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(71) 出願人 (米国を除く全ての指定国について): トヨタ自動車株式会社 (TOYOTA JIDOSHA KABUSHIKI KAISHA) [JP/JP]; 〒4718571 愛知県豊田市トヨタ町１番地 Aichi (JP). 国立大学法人筑波大学 (UNIVERSITY OF TSUKUBA) [JP/JP]; 〒3058577 茨城県つくば市天王台一丁目１番１ Ibaraki (JP).

(72) 発明者; および

(75) 発明者/出願人 (米国についてのみ): 村上和雄 (MURAKAMI, Kazuo) [JP/JP]; 〒3050062 茨城県つくば市赤塚字牛ヶ淵５８６－９財団法人国際科学振興財団内 Ibaraki (JP). 林隆志 (HAYASHI, Takashi) [JP/JP]; 〒3050062 茨城県つくば市赤塚字牛ヶ淵５８６－９財団法人国際科学振興財団内 Ibaraki (JP). 堀美代 (HORI, Miyo) [JP/JP]; 〒3050062 茨城県つくば市赤塚字牛ヶ淵５８６－９財団法人国際科学振興財団内 Ibaraki (JP). 坂本成子 (SAKAMOTO, Shigeko) [JP/JP]; 〒3050062 茨城県つくば市赤塚字牛ヶ淵５８６－９財団法人国際科学振興財団内 Ibaraki (JP). 浦山修 (URAYAMA, Osamu) [JP/JP]; 〒3058577 茨城県つくば市天王台一丁目１番１国立大学法人筑波大学内 Ibaraki (JP). 中川嘉 (NAKAGAWA, Yoshimi) [JP/JP]; 〒3058577 茨城県つくば市天王台一丁目１番１国立大学法人筑波大学内 Ibaraki (JP). 山中陽子 (YAMANAKA, Yoko) [JP/JP]; 〒4718571 愛知県豊田市トヨタ町 1 番地トヨタ自動車株式会社内 Aichi (JP). 原康弘 (HARA, Yasuhiro) [JP/JP]; 〒4718571 愛知県豊田市トヨタ町 1 番地トヨタ自動車株式会社内 Aichi (JP).

(74) 代理人: 平木祐輔, 外 (HIRAKI, Yusuke et al.); 〒1050001 東京都港区虎ノ門 4 丁目 3 番 20 号 神谷町 MT ビル 19 階 Tokyo (JP).

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(54) **Title**: POSITIVE AFFECT MARKER GENE AND USE THEREOF

(54) 発明の名称: 陽性感情マーカー遺伝子及びその利用方法

(57) **Abstract**: Disclosed is a system for evaluating positive affect or the degree of health, which relies on a gene marker that enables the evaluation of positive affect or the degree of health in a subject conveniently and with high reliability. Specifically disclosed is a method for evaluating positive affect or the degree of health in a rat or a human body, which comprises the following steps (a) and (b): (a) measuring the level of expression of a rat positive affect marker gene or a human positive affect marker gene in the rat or the human body; and (b) evaluating the positive affect or the degree of health in the rat or the human body based on the level of expression measured in step (a).

(57) 要約: 被験体の陽性感情又は健康度を簡便且つ高い信頼性をもって評価することができる遺伝子マーカーに基づく陽性感情又は健康度の評価系を提供する。ラット又はヒトにおいてラット陽性感情マーカー遺伝子又はヒト陽性感情マーカー遺伝子の発現量を測定するステップ a と、ステップ a で測定した発現量に基づいて、ラット又はヒトの陽性感情又は健康度を評価するステップ b とを含む、ラット又はヒトの陽性感情又は健康度の評価方法を提供する。

WO 2010/001600 A1

明　細　書

発明の名称 ： 陽性感情マーカー遺伝子及びその利用方法

技術分野

[0001] 本発明は、陽性感情の客観的な指標となる遺伝子マーカー及びその利用方法に関する。

背景技術

[0002] 社会の複雑化に伴い、ストレス及びそれに起因する人体への健康障害が社会問題として提起されつつある。快・不快の心理状態の推定方法としては、心理テスト、心拍・体温解析、脳波解析やfMRI、脳内情報伝達物質の推定などが開発されているが、実施難易度と得られる情報の信頼性はトレードオフの関係にあり、簡便かつ信頼性の高い方法はない。

[0003] 近年、ゲノム情報の解明や遺伝子診断技術の進歩により、ストレスのように人が感じている心理状態や、発癌、生活習慣病などの身体状態を、遺伝子の発現状態から推定することが可能になってきている。しかし、これらの推定技術は、全て陰性の心理状態・身体状態に関するものであり、陽性の心理・身体状態、即ち、快感情やリラックスといった心理状態、身体活性化や健康といった身体状態に関する推定技術はほとんどない。笑いがNK細胞の活性化（特許文献１）や糖尿病患者の食後血糖値を抑えることは知られているが（非特許文献１）、NK細胞や血糖値だけで個体レベルでの評価を実施することはできない。

[0004] 陰性の心理状態や身体状態は、モデル動物などを用いた実験系の確立が容易であり、対照との比較により、その遺伝子発現の差の解析も比較的容易である。一方、陽性の心理状態や身体状態は、個人の感覚的なものであるため、定義づけが困難であり、モデル動物を用いた実験系も長く開発されなかった。したがって、陽性の心理状態にあると、健康になれるといった漠然とした思いはあっても、これまで研究の対象にはならなかった。

特許文献1：特開平8-266632

非特許文献1：Journal of Psychosomatic Research 62 (2007) 703-706: Laughter regulates gene expression in patient with type 2 dabetes

発明の開示

発明が解決しようとする課題

[0005] このように、現在までに陽性の心理状態（以下、「陽性感情」とも称する）を遺伝子発現レベルで客観的に推定する試みはなされていない。

[0006] いったん陽性感情の客観的な指標たる遺伝子マーカーを見出すことができれば、かかる指標に基づき、所与の刺激が被験体を陽性感情又は健康増進に導くものであるか否かを評価することができ、快適さを追求する製品開発の分野での利用が期待できる。

[0007] したがって、本発明は、被験体の陽性感情又は健康度を簡便且つ高い信頼性をもって評価することができる遺伝子マーカーを提供すること、及び該遺伝子マーカーに基づく陽性感情又は健康度の評価系を提供することを目的とする。

課題を解決するための手段

[0008] ラットにおいて、50KHz近傍の超音波は、遊び行動、交尾及び報酬事象の際に発せられる感情指標であり、22KHz近傍の超音波は嫌悪事象、薬物離脱の際に発せられる感情指標であることが報告されている（J. Burgdorf et al., Breeding for 50-kHz Positive Affective Vocalization in Rats. Behavior Genetics, Vol.35 No.1, January 2005）。そこで、本発明者らは、50KHz近傍の発生音声を指標とした陽性感情下にあるラットにおいて遺伝子発現量の網羅的解析を行ったところ、かかる陽性感情ラットで発現量が有意に増大している遺伝子(以下、「ラット陽性感情マーカー遺伝子」とも称する)が存在することを見出した。なお、本明細書で使用する50KHz近傍とは、45～65KHz、好ましくは45～55KHzの音域を指す。

[0009] さらに本発明者らは、笑いを誘発させた陽性感情下にあるヒトにおいて遺伝子発現量の網羅的解析を行ったところ、かかる陽性感情のヒトで発現量が有意に増大している遺伝子(以下、「ヒト陽性感情マーカー遺伝子」とも称す

る)が存在することを見出した。

[0010] 本発明は上記知見を基に完成されたものであり、以下の特徴を包含するものである。

[0011] すなわち、本発明は、ラット又はヒトに評価対象である刺激を負荷する第1のステップと、少なくとも1種のラット陽性感情マーカー遺伝子又はヒト陽性感情マーカー遺伝子の発現量を生体由来試料において測定する第2のステップと、測定した前記遺伝子の発現量に基づいて、対象刺激が陽性刺激であるか否かを評価する第3のステップとを含む、所与の刺激がラット又はヒトに対する陽性刺激であるか否かを評価する方法に関する。

[0012] 上記方法では、第2のステップにおいて、測定対象の遺伝子の塩基配列の少なくとも一部を含む核酸を固定化した支持体を用いて、当該遺伝子の発現量を測定することができる。

[0013] 本発明はまた、ラット陽性感情マーカー遺伝子又はヒト陽性感情マーカー遺伝子の塩基配列の少なくとも一部を含む核酸からなる群から選ばれる少なくとも1種の核酸、又はラット陽性感情マーカー遺伝子又はヒト陽性感情マーカー遺伝子によってコードされるタンパク質に対して特異的に結合する分子からなる群から選択される少なくとも1種の分子を含む、ラット又はヒトの陽性感情、又はヒトの健康度を評価するための検査キットに関する。

[0014] 本発明に係る検査キットにおいて、前記分子は抗体、リガンドタンパク質又は受容体タンパク質であることができる。

[0015] 本発明に係る検査キットにおいて、前記核酸又は分子は支持体に固定されていてもよい。

発明の効果

[0016] 本発明によれば、陽性感情マーカー遺伝子を指標とするラット又はヒトの陽性感情又は健康度の評価系、及びラット又はヒトにおいて陽性感情評価を行うための検査キット、及びヒトにおいて健康度の評価を行うための検査キットが提供される。

図面の簡単な説明

[0017] [図1]図1は、実施例で採用したTickling刺激負荷時程図を示す。

[図2]図2は、刺激開始日におけるTickling(+)4週令ラット発生音声の周波数成分解析図である。

[図3]図3は、刺激開始日におけるTickling(-)4週令ラット発生音声の周波数成分解析図である。

[図4]図4は、刺激開始日におけるLight Touch(+)4週令ラット発生音声の周波数成分解析図である。

[図5]図5は、刺激開始日におけるLight Touch(-)4週令ラット発生音声の周波数成分解析図である。

[図6]図6は、刺激開始日における対照(+)4週令ラット発生音声の周波数成分解析図である。

[図7]図7は、刺激開始日における対照(-)4週令ラット発生音声の周波数成分解析図である。

[図8]図8は、刺激開始日におけるTickling(+)6週令ラット発生音声の周波数成分解析図である。

[図9]図9は、刺激開始日におけるTickling(-)6週令ラット発生音声の周波数成分解析図である。

[図10]図10は、刺激開始日におけるTickling(+)8週令ラット発生音声の周波数成分解析図である。

[図11]図11は、刺激開始日におけるTickling(-)8週令ラット発生音声の周波数成分解析図である。

[図12]図12は、刺激開始翌日におけるTickling(+)4週令ラット発生音声の周波数成分解析図である。

[図13]図13は、刺激開始翌日におけるTickling(-)4週令ラット発生音声の周波数成分解析図である。

[図14]図14は、刺激開始翌日におけるLight Touch(+)4週令ラット発生音声の周波数成分解析図である。

[図15]図15は、刺激開始翌日におけるLight Touch(-)4週令ラット発生音声の

周波数成分解析図である。

[図16]図16は、刺激開始翌日における対照(+)4週令ラット発生音声の周波数成分解析図である。

[図17]図17は、刺激開始翌日における対照(-)4週令ラット発生音声の周波数成分解析図である。

[図18]図18は、刺激開始翌日におけるTickling(+)6週令ラット発生音声の周波数成分解析図である。

[図19]図19は、刺激開始翌日におけるTickling(-)6週令ラット発生音声の周波数成分解析図である。

[図20]図20は、刺激開始翌日におけるTickling(+)8週令ラット発生音声の周波数成分解析図である。

[図21]図21は、刺激開始翌日におけるTickling(-)8週令ラット発生音声の周波数成分解析図である。

[図22]図22は、刺激開始2週目におけるTickling(+)4週令ラット発生音声の周波数成分解析図である。

[図23]図23は、刺激開始2週目におけるTickling(-)4週令ラット発生音声の周波数成分解析図である。

[図24]図24は、刺激開始2週目におけるLight Touch(+)4週令ラット発生音声の周波数成分解析図である。

[図25]図25は、刺激開始2週目におけるLight Touch(-)4週令ラット発生音声の周波数成分解析図である。

[図26]図26は、刺激開始2週目における対照(+)4週令ラット発生音声の周波数成分解析図である。

[図27]図27は、刺激開始2週目における対照(-)4週令ラット発生音声の周波数成分解析図である。

[図28]図28は、刺激開始2週目におけるTickling(+)6週令ラット発生音声の周波数成分解析図である。

[図29]図29は、刺激開始2週目におけるTickling(-)6週令ラット発生音声の周

波数成分解析図である。

[図30]図30は、刺激開始2週目におけるTickling(+)8週令ラット発生音声の周波数成分解析図である。

[図31]図31は、刺激開始2週目におけるTickling(-)8週令ラット発生音声の周波数成分解析図である。

[図32]図32は、刺激開始4週目におけるTickling(+)4週令ラット発生音声の周波数成分解析図である。

[図33]図33は、刺激開始4週目におけるTickling(-)4週令ラット発生音声の周波数成分解析図である。

[図34]図34は、刺激開始4週目におけるLight Touch(+)4週令ラット発生音声の周波数成分解析図である。

[図35]図35は、刺激開始4週目におけるLight Touch(-)4週令ラット発生音声の周波数成分解析図である。

[図36]図36は、刺激開始4週目における対照(+)4週令ラット発生音声の周波数成分解析図である。

[図37]図37は、刺激開始4週目における対照(-)4週令ラット発生音声の周波数成分解析図である。

[図38]図38は、刺激開始4週目におけるTickling(+)6週令ラット発生音声の周波数成分解析図である。

[図39]図39は、刺激開始4週目におけるTickling(-)6週令ラット発生音声の周波数成分解析図である。

[図40]図40は、刺激開始4週目におけるTickling(+)8週令ラット発生音声の周波数成分解析図である。

[図41]図41は、刺激開始4週目におけるTickling(-)8週令ラット発生音声の周波数成分解析図である。

[図42]図42は、刺激開始直後における４週令ラットへの各処置直後の接近待機時間を示す。

[図43]図43は、刺激開始翌日における４週令ラットへの各処置直後の接近待

機時間を示す。

[図44]図44は、刺激開始２週目における４週令ラットへの各処置直後の接近待機時間を示す。

[図45]図45は、刺激開始４週目における４週令ラットへの各処置直後の接近待機時間を示す。

[図46]図46は、Tickling／対照間、Tickling／Light Touch間の遺伝子発現の差をDNAチップ法にて解析した際の、DNAチップ上の各プローブの信号強度の分布を示す。

[図47]図47は、いずれか２組の解析においてCy3およびCy5の信号強度が50以上あったプローブをクラスタリングした像である。

[図48]図48は、少なくとも２組の解析において２倍超あるいは0.5倍未満の発現差を認めたプローブのクラスタリング像である。

[図49]図49は、対照群と比較してTickling群の唾液腺組織で1.5倍超の発現差を認めた593プローブのクラスタリング像である。

[図50]図50は、Light Touch群と比較してTickling群の唾液腺組織で1.5倍超の発現差を認めた171プローブのクラスタリング像である。

[図51]図51は、対照群あるいはLight Touch群と比較してTickling群において発現差を認めた遺伝子(トランスクリプトを含む)の数を示したベン図である。

[図52]図52は、対照群と比較してTickling群の唾液腺組織で1/1.5倍未満の発現差を認めた525プローブのクラスタリング像である。

[図53]図53は、Light Touch群と比較してTickling群の唾液腺組織で1/1.5倍未満の発現差を認めた166プローブのクラスタリング像である。

[図54]図54は、対照群あるいはLight Touch群と比較してTickling群において発現差を認めた唾液腺組織の遺伝子の数を示すベン図である。

[図55]図55は、対照群と比較してTickling群の視床下部組織で1.5倍超の発現差を認めた157プローブのクラスタリング像である。

[図56]図56は、Light Touch群と比較してTickling群の視床下部組織で1.5倍

超の発現差を認めた136プローブのクラスタリング像である。

[図57]図57は、対照群あるいはLight Touch群と比較してTickling群において発現差を認めた視床下部の遺伝子(トランスクリプトを含む)の数を示すベン図である。

[図58]図58は、対照群と比較してTickling群の視床下部で1/1.5倍未満の発現差を認めた57プローブのクラスタリング像である。

[図59]図59は、Light Touch群と比較してTickling群の視床下部組織で1/1.5倍未満の発現差を認めた185プローブのクラスタリング像である。

[図60]図60は、対照群あるいはLight Touch群と比較してTickling群において1/1.5倍未満の発現差を認めた視床下部の遺伝子の数を示すベン図である。

[図61]図61は、GO階層図の色の濃淡とP値を示す。

[図62]図62は、対照群と比較してTickling群で発現が増加した脳及び血液の遺伝子のGO階層図である。

[図63]図63は、Light Touch群と比較してTickling群で発現が増加した脳及び血液の遺伝子のGO階層図である。

[図64]図64は、Light Touch群と比較してTickling群で発現が減少した脳及び血液の遺伝子のGO階層図である。

[図65]図65は、対照群と比較してTickling群で発現が増加した唾液腺の遺伝子のGO階層図である。

[図66]図66は、対照群と比較してTickling群で発現が減少した唾液腺の遺伝子のGO階層図である。

[図67]図67は、Light Touch群と比較してTickling群で発現が増加した唾液腺の遺伝子のGO階層図である。

[図68]図68は、Light Touch群と比較してTickling群で発現が減少した唾液腺の遺伝子のGO階層図である。

[図69]図69は、対照群と比較してTickling群で発現が増加した視床下部の遺伝子のGO階層図である。

[図70]図70は、対照群と比較してTickling群で発現が減少した視床下部の遺

伝子のGO階層図である。

[図71]図71は、Light Touch群と比較してTickling群で発現が増加した視床下部の遺伝子のGO階層図である。

[図72]図72は、Light Touch群と比較してTickling群で発現が減少した視床下部の遺伝子のGO階層図である。

[図73]図73は、Tickling負荷２日目のラット発生音声の周波数成分解析図である。

[図74]図74は、Light Touch負荷開始目のラット発生音声の周波数成分解析図である。

[図75]図75は、Tickling／Light Touch間の遺伝子発現の差をDNAチップ法にて解析した際の、DNAチップ上の各プローブの信号強度の分布を示す。

[図76]図76は、いずれかの解析においてCy3およびCy5の信号強度が50以上あったプローブをクラスタリングした像である。

[図77]図77は、いずれかの解析において1.5倍以上あるいは1/1.5倍以下の発現差を認めた868プローブのクラスタリング像である。

[図78]図78は、２倍以上あるいは0.5倍以下の発現差を認めた88プローブのクラスタリング像である。

[図79]図79は、いずれかの解析において1.5倍以上あるいは1/1.5倍以下の発現差を認めた4,397プローブのクラスタリング像（プローブの並びは長期刺激を基準)である。

[図80]図80は、いずれかの解析において1.5倍以上あるいは1/1.5倍以下の発現差を認めた4,397プローブのクラスタリング像(プローブの並びは短期刺激を基準)である。

[図81]図81は、いずれかの解析において２倍以上あるいは0.5倍以下の発現差を認めた865プローブのクラスタリング像(プローブの並びは長期刺激を基準)である。

[図82]図82は、いずれかの解析において２倍以上あるいは0.5倍以下の発現差を認めた865プローブのクラスタリング像(プローブの並びは短期刺激を基準)

である。

[図83]図83は、GO階層図の色の濃淡とP値を示す。

[図84]図84は、脳と擦過細胞で共通して発現増加した遺伝子のGO階層図である。

[図85]図85は、視床下部で発現増加した遺伝子のGO階層図である。

[図86]図86は、視床下部で発現が減少した遺伝子のGO階層図である。

[図87]図87は、線条体で発現増加した遺伝子のGO階層図である。

[図88]図88は、線条体で発現が減少した遺伝子のGO階層図である。

[図89]図89は、リアルタイムPCRによる遺伝子発現定量解析のフローを示す。

[図90]図90は、笑いによる遺伝子発現の変化に関する研究における実験時程図である。

[図91]図91は、糖尿病罹病者群及び糖尿病非罹病者群における、講義前後、コント前後の唾液中アミラーゼ活性をプロットした図である。

[図92]図92は、糖尿病罹病者群及び糖尿病非罹病者群における、講義前後、コント前後の唾液中酸化還元電位(ORP)をプロットした図である。

[図93]図93は、糖尿病罹病者群及び糖尿病非罹病者群における、講義前後、コント前後の唾液量をプロットした図である。

[図94]図94は、糖尿病罹病者群及び糖尿病非罹病者群における、講義前後、コント前後の唾液緩衝能をプロットした図である。

[図95]図95は、糖尿病罹病者群及び糖尿病非罹病者群における、講義前後、コント前後の総合感情障害度(TMD)をプロットした図である。

[図96]図96は、糖尿病罹病者群及び糖尿病非罹病者群における、講義前後、コント前後の不安傾向(STAI)をプロットした図である。

[図97]図97は、糖尿病罹病者群及び糖尿病非罹病者群における、講義前後、コント前後の唾液中分泌型イムノグロブリン(s-IgA)をプロットした図である。

[図98]図98は、糖尿病罹病者群及び糖尿病非罹病者群における、講義前後、コント前後の唾液中コルチゾールをプロットした図である。

[図99]図99は、糖尿病罹病者群及び糖尿病非罹病者群における、講義前後、コント前後の血糖値をプロットした図である。

[図100]図100は、糖尿病罹病者群及び糖尿病非罹病者群における、講義前後、コント前後の白血球数をプロットした図である。

[図101]図101は、糖尿病罹病者群及び糖尿病非罹病者群における、講義前後、コント前後の好中球比をプロットした図である。

[図102]図102は、糖尿病罹病者群及び糖尿病非罹病者群における、講義前後、コント前後のリンパ球比をプロットした図である。

[図103]図103は、糖尿病罹病者群及び糖尿病非罹病者群における、講義前後、コント前後のNK細胞活性をプロットした図である。

[図104]図104は、糖尿病罹病者群及び糖尿病非罹病者群における、講義前後、コント前後の血中コルチゾールをプロットした図である。

[図105]図105は、糖尿病罹病者群及び糖尿病非罹病者群における、講義前後、コント前後のC反応性蛋白をプロットした図である。

[図106]図106は、糖尿病罹病者群及び糖尿病非罹病者群における、血糖値の講義前後差及びコント前後差をプロットした図である。

[図107]図107は、歯周病罹病者群及び歯周病非罹病者群における、講義前後、コント前後の唾液アミラーゼ活性をプロットした図である。

[図108]図108は、歯周病罹病者群及び歯周病非罹病者群における、講義前後、コント前後の唾液中酸化還元電位をプロットした図である。

[図109]図109は、歯周病罹病者群及び歯周病非罹病者群における、講義前後、コント前後の唾液量をプロットした図である。

[図110]図110は、歯周病罹病者群及び歯周病非罹病者群における、講義前後、コント前後の唾液緩衝能をプロットした図である。

[図111]図111は、歯周病罹病者群及び歯周病非罹病者群における、講義前後、コント前後の総合感情障害度(TMD)をプロットした図である。

[図112]図112は、歯周病罹病者群及び歯周病非罹病者群における、講義前後、コント前後の不安傾向(STAI)をプロットした図である。

[図113]図113は、歯周病罹病者群及び歯周病非罹病者群における、講義前後、コント前後の唾液中分泌型イムノグロブリンAをプロットした図である。

[図114]図114は、歯周病罹病者群及び歯周病非罹病者群における、講義前後、コント前後の唾液中コルチゾールをプロットした図である。

[図115]図115は、歯周病罹病者群及び歯周病非罹病者群における、講義前後、コント前後の血糖値をプロットした図である。

[図116]図116は、歯周病罹病者群及び歯周病非罹病者群における、講義前後、コント前後の白血球数をプロットした図である。

[図117]図117は、歯周病罹病者群及び歯周病非罹病者群における、講義前後、コント前後の好中球比をプロットした図である。

[図118]図118は、歯周病罹病者群及び歯周病非罹病者群における、講義前後、コント前後のリンパ球比をプロットした図である。

[図119]図119は、歯周病罹病者群及び歯周病非罹病者群における、講義前後、コント前後のNK細胞活性をプロットした図である。

[図120]図120は、歯周病罹病者群及び歯周病非罹病者群における、講義前後、コント前後の血中コルチゾールをプロットした図である。

[図121]図121は、歯周病罹病者群及び歯周病非罹病者群における、講義前後、コント前後のCRPをプロットした図である。

[図122]図122は、歯周病罹病者群及び歯周病非罹病者群における、血糖値の講義前後差及びコント前後差をプロットした図である。

[図123]図123は、実施例4の解析2、4～10において、1.5倍以上あるいは1/1.5倍以下の発現変化を認めた遺伝子のヒストグラムを示す。縦軸に発現変化倍数のLog2値を表し、横軸にサンプル名を表した。

[図124]図124は、対応する解析ごとの発現変化の相対差を比較により示す。

[図125]図125は、糖尿病非罹病者群と糖尿病罹病者群で笑いにより1.5倍以上の発現変化を認めた遺伝子のベン図を示す。

[図126]図126は、糖尿病非罹病者群と糖尿病罹病者群で笑いにより1.5倍以下の発現変化を認めた遺伝子のベン図を示す。

[図127]図127は、糖尿病非罹病・歯周病非罹病者群と糖尿病非罹病・歯周病罹病者群で笑いにより1.5倍以上の発現変化を認めた遺伝子のベン図を示す。

[図128]図128は、糖尿病非罹病・歯周病非罹病者群と糖尿病非罹病・歯周病罹病者群で笑いにより1.5倍以下の発現変化を認めた遺伝子のベン図を示す。

[図129]図129は、糖尿病非罹病・歯周病非罹病者群と糖尿病罹病・歯周病非罹病者群で笑いにより1.5倍以上の発現変化を認めた遺伝子のベン図を示す。

[図130]図130は、糖尿病非罹病・歯周病非罹病者群と糖尿病罹病・歯周病非罹病者群で笑いにより1/1.5倍以下の発現変化を認めた遺伝子のベン図を示す。

[図131]図131は、糖尿病非罹病・歯周病罹病者群と糖尿病罹病・歯周病罹病者群で笑いにより1.5倍以上の発現変化を認めた遺伝子のベン図を示す。

[図132]図132は、糖尿病非罹病・歯周病罹病者群と糖尿病罹病・歯周病罹病者群で笑いにより1/1.5倍以下の発現変化を認めた遺伝子のベン図を示す。

[図133]図133は、糖尿病罹病・歯周病非罹病者群と糖尿病罹病・歯周病罹病者群で笑いにより1.5倍以上の発現変化を認めた遺伝子のベン図を示す。

[図134]図134は、糖尿病罹病・歯周病非罹病者群と糖尿病罹病・歯周病罹病者群で笑いにより1/1.5倍以下の発現変化を認めた遺伝子のベン図を示す。

[図135]図135は、歯周病非罹病者群と歯周病罹病者群で笑いにより1.5倍以上の発現変化を認めた遺伝子のベン図を示す。

[図136]図136は、歯周病非罹病者群と歯周病罹病者群で笑いにより1/1.5倍以下の発現変化を認めた遺伝子のベン図を示す。

発明を実施するための形態

[0018] 本明細書は本願の優先権の基礎である日本国特許出願2008-170854号の明細書及び/又は図面に記載される内容を包含する。

[0019] <u>１－１．ラット陽性感情マーカー遺伝子及びそれを用いたラット陽性感情評価系</u>

本発明は、ラットの陽性感情評価方法を提供する。具体的に、本発明に係るラットの陽性感情評価方法は、ラットにおいてラット陽性感情マーカー遺

伝子の発現量を測定するステップaと、ステップaで測定した発現量に基づいて、ラットの陽性感情を評価するステップbとを含んでいる。

[0020] 本明細書で使用する「陽性感情」（positive emotion/affect）とは、例えば、嬉しい、快活、愉快、楽しい、温和、穏やか、といった心理状態や、幸せ、喜び、愛、希望、満足、意欲、興味、信頼などのプラスの感情、心身を健康状態又は健康増進に導く任意の感情を指す。健康増進とは、WHO定義のうち、身体的、精神的なものにおいて、外界からの刺激に対する心身の適応能力を高めることをいう。一方、本明細書で使用する「陰性感情」（negative emotion/affect）とは、緊張、不安、悲しみ、うつ、怒り、恐怖、困惑といった心理状態やマイナスの感情、心身を病的状態に導く任意の感情を指す。

[0021] 本明細書で使用する「陽性感情マーカー遺伝子」とは、被験体の陽性感情の指標となる遺伝子であって、被験体が陽性感情にある場合に、発現量が有意に増加するか又は減少する任意の遺伝子を指す。

[0022] 特に本発明で提供する「ラット陽性感情マーカー遺伝子」は、50KHz近傍の発生音声を指標とした陽性感情下にあるラットにおいて、そのような陽性感情特性を示さないラットに比較して、発現量が1.5倍以上、好ましくは2.0倍以上増加するか又は減少する遺伝子として定義される。言い換えれば、ラット陽性感情マーカー遺伝子は、ラットの50KHz近傍の発生音声と連動して発現量が1.5倍以上、好ましくは2.0倍以上増減する遺伝子である。

[0023] 陽性感情ラットにおいて2.0倍以上の発現量の増減を示す本発明のラット陽性感情マーカー遺伝子を下記の表1、表2に示す。

[表1]

No	Target(Gene)Symbol	Target Accession	UniGene	Up/Down	生体由来試料
1	Gsta5	NM_031509	Rn.10460	Up	Bc
2	-	AA858768	-	Up	Bc
3	Aldh1a1	NM_022407	Rn.6132	Up	Bc
4	Yc2	NM_001009920	Rn.120929	Up	Bc
5	-	TC536876	-	Up	Bc
6	Ttc6_predicted	XM_216713	Rn.82576	Up	Bc
7	Gsta2	NM_017013	Rn.144550	Up	Bc
8	-	BQ200056	-	Up	Bc
9	Gsta2	BQ199390	Rn.144550	Up	Bc
10	LOC307767	XM_226381	Rn.41880	Up	Bc
11	Cdig11	NM_153623	Rn.160166	Up	Bc
12	Selenbp1	NM_080892	Rn.16617	Up	Bc
13	-	TC561220	-	Down	Bc
14	Cdkn1c	XM_341966	-	Down	Bc
15	Cdkn1c	NM_182735	Rn.162507	Down	Bc
16	-	NM_001013853	Rn.163132	Down	Bc
17	Cdkn1c	NM_182735	Rn.162507	Down	Bc
18	MGC72973	NM_198776	Rn.36966	Down	Bc
19	-	AI045044	Rn.166087	Down	Bc
20	Me2_predicted	XM_225729	Rn.38235	Down	Bc
21	Gda	NM_031776	Rn.161897	Down	Bc
22	LOC300760	XM_236308	-	Down	Bc
23	Susd2_predicted	XM_215372	Rn.161744	Down	Bc
24	Susd2_predicted	XM_215372	Rn.161744	Down	Bc
25	Hpd	NM_017233	Rn.3664	Down	Bc
26	Slfn3	NM_053687	-	Up	Bl
27	-	AA963075	Rn.73451	Up	Bl
28	S100a9	NM_053587	Rn.6703	Up	Bl
29	Bnc1_predicted	XM_344917	-	Down	Bl
30	Slc6a3	NM_012694	Rn.10093	Up	Hy
31	Cga	J00757	Rn.10589	Up	Hy
32	Cga	NM_053918	Rn.10589	Up	Hy
33	-	AI044887	Rn.5827	Down	Hy
34	-	BF398607	Rn.45255	Down	Hy
35	Avp	NM_016992	Rn.9976	Up	St
36	Neurod2	NM_019326	Rn.10724	Up	St
37	-	AW914894	Rn.10267	Up	St
38	Vip	XM_217838	Rn.18675	Up	St
39	-	XM_576570	Rn.22624	Up	St
40	-	TC524999	-	Up	St
41	Slc17a7	NM_053859	Rn.10267	Up	St
42	-	BF281936	-	Up	St
43	-	CO403684	-	Up	St
44	-	CB582871	Rn.13498	Up	St
45	Cck	BM382824	Rn.9781	Up	St
46	Sstr1	NM_012719	#N/A	Up	St
47	Cort	NM_012835	Rn.42915	Up	St
48	Nrn1	NM_053346	Rn.10490	Up	St
49	C1ql3_predicted	XM_225579	Rn.3546	Up	St
50	Prss12	NM_053504	-	Up	St
51	-	TC558785	Rn.86653	Up	St
52	-	TC562720	-	Up	St
53	-	TC519964	-	Up	St

[0024]

No	Target(Gene)Symbol	Target Accession	UniGene	Up/Down	生体由来試料
54	Nov	NM_030868	-	Up	St
55	-	XM_575489	Rn.162955	Up	St
56	Cck	NM_012829	Rn.162754	Up	St
57	Nptx1	NM_153735	Rn.9781	Up	St
58	RGD1308977_predicted	XM_214510	Rn.139226	Up	St
59	-	CB544275	Rn.54707	Up	St
60	-	BF398607	Rn.45255	Down	St
61	Ttr	NM_012681	Rn.1404	Down	St

[表2]

No	Target(Gene)Symbol	Target Accession	UniGene	Up/Down	生体由来試料
62	-	NM_001013853	Rn.163132	Up	BI
63	RGD1308591_predicted	XM_230631	Rn.22314	Up	BI
64	-	TC545861	-	Up	BI
65	-	TC559380	-	Up	BI
66	-	TC551459	-	Up	BI
67	-	TC560203	-	Up	BI
68	RGD1309846_predicted	XM_231625	-	Up	BI
69	-	TC532273	-	Up	BI
70	-	TC568188	-	Up	BI
71	-	XM_343940	-	Up	BI
72	-	TC549515	-	Up	BI
73	-	TC555328	-	Up	BI
74	MGC72973	NM_198776	Rn.36966	Up	BI
75	-	TC549495	-	Up	BI
76	-	CB544341	Rn.6526	Up	BI
77	Gabrd	NM_017289	Rn.10927	Up	BI
78	-	TC542956	-	Up	BI
79	Olr1572_predicted	XM_221921	-	Up	BI
80	-	TC525431	-	Up	BI
81	Strn4_predicted	XM_218432	Rn.137083	Up	BI
82	-	A_44_P337592	-	Up	BI
83	-	AW143701	Rn.17098	Up	BI
84	Rnf40	NM_153471	Rn.162466	Up	BI
85	-	TC544981	-	Up	BI
86	Bst2	NM_198134	Rn.32168	Up	BI
87	LOC361100	XM_341386	Rn.104585	Up	BI
88	-	BQ211845	Rn.165621	Up	BI
89	-	AA900394	Rn.165621	Up	BI
90	Olr1234_predicted	NM_001000446	Rn.143535	Up	BI
91	-	AW918996	Rn.7470	Up	BI
92	RGD1307160_predicted	XM_219953	Rn.61235	Up	BI
93	-	BI395434	-	Up	BI
94	-	XM_215067	-	Up	BI
95	-	TC561947	-	Up	BI
96	-	A_44_P426640	-	Up	BI
97	-	A_44_P368450	-	Up	BI
98	Cox6a2	NM_012812	Rn.5119	Up	BI
99	-	AA925776	Rn.11283	Up	BI
100	-	TC528645	Rn.14945	Up	BI
101	Ltap_predicted	XM_222896	Rn.19850	Up	BI
102	-	XM_346943	Rn.22985	Up	BI
103	-	AA900371	Rn.161752	Down	BI
104	-	AA900000	Rn.103172	Down	BI
105	-	AA899215	-	Down	BI
106	-	TC555778	-	Down	BI
107	Jund	NM_138875	Rn.46225	Down	BI
108	-	AI556201	Rn.48701	Down	BI
109	-	BI302367	Rn.94935	Down	BI
110	-	BI277534	Rn.122326	Down	BI
111	-	BF416864	Rn.161752	Down	BI
112	RGD1311005_predicted	XM_341099	Rn.65800	Down	BI
113	-	XM_575687	Rn.162772	Down	BI
114	-	BI277534	Rn.122326	Down	BI
115	-	BI277534	Rn.122326	Down	BI
116	Rpl26_predicted	XM_213346	Rn.144702	Down	BI
117	-	BI277534	Rn.122326	Down	BI
118	Mrps18c_predicted	XM_214003	Rn.105741	Down	BI
119	Plp	NM_030990	Rn.4550	Down	BI

[0025]

No	Target(Gene)Symbol	Target Accession	UniGene	Up/Down	生体由来試料
120	-	BI277534	Rn.7999	Down	B I
121	Polr2k_predicted	XM_219604	-	Down	B I
122	-	BI277534	-	Down	B I
123	-	BI277534	-	Down	B I
124	-	NM_001014207	Rn.137575	Down	B I
125	-	TC559328	-	Down	B I
126	-	BI277534	Rn.122326	Down	B I
127	Cma1	NM_013092	Rn.10182	Down	B I
128	Rpl37	BI277661	Rn.129486	Down	B I
129	-	TC559328	Rn.122326	Down	B I
130	-	BE098803	Rn.122326	Down	B I
131	-	BI277534	Rn.122326	Down	B I
132	-	AI231572	Rn.1180	Down	B I
133	Slpi	NM_053372	Rn.18560	Up	B I
134	Slpi	NM_053372	Rn.18560	Up	B I
135	LOC296356	XM_215940	Rn.144851	Up	B I
136	Fn1	NM_019143	Rn.1604	Up	B I
137	-	NM_001013853	Rn.163132	Up	B I
138	-	TC551459	-	Up	B I
139	Adn	XM_343169	Rn.16172	Up	B I
140	Timp2	NM_021989	Rn.10161	Up	B I
141	-	NM_001013110	Rn.91296	Up	B I
142	Ptpn11	NM_013088	Rn.98209	Up	B I
143	LOC298270	XM_233230	Rn.162076	Down	B I
144	LOC292088	XM_238058	-	Down	B I
145	Slc6a3	NM_012694	Rn.10093	Up	Hy
146	-	TC543527	-	Up	Hy
147	-	BE108176	Rn.3464	Up	Hy
148	Galp	NM_022633	Rn.48754	Up	Hy
149	Pomc2	NM_139326	Rn.108195	Up	Hy
150	-	BF398607	Rn.45255	Down	Hy
151	Chrna3	NM_052805	Rn.10996	Down	Hy
152	-	AW914894	Rn.10267	Down	Hy
153	Shox2	NM_013028	Rn.11258	Down	Hy
154	LOC289633	XM_223426	Rn.123835	Down	Hy
155	Prpf31_predicted	XM_218173	Rn.99310	Down	Hy
156	-	TC530743	-	Down	Hy
157	Slc5a7	NM_053521	Rn.44872	Down	Hy
158	Ttr	NM_012681	Rn.1404	Down	Hy
159	Lhx9	NM_181367	Rn.75111	Down	Hy
160	-	AW527509	Rn.41179	Down	Hy
161	Shox2	NM_013028	Rn.11258	Down	Hy
162	Grifin	NM_057187	Rn.26894	Down	Hy
163	-	TC556932	-	Down	Hy
164	Zic1	NM_022677	Rn.161923	Down	Hy
165	Prkcd	NM_133307	Rn.98279	Down	Hy
166	Slc18a3	NM_031663	Rn.9987	Down	Hy
167	Cpne4_predicted	XM_345977	Rn.124862	Down	Hy
168	-	TC519964	-	Down	Hy
169	RGD1311951_predicted	XM_237334	Rn.70007	Down	Hy
170	-	AI178665	Rn.58356	Down	Hy
171	-	BC092605	Rn.22271	Down	Hy
172	-	TC543142	-	Down	Hy
173	-	TC567761	-	Down	Hy
174	Ramp3	NM_020100	Rn.48672	Down	Hy
175	Lef1	NM_130429	Rn.21926	Down	Hy
176	Irx5_predicted	XM_225077	-	Down	Hy
177	MGC95205	NM_001005540	Rn.12833	Down	Hy
178	-	BE126741	-	Down	Hy
179	-	TC551026	-	Down	Hy

[0026]

No	Target(Gene)Symbol	Target Accession	UniGene	Up/Down	生体由来試料
180	Cga	J00757	Rn. 10589	Up	Hy
181	Cga	NM_053918	Rn. 10589	Up	Hy
182	Shox2	NM_013028	Rn. 11258	Up	Hy
183	-	BC092605	Rn. 22271	Up	Hy
184	-	BE108176	Rn. 3464	Up	Hy
185	Prkcd	NM_133307	Rn. 98279	Up	Hy
186	-	TC543263	-	Up	Hy
187	Vip	XM_217838	Rn. 18675	Up	Hy
188	Grifin	NM_057187	Rn. 26894	Up	Hy
189	-	TC530743	-	Up	Hy
190	Nexn	NM_139230	Rn. 107975	Up	Hy
191	Ramp3	NM_020100	Rn. 48672	Up	Hy
192	-	XM_575030	Rn. 7078	Up	Hy
193	Ttr	NM_012681	Rn. 1404	Down	Hy
194	-	BF398607	Rn. 45255	Down	Hy
195	Gnrh1	NM_012767	Rn. 59459	Down	Hy
196	Foxg1	NM_012560	Rn. 9864	Down	Hy
197	Prpf31_predicted	XM_218173	Rn. 99310	Down	Hy
198	Slc18a3	NM_031663	Rn. 9987	Down	Hy
199	Ngfr	NM_012610	Rn. 10980	Down	Hy
200	Zfyve9_predicted	XM_233341	Rn. 23612	Down	Hy
201	Avp	NM_016992	Rn. 9976	Down	Hy
202	-	AI013718	-	Down	Hy
203	Slc5a7	NM_053521	Rn. 44872	Down	Hy
204	-	BQ194469	Rn. 161764	Up	St
205	LOC290372	XM_237952	Rn. 19611	Up	St
206	-	BG672648	-	Up	St
207	-	BF398607	Rn. 45255	Down	St
208	Prpf31_predicted	XM_218173	Rn. 99310	Down	St
209	Vip	XM_217838	Rn. 18675	Down	St
210	Slc17a7	NM_053859	Rn. 10267	Down	St
211	Cck	BM382824	Rn. 9781	Down	St
212	-	AW914894	#N/A	Down	St
213	Homer1	U92079	Rn. 10267	Down	St
214	Cck	NM_012829	-	Down	St
215	Tjp1_predicted	XM_218747	Rn. 101871	Up	St
216	Tjp1_predicted	XM_218747	Rn. 101871	Up	St
217	Tjp1_predicted	XM_218747	Rn. 101871	Up	St
218	-	AW144721	Rn. 3039	Up	St
219	-	AA963075	Rn. 73451	Up	St
220	Sv2b	NM_057207	Rn. 58137	Up	St
221	-	BG672648	-	Up	St
222	Avp	NM_016992	Rn. 9976	Up	St
223	-	BF398607	Rn. 45255	Down	St
224	Prpf31_predicted	XM_218173	Rn. 99310	Down	St
225	-	TC560395	-	Down	St
226	RGD:1303100	NM_001003929	Rn. 55036	Down	St
227	Slc17a7	NM_053859	Rn. 10267	Down	St
228	-	A_44_P302611	-	Down	St
229	-	BF546193	Rn. 174580	Down	St
230	RGD1309846_predicted	XM_231625	-	Down	St
231	Bhlhb3	NM_133303	Rn. 10784	Down	St
232	Cck	NM_012829	Rn. 9781	Down	St
233	-	AW914894	Rn. 10267	Down	St
234	Homer1	U92079	-	Down	St
235	Crisp1	NM_022859	Rn. 10102	Up	Sg
236	-	ENSRNOT00000040037	-	Up	Sg
237	Prpg2	NM_172065	Rn. 29950	Up	Sg
238	Psp	NM_052808	Rn. 9766	Up	Sg
239	-	BF415117	Rn. 2635	Up	Sg

[0027]

No	Target(Gene)Symbol	Target Accession	UniGene	Up/Down	生体由来試料
240	Mgat3	NM_019239	Rn.9803	Up	Sg
241	-	TC519989	-	Up	Sg
242	-	XM_341973	-	Up	Sg
243	Scgb2a1	NM_080770	Rn.144559	Up	Sg
244	-	A_44_P875993	-	Up	Sg
245	-	M87788	Rn.118336	Up	Sg
246	Amy2_predicted	XM_345278	Rn.67070	Up	Sg
247	Amy1	NM_001010970	Rn.116361	Up	Sg
248	-	XM_342323	-	Up	Sg
249	-	CB545830	Rn.157214	Up	Sg
250	RGD1311424_predicted	XM_343001	Rn.57800	Up	Sg
251	-	BI288013	Rn.40911	Up	Sg
252	Mycl1	XM_233490	Rn.41400	Up	Sg
253	-	NM_001013941	Rn.161900	Up	Sg
254	Dusp1	NM_053769	Rn.98260	Up	Sg
255	LOC366764	XM_345751	-	Up	Sg
256	-	L07402	Rn.119901	Down	Sg
257	LOC314509	XM_234661	Rn.110660	Down	Sg
258	-	Z93368	Rn.110663	Down	Sg
259	LOC299469	XM_234749	-	Down	Sg
260	LOC366769	XM_345756	Rn.126669	Down	Sg
261	-	Z93350	Rn.10956	Down	Sg
262	-	ENSRNOT00000043097	-	Down	Sg
263	-	XM_575540	Rn.117940	Down	Sg
264	LOC299551	XM_234830	-	Down	Sg
265	LOC366758	XM_345745	Rn.112181	Down	Sg
266	-	XM_345746	-	Down	Sg
267	Prpf31_predicted	XM_218173	Rn.99310	Down	Sg
268	-	NM_001014264	Rn.102149	Down	Sg
269	-	BE098883	Rn.15951	Down	Sg
270	LOC314512	XM_234676	Rn.110661	Down	Sg
271	LOC297260	XM_231999	-	Down	Sg
272	Fetub	NM_053348	Rn.2464	Down	Sg
273	-	BC092624	Rn.163825	Down	Sg
274	LOC366758	XM_345745	Rn.112181	Down	Sg
275	-	XM_234741	-	Down	Sg
276	Igkv28	L17078	Rn.92371	Down	Sg
277	-	BF560128	Rn.28431	Down	Sg
278	-	XM_345749	-	Up	Sg
279	Klk1c10	XM_214947	Rn.136578	Up	Sg
280	Klks3	NM_175759	Rn.34527	Up	Sg
281	Ton	NM_012677	Rn.9882	Up	Sg
282	Vcsa1	NM_012684	Rn.9927	Up	Sg
283	RGD:619853	NM_022709	Rn.162774	Up	Sg
284	Klk12	NM_001005382	Rn.141980	Up	Sg
285	Olr1223_predicted	NM_001000441	Rn.143544	Up	Sg
286	RGD:735032	XM_214931	Rn.107068	Up	Sg
287	-	XM_341973	-	Up	Sg
288	Vcsa1	NM_012684	Rn.9927	Up	Sg
289	Acaca	NM_022193	Rn.44372	Up	Sg
290	-	NM_001013067	Rn.79264	Up	Sg
291	Egf	NM_012842	Rn.6075	Up	Sg
292	RGD:735160	NM_198685	Rn.79319	Up	Sg
293	Svs6_predicted	XM_342575	Rn.145207	Up	Sg
294	-	CB545830	Rn.157214	Up	Sg
295	Klk7	NM_012593	Rn.144553	Up	Sg
296	Pip	NM_022708	Rn.78367	Up	Sg
297	RGD:735032	XM_214931	Rn.107068	Up	Sg
298	Muc10	NM_133513	Rn.10113	Up	Sg
299	RGD:1303220	NM_001003977	Rn.141979	Up	Sg

[0028]

No	Target(Gene)Symbol	Target Accession	UniGene	Up/Down	生体由来試料
300	Grpca	NM_181440	Rn.10942	Up	Sg
301	-	TC524810	-	Up	Sg
302	-	AA963004	Rn.24539	Up	Sg
303	Scgb2a1	NM_080770	Rn.144559	Up	Sg
304	Ngfg	NM_031523	Rn.11331	Up	Sg
305	-	ENSRNOT00000042436	-	Up	Sg
306	RGD:735228	XM_214939	Rn.21391	Up	Sg
307	Gpr83	NM_080411	Rn.63075	Up	Sg
308	-	NM_001013941	Rn.161900	Up	Sg
309	Tgfb2	NM_031131	Rn.24539	Up	Sg
310	Prpg2	NM_172065	Rn.29950	Up	Sg
311	Mpv17l_predicted	XM_340739	Rn.22842	Up	Sg
312	Npas3_predicted	XM_234124	Rn.135138	Up	Sg
313	LOC290262	XM_224224	-	Up	Sg
314	LOC287803	XM_221081	Rn.163171	Up	Sg
315	LOC362603	XM_347064	Rn.91410	Up	Sg
316	Oxt	NM_012996	Rn.48915	Up	Sg
317	Vgll2_predicted	XM_228170	Rn.17643	Up	Sg
318	Th	NM_012740	Rn.11082	Up	Sg
319	RGD1309050_predicted	XM_240734	Rn.6819	Up	Sg
320	B4galt6	NM_031740	-	Up	Sg
321	LOC361702	XM_341985	Rn.61872	Up	Sg
322	-	AA956502	-	Up	Sg
323	-	CK595775	Rn.125806	Up	Sg
324	Rbp3	XM_341400	Rn.41214	Up	Sg
325	Lrrc27_predicted	XM_341954	Rn.162479	Up	Sg
326	RGD1308967_predicted	XM_232748	Rn.143980	Up	Sg
327	Fmo5	NM_144739	Rn.7038	Up	Sg
328	LOC361340	XM_341623	Rn.132740	Up	Sg
329	Tbx5_predicted	NM_001009964	Rn.6327	Up	Sg
330	-	X89700	-	Up	Sg
331	Kif23_predicted	XM_236313	Rn.63734	Up	Sg
332	-	ENSRNOT00000016430	-	Up	Sg
333	LOC309745	XM_228133	Rn.84956	Up	Sg
334	Riok3_predicted	XM_341578	Rn.4181	Up	Sg
335	Lyl1	NM_001007677	Rn.17352	Up	Sg
336	Zfp393_predicted	XM_233437	Rn.159750	Up	Sg
337	Mxi1	NM_013160	Rn.37510	Up	Sg
338	Gdf5	AB087404	Rn.127822	Up	Sg
339	-	AW917276	Rn.7332	Up	Sg
340	B4galt6	NM_031740	-	Up	Sg
341	LOC313633	XM_233574	Rn.27233	Up	Sg
342	-	TC541862	-	Up	Sg
343	-	NM_001024751	Rn.76073	Up	Sg
344	Erabp	NM_024136	Rn.10362	Up	Sg
345	-	XM_345742	-	Up	Sg
346	Limd1_predicted	XM_236734	Rn.161977	Up	Sg
347	RGD1309038_predicted	XM_225887	Rn.24687	Up	Sg
348	-	TC562194	-	Up	Sg
349	Actn3	NM_133424	Rn.17592	Up	Sg
350	-	CB547130	Rn.179696	Up	Sg
351	Cart1	NM_012921	Rn.9282	Up	Sg
352	RGD1311019_predicted	XM_238442	Rn.18688	Up	Sg
353	Znf507_predicted	XM_218515	Rn.141981	Up	Sg
354	LOC310631	XM_227403	Rn.104095	Up	Sg
355	-	AI045861	Rn.10526	Up	Sg
356	Ccl17	NM_057151	Rn.46679	Up	Sg
357	Arl12_predicted	XM_220907	Rn.18110	Up	Sg
358	-	TC559056	Rn.147866	Up	Sg
359	Mobp	NM_012720	Rn.91185	Up	Sg

[0029]

No	Target(Gene)Symbol	Target Accession	UniGene	Up/Down	生体由来試料
360	Golph2_predicted	XM_225147	Rn.1545	Up	Sg
361	-	ENSRNOT00000038788	-	Up	Sg
362	-	AA800803	Rn.102152	Up	Sg
363	Mospd4_predicted	BF400026	Rn.63770	Up	Sg
364	-	XM_578308	-	Up	Sg
365	Rasgrp4	NM_130824	Rn.81227	Up	Sg
366	-	NM_001024273	Rn.14280	Up	Sg
367	-	A_44_P882921	-	Up	Sg
368	-	A_44_P729420	-	Up	Sg
369	Hsf4_predicted	XM_214668	Rn.163399	Up	Sg
370	Znf297	NM_001009172	Rn.17135	Up	Sg
371	-	TC540693	-	Up	Sg
372	LOC301121	XM_236777	Rn.35756	Up	Sg
373	Spata18	NM_199374	Rn.27773	Up	Sg
374	LOC367391	XM_346122	Rn.83054	Up	Sg
375	P2rx2	NM_053656	Rn.88799	Up	Sg
376	-	TC545251	-	Up	Sg
377	-	A_44_P278941	-	Up	Sg
378	Andpro	NM_012718	Rn.9977	Up	Sg
379	Sult1a2	NM_031732	Rn.9937	Up	Sg
380	-	NM_001014232	Rn.8173	Up	Sg
381	Sprr3_predicted	XM_227339	Rn.19820	Up	Sg
382	Mgat4a_predicted	NM_001012225	Rn.145359	Up	Sg
383	Hapln1	NM_019189	Rn.50531	Up	Sg
384	-	BM388083	Rn.41133	Up	Sg
385	-	BG380409	Rn.143966	Up	Sg
386	Sds	NM_053962	Rn.9918	Up	Sg
387	Cngb1	AJ224680	Rn.10733	Up	Sg
388	-	NM_001024983	Rn.152074	Up	Sg
389	LOC365807	XM_345218	Rn.111884	Up	Sg
390	RGD:628846	NM_031605	Rn.10034	Up	Sg
391	-	BF567941	Rn.169222	Up	Sg
392	RGD:727806	NM_001001508	Rn.58355	Up	Sg
393	Pex11a	NM_053487	Rn.14519	Up	Sg
394	-	AA963232	Rn.1053	Up	Sg
395	-	AW142782	Rn.43391	Up	Sg
396	-	A_44_P260574	Rn.43391	Up	Sg
397	Adcyap1	NM_016989	Rn.37400	Up	Sg
398	Nr4a1	NM_024388	Rn.10000	Up	Sg
399	Spt2_predicted	XM_238528	-	Up	Sg
400	-	TC538568	-	Up	Sg
401	-	BF290953	Rn.24673	Up	Sg
402	LOC296782	XM_216075	-	Up	Sg
403	-	XM_343522	-	Up	Sg
404	Akr1c11_predicted	XM_341550	Rn.132469	Up	Sg
405	-	A_44_P304740	-	Up	Sg
406	-	AW142587	Rn.9491	Up	Sg
407	Itm2c_predicted	NM_001009674	Rn.8450	Up	Sg
408	-	AW916070	Rn.167735	Up	Sg
409	-	TC531872	Rn.167735	Up	Sg
410	LOC300150	XM_235563	-	Up	Sg
411	-	ENSRNOT00000049913	-	Up	Sg
412	Nr1d1	NM_145775	Rn.29848	Up	Sg
413	RGD1308684_predicted	XM_341641	Rn.41567	Up	Sg
414	LOC365316	XM_344926	-	Up	Sg
415	Scnn1g	NM_017046	Rn.10360	Up	Sg
416	Gpx6	NM_147165	Rn.9852	Up	Sg
417	Lrp2	NM_030827	Rn.26430	Up	Sg
418	-	TC566080	-	Up	Sg
419	-	NM_001017383	Rn.22468	Up	Sg

[0030]

No	Target(Gene)Symbol	Target Accession	UniGene	Up/Down	生体由来試料
420	-	BI279326	Rn.48786	Up	Sg
421	LOC297757	XM_216317	Rn.144410	Up	Sg
422	Pex11a	BC061835	Rn.14519	Up	Sg
423	Cdh11	XM_341639	Rn.8900	Up	Sg
424	RGD1306750_predicted	XM_347055	Rn.48786	Up	Sg
425	LOC313589	XM_233520	Rn.162826	Up	Sg
426	-	AA875449	Rn.2923	Up	Sg
427	Duox2	NM_024141	Rn.55542	Up	Sg
428	LOC474169	NM_001007015	Rn.87496	Up	Sg
429	-	BC091324	Rn.13679	Up	Sg
430	RGD:708361	NM_138547	Rn.10021	Up	Sg
431	-	X55180	Rn.117936	Up	Sg
432	LOC288979	XM_222564	Rn.24014	Up	Sg
433	-	AW918545	Rn.13679	Up	Sg
434	-	TC542673	Rn.13679	Up	Sg
435	-	BG672648	-	Up	Sg
436	RGD:735199	NM_198734	Rn.154471	Up	Sg
437	RGD1309403_predicted	XM_227140	Rn.38949	Up	Sg
438	-	CO556754	Rn.15953	Up	Sg
439	Muc19_predicted	XM_235593	Rn.162964	Down	Sg
440	Smgb	NM_080775	Rn.9925	Down	Sg
441	Rasl12_predicted	XM_236351	Rn.147874	Down	Sg
442	Cdh22	NM_019161	Rn.145674	Down	Sg
443	LOC314509	XM_234661	Rn.110660	Down	Sg
444	RGD:708577	NM_133622	Rn.9752	Down	Sg
445	Lman1l_predicted	XM_217166	-	Down	Sg
446	-	XM_214055	-	Down	Sg
447	Bpil1_predicted	XM_215892	Rn.162713	Down	Sg
448	LOC362442	XM_342764	Rn.77935	Down	Sg
449	LOC362442	XM_342764	Rn.77935	Down	Sg
450	RGD:1303308	NM_001004236	Rn.33830	Down	Sg
451	LOC292801	XM_218497	-	Down	Sg
452	-	A_44_P950925	-	Down	Sg
453	RGD1311224_predicted	XM_215767	Rn.47550	Down	Sg
454	Kcne1	NM_012973	Rn.9734	Down	Sg
455	Kntc1_predicted	XM_222157	Rn.47918	Down	Sg
456	Mme	NM_012608	Rn.33598	Down	Sg
457	Fetub	NM_053348	Rn.2464	Down	Sg
458	Galnt12_predicted	XM_223905	-	Down	Sg
459	-	XM_344059	-	Down	Sg
460	-	NM_001013180	Rn.30648	Down	Sg
461	Cox4i2	NM_053472	Rn.7214	Down	Sg
462	Gnas	L10326	Rn.31	Down	Sg
463	Runx3	NM_130425	Rn.34220	Down	Sg
464	Olr1654_predicted	NM_021860	Rn.138118	Down	Sg
465	Serpina1	NM_022519	Rn.1419	Down	Sg
466	Igkv28	L17078	Rn.92371	Down	Sg
467	Dlk1	NM_053744	Rn.14547	Down	Sg
468	LOC299434	XM_234680	Rn.134951	Down	Sg
469	LOC366769	XM_345756	Rn.126669	Down	Sg
470	-	TC527103	Rn.107412	Down	Sg
471	Creb3l4	XM_227391	Rn.107412	Down	Sg
472	-	TC539429	Rn.107412	Down	Sg
473	Galnt7	NM_022926	Rn.144577	Down	Sg
474	Oit1_predicted	XM_214143	Rn.38497	Down	Sg
475	-	L07410	-	Down	Sg
476	RGD1311701_predicted	XM_230278	Rn.34843	Down	Sg
477	-	AF217591	Rn.134336	Down	Sg
478	-	AW144181	-	Down	Sg
479	-	TC539049	-	Down	Sg

[0031]

No	Target(Gene)Symbol	Target Accession	UniGene	Up/Down	生体由来試料
480	RGD:1303068	NM_203337	Rn.24125	Down	Sg
481	-	Z93368	Rn.167718	Down	Sg
482	-	AW144454	Rn.167718	Down	Sg
483	-	NM_001014264	Rn.102149	Down	Sg
484	RGD:620649	CA509211	Rn.3517	Down	Sg
485	-	XM_573320	Rn.163185	Down	Sg
486	Dnajc10_predicted	XM_215751	Rn.8642	Down	Sg
487	-	NM_001025041	Rn.162656	Down	Sg
488	-	M84148	Rn.134335	Down	Sg
489	Ces3	NM_133295	Rn.2549	Down	Sg
490	Dnajc10_predicted	XM_215751	Rn.8642	Down	Sg
491	Cdh22	NM_019161	Rn.145674	Down	Sg
492	-	L07402	-	Down	Sg
493	RGD:1303167	NM_212541	Rn.27480	Down	Sg
494	Ca3	NM_019292	Rn.1647	Down	Sg
495	Cyp2f2	NM_019303	Rn.10817	Down	Sg
496	LOC299469	XM_234749	-	Down	Sg
497	Sectm1	NM_199082	-	Down	Sg
498	-	NM_001013219	Rn.104514	Down	Sg
499	RGD:708486	NM_020091	Rn.48676	Down	Sg
500	-	XM_575093	Rn.116833	Down	Sg
501	Fam3b_predicted	XM_221623	Rn.162007	Down	Sg
502	Gm1012	XM_342493	Rn.44656	Down	Sg
503	-	XM_234741	-	Down	Sg
504	LOC314512	XM_234676	Rn.110661	Down	Sg
505	Acdc	NM_144744	Rn.24299	Down	Sg
506	Bf	NM_212466	Rn.109148	Down	Sg
507	Olr197_predicted	NM_001000188	Rn.141814	Down	Sg
508	LOC299551	XM_234830	-	Down	Sg
509	-	Z93354	Rn.179369	Down	Sg
510	Sec23b_predicted	XM_342531	Rn.8735	Down	Sg
511	Amy1	NM_001010970	Rn.116361	Down	Sg
512	Cxadrl1	NM_199406	Rn.162547	Down	Sg
513	Galnt5	NM_031796	Rn.30048	Down	Sg
514	-	XM_344373	-	Down	Sg
515	-	TC525800	-	Down	Sg
516	-	XM_575540	Rn.117940	Down	Sg
517	C1ql3_predicted	BF391573	Rn.39092	Down	Sg
518	Igfbp2	NM_013122	Rn.6813	Down	Sg
519	Cnnm4_predicted	XM_343554	Rn.857	Down	Sg
520	RGD:1303241	NM_001002802	Rn.38581	Down	Sg
521	-	BC091425	-	Down	Sg
522	Creb3l1	NM_001005562	Rn.24541	Down	Sg
523	-	U75411	-	Down	Sg
524	LOC366733	XM_345725	Rn.8473	Down	Sg
525	Galnt12_predicted	XM_223905	-	Down	Sg
526	-	XM_342323	-	Down	Sg
527	Akr1b8	NM_173136	Rn.23676	Down	Sg
528	-	XM_575775	Rn.23267	Down	Sg
529	Dnase1	NM_013097	Rn.6077	Down	Sg
530	Tgoln2	NM_138840	Rn.11349	Down	Sg
531	Prpf31_predicted	XM_218173	Rn.99310	Down	Sg
532	-	XM_234755	-	Down	Sg
533	Cd14	NM_021744	-	Down	Sg
534	F3	NM_013057	Rn.9980	Down	Sg
535	-	XM_575534	-	Down	Sg
536	-	TC554663	-	Down	Sg
537	Tgoln2	NM_138840	Rn.11349	Down	Sg
538	-	NM_001025683	Rn.16921	Down	Sg
539	Hcn3	NM_053685	Rn.48801	Down	Sg

[0032]

No	Target(Gene)Symbol	Target Accession	UniGene	Up/Down	生体由来試料
540	-	NM_001025683	Rn.16921	Down	Sg
541	-	AF468681	-	Down	Sg
542	-	BF524215	-	Down	Sg
543	Ddc	NM_012545	Rn.11064	Down	Sg
544	-	TC538655	-	Down	Sg
545	Cnn1	NM_031747	Rn.31788	Down	Sg
546	LOC366765	XM_345752	Rn.112186	Down	Sg
547	-	BQ200884	Rn.11349	Down	Sg
548	Amy2_predicted	XM_345278	Rn.67070	Down	Sg
549	-	BE103448	Rn.165522	Down	Sg
550	RGD:1303221	NM_001004215	Rn.144176	Down	Sg
551	-	L07408	Rn.117930	Down	Sg
552	Pcsk3	NM_019331	Rn.3220	Down	Sg
553	LOC301711	XM_237538	-	Down	Sg
554	LOC363618	XM_343911	Rn.72525	Down	Sg
555	Mapt	NM_017212	Rn.2455	Down	Sg
556	-	TC555084	-	Down	Sg
557	Retn	NM_144741	Rn.16746	Down	Sg
558	LOC310429	XM_227167	-	Down	Sg
559	RGD1304977_predicted	XM_238325	Rn.101794	Down	Sg
560	Srebf1	XM_213329	Rn.801	Down	Sg
561	-	AW520826	-	Down	Sg
562	LOC307231	XM_225713	Rn.148475	Down	Sg
563	LOC366733	XM_345725	Rn.8473	Down	Sg
564	Arg2	NM_019168	Rn.11055	Down	Sg
565	Cd14	NM_021744	-	Down	Sg
566	Gpx2	NM_183403	Rn.3503	Down	Sg
567	Frmpd1_predicted	XM_233002	Rn.37934	Down	Sg
568	-	TC555358	-	Down	Sg
569	Acsl1	NM_012820	Rn.6215	Down	Sg
570	RGD:1303180	NR_002149	-	Down	Sg
571	LOC362348	XM_342669	Rn.91492	Down	Sg
572	-	BE110753	Rn.8285	Down	Sg
573	-	TC540316	Rn.8285	Down	Sg
574	-	AW917167	Rn.18668	Down	Sg
575	Nid67	NM_173126	Rn.8865	Down	Sg
576	Rhoc_predicted	XM_215659	Rn.162614	Down	Sg
577	Acsl1	NM_012820	Rn.6215	Down	Sg
578	Lama5	XM_215963	Rn.62616	Down	Sg
579	Gpr2_predicted	XM_343968	Rn.49607	Down	Sg
580	Scn11a	NM_019265	Rn.30023	Down	Sg
581	-	NM_001013232	Rn.111376	Down	Sg

[0033] 表1及び2において、「No.」の欄は各遺伝子に割り振った番号を意味し、「Target Symbol」の欄は一般的な遺伝子表記である。また、「Target Accession」の欄は公共のデータベースに登録されている登録ID（アクセッション番号）であり、「UniGene」とは、NCBIが提供する配列データの重複をなくした核酸配列データベースであり、「UniGene」の欄は、データベース（UniGene）に登録されているUiGeneIDである。さらに、「Up/down」は、陽性感情ラットにおいて発現量が増加（Up）しているか、発現量が減少（Down）しているかを意味している。さらに「生体由来試料」は、陽性感情ラットにおいて各ラット陽性感情マーカー遺伝子が陽性感情の指標として機能することができ

る試料を示す。

[0034] 表1に示すラット陽性感情マーカー遺伝子は、2日間の短期間で陽性刺激を負荷した際に発現量の顕著な増減を認めた遺伝子のリストであり、表2に示すラット陽性感情マーカー遺伝子は、陽性刺激を4週間の長期間で負荷した際に発現量の顕著な増減を認めた遺伝子のリストである。表1及び2から分かるとおり、短期間の陽性刺激による場合と、長期間の陽性刺激による場合とで、発現量の顕著な増減が認められる遺伝子が異なる。

[0035] すなわち、表1に示すラット陽性感情マーカー遺伝子は、一過性の陽性感情を検出することができるマーカーであり、表2に示すラット陽性感情マーカー遺伝子は、体質の変化を生じさせるような持続的な陽性感情の結果を検出することができるマーカーである。

[0036] 本発明に係るラットの陽性感情評価方法においては、先ずステップaにおいて、表1及び/又は2に示す遺伝子群から選択される少なくとも1種の遺伝子の発現量を、指定の生体由来試料において測定する。ここで、「指定の生体由来試料」とは、表1及び/又は2に示す各遺伝子に対応する「生体由来試料」の欄に記載の試料（すなわち、血液、視床下部、線条体、口腔内細胞又は唾液腺）を指す。なお、下記に記載の表81～84及び表45～59に列挙する遺伝子は、それぞれ短期刺激、長期刺激において見出されたラット陽性感情マーカー遺伝子の中でも、種々の生物学的活性に関連する遺伝子であり、ステップaにおいては、上記表1及び/又は表2に示す遺伝子群に加えて、又はこれに代えて、表81～84及び/又は45～59に列挙する遺伝子の発現量を、指定の生体由来試料において測定してもよい。

[0037] 遺伝子発現量の測定は、対象の遺伝子の発現量を特異的に定量できる方法であれば特に制限はなく、対象遺伝子のmRNA量(又はcDNA)を測定することによってもよいし、対象遺伝子がコードするタンパク質量を測定することによってもよい。

[0038] 対象遺伝子のmRNA量（又はcDNA）の測定には、該mRNA(又はcDNA)に対して相補的な塩基配列を有する核酸を使用することができる。具体的には、ラッ

ト生体由来試料から全mRNAを単離し、測定対象の遺伝子の塩基配列の少なくとも一部（好ましくはコード領域）を含む核酸をプローブ又はプライマーとして用いることによって行う。測定に使用する核酸は必ずしもDNAである必要はなく、RNA、DNA/RNAキメラ、他の人工核酸などであってもよい。かかる核酸は、当業者に周知の方法、例えば適当な配列のクローニング及び制限酵素による切断、ホスホトリエステル法（例えばNarangら，1979年，Meth.Enzymol.，第68巻，p90～99参照）、ホスホジエステル法（例えばBrownら，1979年、Meth.Enzymol.，第68巻，p109～151参照）、エチルホスホアミダイト法（例えばBeaucageら，1981年，Tetrahedron Lett.，第22巻，p1859～1862参照）などの方法により、直接合成することができる。また市販の自動DNA合成装置を使用することによって合成してもよい。

[0039] ラット生体由来試料からの全mRNAの単離は、当業者に公知の手法によって行うことができる。例えば、ラット生体由来試料の破壊液から定法に従って全RNAを取得し、オリゴdTカラムにてmRNAを回収することができる。

[0040] mRNA量の測定には、当業者に公知のいずれの方法を用いてもよい。そのような方法として例えば、DNAマイクロアレイ法、RT-PCR、定量PCR、ノーザンブロット等を使用することができる。一般的には、1個～数種類の遺伝子に関してmRNA量を測定する場合には、RT-PCR、定量PCR、ノーザンブロット等を使用することが好ましい。この場合、上記核酸プローブ又はプライマーを標識することにより、mRNA量を測定することができる。一方、100種以上といった多数の遺伝子についてmRNA量を測定する場合には、DNAマイクロアレイ法を使用することが好ましい。DNAマイクロアレイ法でmRNA量を測定する場合には、上記核酸プローブを固定化した支持体に、測定試料である全mRNAを接触させることによって行う。この場合、一般的には、測定試料のmRNAを標識し、各プローブとのハイブリダイゼーションの有無を蛍光強度によって検出することにより、mRNA量を測定することができる。なお、ハイブリダイゼーション条件は、各プローブと対象のmRNAとの特異的なハイブリダイゼーションが担保される条件であれば特に制限されないが、ストリンジェントな条件である

ことが好ましい。そのような条件は当業者に公知であり、例えばSambrookらMolecular Cloning: A Laboratory Manual 2nd Ed. Cold Spring Harbor Laboratory Press (1989)等に記載の条件が挙げられる。

[0041] 一方、対象遺伝子の発現量の測定を該遺伝子がコードするタンパク質量を測定することによって行う場合には、該タンパク質に対して特異的に結合する分子、例えば該タンパク質に特異的に結合する抗体を使用することができる。なお、測定対象の遺伝子がコードするタンパク質を抗原とし、当該抗原に特異的に結合する限り、前記抗体としては特に制限はなく、マウス抗体、ラット抗体、ウサギ抗体、ヒツジ抗体等を適宜用いることができる。抗体は、ポリクローナル抗体であってもモノクローナル抗体であってもよいが、均質な抗体を安定に生産できる点でモノクローナル抗体が好ましい。ポリクローナル抗体およびモノクローナル抗体は当業者に周知の方法により作製することができる。

[0042] モノクローナル抗体を産生するハイブリドーマは、基本的には公知技術を使用し、以下のようにして作製できる。すなわち、所望の抗原や所望の抗原を発現する細胞を感作抗原として使用して、これを通常の免疫方法にしたがって免疫し、得られる免疫細胞を通常の細胞融合法によって公知の親細胞と融合させ、通常のスクリーニング法により、モノクローナルな抗体産生細胞（ハイブリドーマ）をスクリーニングすることによって作製できる。ハイブリドーマの作製は、たとえば、ミルステインらの方法 (Kohler. G. and Milstein, C., Methods Enzymol. (1981) 73: 3-46) 等に準じて行うことができる。

[0043] 得られたモノクローナル抗体は、測定対象のタンパク質の定量用に、エンザイムーリンクイムノソルベントアッセイ（ELISA）、酵素イムノドットアッセイ、ラジオイムノアッセイ、凝集に基づいたアッセイ、あるいは他のよく知られているイムノアッセイ法で検査試薬として用いることができる。また、モノクローナル抗体は標識化されることが好ましい。標識化を行う際、標識化合物としては例えば当分野で公知の酵素、蛍光物質、化学発光物質、放

射性物質、染色物質などを使用することができる。

[0044] その他、タンパク質量の測定には、該タンパク質に特異的に結合可能なリガンドタンパク質又は受容体タンパク質を使用することもできる。

[0045] 一方、本発明に係るラットの陽性感情を評価するための検査キットは、上記表1及び/若しくは2に示す遺伝子（並びに/又は表81～84及び/若しくは表45～59に示す遺伝子）の塩基配列の少なくとも一部を含む核酸からなる群から選ばれる少なくとも1種の核酸、或いは、上記表1及び/又は2に示す遺伝子によってコードされるタンパク質に特異的に結合する分子（例えば抗体）からなる群から選ばれる少なくとも1種の分子を備える。本発明の検査キットが備える核酸又は分子の種類は、測定対象の遺伝子の種類に応じて変化する。

[0046] 例えば、当該検査キットは、支持体に上述した核酸又は分子(若しくはその一部)を被覆したものを挙げることができる。支持体としてはポリスチレンやポリカーボネート、ポリプロピレン、ポリビニール製のマイクロタイタープレート、試験管、キャピラリー、ビーズ、膜、フィルターなどが挙げられる。

[0047] 以上のようにして、上記表1及び/又は2に示す遺伝子群から選択される少なくとも1種の遺伝子の発現量を指定の生体由来試料において測定した後、ステップbにおいて、当該発現量に基づいて、ラットの陽性感情の評価を行う。

[0048] ステップbにおける評価は、表1、2に挙げる遺伝子についての基準値に対して、ステップaで測定した遺伝子の発現量から算出されるスコアが異なるかを判断することによって行うことができる。

[0049] 具体的には、表1、2に挙げる遺伝子のうち、発現量から算出されるスコアが、「Up/down」の欄がUpの遺伝子については基準値より高くなっているか否かを判断し、Downの遺伝子については基準値より低くなっている否かを判断する。

[0050] 上記「基準値」は、表1、2に挙げる陽性感情マーカー遺伝子ごとに設定される。本発明において、基準値は、例えば、約50KHz近傍の超音波を発していない対照ラットにおけるラット陽性感情マーカー遺伝子の発現量を、対照ラ

ットと陽性感情にあるラットとの間で発現量の有意な差が認められない任意の遺伝子Xの発現量に対する相対値として示した値とすることができる。この場合、上記スコアは、ステップaで測定したラット陽性感情マーカー遺伝子の発現量を、遺伝子Xの発現量で除算することによって算出することができる。かかる基準値は、表1、2に記載の各遺伝子について予め求めておいてもよいし、対照ラットにおける基準値の測定を本発明のステップaと平行して行ってもよい。基準値は、複数の対照ラットで算出することにより、基準値±標準偏差とすることが好ましい。これにより基準値に対する個体差の影響を排除することができる。またこれに関連して、本発明に係る検査キットは、上記遺伝子Xの塩基配列を有する核酸又は遺伝子Xがコードするタンパク質に対する抗体をさらに含むことができる。これにより、対照ラットにおいて基準値を測定するために、及び評価対象のラットにおいて上記スコアを算出するために、遺伝子Xの発現量を求めることができる。また、本発明に係る検査キットは、表1、2に示す陽性感情マーカー遺伝子のそれぞれについて予め算出された基準値（±標準偏差）の対応表を含むことが好ましい。これにより、対照ラットを用いた基準値の算出を省略することができる。

[0051] ここで、評価の一例を挙げると、例えば、表1、2に記載されるラット陽性感情マーカー遺伝子のうち、発現量が「Up」の遺伝子から遺伝子を選択し、選択した遺伝子の発現量及び遺伝子Xの発現量を測定し、この選択した遺伝子の発現量を遺伝子Xの発現量で除算した値が、該遺伝子について予め算出しておいた基準値を有意に上回っている場合に、ラットは陽性感情であると評価することができる。なお、かかる評価の信頼度を高めるために、複数の遺伝子について上記判断を行い、50%以上、より好ましくは60%以上、より好ましくは70%以上、より好ましくは80%以上、より好ましくは90%以上、最も好ましくは100%の遺伝子において基準値を有意に上回っている場合に、ラットは陽性感情であると評価することとしてもよい。あるいは、対照に対する遺伝子発現量の増加率又は減少率を、選択した複数の遺伝子のそれぞれについて求め、その百分比合計が所定の数値を超える場合に、ラットは陽性感情

であると評価してもよい。

[0052] 本発明に係るラットの陽性感情評価方法及び検査キットによれば、陽性感情を簡便且つ高い信頼性をもって評価することができる。特に、本発明に係るラットの陽性感情評価方法において、測定対象の遺伝子の種類を増やすこと（例えば10種～100種又はそれ以上）によって、より優れた信頼度をもって、ラットの陽性感情を評価することができる。

[0053] １－２．ヒト陽性感情マーカー遺伝子及びそれを用いたヒトの陽性感情又は健康度の評価系

本発明はまた、ヒトの陽性感情又は健康度の評価方法を提供する。この方法は、原理的には、上記ラット陽性感情評価方法と同様にして行うことができる。したがって、本発明のヒト陽性感情又はヒト健康度の評価方法は、ヒト陽性感情マーカー遺伝子の発現量を生体由来試料、例えば血液、において測定するステップaと、ステップaで測定した発現量に基づいて、ヒトの陽性感情又は健康度を評価するステップbとを含んでいる。

[0054] 本明細書で使用する「ヒト陽性感情マーカー遺伝子」は、笑いを誘発する刺激（本明細書中、「笑い刺激」ともいう）を負荷したヒトにおいて、そのような刺激を負荷していないヒトに比較して、発現量が増加するか又は減少する遺伝子として定義される。言い換えれば、ヒト陽性感情マーカー遺伝子は、ヒトの笑いと連動して発現量が増減する遺伝子である。

[0055] また「健康」とは、WHO定義より、「完全な肉体的、精神的及び社会的福祉の状態であり、単に疾病又は病弱の存在しないことではない」を指し、「健康度」とはその程度を指す。ヒトにおいて、笑いがNK細胞の活性化や糖尿病患者の食後血糖値を抑えることが知られている。本発明では、s-IgAなどの免疫機能の活性化、ストレス指標である唾液アミラーゼ、好中球などから見られるストレス状態の改善、感染や炎症時に増加するC反応性蛋白の減少、糖尿病患者の食後血糖値抑制などを、笑い刺激により確認し、笑いが健康維持・増進や、疾病の機能回復に効果があるという結果を得た。これらの健康維持・増進や、疾病の機能回復の効果と、陽性感情マーカー遺伝子の各遺伝子セ

ットとは、対応付けすることができている。そのため、ヒト陽性感情マーカー遺伝子の発現量に基づくヒト陽性感情の評価は、ヒトの健康度の評価と考えることもできる。

[0056] ヒト陽性感情マーカー遺伝子のうち、機能面で注目される遺伝子と、顕著な発現量の増減を示す遺伝子の上位15遺伝子とからなる遺伝子群は、それぞれ遺伝子セット1～8と称し、下記表に要約されている：遺伝子セット1、表164；遺伝子セット2、表172；遺伝子セット3、表178；遺伝子セット4、表185；遺伝子セット5、表155；遺伝子セット6、表159；遺伝子セット7、表190；遺伝子セット8、表198。これらの表中、「No.」の欄は各遺伝子セット中の各遺伝子に割り振った番号を意味し、「Target(Gene) Symbol」の欄は一般的な遺伝子表記である。また、「Target Accession」の欄は公共のデータベースに登録されている登録ID（アクセッション番号）であり、「UniGene」とは、NCBIが提供する配列データの重複をなくした核酸配列データベースであり、「UniGene」の欄は、データベース（UniGene）に登録されているUiGeneIDである。さらに、「Up/down」は、笑いを誘導した陽性感情下のヒトにおいて発現量が増加（Up）しているか、発現量が減少（Down）しているかを意味している。

[0057] また「被験者群」は、各遺伝子セットに含まれる遺伝子の発現の増減が確認された被験者の種類を示している：A、糖尿病非罹病かつ歯周病非罹病者；B、糖尿病非罹病かつ歯周病罹病者；C、糖尿病罹病かつ歯周病非罹病者；D、糖尿病罹病かつ歯周病罹病者；A＋B、糖尿病非罹病者；C＋D、糖尿病罹病者；A＋C、歯周病非罹病者；B＋D、歯周病罹病者。

[0058] 遺伝子セット1、2、5は、広く一般の人に対して利用できる陽性感情又は健康度評価のための遺伝子セットであり、その中でも特に遺伝子セット1は広く一般の人に対して陽性感情又は健康度評価を行うのに適した遺伝子セットである。遺伝子セット3、4、6は、糖尿病罹病者に適した遺伝子セットであるが、他の疾病に罹病している人、疾病に罹病していない人の陽性感情又は健康度評価に利用できる。遺伝子セット2、4、8は、歯周病罹病者に適した遺伝子

セットであるが、他の疾病に罹病している人、疾病に罹病していない人の陽性感情又は健康度評価に利用できる。これらの遺伝子セットは、単独でも、それぞれを組み合わせても陽性感情又は健康度評価に利用できる。

[0059] 本発明に係るヒトの陽性感情又は健康度の評価方法においては、先ずステップaにおいて、遺伝子セット1～8に示す遺伝子セット中の少なくとも1種の遺伝子の発現量を、生体由来試料、例えば血液、において測定する。測定する生体由来試料は、血液のほか、生体由来の組織、細胞、体液、排泄物等をいい、体液には血漿、血清等の血液由来試料、唾液、乳等が含まれる。排泄物には尿、便等が含まれる。細胞には血液から分離した白血球、口腔内粘膜擦過細胞、鼻粘膜細胞等が含まれるが、これらに限定されるものではなく、生体から採取できるものであれば試料として利用できる。

[0060] 遺伝子発現量の測定は、上記ラット陽性感情評価方法の節に記載されるようにして行えばよい。この関連で、本発明に係るヒトの陽性感情又は健康度を評価するための検査キットは、上記遺伝子セット1～8に示す遺伝子セット中の遺伝子の塩基配列の少なくとも一部を含む核酸からなる群から選ばれる少なくとも1種の核酸、或いは、上記遺伝子セット1～8に示す遺伝子セット中の遺伝子によってコードされるタンパク質に特異的に結合する分子（例えば抗体）からなる群から選ばれる少なくとも1種の分子を備えている。

[0061] 次いで、上記測定結果に基づき、ステップbにおいて、ヒトの陽性感情又は健康度の評価を行う。

[0062] ステップbにおける評価は、遺伝子セット1～8中の遺伝子についての基準値に対して、ステップaで測定した遺伝子の発現量から算出されるスコアが異なるかを判断することによって行うことができる。

[0063] 具体的には、遺伝子セット1～8に挙げる遺伝子のうち、発現量から算出されるスコアが、「Up/down」の欄がUpの遺伝子については基準値より高くなっているか否かを判断し、Downの遺伝子については基準値より低くなっている否かを判断する。

[0064] 上記「基準値」は、遺伝子セット1～8に挙げる陽性感情マーカー遺伝子ご

とに設定される。本発明において、基準値は、例えば、笑いを誘発する刺激を負荷していない対照ヒトにおけるヒト陽性感情マーカー遺伝子の発現量を、対照ヒトと陽性感情にあるヒトとの間で発現量の有意な差が認められない任意の遺伝子Xの発現量に対する相対値として示した値とすることができる。この場合、上記スコアは、ステップaで測定したヒト陽性感情マーカー遺伝子の発現量を、遺伝子Xの発現量で除算することによって算出することができる。かかる基準値は、遺伝子セット1～8に記載の各遺伝子について予め求めておいてもよいし、対照ヒトにおける基準値の測定を本発明のステップaと平行して行ってもよい。基準値は、複数の対照ヒトで算出することにより、基準値±標準偏差とすることが好ましい。これにより基準値に対する個体差の影響を排除することができる。またこれに関連して、本発明に係るヒトの陽性感情又は健康度を評価するための検査キットは、上記遺伝子Xの塩基配列を有する核酸又は遺伝子Xがコードするタンパク質に対する抗体をさらに含むことができる。これにより、対照ヒトにおいて基準値を測定するために、及び評価対象のヒトにおいて上記スコアを算出するために、遺伝子Xの発現量を求めることができる。また、本発明に係るヒトの陽性感情又は健康度を評価するための検査キットは、遺伝子セット1～8に示す陽性感情マーカー遺伝子のそれぞれについて予め算出された基準値（±標準偏差）の対応表を含むことが好ましい。これにより、対照ヒトを用いた基準値の算出を省略することができる。

[0065] ここで、評価の一例を挙げると、例えば、遺伝子セット1～8に記載されるヒト陽性感情マーカー遺伝子のうち、発現量が「Up」の遺伝子から遺伝子を選択し、選択した遺伝子の発現量及び遺伝子Xの発現量を測定し、この選択した遺伝子の発現量を遺伝子Xの発現量で除算した値が、該遺伝子について予め算出しておいた基準値を有意に上回っている場合に、ヒトは陽性感情である又は健康度が高いと評価することができる。なお、かかる評価の信頼度を高めるために、複数の遺伝子について上記判断を行い、50%以上、より好ましくは60%以上、より好ましくは70%以上、より好ましくは80%以上、より好

ましくは90%以上、最も好ましくは100%の遺伝子において基準値を有意に上回っている場合に、ヒトは陽性感情である又は健康度が高いと評価することとしてもよい。あるいは、対照に対する遺伝子発現量の増加率又は減少率を、選択した複数の遺伝子のそれぞれについて求め、その百分比合計が所定の数値を超える場合に、ヒトは陽性感情である又は健康度が高いと評価してもよい。

[0066] 本発明に係るヒトの陽性感情又は健康度の評価方法及び検査キットによれば、陽性感情又は健康度を簡便且つ高い信頼性をもって評価することができる。特に、本発明に係るヒトの陽性感情又は健康度の評価方法において、測定対象の遺伝子の種類を増やすこと（例えば10種～100種又はそれ以上）によって、より優れた信頼度をもって、ヒトの陽性感情又は健康度を評価することができる。

[0067] １－３．ラット共通遺伝子及びヒト共通遺伝子

ヒトにおけるTicking刺激およびユーモア刺激により誘発される笑いには、共通性があることが分かってきている。（文献 Biological Psychology 30(1990)141-150, 笑いの科学 2008/05/12 vol.1）。

[0068] また、ラットにおいて、Ticking刺激により50kHz近傍の発生音声を誘発する行為が、ヒトの笑いの原型ではないかと提案している。（文献 Psychology & Behaivior 79 (2003)533-547）これらのことから、ラットのTicking刺激とヒトの笑いとの関係については、共通する生体への生理作用があり、遺伝子発現が類似していることが推測できる。

[0069] そこで本願発明者らは、上記ラット陽性感情マーカー遺伝子及び上記ヒト陽性感情マーカー遺伝子間で、それぞれTickling刺激及び笑い刺激負荷後に、同様の遺伝子発現挙動を示す遺伝子が存在するかどうかを調べたところ、40種の共通遺伝子が存在することを見出した（本明細書中、それぞれラット共通遺伝子、ヒト共通遺伝子と称する）。かかるラット共通遺伝子及びヒト共通遺伝子は、ラット及びヒトの陽性感情評価系で、及びヒトの健康度評価系で、特に有用な陽性感情評価マーカーとして利用できると考えられる。

[0070] したがって、本発明のラット又はヒトの陽性感情評価方法、又はヒトの健康度評価方法において、上記ヒト陽性感情マーカー遺伝子又はラット陽性感情マーカー遺伝子に加えて又はこれに代えて、ラット共通遺伝子又はヒト共通遺伝子を使用することができる。

[0071] これらヒト共通遺伝子及びラット共通遺伝子は、それぞれ下記表202及び205に要約されている。

[0072] １－４．他の評価手法

本発明の陽性感情又は健康度の評価方法において、好ましくは、評価の信頼度を高めるために、複数の陽性感情マーカー遺伝子を1つの遺伝子群として使用し、該遺伝子群の遺伝子発現量を網羅的に解析することによって、陽性感情又は健康度を評価する。

[0073] ラット陽性感情評価方法において、上記遺伝子群として、例えば次のものを使用することができる：表1に列挙される遺伝子群；表2に列挙される遺伝子群；表81～84のいずれかに列挙される遺伝子群；表45～59のいずれかに列挙される遺伝子群；及び表205に列挙される遺伝子群；又はこれらの遺伝子群の組合せ。

[0074] またヒト陽性感情又はヒト健康度の評価方法において、上記遺伝子群として、例えば次のものを使用することができる：表164に列挙される遺伝子群（又は遺伝子セット1）；表172（又は遺伝子セット2）；表178に列挙される遺伝子群（又は遺伝子セット3）；表185に列挙される遺伝子群（又は遺伝子セット4）；表155に列挙される遺伝子群（又は遺伝子セット5）；表159に列挙される遺伝子群（又は遺伝子セット6）；表190に列挙される遺伝子群（又は遺伝子セット7）；表198に列挙される遺伝子群（又は遺伝子セット8）；表202に列挙される遺伝子群；又はこれらの遺伝子群の組合せ。

[0075] １－４－１．発現方向の一致率の評価

本発明の陽性感情又は健康度の評価方法において、陽性感情又は健康度の評価は、上記のような遺伝子群に含まれる全遺伝子の発現量を生体由来試料にて測定し、各遺伝子の発現増減の方向の一致率を評価することによって行

われる。一致率(%)は、各遺伝子について示されている発現方向(Up/Down)に向かって基準値に対して有意に増減している遺伝子数を、遺伝子群に含まれる遺伝子の総数で割った値に100を乗じることによって求めることができる。

[0076] この場合、例えば、一致率(%)が50%以上、より好ましくは60%以上、より好ましくは70%以上、より好ましくは80%以上、より好ましくは90%以上、最も好ましくは100%である場合に、被験体は陽性感情である又は健康度が高いと評価することができる。

[0077] あるいは、かかる評価手法を後述する陽性刺激評価系にて使用する場合には、評価対象刺激負荷後の上記一致率を複数の評価対象刺激について求め、最も高い一致率を生じさせた評価対象刺激を陽性感情又は健康増進に導く良好な刺激として選択することができる。

[0078] 1－4－2．発現強度のスコア化

本発明の陽性感情又は健康度の評価方法において、陽性感情又は健康度の評価は、上記のような遺伝子群に含まれる全遺伝子の発現量を生体由来試料にて測定し、測定した遺伝子の発現量とTickling刺激又は笑い刺激負荷後の(すなわち陽性感情の被験体の)該遺伝子の発現量との差を、遺伝子群に含まれる全遺伝子について比較することによって行うことができる。具体的には、測定した遺伝子発現量とTickling刺激又は笑い刺激負荷後の遺伝子発現量との差を二乗したスコアの総和を次式に従って取得する。

[数1]

$$\sum_{i=1}^{n}(a_i - b_i)^2$$

[0079] [式中、nは遺伝子群に含まれる遺伝子の総数であり；a_iは生体由来試料にて測定された遺伝子iの発現量であり；b_iはTickling刺激又は笑い刺激負荷後の遺伝子iの発現量である]

このスコアは、測定された遺伝子発現量と、Tickling刺激又は笑い刺激負荷後の遺伝子発現量との差が小さいほど小さくなる。したがって、被験体の陽性感情の程度又は健康度をこのスコアを指標にして推定することができる

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[0080] 例えば、かかる評価手法を後述する陽性刺激評価系にて使用する場合には、評価対象刺激負荷後の上記スコアを複数の評価対象刺激について求め、最も低いスコアを生じさせた評価対象刺激を陽性感情又は健康増進に導く良好な刺激として選択することができる。

[0081] 1－4－3．発現方向の一致率の評価と発現強度のスコア化の組合せ

本発明の陽性感情又は健康度の評価方法において、陽性感情又は健康度の評価は、上記(1－4－1)と(1－4－2)の手法を組合わせることによって行うことができる。具体的には、上記のような遺伝子群に含まれる全遺伝子の発現量を生体由来試料にて測定し、各遺伝子について示されている発現方向(Up/Down)に向かって基準値に対して有意に増減している遺伝子を選別し、測定した遺伝子発現量とTickling刺激又は笑い刺激負荷後の遺伝子発現量との差を二乗したスコアを選別した各遺伝子について求め、これを総和したスコアを次式に従って取得する。

[数2]

$$\sum_{i=1}^{m}(a_i - b_i)^2$$

[0082] [式中、mは、生体由来試料にて測定された遺伝子群中の遺伝子のうち、Tickling刺激又は笑い刺激負荷後の遺伝子発現方向と同方向に向かって基準値に対して有意に増減している遺伝子の数であり；a_iは生体由来試料にて測定された遺伝子iの発現量であり；b_iはTickling刺激又は笑い刺激負荷後の遺伝子iの発現量である]

このスコアは、測定された遺伝子発現量と、Tickling刺激又は笑い刺激負荷後の遺伝子発現量との差が小さいほど小さくなる。したがって、被験体の陽性感情の程度又は健康度をこのスコアを指標にして推定することができる。

[0083] 例えば、かかる評価手法を後述する陽性刺激評価系にて使用する場合には、評価対象刺激負荷後の上記スコアを複数の評価対象刺激について求め、最

も低いスコアを生じさせた評価対象刺激を陽性感情又は健康増進に導く良好な刺激として選択することができる。

[0084] 1－4－4．カルバック・ライブラー（Kullback-Leibler）相互情報量

本発明の陽性感情又は健康度の評価方法において、陽性感情又は健康度の評価は、カルバック・ライブラー(Kullback-Leibler)相互情報量に基づいて行うことができる。本発明において、カルバック・ライブラー相互情報量は、上記のような遺伝子群の生体由来試料における発現量及び発現パターンと、Tickling刺激又は笑い刺激負荷後の(すなわち陽性感情の被験体の)前記遺伝子群の発現量及び発現パターンとの差の尺度として取得される。具体的には、a_iを次式：

[数3]

$$\tilde{a}_i = \frac{a_i}{\sum_{i=1}^{n} a_i}$$

[式中、n は遺伝子群に含まれる遺伝子の総数であり；$\tilde{a}_i$は生体由来試料にて測定された遺伝子 i の発現量を遺伝子群の総発現量で除した値である]

[0085] に従い正規化することで、

[数4]

$$\sum_{i=1}^{n} \tilde{a}_i = 1$$

となる。$\tilde{b}_i$も同様に定義する。$\tilde{a}_1 \cdots\cdots \tilde{a}_n$ を、$\tilde{a} = (\tilde{a}_1, \cdots\cdots \tilde{a}_n)$、$\tilde{b}_1 \cdots\cdots \tilde{b}_n$ を、$\tilde{b} = (\tilde{b}_1, \cdots\cdots \tilde{b}_n)$ と定義する。$\tilde{a}$, $\tilde{b}$ に対してカルバック・ライブラー相互情報量は下記式で求めることができる。

$$KL(\tilde{a}, \tilde{b}) = \sum_{i=1}^{n} \tilde{a}_i \log \frac{\tilde{a}_i}{\tilde{b}_i}$$

[式中、n は遺伝子群に含まれる遺伝子の総数であり；$\tilde{a}_i$は生体由来試料にて測定された遺伝子 i の発現量を遺伝子群の総発現量で除した値であり；$\tilde{b}_i$は Tickling 刺激又は笑い刺激負荷後の遺伝子 i の発現量を遺伝子群の総発現量で除した値である]

[0086] カルバック・ライブラー相互情報量は、その値が小さいほど、比較される2

群間の遺伝子発現量及び遺伝子発現パターンがより近似していることを示す。したがって、被験体の陽性感情の程度又は健康度は、Tickling刺激又は笑い刺激負荷後の発現量及び発現パターンを基準にして推定することができる。

[0087] 例えば、かかる評価手法を後述する陽性刺激評価系にて使用する場合には、Tickling刺激又は笑い刺激負荷後の発現量及び発現パターンを基準とした評価対象刺激後のカルバック・ライブラー相互情報量を、複数の評価対象刺激について求め、最も小さいカルバック・ライブラー相互情報量を生じさせた評価対象刺激を陽性感情又は健康増進に導く良好な刺激として選択することができる。

[0088] なお、カルバック・ライブラー相互情報量を、下記式によって定義してもよい。

[数5]

$$KL(\tilde{b},\tilde{a}) = \sum_{i=1}^{n} \tilde{b}_i \log \frac{\tilde{b}_i}{\tilde{a}_i}$$

[式中、n は遺伝子群に含まれる遺伝子の総数であり；$\tilde{a}_i$は生体由来試料にて測定された遺伝子 i の発現量を遺伝子群の総発現量で除した値であり；$\tilde{b}_i$は Tickling 刺激又は笑い刺激負荷後の遺伝子 i の発現量を遺伝子群の総発現量で除した値である]

[0089] さらに、下記式:

[数6]

$$J(\tilde{a},\tilde{b}) = KL(\tilde{a},\tilde{b}) + KL(\tilde{b},\tilde{a})$$

[0090] と対称化した相互情報量Jをカルバック・ライブラー相互情報量の代わりに使ってもよい。なお、カルバック・ライブラー相互情報量ではなく、その他の相互情報量、例えば、Hellinger相互情報量など、を使ってもよい。

[0091] 2．陽性刺激評価系

本発明はまた、所与の刺激がラット及びヒトに対する陽性刺激であるか否かを評価する方法（以下、それぞれ「ラット陽性刺激評価方法」及び「ヒト陽性刺激評価方法」とも称する）を提供する。

[0092] 本明細書で使用する「陽性刺激」とは、被験体（すなわちラット又はヒト）を陽性感情に導くか又は被験体(すなわちヒト)を健康増進に導く、任意の刺激を指す。また本発明で使用する「刺激」とは、生体に作用してなんらかの現象や反応を起こさせるものを指し、外的な刺激と、内的な刺激を含む。刺激の種類には、物理的、化学的、生物的、心理的な刺激が挙げられる。これらの刺激は、視覚的、聴覚的、味覚的、嗅覚的、前庭感覚的、体性感覚的、内臓感覚的、運動感覚的刺激の１種以上である。また、陽性刺激であるか否かの評価対象となる刺激は、その種類だけではなく、断続的又は継続的な刺激といった刺激の負荷様式についても評価される。

[0093] ２－１．ラット陽性刺激評価方法

本発明に係るラット陽性刺激評価方法は、ラットに評価対象である刺激を負荷する第1のステップと、少なくとも1種のラット陽性感情マーカー遺伝子の発現量を測定する第2のステップと、測定した前記ラット陽性感情マーカー遺伝子の発現量に基づいて、対象刺激がラットに対する陽性刺激であるか否かを判断する第3のステップとを含んでいる。

[0094] 第1のステップでは、ラットに評価対象である刺激を負荷する。刺激の負荷期間は特に制限されないが、ラット陽性感情マーカー遺伝子として表1に示す遺伝子群を使用する場合には短期間で負荷し、ラット陽性感情マーカー遺伝子として表2に示す遺伝子群を使用する場合には長期間で負荷することが好ましい。なお、本発明において、用語「短期間」は1～数日間（例えば2日、3日、4日又は5日）を、「長期間」は3週間～4週間を指す。

[0095] 次いで第2のステップでは、表1、2に示されるラット陽性感情マーカー遺伝子の少なくとも1種の遺伝子の発現量を指定の生体由来試料において測定する。なお、測定対象のラット陽性感情マーカー遺伝子として、表1、2に加えて又はこれに代えて表81～84及び/又は45～59に示す遺伝子の少なくとも1種の発現量を測定してもよいこと、及び表1、2、81～84及び45～59のいずれかに列挙される遺伝子群の発現量を測定してもよいこと、については上記と同様であり、その測定方法についても上記の通りである。

[0096] 次いで第3のステップで、第2のステップで測定したラット陽性感情マーカー遺伝子の発現量に基づいて、対象刺激がラット陽性刺激であるか否かを評価する。評価は、上記の通り、第2のステップで測定したラット陽性感情マーカー遺伝子の発現量から算出されるスコアが、当該遺伝子の基準値と異なるかを判定することによって行うことができる。

[0097] 第3のステップにおける対象刺激の評価は、対象刺激の負荷前後のラット陽性感情マーカー遺伝子の発現量を比較することによって行ってもよい。すなわち、対象刺激の負荷前に測定したラット陽性感情マーカー遺伝子の発現量に比較して、刺激負荷後に当該遺伝子の発現量が増加又は減少していれば、当該刺激はラット陽性刺激であると評価することができる。

[0098] したがって、本発明に係るラット陽性刺激評価方法は、ラットに評価の対象である刺激を負荷する第1のステップの前にラット陽性感情マーカー遺伝子の発現量を測定するステップをさらに含むことができる。なおこの場合、生体由来試料として血液、口腔粘膜細胞又は唾液腺を利用する必要があるため、測定対象の陽性感情マーカー遺伝子は、これらの生体由来試料においてラット陽性感情マーカー遺伝子として機能するものを選択する。

[0099] また第3のステップにおける対象刺激の評価は、対照ラットとの比較によって行ってもよい。すなわち、対象刺激を負荷したラットと、対象刺激を負荷しない対照ラットの両者で同一の陽性感情マーカー遺伝子の発現量を測定し、対象刺激を負荷したラットにおいて当該遺伝子の発現量が増加又は減少していれば、対象刺激はラット陽性刺激であると評価することができる。

[0100] ２－２．ヒト陽性刺激評価方法

本発明に係るヒト陽性刺激評価方法は、ヒトに評価対象である刺激を負荷する第1のステップと、少なくとも1種のヒト陽性感情マーカー遺伝子の発現量を測定する第2のステップと、測定した前記ヒト陽性感情マーカー遺伝子の発現量に基づいて、対象刺激がヒトに対する陽性刺激であるか否かを判断する第3のステップとを含んでいる。

[0101] 第1のステップでは、ヒトに評価対象である刺激を負荷する。刺激の負荷期

間は特に制限されないが、短期間で負荷することがより好ましい。なお、ヒト陽性刺激評価方法の関連で使用する用語「短期間」は１秒～数分又は数時間を指す。

[0102] 次いで第2のステップでは、遺伝子マーカー1～8に示されるヒト陽性感情マーカー遺伝子の少なくとも1種の遺伝子の発現量を生体由来試料、例えば血液、において測定する。なお、測定対象のヒト陽性感情マーカー遺伝子として、遺伝子マーカー1～8に加えて又はこれに代えてヒト共通遺伝子の少なくとも1種の発現量を測定してもよいこと、及び遺伝子マーカー1～8のいずれかの遺伝子群、又はヒト共通遺伝子の遺伝子群の発現量を網羅的に測定してもよいこと、については上記と同様であり、その測定方法についても上記の通りである。

[0103] 次いで第3のステップで、第2のステップで測定したヒト陽性感情マーカー遺伝子の発現量に基づいて、対象刺激がヒト陽性刺激であるか否かを評価する。評価は、上記の通り、第2のステップで測定したヒト陽性感情マーカー遺伝子の発現量から算出されるスコアが、当該遺伝子の基準値と異なるかを判定することによって行うことができる。

[0104] 第3のステップにおける対象刺激の評価は、対象刺激の負荷前後のヒト陽性感情マーカー遺伝子の発現量を比較することによって行ってもよい。すなわち、対象刺激の負荷前に測定したヒト陽性感情マーカー遺伝子の発現量に比較して、刺激負荷後に当該遺伝子の発現量が増加又は減少していれば、当該刺激はヒト陽性刺激であると評価することができる。

[0105] したがって、本発明に係るヒト陽性刺激評価方法は、ヒトに評価の対象である刺激を負荷する第1のステップの前にヒト陽性感情マーカー遺伝子の発現量を測定するステップをさらに含むことができる。

[0106] また第3のステップにおける対象刺激の評価は、対照ヒトとの比較によって行ってもよい。すなわち、対象刺激を負荷したヒトと、対象刺激を負荷しない対照ヒトの両者で同一の陽性感情マーカー遺伝子の発現量を測定し、対象刺激を負荷したヒトにおいて当該遺伝子の発現量が増加又は減少していれば

、対象刺激はヒト陽性刺激であると評価することができる。

[0107] ２－３．ラット共通遺伝子を用いたヒト陽性刺激探索方法

上記の通り、ラット陽性感情マーカー遺伝子及びヒト陽性感情マーカー遺伝子間で、それぞれTickling刺激及び笑い刺激負荷後に、同様の遺伝子発現挙動を示す40種の共通遺伝子（それぞれラット共通遺伝子、ヒト共通遺伝子と称する）が存在することが見出された。かかるラット共通遺伝子及びヒト共通遺伝子は、ラット及びヒトの陽性感情評価系で特に有用な陽性感情評価マーカーとして利用できると考えられる。さらに、ラットにおいて評価の対象である刺激を負荷し、ラット共通遺伝子の発現量が増加又は減少していれば、対象刺激はラット陽性刺激であることが評価できるとともに、ヒトにおいても同様の効果がある刺激と推測できる。ヒト陽性刺激の探索を行う際、ラット共通遺伝子を用いたラットでの刺激評価は、ヒト陽性刺激の探索ツールとして利用できる。

[0108] したがって、本発明のヒトの陽性刺激評価方法は、ラット共通遺伝子を用いて上記ラット陽性刺激評価を行うステップと、陽性刺激であると評価された刺激をヒト陽性刺激であると認定するステップとを含むことができる。

[0109] ２－４．ラット陽性感情マーカー遺伝子を用いたヒト陽性感情マーカー遺伝子の探索方法

ラットのTicking刺激とヒトの笑いについては、共通する生体への生理作用があり、遺伝子発現が類似していることが推測できる。また、Tickling刺激及び笑い刺激負荷後に、同様の遺伝子発現挙動を示す共通遺伝子が存在する。これらのことから、ラット陽性感情マーカー遺伝子のヒトホモログ遺伝子は、負荷した刺激に対してヒトにおいて遺伝子の発現変動が期待できる。そのため、ヒトホモログ遺伝子に注目した陽性感情評価実験を実施することにより、新たなヒト陽性感情マーカーおよびヒト陽性刺激評価方法を構築することができる。したがって、ラット陽性感情マーカーは、新たなヒト陽性感情マーカー遺伝子の探索方法となる。なお、ラット陽性感情マーカーのヒトホモログ遺伝子は、ラット遺伝子のアノテーションの表の「Homology」の欄

に記載されている。

実施例

[0110] [実施例1]

発生音声の周波数解析によるラットへの陽性刺激負荷方法の確立

１－１．ラット飼育法の検討実験

6週令のWistar系雄性ラットの単独飼育群(Single Housing)と集団飼育群(Social Housing、３匹飼い)に対し、陽性刺激であるTickling(下記1-2-1参照)を施行した。単独飼育群は、社会的孤立性を高めるため、ケージ間に衝立を設置した。その結果、単独飼育群ではラット陽性感情の指標である50KHz近傍の高周波音声(physiology & Behavior, 72:167-173, 2001)を確認したのに対し、集団飼育群では当音声は確認できなかった。このことは、単独飼育群では、術者によるTicklingのみが陽性刺激となっているため、Tickling刺激負荷時に陽性感情指標の50KHz近傍の高周波音声が確認できるのに対し、集団飼育群では同居ラット同士でじゃれ合うことによる陽性刺激が術者によるTicklingによる陽性刺激を上回るため、Tickling負荷では50KHz近傍の高周波音声が確認できないと結論付けた。

[0111] 以上の結果より、本研究ではラット単独飼育法を採用し、陽性感情指標である50KHz近傍の高周波音声による陽性感情評価を容易にすることにした。

[0112] １－２．ラットへのTickling刺激負荷の検討

１－２－１．実験方法（Tickling法、Light Touch法、対照）

1) Tickling刺激負荷法

Ticklingとは触覚刺激負荷法であり、げっ歯類のRough-and-Tumble Playを模倣した方法である(J. Panksepp: Behavior Genetics 35, 2005)。具体的には、ラットの後から右手で回りこんで、コンピュータのマウスを握るようにラットをつかみ(Dorsal Contact)、ラットの後首筋を指でくすぐる。引き続き直ちにひっくり返し、ラットを床に押し付け(Pinning Behavior)、お腹を全体的に激しくくすぐり(この時、ラットの前足が中に浮くように、腰を床につけるように返すと抵抗がない)、解放する。これらの操作は2秒以内で行な

い、15秒間継続する。

[0113] 本実験では、ラットをTickling用クリーンケージ(内面は黒色フェルトを貼付)に移し、15秒間放置後、15秒のTickling刺激負荷を行なう操作を4回繰り返し、これを１Tickling Sessionとした。１Session終了後1分間の休憩を挟み、さらに２Session目(2分間)を行なった。図1にTickling刺激負荷時程図を示す。

[0114] 2) Light Touch刺激負荷法

ラットをTickling用クリーンケージ(上述)に移し15秒間放置の後、Ticklingの変わりに3秒に1回、ラット背部にやさしく触れる。刺激負荷時程は図1の通りとした。

[0115] 3) 対照

ラットをTickling用クリーンケージ(上述)に移し、5分間(Tickling Session2回＋休憩1分間に相当)放置した。

[0116] １－２－２．実験方法（負荷週令、負荷期間）

３週令(離乳直後)のWistar系雄性ラットを実験スケジュールに合わせ購入、単独飼育(ケージ間には衝立を設置)を開始した。単独飼育4週令目のラットをTickling群4匹、Light Touch群2匹、対照群2匹に、6週令目のラットをTickling群2匹、8週令目のラットをTickling群2匹に割り付けた。Tickling、Light Touchの刺激負荷方法および対照は上述１－２－１記載の方法とし、4週間(月曜～金曜、午後16:30～)継続して行なった。

[0117] １－２－３．実験方法（超広帯域音声の収録）

Tickling、Light Touchの刺激負荷時と休憩時、および対照実験の相当時点において、ラット陽性刺激の指標として50KHz近傍の音声を解析するため、個体毎に超広帯域音響解析システム(小野測器社製、DS-2100)で音声収録し、周波数解析を行った。高周波マイクロホン(小野測器社製、MI-3140)でラット音声を収録し、超広帯域音響解析システム(小野測器社製、DS-2100)でその時の時間波形をフーリエ変換の後、各周波数成分のピーク値をグラフ化して解析に供した。

[0118] 1-2-4. 実験方法（接近待機時間の測定）

Tickling、Light Touch刺激負荷の2Session終了後(対照は5分間放置後)、ラットをTickling用ケージ(上述)のコーナーに置き、対角線上(距離50cm)にある術者の手に接近接触するまでの時間を測定した。各刺激が快であれば、接近待機時間は短縮される。30秒以上経過しても接近接触しない場合は「30秒」とした。

[0119] 1-2-5. 結果

1)超広帯域音声の解析

超広帯域音響解析システムでフーリエ変換した各周波数成分のピーク値を下表４の通り示す。

[表3]

	4週令						6週令		8週令	
	Tickling		LightTouch		対照		Tickling		Tickling	
	＋	－	＋	－	＋	－	＋	－	＋	－
刺激開始日	図2	図3	図4	図5	図6	図7	図8	図9	図10	図11
刺激開始翌日	図12	図13	図14	図15	図16	図17	図18	図19	図20	図21
刺激開始2週目	図22	図23	図24	図25	図26	図27	図28	図29	図30	図31
刺激開始４週目	図32	図33	図34	図35	図36	図37	図38	図39	図40	図41

＋:刺激負荷時、－:刺激非負荷時(休憩待機時)

[0120] ４週令ラット及び６週令ラットでは、Tickling刺激初日から50KHz近傍(本実験では、FFT解析装置を使用したため、先行研究より10KHz程度高周波側にシフト)の音声を発したが、８週令ラットでは、全期間を通じ該音声を発しなかった。また、4週令ラットと６週令ラットでは、刺激開始２週目でTickling休憩時(15秒)にも陽性感情の表す該音声を発するようになった。Light Touchあるいは対照ラットでは、全期間を通じ発生音声は認められなかった。なお、本報告書には全データを記載できないが、刺激開始２週目が音声発生のピークであった。

[0121] 2)接近待機時間の測定

刺激開始直後、刺激開始翌日、刺激開始２週目、刺激開始４週目における

４週令ラットへの各処置直後の接近待機時間をそれぞれ図42、図43、図44、図45に示す。Tickling群の接近待機時間は、Light Touch群、対照群と比較すると有意に短縮(2週目のLight Touch群に対してはP=0.4)していた。刺激開始4週目になると３群間で差を認めなくなった。

[0122] １－２－６．考察・結論

Tickling刺激は、離乳直後(３週令)から６週目までの施行が有効であり、８週目まで個別飼育するとTickling刺激に反応して発する50KHz近傍の音声を確認できなかった。これは、ラットの成長に伴う心身の変化や個別飼育に伴う過剰な慢性ストレスによるものと考えられた。また、Light Touch群では該音声を発しないことから、Tickling刺激は弁別刺激となっている。刺激開始２週目が最も反応する時期であり、Tickling刺激の休憩中(15秒間)でも陽性感情指標である該音声を発するようになり、接近待機時間も短縮されている。しかし、2週目になるとLight Touch群、対照群でも接近待機時間が短縮し、４週目で３群間に差を認めなくなるのは術者にラットが馴れてくるためであると推測された。

[0123] これらの結果より、Tickling刺激はラットにとって陽性感情をもたらす刺激であると結論付けた。

[0124] [実施例２]

遺伝子発現解析実験

上記１－２－２の４週令(離乳直後[３週令]から個別飼育)からTickling刺激を負荷したラット、Light Touch刺激を負荷したラット、対照ラットについて遺伝子発現解析を行なった。

[0125] ２－１．長期間（４週間）のTickling刺激

２－１－１．実験方法（解析対象臓器の摘出）

臓器摘出の順番は、開胸→心採血→生食灌流(腎動脈瀉血)→断頭→開頭→脳摘出→唾液腺摘出の順とした。

[0126] 1) 心採血・生食灌流

エーテル麻酔下に開胸し心採血(約1mLをPAXgene専用採血管に採取)を行な

い、留置針にて生食(約20mL)灌流／腎動脈瀉血を行なった。

[0127] 2) 脳摘出

頭頂部から開頭、脳を摘出し、Glowinski(J Neurochem, 1966)の脳7分割法に従い、氷冷したアルミ板上で線条体、海馬、視床下部、皮質を分けた。脳下垂体はトルコ鞍より直接摘出した。摘出組織は約3mm角にトリミングし、RNA安定化試薬RNAlater(QIAGEN社製)に浸漬、-80℃で保存した。

[0128] 3) 唾液腺摘出

大唾液腺２部位(顎下腺、耳下腺)を摘出、約3mm角にトリミングし、RNA安定化試薬RNAlater(QIAGEN社製)に浸漬、-80℃で保存した。

[0129] ２－１－２．実験方法（ラット組織からのRNA調製・検定）

1) 血液試料からの全RNA調製

PAXgene Blood RNA Kit (QIAGEN社製)を用いて全RNA標品を調製した。

[0130] 2) 組織からの全RNA調製

RNAlater浸漬組織(遺伝子発現解析対象である視床下部、線条体、２唾液腺のみ)を、RNeasy Buffer RLT中でホモジナイズ〔TissueLyzer(QIAGEN社製)使用〕し、以下Kitプロトコールに従い全RNA標品を調製した。各群(Tickling、Light Touch、対照)の試料は部位毎に、全RNAを等量混合した。

[0131] 3) 全RNA純度と無傷度の検定

個体毎(全RNA標品混合前)に、全RNA標品の濃度とA260/280比、28S/18S rRNA比を求めた。28S/18S rRNA比は、マイクロチップ型電気泳動システム(日立コスモアイ、SV1210)により検定・算出した。

[0132] ２－１－３．実験方法（DNAチップ解析）

上記(２－１－２)の全RNA標品を出発材料として、T7RNA Polymerase Promoter配列を付加したOligo(dT)24をプライマーとしたcDNA合成を行った。引き続き、これを鋳型としてアミノアリル-dUTP 存在下にT7RNA PolymeraseによるmRNA増幅を行って、cRNAにアミノ基を導入し、Cyanine 3[Cy3と略](Light Touch群、対照群)あるいはCyanine 5[Cy5と略] (Tickling群)のサクシニミド誘導体とカップリング反応させることにより蛍光標識を行いDNAチップ解析に供

した。

[0133] DNAチップ解析は以下の通り行った。各Cyanine色素で蛍光標識したRNA標品を等量混合し、DNAチップ〔Agilent社製(約41,012オリゴDNA搭載)、Whole Rat Genome DNA Microarray〕上で65℃、17時間ハイブリダイゼーション反応を行い(未反応分子はハイブリダイゼーション反応後洗浄除去)、共焦点レーザースキャナー(Agilent社製、G2565)で各色素に由来する蛍光強度を測定した。バックグランド補正とグローバル正規化の後、信号強度50未満の遺伝子(トランスクリプトを含む)を除外し、Cy5/Cy3比を求めた。

[0134] ２－１－３．結果

本結果で用いる「プローブ」と「遺伝子(トランスクリプトを含む)」の用語は同義であり、図表で用いる凡例は以下の通りである。

[0135] T：Tickling

L：Light Touch

C：対照

Bl：血液

Hy：視床下部

St：線条体

Sg：唾液腺

２－１－４－１．信号強度分布

Tickling／対照間、Tickling／Light Touch間の遺伝子発現の差をDNAチップ法にて解析した際の、DNAチップ上の各プローブの信号強度の分布を図46に示す。縦軸は信号強度、横軸はその信号強度を示す遺伝子数を示すが、組織試料は相互に類似の信号強度分布を示したが、血液試料では、高信号強度を示す遺伝子数が少なかった。これは、網状赤血球由来のグロビン遺伝子の影響を受けているためである。

[0136] ２－１－４－２．発現変化を認めた遺伝子

対照群と比較してTickling群で1.5倍超の発現を認めた末梢血液(Bl)の遺伝子の「Target Accession」及び「UniGene」を下記表4に示す。

[表4]

表4 発現データ T-BI(Cy5) v.s. C-BI(Cy3)
1.5倍超

Target Accession	UniGene
NM_053372	Rn.18560
NM_053372	Rn.18560
NM_001012211	Rn.24375
NM_001009639	Rn.41274
TC542639	-
XM_225457	Rn.15650
XM_215940	Rn.144851
NM_019143	Rn.1604
NM_019143	Rn.1604
XM_215939	Rn.117434
CB547952	-
NM_001013853	Rn.163132
TC565746	-
XM_233798	Rn.54364
NM_053383	Rn.162695
XM_221383	Rn.93766
NM_001025737	Rn.13596
NM_023970	Rn.64508
XM_236932	Rn.18395
XM_573978	Rn.154745
TC551459	-
XM_223533	Rn.3100
NM_001004214	Rn.7882
NM_012550	Rn.10915
TC525117	-
XM_343169	Rn.16172
AW915659	Rn.12530
NM_021989	Rn.10161
XM_340905	Rn.9000
XM_229422	Rn.136325
NM_021587	Rn.40942
Y15685	Rn.17491
NM_013189	Rn.10943
TC531145	-
XM_242005	-
M54999	-
NM_001013110	Rn.91296
NM_001000232	Rn.141742
TC560767	-
XM_343189	Rn.99508
NM_013088	Rn.98209
AW915605	Rn.3496
NM_001025708	Rn.35627
TC529832	-
AI044232	-
AA956382	Rn.8913
CB548114	Rn.163309
XM_231625	-
BM385724	Rn.32253
NM_001014203	Rn.34654
TC545356	-
A_44_P950925	-
TC550311	-

Target Accession	UniGene
NM_001008314	Rn.129070
NM_001013128	Rn.19584
BI282062	-
XM_342967	-
BF550405	Rn.126330
BI291861	Rn.170925
NM_001009717	Rn.17847
NM_021664	Rn.41640
XM_216324	-
XM_217570	Rn.107838
NM_172334	Rn.18229
NM_013176	Rn.9916
BQ196053	Rn.75726
XM_236362	Rn.77165
XM_343919	Rn.16981
NM_019296	Rn.6934
NM_031713	Rn.129434
NM_022281	Rn.10495
NM_017321	Rn.35934
TC543219	-
NM_012824	Rn.8887
TC561006	-
XM_573502	Rn.6050
NM_053356	Rn.107239
TC540507	-
NM_019349	Rn.33275
NM_021775	Rn.45601
BI302517	Rn.80
NM_001025626	Rn.16586
NM_134390	Rn.26876
XM_342068	Rn.162541
XM_227398	-
A_44_P452570	-
NM_172031	Rn.19272
NM_019241	Rn.16074
NM_053634	Rn.48281
AW913892	Rn.93200
NM_001000174	Rn.141836
TC523015	-
NM_012867	Rn.11245
XM_576400	Rn.163014
XM_573983	Rn.1046
XM_219401	Rn.38292
XM_576440	Rn.35504
XM_341584	Rn.51875
NM_130409	Rn.101777
A_44_P417333	-
NM_001025411	Rn.27927
A_44_P288785	-
NM_053471	Rn.87343
XM_236362	Rn.77165
NM_001017472	Rn.154816
TC543877	-

[0137]

Target Accession	UniGene
XM_216446	Rn. 14712
XM_343688	-
XM_235497	Rn. 106726
TC558217	-
XM_215013	Rn. 8801
BF404531	Rn. 21519
NM_013414	Rn. 9722
AA964725	Rn. 144698
NM_031766	Rn. 11056
XM_222831	Rn. 82910
AW144389	Rn. 146578
XM_227140	Rn. 38949
XM_214459	-
XM_219235	-
NM_017080	Rn. 888
NM_017227	Rn. 11155
NM_012823	Rn. 6589
A_44_P128848	-
AW917512	Rn. 6620
NM_212546	Rn. 187184
NM_001013875	Rn. 9606
AA818893	-
NM_022386	Rn. 17361
AA943056	Rn. 7020
NM_001009623	Rn. 19955
ENSRNOT00000017769	-
XM_230631	Rn. 22314
ENSRNOT00000027445	-
NM_001001969	Rn. 144818
XM_216784	Rn. 1714
TC526534	-
XM_341326	Rn. 139095
XM_341544	Rn. 107058
NM_053546	Rn. 161953
XM_215905	Rn. 6870
NM_145878	Rn. 98269
BI395655	Rn. 9561
AW141130	Rn. 164677
NM_012687	Rn. 16283
AY325162	Rn. 163804
XM_220122	Rn. 54595
NM_053325	Rn. 46519
NM_214833	Rn. 142180
XM_216605	Rn. 2163
NM_024140	Rn. 11236
NM_031598	Rn. 11346
TC545363	-
NM_001001119	Rn. 142667
XM_220398	Rn. 99384
NM_017247	Rn. 10246
AW916109	Rn. 17129
TC540416	-
BF405054	Rn. 164738
TC558017	-
XM_236656	Rn. 110737

Target Accession	UniGene
NM_001025136	Rn. 162201
AA900893	-
XM_220996	-
XM_232354	Rn. 63247
XM_223587	Rn. 163258
BG664107	Rn. 40821
XM_234942	Rn. 135600
NM_053734	-
CB547165	Rn. 103609
NM_184045	Rn. 72618
NM_001029901	Rn. 72599
NM_031627	Rn. 11209
NM_181084	Rn. 48267
XM_225188	-
NM_017154	Rn. 9938
NM_053822	Rn. 31839
NM_022199	Rn. 44407
AA858651	Rn. 40130
XM_222160	Rn. 144729
NM_001013916	Rn. 98436
NM_017196	Rn. 32080
NM_012580	Rn. 3160
NM_207609	Rn. 22665
BQ209292	Rn. 34493
NM_031537	-
XM_218412	Rn. 161810
NM_001012025	Rn. 2022
A_44_P459484	-
NM_017022	Rn. 25733
BI395434	-
NM_022534	Rn. 1829
NM_001014803	-
XM_238649	Rn. 1644
NM_001024790	Rn. 72721
XM_341141	Rn. 131566
NM_001005890	Rn. 47351
XM_340920	-
XM_222745	Rn. 58980
XM_237060	Rn. 70110
XM_226529	Rn. 71484
AI136185	Rn. 3287
BG667918	Rn. 98831
NM_001024254	Rn. 162145
XM_342002	Rn. 11238
NM_031822	Rn. 49136
CB547615	Rn. 5854
NM_001000210	Rn. 141783
XM_573505	Rn. 99666
NM_021859	Rn. 44303
TC532172	-
AF218849	Rn. 93208
TC561906	-
NM_001007694	Rn. 35775
AW143701	Rn. 17098
XM_341727	Rn. 21237

[0138]

Target Accession	UniGene
XM_341877	Rn. 162441
BF406540	Rn. 45046
TC541278	-
TC534199	-
AF071214	-
BI395598	Rn. 4034
XM_342961	-
NM_017103	Rn. 37427
TC556853	-
A_44_P110129	-
AA997829	Rn. 4166
XM_233514	Rn. 134664
NM_053587	Rn. 6703
BM385476	Rn. 32168
AI406967	Rn. 11257
XM_227828	Rn. 158385
NM_053560	Rn. 68940
NM_012529	Rn. 1472
NM_138515	Rn. 26060
A_44_P109907	-
XM_224360	-
CO570092	Rn. 20252
CA507495	Rn. 31839
NM_001009682	-
XM_343121	Rn. 10956
XM_223745	Rn. 6715
AI044674	Rn. 166059
CB545600	-
NM_198134	Rn. 32168
NM_053930	Rn. 96497
ENSRNOT00000029749	-
NM_016988	Rn. 9816
XM_218432	Rn. 137083
AA899852	Rn. 5820
AF486617	-
XM_218951	Rn. 99218
TC524990	-
NM_001012345	Rn. 9523
XM_342309	Rn. 105967
XM_341168	Rn. 39189
BC070930	Rn. 162640
AW914026	Rn. 4205
NM_031832	Rn. 764
BF553675	Rn. 105837
NM_022303	Rn. 64486
XM_220520	Rn. 163121
NM_080576	Rn. 48763
XM_218737	-
AA946368	Rn. 102418
NM_001000571	Rn. 142805
NM_001013148	Rn. 9380
NM_017016	Rn. 48653
AI717736	Rn. 2438
XM_341876	Rn. 27239
TC549515	-

Target Accession	UniGene
A_44_P781967	-
XM_342787	Rn. 41612
XM_225999	Rn. 100014
NM_001001001	Rn. 141928
NM_181362	Rn. 118129
NM_012793	Rn. 33890
BM384318	Rn. 1253
S74324	-
NM_001025649	Rn. 98601
AI009484	Rn. 103770
XM_343940	-
BF406112	Rn. 125669
NM_001008776	Rn. 7875
BE108148	Rn. 1292
NM_001011559	Rn. 20252
XM_221188	Rn. 144935
XM_576511	Rn. 12212
NM_182735	Rn. 162507
AI071921	Rn. 137266
NM_138896	Rn. 18446
AF322224	Rn. 20691
XM_573787	Rn. 154855
XM_340889	Rn. 12214
NM_001011991	Rn. 153992
NM_012613	Rn. 10463
XM_216497	Rn. 134695
AI172074	Rn. 95170
NM_133542	Rn. 102247
NM_001000525	Rn. 142140
XM_221048	Rn. 162209
NM_001012217	Rn. 12068
XM_235500	Rn. 9374
NM_139260	Rn. 144673
XM_237967	Rn. 103148
AI232145	Rn. 2550
XM_220219	Rn. 38406
XM_574359	Rn. 41379
NM_053021	Rn. 1780
AW920454	Rn. 18516
XM_214790	Rn. 14443
XM_575518	Rn. 117928
NM_021997	Rn. 10893
XM_216499	Rn. 23067
XM_220173	Rn. 162028
A_44_P250371	-
AF370447	Rn. 28947
NM_173339	Rn. 92160
XM_221034	Rn. 72680
BF550565	Rn. 96000
XM_238138	Rn. 40895
A_44_P739855	-
BI303371	Rn. 12688
NM_176077	Rn. 66254
TC529691	-
NM_022800	Rn. 64592

[0139]

Target Accession	UniGene
XM_220996	-
D64062	-
XM_236574	Rn. 29899
NM_153733	Rn. 59484
NM_172336	Rn. 30491
TC541479	-
TC523614	-
XM_214245	Rn. 13538
NM_198132	Rn. 107690
NM_053843	Rn. 154415
TC560203	-
XM_341251	Rn. 22169
AA899814	Rn. 164538
NM_022960	Rn. 30018
BF523163	Rn. 12212
NM_012701	Rn. 87064
AW143870	-
NM_172077	Rn. 11222
NM_138913	Rn. 10383
XM_217218	Rn. 788
NM_024145	Rn. 11309
NM_019370	Rn. 44
NM_019166	Rn. 88235
BI395522	-
NM_001013138	Rn. 39086
XM_218295	Rn. 16765
NM_057188	Rn. 3862
TC556658	-
TC527564	-
XM_237383	Rn. 45037
AA818951	Rn. 115631
XM_573131	Rn. 126683
XM_220207	Rn. 162027
DN931809	Rn. 9167
TC556010	-
NM_181387	Rn. 145133
XM_213211	Rn. 17380
XM_341620	Rn. 137956
XM_573540	Rn. 59403
XM_214905	-
BF521788	Rn. 47031
XM_214648	Rn. 137980
L04739	-
NM_031691	Rn. 34728
CB544341	Rn. 6526
CF110950	Rn. 104756
XM_341714	Rn. 41391
TC544290	-
NM_017087	Rn. 783
NM_022005	Rn. 839
XM_226278	-
XM_573503	Rn. 6050
BF408265	Rn. 23050
XM_215067	-
A_44_P295565	-

Target Accession	UniGene
XM_213372	-
BF547677	Rn. 3017
TC542260	-
ENSRNOT00000013636	-
NM_031765	Rn. 40816
NM_053619	Rn. 10680
NM_031776	Rn. 161897
NM_001000719	Rn. 142089
TC526044	-
TC521398	-
TC542486	-
XM_344874	-
XM_342276	Rn. 102567
BF285291	Rn. 105722
XM_215517	Rn. 2039
NM_001008321	Rn. 35886
A_44_P356345	-
XM_343373	Rn. 21775
TC549325	-
BF406342	Rn. 153636
XM_341102	Rn. 40960
BF522750	Rn. 44913
TC544901	-
TC542149	-
NM_053311	Rn. 7208
XM_219518	-
XM_226738	Rn. 106845
BC081802	Rn. 107869
XM_218592	Rn. 162417
XM_215247	Rn. 106138
AW915292	-
NM_001008751	Rn. 153972
NM_019311	Rn. 10659
TC544794	-
M84148	Rn. 134335
TC544790	-
NM_001004082	Rn. 98667
BF550847	Rn. 26489
AW144111	Rn. 11061
TC525768	-
XM_342759	Rn. 35561
XM_575074	-
AA955669	Rn. 10241
XM_215564	Rn. 162576
XM_220748	-
XM_342979	Rn. 915

[0140] 対照群と比較してTickling群で1/1.5倍未満の発現を認めた末梢血液(BI)の

遺伝子の「Target Accession」及び「UniGene」を下記表5に示す。

[表5]

表5 発現データ T-B I (Cy5) v.s. C-BI(Cy3)
1/1.5倍未満

Target Accession	UniGene
TC523242	-
NM_001002289	Rn.1717
XM_579763	Rn.156570
A_44_P929321	-
TC528483	-
NM_019149	Rn.29774
XM_225993	-
TC520606	-
XM_216135	Rn.2350
XM_342692	Rn.32245
XM_341374	Rn.105750
TC522919	-
XM_346206	-
NM_031782	Rn.10846
XM_215439	Rn.16647
XM_227719	-
NM_001007734	Rn.4220
NM_178097	Rn.35223
XM_235338	Rn.62343
XM_573994	Rn.100575
AW914824	Rn.163644
NM_001009671	Rn.101706
BX883047	-
U56823	-
XM_343788	-
BF289572	Rn.2497
TC540214	-
NM_053529	Rn.162013
AI045798	Rn.164217
BF289572	Rn.2497
XM_217086	Rn.17278
TC524256	-
XM_216408	-
XM_341374	Rn.105750
NM_019251	Rn.3953
A_44_P284169	-
BF283485	Rn.6459
XM_341374	Rn.105750
XM_214147	Rn.103233
XM_580169	Rn.121165
AI137547	Rn.166786
NM_001004253	Rn.63210
TC522219	-
TC556608	-
AA900054	Rn.29900
NM_001009635	Rn.163304
XM_341919	Rn.11830
BF561525	Rn.23284
XM_213295	-
TC540306	-
AA899215	Rn.144605
XM_342672	-
U06102	-

Target Accession	UniGene
TC523012	-
TC522621	-
XM_216102	Rn.14059
BF556870	Rn.19747
CA508266	Rn.8706
XM_234835	Rn.110671
XM_341060	Rn.163207
NM_001025407	Rn.155539
XM_342534	Rn.30327
XM_225150	Rn.22107
NM_001007608	Rn.3477
XM_345433	Rn.162704
AI102738	Rn.112601
AW144706	Rn.3540
NM_001004270	Rn.46302
XM_236238	-
AW917747	Rn.133346
XM_217405	Rn.36770
AW143240	Rn.2778
AW917872	Rn.11063
XM_345788	-
XM_226652	Rn.20164
AA957114	Rn.31965
AA850595	Rn.164498
XM_224894	Rn.101873
A_44_P189854	-
XM_215401	Rn.101115
XM_216893	Rn.162954
TC527896	-
A_44_P637047	-
NM_153472	Rn.15168
TC528630	-
BF557300	Rn.165295
AI136136	Rn.39132
XM_342940	Rn.20146
XM_222468	-
NM_001013055	Rn.23660
TC544427	-
TC539128	-
XM_226249	Rn.158155
TC521901	-
A_44_P989737	-
BF289572	Rn.2497
XM_574577	Rn.16562
AA997980	Rn.165465
NM_001017467	Rn.3321
BC091428	Rn.34871
NM_001011557	Rn.143768
XM_215485	Rn.33325
AF452647	Rn.89150
XM_573460	-
NM_153726	Rn.83631
NM_024362	Rn.14532

[0141]

Target Accession	UniGene
ENSRNOT00000045943	-
AW142643	-
XM_238213	Rn. 11589
NM_138509	Rn. 7652
NM_001009391	Rn. 98105
AW918202	Rn. 165133
NM_022231	Rn. 91239
XM_579926	Rn. 4131
NM_031113	Rn. 106034
M89646	Rn. 979
BG669046	-
XM_217233	Rn. 13214
AABR03057162	-
XM_213969	-
NM_001013152	Rn. 22496
XM_233984	-
NM_019182	Rn. 30015
XM_216485	Rn. 8332
XM_219600	-
NM_020075	Rn. 40123
XM_213898	Rn. 36174
ENSRNOT00000042274	-
TC522204	-
AI071563	Rn. 20559
CF110545	Rn. 3327
AI010816	Rn. 165682
XM_343253	Rn. 21009
XM_578017	Rn. 57973
NM_001024775	Rn. 155153
AA900363	Rn. 164625
XM_226824	Rn. 103615
NM_053353	Rn. 44218
NM_173153	Rn. 147491
NM_001008372	Rn. 98477
XM_227820	Rn. 16644
A_44_P958992	-
NM_001025115	Rn. 131904
AA925252	Rn. 164901
NM_001024787	Rn. 136186
AI535415	Rn. 136915
NM_001025124	Rn. 1273
XM_216097	Rn. 94940
NM_053974	Rn. 11275
BG371880	Rn. 3907
TC536840	-
NM_001024885	Rn. 160643
AW920687	Rn. 102002
AJ271834	Rn. 4143
NM_001013918	Rn. 154938
XM_223579	-
XM_341639	Rn. 8900
XM_233452	Rn. 45006
BF284864	Rn. 164392
XM_574891	Rn. 145579
XM_344695	-

Target Accession	UniGene
XM_216903	Rn. 61651
A_44_P408033	-
AW143330	Rn. 16886
BF551370	Rn. 18104
NM_001004267	Rn. 106000
TC567071	-
BG662522	Rn. 169395
NM_057119	Rn. 8538
XM_224138	Rn. 105824
TC549612	-
NM_133293	Rn. 92350
TC542651	-
XM_221977	Rn. 144939
XM_225658	-
NM_031329	Rn. 31429
BM391657	Rn. 11832
BU759069	Rn. 1637
BF522056	Rn. 147253
TC523122	-
NM_001014235	Rn. 140721
ENSRNOT00000026964	-
XM_223504	-
U78143	-
XM_345296	Rn. 145322
XM_344823	-
TC558675	-
XM_345098	-
XM_215389	Rn. 163427
TC552020	-
XM_343560	Rn. 22860
NM_053588	Rn. 6814
NM_021846	Rn. 161889
XM_341259	Rn. 163262
AABR03063179	-
NM_138911	Rn. 22614
XM_576864	Rn. 162370
BF289572	Rn. 2497
TC541702	-
NM_173314	Rn. 10664
TC556638	-
BM382988	Rn. 165453
NM_001030033	Rn. 110010
XM_575227	Rn. 22737
NM_001013863	Rn. 144719
XM_235376	-
TC538702	-
AI179535	Rn. 162500
U75399	-
TC517804	-
XM_573797	Rn. 76647
XM_213132	-
BG667930	Rn. 164410
XM_213636	Rn. 13590
AA850242	Rn. 164349
TC551486	-

[0142]

Target Accession	UniGene
NM_022541	Rn. 3792
NM_153306	Rn. 15281
XM_342168	Rn. 3974
XM_224929	Rn. 103659
NM_031021	Rn. 137692
XM_576251	Rn. 40403
AW140893	Rn. 7477
XM_216709	Rn. 58607
XM_213440	Rn. 2953
XM_342710	Rn. 161846
XM_227809	Rn. 136946
NM_022602	Rn. 6343
XM_215251	Rn. 4050
AW144359	Rn. 166200
NM_001013252	Rn. 138078
XM_575783	-
XM_214649	Rn. 12969
NM_201562	Rn. 3210
AW914977	Rn. 24394
XM_217208	Rn. 23803
AW143108	Rn. 3858
XM_216225	Rn. 11876
AW918608	Rn. 7349
XM_219604	-
AW140804	-
XM_220196	Rn. 124783
XM_231251	Rn. 161768
NM_001024892	Rn. 85539
NM_001008313	-
XM_242065	Rn. 154614
XM_213346	Rn. 144702
NM_017107	Rn. 82705
XM_341374	Rn. 105750
XM_341042	Rn. 145151
BF564461	Rn. 169183
NM_181475	Rn. 163044
S63519	-
TC524089	-
C0383501	Rn. 3052
TC522491	-
XM_577990	Rn. 98472
NM_001012086	Rn. 23425
NM_017364	Rn. 98773
XM_216504	Rn. 105772
AW917579	Rn. 785
XM_342909	Rn. 2252
XM_221656	Rn. 7967
BI292115	Rn. 3271
TC521231	-
XM_575931	Rn. 62309
XM_233022	Rn. 162812
NM_134456	Rn. 11069
XM_243815	Rn. 154647
NM_131907	Rn. 5805
XM_224241	Rn. 22885

Target Accession	UniGene
NM_019257	Rn. 162871
XM_227018	-
XM_233982	Rn. 162852
XM_342482	-
XM_341796	Rn. 56086
NM_057205	Rn. 162761
NM_013006	Rn. 3594
TC562387	-
BI294262	Rn. 76368
NM_001025701	Rn. 3991
NM_017151	Rn. 3391
AW530795	Rn. 169873
NM_001013041	Rn. 23593
NM_001009290	Rn. 62471
A_44_P621304	-
NM_031152	Rn. 1016
BF286916	Rn. 165738
A_44_P560036	-
NM_001008324	Rn. 95954
XM_217592	Rn. 12944
AW141147	-
NM_175761	Rn. 119867
XM_219680	Rn. 112772
AW528582	Rn. 8167
XM_214991	Rn. 35776
AI556201	Rn. 48701
XM_346074	-
NM_017268	Rn. 5106
XM_343570	Rn. 17734
NM_001014235	Rn. 140721
XM_574233	Rn. 18683
XM_574942	Rn. 24450
XM_227107	-
XM_214168	-
BG668811	Rn. 64562
TC539303	-
BF565803	Rn. 164480
TC521072	-
XM_219594	Rn. 86176
XM_215082	Rn. 14633
XM_216757	Rn. 3465
AI102620	Rn. 165053
XM_214503	Rn. 96111
XM_340742	Rn. 15835
ENSRNOT00000042478	-
XM_216708	Rn. 22788
NM_001030033	Rn. 110010
XM_345167	Rn. 161785
AW143333	Rn. 19335
XM_217181	Rn. 73451
XM_345431	Rn. 14868
NM_032072	Rn. 4279
XM_236745	Rn. 45886
NM_017234	Rn. 4065
AI105192	-

[0143]

Target Accession	UniGene
XM_236599	Rn. 8687
TC539236	-
NM_001005765	Rn. 106321
NM_133512	Rn. 14544
NM_001008335	Rn. 143972
BN000326	-
NM_133600	Rn. 2789
XM_575612	Rn. 27395
XM_215466	Rn. 144260
AW918514	Rn. 1772
ENSRNOT00000030924	-
NM_173098	Rn. 9707
NM_138504	Rn. 15599
NM_001004243	Rn. 49051
AY316590	Rn. 3366
BF543787	Rn. 160395
NM_001014061	Rn. 42180
AY083459	Rn. 5762
AB005540	-
BG671006	Rn. 3844
NM_053623	Rn. 87821
XM_342982	Rn. 22493
ENSRNOT00000001255	-
NM_001024742	Rn. 125240
NM_001012030	Rn. 22691
BQ202972	Rn. 112513
TC538538	-
XM_231176	Rn. 2745
XM_232775	Rn. 15351
XM_341374	Rn. 105750
NM_001004256	Rn. 137920
XM_345405	-
A_44_P105566	-
XM_226722	Rn. 16711
BU760183	Rn. 927
NM_021766	Rn. 102356
NM_001012128	Rn. 12040
TC538830	-
A_44_P354420	-
NM_173322	Rn. 10967
XM_575780	-
NM_001025701	Rn. 3991
NM_001012184	Rn. 98522
XM_216704	Rn. 87025
BG671963	Rn. 18605
ENSRNOT00000044933	-
NM_138978	Rn. 82760
XM_213393	Rn. 20884
BF559145	Rn. 17789
XM_218267	-
XM_575446	Rn. 118366
NM_133423	Rn. 48752
NM_053662	Rn. 12962
XM_341883	Rn. 27595
NM_001011997	Rn. 146101

Target Accession	UniGene
XM_215213	Rn. 3420
ENSRNOT00000037382	-
AA874812	Rn. 16886
NM_022186	Rn. 44867
XM_225950	-
AA957047	Rn. 11727
BF396386	Rn. 172843
NM_001012089	Rn. 136933
NM_001007618	Rn. 2007
TC560183	-
XM_342642	Rn. 103328
A_44_P575763	-
NM_138823	Rn. 4016
NM_013134	Rn. 9437
XM_342565	Rn. 118078
XM_219594	Rn. 86176
XM_345703	Rn. 95285
AA899996	-
AA963084	Rn. 9450
XM_341921	-
XM_213548	Rn. 86986
A_44_P377593	-
XM_575360	Rn. 162727
A_44_P431358	-
AW915838	Rn. 165769
TC517984	-
XM_573212	Rn. 143962
XM_226722	Rn. 16711
XM_344326	Rn. 124838
XM_221003	-
ENSRNOT00000031239	-
AA819664	Rn. 107401
XM_344565	-
TC520429	-
ENSRNOT00000046166	-
XM_215889	-
XM_233679	Rn. 19289
XM_343551	Rn. 17453
A_44_P762670	-
XM_344478	-
TC561295	-
AI555307	Rn. 101796
XM_227268	Rn. 24186
AW918276	Rn. 162118
NM_001024744	Rn. 66098
TC555779	-
NM_001008773	Rn. 3361
XM_224620	Rn. 11536
XM_342693	Rn. 21921
AI511097	Rn. 167988
A_44_P855945	-
A_44_P476180	-
XM_343405	Rn. 29863
ENSRNOT00000036737	-
TC550760	-

[0144]

Target Accession	UniGene
XM_223981	Rn. 93187
NM_001012182	Rn. 9125
XM_217235	Rn. 2768
XM_216917	Rn. 3694
BE100578	Rn. 164339
TC556501	-
A_44_P384688	-
XM_221450	Rn. 131191
XM_218063	-
NM_053853	Rn. 37420
AW142444	Rn. 2344
XM_216310	Rn. 162764
AW142420	Rn. 93562
NM_001007608	Rn. 3477
AW920837	Rn. 55758
NM_001006980	Rn. 19451
XM_215145	Rn. 109066
XM_232762	-
XM_232769	-
TC556497	-
AA900000	Rn. 103172
TC517445	-
NM_130405	Rn. 162107
XM_343503	Rn. 8675
NM_001007623	Rn. 29892
NM_019620	Rn. 10663
NM_001013245	Rn. 185799
NM_052804	Rn. 40595
NM_199092	Rn. 144844
CO573318	Rn. 164425
XM_226334	Rn. 22363
NM_013138	Rn. 11242
XM_344962	-
NM_001013044	Rn. 145951
NM_001013191	Rn. 7308
NM_017279	Rn. 1617
BE101783	Rn. 164763
NM_053682	Rn. 8153
TC537997	-
BF289572	Rn. 2497
TC540547	-
XM_342107	Rn. 9002
NM_153297	Rn. 11556
NM_001014092	Rn. 18098
AA801187	Rn. 117620
AA964050	Rn. 6975
AW141280	Rn. 92325
XM_224581	Rn. 4177
A_44_P760225	-
AW919175	Rn. 18892
AW143880	Rn. 95188
XM_214982	Rn. 21208
NM_031042	Rn. 11000
NM_001024984	Rn. 11521
AW143503	Rn. 168891

Target Accession	UniGene
ENSRNOT00000049792	-
CB544382	Rn. 7446
AW918130	Rn. 4019
S74331	-
TC547847	-
TC524465	-
NM_153740	Rn. 24729
XM_227635	-
XM_215553	Rn. 162585
NM_001012746	Rn. 162116
XM_238058	-
NM_001012090	Rn. 137486
TC520825	-
XM_233230	Rn. 162076
AW915435	Rn. 170228
XM_214996	Rn. 3939
XM_578123	-
AA926300	-
TC552147	-
XM_234728	-
NM_133563	Rn. 107259
NM_173105	Rn. 20144

[0145] Light Touch群と比較してTickling群で1.5倍超の発現を認めた末梢血液(Bl

)の遺伝子の「Target Accession」及び「UniGene」を下記表6に示す。

[表6]

表6 T-Bl(Cy5) v.s. L-Bl(Cy3) :up regulation(Cy5>Cy3)

Target Accession	UniGene
NM_001013853	Rn.163132
XM_230631	Rn.22314
TC545861	-
TC559380	-
TC551459	-
TC560203	-
XM_231625	-
TC532273	-
TC568188	-
XM_343940	-
TC549515	-
TC555328	-
NM_198776	Rn.36966
TC549495	-
CB544341	Rn.6526
NM_017289	Rn.10927
TC542956	-
XM_221921	-
TC525431	-
XM_218432	Rn.137083
A_44_P337592	-
AW143701	Rn.17098
NM_153471	Rn.162466
TC544981	-
NM_198134	Rn.32168
XM_341386	Rn.104585
BQ211845	Rn.165621
AA900394	Rn.159005
NM_001000446	Rn.143535
AW918996	Rn.7470
XM_219953	Rn.61235
BI395434	-
XM_215067	-
TC561947	-
A_44_P426640	-
A_44_P368450	-
NM_012812	Rn.5119
AA925776	Rn.11283
TC528645	-
XM_222896	Rn.19850
XM_346943	-
TC551985	-
AI548160	Rn.1427
XM_215580	-
XM_344985	-
S58644	-
TC540840	-
XM_221698	-
XM_237794	Rn.46621
XM_343099	Rn.99685
TC529719	-
AA957322	Rn.144531
AW914894	Rn.10267

Target Accession	UniGene
XM_221107	-
NM_182842	Rn.91453
NM_001009676	Rn.23071
XM_236685	Rn.99291
XM_227427	Rn.139466
XM_226439	Rn.20659
XM_346076	Rn.20532
AA818877	Rn.105655
XM_234245	Rn.159753
XM_226421	Rn.144988
NM_001009719	Rn.185816
BI276555	Rn.3702
NM_001014255	Rn.22786
XM_218846	Rn.162433
XM_224877	-
XM_221104	Rn.130739
XM_220207	Rn.162027
XM_340760	Rn.49088
XM_344780	Rn.94784
NM_133406	Rn.41595
BF391440	Rn.36104
XM_343664	Rn.162357
A_44_P959751	-
XM_220370	-
TC533990	-
XM_340955	Rn.99410
NM_031981	Rn.2771
XM_233606	Rn.12602
NM_001030028	Rn.151249
AA998476	Rn.98819
XM_231730	-
TC556097	-
XM_232864	Rn.43474
NM_001008845	Rn.145377
XM_222876	Rn.144949
NM_053698	Rn.31765
AI008579	-
BG664147	Rn.13589
NM_177421	Rn.7312
XM_342671	-
XM_345864	Rn.7336
NM_001000781	Rn.142152
XM_346356	-
AW917567	Rn.2378
TC521279	-
XM_342565	Rn.118078
BC090353	Rn.119131
XM_215174	-
XM_577310	Rn.131934
NM_013224	Rn.144566
AW918701	Rn.36635
XM_237451	-
NM_001017377	Rn.11767

[0146]

Target Accession	UniGene
NP798074	-
NM_001012110	Rn. 15926
XM_345097	-
XM_215206	Rn. 40762
A_44_P852241	-
NM_012818	Rn. 88180
A_44_P898125	-
NM_019630	Rn. 10446
AW915151	-
TC565812	-
XM_214321	Rn. 38446
NM_133522	Rn. 10458
XM_237093	Rn. 50710
NM_198132	Rn. 107690
XM_238571	Rn. 107303
NM_012582	Rn. 10950
AF010444	-
XM_575556	Rn. 46644
NM_019155	Rn. 98191
XM_225768	Rn. 163375
TC566971	-
XM_233793	-
XM_343919	Rn. 16981
NM_139113	Rn. 25840
BC070930	Rn. 162640
NM_030656	Rn. 9931
XM_344072	-
XM_220207	Rn. 162027
AW252149	Rn. 55564
TC567245	-
XM_234528	Rn. 29348
XM_232247	Rn. 106209
AI145252	Rn. 147492
BC061751	Rn. 17120
NM_153722	Rn. 9848
TC524295	-
AY425759	Rn. 9824
A_44_P548286	-
XM_215196	Rn. 65866
AW142805	Rn. 168863
TC568274	-
BF552049	Rn. 157381
NM_053477	Rn. 13468
NM_020091	Rn. 48676
NM_213626	Rn. 103817
NM_030988	Rn. 10429
A_44_P232113	-
NM_022925	Rn. 30011
AA819112	Rn. 163598
NM_001000113	Rn. 142001
XM_347010	Rn. 27529
XM_345190	Rn. 161818
XM_345884	-
XM_236308	-
NM_001000105	Rn. 142506

Target Accession	UniGene
NM_153629	Rn. 163092
NM_001015034	Rn. 14734
A_44_P520403	-
XM_344144	-
XM_235075	-
XM_213440	Rn. 2953
NM_001012174	Rn. 144288
XM_344713	-
XM_219510	Rn. 22113
XM_344751	-
BF284137	Rn. 165309
XM_218185	Rn. 44782
XM_576071	Rn. 18840
XM_223490	-
X62329	-
XM_345932	Rn. 81627
NM_153301	Rn. 86437
NM_001000771	Rn. 142123
NM_053373	Rn. 2834
XM_221479	-
XM_220357	Rn. 79871
NM_001000111	Rn. 142005
NM_130401	Rn. 3605
NM_021759	Rn. 38434
TC564474	-
BM390141	Rn. 9198
NM_139188	Rn. 56698
NM_017269	Rn. 10278
XM_224084	Rn. 137893
TC562194	-
XM_340835	Rn. 12490
CO564048	Rn. 21249
NM_024161	Rn. 100120
AI043579	Rn. 163899
NM_001024249	-
NM_001009674	Rn. 8450
A_44_P342606	-
XM_222031	Rn. 86017
TC522538	-
NM_012489	Rn. 8913
XM_226796	-
BF566441	Rn. 155976
A_44_P438539	-
XM_342832	Rn. 7748
TC517939	-
NM_001000748	Rn. 141919
XM_232779	Rn. 56739
TC546204	-
CB547594	Rn. 6408
XM_342961	-
XM_220509	-
AA899661	Rn. 164596
XM_342159	-
XM_213365	Rn. 2165
NM_212525	Rn. 11534

[0147]

Target Accession	UniGene
XM_232671	Rn. 37783
XM_218203	Rn. 68344
BF523160	Rn. 101923
AA998118	Rn. 6534
XM_232762	-
TC520760	-
NM_053566	Rn. 102312
XM_215061	Rn. 27295
NM_053997	Rn. 9885
DN935747	Rn. 127685
XM_231469	-
XM_343327	Rn. 84274
XM_233230	Rn. 162076
XM_342569	-
XM_224098	Rn. 124444
XM_573505	Rn. 99666
XM_575965	Rn. 106560
A_44_P323955	-
ENSRNOT00000018127	-
NM_001000812	Rn. 143534
AF321132	Rn. 23483
XM_345405	-
XM_344684	Rn. 154752
AF406815	Rn. 15468
XM_218061	-
XM_221119	Rn. 3360
ENSRNOT00000010055	-
XM_222187	Rn. 128427
TC559283	-
TC533942	-
ENSRNOT00000048665	-
NM_019322	Rn. 10699
TC543374	-
XM_342995	-
BF398551	Rn. 173000
XM_345326	-
NM_001000993	Rn. 143285
XM_341857	Rn. 107060
NP798075	-
XM_238278	Rn. 142736
BF521788	Rn. 47031
TC525942	-
NM_181382	Rn. 38054
NM_019146	Rn. 29999
TC562016	-
TC566645	-
XM_230811	Rn. 162723
TC526771	-
NM_001008843	Rn. 40130
TC565055	-
XM_345272	-
TC568157	-
AA926191	-
NM_024145	Rn. 11309
XM_236351	Rn. 147874

Target Accession	UniGene
TC559490	-
XM_231109	Rn. 162654
NM_001017485	Rn. 3988
XM_346329	Rn. 102180
BC059157	Rn. 162644
XM_224673	Rn. 26828
NM_053857	Rn. 11161
XM_341741	Rn. 60559
XM_213381	Rn. 17735
XM_213066	-
NM_001002291	Rn. 142181
XM_222276	-
XM_232602	-
XM_226020	Rn. 27003
NM_053406	Rn. 162659
NM_030585	Rn. 3228
NM_001007725	Rn. 162206
XM_341121	Rn. 162325
NM_001024781	Rn. 22446
NM_181639	Rn. 15870
A_44_P698199	-

[0148] Light Touch群と比較してTickling群で1/1.5倍未満の発現を認めた末梢血

液(BI)の遺伝子の「Target Accession」及び「UniGene」を下記表7に示す。

[表7]

表7 T-BI(Cy5) v.s. L-BI(Cy3) :down regulation(Cy5<Cy3)

Target Accession	UniGene
AA900371	Rn.161752
AA900000	Rn.103172
AA899215	Rn.144605
TC555778	-
NM_138875	Rn.46225
AI556201	Rn.48701
BI302367	Rn.94935
BI277534	Rn.122326
BF416864	Rn.161752
XM_341099	Rn.65800
XM_575687	Rn.162772
BI277534	Rn.122326
BI277534	Rn.122326
XM_213346	Rn.144702
BI277534	Rn.122326
XM_214003	Rn.105741
NM_030990	Rn.4550
BI277534	Rn.122326
XM_219604	-
BI277534	Rn.122326
BI277534	Rn.122326
NM_001014207	Rn.137575
TC559328	-
BI277534	Rn.122326
NM_013092	Rn.10182
BI277661	Rn.129486
TC559328	-
BE098803	Rn.170677
BI277534	Rn.122326
AI231572	Rn.1180
XM_213346	Rn.144702
BI277534	Rn.122326
BM986553	Rn.107561
NM_001025686	Rn.102384
AA963075	Rn.73451
XM_344404	-
NM_012583	Rn.47
AA899664	Rn.162104
AABR03063179	-
XM_343234	Rn.21405
XM_342607	-
TC538830	-
AI717054	Rn.156004
BM389289	Rn.60855
NM_012963	Rn.144565
AB005540	-
AABR03001498	-
XM_217560	Rn.3070
XM_222468	-
TC556885	-
XM_216913	-
XM_576906	Rn.7439
XM_346305	-

Target Accession	UniGene
NM_021766	Rn.102356
AW140820	Rn.164402
AI227823	Rn.7385
NM_012837	Rn.106351
XM_213295	-
NM_021869	Rn.1993
XM_226334	Rn.22363
CF110545	Rn.3327
BF558918	Rn.175256
AW140893	Rn.7477
AI230921	Rn.24537
TC540214	-
BF523472	Rn.34141
TC536843	-
AW253367	Rn.11656
TC538091	-
NM_031561	Rn.102418
NM_053592	Rn.6102
NM_133294	Rn.22633
NM_173153	Rn.147491
AA963823	Rn.2511
XM_341354	Rn.62159
NM_031058	Rn.3174
NM_017276	Rn.1441
M33313	-
XM_580078	-
AJ271834	Rn.4143
XM_216747	Rn.1198
AW141147	-
NM_175761	Rn.119867
AABR03024169	-
XM_216704	Rn.87025
NM_012512	Rn.1868
NM_024149	Rn.28244
XM_343925	Rn.159824
NM_012518	Rn.2892
NM_133381	Rn.108128
XM_224616	-
ENSRNOT00000033714	-
TC543094	-
NM_001007729	Rn.6800
AW917548	Rn.164361
XM_342581	Rn.36664
XM_217061	Rn.3401
NM_139083	Rn.2833
CB547605	Rn.1619
TC541382	-
NM_175764	Rn.10541
XM_232413	Rn.104461
XM_219895	-
AABR03000060	-
XM_214491	Rn.13489
AF072835	Rn.3705

[0149]

Target Accession	UniGene
NM_001024802	Rn. 2779
AI013204	Rn. 112601
AI071866	Rn. 166480
TC523242	-
XM_574891	Rn. 145579
NM_022541	Rn. 3792
XM_342607	-
NM_001013245	Rn. 185799
AW144706	Rn. 3540
XM_573179	Rn. 93919
BC089998	Rn. 36437
XM_579983	-
AI012428	Rn. 23425
AI013718	-
XM_212903	-
XM_216357	Rn. 92601
TC561295	-
XM_227733	-
BF558262	Rn. 15451
TC552330	-
NM_013092	Rn. 10182
ENSRNOT00000026964	-
BG668902	Rn. 112639
TC521072	-
M89646	Rn. 979
NM_012903	Rn. 10123
NM_024359	Rn. 10852
NM_001009671	Rn. 101706
TC562165	-
XM_214147	Rn. 103233
XM_217167	Rn. 163007
U56823	-
U21719	Rn. 100975
NM_019149	Rn. 29774
XM_215401	Rn. 101115
NM_207589	Rn. 103178
NM_001013213	Rn. 91426
TC522491	-
BM389289	Rn. 60855
AW914778	-
NM_053847	Rn. 9939
CB545155	Rn. 19514
U87983	-
NM_053982	Rn. 2890
BF565803	Rn. 164480
BF289360	Rn. 163651
NM_001004199	Rn. 3474
NM_012583	Rn. 47
XM_214099	Rn. 102095
BF389611	-
AW142444	Rn. 2344
NM_012963	Rn. 144565
TC541702	-
NM_031098	Rn. 89756
NM_001013191	Rn. 7308

Target Accession	UniGene
NM_001014272	Rn. 121561
BM388221	Rn. 161950
NM_012555	Rn. 88756
XM_215528	-
AW914778	-
TC557448	-
BC088321	Rn. 1136
XM_216740	Rn. 2696
XM_346997	-
XM_216485	Rn. 8332
XM_216485	Rn. 8332
XM_216330	Rn. 161969
NM_019365	Rn. 36106
BF289572	Rn. 2497
XM_345662	-
CO573873	Rn. 48945
NM_012512	Rn. 1868
AI178672	Rn. 161824
NM_033096	Rn. 4143
TC537630	-
NM_012603	Rn. 12072
NM_023022	Rn. 44480
NM_138875	Rn. 46225
NM_022506	Rn. 1101
NM_001024745	Rn. 99415
TC535264	-
XM_216485	Rn. 8332
NM_001013149	Rn. 162446
CA512711	Rn. 144939
NM_001014148	Rn. 1073
BC081794	Rn. 10266
AA859178	Rn. 92965
AW917590	Rn. 95176
NM_001005528	Rn. 60855
XM_576312	Rn. 12447
XM_216922	Rn. 105890
TC560446	-
XM_341092	Rn. 98280
AW919175	Rn. 18892
BM386104	Rn. 121704
XM_341936	Rn. 23957
BM386861	Rn. 6018
AA900054	Rn. 29900
XM_214034	Rn. 163243
NM_001007678	-
XM_340742	Rn. 15835
XM_228842	-
XM_236263	Rn. 99481
BQ200547	Rn. 6272
NM_032614	Rn. 3578
NM_199380	Rn. 133804
BG668499	Rn. 15170
NM_001015019	Rn. 108412
CA339586	Rn. 164538
AA945152	-

[0150]

Target Accession	UniGene
AI009501	Rn. 137199
NM_153721	Rn. 67082
AA893485	-
BM388896	Rn. 112601
AW916021	Rn. 162877
NM_031113	Rn. 106034
AB062912	-
BF551370	Rn. 18104
NM_031112	Rn. 979
TC544957	-
NM_001005765	Rn. 106321
XM_214991	Rn. 35776
BG661053	Rn. 3990
A_44_P698503	-
XM_345431	Rn. 14868
BG379826	Rn. 119388
TC562387	-
AW143110	Rn. 8014
TC540547	-
XM_238286	Rn. 4025
AI175642	Rn. 156589
XM_579822	-
AI104544	Rn. 162443
AW914778	-
BM986614	Rn. 10615
AI012802	Rn. 11048
S77858	-
NM_001008335	Rn. 143972
A_44_P513635	-
BF289572	Rn. 2497
AI408948	Rn. 26083
NM_133544	Rn. 15277
XM_224241	Rn. 22885
AW915169	Rn. 7993
BF283115	Rn. 1822
XM_216485	Rn. 8332
NM_001008301	Rn. 11790
AI137941	Rn. 162914
XM_340802	Rn. 25201
NM_001017458	Rn. 101085
NM_012924	Rn. 1120
XM_218502	Rn. 3078
AW920832	-
TC545237	-
AW142493	Rn. 7947
NM_052804	Rn. 40595
XM_237521	Rn. 58132
AA899041	Rn. 32366
NM_001007678	-
NM_001024261	Rn. 159746
NM_176857	Rn. 21693
NM_012751	Rn. 1314
XM_216752	-
BC061839	-
NM_001005905	Rn. 2392

Target Accession	UniGene
NM_057207	Rn. 58137
S77858	-
BF394986	Rn. 973
NM_133526	Rn. 6087
XM_213636	Rn. 13590
XM_341342	-
XM_213765	-
TC554503	-
NM_001012353	Rn. 2746
NM_001017374	-
A_44_P899704	-
NM_184048	Rn. 8139
NM_019376	Rn. 29936
NM_031631	Rn. 162275
TC537371	-
AW914778	-
BI291905	Rn. 8562
AI717054	Rn. 156004
XM_221893	-
XM_344962	-
AW917588	Rn. 170291
NM_021597	Rn. 35512
NM_001009696	Rn. 103938

[0151]

Target Accession	UniGene
NM_017293	Rn. 89229
NM_001007714	Rn. 6961
TC520163	-
AW917981	Rn. 13287
CF108752	Rn. 160510
AW914778	-
XM_214600	-
NM_017153	Rn. 94935
TC552040	-
NM_173313	Rn. 10627
BC085914	Rn. 95841
NM_199380	Rn. 133804
BG671006	Rn. 3844
XM_341386	Rn. 104585
L25785	Rn. 3545
AW914793	Rn. 147001
TC520121	-
DN931809	Rn. 9167
NM_173291	Rn. 10564
NM_001009618	Rn. 8706
TC545241	-
NM_001012149	Rn. 40424
BI277661	Rn. 129486
NM_024403	Rn. 2423
XM_216102	Rn. 14059
NM_001008337	Rn. 47359
NM_017172	Rn. 6142
NM_001004238	Rn. 162952
NM_012839	Rn. 161841
BF289572	Rn. 2497
XM_215739	Rn. 95204
NM_138854	Rn. 81033
XM_341622	Rn. 92711
AA925252	Rn. 164901
AI137547	Rn. 166786
XM_215939	Rn. 117434
BI284904	Rn. 5898
NM_001014148	Rn. 1073
XM_230510	Rn. 17258
AB013454	Rn. 110865
TC559042	-
XM_232413	Rn. 104461
L25785	Rn. 3545
AA964809	Rn. 165314
NM_013011	Rn. 1292
BM390738	Rn. 162443
BG374422	Rn. 156566
NM_153628	Rn. 16883
AW921546	Rn. 67055
NM_001014092	Rn. 18098
XM_216485	Rn. 8332
XM_579926	Rn. 4131
NM_012837	Rn. 106351
NM_022506	Rn. 1101
AI411753	Rn. 164361

[0152] 対照群と比較してTickling群で1.5倍超の発現を認めた視床下部(Hy)の遺伝子の「Target Accession」及び「UniGene」を下記表8に示す。

[表8]

Target Accession	UniGene
J00757	Rn. 10589
NM_053918	Rn. 10589
BC087706	Rn. 172334
S43941	-
CB547196	Rn. 101909
TC567231	-
TC523565	-
AI102061	Rn. 13679
TC534363	-
XM_226803	Rn. 33787
NM_001000379	Rn. 143038
XM_232587	Rn. 110583
XM_227314	Rn. 102416
XM_227314	Rn. 102416
XM_236348	Rn. 163026
XM_573975	Rn. 7778
XM_221134	-
NM_177936	Rn. 41687
XM_227314	Rn. 102416
AI233261	Rn. 2460
NM_134331	Rn. 10181
BI277629	Rn. 92548
NM_001004274	Rn. 160666
AW914057	Rn. 1664
AI170406	-
NM_139090	Rn. 10580
AW918545	Rn. 170325
NM_021653	Rn. 87549
TC560804	-
TC524810	-
AA956502	Rn. 165040
NM_001024273	Rn. 14280
XM_573856	Rn. 48445
BG672648	-
X72758	-
XM_575873	Rn. 92964
TC531218	-
NM_012789	Rn. 91364
NM_001007684	Rn. 92653
NM_001014058	Rn. 160098
XM_342820	Rn. 17157
NM_001004424	Rn. 58838
BF564301	Rn. 144051
XM_577816	Rn. 62294
TC536876	-
XM_578731	Rn. 15298
NM_013195	Rn. 5832
AA997472	Rn. 98363
BI285141	Rn. 6007
NM_022224	Rn. 44484
XM_226534	Rn. 104869
BQ190235	Rn. 107678
XM_228345	Rn. 24209
NM_022274	Rn. 54471
NM_001003959	Rn. 117353
AI411835	Rn. 148350
TC543527	-
NM_133542	Rn. 102247
BF414994	Rn. 45721
XM_236534	Rn. 8284
AI231302	Rn. 2119
XM_225250	Rn. 162219
NM_139326	Rn. 108195
NM_001025737	Rn. 13596
XM_232776	-
ENSRNOT00000048767	-

Target Accession	UniGene
XM_345047	Rn. 105849
AW143334	Rn. 17619
TC521315	-
TC550311	-
NM_181367	Rn. 75111
TC537100	-
XM_227605	Rn. 162628
NM_017289	Rn. 10927
NM_013028	Rn. 11258
NM_001024791	Rn. 26582
AI137045	Rn. 166746
TC552040	-
XM_347233	Rn. 19133
XM_215668	Rn. 35269
NM_019230	Rn. 24231
NM_012829	Rn. 9781
XM_227605	Rn. 162628
BM382824	Rn. 9781
NM_021698	Rn. 42925
AW914894	Rn. 10267
BC092605	Rn. 22271
NM_001005540	Rn. 12833
AW916327	Rn. 14770

[0153]

Target Accession	UniGene
BE108176	Rn. 3464
XM_343891	Rn. 106335
XM_214856	Rn. 68084
NM_147205	Rn. 54567
XM_341480	Rn. 12539
AA956563	Rn. 106939
XM_341549	Rn. 163359
XM_225544	Rn. 16371
AW920871	-
XM_216520	Rn. 25300
AW527267	Rn. 90283
XM_342028	Rn. 101878
NM_001000543	Rn. 141899
NM_001001016	Rn. 143579
BF420040	Rn. 3321
TC559286	-
AA686784	Rn. 43930
XM_228509	Rn. 18216
NM_001011898	Rn. 15578
XM_233277	Rn. 104966
XM_215424	Rn. 106944
AA818707	Rn. 1438
XM_344194	Rn. 12385
NM_001025773	Rn. 22307
NM_022633	Rn. 48754
TC523387	-
AA956727	Rn. 9002
TC560767	-
BF564866	Rn. 28360
XM_236988	Rn. 12916
TC550302	-
NM_030850	Rn. 11406
NM_013116	Rn. 9966
NM_012596	Rn. 9891
XM_217838	Rn. 18675
NM_057187	Rn. 26894
TC540316	-
NM_183403	Rn. 3503
Z93354	Rn. 179369
NM_013002	Rn. 9736
XM_575396	-
XM_213611	Rn. 131171
XM_343196	Rn. 9153
NM_001004268	Rn. 106844
AI112716	Rn. 21134
NM_013026	Rn. 11176
XM_340809	Rn. 54720
BI274128	Rn. 164887
TC551397	-
TC548300	-
NM_013028	Rn. 11258
NM_139230	Rn. 107975
XM_343983	Rn. 63010
TC543263	-
XM_221133	Rn. 163178
BQ198978	Rn. 105849
AW143596	Rn. 105849
NM_021843	Rn. 44216
NM_133307	Rn. 98279
NM_020100	Rn. 48672
XM_575030	Rn. 7078
TC530743	-
NM_022268	Rn. 21399
BG665051	Rn. 34582
TC518879	-
AA858877	Rn. 21926
NM_001024982	Rn. 87286
TC556987	-

[0154] 対照群と比較してTickling群で1/1.5倍未満の発現を認めた視床下部(Hy)の遺伝子の「Target Accession」及び「UniGene」を下記表9に示す。

[表9]

Target Accession	UniGene
BI292028	Rn.24783
NM_013197	Rn.32517
AW144011	Rn.166761
NM_033234	Rn.36966
XM_341141	Rn.131566
AABR03001498	-
AI013718	-
XM_238366	Rn.8162
TC523759	-
NM_198776	Rn.36966
AI178665	Rn.58356
XM_218173	Rn.99310
BF398607	Rn.45255
NM_001013853	Rn.163132
XM_224783	-
AI763826	Rn.17349
XM_218649	Rn.127690
NM_031971	Rn.1950
BF388189	Rn.7511
XM_222831	Rn.82910
NM_012610	Rn.10980
XM_227492	-
NM_021589	Rn.39098
XM_238451	Rn.51047
NM_012560	Rn.9864
XM_226861	-
CB605666	Rn.9039
NM_001029908	Rn.123175
NM_012681	Rn.1404
AA996491	Rn.148105
NM_172329	Rn.91140
NM_001012219	Rn.133072
NM_021589	Rn.39098
TC546549	-
NM_153737	Rn.2415
NM_053521	Rn.44872
NM_031663	Rn.9987
A_44_P698793	-
TC548611	-
XM_219592	-
XM_233341	Rn.23612
AI511069	Rn.87363
TC528188	-
NM_012767	Rn.59459
XM_340969	-
XM_221375	Rn.101441
XM_575596	Rn.22776
XM_232595	Rn.58803
NM_031696	Rn.59513
XM_341191	Rn.162243
NM_001008555	Rn.79638
XM_341966	-
NM_016992	Rn.9976
NM_016992	Rn.9976
XM_219062	-
NM_133513	Rn.10113
XM_238528	-

[0155] Light Touch群と比較してTickling群で1.5倍超の発現を認めた視床下部(Hy)の遺伝子の「Target Accession」及び「UniGene」を下記表10に示す。

[表10]

Target Accession	UniGene
BF414994	Rn. 45721
CA945782	Rn. 98697
NM_173839	Rn. 28510
NM_145880	Rn. 127825
AI548201	Rn. 149292
AA900680	Rn. 7939
TC552055	-
AA849876	Rn. 19220
XM_234288	Rn. 21301
TC543527	-
AA892259	Rn. 3765
TC561906	-
TC524444	-
NM_031577	Rn. 10693
AW915359	Rn. 24461
TC542689	-
XM_574544	Rn. 138267
A_44_P791286	-
TC526534	-
BF546819	Rn. 788
TC546683	-
NM_001009645	Rn. 8601
NM_013088	Rn. 98209
XM_236534	Rn. 8284
AI231302	Rn. 2119
NM_001025034	Rn. 105966
XM_225250	Rn. 162219
XM_236253	Rn. 3207
NM_139326	Rn. 108195
NM_013179	Rn. 7628
NM_001003959	Rn. 117353
XM_230634	Rn. 162692
NM_012904	Rn. 1792
XM_574228	Rn. 137597
XM_228038	Rn. 53046
XM_341540	Rn. 36337
BF394697	Rn. 3857
AI411835	Rn. 148350
XM_216130	Rn. 101843
XM_344782	-
NM_001005565	Rn. 163457
NM_012614	Rn. 9714
XM_236320	Rn. 64478
XM_578731	Rn. 15298
BE108176	Rn. 3464
NM_013195	Rn. 5832
XM_218935	Rn. 48217
BI285141	Rn. 6007
XM_220473	-
NM_001024326	Rn. 53184
NM_022224	Rn. 44484
XM_226534	Rn. 104869
BQ190235	Rn. 107678
NM_022274	Rn. 54471
XM_213338	Rn. 163126
XM_228345	Rn. 24209
NM_001009470	Rn. 6743
NM_022633	Rn. 48754
M27315	-
BF420040	Rn. 3321
XM_232776	-

Target Accession	UniGene
NM_053753	Rn. 9886
BF564866	Rn. 28360
XM_341045	Rn. 144010
XM_220783	-
X72758	-
AI059427	Rn. 8068
AI233261	Rn. 2460
NM_133295	Rn. 2549
NM_053730	Rn. 18997
TC550302	-
NM_139342	Rn. 7110
BQ194469	Rn. 161764
AI009774	Rn. 146101
TC541563	-
TC539036	-
NM_001007691	Rn. 137661
XM_341623	Rn. 132740
NM_198780	Rn. 104376
NM_012740	Rn. 11082
AI012802	Rn. 11048
BF549735	Rn. 38972
BG672648	-
XM_219001	Rn. 22111
NM_001024273	Rn. 14280
AW918545	Rn. 170325
TC523387	-
AI233208	Rn. 14584
XM_228059	-
TC551900	-
NM_012659	Rn. 34418
NM_134378	Rn. 161961
AF112446	Rn. 104291
NM_053753	Rn. 9886
BF564866	Rn. 28360
XM_341045	Rn. 144010
XM_220783	-
X72758	-
AI059427	Rn. 8068
AI233261	Rn. 2460
NM_133295	Rn. 2549
NM_053730	Rn. 18997
TC550302	-
NM_139342	Rn. 7110
BQ194469	Rn. 161764

[0156]

Target Accession	UniGene
XM_343891	Rn. 106335
NM_001001016	Rn. 143579
NM_001000543	Rn. 141899
TC531218	-
XM_214856	Rn. 68084
AA956563	Rn. 106939
XM_341549	Rn. 163359
C0564048	Rn. 21249
AA686784	Rn. 43930
L20998	Rn. 111420
BF564301	Rn. 144051
NM_133542	Rn. 102247
XM_235224	Rn. 161939
NM_012625	Rn. 9675
NM_001005384	Rn. 92110
TC544476	-
NM_053955	Rn. 24561
NM_001025737	Rn. 13596
CK595775	Rn. 125806
NM_053870	Rn. 10197
TC543039	-
TC525068	-
NM_021697	Rn. 42920
BE102060	Rn. 170815
NM_053372	Rn. 18560
NM_019374	Rn. 44471
BF284544	Rn. 169359
A_44_P753601	-
XM_219262	Rn. 92644
NM_001005890	Rn. 47351
NM_017016	Rn. 48653
NM_012694	Rn. 10093
TC559451	-
NM_012852	Rn. 34834
NM_012760	Rn. 6977
TC524051	-
A_44_P152317	-
BF563404	Rn. 171004
XM_218484	Rn. 144998
NM_017110	Rn. 89164
XM_341188	Rn. 2649
NM_013031	Rn. 9686
NM_013031	Rn. 9686
AI009774	Rn. 146101
TC541563	-
TC539036	-
NM_001007691	Rn. 137661
XM_341623	Rn. 132740
NM_198780	Rn. 104376
NM_012740	Rn. 11082
AI012802	Rn. 11048
BF549735	Rn. 38972
BG672648	-
XM_219001	Rn. 22111
NM_001024273	Rn. 14280
AW918545	Rn. 170325
TC523387	-
AI233208	Rn. 14584
XM_228059	-
TC551900	-
NM_012659	Rn. 34418
NM_134378	Rn. 161961
AF112446	Rn. 104291

[0157] Light Touch群と比較してTickling群で1/1.5倍未満の発現を認めた視床下部(Hy)の遺伝子の「Target Accession」及び「UniGene」を下記表11に示す。

[表11]

Target Accession	UniGene
AW142828	Rn. 23342
NM_016991	Rn. 10032
TC556987	-
AA858877	Rn. 21926
XM_227605	Rn. 162628
TC537100	-
TC543263	-
BG665051	Rn. 34582
NM_139230	Rn. 107975
NM_013028	Rn. 11258
TC552040	-
AI137045	Rn. 166746
XM_343196	Rn. 9153
AA800765	Rn. 3576
NM_021843	Rn. 44216
AW143596	Rn. 105849
BF393607	Rn. 118853
BQ198978	Rn. 105849
TC567087	-
NM_022268	Rn. 21399
TC530743	-
XM_575030	Rn. 7078
NM_020100	Rn. 48672
XM_343196	Rn. 9153
NM_133307	Rn. 98279
C0397565	Rn. 24009
XM_219747	Rn. 104760
TC540415	-
NM_013028	Rn. 11258
NM_021676	Rn. 42876
U90444	Rn. 89675
BM986371	Rn. 48830
XM_574845	Rn. 32812
XM_574845	Rn. 32812
NM_172224	Rn. 856
NM_130429	Rn. 21926
NM_053324	Rn. 10194
XM_576437	Rn. 161915
TC525061	-
XM_232732	Rn. 106759
A_44_P1038489	-
NM_031828	Rn. 30616
XM_217827	-
XM_223616	Rn. 41145
XM_225077	-
NM_181367	Rn. 75111
TC555919	-
XM_224480	Rn. 99063
NM_021771	Rn. 45385
AB105879	Rn. 44216
NM_019340	Rn. 53900
NM_001024791	Rn. 26582
XM_342643	Rn. 16336
NM_001025680	Rn. 23364
NM_080587	Rn. 81205
NM_017289	Rn. 10927
AW918031	Rn. 7595
TC567793	-
TC560446	-
TC556147	-
NM_019372	Rn. 31799
AI168986	Rn. 79033
TC556932	-
XM_341111	-
AJ517196	Rn. 30616
XM_341553	Rn. 8227
BF389753	Rn. 15176
XM_341499	-

Target Accession	UniGene
NM_147211	Rn. 11272
NM_133581	Rn. 3193
AI176008	-
AABR03057162	-
XM_238528	-
NM_031590	Rn. 53991
BF398607	Rn. 45255
A_44_P260655	-
AA800059	Rn. 2029
AW142932	Rn. 35842
NM_012597	Rn. 1195
NM_138838	Rn. 82720
BF397301	-
NM_031663	Rn. 9987
AA858621	Rn. 12600
XM_228172	Rn. 139633
TC558667	-
TC557723	-
XM_213993	Rn. 47771
NM_013217	Rn. 58
TC541594	-
NM_145683	Rn. 10160
BC098071	Rn. 54711
TC526324	-
TC540619	-
BG376309	Rn. 6873
NM_021589	Rn. 39098
NM_001012219	Rn. 133072
NM_153737	Rn. 2415
NM_012681	Rn. 1404
NM_019292	Rn. 1647
NM_053521	Rn. 44872
XM_235312	-
XM_221387	Rn. 18397
NM_053859	Rn. 10267
AI176129	Rn. 9154
XM_342781	Rn. 118736
XM_218423	-
XM_238366	Rn. 8162
NM_053994	Rn. 11126
XM_221901	-
XM_233354	-
XM_213470	-
AW920863	Rn. 30828
NM_001007615	Rn. 163194
XM_218173	Rn. 99310
AI178665	Rn. 58356

[0158]

Target Accession	UniGene
TC520453	-
XM_341134	Rn. 1141
NM_052806	Rn. 9695
NM_017214	Rn. 11065
TC520825	-
TC556556	-
NM_133415	Rn. 62703
NM_001014035	Rn. 162435
XM_224009	Rn. 35222
BE126741	-
XM_237334	Rn. 70007
AI045171	Rn. 166099
NM_022864	Rn. 10133
XM_214459	-
NM_001007675	Rn. 53880
TC519964	-
NM_019211	Rn. 162685
NM_053981	Rn. 10406
AW527509	Rn. 41179
ENSRNOT00000032841	-
XM_223203	Rn. 150520
NM_023960	Rn. 162953
XM_224009	Rn. 35222
NM_022677	Rn. 161923
XM_345977	Rn. 124862
XM_217648	Rn. 148012
XM_230042	Rn. 154491
XM_343785	Rn. 106251
XM_343055	Rn. 76536
NM_057207	Rn. 58137
TC551026	-
XM_342652	Rn. 117708
TC542844	-
NM_022302	Rn. 64485
AF366899	-
NM_057190	Rn. 7504
AJ517195	-
NM_001029909	Rn. 89150
TC566774	-
NM_147211	Rn. 11272
AI101494	Rn. 136571
NM_001012459	Rn. 162423
BF392884	Rn. 17619
XM_219695	Rn. 162509
NM_139185	Rn. 11233
TC567761	-
AW533914	Rn. 41179
NM_001025042	Rn. 43451
NM_053402	Rn. 34782
XM_230761	Rn. 145056
NM_139217	Rn. 9733
AW914894	Rn. 10267
XM_342172	Rn. 11207
XM_343983	Rn. 63010
BM382824	Rn. 9781
NM_053346	Rn. 3546
XM_226142	Rn. 144765
TC541875	-
BC092605	Rn. 22271
NM_021698	Rn. 42925
XM_227605	Rn. 162628
NM_012829	Rn. 9781
NM_013002	Rn. 9736
BQ193921	Rn. 89675
NM_057187	Rn. 26894
NM_001005540	Rn. 12833
BQ196242	Rn. 8285
AW919005	Rn. 15453
TC524618	-
XM_344284	Rn. 52205

[0159] 対照群と比較してTickling群で1.5倍超の発現を認めた線条体(St)の遺伝子の「Target Accession」及び「UniGene」を下記表12に示す。

[表12]

表12 発現データ T-St(Cy5) v.s. C-St(Cy3)
1.5倍超

Target Accession	UniGene
XM_218747	Rn.101871
XM_218747	Rn.101871
XM_218747	Rn.101871
AW144721	Rn.3039
BE108176	Rn.3464
NM_024390	Rn.6386
XM_218747	Rn.101871
BF391279	Rn.1119
AA963075	Rn.73451
NM_057207	Rn.58137
NM_012996	Rn.48915
NM_021669	Rn.42103
NM_057187	Rn.26894
BG672648	-
BE121329	Rn.25221
NM_016992	Rn.9976
AI011483	Rn.83595
AI511358	Rn.168013
NM_001025679	Rn.161808
TC536876	-
XM_578123	-
BF390414	Rn.154429
XM_344382	-
AW143472	Rn.21549
XM_342036	-
XM_217680	Rn.139570
XM_343562	Rn.16593
BF549735	Rn.38972
TC565530	-
TC525892	-
AI045568	-
BE110241	-
AI230396	Rn.19361
BI395434	-
BF402400	Rn.59637
BF289693	Rn.15475
A_44_P785080	-
BQ202862	-
AA964921	Rn.3661
AA899253	Rn.9560
BF418835	Rn.19353
BF283967	Rn.2740
AI235576	Rn.128814
AI406616	Rn.7349
TC520700	-
NM_001014058	Rn.160098
NM_012643	Rn.93200
BE104250	Rn.9560
AF247818	Rn.48802
BF414994	Rn.45721
BF564301	Rn.144051
AI137553	Rn.12284
BM392158	Rn.29288

Target Accession	UniGene
XM_232757	Rn.20891
TC543527	-
XM_236124	Rn.106147
AA850752	Rn.7043
XM_232983	Rn.43359
NM_138831	Rn.21992
TC559524	-
XM_219001	Rn.22111
XM_220950	-
TC528231	-
TC566043	-
NM_001007694	Rn.35775
BI288769	Rn.165022
XM_223945	Rn.137329
NM_053713	Rn.7719
AI013149	Rn.14890
TC546786	-
NM_199101	Rn.99114
NM_001000484	Rn.143632
BE108919	Rn.2914
NM_001025415	Rn.155971
TC560662	-
AI011505	Rn.165714
AI059481	Rn.166264
TC541160	-
NM_001011977	Rn.47921
XM_344039	Rn.39369
TC521972	-
NM_001001071	Rn.143176
XM_219560	Rn.105761
AI412231	-
BQ195765	Rn.24358
NM_080400	Rn.33267
BF550822	Rn.17900
BE116009	Rn.22987
Y17323	-
XM_576069	-
M26686	-
BM388083	Rn.41133
A_44_P859795	-
AA955478	Rn.47249
BM986267	Rn.11046
XM_574231	Rn.146007
TC566188	-
AI073017	Rn.16489
AI548201	Rn.149292
AW143194	Rn.107690
AW144301	Rn.8938
NM_001000756	Rn.141685
TC552055	-
NM_053754	Rn.74258
TC547414	-
M54999	-

[0160]

Target Accession	UniGene
AW141857	Rn. 18249
TC523243	-
BF408765	Rn. 161936
XM_343875	-
NM_012907	Rn. 10002
XM_219062	-
XM_577757	Rn. 32631
NM_153299	Rn. 57072
TC559144	-
XM_344146	-
AI412054	Rn. 162966
BF394800	Rn. 58355
TC545861	-
XM_341549	Rn. 163359
NM_013088	Rn. 98209
AW143917	Rn. 1097
AA849876	Rn. 19220
AA900854	Rn. 155571
AA925373	Rn. 164909
BE113115	Rn. 166236
XM_223730	Rn. 125227
AI237243	Rn. 96234
TC534125	-
XM_347017	Rn. 138005
TC567669	-
XM_225544	Rn. 16371
BG373356	Rn. 29869
XM_220775	Rn. 113556
AI227908	Rn. 60443
AW915151	-
A_44_P475663	-
XM_223466	-
XM_220611	-
XM_227544	-
AI072072	Rn. 101730
BE110150	Rn. 6307
XM_227230	Rn. 54860
AI178668	Rn. 130237
CA506887	Rn. 33802
AA945574	Rn. 164794
XM_347206	Rn. 1237
TC524205	-
AI136114	Rn. 154557
A_44_P140233	-
TC560558	-
BE111604	Rn. 9560
BC090353	Rn. 119131
BF563517	Rn. 47043
AW528486	Rn. 147770
NM_001017490	Rn. 41478
AA818306	Rn. 16505
AY156086	Rn. 16736
BG381120	Rn. 12899
CA508705	Rn. 179157
BE102354	Rn. 13538

Target Accession	UniGene
NM_021664	Rn. 41640
AA957814	Rn. 152719
NM_031511	Rn. 118681
XM_343658	Rn. 160695
M95791	-
NM_022407	Rn. 6132
BF411904	Rn. 6202
NM_012850	Rn. 10936
CA507578	Rn. 14632
AI103284	Rn. 34387
NM_001009645	Rn. 8601
A_44_P892848	-
BQ193503	Rn. 164414
AW142399	Rn. 163326
AA925323	Rn. 15497
TC556438	-
AW524412	Rn. 17067
NM_133304	Rn. 43849
XM_233526	Rn. 145085

[0161]

Target Accession	UniGene
AI111912	Rn. 6635
A_44_P452570	-
CA504714	Rn. 92051
AABR03062916	-
TC538420	-
AA818893	-
BI279384	Rn. 146573
XM_345799	Rn. 101959
ENSRNOT00000039453	-
BQ211506	Rn. 17458
AA818089	Rn. 3338
NM_001008725	Rn. 12138
AW252746	Rn. 108090
NM_031817	Rn. 30124
AW918531	Rn. 23810
BF558575	Rn. 174745
XM_577424	-
AI059427	Rn. 8068
AW532469	Rn. 147450
NM_031138	Rn. 20766
AI101373	Rn. 9024
XM_236325	Rn. 14593
XM_574271	Rn. 65514
NM_001008884	Rn. 33311
XM_342702	Rn. 47690
BQ200927	Rn. 8096
AW914875	Rn. 9
BM386777	Rn. 18047
AA899782	Rn. 159792
BM387047	Rn. 22461
AA963975	Rn. 23216
XM_223835	-
AI598434	Rn. 163791
XM_225849	Rn. 151076
NP798075	-
XM_213440	Rn. 2953
AI171211	Rn. 15010
BG671786	Rn. 9183
TC542260	-
A_44_P898805	-
XM_344057	Rn. 14920
BE112523	Rn. 14724
BQ202476	Rn. 6249
NM_053960	Rn. 10736
BQ205131	Rn. 168984
AI412542	Rn. 31762
XM_224615	-
BI291861	Rn. 170925
BQ211578	Rn. 21009
BE099435	Rn. 16802
X72758	-
BE102568	Rn. 126427
ENSRNOT00000030924	-
XM_345327	Rn. 107008
BF396509	Rn. 162027

[0162] 対照群と比較してTickling群で1/1.5倍未満の発現を認めた線条体(St)の遺伝子の「Target Accession」及び「UniGene」を下記表13に示す。

[表13]

表13 発現データ T-St(Cy5) v.s. C-St(Cy3)
1/1.5倍未満

Target Accession	UniGene
AI145976	Rn. 121393
XM_575179	Rn. 22639
BQ211747	Rn. 50364
TC564799	-
XM_220066	Rn. 145025
XM_215593	-
BM384240	Rn. 177293
NM_013099	Rn. 10620
TC562408	-
ENSRNOT00000039392	-
AA925221	Rn. 164898
BQ209483	Rn. 98258
NM_134370	-
A_44_P677914	-
AA874934	Rn. 3179
XM_234162	Rn. 100658
XM_342147	Rn. 57442
XM_234399	Rn. 11326
XM_221376	Rn. 19056
XM_221901	-
BM382869	Rn. 24708
BF564733	Rn. 91597
AI113042	-
NM_133381	Rn. 108128
ENSRNOT00000018201	-
AI172204	Rn. 19451
XM_575110	Rn. 125706
XM_343200	Rn. 162946
NM_030868	Rn. 162955
ENSRNOT00000030885	-
XM_236228	Rn. 127055
XM_344970	Rn. 154758
XM_344158	-
NM_001013151	Rn. 35127
NM_001007615	Rn. 163194
NP516919	-
A_44_P982114	-
NM_031075	Rn. 10388
NM_013133	Rn. 10109
XM_222597	Rn. 65707
XM_342431	-
XM_341802	Rn. 144640
CK600488	Rn. 158491
XM_340792	Rn. 46134
XM_228806	Rn. 23446
XM_222031	Rn. 86017
XM_573948	Rn. 102309
XM_225971	Rn. 38640
XM_237792	Rn. 72554
ENSRNOT00000046943	-
AW915996	Rn. 19250
NM_001008558	Rn. 3096
A_44_P775694	-

Target Accession	UniGene
NM_153735	Rn. 54707
XM_345319	Rn. 16387
XM_230761	Rn. 145056
NM_133573	Rn. 9806
NM_001007615	Rn. 163194
AW521749	Rn. 156710
NM_181370	Rn. 49010
XM_217517	Rn. 44797
NM_001014216	Rn. 21433
XM_229186	Rn. 105358
NM_053504	Rn. 86653
NM_012736	Rn. 89705
NM_145675	Rn. 85477
NM_019328	Rn. 88129
TC562144	-
BF401621	Rn. 6987
BF406424	Rn. 48532
NM_138921	Rn. 76362
NM_024483	Rn. 11314
NM_019172	Rn. 9789
XM_574210	Rn. 24402
TC551967	-
NM_053903	Rn. 10714
BQ195982	Rn. 3192
NM_001025422	Rn. 17123
NM_198727	Rn. 107043
NM_013192	-
XM_230789	Rn. 136947
TC543926	-
XM_224318	Rn. 3259
TC541875	-
NM_001013853	Rn. 163132
XM_576570	Rn. 22624
NM_022953	Rn. 30002
XM_575489	Rn. 162754
NM_012612	Rn. 2004
CB582871	Rn. 13498
NM_021679	Rn. 19736
K02111	Rn. 10092
NM_031601	Rn. 86960
XM_345102	Rn. 133599
CA506147	Rn. 1779
CB544275	Rn. 179582
BE117009	Rn. 146484
XM_224318	Rn. 3259
U92079	-
TC558785	-
XM_231354	Rn. 104731
AW914894	Rn. 10267
XM_215523	-
NM_012829	Rn. 9781
XM_234902	Rn. 141564
BC092605	Rn. 22271

[0163]

表13 発現データ T-St(Cy5) v.s. C-St(Cy3)
1/1.5倍未満

Target Accession	UniGene
XM_222253	Rn.105079
BF406637	Rn.7586
NM_001013433	Rn.23090
NM_019270	Rn.44292
XM_234775	Rn.154519
A_44_P621268	-
XM_573948	Rn.102309
XM_222996	-
BG672591	Rn.32103
XM_231125	Rn.19250
AI178665	Rn.58356
NM_001025128	Rn.155378
XM_236975	Rn.163046
TC551575	-
XM_573992	Rn.6116
XM_217825	Rn.36118
XM_226475	Rn.21088
XM_213470	-
XM_219468	-
XM_578193	Rn.74088
NM_139183	Rn.34568
TC531846	-
XM_236914	Rn.47365
AA956799	Rn.23120
NM_033234	Rn.36966
NM_133289	Rn.88082
XM_341342	-
XM_227064	Rn.14848
NM_017119	Rn.11190
BM382824	Rn.9781
XM_237296	Rn.18155
A_44_P445556	-
XM_234394	-
NM_031664	Rn.10140
TC559115	-
XM_230472	Rn.147393
NM_012765	Rn.9935
NM_198776	Rn.36966
NM_030841	Rn.34907
NM_130820	Rn.81186
XM_219665	-
XM_576094	Rn.135003
TC562720	-
XM_342147	Rn.57442
AI502646	Rn.26766
AI228437	Rn.24326
AI232101	Rn.105999
NM_147141	Rn.85880
TC537427	-
XM_225450	Rn.115879
TC526462	-
XM_235397	Rn.33421
XM_231028	Rn.145062

Target Accession	UniGene
TC563514	-
NM_133303	Rn.10784
NM_017358	Rn.10818
NM_001012740	Rn.16398
NM_012513	Rn.11266
XM_231625	-
BF546193	Rn.174580
BF281936	Rn.8247
A_44_P302611	-
NM_053859	Rn.10267
XM_229981	-
NM_001003929	Rn.55036
TC560395	-
NM_001001082	Rn.143554
NM_012513	Rn.11266
XM_218173	Rn.99310
BF398607	Rn.45255

[0164]

表13 発現データ T-St(Cy5) v.s. C-St(Cy3)
1/1.5倍未満

Target Accession	UniGene
XM_235409	Rn.135417
XM_216941	Rn.100742
C0403684	Rn.13498
XM_218227	Rn.162411
AA899896	-
NM_012757	Rn.21943
XM_342247	-
AA999167	Rn.47443
XM_575725	Rn.134121
TC529378	-
CB547154	Rn.51026
XM_233354	-
XM_234108	Rn.144619
NM_021869	Rn.1993
BF393089	Rn.11715
XM_342856	Rn.162041
NM_031971	Rn.1950
NM_012835	Rn.10490
XM_221455	Rn.138746
AI101841	Rn.18085
XM_233196	Rn.96284
NM_012524	Rn.153603
NM_053994	Rn.11126
NM_001013997	Rn.139140
S69671	-
BM986253	Rn.2290
TC546118	-
XM_342933	Rn.100470
XM_238366	Rn.8162
NM_199406	Rn.162547
NM_031010	Rn.11318
XM_342958	Rn.41973
NM_001015008	Rn.11547
BE108930	Rn.124042
XM_222637	-
XM_345018	Rn.62443
AI501923	Rn.167909
NM_001012129	Rn.21462
XM_235694	Rn.31965
NM_133522	Rn.10458
XM_231528	Rn.91746
BQ196178	Rn.9335
XM_236914	Rn.47365
XM_217838	Rn.18675
NM_024354	Rn.9697
XM_223688	Rn.106948
NM_053750	Rn.10637
XM_236616	Rn.120727
NM_001001801	Rn.124802
NM_080696	Rn.81217
XM_217167	Rn.163007
TC532010	-
NM_053346	Rn.3546

[0165] Light Touch群と比較してTickling群で1.5倍超の発現を認めた線条体(St)の遺伝子の「Target Accession」及び「UniGene」を下記表14に示す。

[表14]

表14 T-St(Cy5) v.s. L-St(Cy3) :up regulation(Cy5>Cy3)

Target Accession	UniGene
BQ194469	Rn.161764
XM_237952	Rn.19611
BG672648	-
XM_238550	-
TC529421	-
BF549735	Rn.38972
TC523577	-
NM_001013953	Rn.15323
NM_033237	Rn.8929
TC552854	-
XM_341694	Rn.27744
XM_217175	-
BQ200469	Rn.22330
NM_012907	Rn.10002
NM_053832	Rn.1419

[0166] Light Touch群と比較してTickling群で1/1.5倍未満の発現を認めた線条体(St)の遺伝子の「Target Accession」及び「UniGene」を下記表15に示す。

[表15]

表15 T-St(Cy5) v.s. L-St(Cy3) :down regulation(Cy5<Cy3)

Target Accession	UniGene
BF398607	Rn.45255
XM_218173	Rn.99310
XM_217838	Rn.18675
NM_053859	Rn.10267
BM382824	Rn.9781
AW914894	Rn.10267
U92079	-
NM_012829	Rn.9781
NM_053346	Rn.3546
BF285291	Rn.105722
AI178665	Rn.58356
CB582871	Rn.13498
NM_133522	Rn.10458
NM_012835	Rn.10490
XM_343597	Rn.776
NM_181370	Rn.49010
TC541875	-
XM_575489	Rn.162754
XM_576570	Rn.22624
CO403684	Rn.13498
CB547989	Rn.33084
NM_153735	Rn.54707
NM_053750	Rn.10637
TC528645	-
XM_222253	Rn.105079
NM_031601	Rn.86960
NM_030841	Rn.34907
XM_342967	-
NM_030868	Rn.162955
NM_019326	Rn.10724
NM_019328	Rn.88129
NM_138849	Rn.31973
AA943842	-
TC562720	-
AI103511	Rn.163014
NM_001004282	Rn.17530
AA925539	Rn.6389
XM_225579	-
NM_139183	Rn.34568
XM_230761	Rn.145056
XM_221901	-
XM_343512	-
NM_053504	Rn.86653
TC526462	-

[0167] 対照群と比較してTickling群で1.5倍超の発現を認めた唾液腺(Sg)の遺伝子の「Target Accession」及び「UniGene」を下記表16に示す。

[表16]

Target Accession	UniGene
XM_214947	Rn. 136578
XM_236313	Rn. 63734
NM_012677	Rn. 9882
NM_012842	Rn. 6075
NM_031732	Rn. 9937
NM_031523	Rn. 11331
BF545837	Rn. 98481
XM_576608	Rn. 12811
XM_230827	Rn. 107822
NM_031798	Rn. 11523
NM_001001508	Rn. 58355
NM_175759	Rn. 34527
AI548588	Rn. 41443
NM_001009964	Rn. 6327
NM_017046	Rn. 10360
NM_133424	Rn. 17592
NM_013160	Rn. 37510
AW142685	Rn. 164339
XM_214931	Rn. 107068
XM_223837	Rn. 98363
NM_057116	Rn. 54550
XM_341578	Rn. 4181
NM_001007677	Rn. 17352
XM_218515	Rn. 141981
XM_214931	Rn. 107068
XM_573179	Rn. 93919
NM_023962	Rn. 64493
NM_012684	Rn. 9927
NM_001017383	Rn. 22468
NM_024136	Rn. 10362
XM_236777	Rn. 35756
A_44_P260574	-
TC525855	-
NM_199374	Rn. 27773
BF567941	Rn. 169222
NM_022193	Rn. 44372
AW917276	Rn. 7332
AA963004	Rn. 24539
XM_233437	Rn. 159750
XM_236734	Rn. 161977
AI231342	Rn. 24539
NM_031131	Rn. 24539
ENSRNOT00000016430	-
NM_031740	-
NM_019622	Rn. 91373
XM_231787	Rn. 106207
X89700	-
NM_019189	Rn. 50531
CF110082	Rn. 117936
TC521707	-
NM_001024781	Rn. 22446
BQ196033	Rn. 33794
XM_220907	Rn. 18110
ENSRNOT00000038788	-
XM_344926	-
NM_053656	Rn. 88799
XM_233520	Rn. 162826
NM_198734	Rn. 154471
NM_017081	Rn. 10186
XM_222251	Rn. 76053
A_44_P882921	-

Target Accession	UniGene
XM_237588	Rn. 94994
AW433952	Rn. 16874
BF284032	Rn. 107246
NM_001014068	Rn. 9366
NM_172328	Rn. 91139
A_44_P304740	-
XM_230605	Rn. 162720
XM_218428	-
NM_031348	Rn. 20051
NM_053595	Rn. 6960
XM_225644	Rn. 7963
XM_213491	Rn. 64787
TC525053	-
BG375265	Rn. 16486
NM_024388	Rn. 10000
NM_001007015	Rn. 87496
NM_199266	Rn. 43503
AW522944	Rn. 45519
A_44_P258158	-
BF289878	Rn. 137704
NM_019193	Rn. 10883
NM_017227	Rn. 11155
AI233863	Rn. 22788
XM_225137	-
BG377341	Rn. 28882
NM_019291	Rn. 26083
XM_576608	Rn. 12811
BF545957	Rn. 24778
TC556399	-
NM_001001970	Rn. 145399
NM_031853	Rn. 3285
AI704873	Rn. 17738
XM_341985	Rn. 61872
XM_217293	Rn. 37030
XM_230449	Rn. 45546
XM_346464	Rn. 46211
AW142962	Rn. 9757
XM_341098	-
NM_133578	Rn. 10877
CK595775	Rn. 125806
NM_022634	Rn. 91085
TC543039	-
XM_341973	-
NM_080411	Rn. 63075
NM_199407	Rn. 47255
NM_201422	Rn. 22308
CB545830	Rn. 157214
XM_344305	-
XM_233562	-
NM_001017497	Rn. 113967
ENSRNOT00000043791	-
XM_576813	Rn. 145750
TC559056	-
XM_226853	Rn. 27637
M15402	Rn. 117923
XM_576842	-
NM_024128	Rn. 2865
TC520009	-
AI070114	Rn. 6374
NM_053738	Rn. 74256
TC537554	-

[0168]

Target Accession	UniGene
NM_012718	Rn. 9977
NM_177425	Rn. 94754
XM_216075	-
NM_013156	Rn. 1294
TC531872	-
NM_178333	Rn. 92480
NM_031740	-
XM_221081	Rn. 163171
XM_345742	-
NM_153470	Rn. 3213
NM_001024751	Rn. 76073
A_44_P729420	-
NM_019362	Rn. 34414
XM_240734	Rn. 6819
TC540693	-
NM_001013045	Rn. 138822
XM_341148	Rn. 46306
XM_341954	Rn. 162479
AA800803	Rn. 102152
TC541862	-
NM_130824	Rn. 81227
NM_053674	Rn. 7279
XM_341400	Rn. 41214
C0556754	Rn. 15953
NM_057151	Rn. 46679
NM_031672	Rn. 89268
NM_147165	Rn. 9852
NM_012720	Rn. 91185
CA510810	Rn. 47334
AY007370	Rn. 127827
XM_345643	-
NM_031701	Rn. 17420
TC540359	-
NM_030831	Rn. 88417
BF560064	Rn. 105044
NM_017066	Rn. 1653
NM_181440	Rn. 10942
XM_341641	Rn. 41567
XM_228133	Rn. 84956
NM_024358	Rn. 65930
NM_001012225	Rn. 145359
XM_233574	Rn. 27233
BF565121	Rn. 46977
AF475093	Rn. 3040
NM_001009172	Rn. 17135
NM_001014232	Rn. 8173
XM_341639	Rn. 8900
XM_217031	Rn. 48052
NM_023022	Rn. 44480
XM_344823	-
XM_214499	Rn. 3970
XM_234272	Rn. 96357
NM_199085	Rn. 12754
NM_001009674	Rn. 8450
XM_343871	-
NM_001013923	Rn. 93910
NM_019169	Rn. 1827
XM_217285	Rn. 101391
NM_022709	Rn. 162774
BE113172	Rn. 20331
TC562194	-
XM_235563	-
NM_198685	Rn. 79319

Target Accession	UniGene
XM_342507	Rn. 40950
XM_575834	-
TC538192	-
TC528434	-
NM_021682	Rn. 42884
XM_346023	-
BG664056	Rn. 107963
NM_001012174	Rn. 144288
NM_147215	Rn. 86413
AI170356	Rn. 139327
AW915757	Rn. 164843
XM_219482	-
TC540161	-
TC539827	-
L14933	Rn. 104002
BF548648	Rn. 12094
BQ203725	Rn. 47
AW142782	Rn. 43391
NM_020073	Rn. 48025
AI145603	Rn. 36585
XM_575671	Rn. 162791
NM_013107	Rn. 40476
NM_173094	Rn. 29594
NM_019169	Rn. 1827
NM_175578	Rn. 24428
NM_031069	Rn. 10695
BC091324	Rn. 13679
TC542673	-
TC523471	-
XM_342788	Rn. 107176
NM_022177	Rn. 54439
NM_001012174	Rn. 144288
XM_240449	Rn. 101393
XM_577401	-
NM_001014059	Rn. 13411
AA875032	Rn. 163703
TC558499	-
NM_139325	Rn. 10828
NM_170718	-
M87788	Rn. 118336
AI101197	Rn. 166995
AA924847	Rn. 9470
XM_345584	Rn. 74081
NM_181377	Rn. 163152
NM_147214	Rn. 86422
NM_021698	Rn. 42925
XM_213732	Rn. 94103
XM_222031	Rn. 86017
NM_053769	Rn. 98260
NM_001012459	Rn. 162423
NM_053504	Rn. 86653
NM_031561	Rn. 102418
AW141926	Rn. 10787
NM_016989	Rn. 37400
AI071406	Rn. 8538
XM_345190	Rn. 161818
NM_031778	Rn. 10878
NM_080770	Rn. 144559
TC563058	-
AI169615	Rn. 162275
AA891669	Rn. 124832
NM_080778	Rn. 17815
XM_219001	Rn. 22111

[0169]

Target Accession	UniGene
TC558884	-
XM_347055	Rn. 48786
AA850364	Rn. 24214
XM_343919	Rn. 16981
NM_023962	Rn. 64493
BM390141	Rn. 9198
XM_232226	Rn. 3111
XM_238442	Rn. 18688
AA875647	Rn. 147866
XM_574554	Rn. 112669
NM_024396	Rn. 13115
NM_145717	Rn. 6700
XM_234124	Rn. 135138
XM_345276	-
BF400026	Rn. 63770
TC544280	-
NM_001024983	Rn. 152074
BG380409	Rn. 143966
TC565292	-
A_44_P799008	-
TC544663	-
XM_227403	Rn. 104095
CB545272	Rn. 24090
BE111679	Rn. 13642
XM_574715	-
XM_216317	Rn. 144410
A_44_P110129	-
XM_227140	Rn. 38949
BF567508	Rn. 164219
NM_001000441	Rn. 143544
BE099808	Rn. 161419
XM_213687	Rn. 138846
NM_031798	Rn. 11523
XM_230608	Rn. 80962
TC527065	-
XM_213416	Rn. 47764
NM_172065	Rn. 29950
BF559333	Rn. 164776
AA963232	Rn. 1053
TC538650	-
NM_053674	Rn. 7279
NM_021835	Rn. 93714
XM_575387	Rn. 19785
TC525422	-
NM_133513	Rn. 10113
BG664685	-
NM_012996	Rn. 48915
NM_138902	Rn. 10626
XM_230050	Rn. 35465
BF420279	Rn. 143962
BF558648	Rn. 19093
XM_344463	-
CB547130	Rn. 179696
NM_138979	Rn. 22715
CB547735	Rn. 99537
XM_238544	Rn. 107376
XM_576406	Rn. 57310
NM_031736	Rn. 3608
NM_001013955	Rn. 109830
TC542429	-
NM_012684	Rn. 9927
NM_012740	Rn. 11082
TC543922	-

Target Accession	UniGene
XM_574867	Rn. 161787
XM_236477	Rn. 107533
AA891661	Rn. 1618
NM_031031	Rn. 17661
BF556255	Rn. 175161
XM_227454	Rn. 103871
TC545913	-
A_44_P292951	-
XM_344096	-
NM_019192	Rn. 1451
TC544844	-
XM_573983	Rn. 1046
TC524893	-
NM_053630	Rn. 30035
XM_231478	Rn. 34471
XM_223556	Rn. 40484
XM_225585	Rn. 9197
NM_147213	Rn. 107041
XM_343121	Rn. 10956
TC544040	-
BI304040	Rn. 103275
XM_220783	-
XM_577233	-
NM_022199	Rn. 44407
NM_133538	Rn. 162308
CB547165	Rn. 103609
AW919920	Rn. 154616
XM_341045	Rn. 144010
NM_001013941	Rn. 161900
NM_001008514	Rn. 106342
AW915407	-
XM_238550	-
XM_342316	Rn. 6456
XM_577380	-
XM_214631	Rn. 28599
A_44_P452570	-
TC522992	-
NM_134330	Rn. 22745
XM_236724	Rn. 105334
XM_345570	Rn. 105585
AA956092	Rn. 164998
XM_573726	Rn. 156730
BE106074	Rn. 14606
BG672648	-
BF549735	Rn. 38972
AI233208	Rn. 14584
NM_001001024	Rn. 141892
X72758	-
NM_053289	Rn. 9727
TC525892	-
TC551900	-
NM_024390	Rn. 6386
XM_232757	Rn. 20891
AI235576	Rn. 128814
AW916070	Rn. 167735
NM_022602	Rn. 6343
TC538830	-
AI071874	Rn. 1653
NM_001007627	Rn. 156353
XM_576628	Rn. 121539
NM_147213	Rn. 107041
XM_343658	Rn. 160695
NM_001025415	Rn. 155971

[0170]

Target Accession	UniGene
NM_031605	Rn. 10034
NM_012550	Rn. 10915
BG672252	Rn. 33045
NM_053487	Rn. 14519
BC061835	Rn. 14519
XM_341623	Rn. 132740
NM_031509	Rn. 10460
NM_001012235	Rn. 190651
NM_022708	Rn. 78367
NM_053587	Rn. 6703
TC545251	-
XM_340776	Rn. 137767
XM_227339	Rn. 19820
TC566080	-
XM_213253	Rn. 98412
TC561055	-
XM_347064	Rn. 91410
NM_053453	Rn. 1892
NM_012921	Rn. 9282
XM_343373	Rn. 21775
AW921534	Rn. 164417
NM_001005382	Rn. 141980
NM_001013067	Rn. 79264
AW918545	Rn. 170325
XM_214939	Rn. 21391
XM_344947	Rn. 19594
NM_001024273	Rn. 14280
TC524810	-
AB007601	Rn. 13660
AA956502	Rn. 165040
BF290953	Rn. 24673
NM_198729	Rn. 107044
XM_575887	Rn. 7910
XM_225887	Rn. 24687
A_44_P543576	-
XM_342877	Rn. 91778
XM_345218	Rn. 111884
NM_207597	Rn. 120045
TC542264	-
AI045861	Rn. 10526
XM_230530	Rn. 3346
NM_019316	Rn. 10725
TC542702	-
XM_219001	Rn. 22111
XM_218285	-
XM_218772	Rn. 140572
BM388083	Rn. 41133
XM_341550	Rn. 132469
XM_223730	Rn. 125227
XM_342027	Rn. 143854
XM_340943	Rn. 101656
XM_217680	Rn. 139570
NM_001001071	Rn. 143176
ENSRNOT00000042436	-
CO566330	Rn. 137612
XM_340739	Rn. 22842
NM_053962	Rn. 9918
TC522108	-
AB087404	Rn. 127822
XM_573463	Rn. 137612
XM_573983	Rn. 1046
XM_216386	Rn. 33021
AI233877	Rn. 129700

Target Accession	UniGene
AI412542	Rn. 31762
NM_022798	Rn. 48706
NM_024159	Rn. 161784
AI044267	Rn. 19106
NM_012643	Rn. 93200
TC539426	-
XM_577424	-
XM_232748	Rn. 143980
BI282960	Rn. 107358
XM_346122	Rn. 83054
NM_053634	Rn. 48281
XM_343875	-
XM_215707	Rn. 35486
XM_213775	-
TC557397	-
BF557098	Rn. 9434
XM_576406	Rn. 57310
NM_001025680	Rn. 23364
XM_216584	Rn. 43383
NM_012828	Rn. 2808
TC525688	-
NM_199408	Rn. 103639
NM_031684	Rn. 5814
XM_347233	Rn. 19133
NM_019230	Rn. 24231
XM_342575	Rn. 145207
NM_022005	Rn. 839
XM_213523	Rn. 113761
NM_017180	Rn. 40778
AF217588	Rn. 118446
NM_019328	Rn. 88129
NM_173103	Rn. 10339
TC528328	-
NM_012593	Rn. 144553
BF545837	Rn. 98481
NM_001003977	Rn. 141979
TC521008	-
XM_214668	Rn. 163399
XM_578308	-
NM_001013913	Rn. 72489
CF108834	Rn. 140915
XM_574554	Rn. 112669
XM_221354	Rn. 58246
XM_228797	-
ENSRNOT00000004342	-
NM_053785	Rn. 13425
NM_053951	Rn. 81062
XM_343522	-
XM_234579	Rn. 17349
A_44_P278941	-
NM_001011995	Rn. 154526
NM_001013943	Rn. 122663
A_44_P729229	-
ENSRNOT00000049913	-
NM_031010	Rn. 11318
AA875449	Rn. 2923
X55180	Rn. 117936
A_44_P426578	-
NM_001025147	Rn. 139484
NM_013018	Rn. 44409
NM_133559	Rn. 2899
TC527418	-
NM_001009662	Rn. 22066

[0171]

Target Accession	UniGene
XM_228170	Rn. 17643
NM_138547	Rn. 10021
XM_225147	Rn. 1545
NM_017024	Rn. 10481
NM_131906	Rn. 5641
TC522093	-
XM_226066	-
NM_001003404	Rn. 13127
TC568082	-
TC556357	-
TC538568	-
BF556567	Rn. 9251
XM_222564	Rn. 24014
AW917577	Rn. 154616
TC522904	-
NM_030827	Rn. 26430
NM_017149	Rn. 34890
TC541234	-
TC538087	-
X61479	-
NM_012792	Rn. 867
NM_001000217	Rn. 141776
NM_144739	Rn. 7038
NM_024141	Rn. 55542
XM_213687	Rn. 138846
AA944253	Rn. 7704
XM_228462	Rn. 121914
TC540507	-
NM_012507	Rn. 10624
BI286738	Rn. 79194
XM_573943	Rn. 11716
XM_216751	Rn. 2885
XM_346976	-
AA957139	Rn. 9197
XM_578739	Rn. 98325
NM_133296	Rn. 161982
NM_013040	Rn. 10528
NM_012507	Rn. 10624
NM_175766	Rn. 91314
BF548548	Rn. 170224
NM_012653	Rn. 11047
BF551074	Rn. 13180
NM_001000447	Rn. 163012
XM_214992	-
NM_053856	Rn. 11093
XM_224224	-
NM_022293	Rn. 53793
BC078749	Rn. 10326
NM_175578	Rn. 24428
NM_024484	Rn. 97126
AJ224680	Rn. 10733
BE112231	Rn. 20051
NM_017354	Rn. 10075
XM_214918	Rn. 29166
NM_145775	Rn. 29848
NM_001004021	Rn. 102517
XM_214279	Rn. 144136
CB547704	-
XM_219247	-
NM_138826	Rn. 16133
NM_001003404	Rn. 13127
AA955229	Rn. 164955
AW918168	Rn. 17340

Target Accession	UniGene
AW142587	Rn. 9491
NM_022960	Rn. 30018
NM_080394	Rn. 161777
NM_080394	Rn. 161777
NM_138843	Rn. 32263
XM_222564	Rn. 24014
XM_573122	Rn. 148168
BI279326	Rn. 48786
AI763826	Rn. 17349
NM_031971	Rn. 1950
NM_017178	Rn. 90931
TC551459	-
D00634	-
AI170603	Rn. 121465
NM_022215	Rn. 44452
XM_341114	Rn. 25191
BI277629	Rn. 92548
NM_147212	Rn. 86412
AW914057	Rn. 1664
AI170406	-
NM_012543	Rn. 11274
XM_221134	-
NM_021653	Rn. 87549
TC560804	-
XM_226803	Rn. 33787
AI233261	Rn. 2460
TC556438	-
XM_238528	-
NM_031590	Rn. 53991
NM_012767	Rn. 59459

[0172] 対照群と比較してTickling群で1/1.5倍未満の発現を認めた唾液腺(Sg)の遺伝子の「Target Accession」及び「UniGene」を下記表17に示す。

[表17]

Target Accession	UniGene
NM_013003	Rn. 9875
NM_053882	Rn. 97792
NM_053348	Rn. 2464
U70050	Rn. 22459
TC548855	-
XM_213685	-
XM_234661	Rn. 110660
NM_175762	Rn. 10483
XM_234676	Rn. 110661
NM_019331	Rn. 3220
NM_001014274	Rn. 15754
XM_228708	Rn. 106891
NM_017307	Rn. 8368
NM_001004097	Rn. 91492
XM_232716	Rn. 101678
NM_053765	Rn. 18753
NM_080479	Rn. 14890
XM_215963	Rn. 62616
NM_001005879	Rn. 161844
XM_343191	Rn. 61775
XM_575093	Rn. 116833
NM_019303	Rn. 10817
M84148	Rn. 134335
XM_341319	Rn. 35508
NM_031742	Rn. 11071
XM_226732	Rn. 27737
NM_001024257	Rn. 140802
S82585	-
XM_345725	Rn. 8473
XM_216968	Rn. 6606
XM_221867	Rn. 36184
NM_001007645	Rn. 92940
NM_080783	Rn. 29908
XM_345981	Rn. 8891
NM_001024751	Rn. 76073
NM_001014083	Rn. 79019
XM_216398	Rn. 17006
NM_201420	Rn. 16142
XM_344868	-
XM_344708	Rn. 99341
L17080	-
XM_341190	Rn. 20251
XM_243980	Rn. 154650
NM_198731	Rn. 22857
TC541702	-
NM_182844	Rn. 161974
XM_218995	Rn. 73147
XM_220141	Rn. 58278
NM_001025683	Rn. 16921
NM_013132	Rn. 3318
XM_574957	Rn. 145585
NM_001012034	Rn. 4077
XM_233231	Rn. 23812
XM_574210	Rn. 24402
NM_012615	Rn. 874
NM_013186	Rn. 26724
NM_001002802	Rn. 38581
TC529126	-
XM_218816	Rn. 41796
NM_198749	Rn. 24234
XM_341691	-

Target Accession	UniGene
XM_342531	Rn. 8735
XM_237514	Rn. 162282
XM_237538	-
AF468681	-
XM_230278	Rn. 34843
XM_341519	Rn. 48738
NM_012820	Rn. 6215
NM_173136	Rn. 23676
NM_012820	Rn. 6215
NM_212466	Rn. 109148
AI136348	Rn. 13826
XM_342486	Rn. 35496
XM_340798	Rn. 79891
NM_001024267	Rn. 162344
XM_234810	Rn. 127912
NM_173114	Rn. 127830
TC554663	-
XM_215922	Rn. 20824
XM_341808	Rn. 91353
NM_001008334	Rn. 20057
XM_215359	-
NM_138912	Rn. 30046
XM_218497	-
CA509211	Rn. 3517
XM_343968	Rn. 49607
AI575641	Rn. 26749
NM_145096	Rn. 17310
XM_235478	Rn. 161994
NM_019161	Rn. 145674
TC527103	-
BI295768	Rn. 98178
NM_001025688	Rn. 24602
NM_001000188	Rn. 141814
BF289560	Rn. 42977
NM_001024240	Rn. 19595
XM_342493	Rn. 44656
XM_575775	Rn. 23267
AW144454	Rn. 167718
NM_020091	Rn. 48676
NM_001009430	Rn. 13471
A_44_P951632	-
XM_342668	Rn. 154705
AA926058	-
TC547897	-
AI639532	Rn. 43529
NM_080479	Rn. 14890
TC538578	-
BQ198977	Rn. 117926
NM_138887	Rn. 3201
XM_228452	Rn. 141102
NM_175582	Rn. 22987
BE110753	Rn. 22382
NM_175582	Rn. 22987
XM_215767	Rn. 47550
XM_343911	Rn. 72525
NM_031796	Rn. 30048
NM_138904	Rn. 10202
XM_220114	-
NM_001005562	Rn. 24541
NM_145786	Rn. 45119
NM_001024345	Rn. 17580

[0173]

Target Accession	UniGene
TC536419	-
XM_238325	Rn. 101794
NM_052809	Rn. 2589
NM_017302	Rn. 10524
BM387057	Rn. 166955
XM_240417	Rn. 12785
XM_342391	Rn. 6975
NM_214825	Rn. 142200
XM_235261	Rn. 17834
AA997357	Rn. 127118
XM_232197	Rn. 7350
NM_001012082	Rn. 162630
XM_345725	Rn. 8473
XM_214185	-
BF402596	Rn. 171386
XM_227167	-
XM_233002	Rn. 37934
X78689	Rn. 24569
NM_053685	Rn. 48801
ENSRNOT00000037995	-
CA508578	Rn. 116386
NM_031238	Rn. 5909
XM_226874	Rn. 20775
A_44_P400591	-
NM_030873	Rn. 17153
BF290374	Rn. 118522
AW916533	Rn. 118522
NM_021860	Rn. 138118
NM_017212	Rn. 2455
NM_031565	Rn. 161717
NM_013111	Rn. 9439
TC559328	-
NM_013131	Rn. 9678
NM_017212	Rn. 2455
BF287625	Rn. 6762
TC549528	-
NM_001014125	Rn. 162053
XM_214553	Rn. 163386
TC523891	-
XM_224322	Rn. 150631
XM_216800	Rn. 968
AA965220	Rn. 2460
XM_342688	Rn. 161004
AY724517	Rn. 6866
XM_219346	Rn. 32501
A_44_P713490	-
XM_342293	Rn. 136919
AA996470	Rn. 138055
TC554294	-
XM_235609	Rn. 86665
BM391734	Rn. 11875
CA506323	Rn. 3327
XM_575546	Rn. 92527
BF559342	Rn. 23138
XM_221941	Rn. 20495
XM_575888	Rn. 59706
NM_001014081	Rn. 10956
XM_234741	-
NM_001012068	Rn. 22945
XM_243040	Rn. 99876
XM_220629	Rn. 141184
BE110339	Rn. 16928
NM_172333	Rn. 9468

Target Accession	UniGene
XM_343554	Rn. 857
NM_021744	-
XM_224853	Rn. 8484
AW917167	Rn. 18668
NM_013057	Rn. 9980
NM_057201	Rn. 28035
L42293	-
TC555084	-
BC094306	Rn. 154429
XM_225016	Rn. 59630
TC539429	-
NM_001004215	Rn. 144176
NM_173126	Rn. 8865
TC533697	-
XM_344373	-
CO386096	Rn. 25499
NR_002149	-
NM_173114	Rn. 127830
BF558512	Rn. 166248
BQ211607	Rn. 9246
XM_215659	Rn. 162614
XM_223905	-
BE103448	Rn. 137820
NM_001013219	Rn. 104514
NM_053744	Rn. 14547
XM_344059	-
NM_153724	Rn. 12942
NM_012973	Rn. 9734
NM_017297	Rn. 10047
XM_573320	Rn. 163185
TC543345	-
XM_576118	-
NM_019265	Rn. 30023
L07410	Rn. 117938
NM_176074	Rn. 16145
NM_019168	Rn. 11055
CA508578	Rn. 116386
NM_198733	Rn. 38261
BF411962	Rn. 164850
AA924327	Rn. 164850
BF391573	Rn. 39092
NM_012774	Rn. 9717
XM_343599	Rn. 776
NM_001008776	Rn. 7875
XM_340966	Rn. 2895
BQ209232	Rn. 37805
AW520826	-
BM392235	Rn. 105040
TC555358	-
NM_133622	Rn. 9752
NM_201418	Rn. 7233
NM_183403	Rn. 3503
NM_031598	Rn. 11346
XM_230773	Rn. 162716
NM_012723	Rn. 54456
XM_340769	Rn. 59746
NM_001011944	Rn. 138019
NM_053591	Rn. 6051
TC540316	-
XM_343414	Rn. 53443
XM_580199	-
Z93354	Rn. 179369
AW920845	Rn. 145122

[0174]

Target Accession	UniGene
A_44_P309523	-
AW142807	Rn. 22959
XM_230807	Rn. 55931
XM_236560	Rn. 18668
AW144011	Rn. 166761
XM_342669	Rn. 91492
A_44_P267185	-
XM_225599	-
M12822	-
L22655	Rn. 117926
XM_341782	Rn. 138370
XM_233196	Rn. 96284
NM_022284	Rn. 97593
XM_575534	-
XM_231381	Rn. 136960
NM_021751	Rn. 144589
BU760219	Rn. 129
NM_031697	Rn. 44390
NM_031688	Rn. 2883
NM_001025740	Rn. 144946
TC557065	-
BG373526	Rn. 99508
AA955151	Rn. 55275
NM_019131	Rn. 87540
XM_340773	Rn. 94890
XM_341201	Rn. 24569
NM_001024743	Rn. 3415
NM_171991	Rn. 9232
NM_001014041	Rn. 162620
BF401675	Rn. 10721
XM_231999	-
XM_343745	-
XM_345752	Rn. 112186
XM_343646	-
XM_343690	Rn. 124726
Z93368	Rn. 110663
XM_576693	-
TC540819	-
NM_017353	Rn. 32261
AA891889	Rn. 85462
XM_234332	Rn. 35024
XM_345756	Rn. 126669
AI102819	Rn. 164286
AI010642	Rn. 17603
XM_234749	-
AW914888	Rn. 165522
XM_340999	Rn. 98672
M58040	Rn. 98672
NM_207586	Rn. 43692
XM_575540	Rn. 117940
BF560887	Rn. 175369
AI230431	Rn. 163588
L07402	Rn. 119901
ENSRNOT00000043097	-
XM_341675	-
NM_024362	Rn. 14532
AA956465	Rn. 165038
NM_172047	Rn. 20681
XM_230513	Rn. 17049
NM_001013137	Rn. 3130
TC543281	-
AI009597	Rn. 3896
AI043862	Rn. 3130

Target Accession	UniGene
NM_001024345	Rn. 17580
XM_234680	Rn. 134951
NM_133551	Rn. 10162
TC560122	-
XM_224098	Rn. 124444
XM_340984	Rn. 138774
CB547594	Rn. 6408
XM_226545	Rn. 8884
XM_215924	Rn. 3102
NM_001008882	Rn. 54318
XM_214861	-
XM_224987	Rn. 163333
NM_134432	Rn. 6319
NM_171991	Rn. 9232
CA510548	Rn. 28387
XM_237190	-
NM_031118	Rn. 59
XM_215624	-
NM_031747	Rn. 31788
XM_215562	Rn. 7854
NM_012760	Rn. 6977
AI412958	Rn. 106916
ENSRNOT00000037223	-
AB072614	-
NM_001014235	Rn. 140721
BE116009	Rn. 22987
TC521549	-
BF388415	Rn. 39181
XM_343189	Rn. 99508
NM_001017500	Rn. 29370
XM_345494	-
XM_227391	-
CA508891	Rn. 17734
TC560609	-
TC555778	-
NM_001013232	Rn. 111376
CB547706	-
BG668242	Rn. 55482
XM_575600	Rn. 2931
XM_213211	Rn. 17380
XM_214143	Rn. 38497
NM_017204	Rn. 37490
XM_226094	-
NM_199406	Rn. 162547
U39609	Rn. 82721
XM_225667	Rn. 8206
TC524618	-
TC557658	-
NM_001000062	Rn. 143341
NM_021664	Rn. 41640
NM_001025740	Rn. 144946
NM_183333	Rn. 162014
NM_080698	Rn. 8778
XM_219490	Rn. 41707
XM_573321	Rn. 114048
NM_012596	Rn. 9891
XM_231042	Rn. 162651
AI501919	Rn. 167908
NM_001008890	Rn. 36966
AA819918	Rn. 1836
XM_230592	Rn. 46791
XM_342323	-
NM_019292	Rn. 1647

[0175]

Target Accession	UniGene
XM_213329	Rn. 801
NM_013080	Rn. 10088
XM_346293	-
AA925099	Rn. 55127
NM_031022	Rn. 10381
S79307	-
NM_022931	Rn. 54466
NM_013122	Rn. 6813
NM_177929	Rn. 64427
XM_234755	-
XM_343841	Rn. 101173
XM_230036	Rn. 162666
M12981	-
XM_233016	Rn. 25240
BE117446	Rn. 169246
NM_001014264	Rn. 102149
XM_342055	Rn. 1645
NM_001009632	Rn. 1040
NM_032616	Rn. 48696
NM_001005383	Rn. 3679
NM_012870	-
XM_237514	Rn. 162282
TC539775	-
M61884	Rn. 126981
XM_236411	Rn. 162989
XM_344882	-
NM_138533	Rn. 6699
XM_575518	Rn. 117928
XM_213313	-
XM_216376	-
AW142608	Rn. 7792
AA858448	Rn. 10346
XM_234830	-
XM_347322	Rn. 21421
XM_213329	Rn. 801
BE117300	Rn. 165611
L26525	-
BQ196242	Rn. 8285
NM_153625	Rn. 15381
XM_574212	Rn. 111615
TC543048	-
TC539270	-
X59864	-
NM_017131	Rn. 10111
NM_147211	Rn. 11272
XM_217195	Rn. 57528
NM_012545	Rn. 11064
NM_012729	Rn. 1584
AY580165	Rn. 3679
NM_134349	Rn. 2580
AA894304	Rn. 112831
NM_031640	Rn. 17112
XM_573320	Rn. 163185
NM_133295	Rn. 2549
NM_019905	Rn. 90546
TC541438	-
AI102812	Rn. 166955
XM_213639	Rn. 23475
NM_212541	Rn. 27480
XM_223905	-
BG670971	-
XM_235261	Rn. 17834
NM_001012018	Rn. 143976

Target Accession	UniGene
U06230	Rn. 2888
NM_001010970	Rn. 116361
XM_345278	Rn. 67070
XM_238028	Rn. 162301
L07408	Rn. 117930
NM_053601	Rn. 5785
AW143134	Rn. 7530
XM_216539	Rn. 93581
AF217591	Rn. 134336
NM_057188	Rn. 3862
NM_052808	Rn. 9766
TC548591	-
ENSRNOT00000017568	-
CB546243	Rn. 179609
TC521964	-
XM_214861	-
NM_057187	Rn. 26894
NM_013002	Rn. 9736
AW916327	Rn. 14770
NM_001005540	Rn. 12833
NM_033234	Rn. 36966
L17078	Rn. 92371
AI013718	-
NM_001013853	Rn. 163132
XM_218173	Rn. 99310

[0176]

Target Accession	UniGene
NM_031520	Rn. 98166
NM_012820	Rn. 6215
BF524215	Rn. 161403
NM_022519	Rn. 1419
M62828	Rn. 179389
AW144240	Rn. 107412
NM_021744	-
NM_139087	Rn. 31842
BQ195755	Rn. 94102
TC524058	-
NM_001013180	Rn. 30648
AF217587	Rn. 179370
NM_019161	Rn. 145674
NM_199082	-
NM_001004236	Rn. 33830
AI178495	Rn. 165523
XM_215892	Rn. 162713
XM_236351	Rn. 147874
NM_053472	Rn. 7214
NM_130425	Rn. 34220
NM_001025683	Rn. 16921
L10326	Rn. 31
BG665180	-
CB544349	Rn. 162680
NM_203337	Rn. 24125
U75411	-
XM_217166	-
NM_022926	Rn. 144577
XM_215751	Rn. 8642
XM_222157	Rn. 47918
XM_342764	Rn. 77935
XM_215751	Rn. 8642
AW144181	Rn. 2723
NM_001007729	Rn. 6800
XM_342764	Rn. 77935
XM_214055	-
XM_238285	-
NM_130742	Rn. 60224
BQ200884	Rn. 11349
NM_080775	Rn. 9925
NM_001025041	Rn. 162656
A_44_P950925	-
NM_012608	Rn. 33598
XM_573030	Rn. 94969
NM_012820	Rn. 6215
NM_031623	Rn. 30028
L22655	Rn. 117926
TC531031	-
BF556210	Rn. 11709
NM_001024743	Rn. 3415
BC091425	Rn. 8110
TC538655	-
TC554985	-
NM_001017479	Rn. 18850
NM_001024345	Rn. 17580
XM_221623	Rn. 162007
NM_013097	Rn. 6077
TC539049	-
XM_215963	Rn. 62616
XM_226060	Rn. 107191
TC525800	-
NM_138840	Rn. 11349
NM_138840	Rn. 11349

[0177] Light Touch群と比較してTickling群で1.5倍超の発現を認めた唾液腺(Sg)の遺伝子の「Target Accession」及び「UniGene」を下記表18に示す。

[表18]

Target Accession	UniGene
BI275926	Rn. 5789
TC555518	–
AW917961	Rn. 30788
XM_233490	Rn. 41400
NM_052808	Rn. 9766
AW916363	Rn. 1961
BQ207606	Rn. 136636
XM_341806	–
AI407991	–
NM_139328	–
XM_343001	Rn. 57800
TC555071	–
XM_347125	Rn. 140709
NM_080477	Rn. 44844
NM_001011984	Rn. 98677
BF415117	Rn. 2635
BQ200021	Rn. 98708
XM_341702	Rn. 144207
XM_573100	Rn. 93735
NM_019174	Rn. 51389
NM_019239	Rn. 9803
NM_053801	Rn. 46850
AA859335	Rn. 4035
BF547206	Rn. 12810
BI288013	Rn. 40911
CA508481	Rn. 91523
A_44_P644091	–
BQ192480	Rn. 8959
TC519989	–
U67915	Rn. 10698
BQ203768	Rn. 16646
NM_001024769	Rn. 162332
TC556613	–
BF392782	Rn. 160959
XM_573948	Rn. 102309
BQ206540	Rn. 20866
AJ006522	Rn. 145553
NM_001011903	Rn. 144004
XM_213964	Rn. 41748
XM_226334	Rn. 22363
AA818541	Rn. 101713
XM_578982	–
NM_001008558	Rn. 3096
XM_217648	Rn. 148012
NM_017179	Rn. 10710
XM_219683	–
TC540103	–
NM_053769	Rn. 98260
TC538904	–
NM_001012459	Rn. 162423
NM_017102	Rn. 95055
AI072569	Rn. 166533
XM_227605	Rn. 162628
XM_344971	Rn. 8618
XM_345751	–
XM_225280	–
NM_053788	Rn. 9943
XM_239336	Rn. 17949
XM_342219	Rn. 10700
AI600124	Rn. 1696
XM_342127	Rn. 137452

Target Accession	UniGene
TC556681	–
TC543536	–
BG673169	–
BQ529285	–
XM_230955	Rn. 161879
TC554028	–
TC558499	–
NM_170718	–
NM_020084	Rn. 48680
NM_001009690	Rn. 145021
AA924847	Rn. 9470
BM383380	Rn. 11404
BF417010	Rn. 23448
NM_001013941	Rn. 161900
NM_001008514	Rn. 106342
A_44_P452570	–
BG672648	–
BF549735	Rn. 38972
X72758	–
NM_053289	Rn. 9727
ENSRNOT00000028551	–
TC525892	–
XM_344039	Rn. 39369
NM_031817	Rn. 30124
NM_001001024	Rn. 141892
TC559298	–
NM_001000257	Rn. 141686
NM_017074	Rn. 3881
XM_228059	–
XM_216459	Rn. 61954
BF402400	Rn. 59637
AI235576	Rn. 128814
BQ211578	Rn. 21009
TC523387	–
AI233208	Rn. 14584
NM_053630	Rn. 30035
TC551900	–
TC544315	–
NM_022199	Rn. 44407
BI277629	Rn. 92548
NM_147212	Rn. 86412
AI233261	Rn. 2460
BQ194469	Rn. 161764
TC550302	–
AW914894	Rn. 10267
CB545613	Rn. 179591
XM_238528	–

[0178]

Target Accession	UniGene
AI171692	Rn. 110564
XM_342204	Rn. 45065
BG381647	Rn. 26832
NM_001014042	Rn. 139442
BF290303	Rn. 3602
ENSRNOT00000038976	-
NM_019292	Rn. 1647
NM_001010970	Rn. 116361
BC086330	Rn. 155340
XM_341392	Rn. 19511
AI228422	Rn. 14665
XM_345278	Rn. 67070
NM_130822	Rn. 17279
XM_342323	-
NM_053601	Rn. 5785
L07408	Rn. 117930
XM_238028	Rn. 162301
AF217591	Rn. 134336
XM_573382	-
XM_215660	Rn. 44158
TC551373	-
XM_575511	Rn. 117923
NM_012596	Rn. 9891
XM_216539	Rn. 93581
XM_341973	-
NM_020073	Rn. 48025
CB545830	Rn. 157214
XM_233562	-
XM_346023	-
NM_139325	Rn. 10828
NM_080411	Rn. 63075
NM_053738	Rn. 74256
TC559056	-
TC522904	-
NM_053504	Rn. 86653
NM_080770	Rn. 144559
TC563058	-
AI169615	Rn. 162275
AA891661	Rn. 1618
XM_236477	Rn. 107533
TC545913	-
BF556255	Rn. 175161
XM_227454	Rn. 103871
XM_345584	Rn. 74081
BF283584	Rn. 160119
NM_001013944	Rn. 122003
AI763958	Rn. 168679
XM_341012	-
AW142782	Rn. 43391
NM_013107	Rn. 40476
NM_145775	Rn. 29848
A_44_P875993	-
BF390586	Rn. 41897
XM_347101	Rn. 15978
A_44_P210507	-
AW918267	Rn. 55264
TC556031	-
TC525755	-
NM_032063	Rn. 10628
NM_173097	Rn. 9729
NM_153732	Rn. 64641
M87788	Rn. 118336
AI101197	Rn. 166995

[0179] Light Touch群と比較してTickling群で1/1.5倍未満の発現を認めた唾液腺(Sg)の遺伝子の「Target Accession」及び「UniGene」を下記表19に示す。

[表19]

Target Accession	UniGene
XM_575518	Rn. 117928
NM_147141	Rn. 85880
XM_234830	-
TC560753	-
NM_207586	Rn. 43692
TC524768	-
AA891889	Rn. 85462
XM_234676	Rn. 110661
XM_234332	Rn. 35024
XM_345756	Rn. 126669
XM_344882	-
NM_001014264	Rn. 102149
XM_234755	-
XM_343841	Rn. 101173
AI102819	Rn. 164286
AI010642	Rn. 17603
XM_234749	-
XM_343745	-
XM_345752	Rn. 112186
XM_343646	-
XM_343690	Rn. 124726
Z93368	Rn. 110663
BG666908	Rn. 1695
XM_233470	Rn. 162830
BI300279	Rn. 167449
XM_231999	-
NM_001000482	Rn. 143462
XM_216071	Rn. 129992
M58040	Rn. 98672
AW914888	Rn. 165522
XM_340999	Rn. 98672
AA943135	Rn. 160939
XM_575540	Rn. 117940
XM_230278	Rn. 34843
XM_218497	-
NM_013122	Rn. 6813
NM_053348	Rn. 2464
XM_575093	Rn. 116833
NM_019303	Rn. 10817
M84148	Rn. 134335
NM_021860	Rn. 138118
NM_013080	Rn. 10088
L17078	Rn. 92371
XM_234661	Rn. 110660
XM_232716	Rn. 101678
XM_347322	Rn. 21421
TC548855	-
BC086388	Rn. 14694
BF401675	Rn. 10721
XM_343695	-
XM_346121	-
NM_139115	Rn. 28432
BF550562	Rn. 120440
XM_345745	Rn. 112181
BE116076	Rn. 16973
CA504956	Rn. 98209
XM_340912	Rn. 44271
NM_019331	Rn. 3220
AY724517	Rn. 6866
XM_219346	Rn. 32501
A_44_P713490	-
XM_342293	Rn. 136919
XM_235609	Rn. 86665
AA848453	Rn. 2

Target Accession	UniGene
XM_345850	Rn. 19092
XM_236268	Rn. 20269
NM_001004201	Rn. 26693
NM_019329	Rn. 10043
NM_053822	Rn. 31839
TC539270	-
TC543894	-
NM_001014145	Rn. 146844
TC528464	-
TC527116	-
TC543675	-
BG376309	Rn. 6873
BF287768	Rn. 17793
NM_012945	Rn. 10148
NM_178103	Rn. 50065
AI104291	Rn. 1668
TC545358	-
XM_345746	-
BF288445	Rn. 4108
AW914018	Rn. 155069
TC522641	-
BC092624	Rn. 163825
AA957713	Rn. 1880
A_44_P531925	-
BF560128	Rn. 28431
ENSRNOT00000029763	-
AY325227	-
XM_217851	Rn. 143821
XM_230519	Rn. 20545
XM_574921	Rn. 13649
XM_234928	Rn. 12319
NM_031091	Rn. 3788
BG665385	-
XM_231157	Rn. 61607
NM_001007615	Rn. 163194
XM_218173	Rn. 99310
AI178665	Rn. 58356
NM_022215	Rn. 44452
AABR03057162	-

[0180]

Target Accession	UniGene
BF416744	Rn. 173768
XM_576959	Rn. 141110
BG672591	Rn. 32103
XM_220549	-
TC531846	-
XM_240734	Rn. 6819
NM_001014190	Rn. 161029
XM_234272	Rn. 96357
XM_226262	Rn. 140808
NM_022925	Rn. 30011
BF560887	Rn. 175369
XM_341675	-
AI230431	Rn. 163588
L07402	Rn. 119901
XM_347119	Rn. 121539
ENSRNOT00000046211	-
XM_234781	Rn. 104989
XM_223808	Rn. 46995
XM_221874	Rn. 6774
XM_345273	Rn. 15953
XM_345708	-
XM_214696	Rn. 69429
S81289	-
TC561351	-
AI104253	Rn. 155385
AW533905	Rn. 113868
AA956465	Rn. 165038
NM_001014081	Rn. 10956
XM_234741	-
XM_342749	Rn. 162784
A_44_P951089	-
XM_341043	-
TC541564	-
BF559590	Rn. 175298
AI171778	Rn. 49088
CA504571	Rn. 16806
XM_577777	Rn. 160773
TC527654	-
BF553260	Rn. 174985
BM387035	Rn. 146373
AI230614	Rn. 8925
NM_022213	Rn. 44448
TC545016	-
XM_342968	Rn. 134593
TC545343	-
TC519270	-
A_44_P715612	-
NM_053727	Rn. 54147
AA817948	Rn. 29157
TC567885	-
BE098157	Rn. 16844
NM_024362	Rn. 14532
XM_216005	Rn. 27698
BQ191078	Rn. 17106
ENSRNOT00000043097	-
AA924012	Rn. 23232
XM_232928	-
XM_345745	Rn. 112181
BF556558	Rn. 12210
XM_215932	Rn. 40998
BX883048	-
AA944455	Rn. 3775
AI549412	Rn. 108143

[0181] 対照群と比較してTickling群で2.0倍超の発現を認めた末梢血液(BI)の遺伝

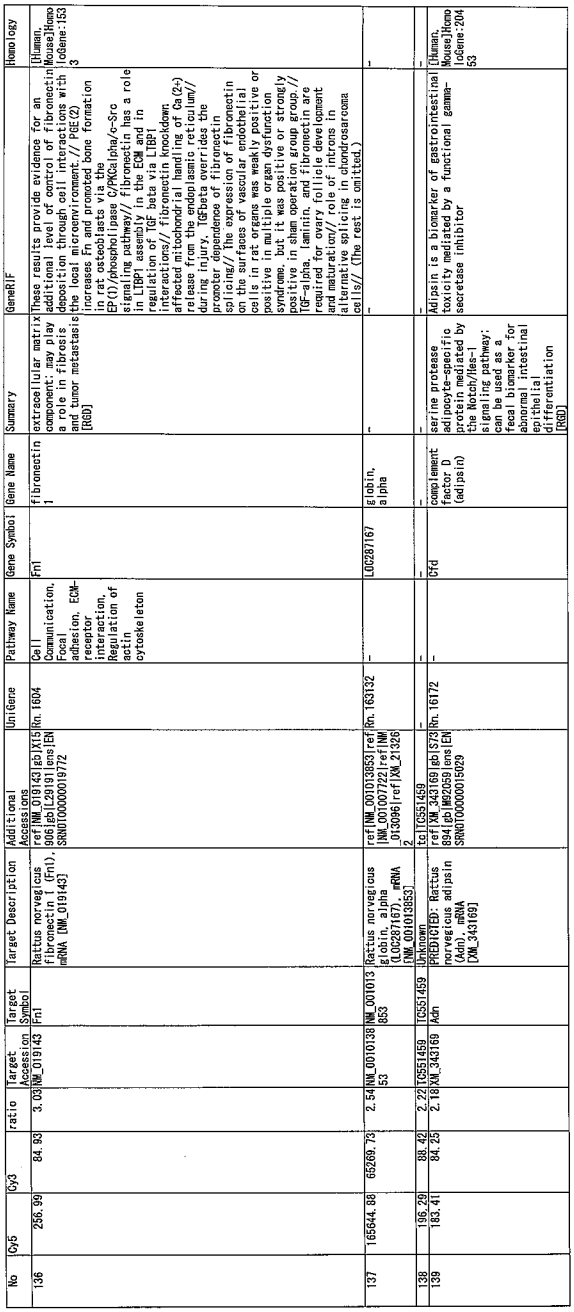
子のアノテーションを下記表20に示す。

[表20]

表20 T-B1(Cy5) v.s. C-B1(Cy3) :up regulation(Cy5>Cy3)

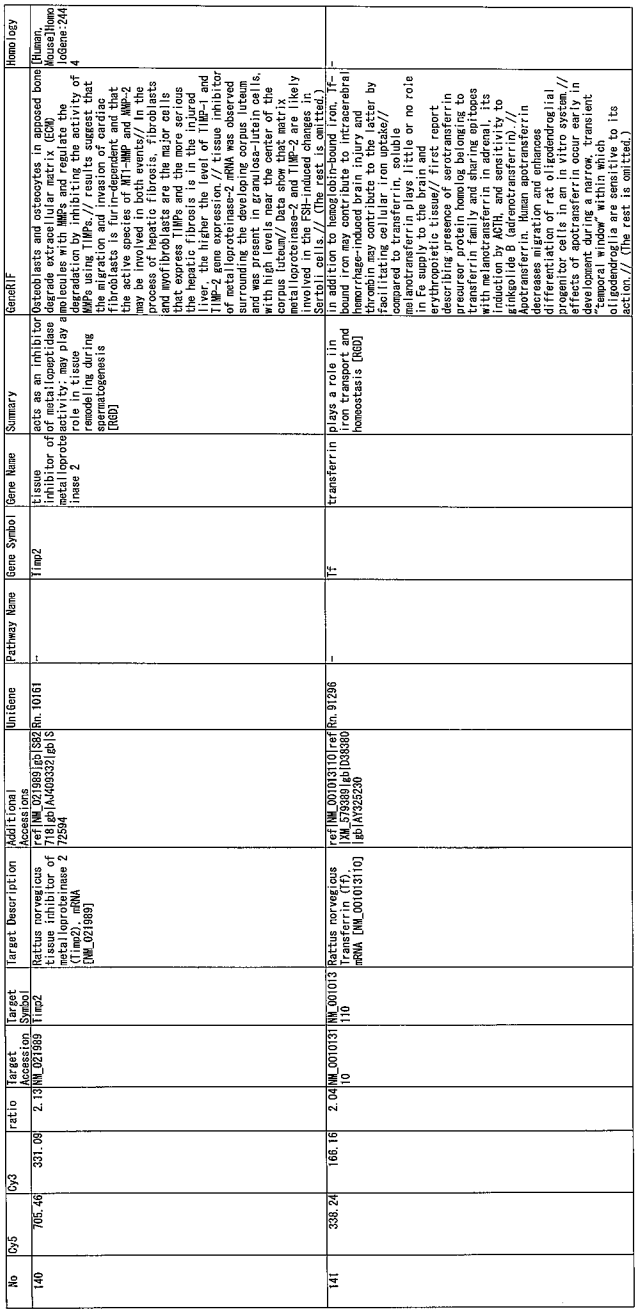
No	Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Pathway Name	Gene Symbol	Gene Name	Summary	GeneRIF	Homology
133	1067.38	180.53	5.63	NM_053372	Slpi	Rattus norvegicus secretory leukocyte peptidase inhibitor (Slpi), mRNA [NM_053372]	ref|NM_053372|gb|AF424377|gb|AF151982|tc|TC105770|2	Rn.18560	-	Slpi	secretory leukocyte peptidase inhibitor	suppresses the inflammation and joint damage caused by bacterial cell wall-induced arthritis [RGD]	SLPI inhibition of NF-kappaB activation is mediated, in part, by competitive binding (blocking p65 binding) to the NF-kappaB consensus-binding site.// plays an important role in controlling excessive proteolysis and inflammation during a critical phase of early pregnancy.// the ischemia-induced expression of SLPI might play a neuroprotective role in focal stroke, possibly because of rapid inhibition of activated proteases and its suppression in inflammatory response.// REVIEW: Endogenous generation of IL- 10 and IL- 13 as well as secretory leukocyte protease inhibitor (SLPI), significantly regulates the inflammatory response	[Human, Mouse]Homologene:2305
134	406.86	96.66	4.21	NM_053372	Slpi	Rattus norvegicus secretory leukocyte peptidase inhibitor (Slpi), mRNA [NM_053372]	ref|NM_053372|gb|AF424377|gb|AF151982|tc|TC105770|2	Rn.18560	-	Slpi	secretory leukocyte peptidase inhibitor	suppresses the inflammation and joint damage caused by bacterial cell wall-induced arthritis [RGD]	SLPI inhibition of NF-kappaB activation is mediated, in part, by competitive binding (blocking p65 binding) to the NF-kappaB consensus-binding site.// plays an important role in controlling excessive proteolysis and inflammation during a critical phase of early pregnancy.// the ischemia-induced expression of SLPI might play a neuroprotective role in focal stroke, possibly because of rapid inhibition of activated proteases and its suppression in inflammatory response.// REVIEW: Endogenous generation of IL- 10 and IL- 13 as well as secretory leukocyte protease inhibitor (SLPI), significantly regulates the inflammatory response	[Human, Mouse]Homologene:2305
135	276.13	89.28	3.09	XM_215940	LOC296356	PREDICTED: Rattus norvegicus similar to secretory leukocyte protease inhibitor (LOC296356), mRNA [XM_215940]	ref|XM_215940	Rn.144651	-	RGD1563818_predicted	similar to secretory leukocyte protease inhibitor (predicted)	-	-	-

[0182]



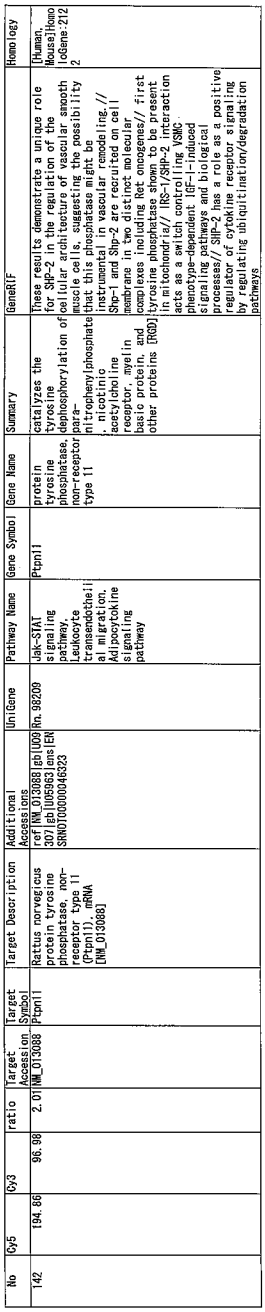
No	Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Pathway Name	Gene Symbol	Gene Name	Summary	GeneRIF	Homology
136	256.99	84.93	3.03	NM_019143	Fn1	Rattus norvegicus fibronectin 1 (Fn1), mRNA [NM_019143]	ref|NM_019143|gb|X15906|gb|L29191|ens|ENSRNOT00000019772	Rn.1604	Cell Communication, Focal adhesion, ECM-receptor interaction, Regulation of actin cytoskeleton	Fn1	fibronectin 1	extracellular matrix component: may play a role in fibrosis and tumor metastasis [RGD]	These results provide evidence for an additional level of control of fibronectin deposition through cell interactions with the local microenvironment.// PGE(2) increases osteoblast bone formation in part via the Ptsr2 subtype of the EP(1)/phospholipase C/PKCalpha/c-Src signaling pathway// fibronectin has a role in LTBP1 assembly in the ECM and in regulation of TGF beta via LTBP1 interactions// fibronectin knockdown affected mitochondrial handling of Ca(2+) release from the endoplasmic reticulum// during injury, TGFbeta overrides the promoter dependence of fibronectin splicing// The expression of fibronectin on the surfaces of vascular endothelial cells in rat corpora was markedly positive or positive in multiple organ dysfunction syndrome, but it was positive or strongly positive in sham operation group group.// TGF-alpha, laminin, and fibronectin are required for ovary follicle development and maturation// role of introns in alternative splicing in chondrosarcoma cells// (The rest is omitted.)	[Human, Mouse]Homologene:1533
137	165644.88	65269.73	2.54	NM_001013853	Fn1	Rattus norvegicus globin, alpha (LOC287167), mRNA [NM_001013853]	ref|NM_001013853|ref|NM_001007721|ref|NM_013096|ref|XM_213261	Rn.163132	-	LOC287167	globin, alpha 2	-	-	-
138	196.20	88.42	2.22	TC551459	TC551459	Unknown	tc|TC551459	-	-	-	-	-	-	-
139	183.41	84.25	2.18	XM_343169	Adn	PREDICTED: Rattus norvegicus adipsin (Adn), mRNA [XM_343169]	ref|XM_343169|gb|S73894|gb|M92059|ens|ENSRNOT00000015029	Rn.16172	-	Cfd	complement factor D (adipsin)	serine protease adipocyte-specific protein mediated by the Notch/Hes-1 signaling pathway: can be used as a fecal biomarker for abnormal intestinal epithelial differentiation [RGD]	Adipsin is a biomarker of gastrointestinal toxicity mediated by a functional gamma-secretase inhibitor	[Human, Mouse]Homologene:20453

[0183]



No	Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Pathway Name	Gene Symbol	Gene Name	Summary	GeneRIF	Homology
140	705.46	331.09	2.13	NM_021989	Timp2	Rattus norvegicus tissue inhibitor of metalloproteinase 2 (Timp2), mRNA [NM_021989]	ref|NM_021989|gb|S82718|gb|AA043532|gb|S72594	Rn.10161	--	Timp2	tissue inhibitor of metalloproteinase 2	acts as an inhibitor of metalloproteinase activity and as a cell growth factor; may play a role in tissue remodeling during spermatogenesis [RGD]	Osteoblasts and osteocytes in apposed bone degrade extracellular matrix (ECM) mediated with MMPs and results in the degradation by inhibiting the activity of MMPs using TIMPs.// results suggest that the migration and invasion of cardiac fibroblasts is furin-dependent and that the active species of MT1-MMP and MMP-2 may be involved in both events// In the process of hepatic fibrosis, fibroblasts and myofibroblasts are the major cells that express TIMPs and the more serious the hepatic fibrosis is in the injured liver, the higher the level of TIMP-1 and TIMP-2 expression// tissue inhibitor of metalloproteinase-2 mRNA was observed surrounding the developing corpus luteum and was present in granulosa-lutein cells, with high levels near the center of the corpus luteum// Data show that matrix metalloproteinase-2 and TIMP-2 are likely involved in the FSH-induced changes in Sertoli cells.// (The rest is omitted.)	[Human, Mouse]Homo (Gene:24 4
141	338.24	166.16	2.04	NM_001013110	Tf	Rattus norvegicus Transferrin (Tf), mRNA [NM_001013110]	ref|NM_001013110|ref|XM_573089|gb|D38380|gb|AY325230	Rn.91296	-	Tf	transferrin	plays a role in iron transport and homeostasis [RGD]	in addition to hemoglobin-bound iron. Tf-bound iron may contribute to intracerebral hemorrhage-induced brain injury and thrombin may contribute to the latter by facilitating cellular iron uptake// compared to transferrin, soluble melanotransferrin plays little or no role in Fe supply to the brain and erythropoietic tissue// first report describing presence of serotransferrin precursor protein homolog belonging to transferrin family and sharing epitopes with melanotransferrin in adrenal. Its induction by ACTH, and sensitivity to galactosyl & N-acetylgalactosaminyl// Melanotransferrin/human p97/ferrin decreases migration and enhances differentiation of rat oligodendroglial progenitor cells in an in vitro system.// effects of apotransferrin occur early in development during a narrow, transient "temporal window" within which oligodendroglia are sensitive to its action.// (The rest is omitted.)	-

[0184]



No	Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Pathway Name	Gene Symbol	Gene Name	Summary	GeneRIF	Homology
142	194.86	96.98	2.01	NM_013088	Ptpn11	Rattus norvegicus protein tyrosine phosphatase, non-receptor type 11 (Ptpn11), mRNA [NM_013088]	ref|NM_013088|gb|U00738|RATSHPTPA|U06863|emb|CAA48323 SRN0700000046323	Rn.98209	Jak-STAT signaling pathway// Leukocyte transendothelial migration// Adipocytokine signaling pathway	Ptpn11	protein tyrosine phosphatase, non-receptor type 11	catalyzes the dephosphorylation of para-nitrophenylphosphate, nicotinic acetylcholine receptor, myelin basic protein, and other proteins [RGD]	These results demonstrate a unique role for SHP-2 in the regulation of the vascular architecture of vascular smooth muscle cells, suggesting the possibility that this phosphatase might be instrumental in vascular remodeling.// Shp-1 and Shp-2 are recruited on cell membrane in two distinct molecular complexes including Ret oncogenes// first tyrosine phosphatase shown to be present in mitochondria// IRS-1/SHP-2 interaction acts as a switch controlling VSMC phenotype-dependent IGF-1-induced signaling pathway and biological processes// SHP-2 has a role as a positive regulator of cytokine receptor signaling by regulating ubiquitination/degradation pathways	[Human; Mouse]Homologene:2122

[0185] 対照群と比較してTickling群で0.5倍未満の発現を認めた末梢血液(BI)の遺伝子のアノテーションを下記表21に示す。

[表21]

表21 T-BI(Cy5) v.s. O-BI(Cy3) :down regulation(Cy5<Cy3)

No	Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Pathway Name	Gene Symbol	Gene Name	Summary	GeneRIF	Homology
143	105.31	223.94	0.47	XM_233230	LOC298270	PREDICTED: Rattus norvegicus similar to 60S ribosomal protein L9 (LOC298270), mRNA [XM_233230]	ref|XM_233230	Rn.162076	-	RGD1561395_predicted	similar to 60S ribosomal protein L9 (predicted)	-	-	-
144	100.27	210.48	0.48	XM_238058	LOC292088	PREDICTED: Rattus norvegicus hypothetical LOC292088 (LOC292088), mRNA [XM_238058]	ref|XM_238058	-	-	RGD1563459_predicted	RGD1563459 (predicted)	-	-	-

[0186] Light Touch群と比較してTickling群で2.0倍超の発現を認めた末梢血液(BI)の遺伝子のアノテーションを下記表22に示す。

[表22]

表22 T-BI (Cy5) v.s. L-BI (Cy3) :up regulation(Cy5>Cy3)

No	Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	Unigene	Pathway Name	Gene Symbol	Gene Name	Summary	GeneRIF	Homology
62	404614.83	65276.98	6.20	NM_001013853	NM_001013853	Rattus norvegicus globin, alpha (LOC287167), mRNA [NM_001013853]	ref|NM_001013853|ref|NM_017309|ref|XM_213262	Rn.16313	-	LOC287167	globin, alpha	-	-	-
63	378.66	100.94	3.75	XM_230631	RGD1309659_predicted	PREDICTED: Rattus norvegicus similar to 4930465D02Rik protein (predicted) (LOC314468), mRNA [XM_230631]	ref|XM_230631|gb|AI171564|TC523664	Rn.22314	-	Taspl_predicted	taspase, threonine aspartase 1 (predicted)	-	-	[Human, Mouse]Homologene:9795
64	443.46	132.56	3.35	TC545861	TC545861	Q940M3 (Q940M3) AI5ge00530/murF9_180, partial (4%) [TC545861]	tc|TC545861	-	-	-	-	-	-	-
65	231.68	73.61	3.15	TC559380	TC559380	Unknown	tc|TC559380	-	-	-	-	-	-	-
66	209.08	67.42	3.10	TC551459	TC551459	Unknown	tc|TC551459	-	-	-	-	-	-	-
67	149.31	53.76	2.78	TC560203	TC560203	Unknown	tc|TC560203	-	-	-	-	-	-	-
68	516.44	186.03	2.78	XM_231625	RGD1309884_predicted	PREDICTED: Rattus norvegicus similar to 2010012F05Rik protein (LOC500373), mRNA [XM_231625]	ref|XM_231625|gb|BF418724|gb|AI639434|ens|ENSRNOT00000052393	-	-	-	similar to 2010012F05Rik protein	-	-	[Human, Mouse]Homologene:57102
69	162.18	58.96	2.75	TC532273	TC532273	Q14886 (Q14886) Mucin (Fragment), partial (10%) [TC532273]	tc|TC532273	-	-	-	-	-	-	-
70	141.09	52.78	2.67	TC568188	TC568188	Unknown	tc|TC568188	-	-	-	-	-	-	-
71	2866.54	1094.87	2.62	XM_343940	XM_343940	Rattus norvegicus similar to protein kinase related to Raf protein kinases; Method: conceptual translation supplied by author (LOC363649), mRNA [XM_343940]	gb|XM_343940	-	-	-	-	-	-	-
72	174.97	67.76	2.58	TC549515	TC549515	Unknown	tc|TC549515	-	-	-	-	-	-	-
73	220.49	86.67	2.54	TC555328	TC555328	CIRP_CRIGR (P60826) Cold-inducible RNA-binding protein (Glycine-rich RNA-binding protein CIRP) (A18 hnRNP), partial (89%) [TC555328]	tc|TC555328|tc|TC556471	-	-	-	-	-	-	-

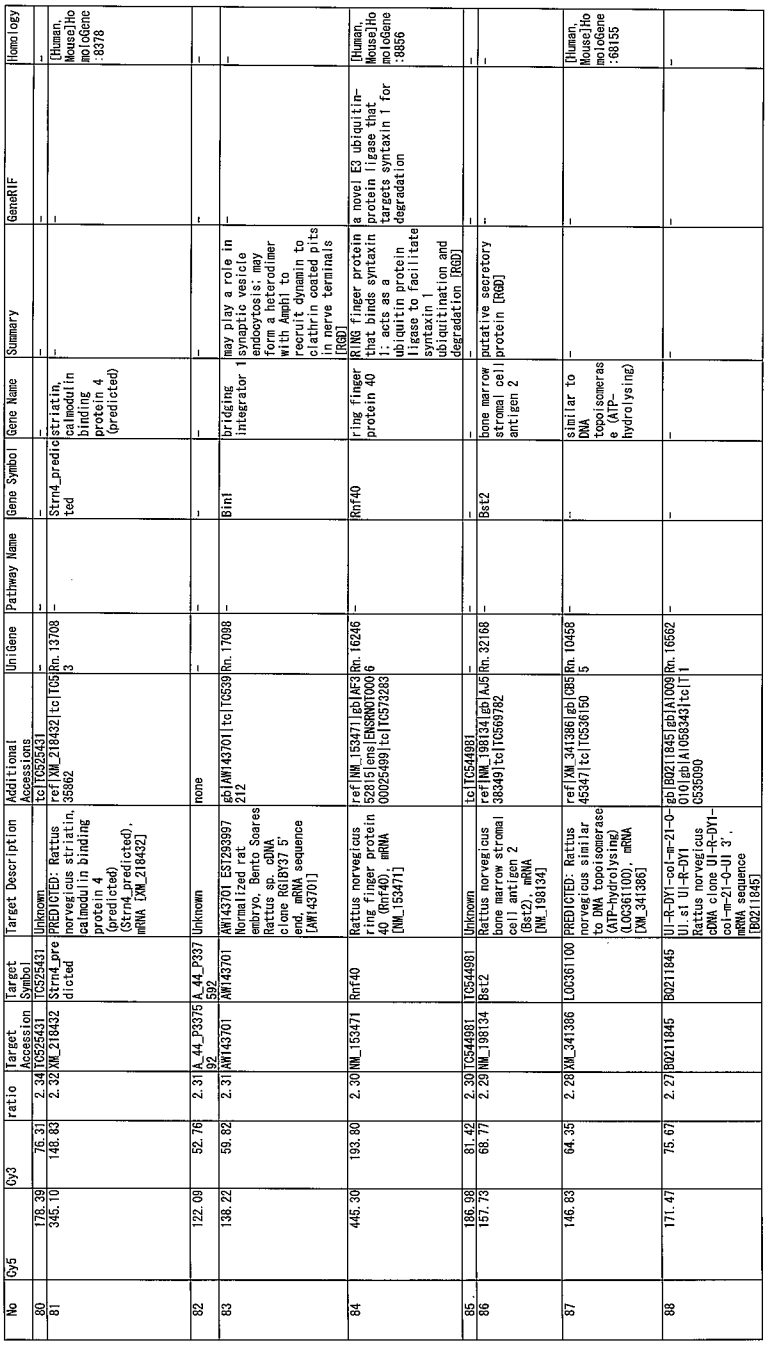
[0187]

No	Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Pathway Name	Gene Symbol	Gene Name	Summary	GeneRIF	Homology
74	164828.15	65277.85	2.53	NM_198776	MGC72973	Rattus norvegicus beta-glo (MGC72973), mRNA [NM_198776]	ref|NM_198776|ref|NM_033234|gb|X05080|gb|BC058502	Rn.36966	-	-	beta-glo	-	-	[Human, Mouse]Homologene:73881
75	181.66	72.49	2.51	TC549495	TC549495	Unknown	tc|TC549495	-	-	-	-	-	-	-
76	693.78	285.91	2.43	C8544341	C8544341	AMGNNUC:NRNHW-00288-E10-A W rat hypo-pit (10478) Rattus norvegicus cDNA clone nrnw-00288-e10 5, mRNA sequence [C8544341]	gb|C8544341	Rn.6526	-	Kif1b	kinesin family member 1B	putative mycogenic mitochondrial transporter [RGD]	KIF1Bbeta3 is involved in the translocation of lysosomes from perinuclear regions to the cell periphery// localization to synaptic vesicles	[Human, Mouse]Homologene:69177
77	126.21	52.08	2.42	NM_017289	Gabrd	Rattus norvegicus gamma-aminobutyric acid A receptor, delta (Gabrd), mRNA [NM_017289]	ref|NM_017289|gb|M35162|gb|BC087714|ens|ENSRNOT00000022246	Rn.10927	Neuroactive ligand-receptor interaction	Gabrd	gamma-aminobutyric acid A receptor, delta	GABA-A receptor subunit that contributes to slow phases of GABA-induced desensitization: plays a role in synaptic transmission [RGD]	Increased expression of GABA(A) receptor delta subunit in the interneurones of the periaqueductal gray matter could render the panic circuitry abnormally excitable by disinhibiting ongoing GABAergic inhibition.// Low pH enhances Gaba A delta receptor steady-state currents by modifying GABA(A) receptor gating properties.// conclude that receptors can accumulate in slowly equilibrating desensitized states during repetitive receptor activation: results may indicate role for slow phases of desensitization for synaptic function under conditions of repeated receptor activation	[Human, Mouse]Homologene:55489
78	145.24	61.35	2.37	TC542956	TC542956	08BL02 (08BL02) Mus musculus adult male corpora quadrigemina cDNA, RIKEN full-length enriched library, clone:B230215E15 product:RAP2 INTERACTING PROTEIN X homolog, partial (10%) [TC542956]	tc|TC542956	-	-	-	-	-	-	-

[0188]

No	Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Pathway Name	Gene Symbol	Gene Name	Summary	GeneRIF	Homology
79	530.81	226.10	2.35	XM_221921	Olr1572_predicted	PREDICTED: Rattus norvegicus olfactory receptor 1572 (predicted) (Olr1572_predicted), mRNA [XM_221921]	ref|XM_221921|ens|ENSRNOT00000048051|ens|ENSRNOT00000043537|ens|ENSRNOT00000009445.49	-	-	Olr1572_predicted	olfactory receptor 1572 (predicted)	Olfactory receptors interact with odorant molecules in the nose, to initiate a neuronal response that triggers the perception of a smell. The olfactory receptor proteins are members of a large family of G-protein-coupled receptors (GPCR) arising from single coding-exon genes. Olfactory receptors share a 7-transmembrane domain structure with many neurotransmitter and hormone receptors and are responsible for the recognition and G protein-mediated transduction of odorant signals. The olfactory receptor gene family is the largest in the genome. The nomenclature assigned to the olfactory receptor genes and proteins for this organism is independent of other organisms.	-	-

[0189]

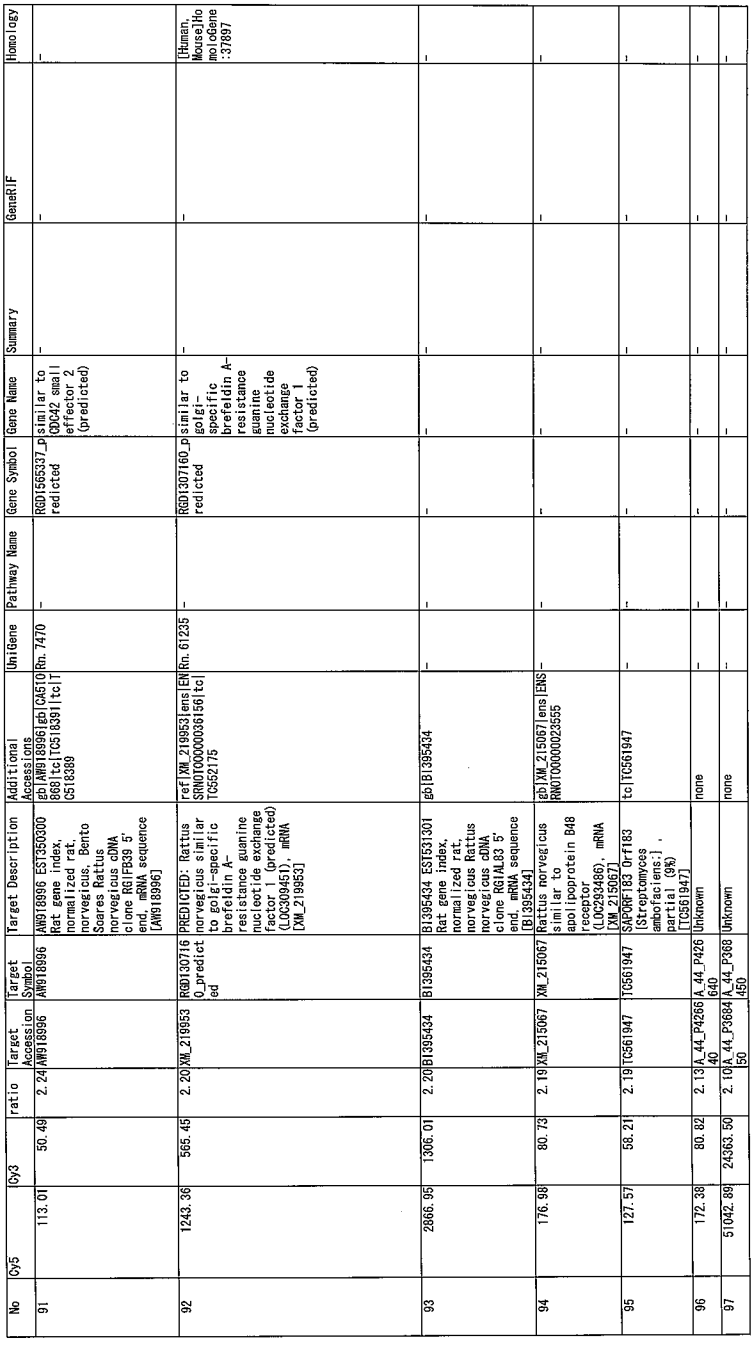


No	Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Pathway Name	Gene Symbol	Gene Name	Summary	GeneRIF	Homology
80	178.39	76.31	2.34	tc|TC525431	tc|TC525431	Unknown	tc|TC525431	-	-	-	-	-	-	-
81	345.10	148.83	2.32	XM_218432	Strn4_predicted	PREDICTED: Rattus norvegicus striatin, calmodulin binding protein 4 (predicted) (Strn4_predicted), mRNA [XM_218432]	ref|XM_218432|tc|TC525431 35862	Rn.137083	-	Strn4_predicted	striatin, calmodulin binding protein 4 (predicted)	-	-	[Human, Mouse]HomoloGene:8378
82	122.09	52.76	2.31	A_44_P33759292	A_44_P337592	Unknown	none	-	-	-	-	-	-	-
83	138.22	59.82	2.31	AW143701	AW143701	AW143701 EST293997 Normalized rat embryo, Bento Soares Rattus sp. cDNA clone RGIBY37 5', mRNA sequence [AW143701]	gb|AW143701|tc|TC539212	Rn.17098	-	Bin1	bridging integrator 1	may play a role in synaptic vesicle endocytosis; may form a heterodimer with Amphi to recruit dynamin to clathrin coated pits in nerve terminals [RGD]	-	-
84	446.30	193.80	2.30	NM_153471	Rnf40	Rattus norvegicus ring finger protein 40 (Rnf40), mRNA [NM_153471]	ref|NM_153471|gb|AF352815|ens|ENSRNOT00000600255499|tc|TC573283	Rn.16246	-	Rnf40	ring finger protein 40	RING finger protein that binds syntaxin 1; acts as a ubiquitin protein ligase to facilitate syntaxin 1 ubiquitination and degradation [RGD]	a novel E3 ubiquitin-protein ligase that targets syntaxin 1 for degradation	[Human, Mouse]HomoloGene:8856
85	186.98	81.42	2.30	TC544981	TC544981	Unknown	tc|TC544981	-	-	-	-	-	-	-
86	157.73	68.77	2.28	NM_198134	Bst2	Rattus norvegicus bone marrow stromal cell antigen 2 (Bst2), mRNA [NM_198134]	ref|NM_198134|gb|AJ538349|tc|TC569782	Rn.32168	-	Bst2	bone marrow stromal cell antigen 2	putative secretory protein [RGD]	-	-
87	146.83	64.35	2.28	XM_341386	LOC361100	PREDICTED: Rattus norvegicus similar to DNA topoisomerase (ATP-hydrolysing) (LOC361100), mRNA [XM_341386]	ref|XM_341386|gb|CB545347|tc|TC536150	Rn.104585	-	-	similar to DNA topoisomerase (ATP-hydrolysing)	-	-	[Human, Mouse]HomoloGene:68155
88	171.47	75.67	2.27	BI021845	BI021845	UI-R-DY1-col-m-21-0-UI.s1 UI-R-DY1 Rattus norvegicus cDNA clone UI-R-DY1-col-m-21-0-UI 3', mRNA sequence [BI021845]	gb|BI021845|gb|AI009010|gb|AI058343|tc|TC535090	Rn.16562	-	-	-	-	-	-

[0190]

No	Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Pathway Name	Gene Symbol	Gene Name	Summary	GeneRIF	Homology
89	127.97	56.60	2.26	AA900394	AA900394	AA900394 UI-R-ED-cm-h-03-0-UI.s2 UI-R-ED Rattus norvegicus cDNA clone UI-R-ED-cm-h-03-0-UI 3', mRNA sequence [AA900394]	gb|AA900394	Rn.16562 1	-	-	-	-	-	-
90	119.45	52.93	2.26	NM_001000446	Olr1234_predicted	Rattus norvegicus olfactory receptor 1234 (predicted) (Olr1234_predicted), mRNA [NM_001000446]	ref|NM_001000446|gb|XM_236077|ens|ENSRNOT00000049107	Rn.14353	-	Olr1234_predicted	olfactory receptor 1234 (predicted)	Olfactory receptors interact with odorant molecules in the nose, to initiate a neuronal response that triggers the perception of a smell. The olfactory receptor proteins are members of a large family of G-protein-coupled receptors (GPCR) arising from single coding-exon genes. Olfactory receptors share a 7-transmembrane domain structure with many neurotransmitter and hormone receptors and are responsible for the recognition and G protein-mediated transduction of odorant signals. The olfactory receptor gene family is the largest in the genome. The nomenclature assigned to the olfactory receptor genes and proteins for this organism is independent of other organisms.	-	[Mouse]HomoloGene:74016

[0191]

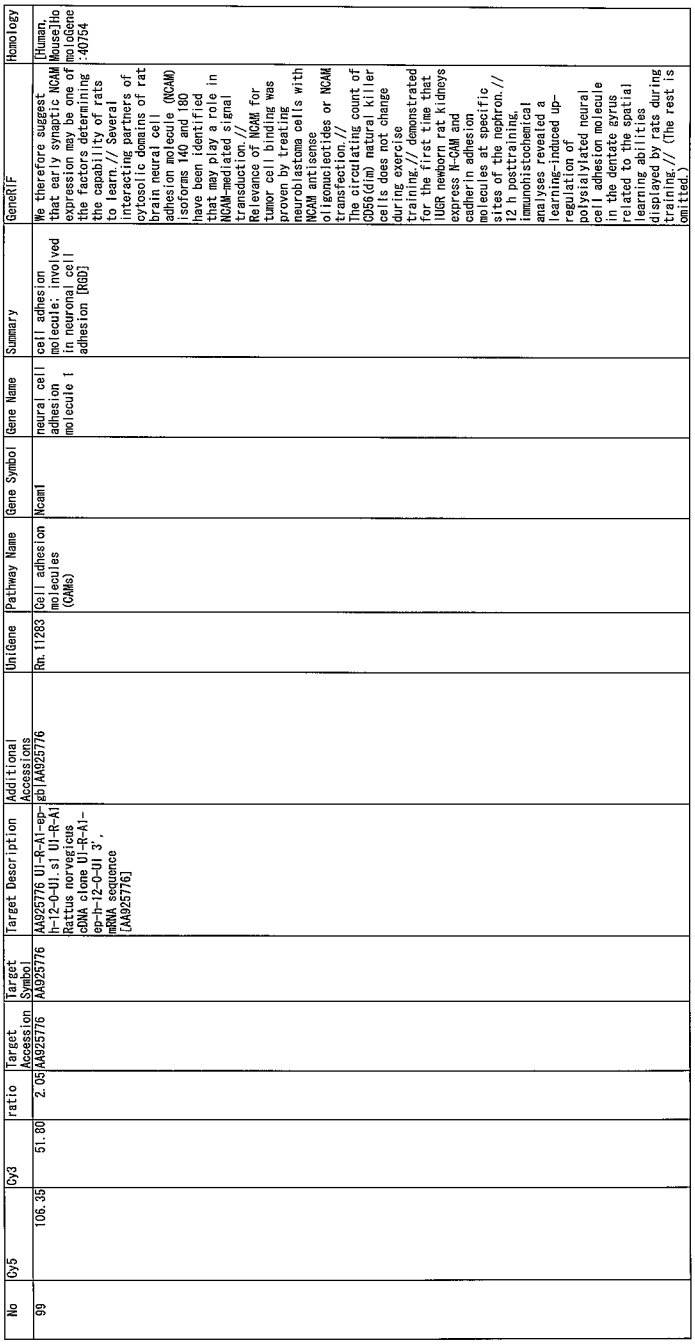


No	Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Pathway Name	Gene Symbol	Gene Name	Summary	GeneRIF	Homology
91	113.01	50.49	2.24	AW918996	AW918996	AW918996 EST350300 Rat gene index, normalized rat, norvegicus, Bento Soares Rattus norvegicus cDNA clone RGIFB39 5' end, mRNA sequence [AW918996]	gb|AW918996|gb|CA510868|tc|TC518391|tc|TC518389	Rn.7470	-	RGD1565337_predicted	similar to CDC42 small effector 2 (predicted)	-	-	-
92	1243.36	565.45	2.20	XM_219953	RGD1307160_predicted	PREDICTED: Rattus norvegicus similar to golgi-specific brefeldin A-resistance guanine nucleotide exchange factor 1 (predicted) (LOC310945), mRNA [XM_219953]	ref|XM_219953|ens|ENSRNOT00000036156|tc|TC552175	Rn.61235	-	RGD1307160_predicted	similar to golgi-specific brefeldin A-resistance guanine nucleotide exchange factor 1 (predicted)	-	-	(Human, Mouse)Homolog:37897
93	2866.95	1306.01	2.20	BI395434	BI395434	BI395434 EST531301 Rat gene index, normalized rat, norvegicus Rattus norvegicus cDNA clone RGIAL83 5' end, mRNA sequence [BI395434]	gb|BI395434	-	-	-	-	-	-	-
94	176.98	80.73	2.19	XM_215067	XM_215067	Rattus norvegicus similar to apolipoprotein B48 receptor (LOC293486), mRNA [XM_215067]	gb|XM_215067|ens|ENSRNOT00000022555	-	-	-	-	-	-	-
95	127.57	58.21	2.19	TC561947	TC561947	SAPORF183 Orf183 [Streptomyces ambofaciens:], partial (9%) [TC561947]	tc|TC561947	-	-	-	-	-	-	-
96	172.38	80.82	2.13	A_44_P426640	A_44_P426640	Unknown	none	-	-	-	-	-	-	-
97	51042.89	24363.50	2.10	A_44_P368450	A_44_P368450	Unknown	none	-	-	-	-	-	-	-

[0192]

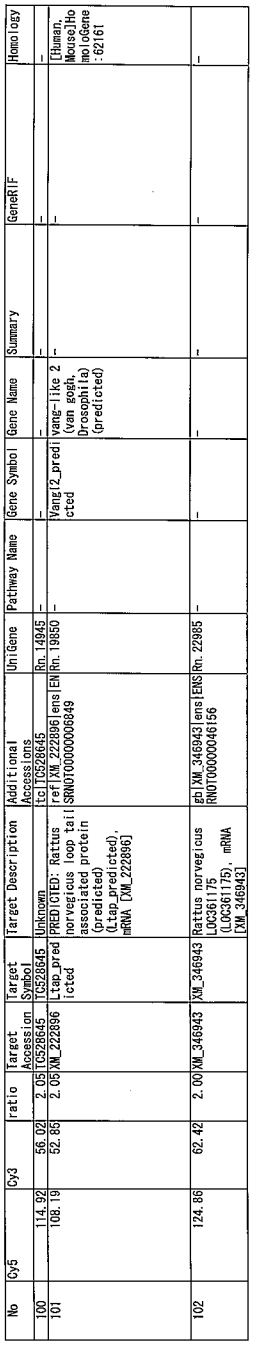
No	Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Pathway Name	Gene Symbol	Gene Name	Summary	GeneRIF	Homology
98	1796.58	874.03	2.06	NM_012812	Cox6a2	Rattus norvegicus cytochrome c oxidase, subunit VIa, polypeptide 2 (Cox6a2), mRNA [NM_012812]	ref|NM_012812|gb|X12554|gb|X72758|ens|ENSRNOT00000026908	Rn.5119	Oxidative phosphorylation	Cox6a2	cytochrome c oxidase, subunit VIa, polypeptide 2	heart isoform of subunit VIa of cytochrome c oxidase [RGD]	-	[Human, Mouse]Homologene:38020

[0193]



No	Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Pathway Name	Gene Symbol	Gene Name	Summary	GeneRIF	Homology
99	106.35	51.80	2.05	AA925776	AA925776	AA925776 UI-R-A1-ep-h-12-0-UI.s1 UI-R-A1 Rattus norvegicus cDNA clone UI-R-A1-ep-h-12-0-UI 3', mRNA sequence [AA925776]	gb|AA925776	Rn.11283	Cell adhesion molecules (CAMs)	Ncam1	neural cell adhesion molecule 1	cell adhesion molecule; involved in neuronal cell adhesion [RGD]	We therefore suggest that early synaptic NCAM expression may be one of the factors determining the capability of rats to learn.// Several interacting partners of cytosolic domains of rat brain neural cell adhesion molecule (NCAM) isoforms 140 and 180 have been identified that may play a role in NCAM-mediated signal transduction.// Relevance of NCAM for tumor cell binding was proven by treating neuroblastoma cells with NCAM antisense oligonucleotides or NCAM transfection.// The circulating count of CD56(dim) natural killer cells does not change during exercise training.// demonstrated for the first time that IUGR newborn rat kidneys express N-CAM and cadherin adhesion molecules at specific sites of the nephron.// 12 h posttraining, immunohistochemical analyses revealed a learning-induced up-regulation of polysialylated neural cell adhesion molecule in the dentate gyrus related to the spatial learning abilities displayed by rats during training.// (The rest is omitted.)	[Human, Mouse]Ho molecule; molGene ID:40754

[0194]



No	Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Pathway Name	Gene Symbol	Gene Name	Summary	GeneRIF	Homology
100	114.92	56.02	2.05	TC528645	TC528645	Unknown	tc|TC528645	Rn.14945	-	-	-	-	-	-
101	108.19	52.85	2.05	XM_222896	Ltap_predicted	PREDICTED: Rattus norvegicus loop tail associated protein (predicted) (Ltap_predicted), mRNA [XM_222896]	ref|XM_222896|ens|ENSRNOT00000006849	Rn.19850	-	Vangl2_predicted	vang-like 2 (van gogh, Drosophila) (predicted)	-	-	[Human, Mouse]HomoloGene:62161
102	124.86	62.42	2.00	XM_346943	XM_346943	Rattus norvegicus LOC361175 (LOC361175), mRNA [XM_346943]	gb|XM_346943|ens|ENSRNOT00000046156	Rn.22985	-	-	-	-	-	-

[0195] Light Touch群と比較してTickling群で0.5倍未満の発現を認めた末梢血液(BI)の遺伝子のアノテーションを下記表23に示す。

[表23]

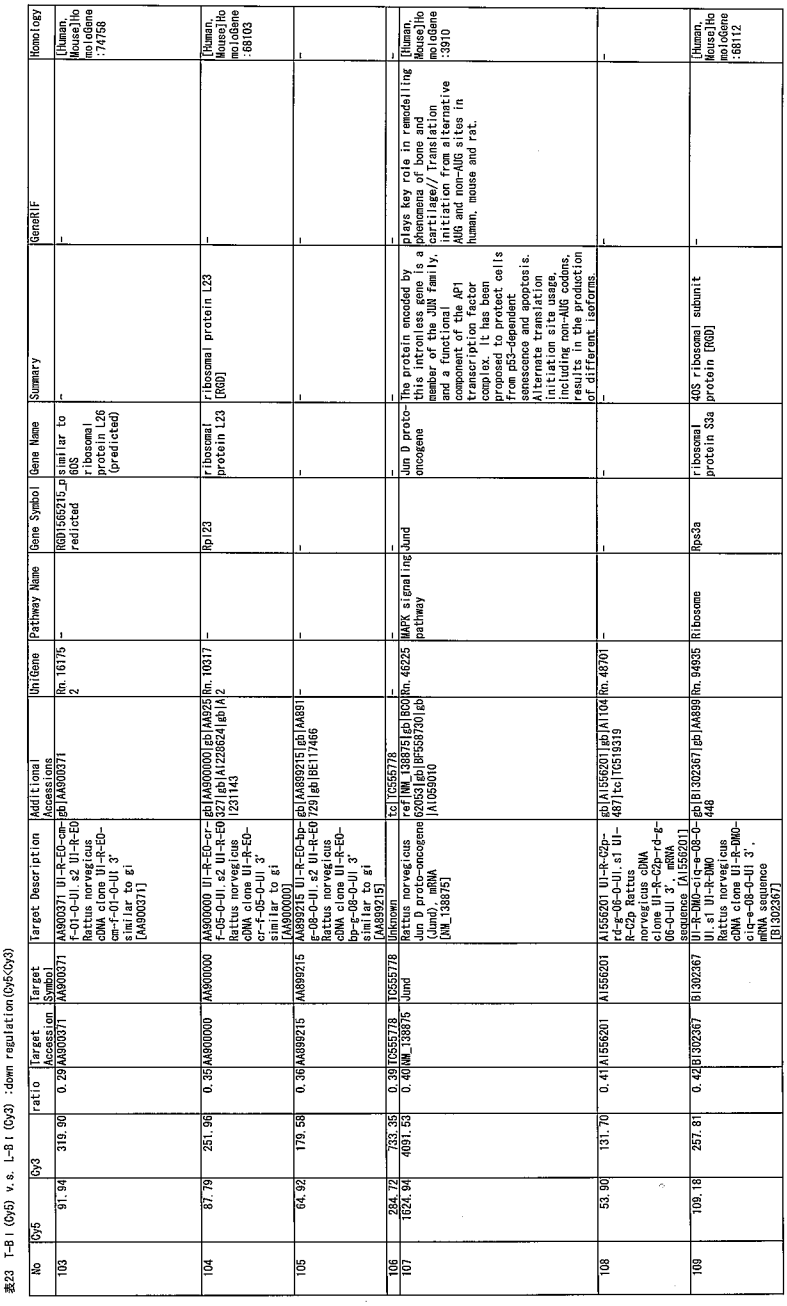
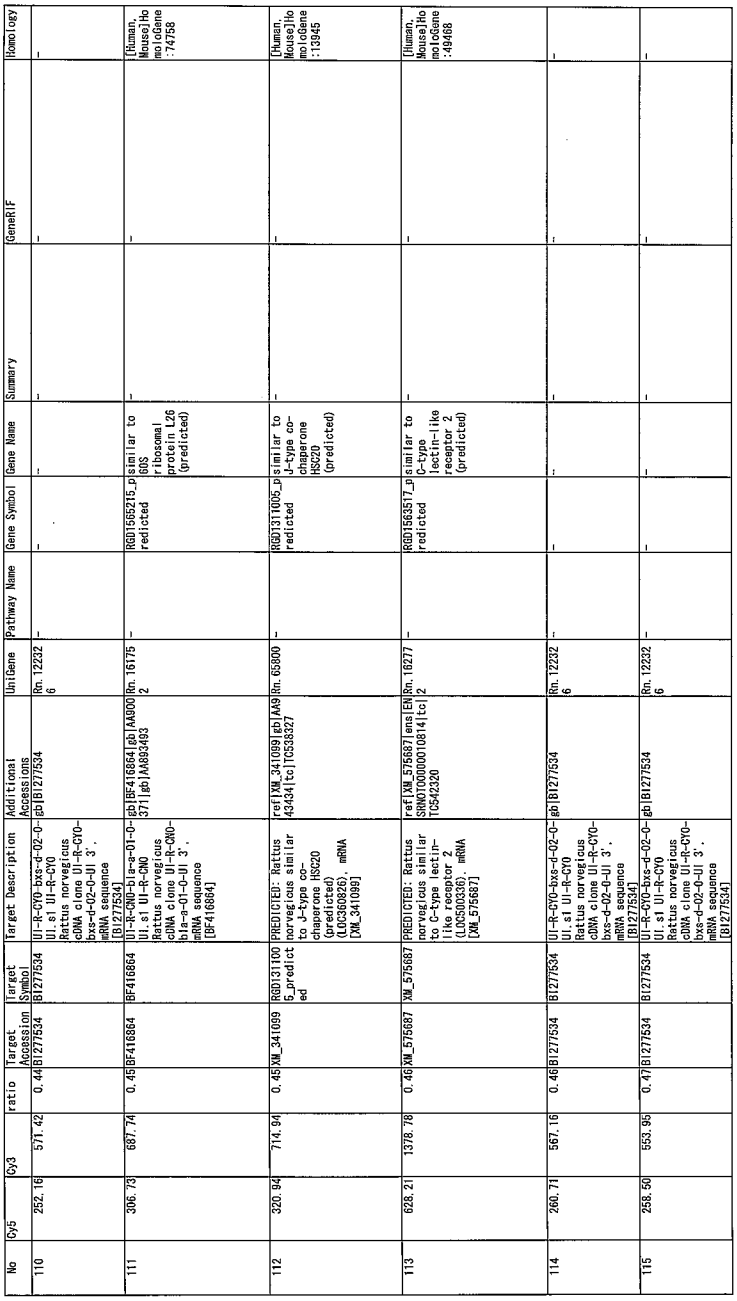


表23 T-B1 (Cy5) v.s. L-B1 (Cy3) :down regulation(Cy5<Cy3)

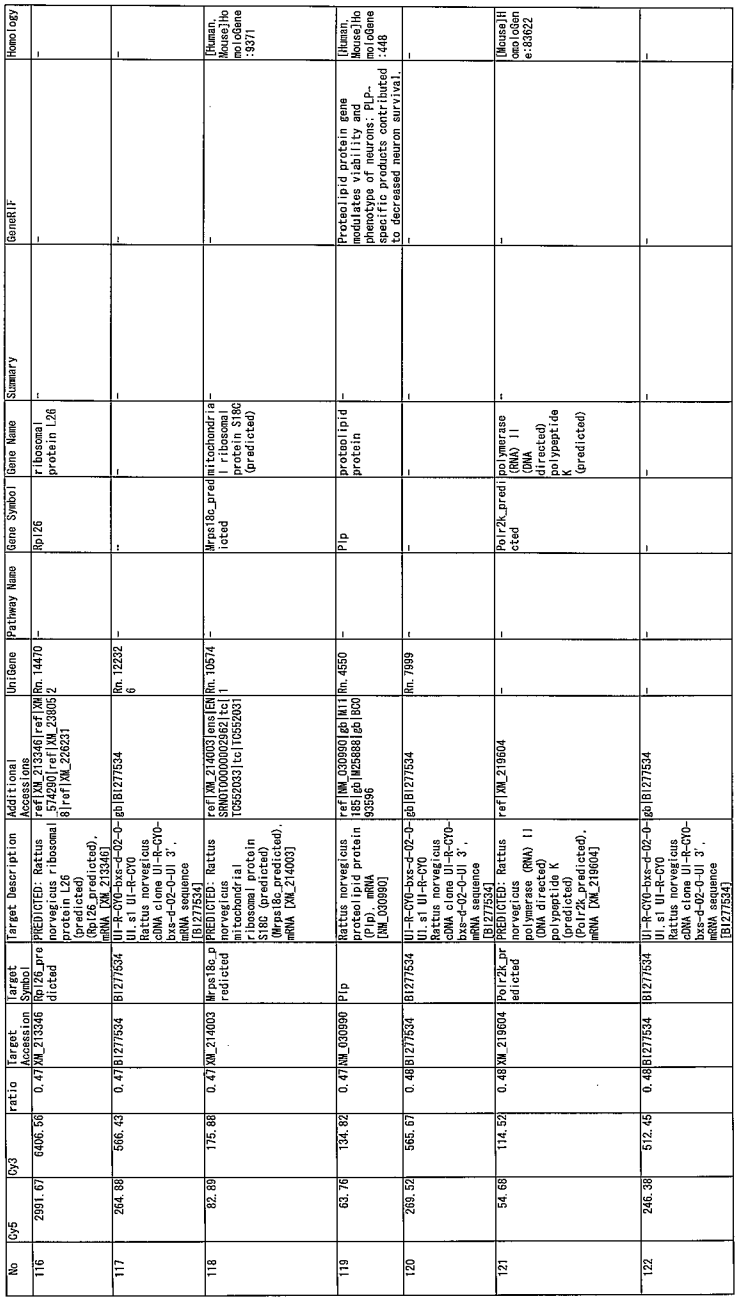
No	Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Pathway Name	Gene Symbol	Gene Name	Summary	GeneRIF	Homology
103	91.94	319.90	0.29	AA900371	AA900371	AA900371 UI-R-E0-dm-f-01-0-UI.s2 UI-R-E0 Rattus norvegicus cDNA clone UI-R-E0-cm-f-01-0-UI 3' similar to gi [AA900371]	gb|AA900371	Rn.16175 2	-	RGD1565215_predicted	similar to 60S ribosomal protein L26 (predicted)	-	-	[Human, Mouse]HomoloGene:74758
104	87.79	251.96	0.35	AA900000	AA900000	AA900000 UI-R-E0-cr-f-05-0-UI.s2 UI-R-E0 Rattus norvegicus cDNA clone UI-R-E0-cr-f-05-0-UI 3' similar to gi [AA900000]	gb|AA900000|gb|AA925327|gb|AI228624|gb|AI231143	Rn.10317	-	Rpl23	ribosomal protein L23	ribosomal protein L23 [RGD]	-	[Human, Mouse]HomoloGene:68103
105	64.92	179.58	0.36	AA899215	AA899215	AA899215 UI-R-E0-bp-g-08-0-UI.s2 UI-R-E0 Rattus norvegicus cDNA clone UI-R-E0-bp-g-08-0-UI 3' similar to gi [AA899215]	gb|AA899215|gb|AA891729|gb|BE117466	-	-	-	-	-	-	-
106	284.72	733.35	0.39	TC555778	TC555778	Unknown	tc|TC555778	-	-	-	-	-	-	-
107	1624.94	4091.53	0.40	NM_138875	Jund	Rattus norvegicus Jun D proto-oncogene (Jund), mRNA [NM_138875]	ref|NM_138875|gb|BG620563|gb|BF558730|gb|AI059010	Rn.46225	MAPK signaling pathway	Jund	Jun D proto-oncogene	The protein encoded by this intronless gene is a member of the JUN family, and a functional component of the AP1 transcription factor complex. It has been proposed to protect cells from p53-dependent senescence and apoptosis. Alternate translation initiation site usage, including non-AUG codons, results in the production of different isoforms.	plays key role in remodelling phenomena of bone and cartilage// Translation initiation from alternative AUG and non-AUG sites in human, mouse and rat.	[Human, Mouse]HomoloGene:3910
108	53.90	131.70	0.41	AI556201	AI556201	AI556201 UI-R-C2p-rd-g-06-0-UI.s1 UI-R-C2p Rattus norvegicus cDNA clone UI-R-C2p-rd-g-06-0-UI 3', mRNA sequence [AI556201]	gb|AI556201|gb|AI104487|tc|TC519319	Rn.48701	-	-	-	-	-	-
109	109.18	257.81	0.42	BI302367	BI302367	UI-R-DMO-ciq-e-08-0-UI.s1 UI-R-DMO Rattus norvegicus cDNA clone UI-R-DMO-ciq-e-08-0-UI 3', mRNA sequence [BI302367]	gb|BI302367|gb|AA899448	Rn.94935	Ribosome	Rps3a	ribosomal protein S3a	40S ribosomal subunit protein [RGD]	-	[Human, Mouse]HomoloGene:68112

[0196]



No	Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Pathway Name	Gene Symbol	Gene Name	Summary	GeneRIF	Homology
110	252.16	571.42	0.44	BI277534	BI277534	UI-R-CY0-bxs-d-02-0-UI.s1 UI-R-CY0 Rattus norvegicus cDNA clone UI-R-CY0-bxs-d-02-0-UI 3', mRNA sequence [BI277534]	gb|BI277534	Rn.12232	-	-	-	-	-	-
111	306.73	687.74	0.45	BF416864	BF416864	UI-R-CN0-bla-a-01-0-UI.s1 UI-R-CN0 Rattus norvegicus cDNA clone UI-R-CN0-bla-a-01-0-UI 3', mRNA sequence [BF416864]	gb|BF416864|gb|AA900371|gb|AA893493	Rn.16175	-	RGD1565215_predicted	similar to 60S ribosomal protein L26 (predicted)	-	-	[Human, Mouse]HomoloGene:74758
112	320.94	714.91	0.45	XM_341099	RGD1311005_predicted	PREDICTED: Rattus norvegicus similar to J-type co-chaperone HSC20 (LOC360920), mRNA [XM_341099]	ref|XM_341099|gb|AA943431|tc|TC538327	Rn.65800	-	RGD1311005_predicted	similar to J-type co-chaperone HSC20 (predicted)	-	-	[Human, Mouse]HomoloGene:13945
113	628.21	1378.78	0.46	XM_575687	XM_575687	PREDICTED: Rattus norvegicus similar to C-type lectin-like receptor 2 (LOC500336), mRNA [XM_575687]	ref|XM_575687|ens|ENSRNOT00000010814|tc|TC542320	Rn.16277	-	RGD1563517_predicted	similar to C-type lectin-like receptor 2 (predicted)	-	-	[Human, Mouse]HomoloGene:49468
114	260.71	567.16	0.46	BI277534	BI277534	UI-R-CY0-bxs-d-02-0-UI.s1 UI-R-CY0 Rattus norvegicus cDNA clone UI-R-CY0-bxs-d-02-0-UI 3', mRNA sequence [BI277534]	gb|BI277534	Rn.12232	-	-	-	-	-	-
115	258.50	553.95	0.47	BI277534	BI277534	UI-R-CY0-bxs-d-02-0-UI.s1 UI-R-CY0 Rattus norvegicus cDNA clone UI-R-CY0-bxs-d-02-0-UI 3', mRNA sequence [BI277534]	gb|BI277534	Rn.12232	-	-	-	-	-	-

[0197]

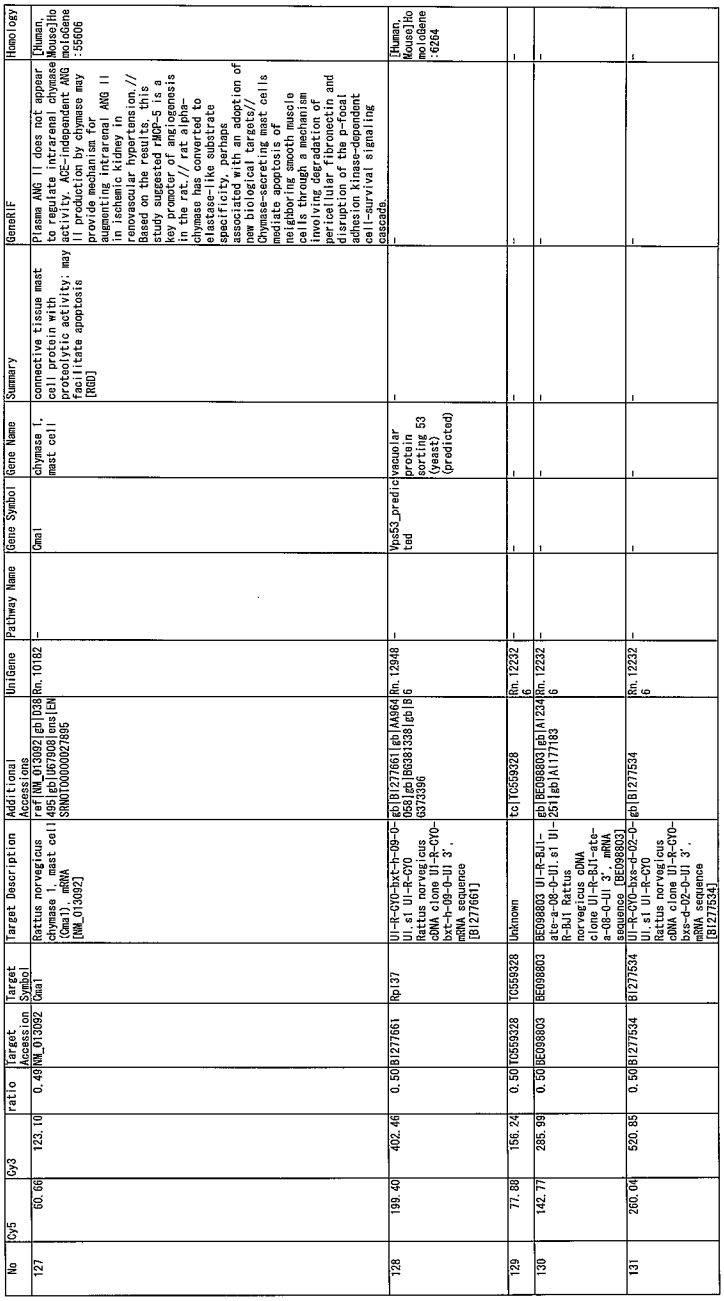


No	Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Pathway Name	Gene Symbol	Gene Name	Summary	GeneRIF	Homology
116	2991.67	6406.56	0.47	XM_213346	Rpl26_predicted	PREDICTED: Rattus norvegicus ribosomal protein L26 (predicted) (Rpl26_predicted), mRNA [XM_213346]	ref|XM_213346|ref|XM_574290|ref|XM_238058|ref|XM_226231	Rn.14470	-	Rpl26	ribosomal protein L26	-	-	-
117	264.88	566.43	0.47	B1277534	B1277534	UI-R-CY0-bxs-d-02-0-UI.s1 UI-R-CY0 Rattus norvegicus cDNA clone UI-R-CY0-bxs-d-02-0-UI 3', mRNA sequence [B1277534]	gb|B1277534	Rn.12232 6	-	-	-	-	-	-
118	82.89	175.88	0.47	XM_214003	Mrps18c_predicted	PREDICTED: Rattus norvegicus mitochondrial ribosomal protein S18C (predicted) (Mrps18c_predicted), mRNA [XM_214003]	ref|XM_214003|ens|ENSRNOT00000029621|tc|TC652033|tc|TC652031	Rn.10574	-	Mrps18c_predicted	mitochondrial ribosomal protein S18C (predicted)	-	-	[Human, Mouse]Homologene:9371
119	63.76	134.82	0.47	XM_030990	Plp	Rattus norvegicus proteolipid protein (Plp), mRNA [XM_030990]	ref|XM_030990|gb|M11185|gb|M25888|gb|M93596	Rn.4550	-	Plp	proteolipid protein	-	Proteolipid protein gene modulates viability and phenotype of neurons: PLP-specific products contributed to decreased neuron survival.	[Human, Mouse]Homologene:448
120	269.52	565.67	0.48	B1277534	B1277534	UI-R-CY0-bxs-d-02-0-UI.s1 UI-R-CY0 Rattus norvegicus cDNA clone UI-R-CY0-bxs-d-02-0-UI 3', mRNA sequence [B1277534]	gb|B1277534	Rn.7999	-	-	-	-	-	-
121	54.68	114.52	0.48	XM_219604	Polr2k_predicted	PREDICTED: Rattus norvegicus polymerase (RNA) II (DNA directed) polypeptide K (predicted) (Polr2k_predicted), mRNA [XM_219604]	ref|XM_219604	-	-	Polr2k_predicted	polymerase (RNA) II (DNA directed) polypeptide K (predicted)	-	-	[Mouse]Homologene:83622
122	246.38	512.45	0.48	B1277534	B1277534	UI-R-CY0-bxs-d-02-0-UI.s1 UI-R-CY0 Rattus norvegicus cDNA clone UI-R-CY0-bxs-d-02-0-UI 3', mRNA sequence [B1277534]	gb|B1277534	-	-	-	-	-	-	-

[0198]

No	Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Pathway Name	Gene Symbol	Gene Name	Summary	GeneRIF	Homology
123	253.63	525.25	0.48	B1277534	B1277534	UI-R-CY0-bxs-d-02-0-UI.s1 UI-R-CY0 Rattus norvegicus cDNA clone UI-R-CY0-bxs-d-02-0-UI 3', mRNA sequence [B1277534]	gb|B1277534	-	-	-	-	-	-	-
124	139.70	288.64	0.48	NM_0010142 07	NM_001014207	Rattus norvegicus similar to RIKEN cDNA 4930553M18 (predicted) (LOC712027), mRNA [NM_001014207]	ref|NM_001014207|gb|CB548312|gb|BC087647|ens|ENSRNOT00000000605	Rn.137575	-	Josd3	Josephin domain containing 3	-	-	(Human, Mouse)Homolo gene:11472
125	207.27	424.59	0.49	TC559328	TC559328	Unknown	tc|TC559328	-	-	-	-	-	-	-
126	252.71	513.87	0.49	B1277534	B1277534	UI-R-CY0-bxs-d-02-0-UI.s1 UI-R-CY0 Rattus norvegicus cDNA clone UI-R-CY0-bxs-d-02-0-UI 3', mRNA sequence [B1277534]	gb|B1277534	Rn.122326	-	-	-	-	-	-

[0199]



No	Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Pathway	Gene Symbol	Gene Name	Summary	GeneRIF	Homology
127	60.66	123.10	0.49	NM_013092	Cma1	Rattus norvegicus chymase 1, mast cell (Cma1), mRNA [NM_013092]	ref|NM_013092|gb|D38495|gb|U67908|ens|ENSRNOT00000027895	Rn.10182	-	Cma1	chymase 1, mast cell	connective tissue mast cell protein with proteolytic activity; may facilitate apoptosis [RGD]	Plasma ANG II does not appear to regulate intrarenal chymase activity. ACE-independent ANG II production by chymase may provide mechanism for augmenting intrarenal ANG II in ischemic kidney in renovascular hypertension.// Based on the results, this study suggested rMCP-5 is a key promoter of angiogenesis in the rat.// rat alpha-chymase has converted to elastase-like substrate specificity, perhaps associated with an adoption of new biological targets// Chymase-secreting mast cells mediate apoptosis of neighboring smooth muscle cells through a mechanism involving degradation of pericellular fibronectin and disruption of the p-focal adhesion kinase-dependent cell-survival signaling cascade.	[Human, Mouse]Homolo gene :55606
128	199.40	402.46	0.50	BI277661	Rpl37	UI-R-CY0-bxt-h-09-0-UI.s1 UI-R-CY0 Rattus norvegicus cDNA clone UI-R-CY0-bxt-h-09-0-UI 3', mRNA sequence [BI277661]	gb|BI277661|gb|AA964658|gb|BG381338|gb|6372396	Rn.12948	-	Vps53_predicted	vacuolar protein sorting 53 (yeast) (predicted)	-	-	[Human, Mouse]Homolo gene :6264
129	77.88	156.24	0.50	TC559328	TC559328	Unknown	tc|TC559328	Rn.122326	-	-	-	-	-	-
130	142.77	285.99	0.50	BE098803	BE098803	BE098803 UI-R-BJ1-ate-a-08-0-UI.s1 UI-R-BJ1 Rattus norvegicus cDNA clone UI-R-BJ1-ate-a-08-0-UI 3', mRNA sequence [BE098803]	gb|BE098803|gb|AI232511|gb|AI177183	Rn.122326	-	-	-	-	-	-
131	260.04	520.85	0.50	BI277534	BI277534	UI-R-CY0-bxs-d-02-0-UI.s1 UI-R-CY0 Rattus norvegicus cDNA clone UI-R-CY0-bxs-d-02-0-UI 3', mRNA sequence [BI277534]	gb|BI277534	Rn.122326	-	-	-	-	-	-

[0200]

No	Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Pathway Name	Gene Symbol	Gene Name	Summary	GeneRIF	Homology
132	298.52	597.52	0.50	AI231572	AI231572	AI231572 EST228260 Normalized rat embryo, Bento Soares Rattus sp. cDNA clone RBENW20.3 5' end, mRNA sequence [AI231572]	gb|AI231572|gb|BE113204|gb|BE112204	Rn.1180	-	Hbld2	HESB like domain containing 2	probably a mitochondrial protein involved in the biogenesis of iron?sulfur clusters [RGD]	-	[Human, Mouse]Homologene:12297

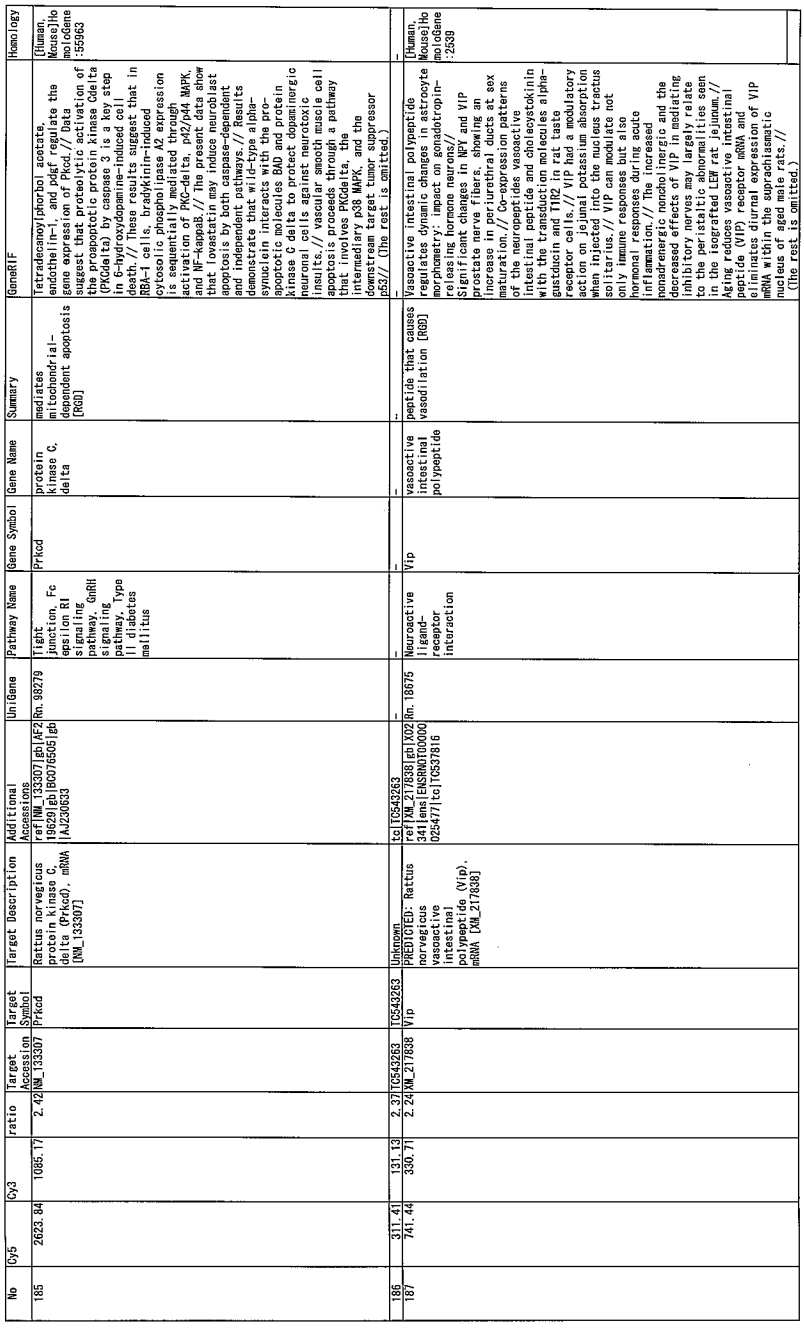
[0201] 対照群と比較してTickling群で2.0倍超の発現を認めた視床下部(Hy)の遺伝子のアノテーションを下記表24に示す。

[表24]

表24 T-Hy(Cy5) v.s. C-Hy(Cy3) :up regulation(Cy5>Cy3)

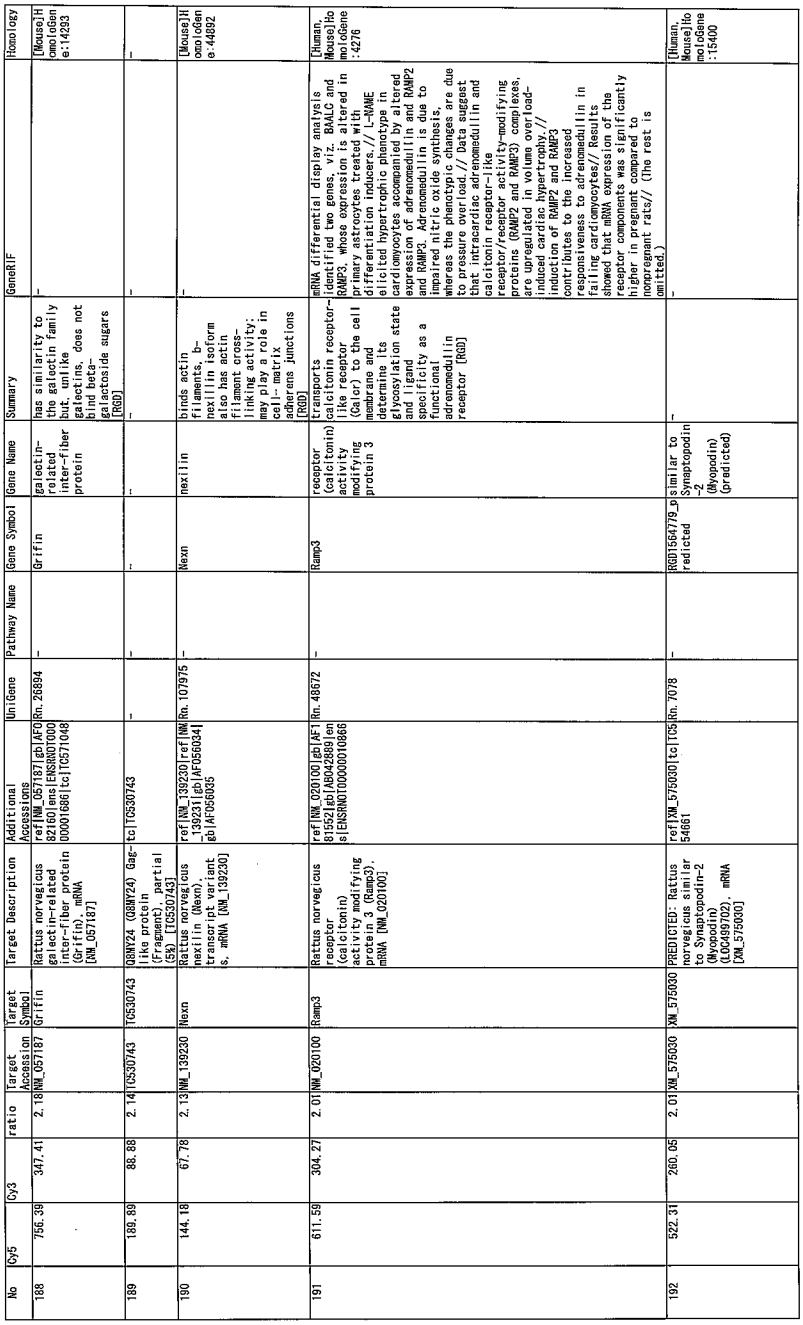
No	Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Pathway Name	Gene Symbol	Gene Name	Summary	GeneRIF	Homology
180	1174.60	62.88	18.68	J00757	Cga	Rattus norvegicus glycoprotein hormone alpha subunit precursor mRNA, complete cds. [J00757]	gb|J00757|gb|D85694O|Rn.10589 21|gb|D00575|ens|ENSR NOT00000012385	Rn.10589	Neuroactive ligand-receptor interaction, GnRH signaling pathway	Cga	glycoprotein hormones, alpha subunit	alpha subunit of pituitary glycoprotein hormones [RGD]	-	[Human, Mouse]Homolo Gene:587
181	968.26	350.78	2.76	NM_053918	Cga	Rattus norvegicus glycoprotein hormones, alpha subunit (Cga), mRNA [NM_053918]	ref|NM_053918|gb|V01 253	Rn.10589	Neuroactive ligand-receptor interaction, GnRH signaling pathway	Cga	glycoprotein hormones, alpha subunit	alpha subunit of pituitary glycoprotein hormones [RGD]	-	[Human, Mouse]Homolo Gene:587
182	146.60	53.48	2.74	NM_013028	Shox2	Rattus norvegicus short stature homeobox 2 (Shox2), mRNA [NM_013028]	ref|NM_013028|gb|AJ0 02258|gb|AJ002258|gb |AJ002260	Rn.11258	-	Shox2	short stature homeobox 2	putative homeobox gene; human homolog encodes a putative homeobox gene involved in embryonic development [RGD]	-	-
183	437.63	169.56	2.58	BC092605	BC092605	Rattus norvegicus protein tyrosine phosphatase, non-receptor type 3 (predicted), mRNA (cDNA clone IMAGE:7308722), partial cds. [BC092605]	gb|BC092605|gb|AW918 679|tc|TC520643|tc|T C520642	Rn.22271	-	Ptpn3	protein tyrosine phosphatase, non-receptor type 3	-	-	-
184	125.12	51.44	2.43	BE108176	BE108176	gb|BE108176|BE108176 UI-R-BS1-ayw-g-04-0-UI.s1 UI-R-BS1 Rattus norvegicus cDNA clone UI-R-BS1-ayw-g-04-0-UI 3', mRNA sequence [BE108176]	gb|BE108176	Rn.3464	-	Ddt	D-dopachrome tautomerase	converts D-dopachrome into 5,6-dihydroxyindole [RGD]	-	[Human, Mouse]Homolo Gene:1038

[0202]



No	Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Pathway Name	Gene Symbol	Gene Name	Summary	GenoMIF	Homology
185	2623.84	1085.17	2.42	NM_133307	Prkcd	Rattus norvegicus protein kinase C, delta (Prkcd), mRNA [NM_133307]	ref|NM_133307|gb|AF2 19629|gb|BC076505|gb |AJ230633	Rn.98279	Tight junction, Fc epsilon RI signaling pathway, GnRH signaling pathway, Type II diabetes mellitus	Prkcd	protein kinase C, delta	mediates mitochondrial-dependent apoptosis [RGD]	Tetradecanoylphorbol acetate, endothelin-1, and pdgf regulate the gene expression of Prkcd.// Data suggest that proteolytic activation of the proapoptotic protein kinase Cdelta (PKCdelta) by caspase 3 is a key step in 6-hydroxydopamine-induced cell death.// These results suggest that in RBA-1 cells, bradykinin-induced cytosolic phospholipase A2 expression is sequentially mediated through activation of PKC-delta, p42/p44 MAPK, and NF-kappaB.// The present data show that lovastatin may induce neuroblast apoptosis by both caspase-dependent and independent pathways.// Results demonstrate that wild-type alpha-synuclein interacts with the pro-apoptotic molecules Bad and protein kinase C delta to protect dopaminergic neuronal cells against neurotoxic insults.// vascular smooth muscle cell apoptosis proceeds through a pathway that involves PKCdelta, the intermediary p38 MAPK, and the downstream target tumor suppressor p53// (The rest is omitted.)	[Human, Mouse]Homologene:55963
186	311.41	131.13	2.37	TC543263	Vip	Unknown	tc|TC543263	-	-	-	-	-	-	-
187	741.44	330.71	2.24	XM_217838	Vip	PREDICTED: Rattus norvegicus vasoactive intestinal polypeptide (Vip), mRNA [XM_217838]	ref|XM_217838|gb|X02 341|ens|ENSRNOT00000 025477|tc|TC537816	Rn.18675	Neuroactive ligand-receptor interaction	Vip	vasoactive intestinal polypeptide	peptide that causes vasodilation [RGD]	Vasoactive intestinal polypeptide regulates dynamic changes in astrocyte morphometry: impact on gonadotropin-releasing hormone neurons// Significant changes in NPY and VIP prostate nerve fibers, showing an increase in periurethral ducts at sex maturation.// Co-expression patterns of the neuropeptide vasoactive intestinal peptide and cholecystokinin with the transduction molecules alpha-gustducin and T1R2 in rat taste receptor cells.// VIP had a modulatory action on jejunal potassium absorption when injected into the nucleus tractus solitarius.// VIP can modulate not only immune responses but also hormonal responses during acute inflammation.// The increased nonadrenergic noncholinergic and the decreased effects of VIP in mediating inhibitory nerves may largely relate to the peristaltic abnormalities seen in the isografted LEW rat jejunum.// Aging reduces vasoactive intestinal peptide (VIP) receptor mRNA and peptide (VIP)-immunoreactivity but not mRNA within the suprachiasmatic nucleus of aged male rats.// (The rest is omitted.)	[Human, Mouse]Homologene:2539

[0203]



No	Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Pathway Name	Gene Symbol	Gene Name	Summary	GeneRIF	Homology
188	756.39	347.41	2.18	NM_057187	Grifin	Rattus norvegicus galactin-related inter-fiber protein (Grifin), mRNA [NM_057187]	ref|NM_057187|gb|AF0 82160|ens|ENSRNOT000 00001686|tc|TC571048	Rn.26894	-	Grifin	galectin-related inter-fiber protein	has similarity to the galactin family but, unlike galectins, does not bind beta-galactoside sugars [RGD]	-	[Mouse]H omoloGen e:14293
189	189.89	88.88	2.14	TC530743	TC530743	Q8WY24 (Q8WY24) Gag-like protein (Fragment), partial (5%) [TC530743]	-	-	-	Mexn	mexilin	binds actin filaments, b-mexilin isoform also has actin filament cross-linking activity; may play a role in cell-matrix adherens junctions [RGD]	-	-
190	144.18	67.78	2.13	NM_139230	Mexn	Rattus norvegicus mexilin (Mexn), transcript variants, mRNA [NM_139230]	ref|NM_139230|ref|NM 139231|gb|AF056034| gb|AF056035	Rn.107975	-	Ramp3	receptor (calcitonin) activity modifying protein 3	transports calcitonin receptor-like receptor (Calcr) to the cell membrane and determine its glycosylation state and ligand specificity as a functional adrenomedullin receptor [RGD]	mRNA differential display analysis identified two genes, viz. BAALC and RAMP3, whose expression is altered in primary astrocytes treated with differentiation inducers.// L-NAME elicited hypertrophic phenotype in cardiomyocytes accompanied by altered expression of adrenomedullin and RAMP2 and RAMP3. Adrenomedullin is due to impaired nitric oxide synthesis whereas the phenotypic changes are due to pressure overload.// Data suggest that intracardiac adrenomedullin and calcitonin receptor-like receptor/receptor activity-modifying proteins (RAMP2 and RAMP3) complexes, are upregulated in volume overload-induced cardiac hypertrophy.// induction of RAMP2 and RAMP3 contributes to the increased responsiveness to adrenomedullin in failing cardiomyocytes// Results showed that mRNA expression of the receptor components was significantly higher in pregnant compared to nonpregnant rats// (The rest is omitted.)	[Human, Mouse]Ho moloGene :4276
191	611.59	304.27	2.01	NM_020100	Ramp3	Rattus norvegicus receptor (calcitonin) activity modifying protein 3 (Ramp3), mRNA [NM_020100]	ref|NM_020100|gb|AF1 81562|gb|AB042889|en s1|ENSRNOT00000010866	Rn.48672	-	RGD1564779_predicted	similar to Synaptopodin-2 (Myopodin) (predicted)	-	-	[Human, Mouse]Ho moloGene :15400
192	522.31	260.05	2.01	XM_575030	XM_575030	PREDICTED: Rattus norvegicus similar to Synaptopodin-2 (Myopodin) (LOC499702), mRNA [XM_575030]	ref|XM_575030|tc|TC5 54661	Rn.7078	-					

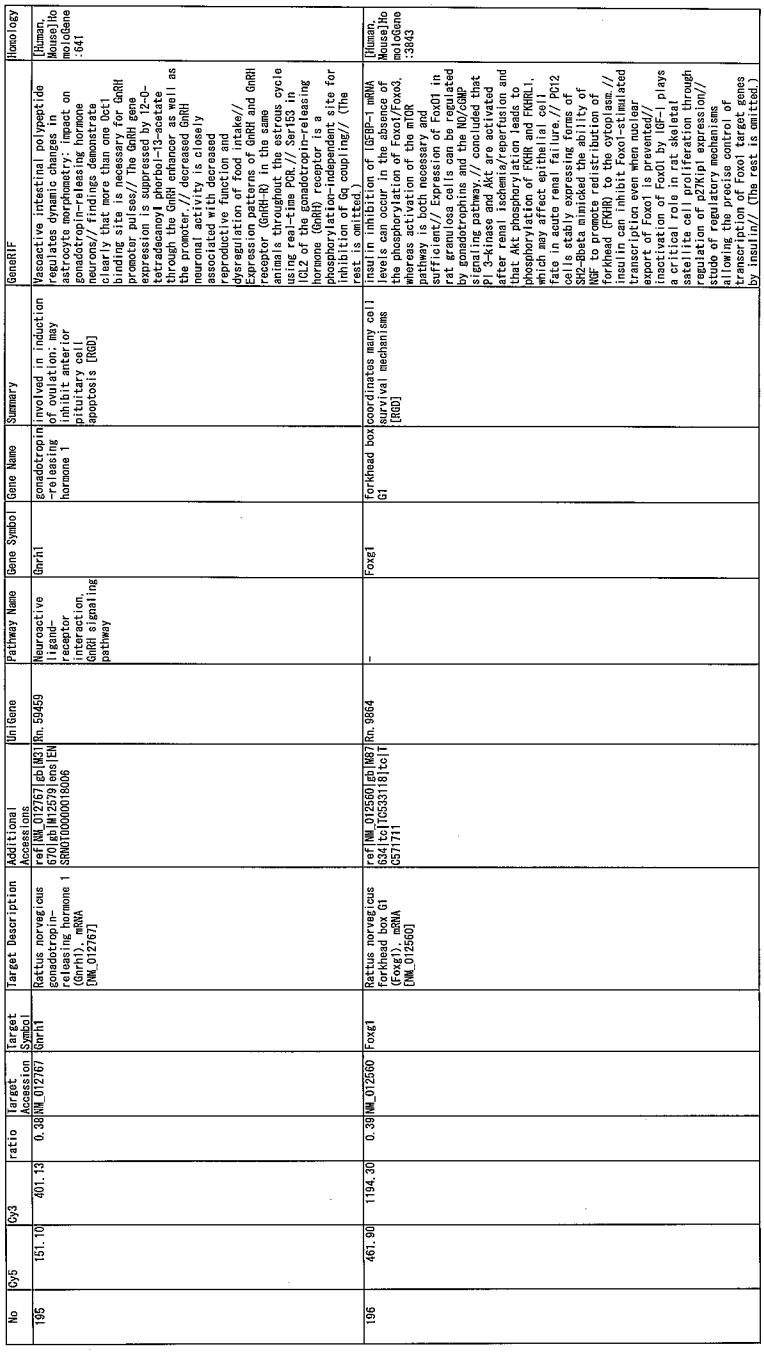
[0204] 対照群と比較してTickling群で0.5倍未満の発現を認めた視床下部(Hy)の遺伝子のアノテーションを下記表25に示す。

[表25]

表25 T-Hy(Cy5) v.s. C-Hy(Cy3) :down regulation(Cy5<Cy3)

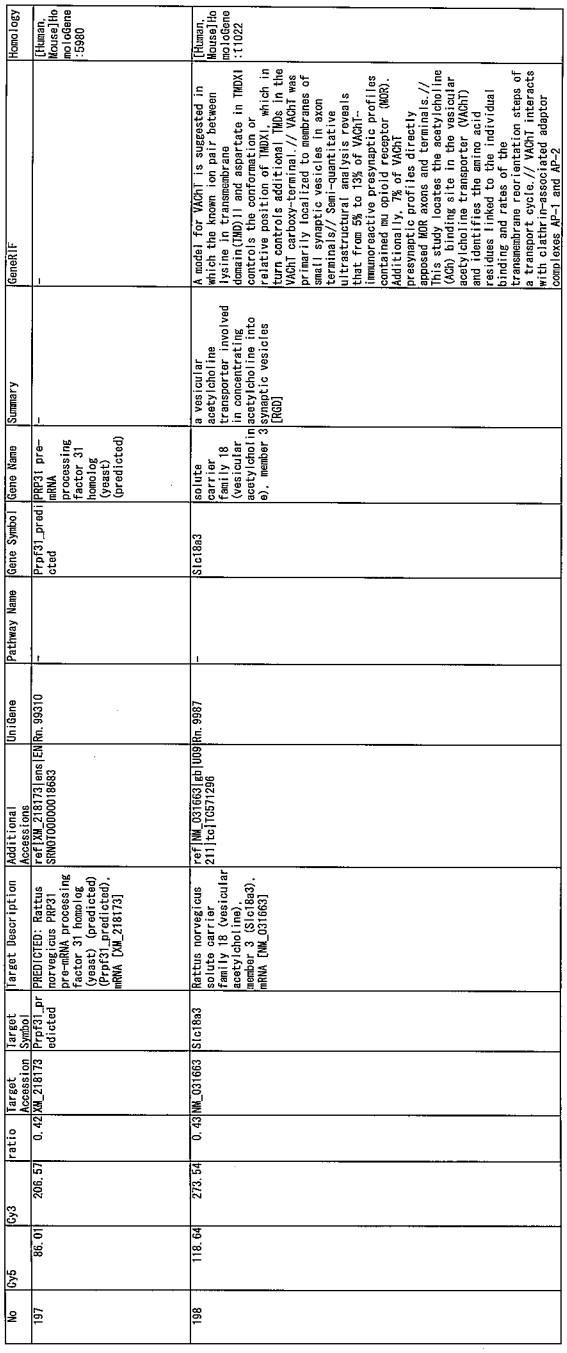
No	Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Pathway Name	Gene Symbol	Gene Name	Summary	GeneRIF	Homology
193	121.48	1484.54	0.08	NM_012681	Ttr	Rattus norvegicus transthyretin (Ttr), mRNA [NM_012681]	ref|NM_012681|gb|X14876|gb|K03252|gb|AF479660	Rn.1404	-	Ttr	transthyretin	Binds thyroxine (T4) and 3,5,3' triiodothyronine (T3); plays a role in thyroid hormone transport in serum [RGD]	Data suggest that monomeric transthyretin may represent an ischemia-specific CSF marker to indicate the sequential changes according to ischemic insults of the brain.// data show the LRI gene is up-regulated following short interval successive partial hepatectomy; it may play an important role in liver regeneration// Amyloid formation in rat transthyretin: effect of oxidative stress// Comparison of binding interactions of dibromoflavonoids with transthyretin// Complex of rat transthyretin with tetraiodothyroacetic acid refined at 2.1 and 1.8 A resolution// Structural basis of negative cooperativity in transthyretin	[Human, Mouse]HomoloGene:317
194	132.74	1001.04	0.13	BF398607	BF398607	BF398607 UI-R-BS2-baq-g-09-0-UI.s1 UI-R-BS2 Rattus norvegicus cDNA clone UI-R-BS2-baq-g-09-0-UI 3', mRNA sequence [BF398607]	gb|BF398607|gb|BF285611	Rn.45255	-	RGD1564156_predicted	similar to teratocyte-specific carboxylesterase (predicted)	-	-	-

[0205]



No	Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Pathway Name	Gene Symbol	Gene Name	Summary	GenoRIF	Homology
195	151.10	401.13	0.38	NM_012767	Gnrh1	Rattus norvegicus gonadotropin-releasing hormone 1 (Gnrh1), mRNA [NM_012767]	ref|NM_012767|gb|M31670|gb|M12579|ens|ENSRNOT00000018006	Rn.59459	Neuroactive ligand-receptor interaction, GnRH signaling pathway	Gnrh1	gonadotropin-releasing hormone 1	involved in induction of ovulation; may inhibit anterior pituitary cell apoptosis [RGD]	Vasoactive intestinal polypeptide regulates dynamic changes in astrocyte morphometry: impact on gonadotropin-releasing hormone neurons// findings demonstrate clearly that more than one Oct1 binding site is necessary for GnRH promotor pulses// The GnRH gene expression is suppressed by 12-O-tetradecanoyl phorbol-13-acetate through the GnRH enhancer as well as the promoter.// decreased GnRH neuronal activity is closely associated with decreased reproductive function and dysregulation of feed intake// Expression patterns of GnRH and GnRH receptor (GnRH-R) in the same animals throughout the estrous cycle using real-time PCR.// Ser153 in IQL2 of the gonadotropin-releasing hormone (GnRH) receptor is a phosphorylation-independent site for inhibition of Gq coupling// (The rest is omitted.)	[Human, Mouse]Homologene:641
196	461.90	1194.30	0.39	NM_012560	Foxg1	Rattus norvegicus forkhead box G1 (Foxg1), mRNA [NM_012560]	ref|NM_012560|gb|M87634|tc|TCG5331180571711|tc|T	Rn.9864	-	Foxg1	forkhead box G1	coordinates many cell survival mechanisms [RGD]	insulin inhibition of IGFBP-1 mRNA levels can occur in the absence of the phosphorylation of Foxo1/Foxo3, whereas activation of the mTOR pathway is both necessary and sufficient// Expression of Foxo1 in rat granulosa cells can be regulated by gonadotrophins and the MAPK signaling pathway// constitutively activated PI 3-kinase and Akt are activated after renal ischemia/reperfusion and that Akt phosphorylation leads to phosphorylation of FKHR and FKHRL1, which may affect epithelial cell fate in acute renal failure.// PC12 cells stably expressing forms of Sh2-Bbeta mimicked the ability of NGF to promote redistribution of forkhead (FKHR) to the cytoplasm.// insulin can inhibit Foxo1-stimulated transcription even when nuclear export of Foxo1 is prevented// inactivation of Foxo1 by IGF-1 plays a critical role in rat skeletal satellite cell proliferation through regulation of p27Kip1 expression// results suggest a regulatory mechanism allowing the precise control of transcription of Foxo1 target genes by insulin// (The rest is omitted.)	[Human, Mouse]Homologene:3843

[0206]

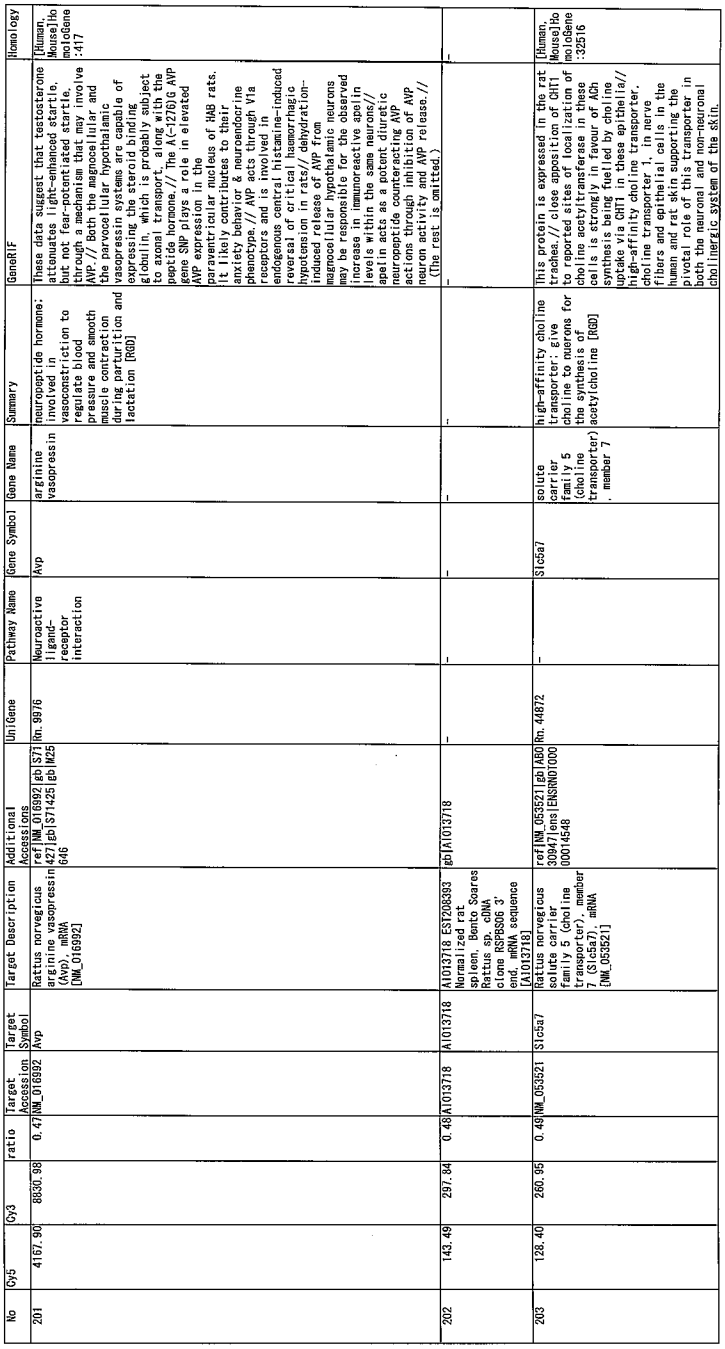


No	Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Pathway Name	Gene Symbol	Gene Name	Summary	GeneRIF	Homology
197	86.01	206.57	0.42	XM_218173	Prp31_predicted	PREDICTED: Rattus norvegicus PRP31 pre-mRNA processing factor 31 homolog (yeast) (predicted) (Prp31_predicted), mRNA [XM_218173]	ref|XM_218173|ens|ENSRNOT00000018683	Rn.99310	-	Prp31_predicted	PRP31 pre-mRNA processing factor 31 homolog (yeast) (predicted)	-	-	[Human, Mouse]HomoloGene:5980
198	118.64	273.54	0.43	NM_031663	Slc18a3	Rattus norvegicus solute carrier family 18 (vesicular acetylcholine), member 3 (Slc18a3), mRNA [NM_031663]	ref|NM_031663|gb|U09211|tc|TC57129|	Rn.9987	-	Slc18a3	solute carrier family 18 (vesicular acetylcholine), member 3	a vesicular acetylcholine transporter involved in concentrating acetylcholine into synaptic vesicles [RGD]	A model for VAChT is suggested in which the known ion pair between lysine in transmembrane domain(TMD)II and aspartate in TMDXI controls the conformation or relative position of TMDXI, which in turn controls additional TMDs in the VAChT carboxy-terminal.// VAChT was primarily localized to membranes of small synaptic vesicles in axon terminals// Semi-quantitative ultrastructural analysis reveals that from 5% to 13% of VAChT-immunoreactive presynaptic profiles contained mu opioid receptor (MOR). Additionally, 7% of VAChT presynaptic profiles directly apposed MOR axons and terminals.// This study locates the acetylcholine (ACh) binding site in the vesicular acetylcholine transporter (VAChT) and identifies the amino acid residues linked to the individual binding and rates of the transmembrane reorientation steps of a transport cycle.// VAChT interacts with clathrin-associated adaptor complexes AP-1 and AP-2	[Human, Mouse]HomoloGene:11022

[0207]

No	Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Pathway Name	Gene Symbol	Gene Name	Summary	GeneRIF	Homology
199	100.28	222.62	0.45	NM_012610	Ngfr	Rattus norvegicus nerve growth factor receptor (TNFR superfamily, member 16) (Ngfr), mRNA [NM_012610]	ref|NM_012610|gb|X05 137.1|M14164|ens| ENSRNOT00000007268	Rn.10980	Neurodegenerative Disorders	Ngfr	nerve growth factor receptor (TNFR superfamily, member 16)	receptor that can bind NGF, BDNF, NT-3, and NT-4 [RGD]	NGF-receptor complexes have two distinct diffusive states, characterized as mobile and immobile phase// The results indicate that the NGF/NGF receptor system plays a role in the pathogenesis of EV-induced POD in rats.// diminished p75NTR expression by chronic estrogen administration may exert long-term effects on survival or axonal outgrowth in symapathetic neurons// This implicates different mechanisms of neurotrophin action on kindling (mediated by TrkA) and neuronal sprouting (mediated by both TrkA and p75NTR) and suggests that sprouting involves kindling-independent neurotrophin action via p75NTR.// p75(NTR) mediates survival of embryonic pr// Nuclear translocation of p75(CD may represent a novel neurotrophin-mediated signaling pathway.// (The rest is omitted.)	[Human, Mouse]Homologene:1877
200	129.99	277.46	0.47	XM_233341	Zfyve9_predicted	PREDICTED: Rattus norvegicus zinc finger, FYVE domain containing 9 (predicted) (Zfyve9_predicted), mRNA [XM_233341]	ref|XM_233341|ens|ENSRNOT00000037523|tc| TC523508	Rn.23612	-	Zfyve9_predicted	zinc finger, FYVE domain containing 9 (predicted)	-	-	[Human, Mouse]Homologene:3527

[0208]



No	Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Pathway Name	Gene Symbol	Gene Name	Summary	GeneRIF	Homology
201	4167.90	8830.98	0.47	NM_016992	Avp	Rattus norvegicus arginine vasopressin (Avp), mRNA [NM_016992]	ref|NM_016992|gb|S71427|gb|S71425|gb|M25646	Rn.9976	Neuroactive ligand-receptor interaction	Avp	arginine vasopressin	neuropeptide hormone: involved in vasoconstriction to regulate blood pressure and smooth muscle contraction during parturition and lactation [RGD]	These data suggest that testosterone attenuates light-enhanced startle, but not fear-potentiated startle, through a mechanism that may involve AVP.// Both the magnocellular and the parvocellular hypothalamic vasopressin systems are capable of expressing the steroid binding globulin, which is probably subject to axonal transport, along with the peptide hormone.// The A(-1270)G AVP gene SNP plays a role in elevated AVP expression in the parvocellular nucleus of HAB rats. It likely contributes to their anxiety behavior & neuroendocrine phenotype.// AVP acts through V1a receptors and is involved in endogenous central histamine-induced reversal of critical haemorrhagic hypotension in rats// dehydration-induced release of AVP from magnocellular hypothalamic neurons may be responsible for the observed increase in immunoreactive apelin levels within the same neurons// apelin acts as a potent diuretic neuropeptide counteracting AVP actions through inhibition of AVP motion activity and AVP release.// (The rest is omitted.)	[Human, Mouse]HomoloGene :417
202	143.49	297.84	0.48	AI013718	AI013718	AI013718 EST208393 Normalized rat spleen, Bento Soares Rattus sp. cDNA clone RSPBS06 3' end, mRNA sequence [AI013718]	gb|AI013718	-	-	-	-	-	-	-
203	128.40	260.95	0.49	NM_053521	Slc5a7	Rattus norvegicus solute carrier family 5 (choline transporter), member 7 (Slc5a7), mRNA [NM_053521]	ref|NM_053521|gb|AB030947|ens|ENSRNOT00000014548	Rn.44872	-	Slc5a7	solute carrier family 5 (choline transporter), member 7	high-affinity choline transporter: give choline to nuerons for the synthesis of acetylcholine [RGD]	This protein is expressed in the rat trachea.// close apposition of ChT1 to reported sites of localization of choline acetyltransferase in these cells is strongly in favour of Ach synthesis being fuelled by choline uptake via ChT1 in these epithelia// high-affinity choline transporter. choline transporter-1, in nerve fibers and epithelial cells in the human and rat skin suggesting the pivotal role of this transporter in both the neuronal and non-neuronal cholinergic system of the skin.	[Human, Mouse]HomoloGene :32516

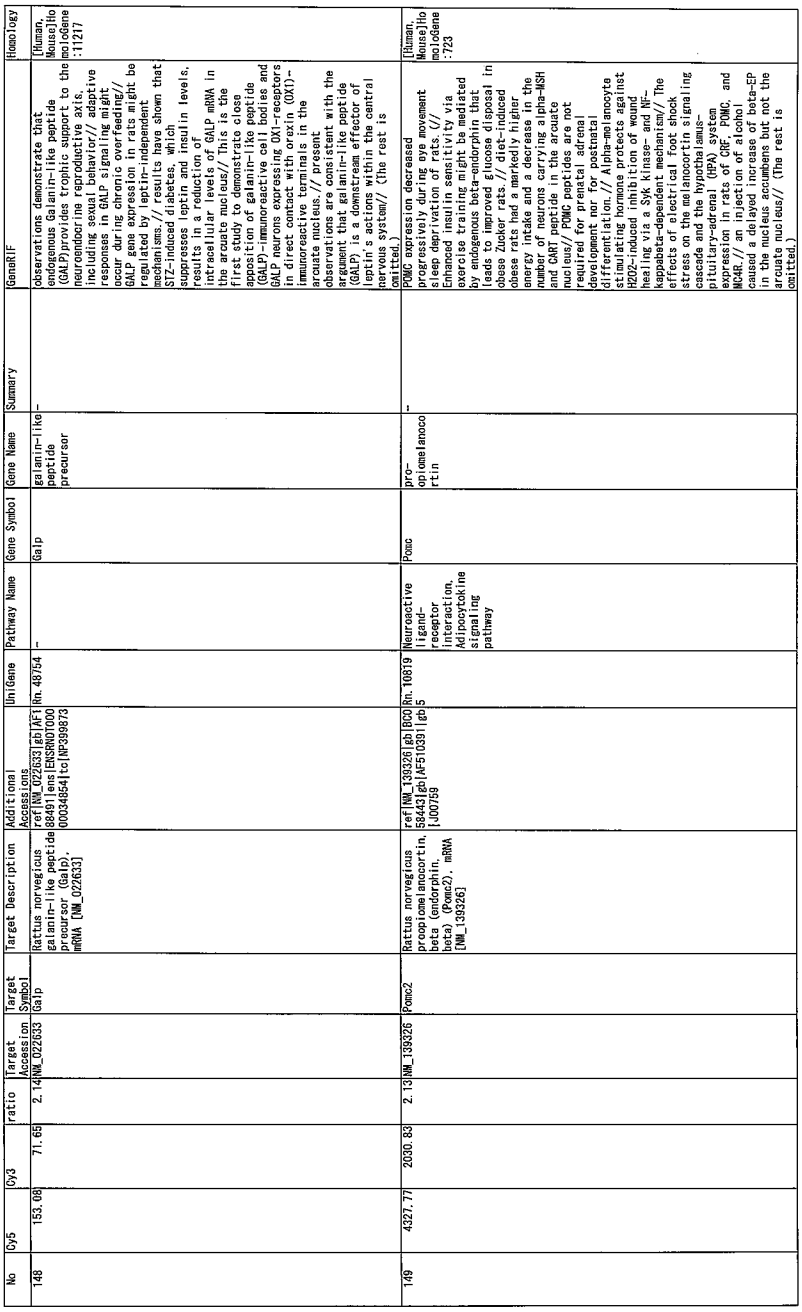
[0209] Light Touch群と比較してTickling群で2.0倍超の発現を認めた視床下部(Hy)の遺伝子のアノテーションを下記表26に示す。

[表26]

表26 T-Hy(Cy5) v.s. L-Hy(Cy3) :up regulation(Cy5>Cy3)

No	Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Pathway Name	Gene Symbol	Gene Name	Summary	GeneRIF	Homology
145	275.61	111.83	2.46	NM_012694	Slc6a3	Rattus norvegicus solute carrier family 6 (neurotransmitter transporter, dopamine), member 3 (Slc6a3), mRNA [NM_012694]	ref|NM_012694|gb|M80 570|ens|ENSRNOT00000 024015|tc|TC569830	Rn.10093	-	Slc6a3	solute carrier family 6 (neurotransmitter transporter, dopamine), member 3	acts as a sodium-dependent dopamine transporter; may play a role in regulation of dopamine metabolism and signaling [RGD]	The decrease in DAT cell surface expression in the mPFC may be responsible for decreased DAT function in the mPFC of stimulated compared with deprived rats; there is plasticity in this regulatory mechanism mediating DAT trafficking and function.// the carboxyl terminus regulates dopamine transporter export from endoplasmic reticulum// tyrosine hydroxylase and the dopamine transporter are differentially distributed in the medial- versus the lateral ventral pallidum.// Observed differences in density and distribution of DAT1 sites in Wistar Kyoto rats may lead to altered modulation of synaptic dopamine levels in cell body and mesolimbic regions, contributing to the depression-like behaviors reported in this rat strain.// dopamine transporter constitutively internalizes and recycles in a protein kinase C-regulated manner in stably transfected PC12 cell lines// dopamine membrane transporter (DAT) protein density and mRNA expression is upregulated in restricted-fed adult male rats// (The rest is omitted.)	-
146	2366.68	973.65	2.43	TC543527	TC543527	COL1_MOUSE (P01193) Corticotropin-lipotropin precursor (Pro-opiomelanocortin) (POMC) [Contains: NPP; Melanotropin gamma (Gamma-MSH); Corticotropin (Adrenocorticotropic hormone) (ACTH); Melanotropin alpha (Alpha-MSH); Corticotropin-like intermediary	tc|TC543527	-	-	-	-	-	-	-
147	120.18	55.09	2.18	BE108176	BE108176	BE108176 UI-R-BS1-ayw-g-04-0-UI.s1 UI-R-BS1 Rattus norvegicus cDNA clone UI-R-BS1-ayw-g-04-0-UI 3', mRNA sequence [BE108176]	gb|BE108176	Rn.3464	-	Ddt	D-dopachrome tautomerase	converts D-dopachrome into 5,6-dihydroxyindole [RGD]	-	[Human, Mouse]HomoloGene:1038

[0210]



No	Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Pathway Name	Gene Symbol	Gene Name	Summary	GeneRIF	Homology
148	153.08	71.65	2.14	NM_022633	Galp	Rattus norvegicus galanin-like peptide precursor (Galp), mRNA [NM_022633]	ref|NM_022633|gb|AF1 88491|ens|ENSRNOT000 00034854|tc|NP399873	Rn.48754	-	Galp	galanin-like peptide precursor	-	observations demonstrate that endogenous Galanin-like peptide (GALP)provides trophic support to the neuroendocrine reproductive axis, including sexual behavior// adaptive responses in GALP signaling might occur during chronic overfeeding// GALP gene expression in rats might be regulated by leptin-independent mechanisms.// results have shown that STZ-induced diabetes, which suppresses leptin and insulin levels, results in a reduction of intracellular levels of GALP mRNA in the arcuate nucleus// This is the first study to demonstrate close apposition of galanin-like peptide (GALP)-immunoreactive cell bodies and GALP neurons expressing OXI-receptors in direct contact with orexin (OXI)-immunoreactive terminals in the arcuate nucleus.// present observations are consistent with the argument that galanin-like peptide (GALP) is a downstream effector of leptin's actions within the central nervous system// (The rest is omitted.)	[Human, Mouse]Ho mologene :11217
149	4327.77	2030.83	2.13	NM_139326	Pomc2	Rattus norvegicus proopiomelanocortin, beta (endorphin, beta) (Pomc2), mRNA [NM_139326]	ref|NM_139326|gb|BC0 58443|gb|AF510391|gb| AJ00799	Rn.10819	Neuroactive ligand-receptor interaction, Adipocytokine signaling pathway	Pomc	pro-opiomelanocortin	-	POMC expression decreased progressively during eye movement sleep deprivation of rats.// Enhanced insulin sensitivity via exercise training might be mediated by endogenous beta-endorphin that leads to improved fuel disposal in obese Zucker rats.// diet-induced obese rats had a markedly higher energy intake and a decrease in the number of neurons carrying alpha-MSH and CART peptide in the arcuate nucleus// POMC peptides are not required for prenatal adrenal development nor for postnatal differentiation.// Alpha-melanocyte stimulating hormone protects against H2O2-induced inhibition of wound healing via a Syk kinase- and NF-kappabeta-dependent mechanism// The effects of electrical foot shock stress on the melanocortin signaling cascade and the hypothalamus-pituitary-adrenal (HPA) system were assessed// effects of CRF, POMC, and MC4R.// an injection of alcohol caused a delayed increase of beta-EP in the nucleus accumbens but not the arcuate nucleus// (The rest is omitted.)	[Human, Mouse]Ho mologene :723

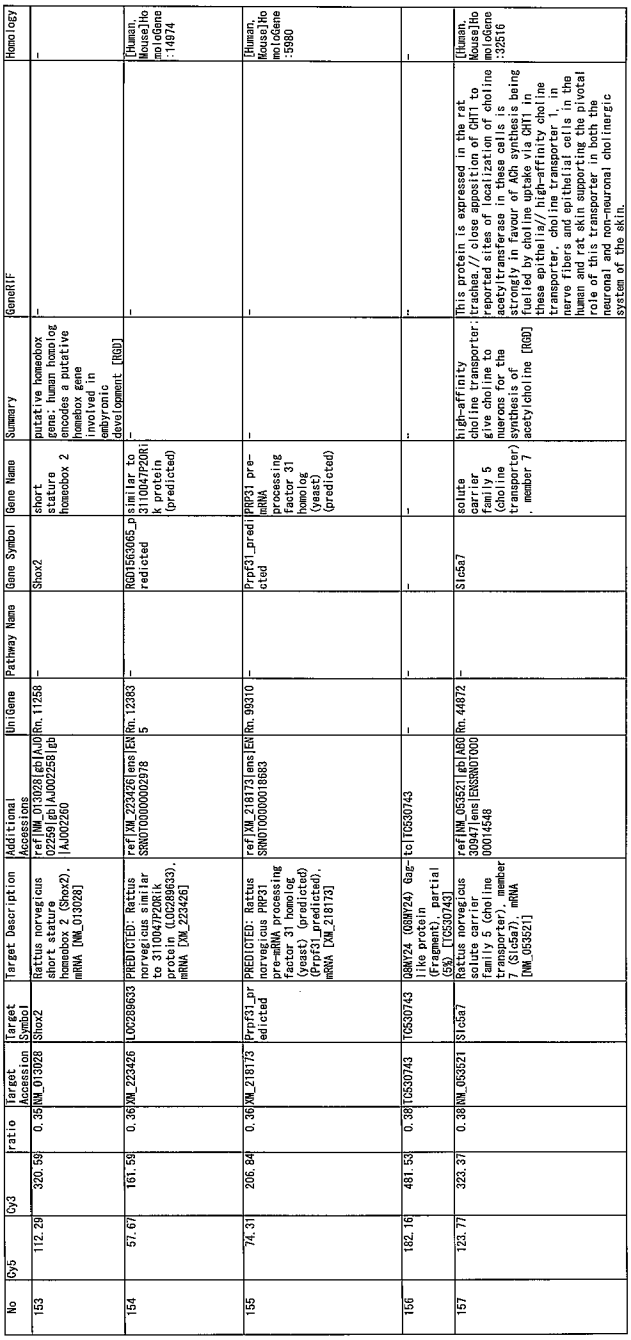
[0211] Light Touch群と比較してTickling群で0.5倍未満の発現を認めた視床下部(Hy)の遺伝子のアノテーションを下記表27に示す。

[表27]

表27 T-Hy(Cy5) v.s. L-Hy(Cy3) :down regulation(Cy5<Cy3)

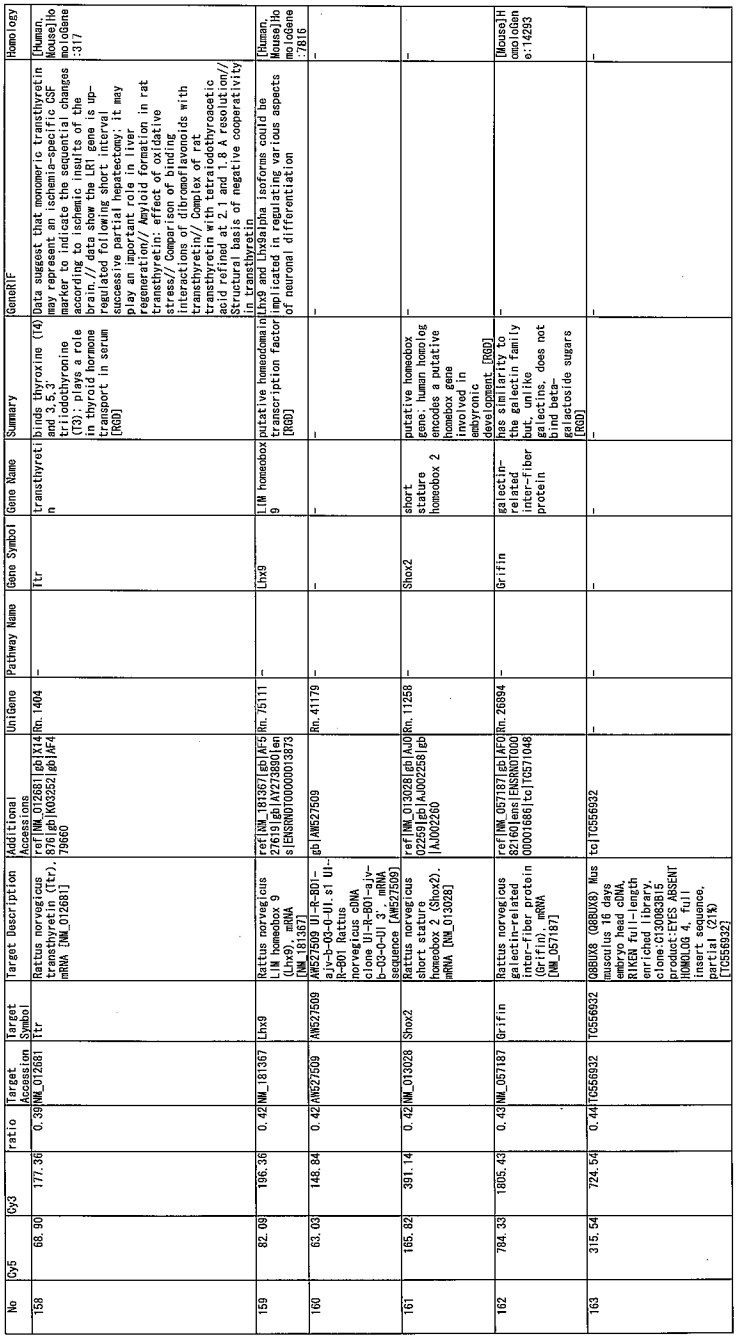
No	Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Pathway Name	Gene Symbol	Gene Name	Summary	GeneRIF	Homology
150	136.84	1121.56	0.12	BF398607	BF398607	BF398607 UI-R-BS2-beg-09-0-UI.s1 UI-R-BS2 Rattus norvegicus cDNA clone UI-R-BS2-beg-09-0-UI 3', mRNA sequence [BF398607]	gb|BF398607|gb|BF285611	Rn.45255	-	RGD1564156_predicted	similar to teratocyte-specific carboxylesterase (predicted)	-	-	-
151	56.03	317.04	0.18	NM_052805	Chrna3	Rattus norvegicus cholinergic receptor, nicotinic, alpha polypeptide 3 (Chrna3), mRNA [NM_052805]	ref|NM_052805|gb|L31621|gb|AY674284|gb|X03440	Rn.10996	-	Chrna3	cholinergic receptor, nicotinic, alpha polypeptide 3	subunit of nicotinic acetylcholine receptor that is specific to the brain and peripheral nervous system [RGD]	analysis of nicotinic acetylcholine receptor subunit binding to 4/7 alpha-conotoxins// Increased expression of the alpha 3 nicotinic receptor subunit may contribute to the mechanical hypersensitivity observed following spinal nerve ligation.// In living cells the receptor came to the plasma membrane primarily distributed in the endoplasmic reticulum.// Immunocytochemistry revealed most chromaffin cells positive for alpha3 proteins. And suggest that the most frequently encountered receptors of rat chromaffin cells should comprise alpha3beta4, alpha3beta2 with the addition of alpha5 subunits.	[Human,Mouse]HomoloGene:591
152	217.82	639.73	0.34	AW914894	AW914894	AW914894 EST346198 Normalized rat ovary, Bento Soares Rattus sp. cDNA clone RGIBM01 5' end, mRNA sequence [AW914894]	gb|AW914894|gb|BF567766|tc|TC521958	Rn.10267	-	Slc17a7	solute carrier family 17 (sodium-dependent inorganic phosphate cotransporter), member 7	a Na(+)-dependent inorganic phosphate cotransporter; may be involved in neuronal Na+ transport [RGD]	A newly proposed mechanism for altering the strength of glutamatergic synapses based on the recently identified vesicular glutamate transporter VGLUT1.// Intracortical VGLUT1/VGLUT2 coexpressing neurons can independently modulate level of expression of either transporter at discrete synapses. May serve as plastic interface between subcortical inputs (VGLUT2) and cortical inputs (VGLUT1) neurons.// a high proportion of cardiac neurones appear to be glutamatergic, but differ from other vagal afferents in expressing vesicular glutamate transporter 1// VGLUT1 and VGLUT2 proteins may often transport glutamate into vesicles within the same neuron, especially during early postnatal development, and that they are expressed widely in presumed glutamatergic, GABAergic, and cholinergic neurons, and astrocytes// the coupling of zinc transporter 3 and Vglut1 transport mechanisms regulates neurotransmitter content in secretory vesicles// (The rest is omitted.)	[Human]HomoloGene:69302

[0212]



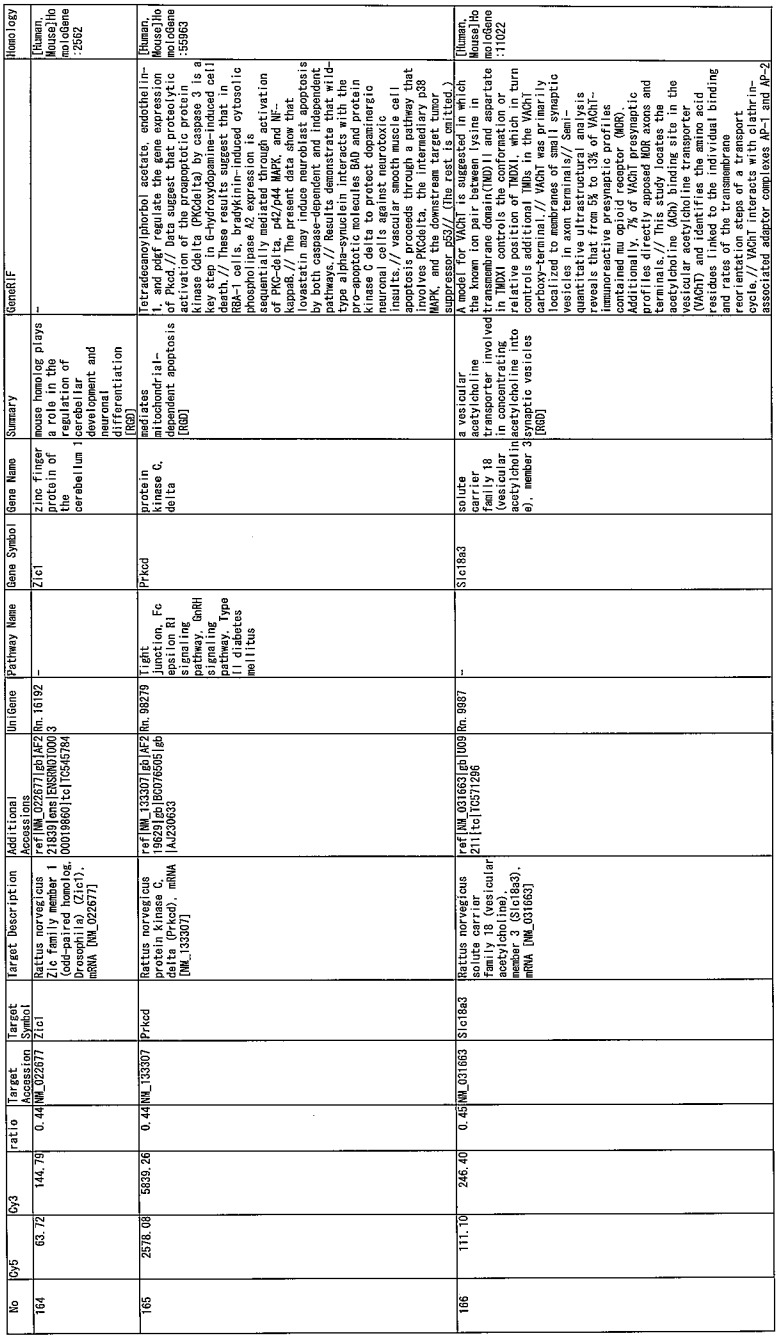
No	Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Pathway Name	Gene Symbol	Gene Name	Summary	GeneRIF	Homology
153	112.29	320.59	0.35	NM_013028	Shox2	Rattus norvegicus short stature homeobox 2 (Shox2), mRNA [NM_013028]	ref|NM_013028|gb|AJ0 02239|gb|AJ002258|gb |AJ002260	Rn.11258	-	Shox2	short stature homeobox 2	putative homeobox gene; human homolog encodes a putative homeobox gene involved in embryonic development. [RGD]	-	-
154	57.67	161.59	0.36	XM_223426	LOC289633	PREDICTED: Rattus norvegicus similar to 3110047P20Rik protein (LOC289633), mRNA [XM_223426]	ref|XM_223426|ens|EN SRNOT00000002978	Rn.12383 5	-	RGD1563065_p redicted	similar to 3110047P20Ri k protein (predicted)	-	-	[Human, Mouse]Ho moloGene :14974
155	74.31	206.84	0.36	XM_218173	PrpF31_pr edicted	PREDICTED: Rattus norvegicus PRP31 pre-mRNA processing factor 31 homolog (yeast) (predicted) (Prpf31_predicted), mRNA [XM_218173]	ref|XM_218173|ens|EN SRNOT00000018683	Rn.99310	-	PrpF31_predi cted	PRP31 pre-mRNA processing factor 31 homolog (yeast) (predicted)	-	-	[Human, Mouse]Ho moloGene :9980
156	182.16	481.53	0.38	TC530743	TC530743	Q8NY24 Q8NY24) Gag-to like protein (Fragment), partial (5%) [TC530743]	TC530743	-	-	-	-	-	-	-
157	123.77	323.37	0.38	NM_053521	Slc5a7	Rattus norvegicus solute carrier family 5 (choline transporter), member 7 (Slc5a7), mRNA [NM_053521]	ref|NM_053521|gb|AB0 30947|ens|ENSRNOT000 00014548	Rn.44872	-	Slc5a7	solute carrier family 5 (choline transporter) , member 7	high-affinity choline transporter: give choline to nuerons for the synthesis of acetylcholine [RGD]	This protein is expressed in the rat trachea.// close apposition of CHT1 to reported sites of localization of choline acetyltransferase in these cells is strongly in favour of ACh synthesis being fuelled by choline uptake via CHT1 in these epithelia//high-affinity choline transporter, choline transporter 1, in nerve fibres and epithelial cells in the human and rat, supports the pivotal role of this transporter in both the neuronal and non-neuronal cholinergic system of the skin.	[Human, Mouse]Ho moloGene :32516

[0213]



No	Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Pathway Name	Gene Symbol	Gene Name	Summary	GeneRIF	Homology
158	68.90	177.36	0.39	NM_012681	Ttr	Rattus norvegicus transthyretin (Ttr), mRNA [NM_012681]	ref|NM_012681|gb|X14876|gb|K03252|g79660|AF4	Rn.1404	-	Ttr	transthyretin	binds thyroxine (T4) and 3,5,3' triiodothyronine (T3); plays a role in thyroid hormone transport in serum [RGD]	Data suggest that monomeric transthyretin may represent an ischemia-specific CSF marker to indicate the sequential changes according to ischemic insults of the brain.// data show the LRI gene is up-regulated following short interval successive partial hepatectomy: it may play an important role in liver regeneration// Amyloid formation in rat transthyretin: effect of oxidative stress// Comparison of binding interactions of dibromoflavonoids with transthyretin// Complex of rat transthyretin with tetraiodothyroacetic acid refined at 2.1 and 1.8 A resolution// Structural basis of negative cooperativity in transthyretin	[Human, Mouse]Homologene:317
159	82.09	196.36	0.42	NM_181367	Lhx9	Rattus norvegicus LIM homeobox 9 (Lhx9), mRNA [NM_181367]	ref|NM_181367|gb|AF527609|ens|ENSRNOT00000013873	Rn.75111	-	Lhx9	LIM homeobox 9	putative homeodomain transcription factor [RGD]	Lhx9 and Lhx9alpha isoforms could be implicated in regulating various aspects of neuronal differentiation	[Human, Mouse]Homologene:7816
160	63.03	148.84	0.42	AM527609	AM527609	AM527609 U1-A-B01-a1y-b-03-0-U1.s1 U1-A-B01 Rattus norvegicus cDNA clone a1y-b-03-0-U1 3', mRNA sequence [AM527609]	gb|AM527609	Rn.41179	-	-	-	-	-	-
161	165.82	391.14	0.42	NM_013028	Shox2	Rattus norvegicus short stature homeobox 2 (Shox2), mRNA [NM_013028]	ref|NM_013028|gb|AJ002258|gb|AJ002260	Rn.11258	-	Shox2	short stature homeobox 2	putative homeobox gene; human homolog encodes a putative homeobox gene involved in embryonic development [RGD]	-	-
162	784.33	1805.43	0.43	NM_057187	Grifin	Rattus norvegicus galectin-related inter-fiber protein (Grifin), mRNA [NM_057187]	ref|NM_057187|gb|AF082160|ens|ENSRNOT00000010686|tc|TC571048	Rn.26894	-	Grifin	galectin-related inter-fiber protein	has similarity to the galectin family but, unlike galectins, does not bind beta-galactoside sugars [RGD]	-	[Mouse]Homologene:14293
163	315.54	724.54	0.44	TC556932	TC556932	Q8BUX8 (Q8BUX8) Mus musculus 16 days embryo head cDNA, RIKEN full-length enriched library, clone:C130083B15 product:EYES ABSENT HOMOLOG 4, full insert sequence, partial (21%) [TC556932]	tc|TC556932	-	-	-	-	-	-	-

[0214]

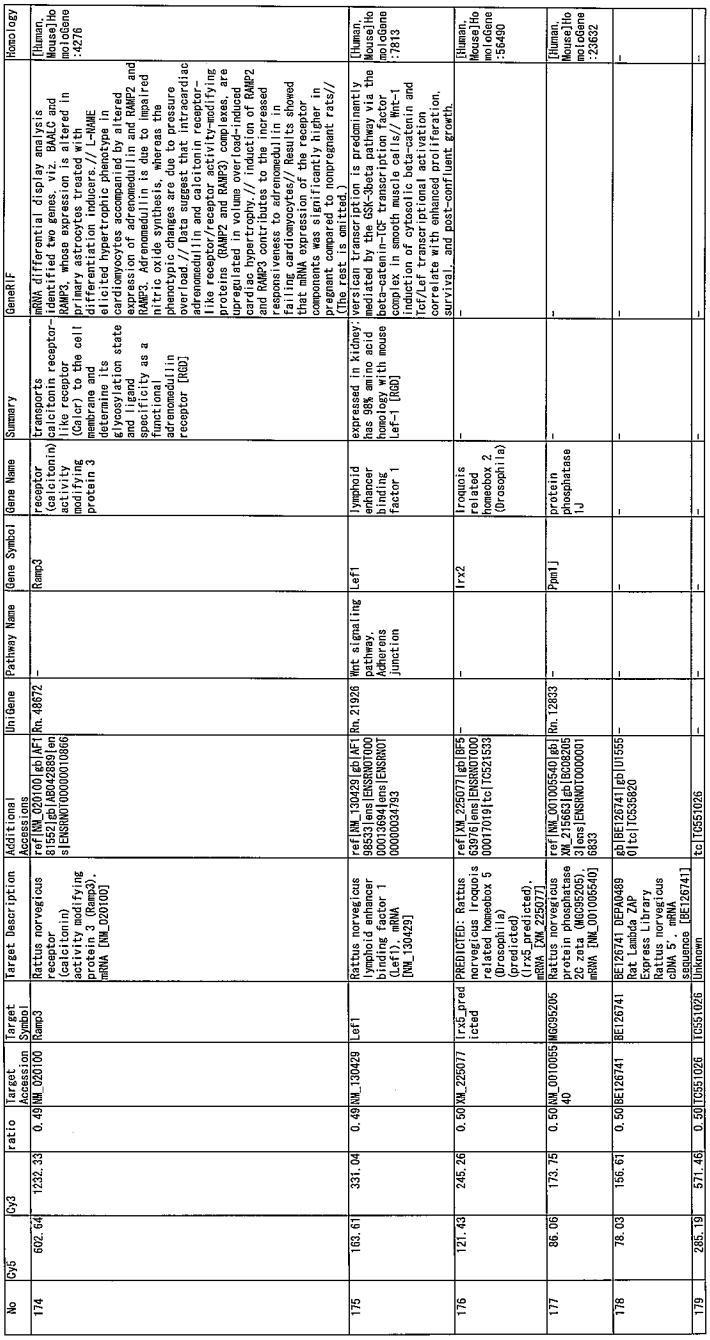


No	Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accession Nos	UniGene	Pathway Name	Gene Symbol	Gene Name	Summary	GeneRIF	Homology
164	63.72	144.79	0.44	NM_022677	Zic1	Rattus norvegicus Zic family member 1 (odd-paired homolog, Drosophila) (Zic1), mRNA [NM_022677]	ref|NM_022677|gb|AF2 21839|ens|ENSRNOT0000 0019860|tc|TC545784	Rn.16192	-	Zic1	zinc finger protein of the cerebellum 1	mouse homolog plays a role in the regulation of cerebellar development and neuronal differentiation [RGD]	-	[Human, Mouse]Homologene:2562
165	2578.08	5839.26	0.44	NM_133307	Prkcd	Rattus norvegicus protein kinase C, delta (Prkcd), mRNA [NM_133307]	ref|NM_133307|gb|AF2 19629|gb|BC076505|gb |AJ230633	Rn.98279	Tight junction, Fc epsilon RI signaling pathway, GnRH signaling pathway, Type II diabetes mellitus	Prkcd	protein kinase C, delta	mediates mitochondrial-dependent apoptosis [RGD]	Tetradecanoylphorbol acetate, endothelin-1, and pdgf regulate the gene expression of Pkcd.// Data suggest that proteolytic activation of the proapoptotic protein kinase Cdelta (PKCdelta) by caspase 3 is a key step in 6-hydroxydopamine-induced cell death.// These results suggest that in RBA-1 cells, bradykinin-induced cytosolic phospholipase A2 expression is sequentially mediated through activation of PKCdelta and MAPK and NF-kappaB.// The present data show that lovastatin may induce neuroblast apoptosis by both caspase-dependent and independent pathways.// Results demonstrate that wild-type alpha-synuclein interacts with the pro-apoptotic molecules BAD and protein kinase C delta to protect dopaminergic neuronal cells against neurotoxic insults.// vascular smooth muscle cell apoptosis proceeds through a pathway that involves PKCdelta, the intermediary p38 MAPK, and the downstream target tumor suppressor p53// (the rest is omitted.)	[Human, Mouse]Homologene:55963
166	111.10	246.40	0.45	NM_031663	Slc18a3	Rattus norvegicus solute carrier family 18 (vesicular acetylcholine), member 3 (Slc18a3), mRNA [NM_031663]	ref|NM_031663|gb|U09 211|tc|TC571296	Rn.9987	-	Slc18a3	solute carrier family 18 (vesicular acetylcholine), member 3	a vesicular acetylcholine transporter involved in concentrating acetylcholine into synaptic vesicles [RGD]	A model for VAChT is suggested in which the known ion pair between lysine in transmembrane domain(MD) 1 and aspartate in MD10 controls the conformation or relative position of TMD1, which in turn controls additional TMDs in the VAChT carboxy-terminal.// VAChT was primarily localized to membranes of small synaptic vesicles in axon terminals// Semi-quantitative ultrastructural analysis reveals that from 5% to 13% of VAChT-immunoreactive presynaptic profiles contained mu opioid receptor (MOR). Additionally, 7% of VAChT presynaptic profiles directly apposed MOR axons and terminals.// This study locates the acetylcholine (ACh) binding site in the vesicular acetylcholine transporter (VAChT) and identifies the amino acid residues linked to the individual binding and rates of the transmembrane conformational steps of a transport cycle.// VAChT interacts with clathrin-associated adaptor complexes AP-1 and AP-2	[Human, Mouse]Homologene:11022

[0215]

No	Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accession	UniGene	Pathway Name	Gene Symbol	Gene Name	Summary	GeneRIF	Homology
167	197.55	435.66	0.45	XM_345977	Cpne4_predicted	PREDICTED: Rattus norvegicus copine IV (predicted) (Cpne4_predicted), mRNA [XM_345977]	ref|XM_345977|ens|ENSRNOT00000016749	Rn.124862	-	Cpne4_predicted	copine IV (predicted)	-	-	(Human, Mouse)HomoloGene:26078
168	261.64	570.19	0.46	TC519964	TC519964	Unknown	tc|TC519964	-	-	-	-	-	-	-
169	76.38	164.56	0.46	XM_237334	RGD1311195_predicted	PREDICTED: Rattus norvegicus similar to sphingosine kinase type 1-interacting protein (predicted) (LOC316661), mRNA [XM_237334]	ref|XM_237334|ens|ENSRNOT00000022051|ENSRNOT00000022039	Rn.70007	-	RGD1311195_predicted	similar to sphingosine kinase type 1-interacting protein (predicted)	-	-	(Human, Mouse)HomoloGene:18172
170	250.19	533.43	0.47	AI178665	AI178665	AI178665 EST2223346 Normalized rat placenta, Bento Soares Rattus sp. cDNA clone RPLCU10 3' end, mRNA sequence [AI178665]	gb|AI178665|gb|AA955733|gb|BF400873	Rn.58356	-	-	similar to adaptin-ear-binding coat-associated protein 1	-	-	(Human, Mouse)HomoloGene:22902
171	431.34	911.40	0.47	BC092605	BC092605	Rattus norvegicus protein tyrosine phosphatase, non-receptor type 3 (predicted), mRNA (cDNA clone IMAGE:7309722), partial cds. [BC092605]	gb|BC092605|gb|AW918679|tc|TC520643|tc|TC520642	Rn.22271	-	Ptpn3	protein tyrosine phosphatase, non-receptor type 3	-	-	-
172	55.20	114.40	0.48	TC543142	TC543142	Unknown	tc|TC543142	-	-	-	-	-	-	-
173	1060.89	2172.29	0.49	TC567761	TC567761	Unknown	tc|TC567761	-	-	-	-	-	-	-

[0216]



No	Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Pathway Name	Gene Symbol	Gene Name	Summary	GeneRIF	Homology
174	602.64	1232.33	0.49	NM_020100	Ramp3	Rattus norvegicus receptor (calcitonin) activity modifying protein 3 (Ramp3), mRNA [NM_020100]	ref|NM_020100|gb|AF1 81562|gb|AB042889|en s|ENSRNOT00000010866	Rn.48672	-	Ramp3	receptor (calcitonin) activity modifying protein 3	transports calcitonin receptor-like receptor (Calcr) to the cell membrane and determine its glycosylation state and ligand specificity as a functional adrenomedullin receptor [RGD]	mRNA differential display analysis identified two genes, viz. BAALC and RAMP3, whose expression is altered in primary astrocytes treated with differentiation inducers.// L-NAME elicited hypertrophic phenotype in cardiomyocytes accompanied by altered expression of adrenomedullin and impaired RAMP3. Adrenomedullin is also an impaired nitric oxide synthesis, whereas the phenotypic changes are due to pressure overload.// Data suggest that intracardiac adrenomedullin and calcitonin receptor-like receptor/receptor activity-modifying proteins (RAMP2 and RAMP3) complexes, are upregulated in volume overload-induced cardiac hypertrophy.// induction of RAMP2 and RAMP3 contributes to the increased responsiveness to adrenomedullin in failing cardiomyocytes.// Results showed that mRNA expression of the receptor components was significantly higher in pregnant compared to nonpregnant rats// (The rest is omitted.)	[Human, Mouse]Ho molecGene :4276
175	163.61	331.04	0.49	NM_130429	Lef1	Rattus norvegicus lymphoid enhancer binding factor 1 (Lef1), mRNA [NM_130429]	ref|NM_130429|gb|AF1 98533|emb|ENSRNOT000 00013694|ens|ENSRNOT 00000034793	Rn.21926	Wnt signaling pathway, Adherens junction	Lef1	lymphoid enhancer binding factor 1	expressed in kidney; vertebrate transcription factor; 399 aa; contains a HMG box homology with mouse Lef-1 [RGD]	Lef1 is predominantly activated by the Wnt signaling pathway via the beta-catenin-TCF transcription factor complex in smooth muscle cells.// Wnt-1 induction of cytosolic beta-catenin and Tcf/Lef transcriptional activation correlate with enhanced proliferation, survival, and post-confluent growth.	[Human, Mouse]Ho molecGene :7813
176	121.43	245.26	0.50	XM_225077	Irx5_predicted	PREDICTED: Rattus norvegicus Iroquois related homeobox 5 (Drosophila) (predicted) (Irx5_predicted), mRNA [XM_225077]	ref|XM_225077|gb|BF5 63976|ens|ENSRNOT000 00017019|tc|TC521533	-	-	Irx2	Iroquois related homeobox 2 (Drosophila)	-	-	[Human, Mouse]Ho molecGene :56490
177	86.06	173.75	0.50	NM_0010055 40	MGI95205	Rattus norvegicus protein phosphatase 2C zeta (MGI95205), mRNA [NM_001005540]	ref|NM_001005540|gb| XM_215663|gb|BC08620 3|ens|ENSRNOT000000 6833	Rn.12633	-	Ppm1j	protein phosphatase 1J	-	-	[Human, Mouse]Ho molecGene :20632
178	78.03	156.61	0.50	BE126741	BE126741	BE126741 DEPAO489 Rat Lambda ZAP Express Library Rattus norvegicus cDNA 5' mRNA sequence [BE126741]	gb|BE126741|gb|U1555 0|tc|TC535820	-	-	-	-	-	-	-
179	285.19	571.46	0.50	TC551026	TC551026	Unknown	tc|TC551026	-	-	-	-	-	-	-

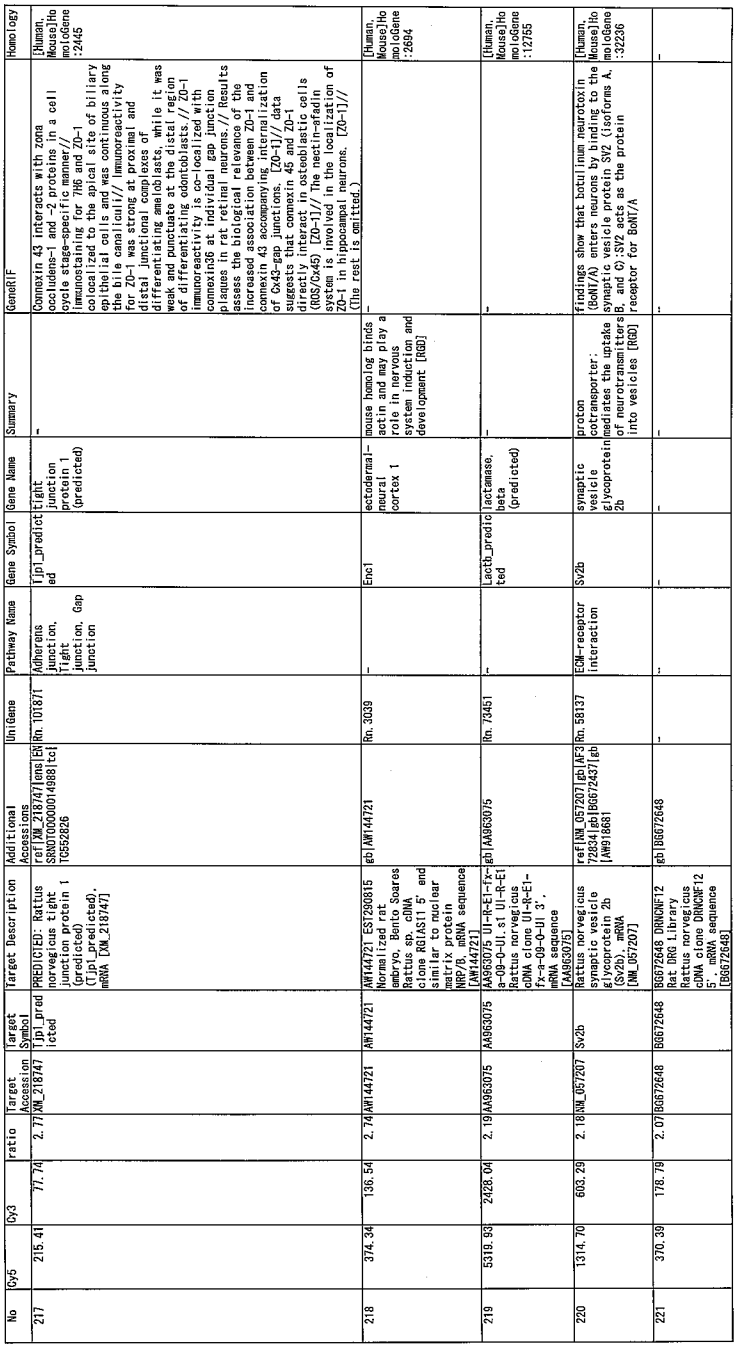
[0217] 対照群と比較してTickling群で2.0倍超の発現を認めた線条体(St)の遺伝子のアノテーションを下記表28に示す。

[表28]

表28 T-St(Cy5) v.s. C-St(Cy3) :up regulation(Cy5>Cy3)

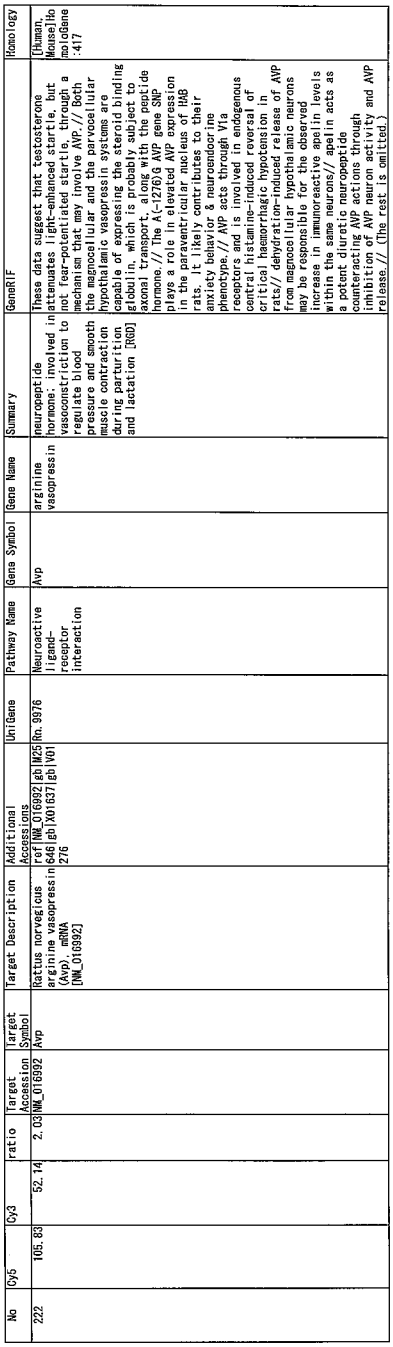
No	Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Pathway Name	Gene Symbol	Gene Name	Summary	GeneRIF	Homology
215	544.39	134.97	4.03	XM_218747	Tjp1_predicted	PREDICTED: Rattus norvegicus tight junction protein 1 (predicted) (Tjp1_predicted), mRNA (XM_218747)	ref|XM_218747|tc|TC652826	Rn.101871	Adherens junction, Tight junction, Gap junction	Tjp1_predicted	tight junction protein 1 (predicted)	-	Connexin 43 interacts with zonula occludens-1 and -2 proteins in a cell cycle stage-specific manner// immunostaining for 7H6 and ZO-1 colocalized to the apical site of biliary epithelial cells and was continuous along the bile canaliculi// Immunoreactivity for ZO-1 was strong at proximal and distal junctional complexes of differentiating ameloblasts, while it was weak and punctuate at the distal region of differentiating odontoblasts.// ZO-1 immunoreactivity is co-localized with connexin36 at individual gap junction plaques in rat retinal neurons.// Results assess the biological relevance of the increased association between ZO-1 and connexin 43 accompanying internalization of Cx43-gap junctions. [ZO-1]// data suggests that connexin 45 and ZO-1 directly interact in osteoblastic cells (ROS/Cx45) [ZO-1]// The nectin-afadin system is involved in the localization of ZO-1 in hippocampal neurons. [ZO-1]// (The rest is omitted.)	[Human, Mouse]Homologene:2445
216	534.39	147.28	3.63	XM_218747	Tjp1_predicted	PREDICTED: Rattus norvegicus tight junction protein 1 (predicted) (Tjp1_predicted), mRNA (XM_218747)	ref|XM_218747|tc|TC652826	Rn.101871	Adherens junction, Tight junction, Gap junction	Tjp1_predicted	tight junction protein 1 (predicted)	-	Connexin 43 interacts with zonula occludens-1 and -2 proteins in a cell cycle stage-specific manner// immunostaining for 7H6 and ZO-1 colocalized to the apical site of biliary epithelial cells and was continuous along the bile canaliculi// Immunoreactivity for ZO-1 was strong at proximal and distal junctional complexes of differentiating ameloblasts, while it was weak and punctuate at the distal region of differentiating odontoblasts.// ZO-1 immunoreactivity is co-localized with connexin36 at individual gap junction plaques in rat retinal neurons.// Results assess the biological relevance of the increased association between ZO-1 and connexin 43 accompanying internalization of Cx43-gap junctions. [ZO-1]// data suggests that connexin 45 and ZO-1 directly interact in osteoblastic cells (ROS/Cx45) [ZO-1]// The nectin-afadin system is involved in the localization of ZO-1 in hippocampal neurons. [ZO-1]// (The rest is omitted.)	[Human, Mouse]Homologene:2445

[0218]



No	Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Pathway Name	Gene Symbol	Gene Name	Summary	GenoFIF	Homology
217	215.41	77.74	2.77	XM_218747	Tjp1_predicted	PREDICTED: Rattus norvegicus tight junction protein 1 (predicted) (Tjp1_predicted), mRNA [XM_218747]	ref|XM_218747|ens|ENSRNOT00000014988|tc|TC552826	Rn.101871	Adherens junction, Tight junction, Gap junction	Tjp1_predicted	tight junction protein 1 (predicted)	-	Connexin 43 interacts with zona occludens-1 and -2 proteins in a cell cycle stage-specific manner// immunostaining for 7H6 and ZO-1 colocalized to the apical site of biliary epithelial cells and was continuous along the bile canaliculi// Immunoreactivity for ZO-1 was strong at proximal and distal junctional complexes of differentiating ameloblasts, while it was weak and punctuate at the distal region of differentiating odontoblasts.// ZO-1 immunoreactivity is co-localized with connexin30 at individual gap junction plaques in retinal neurons.// Results suggest the horizontal neurons of the increased association between ZO-1 and connexin 43 accompanying internalization of Cx43-gap junctions. [ZO-1]// data suggests that connexin 45 and ZO-1 directly interact in osteoblastic cells (ROS/Cx45) [ZO-1]// The nectin-afadin system is involved in the localization of ZO-1 in hippocampal neurons. [ZO-1]// (The rest is omitted.)	[Human, Mouse]Homolodene :2445
218	374.34	136.54	2.74	AW144721	AW144721	AW144721 EST290815 Normalized rat embryo, Bento Soares Rattus sp. cDNA clone RGIAS11 5' end similar to nuclear matrix protein NMP200, mRNA sequence [AW144721]	gb|AW144721	Rn.3039	-	Encl	ectodermal-neural cortex 1	mouse homolog binds actin and may play a role in nervous system induction and development [RGD]	-	[Human, Mouse]Homolodene :2694
219	5316.93	2428.04	2.19	AA963075	AA963075	AA963075 Ui-R-E1-fx-a-09-0-Ui.s1 Ui-R-E1-fx-a-09-0-Ui 3', mRNA sequence [AA963075]	gb|AA963075	Rn.73451	-	Lactb_predicted	lactamase, beta (predicted)	-	-	[Human, Mouse]Homolodene :12755
220	1314.70	603.29	2.18	NM_057207	Sv2b	Rattus norvegicus synaptic vesicle glycoprotein 2b (Sv2b), mRNA [NM_057207]	ref|NM_057207|gb|AF372834|gb|BG672437|AW918681	Rn.58137	ECM-receptor interaction	Sv2b	synaptic vesicle glycoprotein 2b	proton cotransporter: mediates the uptake of neurotransmitters into vesicles [RGD]	findings show that botulinum neurotoxin (BoNT/A) enters neurons by binding to the synaptic vesicle protein SV2 (isoforms A, B, and C).SV2 acts as the protein receptor for BoNT/A	[Human, Mouse]Homolodene :32236
221	370.39	178.79	2.07	BG672648	BG672648	BG672648 DRNGNF12 Rat DRG Library Rattus norvegicus cDNA clone DRNGNF12 5', mRNA sequence [BG672648]	gb|BG672648	-	-	-	-	-	-	-

[0219]



No	Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Pathway Name	Gene Symbol	Gene Name	Summary	GeneRIF	Homology
222	105.83	52.14	2.03	NM_016992	Avp	Rattus norvegicus arginine vasopressin (Avp), mRNA [NM_016992]	ref|NM_016992|gb|M25646|gb|X01637|gb|V01276	Rn.9976	Neuroactive ligand-receptor interaction	Avp	arginine vasopressin	neuropeptide hormone: involved in vasoconstriction to regulate blood pressure and smooth muscle contraction during parturition and lactation [KOD]	These data suggest that testosterone attenuates light-enhanced startle, but not fear-potentiated startle, through a mechanism that may involve AVP.// Both the magnocellular and the parvocellular hypothalamic vasopressin systems are capable of expressing the steroid binding globulin, which is probably subject to normal transport along with the steroid hormone.// The A(-1276)G AVP gene SNP plays a role in elevated AVP expression in the paraventricular nucleus of IHB rats. It likely contributes to their anxiety behavior & neuroendocrine phenotype.// AVP acts through V1a receptors and is involved in endogenous central histamine-induced reversal of critical haemorrhagic hypotension in rats// dehydration-induced release of AVP from magnocellular hypothalamic neurons may be responsible for the observed increase in immunoreactive apelin levels within the same neurons// apelin acts as a potent diuretic neuropeptide counteracting AVP actions through inhibition of AVP neuron activity and AVP release.// (The rest is omitted.)	[Human, Mouse]Homologene:417

[0220] 対照群と比較してTickling群で0.5倍未満の発現を認めた線条体(St)の遺伝子のアノテーションを下記表29に示す。

[表29]

表29 T-St(Cy5) v.s. C-St(Cy3) :down regulation(Cy5<Cy3)

No	Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Pathway Name	Gene Symbol	Gene Name	Summary	GeneRIF	Homology
223	73.41	657.87	0.11	BF398607	BF398607	BF398607 UI-R-BS2-baq-g-09-0-UI.s1 UI-R-BS2 Rattus norvegicus cDNA clone UI-R-BS2-baq-g-09-0-UI 3', mRNA sequence [BF398607]	gb|BF398607|gb|BF285611	Rn.45255	-	RGD1564156_predicted	similar to tetraocyte-specific carboxylesterase (predicted)	-	-	-
224	62.56	185.65	0.34	XM_218173	Prpf31_predicted	PREDICTED: Rattus norvegicus PRP31 pre-mRNA processing factor 31 homolog (yeast) (Prpf31_predicted), mRNA [XM_218173]	ref|XM_218173|ens|ENSRNOT00000018883	Rn.99310	-	Prpf31_predicted	PRP31 pre-mRNA processing factor 31 homolog (yeast) (predicted)	-	-	[Human, Mouse]HomoloGene:5980
225	229.58	616.27	0.37	TC560395	TC560395	Unknown	tc|TC560395	-	-	-	-	-	-	-
226	108.59	290.89	0.37	NM_001003929	RGD:1303100	Rattus norvegicus ciliary neurotrophic factor receptor (Cntfr), mRNA [NM_001003929]	ref|NM_001003929|gb|S54212|tc|TC573254	Rn.55036	Cytokine-cytokine receptor interaction. Jak-STAT signaling pathway	Cntfr	ciliary neurotrophic factor receptor	acts as a receptor for ciliary neurotrophic factor; may play a role in motor neuron function [RGD]	CNTF receptor-alpha is transiently expressed in the cerebral cortex surrounding the hematoma following induction of intracerebral hemorrhage, with a peak at 5 days.// CNTF-CNTFRalpha activates the JAK/STAT pathway leading to enhanced Cx43 expression and intercellular coupling.// Results show that ciliary neurotrophic factor (CNTF) and its receptor (CNTFRalpha) are differentially regulated in hippocampal neurons and reactive astrocytes following kainic acid injection.	[Human, Mouse]HomoloGene:9619

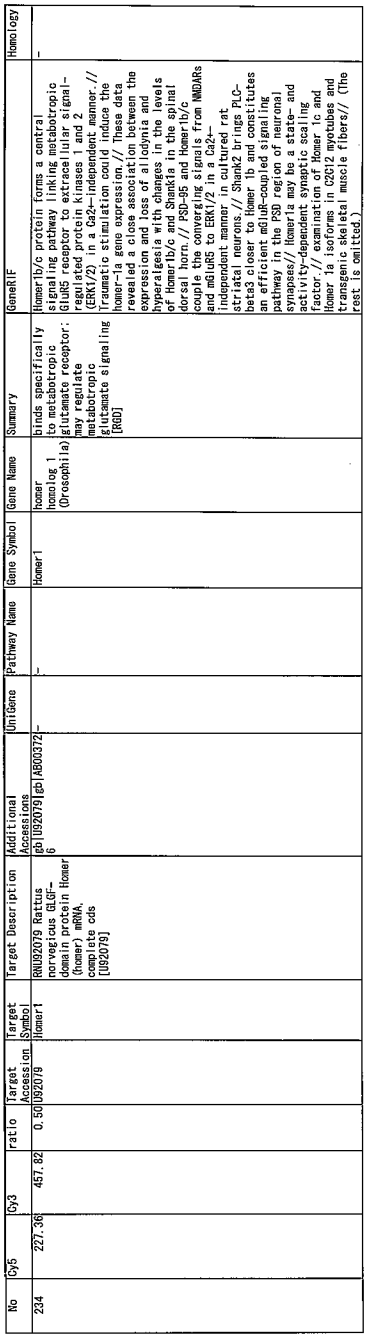
[0221]

No	Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accession	UniGene	Pathway Name	Gene Symbol	Gene Name	Summary	GeneRIF	Homology
227	147.03	378.82	0.39	NM_053859	Slc17a7	Rattus norvegicus solute carrier family 17 (sodium-dependent inorganic phosphate cotransporter), member 7 (Slc17a7), mRNA [NM_053859]	ref|NM_053859.1|gb|U07609.1|m|ENSRNOT00000028064|tc|TC568551	Rn.10267	-	Slc17a7	solute carrier family 17 (sodium-dependent inorganic phosphate cotransporter), member 7	a Na(+)-dependent inorganic phosphate cotransporter; may be involved in neuronal Na+ transport [RGD]	A newly proposed mechanism for altering the strength of glutamatergic synapses based on the recently identified vesicular glutamate transporter VGLUT1, // intracortical VGLUT1/VGLUT2 coexpressing neurons can independently modulate level of expression of either transporter at discrete synapses. May serve as plastic interface between subcortical thalamic input (VGLUT2) and cortical output (VGLUT1) neurons.// a high proportion of cardiac neurones appear to be glutamatergic, but differ from other vagal afferents in expressing vesicular glutamate transporter 1// VGLUT1 and VGLUT2 proteins may often transport glutamate into vesicles within the same neuron, especially during early postnatal development, and that they are expressed widely in presumed glutamatergic, GABAergic and glycinergic neurons, and astrocytes,// the coupling of zinc transporter 3 and Vglut1 transport mechanisms regulates neurotransmitter content in secretory vesicles// (The rest is omitted.)	[Human]HomoloGene:69302
228	138.21	345.06	0.40	A_44_P30261	A_44_P302611	Unknown	none	-	-	-	-	-	-	-
229	575.44	1368.10	0.42	BF546193	BF546193	UI-R-C1-km-d-04-0-UI.r1 UI-R-C1 Rattus norvegicus cDNA clone UI-R-C1-km-d-04-0-UI 5', mRNA sequence [BF546193]	gb|BF546193|tc|TC6560395	Rn.174580	-	-	-	-	-	-
230	540.01	1257.47	0.43	XM_231625	RGD1309884_predicted	PREDICTED: Rattus norvegicus similar to 2010012F05Rik protein (LOC500373), mRNA [XM_231625]	ref|XM_231625.1|gb|BF418724.1|AI639434|en|ENSRNOT00000052393	-	-	-	similar to 2010012F05Rik protein	-	-	[Human, Mouse]HomoloGene:57102
231	74.03	162.94	0.45	NM_133303	Bhlhb3	Rattus norvegicus basic helix-loop-helix domain containing, class B3 (Bhlhb3), mRNA [NM_133303]	ref|NM_133303.1|ref|XM_578618|gb|AF009329.1|tc|TC569016	Rn.10784	-	Bhlhb3	basic helix-loop-helix domain containing, class B3	may play a role in regulating neuronal differentiation during development and adaptive neuronal plasticity and neurite outgrowth in the adult [RGD]	Dec1 and Dec2 are regulators of the mammalian molecular clock, and form a fifth clock-gene family [dec1 & dec2]	[Human, Mouse]HomoloGene:11549

[0222]

No	Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Pathway Name	Gene Symbol	Gene Name	Summary	GeneRIF	Homology
232	1401.33	2918.25	0.48	NM_012829	Cck	Rattus norvegicus cholecystokinin (Cck), mRNA [NM_012829]	ref|NM_012829|gb|X01032|gb|K01259|gb|M25942	Rn.9781	Neuroactive ligand-receptor interaction	Cck	cholecystokinin	brain-gut peptide with hemacrine and autocrine function in the gut [RGD]	CCK preadministration to obese rats did not affect ghrelin-induced food intake.// A study of the hypothesis that CCK in the rostral ventromedial medulla may engage descending pain facilitatory pathways to enhance spinal nociceptive transmission and attenuate morphine antinociception.// Co-expression patterns of the neuropeptides vasoactive intestinal peptide and cholecystokinin with the transduction molecules alpha-gustducin and T1R2 in rat taste receptor cells.// Data suggest that cholecystokinin may play a role in the generation of negative affective states indexed by 22-kilohertz (kHz) ultrasonic calls in certain regions of the brain.// procholecystokinin undergoes parallel pathways of proteolytic cleavages// Plasma levels CCK and CGRP were significantly increased through 3 hours and 7 days postinjury, with the peak at 72 hours. CCK in jejunum changed as in plasma.// The degree of colocalization of the prohormone convertase (PC) enzymes PC1, PC2, and PC5 with CCK in rat brain is regionally specific.// (The rest is omitted.)	[Human, Mouse]HomoloGene:583
233	1336.22	2730.74	0.49	AW914894	AW914894	AW914894 EST346198 Normalized rat ovary, Bento Soares Rattus sp. cDNA clone RGIBM01 5' end, mRNA sequence [AW914894]	gb|AW914894|gb|BF567766|tc|TC521958	Rn.10267	-	Slc17a7	solute carrier family 17 (sodium-dependent inorganic phosphate cotransporter), member 7	a Na(+)-dependent inorganic phosphate cotransporter; may be involved in neuronal Na+ transport [RGD]	A newly proposed mechanism for altering the strength of glutamatergic synapses based on the recently identified vesicular glutamate transporter VGLUT1.// Intracortical VGLUT1/VGLUT2 coexpressing neurons can independently modulate level of expression of either transporter at discrete synapses. May serve as plastic interface between subcortical thalamic input (VGLUT2) and cortical output (VGLUT1) neurons.// a high proportion of cardiac neurones appear to be glutamatergic, but differ from other vagal afferents in expressing vesicular glutamate transporter 1// VGLUT1 and VGLUT2 proteins may often transport glutamate into vesicles within the same neuron, especially during early postnatal development, and that they are expressed widely in presumed glutamatergic, GABAergic, and cholinergic neurons, and astrocytes// the coupling of zinc transporter 3 and Vglut1 transport mechanisms regulates neurotransmitter content in secretory vesicles// (The rest is omitted.)	[Human]HomoloGene:69302

[0223]



No	Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Pathway Name	Gene Symbol	Gene Name	Summary	GeneRIF	Homology
234	227.36	457.82	0.50	U92079	Homer1	RNU92079 Rattus norvegicus GLGF-domain protein Homer (homer) mRNA, complete cds [U92079]	gb|U92079|gb|AB003723	-	-	Homer1	homer homolog 1 (Drosophila)	binds specifically to metabotropic glutamate receptor: may regulate metabotropic glutamate signaling [RGD]	Homer1b/c protein forms a central signaling pathway linking metabotropic GluR5 receptor to extracellular signal-regulated protein kinases 1 and 2 (ERK1/2) in a Ca(2+)-independent manner.// Traumatic stimulation could induce the homer-1a gene expression.// These data revealed a close association between the expression and loss of allodynia and hyperalgesia with changes in the levels of Homer1b/c and Shank1a in the spinal dorsal horn.// PSD-95 and Homer1b/c couple the converging signals from NMDARs and mGluR5 to ERK1/2 in a Ca(2+)-independent manner in cultured rat cortical neurons.// Shank2 brings beta3 class Pix to Homer 1b and constitutes an efficient mGluR-coupled signaling pathway in the PSD region of neuronal synapses.// Homer1a may be a state- and activity-dependent synaptic scaling factor.// examination of Homer 1c and Homer 1a isoforms in C2C12 myotubes and transgenic skeletal muscle fibers// (The rest is omitted.)	-

[0224] Light Touch群と比較してTickling群で2.0倍超の発現を認めた線条体(St)の遺伝子のアノテーションを下記表30に示す。

[表30]

表30 T-St(Cy5) v.s. L-St(Cy3) :up regulation(Cy5>Cy3)

No	Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Pathway Name	Gene Symbol	Gene Name	Summary	GeneRIF	Homology
204	203.75	95.09	2.14	BG194469	BG194469	BG194469 UI-R-CN1-cma-l-10-0-UI.s1 UI-R-CN1 Rattus norvegicus cDNA clone UI-R-CN1-cma-l-10-0-UI 3', mRNA sequence [BG194469]	gb|BG194469|gb|AW142499	Rn.16176	-	RGD1563824_predicted	similar to Wilms tumor 1-associating protein (WT1-associated protein) homolog) (predicted)	-	-	[Human, Mouse]HomoloGene:68422
205	108.13	52.68	2.05	XM_237952	LOC290372	PREDICTED: Rattus norvegicus similar to expressed sequence AU021034 (LOC290372), mRNA [XM_237952]	ref|XM_237952|gb|BF544533|tc|TC54189	Rn.19611	-	RGD1560137_predicted	similar to expressed sequence AU021034 (predicted)	-	-	[Human, Mouse]HomoloGene:52240
206	271.17	132.24	2.05	BG672648	BG672648	BG672648 DRNGWF12 Rat DRG Library Rattus norvegicus cDNA clone DRNGWF12 5', mRNA sequence [BG672648]	gb|BG672648	-	-	-	-	-	-	-

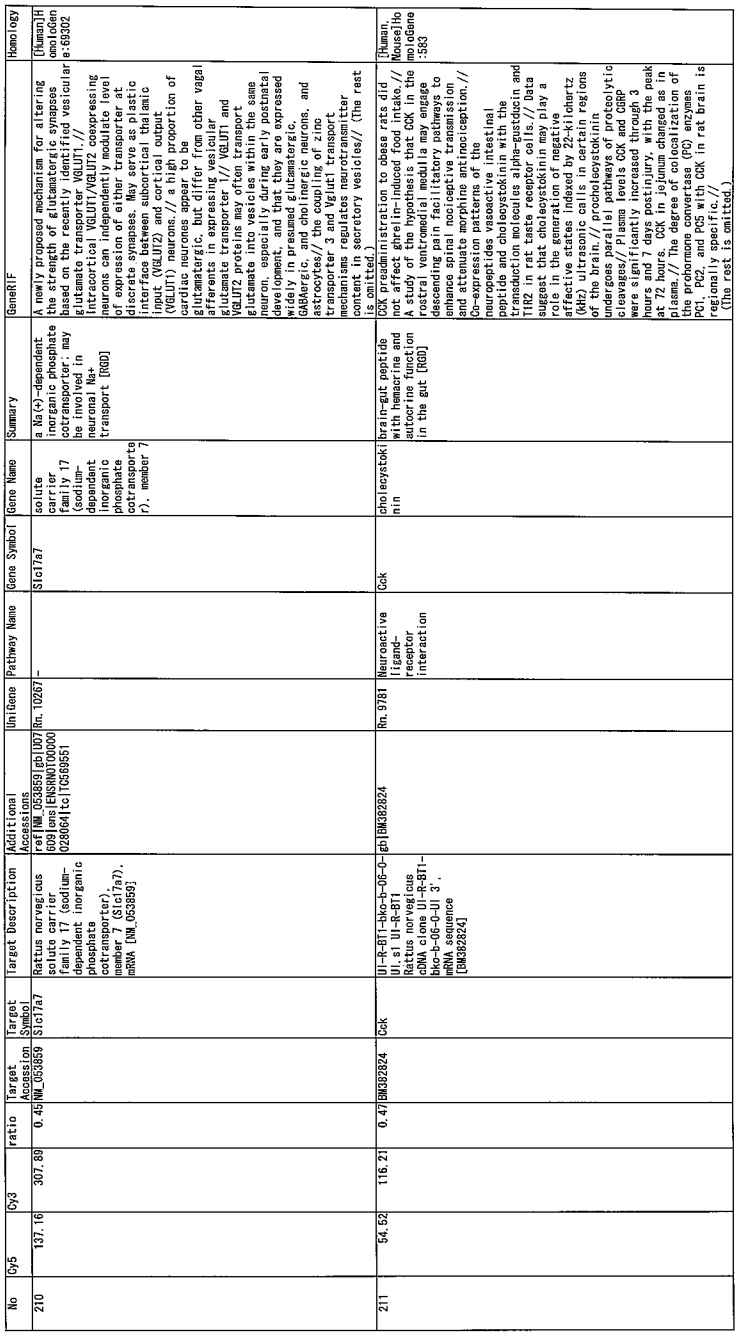
[0225] Light Touch群と比較してTickling群で0.5倍未満の発現を認めた線条体(St)の遺伝子のアノテーションを下記表31に示す。

[表31]

表31 T-St(Cy5) v.s. L-St(Cy3) :down regulation(Cy5<Cy3)

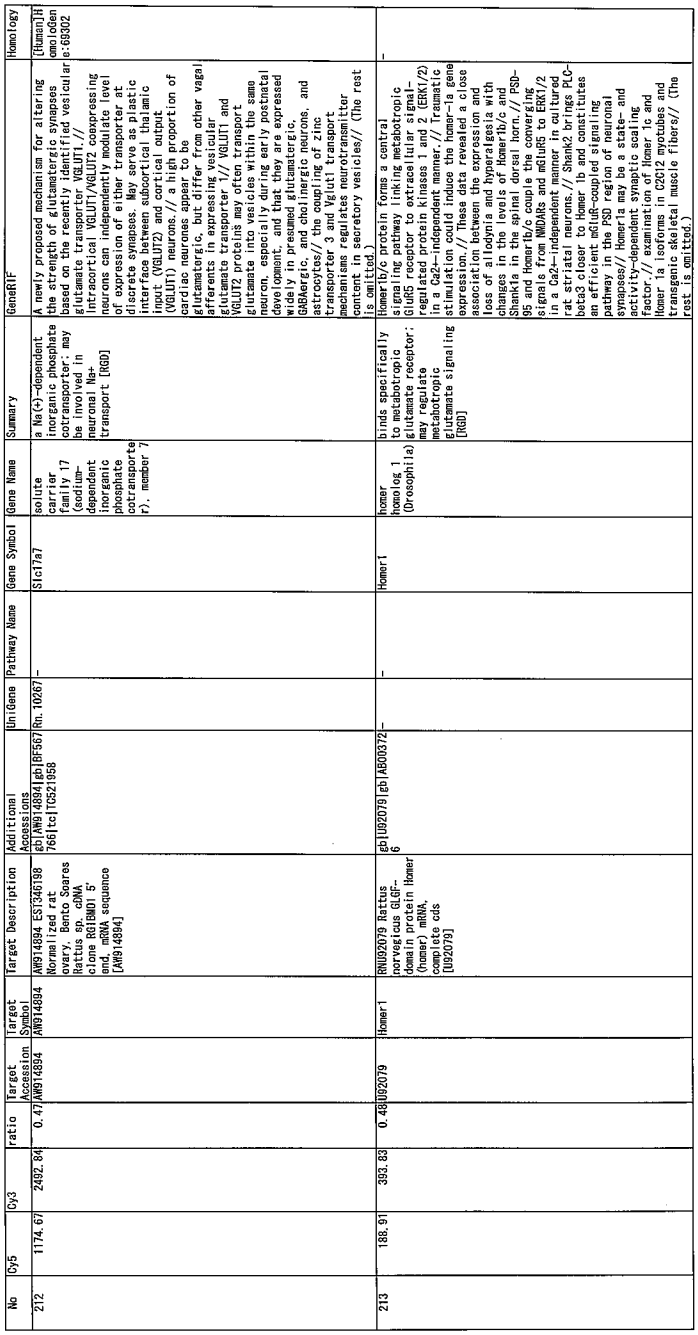
No	Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Pathway Name	Gene Symbol	Gene Name	Summary	GeneRIF	Homology
207	62.08	591.13	0.11	BF398607	BF398607	BF398607 UI-R-BS2-baq-g-09-0-UI.s1 UI-R-BS2 Rattus norvegicus cDNA clone UI-R-BS2-baq-g-09-0-UI 3', mRNA sequence [BF398607]	gb|BF398607|gb|BF285611	Rn.45255	-	RGD1564156_predicted	similar to teratocyte-specific carboxylesterase (predicted)	-	-	-
208	55.32	141.38	0.39	XM_218173	Prpf31_predicted	PREDICTED: Rattus norvegicus PRP31 pre-mRNA processing factor 31 homolog (yeast) (predicted) (Prpf31_predicted), mRNA [XM_218173]	ref|XM_218173|ens|ENSRNOT00000018683	Rn.99310	-	Prpf31_predicted	PRP31 pre-mRNA processing factor 31 homolog (yeast) (predicted)	-	-	[Human, Mouse]HomoloGene:5980
209	83.97	190.00	0.44	XM_217838	Vip	PREDICTED: Rattus norvegicus vasoactive intestinal polypeptide (Vip), mRNA [XM_217838]	ref|XM_217838|gb|AY029341|ens|ENSRNOT00000025477|tc|TC537816	Rn.18675	Neuroactive ligand-receptor interaction	Vip	vasoactive intestinal polypeptide	peptide that causes vasodilation [RGD]	Vasoactive intestinal polypeptide regulates dynamic changes in estrous cycle morphometry: impact on gonadotropin-releasing hormone neurons// Significant changes in NPY and VIP prostate nerve fibers, showing an increase in periurethral ducts at sex maturation.// Co-expression patterns of the neuropeptides vasoactive intestinal peptide and cholecystokinin with the transduction molecules alpha-gustducin and TTR2 in rat taste receptor cells.// VIP had a modulatory action on jejunal potassium absorption when injected into the nucleus tractus solitarius.// VIP can modulate not only immune responses but also hormonal responses during acute inflammation.// The increased noradrenergic innervation and the decreased effects of VIP in mediating inhibitory nerves may largely relate to the peristaltic abnormalities seen in the isogrefted LEW rat jejunum.// Aging reduces vasoactive intestinal peptide (VIP) receptor mRNA and eliminates diurnal expression of VIP mRNA within the suprachiasmatic nucleus of aged male rats.// (The rest is omitted.)	[Human, Mouse]HomoloGene:2539

[0226]



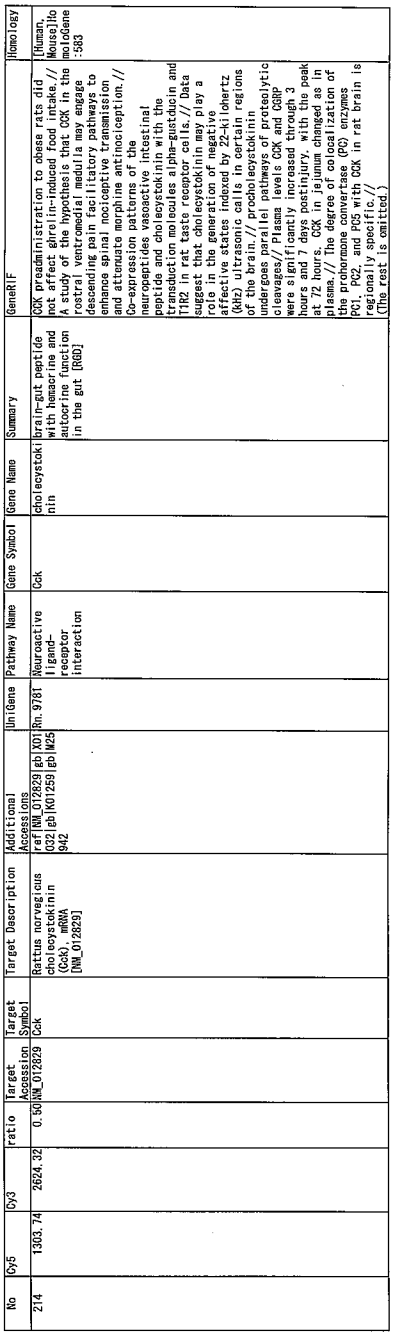
No	Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Pathway Name	Gene Symbol	Gene Name	Summary	GeneRIF	Homology
210	137.16	307.89	0.45	NM_053859	Slc17a7	Rattus norvegicus solute carrier family 17 (sodium-dependent inorganic phosphate cotransporter), member 7 (Slc17a7), mRNA [NM_053859]	ref|NM_053859|gb|U07609|ens|ENSRNOT00000028064|tc|TC569551	Rn.10267	-	Slc17a7	solute carrier family 17 (sodium-dependent inorganic phosphate cotransporter), member 7	a Na(+)-dependent inorganic phosphate cotransporter; may be involved in neuronal Na+ transport [RGD]	A newly proposed mechanism for altering the strength of glutamatergic synapses based on the recently identified vesicular glutamate transporter VGLUT1.// Intracortical VGLUT1/VGLUT2 coexpressing neurons can independently modulate level of expression of either transporter at discrete synapses. May serve as plastic interface between subcortical thalamic (VGLUT2) and cortical output (VGLUT1) neurons.// a gh proportion of cardiac neurons appear to be synthesize glutamatergic, but differ from other vagal afferents in expressing vesicular glutamate transporter 1// VGLUT1 and VGLUT2 proteins may often transport glutamate into vesicles within the same neuron, especially during early postnatal development, and that they are expressed widely in presumed glutamatergic, GABAergic, and cholinergic neurons, and astrocytes// the coupling of zinc transporter 3 and Vglut1 transport mechanisms regulates neurotransmitter content in secretory vesicles// (The rest is omitted.)	[Human]Homologene:69302
211	54.52	116.21	0.47	BM382824	Cck	UI-R-BT1-bko-b-06-0-UI.s1 UI-R-BT1 Rattus norvegicus cDNA clone UI-R-BT1-bko-b-06-0-UI 3', mRNA sequence [BM382824]	gb|BM382824	Rn.9781	Neuroactive ligand-receptor interaction	Cck	cholecystokinin	brain-gut peptide with hormactine and autocrine function in the gut [RGD]	CCK preadministration to obese rats did not affect ghrelin-induced food intake.// A study of the hypothesis that CCK in the rostral nucleus tractus solitarii may engage descending pain facilitatory pathways to enhance spinal nociceptive transmission and attenuate morphine antinociception.// Co-expression patterns of the neuropeptides vasoactive intestinal peptide and cholecystokinin with the transduction molecules alpha-gustducin and T1R2 in rat taste receptor cells.// Data suggest that cholecystokinin may play a role in the generation of negative affective states indexed by 22-kilohertz (kHz) ultrasonic calls in certain regions of the brain.// procholecystokinin undergoes parallel pathways of proteolytic cleavages// Plasma levels CCK and CGRP were significantly increased through 3 hours and 7 days postinjury, with the peak at 72 hours// CCK in jejunum changed as in plasma// The degree of conversion of the prohormone convertase (PC) enzymes PC1, PC2, and PC5 with CCK in rat brain is regionally specific.// (The rest is omitted.)	[Human, Mouse]Homologene:583

[0227]



No	Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Pathway Name	Gene Symbol	Gene Name	Summary	GeneRIF	Homology
212	1174.67	2492.84	0.47	AW914894	AW914894	AW914894 ES1346198 Normalized rat ovary, Bento Soares Rattus sp. cDNA clone rBS1BN01 5' end, mRNA sequence [AW914894]	gb|AW914894|gb|BF567766|tc|TCG21958	Rn. 10267	-	Slc17a7	solute carrier family 17 (sodium-dependent inorganic phosphate cotransporter), member 7	a Na(+)-dependent inorganic phosphate cotransporter; may be involved in neuronal Na+-dependent transport [RGD]	A newly proposed mechanism for altering the strength of glutamatergic synapses based on the recently identified vesicular glutamate transporter VGLUT1.// Intracortical VGLUT1/VGLUT2 coexpressing neurons can independently modulate level of excitation either through their discrete synapses. May serve as plastic interface between subcortical thalamic input (VGLUT2) and cortical output (VGLUT1) neurons.// a high proportion of cardiac neurones appear to be glutamatergic, but differ from other vagal afferents in expressing vesicular glutamate transporter 1// VGLUT1 and VGLUT2 proteins may often transport glutamate into vesicles within the same neuron, especially during early postnatal development, and that they are expressed widely in presumed glutamatergic, GABAergic, and cholinergic neurons, and astrocytes// the coupling of zinc transporter 3 and Vglut1 transport mechanisms regulates neurotransmitter content in secretory vesicles// (The rest is omitted.)	[Human]Homologene:69302
213	188.91	393.83	0.48	U92079	Homer1	RNU92079 Rattus norvegicus GLGF-domain protein Homer (homer) mRNA, complete cds [U92079]	gb|U92079|gb|AB006372	-	-	Homer1	homer homolog 1 (Drosophila)	binds specifically to metabotropic glutamate receptor; may regulate metabotropic glutamate signaling [RGD]	Homer1b/c protein forms a central signaling pathway linking metabotropic GluR5 receptor to extracellular signal-regulated protein kinases 1 and 2 (ERK1/2) in a Ca2+-independent manner.// Traumatic stimulation could induce the homer-1a gene expression.// These data revealed a close association between the expression and loss of allodynia and hyperalgesia with changes in the levels of Homer1b/c and Shank1a in the spinal dorsal horn.// PSD-95 and Homer1b/c couple the converging signals from NMDARs and mGluR5 to ERK1/2 in a Ca2+-independent manner in cultured rat striatal neurons.// Shank2 brings PLC-beta1 closer to Homer1b and constitutes an efficient mGluR-coupled signaling pathway in the PSD region of neuronal synapses// Homer1a may be a state- and activity-dependent synaptic scaling factor.// examination of Homer 1c and Homer 1a isoforms in C2C12 myotubes and transgenic skeletal muscle fibers// (The rest is omitted.)	-

[0228]



No	Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Pathway Name	Gene Symbol	Gene Name	Summary	GeneRIF	Homology
214	1303.74	2624.32	0.50	NM_012829	Cck	Rattus norvegicus cholecystokinin (Cck), mRNA [NM_012829]	ref|NM_012829|CO32|gb|K01259|942 gb|X01|gb|M25	Rn.9781	Neuroactive ligand-receptor interaction	Cck	cholecystokinin	brain-gut peptide with hemaorine and autocorine function in the gut [RGD]	CCK preadministration to obese rats did not affect ghrelin-induced food intake.// A study of the hypothesis that CCK in the rostral ventromedial medulla may engage descending pain facilitatory pathways to enhance spinal nociceptive transmission and attenuate morphine antinociception.// Co-expression patterns of the neuropeptides vasoactive intestinal peptide and cholecystokinin with the transduction molecules alpha-gustducin and T1R2 in rat taste receptor cells.// Data suggest that cholecystokinin may play a role in the generation of negative affective states induced by 22-kilohertz (kHz) ultrasonic calls in certain regions of the brain.// procholecystokinin undergoes parallel pathways of proteolytic cleavages.// Plasma levels CCK and CGRP were significantly increased through 3 hours and 7 days postinjury. with the peak at 72 hours. CCK in jejunum changed as in plasma.// The degree of colocalization of the prohormone convertase (PC) enzymes PC1, PC2, and PC5 with CCK in rat brain is regionally specific.// (The rest is omitted.)	[Human, Mouse]Ho molOGene :583

[0229] 対照群と比較してTickling群で2.0倍超の発現を認めた唾液腺(Sg)の遺伝子のアノテーションを下記表32に示す。

[表32]

表32 T-Sg(Cy5) v.s. C-Sg(Cy3) up regulation(Cy5>Cy3)

No	Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accession	UniGene	Pathway Name	Gene Symbol	Gene Name	Summary	GeneRIF	Homology
278	3234.68	141.42	22.87	XM_345749	XM_345749	Rattus norvegicus similar to immunoglobulin heavy chain (LOC366782), mRNA [XM_345749].	gb|XM_345749	-	-	-	-	-	-	-
279	27702.10	1848.55	14.99	XM_214947	Klk1c10	PREDICTED: Rattus norvegicus T-kininogenase (Klk1c10), mRNA [XM_214947]	ref|XM_214947|gb|AY041899|tc|TC565528	Rn.136578	-	-	T-kininogenase	-	-	[Mouse]Homologene.83264
280	32731.46	2472.09	13.24	NM_175759	Klks3	Rattus norvegicus kallikrein, submaxillary gland S3 (Klks3), mRNA [NM_175759]	ref|NM_175759|gb|AY056616|ens|ENSRNOT00000025723	Rn.34527	-	Klks3	kallikrein, submaxillary gland S3	a kallikrein-related serine protease; first isolated from the rat submaxillary gland; acts as a potent enzymatic vasoconstrictor [RGD]	-	-
281	70828.46	5776.93	12.26	NM_012677	Ton	Rattus norvegicus tonin (Ton), mRNA [NM_012677]	ref|NM_012677|gb|M11565|M23378|ens|ENSRNOT00000025701	Rn.9882	-	Ton	tonin	serine protease involved in generating the vasoconstrictor angiotensin II from precursors [RGD]	tonin may play a role in the process of heart hypertrophy// expression in the rat adult and modulation of the central production of angiotensin II	-
282	205523.92	18028.99	11.40	NM_012684	Vcsa1	Rattus norvegicus variable coding sequence A1 (Vcsa1), mRNA [NM_012684]	ref|NM_012684|gb|M63112|gb|X52467|gb|M59467	Rn.9927	-	Vcsa1	variable coding sequence A1	a prochormone-like protein [RGD]	Sialorphin increased, in a dose-related manner, the occurrence of intromissions across the successive ejaculatory sequences.// Sialorphin protects endogenous enkephalins released after nociceptive stimuli by inhibiting neprilysin in vivo. It is a natural systemically active regulator of NEP activity & is a physiological modulator of pain perception after injury	-
283	152232.51	17414.66	8.74	NM_022709	RGD:61985	Rattus norvegicus SMR2 (Smr2), mRNA [NM_022709]	ref|NM_022709|gb|J05490|tc|TC514	Rn.16277	-	-	SMR2	mRNA expression is significantly higher in males than in females; has similarity to the salivary glutamine-rich proteins (GRP) expressed in submaxillary gland; may also be related to proline rich proteins [RGD]	-	-

[0230]

No	Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accession	UniGene	Pathway Name	Gene Symbol	Gene Name	Summary	GeneRIF	Homology
284	1543.60	182.10	8.48	NM_001005382	Klk12	Rattus norvegicus glandular kallikrein 12 submandibular/renal (Klk12), mRNA [NM_001005382]	NM_001005382|pb|NM_213567|pb|NM_191648|ens|ENSRNOT00000009256	Rn.14198	-	Klk12	glandular kallikrein 12 submandibular/renal	-	-	(Human, Mouse)Homologene:81694
285	3257.87	451.12	7.22	NM_001000441	Olr1223_predicted	Rattus norvegicus olfactory receptor 1223 (predicted) (Olr1223_predicted), mRNA [NM_001000441]	ref|NM_001000441|pb|XM_236067|ens|ENSRNOT00000049709	Rn.14354	-	Olr1223_predicted	olfactory receptor 1223 (predicted)	Olfactory receptors interact with odorant molecules in the nose, to initiate a neuronal response that triggers the perception of a smell. The olfactory receptor proteins are members of a large family of G-protein-coupled receptors (GPCR) arising from single coding-exon genes. Olfactory receptors share a 7-transmembrane domain structure with many neurotransmitter and hormone receptors and are responsible for the recognition and G protein-mediated transduction of odorant signals. The olfactory receptor gene family is the largest in the genome. The nomenclature assigned to the olfactory receptor genes and proteins for this organism is independent of other organisms.	-	[Mouse]HomoloGene:17420

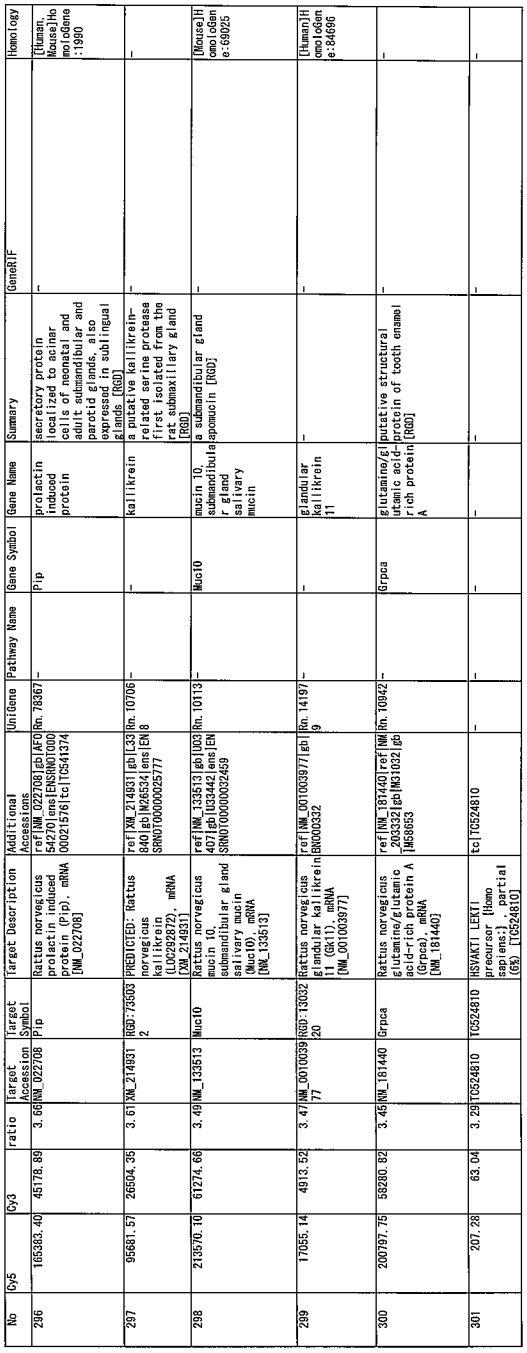
[0231]

No	Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Pathway Name	Gene Symbol	Gene Name	Summary	GeneRIF	Homology
286	86887.34	13877.73	6.41	XM_214931	RGD:735032	PREDICTED: Rattus norvegicus kallikrein (LOC292872), mRNA [XM_214931]	ref|XM_214931|gb|L33940|gb|M11564|ens|ENSRNOT00000025777	Rn.10706	-	-	kallikrein	a putative kallikrein-related serine protease first isolated from the rat submaxillary gland [RGD]	-	-
287	343.56	56.00	6.13	XM_341973	XM_341973	Rattus norvegicus similar to Aldehyde dehydrogenase 7 (LOC361680), mRNA [XM_341973]	gb|XM_341973|ens|ENSRNOT00000024034	-	-	-	-	-	-	-
288	1815.47	311.57	5.83	NM_012684	Vcsa1	Rattus norvegicus variable coding sequence A1 (Vcsa1), mRNA [NM_012684]	ref|NM_012684|X84997|cl|TC569703	Rn.9927	-	Vcsa1	variable coding sequence A1	a prohormone-like protein [RGD]	Stalorphin increased, in a dose-related manner, the occurrence of intromissions across the successive ejaculatory sequences.// Stalorphin products endogenous enkephalins released after copulation activate, by inhibiting enkephalin-degrading enzymes, a natural systemically active regulator of NEP activity & is a physiological modulator of pain perception after injury	-	-
289	8263.27	1424.57	5.80	NM_022193	Acaca	Rattus norvegicus acetyl-coenzyme A carboxylase alpha (Acaca), mRNA [NM_022193]	ref|NM_022193|gb|J03808|ens|ENSRNOT00000050175|ens|ENSRNOT00000044366	Rn.44372	Fatty acid biosynthesis, Pyruvate metabolism, Propanoate metabolism, Insulin signaling pathway	Acaca	acetyl-coenzyme A carboxylase alpha	catalyzes the rate-limiting carboxylation of acetyl CoA to malonyl CoA during long-chain fatty acid synthesis [RGD]	-	(Human, Mouse)Homologene:31015
290	42529.56	9583.96	4.44	NM_001013067	NM_001013067	Rattus norvegicus kallikrein 6 (neurosin) (Klk6_predicted), mRNA [NM_001013067]	ref|NM_001013067|gb|AF276221|mms|ENSRNOT00000000257|5	Rn.79264	-	Klk6_predicted	kallikrein 6 (predicted)	-	-	(Mouse)Homologene:83265

[0232]

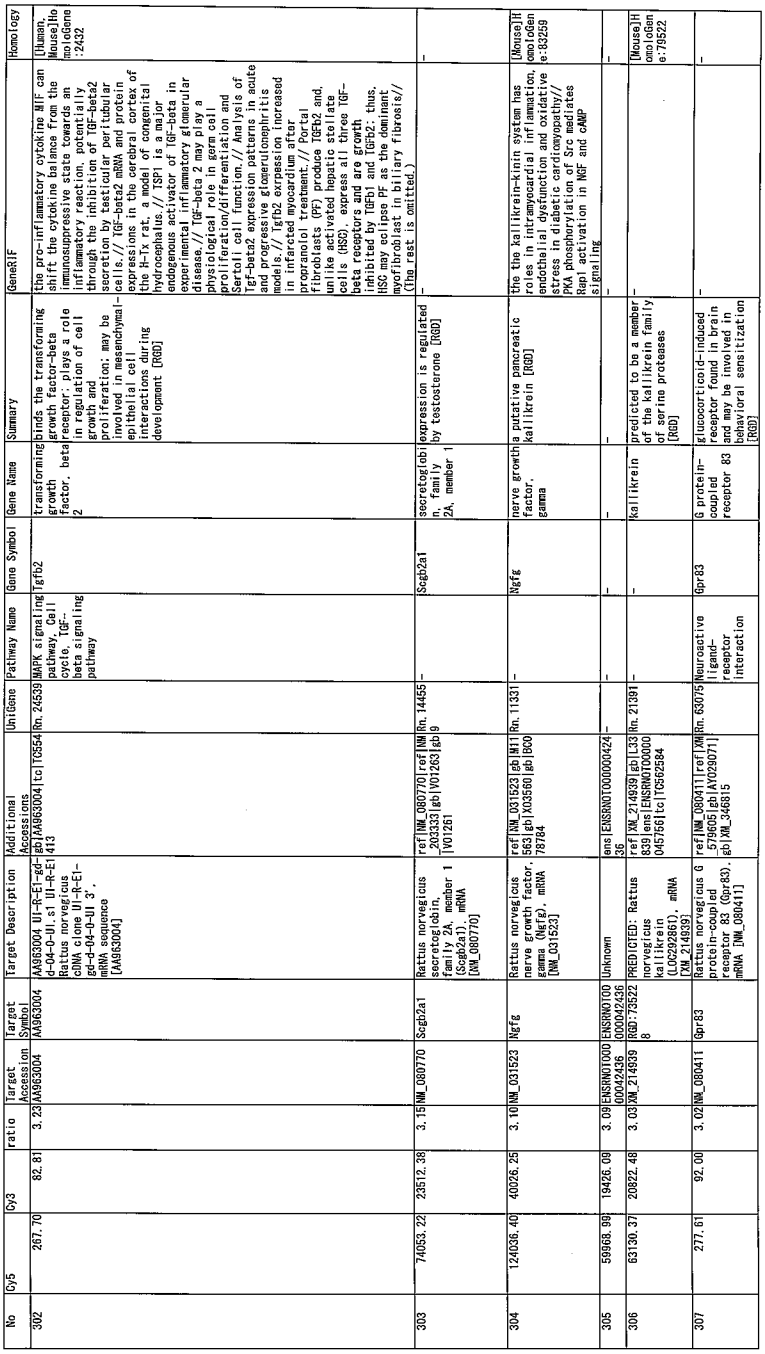
No	Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Pathway Name	Gene Symbol	Gene Name	Summary	GeneRIF	Homology
291	6218.28	1414.59	4.40	NM_012842	Egf	Rattus norvegicus epidermal growth factor (Egf), mRNA [NM_012842]	ref|NM_012842|gb|U04842|gb|BC062030|gb|AW140863	Rn.6075	MAPK signaling pathway, Cytokine-cytokine receptor interaction, Focal adhesion, Gap junction, Regulation of actin cytoskeleton	Egf	epidermal growth factor	binds the epidermal growth factor receptor; may play a role in MAP kinase mediated signaling pathways [RGD]	EGF-based signaling cascades phosphorylate Cav1 and have roles in caveolae assembly// ERK1/2 mediates EGF-induced rapid Rb phosphorylation at Ser780 and Ser795// Neo-natal rats with intestinal injury have significantly lower levels of ileum EGF.// Linear signal transduction pathway involving PI3-kinase-dependent MAPK activation mediates EGF-induced DNA synthesis in mesangial cells by regulating c-fos and p27(Kip1) expression.// The epidermal growth factor acts to cell differentiate and proliferate of PC12 cells.// The Epidermal Growth Factor induces transient and sustained ERK activation.// These results suggest that increases in transepithelial resistance accompanying AEC transdifferentiation and/or EGF exposure are mediated, at least in part, by changes in the pattern of expression of specific claudin isoforms.// Epidermal growth factor triggers caspase-independent pituitary cell death// This entire ectodomain is further processed into a 70-kDa receptor and finally into the mature 5.9 kDa urinary EGF.// (The rest is omitted.)	-	-
292	900.62	208.52	4.32	NM_198685	RGD:735160	Rattus norvegicus cystatin S (CystS), mRNA [NM_198685]	ref|NM_198685|gb|U04206|gb|XM_215879|ens|ENSRNOT00000044345	Rn.79319	-	-	cystatin S	cysteine proteinase inhibitor; may be regulated by cAMP mediated signaling and by estrogen [RGD]	-	-
293	2022.83	528.42	3.83	XM_342575	Svs6_predicted	PREDICTED: Rattus norvegicus seminal vesicle secretion 6 (predicted) (Svs6_predicted), mRNA [XM_342575]	ref|XM_342575|ens|ENSRNOT00000018510|tc|TC518977|tc|TC518976	Rn.14520	-	Svs6_predicted	seminal vesicle secretion 6 (predicted)	-	-	[Mouse]Homologene:49347
294	246.10	65.56	3.75	CB546830	CB546830	CB546830 AMONIC:MRPE4-00028-H9-A mrpe4 (10380) Rattus norvegicus cDNA clone mrpe4-00028-h9 5', mRNA sequence [CB546830]	gb|CB546830	Rn.15721	-	-	-	-	-	-
295	71213.81	19366.14	3.68	NM_012593	Klk7	Rattus norvegicus kallikrein 7 (Klk7), mRNA [NM_012593]	ref|NM_012593|ens|ENSRNOT00000025750|gb|M19947|tc|TC521340	Rn.14455	-	-	kallikrein 7	serine protease; involved in processing of bioactive peptides [RGD]	-	-

[0233]



No	Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Pathway Name	Gene Symbol	Gene Name	Summary	GeneRIF	Homology
296	165383.40	45178.89	3.66	NM_022708	Pip	Rattus norvegicus prolactin induced protein (Pip), mRNA [NM_022708]	ref|NM_022708|gb|AF0 54270|ens|ENSRNOT000 00021576|tc|TC541374	Rn.78367	-	Pip	prolactin induced protein	secretory protein localized to acinar cells of neonatal and adult submandibular and parotid glands, also expressed in sublingual glands [RGD]	-	[Human, Mouse]Homoloene:1990
297	95681.57	26504.35	3.61	XM_214931	RGD:73503 2	PREDICTED: Rattus norvegicus kallikrein (LOC298872), mRNA [XM_214931]	ref|XM_214931|gb|L33 840|gb|M26534|ens|EN SRNOTG00000025777	Rn.10706	-	-	kallikrein	a putative kallikrein-related serine protease first isolated from the rat submaxillary gland [RGD]	-	-
298	213570.10	61274.66	3.49	NM_133513	Muc10	Rattus norvegicus mucin 10, submandibular gland salivary mucin (Muc10), mRNA [NM_133513]	ref|NM_133513|gb|U03 407|gb|U33442|ens|EN SRNOT00000002459	Rn.10113	-	Muc10	mucin 10, submandibular gland salivary mucin	a submandibular gland apomucin [RGD]	-	[Mouse]Homoloene:69025
299	17055.14	4913.52	3.47	NM_001003977	RGD:13032 20	Rattus norvegicus glandular kallikrein 11 (Gkl1), mRNA [NM_001003977]	ref|NM_001003977|gb|BN 000332	Rn.14197	-	-	glandular kallikrein 11	-	-	[Human]Homoloene:84696
300	200797.75	58280.82	3.45	NM_181440	Grpca	Rattus norvegicus glutamine/glutamic acid-rich protein A (Grpca), mRNA [NM_181440]	ref|NM_181440|ref|NM 203232|gb|M31032|gb M59863	Rn.10942	-	Grpca	glutamine/glutamic acid-rich protein A	putative structural protein of tooth enamel [RGD]	-	-
301	207.28	63.04	3.29	TC524810	TC524810	HSYAK11 LEK11 precursor (Homo sapiens), partial (6%) [TC524810]	tc|TC524810	-	-	-	-	-	-	-

[0234]



No	Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Pathway Name	Gene Symbol	Gene Name	Summary	GeneRIF	Homology
302	267.70	82.81	3.23	AA963004	AA963004	AA963004 UI-R-E1-gd-d-04-0-UI.s1 UI-R-E1-gd-d-04-0-UI 3', mRNA sequence [AA963004]	ref|NM_080770|gb|AA963004|tc|TC554 413	Rn.24539	MAPK signaling pathway, Cell cycle, TGF-beta signaling pathway	Tgfb2	transforming growth factor, beta 2	binds the transforming growth factor-beta receptor. plays a role in regulation of cell growth and proliferation; may be involved in mesenchymal-epithelial cell interactions during development [RGD]	the pro-inflammatory cytokine MIF can shift the cytokine balance from the immunosuppressive state towards inflammatory reaction. potentially through the inhibition of TGF-beta2 secretion by testicular peritubular cells.// TGF-beta2 mRNA and protein expressions in the cerebral cortex of the H-Tx rat, a model of congenital hydrocephalus.// TSP1 is a major endogenous activator of TGF-beta in experimental inflammatory glomerular disease.// TGF-beta 2 may play a physiological role in germ cell proliferation/differentiation and Sertoli cell function.// Analysis of Tgf-beta2 expression patterns in acute and progressive glomerulonephritis models.// Tgfb2 expression increased in infarcted myocardium.// Portal fibroblasts (PF) produce TGFb2 and, unlike activated hepatic stellate cells (HSC), express all three TGF-beta receptors and are growth inhibited by TGFb1 and TGFb2: thus, HSC may eclipse PF as the dominant myofibroblast in biliary fibrosis// (The rest is omitted.)	[Human, Mouse]Homologene:2432
303	74053.22	23512.38	3.15	NM_080770	Scgb2a1	Rattus norvegicus secretoglobin, family 2A, member 1 (Scgb2a1), mRNA [NM_080770]	ref|NM_080770|ref|NM_203333|gb|V01263|gb|V01261	Rn.14455	-	Scgb2a1	secretoglobin, family 2A, member 1	expression is regulated by testosterone [RGD]	-	-
304	124036.40	40026.25	3.10	NM_031523	Ngfg	Rattus norvegicus nerve growth factor gamma (Ngfg), mRNA [NM_031523]	ref|NM_031523|gb|M11563|gb|X03560|gb|B00787|84	Rn.11331	-	Ngfg	nerve growth factor, gamma	a putative pancreatic kallikrein [RGD]	the the kallikrein-kinin system has role in intramyocardial inflammation, endothelial dysfunction and cardiac stress in diabetic cardiomyopathy// PKA phosphorylation of Src mediates Rap1 activation in NGF and cAMP signaling	[Mouse]Homologene:50239
305	59968.99	19426.00	3.09	ENSRNOT00000042436	ENSRNOT00000042436	Unknown	ens|ENSRNOT00000042436	-	-	-	-	-	-	-
306	63130.37	20822.48	3.03	XM_214939	RGD:735228	PREDICTED: Rattus norvegicus kallikrein (LOC229861), mRNA [XM_214939]	ref|XM_214939|gb|L33839|ens|ENSRNOT00000045766|tc|TC562584	Rn.21391	-	-	kallikrein	predicted to be a member of the kallikrein family of serine proteases [RGD]	-	[Mouse]Homologene:79522
307	277.61	92.00	3.02	NM_080411	Gpr83	Rattus norvegicus G protein-coupled receptor 83 (Gpr83), mRNA [NM_080411]	ref|NM_080411|ref|XM_579605|gb|AY029071|gb|XM_346815	Rn.63075	Neuroactive ligand-receptor interaction	Gpr83	G protein-coupled receptor 83	glucocorticoid-induced receptor found in brain and may be involved in behavioral sensitization [RGD]	-	-

[0235]



No	Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Pathway Name	Gene Symbol	Gene Name	Summary	GeneRIF	Homology
308	4492.24	1493.90	3.01	NM_001013941	NM_001013941	Rattus norvegicus similar to 14-3-3 protein sigma (LOC298795), mRNA [NM_001013941]	ref|NM_001013941|ref|XM_233085|ens|ENSRNOT00000043959	Rn.16190	Cell cycle	-	similar to 14-3-3 protein sigma	-	-	-
309	291.87	100.16	2.91	NM_031131	Tgfb2	Rattus norvegicus transforming growth factor, beta 2 (Tgfb2), mRNA [NM_031131]	ref|NM_031131|gb|AF153013|AF153013|ens|ENSRNOT00000003313	Rn.24539	MAPK signaling pathway, Cell cycle, TGF-beta signaling pathway	Tgfb2	transforming growth factor, beta 2	binds the transforming growth factor beta receptor, plays a role in regulation of cell growth and proliferation; may be involved in mesenchymal-epithelial cell interactions during development [RGD]	the pro-inflammatory cytokine MIF can shift the cytokine balance from the immunosuppressive state to an inflammatory reaction, potentially through the inhibition of TGF-beta2 secretion by testicular peritubular cells. // TGF-beta2 mRNA and protein expressions in the cerebral cortex of the H-Tx rat, a model of congenital hydrocephalus. // TSP1 is a major endogenous activator of TGF-beta in experimental inflammatory glomerular disease. // TGF-beta 2 may play a physiological role in germ cell proliferation/differentiation and Sertoli cell function. // Analysis of Tgf-beta2 expression patterns in acute and progressive glomerulonephritis models. // Tgfb2 expression increased in infarcted myocardium after permanent ligation treatment. // Portal fibroblasts (PF) produce TGFb2 and, unlike activated hepatic stellate cells (HSC), express all three TGF-beta receptors and are growth inhibited by TGFb1 and TGFb2; thus, HSC may eclipse PF as the dominant myofibroblast in biliary fibrosis// (The rest is omitted.)	[Human, Mouse]Homologene:2492
310	164227.44	57850.42	2.84	NM_172065	Prpg2	Rattus norvegicus proline-rich proteoglycan 2 (Prpg2), mRNA [NM_172065]	ref|NM_172065|gb|M11899|gb|L17318|ens|ENSRNOT00000013943	Rn.29950	-	Prpg2	proline-rich proteoglycan 2	member of a family of proline rich proteins that are induced in salivary gland by isoproterenol treatment and by feeding tannins [RGD]	-	-
311	145.34	52.12	2.79	XM_340739	Mpv17l_predicted	PREDICTED: Rattus norvegicus Mpv17 transgene, kidney disease mutant-like (predicted) (Mpv17l_predicted), mRNA [XM_340739]	ref|XM_340739|ens|ENSRNOT00000043841|c|TC540192	Rn.22842	-	Mpv17l_predicted	Mpv17 transgene, kidney disease mutant-like (predicted)	-	-	[Mouse]Homologene:13547

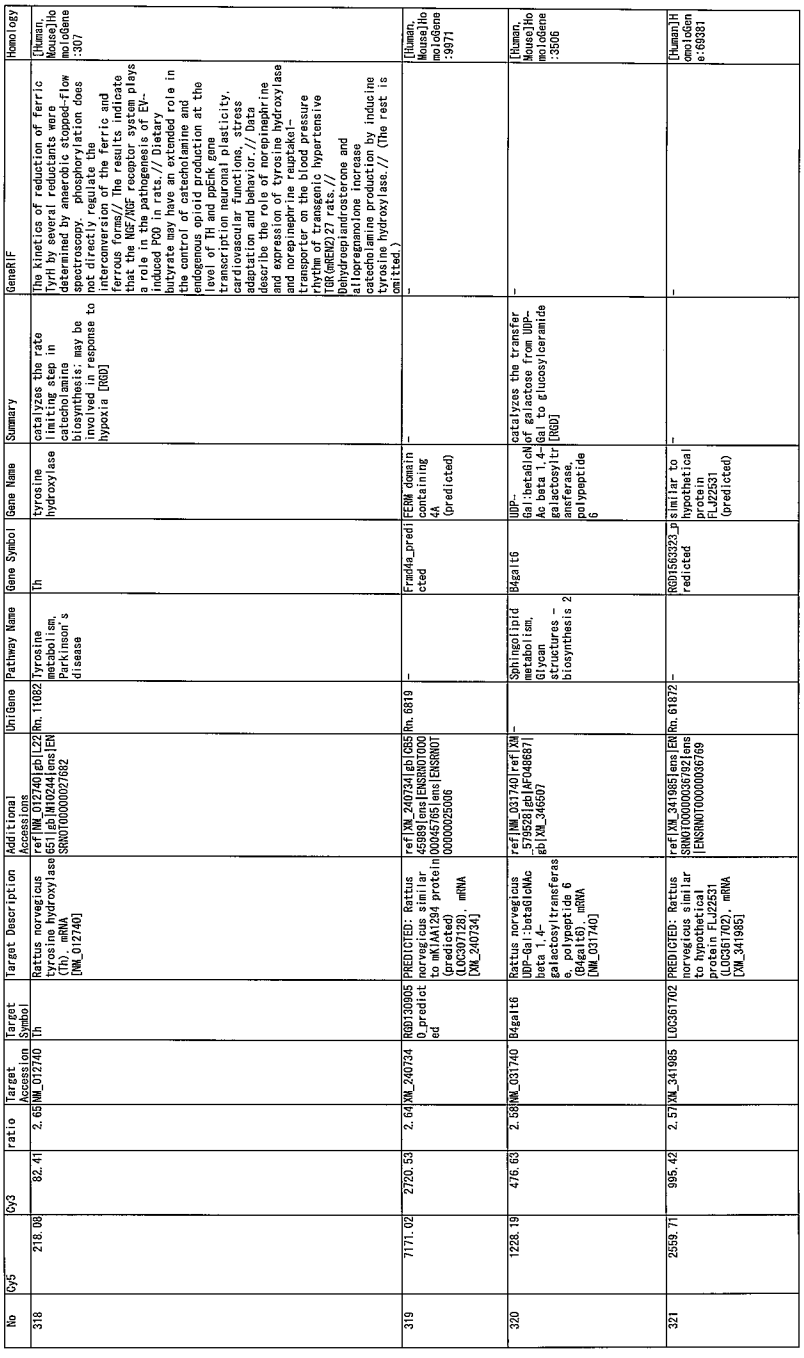
[0236]

No	Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Pathway Name	Gene Symbol	Gene Name	Summary	GeneRIF	Homology
312	20380.80	7339.94	2.78	XM_234124	Npas3_predicted	PREDICTED: Rattus norvegicus neuronal PAS domain protein 3 (predicted) (Npas3_predicted), mRNA [XM_234124]	ref|XM_234124|ens|ENSRNOT00000049945	Rn.135138	-	RGD1563961_predicted	Npas3_predicted neuronal PAS domain protein 3 (predicted)	-	-	[Human, Mouse]HomoloGene:8461
313	3122.88	1125.48	2.77	XM_224224	LOC290262	PREDICTED: Rattus norvegicus similar to natural killer cell protease 1 precursor (RNKP-1) (Granzyme B) (LOC290262), mRNA [XM_224224]	ref|XM_224224|ref|XM_577431|ref|XM_577432|gb|AA66893	-	-	RGD1563961_predicted	similar to Natural Killer cell protease 1 precursor (RNKP-1) (Granzyme B) (predicted)	-	-	-
314	6270.03	2271.28	2.76	XM_221081	LOC287603	Rattus norvegicus similar to tweety homolog 2 (LOC287603), mRNA [XM_221081]	gb|XM_221081	Rn.163171	-	RGD1562869_predicted	similar to Tweety homolog 2 (predicted)	-	-	[Human, Mouse]HomoloGene:41882
315	4662.43	1714.21	2.72	XM_347064	LOC362603	PREDICTED: Rattus norvegicus hypothetical LOC362603 (LOC362603), mRNA [XM_347064]	ref|XM_347064|tc|TC5|Rn.91410|67561	Rn.91410	-	RGD1559801_predicted	RGD1559801 (predicted)	-	-	-

[0237]

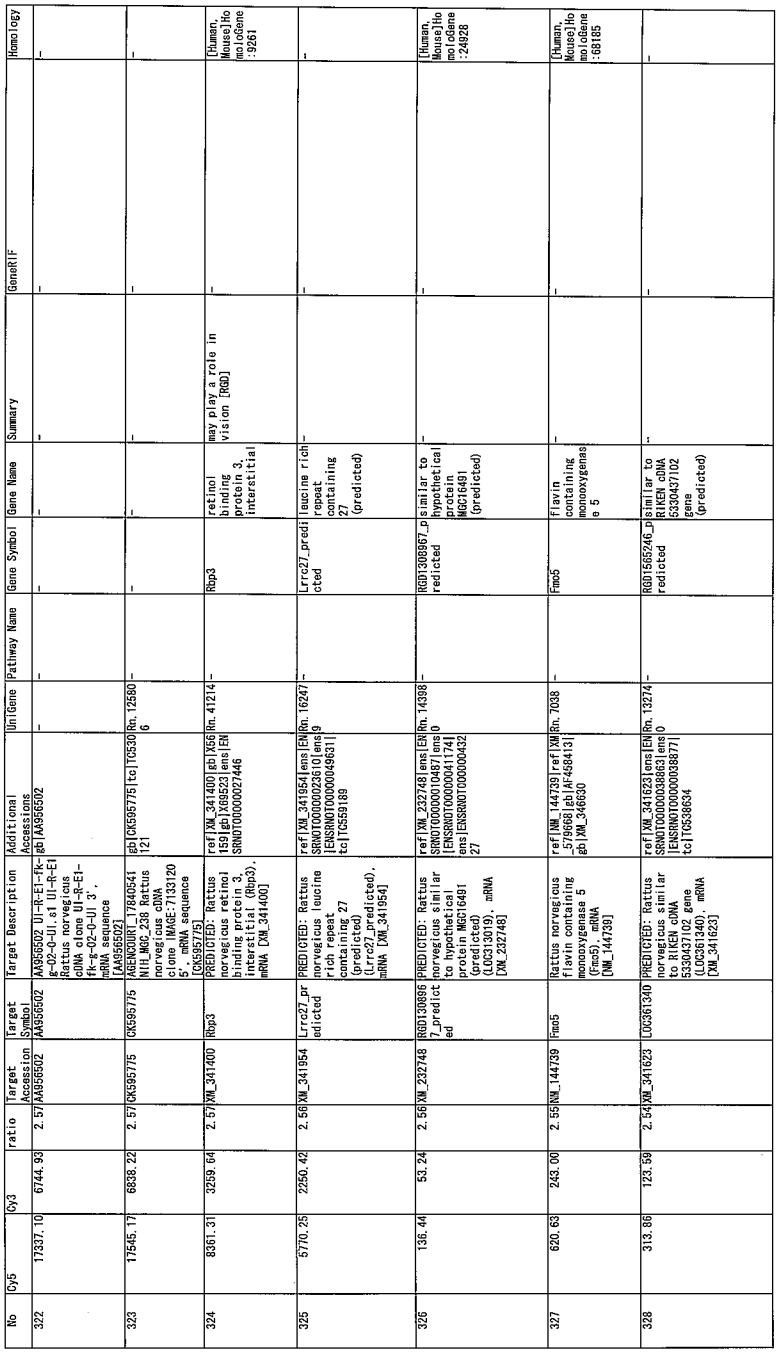
No	Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Pathway Name	Gene Symbol	Gene Name	Summary	GeneRIF	Homology
316	144.02	53.99	2.67	NM_012996	Oxt	Rattus norvegicus oxytocin (Oxt), mRNA [NM_012996]	ref|NM_012996|gb|M25649.1|RATOXY|D00800|Q28629|tc|TC572906	Rn.46915	Neuroactive ligand-receptor interaction	Oxt	oxytocin	hormone involved in contraction of smooth muscle during parturition and lactation; gene encodes two proteins, oxytocin and neurophysin I [RGD]	oxytocin has a role in gonadal steroid modulation of stress-induced hypothalamo-pituitary-adrenal activity and anxiety behavior// Oxytocin may stimulate mother-infant bond formation partly by acting through brain areas involved in regulating olfactory discrimination, emotions, and reward.// differences in intracerebral release patterns of oxytocin, rather than differences at the level of oxytocin receptors, are critical for the regulation of maternal aggressive behavior// Changes in oxytocin content (but not receptor expression) within the nucleus tractus solitarii may constitute functional mechanism by which training improves cardiovascular control in normotensive and hypertensive individuals.// excitatory responses to oxytocin vary markedly between bed nuclei of stria terminalis subdivisions and may reflect local circuitry within the extended amygdala// (the rest is omitted.)	[Human, Mouse]Homologene:35494
317	3903.91	1473.77	2.65	XM_228170	Vgll2_predicted	PREDICTED: Rattus norvegicus vestigial like 2 homolog (Drosophila) (predicted) (Vgll2_predicted), mRNA [XM_228170]	ref|XM_228170|ens|ENSRNOT00000000456|tc|TC565825	Rn.17643	-	Vgll2_predicted	vestigial like 2 homolog (Drosophila) (predicted)	-	-	[Human, Mouse]Homologene:35066

[0238]



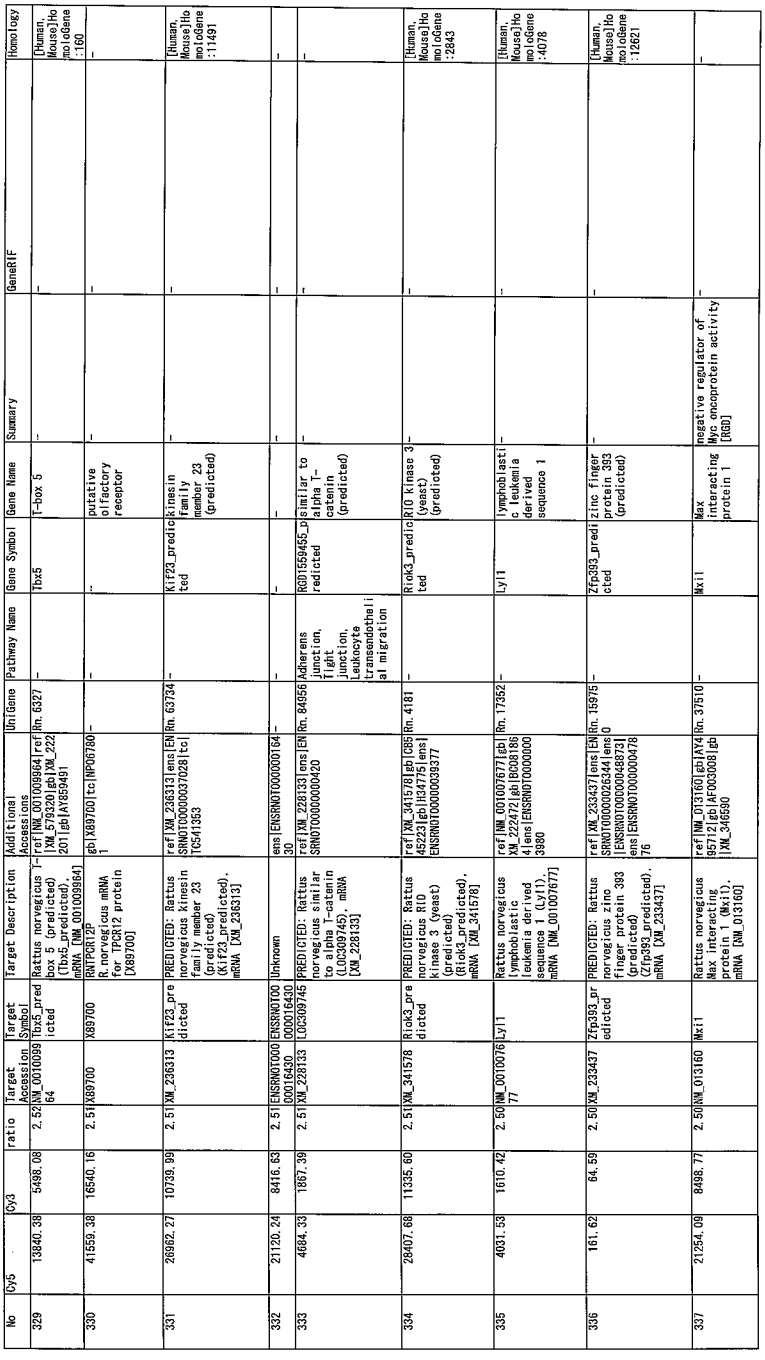
No	Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Pathway Name	Gene Symbol	Gene Name	Summary	GeneRIF	Homology
318	218.08	82.41	2.65	NM_012740	Th	Rattus norvegicus tyrosine hydroxylase (Th), mRNA [NM_012740]	ref|NM_012740|gb|L22651|gb|M10244|ens|ENSRNOT00000027682	Rn.11082	Tyrosine metabolism, Parkinson's disease	Th	tyrosine hydroxylase	catalyzes the rate limiting step in catecholamine biosynthesis; may be involved in response to hypoxia [RGD]	The kinetics of reduction of ferric [Tyrh] by several reductants were determined by anaerobic stopped-flow spectroscopy. phosphorylation does not directly regulate the interconversion of the ferric and ferrous forms// The results indicate that the NGF/NGF receptor system plays a role in the pathogenesis of EV-induced POD in rats.// Dietary butyrate may have an extended role in the control of catecholamine and endogenous opioid production at the level of TH and pdnk gene transcription neuronal plasticity. cardiovascular functions, stress adaptation, behavior.// Data describe the role of norepinephrine and expression of tyrosine hydroxylase and norepinephrine reuptake1-transporter on the blood pressure rhythm of transgenic hypertensive [TGR(mREN2)27 rats.// Dehydroepiandrosterone and allopregnanolone increase catecholamine production by inducine tyrosine hydroxylase.// (The rest is omitted.)	[Human, Mouse]Homologene:9971
319	7171.02	2720.53	2.64	XM_240734	RGD1300050_predicted	PREDICTED: Rattus norvegicus similar to mKIAA1234 protein (predicted) (LOC300730), mRNA [XM_240734]	ref|XM_240734|gb|CB545889|ens|ENSRNOT00000045765|ens|ENSRNOT00000025006	Rn.6819	-	Frmd4a_predicted	FERM domain containing 4A (predicted)	-	-	[Human, Mouse]Homologene:3506
320	1228.19	476.63	2.58	NM_031740	B4galt6	Rattus norvegicus UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 6 (B4galt6), mRNA [NM_031740]	ref|NM_031740|ref|XM_579528|gb|AF048687|gb|XM_346507	-	Sphingolipid metabolism, Glycan structures - biosynthesis 2	B4galt6	UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 6	catalyzes the transfer of galactose from UDP-Gal to glucosylceramide [RGD]	-	[Human, Mouse]Homologene:3506
321	2559.71	995.42	2.57	XM_341985	LOC361702	PREDICTED: Rattus norvegicus similar to hypothetical protein FLJ22531 (LOC361702), mRNA [XM_341985]	ref|XM_341985|ens|ENSRNOT00000067921|ens|ENSMUST00000036769	Rn.61872	-	RGD1563323_predicted	similar to hypothetical protein FLJ22531 (LOC361702) (predicted)	-	-	[Human]Homologene:69381

[0239]



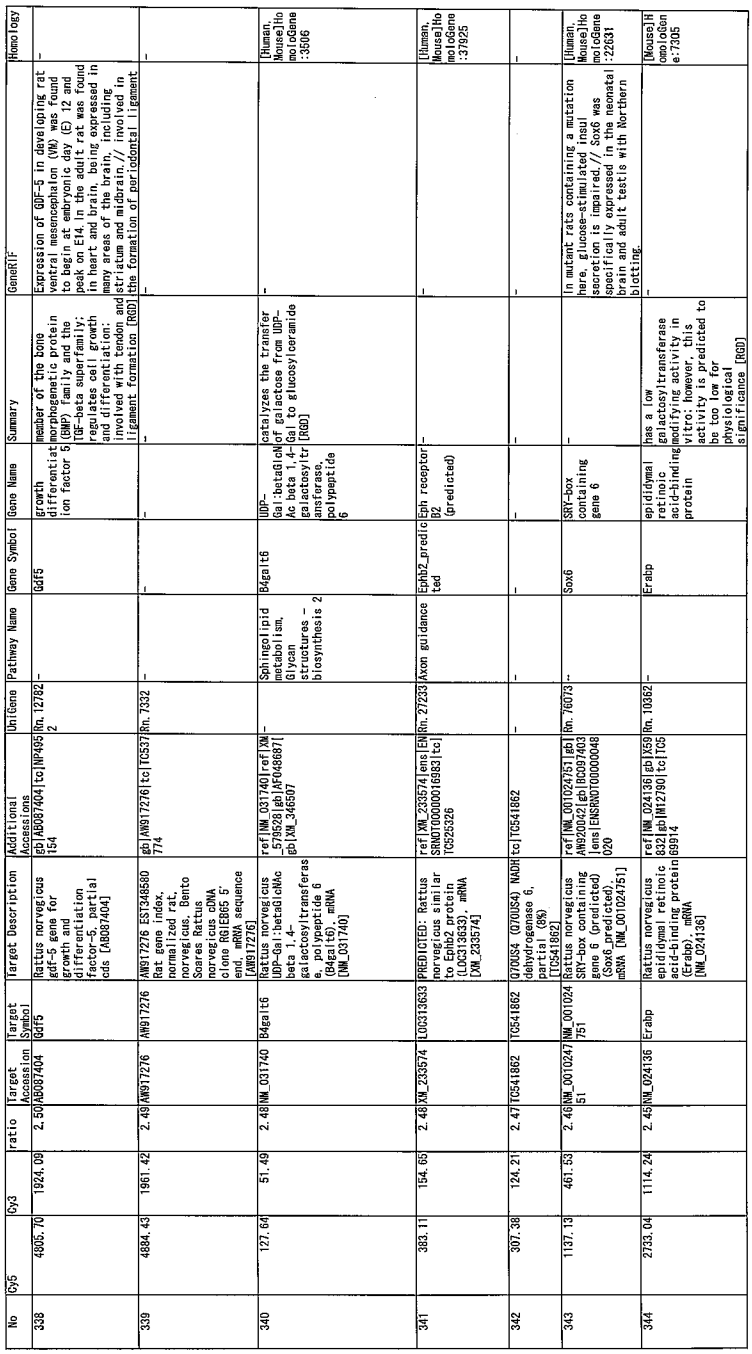
No	Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Pathway Name	Gene Symbol	Gene Name	Summary	GeneRIF	Homology
322	17337.10	6744.93	2.57	AA956502	AA956502	AA956502 UI-R-E1-fk-g-02-0-UI.s1 UI-R-E1 Rattus norvegicus cDNA clone UI-R-E1-fk-g-02-0-UI 3', mRNA sequence [AA956502]	gb|AA956502	-	-	-	-	-	-	-
323	17545.17	6838.22	2.57	CK595775	CK595775	AGENCOURT_17840541 NIH_MGC_238 Rattus norvegicus cDNA clone IMAGE:7133120 5', mRNA sequence [CK595775]	gb|CK595775|tc|TC6330121	Rn.12580.6	-	-	-	-	-	-
324	8361.31	3259.64	2.57	XM_341400	Rbp3	PREDICTED: Rattus norvegicus retinol binding protein 3, interstitial (Rbp3), mRNA [XM_341400]	ref|XM_341400|gb|X56159|gb|X69523|ens|ENSRNOT00000027446	Rn.41214	-	Rbp3	retinol binding protein 3, interstitial	may play a role in vision [RGD]	-	[Human, Mouse]Homologene:9261
325	5770.25	2250.42	2.56	XM_341954	Lrrc27_predicted	PREDICTED: Rattus norvegicus leucine rich repeat containing 27 (predicted) (Lrrc27_predicted), mRNA [XM_341954]	ref|XM_341954|ens|ENSRNOT00000023610|ens|ENSRNOT00000049631|tc|TC559189	Rn.16247	-	Lrrc27_predicted	leucine rich repeat containing 27 (predicted)	-	-	-
326	136.44	53.24	2.56	XM_232748	RGD1306895_predicted	PREDICTED: Rattus norvegicus similar to hypothetical protein MGC16491 (predicted) (LOC313019), mRNA [XM_232748]	ref|XM_232748|ens|ENSRNOT00000019487|ens|ENSRNOT00000041724|ens|ENSRNOT00000000432	Rn.14398	-	RGD1306967_predicted	similar to hypothetical protein MGC16491 (predicted)	-	-	[Human, Mouse]Homologene:24928
327	620.63	243.00	2.55	XM_144739	Fmo5	Rattus norvegicus flavin containing monooxygenase 5 (Fmo5), mRNA [XM_144739]	ref|XM_144739|ref|XM_579668|gb|AF468413|gb|XM_346630	Rn.7038	-	Fmo5	flavin containing monooxygenase 5	-	-	[Human, Mouse]Homologene:68185
328	313.86	123.59	2.54	XM_341623	LOC361340	PREDICTED: Rattus norvegicus similar to RIKEN cDNA 5330437102 gene (LOC361340), mRNA [XM_341623]	ref|XM_341623|ens|ENSRNOT00000038862|ens|ENSRNOT00000038971|tc|TC538634	Rn.13274	-	RGD1565246_predicted	similar to RIKEN cDNA 5330437102 gene (predicted)	-	-	-

[0240]



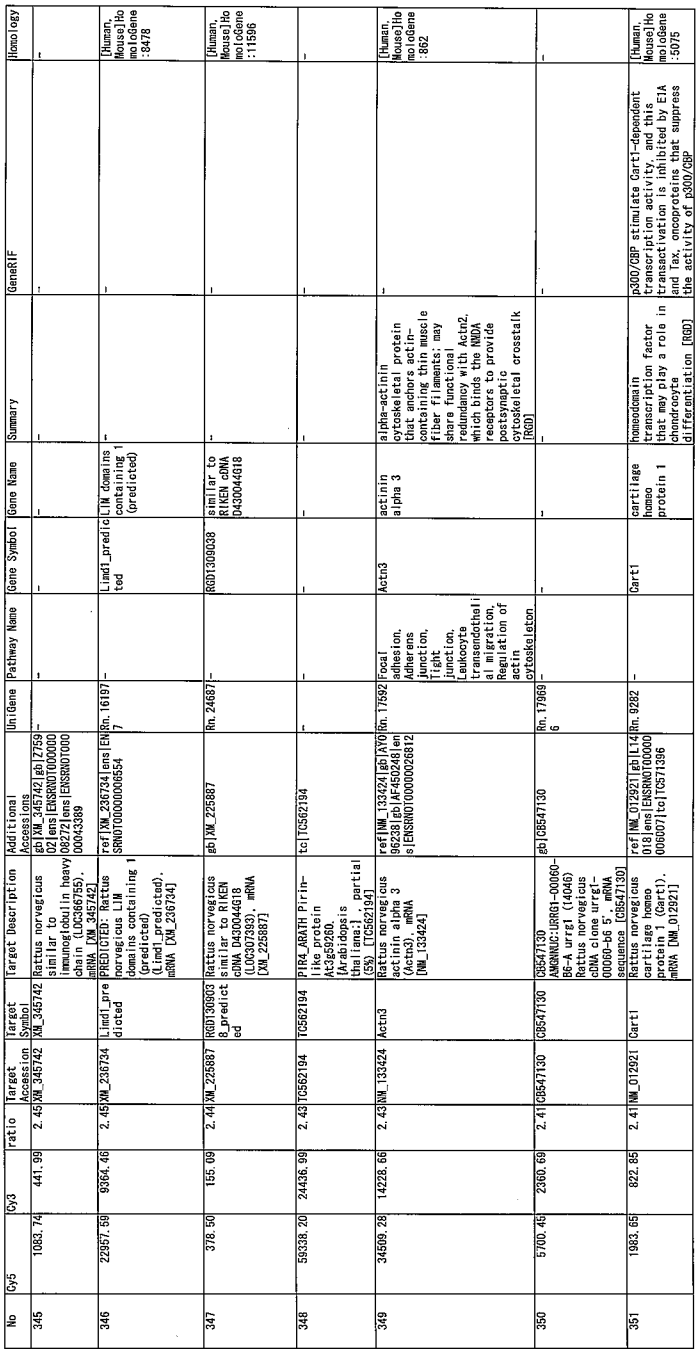
No	Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Pathway Name	Gene Symbol	Gene Name	Summary	GeneRIF	Homology
329	13840.38	5498.08	2.52	XM_0010099 64	Tbx5_predicted	Rattus norvegicus T-box 5 (predicted) (Tbx5_predicted), mRNA [XM_0010099 64]	ref|XM_0010099 64|ref|XM_222 201|gb|AY859491	Rn. 6327	-	Tbx5	T-box 5	-	-	[Human, Mouse]Homolodene :160
330	41559.38	16540.16	2.51	X89700	RATPCR12P	R.norvegicus mRNA for TPCR12 protein [X89700]	gb|X89700|tc|NP006780 1	-	-	-	putative olfactory receptor	-	-	-
331	26962.27	10739.99	2.51	XM_236313	Kif23_predicted	PREDICTED: Rattus norvegicus kinesin family member 23 (predicted) (Kif23_predicted), mRNA [XM_236313]	ref|XM_236313|ens|ENSRNOT00000037028|tc|TC41353	Rn. 63734	-	Kif23_predicted	kinesin family member 23 (predicted)	-	-	[Human, Mouse]Homolodene :11491
332	21120.24	8416.63	2.51	ENSRNOT0000 0016430	ENSRNOT0000 0016430	Unknown	ens|ENSRNOT00000016430	-	-	-	-	-	-	-
333	4684.33	1867.39	2.51	XM_228133	LOC309745	PREDICTED: Rattus norvegicus similar to alpha T-catenin (LOC309745), mRNA [XM_228133]	ref|XM_228133|ens|ENSRNOT00000000420	Rn. 84956	Adherens junction, Tight junction, Leukocyte transendothelial migration	RGD1559455_predicted	similar to alpha T-catenin (predicted)	-	-	-
334	28407.68	11335.60	2.51	XM_341578	Riok3_predicted	PREDICTED: Rattus norvegicus RIO kinase 3 (yeast) (predicted) (Riok3_predicted), mRNA [XM_341578]	ref|XM_341578|gb|CB545223|gb|AI347751|ens|ENSRNOT00000039377	Rn. 4181	-	Riok3_predicted	RIO kinase 3 (yeast) (predicted)	-	-	[Human, Mouse]Homolodene :2843
335	4031.53	1610.42	2.50	NM_0010076 77	Lyl1	Rattus norvegicus lymphoblastic leukemia derived sequence 1 (Lyl1), mRNA [NM_0010076 77]	ref|NM_0010076 77|gb|XM_222472|gb|BG038186|ens|ENSRNOT00000003980	Rn. 17352	-	Lyl1	lymphoblastic leukemia derived sequence 1	-	-	[Human, Mouse]Homolodene :4078
336	161.62	64.59	2.50	XM_233437	Zfp393_predicted	PREDICTED: Rattus norvegicus zinc finger protein 393 (predicted) (Zfp393_predicted), mRNA [XM_233437]	ref|XM_233437|ens|ENSRNOT00000026344|ens|ENSRNOT00000048873|ens|ENSRNOT00000049478 76	Rn. 15975	-	Zfp393_predicted	zinc finger protein 393 (predicted)	-	-	[Human, Mouse]Holodene :12621
337	21254.09	8498.77	2.50	NM_013160	Mxi1	Rattus norvegicus Max interacting protein 1 (Mxi1), mRNA [NM_013160]	ref|NM_013160|gb|AY4 05712|gb|AF003008|gb|XM_346590	Rn. 37510	-	Mxi1	Max interacting protein 1	negative regulator of Myc oncoprotein activity [RGD]	-	-

[0241]



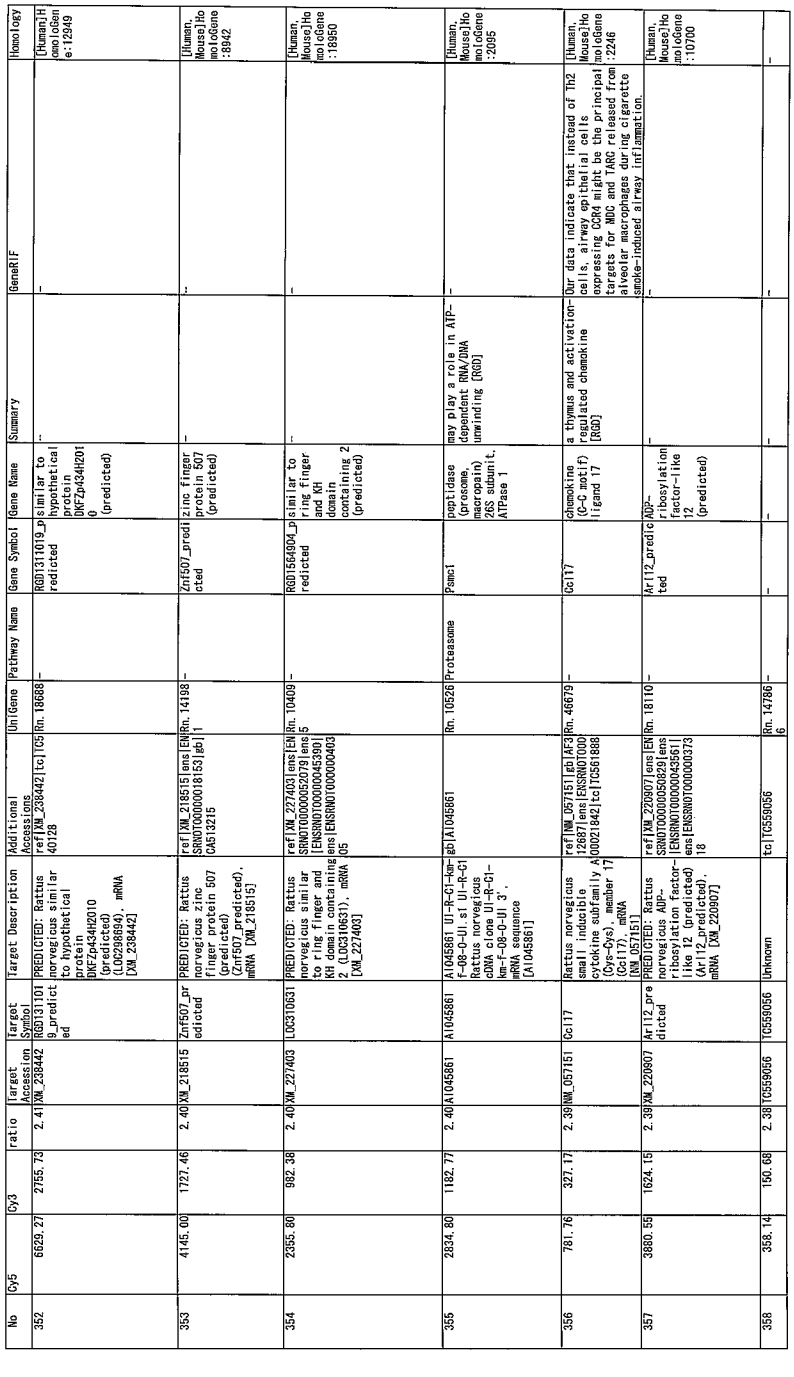
No	Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Pathway Name	Gene Symbol	Gene Name	Summary	GeneRif	Homology
338	4805.70	1924.09	2.50	AB087404	Gdf5	Rattus norvegicus gdf-5 gene for growth and differentiation factor-5, partial cds [AB087404]	gb|AB087404|tc|NP495154	Rn.127822	-	Gdf5	growth differentiation factor 5	member of the bone morphogenetic protein (BMP) family and the TGF-beta superfamily; regulates cell growth and differentiation: involved with tendon and ligament formation [RGD]	Expression of GDF-5 in developing rat ventral mesencephalon (VM) was found to begin at embryonic day (E) 12 and peak on E14. in the adult rat was found in heart and brain, being expressed in many areas of the brain, including striatum and midbrain.// involved in the formation of periodontal ligament	-
339	4884.43	1961.42	2.49	AW917276	AW917276	AW917276 EST348580 Rat gene index, normalized rat, norvegicus, Bento Soares Rattus norvegicus cDNA clone RGIBE65 5' end, mRNA sequence [AW917276]	gb|AW917276|tc|TC6537774	Rn.7332	-	-	-	-	-	-
340	127.64	51.49	2.48	NM_031740	B4galt6	Rattus norvegicus UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 6 (B4galt6), mRNA [NM_031740]	ref|NM_031740|ref|XM_575528|gb|AF048687|gb|XM_346507	-	Sphingolipid metabolism, Glycan structures - biosynthesis 2	B4galt6	UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 6	catalyzes the transfer of galactose from UDP-Gal to glucosylceramide [RGD]	-	[Human, Mouse]HomoloGene:3506
341	383.11	154.65	2.48	XM_233574	LOC313633	PREDICTED: Rattus norvegicus similar to EphA2 protein, (LOC313633), mRNA [XM_233574]	ref|XM_233574|ens|ENSRNOT00000016983|tc|TC6225326	Rn.27233	Axon guidance	Epha2_predicted	Eph receptor B2 (predicted)	-	-	[Human, Mouse]HomoloGene:37925
342	307.38	124.21	2.47	TC541862	TC541862	Q70US4 (Q70US4) NADH dehydrogenase 6, partial (8%) [TC541862]	tc|TC541862	-	-	-	-	-	-	-
343	1137.13	461.53	2.46	NM_001024751	NM_001024751	Rattus norvegicus SRY-box containing gene 6 (predicted) (Sox6_predicted), mRNA [NM_001024751]	ref|NM_001024751|gb|AW920042|gb|BC097403|ens|ENSRNOT00000048020	Rn.76073	-	Sox6	SRY-box containing gene 6	-	In mutant rats containing a mutation hare, glucose-stimulated insulin secretion is impaired.// Sox6 was specifically expressed in the neonatal brain and adult testis with Northern blotting.	[Human, Mouse]HomoloGene:22631
344	2733.04	1114.24	2.45	NM_024136	Erabp	Rattus norvegicus epididymal retinoic acid-binding protein (Erabp), mRNA [NM_024136]	ref|NM_024136|gb|X59832|gb|M12790|tc|TC69914	Rn.10362	-	Erabp	epididymal retinoic acid-binding protein	has a low galactosyltransferase modifying activity in vitro; however, this activity is predicted to be too low for physiological significance [RGD]	-	[Mouse]HomoloGene:7305

[0242]

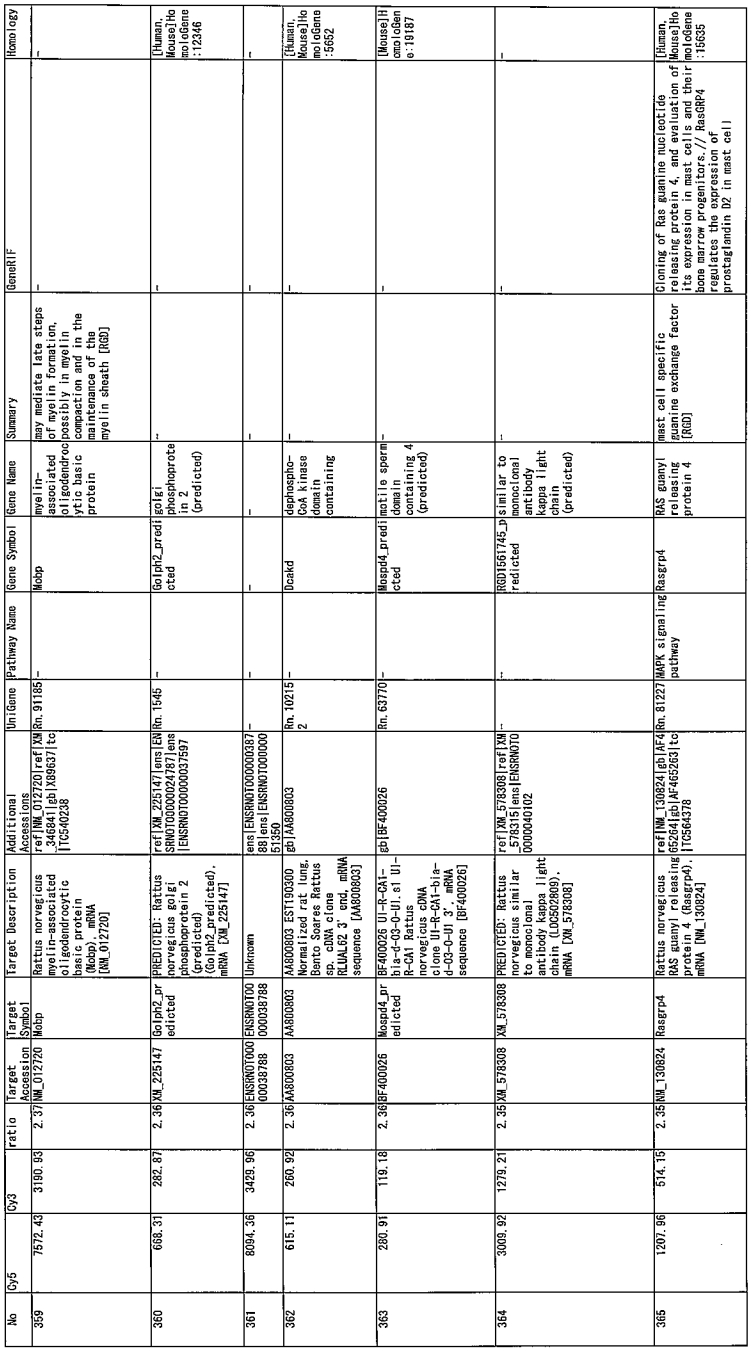


No	Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Pathway Name	Gene Symbol	Gene Name	Summary	GeneRIF	Homology
345	1083.74	441.99	2.45	XM_345742	XM_345742	Rattus norvegicus similar to immunoglobulin heavy chain (LOC366755), mRNA (XM_345742)	gb|XM_345742|gb|I7559022|ens|ENSRNOT00000008027|ens|ENSRNOT00000043389	-	-	-	-	-	-	-
346	22957.59	9364.46	2.45	XM_236734	Limd1_predicted	PREDICTED: Rattus norvegicus LIM domains containing 1 (predicted) (Limd1_predicted), mRNA (XM_236734)	ref|XM_236734|ens|ENSRNOT00000060554	Rn.161977	-	Limd1_predicted	LIM domains containing 1 (predicted)	-	-	[Human, Mouse]Homologene:8478
347	378.50	155.09	2.44	XM_225887	RGD1309003_predicted	Rattus norvegicus similar to RIKEN cDNA D430044618 (LOC307393), mRNA (XM_225887)	gb|XM_225887	Rn.24687	-	RGD1309038	similar to RIKEN cDNA D430044618	-	-	[Human, Mouse]Homologene:11596
348	59338.20	24436.99	2.43	TC562194	TC562194	PIR4_ARATH Pirin-like protein At3g59260. [Arabidopsis thaliana] [1 (SA) [TC562194]	tc|TC562194	-	-	-	-	-	-	-
349	34699.28	14228.66	2.43	NM_133424	Actn3	Rattus norvegicus actinin alpha 3 (Actn3), mRNA [NM_133424]	ref|NM_133424|gb|AY096238|gb|AF450248|ens|ENSRNOT00000026812	Rn.17592	Focal adhesion, Adherens junction, Tight junction, Leukocyte transendothelial migration, Regulation of actin cytoskeleton	Actn3	actinin alpha 3	alpha-actinin cytoskeletal protein that anchors actin-containing thin muscle fiber filaments; may share functional redundancy with Actn2, which binds the NMDA receptors to provide postsynaptic cytoskeletal crosstalk [RGD]	-	[Human, Mouse]Homologene:862
350	5700.46	2360.69	2.41	CB547130	CB547130	CB547130 AMGNNUC:UGRG1-00060-BF-A ugrg1 (14046) Rattus norvegicus cDNA clone ugrg1-00060-bf-a 5, mRNA sequence [CB547130]	gb|CB547130	Rn.179696	-	-	-	-	-	-
351	1983.65	822.85	2.41	NM_012921	Cart1	Rattus norvegicus cartilage homeo protein 1 (Cart1), mRNA [NM_012921]	ref|NM_012921|gb|L14018|ens|ENSRNOT00000006007|tc|TC571396	Rn.9282	-	Cart1	cartilage homeo protein 1	homeodomain transcription factor that may play a role in chondrocyte differentiation [RGD]	p300/CBP stimulates Cart1-dependent transcription activity, and this transactivation is inhibited by E1A and Tax, oncoproteins that suppress the activity of p300/CBP	[Human, Mouse]Homologene:5075

[0243]

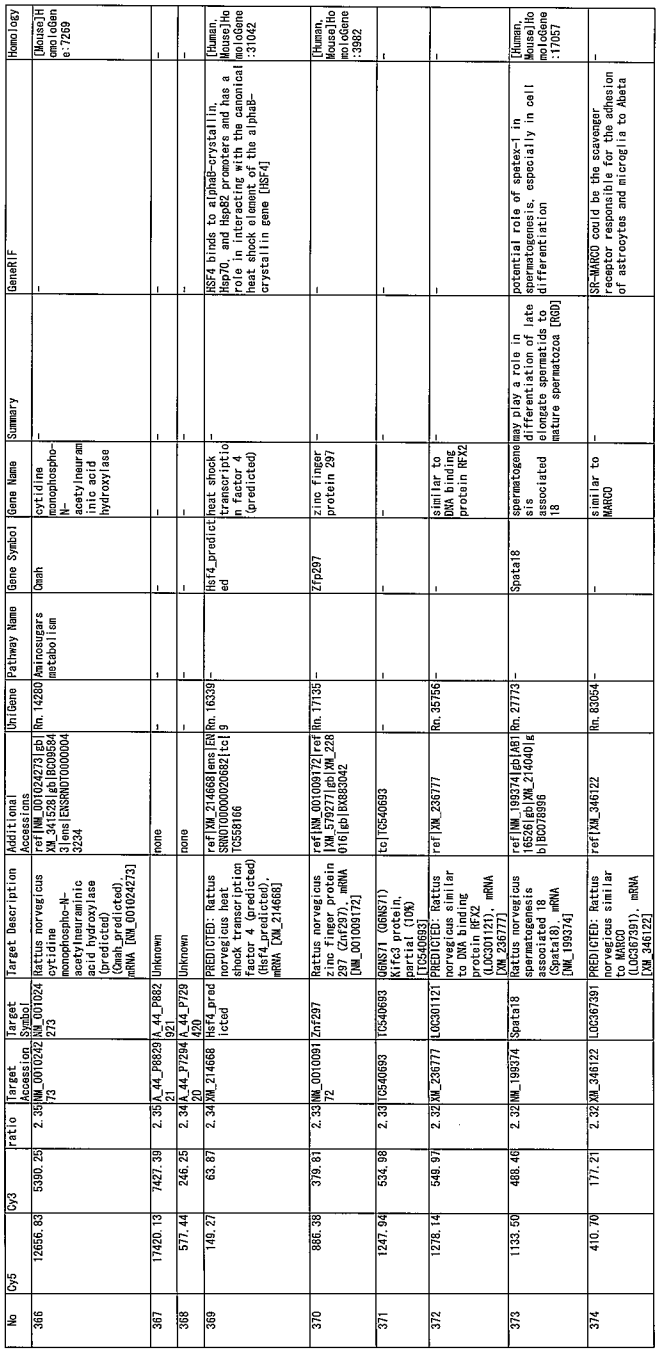


No	Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Pathway Name	Gene Symbol	Gene Name	Summary	GeneRIF	Homology
352	6629.27	2755.73	2.41	XM_238442	RGD1311101_predicted	PREDICTED: Rattus norvegicus similar to hypothetical protein DKFZp434H2010 (predicted) (LOC298894), mRNA [XM_238442]	ref|XM_238442|tc|TC65|Rn.18688		–	RGD1311019_predicted	similar to hypothetical protein DKFZp434H2010 (predicted)	–	–	[Human] HomoloGene:12949
353	4145.00	1722.46	2.40	XM_218515	Znf507_predicted	PREDICTED: Rattus norvegicus zinc finger protein 507 (predicted) (Znf507_predicted), mRNA [XM_218515]	ref|XM_218515|ens|ENSRNOT00000018153|gb||CA513216	Rn.14198	–	Znf507_predicted	zinc finger protein 507 (predicted)	–	–	[Human, Mouse] HomoloGene:8942
354	2355.80	982.38	2.40	XM_227403	LOC310631	PREDICTED: Rattus norvegicus similar to ring finger and KH domain containing 2 (LOC310631), mRNA [XM_227403]	ref|XM_227403|ens|ENSRNOT00000052079|ens|ENSRNOT00000045390|ens|ENSRNOT00000000403	Rn.10409	–	RGD1564904_predicted	similar to ring finger and KH domain containing 2 (predicted)	–	–	[Human, Mouse] HomoloGene:18950
355	2834.80	1182.77	2.40	AI045861	AI045861	AI045861 UI-R-C1-km-F-08-0-UI.s1 UI-R-C1 Rattus norvegicus cDNA clone UI-R-C1-km-F-08-0-UI 3', mRNA sequence [AI045861]	gb|AI045861	Rn.10526	Proteasome	Psmc1	peptidase (prosome, macropain) 26S subunit, ATPase 1	may play a role in ATP-dependent RNA/DNA unwinding [RGD]	–	[Human, Mouse] HomoloGene:2095
356	781.76	327.17	2.39	NM_057151	Ccl17	Rattus norvegicus small inducible cytokine subfamily A (Cys-Cys), member 17 (Ccl17), mRNA [NM_057151]	ref|NM_057151|gb|AF3|AF3|ens|ENSRNOT00000021842|tc|TC65|Rn.46679	–		Ccl17	chemokine (C-C motif) ligand 17	a thymus and activation-regulated chemokine [RGD]	Our data indicate that instead of Th2 cells, airway epithelial cells expressing CCR4 might be the principal targets for MDC and TARC released from alveolar macrophages during cigarette smoke-induced airway inflammation.	[Human, Mouse] HomoloGene:2246
357	3880.55	1624.15	2.39	XM_220907	Arl12_predicted	PREDICTED: Rattus norvegicus ADP-ribosylation factor-like 12 (predicted) (Arl12_predicted), mRNA [XM_220907]	ref|XM_220907|ens|ENSRNOT00000056829|ens|ENSRNOT00000045561|ens|ENSRNOT00000000373|ens|ENSRNOT00000000373	Rn.18110	–	Arl12_predicted	ADP-ribosylation factor-like 12 (predicted)	–	–	[Human, Mouse] HomoloGene:10700
358	368.14	150.68	2.38	TC659056	TC659056	Unknown	tc|TC659056	Rn.14786	–	–	–	–	–	–



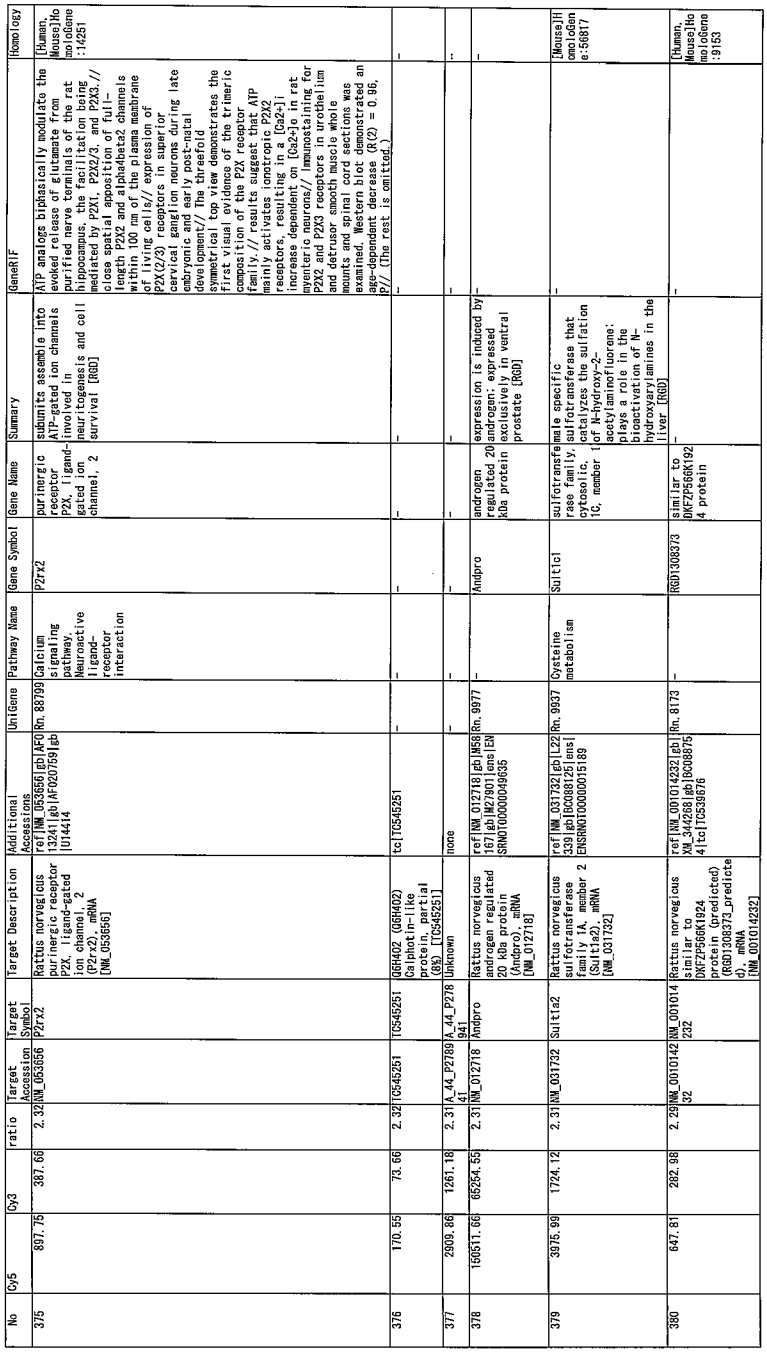
No	Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Pathway Name	Gene Symbol	Gene Name	Summary	GeneRIF	Homology
359	7572.43	3190.93	2.37	NM_012720	Mobp	Rattus norvegicus myelin-associated oligodendrocytic basic protein (Mobp), mRNA [NM_012720]	ref|NM_012720|ref|XM_346841|gb|X86637|to|TC540238	Rn. 91185	-	Mobp	myelin-associated oligodendrocytic basic protein	may mediate late steps of myelin formation, possibly in myelin compaction and in the maintenance of the myelin sheath [RGD]	-	-
360	668.31	282.87	2.36	XM_225147	Golph2_predicted	PREDICTED: Rattus norvegicus golgi phosphoprotein 2 (predicted) (Golph2_predicted), mRNA [XM_225147]	ref|XM_225147|ens|ENSRNOT00000024787|ens|ENSRNOT00000037597	Rn. 1545	-	Golph2_predicted	golgi phosphoprotein 2 (predicted)	-	-	[Human, Mouse]HomoloGene:12346
361	8094.36	3429.96	2.36	ENSRNOT00000038788	ENSRNOT00000038788	Unknown	ens|ENSRNOT00000038788|ens|ENSRNOT00000051360	-	-	-	-	-	-	-
362	615.11	260.92	2.36	AA800803	AA800803	AA800803 EST190300 Normalized rat lung, Bento Soares Rattus sp. cDNA clone RLUAL62 3' end, mRNA sequence [AA800803]	gb|AA800803	Rn. 10215-2	-	Dcakd	dephospho-CoA kinase domain containing	-	-	[Human, Mouse]HomoloGene:5652
363	280.91	119.18	2.36	BF400026	Mospd4_predicted	BF400026 UI-R-CA1-bia-d-03-0-UI.s1 UI-R-CA1 Rattus norvegicus cDNA clone UI-R-CA1-bia-d-03-0-UI 3', mRNA sequence [BF400026]	gb|BF400026	Rn. 63770	-	Mospd4_predicted	motile sperm domain containing 4 (predicted)	-	-	[Mouse]HomoloGene:19187
364	3009.92	1279.21	2.35	XM_578308	XM_578308	PREDICTED: Rattus norvegicus similar to monoclonal antibody kappa light chain (LOC502800), mRNA [XM_578308]	ref|XM_578308|ref|XM_575215|ens|ENSRNOT00000043102	-	-	RGD1561745_predicted	similar to monoclonal antibody kappa light chain (predicted)	-	-	-
365	1207.96	514.15	2.35	NM_130824	Rasgrp4	Rattus norvegicus RAS guanyl releasing protein 4 (Rasgrp4), mRNA [NM_130824]	ref|NM_130824|gb|AF462641|gb|AF462643|to|TC564378	Rn. 81227	MAPK signaling pathway	Rasgrp4	RAS guanyl releasing protein 4	mast cell specific guanine exchange factor [RGD]	Cloning of Ras guanine nucleotide releasing protein 4, and evaluation of its expression in mast cells and their bone marrow progenitors.// RasGRP4 regulates the expression of prostaglandin D2 in mast cell	[Human, Mouse]HomoloGene:15635

[0245]



No	Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Pathway Name	Gene Symbol	Gene Name	Summary	GeneRIF	Homology
366	12656.83	5390.25	2.35	NM_0010242 73	NM_0010242 73	Rattus norvegicus cytidine monophospho-N-acetylneuraminic acid hydroxylase (predicted) (Cmah_predicted), mRNA [XM_0010242 73]	ref|NM_0010242 73|gb|XM_341528|gb|BC009544|ens|ENSRNOT0000004 3234	Rn. 14280	Aminosugars metabolism	Cmah	cytidine monophospho-N-acetylneuraminic acid hydroxylase	-	-	[Mouse]H omoloGen e:7269
367	17420.13	7427.39	2.35	A_44_P8829 21	A_44_P882 921	Unknown	none	-	-	-	-	-	-	-
368	577.44	246.25	2.34	A_44_P7294 20	A_44_P729 420	Unknown	none	-	-	-	-	-	-	-
369	149.27	63.87	2.34	XM_214668	Hsf4_pred icted	PREDICTED: Rattus norvegicus heat shock transcription factor 4 (predicted) (Hsf4_predicted), mRNA [XM_214668]	ref|XM_214668|ens|ENSRNOT00000020682|tc|TC558106	Rn. 16339	-	Hsf4_predicted	heat shock transcription factor 4 (predicted)	-	HSF4 binds to alphaB-crystallin, Hsp70, and Hsp82 promoters and has a role in interacting with the canonical heat shock element of the alphaB-crystallin gene [HSF4]	[Human, Mouse]Ho moloGene :31042
370	866.38	378.81	2.33	NM_0010091 72	Znf297	Rattus norvegicus zinc finger protein 297 (Znf297), mRNA [NM_0010091 72]	ref|NM_0010091 72|ref|XM_579277|gb|XM_228016|gb|BX883042	Rn. 17135	-	Zfp297	zinc finger protein 297	-	-	[Human, Mouse]Ho moloGene :3982
371	1247.94	534.98	2.33	TC540693	TC540693	Q6NS71 (Q6NS71) Kifc3 protein, partial (10%) [TC540693]	tc|TC540693	-	-	-	-	-	-	-
372	1278.14	548.97	2.32	XM_236777	LOC3011121	PREDICTED: Rattus norvegicus similar to DNA binding protein RFX2 (LOC3011121), mRNA [XM_236777]	ref|XM_236777	Rn. 35756	-	-	similar to DNA binding protein RFX2	-	-	-
373	1133.50	488.46	2.32	NM_199374	Spata18	Rattus norvegicus spermatogenesis associated 18 (Spata18), mRNA [NM_199374]	ref|NM_199374|gb|AB1656 26|gb|XM_214040|gb|BC078996	Rn. 27773	-	Spata18	spermatogenesis associated 18	may play a role in differentiation of late spermatids to mature spermatozoa [RGD]	potential role of spatex-1 in spermatogenesis, especially in cell differentiation	[Human, Mouse]Ho moloGene :17057
374	410.70	177.21	2.32	XM_346122	LOC367391	PREDICTED: Rattus norvegicus similar to MARCO (LOC367391), mRNA [XM_346122]	ref|XM_346122	Rn. 83054	-	-	similar to MARCO	-	SR-MARCO could be the scavenger receptor responsible for the adhesion of astrocytes and microglia to Abeta	-

[0246]

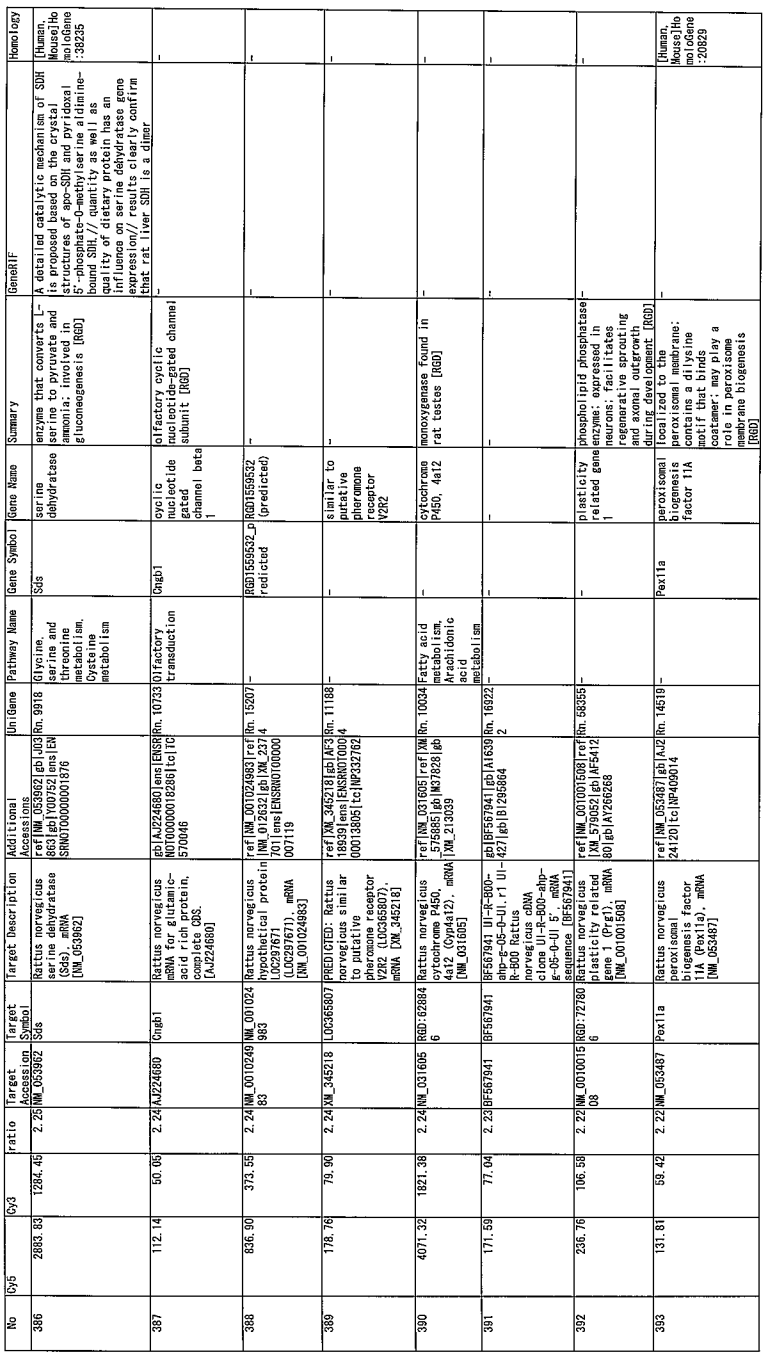


No	Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Pathway Name	Gene Symbol	Gene Name	Summary	GeneRIF	Homology
375	897.76	387.66	2.32	NM_053656	P2rx2	Rattus norvegicus purinergic receptor P2X, ligand-gated ion channel, 2 (P2rx2), mRNA [NM_053656]	ref|NM_053656|gb|AF0 13241|gb|AF020759|gb |U14414	Rn. 88799	Calcium signaling pathway, Neuroactive ligand-receptor interaction	P2rx2	purinergic receptor P2X, ligand-gated ion channel, 2	subunits assemble into ATP-gated ion channels involved in neurotogenesis and cell survival [RGD]	ATP analogs biphasically modulate the evoked release of glutamate from purified nerve terminals of the rat hippocampus, the facilitation being mediated by P2X1, P2X2/3, and P2X3.// close spatial apposition of full-length P2X2 and alphabeta2 channels within 100 nm of the plasma membrane of living cells// expression of P2X(2/3) receptors in superior cervical ganglion neurons during late embryonic and early post-natal development// The threefold symmetrical top view demonstrates the first visual evidence of the trimeric composition of the P2X receptor family.// results suggest that ATP mainly activates ionotropic P2X2 receptors, resulting in a [Ca2+]i increase dependent on [Ca2+]o in rat myenteric neurons// immunostaining for P2X2 and P2X3 receptors in urothelium and detrusor smooth muscle whole mounts and spinal cord sections was examined. Western blot demonstrated an age-dependent decrease (R(2) = 0.96. P// (The rest is omitted.)	-	[Human, Mouse]Ho moloGene :14251
376	170.55	73.66	2.32	TC545251		QGH402 (QGH402) Calphotin-like protein, partial (6%) [TC545251]	tc|TC545251	-	-	-	-	-	-	-
377	2909.86	1261.18	2.31	A_44_P27894 1	A_44_P278941	Unknown	none	-	-	-	-	-	-	-
378	160511.66	66264.55	2.31	NM_012718	Andpro	Rattus norvegicus androgen regulated 20 kDa protein (Andpro), mRNA [NM_012718]	ref|NM_012718|gb|M58 157|gb|M27301|ens|EN SRNOT00000049635	Rn. 9977	-	Andpro	androgen regulated 20 kDa protein	expression is induced by androgen; expressed exclusively in ventral prostate [RGD]	-	-
379	3976.99	1724.12	2.31	NM_031732	Sult1a2	Rattus norvegicus sulfotransferase family 1A, member 2 (Sult1a2), mRNA [NM_031732]	ref|NM_031732|gb|L22 330|gb|BC088125|ens| ENSRNOT00000015189	Rn. 9937	Cysteine metabolism	Sult1c1	sulfotransferase family, cytosolic, 1C, member 1	male specific sulfotransferase that catalyzes the sulfation of N-hydroxy-2-acetylaminofluorene; plays a role in the bioactivation of N-hydroxyarylamines in the liver [RGD]	-	[Mouse]Hom oloGene :56817
380	647.81	282.98	2.29	NM_001014232	NM_001014232	Rattus norvegicus similar to ZNFZP566K1924 protein (predicted) (RGD1308373_predicted), mRNA [NM_001014232]	ref|NM_001014232|gb| XM_344288|gb|BC088875 .4|tc|TC539676	Rn. 8173	-	RGD1308373	similar to ZNFZP566K1924 protein	-	-	[Human, Mouse]Ho moloGene :9153

[0247]

No	Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accession	UniGene	Pathway Name	Gene Symbol	Gene Name	Summary	GeneRIF	Homology
381	397.95	173.85	2.29	XM_227339	Sprr3_predicted	PREDICTED: Rattus norvegicus small proline-rich protein 3 (predicted) (Sprr3_predicted), mRNA [XM_227339]	ref|XM_227339|ens|ENSRNOT00000030295	Rn.19820	-	Sprr3_predicted	small proline-rich protein 3 (predicted)	-	-	[Human, Mouse]HomoloGene:22638
382	233.71	102.35	2.28	NM_001012225	Mgat4a_predicted	Rattus norvegicus mannoside acetylglucosaminyltransferase 4, isoenzyme A (predicted) (Mgat4a_predicted), mRNA [NM_001012225]	ref|NM_001012225|ref|XM_215875|ens|ENSRNOT00000032000	Rn.14535	N-Glycan biosynthesis, Glycan structures - biosynthesis 1	Mgat4a	mannoside acetylglucosaminyltransferase 4, isoenzyme A	-	-	[Human, Mouse]HomoloGene:8153
383	200.79	88.11	2.28	NM_019189	Hapln1	Rattus norvegicus hyaluronan and proteoglycan link protein 1 (Hapln1), mRNA [NM_019189]	ref|NM_019189|ens|ENSRNOT00000042958|ens|ENSRNOT00000043196|gb|M22340	Rn.50531	-	Hapln1	hyaluronan and proteoglycan link protein 1	stabilizs cartilage proteoglycan/hyaluronic acid aggregates by binding to each component [RGD]	study represents the first report that follicle stimulating hormone amplifies insulin-like growth factor-1-mediated cartilage link protein Crtl1 production, possibly via phosphatidylinositol 3-kinase-Akt signaling cascades in rat granulosa cells	[Human, Mouse]HomoloGene:1420
384	395.11	173.49	2.28	BM388083	BM388083	BM388083 UI-R-DM1-cjz-d-11-0-UI.s1 UI-R-DM1 Rattus norvegicus cDNA clone UI-R-DM1-cjz-d-11-0-UI 3', mRNA sequence [BM388083]	gb|BM388083|gb|BF416877|gb|BF416877	Rn.41133	-	Sorcs2_predicted	sortilin-related VPS10 domain containing receptor 2 (predicted)	-	-	[Mouse]HomoloGene:75305
385	286.67	126.13	2.27	BG380409	BG380409	BG380409 UI-R-CTO-btw-h-07-0-UI.s1 UI-R-CTO Rattus norvegicus cDNA clone UI-R-CTO-btw-h-07-0-UI 3', mRNA sequence [BG380409]	gb|BG380409	Rn.14396	-	RGD1560070_predicted	similar to ataxin 2-binding protein 1 isoform 2 (predicted)	-	-	[Mouse]HomoloGene:53459

[0248]

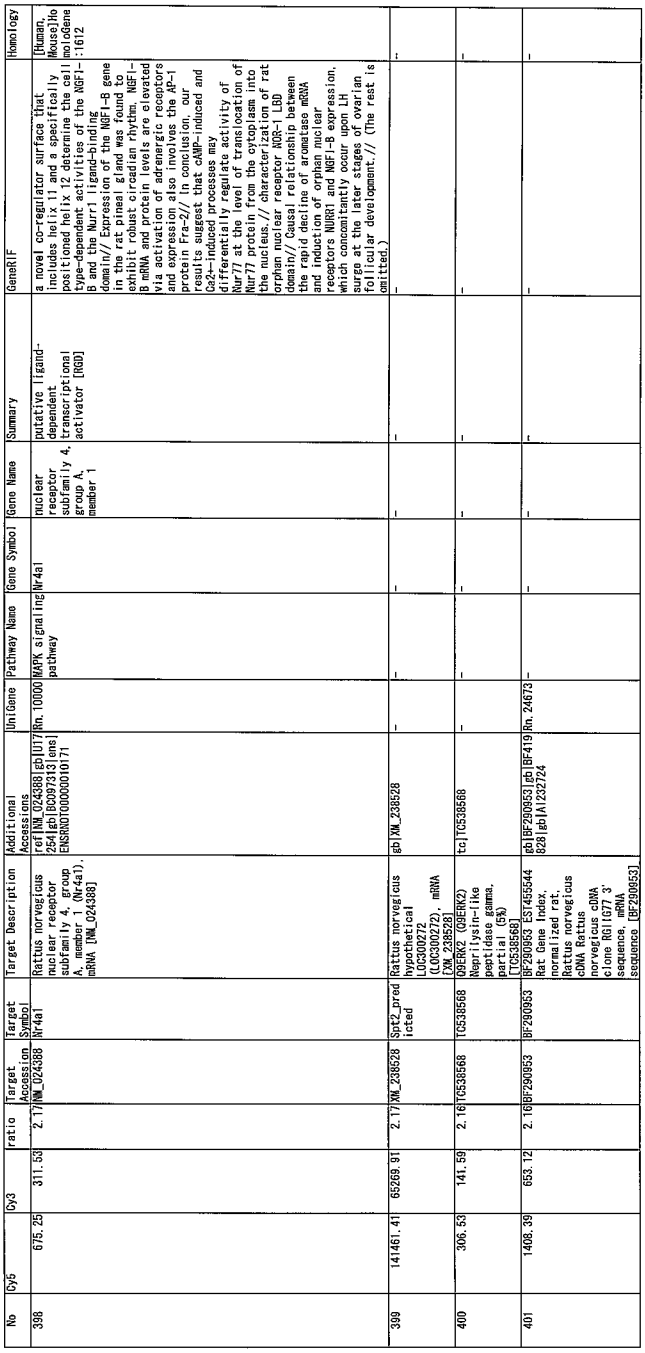


No	Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Pathway Name	Gene Symbol	Gene Name	Summary	GeneRIF	Homology
386	2883.83	1284.45	2.25	NM_053962	Sds	Rattus norvegicus serine dehydratase (Sds), mRNA [NM_053962]	ref|NM_053962|gb|U07752|ens|ENSRNOT00000001876	Rn.9918	Glycine, serine and threonine metabolism, Cysteine metabolism	Sds	serine dehydratase	enzyme that converts L-serine to pyruvate and ammonia. involved in gluconeogenesis [RGD]	A detailed catalytic mechanism of SDH is proposed based on the crystal structures of apo-SDH and pyridoxal 5'-phosphate-D-methylserine aldimine-bound SDH.// quantity as well as quality of dietary protein has an influence on serine dehydratase gene expression.// results clearly confirm that rat liver SDH is a dimer	[Human, Mouse]Homologene:38235
387	112.14	50.05	2.24	AJ224680	Cngb1	Rattus norvegicus mRNA for glutamic-acid rich protein, complete CDS. [AJ224680]	gb|AJ224680|ens|ENSRNOT00000018286|tc|TC5700046	Rn.10733	Olfactory transduction	Cngb1	cyclic nucleotide gated channel beta 1	olfactory cyclic nucleotide-gated channel subunit [RGD]	-	-
388	836.90	373.55	2.24	NM_001024983	NM_001024983	Rattus norvegicus hypothetical protein (LOC297671), mRNA [NM_001024983]	ref|NM_001024983|ref|NM_012632|gb|M27374|ens|ENSRNOT00000007119	Rn.15207	-	RGD1559532_predicted	RGD1559532 (predicted)	-	-	-
389	178.76	79.90	2.24	XM_345218	LOC365807	PREDICTED: Rattus norvegicus similar to putative pheromone receptor V2R2 (LOC365807), mRNA [XM_345218]	ref|XM_345218|gb|AF3|ens|ENSRNOT00000013805|tc|NP232762	Rn.11188	-	-	similar to putative pheromone receptor V2R2	-	-	-
390	4071.32	1821.38	2.24	NM_031605	RGD:62884 6	Rattus norvegicus cytochrome P450, 4a12 (Cyp4a12), mRNA [NM_031605]	ref|NM_031605|ref|XM_575885|gb|M27828|gb|XM_213039	Rn.10034	Fatty acid metabolism, Arachidonic acid metabolism	-	cytochrome P450, 4a12	monooxygenase found in rat testes [RGD]	-	-
391	171.59	77.04	2.23	BF567941	BF567941	BF567941 UI-R-B00-ahp-g-05-0-UI.r1 UI-R-B00-ahp-g-05-0-UI 5', mRNA sequence [BF567941]	gb|BF567941|gb|AI639427|gb|BI295864	Rn.169222	-	-	-	-	-	-
392	236.76	106.58	2.22	NM_001001508	RGD:72780 6	Rattus norvegicus plasticity related gene 1 (Prg1), mRNA [NM_001001508]	ref|NM_001001508|ref|XM_579052|gb|AF541280|gb|AY266268	Rn.58355	-	-	plasticity related gene 1	phospholipid phosphatase-related enzyme; expressed in neurons; facilitates regenerative sprouting and axonal outgrowth during development [RGD]	-	-
393	131.81	59.42	2.22	NM_053487	Pex11a	Rattus norvegicus peroxisomal biogenesis factor 11A (Pex11a), mRNA [NM_053487]	ref|NM_053487|gb|AA241201|tc|NP409014	Rn.14519	-	Pex11a	peroxisomal biogenesis factor 11A	localized to the peroxisomal membrane; contains a dilysine motif that binds coatamer; may play a role in peroxisome membrane biogenesis [RGD]	-	[Human, Mouse]Homologene:20829

[0249]

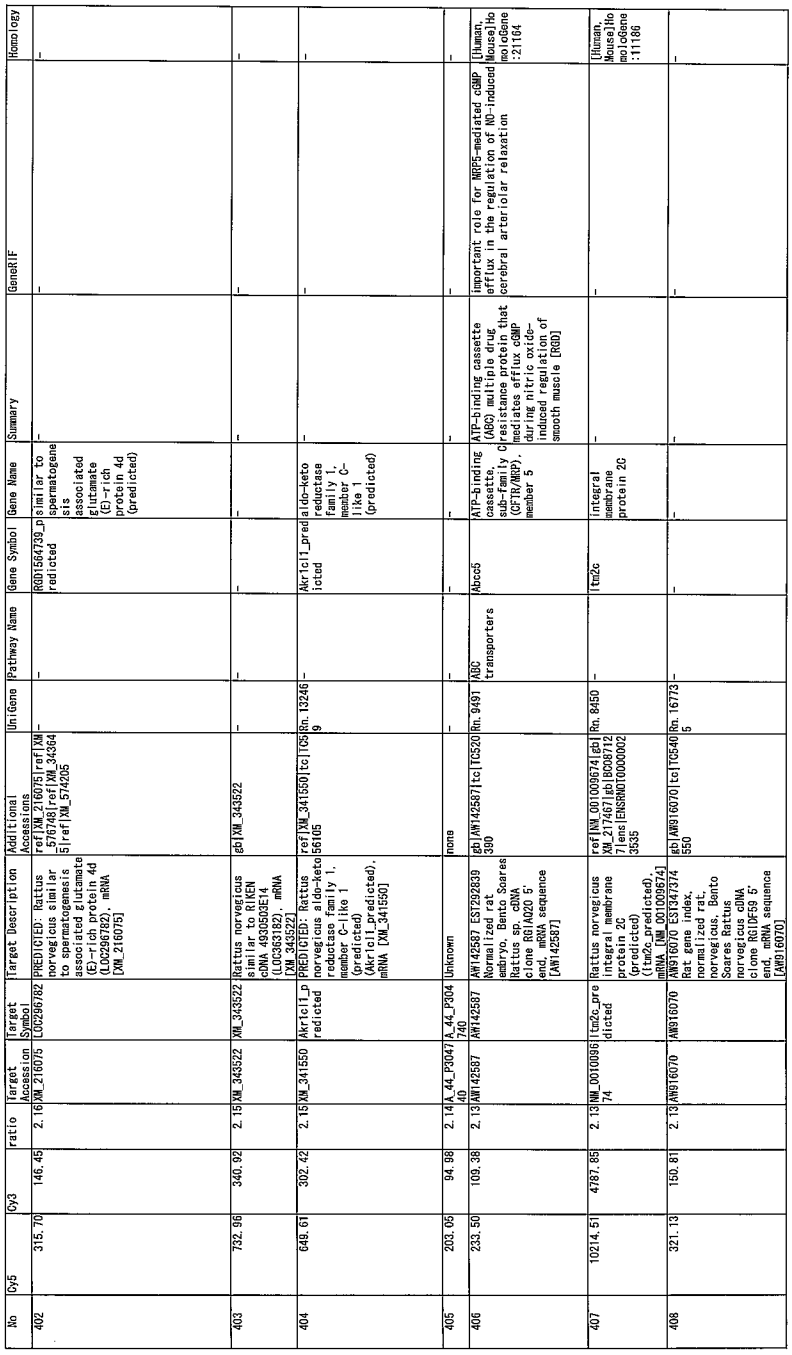
No	Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accession	UniGene	Pathway Name	Gene Symbol	Gene Name	Summary	GeneRIF	Homology
394	886.25	401.06	2.21	AA963232	AA963232	AA963232 UI-R-EI-gj-c-12-0-UI.s1 UI-R-EI Rattus norvegicus cDNA clone UI-R-EI-gj-c-12-0-UI 3', mRNA sequence [AA963232]	gb|AA963232|gb|AI177314|gb|AI406499	Rn.1063	-	S100a16_predicted	S100 calcium binding protein A16 (predicted)	-	-	(Human, Mouse)No motodome :12291
395	111.95	51.21	2.19	AW142782	AW142782	AW142782 EST293035 Normalized rat kidney, Bento Soares Rattus sp. cDNA clone RGIAV52 5' end, mRNA sequence [AW142782]	gb|AW142782|tc|TC543868	Rn.43391	-	-	-	-	-	-
396	975.91	446.45	2.19	A_44_P2605 74	A_44_P260574	Unknown	none	Rn.43391	-	-	-	-	-	-
397	348.49	159.56	2.18	NM_016989	Adcyap1	Rattus norvegicus adenylate cyclase activating polypeptide 1 (Adcyap1), mRNA [NM_016989]	ref|NM_016989|ref|NM_578383|gb|M63006|gb|XM_346860	Rn.37400	Neuroactive ligand-receptor interaction	Adcyap1	adenylate cyclase activating polypeptide 1	regulatory protein that stimulates cell proliferation, induces differentiation, modulates neurotransmitter release, vasodilation, bronchodilation, and hormone release, and suppresses inflammatory responses [RGD]	These results indicate that a large number of PACAP neurons and a small number of GnRH neurons project to the NGS // The specificity of PAC1 receptor participation in pituitary adenylate cyclase-activating polypeptide (PACAP)-facilitated sex behavior was demonstarted.// gastrin- and PACAP-stimulated secretion of histamine and pancreastatin is inhibited by somatostatin, misoprostol and galanin in enterochromaffin-like cells// PACAP is involved in the gonadotropin surge during estrus, perhaps through increased gonadotroph sensitivity to GnRH and suppression of Fshb subunit expression through increased follistatin.// Gastric enterochromaffin cells can be isolated to homogeneity by using a combination of density gradient centrifugation, followed by gradient sorting using PACAP.// PACAP priming of immature rat granulosa cells for 12 h increases subsequent FSH induced estradiol production and that PACAP could be involved in the cyclic recruitment of immature follicles// (The rest is omitted.)	(Human, Mouse)No motodome :569

[0250]



No	Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Pathway Name	Gene Symbol	Gene Name	Summary	GeneRIF	Homology
398	675.25	311.53	2.17	NM_024388	Nr4a1	Rattus norvegicus nuclear receptor subfamily 4, group A, member 1 (Nr4a1), mRNA [NM_024388]	ref|NM_024388|gb|U17254|gb|BC097313|ens|ENSRNOT00000010171	Rn. 10000	MAPK signaling pathway	Nr4a1	nuclear receptor subfamily 4, group A, member 1	putative ligand-dependent transcriptional activator [RGD]	a novel co-regulator surface that includes helix 11 and a specifically positioned helix 12 determine the cell type-dependent activities of the NGFI-B and the Nurr1 ligand-binding domain// Expression of the NGFI-B gene in the rat pineal gland was found to exhibit robust circadian rhythm, NGFI-B mRNA and protein levels are elevated via activation of adrenergic receptors and expression is mediated by the AP-1 protein Fra-2// In conclusion, our results suggest that cAMP-induced and Ca2+-induced processes may differentially regulate activity of Nur77 at the level of translocation of Nur77 protein from the cytoplasm into the nucleus.// characterization of rat orphan nuclear receptor NOR-1 LBD domain// Causal relationship between the rapid decline of aromatase mRNA and induction of orphan nuclear receptors NURR1 and NGFI-B expression, which concomitantly occur upon LH surge at the later stages of ovarian follicular development.// (The rest is omitted.)	[Human, Mouse]HomoloGene:1612
399	141461.41	65269.91	2.17	XM_238528	Sgtb2_predicted	Rattus norvegicus hypothetical LOC300272 (LOC300272), mRNA [XM_238528]	gb|XM_238528	-	-	-	-	-	-	-
400	306.53	141.59	2.16	TC538568	Q9ERK2 (Q9ERK2) Neprilysin-like peptidase gamma, partial (5%) [TC538568]	tc|TC538568	-	-	-	-	-	-	-	-
401	1408.39	653.12	2.16	BF290953	BF290953 EST455544 Rat Gene Index, normalized rat, Rattus norvegicus cDNA Rattus norvegicus cDNA clone RGIFD77 3' sequence, mRNA sequence [BF290953]	gb|BF290953|gb|BF419828|gb|AI232724	Rn. 24673	-	-	-	-	-	-	-

[0251]

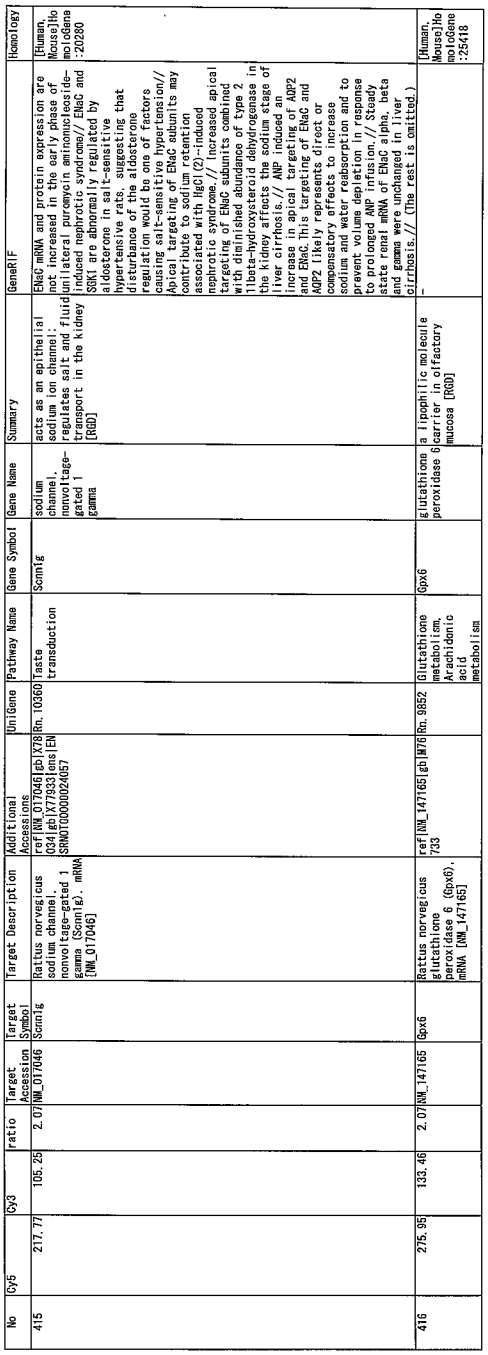


No	Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Pathway Name	Gene Symbol	Gene Name	Summary	GeneRIF	Homology
402	315.70	146.45	2.16	XM_216075	LOC296782	PREDICTED: Rattus norvegicus similar to spermatogenesis associated glutamate (E)-rich protein 4d (LOC296782), mRNA [XM_216075]	ref|XM_216075|ref|XM_576746|ref|XM_345365|ref|XM_574205	-	-	RGD1564739_predicted	similar to spermatogenesis associated glutamate (E)-rich protein 4d (predicted)	-	-	-
403	732.96	340.92	2.15	XM_343522	XM_343522	Rattus norvegicus similar to KIAA1530 protein, mRNA (cDNA clone MGC:109182 IMAGE:7393522), complete cds.	gb|XM_343522	-	-	-	-	-	-	-
404	648.61	302.42	2.15	XM_341550	Akr1cl1_predicted	PREDICTED: Rattus norvegicus aldo-keto reductase family 1, member C-like 1 (predicted) (Akr1cl1_predicted), mRNA [XM_341550]	ref|XM_341550|tc|TC56105	Rn.132469	-	Akr1cl1_predicted	aldo-keto reductase family 1, member C-like 1 (predicted)	-	-	-
405	203.05	94.98	2.14	A_44_P30447409	A_44_P304740	Unknown	none	-	-	-	-	-	-	-
406	233.50	109.38	2.13	AW142587	AW142587	AW142587 EST292839 Normal 2day rat hemisphere Bento Soares Rattus sp. cDNA clone RGIAQ20 5', end, mRNA sequence [AW142587]	gb|AW142587|tc|TC6520	Rn.94913080	ABC transporters	Abcc5	ATP-binding cassette, sub-family C (CFTR/MRP), member 5	ATP-binding cassette (ABC) multiple drug resistance protein that mediates efflux of cGMP during nitric oxide-induced regulation of smooth muscle [RGD]	important role for MRP5-mediated cGMP efflux in the regulation of NO-induced cerebral arteriolar relaxation	[Human, Mouse]HomoloGene:21164
407	10214.51	4787.86	2.13	NM_001009674	Ttn2c_predicted	Rattus norvegicus integral membrane protein 2C (predicted) (Ttn2c_predicted), mRNA [NM_001009674]	ref|NM_001009674|gb|XM_217467|gb|BC098712|ens|ENSRNOT00000023535	Rn.84503	-	Ttn2c	integral membrane protein 2C	-	-	[Human, Mouse]HomoloGene:11186
408	321.13	150.81	2.13	AW916070	AW916070	AW916070 EST347374 Rat gene index, normalized rat, norvegicus, Bento Soares Rattus norvegicus cDNA clone RGIDF59 5', end, mRNA sequence [AW916070]	gb|AW916070|tc|TC6540	Rn.167735	-	-	-	-	-	-

[0252]

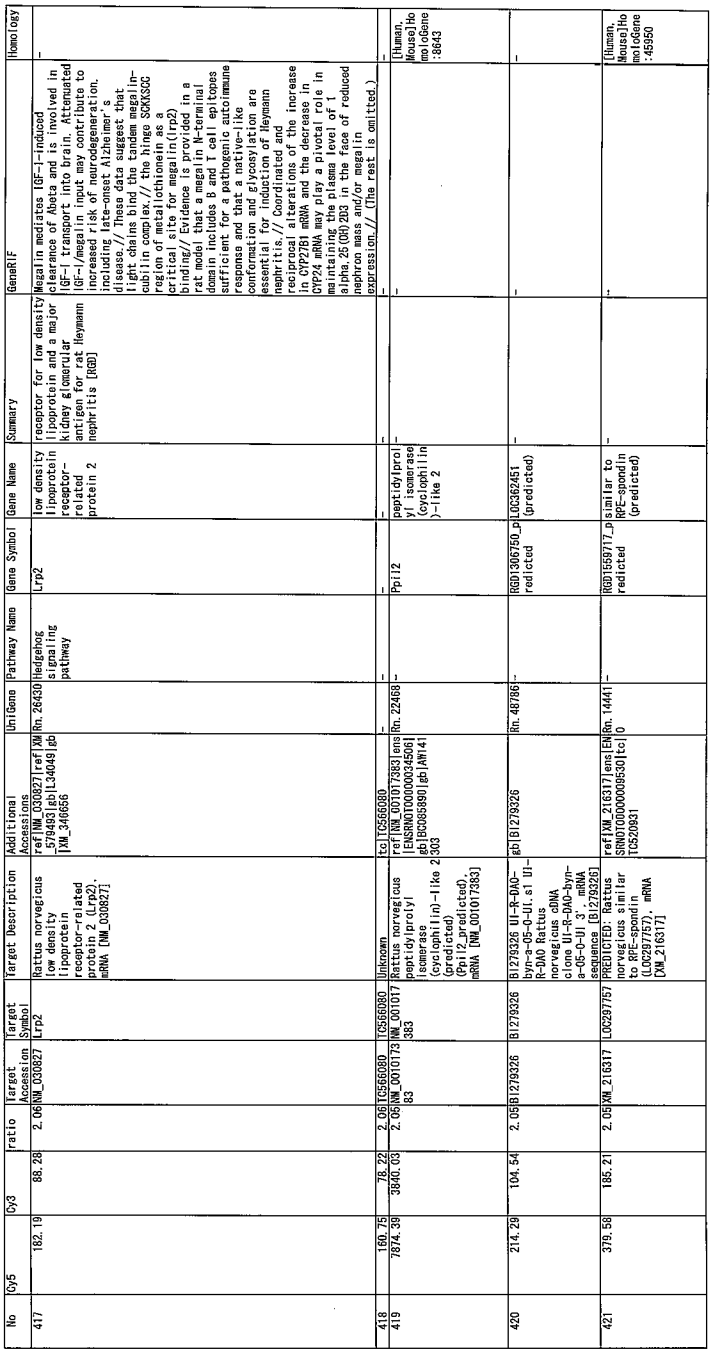
No	Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Pathway Name	Gene Symbol	Gene Name	Summary	GeneRIF	Homology
409	226.86	106.72	2.13	TC531872	TC531872	Q7TPA6 (Q7TPA6) Abi-1a2 partial (10%) [TC531872]	tc|TC531872	Rn.16773.5	-	-	-	-	-	-
410	306.03	144.66	2.12	XM_235563	LOC300150	PREDICTED: Rattus norvegicus similar to hypothetical protein BC009980 (LOC300150), mRNA [XM_235563]	ref|XM_235563|ens|ENSRNOT00000043911|ens|ENSRNOT00000040769	-	-	RGD1562257_predicted	similar to hypothetical protein BC009980 (predicted)	-	-	[Human, Mouse]Homolo gene:34707
411	392.25	196.35	2.10	ENSRNOT00000049913	ENSRNOT00000049913	Unknown	ens|ENSRNOT00000000499	-	-	-	-	-	-	-
412	260.26	123.91	2.10	NM_145775	Nr1d1	Rattus norvegicus nuclear receptor subfamily 1, group D, member 1 (Nr1d1), mRNA [NM_145775]	ref|NM_145775|gb|BC062047|gb|M22804|ens|ENSRNOT00000012537	Rn.29848	Circadian rhythm	Nr1d1	nuclear receptor subfamily 1, group D, member 1	member of tha steroid hormone receptor superfamily [RGD]	Rev-Erbalpha as a target gene of PPARgamma in adipose tissue and demonstrate a role for this nuclear receptor as a promoter of adipocyte differentiation.	[Human, Mouse]Homolo gene:23324
413	1146.71	551.72	2.08	XM_341641	RGD1306668_predicted	Rattus norvegicus similar to hypothetical protein LOC392922 (LOC3613363), mRNA [XM_341641]	gb|XM_341641|ens|ENSRNOT00000012291|tc1|CS539381|tc1|TC539382	Rn.41567	-	RGD1306668_predicted	similar to hypothetical protein LOC392922 (predicted)	-	-	[Human, Mouse]Homolo gene:13240
414	1378.02	664.06	2.08	XM_344926	LOC365316	PREDICTED: Rattus norvegicus similar to Hornerin (LOC365316), mRNA [XM_344926]	ref|XM_344926	-	-	RGD1565802_predicted	similar to Hornerin (predicted)	-	-	-

[0253]



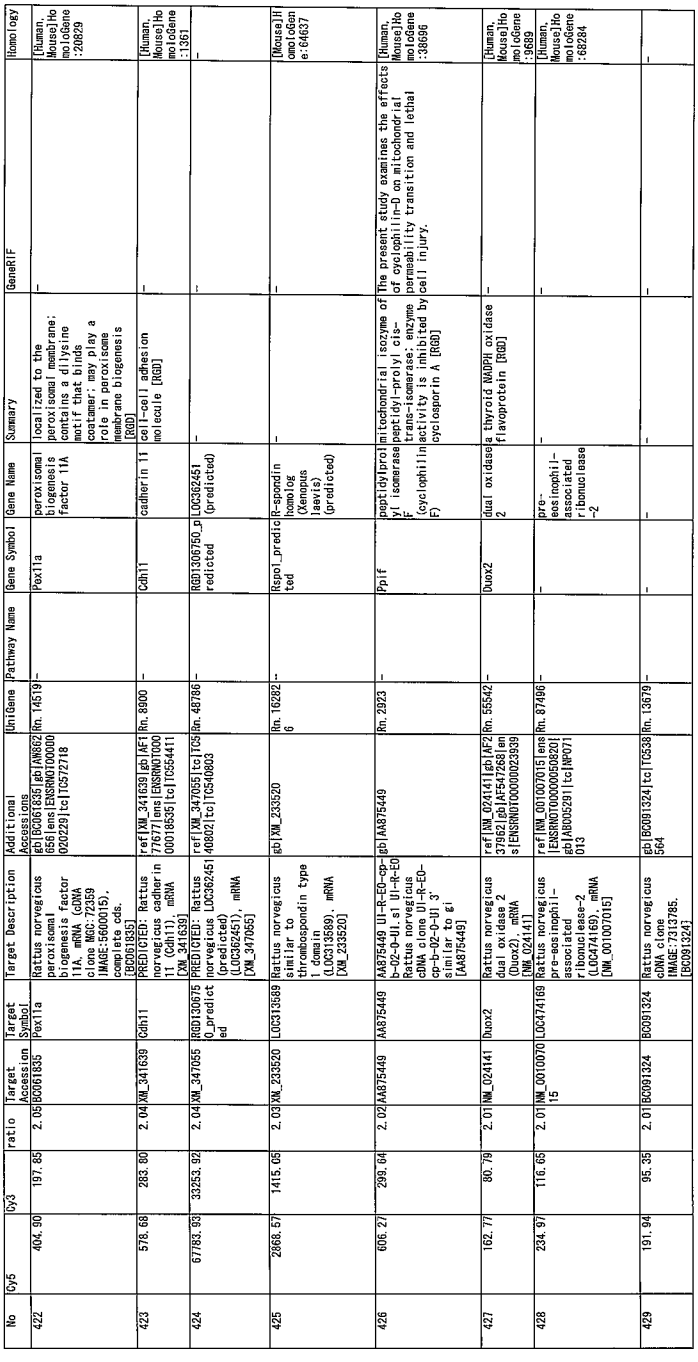
No	Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accession	UniGene	Pathway Name	Gene Symbol	Gene Name	Summary	GeneRIF	Homology
415	217.77	105.25	2.07	NM_017046	Scnn1g	Rattus norvegicus sodium channel, nonvoltage-gated 1 gamma (Scnn1g), mRNA [NM_017046]	ref|NM_017046|gb|M70034|gb|X77833|ens|ENSRNOT00000024057	Rn.10360	Taste transduction	Scnn1g	sodium channel, nonvoltage-gated 1 gamma	acts as an epithelial sodium channel; regulates salt and fluid transport in the kidney [RGD]	ENaG mRNA and protein expression are not increased in the early phase of urinary concentrating defect in mice with diabetes insipidus and nephrotic syndrome.// ENaG and SGK1 are abnormally regulated by aldosterone in salt-sensitive hypertensive rats, suggesting that disturbance of the aldosterone regulation would be one of factors causing salt-sensitive hypertension// Apical targeting of ENaC subunits may contribute to sodium retention associated with HgCl(2)-induced nephrotic syndrome.// Increased apical targeting of ENaC subunits combined with diminished abundance of type 2 11beta-hydroxysteroid dehydrogenase in the kidney affects the sodium stage of liver cirrhosis.// ANP induced an increase in apical targeting of AQP2 and ENaC. This targeting effect on AQP2 likely represents a critical compensatory effects to increase sodium and water reabsorption and to prevent volume depletion in response to prolonged ANP infusion.// Steady state renal mRNA of ENaC alpha, beta and gamma were unchanged in liver cirrhosis.// (The rest is omitted.)	[Human, Mouse]HomoloGene:20280
416	275.95	133.46	2.07	NM_147165	Gpx6	Rattus norvegicus glutathione peroxidase 6 (Gpx6), mRNA [NM_147165]	ref|NM_147165|gb|AW761733	Rn.9852	Glutathione metabolism, Arachidonic acid metabolism	Gpx6	glutathione peroxidase 6	a lipophilic molecule carrier in olfactory mucosa [RGD]	-	[Human, Mouse]HomoloGene:25418

[0254]



No	Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Pathway Name	Gene Symbol	Gene Name	Summary	GeneRIF	Homology
417	182.19	88.28	2.06	NM_030827	Lrp2	Rattus norvegicus low density lipoprotein receptor-related protein 2 (Lrp2), mRNA [NM_030827]	ref|NM_030827|ref|XM_579493|gb|L34049|gb|XM_346656	Rn. 26430	Hedgehog signaling pathway	Lrp2	low density lipoprotein receptor-related protein 2	receptor for low density lipoprotein and a major kidney glomerular antigen for rat Heymann nephritis [RGD]	Megalin mediates IGF-I-induced clearance of Abeta and is involved in IGF-I transport into brain. Attenuated IGF-I/megalin input may contribute to increased risk of neurodegeneration including late-onset Alzheimer's disease.// These data suggest that light chains bind the tandem megalin-cubilin complex.// the hinge SCKKSGC region of metallothionein as a critical site for megalin(Lrp2) binding// Evidence is provided in a rat model that a megalin N-terminal domain includes B and T cell epitopes sufficient for a pathogenic autoimmune response and that a native-like conformation and glycosylation are essential for induction of Heymann nephritis.// Coordinated and reciprocal alterations of the increase in CYP27B1 mRNA and the decrease in CYP24 mRNA may play a pivotal role in maintaining the plasma level of 1 alpha,25(OH)2D3 in the face of reduced nephron mass and/or megalin expression.// (The rest is omitted.)	-
418	160.75	78.22	2.06	TC566080	TC566080	Unknown	tc|TC566080	-	-	-	-	-	-	-
419	7874.39	3840.03	2.05	NM_001017383	Rattus norvegicus peptidyprolyl isomerase (cyclophilin)-like 2 (predicted) (Ppil2 predicted), mRNA [NM_001017383]	ref|NM_001017383|ens|ENSRNOT00000034506|gb|BC085890|gb|AH141303	Rn. 22468	-	Ppil2	peptidylprolyl isomerase (cyclophilin)-like 2	-	-	[Human, Mouse]HomoloGene:8643
420	214.29	104.54	2.05	B1279326	B1279326	B1279326 UI-R-DAO-byn-a-05-0-UI.s1 UI-R-DAO Rattus norvegicus cDNA clone UI-R-DAO-byn-a-05-0-UI 3', mRNA sequence [B1279326]	gb|B1279326	Rn. 46786	-	RGD1306750_predicted	LOC362451 (predicted)	-	-	-
421	379.58	185.21	2.05	XM_216317	LOC297757	PREDICTED: Rattus norvegicus similar to RPE-spondin (LOC297757), mRNA [XM_216317]	ref|XM_216317|ens|ENSRNOT00000009530|tc|TC520931	Rn. 14441	-	RGD1559717_predicted	similar to RPE-spondin (predicted)	-	-	[Human, Mouse]HomoloGene:45950

[0255]

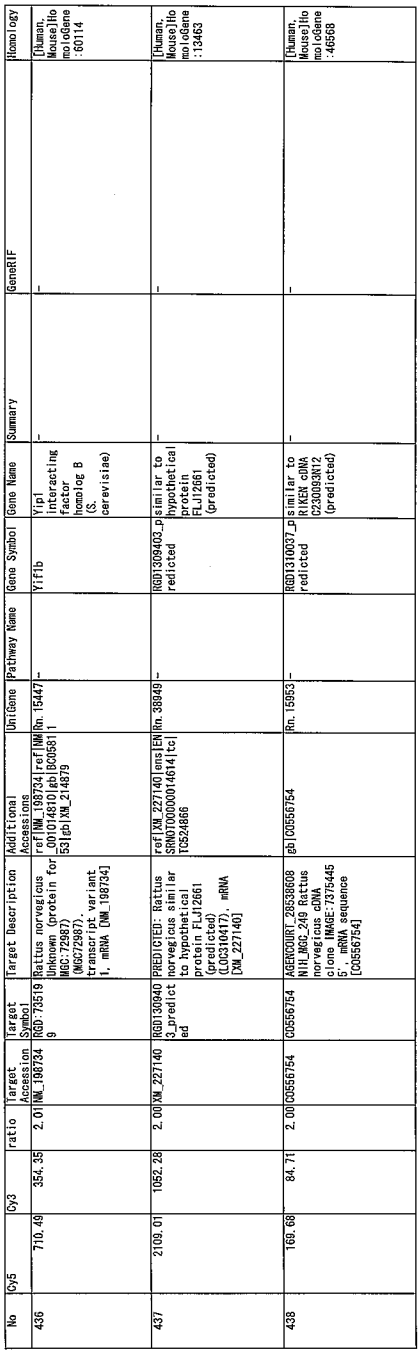


No	Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Pathway Name	Gene Symbol	Gene Name	Summary	GeneRIF	Homology
422	404.90	197.85	2.05	BC061835	Pex11a	Rattus norvegicus peroxisomal biogenesis factor 11A, mRNA (cDNA clone MGC:72339 IMAGE:7360015), complete cds. [BC061835]	gb|BC061835|gb|AN682650|ens|ENSRNOT00000020229|tc|TC572718	Rn.14519	-	Pex11a	peroxisomal biogenesis factor 11A	localized to the peroxisomal membrane; contains a diLysine motif that binds coatamer; may play a role in peroxisome membrane biogenesis [RGD]	-	[Human, Mouse]Homolodene:20829
423	578.68	283.80	2.04	XM_341639	Cdh11	PREDICTED: Rattus norvegicus cadherin 11 (Cdh11), mRNA [XM_341639]	ref|XM_341639|gb|AF177677|ens|ENSRNOT00000018635|tc|TC554411	Rn.8900	-	Cdh11	cadherin 11	cell-cell adhesion molecule [RGD]	-	[Human, Mouse]Homolodene:1361
424	67783.93	33253.92	2.04	XM_347055	RGD1306750_predicted	PREDICTED: Rattus norvegicus LOC362451 (predicted), mRNA [XM_347055]	ref|XM_347055|tc|TC540802|tc|TC540803	Rn.48786	-	RGD1306750_predicted	LOC362451 (predicted)	-	-	-
425	2868.57	1415.05	2.03	XM_233520	LOC313589	Rattus norvegicus similar to thrombospondin type 1 domain (LOC313589), mRNA [XM_233520]	gb|XM_233520	Rn.162826	-	Rspo1_predicted	R-spondin homolog (Xenopus laevis) (predicted)	-	-	[Mouse]Homolodene:64637
426	606.27	299.64	2.02	AA875449	AA875449	AA875449 UI-R-E0-cp-b-02-0-UI.s1 UI-R-E0-Rattus norvegicus cDNA clone UI-R-E0-cp-b-02-0-UI 3' similar to gi [AA875449]	gb|AA875449	Rn.2923	-	Ppif	peptidylprolyl isomerase F (cyclophilin F)	mitochondrial isozyme of peptidyl-prolyl cis-trans-isomerase, enzyme activity is inhibited by cyclosporin A [RGD]	The present study examines the effects of cyclophilin-D on mitochondrial permeability transition and lethal cell injury.	[Human, Mouse]Homolodene:386696
427	162.77	80.79	2.01	NM_024141	Duox2	Rattus norvegicus dual oxidase 2 (Duox2), mRNA [NM_024141]	ref|NM_024141|gb|AF237962|gb|AF547268|ens|ENSRNOT00000023939	Rn.55542	-	Duox2	dual oxidase 2	a thyroid NADPH oxidase flavoprotein [RGD]	-	[Human, Mouse]Homolodene:9689
428	234.97	116.65	2.01	NM_0010070 15	LOC474169	Rattus norvegicus pre-eosinophil-associated ribonuclease-2 (LOC474169), mRNA [NM_0010070 15]	ref|NM_0010070 15|ens|ENSRNOT00000059820|gb|AB005291|tc|NM071013	Rn.87496	-	-	pre-eosinophil-associated ribonuclease-2	-	-	[Human, Mouse]Homolodene:88284
429	191.94	95.35	2.01	BC091324	BC091324	Rattus norvegicus cDNA clone IMAGE:7313785. [BC091324]	gb|BC091324|tc|TC563805644	Rn.13679	-	-	-	-	-	-

[0256]

No	Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Pathway Name	Gene Symbol	Gene Name	Summary	GeneRIF	Homology
430	151.20	75.12	2.01	NM_138547	RGD:70836	Rattus norvegicus 3-alpha-hydroxysteroid dehydrogenase (LOC191574), mRNA [NM_138547]	ref|NM_138547|ref|NP_579650|gb|D17310|gb|XM_346501	Rn.10021	-	-	3-alpha-hydroxysteroid dehydrogenase	catalyzes the conversion of 5 alpha-dihydrotestosterone to 3alpha-androstanediol in steroid metabolism [RGD]	Burst phase kinetics for the NADP(+)-dependent turnover of 3alpha-diol by M227A of 3Alpha-hydroxysteroid dehydrogenase was also abolished// 3alpha-HSD immunoreactivity was largely distributed in the white matter and gray matter, but the highest density was found in sensory areas of the dorsal horn.// Binding cavity residues of 3-alpha-hydroxysteroid dehydrogenase not only control steroid hormone affinity but also affect the rates of oxidation which becomes rate-limiting when the steroid fails to make proper contact with these residues.	[Mouse]Homologene:64472
431	1303.34	647.58	2.01	X55180	X55180	Rattus norvegicus mRNA for monoclonal antibody Y13-259 Vk. [X55180]	gb|X55180|tc|NP06837 4	Rn.11783	-	RGD1560438_predicted	similar to IG light chain VK region Y13-259 (predicted)	-	-	-
432	444.77	221.08	2.01	XM_222564	LOC288979	PREDICTED: Rattus norvegicus similar to complement 1, q subcomponent-like 2 (LOC288979), mRNA [XM_222564]	ref|XM_222564|tc|TC5 40456	Rn.24014	-	-	similar to complement 1, q subcomponent-like 2	-	-	-
433	371.25	184.56	2.01	AW918545	AW918545	AW918545 EST348849 Rat gene index, normalized rat, norvegicus, Bento Soares Rattus norvegicus cDNA clone RGIEU57 5', end, mRNA sequence [AW918545]	gb|AW918545|tc|TC654 334	Rn.13679	-	-	-	-	-	-
434	101.58	50.52	2.01	TC542673	TC542673	QBJ4S2 (QBJ4S2) PCRET partial (3%) [TC542673]	tc|TC542673	Rn.13679	-	-	-	-	-	-
435	438.22	218.04	2.01	B66726648	B66726648	B66726648 DRNCNF12 Rat DRG Library Rattus norvegicus cDNA clone DRNCNF12 5', mRNA sequence [B66726648]	gb|B66726648	-	-	-	-	-	-	-

[0257]



No	Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Pathway Name	Gene Symbol	Gene Name	Summary	GeneRIF	Homology
436	710.49	354.35	2.01	NM_198734	RGD:73519 9	Rattus norvegicus Unknown (protein for MGC:72987). (MGC:72987), transcript variant 1, mRNA [NM_198734]	ref|NM_198734|ref|NM_001005811|gb|AK214879	Rn.15447	-	Yif1b	Yip1 interacting factor homolog B (S. cerevisiae)	-	-	[Human, Mouse]Homologene:60114
437	2109.01	1052.28	2.00	XM_227140	RGD1309403_predicted	PREDICTED: Rattus norvegicus similar to hypothetical protein FLJ12661 (predicted) (LOC310417), mRNA [XM_227140]	ref|XM_227140|ens|ENSRNOT00000014614|tc|TC524866	Rn.38949	-	RGD1309403_predicted	similar to hypothetical protein FLJ12661 (predicted)	-	-	[Human, Mouse]Homologene:13463
438	168.68	84.71	2.00	C05567754	C05567754	AGENCOURT_29536608 NIH_MGC_246 Rattus norvegicus cDNA clone IMAGE:7375445 5', mRNA sequence [C05567754]	gb|C05567754	Rn.15953	-	RGD1310037_predicted	similar to RIKEN cDNA C230093H12 (predicted)	-	-	[Human, Mouse]Homologene:46568

[0258] 対照群と比較してTickling群で0.5倍未満の発現を認めた唾液腺(Sg)の遺伝子のアノテーションを下記表33に示す。

[表33]

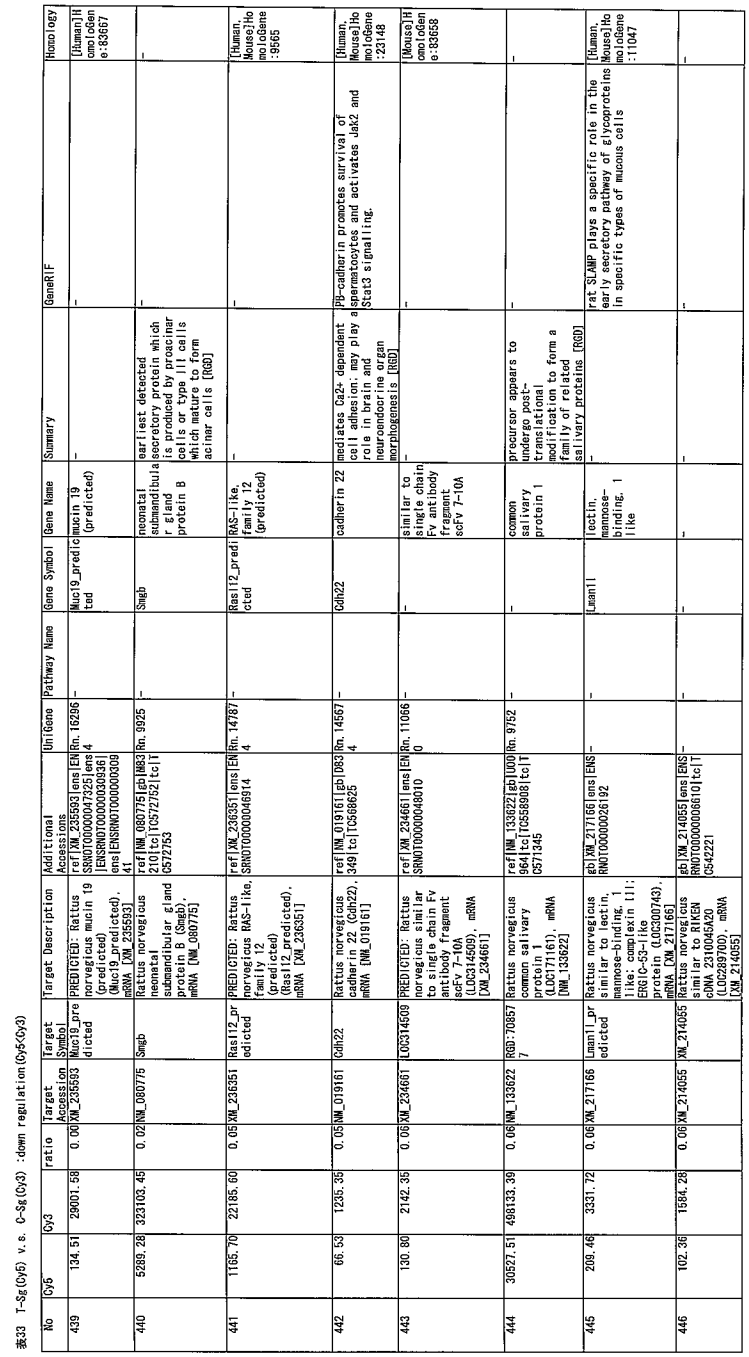
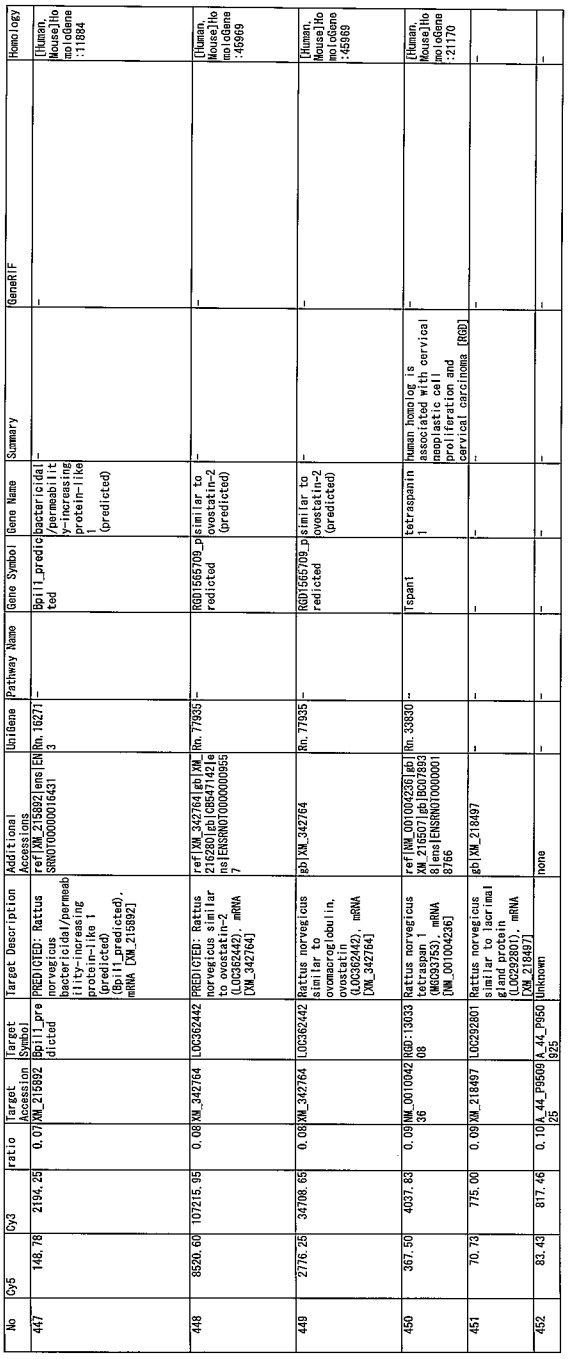


表33 T-Sg(Cy5) v.s. C-Sg(Cy3) :down regulation(Cy5<Cy3)

No	Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Pathway Name	Gene Symbol	Gene Name	Summary	GeneRIF	Homology
439	134.51	29001.58	0.00	XM_235593	Muc19_predicted	PREDICTED: Rattus norvegicus mucin 19 (predicted) (Muc19_predicted), mRNA [XM_235593]	ref|XM_235593|ens|ENSRNOT00000047325|ens|ENSRNOT00000030936|ens|ENSRNOT00000000309 41	Rn.16256	-	Muc19_predicted	mucin 19 (predicted)	-	-	[Human]Homolo Gene:83657
440	5289.28	323103.45	0.02	NM_080775	Smgb	Rattus norvegicus neonatal submandibular gland protein B (Smgb), mRNA [NM_080775]	ref|NM_080775|gb|M83210|tc|TC572752|tc|TC572753	Rn.9925	-	Smgb	neonatal submandibular gland protein B	earliest detected secretory protein which is produced by proacinar cells or type III cells which mature to form acinar cells [RGD]	-	-
441	1168.70	22195.60	0.05	XM_236351	Rasl12_predicted	PREDICTED: Rattus norvegicus RAS-like, family 12 (predicted) (Rasl12_predicted), mRNA [XM_236351]	ref|XM_236351|ens|ENSRNOT00000046914	Rn.14787	-	Rasl12_predicted	RAS-like, family 12 (predicted)	-	-	[Human, Mouse]Homolo Gene:9565
442	66.53	1235.35	0.05	NM_019161	Cdh22	Rattus norvegicus cadherin 22 (Cdh22), mRNA [NM_019161]	ref|NM_019161|gb|D83349|tc|TC568625	Rn.14567	-	Cdh22	cadherin 22	mediates Ca2+ dependent cell adhesion: may play a role in brain and neuroendocrine organ morphogenesis [RGD]	PB-cadherin promotes survival of spermatocytes and activates Jak2 and Stat3 signalling.	[Human, Mouse]Homolo Gene:23148
443	130.80	2142.35	0.06	XM_234661	LOC314509	PREDICTED: Rattus norvegicus similar to single chain Fv antibody fragment scFv 7-10A (LOC314509), mRNA [XM_234661]	ref|XM_234661|ens|ENSRNOT00000048010	Rn.11066	-	-	similar to single chain Fv antibody fragment scFv 7-10A	-	-	[Mouse]Homolo Gene:83658
444	30527.51	498133.39	0.06	NM_133622	RGD:70857	Rattus norvegicus common salivary protein 1 (LOC171161), mRNA [NM_133622]	ref|NM_133622|gb|U00964|tc|TC558908|tc|TC571345	Rn.9752	-	-	common salivary protein 1	precursor appears to undergo post-translational modification to form a family of related salivary proteins [RGD]	-	-
445	209.46	3331.72	0.06	XM_217166	Lmanl1_predicted	Rattus norvegicus similar to lectin, mannose-binding, 1 like; complexin III; ERGIC-53-like protein (LOC300743), mRNA [XM_217166]	gb|XM_217166|ens|ENSRNOT00000026192	-	-	Lmanl1	lectin, mannose-binding, 1 like	-	rat SLAMP plays a specific role in the early secretory pathway of glycoproteins in specific types of mucous cells	[Human, Mouse]Homolo Gene:11047
446	102.36	1584.28	0.06	XM_214055	XM_214055	Rattus norvegicus similar to RIKEN cDNA 2310045A20 (LOC298700), mRNA [XM_214055]	gb|XM_214055|ens|ENSRNOT00000066010|tc|TC542221	-	-	-	-	-	-	-

[0259]

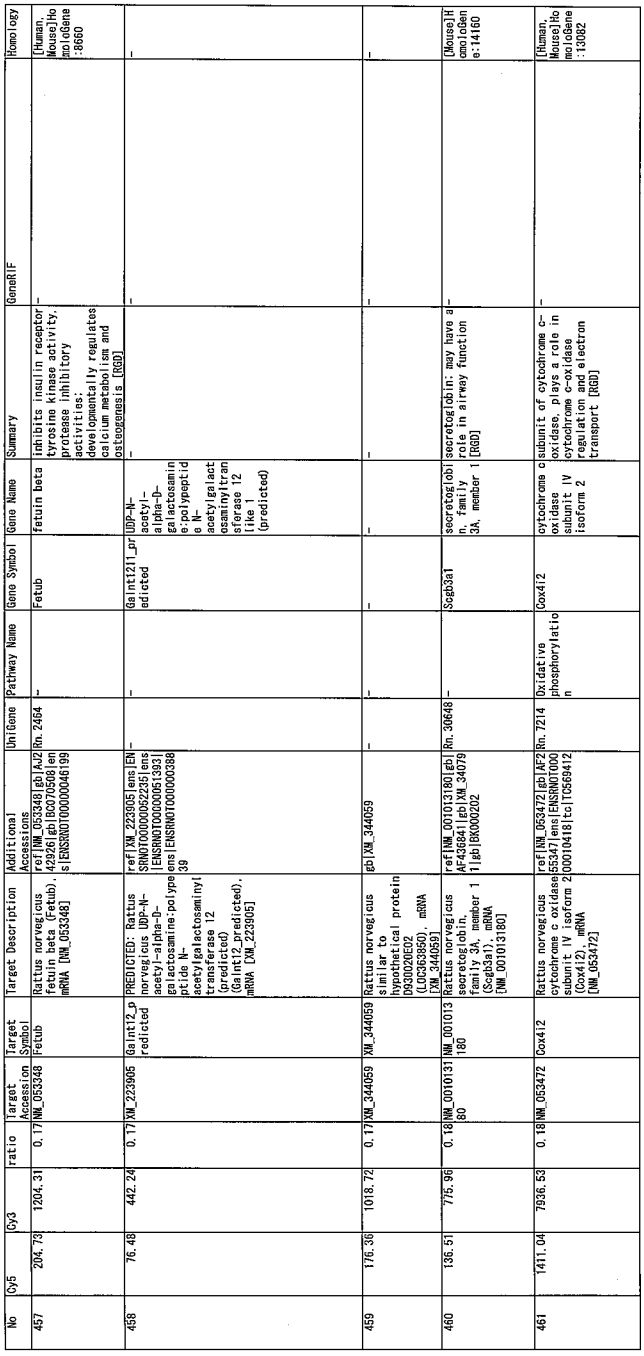


No	Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accession	UniGene	Pathway Name	Gene Symbol	Gene Name	Summary	GeneRIF	Homology
447	148.78	2194.25	0.07	XM_215892	Bpil1_predicted	PREDICTED: Rattus norvegicus bactericidal/permeability-increasing protein-like 1 (predicted) (Bpil1_predicted), mRNA [XM_215892]	ref|XM_215892|ens|ENSRNOT00000016431	Rn.162713	-	Bpil1_predicted	bactericidal/permeability-increasing protein-like 1 (predicted)	-	-	[Human, Mouse]HomoloGene:11884
448	8520.60	107215.95	0.08	XM_342764	LOC362442	PREDICTED: Rattus norvegicus similar to ovostatin-2 (LOC362442), mRNA [XM_342764]	ref|XM_342764|gb|XM_216280|gb|CB547142|ens|ENSRNOT00000009557	Rn.77935	-	RGD1565709_predicted	similar to ovostatin-2 (predicted)	-	-	[Human, Mouse]HomoloGene:45969
449	2776.25	34708.65	0.08	XM_342764	LOC362442	Rattus norvegicus similar to ovomacroglobulin, ovostatin (LOC362442), mRNA [XM_342764]	gb|XM_342764	Rn.77935	-	RGD1565709_predicted	similar to ovostatin-2 (predicted)	-	-	[Human, Mouse]HomoloGene:45969
450	367.50	4037.83	0.09	NM_001100942	RGD:1303308	Rattus norvegicus tetraspan 1 (MGC93753), mRNA [NM_001004236]	ref|NM_001004236|gb|XM_216507|gb|BC078938|ens|ENSRNOT00000018766	Rn.33830	-	Tspan1	tetraspanin 1	human homolog is associated with cervical neoplastic cell proliferation and cervical carcinoma [RGD]	-	[Human, Mouse]HomoloGene:21170
451	70.73	775.00	0.09	XM_218497	LOC292801	Rattus norvegicus similar to lacrimal gland protein (LOC292801), mRNA [XM_218497]	gb|XM_218497	-	-	-	-	-	-	-
452	83.43	817.46	0.10	A_44_P9509825	A_44_P9509825	Unknown	none	-	-	-	-	-	-	-

[0260]

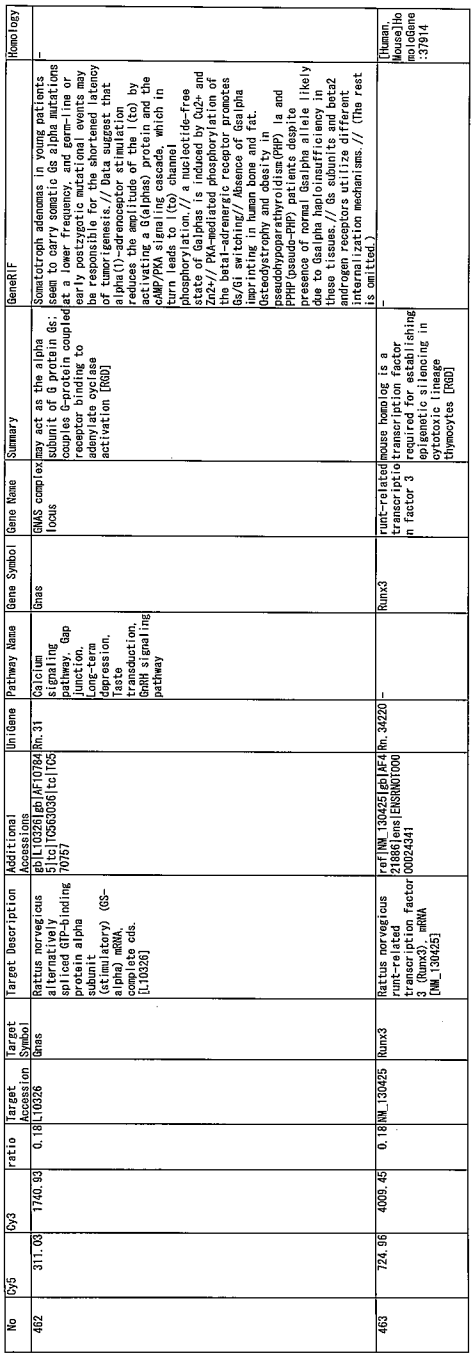
No	Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Pathway Name	Gene Symbol	Gene Name	Summary	GenaRIF	Homology
453	63.07	545.73	0.12	XM_215767	RGD1311224_predicted	PREDICTED: Rattus norvegicus similar to fatty acid desaturase 2; linoleoyl-CoA desaturase (delta-6-desaturase)-like 2; delta-6 fatty acid desaturase (predicted) (LOC295714), mRNA [XM_215767]	ref|XM_215767|ens|ENSRNOT00000012560|col|10546733	Rn. 47560	-	RGD1311224_predicted	similar to fatty acid desaturase 2; linoleoyl-CoA desaturase (delta-6-desaturase)-like 2; delta-6 fatty acid desaturase (predicted)	-	-	[Mouse]Homologene:72650
454	348.21	2901.71	0.12	NM_012973	Kcnel	Rattus norvegicus potassium voltage-gated channel, isk-related subfamily, member 1 (Kcnel), mRNA [NM_012973]	ref|NM_012973|gb|M22412|gb|M36461|ens|ENSRNOT00000002717	Rn. 6734	-	Kcnel	potassium voltage-gated channel, isk-related subfamily, member 1	beta subunit of the voltage-gated potassium channel complex: involved in modulating channel kinetics [RGD]	Expression of KCNQ1 and KCNE1 associated with early stages of spermatogenesis and with presence of undifferentiated healthy or neoplastic germ cells. KCNQ1/KCNE1 may be involved in K+ transport, probably during germ-cell development.// may play a role in the negative regulation of the exocrine pancreas by somatostatin.// resting membrane potential in stomach SMCs	[Human, Mouse]Homologene:185
455	64.90	505.88	0.13	XM_222157	Kntc1_predicted	PREDICTED: Rattus norvegicus kinetochore associated 1 (predicted) (Kntc1_predicted), mRNA [XM_222157]	ref|XM_222157|gb|BF564273|ens|ENSRNOT00000040513|ens|ENSRNOT00000047092	Rn. 47918	-	Kntc1_predicted	kinetochore associated 1 (predicted)	-	-	[Human, Mouse]Homologene:32227
456	107.58	648.15	0.17	NM_012608	Mme	Rattus norvegicus membrane metallo endopeptidase (Mme), mRNA [NM_012608]	ref|NM_012608|gb|M15944|ens|ENSRNOT00000013169|ens|ENSRNOT00000042576	Rn. 33598	Hematopoietic cell lineage, Alzheimer's disease	Mme	membrane metallo endopeptidase	zinc-containing metallo-enzyme: involved in degradation of cardiac peptides [RGD]	neutral endopeptidase activity is decreased by ascorbic acid in cultured osteoblastic cells// Neutral endopeptidase inactivity induces an exaggerated neurogenic inflammation mediated by neurokinin-1 receptor, which may lead to edema in pulmonary alveoli.// Intracardiac expression of neutral endopeptidase// In spontaneously hypertensive rats, the local concentration and action of adrenomedullin in the tissues may be differentially regulated by NEP.	[Human, Mouse]Homologene:5275

[0261]



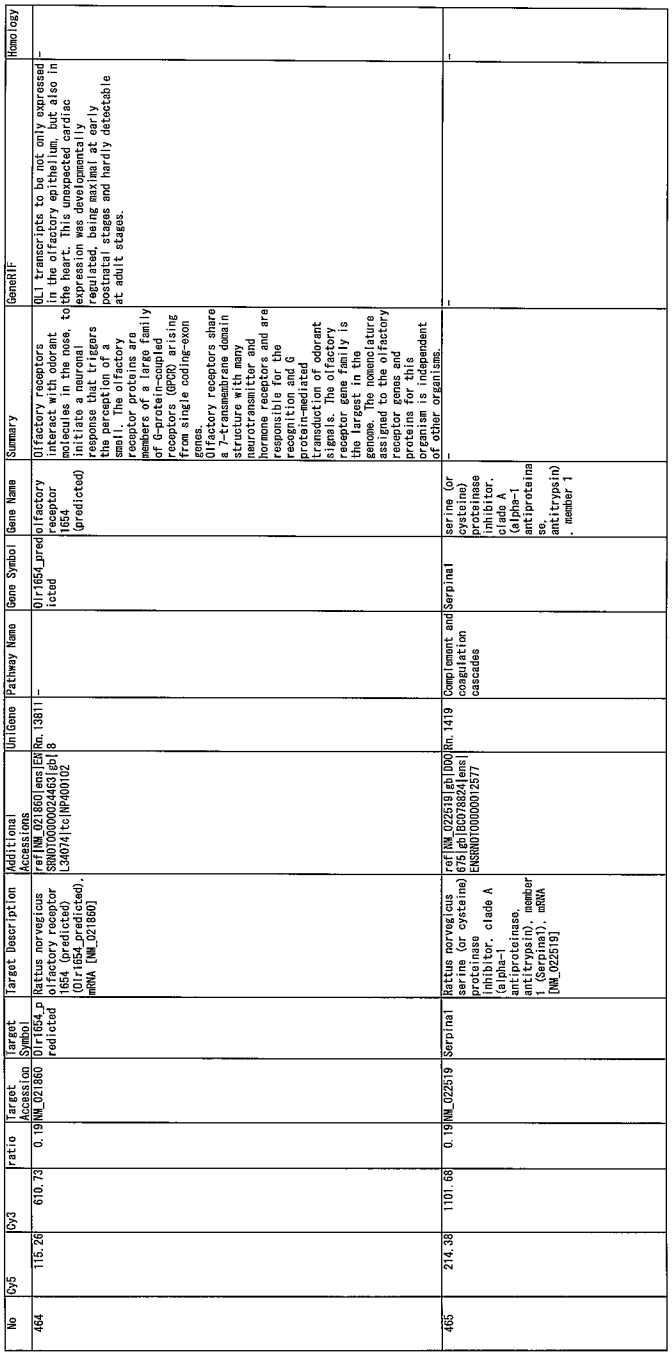
No	Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Pathway Name	Gene Symbol	Gene Name	Summary	GeneRIF	Homology
457	204.73	1204.31	0.17	NM_053348	Fetub	Rattus norvegicus fetuin beta (Fetub), mRNA [NM_053348]	ref|NM_053348|gb|AA2 42966|gb|BQ073508|en s|ENSRNOT00000046199	Rn.2464	-	Fetub	fetuin beta	inhibits insulin receptor tyrosine kinase activity, protease inhibitory activities, developmentally regulates calcium metabolism and osteogenesis [RGD]	-	[Human, Mouse]Homologene:8660
458	76.48	442.24	0.17	XM_223905	Galnt12_predicted	PREDICTED: Rattus norvegicus UDP-N-acetyl-alpha-D-galactosamine-polypeptide N-acetylgalactosaminyltransferase 12 (predicted) (Galnt12_predicted), mRNA [XM_223905]	ref|XM_223905|ens|ENSRNOG00000022356|ens|ENSRNOG00000051393|ens|ENSRNOT00000000388|ens|ENSRNOT00000000388|39	-	-	Galnt12_predicted	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 12 (predicted)	-	-	-
459	176.36	1018.72	0.17	XM_344059	XM_344059	Rattus norvegicus similar to hypothetical protein DKFZp434D0220 (LOC363860), mRNA [XM_344059]	gb|XM_344059	-	-	-	-	-	-	-
460	136.51	776.96	0.18	NM_001013180	NM_001013180	Rattus norvegicus secretoglobin, family 3A, member 1 (Scgb3a1), mRNA [NM_001013180]	ref|NM_001013180|gb|AF436841|gb|AAL34079|gb|BK000202	Rn.30648	-	Scgb3a1	secretoglobin, family 3A, member 1	secretoglobin: may have a role in airway function [RGD]	-	[Mouse]Homologene:14160
461	1411.04	7936.53	0.18	NM_053472	Cox4i2	Rattus norvegicus cytochrome c oxidase subunit IV isoform 2 (Cox4i2), mRNA [NM_053472]	ref|NM_053472|gb|AF2 65317|emb|CAJ43407|ens|ENSRNOT00000010411|ens|ENSRNOT00000010411|tc|TIGR9412	Rn.7214	Oxidative phosphorylation	Cox4i2	cytochrome c oxidase subunit IV isoform 2	subunit of cytochrome c-oxidase, plays a role in cytochrome c oxidase regulation and electron transport [RGD]	-	[Human, Mouse]Homologene:13082

[0262]



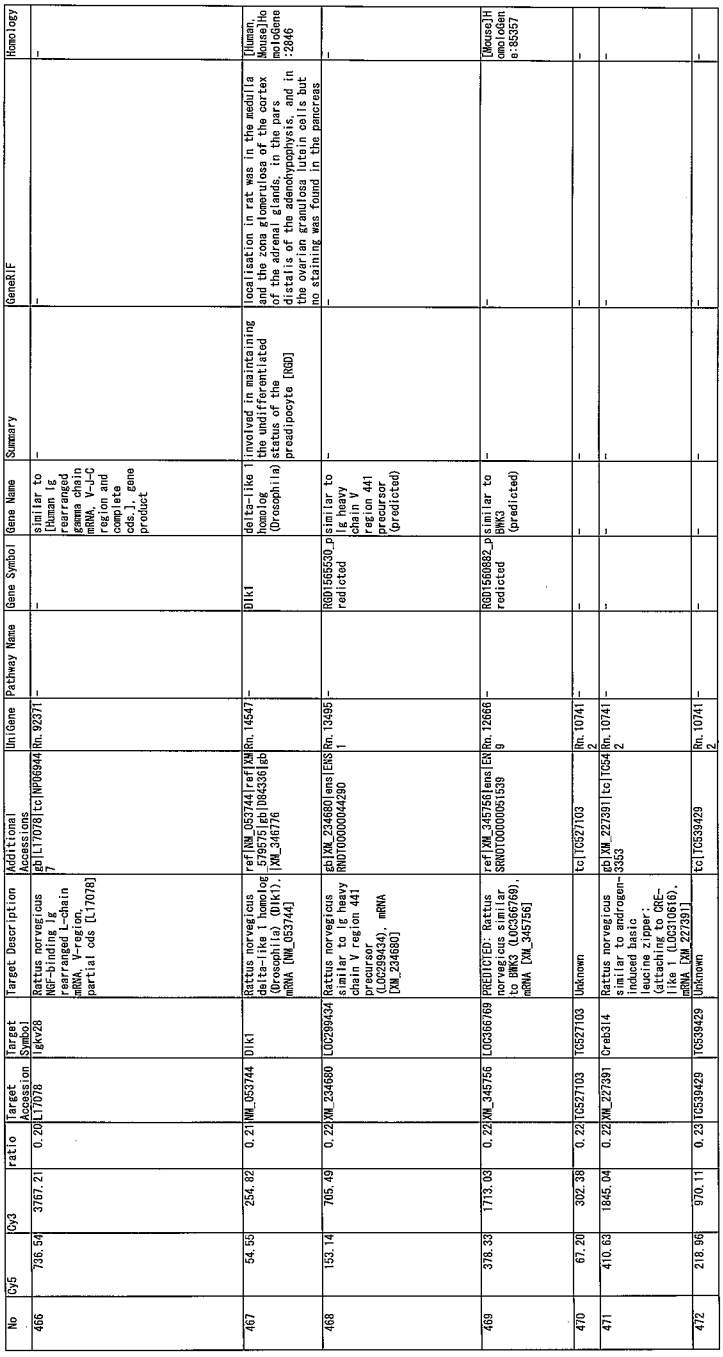
No	Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Pathway Name	Gene Symbol	Gene Name	Summary	GeneRIF	Homology
462	311.03	1740.93	0.18	L10326	Gnas	Rattus norvegicus alternatively spliced GTP-binding protein alpha subunit (stimulatory) (GS-alpha) mRNA, complete cds. [L10326]	gb|L10326|gb|AF10784 5|c1|T05630361|c1|T05 7075)	Rn.31	Calcium signaling pathway, Gap junction, Long-term depression, Tight junction, transduction, GnRH signaling pathway	Gnas	GNAS complex locus	may act as the alpha subunit of G protein Gs: couples G-protein coupled receptor binding to adenylate cyclase activation [RGD]	Somatotroph adenomas in young patients seem to carry somatic Gs alpha mutations at a lower frequency, and germ-line or early postzygotic mutational events may be responsible for the shortened latency of tumorigenesis.// Data suggest that activating mutations of the Gs alpha (Gs) by reduces the amplitude of the cAMP response to activating a G(alpha) protein and the turn leads to l (to) channel phosphorylation.// a nucleotide-free state of Galphas is induced by Cu2+ and Zn2+// PKA-mediated phosphorylation of the beta1-adrenergic receptor promotes Gs/Gi switching// Absence of Gsalpha imprinting in human bone and fat. Osteodystrophy and obesity in pseudohypoparathyroidism(PHP) Ia and PPHP(pseudo-PHP) patients despite presence of normal Gsalpha allele likely due to Gsalpha Haploinsufficiency in these tissues.// Gs subunits and beta2 androgen receptors utilize different internalization mechanisms.// (The rest is omitted.)	-
463	724.96	4008.45	0.18	NM_130425	Runx3	Rattus norvegicus runt-related transcription factor 3 (Runx3), mRNA [NM_130425]	ref|NM_130425|gb|AF4 21886|ens|ENSRNOT000 00024341	Rn.34220	-	Runx3	runt-related transcription factor 3	mouse homolog is a transcription factor required for establishing epigenetic silencing in cytotoxic lineage thymocytes [RGD]	-	[Human, Mouse]Ho moloGene :37914

[0263]



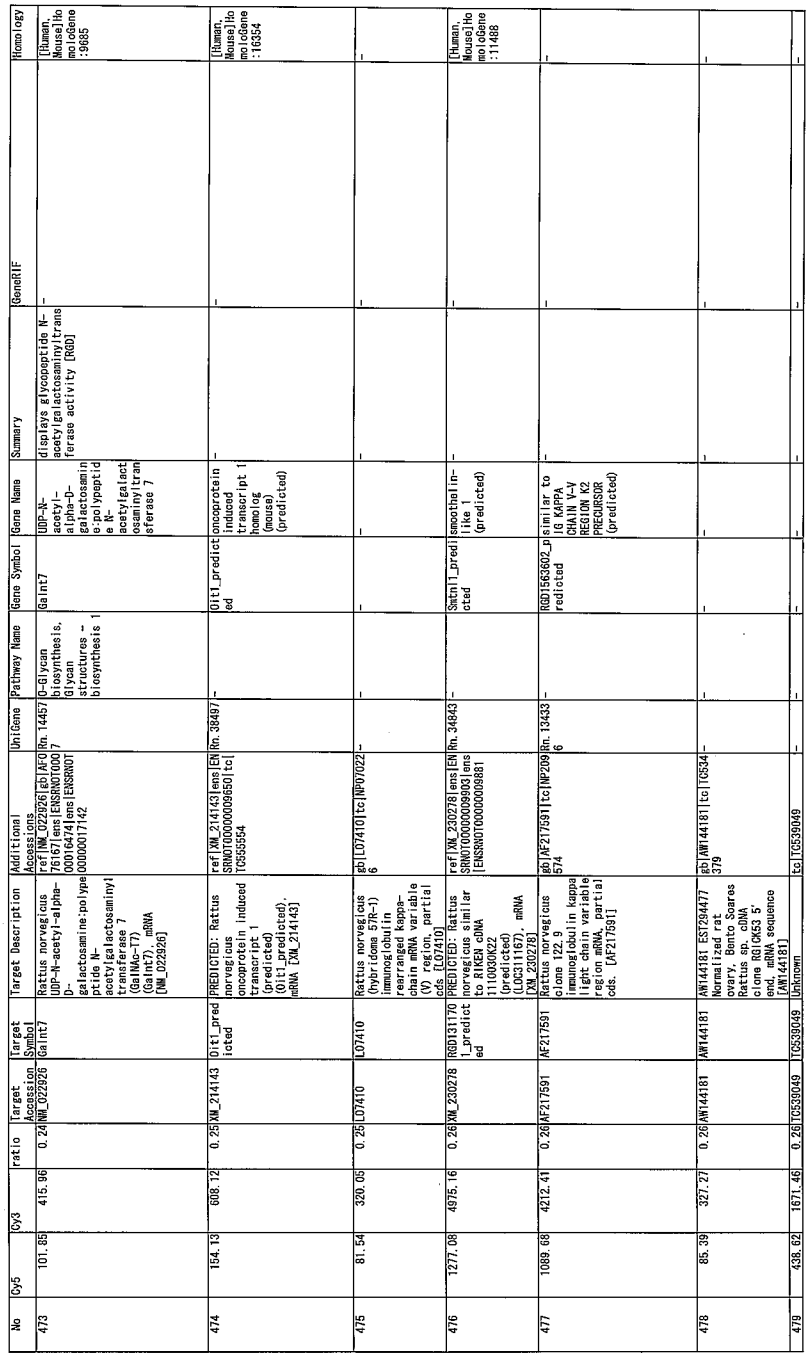
No	Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Pathway Name	Gene Symbol	Gene Name	Summary	GeneRIF	Homology
464	115.26	610.73	0.19	NM_021860	Olr1654_predicted	Rattus norvegicus olfactory receptor 1654 (predicted) (Olr1654_predicted), mRNA [NM_021860]	ref|NM_021860|ens|ENSRNOT00000024463|gb|L34074|tc|NP400102	Rn.13811	-	Olr1654_predicted	olfactory receptor 1654 (predicted)	Olfactory receptors interact with odorant molecules in the nose, to initiate a neuronal response that triggers the perception of a smell. The olfactory receptor proteins are members of a large family of G-protein-coupled receptors (GPCR) arising from single coding-exon genes. Olfactory receptors share a 7-transmembrane domain structure with many neurotransmitter and hormone receptors and are responsible for the recognition and G protein-mediated transduction of odorant signals. The olfactory receptor gene family is the largest in the genome. The nomenclature assigned to the olfactory receptor genes and proteins for this organism is independent of other organisms.	OL1 transcripts to be not only expressed in the olfactory epithelium, but also in the heart. This unexpected cardiac expression was developmentally regulated, being maximal at early postnatal stages and hardly detectable at adult stages.	-
465	214.38	1101.68	0.19	NM_022519	Serpina1	Rattus norvegicus serine (or cysteine) proteinase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 1 (Serpina1), mRNA [NM_022519]	ref|NM_022519|gb|D00675|gb|S60738|ens|ENSRNOT00000012577	Rn.1419	Complement and coagulation cascades	Serpina1	serine (or cysteine) proteinase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 1	-	-	-

[0264]



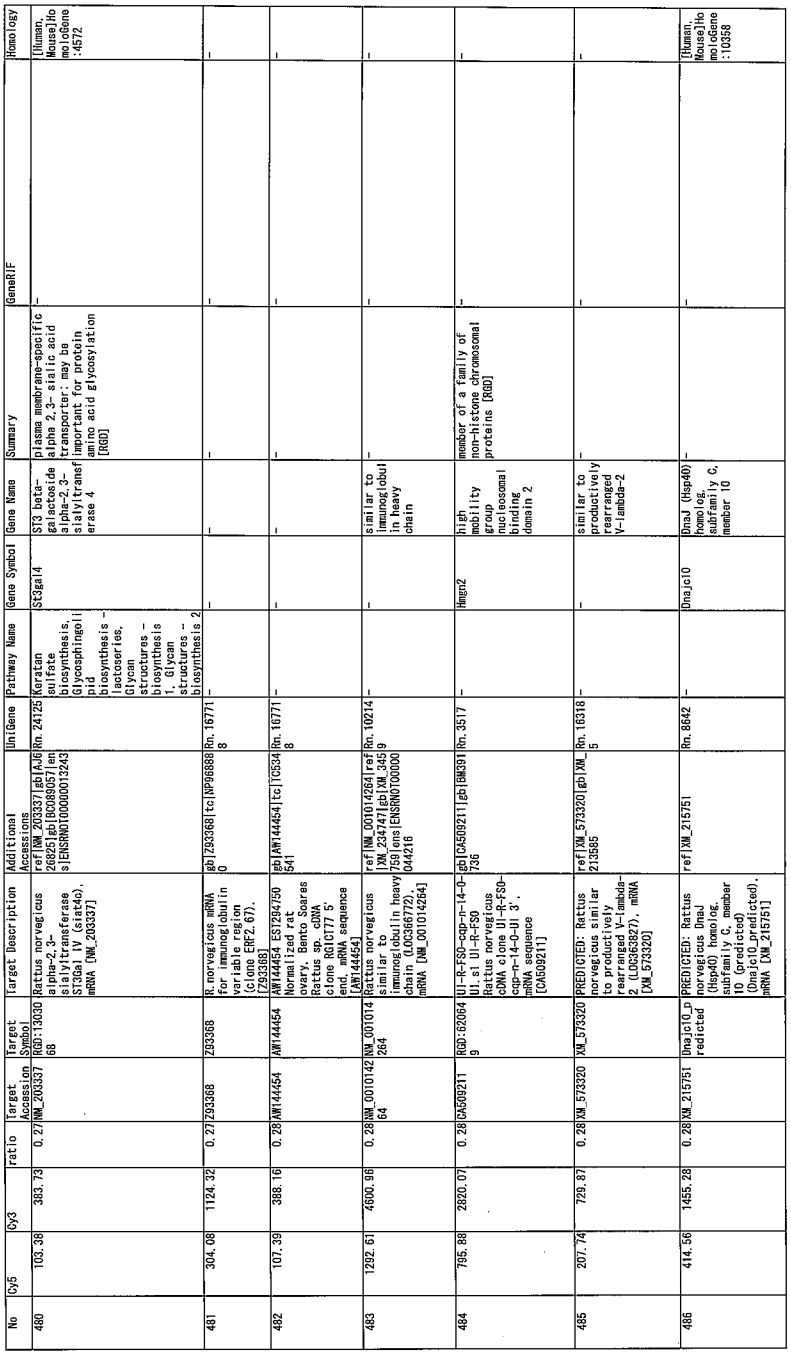
No	Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Pathway Name	Gene Symbol	Gene Name	Summary	GeneRIF	Homology
466	736.54	3767.21	0.20	L17078	Igkv28	Rattus norvegicus NGF-binding Ig rearranged L-chain mRNA, V-region, partial cds [L17078]	gb|L17078|tc|NP06944 7	Rn.92371	-	-	similar to [Human Ig rearranged gamma chain mRNA, V-J-C region and complete cds.], gene product	-	-	-
467	54.55	254.82	0.21	NM_053744	Dlk1	Rattus norvegicus delta-like 1 homolog (Drosophila) (Dlk1), mRNA [NM_053744]	ref|NM_053744|ref|XM_579675|gb|D84336|gb|AM_346776	Rn.14547	-	Dlk1	delta-like 1 homolog (Drosophila)	involved in maintaining the undifferentiated status of the preadipocyte [RGD]	localisation in rat was in the medulla and the zona glomerulosa of the cortex of the adrenal glands, in the pars distalis of the adenohypophysis, and in the ovarian granulosa lutein cells but no staining was found in the pancreas	[Human, Mouse]HomoloGene:2846
468	153.14	705.49	0.22	XM_234680	LOC299434	Rattus norvegicus similar to Ig heavy chain V region 441 precursor (LOC299434), mRNA [XM_234680]	gb|XM_234680|ens|ENSRNOT00000044290	Rn.13495 1	-	RGD1565530_predicted	similar to Ig heavy chain V region 441 precursor (predicted)	-	-	-
469	378.33	1713.03	0.22	XM_345756	LOC366769	PREDICTED: Rattus norvegicus similar to BMK3 (LOC366769), mRNA [XM_345756]	ref|XM_345756|ens|ENSRNOT00000051539	Rn.12666 9	-	RGD1560882_predicted	similar to BMK3 (predicted)	-	-	[Mouse]Homoloden e:85357
470	67.20	302.38	0.22	TC527103	TC527103	Unknown	tc|TC527103	Rn.10741 2	-	-	-	-	-	-
471	410.63	1845.04	0.22	XM_227391	Crab3l4	Rattus norvegicus similar to androgen-induced basic leucine zipper; (attaching to CRE-like 1 (LOC310616), mRNA [XM_227391]	gb|XM_227391|tc|TC543353	Rn.10741 2	-	-	-	-	-	-
472	218.96	970.11	0.23	TC539429	TC539429	Unknown	tc|TC539429	Rn.10741 2	-	-	-	-	-	-

[0265]



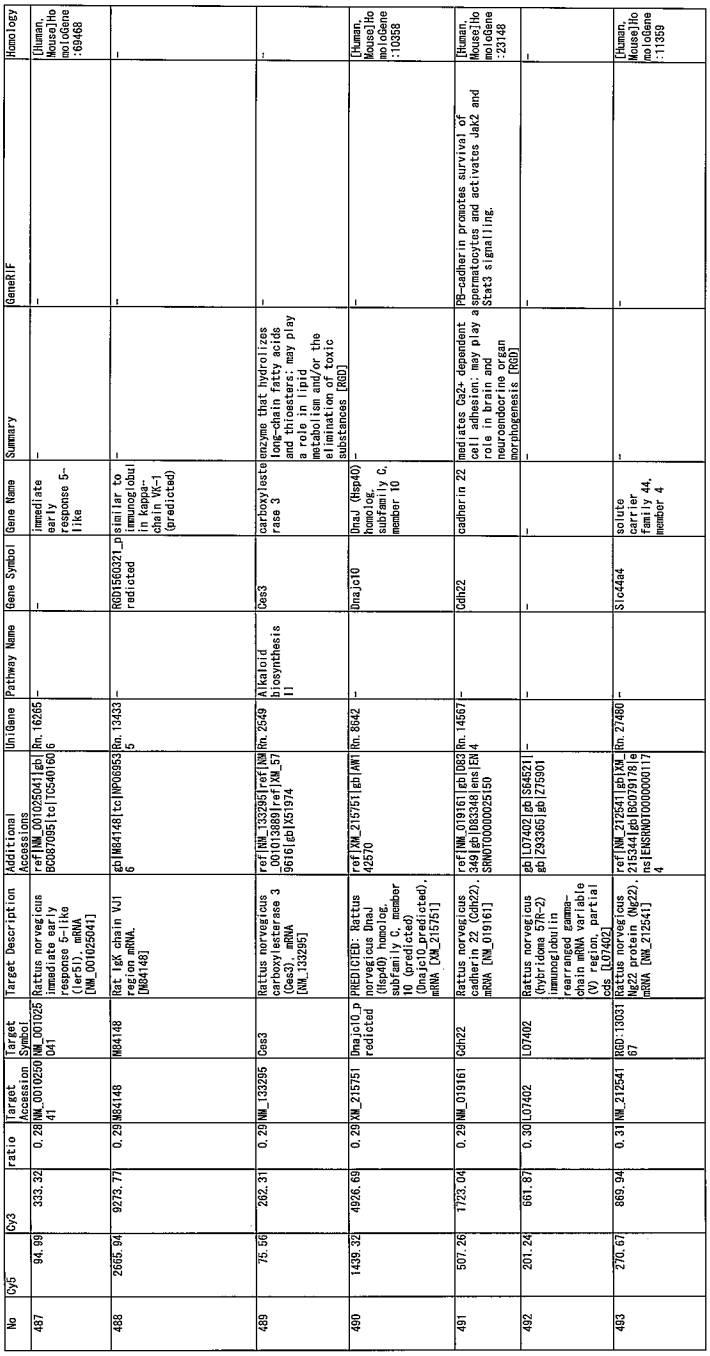
No	Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Pathway Name	Gene Symbol	Gene Name	Summary	GeneRIF	Homology
473	101.85	415.96	0.24	NM_022926	Galnt7	Rattus norvegicus UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 7 (GalNAc-T7) (Galnt7), mRNA [NM_022926]	ref|NM_022926|gb|AF0|Rn.144576 7|ens|ENSRNOT00000016474|ens|ENSRNOT00000017142	Rn.38497	O-Glycan biosynthesis, Glycan structures - biosynthesis 1	Galnt7	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 7	displays glycopeptide N-acetylgalactosaminyltransferase activity [RGD]	-	[Human, Mouse]Homologene:9885
474	164.13	608.12	0.25	XM_214143	Olil_predicted	PREDICTED: Rattus norvegicus oncoprotein induced transcript 1 (predicted) (Olil_predicted), mRNA [XM_214143]	ref|XM_214143|ens|ENSRNOT00000006650|tc|TC555554	Rn.38497	-	Olil_predicted	oncoprotein induced transcript 1 homolog (mouse) (predicted)	-	-	[Human, Mouse]Homologene:16354
475	81.54	320.05	0.25	L07410	L07410	Rattus norvegicus (hybridoma 57R-1) immunoglobulin rearranged kappa-chain mRNA variable (V) region, partial cds. [L07410]	gb|L07410|tc|NP07022-6	-	-	-	-	-	-	-
476	1277.08	4975.16	0.26	XM_230278	RGD1311700_predicted	PREDICTED: Rattus norvegicus similar to RIKEN cDNA 1110030K22 (predicted) (LOC311167), mRNA [XM_230278]	ref|XM_230278|ens|ENSRNOT00000059093|ens|ENSRNOT00000009881	Rn.34643	-	Smtnl1_predicted	smoothelin-like 1 (predicted)	-	-	[Human, Mouse]Homologene:11488
477	1089.68	4212.41	0.26	AF217591	AF217591	Rattus norvegicus clone 122.9 immunoglobulin kappa light chain variable region mRNA, partial cds. [AF217591]	gb|AF217591|tc|NP2095746	Rn.134336	-	RGD1563602_predicted	similar to IG KAPPA CHAIN V-V REGION K2 PRECURSOR (predicted)	-	-	-
478	85.39	327.27	0.26	AW144181	AW144181	AW144181 EST294477 Normalized rat ovary, Bento Soares Rattus sp. cDNA clone RGICK53 5' end, mRNA sequence [AW144181]	gb|AW144181|tc|TC6534379	-	-	-	-	-	-	-
479	438.62	1671.46	0.26	TC6539049	TC6539049	Unknown	tc|TC6539049	-	-	-	-	-	-	-

[0266]



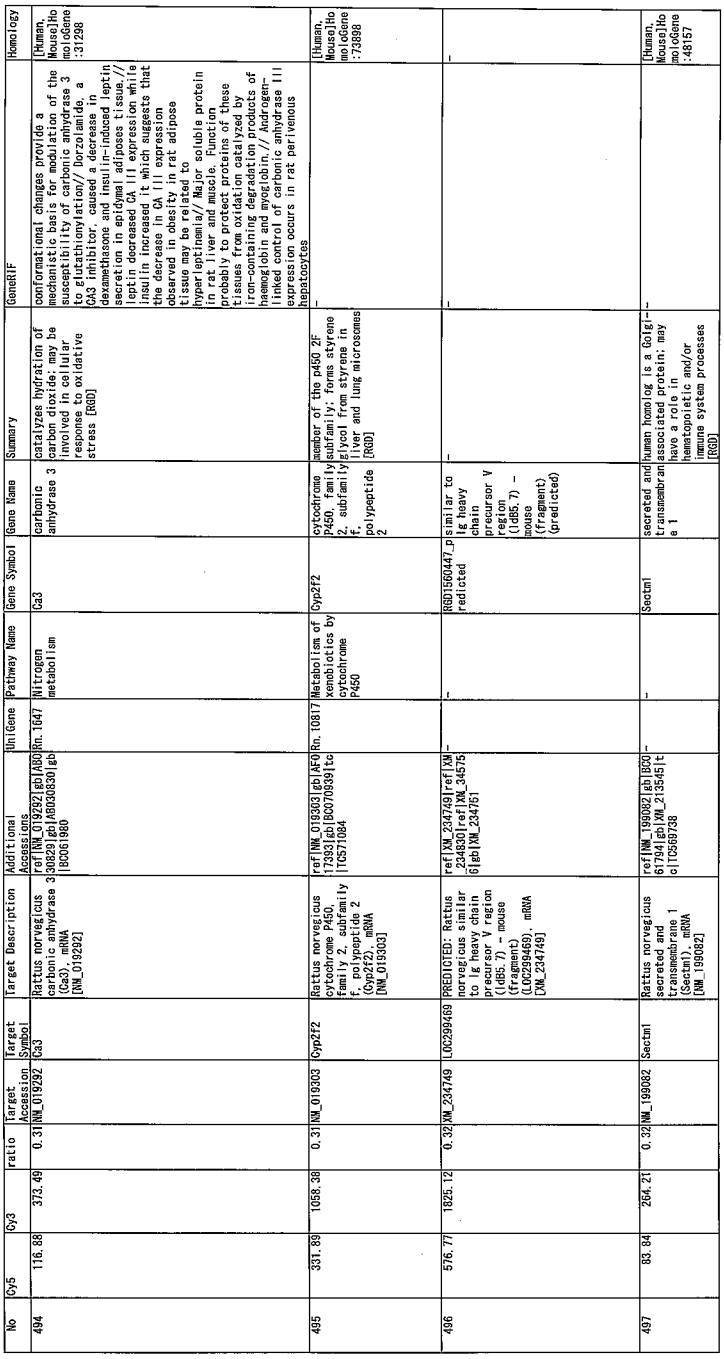
No	Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Pathway Name	Gene Symbol	Gene Name	Summary	GeneRIF	Homology
480	103.38	383.73	0.27	NM_200337	RGD:1303068	Rattus norvegicus alpha-2,3-sialyltransferase ST3Gal IV (sialyltransferase 4) mRNA [NM_200337]	ref|NM_200337|gb|AJ608057|AJ608057|en s|ENSRNOT00000013243	Rn.24125	Keratan sulfate biosynthesis, Glycosphingolipid biosynthesis - lactoseries, Glycan structures - biosynthesis 1, Glycan structures - biosynthesis 2	ST3gal4	ST3 beta-galactoside alpha-2,3-sialyltransferase 4	plasma membrane-specific alpha 2,3- sialic acid transporter; may be involved in formation of amino acid glycosylation [RGD]	-	[Human, Mouse]Homologene:4572
481	304.08	1124.32	0.27	Z93368	Z93368	R.norvegicus mRNA for immunoglobulin variable region (clone ERF2.67). [Z93368]	gb|Z93368|tc|NP96888 0	Rn.167718	-	-	-	-	-	-
482	107.39	388.16	0.28	AW144454	AW144454	AW144454 EST284750 Normalized rat ovary, Bento Soares Rattus sp. cDNA clone RGICT77 5', mRNA sequence [AW144454]	gb|AW144454|tc|T0534 541	Rn.167718	-	-	-	-	-	-
483	1292.61	4690.96	0.28	NM_001014264	NM_001014264	Rattus norvegicus similar to immunoglobulin heavy chain (LOC366772), mRNA [NM_001014264]	ref|NM_001014264|ref|XM_234747|gb|XM_345970|ens|ENSRNOT00000044216	Rn.10214	-	-	similar to immunoglobulin heavy chain	-	-	-
484	795.88	2820.07	0.28	CA509211	RGD:620649	UI-R-F$0-cap-n-14-0-UI 3', mRNA sequence [CA509211]	gb|CA509211|gb|BM391736	Rn.3517	-	Hmgn2	high mobility group nucleosomal binding domain 2	member of a family of non-histone chromosomal proteins [RGD]	-	-
485	207.74	729.87	0.28	XM_573320	XM_573320	PREDICTED: Rattus norvegicus similar to productively rearranged V-lambda-2 (LOC363827), mRNA [XM_573320]	ref|XM_573320|gb|XM_213585	Rn.16318	-	-	similar to productively rearranged V-lambda-2	-	-	-
486	414.56	1455.28	0.28	XM_215751	Dnajc10_predicted	PREDICTED: Rattus norvegicus DnaJ (Hsp40) homolog, subfamily C, member 10 (predicted) (Dnajc10_predicted), mRNA [XM_215751]	ref|XM_215751	Rn.8642	-	Dnajc10	DnaJ (Hsp40) homolog, subfamily C, member 10	-	-	[Human, Mouse]Homologene:10358

[0267]



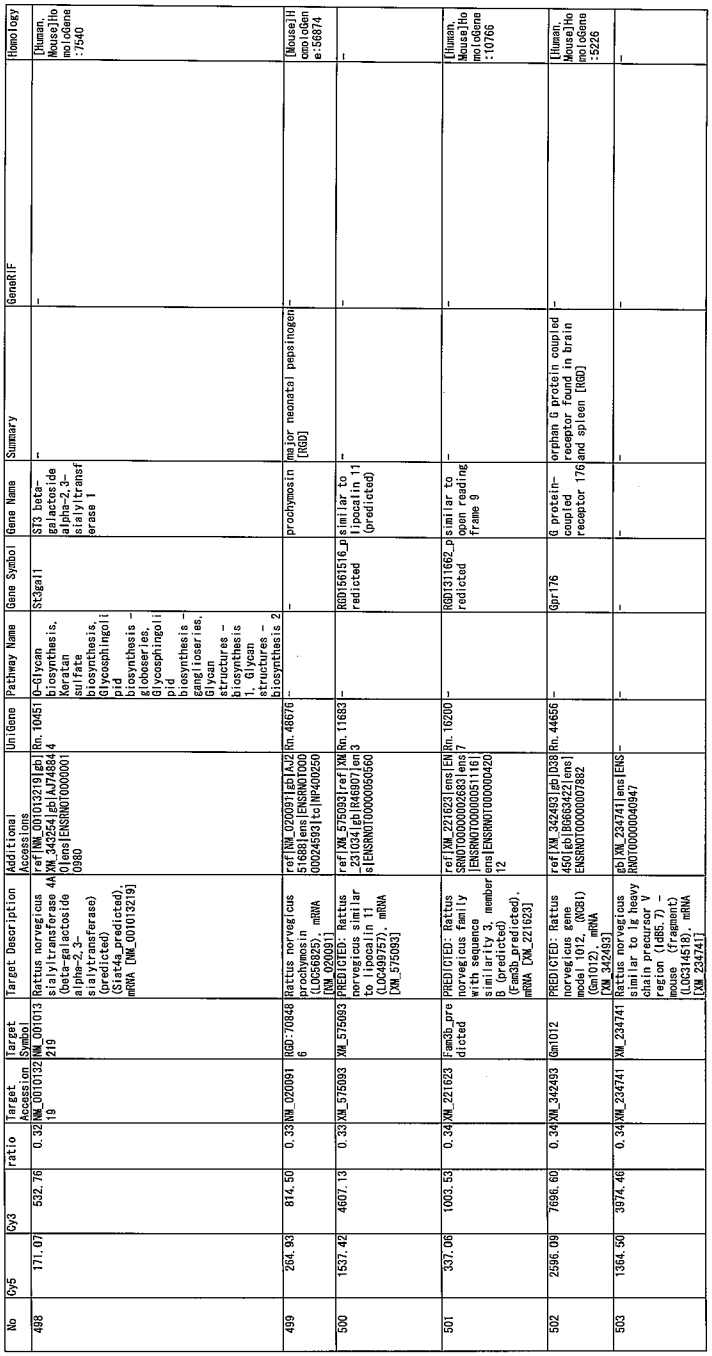
No	Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Pathway Name	Gene Symbol	Gene Name	Summary	GeneRIF	Homology
487	94.99	333.32	0.28	NM_001025041	NM_001025041	Rattus norvegicus immediate early response 5-like (ier5l), mRNA [NM_001025041]	ref|NM_001025041|gb|BC087095|tc|TC540160	Rn.16265	-	-	immediate early response 5-like	-	-	[Human, Mouse]HomoloGene:69468
488	2665.94	9273.77	0.29	M84148	M84148	Rat IgK chain VJ1 region mRNA. [M84148]	gb|M84148|tc|NP06953	Rn.13433	-	RGD1560321_predicted	similar to immunoglobulin kappa-chain VK-1 (predicted)	-	-	-
489	75.56	262.31	0.29	NM_133295	Ces3	Rattus norvegicus carboxylesterase 3 (Ces3), mRNA [NM_133295]	ref|NM_133295|ref|NM_001013089|ref|XM_963616|gb|X51974	Rn.2549	Alkaloid biosynthesis II	Ces3	carboxylesterase 3	enzyme that hydrolizes long-chain fatty acids and thioesters; may play a role in lipid metabolism and/or the elimination of toxic substances [RGD]	-	-
490	1439.32	4926.69	0.29	XM_215751	DnajC10_predicted	PREDICTED: Rattus norvegicus DnaJ (Hsp40) homolog, subfamily C, member 10 (predicted) (DnajC10_predicted), mRNA [XM_215751]	ref|XM_215751|gb|AW1 42570	Rn.8642	-	DnajC10	DnaJ (Hsp40) homolog, subfamily C, member 10	-	-	[Human, Mouse]HomoloGene:10358
491	507.26	1720.04	0.29	NM_019161	Cdh22	Rattus norvegicus cadherin 22 (Cdh22), mRNA [NM_019161]	ref|NM_019161|gb|D83 349|gb|D83348|ens|EM SNVDTOD00025180	Rn.14567	-	Cdh22	cadherin 22	mediates Ca2+ dependent cell adhesion; may play a spermatocytes and activates Jak2 and Stat5 signalling.	PB-cadherin promotes survival of in brain and plays a role in neuronal organ morphogenesis [RGD]	[Human, Mouse]HomoloGene:23148
492	201.24	661.87	0.30	L07402	L07402	Rattus norvegicus (hybridoma 57R-2) immunoglobulin rearranged gamma-chain mRNA variable (V) region, partial cds [L07402]	gb|L07402|gb|S64521|gb|Z93365|gb|Z75901	-	-	-	-	-	-	-
493	270.67	869.94	0.31	XM_212541	RGD:13031767	Rattus norvegicus Ng22 protein (Ng22), mRNA [XM_212541]	ref|XM_212541|gb|XM_215344|gb|BC079178|ens|ENSRNOT00000001174	Rn.27460	-	Slc44a4	solute carrier family 44, member 4	-	-	[Human, Mouse]HomoloGene:11359

[0268]



No	Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Pathway Name	Gene Symbol	Gene Name	Summary	GeneRIF	Homology
494	116.88	373.49	0.31	NM_019292	Ca3	Rattus norvegicus carbonic anhydrase 3 (Ca3), mRNA [NM_019292]	ref|NM_019292|gb|AB0 38829|gb|AB038830|gb |BC061880	Rn.1647	Nitrogen metabolism	Ca3	carbonic anhydrase 3	catalyzes hydration of carbon dioxide; may be involved in cellular response to oxidative stress [RGD]	conformational changes provide a mechanistic basis for modulation of the catalytic efficiency of carbonic anhydrase 3 by glutathionylation// borzolamide, a CA3 inhibitor, caused a decrease in dexamethasone and insulin-induced leptin secretion in epididymal adipose tissue.// leptin decreased CA III expression while insulin increased it which suggests that the decrease in CA III expression observed in obesity in rat adipose tissue may be related to hyperleptinemia// Major soluble protein in rat liver and muscle. Function probably to protect proteins of these tissues from oxidation catalyzed by iron-containing degradation products of haemoglobin and myoglobin.// Androgen-linked control of carbonic anhydrase III expression occurs in rat perivenous hepatocytes	[Human, Mouse]HomoloGene:31290
495	331.89	1058.38	0.31	NM_019303	Cyp2f2	Rattus norvegicus cytochrome P450, family 2, subfamily f, polypeptide 2 (Cyp2f2), mRNA [NM_019303]	ref|NM_019303|gb|AF0 17393|gb|BC070939|tc |TC571084	Rn.10817	Metabolism of xenobiotics by cytochrome P450	Cyp2f2	cytochrome P450, family 2, subfamily f, polypeptide 2	member of the p450 2F subfamily. forms styrene glycol from styrene in liver and lung microsomes [RGD]	-	[Human, Mouse]HomoloGene:73898
496	576.77	1825.12	0.32	XM_234749	LOC299469	PREDICTED: Rattus norvegicus similar to Ig heavy chain precursor V region (idiotype) (fragment) (LOC299469), mRNA [XM_234749]	ref|XM_234749|ref|XM _234830|ref|XM_34575 6|gb|XM_234761	-	-	RGD1560447_predicted	similar to Ig heavy chain precursor V region (idio. 7) - mouse (fragment) (predicted)	-	-	-
497	83.84	264.21	0.32	NM_199082	Sectm1	Rattus norvegicus secreted and transmembrane 1 (Sectm1), mRNA [NM_199082]	ref|NM_199082|gb|BG0 61794|gb|XM_213545|t c|TC569738	-	-	Sectm1	secreted and transmembrane 1	human homolog is a Golgi-associated protein: may have a role in hematopoietic and/or immune system processes [RGD]	-	[Human, Mouse]HomoloGene:48157

[0269]

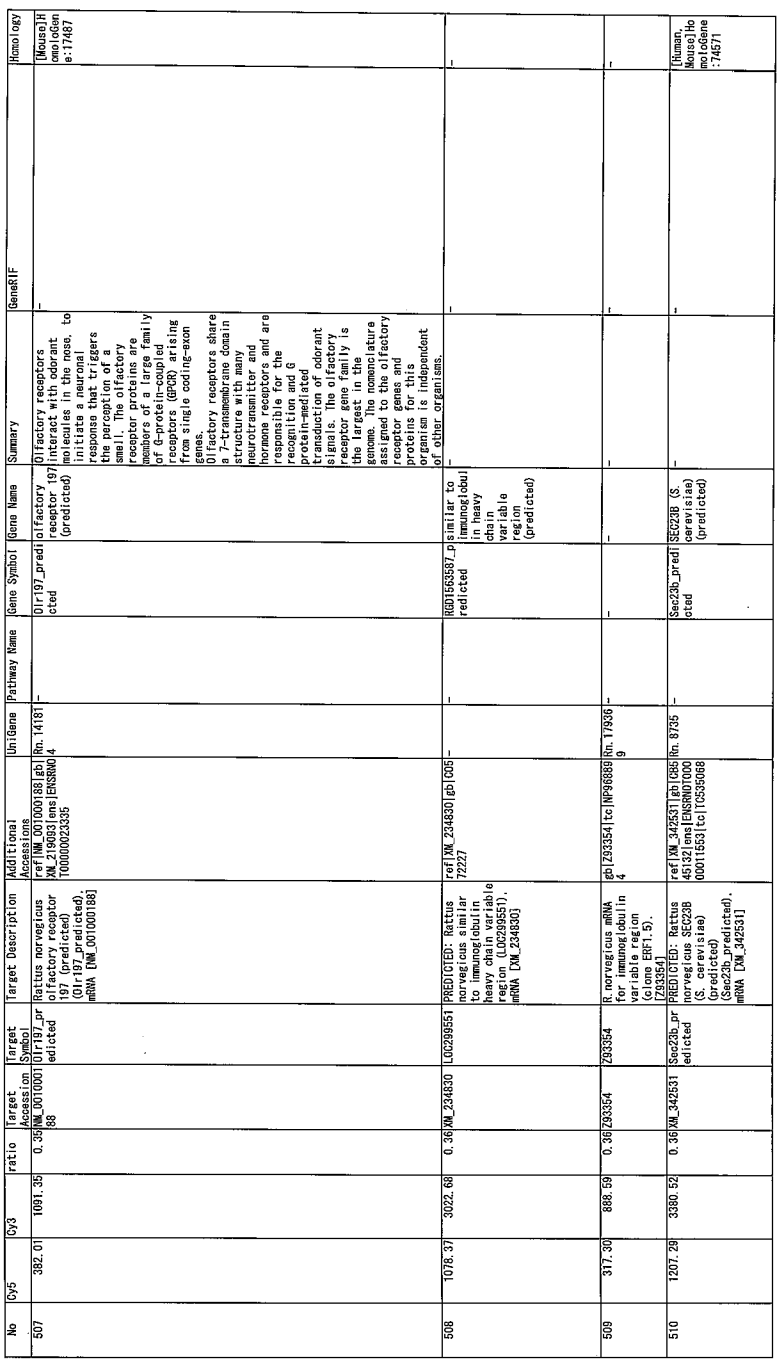


No	Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Pathway Name	Gene Symbol	Gene Name	Summary	GeneRIF	Homology
498	171.07	532.76	0.32	NM_001013219	NM_001013219	Rattus norvegicus sialyltransferase 4A (beta-galactoside alpha-2,3-sialyltransferase) (predicted) (ST4a_predicted), mRNA [NM_001013219]	ref|NM_001013219|gb|AJ2 44254|gb|AJ748844 |gb|AJ748845|ens|EN SRNOT00000001 0980	Rn. 10451	G-Glycan biosynthesis, Keratan sulfate biosynthesis, Glycosphingoli pid biosynthesis - globoseries, Glycosphingoli pid biosynthesis - ganglioseries, Glycan structures - biosynthesis 1, Glycan structures - biosynthesis 2	St3gal1	ST3 beta-galactoside alpha-2,3-sialyltransferase 1	-	-	[Human, Mouse]Homologene:7540
499	264.93	814.50	0.33	NM_020091	RGD:70848	Rattus norvegicus prochymosin (LOC56825), mRNA [NM_020091]	ref|NM_020091|gb|AJ2 51688|ens|ENSRNOT00 000024593|tc|NP400250	Rn. 48676	-	-	prochymosin	major neonatal pepsinogen [RGD]	-	[Mouse]Homologene:56874
500	1537.42	4607.13	0.33	XM_575093	XM_575093	PREDICTED: Rattus norvegicus similar to Lipocalin 11 (LOC499757), mRNA [XM_575093]	ref|XM_575093|ref|XM_ 231034|gb|BI46907|ens|ENSRNOT00000060560	Rn. 11683	-	RGD1561516_predicted	similar to Lipocalin 11 (predicted)	-	-	-
501	337.06	1003.53	0.34	XM_221623	Fam3b_predicted	PREDICTED: Rattus norvegicus family with sequence similarity 3, member B (predicted) (Fam3b_predicted), mRNA [XM_221623]	ref|XM_221623|ens|EN SRNOT00000002683|ens|ENSRNOT00000051116|ens|ENSRNOT00000000420 12	Rn. 16200	-	RGD1311692_predicted	similar to open reading frame 9	-	-	[Human, Mouse]Homologene:10766
502	2596.09	7696.60	0.34	XM_342493	Gpr176	PREDICTED: Rattus norvegicus gene model 176, (NCBI) [XM_342493]	ref|XM_342493|gb|D38 4951|gb|BG663422|ens|ENSRNOT00000007862	Rn. 44656	-	Gpr176	G protein-coupled receptor 176	orphan G protein coupled receptor found in brain and spleen [RGD]	-	[Human, Mouse]Homologene:5226
503	1364.50	3974.46	0.34	XM_234741	XM_234741	Rattus norvegicus similar to Ig heavy chain precursor V region (Id85.7) - mouse (fragment) (LOC314518), mRNA [XM_234741]	gb|XM_234741|ens|ENS RNOT00000040947	-	-	-	-	-	-	-

[0270]

No	Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Pathway Name	Gene Symbol	Gene Name	Summary	GeneRIF	Homology
504	659.60	1906.35	0.35	XM_234676	LOC314512	PREDICTED: Rattus norvegicus similar to immunoglobulin heavy chain (LOC314512), mRNA [XM_234676]	ref|XM_234676|ref|XM_345743|gb|XM_345748|gb|M84149	Rn.110661	-	RGD1565780_predicted	similar to immunoglobulin heavy chain (predicted)	-	-	-
505	76.17	218.03	0.35	NM_144744	Acdc	Rattus norvegicus adipocyte complement related protein of 30 kDa (Acdc), mRNA [NM_144744]	ref|NM_144744|gb|AY033885|gb|BC092565|ens|ENSRNOT00000002492	Rn.24299	Adipocytokine signaling pathway, Type II diabetes mellitus	Adipoq	adiponectin, C1Q and collagen domain containing	adipocyte complement-related factor that plays a role in obesity-related insulin resistance [RGD]	Results suggest that adiponectin does not play any role in regulating changes in insulin sensitivity during pregnancy in rats.// difference between obese (fa/fa) Zucker rats and lean Zucker rats that plasma adiponectin levels of obese (fa/fa) Zucker rats are significantly higher than those of lean Zucker rats// Ectopic expression of the Acrp30 transgene resulted in modulation of hepatic gluconeogenesis and lipogenesis.// There was no major effect on the expression of the adiponectin gene in white or brown fat despite the cold-induced stimulation of sympathetic activity and fatty acid flux. Adiponectin is unlikely to play a key role in metabolic adaptations to cold.// an impaired depot-specific expression of adiponectin is a contributing factor for the development of insulin resistance in Zucker fatty rats// Adiponectin expression is restored to normal levels after body-weight reduction, supporting its link with obesity-related insulin resistance	[Human, Mouse]HomoloGene:3525
506	261.11	747.31	0.35	NM_212466	Bf	Rattus norvegicus B-factor, properdin (Bf), mRNA [NM_212466]	ref|NM_212466|gb|AY325253|gb|XM_215326|ens|ENSRNOT00000033942	Rn.109148	-	Cfb	complement factor B	predicted gene; component of the alternative pathway of complement activation; may be linked to the major histocompatibility complex and thus involved in the immune response [RGD]	-	[Human, Mouse]HomoloGene:1292

[0271]

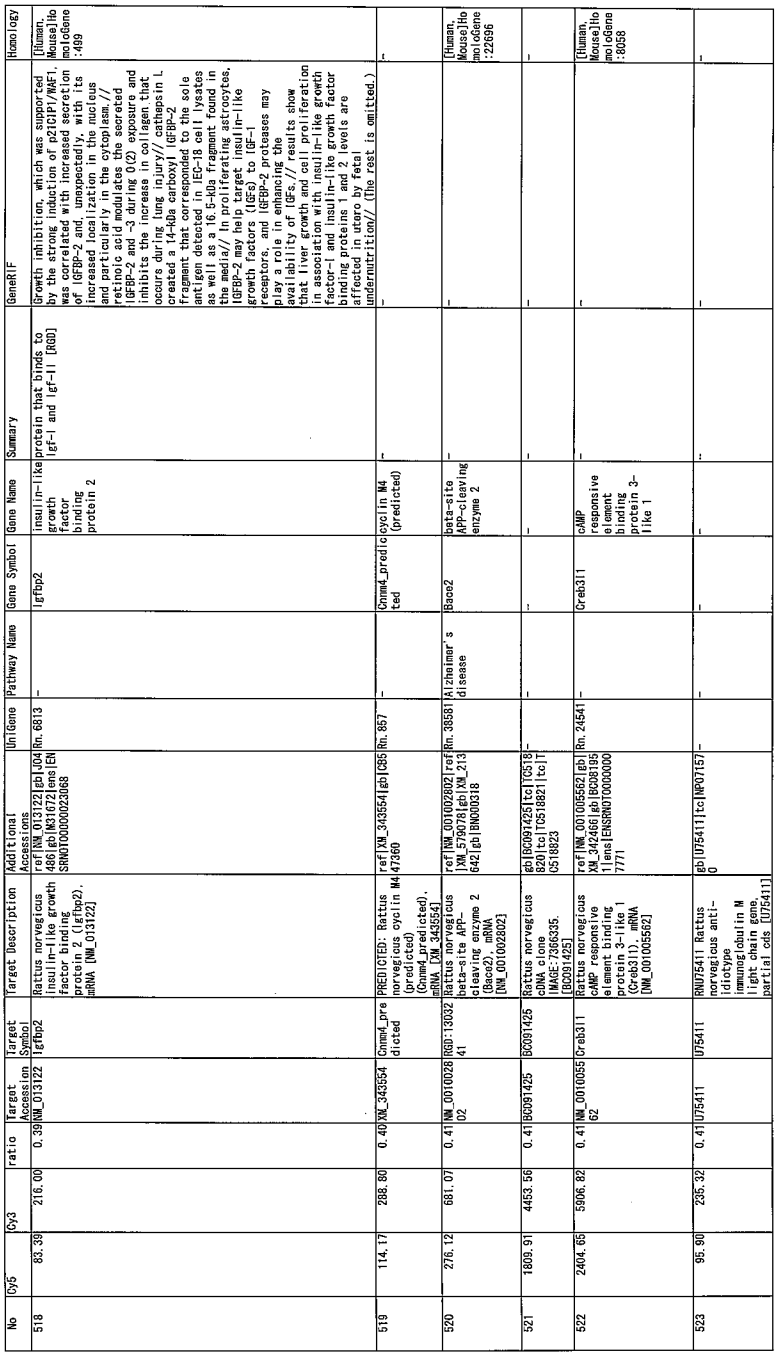


No	Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Pathway Name	Gene Symbol	Gene Name	Summary	GeneRIF	Homology
507	382.01	1091.35	0.35	NM_001000188	Olr197_predicted	Rattus norvegicus olfactory receptor 197 (predicted) (Olr197_predicted), mRNA [NM_001000188]	ref|NM_001000188|gb|XM_219093|ens|ENSRNOT00000023335	Rn.14181	-	Olr197_predicted	olfactory receptor 197 (predicted)	Olfactory receptors interact with odorant molecules in the nose, to initiate a neuronal response that triggers the perception of a smell. The olfactory receptor proteins are members of a large family of G-protein-coupled receptors (GPCR) arising from single coding-exon genes. Olfactory receptors share a 7-transmembrane domain structure with many neurotransmitter and hormone receptors and are responsible for the recognition and G protein-mediated transduction of odorant signals. The olfactory receptor gene family is the largest in the genome. The nomenclature assigned to the olfactory receptor genes and proteins for this organism is independent of other organisms.	-	[Mouse]Homologene:17487
508	1078.37	3022.68	0.36	XM_234830	LOC299551	PREDICTED: Rattus norvegicus similar to immunoglobulin heavy chain variable region (LOC299551), mRNA [XM_234830]	ref|XM_234830|gb|CO5-72227	-	-	RGD1563587_predicted	similar to immunoglobulin heavy chain variable region (predicted)	-	-	-
509	317.30	888.59	0.36	293354	293354	R.norvegicus mRNA for immunoglobulin variable region (clone ERF1.5). [293354]	gb|Z93354|tc|WP96889 4	Rn.17936	-	-	-	-	-	-
510	1207.29	3380.52	0.36	XM_342531	Sec23b_predicted	PREDICTED: Rattus norvegicus SEC23B (S. cerevisiae) (predicted) (Sec23b_predicted), mRNA [XM_342531]	ref|XM_342531|gb|CB5451321|ens|ENSRNOT00000011553|tc|TC6395068	Rn.8735	-	Sec23b_predicted	SEC23B (S. cerevisiae) (predicted)	-	-	[Human, Mouse]Homologene:74671

[0272]

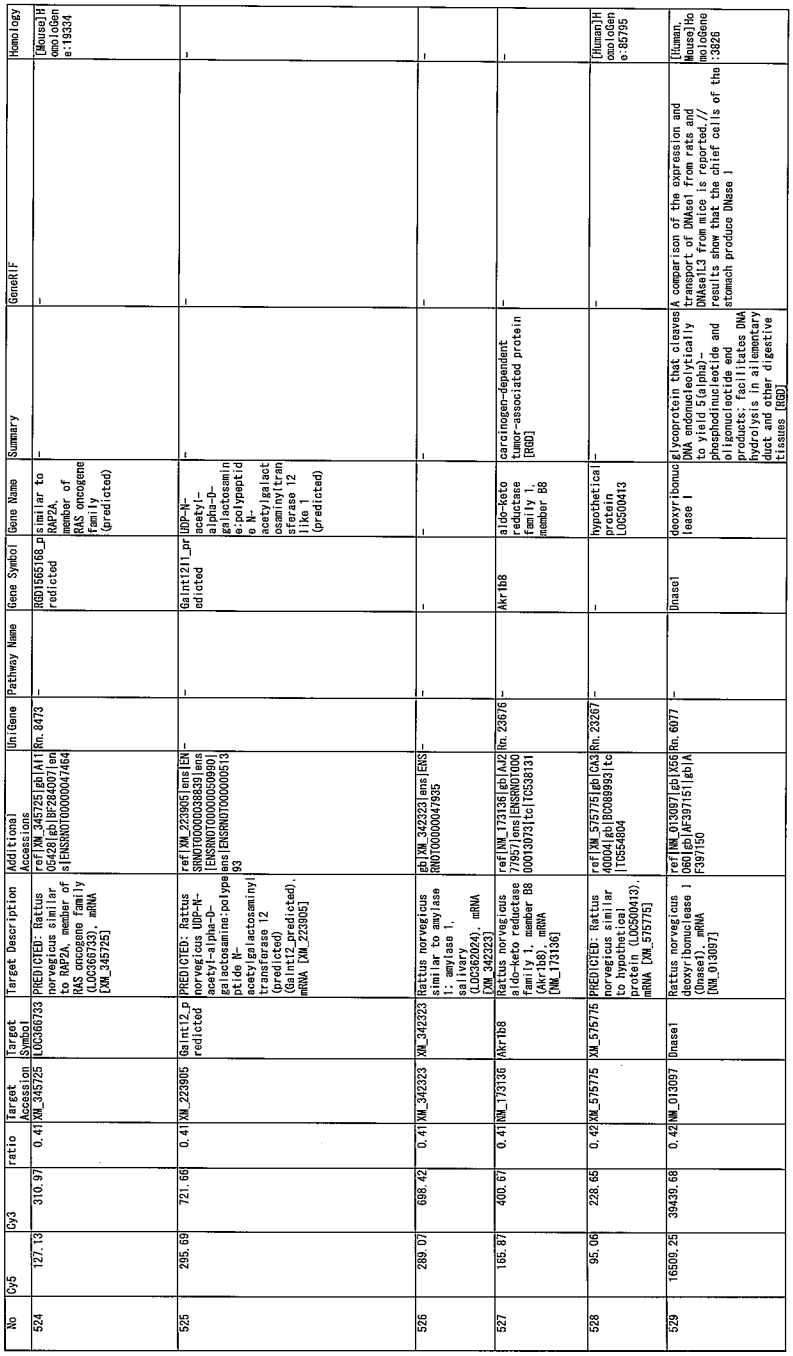
No	Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Pathway Name	Gene Symbol	Gene Name	Summary	GeneRIF	Homology
511	557.00	1647.24	0.36	NM_001010970	Amy1	Rattus norvegicus amylase 1, salivary (Amy1), mRNA (NM_001010970)	ref|NM_001010970|gb|AB057450|gb|BC038228||Ensembl|ENSRNOT00000022496	Rn.11636	Starch and sucrose metabolism	Amy1	amylase 1, salivary	-	the HCO3-anion participates in the secretory response at sites distal to the ion transportation sequence at sites distal to the identified ion transporters in both endocrine and exocrine cells; the absence of extracellular bicarbonate is shown to decrease by about 50% basal alpha-amylase secretion	-
512	206.37	573.02	0.36	NM_199406	Cxadr11	Rattus norvegicus coxsackie virus and adenovirus receptor-like 1 (Cxadr11), mRNA (NM_199406)	ref|NM_199406|gb|BC063181|gb|XM_342167|gb|XM_343453	Rn.16254	-	Cxadr11	coxsackie virus and adenovirus receptor-like 1	-	-	[Mouse]Homologene:30850
513	58.19	159.53	0.36	NM_031796	Galnt5	Rattus norvegicus UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 5 (Galnt5), mRNA (NM_031796)	ref|NM_031796|gb|AF045543|ens|ENSMUST00000006319|tc|TC071636	Rn.30048	O-Glycan biosynthesis, Glycan structures - biosynthesis 1	Galnt5	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 5	recombinant proteins display transferase activity in vitro [RGD]	-	[Human, Mouse]Homologene:8733
514	89.35	241.56	0.37	XM_344373	XM_344373	Rattus norvegicus similar to RIKEN cDNA A430107P09 gene (LOC364350), mRNA (XM_344373)	gb|XM_344373	-	-	-	-	-	-	-
515	79.97	215.82	0.37	TC525800	TC525800	Unknown	tc|TC525800	-	-	-	-	-	-	-
516	3244.72	8611.21	0.38	XM_575540	XM_575540	PREDICTED: Rattus norvegicus similar to immunoglobulin kappa chain (LOC500189), mRNA (XM_575540)	ref|XM_575540|gb|LO7401ens|ENSRNOT00000044112|tc|NEW70229	Rn.11794	-	RGD1565463_predicted	similar to immunoglobulin kappa-chain (predicted)	-	-	-
517	53.36	139.59	0.38	BF391573	C1q13_predicted	UI-R-CA1-bcw-a-06-0-UI.s1 UI-R-CA1 cDNA clone UI-R-CA1-bcw-a-06-0-UI 3', mRNA sequence (BF391573)	gb|BF391573	Rn.39092	-	RGD1562565_predicted	RGD1562565 (predicted)	-	-	-

[0273]



No	Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Pathway Name	Gene Symbol	Gene Name	Summary	GeneRIF	Homology
518	83.39	216.00	0.39	NM_013122	Igfbp2	Rattus norvegicus insulin-like growth factor binding protein 2 (Igfbp2), mRNA [NM_013122]	ref|NM_013122|gb|J04486|gb|M31072|ens|ENSRNOT00000023068	Rn. 6813	-	Igfbp2	insulin-like growth factor binding protein 2	protein that binds to Igf-I and Igf-II [RGD]	Growth inhibition, which was supported by the strong induction of p21CIP1/WAF1, was correlated with increased secretion of IGFBP-2 and, unexpectedly, with its increased localization in the nucleus and particularly in the cytoplasm.// Retinoic acid modulates the secretion of IGFBP-2 and, during G(2), and inhibits the increase in collagen that occurs during lung injury// cathepsin L created a 14-kDa carboxyl IGFBP-2 fragment that corresponded to the sole antigen detected in IEC-18 cell lysates as well as a 16.5-kDa fragment found in the media// In proliferating astrocytes, IGFBP-2 may help target insulin-like growth factors (IGFs) to IGF-I receptors, and IGFBP-2 proteases may play a role in enhancing the availability of IGFs.// results show that liver growth and cell proliferation in association with insulin-like growth factor-I and insulin-like growth factor binding proteins 1 and 2 levels are affected in utero by fetal undernutrition// (The rest is omitted.)	[Human, Mouse]Homologene:499
519	114.17	288.80	0.40	XM_343564	Comm4_predicted	PREDICTED: Rattus norvegicus cyclin M4 (predicted) (Comm4_predicted), mRNA [XM_343564]	ref|XM_343564|gb|D85447360	Rn. 857	-	Comm4_predicted	cyclin M4 (predicted)	-	-	-
520	276.12	681.07	0.41	NM_0010028 02	RGD:1303241	Rattus norvegicus beta-site APP-cleaving enzyme 2 (Baco2), mRNA [NM_001002802]	ref|NM_001002802|ref|XM_579078|gb|XM_213642|gb|BN000318	Rn. 38581	Alzheimer's disease	Baco2	beta-site APP-cleaving enzyme 2	-	-	[Human, Mouse]Homologene:22696
521	1809.91	4453.56	0.41	BC091425	BC091425	Rattus norvegicus cDNA clone IMAGE:7366335. [BC091425]	gb|BC091425|tc|TC5182050|tc|TC518823	-	-	-	-	-	-	-
522	2404.65	5906.82	0.41	NM_0010005 62	Creb311	Rattus norvegicus cAMP responsive element binding protein 3-like 1 (Creb311), mRNA [NM_001005562]	ref|NM_001005562|gb|XM_342461|gb|BG381115|ens|ENSRNOT00000007771	Rn. 24541	-	Creb311	cAMP responsive element binding protein 3-like 1	-	-	[Human, Mouse]Homologene:6038
523	95.90	235.32	0.41	U75411	U75411	RNU75411 Rattus norvegious anti-idiotype immunoglobulin M light chain gene, partial cds [U75411]	gb|U75411|tc|NP07157	-	-	-	-	-	-	-

[0274]



No	Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Pathway Name	Gene Symbol	Gene Name	Summary	GeneRIF	Homology
524	127.13	310.97	0.41	XM_345725	LOC366733	PREDICTED: Rattus norvegicus similar to RAP2A, member of RAS oncogene family (LOC366733), mRNA [XM_345725]	ref|XM_345725|gb|AI1 05428|gb|BF284407|ens|ENSRNOT00000047464	Rn.8473	-	RGD1565168_predicted	similar to RAP2A, member of RAS oncogene family (predicted)	-	-	[Mouse]Homologene:19334
525	295.69	721.66	0.41	XM_223905	Galnt12_predicted	PREDICTED: Rattus norvegicus UDP-N-acetyl-alpha-D-galactosamine-polypeptide N-acetylgalactosaminyltransferase 12 (predicted) (Galnt12_predicted), mRNA [XM_223905]	ref|XM_223905|ens|ENSRNOT00000038839|ens|ENSRNOT00000030990|ens|ENSRNOT00000005139|3	-	-	Galnt12l1_predicted	UDP-N-acetyl-alpha-D-galactosamine-polypeptide N-acetylgalactosaminyltransferase 12 like 1 (predicted)	-	-	-
526	289.07	698.42	0.41	XM_342323	XM_342323	Rattus norvegicus similar to amylase 1, salivary (LOC342323), mRNA [XM_342323]	gb|XM_342323|ens|ENSRNOT00000047935	-	-	-	-	-	-	-
527	165.87	400.67	0.41	NM_173136	Akr1b8	Rattus norvegicus aldo-keto reductase family 1, member B8 (Akr1b8), mRNA [NM_173136]	ref|NM_173136|gb|AA2 77957|ens|ENSRNOT00000013073|tc|TC538131	Rn.23676	-	Akr1b8	aldo-keto reductase family 1, member B8	carcinogen-dependent tumor-associated protein [RGD]	-	-
528	95.06	228.65	0.42	XM_575775	XM_575775	PREDICTED: Rattus norvegicus similar to hypothetical protein (LOC500413), mRNA [XM_575775]	ref|XM_575775|gb|CA3 40004|gb|BG088993|tc|TC554804	Rn.23267	-	-	hypothetical protein LOC500413	-	-	[Human]Homologene:85795
529	16509.25	39439.68	0.42	NM_013097	Dnase1	Rattus norvegicus deoxyribonuclease I (Dnase1), mRNA [NM_013097]	ref|NM_013097|gb|X56 06|gb|AF397151|gb|A F397150	Rn.6077	-	Dnase1	deoxyribonuclease I	glycoprotein that cleaves DNA endonucleolytically to yield 5(alpha)-phosphodinucleotide and oligonucleotide end products; facilitates DNA digestion in alimentary duct and other digestive tissues [RGD]	A comparison of the expression and transport of DNAseI from rats and DNAseIL3 from mice is reported.// results show that the chief cells of the stomach produce DNAse I	[Human,Mouse]Homologene:3826

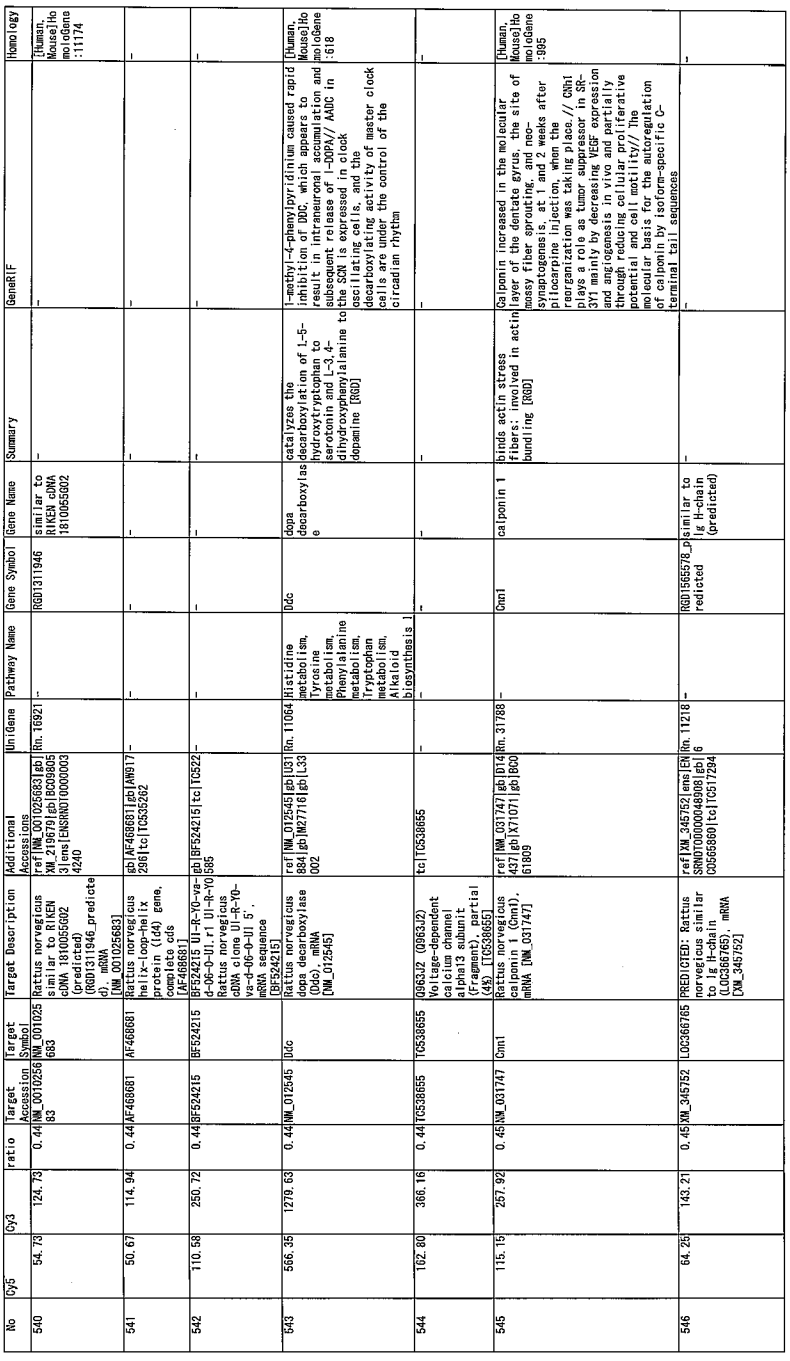
[0275]

No	Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Pathway	Name	Gene Symbol	Gene Name	Summary	GeneRIF	Homology
530	428.66	1005.04	0.43	NM_138840	Tgoln2	Rattus norvegicus trans-golgi network protein 1 (Tgoln2), mRNA [NM_138840]	ref|NM_138840|gb|X64600|gb|X53566|ens|ENSRNOT00000019713	Rn.11349	-		Tgoln2	trans-golgi network protein 2	resident integral membrane proteins of the trans-Golgi network (TGN), cycles constitutively between the TGN and the plasma membrane [RGD]	The results of this study suggest a role for TGN38 in facilitating rapid changes in the protein composition of postsynaptic membranes.	-
531	70.57	165.18	0.43	XM_218173	Prpf31_predicted	PREDICTED: Rattus norvegicus PRP31 pre-mRNA processing factor 31 homolog (yeast) (predicted) (Prpf31_predicted), mRNA [XM_218173]	ref|XM_218173|ens|ENSRNOT00000018603	Rn.99310	-		Prpf31_predicted	PRP31 pre-mRNA processing factor 31 homolog (yeast) (predicted)	-	-	[Human, Mouse]Homologene:5980
532	364.35	849.81	0.43	XM_234755	XM_234755	Rattus norvegicus similar to immunoglobulin heavy chain (LOC299475), mRNA [XM_234755]	gb|XM_234755|ens|ENSRNOT00000042393|ens|ENSRNOT00000049078	-	-		-	-	-	-	-
533	307.85	715.76	0.43	NM_021744	Cd14	Rattus norvegicus CD14 antigen (Cd14), mRNA [NM_021744]	ref|NM_021744|gb|U51804|gb|BC061733|ens|ENSRNOT00000023977	-	MAPK signaling pathway, Toll-like receptor signaling pathway, Hematopoietic cell lineage, Regulation of actin cytoskeleton		Cd14	CD14 antigen	component of the lippopolysaccharide receptor complex; mediates LPS-induced monocyte/macrophage and inflammatory response [RGD]	CD14 glycoprotein is present on the cell membranes of vascular smooth muscle cells of rat aorta. Where it acts as a lippopolysaccharide receptor.// In Kupffer cells, increased TLR4, CD14 expression has been induced by LPS within 1-3 hours, and further increase of TLR4, CD14 expression is correlated with the cytokines produced by KCs.// the CD14 antigen system appeared to be an early trigger for Kupffer cell activation followed by induction of inflammatory cytokine interleukin-1beta synthesis leading to hepatic injury after partial hepatectomy// Ethanol administration led to a significant synthesis of endotoxin receptor CD14 protein and its gene expression in Kupffer cells, which maybe result in the pathological changes of liver tissue and hepatic functional damages.// Although microglial-derived CD14 does not contribute to early events triggered by intracerebral endotoxin treatment, it modulates the duration of inflammation within the cerebral tissue.// (The rest is omitted.)	[Human, Mouse]Homologene:493

[0276]

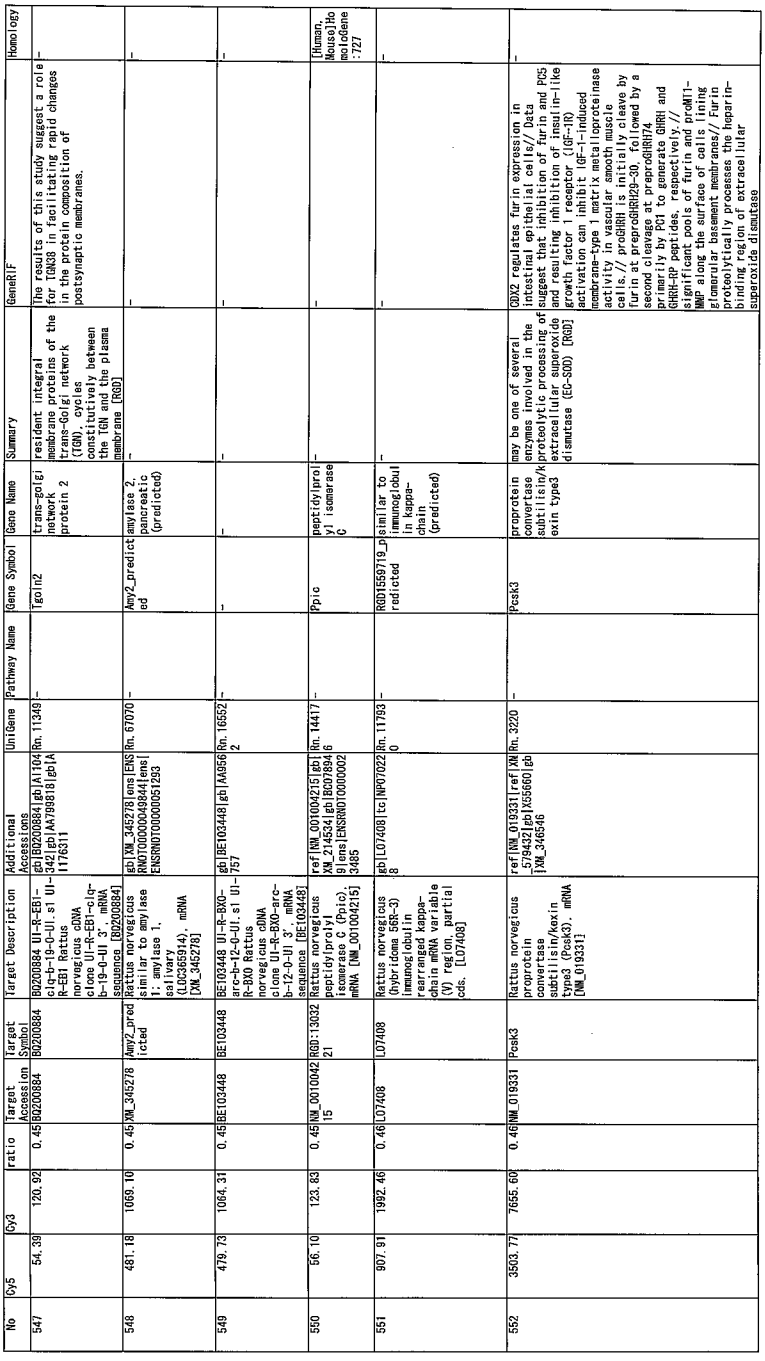
No	Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Pathway Name	Gene Symbol	Gene Name	Summary	GeneRIF	Homology
534	212.79	492.05	0.43	XM_013057	F3	Rattus norvegicus coagulation factor 3 (F3), mRNA [XM_013057]	ref|XM_013057|gb|U07619|gb|BC081846|ens|ENSRNOT00000015836	Rn.9960	Complement and coagulation cascades	F3	coagulation factor III	an initiation factor for blood coagulation: plays a critical role in hepatic ischemic reperfusion injury [RGD]	during aortic smooth muscle cell apoptosis, microparticles (MPs) produced bore intact and functional TF, but the release of TFPI did not change, so that the balance shifted to a procoagulant state// Induction of vascular dysfunctions like nitric oxide and endothelin differs in IPC-reduced and tissue factor-induced disseminated intravascular coagulation models.// Renal ischemic reperfusion injury can by avoided by antisensa oligodeoxynucleotide to the protein.// The expression of tissue factor and tissue factor pathway inhibitor in aortic smooth muscle cells is up-regulated in synthetic compared to contractile phenotype.// Antisense oligonucleotide inhibits hepatic ischemic reperfusion injury	[Human, Mouse]Homoldene :1511
535	1484.53	3422.17	0.43	XM_575534	XM_575534	PREDICTED: Rattus norvegicus similar to NGF-binding Ig light chain (LOC500182), mRNA [XM_575534]	ref|XM_575534|ens|ENSRNOT00000069541|ens|ENSRNOT00000046571	-	-	RGD1565546_predicted	similar to NGF-binding Ig light chain (predicted)	-	-	-
536	86.95	199.49	0.44	TC554663	TC554663	Unknown	tc|TC554663	-	-	-	-	-	-	-
537	974.27	2233.97	0.44	NM_138840	Tgoln2	Rattus norvegicus trans-golgi network protein 1 (Tgoln2), mRNA [NM_138840]	ref|NM_138840|gb|X53565|ens|ENSRNOT00000051608|ens|ENSRNOT00000019713	Rn.11349	-	Tgoln2	trans-golgi network protein 2	resident integral membrane proteins of the trans-Golgi network (TGN), cycles constitutively between the TGN and the plasma membrane [RGD]	The results of this study suggest a role for TGN38 in facilitating rapid changes in the protein composition of postsynaptic membranes.	-
538	170.22	390.09	0.44	NM_001025683	NM_001025683	Rattus norvegicus similar to RIKEN cDNA 1810055G02 (predicted) (RGD1311946_predicted), mRNA [NM_001025683]	ref|NM_001025683|gb|BC098053|tc|TC521627	Rn.16921	-	RGD1311946	similar to RIKEN cDNA 1810055G02	-	-	[Human, Mouse]Homoldene :11174
539	55.82	127.83	0.44	NM_053685	Hcn3	Rattus norvegicus hyperpolarization-activated cyclic nucleotide-gated potassium channel 3 (Hcn3), mRNA [NM_053685]	ref|NM_053685|gb|AF247452|ens|ENSRNOT00000027785	Rn.48801	-	Hcn3	hyperpolarization-activated cyclic nucleotide-gated potassium channel 3	may play a role in generation of neuronal pacemaker activity [RGD]	Of particular importance is that we detected no currents upon hyperpolarization in the ST4A cells at the nonproliferative stage when only HCN3 protein was present.// densely clustered at synaptic terminals of retinal bipolar cells and photoreceptors.// Immunoreactivity for HCN3 in rat brain shows subcortical distribution mainly concentrated in the hypothalamus.	[Human, Mouse]Homoldene :22453

[0277]



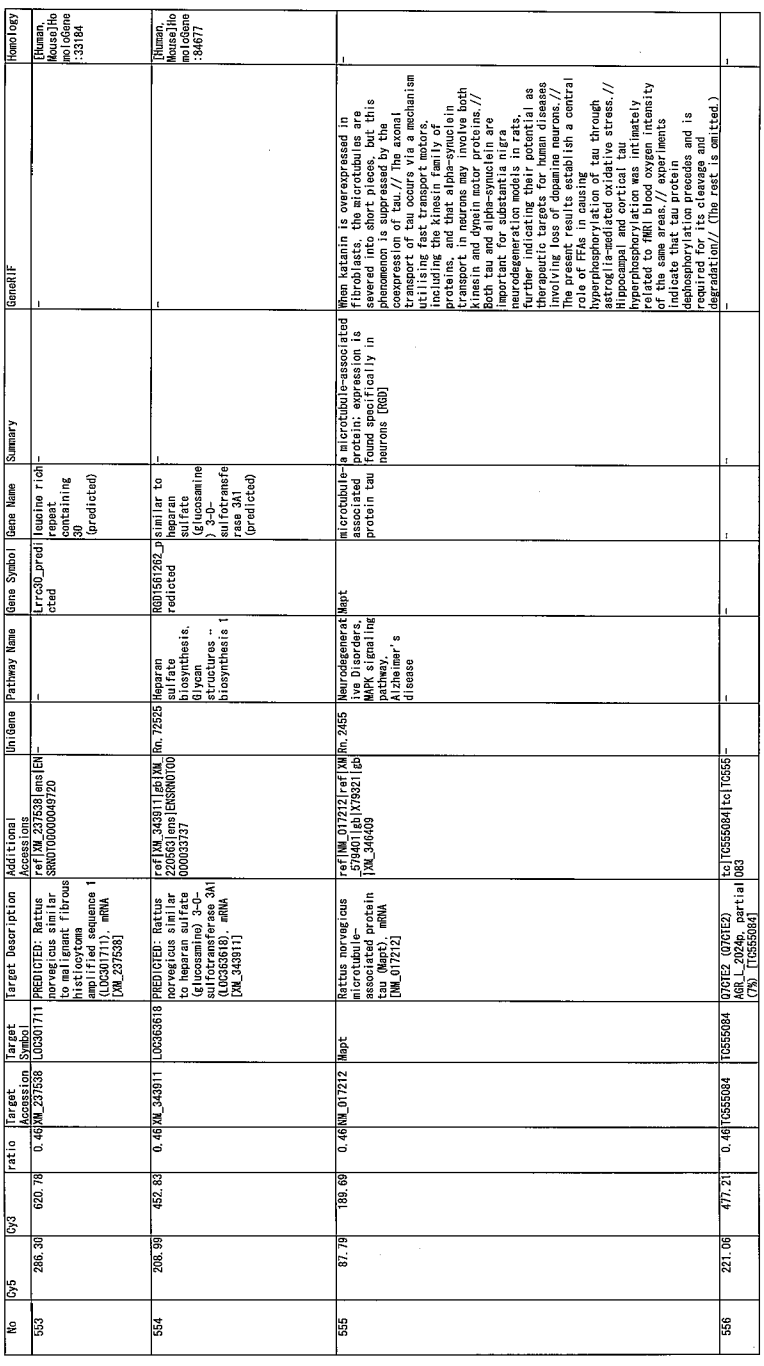
No	Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Pathway Name	Gene Symbol	Gene Name	Summary	GeneRIF	Homology
540	54.73	124.73	0.44	NM_001025683	NM_001025683	Rattus norvegicus similar to RIKEN cDNA 1810055602 (predicted) (RGD1311946_predicted), mRNA [NM_001025683]	ref|NM_001025683|gb|XM_219679|BC039805|ens|ENSMOT00000034240	Rn.16921	-	RGD1311946	similar to RIKEN cDNA 1810055602	-	-	(Human, Mouse)Homologene:11174
541	50.67	114.94	0.44	AF468681	AF468681	Rattus norvegicus helix-loop-helix protein (id4) gene, complete cds [AF468681]	gb|AF468681|gb|AW917296|tc|TC535262	-	-	-	-	-	-	-
542	110.58	250.72	0.44	BF524215	BF524215	BF524215 UI-R-Y0-va-d-06-0-UI.r1 UI-R-Y0-va-d-06-0-UI 5', mRNA sequence [BF524215]	gb|BF524215|tc|TC522585	-	-	-	-	-	-	-
543	566.35	1279.63	0.44	NM_012545	Ddc	Rattus norvegicus dopa decarboxylase (Ddc), mRNA [NM_012545]	ref|NM_012545|gb|U31884|gb|M27716|gb|L33002	Rn.11064	Histidine metabolism, Tyrosine metabolism, Phenylalanine metabolism, Tryptophan metabolism, Alkaloid biosynthesis I	Ddc	dopa decarboxylase	catalyzes the decarboxylation of L-5-hydroxytryptophan to serotonin and L-3,4-dihydroxyphenylalanine to dopamine [RGD]	1-methyl-4-phenylpyridinium caused rapid reduction of DDC, which appears to result in neuronal accumulation and decreased release of L-DOPA// AADC in the SCN is expressed in clock oscillating cells, and the decarboxylating activity of master clock cells are under the control of the circadian rhythm	(Human, Mouse)Homologene:618
544	162.80	366.16	0.44	T65386555	T65386555	Q963J2 (Q963J2) Voltage-dependent calcium channel alpha13 subunit (Fragment), partial (4%) [T65386555]	tc|T65386555	-	-	-	-	-	-	-
545	115.15	257.92	0.45	NM_031747	Cnn1	Rattus norvegicus calponin 1 (Cnn1), mRNA [NM_031747]	ref|NM_031747|gb|D14437|gb|X71071|gb|BC061809	Rn.31788	-	Cnn1	calponin 1	binds actin stress fibers; involved in actin bundling [RGD]	Calponin increased in the molecular layer of the dentate gyrus, the site of mossy fiber sprouting, and neo-synaptogenesis, at 1 and 2 weeks after pilocarpine injection, when the pilocarpine was taking place// Chh1 plays a role as tumor suppressor in SK-3Y1 mainly by decreasing VEGF expression and angiogenesis in vivo and partially through reducing cellular proliferative potential and cell motility// The molecular basis for the autoregulation of calponin by isoform-specific C-terminal tail sequences	(Human, Mouse)Homologene:995
546	64.26	143.21	0.45	XM_345752	LOC366765	PREDICTED: Rattus norvegicus similar to Ig H-chain (LOC366765), mRNA [XM_345752]	ref|XM_345752|ens|ENSRNOT00000048908|gb|CD566860|tc|TC517294	Rn.11218	-	RGD1565578_predicted	similar to Ig H-chain (predicted)	-	-	-

[0278]



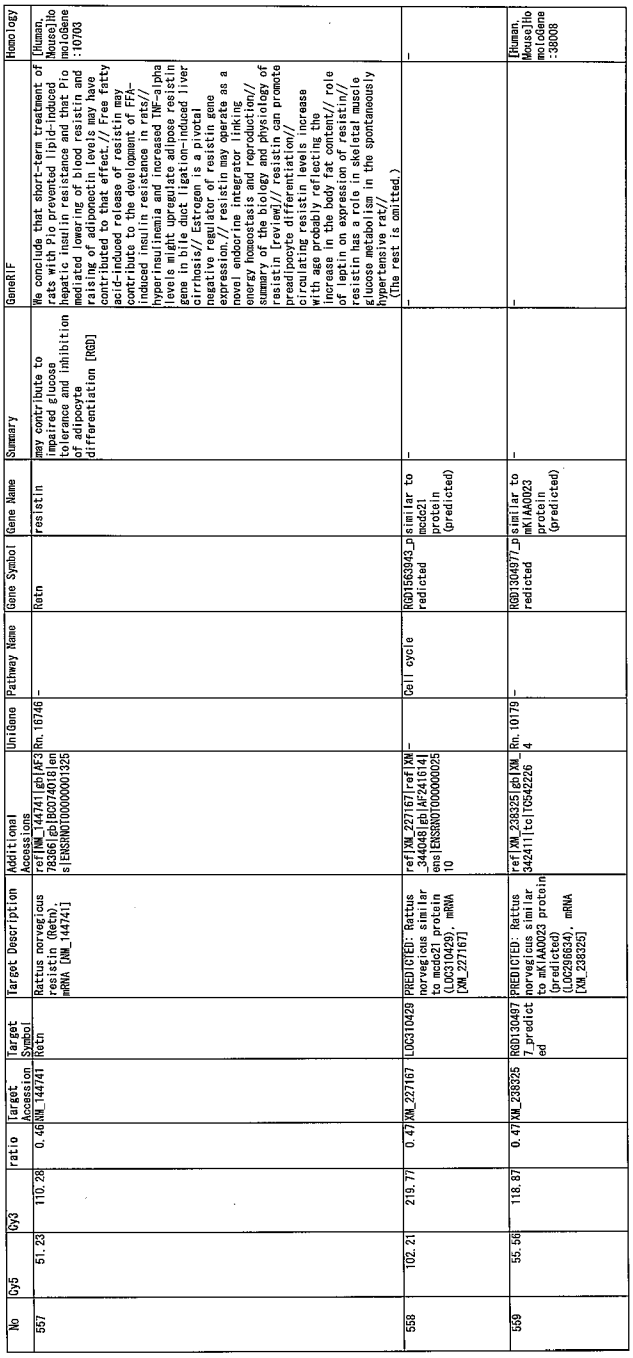
No	Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Pathway Name	Gene Symbol	Gene Name	Summary	GeneRIF	Homology
547	54.39	120.92	0.45	BQ200884	BQ200884	BQ200884 UI-R-EB1-clq-b-19-0-UI.sl UI-R-EB1 Rattus norvegicus cDNA clone UI-R-EB1-clq-b-19-0-UI 3', mRNA sequence [BQ200884]	gb|BQ200884|gb|AI104342|gb|AW799818|gb|AI176311	Rn.11349	-	Tgoln2	trans-golgi network protein 2	resident integral membrane proteins of the trans-Golgi network (TGN); cycles constitutively between the TGN and the plasma membrane [RGD]	The results of this study suggest a role for TGN38 in facilitating rapid changes in the protein composition of postsynaptic membranes.	-
548	481.18	1069.10	0.45	XM_345278	Amy2_predicted	Rattus norvegicus similar to amylase 1; amylase 1, salivary (LOC365914), mRNA [XM_345278]	gb|XM_345278|ENS|ENSRNOT00000049844|ens|ENSRNOT00000051293	Rn.67070	-	Amy2_predicted	amylase 2, pancreatic (predicted)	-	-	-
549	479.73	1064.31	0.45	BE103448	BE103448	BE103448 UI-R-BX0-arc-b-12-0-UI.sl UI-R-BX0 Rattus norvegicus cDNA clone UI-R-BX0-arc-b-12-0-UI 3', mRNA sequence [BE103448]	gb|BE103448|gb|AA956757	Rn.16552	-	-	-	-	-	-
550	56.10	123.83	0.45	NM_001004215	RGD:13032 21	Rattus norvegicus peptidylprolyl isomerase G (Ppic), mRNA [NM_001004215]	ref|NM_001004215|gb|XM_214534|gb|BC071894|ens|ENSRNOT00000023485	Rn.14417	-	Ppic	peptidylprolyl isomerase C	-	-	[Human, Mouse]Homologene:727
551	907.91	1992.46	0.46	LO7408	LO7408	Rattus norvegicus (hybridoma 56R-3) immunoglobulin rearranged kappa-chain mRNA variable (V) region, partial cds. [LO7408]	gb|LO7408|tc|NP07022 8	Rn.11783 0	-	RGD1559719_predicted	similar to immunoglobulin kappa-chain (predicted)	-	-	-
552	3503.77	7655.60	0.46	NM_019331	Pcsk3	Rattus norvegicus proprotein convertase subtilisin/kexin type3 (Pcsk3), mRNA [NM_019331]	ref|NM_019331|ref|NM_153432|gb|X53660|gb|J04546	Rn.3220	-	Pcsk3	proprotein convertase subtilisin/kexin type3	may be one of several enzymes involved in the proteolytic processing of extracellular superoxide dismutase (EC-SOD) [RGD]	CDX2 regulates furin expression in intestinal epithelial cells// Data suggest that inhibition of furin and PC5 and resulting inhibition of insulin-like growth factor I receptor (IGF-IR) activation can inhibit IGF-I-induced matrix-type 1 matrix metalloproteinase activity in vascular smooth muscle cells.// proGHRH is initially cleave by furin at preproGHRH29-30, followed by a second cleavage at preproGHRH74 primarily by PC1 to generate GHRH and GHRH-RP peptides, respectively.// significant pools of furin and proMT1-MMP along the surface of cells lining glomerular basement membranes.// Furin proteolytically processes the heparin-binding region of extracellular superoxide dismutase	-

[0279]



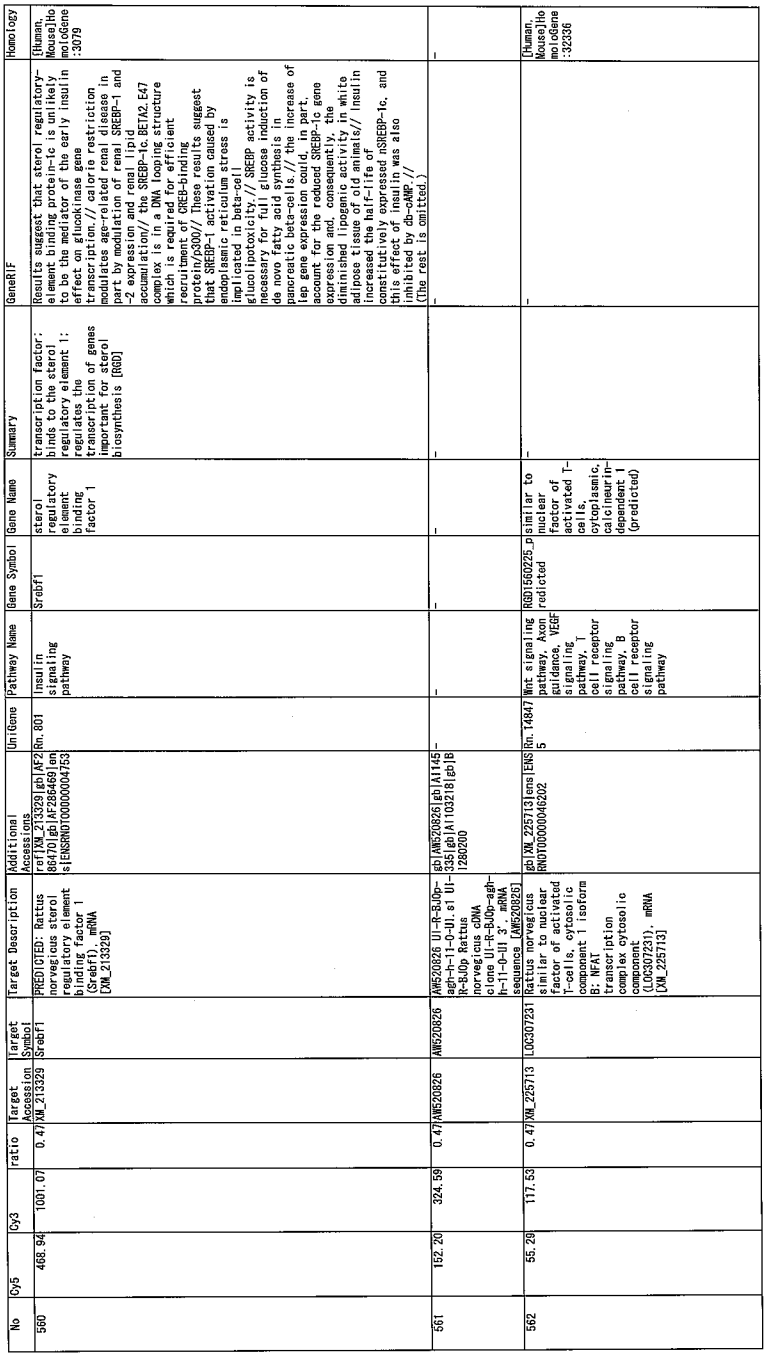
No	Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Pathway Name	Gene Symbol	Gene Name	Summary	GeneRIF	Homology
553	286.30	620.78	0.46	XM_237538	LOC301711	PREDICTED: Rattus norvegicus similar to malignant fibrous histiocytoma amplified sequence 1 (LOC301711), mRNA [XM_237538]	ref|XM_237538|ens|ENSRNOT00000049720	-	-	Lrrc30_predicted	leucine rich repeat containing 30 (predicted)	-	-	[Human, Mouse]HomoloGene:33184
554	208.99	452.83	0.46	XM_343911	LOC363618	PREDICTED: Rattus norvegicus similar to heparan sulfate (glucosamine) 3-O-sulfotransferase 3A1 (LOC363618), mRNA [XM_343911]	ref|XM_343911|gb|XM_220563|ens|ENSRNOT00000033737	Rn.72525	Heparan sulfate biosynthesis. Glycan structures -- biosynthesis 1	RGD1561262_predicted	similar to heparan sulfate (glucosamine) 3-O-sulfotransferase 3A1 (predicted)	-	-	[Human, Mouse]HomoloGene:84677
555	87.79	189.69	0.46	NM_017212	Mapt	Rattus norvegicus microtubule-associated protein tau (Mapt), mRNA [NM_017212]	ref|NM_017212|ref|XM_579401|gb|X79321|gb|XM_340409	Rn.2455	Neurodegenerative Disorders, MAPK signaling pathway, Alzheimer's disease	Mapt	microtubule-associated protein tau	a microtubule-associated protein: expression is found specifically in neurons [RGD]	When katanin is overexpressed in fibroblasts, the microtubules are severed into short pieces, but this phenomenon is suppressed by the coexpression of tau.// The axonal transport of tau occurs via a mechanism utilising fast transport motors, including the kinesin family of proteins, and that alpha-synuclein transport in neurons may involve both Kinesin and dynein motor proteins.// Both tau and alpha-synuclein are important for substantia nigra neurodegeneration models in rats, further indicating their potential as therapeutic targets for human diseases involving loss of dopamine neurons.// The present results establish a central role of FFAs in causing hyperphosphorylation of tau through astroglia-mediated oxidative stress.// Hippocampal and cortical tau hyperphosphorylation was intimately related to fMRI blood oxygen intensity of the same areas.// experiments indicate that tau protein dephosphorylation precedes and is required for its cleavage and degradation// (The rest is omitted.)	-	-
556	221.06	477.21	0.46	TC555084		D7GTE2 (D7GTE2) AGR_L_2024p, partial (7%) [TC555084]	tc|TC555084|tc|TC555	-	-	-	-	-	-	-

[0280]



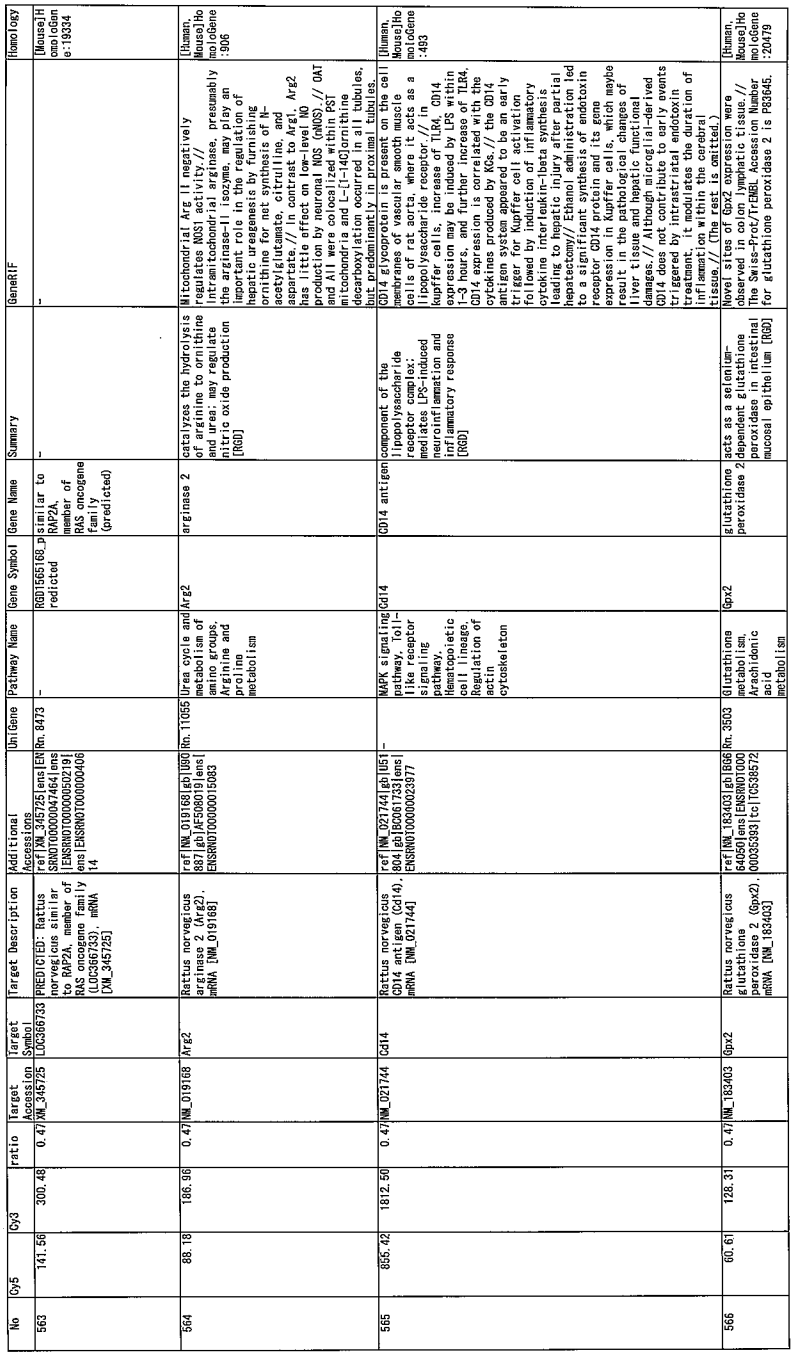
No	Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Pathway Name	Gene Symbol	Gene Name	Summary	GeneRIF	Homology
557	51.23	110.28	0.46	NM_144741	Retn	Rattus norvegicus resistin (Retn), mRNA [NM_144741]	ref|NM_144741|gb|AF3783861|gb|BC074018|ens|ENSRNOT00000001325	Rn.16746	-	Retn	resistin	may contribute to impaired glucose tolerance and inhibition of adipocyte differentiation [RGD]	We conclude that short-term treatment of rats with Pio prevented lipid-induced hepatic insulin resistance and that Pio mediated lowering of blood resistin and raising of adiponectin levels may have contributed to these effects.// resistin may contribute to the development of FFA-induced insulin resistance in rats.// hyperinsulinemia and increased TNF-alpha levels might upregulate adipose resistin gene in bile duct ligation-induced liver cirrhosis.// Estrogen is a pivotal negative regulator of resistin gene expression.// resistin may operate as a novel endocrine integrator linking energy homeostasis and reproduction.// summary of the biology and physiology of resistin [review].// resistin can promote preadipocyte differentiation.// circulating resistin levels increase with age probably reflecting the increase in the body fat content.// role of leptin on expression of resistin.// resistin as a role in skeletal muscle glucose metabolism in the spontaneously hypertensive rat.// (The rest is omitted.)	-	[Human, Mouse]Homologene:10703
558	102.21	219.77	0.47	XM_227167	LOC310429	PREDICTED: Rattus norvegicus similar to mcdc21 protein (LOC310429), mRNA [XM_227167]	ref|XM_227167|ref|XM_344048|gb|AF241614|ens|ENSRNOT00000000025 10	-	Cell cycle	RGD1563943_predicted	similar to mcdc21 protein (predicted)	-	-	-
559	55.56	118.87	0.47	XM_238325	RGD1304977_predicted	PREDICTED: Rattus norvegicus similar to mKIAA0023 protein (predicted) (LOC298634), mRNA [XM_238325]	ref|XM_238325|gb|XM_342411|tc|TC642226	Rn.10179	-	RGD1304977_predicted	similar to mKIAA0023 protein (predicted)	-	-	[Human, Mouse]Homologene:38008

[0281]



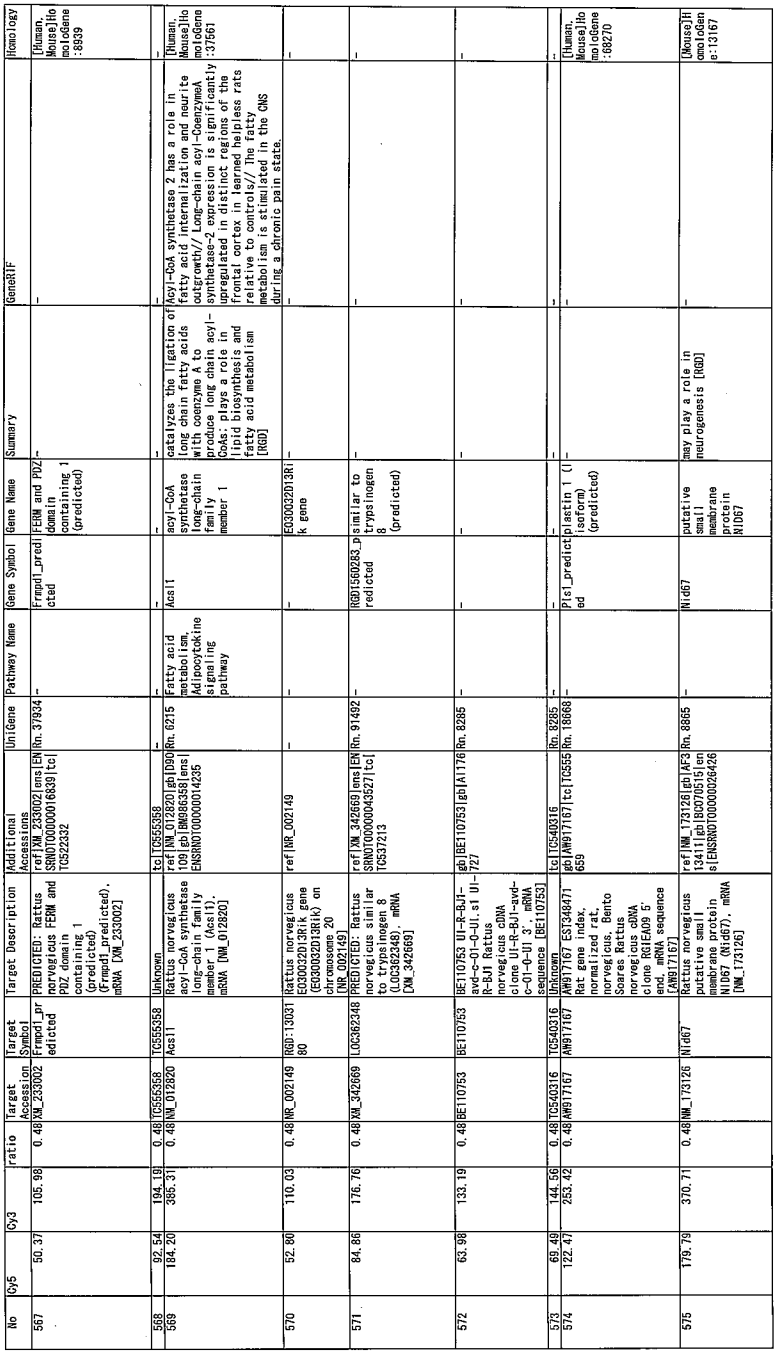
No	Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Pathway Name	Gene Symbol	Gene Name	Summary	GeneRIF	Homology
560	468.94	1001.07	0.47	XM_213329	Srebf1	PREDICTED: Rattus norvegicus sterol regulatory element binding factor 1 (Srebf1), mRNA [XM_213329]	ref|XM_213329|gb|AF2 86470|gb|AF2866469|en s|ENSRNOT00000004753	Rn.801	Insulin signaling pathway	Srebf1	sterol regulatory element binding factor 1	transcription factor; binds to the sterol regulatory element 1; regulates the transcription of genes important for sterol biosynthesis [RGD]	Results suggest that sterol regulatory-element binding protein-1c is unlikely to be the mediator of the early insulin effect on glucokinase gene transcription.// calorie restriction modulates age-related renal disease in part by modulation of renal SREBP-1 and -2 expression and renal lipid accumulation// The SREBP-1c, DETA2.547 complex is a DNA looping structure which is required for efficient recruitment of CREB-binding protein/p300// These results suggest that SREBP-1 activation caused by endoplasmic reticulum stress is implicated in beta-cell glucolipotoxicity.// SREBP activity is necessary for full glucose induction of de novo fatty acid synthesis in pancreatic beta-cells.// the increase of lep gene expression could, in part, account for the reduced SREBP-1c gene expression and, consequently, the diminished lipogenic activity in white adipose tissue of old animals// Insulin increased the half-life of constitutively expressed nSREBP-1c, and this effect of insulin was also mimicked by dbcAMP// (The rest is omitted.)	-	[Human, Mouse]Ho mologene :3079
561	152.20	324.59	0.47	AW520826	AW520826	AW520826 UI-R-BJ0p-agh-h-11-0-UI.s1 UI-R-BJ0p Rattus norvegicus cDNA clone UI-R-BJ0p-agh-h-11-0-UI 3', mRNA sequence [AW520826]	gb|AW520826|gb|AI145 335|gb|AI103218|gb|B I280200	-	-	-	-	-	-	-
562	55.26	117.53	0.47	XM_225713	LOC307231	Rattus norvegicus similar to nuclear factor of activated T-cells, cytosolic component 1 isoform B: NFAT transcription complex cytosolic component (LOC307231), mRNA [XM_225713]	gb|XM_225713|ens|ENS RNOT00000046202	Rn.14847 5	Wnt signaling pathway, Axon guidance, VEGF signaling pathway, T cell receptor signaling pathway, B cell receptor signaling pathway	RGD1560225_p redicted	similar to nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 1 (predicted)	-	-	[Human, Mouse]Ho mologene :32336

[0282]



No	Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Pathway Name	Gene Symbol	Gene Name	Summary	GeneRIF	Homology
563	141.56	300.48	0.47	XM_345725	LOC366733	PREDICTED: Rattus norvegicus similar to RAP2A, member of RAS oncogene family (LOC366733), mRNA [XM_345725]	ref|XM_345725|ens|ENSRNOT00000047464|ens|ENSRNOT00000050219|ens|ENSRNOT00000000406	Rn.8473	-	RGD1565168_predicted	similar to RAP2A, member of RAS oncogene family (predicted)	-	-	[Mouse]Homolo geneID:19334
564	88.18	186.96	0.47	NM_019168	Arg2	Rattus norvegicus arginase 2 (Arg2), mRNA [NM_019168]	ref|NM_019168|gb|U90887|gb|AF508019|ens|ENSRNOT00000015083	Rn.11065	Urea cycle and metabolism of amino groups, Arginine and proline metabolism	Arg2	arginase 2	catalyzes the hydrolysis of arginine to ornithine and urea; may regulate nitric oxide production [RGD]	Mitochondrial Arg II negatively regulates NOS1 activity.// Intramitochondrial arginase, presumably the arginase-II isozyme, may play an important role in the regulation of hepatic ureagenesis by furnishing ornithine for net synthesis of N-acetylglutamate, citrulline, and aspartate.// In contrast to Arg1, Arg2 has little effect on low-level NO production by neuronal NOS (nNOS).// OAT and AII were colocalized within PST mitochondria and L-[1-14C]ornithine decarboxylation occurred in all tubules, but predominantly in proximal tubules.	[Human, Mouse]HomoloGene:906
565	855.42	1812.50	0.47	NM_021744	Cd14	Rattus norvegicus CD14 antigen (Cd14), mRNA [NM_021744]	ref|NM_021744|gb|U51804|gb|BC061233|ens|ENSRNOT00000023977	-	MAPK signaling pathway, Toll-like receptor signaling pathway, Hematopoietic cell lineage, Regulation of actin cytoskeleton	Cd14	CD14 antigen	component of the lipopolysaccharide receptor complex; mediates LPS-induced neuroinflammation and inflammatory response [RGD]	CD14 glycoprotein is present on the cell membranes of monocytes and macrophages. It acts as a receptor for complexes of lipopolysaccharide receptor // in kupffer cells, increase of TLR4, CD14 expression may be induced by LPS within 1-3 hours, and further increase of TLR4, CD14 expression is correlated with the cytokines produced by KCs.// the CD14 antigen system appeared to be an early trigger for Kupffer cell activation followed by induction of inflammatory cytokine interleukin-1beta synthesis leading to hepatic injury after partial hepatectomy.// Ethanol administration led to a significant synthesis of endotoxin receptor CD14 protein and its gene expression in Kupffer cells, which maybe result in the pathological changes of liver tissue and hepatic functional damages.// Liver injury mediated by CD14 does not contribute to early events triggered by intrastriatal endotoxin treatment. it modulates the duration of inflammation within the cerebral tissue.// (The rest is omitted.)	[Human, Mouse]HomoloGene:493
566	60.61	128.31	0.47	NM_183403	Gpx2	Rattus norvegicus glutathione peroxidase 2 (Gpx2), mRNA [NM_183403]	ref|NM_183403|gb|BG640506|ens|ENSRNOT00000035393|tc|TC538572	Rn.3503	Glutathione metabolism, Arachidonic acid metabolism	Gpx2	glutathione peroxidase 2	acts as a selenium-dependent glutathione peroxidase in intestinal mucosal epithelium [RGD]	Novel sites of Gpx2 expression were observed in colon lymphatic tissue.// The Swiss-Prot/TrEMBL Accession Number for glutathione peroxidase 2 is P83645.	[Human, Mouse]HomoloGene:20479

[0283]

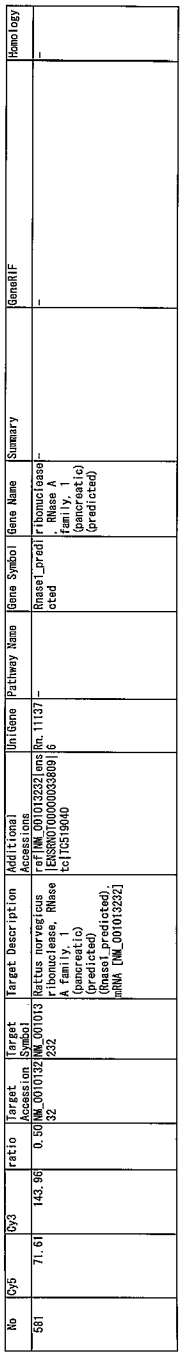


No	Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Pathway Name	Gene Symbol	Gene Name	Summary	GeneRIF	Homology
567	50.37	105.98	0.48	XM_233002	Frmpd1_predicted	PREDICTED: Rattus norvegicus FERM and PDZ domain containing 1 (predicted) (Frmpd1_predicted), mRNA [XM_233002]	ref|XM_233002.1|ens|ENSRNOT00000016839|tc|TC522332	Rn.37934	-	Frmpd1_predicted	FERM and PDZ domain containing 1 (predicted)	-	-	[Human, Mouse]HomoloGene:8939
568	92.54	194.19	0.48	TC555358	TC555358	Unknown	tc|TC555358	-	-	-	-	-	-	-
569	184.20	386.31	0.48	NM_012820	Acsl1	Rattus norvegicus acyl-CoA synthetase long-chain family member 1 (Acsl1), mRNA [NM_012820]	ref|NM_012820.1|gb|D90280.1|mm|gb|BM986358|ens|ENSRNOT00000014235	Rn.6215	Fatty acid metabolism, Adipocytokine signaling pathway	Acsl1	acyl-CoA synthetase long-chain family member 1	catalyzes the ligation of long chain fatty acids with coenzyme A to produce long chain acyl-CoAs; plays a role in lipid biosynthesis and fatty acid metabolism [RGD]	Acyl-CoA synthetase 2 has a role in fatty acid internalization and neurite outgrowth// Long-chain acyl-CoenzymeA synthetase 2 expression is significantly upregulated in distinct regions of the frontal cortex in learned helpless rats relative to controls// The fatty metabolism is stimulated in the CNS during a chronic pain state.	[Human, Mouse]HomoloGene:37561
570	52.80	110.03	0.48	NR_002149	RGD:13031 80	Rattus norvegicus EG30032D13Rik gene (EG30032D13Rik) on chromosome 20 [NR_002149]	ref|NR_002149	-	-	-	EG30032D13Rik gene	-	-	-
571	84.86	176.76	0.48	XM_342669	LOC362348	PREDICTED: Rattus norvegicus similar to trypsinogen 8 (LOC362348), mRNA [XM_342669]	ref|XM_342669.1|ens|ENSRNOT00000043527|tc|TC537213	Rn.91492	-	RGD1560283_predicted	similar to trypsinogen 8 (predicted)	-	-	-
572	63.98	133.19	0.48	BE110753	BE110753	BE110753 UI-R-BJ1-avd-c-01-0-UI.s1 UI-R-BJ1 Rattus norvegicus cDNA clone UI-R-BJ1-avd-c-01-0-UI 3', mRNA sequence [BE110753]	gb|BE110753|gb|AI176727	Rn.8285	-	-	-	-	-	-
573	69.49	144.56	0.48	TC540316	TC540316	Unknown	tc|TC540316	Rn.8285	-	-	-	-	-	-
574	122.47	253.42	0.48	AW917167	AW917167	AW917167 EST348471 Rat gene index, normalized rat, norvegicus, Bento Soares Rattus norvegicus cDNA clone RGIEA09 5' end, mRNA sequence [AW917167]	gb|AW917167|tc|TC555659	Rn.18668	-	Pisl_predicted	plastin 1 (I isoform) (predicted)	-	-	[Human, Mouse]HomoloGene:68270
575	179.79	370.71	0.48	NM_173126	Nid67	Rattus norvegicus nidogen like 1 (Nid67), mRNA [NM_173126]	ref|NM_173126.2|gb|AF3134111|gb|BQ076515|ens|ENSRNOT00000026426	Rn.8865	-	Nid67	putative small membrane protein Nid67	may play a role in neurogenesis [RGD]	-	[Mouse]Homologene:13167

[0284]

No	Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Pathway Name	Gene Symbol	Gene Name	Summary	GeneRIF	Homology
576	201.96	416.31	0.49	XM_215659	Rhoc_predicted	PREDICTED: Rattus norvegicus ras homolog gene family, member C (predicted) (Rhoc_predicted), mRNA [XM_215659]	ref|XM_215659|ens|ENSRNOT00000017254|tc|TC534618|tc|TC534689	Rn. 16261	-	Rhoc_predicted	ras homolog gene family, member C (predicted)	-	-	[Human, Mouse]HomoloGene:56380
577	143.17	291.53	0.49	NM_012820	Acsl1	Rattus norvegicus acyl-CoA synthetase long-chain family member 1 (Acsl1), mRNA [NM_012820]	ref|NM_012820|gb|D90109|gb|AW916542|ens|ENSRNOT00000014235	Rn. 6215	Fatty acid metabolism, Adipocytokine signaling pathway	Acsl1	acyl-CoA synthetase long-chain family member 1	catalyzes the ligation of long chain fatty acids with coenzyme A to produce long chain acyl-CoAs; plays a role in lipid biosynthesis and fatty acid metabolism [RGD]	Acyl-CoA synthetase 2 has a role in fatty acid internalization and neurite outgrowth.// Long-chain acyl-CoenzymeA synthetase-2 expression is significantly upregulated in distinct regions of the frontal cortex in learned helpless rats relative to controls.// The fatty acid-activating enzyme ACSL1 in the CNS during a chronic pain state	[Human, Mouse]HomoloGene:37561
578	130.99	266.25	0.49	XM_215963	Lama5	PREDICTED: Rattus norvegicus laminin, alpha 5 (Lama5), mRNA [XM_215963]	ref|XM_215963|ens|ENSRNOT00000089815|ens|ENSRNOT00000051597|gb|AW141471	Rn. 62616	Cell Communication, Focal adhesion, ECM-receptor interaction	Lama5	laminin, alpha 5	an extracellular matrix glycoprotein involved in cell migration and differentiation [RGD]	Data suggest that the early arrest of tumor cells in the pulmonary vasculature through interaction of alpha3beta1 integrin with laminin-5 in exposed basement membrane provides a basis for cell arrest during pulmonary metastasis.// laminin 6 and 5 have distinct biological activities, but they may cooperatively support cell adhesion.// LN6 and LN5 have distinct biological activities, but they may cooperatively support cell adhesion	[Human, Mouse]HomoloGene:4060
579	62.96	127.75	0.49	XM_343968	Gpr2_predicted	PREDICTED: Rattus norvegicus G protein-coupled receptor 2 (predicted) (Gpr2_predicted), mRNA [XM_343968]	ref|XM_343968|ens|ENSRNOT00000027458|tc|TC560118	Rn. 49607	-	Gpr2_predicted	G protein-coupled receptor 2 (predicted)	-	-	[Human, Mouse]HomoloGene:7271
580	50.20	101.67	0.49	NM_019265	Scn11a	Rattus norvegicus sodium channel, voltage-gated, type11, alpha polypeptide (Scn11a), mRNA [NM_019265]	ref|NM_019265|AF059030|gb|AJ237852|ens|ENSRNOT00000034025	Rn. 30023	-	Scn11a	sodium channel, voltage-gated, type XI, alpha	Na channel alpha-subunit: may be involved in generation of electrical activity in peripheral sensory neurons [RGD]	Examination of lamotrigine block of mutant sodium channel alpha subunits, in which alanine had been substituted for each individual amino acid in IVS6, identified mutations I1760A, F1764A and Y1771A as causing the largest reductions in affinity.// The pattern of expression of the voltage-gated sodium channels Na(v)1.8 and Na(v)1.9 does not change in uninjured primary sensory neurons in experimental neuropathic pain models.	[Human, Mouse]HomoloGene:8041

[0285]



No	Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Pathway Name	Gene Symbol	Gene Name	Summary	GeneRIF	Homology
581	71.61	143.96	0.50	NM_001013232	NM_001013232	Rattus norvegicus ribonuclease, RNase A family, 1 (pancreatic) (predicted) (Rnase1_predicted), mRNA [NM_001013232]	ref|NM_001013232|ens|ENSRNOT00000003809|tc|TC519040	Rn.11137	-	Rnase1_predicted	ribonuclease, RNase A family, 1 (pancreatic) (predicted)	-	-	-

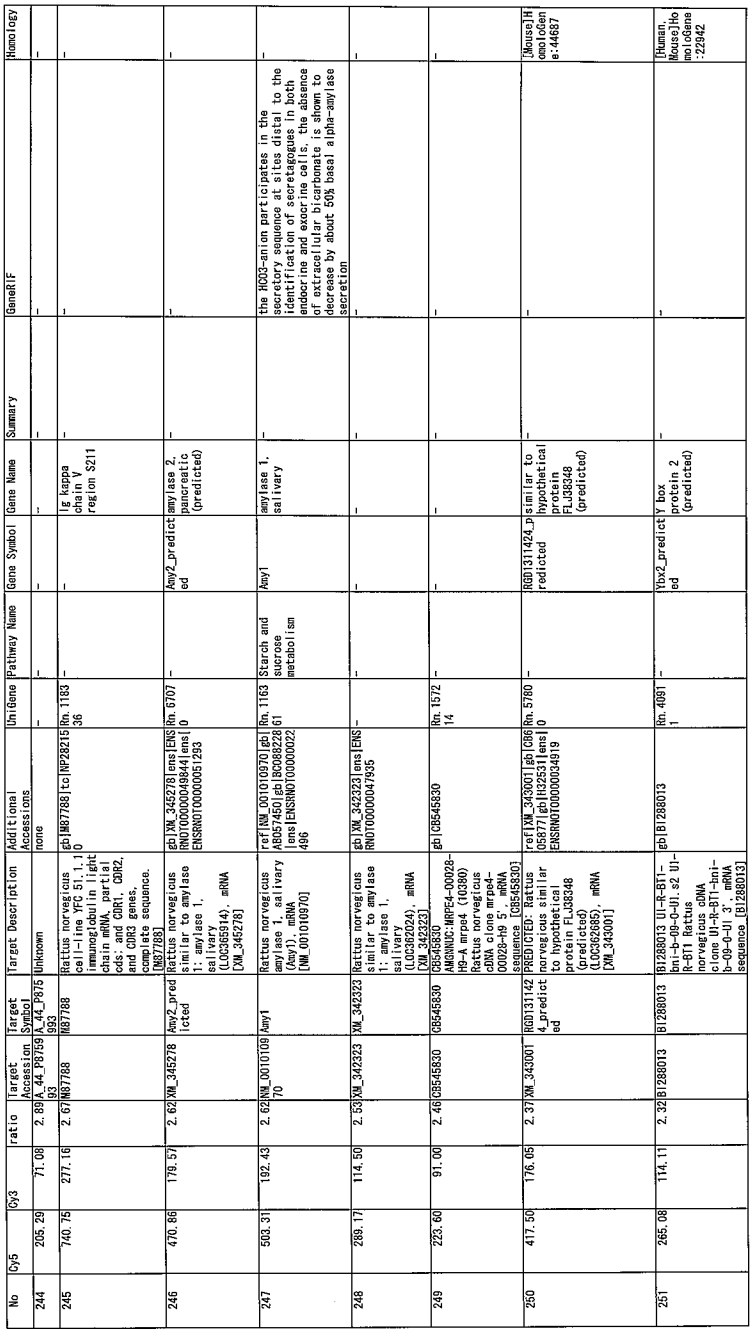
[0286] Light Touch群と比較してTickling群で2.0倍超の発現を認めた唾液腺(Sg)の遺伝子のアノテーションを下記表34に示す。

[表34]

表34 T-Sg(Cy5) v.s. L-Sg(Cy3) :up regulation(Cy5>Cy3)

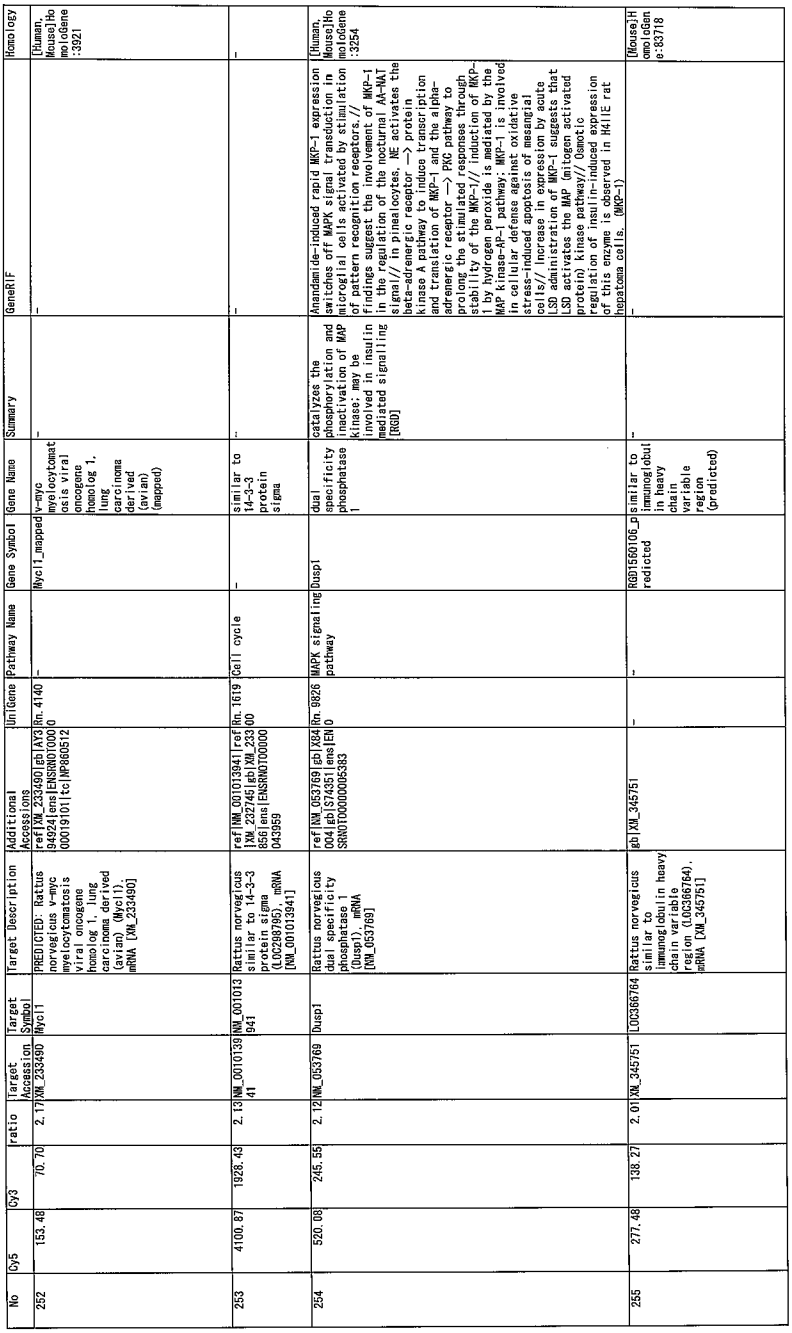
No	Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Pathway Name	Gene Symbol	Gene Name	Summary	GeneRIF	Homology
235	442.52	64.54	6.86	NM_022859	Crisp1	Rattus norvegicus cysteine-rich secretory protein 1 (Crisp1), mRNA [NM_022859]	ref|NM_022859|ref|XM_346949|gb|M31173|gb|X04643	Rn.1010	-	Crisp1	cysteine-rich secretory protein 1	-	In addition to its influence on protein tyrosine phosphorylation, bicarbonate is required to support other rat sperm capacitation-associated events, such as hyperactivation, exocytosis of the acrosomal vesicle, and expression of ability of sperm to fuse with egg.	-
236	521.01	79.25	6.57	ENSRNOT00000040037	ENSRNOT00000040037	R.norvegicus mRNA for immunoglobulin variable region (clone ERF3.23). [Z33370]	ens|ENSRNOT00000040037|gb|Z33370|tc|NP968878	-	-	-	-	-	-	-
237	349.96	65.01	5.38	NM_172065	Prrg2	Rattus norvegicus proline-rich proteoglycan 2 (Prrg2), mRNA [NM_172065]	ref|NM_172065|gb|L17318|ens|ENSRNOT00000013943|tc|TC573282	Rn.2995	-	Prrg2	proline-rich proteoglycan 2	member of a family of proline rich proteins that are induced in salivary gland by isoproterenol treatment and by feeding tannins [ROD]	-	-
238	1220.16	245.33	4.97	NM_052808	Psp	Rattus norvegicus parotid secretory protein (Psp), mRNA [NM_052808]	ref|NM_052808|gb|M93018|ens|ENSRNOT00000018226|tc|TC572606	Rn.9766	-	Psp	parotid secretory protein	secretory protein stored in part of acinar cells [ROD]	PSP co-fractionates with chromogranin A but not with secreted alkaline phosphatase, its sorting is not cell-type specific but the precise mechanism of its sorting is unknown	[Human, Mouse]Homologene:69034
239	238.50	50.03	4.77	BF415117	BF415117	BF415117 UI-R-BJ2-boa-h-09-0-UI.s1 UI-R-BJ2 Rattus norvegicus cDNA clone UI-R-BJ2-boa-h-09-0-UI 3', mRNA sequence [BF415117]	gb|BF415117|gb|BM387156|gb|AA817753	Rn.2635	-	-	-	-	-	-
240	483.22	109.65	4.41	NM_019239	Mgat3	Rattus norvegicus mannoside acetyl glucosaminyltransferase 3 (Mgat3), mRNA [NM_019239]	ref|NM_019239|gb|D10852|ens|ENSRNOT00000023434	Rn.9803	N-Glycan biosynthesis, Glycan structures - biosynthesis 1	Mgat3	mannoside acetyl glucosaminyltransferase 3	enzyme that catalyzes the addition of N-acetylglucosamine to the beta-linked mannose of the trimannosyl core of N-linked sugar chains [ROD]	-	[Human, Mouse]Homologene:31088
241	250.75	59.49	4.22	TC519989	TC519989	Unknown	tc|TC519989	-	-	-	-	-	-	-
242	303.35	80.66	3.76	XM_341973	XM_341973	Rattus norvegicus similar to Aldehyde dehydrogenase 7 (LOC361690), mRNA [XM_341973]	gb|XM_341973|ens|ENSRNOT00000024034	-	-	-	-	-	-	-
243	68772.07	22172.27	3.10	NM_080770	Scgb2a1	Rattus norvegicus secretoglobin, Family 2A, member 1 (Scgb2a1), mRNA [NM_080770]	ref|NM_080770|ref|NM_203333|gb|Y01263|gb|Y01261	Rn.1445	-	Scgb2a1	secretoglobin, family 2A, member 1	expression is regulated by testosterone [ROD]	-	-

[0287]



No	Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Pathway Name	Gene Symbol	Gene Name	Summary	GeneRIF	Homology
244	205.29	71.08	2.89	A_44_P87693	A_44_P875993	Unknown	none	-	-	-	-	-	-	-
245	740.75	277.16	2.67	M87788	M87788	Rattus norvegicus cell-line YFC 51.1.10 immunoglobulin light chain mRNA, partial cds: and CDR1, CDR2, and CDR3 genes, complete sequence. [M87788]	gb|M87788.1|to|NP28215	Rn.118336	-	-	Ig kappa chain V region S211	-	-	-
246	470.86	179.57	2.62	XM_345278	Amy2_predicted	Rattus norvegicus similar to amylase 1, salivary (LOC365914), mRNA [XM_345278]	gb|XM_345278.3|ens|ENSRNOT00000049844|ens|ENSRNOT00000051253	Rn.67070	-	Amy2_predicted	amylase 2, pancreatic (predicted)	-	-	-
247	503.31	192.43	2.62	NM_001010970	Amy1	Rattus norvegicus amylase 1, salivary (Amy1), mRNA [NM_001010970]	ref|NM_001010970.2|gb|AB057450.1|gb|BC088228.1|ens|ENSRNOT00000049496	Rn.116361	Starch and sucrose metabolism	Amy1	amylase 1, salivary	-	the ROS3-anion participates in the secretory sequence at sites distal to the identification of secretagogues in both andocrine and exocrine cells, the absence of extracellular bicarbonate is shown to decrease by about 50% basal alpha-amylase secretion	-
248	289.17	114.50	2.53	XM_342323	XM_342323	Rattus norvegicus similar to amylase 1, salivary (LOC362024), mRNA [XM_342323]	gb|XM_342323.3|ens|ENSRNOT00000047935	-	-	-	-	-	-	-
249	223.60	91.00	2.46	CB545830	CB545830	AMGNNUC:MRP64-00028-H9-A mrp64 (10390) Rattus norvegicus cDNA clone mrp64-00028-h9 5', mRNA sequence [CB545830]	gb|CB545830	Rn.157214	-	-	-	-	-	-
250	417.50	176.05	2.37	XM_343001	RGD1311142_predicted	PREDICTED: Rattus norvegicus similar to hypothetical protein FLJ38348 (predicted) (LOC362685), mRNA [XM_343001]	ref|XM_343001.3|gb|CB605677.1|gb|BI325311.1|ens|ENSRNOT00000034919	Rn.57800	-	RGD1311424_predicted	similar to hypothetical protein FLJ38348 (predicted)	-	-	[Mouse]Homoloden:44687
251	265.08	114.11	2.32	BI288013	BI288013	BI288013 UI-R-BT1-hni-h-09-d-UI.s2 UI-R-BT1 Rattus norvegicus cDNA clone UI-R-BT1-hni-h-09-d-UI 3', mRNA sequence [BI288013]	gb|BI288013	Rn.40911	-	Ybx2_predicted	Y box protein 2 (predicted)	-	-	[Human, Mouse]HomoloGene:22942

[0288]



No	Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Pathway Name	Gene Symbol	Gene Name	Summary	GeneRIF	Homology
252	153.48	70.70	2.17	XM_233490	Mycl1	PREDICTED: Rattus norvegicus v-myc myelocytomatosis viral oncogene homolog 1, lung carcinoma derived (avian) (Mycl1), mRNA [XM_233490]	ref|XM_233490|gb|AY3 94924|ens|ENSRNOT000 00019101|tc|NP860512	Rn.4140	-	Mycl1_mapped	v-myc myelocytomatosis viral oncogene homolog 1, lung carcinoma derived (avian) (mapped)	-	-	[Human, Mouse]Homoldene :3921
253	4100.87	1928.43	2.13	NM_001013941	Dusp1	Rattus norvegicus similar to 14-3-3 protein sigma (LOC298795), mRNA [NM_001013941]	ref|NM_001013941|ref|XM_232746|gb|XM_233000 856|ens|ENSRNOT00000043959	Rn.1619	Cell cycle	-	similar to 14-3-3 protein sigma	-	-	-
254	520.08	245.55	2.12	NM_053769	Dusp1	Rattus norvegicus dual specificity phosphatase 1 (Dusp1), mRNA [NM_053769]	ref|NM_053769|gb|X64 004|gb|S74351|ens|EN SRNOT00000005383	Rn.9826	MAPK signaling pathway	Dusp1	dual specificity phosphatase 1	catalyzes the phosphorylation and inactivation of MAP kinase, may be involved in insulin mediated signalling [RGD]	Anandamide-induced rapid MKP-1 expression switches off MAPK signal transduction in microglial cells activated by stimulation of pattern recognition receptors.// In vitro studies suggest the involvement of MKP-1 in the regulation of the monocyte/ AA-NAT signal// In pinealocytes, NE activates the beta-adrenergic receptor --> protein kinase A pathway to induce transcription and translation of MKP-1 and the alpha-adrenergic receptor --> PKG pathway to prolong the stimulated responses through stability of the MKP-1// induction of MKP-1 by hydrogen peroxide is mediated by the MAP kinase-AP-1 pathway; MKP-1 is involved in cellular defense against oxidative stress-induced apoptosis of mesangial cells// Increase in expression by acute LSD administration of MKP-1 suggests that LSD activates the MAP (mitogen activated protein) kinase pathway// Osmotic regulation of insulin-induced expression of this enzyme is observed in HeLE rat hepatoma cells. (MKP-1)	[Human, Mouse]Homoldene :3254
255	277.48	138.27	2.01	XM_345751	LOC366764	Rattus norvegicus similar to immunoglobulin heavy chain variable region (LOC366764), mRNA [XM_345751]	gb|XM_345751	-	-	RGD1560106_predicted	similar to immunoglobulin heavy chain variable region (predicted)	-	-	[Mouse]Hommo16Gene:83718

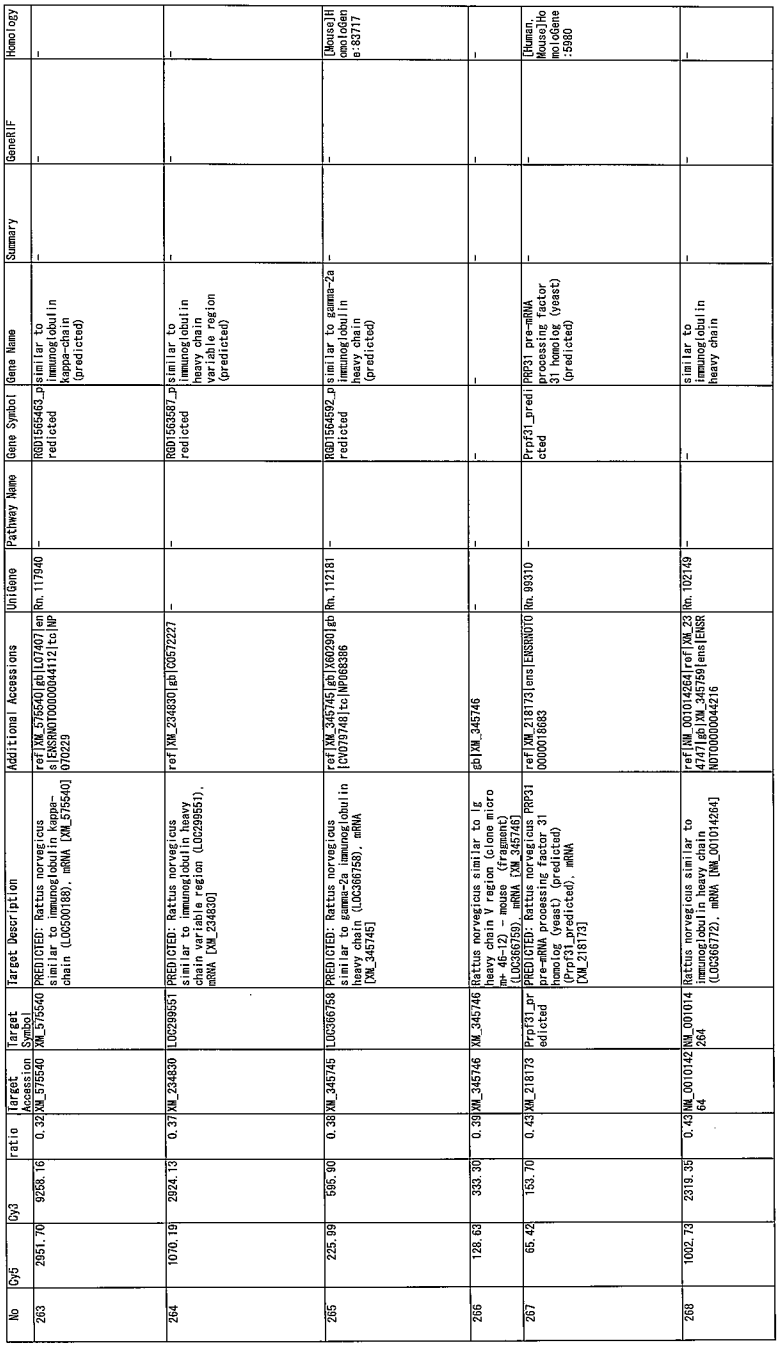
[0289] Light Touch群と比較してTickling群で0.5倍未満の発現を認めた唾液腺(Sg)の遺伝子のアノテーションを下記表35に示す。

[表35]

表35 T-Sg(Cy5) v.s. L-Sg(Cy3) :down regulation(Cy5<Cy3)

No	Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Pathway Name	Gene Symbol	Gene Name	Summary	GeneRIF	Homology
256	184.50	1054.20	0.18	LO7402	LO7402	Rattus norvegicus (hybridoma 57R-2) immunoglobulin rearranged gamma-chain mRNA variable (V) region, partial cds [LO7402]	gb|LO7402|gb|S64527|gb|Z75901	Rn.119901	-	-	-	-	-	-
257	100.15	386.01	0.26	XM_234661	LOC314509	PREDICTED: Rattus norvegicus similar to single chain Fv antibody fragment scFv 7-10A (LOC314509), mRNA [XM_234661]	ref|XM_234661|ens|ENSRNOT0 0000048010	Rn.110660	-	-	similar to single chain Fv antibody fragment scFv 7-10A	-	-	[Mouse]Homologene:83658
258	240.84	829.28	0.29	Z93368	Z93368	R.norvegicus mRNA for immunoglobulin variable region (clone ERF2.67) [Z93368]	gb|Z93368|tc|NP968880	Rn.110663	-	-	-	-	-	-
259	627.99	2146.31	0.29	XM_234749	LOC299469	PREDICTED: Rattus norvegicus similar to Ig heavy chain precursor V region (Id85.7) - mouse (fragment) (LOC299469), mRNA [XM_234749]	ref|XM_234749|ref|XM_23463 0|ref|XM_345756|gb|XM_2347 51	-	-	RGD1560447_predicted	similar to Ig heavy chain precursor V region (Id85.7) - mouse (fragment) (predicted)	-	-	-
260	303.66	1021.59	0.30	XM_345756	LOC366769	PREDICTED: Rattus norvegicus similar to BMK3 (LOC366769), mRNA [XM_345756]	ref|XM_345756|ens|ENSRNOT0 0000051539	Rn.126669	-	RGD1560892_predicted	similar to BMK3 (predicted)	-	-	[Mouse]Homologene:85357
261	51.49	172.33	0.30	Z93360	Z93360	R.norvegicus mRNA for immunoglobulin variable region (clone ERF1.25). [Z93360]	gb|Z93360|tc|NP968898	Rn.10956	-	-	immunoglobulin delta heavy chain constant region	-	-	-
262	2295.84	7368.70	0.31	ENSRNOT0000043097	ENSRNOT0000043097	Unknown	ens|ENSRNOT00000043097	-	-	-	-	-	-	-

[0290]

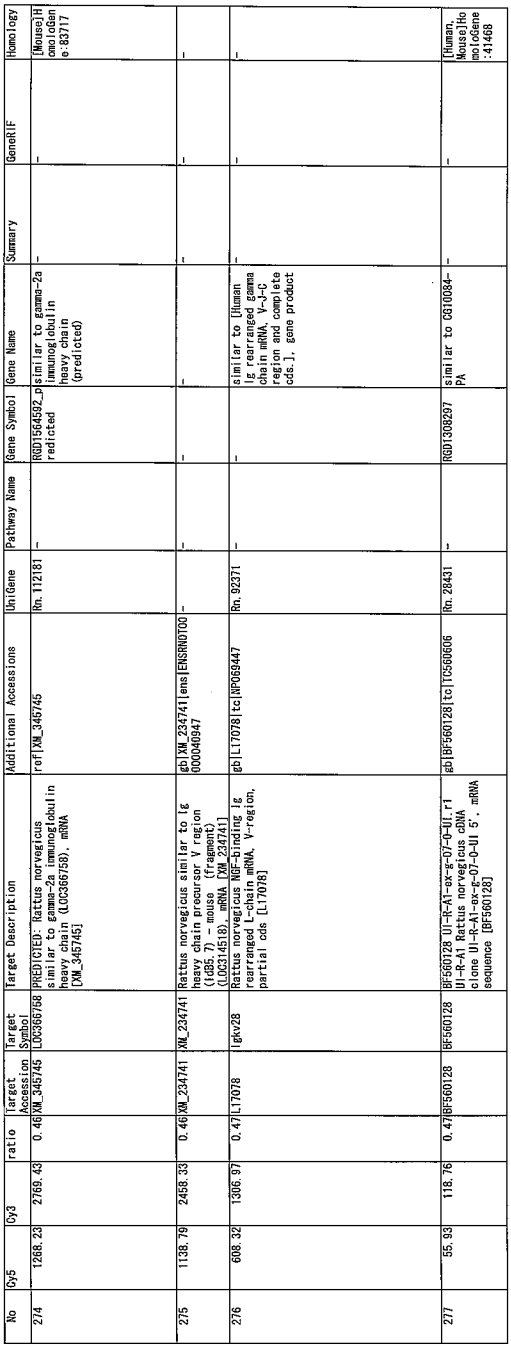


No	Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Pathway Name	Gene Symbol	Gene Name	Summary	GeneRIF	Homology
263	2951.70	9258.16	0.32	XM_576540	XM_576540	PREDICTED: Rattus norvegicus similar to immunoglobulin kappa-chain (LOC500188), mRNA [XM_576540]	ref|XM_576540|gb|LO7407|ensembl|ENSRNOT00000044172|tc|NP070229	Rn.117940	-	RGD1565463_predicted	similar to immunoglobulin Kappa-chain (predicted)	-	-	-
264	1070.19	2924.13	0.37	XM_234830	LOC299551	PREDICTED: Rattus norvegicus similar to immunoglobulin heavy chain variable region (LOC299551), mRNA [XM_234830]	ref|XM_234830|gb|O6572227	-	-	RGD1563587_predicted	similar to immunoglobulin heavy chain variable region (predicted)	-	-	-
265	225.99	986.90	0.38	XM_345745	LOC366758	PREDICTED: Rattus norvegicus similar to gamma-2a immunoglobulin heavy chain (LOC367758), mRNA [XM_345745]	ref|XM_345745|gb|X60290|gb|CV079748|tc|WP068386	Rn.112181	-	RGD1564592_predicted	similar to gamma-2a immunoglobulin heavy chain (predicted)	-	-	[Mouse]Homologene:83717
266	128.63	333.30	0.39	XM_345746	XM_345746	Rattus norvegicus similar to Ig heavy chain V region (clone micro m- 46-12) - mouse (fragment) (LOC367759), mRNA [XM_345746]	gb|XM_345746	-	-	-	-	-	-	-
267	65.42	153.70	0.43	XM_218173	Prp31_predicted	PREDICTED: Rattus norvegicus PRP31 pre-mRNA processing factor 31 homolog (yeast) (predicted), mRNA [XM_218173]	ref|XM_218173|ens|ENSRNOT00000018683	Rn.99310	-	Prp31_predicted	PRP31 pre-mRNA processing factor 31 homolog (yeast) (predicted)	-	-	[Human, Mouse]Homologene:5980
268	1002.73	2319.35	0.43	NM_001014264	NM_001014264	Rattus norvegicus similar to immunoglobulin heavy chain (LOC366772), mRNA [NM_001014264]	ref|NM_001014264|ref|XM_234741|gb|XM_345759|ens|ENSRNOT00000044216	Rn.102149	-	-	similar to immunoglobulin heavy chain	-	-	-

[0291]

No	Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Pathway Name	Gene Symbol	Gene Name	Summary	GeneRIF	Homology
269	67.71	153.03	0.44	BE098883	BE098883	BE098883 UI-R-BJ1-ate-h-09-0-UI.s1 UI-R-BJ1 Rattus norvegicus cDNA clone UI-R-BJ1-ate-h-09-0-UI 3', mRNA sequence [BE098883]	gb|BE098883|gb|AI102264|gb|AI504250	Rn.15951	-	Dhx57	DEAH (Asp-Glu-Ala-Asp/His) box polypeptide 57	-	-	[Human, Mouse]HomoloGene:56267
270	582.66	1314.22	0.44	XM_234676	LOC314512	PREDICTED: Rattus norvegicus similar to immunoglobulin heavy chain (LOC314512), mRNA [XM_234676]	ref|XM_234676|ref|XM_345748|gb|M84149	Rn.110661	-	RGD1565780_predicted	similar to immunoglobulin heavy chain (predicted)	-	-	-
271	2276.00	5079.18	0.45	XM_231999	LOC297260	PREDICTED: Rattus norvegicus similar to Ig variable region, light chain (LOC297260), mRNA [XM_231999]	ref|XM_231999|ref|XM_578306|ref|XM_578344	-	-	RGD1560632_predicted	similar to Ig variable region, light chain (predicted)	-	-	-
272	169.57	378.19	0.45	NM_053348	Fetub	Rattus norvegicus fetuin beta (Fetub), mRNA [NM_053348]	ref|NM_053348|gb|AJ242926|gb|BC079508|ens|ENSRNOT000000046199	Rn.2464	-	Fetub	fetuin beta	inhibits insulin receptor tyrosine kinase activity; protease inhibitory activities; developmentally regulates calcium metabolism and osteogenesis [RGD]	-	[Human, Mouse]HomoloGene:8660
273	81.55	179.22	0.46	BC092624	BC092624	Rattus norvegicus ubiquitin specific protease 33 (predicted), mRNA (cDNA clone MGC:109313 IMAGE:7314029), complete cds. [BC092624]	gb|BC092624|gb|AW142914|tc|TC536202	Rn.163825	-	Usp33	ubiquitin specific peptidase 33	-	-	[Human, Mouse]HomoloGene:8996

[0292]



No	Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Pathway Name	Gene Symbol	Gene Name	Summary	GeneRIF	Homology
274	1268.23	2769.43	0.46	XM_345745	LOC366768	PREDICTED: Rattus norvegicus similar to gamma-2a immunoglobulin heavy chain (LOC366768), mRNA [XM_345745]	ref|XM_345745	Rn.112181	-	RGD1564592_predicted	similar to gamma-2a immunoglobulin heavy chain (predicted)	-	-	[Mouse]Homoloden e:83717
275	1138.79	2458.33	0.46	XM_234741	XM_234741	Rattus norvegicus similar to Ig heavy chain precursor V region (1d85.7) - mouse (fragment) (LOC314518), mRNA [XM_234741]	gb|XM_234741|ens|ENSRNOT00000040947	-	-	-	-	-	-	-
276	608.32	1306.97	0.47	L17078	Igkv28	Rattus norvegicus MGF-binding Ig rearranged L-chain mRNA, V-region, partial cds [L17078]	gb|L17078|tc|NP069447	Rn.92371	-	-	similar to [Human Ig rearranged gamma chain mRNA, V-J-C region and complete cds.], gene product	-	-	-
277	55.93	118.76	0.47	BF560128	BF560128	BF560128 UI-R-A1-ax-g-07-0-UI.r1 UI-R-A1 Rattus norvegicus cDNA clone UI-R-A1-ax-g-07-0-UI 5', mRNA sequence [BF560128]	gb|BF560128|tc|TC560606	Rn.28431	-	RGD1308297	similar to C610084--PA	-	-	[Human, Mouse]HomoloGene:41468

[0293] なお、表20～35中の「No.」は、上記表2中の「No.」に対応している。

[0294] Tickling群において末梢血液で２倍超の発現を認める遺伝子は、Light Touch群と比較した場合は41遺伝子存在し、そのうち未知遺伝子が12、機能推定あるいは構造類似している遺伝子は10、部分配列である遺伝子は５つであった。一方、対照群と比較した場合は10遺伝子存在し、そのうち１遺伝子が未知遺伝子、２遺伝子が機能推定あるいは構造類似している遺伝子であった。

末梢血液で0.5倍未満の発現を認める遺伝子は、Light Touch群と比較した場合は30遺伝子、対照群と比較した場合は２遺伝子存在した。同様に発現差を認める遺伝子をカウントすると、視床下部で２倍超の発現を認める遺伝子は、Light Touch群と比較した場合は５遺伝子、対照群と比較した場合は13遺伝子存在し、0.5倍未満の発現を認める遺伝子は、Light Touch群と比較した場合は30遺伝子、対照群と比較した場合は11遺伝子存在した。また、線条体では２倍超の発現を認める遺伝子は、Light Touch群と比較した場合は３遺伝子、対照群と比較した場合は８遺伝子存在し、0.5倍未満の発現を認める遺伝子は、Light Touch群と比較した場合は８遺伝子、対照群と比較した場合は12遺伝子存在した。唾液腺では、対照群と比較した場合に発現差を認める遺伝子が多く、２倍超の発現を認める遺伝子は161、0.5倍未満の発現を認める遺伝子は143存在した。Light Touch群と比較した場合は、それぞれ21遺伝子、22遺伝子であった。

[0295] 注目すべき遺伝子としては、Ticklingにより視床下部でUp-regulateされたGalp、Slc6a3、Down-regulateされたChrna3、Slc5a7、Slc18a3、Avp、線条体でDown-regulateされたCck、唾液腺でUp-regulateされたAmy1、Klks3、Ton、Klk12、Ngfg、Down-regulateされたFetub、Serpina1等がある。

[0296] ２－１－４－３．クラスタリング解析

いずれか２組の解析におけるCy3およびCy5の信号強度が50以上あったプローブは26,075遺伝子(トランスクリプトを含む)存在し、これらをクラスタリングした像を図47に示し、少なくとも２組の解析において２倍超あるいは0.5倍未満の発現差を認めたプローブのクラスタリング像を図48に示した。発現差の程度は、TicklingによりUp-regulateされた遺伝子(トランスクリプトを含む)は赤色、Down-regulateされた遺伝子(トランスクリプトを含む)は緑色の濃さの程度で表した(カラーバーは図中右側に表示)。また、信号強度が低く(50未満)、発現差を表示できない遺伝子(トランスクリプトを含む)は灰色で表示した。

[0297] 対照群あるいはLight Touch群と比較してTickling群の唾液腺組織でそれぞ

れ1.5倍超の発現差を認めた593プローブと171プローブのクラスタリング像を図49と図50に示した。また、両比較において発現差を認めた遺伝子(トランスクリプトを含む)の数を図51のベン図に示したが、共通して発現差を認める遺伝子は48存在した。一方、両比較でそれぞれ1/1.5倍未満の発現差を認めた525プローブと166プローブのクラスタリング像を図52と図53に示し、図54のベン図には両比較において発現差を認めた遺伝子(トランスクリプトを含む)数を示したが、共通して発現差を認めた遺伝子は56存在した。

[0298] 対照群あるいはLight Touch群と比較してTickling群の視床下部組織でそれぞれ1.5倍超の発現差を認めた157プローブと136プローブのクラスタリング像を図55と図56に示した。また、両比較において発現差を認めた遺伝子(トランスクリプトを含む)の数を図57のベン図に示したが、共通して発現差を認める遺伝子は39存在した。一方、両比較でそれぞれ1/1.5倍未満の発現差を認めた57プローブと185プローブのクラスタリング像を図58と図59に示し、図60のベン図には両比較において発現差を認めた遺伝子(トランスクリプトを含む)数を示したが、共通して発現差を認めた遺伝子は11存在した。

[0299] 2-1-4-4. オントロジー解析

当解析は、対照群あるいはLight Touch群と比較してTickling群で1.5倍超あるいは1/1.5倍未満の発現差を認める遺伝子を対象とし、該条件にて抽出される視床下部あるいは線条体の遺伝子と共通する末梢血液の遺伝子と、唾液腺、視床下部の遺伝子に関し行なった。抽出されたプローブ数と遺伝子数は下記表36に示す。

[表36]

表36 抽出された遺伝子の数

組織	刺激の組み合わせ	CあるいはLに対する発現量	プローブ数	遺伝子数	GO Term
唾液腺	T-C	UP	593	421	表37
		DOWN	525	349	表38
	T-L	UP	171	107	表39
		DOWN	166	104	表40
視床下部	T-C	UP	157	104	表41
		DOWN	57	39	表42
	T-L	UP	136	98	表43
		DOWN	185	113	表44

[0300] DNAチップ上のプローブと遺伝子(GeneID)との対応付けは、Agilent社の提供する情報とNCBI Entrez(http://www.ncbi.nlm.nih.gov/)の情報に基づいて行なった。GeneIDとGOの対応付けはBiNGO (http://www.psb.ugent.be.cbd/papers/BiNGO/)を用いて行い、GOの階層図はCytoscape (http://www.cytoscape.org/)を用いて描画した。各GO Termについて、Agilent社製Whole Rat Genome Microarray上の全遺伝子中での出現頻度に比べて抽出遺伝子群中での出現頻度が高くなっているかHypergeometric testを用いて有意水準FDR(False Discovery rate)<0.1で検定した。該検定で有意と判定されたGO Termを抽出遺伝子群に特徴的なGOとした。表37から表44に、各試料で抽出された遺伝子(表36参照)のGO解析結果を示す。

[表37]

表37　Cに対しTで発現増加した唾液腺の遺伝子のGO解析結果

	FDR 0.01 以下
	FDR 0.05～0.01
MF:	Molecular Function
CC:	Cellular Component
BP:	Biological Process

分類	GO ID	Description	P値	遺伝子数	
				総数	変動した数
MF	17017	MAP kinase phosphatase activity	6.21E-04	4	4
MF	4293	tissue kallikrein activity	8.94E-04	9	5
CC	5576	extracellular region	1.34E-02	1718	69
CC	44421	extracellular region part	1.34E-02	1622	66
CC	5615	extracellular space	1.34E-02	1567	64
BP	35051	cardiac cell differentiation	1.62E-02	4	3
BP	6629	lipid metabolism	1.62E-02	478	27
BP	42416	dopamine biosynthesis	2.45E-02	5	3
BP	51057	positive regulation of small GTPase mediated signal transduction	2.45E-02	5	3
BP	44255	cellular lipid metabolism	2.45E-02	394	23
BP	42417	dopamine metabolism	6.19E-02	15	4
BP	8202	steroid metabolism	6.51E-02	132	11
BP	35295	tube development	7.19E-02	95	9
CC	5624	membrane fraction	7.19E-02	605	29

[表38]

表38 CIに対しLTで発現減少した唾液腺の遺伝子のGO解析結果

	FDR 0.01 以下
	FDR 0.05～0.01
MF:	Molecular Function
CC:	Cellular Component
BP:	Biological Process

分類	GO ID	Description	P値	遺伝子数	
				総数	変動した数
CC	5576	extracellular region	5.73E-04	1718	66
MF	3779	actin binding	5.73E-04	151	15
BP	9225	nucleotide-sugar metabolism	9.00E-04	11	5
CC	5615	extracellular space	9.63E-04	1567	60
CC	44421	extracellular region part	1.12E-03	1622	61
MF	8092	cytoskeletal protein binding	2.86E-02	255	16
BP	42060	wound healing	9.33E-02	106	9

[表39]

表39 LIに対しTで発現増加した唾液腺の遺伝子のGO解析結果

	FDR 0.01 以下
	FDR 0.05~0.01
MF:	Molecular Function
CC:	Cellular Component
BP:	Biological Process

分類	GO ID	Description	P値	遺伝子数	
				総数	変動した数
MF	17017	MAP kinase phosphatase activity	9.41E-04	4	3
MF	4556	alpha-amylase activity	6.28E-02	4	2
CC	44421	extracellular region part	6.28E-02	1622	23
MF	16160	amylase activity	6.28E-02	5	2
MF	16846	carbon-sulfur lyase activity	6.28E-02	5	2
MF	8138	protein tyrosine/serine/threonine phosphatase activity	6.28E-02	24	3
CC	5615	extracellular space	6.28E-02	1567	22
BP	6534	cysteine metabolism	6.28E-02	6	2
MF	16829	lyase activity	6.28E-02	105	5
CC	5576	extracellular region	6.28E-02	1718	23

[表40]

表40 Lに対しTで発現減少した唾液腺の遺伝子のGO解析結果

FDR 0.01 以下
FDR 0.05～0.01
MF: Molecular Function CC: Cellular Component BP: Biological Process

分類	GO ID	Description	P値	遺伝子数	
				総数	変動した数
BP	15031	protein transport	2.33E-02	365	9
BP	45184	establishment of protein localization	2.33E-02	391	9
BP	8104	protein localization	2.59E-02	418	9
BP	6886	intracellular protein transport	5.83E-02	289	7
MF	158	protein phosphatase type 2A activity	7.25E-02	8	2
BP	51169	nuclear transport	7.73E-02	88	4
MF	5515	protein binding	7.91E-02	3356	27
BP	6913	nucleocytoplasmic transport	7.91E-02	97	4
BP	6605	protein targeting	7.91E-02	170	5
BP	46907	intracellular transport	7.91E-02	466	8
BP	51649	establishment of cellular localization	7.91E-02	476	8
BP	51641	cellular localization	7.91E-02	480	8
MF	4721	phosphoprotein phosphatase activity	7.91E-02	109	4
BP	6606	protein import into nucleus	9.27E-02	56	3
BP	51170	nuclear import	9.27E-02	56	3

[表41]

表41　Cに対しTで発現増加した視床下部の遺伝子のGO解析結果

	FDR 0.01 以下
	FDR 0.05～0.01
MF:	Molecular Function
CC:	Cellular Component
BP:	Biological Process

分類	GO ID	Description	P値	遺伝子数	
				総数	変動した数
BP	51235	maintenance of localization	9.18E-02	17	3
BP	42992	negative regulation of transcription factor import into nucleus	9.18E-02	6	2
BP	42994	cytoplasmic sequestering of transcription factor	9.18E-02	6	2
BP	51220	cytoplasmic sequestering of protein	9.18E-02	6	2
BP	42308	negative regulation of protein import into nucleus	9.18E-02	6	2
BP	46823	negative regulation of nucleocytoplasmic transport	9.18E-02	7	2
BP	51224	negative regulation of protein transport	9.18E-02	7	2

[表42]

表42 CIに対しLTで発現減少した視床下部の遺伝子のGO解析結果

	FDR 0.01 以下
	FDR 0.05~0.01

MF: Molecular Function
CC: Cellular Component
BP: Biological Process

分類	GO ID	Description	P値	遺伝子数	
				総数	変動した数
BP	42475	odontogenesis (sensu Vertebrata)	8.96E-02	19	2
MF	5179	hormone activity	8.96E-02	92	3
BP	42476	odontogenesis	8.96E-02	27	2
MF	5277	acetylcholine transporter activity	8.96E-02	1	1
BP	351	assembly of spliceosomal tri-snRNP U4/U6.U5	8.96E-02	1	1
MF	5183	luteinizing hormone-releasing factor activity	8.96E-02	1	1
BP	8292	acetylcholine biosynthesis	8.96E-02	1	1
MF	46906	tetrapyrrole binding	8.96E-02	39	2
MF	20037	heme binding	8.96E-02	39	2
BP	51234	establishment of localization	8.96E-02	1974	10
BP	51179	localization	8.96E-02	1999	10
BP	6374	nuclear mRNA splicing via U2-type spliceosome	8.96E-02	2	1
MF	16748	succinyltransferase activity	8.96E-02	2	1
BP	7183	SMAD protein heteromerization	8.96E-02	2	1
MF	3870	5-aminolevulinate synthase activity	8.96E-02	2	1
BP	16199	axon midline choice point recognition	8.96E-02	2	1
MF	16749	N-succinyltransferase activity	8.96E-02	2	1
BP	50891	body fluid osmoregulation	8.96E-02	2	1
BP	16198	axon choice point recognition	8.96E-02	2	1
BP	18987	osmoregulation	9.41E-02	3	1
BP	8291	acetylcholine metabolism	9.41E-02	3	1
BP	15870	acetylcholine transport	9.41E-02	3	1
MF	43121	neurotrophin binding	9.41E-02	3	1
BP	7181	transforming growth factor beta receptor complex assembly	9.41E-02	3	1
BP	7184	SMAD protein nuclear translocation	9.41E-02	3	1
BP	244	assembly of spliceosomal tri-snRNP	9.41E-02	3	1

[0301]

分類	GO ID	Description	P値	遺伝子数	
				総数	変動した数
BP	6576	biogenic amine metabolism	9.41E-02	59	2
BP	7178	transmembrane receptor protein serine/threonine kinase signaling pathway	9.41E-02	63	2
MF	5275	amine transporter activity	9.41E-02	67	2
MF	19841	retinol binding	9.41E-02	4	1
MF	15220	choline transporter activity	9.41E-02	4	1
BP	15669	gas transport	9.41E-02	4	1
BP	15671	oxygen transport	9.41E-02	4	1
CC	46540	U4/U6 x U5 tri-snRNP complex	9.41E-02	4	1
MF	15349	thyroid hormone transporter activity	9.41E-02	4	1
BP	387	spliceosomal snRNP biogenesis	9.41E-02	4	1
BP	8040	axon guidance	9.41E-02	68	2
BP	7167	enzyme linked receptor protein signaling pathway	9.49E-02	211	3

[表43]

表43 Lに対しLTで発現増加した視床下部の遺伝子のGO解析結果

FDR 0.01 以下
FDR 0.05~0.01

MF: Molecular Function
CC: Cellular Component
BP: Biological Process

分類	GO ID	Description	P値	遺伝子数	
				総数	変動した数
BP	7631	feeding behavior	8.12E-06	41	7
MF	5184	neuropeptide hormone activity	5.30E-05	20	5
MF	5179	hormone activity	5.30E-05	92	8
BP	7218	neuropeptide signaling pathway	8.61E-04	63	6
BP	42401	biogenic amine biosynthesis	4.88E-03	27	4
BP	42423	catecholamine biosynthesis	4.88E-03	10	3
BP	42398	amino acid derivative biosynthesis	8.36E-03	33	4
BP	42136	neurotransmitter biosynthesis	1.09E-02	14	3
BP	9072	aromatic amino acid family metabolism	1.20E-02	15	3
BP	9308	amine metabolism	1.36E-02	293	9
BP	7268	synaptic transmission	1.63E-02	311	9
MF	16714	oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, reduced pteridine as one donor, and incorporation of one atom of oxygen	1.63E-02	4	2
BP	46717	acid secretion	1.63E-02	4	2
BP	6807	nitrogen compound metabolism	1.63E-02	314	9
BP	7267	cell-cell signaling	1.81E-02	556	12
BP	6584	catecholamine metabolism	1.81E-02	21	3
BP	18958	phenol metabolism	1.81E-02	21	3
BP	6725	aromatic compound metabolism	1.91E-02	93	5
BP	42416	dopamine biosynthesis	1.91E-02	5	2
BP	19226	transmission of nerve impulse	1.91E-02	337	9
BP	1505	regulation of neurotransmitter levels	2.19E-02	101	5
BP	44271	nitrogen compound biosynthesis	2.19E-02	58	4
BP	9309	amine biosynthesis	2.19E-02	58	4
MF	8504	monoamine transporter activity	2.19E-02	6	2
BP	15844	monoamine transport	2.19E-02	6	2
BP	6576	biogenic amine metabolism	2.19E-02	59	4

[0302]

分類	GO ID	Description	P値	遺伝子数	
				総数	変動した数
BP	6570	tyrosine metabolism	2.88E-02	7	2
MF	5102	receptor binding	3.08E-02	540	11
BP	42133	neurotransmitter metabolism	3.41E-02	31	3
MF	15238	drug transporter activity	3.44E-02	8	2
BP	7610	behavior	4.98E-02	258	7
MF	16247	channel regulator activity	7.56E-02	43	3
BP	6575	amino acid derivative metabolism	7.56E-02	90	4
BP	1659	thermoregulation	7.56E-02	13	2
BP	46928	regulation of neurotransmitter secretion	7.56E-02	14	2
MF	15457	auxiliary transport protein activity	7.56E-02	47	3
BP	42417	dopamine metabolism	7.56E-02	15	2
BP	51223	regulation of protein transport	7.56E-02	15	2
CC	44427	chromosomal part	7.56E-02	101	4
MF	16829	lyase activity	7.56E-02	105	4
MF	8493	tetracycline transporter activity	7.56E-02	1	1
BP	19637	organophosphate metabolism	7.56E-02	1	1
MF	4511	tyrosine 3-monooxygenase activity	7.56E-02	1	1
MF	15520	tetracycline:hydrogen antiporter activity	7.56E-02	1	1
CC	31465	Cul4B-RING ubiquitin ligase complex	7.56E-02	1	1
BP	6113	fermentation	7.56E-02	1	1
MF	8473	ornithine cyclodeaminase activity	7.56E-02	1	1
BP	15842	synaptic vesicle amine transport	7.56E-02	1	1
MF	1874	alkyl sulfatase activity	7.56E-02	1	1
BP	51177	meiotic sister chromatid cohesion	7.56E-02	1	1
MF	30338	CMP-N-acetylneuraminate monooxygenase activity	7.56E-02	1	1
MF	5329	dopamine transporter activity	7.56E-02	1	1
MF	4611	phosphoenolpyruvate carboxykinase activity	7.56E-02	1	1
BP	7065	male meiosis sister chromatid cohesion	7.56E-02	1	1
BP	6114	glycerol biosynthesis	7.56E-02	1	1
BP	46327	glycerol biosynthesis from pyruvate	7.56E-02	1	1
BP	46173	polyol biosynthesis	7.56E-02	1	1
BP	50482	arachidonic acid secretion	7.56E-02	1	1
CC	31464	Cul4A-RING ubiquitin ligase complex	7.56E-02	1	1
MF	19788	NEDD8 ligase activity	7.56E-02	1	1
MF	5330	dopamine:sodium symporter activity	7.56E-02	1	1
MF	4416	hydroxyacylglutathione hydrolase activity	7.56E-02	1	1

[0303]

分類	GO ID	Description	P値	遺伝子数	
				総数	変動した数
CC	31467	Cul7-RING ubiquitin ligase complex	7.56E-02	1	1
BP	7066	female meiosis sister chromatid cohesion	7.56E-02	1	1
MF	30354	melanin-concentrating hormone activity	7.56E-02	1	1
MF	15307	drug:hydrogen antiporter activity	7.56E-02	1	1
BP	1706	endoderm formation	7.56E-02	1	1
MF	4167	dopachrome isomerase activity	7.56E-02	1	1
MF	42895	antibiotic transporter activity	7.56E-02	1	1
CC	5900	oncostatin-M receptor complex	7.56E-02	1	1
MF	4613	phosphoenolpyruvate carboxykinase (GTP) activity	7.56E-02	1	1
BP	15904	tetracycline transport	7.56E-02	1	1
MF	4398	histidine decarboxylase activity	7.56E-02	1	1
BP	6585	dopamine biosynthesis from tyrosine	7.56E-02	1	1
MF	16831	carboxy-lyase activity	7.87E-02	19	2
BP	46822	regulation of nucleocytoplasmic transport	7.87E-02	19	2
BP	6520	amino acid metabolism	7.87E-02	178	5
BP	6519	amino acid and derivative metabolism	8.48E-02	256	6

[表44]

表44 Lに対してで発現減少した視床下部の遺伝子のGO解析結果

分類	GO ID	Description	P値	遺伝子数	
				総数	変動した数
MF	5509	calcium ion binding	4.26E-04	361	14
MF	43169	cation binding	6.84E-03	932	20
BP	7267	cell-cell signaling	4.38E-02	556	13
MF	43167	ion binding	4.38E-02	1252	21
MF	46872	metal ion binding	4.38E-02	1252	21
BP	8589	regulation of smoothened signaling pathway	4.38E-02	4	2
BP	42475	odontogenesis (sensu Vertebrata)	4.38E-02	19	3
BP	9653	morphogenesis	4.38E-02	822	16
BP	7399	nervous system development	6.78E-02	620	13
BP	19226	transmission of nerve impulse	6.78E-02	337	9
BP	1505	regulation of neurotransmitter levels	6.78E-02	101	5
MF	4890	GABA-A receptor activity	6.78E-02	27	3
BP	42476	odontogenesis	6.78E-02	27	3
MF	5488	binding	6.78E-02	5647	57
BP	48731	system development	6.78E-02	649	13
MF	16917	GABA receptor activity	9.11E-02	31	3
CC	5886	plasma membrane	9.12E-02	1521	22
MF	4697	protein kinase C activity	9.33E-02	9	2
MF	15269	calcium-activated potassium channel activity	9.33E-02	9	2

FDR 0.01 以下
FDR 0.05～0.01

MF: Molecular Function
CC: Cellular Component
BP: Biological Process

[0304] また、それぞれについてCytoscapeを用いて作図したGO階層図は、図62から図72に示した。なお、図61には色の濃淡とP値の関係を表した。色が濃いほどそのGO Termに割り当てられる有意性が高く、円の大きさが大きいほど割り当

てられる遺伝子数が多いこと示す。

[0305] 対照群と比較してTickling群の唾液腺で相対的に発現変動している遺伝子、およびLight Touch群と比較してTickling群の視床下部で相対的に発現変動している遺伝子のGO解析では、それぞれ新規ストレス指標探索、健康増進遺伝子探索のための遺伝子を特定することができた。

[0306] これらのGO解析で注目される唾液腺でUp-regulateされる遺伝子としては、機能上GO ID: 17017のMAPキナーゼ脱リン酸化酵素に割り当てられる４遺伝子(表45)、組織カリクレイン活性(GO ID: 4293)に割り当てられる５遺伝子(表46)、細胞外成分(GO ID: 5576, 44421, 5615)として割り当てられる67遺伝子(表47)、生物学経路として脂質代謝(GO ID: 6629, 44255)に割り当てられる９遺伝子(表48)、ドーパミン合成(GO ID: 42416)に割り当てられる３遺伝子(表49)が抽出された。Down-regulateされる遺伝子としては、機能上、アクチン結合(GO ID; 3779)に割り当てられる13遺伝子(表50)、細胞外に局在する成分(GO ID: 5576, 44421, 5615)として割り当てられる66遺伝子(表51)、生物学経路として核酸構成糖の代謝(GO ID: 9225)に割り当てられる２遺伝子(表52)が抽出された。

[0307] 視床下部でUp-regulateされる遺伝子としては、機能上、ホルモン活性(GO ID: 5184, 5179)に割り当てられる２遺伝子(表53)、モノアミントランスポーター(GO ID: 8504)に割り当てられる３遺伝子(表54)、受容体結合(GO ID: 5102)に割り当てられる４遺伝子(表55)、生物学的経路として食行動(GO ID: 7631)に割り当てられる６遺伝子(表56)、生体アミン合成(GO ID: 42401, 42426, 42416, 9309)に割り当てられる３遺伝子(表57)、生体アミン代謝(GO ID: 9308, 6584, 6576)に割り当てられる１遺伝子(表58)が抽出された。Down-regulateされる遺伝子としては、機能上、陽イオン結合(GO ID; 5509, 43169)に割り当てられる21遺伝子(表59)が抽出された。

[表45]

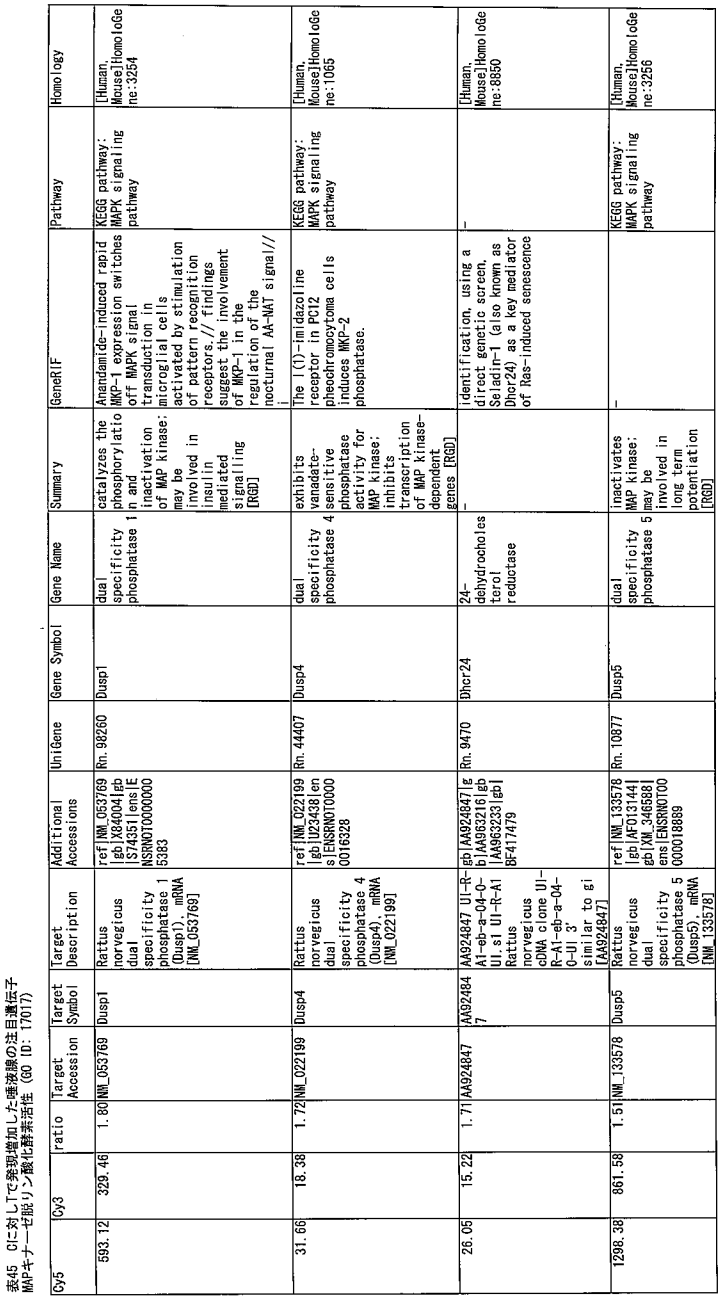


表45 Cに対して発現増加した唾液腺の注目遺伝子
MAPキナーゼ脳リン酸化酵素活性 (GO ID: 17017)

Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Gene Symbol	Gene Name	Summary	GeneRIF	Pathway	Homology
593.12	329.46	1.80	NM_053769	Dusp1	Rattus norvegicus dual specificity phosphatase 1 (Dusp1), mRNA [NM_053769]	ref|NM_053769 |gb|X84004|gb |S74351|ens|E NSRNOT0000000 5383	Rn.98260	Dusp1	dual specificity phosphatase 1	catalyzes the phosphorylation and inactivation of MAP kinase; may be involved in insulin mediated signalling [RGD]	Anandamide-induced rapid MKP-1 expression switches off MAPK signal transduction in microglial cells activated by stimulation of pattern recognition receptors.// findings suggest the involvement of MKP-1 in the regulation of the nocturnal AA-NAT signal// i	KEGG pathway: MAPK signaling pathway	[Human, Mouse]Homologene:3254
31.66	18.38	1.72	NM_022199	Dusp4	Rattus norvegicus dual specificity phosphatase 4 (Dusp4), mRNA [NM_022199]	ref|NM_022199 |gb|U23438|en s|ENSRNOT0000 0016328	Rn.44407	Dusp4	dual specificity phosphatase 4	exhibits vanadate-sensitive phosphatase activity for MAP kinase; inhibits transcription of MAP kinase-dependent genes [RGD]	The 1(1)-imidazoline receptor in PC12 pheochromocytoma cells induces MKP-2 phosphatase.	KEGG pathway: MAPK signaling pathway	[Human, Mouse]Homologene:1065
26.05	15.22	1.71	AA924847	AA924484 7	AA924847 UI-R-A1-eb-a-04-0-UI.s1 UI-R-A1 Rattus norvegicus cDNA clone UI-R-A1-eb-a-04-0-UI 3' similar to gi [AA924847]	gb|AA924847|gb |AA963216|gb |AA963233|gb| BF417479	Rn.9470	Dhcr24	24-dehydrocholesterol reductase	-	identification, using a direct genetic screen, Seladin-1 (also known as Dhcr24) as a key mediator of Ras-induced senescence	-	[Human, Mouse]Homologene:8850
1298.38	861.58	1.51	NM_133578	Dusp5	Rattus norvegicus dual specificity phosphatase 5 (Dusp5), mRNA [NM_133578]	ref|NM_133578 |gb|AF013144| |gb|AW_346588| ens|ENSRNOT00 000018869	Rn.10877	Dusp5	dual specificity phosphatase 5	inactivates MAP kinase; may be involved in long term potentiation [RGD]	-	KEGG pathway: MAPK signaling pathway	[Human, Mouse]Homologene:3256

[表46]

表46 Oに対しTで発現増加した嗅液膜の注目遺伝子
組織カリクレイン活性 (GO ID: 4293)

Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Gene Symbol	Gene Name	Summary	GeneRIF	Pathway	Homology
32731.46	2472.09	13.24	NM_175759	Klks3	Rattus norvegicus kallikrein, submaxillary gland S3 (Klks3), mRNA [NM_175759]	ref|NM_175759 |gb|M11566|gb |BC061771|ens |ENSRNOT00000 025723	Rn.34627	Klks3	kallikrein, submaxillary gland S3	a kallikrein-related serine protease: first isolated from the rat submaxillary gland; acts as a potent enzymatic vasoconstrictor [RGD]	-	-	-
70928.46	5776.93	12.26	NM_012677	Ton	Rattus norvegicus tonin (Ton), mRNA [NM_012677]	ref|NM_012677 |gb|M11565|gb |M23878|ens|E NSRNOT0000002 5701	Rn.9882	Ton	tonin	serine protease involved in generating the octapeptide angiotensin II from precursors [RGD]	tonin may play a role in the process of heart hypertrophy// expression in the rat brain and mediation of the central production of angiotensin II	-	-
1543.60	182.10	8.48	NM_0010053 82	Klk12	Rattus norvegicus glandular kallikrein 12, submandibular/ renal (Klk12), mRNA [NM_0010053 82]	ref|NM_0010053 82|gb|XM_218 567|gb|M19648 |ens|ENSRNOT0 0000025631	Rn.141980	Klk12	glandular kallikrein 12, submandibular/renal	-	-	-	[Human, Mouse]HomoloGene:81694
88887.34	13877.73	6.41	XM_214931	RGD:735032	PREDICTED: Rattus norvegicus kallikrein (LOC292872), mRNA [XM_214931]	ref|XM_214931 |gb|L33840|gb |M11564|ens|E NSRNOT0000002 5777	Rn.107068	-	kallikrein	a putative kallikrein-related serine protease first isolated from the rat submaxillary gland [RGD]	-	-	-

[0308]

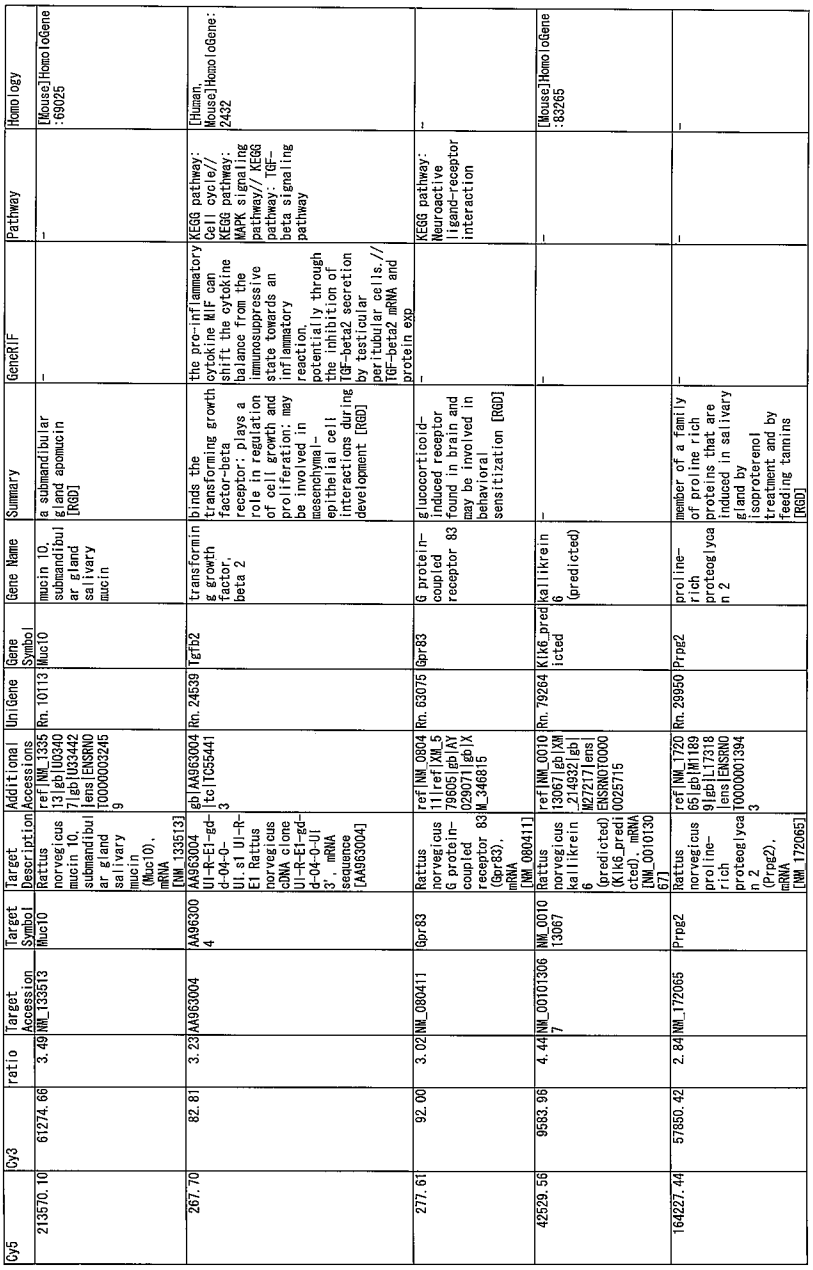
Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Gene Symbol	Gene Name	Summary	GeneRIF	Pathway	Homology
124036.40	40026.25	3.10	NM_031523	Ngfg	Rattus norvegicus nerve growth factor, gamma (Ngfg), mRNA [NM_031523]	ref|NM_031523 |gb|M11563|gb |X03560|gb|BC 078784	Rn.11331	Ngfg	nerve growth factor, gamma	a putative pancreatic kallikrein [RGD]	the the kallikrein-kinin system has roles in intramyocardial inflammation, endothelial dysfunction and oxidative stress in diabetic cardiomyopathy // PKA phosphorylation of Src mediates Rap1 activation in NGF and cAMP signaling	--	[Mouse]HomoloGene:83259

[表47]

表47 Cに対して発現増加した唾液腺の注目遺伝子
細胞外成分 (GO ID: 5576, 44421, 5615)

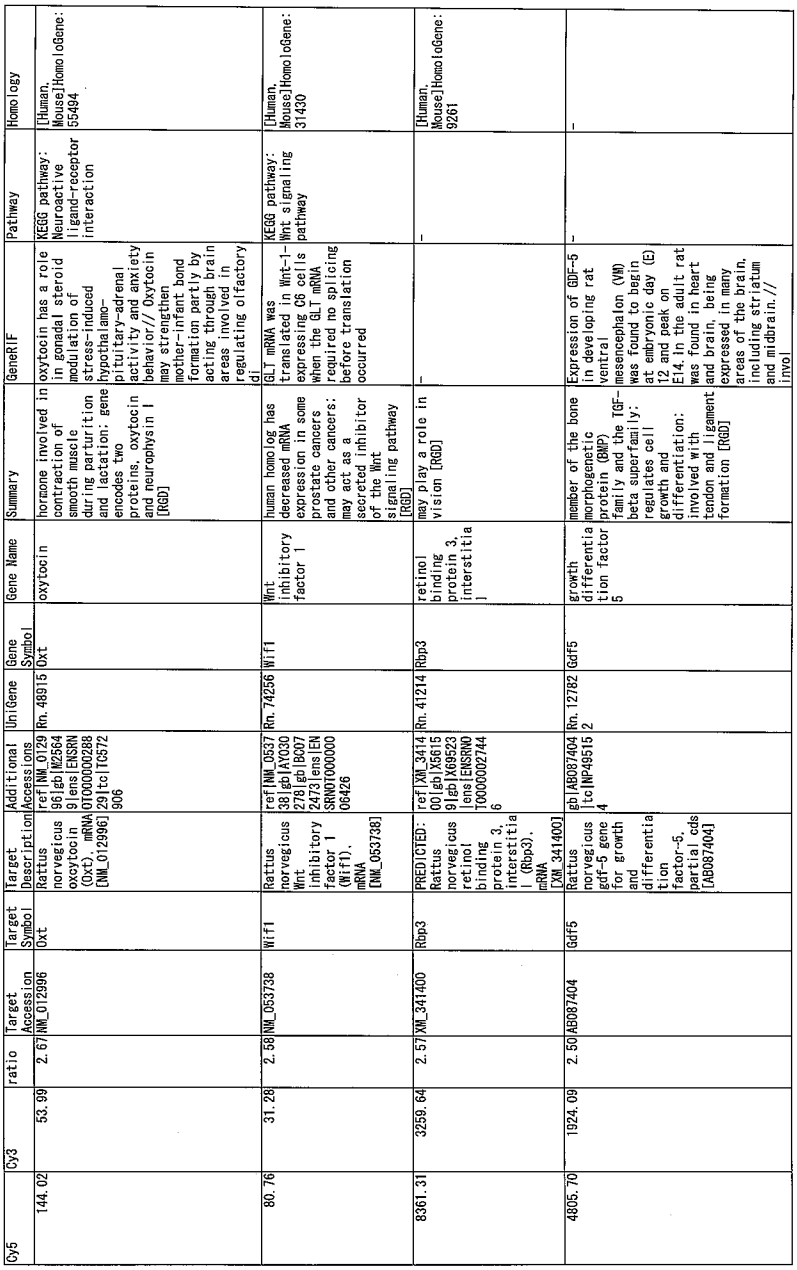
Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Gene Symbol	Gene Name	Summary	GeneRIF	Pathway	Homology
42529.56	9583.96	4.44	NM_00101306 7	NM_00103067	Rattus norvegicus kallikrein 6 (predicted) (Klk6_predicted), mRNA [NM_001013067]	ref|NM_001013067|gb|XM_214932|gb|M27217|ens|ENSRNOT00000025715	Rn.79264	Klk6_predicted	kallikrein 6 (predicted)	-	-	-	[Mouse]HomoloGene:83265
6218.28	1414.59	4.40	NM_012842	Egf	Rattus norvegicus epidermal growth factor (Egf), mRNA [NM_012842]	ref|NM_012842|gb|U04942|BC082042|gb|AW140863	Rn.6075	Egf	epidermal growth factor	binds the epidermal growth factor receptor; may play a role in MAP kinase mediated signaling pathways [RGD]	EGF-based signaling cascades phosphorylate Cavl and have roles in caveolae assembly// ERK1/2 mediates EGF-induced rapid Rb phosphorylation at Ser780 and Ser795// Neo-natal rats with intestinal injury have significantly lower levels of ileum EGF.// Linear	KEGG pathway: Cytokine-cytokine receptor interaction// KEGG pathway: Focal adhesion// KEGG pathway: Gap junction// KEGG pathway: MAPK signaling pathway// KEGG pathway: Regulation of actin cytoskeleton	[Human, Mouse]HomoloGene:1483
2022.83	528.42	3.83	XM_342575	Svs6_predicted	PREDICTED: Rattus norvegicus seminal vesicle secretion 6 (predicted) (Svs6_predicted), mRNA [XM_342575]	ref|XM_342575|ENSRNOT00000001851|tc|TC5189761|tc|TC518976	Rn.145207	Svs6_predicted	seminal vesicle secretion 6 (predicted)	-	-	-	[Mouse]HomoloGene:49347
165383.40	45178.89	3.66	NM_022708	Pip	Rattus norvegicus prolactin induced protein (Pip), mRNA [NM_022708]	ref|NM_022708|gb|AF054081|ens|ENSRNOT00000027015761|tc|TC541374	Rn.78367	Pip	prolactin induced protein	secretory protein localized to acinar cells of neonatal and adult submandibular and parotid glands, also expressed in sublingual glands [RGD]	-	-	[Human, Mouse]HomoloGene:1990

[0309]



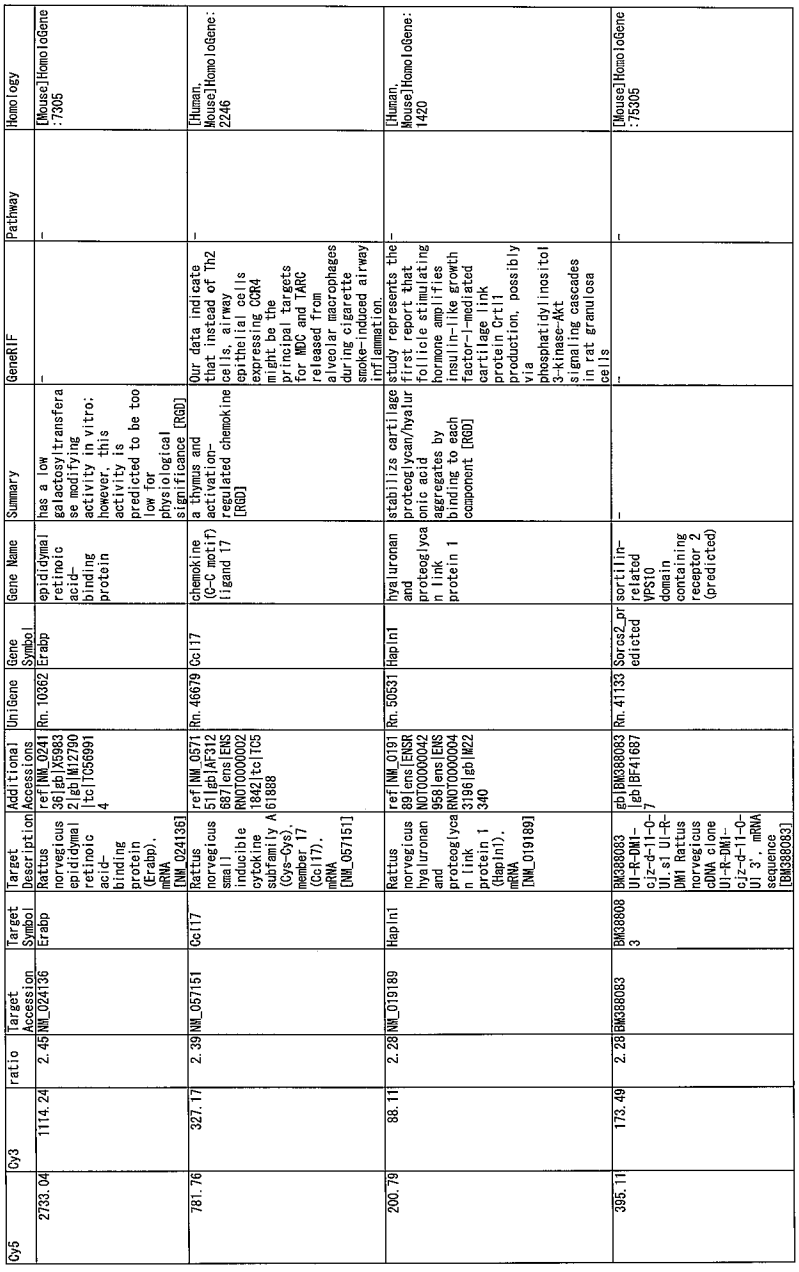
Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Gene Symbol	Gene Name	Summary	GeneRIF	Pathway	Homology
213570.10	61274.66	3.49	NM_133513	Muc10	Rattus norvegicus mucin 10, submandibular gland salivary mucin (Muc10), mRNA [NM_133513]	ref|NM_133513|gb|U03407|gb|U33442|ens|ENSRNOT00000032469	Rn.10113	Muc10	mucin 10, submandibular gland salivary mucin	a submandibular gland apomucin [RGD]	-	-	[Mouse]HomoloGene:69025
267.70	82.81	3.23	AA963004	AA963004	AA963004 UI-R-E1-gd-d-04-0-UI.s1 UI-R-E1 Rattus norvegicus cDNA clone UI-R-E1-gd-d-04-0-UI 3', mRNA sequence [AA963004]	gb|AA963004|tc|TC55441 3	Rn.24539	Tgfb2	transforming growth factor, beta 2	binds the transforming growth factor-beta receptor: plays a role in regulation of cell growth and proliferation; may be involved in mesenchymal-epithelial cell interactions during development [RGD]	the pro-inflammatory cytokine MIF can shift the cytokine balance from the immunosuppressive state towards an inflammatory reaction, potentially through the inhibition of TGF-beta2 secretion by testicular peritubular cells.// TGF-beta2 mRNA and protein exp	KEGG pathway: Cell cycle// KEGG pathway: MAPK signaling pathway// KEGG pathway: TGF-beta signaling pathway	[Human, Mouse]HomoloGene:2432
277.61	92.00	3.02	NM_080411	Gpr83	Rattus norvegicus G protein-coupled receptor 83 (Gpr83), mRNA [NM_080411]	ref|NM_080411|ref|XM_002907|gb|AY029071|gb|X_346815	Rn.63075	Gpr83	G protein-coupled receptor 83	glucocorticoid-induced receptor found in brain and may be involved in behavioral sensitization [RGD]	-	KEGG pathway: Neuroactive ligand-receptor interaction	-
42529.56	9583.96	4.44	NM_001071306	NM_001013067	Rattus norvegicus kallikrein 6 (predicted) (Klk6_predicted), mRNA [NM_001013067]	ref|NM_001013067|gb|XM_214932|gb|M27217|ens|ENSRNOT00000025715	Rn.79264	Klk6_predicted	kallikrein 6 (predicted)	-	-	-	[Mouse]HomoloGene:83265
164227.44	57850.42	2.84	NM_172065	Prpg2	Rattus norvegicus proline-rich proteoglycan 2 (Prpg2), mRNA [NM_172065]	ref|NM_172065|gb|M71893|gb|L17318|ens|ENSRNOT00000013943	Rn.29950	Prpg2	proline-rich proteoglycan 2	member of a family of proline rich proteins that are induced in salivary gland by isoproterenol treatment and by feeding tannins [RGD]	-	-	-

[0310]



Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Gene Symbol	Gene Name	Summary	GeneRIF	Pathway	Homology
144.02	53.99	2.67	NM_012996	Oxt	Rattus norvegicus oxytocin (Oxt), mRNA [NM_012996]	ref|NM_0129 96|gb|M2564 9|ens|ENSRN OTO0000288 29|tc|TC572 906	Rn. 48915	Oxt	oxytocin	hormone involved in contraction of smooth muscle during parturition and lactation; gene encodes two proteins, oxytocin and neurophysin I [RGD]	oxytocin has a role in gonadal steroid modulation of stress-induced hypothalamo-pituitary-adrenal activity and anxiety behavior// Oxytocin may strengthen mother-infant bond formation partly by acting through brain areas involved in regulating olfactory di	KEGG pathway: Neuroactive ligand-receptor interaction	[Human, Mouse]HomoloGene: 55494
80.76	31.28	2.58	NM_053738	Wif1	Rattus norvegicus Wnt inhibitory factor 1 (Wif1), mRNA [NM_053738]	ref|NM_0537 38|gb|AY030 278|gb|BC07 2473|ens|EN SRNOT0000 00426	Rn. 74256	Wif1	Wnt inhibitory factor 1	human homolog has decreased mRNA expression in some prostate cancers; and other cancers; may act as a secreted inhibitor of the Wnt signaling pathway [RGD]	GLT mRNA was translated in Wnt-1-expressing C6 cells when the GLT mRNA required no splicing before translation occurred	KEGG pathway: Wnt signaling pathway	[Human, Mouse]HomoloGene: 31430
8361.31	3259.64	2.57	XM_341400	Rbp3	PREDICTED: Rattus norvegicus retinol binding protein 3, interstitial (Rbp3), mRNA [XM_341400]	ref|XM_3414 00|gb|X56615 9|gb|AY69523 |ens|ENSRNO T0000002744 6	Rn. 41214	Rbp3	retinol binding protein 3, interstitial	may play a role in vision [RGD]	-	-	[Human, Mouse]HomoloGene: 9261
4805.70	1924.09	2.50	AB087404	Gdf5	Rattus norvegicus gdf-5 gene for growth and differentiation factor-5, partial cds [AB087404]	gb|AB087404 |tc|NP49515 4	Rn. 12782	Gdf5	growth differentiation factor 5	member of the bone morphogenetic protein (BMP) family and the TGF-beta superfamily; regulates cell growth and differentiation; involved with tendon and ligament formation [RGD]	Expression of GDF-5 in developing rat ventral mesencephalon (VM) was found to begin at embryonic day (E) 12 and peak on E14. In the adult rat was found in heart and brain, being expressed in many areas of the brain, including striatum and midbrain.// invol	-	-

[0311]

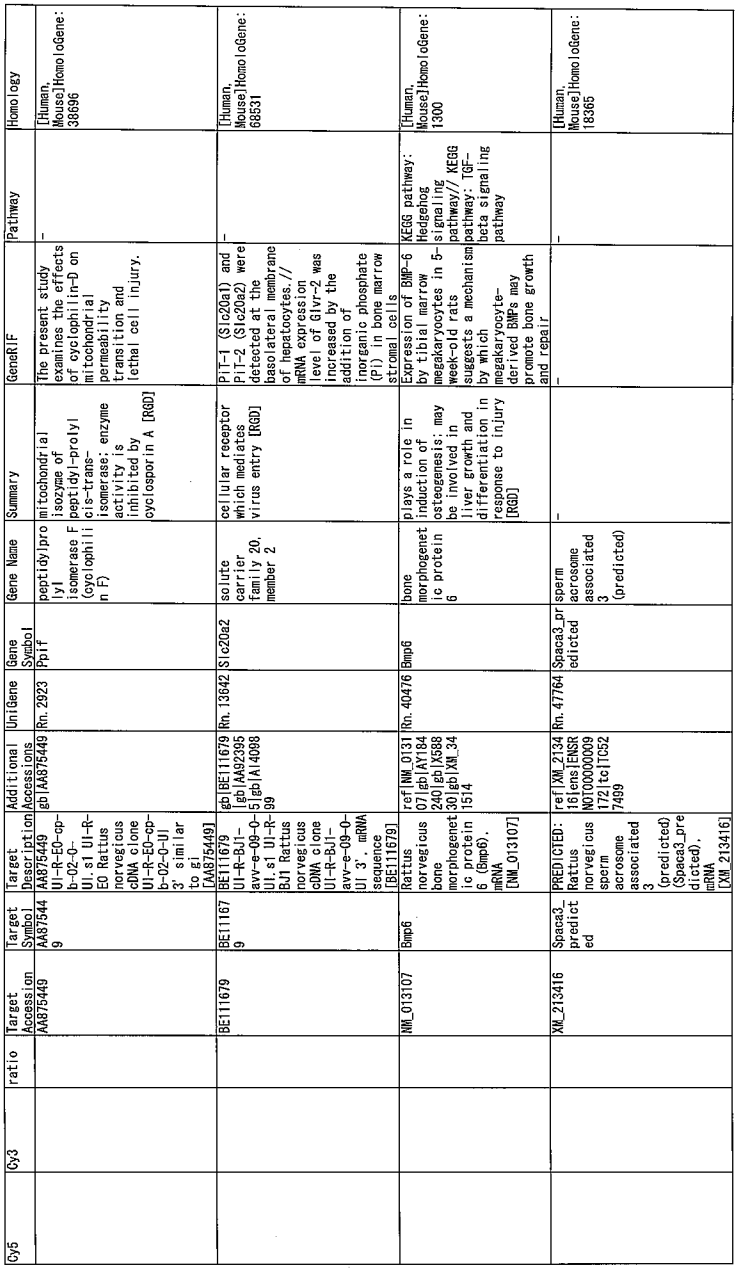


Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Gene Symbol	Gene Name	Summary	GeneRIF	Pathway	Homology
2733.04	1114.24	2.45	NM_024136	Erabp	Rattus norvegicus epididymal retinoic acid-binding protein (Erabp), mRNA [NM_024136]	ref|NM_024136|gb|X59832|gb|M12790|tc|TC56991	Rn.10362	Erabp	epididymal retinoic acid-binding protein	has a low galactosyltransferase modifying activity in vitro; however, this activity is predicted to be too low for physiological significance [RGD]	-	-	[Mouse]HomoloGene:7305
781.76	327.17	2.39	NM_057151	Ccl17	Rattus norvegicus small inducible cytokine subfamily A (Cys-Cys), member 17 (Ccl17), mRNA [NM_057151]	ref|NM_057151|gb|AF312687|ens|ENSRNOT00000021842|tc|TC561888	Rn.46679	Ccl17	chemokine (C-C motif) ligand 17	a thymus and activation-regulated chemokine [RGD]	Our data indicate that instead of Th2 cells, airway epithelial cells expressing CCR4 might be the principal targets for MDC and TARC released from alveolar macrophages during cigarette smoke-induced airway inflammation.	-	[Human,Mouse]HomoloGene:2246
200.79	88.11	2.28	NM_019189	Hapln1	Rattus norvegicus hyaluronan and proteoglycan link protein 1 (Hapln1), mRNA [NM_019189]	ref|NM_019189|ens|ENSRNOT00000042958|ens|ENSRNOT00000043196|gb|M22340	Rn.50531	Hapln1	hyaluronan and proteoglycan link protein 1	stabilizs cartilage proteoglycan/hyaluronic acid aggregates by binding to each component [RGD]	study represents the first report that follicle stimulating hormone amplifies insulin-like growth factor-I-mediated cartilage link protein Crtl1 production, possibly via phosphatidylinositol 3-kinase-Akt signaling cascades in rat granulosa cells	-	[Human,Mouse]HomoloGene:1420
395.11	173.49	2.28	BM388083	BM38808 3	BM388083 UI-R-DM1-cjz-d-11-0-UI.s1 UI-R-DM1 Rattus norvegicus cDNA clone UI-R-DM1-cjz-d-11-0-UI 3', mRNA sequence [BM388083]	gb|BM388083|gb|BF41687	Rn.41133	Sorcs2_predicted	sortilin-related VPS10 domain containing receptor 2 (predicted)	-	-	-	[Mouse]HomoloGene:75305

[0312]

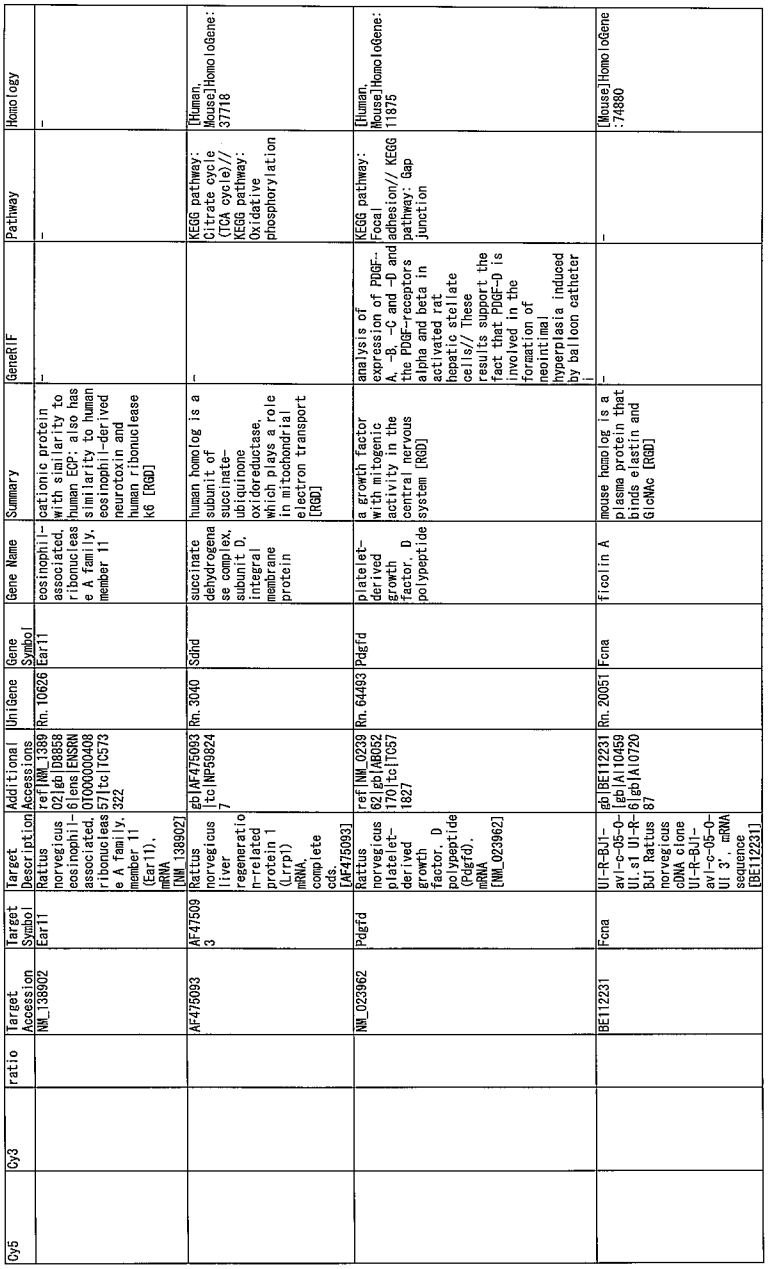
Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Gene Symbol	Gene Name	Summary	GeneRIF	Pathway	Homology
44.00	19.81	2.22	NM_053504	Prss12	Rattus norvegicus protease, serine, 12 (Prss12), mRNA [NM_053504]	ref|NM_053504.1|Ens|ENSRNOT00000002671|Ens|ENSRNOT00000001116	Rn.86653	Prss12	peptidase, serine, 12 (neurotrypsin, motopsin)	mouse homolog is a serine protease; may be involved in learning and memory [RGD]	-	-	[Human, Mouse]HomoloGene: 7490
			NM_016989	Adcyap1	Rattus norvegicus adenylate cyclase activating polypeptide 1 (Adcyap1), mRNA [NM_016989]	ref|NM_016989.2|XM_003906383|gb|M63460|XM_346860	Rn.37400	Adcyap1	adenylate cyclase activating polypeptide 1	regulatory protein that stimulates cell proliferation, induces differentiation, modulates neurotransmitter release, vasodilation, bronchodilation, and hormone release, and suppresses inflammatory responses [RGD]	These results indicate that a large number of PACAP neurons and a small number of BDNF neurons of the VMH project to the MCG.// The specificity of PAC1 receptor participation in pituitary adenylate cyclase-activating polypeptide (PACAP)-facilitated sex be	KEGG pathway: Neuroactive ligand-receptor interaction	[Human, Mouse]HomoloGene: 869
			NM_031736	Slc27a2	Rattus norvegicus solute carrier family 27 (fatty acid transporter), member 2 (Slc27a2), mRNA [NM_031736]	ref|NM_031736.1|XM_003979526|gb|D85100|XM_346669	Rn.3608	Slc27a2	solute carrier family 27 (fatty acid transporter), member 2	has very long-chain acyl-CoA synthetase activity; may play a role in fatty acid metabolism [RGD]	In response to an increase of cellular cholesterol, fatty acid transporter is translocated from cytosol to membranes of type II pneumocytes.	KEGG pathway: Alkaloid biosynthesis II// KEGG pathway: Caprolactam degradation// KEGG pathway: Ethylbenzene degradation// KEGG pathway: Limonene and pinene degradation// KEGG pathway: Propanoate metabolism	-
			NM_147165	Gpx6	Rattus norvegicus glutathione peroxidase 6 (Gpx6), mRNA [NM_147165]	ref|NM_147165.1|gb|AW673653	Rn.9852	Gpx6	glutathione peroxidase 6	a lipophilic molecule carrier in olfactory mucosa [RGD]	-	KEGG pathway: Arachidonic acid metabolism// KEGG pathway: Glutathione metabolism	[Human, Mouse]HomoloGene: 29418

[0313]



Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Gene Symbol	Gene Name	Summary	GeneRIF	Pathway	Homology
			AA875449	AA875449	UI-R-E0-op-b-02-0-UI.s1 UI-R-E0 Rattus norvegicus cDNA clone UI-R-E0-op-b-02-0-UI 3' similar to gi [AA875449]	gb|AA875449	Rn.2923	Ppif	peptidylpro lyl isomerase F (cyclophili n F)	mitochondrial isozyme of peptidyl-prolyl cis-trans-isomerase; enzyme activity is inhibited by cyclosporin A [RGD]	The present study examines the effects of cyclophilin-D on mitochondrial permeability transition and lethal cell injury.	-	[Human, Mouse]HomoloGene: 38696
			BE111679	BE111167 9	BE111679 UI-R-BJ1-avv-e-09-0-UI.s1 UI-R-BJ1 Rattus norvegicus cDNA clone UI-R-BJ1-avv-e-09-0-UI 3', mRNA sequence [BE111679]	gb|BE111679 |gb|AA892395 5|gb|AI4098 99	Rn.13642	Slc20a2	solute carrier family 20, member 2	cellular receptor which mediates virus entry [RGD]	PiT-1 (Slc20a1) and PiT-2 (Slc20a2) were detected at the basolateral membrane of hepatocytes.// mRNA expression level of Glvr-2 was increased by the addition of inorganic phosphate (Pi) in bone marrow stromal cells	-	[Human, Mouse]HomoloGene: 68531
			NM_013107	Bmp6	Rattus norvegicus bone morphogenetic protein 6 (Bmp6), mRNA [NM_013107]	ref|NM_0131 07|gb|AY184 240|gb|X588 30|gb|XM_34 1514	Rn.40476	Bmp6	bone morphogenetic protein 6	plays a role in induction of osteogenesis; may be involved in liver growth and differentiation in response to injury [RGD]	Expression of BMP-6 by tibial marrow megakaryocytes in 5-week-old rats suggests a mechanism by which megakaryocyte-derived BMPs may promote bone growth and repair	KEGG pathway: Hedgehog signaling pathway// KEGG pathway: TGF-beta signaling pathway	[Human, Mouse]HomoloGene: 1300
			XM_213416	Spaca3_predicted	PREDICTED: Rattus norvegicus sperm acrosome associated 3 (predicted) (Spaca3_predicted), mRNA [XM_213416]	ref|XM_2134 16|ens|ENSR NOT0000009 172|tc|TC52 7499	Rn.47764	Spaca3_predicted	sperm acrosome associated 3 (predicted)	-	-	-	[Human, Mouse]HomoloGene: 18365

[0314]



Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Gene Symbol	Gene Name	Summary	GeneRIF	Pathway	Homology
			NM_138902	Ear11	Rattus norvegicus eosinophil-associated, ribonuclease A family, member 11 (Ear11), mRNA [NM_138902]	ref|NM_138902.1|gb|D88582.1|ens|ENSRNOT00000040857|tc|TC57322	Rn.10626	Ear11	eosinophil-associated, ribonuclease A family, member 11	cationic protein with similarity to human ECP; also has similarity to human eosinophil-derived neurotoxin and human ribonuclease K6 [RGD]	-	-	-
			AF475093	AF475093	Rattus norvegicus liver regeneration-related protein 1 (Lrrp1) mRNA, complete cds. [AF475093]	gb|AF475093.1|tc|NP59824.7	Rn.3040	Sdhd	succinate dehydrogenase complex, subunit D, integral membrane protein	human homolog is a subunit of succinate-ubiquinone oxidoreductase, which plays a role in mitochondrial electron transport [RGD]	-	KEGG pathway: Citrate cycle (TCA cycle)// KEGG pathway: Oxidative phosphorylation	[Human, Mouse]HomoloGene: 37718
			NM_023962	Pdgfd	Rattus norvegicus platelet-derived growth factor, D polypeptide (Pdgfd), mRNA [NM_023962]	ref|NM_023962.2|gb|AB052170.1|tc|TC61571827	Rn.64493	Pdgfd	platelet-derived growth factor, D polypeptide	a growth factor with mitogenic activity in the central nervous system [RGD]	analysis of expression of PDGF-A, -B, -C and -D and the PDGF-receptors alpha and beta in activated rat hepatic stellate cells// These results support the fact that PDGF-D is involved in the formation of neointimal hyperplasia induced by balloon catheter i	KEGG pathway: Focal adhesion// KEGG pathway: Gap junction	[Human, Mouse]HomoloGene: 11875
			BE112231	Fcna	UI-R-BJ1-avl-c-05-0-UI.s1 UI-R-BJ1 Rattus norvegicus cDNA clone UI-R-BJ1-avl-c-05-0-UI 3', mRNA sequence [BE112231]	gb|BE112231.1|gb|AI104596.1|gb|AI107208.1	Rn.20051	Fcna	ficolin A	mouse homolog is a plasma protein that binds elastin and GlcNAc [RGD]	-	-	[Mouse]HomoloGene :74880

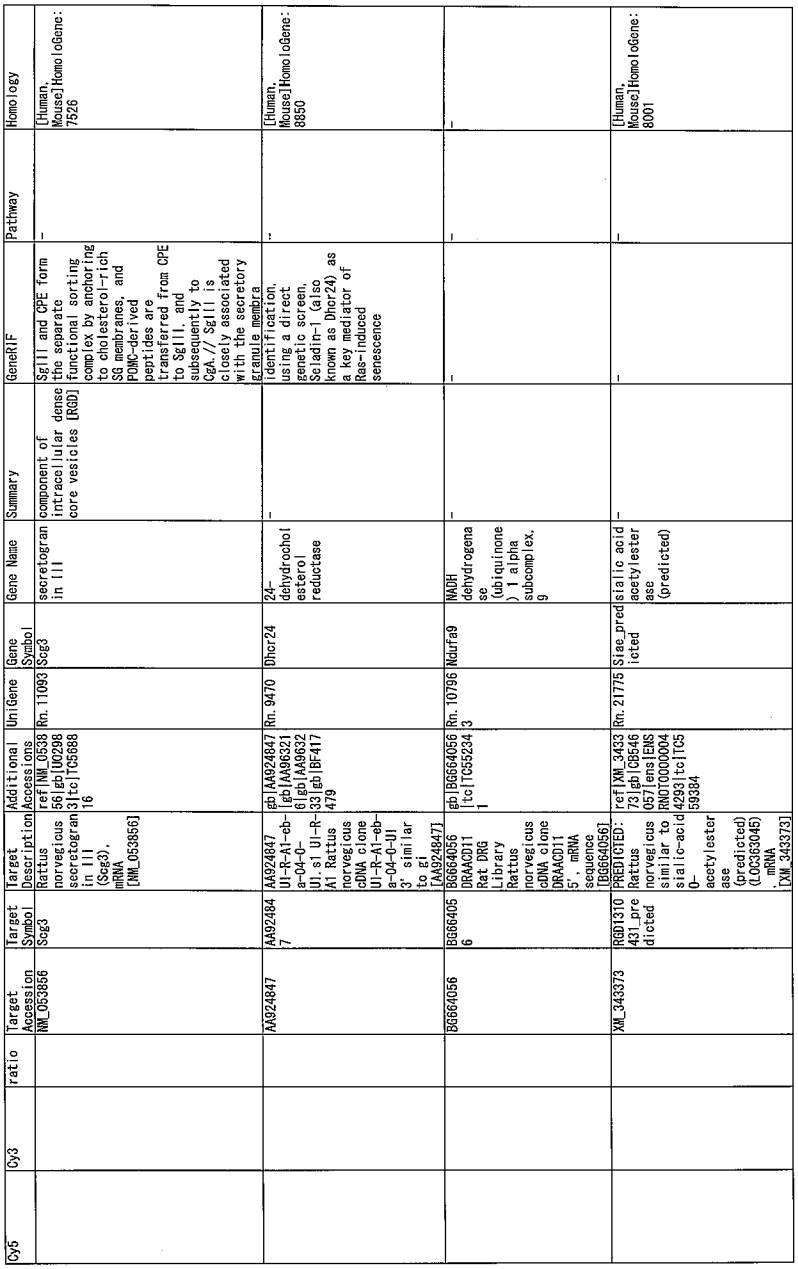
[0315]

Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Gene Symbol	Gene Name	Summary	GeneRIF	Pathway	Homology
			NM_021698	F13a	Rattus norvegicus coagulation factor XIII, A1 subunit (F13a), mRNA [NM_021698]	ref|NM_021698|98|gb|Y1250|2|gb|AW9190|18|ens|ENSRNOT00000002168	Rn.42925	F13a1	coagulation factor XIII, A1 subunit	enhances gastric mucosa healing; reduces endothelial permeability [RGD]	-	KEGG pathway: Complement and coagulation cascades	[Human, Mouse]HomoloGene: 20077
			NM_080394	Reln	Rattus norvegicus reelin (Reln), mRNA [NM_080394]	ref|NM_080394|94|gb|AB062680|gb|AW140590|tc|TC572679	Rn.16177	Reln	reelin	regulates neuronal cell migration during development; plays a role in locomotor behavior [RGD]	reelin, which is expressed along the route of the migrating GnRH neurons, has an inhibitory role in guiding GnRH neurons to the basal forebrain// differentiation factor for radial glial cells of dentate gyrus and as a positional cue for radial fiber orien	KEGG pathway: Cell Communication// KEGG pathway: ECM-receptor interaction// KEGG pathway: Focal adhesion	[Human, Mouse]HomoloGene: 3699
			AA891661	AA891661	AA891661 EST195464 Normalized rat kidney, Bento Soares Rattus sp. cDNA clone RK1AF23 3' end, mRNA sequence [AA891661]	gb|AA891661	Rn.1618	Aqp1	aquaporin 1	integral membrane protein that is a major water transport molecule in the kidney proximal tubule and red blood cells [RGD]	data indicate that the ar/R constriction is a major checkpoint for solute permeability, and that the exquisite electrostatic proton barrier in AQPs comprises both the NPA constriction as well as the ar/R constriction// AQP1 and AQP6, and the heterotrimeri	-	[Human, Mouse]HomoloGene: 68051
			XM_225585	Mrc1_predicted	PREDICTED: Rattus norvegicus mannose receptor, C type 1 (predicted) (Mrc1_predicted), mRNA [XM_225585]	ref|XM_225585|85|gb|CB544894|ens|ENSRNOT00000024736|tc|TC555453	Rn.9197	Mrc1_predicted	mannose receptor, C type 1 (predicted)	-	-	-	-

[0316]

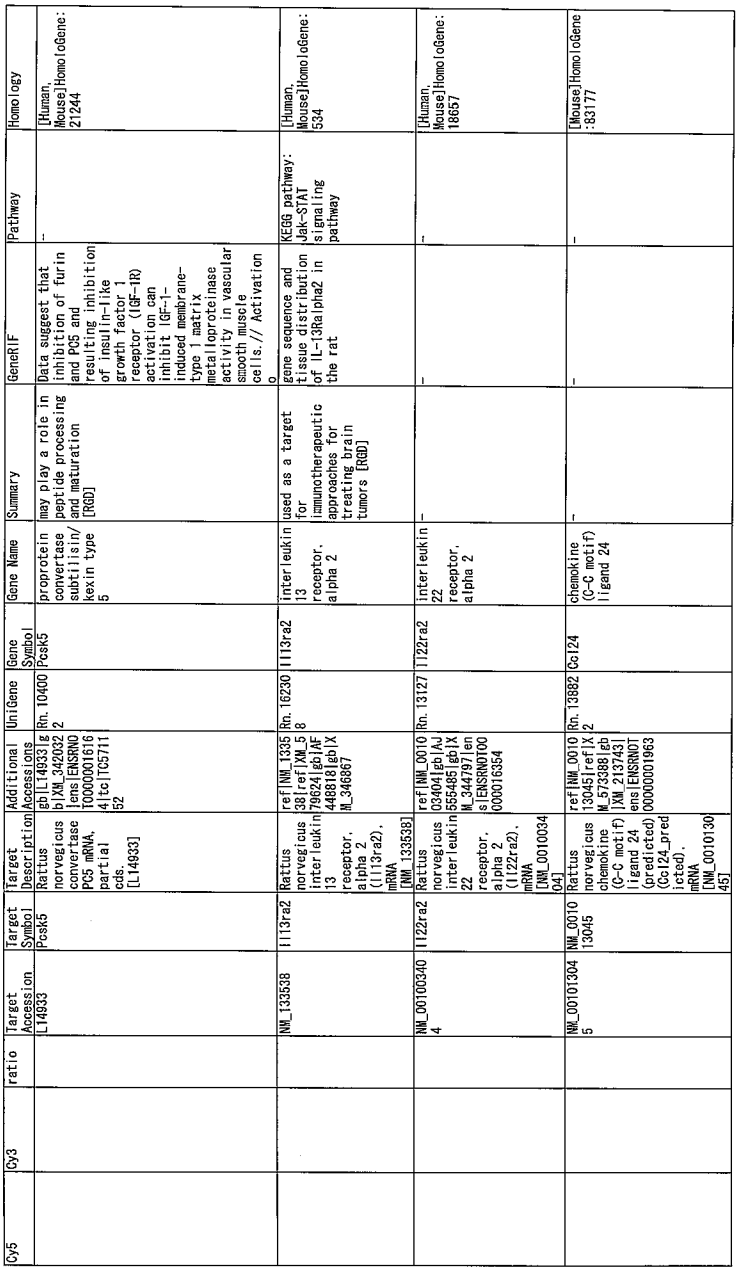
Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Gene Symbol	Gene Name	Summary	GeneRIF	Pathway	Homology
			X61479	X61479	RRGSFi Rat mRNA for CSF-1 receptor [X61479]	gb|X61479	-	OsFlr	colony stimulating factor 1 receptor	may mediate normal and neoplastic growth of muscular cells [RGD]	the CSFiR mutation of Asp-802 to Val confers resistance to kinase inhibitor imatinib	-	[Human, Mouse]HomoloGene: 3817
			XM_573463	XM_5734 63	PREDICTED: Rattus norvegicus similar to complement component factor h (LOC498240), mRNA [XM_573463]	ref|XM_5734 63|gb|BC089 845|ens|ENS RNOT0000002 9281|ens|EN SRNOT000000 29294	Rn.13761 2	Cfh	complement component factor H	regulator of complement cascade activation [RGD]	Glomerular epithelial cells(GEC) and glomeruli express factor H mRNA and protein. Up-regulated in membranous nephropathy. Likely direct response of GEC to complement attack and may represent protective response.// Complement Factor H is highly expressed i	KEGG pathway: Complement and coagulation cascades	[Human, Mouse]HomoloGene: 20086
			NM_021682	Negr1	Rattus norvegicus neuronal growth regulator 1 (Negr1), mRNA [NM_021682]	ref|NM_0216 82|gb|AB017 139|tc|TC57 2970	Rn.42884	Negr1	neuronal growth regulator 1	glycosylphosphatidy linositol-anchored cell adhesion protein [RGD]	-	KEGG pathway: Cell adhesion molecules (CAMs)	[Human, Mouse]HomoloGene: 41447
			NM_031590	Wisp2	Rattus norvegicus WNT1 inducible signaling pathway protein 2 (Wisp2), mRNA [NM_031590]	ref|NM_0315 90|gb|AF259 981|gb|BC08 9187|ens|EN SRNOT000000 14346	Rn.53991	Wisp2	WNT1 inducible signaling pathway protein 2	involved in negative regulation of cell growth: mRNA expression is lost upon cell transformation induced by activated H-ras oncogene and inactivated p53 tumor supressor [RGD]	data indicate that CCN5 protein is positively regulated by estrogen in the rat uterus and suggests that this gene may play an important role in maintaining normal uterine physiology	-	[Human, Mouse]HomoloGene: 2882

[0317]



Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Gene Symbol	Gene Name	Summary	GeneRIF	Pathway	Homology
			NM_053856	Scg3	Rattus norvegicus secretogranin III (Scg3), mRNA [NM_053856]	ref|NM_0538 56|gb|U00298 3|tc|TC5088 16	Rn.11003	Scg3	secretogranin III	component of intracellular dense core vesicles [RGD]	SgIII and CPE form the separate functional sorting complex by anchoring to cholesterol-rich SG membranes, and POMC-derived peptides are transferred from CPE to SgIII, and subsequently to CgA.// SgIII is closely associated with the secretory granule membra	-	[Human, Mouse]HomoloGene: 7526
			AA924847	AA92484 7	UI-R-A1-eb-a-04-0-UI.s1 UI-R-A1 Rattus norvegicus cDNA clone UI-R-A1-eb-a-04-0-UI 3' similar to gi [AA924847]	gb|AA924847 |gb|AA96321 8|gb|AA9632 33|gb|BF417 479	Rn.9470	Dhcr24	24-dehydrocholesterol reductase	-	identification, using a direct genetic screen, Seladin-1 (also known as Dhcr24) as a key mediator of Ras-induced senescence	-	[Human, Mouse]HomoloGene: 8850
			BG664056	BG66405 6	BG664056 DRAACD11 Rat DRG Library Rattus norvegicus cDNA clone DRAACD11 5', mRNA sequence [BG664056]	gb|BG664056 |tc|TC65234 1	Rn.10796 3	Ndufa9	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 9	-	-	-	-
			XM_343373	RGD1310 431_predicted	PREDICTED: Rattus norvegicus similar to sialic-acid O-acetylesterase (predicted) (LOC363045), mRNA [XM_343373]	ref|XM_3433 73|gb|CB546 057|ens|ENS RNOT0000004 4293|tc|TC5 59384	Rn.21775	Siae_predicted	sialic acid acetylesterase (predicted)	-	-	-	[Human, Mouse]HomoloGene: 8001

[0318]

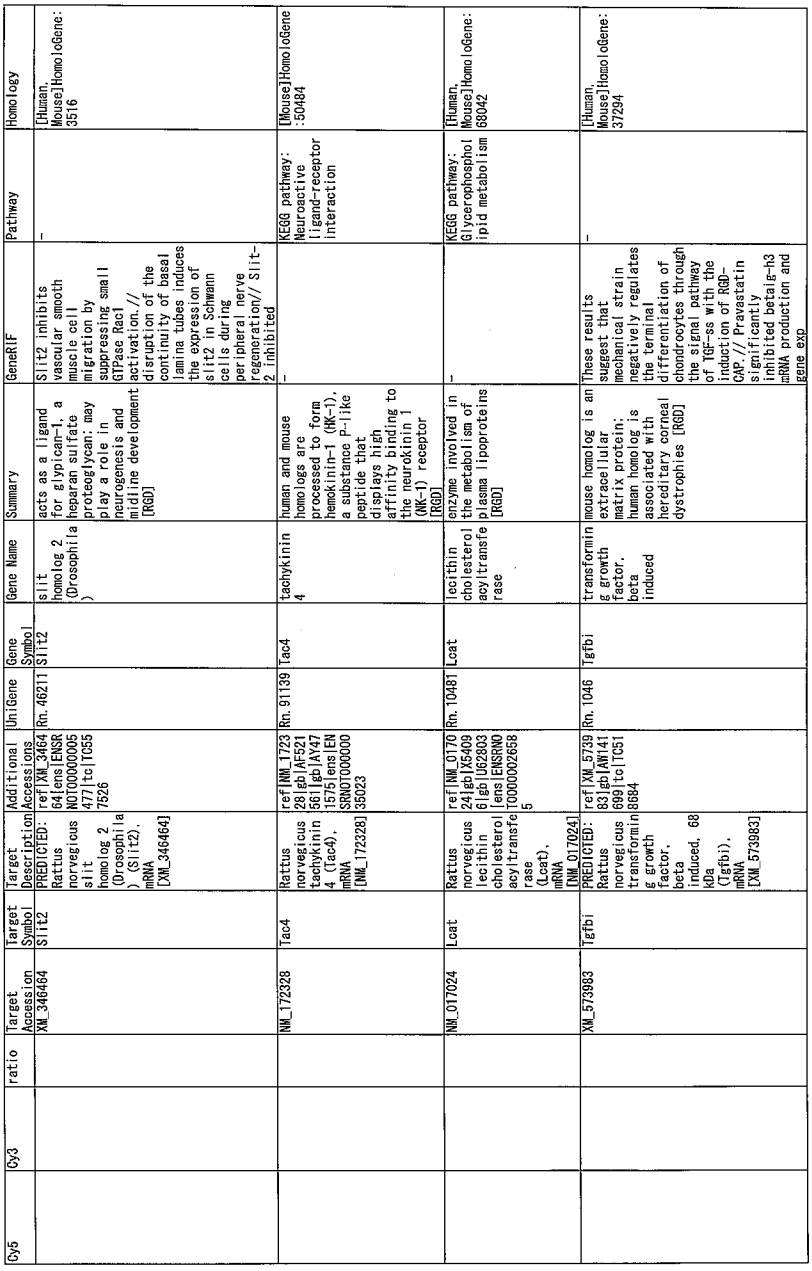


Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Gene Symbol	Gene Name	Summary	GeneRIF	Pathway	Homology
			L14933	Pcsk5	Rattus norvegicus convertase PC5 mRNA, partial cds. [L14933]	gb|L14933|gb|XM_342032|ens|ENSRNOT00000016164|Tc5711452	Rn.10400	Pcsk5	proprotein convertase subtilisin/kexin type 5	may play a role in peptide processing and maturation [RGD]	Data suggest that inhibition of furin and PC5 and resulting inhibition of insulin-like growth factor 1 receptor (IGF-1R) activation can inhibit IGF-1-induced membrane-type 1 matrix metalloproteinase activity in vascular smooth muscle cells.// Activation o	-	[Human, Mouse]HomoloGene: 21244
			NM_133538	Il13ra2	Rattus norvegicus interleukin 13 receptor, alpha 2 (Il13ra2), mRNA [NM_133538]	ref|NM_133538|ref|XM_538|ref|XM_579624|gb|AF448818|gb|XM_346867	Rn.16230	Il13ra2	interleukin 13 receptor, alpha 2	used as a target for immunotherapeutic approaches for treating brain tumors [RGD]	gene sequence and tissue distribution of IL-13Ralpha2 in the rat	KEGG pathway: Jak-STAT signaling pathway	[Human, Mouse]HomoloGene: 534
			NM_001003404	Il22ra2	Rattus norvegicus interleukin 22 receptor, alpha 2 (Il22ra2), mRNA [NM_001003404]	ref|NM_001003404|gb|AJ555485|gb|XM_344791|ens|ENSRNOT00000016354	Rn.13127	Il22ra2	interleukin 22 receptor, alpha 2	-	-	-	[Human, Mouse]HomoloGene: 18657
			NM_001013045	NM_001013045	Rattus norvegicus chemokine (C-C motif) ligand 24 (predicted) (Ccl24_predicted), mRNA [NM_001013045]	ref|NM_001013045|ref|XM_573388|gb|XM_213743|ens|ENSRNOT00000001963	Rn.13882	Ccl24	chemokine (C-C motif) ligand 24	-	-	-	[Mouse]HomoloGene: 83177

[0319]

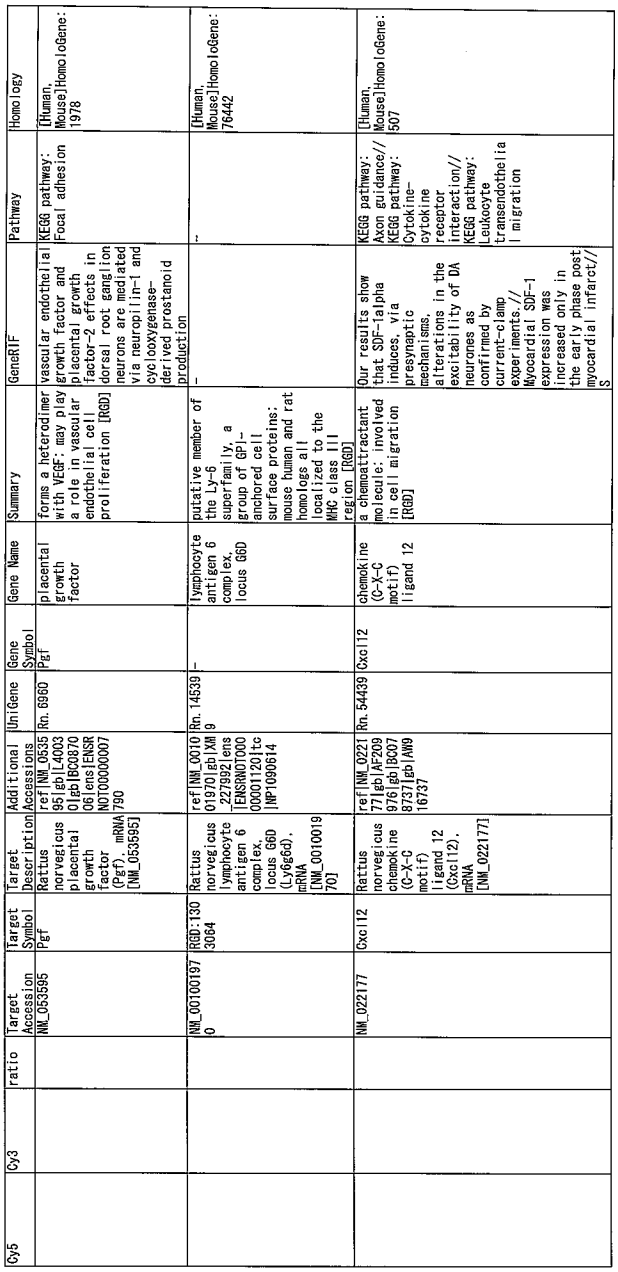
Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Gene Symbol	Gene Name	Summary	GeneRIF	Pathway	Homology
			NM_019192	Sepp1	Rattus norvegicus selenoprotein P, plasma, 1 (Sepp1). mRNA [NM_019192]	ref|NM_019192.2|gb|M63574.1|tc|TC65166	Rn.1451	Sepp1	selenoprotein P, plasma, 1	plasma glycoprotein that contains ten selenocysteine residues: may play a role in response to oxidative stress [RGD]	selenenylsulfide linkages Sec304-Cys314 and Cys306-Sec316 were present: selenoprotein P contains these two selenenylsulfide bonds// mass spectrometric characterization of full-length protein and three isoforms shortened at the C terminus	-	-
			NM_024358	Notch2	Rattus norvegicus notch gene homolog 2, (Drosophila) (Notch2), mRNA [NM_024358]	ref|NM_024358.1|gb|M93661.1|ens|ENSRNOT00000002570|ens|ENSRNOT00000000450|ens|ENSRNOT00000000620	Rn.65930	Notch2	notch gene homolog 2 (Drosophila)	transmembrane protein that may be involved in cellular interactions that specify cell fate [RGD]	-	KEGG pathway: Dorso-ventral axis formation// KEGG pathway: Notch signaling pathway	[Human; Mouse]HomoloGene: 7865
			NM_053289	Pap	Rattus norvegicus pancreatitis-associated protein (Pap), mRNA [NM_053289]	ref|NM_053289.2|gb|S77418.1|gb|S43715.1|ens|ENSRNOT00000008212	Rn.9727	Pap	pancreatitis-associated protein	lectin-related secretory protein: may be involved in stress response to control bacterial proliferation [RGD]	These results suggest that Reg family members would be new mediators among injured neurons and glial cells, and may play pivotal roles during nerve regeneration.// Sepsis resulted in an up-regulation of PAP-1 gene expression and increase in its protein le	-	[Human; Mouse]HomoloGene: 49257

[0320]



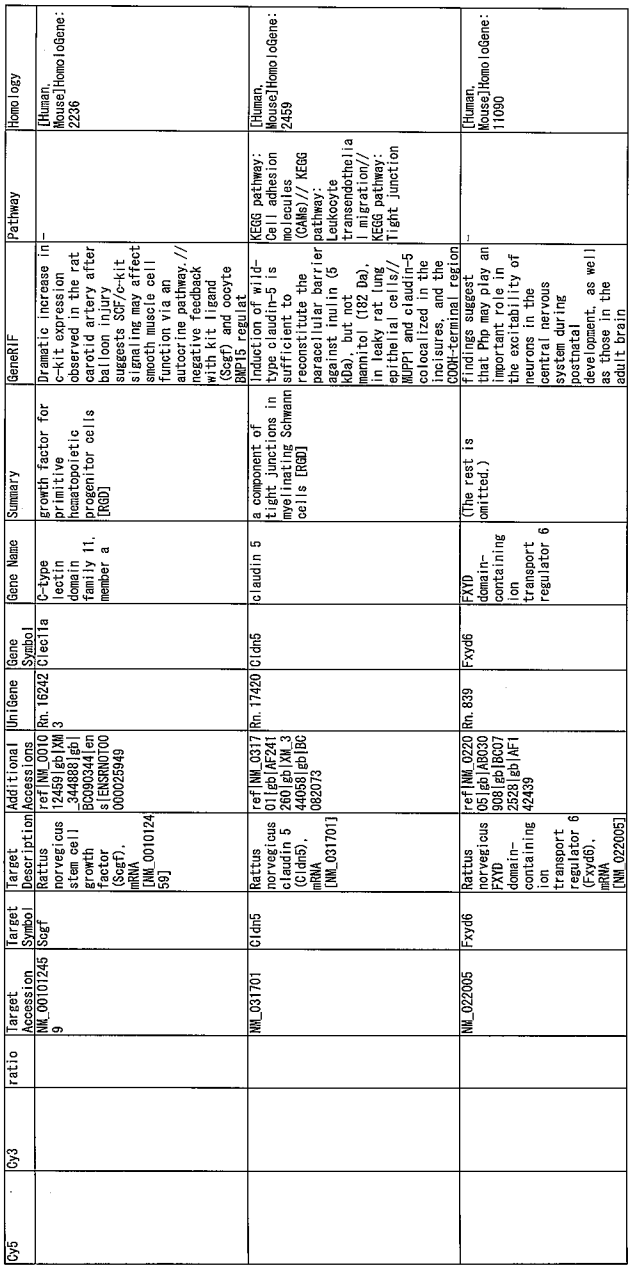
Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Gene Symbol	Gene Name	Summary	GeneRIF	Pathway	Homology
			XM_346464	Slit2	PREDICTED: Rattus norvegicus slit homolog 2 (Drosophila) (Slit2), mRNA [XM_346464]	ref|XM_346464|ENSRNOT00000005477|tc|T0557626	Rn.46211	Slit2	slit homolog 2 (Drosophila)	acts as a ligand for glypican-1, a heparan sulfate proteoglycan: may play a role in neurogenesis and midline development [RGD]	Slit2 inhibits vascular smooth muscle cell migration by suppressing small GTPase Rac1 activation.// disruption of the continuity of basal lamina tubes induces the expression of slit2 in Schwann cells during peripheral nerve regeneration// Slit-2 inhibited	-	[Human, Mouse]HomoloGene: 3516
			NM_172328	Tac4	Rattus norvegicus tachykinin 4 (Tac4), mRNA [NM_172328]	ref|NM_172328|561|gb|AY475575|ens|ENSRNOT00000035023	Rn.91139	Tac4	tachykinin 4	human and mouse homologs are processed to form hemokinin-1 (HK-1), a substance P-like peptide that displays high affinity binding to the neurokinin 1 (NK-1) receptor [RGD]	-	KEGG pathway: Neuroactive ligand-receptor interaction	[Mouse]HomoloGene: 50484
			NM_017024	Lcat	Rattus norvegicus lecithin cholesterol acyltransferase (Lcat), mRNA [NM_017024]	ref|NM_017024|6|gb|U62803|ens|ENSRNOT00000026585	Rn.10481	Lcat	lecithin cholesterol acyltransferase	enzyme involved in the metabolism of plasma lipoproteins [RGD]	-	KEGG pathway: Glycerophospholipid metabolism	[Human, Mouse]HomoloGene: 68042
			XM_573983	Tgfbi	PREDICTED: Rattus norvegicus transforming growth factor, beta induced, 68 kDa (Tgfbi), mRNA [XM_573983]	ref|XM_573983|699|tc|T058834	Rn.1046	Tgfbi	transforming growth factor, beta induced	mouse homolog is an extracellular matrix protein: human homolog is associated with hereditary corneal dystrophies [RGD]	These results suggest that mechanical strain negatively regulates the terminal differentiation of chondrocytes through the signal pathway of TGF-ss with the induction of RGD-CAP.// Pravastatin significantly inhibited betaig-h3 mRNA production and gene exp	-	[Human, Mouse]HomoloGene: 37294

[0321]



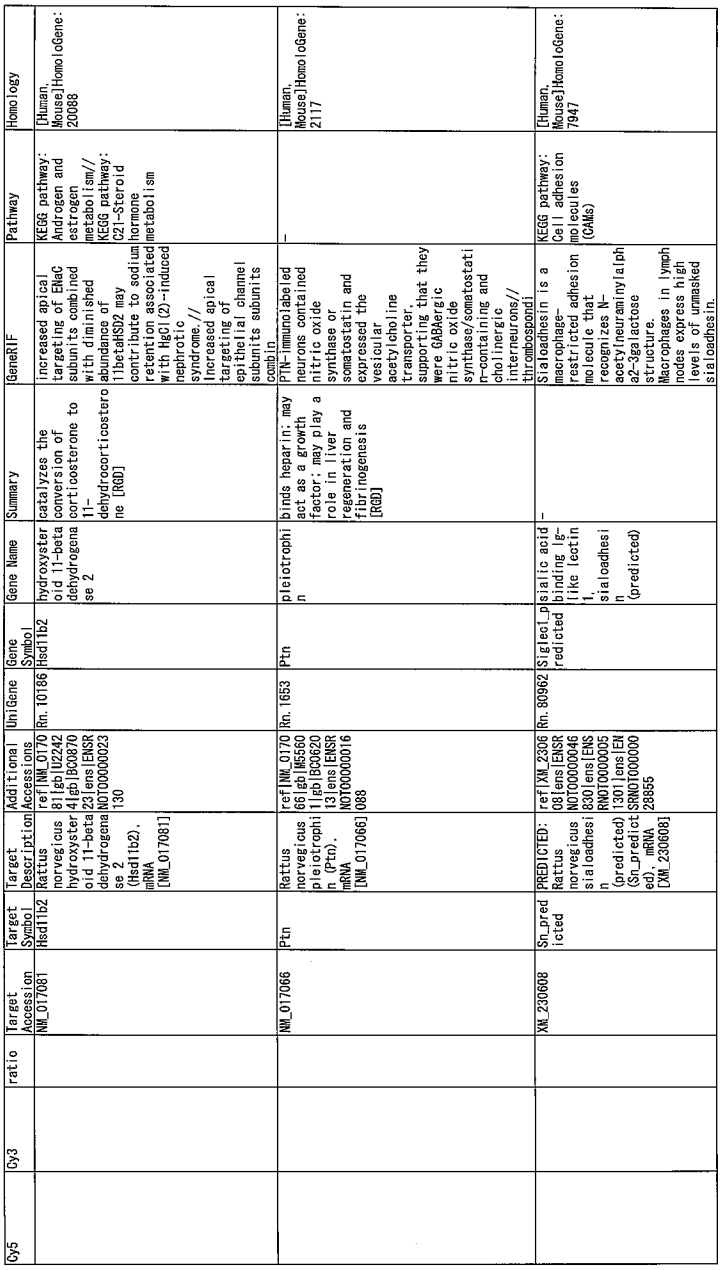
Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Gene Symbol	Gene Name	Summary	GeneRIF	Pathway	Homology
			NM_053595	Pgf	Rattus norvegicus placental growth factor (Pgf), mRNA [NM_053595]	ref|NM_0535 95|gb|L4003 01|gb|BC0870 06|ens|ENSR NOT00000007 790	Rn. 6960	Pgf	placental growth factor	forms a heterodimer with VEGF: may play a role in vascular endothelial cell proliferation [RGD]	vascular endothelial growth factor and placental growth factor-2 effects in dorsal root ganglion neurons are mediated via neuropilin-1 and cyclooxygenase-derived prostanoid production	KEGG pathway: Focal adhesion	[Human, Mouse]HomoloGene: 1978
			NM_001001970	RGD:1303064	Rattus norvegicus lymphocyte antigen 6 complex, locus G6D (Ly6g6d), mRNA [NM_001001970]	ref|NM_0010 01970|gb|XM_ 227992|ens |ENSRNOT000 00001120|to |NP1090614	Rn. 14539	-	lymphocyte antigen 6 complex, locus G6D	putative member of the Ly-6 superfamily, a group of GPI-anchored cell surface proteins: mouse human and rat homologs all localized to the MHC class III region [RGD]	-	-	[Human, Mouse]HomoloGene: 76442
			NM_022177	Cxcl12	Rattus norvegicus chemokine (C-X-C motif) ligand 12 (Cxcl12), mRNA [NM_022177]	ref|NM_0221 77|gb|AF209 976|gb|BC07 8737|gb|AW0 16737	Rn. 54439	Cxcl12	chemokine (C-X-C motif) ligand 12	a chemoattractant molecule: involved in cell migration [RGD]	Our results show that SDF-1alpha induces, via presynaptic mechanisms, alterations in the excitability of DA neurones as confirmed by current-clamp experiments.// Myocardial SDF-1 expression was increased only in the early phase post myocardial infarct// s	KEGG pathway: Axon guidance// KEGG pathway: Cytokine-cytokine receptor interaction// KEGG pathway: Leukocyte transendothelial migration	[Human, Mouse]HomoloGene: 507

[0322]



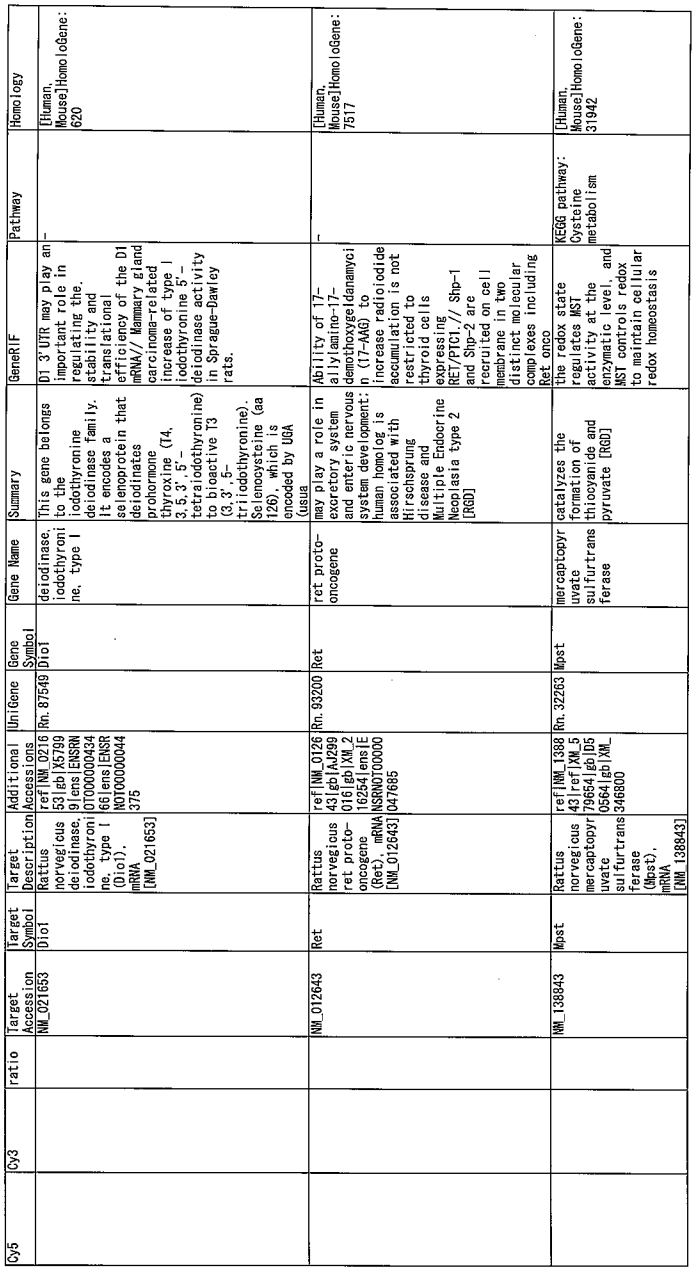
Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Gene Symbol	Gene Name	Summary	GeneRIF	Pathway	Homology
			NM_001012459	Sogf	Rattus norvegicus stem cell growth factor (Sogf), mRNA [NM_001012459]	ref|NM_001012459|XM_344888|gb|BC090344|ENSRNOT00000025949	Rn.16242	C1ecl1a	C-type lectin domain family 11, member a	growth factor for primitive hematopoietic progenitor cells [RGD]	Dramatic increase in c-kit expression observed in the rat carotid artery after balloon injury suggests SCF/c-kit signaling may affect smooth muscle cell function via an autocrine pathway.// negative feedback with kit ligand (Sogf) and oocyte BMP15 regulat	-	[Human, Mouse]HomoloGene: 2236
			NM_031701	Cldn5	Rattus norvegicus claudin 5 (Cldn5), mRNA [NM_031701]	ref|NM_031701|AF241260|gb|AW_344058|gb|BG082073	Rn.17420	Cldn5	claudin 5	a component of tight junctions in myelinating Schwann cells [RGD]	Induction of wild-type claudin-5 is sufficient to reconstitute the paracellular barrier against inulin (5 kDa), but not mannitol (182 Da), in leaky rat lung epithelial cells// MUPP1 and claudin-5 colocalized in the incisures, and the COOH-terminal region	KEGG pathway: Cell adhesion molecules (CAMs)// KEGG pathway: Leukocyte transendothelial migration// KEGG pathway: Tight junction	[Human, Mouse]HomoloGene: 2459
			NM_022005	Fxyd6	Rattus norvegicus FXYD domain-containing ion transport regulator 6 (Fxyd6), mRNA [NM_022005]	ref|NM_022005|AB030652|gb|AB030908|gb|BC072528|gb|AF142439	Rn.839	Fxyd6	FXYD domain-containing ion transport regulator 6	(The rest is omitted.)	findings suggest that Php may play an important role in the excitability of neurons in the central nervous system during postnatal development, as well as those in the adult brain	-	[Human, Mouse]HomoloGene: 11090

[0323]



Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Gene Symbol	Gene Name	Summary	GeneRIF	Pathway	Homology
			NM_017081	Hsd11b2	Rattus norvegicus hydroxysteroid 11-beta dehydrogenase 2 (Hsd11b2), mRNA [NM_017081]	ref|NM_017081|gb|U22424|gb|BC087041|ens|ENSRNOT00000023130	Rn.10186	Hsd11b2	hydroxysteroid 11-beta dehydrogenase 2	catalyzes the conversion of cortiocosterone to 11-dehydrocorticosterone [RGD]	increased apical targeting of EMaC subunits combined with diminished abundance of 11betaHSD2 may contribute to sodium retention associated with HgCl(2)-induced nephrotic syndrome.// Increased apical targeting of epithelial channel subunits combin...	KEGG pathway: Androgen and estrogen metabolism//KEGG pathway: C21-Steroid hormone metabolism	[Human, Mouse]HomoloGene: 20088
			NM_017066	Ptn	Rattus norvegicus pleiotrophin (Ptn), mRNA [NM_017066]	ref|NM_017066|gb|M65560|gb|BC006201|ens|ENSRNOT00000016088	Rn.1653	Ptn	pleiotrophin	binds heparin: may act as a growth factor; may play a role in liver regeneration and fibrinogenesis [RGD]	PTN-immunolabeled neurons contained nitric oxide synthase or somatostatin and expressed the vesicular acetylcholine transporter, supporting that they were GABAergic nitric oxide synthase/somatostatin-containing and cholinergic interneurons// thrombospondi...	-	[Human, Mouse]HomoloGene: 2117
			XM_230608	Sn_predicted	PREDICTED: Rattus norvegicus sialoadhesin (predicted) (Sn_predicted), mRNA [XM_230608]	ref|XM_230608|ens|ENSRNOT00000004630|ens|ENSRNOT00000005130|ens|ENSRNOT00000028855	Rn.80962	Siglecl_predicted	sialic acid binding Ig-like lectin 1, sialoadhesin (predicted)	-	Sialoadhesin is a macrophage-restricted adhesion molecule that recognizes N-acetylneuraminylalpha2-3galactose structure. Macrophages in lymph nodes express high levels of unmasked sialoadhesin.	KEGG pathway: Cell adhesion molecules (CAMs)	[Human, Mouse]HomoloGene: 7947

[0324]



Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Gene Symbol	Gene Name	Summary	GeneRIF	Pathway	Homology
			NM_021653	Dio1	Rattus norvegicus deiodinase, iodothyronine, type I (Dio1), mRNA [NM_021653]	ref|NM_0216 53|gb|X5799 9|ens|ENSRN OT00000434 66|ens|ENSR NOT00000044 375	Rn. 87549	Dio1	deiodinase, iodothyronine, type I	This gene belongs to the iodothyronine deiodinase family. It encodes a selenoprotein that deiodinates prohormone thyroxine (T4, 3,5,3',5'-tetraiodothyronine) to bioactive T3 (3,3',5-triiodothyronine). Selenocysteine (aa 126), which is encoded by UGA (usua	D1 3'UTR may play an important role in regulating the stability and translational efficiency of the D1 mRNA// Mammary gland carcinoma-related increase of type I iodothyronine 5'-deiodinase activity in Sprague-Dawley rats.	-	[Human, Mouse]HomoloGene: 620
			NM_012643	Ret	Rattus norvegicus ret proto-oncogene (Ret), mRNA [NM_012643]	ref|NM_0126 43|gb|AJ299 016|gb|XM_2 16254|ens|E NSRNOT00000 047665	Rn. 93200	Ret	ret proto-oncogene	may play a role in exoretory system and enteric nervous system development: human homolog is associated with Hirschsprung disease and Multiple Endocrine Neoplasia type 2 [RGD]	Ability of 17-allylamino-17-demethoxygeldanamycin (17-AAG) to increase radioiodide accumulation is not restricted to thyroid cells expressing RET/PTC1.// Shp-1 and Shp-2 are recruited on cell membrane in two distinct molecular complexes including Ret onco	-	[Human, Mouse]HomoloGene: 7517
			NM_138843	Mpst	Rattus norvegicus mercaptopyruvate sulfurtransferase (Mpst), mRNA [NM_138843]	ref|NM_1388 43|ref|XM_5 79654|gb|BG 0664|gb|XM_ 346800	Rn. 32263	Mpst	mercaptopyruvate sulfurtransferase	catalyzes the formation of thiocyanide and pyruvate [RGD]	the redox state regulates MST activity at the enzymatic level, and MST controls redox to maintain cellular redox homeostasis	KEGG pathway: Cysteine metabolism	[Human, Mouse]HomoloGene: 31942

[0325]

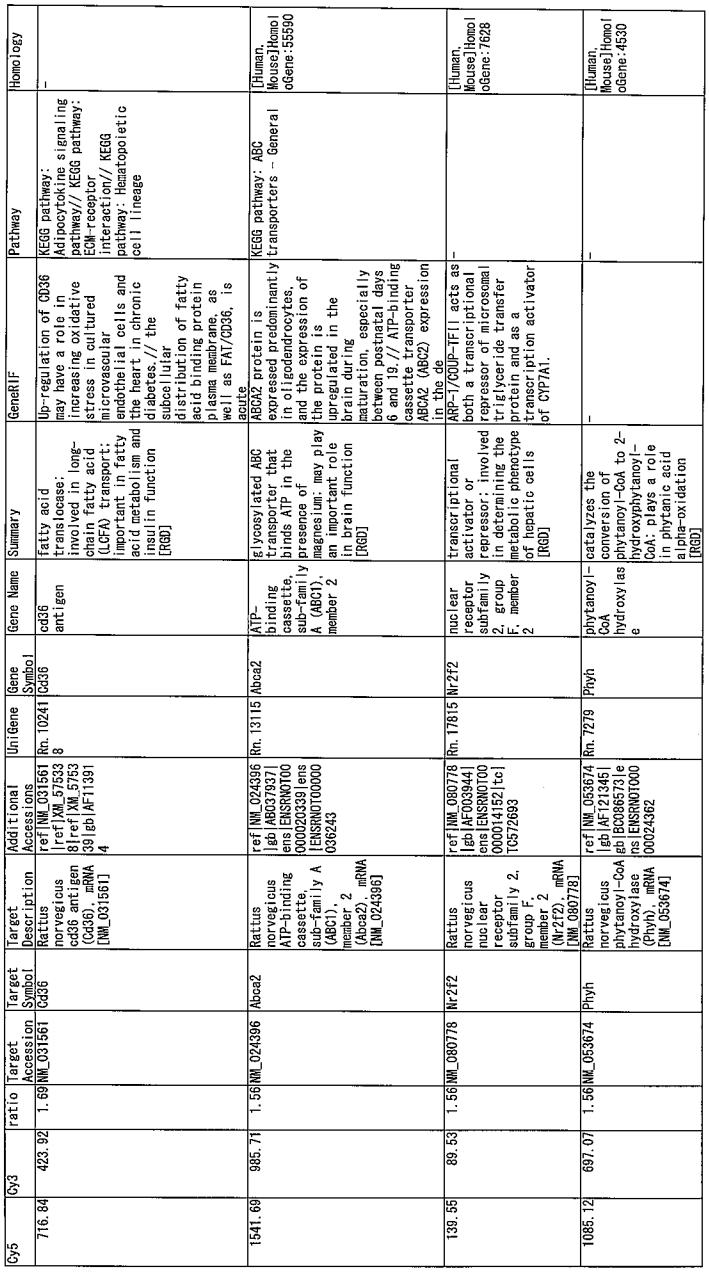
Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Gene Symbol	Gene Name	Summary	GeneRIF	Pathway	Homology
			NM_013156	Ctsl	Rattus norvegicus cathepsin L (Ctsl), mRNA [NM_013156]	ref|NM_013156|gb|BC063462|gb|S85184|ens|ENSRNOT00000000025	Rn. 1284	Ctsl	cathepsin L	mouse homolog is deleted in the CD4 T-cell-deficient mouse mutant nacht (dnt); may play a role in CD4+ T-cell selection in the thymus [RGD]	cathepsin L created a 14-kDa carboxyl IGFBP-2 fragment that corresponded to the sole antigen detected in IEC-18 cell lysates as well as a 16.5-kDa fragment found in the media.// The co-localization of PAP/TRAP and the cysteine protease cathepsin L could su	KEGG pathway: Antigen processing and presentation	[Human, Mouse]HomoloGene: 74296
			NM_017178	Bmp2	Rattus norvegicus bone morphogenetic protein 2 (Bmp2), mRNA [NM_017178]	ref|NM_017178|gb|Z26586|gb|L20678|ens|ENSRNOT00000002890|4	Rn. 90931	Bmp2	bone morphogenetic protein 2	involved in cellular signaling during limb development; induces bone formation [RGD]	(TNF)-alpha induced NF-kappaBeta activation and elicited significant increases in BMP-2 mRNA and protein in primary coronary arterial endothelial cells// The Bmp2 3' UTR contains essential regulatory elements that act post-transcriptionally// Our results	KEGG pathway: Hedgehog signaling pathway// KEGG pathway: TGF-beta signaling pathway	[Human, Mouse]HomoloGene: 926
			XM_216584	Car6_predicted	PREDICTED: Rattus norvegicus carbonic anhydrase 6 (predicted) (Car6_predicted), mRNA [XM_216584]	ref|XM_216584|tc|TC6205057	Rn. 43383	Car6	carbonic anhydrase 6	-	-	-	[Human, Mouse]HomoloGene: 20324

[表48]

表48 Glに対して発現増加した唾液腺の注目遺伝子
脂質代謝 (GO ID: 6629, 44255)

Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Gene Symbol	Gene Name	Summary	GeneRIF	Pathway	Homology
8361.31	3259.64	2.57	XM_341400	Rbp3	PREDICTED: Rattus norvegicus retinol binding protein 3, interstitial (Rbp3), mRNA [XM_341400]	ref|XM_341400|gb|X56159|gb|X69523|ens|ENSRNOT0000007446	Rn.41214	Rbp3	retinol binding protein 3, interstitial	may play a role in vision [RGD]	-	-	[Human, Mouse]HomoloGene:9261
61.95	24.38	2.54	NM_019169	Snca	Rattus norvegicus synuclein, alpha (Snca), mRNA [NM_019169]	ref|NM_019169|gb|AF007758|gb|AY550005|gb|AY550006	Rn.1827	Snca	synuclein, alpha	may play a role in regulation of synaptic vesicle biogenesis and organization: may be involved in neurotransmission [RGD]	we were able to modulate tyrosine hydroxylase-positive neuronal cell death by silencing alpha-synuclein expression, suggesting that down-regulation of alpha-synuclein is important in neuronal cell death of Parkinson's disease// DJ-1 up-regulates glutathio	KEGG pathway: Alzheimer's disease// KEGG pathway: Neurodegenerative Disorders// KEGG pathway: Parkinson's disease	[Human, Mouse]HomoloGene:293
40.56	19.56	2.07	NM_031736	Slc27a2	Rattus norvegicus solute carrier family 27 (fatty acid transporter), member 2 (Slc27a2), mRNA [NM_031736]	ref|NM_031736|ref|XM_579626|gb|D85100|gb|XM_346669	Rn.3608	Slc27a2	solute carrier family 27 (fatty acid transporter), member 2	has very long-chain acyl-CoA synthetase activity: may play a role in fatty acid metabolism [RGD]	In response to an increase of cellular cholesterol, fatty acid transporter is translocated from cytosol to membranes of type II pneumocytes.	KEGG pathway: Alkaloid biosynthesis II// KEGG pathway: Caprolactam degradation// KEGG pathway: Ethylbenzene degradation// KEGG pathway: Limonene and pinene degradation// KEGG pathway: Propanoate metabolism	-
182.19	88.28	2.06	NM_030827	Lrp2	Rattus norvegicus low density lipoprotein receptor-related protein 2 (Lrp2), mRNA [NM_030827]	ref|NM_030827|ref|XM_579493|gb|L34049|gb|XM_346656	Rn.26430	Lrp2	low density lipoprotein receptor-related protein 2	receptor for low density lipoprotein and a major kidney glomerular antigen for rat Heymann nephritis [RGD]	Megalin mediates IGF-I-induced clearance of Abeta and is involved in IGF-I transport into brain. Attenuated IGF-I/megalin input may contribute to increased risk of neurodegeneration, including late-onset Alzheimer's disease.// These data suggest that ligh	KEGG pathway: Hedgehog signaling pathway	-

[0326]



Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Gene Symbol	Gene Name	Summary	GeneRIF	Pathway	Homology
716.84	423.92	1.69	NM_031561	Cd36	Rattus norvegicus cd36 antigen (Cd36), mRNA [NM_031561]	ref|NM_031561|ref|XM_573338|ref|XM_575353|gb|AF113914	Rn.102418	Cd36	cd36 antigen	fatty acid translocase: involved in long-chain fatty acid (LCFA) transport: important in fatty acid metabolism and insulin function [RGD]	Up-regulation of CD36 may have a role in increasing oxidative stress in cultured microvascular endothelial cells and the heart in chronic diabetes.// the subcellular distribution of fatty acid binding protein plasma membrane, as well as FAT/CD36, is acute	KEGG pathway: Adipocytokine signaling pathway// KEGG pathway: ECM-receptor interaction// KEGG pathway: Hematopoietic cell lineage	-
1541.69	985.71	1.56	NM_024396	Abca2	Rattus norvegicus ATP-binding cassette, sub-family A (ABC1), member 2 (Abca2), mRNA [NM_024396]	ref|NM_024396|gb|AB037937|ens|ENSRNOT00000020339|ens|ENSRNOT00000036243	Rn.13115	Abca2	ATP-binding cassette, sub-family A (ABC1), member 2	glycosylated ABC transporter that binds ATP in the presence of magnesium: may play an important role in brain function [RGD]	ABCA2 protein is expressed predominantly in oligodendrocytes, and the expression of the protein is upregulated in the brain during maturation, especially between postnatal days 6 and 19.// ATP-binding cassette transporter ABCA2 (ABC2) expression in the de	KEGG pathway: ABC transporters - General	[Human, Mouse]HomoloGene:55590
139.55	89.53	1.56	NM_080778	Nr2f2	Rattus norvegicus nuclear receptor subfamily 2, group F, member 2 (Nr2f2), mRNA [NM_080778]	ref|NM_080778|gb|AF003944|ens|ENSRNOT00000014152|tc|TC57269	Rn.17815	Nr2f2	nuclear receptor subfamily 2, group F, member 2	transcriptional activator or repressor: involved in determining the metabolic phenotype of hepatic cells [RGD]	ARP-1/COUP-TFII acts as both a transcriptional repressor of microsomal triglyceride transfer protein and as a transcription activator of CYP7A1.	-	[Human, Mouse]HomoloGene:7628
1085.12	697.07	1.56	NM_053674	Phyh	Rattus norvegicus phytanoyl-CoA hydroxylase (Phyh), mRNA [NM_053674]	ref|NM_053674|gb|AF121345|gb|BC086573|ens|ENSRNOT00000024362	Rn.7279	Phyh	phytanoyl-CoA hydroxylase	catalyzes the conversion of phytanoyl-CoA to 2-hydroxyphytanoyl-CoA: plays a role in phytanic acid alpha-oxidation [RGD]	-	-	[Human, Mouse]HomoloGene:4530

[0327]

Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Gene Symbol	Gene Name	Summary	GeneRIF	Pathway	Homology
93.67	60.35	1.55	NM_001025415	NM_001025415	Rattus norvegicus cholesterol 25-hydroxylase (predicted) (Ch25h_predicted), mRNA [NM_001025415]	ref|NM_001025415|gb|XM_220063|gb|BC00979 4|ens|ENSRNOT00000025866	Rn.15697	Ch25h	cholesterol 25-hydroxylase	–	–	–	[Human, Mouse]HomoloGene:2942

[表49]

表49 GICに対して発現増加した唾液腺の注目遺伝子
ドーパミン合成 (GO ID: 42416)

Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Gene Symbol	Gene Name	Summary	GeneRIF	Pathway	Homology
267.70	82.81	3.23	AA963004	AA963004	AA963004 UI-R-E1-gd-d-04-0-UI.s1 UI-R-E1 Rattus norvegicus cDNA clone UI-R-E1-gd-d-04-0-UI 3', mRNA sequence [AA963004]	gb|AA963004|tc|TC554413	Rn.24539	Tgfb2	transforming growth factor, beta 2	binds the transforming growth factor-beta receptor: plays a role in regulation of cell growth and proliferation: may be involved in mesenchymal-epithelial cell interactions during development [RGD]	the pro-inflammatory cytokine MIF can shift the cytokine balance from the immunosuppressive state towards an inflammatory reaction, potentially through the inhibition of TGF-beta2 secretion by testicular peritubular cells.// TGF-beta2 mRNA and protein exp	KEGG pathway: Cell cycle// KEGG pathway: MAPK signaling pathway// KEGG pathway: TGF-beta signaling pathway	[Human, Mouse]Homolo Gene:2432
218.08	82.41	2.65	NM_012740	Th	Rattus norvegicus tyrosine hydroxylase (Th), mRNA [NM_012740]	ref|NM_012740.1|gb|L22651|gb|M11024.1|ens|ENSRNOT00000027682	Rn.11082	Th	tyrosine hydroxylase	catalyzes the rate limiting step in catecholamine biosynthesis: may be involved in response to hypoxia [RGD]	The kinetics of reduction of ferric TyrH by several reductants were determined by anaerobic stopped-flow spectroscopy. phosphorylation does not directly regulate the interconversion of the ferric and ferrous forms// The results indicate that the NGF/NGF	KEGG pathway: Parkinson's disease// KEGG pathway: Tyrosine metabolism	[Human, Mouse]Homolo Gene:307
61.95	24.38	2.54	NM_019169	Snca	Rattus norvegicus synuclein, alpha (Snca), mRNA [NM_019169]	ref|NM_019169.1|gb|AF007758|gb|AY550005.1|gb|AY550006	Rn.1827	Snca	synuclein, alpha	may play a role in regulation of synaptic vesicle biogenesis and organization: may be involved in neurotransmission [RGD]	We were able to modulate tyrosine hydroxylase-positive neuronal cell death by silencing alpha-synuclein expression. suggesting that down-regulation of alpha-synuclein is important in neuronal cell death of Parkinson's disease// DJ-1 up-regulates glutathio	KEGG pathway: Alzheimer's disease// KEGG pathway: Neurodegenerative Disorders// KEGG pathway: Parkinson's disease	[Human, Mouse]Homolo Gene:293

[表50]

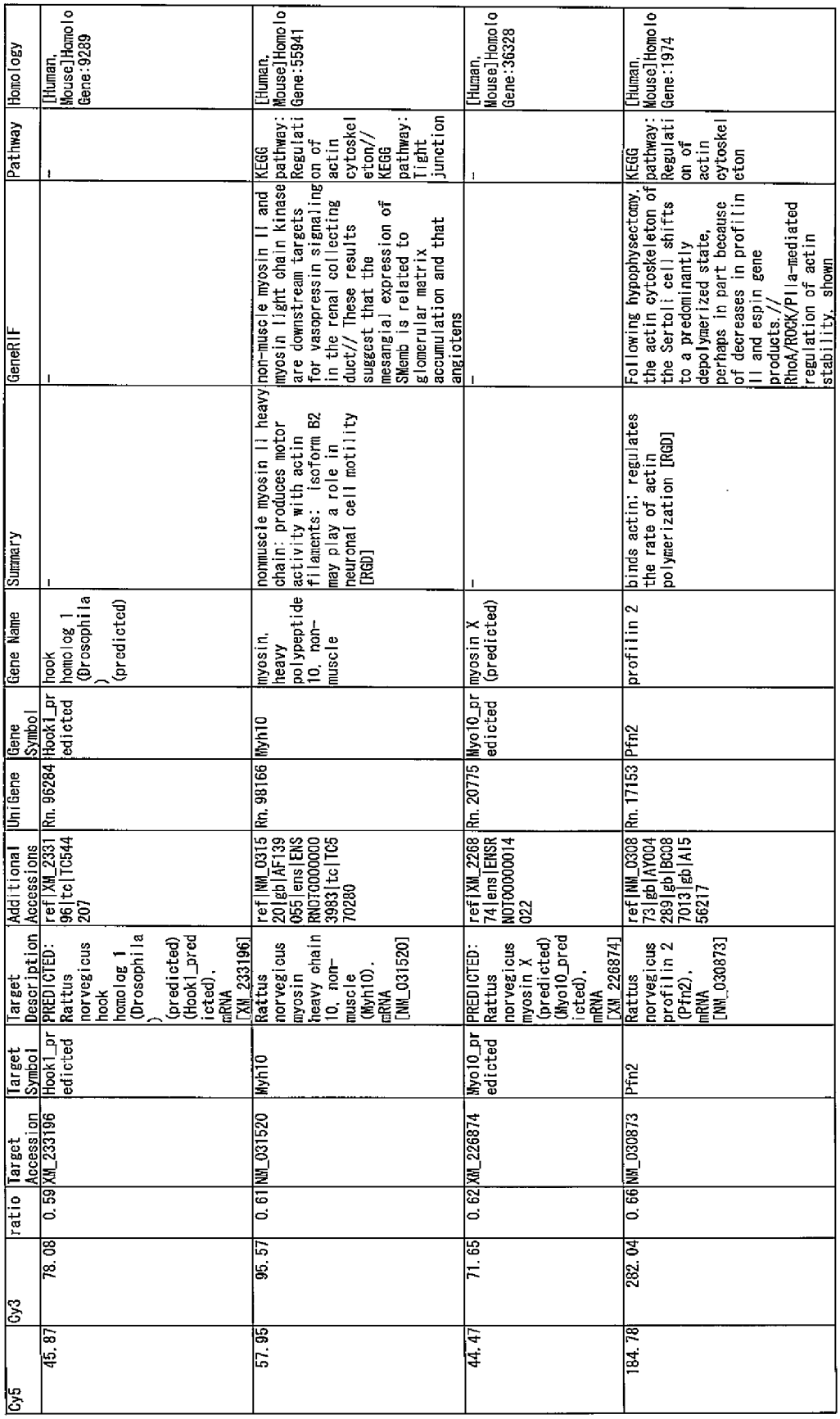
表50 Cに対して発現減少した唾液腺の注目遺伝子
アクチン結合 (GO ID: 3779)

Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Gene Symbol	Gene Name	Summary	GeneRIF	Pathway	Homology
16509.25	39439.68	0.42	NM_013097	Dnase1	Rattus norvegicus deoxyribonuclease I (Dnase1), mRNA [NM_013097]	ref|NM_0130 97|gb|X5606 0|gb|AF3971 51|gb|AF397 150	Rn. 6077	Dnase1	deoxyribonuclease I	glycoprotein that cleaves DNA endonucleolytically to yield 5'(alpha)- phosphodinucleotide and oligonucleotide end products; facilitates hydrolysis in alimentary duct and other digestive tissues [RGD]	A comparison of the expression and transport of DNase I from rats and DNaseIL3 from mice is reported.// results show that the chief cells of the stomach produce DNase I	-	[Human, Mouse]Homolo Gene:3826
115.15	257.92	0.45	NM_031747	Cnn1	Rattus norvegicus calponin 1 (Cnn1), mRNA [NM_031747]	ref|NM_0317 47|gb|D1443 7|gb|X71071 |gb|BC06180 9	Rn. 31788	Cnn1	calponin 1	binds actin stress fibers; involved in actin bundling [RGD]	Calponin increased in the molecular layer of the dentate gyrus, the site of mossy fiber sprouting, and neo-synaptogenesis, at 1 and 2 weeks after pilocarpine injection, when the reorganization was taking place.// CNh1 plays a role as tumor suppressor in S	-	[Human, Mouse]Homolo Gene:995
122.47	253.42	0.48	AW917167	AW917167	AW917167 EST348471 Rat gene index, normalized rat, norvegicus, Bento Soares Rattus norvegicus cDNA clone RGIEA09 5' end, mRNA sequence [AW917167]	gb|AW917167 |tc|TC55565 9	Rn. 18668	Pisl_predicted	plastin 1 (I isoform) (predicted)	-	-	-	[Human, Mouse]Homolo Gene:68270
1910.91	3729.09	0.51	NM_0010243 45	NM_00102 4345	Rattus norvegicus similar to tropomyosin 1, embryonic fibroblast - rat (MGC109519), mRNA [NM_0010243 45]	ref|NM_0010 24345|gb|BC 090009|gb|L 00382|tc|TC 518644	Rn. 17580	--	similar to tropomyosin 1, embryonic fibroblast - rat	-	-	-	[Human, Mouse]Homolo Gene:55509

[0328]

Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Gene Symbol	Gene Name	Summary	GeneRIF	Pathway	Homology
40.70	72.05	0.56	XM_234332	Plekhh1_predicted	PREDICTED: Rattus norvegicus pleckstrin homology domain containing, family H (with MyTH4 domain) member 1 (predicted) (Plekhh1_predicted), mRNA [XM_234332]	ref|XM_234332|ens|ENSRNOT00000001425 7	Rn.35024	Plekhh1_predicted	pleckstrin homology domain containing, family H (with MyTH4 domain) member 1 (predicted)	-	-	-	[Human, Mouse]Homolo Gene:24741
209.62	361.03	0.58	NM_019131	Tpm1	Rattus norvegicus tropomyosin 1, alpha (Tpm1), mRNA [NM_019131]	ref|NM_019131|AF372217|gb|AF372215|gb|M60668	Rn.87540	Tpm1	tropomyosin 1, alpha	This gene is a member of the tropomyosin family and encodes a protein that heterodimerizes with a beta subunit, binding actin in both muscle and nonmuscle cells. In both smooth and striated muscle cells, it plays a role in calcium dependent-regulation of	analysis of tropomyosin bending and binding sites for actin// The stability and energetics of the tropomyosin coiled coil are important for actin affinity.// A splicing silencer that regulates smooth muscle specific alternative splicing is active in multi	-	-
441.61	756.18	0.58	XM_573030	Myh11	PREDICTED: Rattus norvegicus myosin heavy chain 11 (Myh11), mRNA [XM_573030]	ref|XM_573030|gb|X16261|gb|XM_23986 6	Rn.94969	Myh11	myosin, heavy polypeptide 11, smooth muscle	transcription decreases following transformation with mutant p53 [RGD]	-	-	-
91.13	155.56	0.59	NM_182844	Myrip	Rattus norvegicus myosin VIIA and Rab interacting protein (Myrip), mRNA [NM_182844]	ref|NM_182844|AY331984|gb|AY331984|AW915575|tc|TC536770	Rn.16197	Myrip	myosin VIIA and Rab interacting protein	human and mouse homologs form a complex with Rab27A and Myosin VIIa; involved in melanosome trafficking to the actin cytoskeleton [RGD]	the Rab27B-Slac2-c complex is an important constituent of secretory granule exocytosis in parotid acinar cells	-	[Human, Mouse]Homolo Gene:9150

[0329]



Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Gene Symbol	Gene Name	Summary	GeneRIF	Pathway	Homology
45.87	78.08	0.59	XM_233196	Hook1_predicted	PREDICTED: Rattus norvegicus hook homolog 1 (Drosophila) (predicted) (Hook1_predicted), mRNA [XM_233196]	ref|XM_233196|TC544207	Rn.96284	Hook1_predicted	hook homolog 1 (Drosophila) (predicted)	-	-	-	[Human, Mouse]Homolo Gene:9289
57.95	95.57	0.61	NM_031520	Myh10	Rattus norvegicus myosin heavy chain 10, non-muscle (Myh10), mRNA [NM_031520]	ref|NM_031520|BF420155|ens|ENSRNOT00000039383|tc|TC570280	Rn.98166	Myh10	myosin, heavy polypeptide 10, non-muscle	nonmuscle myosin II heavy chain: produces motor activity with actin filaments: isoform B2 may play a role in neuronal cell motility [RGD]	non-muscle myosin II and myosin light chain kinase are downstream targets for vasopressin signaling in the renal collecting duct// These results suggest that the mesangial expression of SMemb is related to glomerular matrix accumulation and that angiotens	KEGG pathway: Regulation of actin cytoskeleton// KEGG pathway: Tight junction	[Human, Mouse]Homolo Gene:55941
44.47	71.65	0.62	XM_226874	Myo10_predicted	PREDICTED: Rattus norvegicus myosin X (predicted) (Myo10_predicted), mRNA [XM_226874]	ref|XM_226874|ENSRNOT00000014022	Rn.20775	Myo10_predicted	myosin X (predicted)	-	-	-	[Human, Mouse]Homolo Gene:36328
184.78	282.04	0.66	NM_030873	Pfn2	Rattus norvegicus profilin 2 (Pfn2), mRNA [NM_030873]	ref|NM_030873|AY004289|gb|BC087013|gb|AI556217	Rn.17153	Pfn2	profilin 2	binds actin: regulates the rate of actin polymerization [RGD]	Following hypophysectomy, the actin cytoskeleton of the Sertoli cell shifts to a predominantly depolymerized state, perhaps in part because of decreases in profilin II and espin gene products.// RhoA/ROCK/PIIa-mediated regulation of actin stability, shown	KEGG pathway: Regulation of actin cytoskeleton	[Human, Mouse]Homolo Gene:1974

[0330]

Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Gene Symbol	Gene Name	Summary	GeneRIF	Pathway	Homology
			XM_240417	Mtmr7_predicted	PREDICTED: Rattus norvegicus myotubularin related protein 7 (predicted) (Mtmr7_predicted), mRNA [XM_240417]	ref|XM_240417|gb|AA998777|ens|ENSRNOT00000015625|tc|TC538804	Rn.12785	Mtmr7_predicted	myotubularin related protein 7 (predicted)	-	-	-	[Human]HomoloGene:56848

[表51]

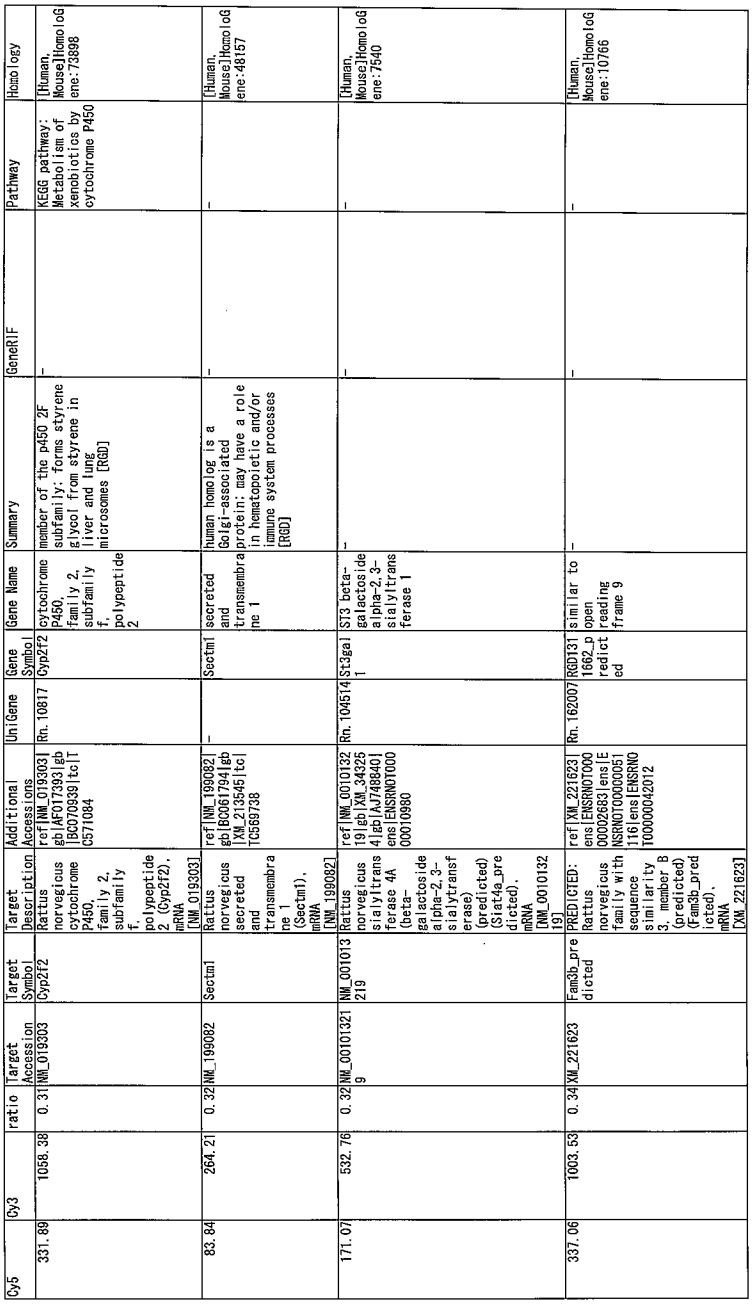
表51 Cに対して発現減少した嗅神経の注目遺伝子
細胞外成分 (GO ID: 5576, 44421, 5615)

Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Gene Symbol	Gene Name	Summary	GeneRIF	Pathway	Homology
66.53	1235.36	0.05	NM_019161	Cdh22	Rattus norvegicus cadherin 22 (Cdh22), mRNA [NM_019161]	ref|NM_019161|gb|D83349|tc|T05688625	Rn.145674	Cdh22	cadherin 22	mediates Ca2+ dependent cell adhesion: may play a role in brain and neuroendocrine organ morphogenesis [RGD]	PB-cadherin promotes survival of spermatocytes and activates Jak2 and Stat3 signalling.	-	[Human, Mouse]HomoloGene:23148
30527.51	498133.39	0.06	NM_133622	RGD:70857 7	Rattus norvegicus common salivary protein 1 (LOC77161), mRNA [NM_133622]	ref|NM_133622|gb|U00964|tc|T05568908|tc|T0571345	Rn.9752	-	common salivary protein 1	precursor appears to undergo post-translational modification to form a family of related salivary proteins [RGD]	-	-	-
25.47	367.35	0.07	NM_139087	Cgrefl	Rattus norvegicus cell growth regulator with EF hand domain 1 (Cgrefl), mRNA [NM_139087]	ref|NM_139087|gb|U66470|gb|AW913954|ens|ENSRNOT00000010586	Rn.31842	Cgrefl	cell growth regulator with EF hand domain 1	inhibits cell growth [RGD]	CGR11 appears to be a primary response gene expressed to moderate levels in functional p53 cells.	-	[Human, Mouse]HomoloGene:4790
37.00	247.55	0.15	NM_001007729	Pf4	Rattus norvegicus platelet factor 4 (Pf4), mRNA [NM_001007729]	ref|NM_001007729|gb|M34119|gb|AW915663|ens|ENSRNOT00000033406	Rn.6800	Cxcl4	chemokine (C-X-C motif) ligand 4	member of low-molecular weight chemokines superfamily: may mediate inflammation and immune response [RGD]	this study identified a novel regulatory element, TME(tandem repeat of MEIS1 binding element)in the PF4 promoter and demonstrated that MEIS1/PBX complexes bind to the TME// A carboxyl-terminal fragment of this protein effects a rapid histamine release from	KEGG pathway: Leukocyte transendothelial migration	[Mouse]HomoloGene:69289
204.73	1204.31	0.17	NM_053348	Fetub	Rattus norvegicus fetuin beta (Fetub), mRNA [NM_053348]	ref|NM_053348|gb|AJ242926|gb|BC070508|ens|ENSRNOT00000046199	Rn.2464	Fetub	fetuin beta	inhibits insulin receptor tyrosine kinase activity, protease inhibitory activities: developmentally regulates calcium metabolism and osteogenesis [RGD]	-	-	[Human, Mouse]HomoloGene:8660

[0331]

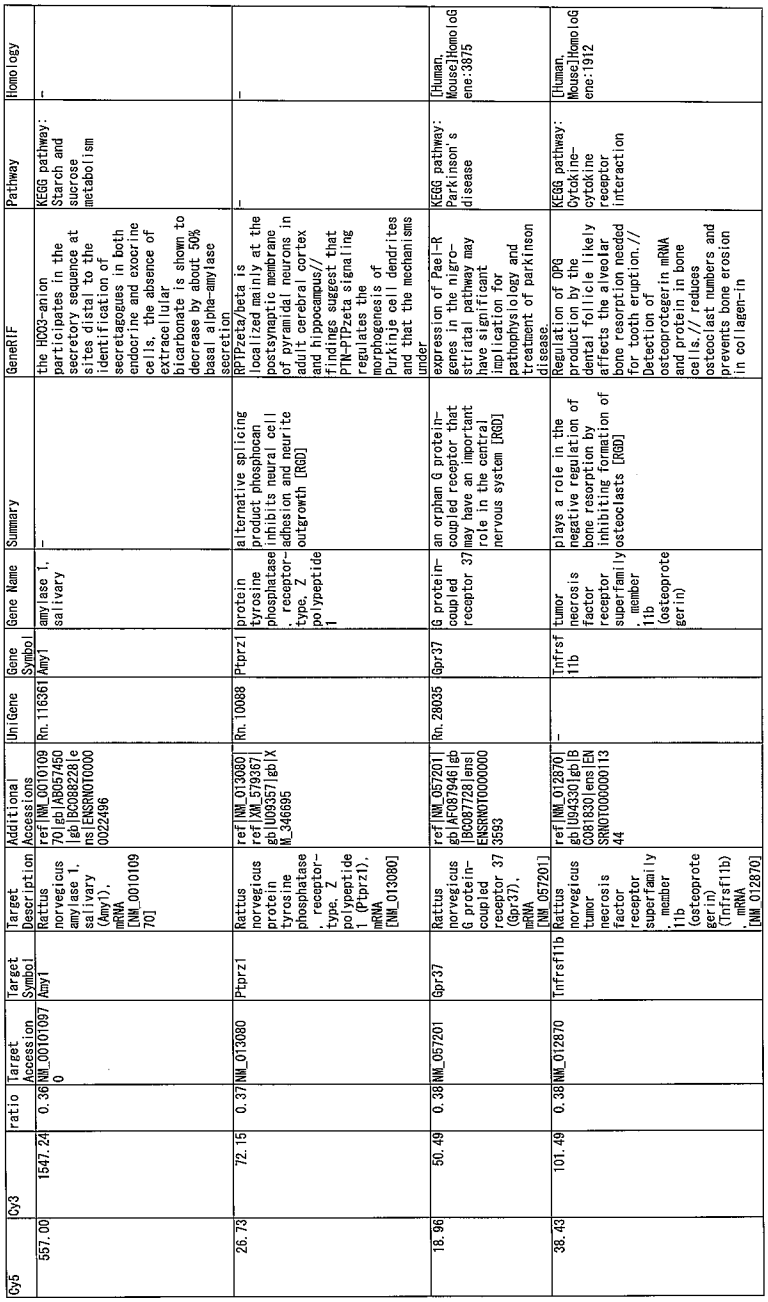
Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Gene Symbol	Gene Name	Summary	GeneRIF	Pathway	Homology
136.51	776.96	0.18	NM_001013180	NM_001013180	Rattus norvegicus secretoglobin family 3A, member 1 (Scgb3a1), mRNA [NM_001013180]	ref|NM_001013180|gb|AF436841|gb|AAL34079|gb|BI600202	Rn.30648	Scgb3a1	secretoglobin family 3A, member 1	secretoglobin: may have a role in airway function [RGD]	-	-	[Mouse]Homolo Gene:14160
54.55	254.82	0.21	NM_053744	Dlk1	Rattus norvegicus delta-like 1 homolog (Drosophila) (Dlk1), mRNA [NM_053744]	ref|NM_053744|ref|XM_579575|gb|D84336|gb|XM_346776	Rn.14547	Dlk1	delta-like 1 homolog (Drosophila)	involved in maintaining the undifferentiated status of the preadipocyte [RGD]	localisation in rat was in the medulla and the zona glomerulosa of the cortex of the adrenal glands, in the pars distalis of the adenohypophysis, and in the ovarian granulosa lutein cells but no staining was found in the pancreas	-	[Human, Mouse]HomoloGene:2846
154.13	608.12	0.25	XM_214143	Oit1_predicted	PREDICTED: Rattus norvegicus oncoprotein induced transcript 1 (predicted) (Oit1_predicted), mRNA [XM_214143]	ref|XM_214143|ens|ENSRNOT00000009650|tc|TC555554	Rn.38497	Oit1_predicted	oncoprotein induced transcript 1 homolog (mouse) (predicted)	-	-	-	[Human, Mouse]HomoloGene:16354
103.38	383.73	0.27	NM_203337	RGD:1303068	Rattus norvegicus alpha-2,3-sialyltransferase ST3Gal IV (siat4c), mRNA [NM_203337]	ref|NM_203337|gb|AJ626825|gb|BC089057|ens|ENSRNOT00000013243	Rn.24125	St3gal4	ST3 beta-galactoside alpha-2,3-sialyltransferase 4	plasma membrane-specific alpha 2,3- sialic acid transporter: may be important for protein amino acid glycosylation [RGD]	-	-	[Human, Mouse]HomoloGene:4572
75.56	262.31	0.29	NM_133295	Ces3	Rattus norvegicus carboxylesterase 3 (Ces3), mRNA [NM_133295]	ref|NM_133295|ref|NM_001013889|ref|XM_579616|gb|X51974	Rn.2549	Ces3	carboxylesterase 3	enzyme that hydrolizes long-chain fatty acids and thioesters; may play a role in lipid metabolism and/or the elimination of toxic substances [RGD]	-	KEGG pathway: Alkaloid biosynthesis II	-

[0332]



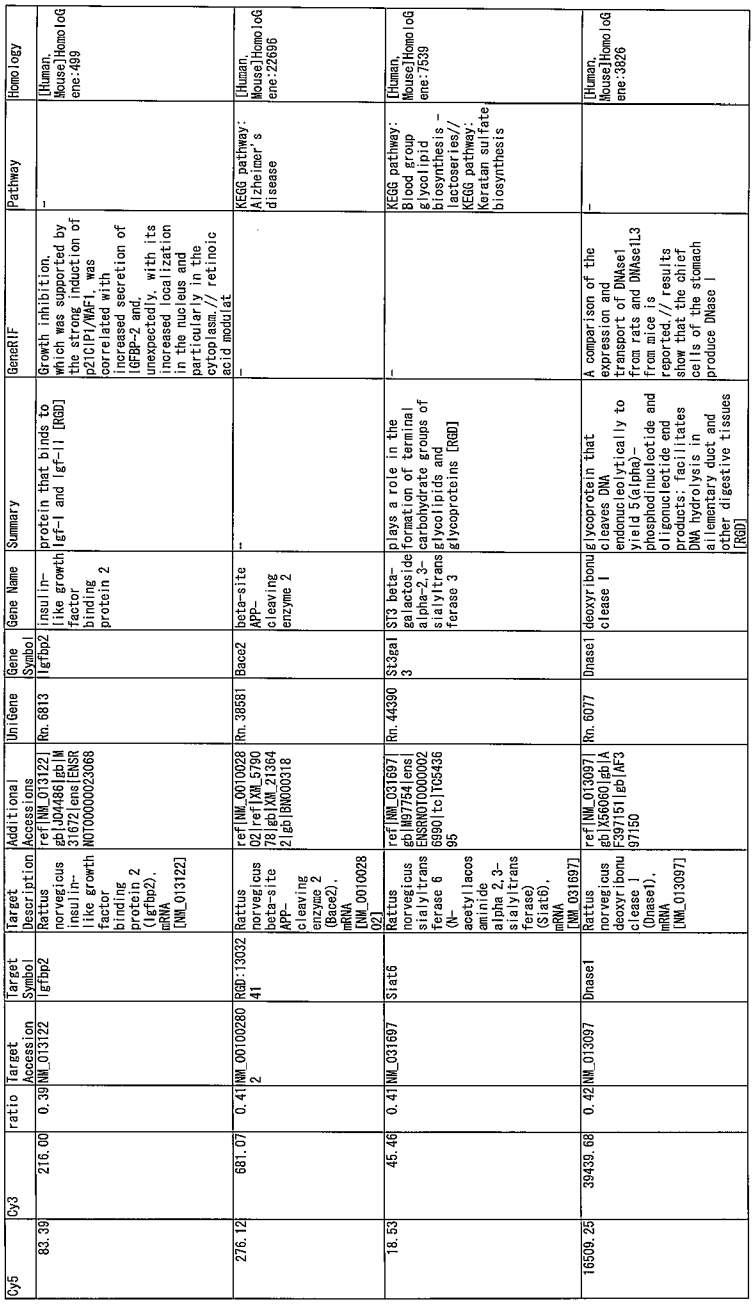
Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Gene Symbol	Gene Name	Summary	GeneRIF	Pathway	Homology
331.89	1058.38	0.31	NM_019303	Cyp2f2	Rattus norvegicus cytochrome P450, family 2, subfamily f, polypeptide 2 (Cyp2f2), mRNA [NM_019303]	ref|NM_019303|gb|AF017393|gb|BC070939|tc|TC571084	Rn.10817	Cyp2f2	cytochrome P450, family 2, subfamily f, polypeptide 2	member of the p450 2F subfamily; forms styrene glycol from styrene in liver and lung microsomes [RGD]	-	KEGG pathway: Metabolism of xenobiotics by cytochrome P450	[Human, Mouse]Homolog ene:73898
83.84	264.21	0.32	NM_199082	Sectm1	Rattus norvegicus secreted and transmembrane 1 (Sectm1), mRNA [NM_199082]	ref|NM_199082|gb|BC061794|gb|XM_213545|tc|TC569738	-	Sectm1	secreted and transmembrane 1	human homolog is a Golgi-associated protein; may have a role in hematopoietic and/or immune system processes [RGD]	-	-	[Human, Mouse]Homolog ene:48157
171.07	532.76	0.32	NM_00101321 9	NM_001013 219	Rattus norvegicus sialyltransferase 4A (beta-galactoside alpha-2,3-sialytransferase) (predicted) (Siat4a_predicted), mRNA [NM_0010132 19]	ref|NM_0010132 19|gb|XM_34325 4|gb|AJ748640|ens|ENSRNOT000 00010980	Rn.104514	St3gal1	ST3 beta-galactoside alpha-2,3-sialyltransferase 1	-	-	-	[Human, Mouse]Homolog ene:7540
337.06	1003.53	0.34	XM_221623	Fam3b_predicted	PREDICTED: Rattus norvegicus family with sequence similarity 3, member B (predicted) (Fam3b_predicted), mRNA [XM_221623]	ref|XM_221623|ens|ENSRNOT000 00002683|ens|ENSRNOT00000005 1116|ens|ENSRNOT00000042012	Rn.162007	RGD1311662_predicted	similar to open reading frame 9	-	-	-	[Human, Mouse]Homolog ene:10766

[0333]



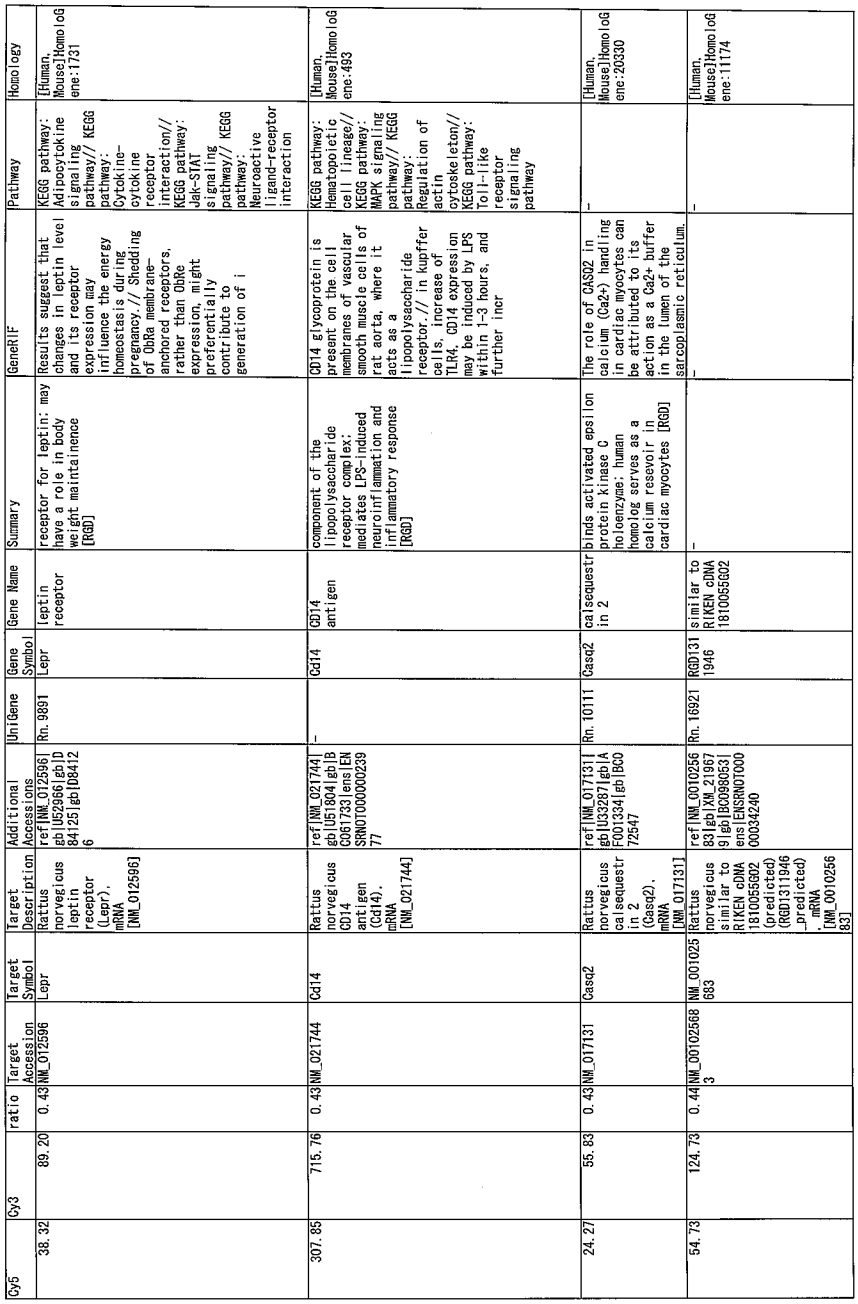
Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Gene Symbol	Gene Name	Summary	GeneRIF	Pathway	Homology
557.00	1547.24	0.36	NM_001010970	Amy1	Rattus norvegicus amylase 1, salivary (Amy1), mRNA [NM_001010970]	ref|NM_001010970|gb|AB057450|gb|BC088228|ens|ENSRNOT00000022496	Rn.116361	Amy1	amylase 1, salivary	-	the HCO3-anion participates in the secretory sequence at sites distal to the identification of secretagogues in both endocrine and exocrine cells, the absence of extracellular bicarbonate is shown to decrease by about 50% basal alpha-amylase secretion	KEGG pathway: Starch and sucrose metabolism	-
26.73	72.15	0.37	NM_013080	Ptprz1	Rattus norvegicus protein tyrosine phosphatase, receptor-type, Z polypeptide 1 (Ptprz1), mRNA [NM_013080]	ref|NM_013080|ref|XM_579367|gb|U09357|gb|XM_346695	Rn.10088	Ptprz1	protein tyrosine phosphatase, receptor-type, Z polypeptide 1	alternative splicing product phosphocan inhibits neural cell adhesion and neurite outgrowth [RGD]	RPTPzeta/beta is localized mainly at the postsynaptic membrane of pyramidal neurons in adult cerebral cortex and hippocampus// findings suggest that PTN-PTPzeta signaling regulates the morphogenesis of Purkinje cell dendrites and that the mechanisms under	-	-
18.96	50.49	0.38	NM_057201	Gpr37	Rattus norvegicus G protein-coupled receptor 37 (Gpr37), mRNA [NM_057201]	ref|NM_057201|gb|AF087946|gb|BC087728|ens|ENSRNOT00000053593	Rn.28035	Gpr37	G protein-coupled receptor 37	an orphan G protein-coupled receptor that may have an important role in the central nervous system [RGD]	expression of Pael-R genes in the nigro-striatal pathway may have significant implication for pathophysiology and treatment of parkinson disease.	KEGG pathway: Parkinson's disease	[Human, Mouse]Homolo Gene:3875
38.43	101.49	0.38	NM_012870	Tnfrsf11b	Rattus norvegicus tumor necrosis factor receptor superfamily, member 11b (osteoprotegerin) (Tnfrsf11b), mRNA [NM_012870]	ref|NM_012870|gb|U94330|gb|BC081830|ens|ENSRNOT00000011344	-	Tnfrsf11b	tumor necrosis factor receptor superfamily, member 11b (osteoprotegerin)	plays a role in the negative regulation of bone resorption by inhibiting formation of osteoclasts [RGD]	Regulation of OPG production by the dental follicle likely affects the alveolar bone resorption needed for tooth eruption.// Detection of osteoprotegerin mRNA and protein in bone cells.// reduces osteoclast numbers and prevents bone erosion in collagen-in	KEGG pathway: Cytokine-cytokine receptor interaction	[Human, Mouse]Homolo Gene:1912

[0334]



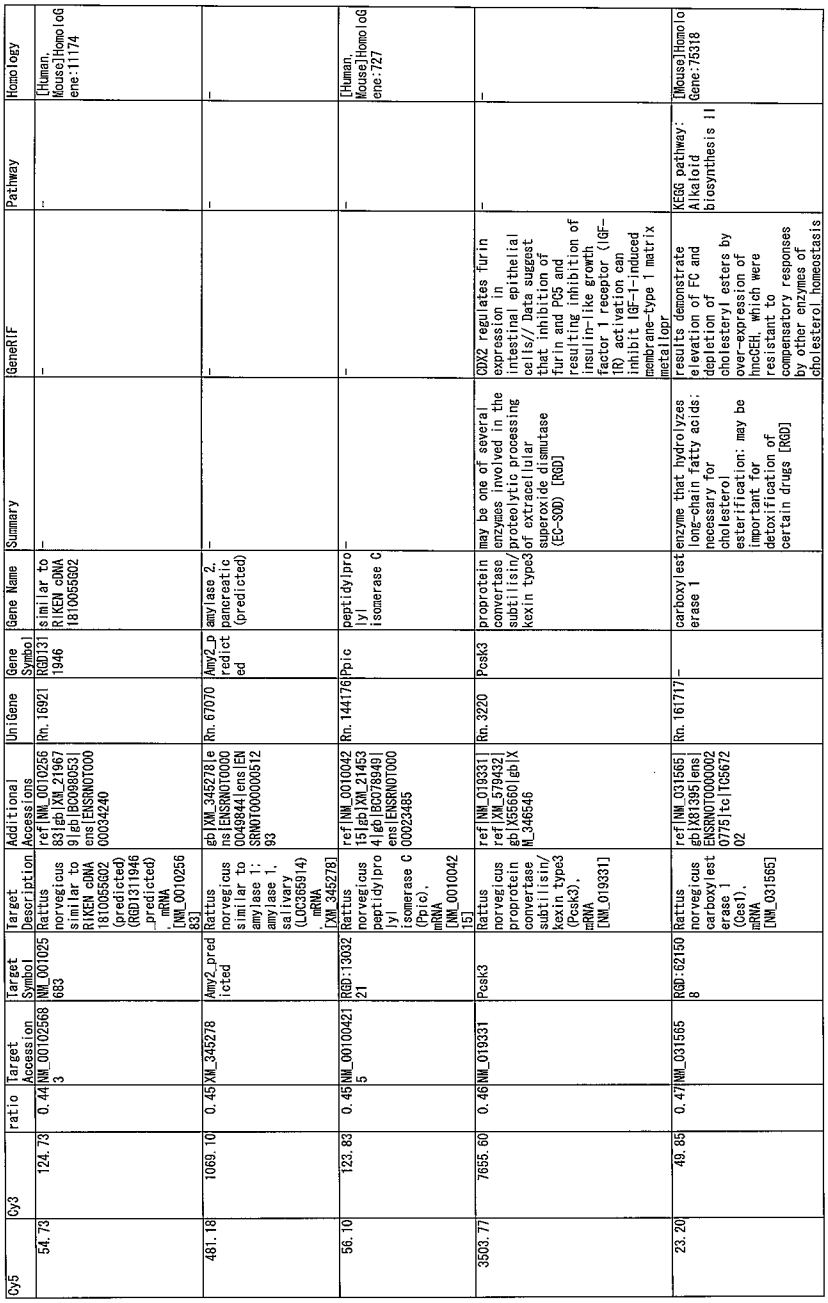
Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Gene Symbol	Gene Name	Summary	GeneRIF	Pathway	Homology
83.39	216.00	0.39	NM_013122	Igfbp2	Rattus norvegicus insulin-like growth factor binding protein 2 (Igfbp2), mRNA [NM_013122]	ref|NM_013122|gb|J04486|gb|M31672|ens|ENSRNOT00000023068	Rn.6813	Igfbp2	insulin-like growth factor binding protein 2	protein that binds to igf-I and igf-II [RGD]	Growth inhibition, which was supported by the strong induction of p21CIP1/WAF1, was correlated with increased secretion of IGFBP-2 and, unexpectedly, with its increased localization in the nucleus and particularly in the cytoplasm.// retinoic acid modulat	-	[Human, Mouse]Homolo Gene:499
276.12	681.07	0.41	NM_001100280 2	RGD:13032 41	Rattus norvegicus beta-site APP-cleaving enzyme 2 (Bace2), mRNA [NM_001100028 02]	ref|NM_001100028 02|ref|XM_579078|gb|XM_213642|gb|BM000318	Rn.38581	Bace2	beta-site APP-cleaving enzyme 2	-	-	KEGG pathway: Alzheimer's disease	[Human, Mouse]Homolo Gene:22696
18.53	45.46	0.41	NM_031697	Siat6	Rattus norvegicus sialyltransferase 6 (N-acetyllacosaminide alpha 2,3-sialyltransferase) (Siat6), mRNA [NM_031697]	ref|NM_031697|gb|M97754|ens|ENSRNOT00000026990|tc|TC54395	Rn.44390	St3gal3	ST3 beta-galactoside alpha-2,3-sialyltransferase 3	plays a role in the formation of terminal carbohydrate groups of glycolipids and glycoproteins [RGD]	-	KEGG pathway: Blood group glycolipid biosynthesis - lactoseries// KEGG pathway: Keratan sulfate biosynthesis	[Human, Mouse]Homolo Gene:7539
16509.25	39439.68	0.42	NM_013097	Dnase1	Rattus norvegicus deoxyribonuclease I (Dnase1), mRNA [NM_013097]	ref|NM_013097|gb|X56060|gb|AF397151|gb|AF397150	Rn.6077	Dnase1	deoxyribonuclease I	glycoprotein that cleaves DNA endonucleolytically to yield 5(alpha)-phosphodinucleotide and oligonucleotide end products; facilitates DNA hydrolysis in alimentary duct and other digestive tissues [RGD]	A comparison of the expression and transport of DNase1 from rats and DNase1L3 from mice is reported.// results show that the chief cells of the stomach produce DNase I	-	[Human, Mouse]Homolo Gene:3826

[0335]



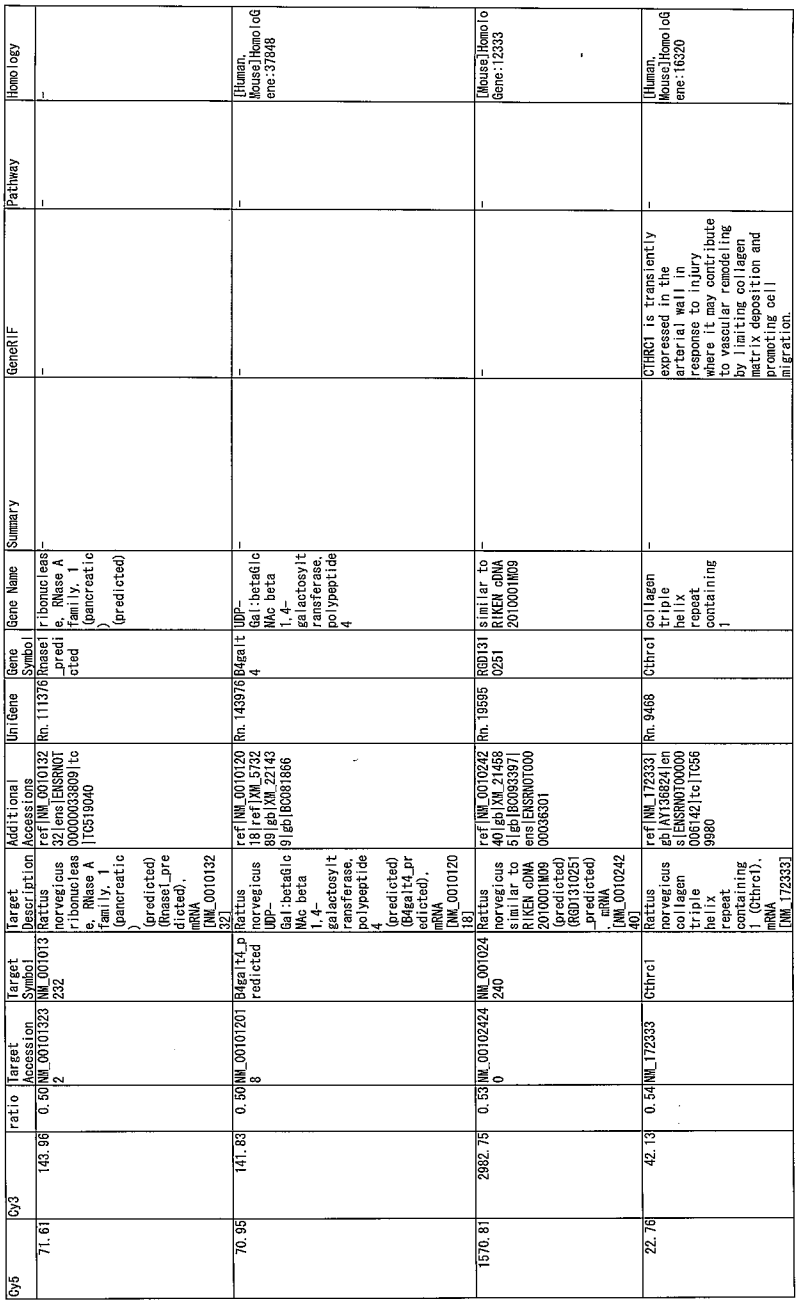
Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Gene Symbol	Gene Name	Summary	GeneRIF	Pathway	Homology
38.32	89.20	0.43	NM_012596	Lepr	Rattus norvegicus leptin receptor (Lepr), mRNA [NM_012596]	ref|NM_012596|gb|U52966|gb|D84125|gb|D84126	Rn.9891	Lepr	leptin receptor	receptor for leptin: may have a role in body weight maintainence [RGD]	Results suggest that changes in leptin level and its receptor expression may influence the energy homeostasis during pregnancy.// Shedding of ObRa membrane-anchored receptors, rather than ObRe expression, might preferentially contribute to generation of i	KEGG pathway: Adipocytokine signaling pathway// KEGG pathway: Cytokine-cytokine receptor interaction// KEGG pathway: Jak-STAT signaling pathway// KEGG pathway: Neuroactive ligand-receptor interaction	[Human, Mouse]Homolo gene:1731
307.85	715.76	0.43	NM_021744	Cd14	Rattus norvegicus CD14 antigen (Cd14), mRNA [NM_021744]	ref|NM_021744|gb|U51804|gb|BC061733|ens|ENSRNOT00000023977	-	Cd14	CD14 antigen	component of the lipopolysaccharide receptor complex: mediates LPS-induced neuroinflammation and inflammatory response [RGD]	CD14 glycoprotein is present on the cell membranes of vascular smooth muscle cells of rat aorta, where it acts as a lipopolysaccharide receptor.// in kupffer cells, increase of TLR4, CD14 expression may be induced by LPS within 1-3 hours, and further incr	KEGG pathway: Hematopoietic cell lineage// KEGG pathway: MAPK signaling pathway// KEGG pathway: Regulation of actin cytoskeleton// KEGG pathway: Toll-like receptor signaling pathway	[Human, Mouse]Homolo gene:493
24.27	55.83	0.43	NM_017131	Casq2	Rattus norvegicus calsequestrin 2 (Casq2), mRNA [NM_017131]	ref|NM_017131|gb|U33287|gb|AF001334|gb|BC072547	Rn.10111	Casq2	calsequestrin 2	binds activated epsilon protein kinase C holoenzyme; human homolog serves as a calcium reservoir in cardiac myocytes [RGD]	The role of CASQ2 in calcium (Ca2+) handling in cardiac myocytes can be attributed to its action as a Ca2+ buffer in the lumen of the sarcoplasmic reticulum.	-	[Human, Mouse]Homolo gene:20330
54.73	124.73	0.44	NM_001025683	Rattus norvegicus similar to RIKEN cDNA 1810055G02 (predicted) (RGD1311946_predicted), mRNA [NM_001025683]	ref|NM_001025683|gb|XM_213677|gb|BC098653|ens|ENSRNOT00000034240	Rn.16921	RGD1311946	similar to RIKEN cDNA 1810055G02	-	-	[Human, Mouse]Homolo gene:11174

[0336]



Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Gene Symbol	Gene Name	Summary	GeneRIF	Pathway	Homology
54.73	124.73	0.44	NM_001025683	NM_001025683	Rattus norvegicus similar to RIKEN cDNA 1810055G02 (predicted) (RGD1311946_predicted), mRNA [NM_0010256 83]	ref|NM_0010256 83|gb|AK_21967 9|gb|BC098053| ens|ENSRNOT000 00034240	Rn. 16921	RGD1311946	similar to RIKEN cDNA 1810055G02	-	-	-	[Human, Mouse]HomoloGene:111174
481.18	1069.10	0.45	XM_345278	Amy2_predicted	Rattus norvegicus similar to amylase 1; amylase 1, salivary (LOC365914), mRNA [XM_345278]	gb|XM_345278|ens|ENSRNOT00000049441ens|ENSRNOT00000005 93	Rn. 67070	Amy2_predicted	amylase 2, pancreatic (predicted)	-	-	-	-
56.10	123.83	0.45	NM_001004215	RGD:1303221	Rattus norvegicus peptidylprolyl isomerase C (Ppic), mRNA [NM_0010042 15]	ref|NM_0010042 15|gb|XM_214534|gb|BC078949| ens|ENSRNOT00000023485	Rn. 144176	Ppic	peptidylprolyl isomerase C	-	-	-	[Human, Mouse]HomoloGene:727
3503.77	7655.60	0.46	NM_019331	Pcsk3	Rattus norvegicus proprotein convertase subtilisin/kexin type3 (Pcsk3), mRNA [NM_019331]	ref|NM_019331|ref|XM_579432|gb|X55660|gb|X_346546	Rn. 3220	Pcsk3	proprotein convertase subtilisin/kexin type3	may be one of several enzymes involved in the proteolytic processing of extracellular superoxide dismutase (EC-SOD) [RGD]	CDX2 regulates furin expression in intestinal epithelial cells// Data suggest that inhibition of furin and PC5 and resulting inhibition of insulin-like growth factor 1 receptor (IGF-1R) activation can inhibit IGF-1-induced membrane-type 1 matrix metalloproteinase	-	-
23.20	49.85	0.47	NM_031565	RGD:621508	Rattus norvegicus carboxylesterase 1 (Ces1), mRNA [NM_0315665]	ref|NM_031565|gb|X81395|ens|ENSRNOT00000020776|tc|TC5672 02	Rn. 161717	-	carboxylesterase 1	enzyme that hydrolyzes long-chain fatty acids: necessary for cholesterol esterification: may be important for detoxification of certain drugs [RGD]	results demonstrate elevation of FC and depletion of cholesteryl esters by over-expression of hmCEH, which were resistant to compensatory responses by other enzymes of cholesterol homeostasis	KEGG pathway: Alkaloid biosynthesis II	[Mouse]HomoloGene:75318

[0337]



Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Gene Symbol	Gene Name	Summary	GeneRIF	Pathway	Homology
71.61	143.96	0.50	NM_001013232	NM_001013232	Rattus norvegicus ribonuclease, RNase A family, 1 (pancreatic) (predicted) (Rnase1_predicted), mRNA [NM_001013232]	ref|NM_001013232|ens|ENSRNOT00000038809|tc|TC519040	Rn.111376	Rnase1_predicted	ribonuclease, RNase A family, 1 (pancreatic) (predicted)	-	-	-	-
70.95	141.83	0.50	NM_001012018	B4galt4_predicted	Rattus norvegicus UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 4 (predicted) (B4galt4_predicted), mRNA [NM_001012018]	ref|NM_001012018|ref|XM_573289|ref|XM_221439|gb|BC081866	Rn.143976	B4galt4	UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 4	-	-	-	[Human, Mouse]HomoloGene:37848
1570.81	2982.75	0.53	NM_001024240	NM_001024240	Rattus norvegicus similar to RIKEN cDNA 2010001M09 (predicted) (RGD1310251_predicted), mRNA [NM_001024240]	ref|NM_001024240|gb|XM_214585|gb|BC093397|ens|ENSRNOT00000036301	Rn.19595	RGD1310251	similar to RIKEN cDNA 2010001M09	-	-	-	[Mouse]HomoloGene:12333
22.76	42.13	0.54	NM_172333	Cthrc1	Rattus norvegicus collagen triple helix repeat containing 1 (Cthrc1), mRNA [NM_172333]	ref|NM_172333|gb|AY368241|ens|ENSRNOT00000006142|tc|TC569980	Rn.9468	Cthrc1	collagen triple helix repeat containing 1	-	CTHRC1 is transiently expressed in the arterial wall in response to injury where it may contribute to vascular remodeling by limiting collagen matrix deposition and promoting cell migration.	-	[Human, Mouse]HomoloGene:16320

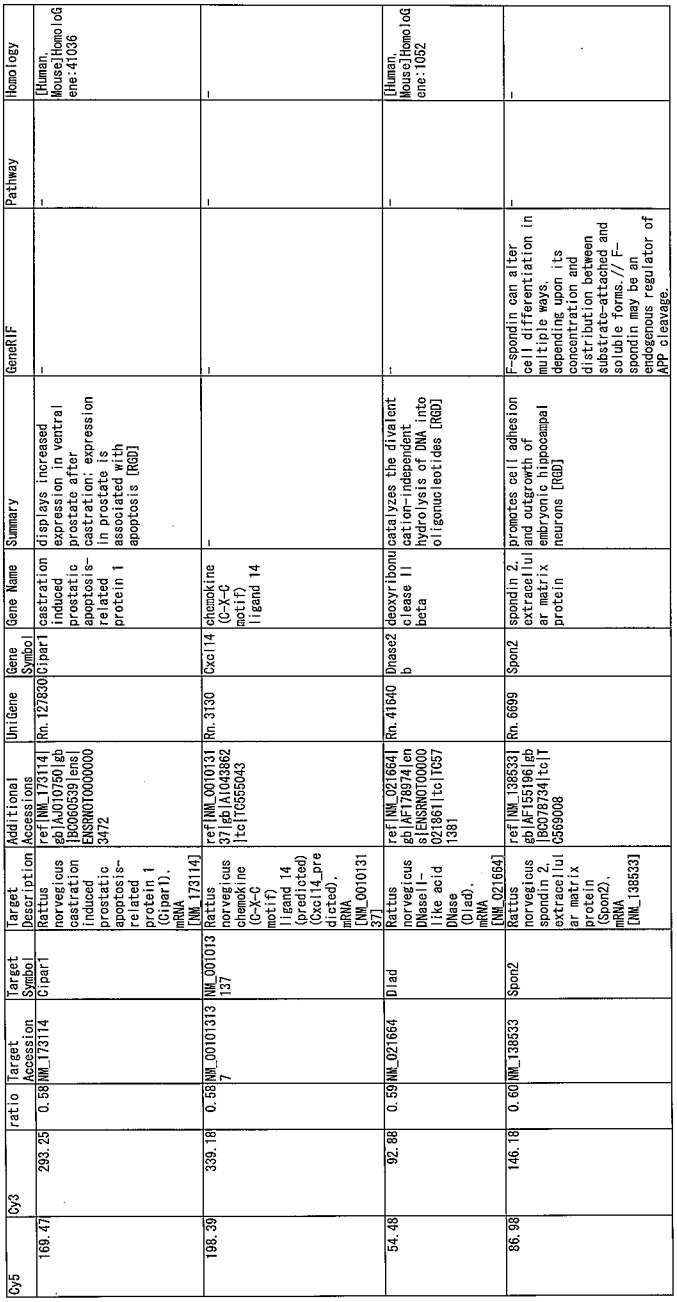
[0338]

Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Gene Symbol	Gene Name	Summary	GeneRIF	Pathway	Homology
92.73	169.69	0.55	XM_215963	Lama5	PREDICTED: Rattus norvegicus laminin, alpha 5 (Lama5), mRNA [XM_215963]	ref|XM_215963|ens|ENSRNOT0000008981|ens|ENSRNOT00000051597|tc|TC51890	Rn.62816	Lama5	laminin, alpha 5	an extracellular matrix glycoprotein involved in cell migration and differentiation [RGD]	Data suggest that the early arrest of tumor cells in the pulmonary vasculature through interaction of alpha3beta1 integrin with laminin-5 in exposed basement membrane provides a basis for cell arrest during pulmonary metastasis.// laminin 6 and 5 have dis	KEGG pathway: Cell Communication//KEGG pathway: ECM-receptor interaction//KEGG pathway: Focal adhesion	[Human, Mouse]HomoloGene:4060
59.27	107.57	0.55	XM_235478	Kdelr3_predicted	PREDICTED: Rattus norvegicus KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 3 (predicted) (Kdelr3_predicted), mRNA [XM_235478]	ref|XM_235478|ens|ENSRNOT00000018174|tc|TC545855	Rn.161994	Kdelr3_predicted	KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 3 (predicted)	-	-	-	[Human, Mouse]HomoloGene:68533
120.04	217.05	0.55	NM_012729	Prss2	Rattus norvegicus protease, serine, 2 (Prss2), mRNA [NM_012729]	ref|NM_012729|ref|XM_342669|gb|V01274|ens|ENSRNOT00000018852	Rn.1584	Prss2	protease, serine, 2	catalyzes the cleavage of Arg-Xaa, Lys-Xaa [RGD]	-	-	-
72.00	130.17	0.55	NM_134432	Agt	Rattus norvegicus angiotensinogen (Agt), mRNA [NM_134432]	ref|NM_134432|gb|BC078741|gb|LO0094|ens|ENSRNOT00000024917	Rn.6319	Agt	angiotensinogen (serpin peptidase inhibitor, clade A, member 8)	plays a role in regulation of blood pressure [RGD]	modification of the critical balance between ANG II and ET-1 systems through variant Dear contributes to hypertension susceptibility in female F2(RxS) intercross rats// the mechanism by which Ang II stimulates IGF-IR expression in VSMCs involves NF-KappaB	-	[Human, Mouse]HomoloGene:14

[0339]

Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Gene Symbol	Gene Name	Summary	GeneRIF	Pathway	Homology
812.47	1464.83	0.55	NM_001008334	RGD1307423_predicted	Rattus norvegicus similar to RIKEN cDNA 1810014L12 (predicted) (RGD1307423_predicted), mRNA [NM_001008334]	ref|NM_001008334|gb|AW523074|gb|BC083344|gb|BF548446	Rn.20057	Tmem97	transmembrane protein 97	-	-	-	[Human, Mouse]Homologene:6443
61.64	110.31	0.56	XM_342668	Prss3_predicted	PREDICTED: Rattus norvegicus protease, serine, 3 (mesotrypsin) (predicted) (Prss3_predicted), mRNA [XM_342668]	ref|XM_342668|ens|ENSRNOT00000041100	Rn.154705	Prss3_predicted	protease, serine, 3 (mesotrypsin) (predicted)	-	-	-	-
47.51	84.12	0.56	NM_176074	C6	Rattus norvegicus complement component 6 (C6), mRNA [NM_176074]	ref|NM_176074|gb|AY230250|ens|ENSRNOT00000033112|tc|TC569389	Rn.16145	C6	complement component 6	component of the complement cascade for immune response., may be a component of the membrane attack complex [RGD]	Lung allografts from C6-deficient donors to C6(-) recipients survive 13-17 days, whereas allografts from C6-sufficient donors to C6(+) recipients are rejected with intense vasoular infiltration and diffuse alveolar hemorrhage 7 days posttransplant. // The	KEGG pathway: Complement and coagulation cascades	[Human, Mouse]Homologene:47
547.92	965.78	0.57	XM_340999	Tfrc	PREDICTED: Rattus norvegicus transferrin receptor (Tfrc), mRNA [XM_340999]	ref|XM_340999|ens|ENSRNOT00000024071ens|ENSRNOT00000004868|ens|ENSRNOT00000041968	Rn.98672	Tfrc	transferrin receptor	receptor for transferrin: involved in regulating stellate cell activation [RGD]	a region of the TfR that can potentially interact with Hso70// These data suggest that alveolar type II (but not type I) cells express functional transferrin receptor in adult rat alveolar epithelium.// MPP(+)-dependent aconitase inactivation, Tf-iron upt	KEGG pathway: Hematopoietic cell lineage	[Human, Mouse]Homologene:2429

[0340]

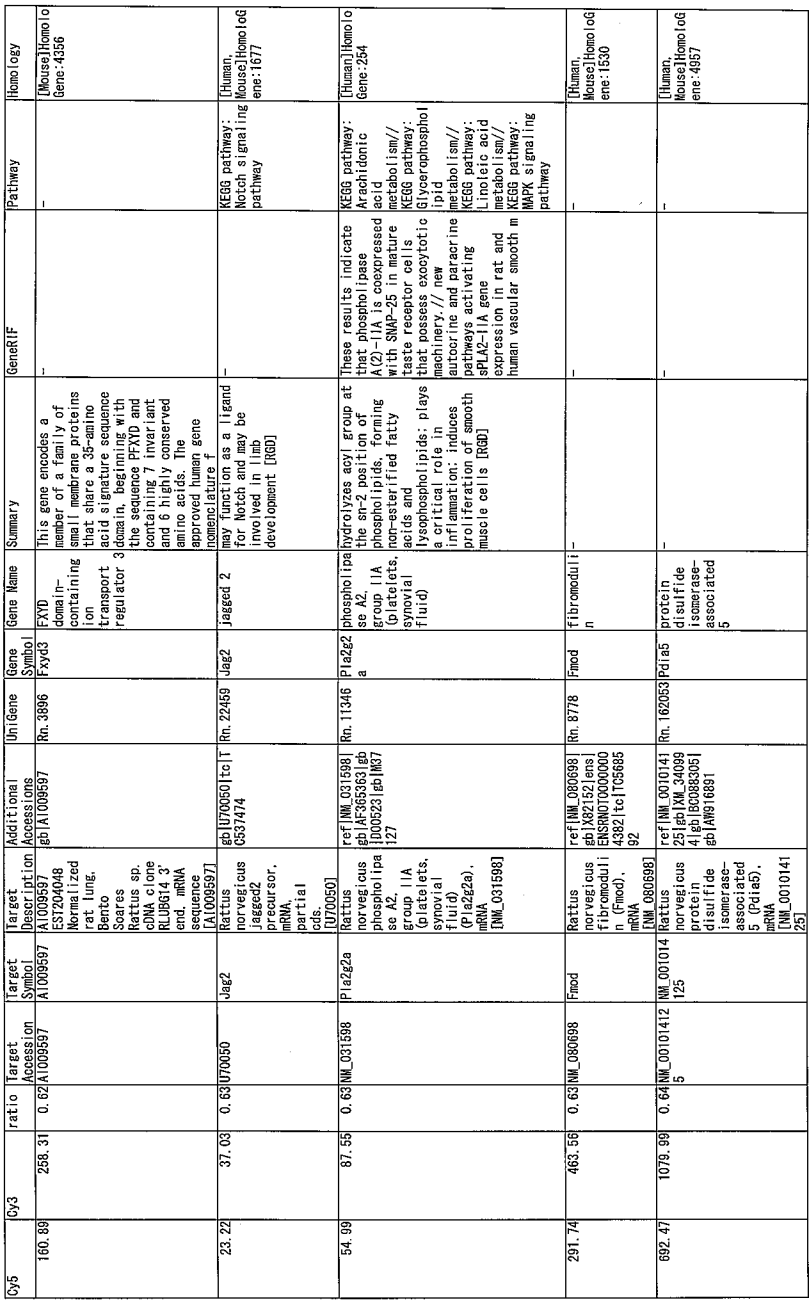


Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Gene Symbol	Gene Name	Summary	GeneRIF	Pathway	Homology
169.47	293.25	0.58	NM_173114	Cipar1	Rattus norvegicus castration induced prostatic apoptosis-related protein 1 (Cipar1), mRNA [NM_173114]	ref|NM_173114|gb|AJ010750|gb|BC060539|ens|ENSRNOT00000003472	Rn.127830	Cipar1	castration induced prostatic apoptosis-related protein 1	displays increased expression in ventral prostate after castration: expression in prostate is associated with apoptosis [RGD]	-	-	(Human, Mouse)Homolog ene:41036
198.39	339.18	0.58	NM_001013137	Rattus norvegicus chemokine (C-X-C motif) ligand 14 (predicted) (Cxcl14_predicted), mRNA [NM_0010131 37]	ref|NM_0010131 37|gb|AJ043862|tc|TC555043	Rn.3130	Cxcl14	chemokine (C-X-C motif) ligand 14	-	-	-	-
54.48	92.88	0.59	NM_021664	Dlad	Rattus norvegicus DNase II-like acid DNase (Dlad), mRNA [NM_021664]	ref|NM_021664|gb|AF179874|ens|ENSRNOT00000021861|tc|TC571381	Rn.41640	Dnase2b	deoxyribonuclease II beta	catalyzes the divalent cation-independent hydrolysis of DNA into oligonucleotides [RGD]	-	-	(Human, Mouse)Homolog ene:1052
86.98	146.18	0.60	NM_138533	Spon2	Rattus norvegicus spondin 2, extracellular matrix protein (Spon2), mRNA [NM_138533]	ref|NM_138533|gb|AF155196|gb|BC078734|tc|TC569008	Rn.6699	Spon2	spondin 2, extracellular matrix protein	promotes cell adhesion and outgrowth of embryonic hippocampal neurons [RGD]	F-spondin can alter cell differentiation in multiple ways, depending upon its concentration and distribution between substrate-attached and soluble forms.// F-spondin may be an endogenous regulator of APP cleavage.	-	-

[0341]

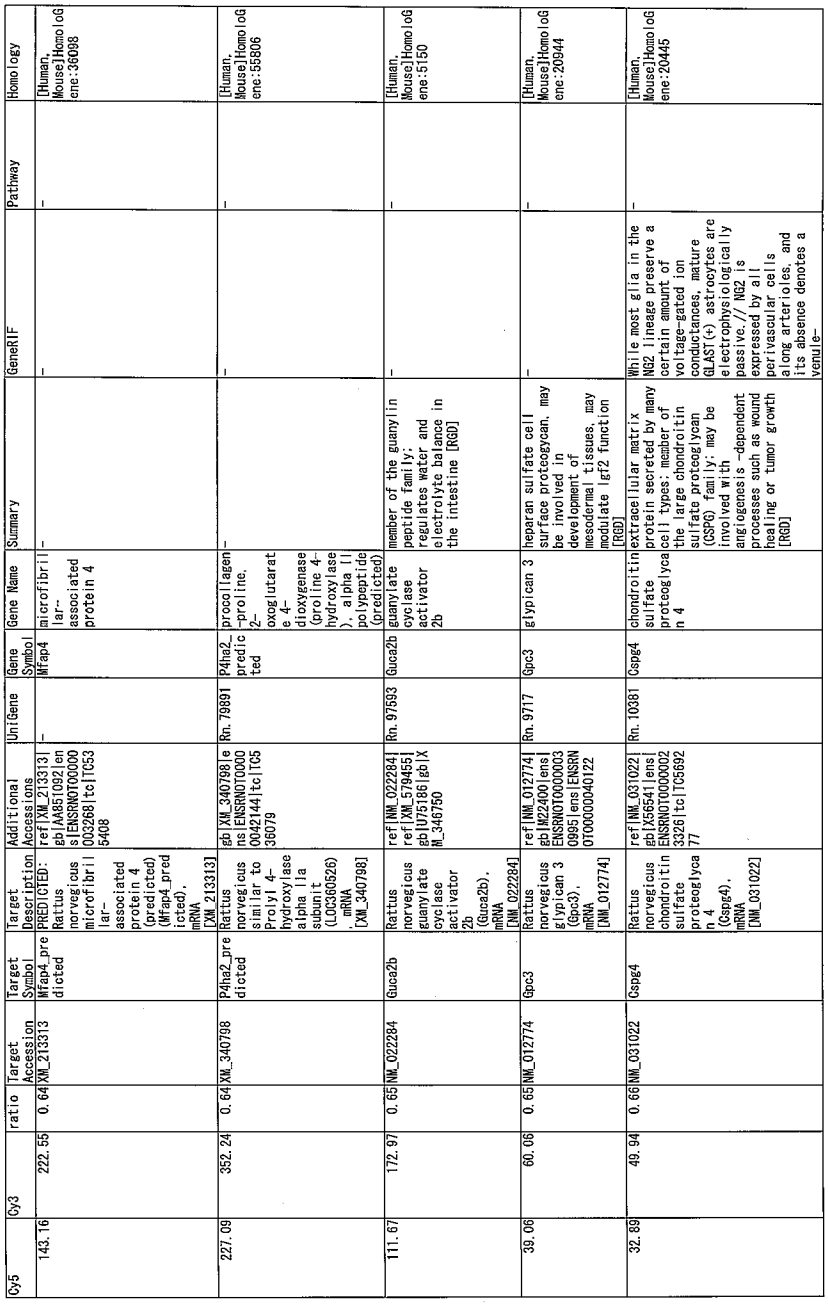
Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Gene Symbol	Gene Name	Summary	GeneRIF	Pathway	Homology
16.93	28.09	0.60	XM_342055	Sema4g_predicted	PREDICTED: Rattus norvegicus sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4G (predicted) (Sema4g_predicted), mRNA [XM_342055]	ref|XM_342055|gb|AW914054|gb|BG088250|tc|TC535808	Rn. 1645	Sema4g_predicted	sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4G (predicted)	-	-	KEGG pathway: Axon guidance	[Human, Mouse]HomoloGene:22682
27.72	45.98	0.60	XM_231381	Sema3c_predicted	Rattus norvegicus similar to semaphorin 3C; semaphorin E (LOC296787), mRNA [XM_231381]	gb|XM_231381|ens|ENSRNOT00000009132|tc|TC559331	Rn. 136960	Sema3c_predicted	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3C (predicted)	-	-	KEGG pathway: Axon guidance	[Human, Mouse]HomoloGene:36201
78.96	128.23	0.62	NM_053591	Dpep1	Rattus norvegicus dipeptidase 1 (renal) (Dpep1), mRNA [NM_053591]	ref|NM_053591|gb|LO73151ens|ENSRNOT00000021397|tc|TC5707 70	Rn. 6051	Dpep1	dipeptidase 1 (renal)	renal enzyme that cleaves proteins [RGD]	carboxypeptidase A, dipeptidase and Na+/K+ ATPase levels in the rat intestine change when exposed to different doses of cadmium	-	[Human, Mouse]HomoloGene:80192
107.57	174.23	0.62	XM_224987	Sfrp1	PREDICTED: Rattus norvegicus secreted frizzled-related protein 1 (Sfrp1), mRNA [XM_224987]	ref|XM_224987|gb|AF167308|ens|ENSRNOT00000024128|tc|TC537124	Rn. 163333	Sfrp1	secreted frizzled-related protein 1	a secreted protein involved in binding Wnt and antagonizing Wnt signaling [RGD]	Sfrp1 gene was identified and characterized by using bioinformatics, consisting of three exons, a signal peptide (codon 1-31), Frizzled domain with ten conserved Cys residues (codon 49-168), and Netrin (NTR) domain with six conserved Cys residues.// findi	KEGG pathway: Wnt signaling pathway	[Human, Mouse]HomoloGene:2266

[0342]



Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Gene Symbol	Gene Name	Summary	GeneRIF	Pathway	Homology
160.89	258.31	0.62	AI009597	AI009597	AI009597 EST204048 Normalized rat lung, Bento Soares Rattus sp. cDNA clone RLUBG14 3' end, mRNA sequence [AI009597]	gb|AI009597	Rn.3896	Fxyd3	FXYD domain-containing ion transport regulator 3	This gene encodes a member of a family of small membrane proteins that share a 35-amino acid signature sequence domain, beginning with the sequence PFXYD and containing 7 invariant and 6 highly conserved amino acids. The approved human gene nomenclature f	-	-	[Mouse]Homolo Gene:4356
23.22	37.03	0.63	U70050	Jag2	Rattus norvegicus jagged2 precursor, mRNA, partial cds. [U70050]	gb|U70050|tc|T C537474	Rn.22459	Jag2	jagged 2	may function as a ligand for Notch and may be involved in limb development [RGD]	-	KEGG pathway: Notch signaling pathway	[Human, Mouse]Homolo Gene:1677
54.99	87.55	0.63	NM_031598	Pla2g2a	Rattus norvegicus phospholipase A2, group IIA (platelets, synovial fluid) (Pla2g2a), mRNA [NM_031598]	ref|NM_031598| gb|AF363863|gb |D00523|gb|M37 127	Rn.11346	Pla2g2a	phospholipase A2, group IIA (platelets, synovial fluid)	hydrolyzes acyl group at the sn-2 position of phospholipids, forming non-esterified fatty acids and lysophospholipids; plays a critical role in inflammation; induces proliferation of smooth muscle cells [RGD]	These results indicate that phospholipase A(2)-IIA is coexpressed with SNAP-25 in mature taste receptor cells that possess exocytotic machinery.// new autocrine and paracrine pathways activating sPLA2-IIA gene expression in rat and human vascular smooth m	KEGG pathway: Arachidonic acid metabolism// KEGG pathway: Glycerophospholipid metabolism// KEGG pathway: Linoleic acid metabolism// KEGG pathway: MAPK signaling pathway	[Human]Homolo Gene:254
291.74	463.56	0.63	NM_080698	Fmod	Rattus norvegicus fibromodulin (Fmod), mRNA [NM_080698]	ref|NM_080698| gb|X82152|ens| ENSRNOT0000000 4382|tc|TC5685 92	Rn.8778	Fmod	fibromodulin	-	-	-	[Human, Mouse]Homolo Gene:1530
692.47	1079.99	0.64	NM_00101412 5	NM_001014125	Rattus norvegicus protein disulfide isomerase-associated 5 (Pdia5), mRNA [NM_0010141 25]	ref|NM_0010141 25|gb|XM_34099 41|gb|BC008305| gb|AW916891	Rn.162053	Pdia5	protein disulfide isomerase-associated 5	-	-	-	[Human, Mouse]Homolo Gene:4957

[0343]



Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Gene Symbol	Gene Name	Summary	GeneRIF	Pathway	Homology
143.16	222.55	0.64	XM_213313	Mfap4_predicted	PREDICTED: Rattus norvegicus microfibrillar-associated protein 4 (predicted) (Mfap4_predicted), mRNA [XM_213313]	ref|XM_213313|gb|AA851092|ens|ENSRNOT00000032268|tc|TC535408	-	Mfap4	microfibrillar-associated protein 4	-	-	-	[Human,Mouse]Homologene:36098
227.09	352.24	0.64	XM_340798	P4ha2_predicted	Rattus norvegicus similar to Prolyl 4-hydroxylase alpha IIa subunit (LOC360526), mRNA [XM_340798]	gb|XM_340798|ens|ENSRNOT00000042144|tc|TC536079	Rn.79891	P4ha2_predicted	procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), alpha II polypeptide (predicted)	-	-	-	[Human,Mouse]Homologene:55806
111.67	172.97	0.65	NM_022284	Guca2b	Rattus norvegicus guanylate cyclase activator 2b (Guca2b), mRNA [NM_022284]	ref|NM_022284|ref|XM_579455|gb|U75186|gb|XM_346750	Rn.97693	Guca2b	guanylate cyclase activator 2b	member of the guanylin peptide family; regulates water and electrolyte balance in the intestine [RGD]	-	-	[Human,Mouse]Homologene:5150
39.06	60.06	0.65	NM_012774	Gpc3	Rattus norvegicus glypican 3 (Gpc3), mRNA [NM_012774]	ref|NM_012774|gb|M22400|ens|ENSRNOT00000030995|ens|ENSRNOT00000040122	Rn.9717	Gpc3	glypican 3	heparan sulfate cell surface proteogycan, may be involved in development of mesodermal tissues, may modulate igf2 function [RGD]	-	-	[Human,Mouse]Homologene:20944
32.89	49.94	0.66	NM_031022	Cspg4	Rattus norvegicus chondroitin sulfate proteoglycan 4 (Cspg4), mRNA [NM_031022]	ref|NM_031022|gb|X56541|ens|ENSRNOT00000033261|tc|TC56927 7	Rn.10381	Cspg4	chondroitin sulfate proteoglycan 4	extracellular matrix protein secreted by many cell types; member of the large chondroitin sulfate proteoglycan (CSPG) family; may be involved with angiogenesis -dependant processes such as wound healing or tumor growth [RGD]	While most glia in the NG2 lineage preserve a certain amount of voltage-gated ion conductances, mature GLAST(+) astrocytes are electrophysiologically passive.// NG2 is expressed by all perivascular cells along arterioles, and its absence denotes a venule-	-	[Human,Mouse]Homologene:20445

[0344]

Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Gene Symbol	Gene Name	Summary	GeneRIF	Pathway	Homology
31.36	47.56	0.66	NM_175762	Ldlr	Rattus norvegicus low density lipoprotein receptor (Ldlr), mRNA [NM_175762]	ref|NM_175762|gb|X13722|gb|X13091|ens|ENSRNOT00000013496	Rn.10483	Ldlr	low density lipoprotein receptor	-	up-regulation and interaction of ezrin and the LDLR serves to augment the delivery of cholesterol and other lipids in support of the hypertrophic and proliferative response of cells to estrogen.// expression pattern of LDL-R in brain microvessels endothel	-	[Human, Mouse]HomoloGene:55469
181.31	274.38	0.66	U06230	Prosl	Rattus norvegicus protein S mRNA, partial cds. [U06230]	gb|U06230|gb|X63650|gb|AW141556|tc|NP066379	Rn.2888	Prosl	protein S (alpha)	component of the Protein C/Protein S anticoagulant system; human homolog interacts with factor Xa, factor Va, and phospholipids to inhibit prothrombin activation [RGD]	-	-	-
64.19	96.72	0.66	NM_053882	Ecml	Rattus norvegicus extracellular matrix protein 1 (Ecm1), mRNA [NM_053882]	ref|NM_053882|gb|U42581|gb|X84740|ens|ENSRNOT00000028740	Rn.97792	Ecml	extracellular matrix protein 1	mouse homolog is an extracellular protein found in a stromal osteogenic cell line [RGD]	-	-	[Human, Mouse]HomoloGene:3260
1473.90	2216.53	0.66	NM_052808	Psp	Rattus norvegicus parotid secretory protein (Psp), mRNA [NM_052808]	ref|NM_052808|gb|M83209|ens|ENSRNOT00000018226|tc|TC57260	Rn.9766	Psp	parotid secretory protein	secretory protein stored in parotid acinar cells [RGD]	PSP co-fractionates with chromogranin A but not with secreted alkaline phosphatase; its sorting is not cell-type specific but the precise mechanism of its sorting is unknown	-	[Human, Mouse]HomoloGene:69034
876.89	1312.03	0.67	NM_021751	Prom1	Rattus norvegicus prominin 1 (Prom1), mRNA [NM_021751]	ref|NM_021751|gb|AF386768|gb|AY262731|gb|AF263368	Rn.144589	Prom1	prominin 1	induces expression of 3-phosphate glyceraldehyde dehydrogenase (GAPDH); may play a role in glucose homeostasis [RGD]	-	-	[Human, Mouse]HomoloGene:4390

[表52]

表52 Cに対して発現減少した唾液腺の注目遺伝子
核酸構成糖の代謝 (GO ID: 9225)

Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Gene Symbol	Gene Name	Summary	GeneRIF	Pathway	Homology
451.09	837.57	0.54	NM_080783	Gale	Rattus norvegicus galactose-4 epimerase, UDP (Gale), mRNA [NM_080783]	ref|NM_080783|gb|X53949|gb|BC097293|ens|ENSRNOT00000001 3322	Rn.29908	Gale	galactose-4-epimerase, UDP	enzyme with galactose-4 epimerase activity [RGD]	-	KEGG pathway: Galactose metabolism// KEGG pathway: Nucleotide sugars metabolism	[Human, Mouse]Homol oGene:347
552.35	846.24	0.65	XM_216968	Tsta3_predicted	PREDICTED: Rattus norvegicus tissue specific transplantation antigen P35B (predicted) (Tsta3_predicted), mRNA [XM_216968]	ref|XM_216968|ens|ENSRNOT00000012306|gb|BF289545|gb|AW917281	Rn.6606	Tsta3_predicted	tissue specific transplantation antigen P35B (predicted)	-	-	-	[Human, Mouse]Homol oGene:2484

[表53]

表53 Lに対して発現増加した視床下部の注目遺伝子
ホルモン活性 (GO ID: 5184, 5179)

Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Gene Symbol	Gene Name	Summary	GeneRIF	Pathway	Homology
37511.36	20083.44	1.87	NM_012625	Pmch	Rattus norvegicus pro-melanin-concentrating hormone (Pmch), mRNA [NM_012625]	ref|NM_012625|gb|M29712|gb|AW262641ens|ENSRNOT00000006174	Rn.9675	Pmch	pro-melanin-concentrating hormone	cyclic neuropeptide; induces hippocampal synaptic transmission [RGD]	MCH is involved in the regulation of LHRH release in the female rat.// glucocorticoids may promote food intake in part by potentiating the orexigenic actions of MCH without affecting the actions of orexin A and glucocorticoids act indirectly to influence	KEGG pathway: Neuroactive ligand-receptor interaction	Human, Mouse|Homologene.37653
793.72	441.05	1.80	XM_574228	XM_574228	PREDICTED: Rattus norvegicus agouti related protein homolog (mouse) (Agrp), mRNA [XM_574228]	ref|XM_574228|gb|AF206017|gb|AW_214672|ens|ENSRNOT00000023606	Rn.13759	Agrp	agouti related protein homolog (mouse)	may interact with melanocortin receptors; may play a role in appetite stimulation [RGD]	Because AGRP is cleaved before secretion, syndecan-3 must influence food intake independently of the MC4-R.// conclude that leptin requires phosphatidylinositol 3-OH-kinase (PI3K) signaling both to inhibit hypothalamic neuropeptide Y and agouti-related pe	-	Human, Mouse|Homologene.7184

[表54]

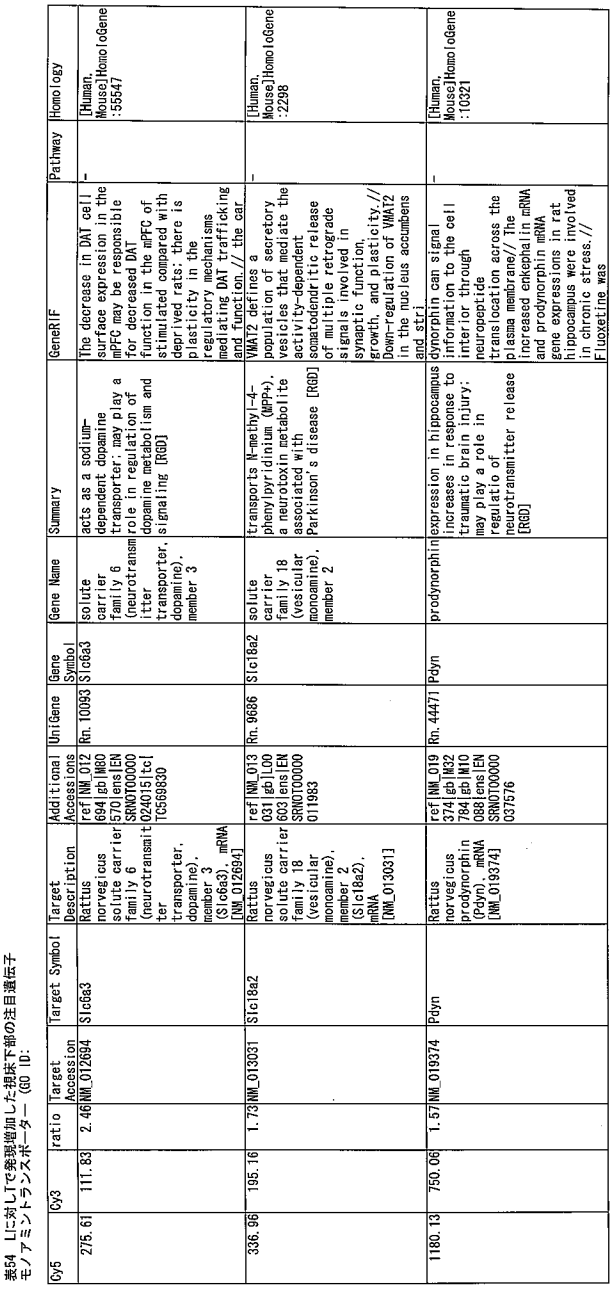


表54 LIに対して発現増加した視床下部の注目遺伝子
モノアミントランスポーター (GO ID:

Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Gene Symbol	Gene Name	Summary	GeneRIF	Pathway	Homology
275.61	111.83	2.46	NM_012694	Slc6a3	Rattus norvegicus solute carrier family 6 (neurotransmitter transporter, dopamine), member 3 (Slc6a3), mRNA [NM_012694]	ref|NM_012694.1|[6] ens|ENSRNOT00000024015|tc|TC669830	Rn.10093	Slc6a3	solute carrier family 6 (neurotransmitter transporter, dopamine), member 3	acts as a sodium-dependent dopamine transporter, may play a role in regulation of dopamine metabolism and signaling [RGD]	The decrease in DAT cell surface expression in the mPFC may be responsible for decreased DAT function in the mPFC of stimulated compared with deprived rats: there is plasticity in the regulatory mechanisms mediating DAT trafficking and function.// the car	-	[Human, Mouse]HomoloGene:55547
336.96	195.16	1.73	NM_013031	Slc18a2	Rattus norvegicus solute carrier family 18 (vesicular monoamine), member 2 (Slc18a2), mRNA [NM_013031]	ref|NM_013031.1|[6] ens|ENSRNOT00000011983	Rn.9686	Slc18a2	solute carrier family 18 (vesicular monoamine), member 2	transports N-methyl-4-phenylpyridinium (MPP+), a neurotoxin metabolite associated with Parkinson's disease [RGD]	VMAT2 defines a population of secretory vesicles that mediate the activity-dependent somatodendritic release of multiple retrograde signals involved in synaptic function, growth, and plasticity.// Down-regulation of VMAT2 in the nucleus accumbens and stri	-	[Human, Mouse]HomoloGene:2298
1180.13	750.06	1.57	NM_019374	Pdyn	Rattus norvegicus prodynorphin (Pdyn), mRNA [NM_019374]	ref|NM_019374.1|[6] ens|ENSRNOT00000037576	Rn.44471	Pdyn	prodynorphin	expression in hippocampus increases in response to traumatic brain injury; may play a role in regulatio of neurotransmitter release [RGD]	dynorphin can signal information to the cell interior through neuropeptide translocation across the plasma membrane.// The increased enkephalin mRNA and prodynorphin mRNA gene expressions in rat hippocampus were involved in chronic stress.// Fluoxetine was	-	[Human, Mouse]HomoloGene:10321

[表55]

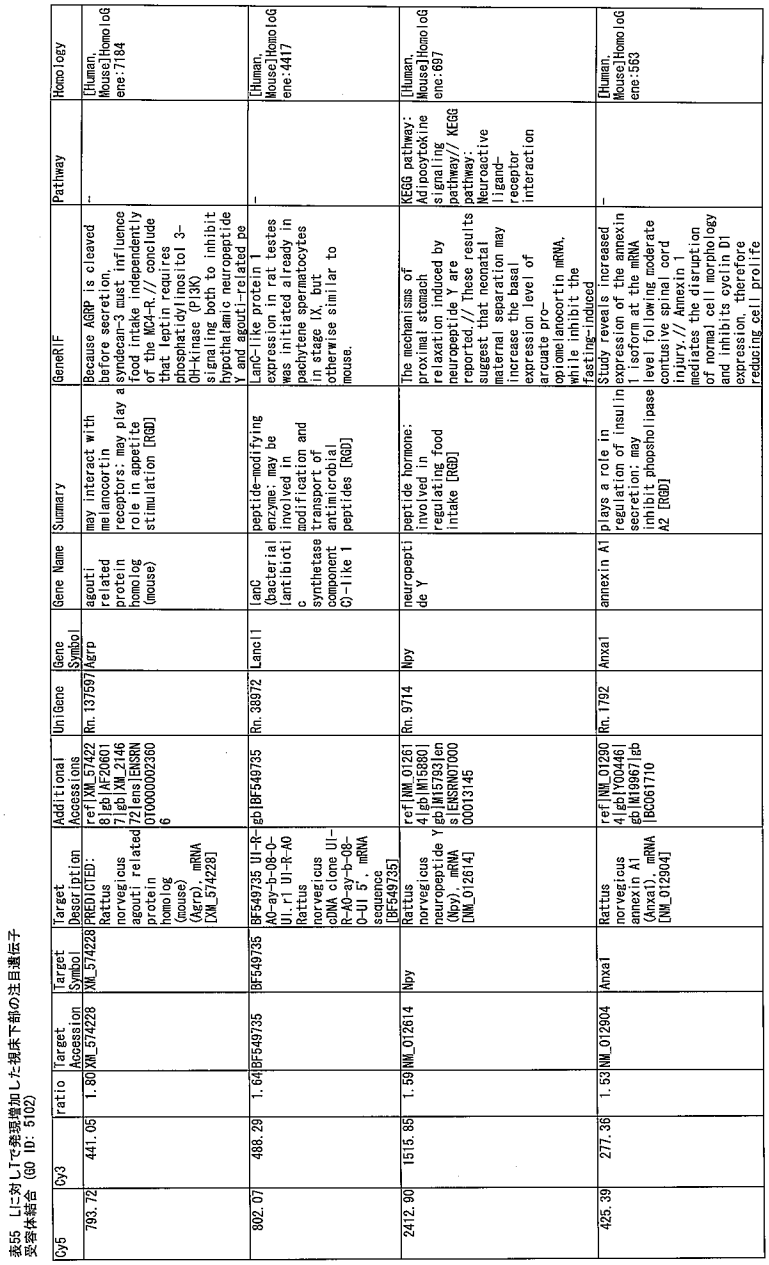


表55 Liに対して発現増加した視床下部の注目遺伝子
受容体結合 (GO ID: 5102)

Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Gene Symbol	Gene Name	Summary	GeneRIF	Pathway	Homology
793.72	441.05	1.80	XM_574228	XM_574228	PREDICTED: Rattus norvegicus agouti related protein homolog (mouse) (Agrp), mRNA [XM_574228]	ref|XM_574228.3|gb|AF20601 7|gb|XM_2146721|ENSRNOT00000002360 6	Rn.137597	Agrp	agouti related protein homolog (mouse)	may interact with melanocortin receptors: may play a role in appetite stimulation [RGD]	Because AGRP is cleaved before secretion, syndecan-3 must influence food intake independently of the MC4-R.// conclude that leptin requires phosphatidylinositol 3-OH-kinase (PI3K) signaling both to inhibit hypothalamic neuropeptide Y and agouti-related pe	-	[Human, Mouse]Homolog ene:7184
802.07	488.29	1.64	BF549735	BF549735	BF549735 UI-R-A0-ay-b-08-0-UI.r1 UI-R-A0 Rattus norvegicus cDNA clone UI-R-A0-ay-b-08-0-UI 5', mRNA sequence [BF549735]	gb|BF549735	Rn.39372	Lancl1	lanC (bacterial lantibiotic synthetase component C)-like 1	peptide-modifying enzyme: may be involved in modification and transport of antimicrobial peptides [RGD]	LanC-like protein 1 expression in rat testes was initiated already in pachytene spermatocytes in stage IX, but otherwise similar to mouse.	-	[Human, Mouse]Homolog ene:4417
2412.90	1515.85	1.59	NM_012614	Npy	Rattus norvegicus neuropeptide Y (Npy), mRNA [NM_012614]	ref|NM_012614|gb|M15880|gb|M15793|ens|ENSRNOT00000013145	Rn.9714	Npy	neuropeptide Y	peptide hormone: involved in regulating food intake [RGD]	The mechanisms of proximal stomach relaxation induced by neuropeptide Y are reported.// These results suggest that neonatal maternal separation may increase the basal expression level of arcuate pro-opiomelanocortin mRNA, while inhibit the fasting-induced	KEGG pathway: Adipocytokine signaling pathway// KEGG pathway: Neuroactive ligand-receptor interaction	[Human, Mouse]Homolog ene:697
425.39	277.36	1.53	NM_012904	Anxa1	Rattus norvegicus annexin A1 (Anxa1), mRNA [NM_012904]	ref|NM_012904.4|gb|Y00446|gb|M19961|gb|BC061710	Rn.1792	Anxa1	annexin A1	plays a role in regulation of insulin secretion; may inhibit phospholipase A2 [RGD]	Study reveals increased expression of the annexin 1 isoform at the mRNA level following moderate contusive spinal cord injury.// Annexin 1 mediates the disruption of normal cell morphology and inhibits cyclin D1 expression, therefore reducing cell prolife	-	[Human, Mouse]Homolog ene:563

[表56]

表56 LIに対して発現増加した視床下部の注目遺伝子
食行動 (GO ID: 7631)

Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Gene Symbol	Gene Name	Summary	GeneRIF	Pathway	Homology
153.08	71.65	2.14	NM_022633	Galp	Rattus norvegicus galanin-like peptide precursor (Galp), mRNA [NM_022633]	ref|NM_022633 |gb|AF188491 |ens|ENSRNOT00 000034854|tc| NP399873	Rn.48754	Galp	galanin-like peptide precursor	-	observations demonstrate that endogenous Galanin-like peptide (GALP)provides trophic support to the neuroendocrine reproductive axis, including sexual behavior// adaptive responses in GALP signaling might occur during chronic overfeeding// GALP gene expre	-	[Human, Mouse]HomoloGene:11217
4327.77	2030.83	2.13	NM_139326	Pomc2	Rattus norvegicus proopiomelanocortin, beta (endorphin, beta) (Pomc2), mRNA [NM_139326]	ref|NM_139326 |gb|BC058443 |gb|AF510391|g bJJ00759	Rn.108195	Pomc	pro-opiomelanocortin	-	POMC expression decreased progressively during eye movement sleep deprivation of rats. // Enhanced insulin sensitivity via exercise training might be mediated by endogenous beta-endorphin that leads to improved glucose disposal in obese Zucker rats.// die	KEGG pathway: Adipocytokine signaling pathway// KEGG pathway: Neuroactive ligand-receptor interaction	[Human, Mouse]HomoloGene:723
37511.36	20083.44	1.87	NM_012625	Pmch	Rattus norvegicus pro-melanin-concentrating hormone (Pmch), mRNA [NM_012625]	ref|NM_012625 |gb|M29712|gb |M62641|ens|E NSRNOT00000006174	Rn.9675	Pmch	pro-melanin-concentrating hormone	cyclic neuropeptide; induces hippocampal synaptic transmission [RGD]	MCH is involved in the regulation of LHRH release in the female rat.// glucocorticoids may promote food intake in part by potentiating the orexigenic actions of MCH without affecting the actions of orexin A and glucocorticoids act indirectly to influence	KEGG pathway: Neuroactive ligand-receptor interaction	[Human, Mouse]HomoloGene:37653
793.72	441.05	1.80	XM_574228	XM_57422 8	PREDICTED: Rattus norvegicus agouti related protein homolog (mouse) (Agrp), mRNA [XM_574228]	ref|XM_574228 |gb|AF206017 |gb|XM_214672 |ens|ENSRNOT00 000023606	Rn.137597	Agrp	agouti related protein homolog (mouse)	may interact with melanocortin receptors; may play a role in appetite stimulation [RGD]	Because AGRP is cleaved before secretion, syndecan-3 must influence food intake independently of the MC4-R.// conclude that leptin requires phosphatidylinositol 3-OH-kinase (PI3K) signaling both to inhibit hypothalamic neuropeptide Y and agouti-related pe	-	[Human, Mouse]HomoloGene:7184

[0345]

Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Gene Symbol	Gene Name	Summary	GeneRIF	Pathway	Homology
2730.85	1705.40	1.60	NM_013179	HcRt	Rattus norvegicus hypocretin (HcRt), mRNA [NM_013179]	ref|NM_013179|gb|AF041241|gb|BF563189|ens|ENSRNOT00000025547	Rn.7628	Hcrt	hypocretin	neuropeptide: involved in feeding behavior and hormone secretion regulation [RGD]	With respect to MCH and orexin neurons, this study emphasizes that these neurons are targets for stimulatory and inhibitory signals from other brain regions including the arcuate nucleus and the general circulation.// These results indicate that hypocreti	KEGG pathway: Neuroactive ligand-receptor interaction	[Human, Mouse]Homolog ene:1166
2412.90	1515.85	1.59	NM_012614	Npy	Rattus norvegicus neuropeptide Y (Npy), mRNA [NM_012614]	ref|NM_012614|gb|M15880|gb|M15793|ens|ENSRNOT00000013145	Rn.9714	Npy	neuropeptide Y	peptide hormone: involved in regulating food intake [RGD]	The mechanisms of proximal stomach relaxation induced by neuropeptide Y are reported.// These results suggest that neonatal maternal separation may increase the basal expression level of arcuate pro-opiomelanocortin mRNA, while inhibit the fasting-induced	KEGG pathway: Adipocytokine signaling pathway// KEGG pathway: Neuroactive ligand-receptor interaction	[Human, Mouse]Homolog ene:697

[表57]

表57 LIに対して発現増加した視床下部の注目遺伝子
生体アミン合成 (GO ID: 42401, 42423, 42416, 9309)

Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Gene Symbol	Gene Name	Summary	GeneRIF	Pathway	Homology
275.61	111.83	2.46	NM_012694	Slc6a3	Rattus norvegicus solute carrier family 6 (neurotransmitter transporter, dopamine), member 3 (Slc6a3), mRNA [NM_012694]	ref|NM_012694|gb|M80570|ens|ENSRNOT00000024015|tc|TC569830	Rn. 10093	Slc6a3	solute carrier family 6 (neurotransmitter transporter, dopamine), member 3	acts as a sodium-dependent dopamine transporter; may play a role in regulation of dopamine metabolism and signaling [RGD]	The decrease in DAT cell surface expression in the mPFG may be responsible for decreased DAT function in the mPFG of stimulated compared with deprived rats; there is plasticity in the regulatory mechanisms mediating DAT trafficking and function.// the ear	-	[Human, Mouse]Homolog ene:55547
1270.69	704.13	1.80	NM_017016	Hdc	Rattus norvegicus histidine decarboxylase (Hdc), mRNA [NM_017016]	ref|NM_017016|gb|M38759|gb|XM_346674|gb|M29591	Rn. 49653	Hdc	histidine decarboxylase	involved in the formation of histamine from its precursor histidine [RGD]	histidine decarboxylase mRNA and protein are found in rat aorta and more specifically in cultured rat aortic smooth muscle, indicative of their capability to synthesize histamine// Identification of catalytically important residues in L-histidine decarbox	KEGG pathway: Histidine metabolism	[Human, Mouse]Homolog ene:20490
888.26	560.95	1.58	NM_012740	Th	Rattus norvegicus tyrosine hydroxylase (Th), mRNA [NM_012740]	ref|NM_012740|gb|L22651|gb|M10244|ens|ENSRNOT00000027682	Rn. 11082	Th	tyrosine hydroxylase	catalyzes the rate limiting step in catecholamine biosynthesis: may be involved in response to hypoxia [RGD]	The kinetics of reduction of ferric tyrH by several reductants were determined by anaerobic stopped-flow spectroscopy. phosphorylation does not directly regulate the interconversion of the ferric and ferrous forms// The results indicate that the NGF/NGF	KEGG pathway: Parkinson's disease// KEGG pathway: Tyrosine metabolism	[Human, Mouse]Homolog ene:307

[表58]

表58 LIに対しTで発現増加した視床下部の注目遺伝子
生体アミン代謝 (GO ID: 9308, 6584, 6576)

Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Gene Symbol	Gene Name	Summary	GeneRIF	Pathway	Homology
275.61	111.83	2.46	NM_012694	Slc6a3	Rattus norvegicus solute carrier family 6 (neurotransmitter transporter, dopamine), member 3 (Slc6a3), mRNA [NM_012694]	ref|NM_0126 94|gb|M90057 0|ens|ENSRN OT00000000240 15|tc|TC0569 930	Rn.10093	Slc6a3	solute carrier family 6 (neurotransmitter transporter, dopamine), member 3	acts as a sodium-dependent dopamine transporter; may play a role in regulation of dopamine metabolism and signaling [RGD]	The decrease in DAT cell surface expression in the mPFC may be responsible for decreased DAT function in the mPFC of stimulated compared with deprived rats. there is plasticity in the regulatory mechanisms mediating DAT trafficking and function.// the car	-	[Human, Mouse]Homo loGene:555 47

[表59]

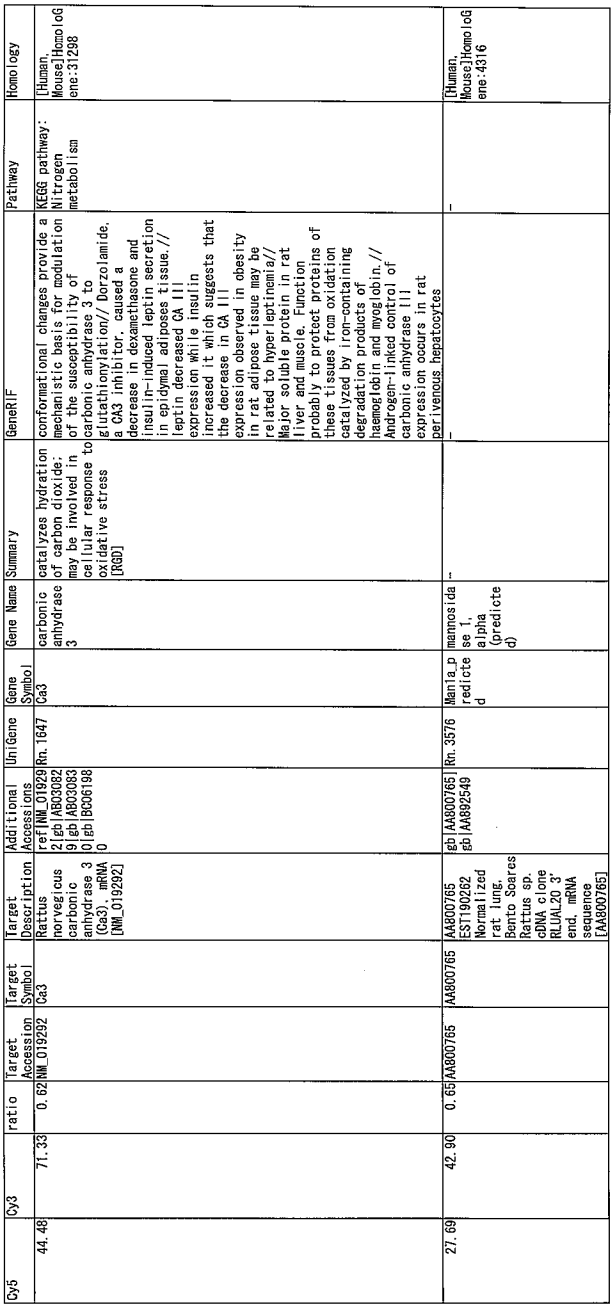
表59 LiにてIで発現減少した視床下部の注目遺伝子
酸イオン結合 (GO ID: 5509, 43169)

Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Gene Symbol	Gene Name	Summary	GeneRIF	Pathway	Homology
192.09	296.29	0.65	NM_172224	Impa2	Rattus norvegicus inositol (myo)-1(or 4)-monophosphatase 2 (Impa2), mRNA [NM_172224]	ref|NM_172224|gb|AY160194|gb|BC083544|ens|ENSRNOT00000025147	Rn.856	Impa2	inositol (myo)-1(or 4)-monophosphatase 2	mouse homolog is an enzyme that catalyzes the synthesis of free myo-inositol from various myo-inositol monophosphates [RGD]	-	KEGG pathway: Inositol phosphate metabolism// KEGG pathway: Phosphatidylinositol signaling system// KEGG pathway: Streptomycin biosynthesis	[Human, Mouse]HomoloGene:22799
390.79	588.19	0.66	NM_133415	Efcbp2	Rattus norvegicus neuronal calcium binding 2 (Efcbp2), mRNA [NM_133415]	ref|NM_133415|gb|AF179375|ens|ENSRNOT00000020341	Rn.62703	Efcbp2	EF hand calcium binding protein 2	may mediate calcium signaling and play a role in neuronal function [RGD]	-	-	[Human, Mouse]HomoloGene:62200

[0346]

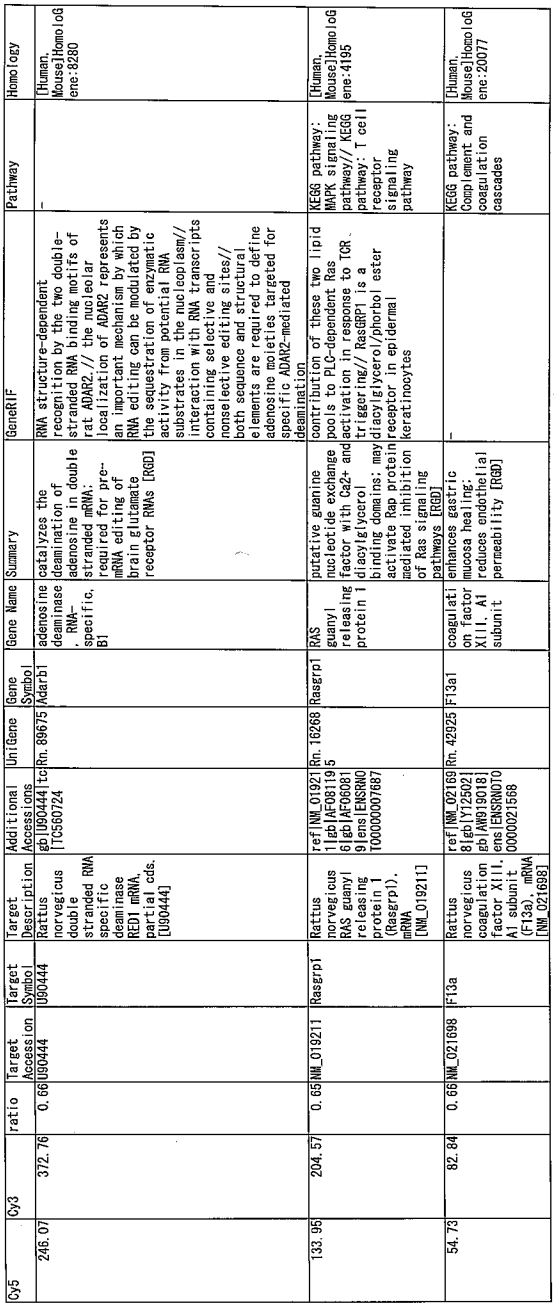
Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Gene Symbol	Gene Name	Summary	GeneRIF	Pathway	Homology
115.10	188.76	0.61	NM_031828	Kcnma1	Rattus norvegicus potassium large conductance calcium-activated channel, subfamily M, alpha member 1 (Kcnma1), mRNA [NM_031828]	ref|NM_03182 8|ref|XM_579 539|gb|AF083 342|gb|AJ517 197	Rn. 30616	Kcnma1	potassium large conduotan ce calcium-activated channel, subfamily M, alpha member 1	large-conductance Ca(2+)-activated K(+) channel: may be involved in the shortened duration of action potential in hippocampal CA1 pyramidal neurons and in channel activity in carotid body chemoreceptor cells [RGD]	Data suggest that the regulation of STREX splicing directed by estrogen and Pg provides a mechanism for Slo's PKA-related phenotypic alteration with pregnancy.// there is a novel interaction between the C-terminal tail of the BKCa channel and the light chain of MAPIA, which enables channel association with and modulation by the cytoskeleton.// Slo gene-encoded BK potassium channels alternative splicing variants are found with and without the 'STREX' exon. In the adrenal medulla, castration increased STREX transcripts slightly and decreased STREX representation in the pituitary.// cAMP-dependent vasodilators activate BK(Ca) channels in PASMC of rats via PKG-dependent and PKA-independent signaling pathways, which suggests cross-activation between cyclic nucleotide-dependent protein kinases in pulmonary arterial smooth muscle// Steady-state and closed-state inactivation properties.// Nitric oxide enhances Ca(2+)-dependent K(+) channel activity in rat carotid body cells.// (The rest is omitted.)	-	[Human, Mouse]Homolo gene:1693

[0347]



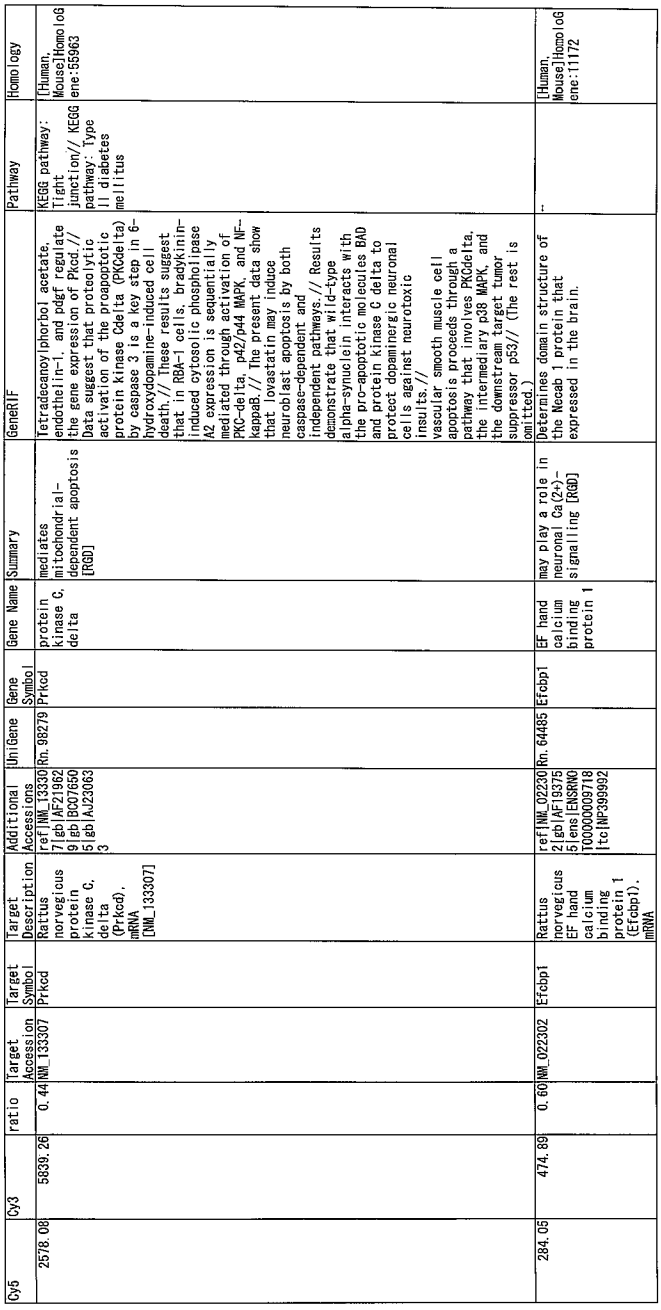
Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Gene Symbol	Gene Name	Summary	GeneRIF	Pathway	Homology
44.48	71.33	0.62	NM_019292	Ca3	Rattus norvegicus carbonic anhydrase 3 (Ca3), mRNA [NM_019292]	ref|NM_019292|gb|AB030829|gb|AB030830|gb|BC006198	Rn.1647	Ca3	carbonic anhydrase 3	catalyzes hydration of carbon dioxide; may be involved in cellular response to oxidative stress [RGD]	conformational changes provide a mechanistic basis for modulation of the susceptibility of carbonic anhydrase 3 to glutathionylation// Dorzolamide, a CA3 inhibitor, caused a decrease in dexamethasone and insulin-induced leptin secretion in epididymal adipose tissue.// leptin decreased CA III expression while insulin increased it which suggests that the decrease in CA III expression observed in obesity in rat adipose tissue may be related to hyperleptinemia// Major soluble protein in rat liver and muscle. Function probably to protect proteins of these tissues from oxidation catalyzed by iron-containing degradation products of haemoglobin and myoglobin.// Androgen-linked control of carbonic anhydrase III expression occurs in rat perivenous hepatocytes	KEGG pathway: Nitrogen metabolism	[Human, Mouse]Homolo gene:31298
27.69	42.90	0.65	AA800765	AA800765	AA800765 EST190262 Normalized rat lung, Bento Soares Rattus sp. cDNA clone RLUAL20 3' end, mRNA sequence [AA800765]	gb|AA800765|gb|AA892549	Rn.3576	Manla_predicted	mannosidase 1, alpha (predicted)	-	-	-	[Human, Mouse]Homolo gene:4316

[0348]



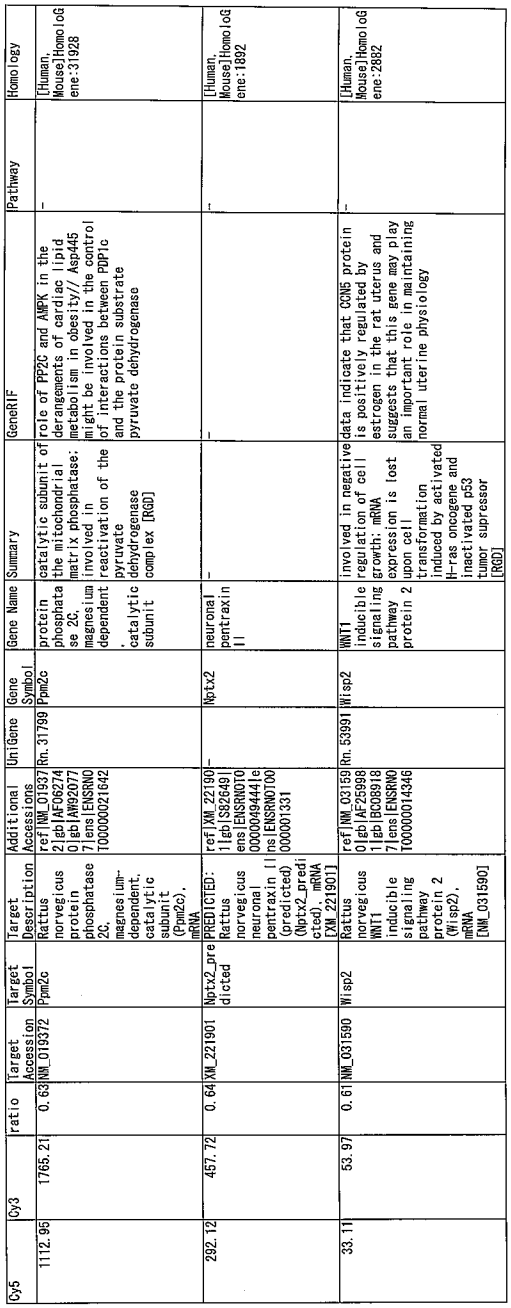
Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Gene Symbol	Gene Name	Summary	GeneRIF	Pathway	Homology
246.07	372.76	0.66	U90444	U90444	Rattus norvegicus double stranded RNA specific deaminase RED1 mRNA, partial cds. [U90444]	gb|U90444|tc|TC560724	Rn.89675	Adarb1	adenosine deaminase, RNA-specific, B1	catalyzes the deamination of adenosine in double stranded mRNA: required for pre-mRNA editing of brain glutamate receptor RNAs [RGD]	RNA structure-dependent recognition by the two double-stranded RNA binding motifs of rat ADAR2.// the nucleolar localization of ADAR2 represents an important mechanism by which RNA editing can be modulated by the sequestration of enzymatic activity from potential RNA substrates in the nucleoplasm// interaction with RNA transcripts containing selective and nonselective editing sites// both sequence and structural elements are required to define adenosine moieties targeted for specific ADAR2-mediated deamination	-	[Human, Mouse]Homolo gene:8280
133.95	204.57	0.65	NM_019211	Rasgrp1	Rattus norvegicus RAS guanyl releasing protein 1 (Rasgrp1). mRNA [NM_019211]	ref|NM_019211|Rn.16268 1|gb|AF081195 6|gb|AF060081 9|ens|ENSRNO T00000007687	Rn.16268	Rasgrp1	RAS guanyl releasing protein 1	putative guanine nucleotide exchange factor with Ca2+ and diacylglycerol binding domains; may activate Rap protein mediated inhibition of Ras signaling pathways [RGD]	contribution of these two lipid pools to PLC-dependent Ras activation in response to TCR triggering// RasGRP1 is a diacylglycerol/phorbol ester receptor in epidermal keratinocytes	KEGG pathway: MAPK signaling pathway// KEGG pathway: T cell receptor signaling pathway	[Human, Mouse]Homolo gene:4195
54.73	82.84	0.66	NM_021698	F13a	Rattus norvegicus coagulation factor XIII, A1 subunit (F13a), mRNA [NM_021698]	ref|NM_021698|Rn.42925 6|gb|Y12502 1|gb|AW960018|ens|ENSRNOT0 0000021568	Rn.42925	F13a1	coagulation factor XIII, A1 subunit	enhances gastric mucosa healing; reduces endothelial permeability [RGD]	-	KEGG pathway: Complement and coagulation cascades	[Human, Mouse]Homolo gene:20077

[0349]



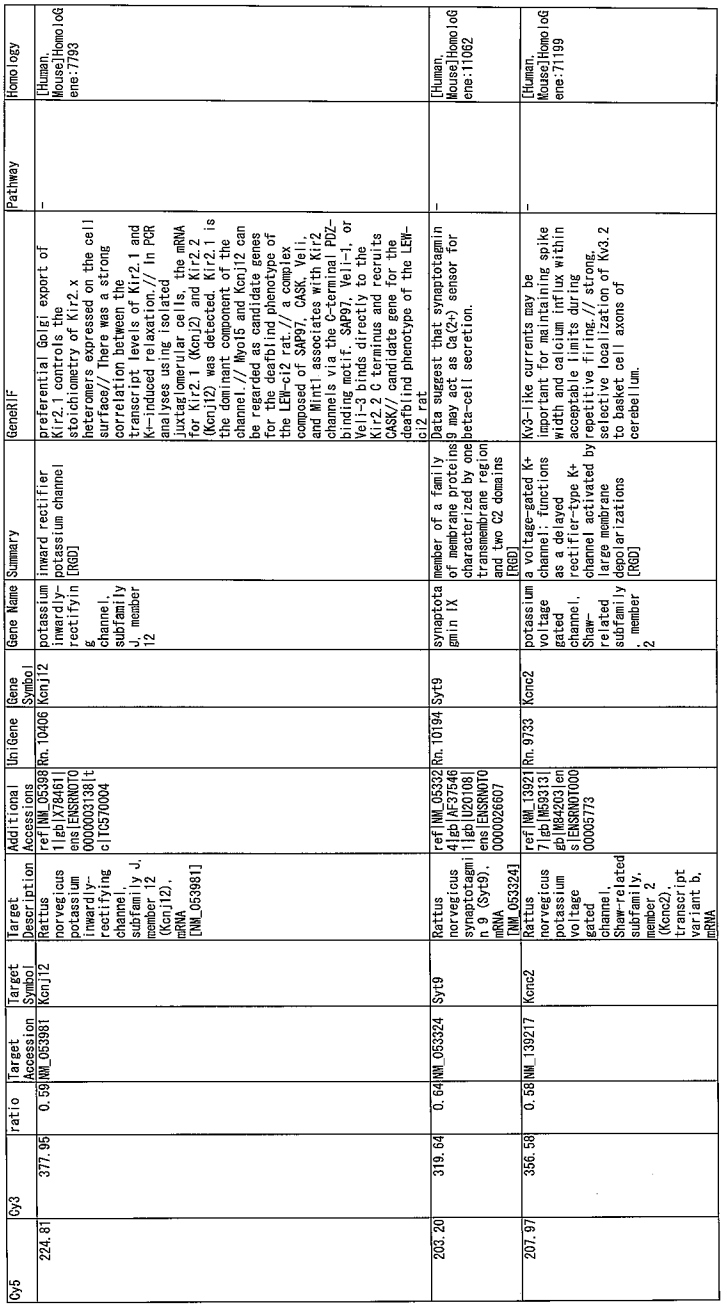
Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Gene Symbol	Gene Name	Summary	GeneRIF	Pathway	Homology
2578.08	5839.26	0.44	NM_133307	Prkcd	Rattus norvegicus protein kinase C, delta (Prkcd), mRNA [NM_133307]	ref|NM_133307.3|gb|AF21962|gb|BC007650|gb|AJ23063	Rn.98279	Prkcd	protein kinase C, delta	mediates mitochondrial-dependent apoptosis [RGD]	Tetradecanoylphorbol acetate, endothelin-1 and pdgf regulate the gene expression of Prkcd.// Data suggest that proteolytic activation of the proapoptotic protein kinase Cdelta (PKCdelta) by caspase 3 is a key step in 6-hydroxydopamine-induced cell death.// These results suggest that in RBA-1 cells, bradykinin-induced cytosolic phospholipase A2 expression is sequentially mediated through activation of PKC-delta, p42/p44 MAPK, and NF-kappaB.// The present data show that lovastatin may induce neuroblast apoptosis by both caspase-dependent and independent pathways.// Results demonstrate that wild-type alpha-synuclein interacts with the pro-apoptotic molecules BAD and protein kinase C delta to protect dopaminergic neuronal cells against neurotoxic insults.// vascular smooth muscle cell apoptosis proceeds through a pathway that involves PKCdelta, the intermediary p38 MAPK, and the downstream target tumor suppressor p53// (the rest is omitted.)	KEGG pathway: Tight junction// KEGG pathway: type II diabetes mellitus	[Human, Mouse]Homologene:55963
284.05	474.89	0.60	NM_022302	Efcbp1	Rattus norvegicus EF hand calcium binding protein 1 (Efcbp1), mRNA	ref|NM_022302.2|gb|AF193755|ens|ENSRNOT00000009718|tc|NP399992	Rn.64485	Efcbp1	EF hand calcium binding protein 1	may play a role in neuronal Ca(2+)-signalling [RGD]	Determines domain structure of the Necab 1 protein that expressed in the brain.	--	[Human, Mouse]Homologene:11172

[0350]



Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Gene Symbol	Gene Name	Summary	GeneRIF	Pathway	Homology
1112.95	1765.21	0.63	NM_019372	Ppm2c	Rattus norvegicus protein phosphatase 2C, magnesium-dependent, catalytic subunit (Ppm2c), mRNA	ref|NM_019372|gb|AF062742|gb|AW920770|ens|ENSRNOT00000021642	Rn. 31799	Ppm2c	protein phosphatase 2C, magnesium dependent, catalytic subunit	catalytic subunit of the mitochondrial matrix phosphatase: involved in reactivation of the pyruvate dehydrogenase complex [RGD]	role of PP2C and AMPK in the derangements of cardiac lipid metabolism in obesity// Asp445 might be involved in the control of interactions between PDP1c and the protein substrate pyruvate dehydrogenase	-	[Human, Mouse]HomoloGene:31928
292.12	457.72	0.64	XM_221901	Nptx2_predicted	PREDICTED: Rattus norvegicus neuronal pentraxin II (predicted) (Nptx2_predicted), mRNA [XM_221901]	ref|XM_221901|-1|gb|S82649|ens|ENSRNOT00000049444|ens|ENSRNOT00000001331	-	Nptx2	neuronal pentraxin II	-	-	-	[Human, Mouse]HomoloGene:1892
33.11	53.97	0.61	NM_031590	Wisp2	Rattus norvegicus WNT1 inducible signaling pathway protein 2 (Wisp2), mRNA [NM_031590]	ref|NM_031590|gb|AF259980|gb|BC089181|ens|ENSRNOT00000014346	Rn. 53991	Wisp2	WNT1 inducible signaling pathway protein 2	involved in negative regulation of cell growth: mRNA expression is lost upon cell transformation induced by activated H-ras oncogene and inactivated p53 tumor supressor [RGD]	data indicate that CCN5 protein is positively regulated by estrogen in the rat uterus and suggests that this gene may play an important role in maintaining normal uterine physiology	-	[Human, Mouse]HomoloGene:2862

[0351]

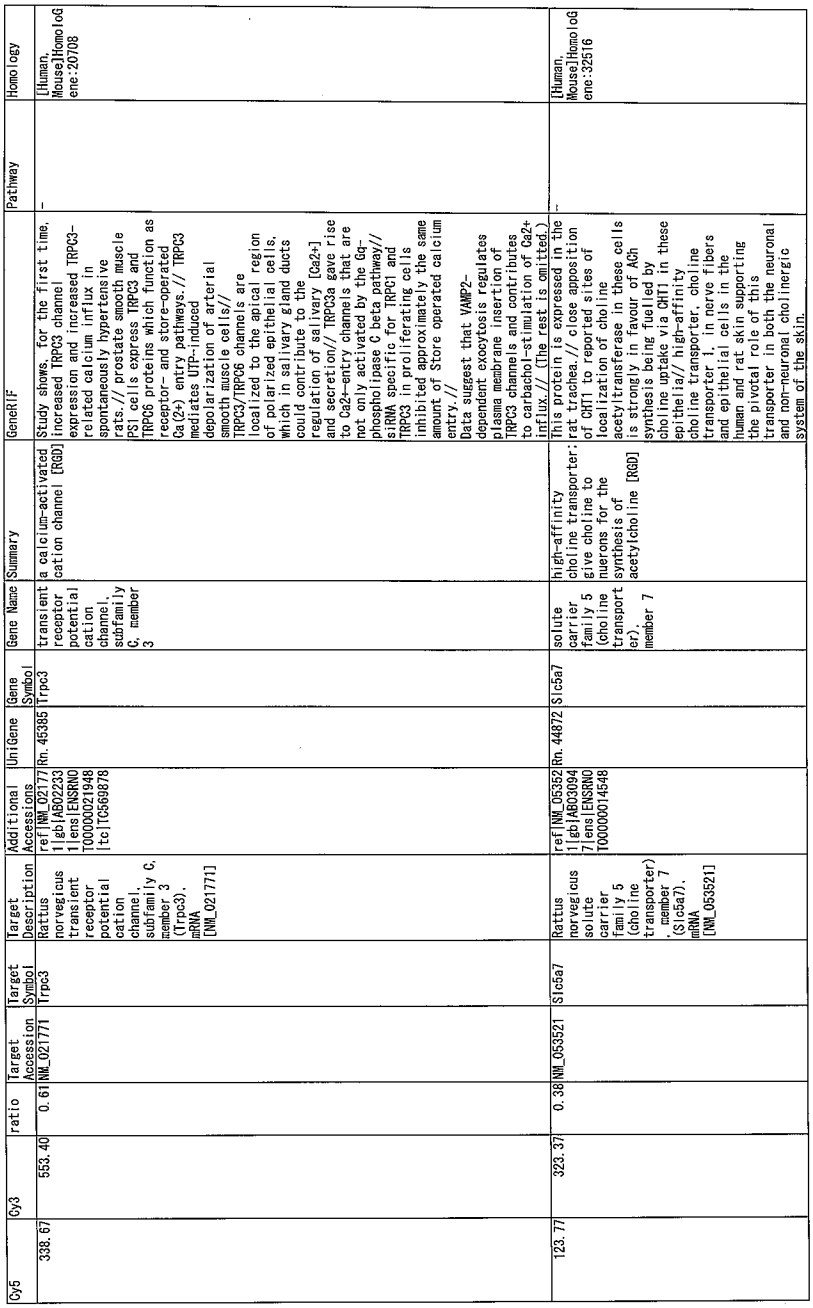


Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Gene Symbol	Gene Name	Summary	GeneRIF	Pathway	Homology
224.81	377.95	0.59	NM_053981	Kcnj12	Rattus norvegicus potassium inwardly-rectifying channel, subfamily J, member 12 (Kcnj12), mRNA [NM_053981]	ref|NM_053981|gb|X78461|ens|ENSRNOT00000003381|tc|TC570004	Rn.10406	Kcnj12	potassium inwardly-rectifying channel, subfamily J, member 12	inward rectifier potassium channel [RGD]	preferential Golgi export of Kir2.1 controls the stoichiometry of Kir2.x heteromers expressed on the cell surface// There was a strong correlation between the transcript levels of Kir2.1 and K+-induced relaxation.// In PCR analyses using isolated juxtaglomerular cells, the mRNA for Kir2.1 (Kcnj2) and Kir2.2 (Kcnj12) was detected. Kir2.1 is the dominant component of the channel.// Myo1b and Kcnj12 can be regarded as candidate genes for the deafblind phenotype of the LEW-cl2 rat.// A complex composed of SAP97, CASK, Veli, and Mint1 associates with Kir2 channels via the C-terminal PDZ-binding motif. SAP97, Veli-1, or Veli-3 binds directly to the Kir2.2 C terminus and recruits CASK// candidate gene for the deafblind phenotype of the LEW-cl2 rat.	-	[Human, Mouse]Homolo gene:7793
203.20	319.64	0.64	NM_053324	Syt9	Rattus norvegicus synaptotagmin 9 (Syt9), mRNA [NM_053324]	ref|NM_053324|gb|AF37546 1|gb|U20108|ens|ENSRNOT00000026607	Rn.10194	Syt9	synaptotagmin IX	member of a family of membrane proteins characterized by one transmembrane region and two C2 domains [RGD]	Data suggest that synaptotagmin 9 may act as Ca(2+) sensor for beta-cell secretion.	-	[Human, Mouse]Homolo gene:11062
207.97	356.58	0.58	NM_139217	Kcnc2	Rattus norvegicus potassium voltage gated channel, Shaw-related subfamily, member 2 (Kcnc2), transcript variant b, mRNA	ref|NM_139217|gb|M59313|gb|M84203|ens|ENSRNOT00000005773	Rn.9733	Kcnc2	potassium voltage gated channel, Shaw-related subfamily, member 2	a voltage-gated K+ channel: functions as a delayed rectifier-type K+ channel activated by large membrane depolarizations [RGD]	Kv3-like currents may be important for maintaining spike width and calcium influx within acceptable limits during repetitive firing.// strong, selective localization of Kv3.2 to basket cell axons of cerebellum.	-	[Human, Mouse]Homolo gene:71199

[0352]

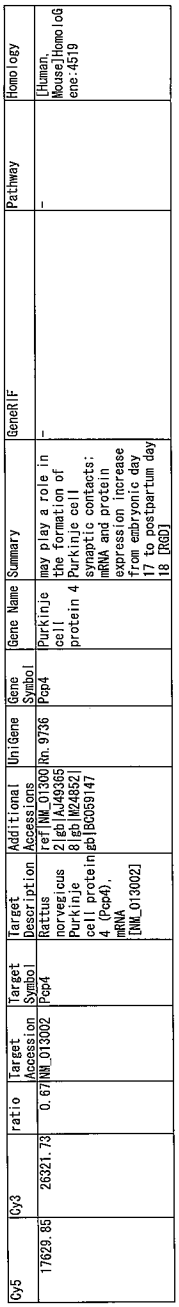
Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Gene Symbol	Gene Name	Summary	GeneRIF	Pathway	Homology
481.00	905.44	0.53	XM_230761	Abpa2bp_predicted	PREDICTED: Rattus norvegicus amyloid beta (A4) precursor protein-binding, family A, member 1 binding protein (predicted) (Abpa2bp_predicted). mRNA	ref|XM_230761|ens|ENSRNOT00000022115|ens|ENSRNOT00000047894|ens|ENSRNOT00000043456	Rn.14505	Abpa2bp_predicted	amyloid beta (A4) precursor protein-binding, family A, member 1 binding protein (predicted)	-	-	-	[Human, Mouse]HomoloGene:10392
24.31	39.73	0.61	XM_342172	Thbs4	PREDICTED: Rattus norvegicus thrombospondin 4 (Thbs4). mRNA [XM_342172]	ref|XM_342172|gb|X89963|gb|AW916235|ens|ENSRNOT00000017078	Rn.11207	Thbs4	thrombospondin 4	extracellular matrix protein: involved in neuronal development [RGD]	-	KEGG pathway: Cell Communication// KEGG pathway: ECM-receptor interaction// KEGG pathway: Focal adhesion// KEGG pathway: TGF-beta signaling pathway	[Human, Mouse]HomoloGene:20691

[0353]



Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Gene Symbol	Gene Name	Summary	GeneRIF	Pathway	Homology
338.67	553.40	0.61	NM_021771	Trpc3	Rattus norvegicus transient receptor potential cation channel, subfamily C, member 3 (Trpc3), mRNA [NM_021771]	ref|NM_021771|Rn.45385|gb|AB022233|ens|ENSRNOT00000021948|tc|TC69078	Rn.45385	Trpc3	transient receptor potential cation channel, subfamily C, member 3	a calcium-activated cation channel [RGD]	Study shows, for the first time, increased TRPC3 channel expression and increased TRPC3-related calcium influx in spontaneously hypertensive rats.// prostate smooth muscle PS1 cells express TRPC3 and TRPC6 proteins which function as receptor- and store-operated Ca(2+) entry pathways.// TRPC3 mediates UTP-induced depolarization of arterial smooth muscle cells// TRPC3/TRPC6 channels are localized to the apical region of polarized epithelial cells, which in salivary gland ducts could contribute to the regulation of salivary [Ca2+] and secretion// TRPC3a gave rise to Ca2+-entry channels that are not only activated by the Gq-phospholipase C beta pathway// siRNA specific for TRPC1 and TRPC3 in proliferating cells inhibited approximately the same amount of Store operated calcium entry.// Data suggest that VAMP2-dependent exocytosis regulates plasma membrane insertion of TRPC3 channels and contributes to carbachol-stimulation of Ca2+ influx.// (The rest is omitted.)	-	[Human, Mouse]HomoloGene:20708
123.77	323.37	0.38	NM_053521	Slc5a7	Rattus norvegicus solute carrier family 5 (choline transporter), member 7 (Slc5a7), mRNA [NM_053521]	ref|NM_053521|Rn.44872|gb|ABO3094 7|ens|ENSRNOT00000014548	Rn.44872	Slc5a7	solute carrier family 5 (choline transporter), member 7	high-affinity choline transporter: give choline to nuerons for the synthesis of acetylcholine [RGD]	This protein is expressed in the rat trachea.// close apposition of CHT1 to reported sites of localization of choline acetyltransferase in these cells is strongly in favour of ACh synthesis being fuelled by choline uptake via CHT1 in these epithelia// high-affinity choline transporter, choline transporter 1, in nerve fibers and epithelial cells in the human and rat skin supporting the pivotal role of this transporter in both the neuronal and non-neuronal cholinergic system of the skin.	-	[Human, Mouse]HomoloGene:32516

[0354]



Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Gene Symbol	Gene Name	Summary	GeneRIF	Pathway	Homology
17629.85	26321.73	0.67	NM_013002	Pcp4	Rattus norvegicus Purkinje cell protein 4 (Pcp4), mRNA [NM_013002]	ref|NM_013002|gb|AJ49365 2|gb|M24852 8|gb|BG059147	Rn.9736	Pcp4	Purkinje cell protein 4	may play a role in the formation of Purkinje cell synaptic contacts: mRNA and protein expression increase from embryonic day 17 to postpartum day 18 [RGD]	-	-	[Human, Mouse]Homolo Gene:4519

[0355] 2－1－5．考察・結論

今回の実験ではラットへのTickling刺激を４週間の長期に渡り施しているため、刺激による即時反応の結果というより体質の変化に伴う各組織の遺伝子の発現差を主に観察していると推測される。すなわち、外界から一時的な刺激に対して、生体は恒常性維持のため神経－内分泌－免疫系を介して各組織が協調反応するので遺伝子の発現レベルでは連動することが予測できたが、長期の刺激は各組織の本来の機能に対して作用するため、その結果は体質

の変化として表出するものと考えられ、組織間で連動して変化する遺伝子は少なかった。

[0356] クラスタリング解析において、視床下部における対照群/Tickling群、Light Touch群/Tickling群で観察される発現差が一部の遺伝子クラスターで逆のパターンを描くことが明らかになった(図55)。線条体および唾液腺(軽度な差異は図50で認めるが)では、これら２比較間で顕著な差は観察されなかった。すなわち、視床下部では対照とLight Touchの差がTickling刺激のベースとして他組織より大きく反映されるものと考えられた。

[0357] 視床下部は生命維持の中枢であるため、GO解析において他組織と比較して多くのGO Termに抽出遺伝子が割り当てられる結果となった。興味ある結果としては、対照群/Tickling群間の解析ではTicklingでDown-regulateされる遺伝子が広範囲のTermに割り当てられるのに対し、Up-regulateされる遺伝子は限局したTermに割り当てられたことである。一方、Light Touch群/Tickling群間の解析では、TicklingでUp-regulateされる遺伝子が広範囲のTermに割り当てられるのに対し、Down-regulateされる遺伝子は狭い範囲のTermに割り当てられたことである。すなわち、一方向に対しては、非特異的なTermに割り当てられる遺伝子により生体反応がマクロに反応し、それとは逆方向のregulationを受ける特異的なTermに割り当てられた遺伝子により微調節を受けていることである。例えば、Light Touch群と比較してTickling群でDown-regulateされる遺伝子群は陰イオン結合に関するTermに属し、Ticklingによる視床下部のCaイオンを介した細胞内刺激伝達、コリン作動性神経による異常興奮を非特異的に制御しているものと考えられる。逆に、Up-regulateされる遺伝子群は食行動や生体アミン合成・代謝に関与する限局した作用を有するTermに属し、特異的に働いていることが特徴的である。特に、食行動に関与する具体的遺伝子は、ガラニン様ペプチド(Galp)、オピオメラノコルチン前駆体(Pomc)、メラニン濃縮ホルモン(Pmch)、Agouti関連蛋白(Agrp)、ハイポクレチン(Hcrt)、ニューロペプチドY(Npy)が抽出されたが、いずれも食行動を活性化する作用を有している。また、対照群/Tickling群間の比較において、Tickli

ng群でストレスホルモン(Avp)が抽出されたことは、本実験において対照として採用したラットの個別飼育は、負のストレス刺激になっていることを検証する結果となった。

[0358] 唾液腺の解析では、多くの遺伝子がTicklingにより発現変動しており、この結果から演繹される唾液成分が新規なストレス指標となる可能性を示唆している。例えば、対照群と比較してTickling群でUp-regulateされたトニン(Ton)、顎下腺カリクレイン(Klks2)、腺性カリクイレイン(Klk12)、神経成長因子(Ngfg)や、Down-regulateされるセリンプロテアーゼインヒビター(Serpina1)、フェツイン(Fetub)はその第一候補となりえる。その他、多くの構造蛋白をコードする遺伝子がUp-regulateされており、これらの成分もストレス指標として利用できる可能性を示唆している。

[0359] ２－１－５－１．健康Responsible遺伝子候補

生命維持の中枢としての視床下部の役割を考えると、Light Touch群と比較してTickling群で発現差を認める遺伝子が健康Responsible遺伝子の第１候補として位置づけられる。非特異的なGO Termに割り当てられるDown-regulateされた遺伝子よりも、特異的なGO Termに割り当てられるUp-regulateされた遺伝子に注目すると、食行動に関与する上記６遺伝子とドーパミントランスポータ(Slc6a3)、チロシン水酸化酵素(Th)がその候補であるが、今後の課題として、短期的なTickling、末梢細胞での発現変化との関連性解析が待たれる。

[0360] ２－１－５－２．新規ストレス指標の推定

今後の体外診断用医薬品には非侵襲・非拘束であることが要求されていることを鑑みると、唾液成分を測定することの臨床的意義が拡大することは容易に推測できる。本研究で実施したTicklingによる唾液腺の遺伝子発現解析から新規ストレス指標を提案するためには、ラットにおける陽性感情と陰性感情の隔たりが大きい対照群/Tickling群間で発現差を認める唾液腺遺伝子から演繹される唾液成分がその候補として適切であると判断する。この選択基準に合致する具体的唾液成分としては、前項記載のトニン(Ton)、顎下腺カリ

クレイン(Klks2)、腺性カリクイレイン(Klk12)、神経成長因子(Ngfg)、セリンプロテアーゼインヒビター(Serpina1)、フェツイン(Fetub)をはじめとして、唾液中の多くの分泌蛋白が候補として挙げられる。刺激負荷後のこれら遺伝子発現の時間変化を予め調べておけば、或る時点での複数の唾液腺遺伝子由来の唾液成分濃度により生体がストレス状態に向かうのか回復期にあるのか判断することが可能になる。また、本実験により特定した複数の唾液成分濃度をパターン解析することによりストレスの種類を判定することも可能になり応用範囲は広い。

[0361] ２－１－６．総括

Ticklingがラットに対して陽性感情を表出する刺激となることを、50KHz近傍の発生音声の解析により検証し、Tickling(4週間)により発現変化する遺伝子群を血液、脳組織(視床下部、線条体)、唾液腺で解析した。

[0362] その結果、長期(4週間)に渡るTicklingによる遺伝子の発現変化は中枢/末梢血液では連動せず、また線条体での発現変化も少ないことが明らかとなった。これは、Ticklingの効果が体質の変化として現れるためであると考察した。Ticklingの長期効果がより多く認められた組織は視床下部と唾液腺であり、前者における遺伝子発現解析より食行動とドーパミン代謝に関わる健康Responsible遺伝子、後者より新規ストレス指標の候補となる唾液成分をコード化する遺伝子を特定することができた。

[0363] ２－２．短期間（２日間）のTickling刺激

６週令(離乳直後[３週令]から個別飼育)になってから２日間、Tickling刺激を負荷したラット、Light Touch刺激(対照)を負荷したラットついて遺伝子発現解析を行なった。Tickling刺激は上記１-２-２記載の方法に従い、ラットをTickling用クリーンケージ(内面は黒色フェルトを貼付)に移し、15秒間放置後、15秒のTickling刺激負荷を行なう操作を4回繰り返して１Tickling Sessionとし、１Session終了後1分間の休憩を挟み、さらに２Session目(2分間)のTicklingを行なった。Tickling刺激負荷時程図は図１に示す通りである。

[0364] 一方、Light Touch刺激は、ラットをTickling用クリーンケージ(上述)に移

し15秒間放置の後、Ticklingの変わりに3秒に1回、ラット背部にやさしく触れることにより負荷した。刺激負荷時程はTickling刺激負荷と同様(図1)とした。

[0365] Tickling負荷２日目及びLight Touch負荷２日目のラット発生音声の周波数成分解析図をそれぞれ図73と図74に示す。Tickling刺激時には50KHz近傍(60KHz)の音声を確認することができたが、対照であるLight Touch刺激では当音声は確認できず、１－２－５．の結果を再現した。

[0366] ２－２－１．実験方法（解析対象臓器の摘出）

臓器摘出の順番は、開胸→心採血→生食灌流(腎動脈瀉血)→口腔内粘膜細胞擦過→断頭→開頭→脳摘出の順とした。

[0367] 1) 心採血・生食灌流

エーテル麻酔下に開胸し心採血(約1mLをPAXgene専用採血管に採取)を行ない、留置針にて生食(約20mL) 灌流／腎動脈瀉血を行なった。

[0368] 2) 口腔内粘膜細胞擦過

生食にて口腔内を洗浄、キムワイプにて口腔内残液を吸収後、マイクロスパーテルで口腔内粘膜細胞を擦過採取し、RNA安定化試薬RNAlater(QIAGEN社製)に浸漬、-80℃で保存した。

[0369] 3) 脳摘出

頭頂部から開頭、脳を摘出し、Glowinski(J Neurochem, 1966)の脳7分割法に従い、氷冷したアルミ板上で線条体、海馬、視床下部、皮質を分けた。脳下垂体はトルコ鞍より直接摘出した。摘出組織は約3mm角にトリミングし、RNA安定化試薬RNAlater(QIAGEN社製)に浸漬、-80℃で保存した。

[0370] ２－２－２．実験方法（ラット組織からのRNA調製・検定）

1) 血液試料からの全RNA調製

PAXgene Blood RNA Kit (QIAGEN社製)を用いて全RNA標品を調製した。

[0371] 2) 口腔内粘膜擦過細胞および脳組織からの全RNA調製

RNAlater浸漬組織(遺伝子発現解析対象である擦過細胞、視床下部、線条体のみ)を、RNeasy Buffer RLT中でホモジナイズ〔TissueLyzer(QIAGEN社製)使

用〕し、以下Kitプロトコールに従い全RNA標品を調製した。各群(Tickling、Light Touch)の口腔粘膜擦過細胞は全RNAを全量混合、脳組織は等量混合した。

[0372] 3) 全RNA純度と無傷度の検定

個体毎(全RNA標品混合前)に、全RNA標品の濃度とA260/280比、28S/18S rRNA比を求めた。28S/18S rRNA比は、マイクロチップ型電気泳動システム(日立コスモアイ、SV1210)により検定・算出した。

[0373] ２－２－３．実験方法（DNAチップ解析）

上記２－２－２の全RNA標品を出発材料として、T7RNA Polymerase Promoter配列を付加したOligo(dT)24をプライマーとしたcDNA合成を行った。引き続き、これを鋳型としてアミノアリル-dUTP 存在下にT7RNA PolymeraseによるmRNA増幅を行って、cRNAにアミノ基を導入し、Cyanine 3[Cy3と略](Light Touch群)あるいはCyanine 5[Cy5と略] (Tickling群)のサクシニミド誘導体とカップリング反応させることにより蛍光標識を行いDNAチップ解析に供した。

[0374] DNAチップ解析は以下の通り行った。各Cyanine色素で蛍光標識したRNA標品を等量混合し、DNAチップ〔Agilent社製(約41,012オリゴDNA搭載)、Whole Rat Genome DNA Microarray〕上で65℃、17時間ハイブリダイゼーション反応を行い(未反応分子はハイブリダイゼーション反応後洗浄除去)、共焦点レーザースキャナー(Agilent社製、G2565)で各色素に由来する蛍光強度を測定した。バックグランド補正とグローバル正規化の後、信号強度50未満の遺伝子(トランスクリプトを含む)を除外し、Cy5/Cy3比を求めた。

[0375] ２－２－４．結果

本結果で用いる「プローブ」と「遺伝子(トランスクリプトを含む)」の用語は同義であり、図表で用いる凡例は以下の通りである。

[0376] T：Tickling

L：Light Touch

Bl：血液

Bc：口腔内粘膜擦過細胞

Hy：視床下部

St：線条体

２－２－４－１．信号強度分布

Tickling／Light Touch間の遺伝子発現の差をDNAチップ法にて解析した際の、DNAチップ上の各プローブの信号強度の分布を図75に示す。縦軸は信号強度、横軸はその信号強度を示す遺伝子数を示すが、脳組織試料は相互に類似の信号強度分布を示したが、血液試料及び口腔粘膜擦過細胞試料では、高信号強度を示す遺伝子数が少なかった。

[0377] ２－２－４－２．発現変化を認めた遺伝子

Light Touch群と比較してTickling群で1.5倍超の発現を認めた末梢血液(BI)の遺伝子の「Target Accession」及び「UniGene」を下記表60に示す。

[表60]

表60 #17 T-Bl(Cy5) v.s. #17 L-Bl(Cy3) :up regulation(Cy5>Cy3)

Target Accession	UniGene
NM_053687	-
AA963075	Rn.73451
NM_053587	Rn.6703
NM_057207	Rn.58137
XM_343234	Rn.21405
NM_053822	Rn.31839
BF558825	Rn.175245
NM_001009353	Rn.90768
NM_031512	Rn.9869
XM_574891	Rn.145579
XM_216485	Rn.8332
NM_001007599	Rn.103172
XM_213346	Rn.144702
NM_012904	Rn.1792
TC559977	-
XM_219604	-
NM_031512	Rn.9869
NM_031537	-
NM_053953	Rn.10758
XM_216485	Rn.8332
XM_216485	Rn.8332
XM_216485	Rn.8332
XM_216485	Rn.8332
XM_216485	Rn.8332
CF108931	Rn.36964
AW144706	Rn.3540
TC537861	-
XM_216485	Rn.8332
TC538830	-
XM_216485	Rn.8332
XM_226929	Rn.42111
XM_216485	Rn.8332
AA900000	Rn.103172
XM_216485	Rn.8332
NM_001006975	Rn.17885
NM_031098	Rn.89756
BI395434	-
BF287531	Rn.4334
XM_216102	Rn.14059
XM_217405	Rn.36770
TC521072	-
NM_181091	Rn.15333
XM_227821	Rn.43876
AW141130	Rn.164677
NM_019257	Rn.162871
NM_001009618	Rn.8706
AI137547	Rn.166786
NM_001025274	-
XM_216485	Rn.8332
XM_229422	Rn.136325
XM_345431	Rn.14868
XM_238467	Rn.22509
BF287785	Rn.141646

Target Accession	UniGene
TC553999	-
XM_235459	Rn.2438
XM_221333	Rn.20571
BF565803	Rn.164480
NM_053619	Rn.10680
NM_175761	Rn.119867
XM_221003	-
XM_215643	Rn.16643
NM_022205	Rn.44431
NM_017340	Rn.31796
NM_001007702	Rn.13725
NM_053847	Rn.9939
AW144410	Rn.91446
XM_340742	Rn.15835
NM_019149	Rn.29774
NM_030848	Rn.10728
NM_001013245	Rn.185799
XM_575368	Rn.41216

[0378] Light Touch群と比較してTickling群で1/1.5倍未満の発現を認めた末梢血液(Bl)の遺伝子の「Target Accession」及び「UniGene」を下記表61に示す。

[表61]

表61 #17 T-BI(Cy5) v.s. #17L-BI(Cy3) :down regulation(Cy5<Cy3)

Target Accession	UniGene
XM_344917	-
ENSRNOT00000046211	-
NM_013092	Rn.10182
NM_017238	Rn.10011
NM_001015008	Rn.11547
XM_221527	Rn.7765
NM_178144	Rn.12347
TC560346	-
XM_341846	-
NM_172336	Rn.30491
XM_342204	Rn.45065
XM_228492	-
NM_001014275	Rn.3795
NM_145773	Rn.10214
AA866223	-
NM_057188	Rn.3862
AA925697	Rn.50843
XM_234377	Rn.105640
XM_228475	-
NM_001010953	Rn.22162
CB772584	Rn.17965
NM_023964	Rn.64496
XM_218592	Rn.162417
XM_344770	-
NM_001000896	Rn.142668
XM_217869	Rn.144777
BQ203920	Rn.2361
XM_219510	Rn.22113
AA818576	Rn.63458
NM_001014264	Rn.102149
XM_342315	Rn.67979
NM_012597	Rn.1195
AW528833	Rn.11046
ENSRNOT00000021215	-
NM_031577	Rn.10693
NM_017100	Rn.11034
NM_022196	Rn.44379
AA851436	Rn.101545
XM_341997	Rn.37338
NM_181625	Rn.90340
AI411618	Rn.2393
XM_234433	-
NM_001014074	Rn.140455
XM_233779	Rn.104223
XM_341746	Rn.138388
BF397707	Rn.148228
A_44_P806369	-
XM_214196	Rn.137882
TC523980	-
XM_219785	Rn.17101
XM_217094	Rn.13486
ENSRNOT00000013882	-
XM_342493	Rn.44656

Target Accession	UniGene
A_44_P558064	-
A_44_P806297	-
NM_053342	Rn.52859
XM_238528	-
AI715122	Rn.22560
NM_019287	Rn.33815
XM_241632	Rn.12030
A_44_P485409	-
XM_218761	-
XM_216425	Rn.162821
XM_218706	Rn.162343
NM_053303	Rn.127121
TC543622	-
A_44_P412349	-
XM_345096	-
XM_215939	Rn.117434
NM_022925	Rn.30011
NM_001001060	Rn.142839
BI281796	Rn.105655
BF406235	Rn.107043
CB547833	Rn.145144
NM_019145	Rn.44634
AI230784	Rn.111805
NM_012580	Rn.3160

[0379] Light Touch群と比較してTickling群で1.5倍超の発現を認めた視床下部(Hy)の遺伝子の「Target Accession」及び「UniGene」を下記表62に示す。

[表62]

Target Accession	UniGene
NM_053918	Rn.10589
NM_013116	Rn.9966
CR475266	Rn.157287
NM_153294	Rn.14575
AI012802	Rn.11048
NM_022239	Rn.47720
NM_001008884	Rn.33311
NM_031334	Rn.1303
TC524999	-
XM_233526	Rn.145085
XM_215498	Rn.126604
BF549735	Rn.38972
NM_013015	Rn.11400
XM_580165	-
NM_012778	Rn.1618
NM_144737	Rn.3928
XM_216018	Rn.85879
NM_001008555	Rn.79638
NM_012694	Rn.10093
J00757	Rn.10589
TC534031	-

[0380] Light Touch群と比較してTickling群で1/1.5倍未満の発現を認めた視床下部(Hy)の遺伝子の「Target Accession」及び「UniGene」を下記表63に示す。

[表63]

Target Accession	UniGene
BQ194469	Rn.161764
NM_012681	Rn.1404
BF398607	Rn.45255
AI010332	Rn.164882
AI044887	Rn.5827
TC522684	-
XM_231730	-
NM_001014207	Rn.137575
BG376285	Rn.6228
TC523509	-
AW918626	Rn.170329

[0381] Light Touch群と比較してTickling群で1.5倍超の発現を認めた線条体(St)の遺伝子の「Target Accession」及び「UniGene」を下記表64に示す。

[表64]

Target Accession	UniGene
NM_024483	Rn. 11314
NM_030841	Rn. 34907
BF285957	Rn. 129513
CB544275	Rn. 179582
NM_133522	Rn. 10458
CB582871	Rn. 13498
TC555778	-
NM_030868	Rn. 162955
NM_012625	Rn. 9675
NM_013192	-
NM_133559	Rn. 2899
XM_576570	Rn. 22624
XM_221455	Rn. 138746
AW914778	-
NM_019328	Rn. 88129
CO403684	Rn. 13498
NM_012719	Rn. 42915
NM_031628	Rn. 62694
TC558767	-
XM_214510	Rn. 139226
XM_342857	Rn. 10787
NM_053504	Rn. 86653
AI227991	Rn. 105934
TC545153	-
XM_576570	Rn. 22624
NM_022202	Rn. 44420
NM_022937	Rn. 162465
TC558785	-
TC519964	-
ENSRNOT00000046943	-
AA874934	Rn. 3179
XM_575489	Rn. 162754
XM_223820	Rn. 69050
XM_215066	Rn. 128103
NM_001005871	Rn. 9986
NM_138849	Rn. 31973
XM_340792	Rn. 46134
XM_574851	Rn. 155530
XM_344562	Rn. 162163
XM_230296	Rn. 22267
XM_231528	Rn. 91746
AA801434	Rn. 3216
XM_217838	Rn. 18675
BQ210081	Rn. 3081
NM_001004282	Rn. 17530
NM_181370	Rn. 49010
XM_231381	Rn. 136960
AW916327	Rn. 14770
NM_001013243	Rn. 9297
XM_340792	Rn. 46134
AW914913	Rn. 21006
XM_236914	Rn. 47365
NM_053514	Rn. 31766
NM_031817	Rn. 30124
NM_133570	Rn. 10930
XM_231528	Rn. 91746
NM_053750	Rn. 10637
XM_230296	Rn. 22267
NM_013165	Rn. 90997
AI556229	Rn. 161436
XM_230639	Rn. 104639

Target Accession	UniGene
XM_224673	Rn. 26828
XM_229981	-
AF091111	Rn. 48687
BC092605	Rn. 22271
AW914891	Rn. 8590
TC544290	-
NM_001012022	Rn. 6830
TC523200	-
NM_030850	Rn. 11406
NM_012789	Rn. 91364
AW918626	Rn. 170329
NM_019326	Rn. 10724
NM_053859	Rn. 10267
NM_012835	Rn. 10490
XM_343507	Rn. 46028
XM_345102	Rn. 133599

[0382]

Target Accession	UniGene
NM_022292	Rn. 64577
BF281936	Rn. 8247
NM_001009353	Rn. 90768
NM_153735	Rn. 54707
XM_236376	Rn. 163030
TC551967	-
NM_012996	Rn. 48915
S74320	-
NM_053573	Rn. 11005
NM_016992	Rn. 9976
XM_231528	Rn. 91746
NM_012757	Rn. 21943
TC562720	-
XM_216568	Rn. 38448
XM_223205	Rn. 162242
NM_031778	Rn. 10878
NM_012513	Rn. 11266
AI549455	Rn. 9411
NM_016991	Rn. 10032
XM_216471	Rn. 134702
XM_230761	Rn. 145056
NM_053788	Rn. 9943
TC537129	-
NM_134374	Rn. 144662
XM_574210	Rn. 24402
TC560122	-
AW914894	Rn. 10267
BM382824	Rn. 9781
NM_016989	Rn. 37400
NM_019339	Rn. 9796
S82649	-
NM_053996	Rn. 9663
A_44_P950925	-
NM_024354	Rn. 9697
TC530678	-
NM_053346	Rn. 3546
NM_012612	Rn. 2004
NM_080778	Rn. 17815
A_44_P722152	-
XM_225579	-
NM_001012740	Rn. 16398
NM_053613	Rn. 45686
NM_012513	Rn. 11266
XM_575616	Rn. 50757
NM_012829	Rn. 9781
NM_177927	Rn. 16993
TC541875	-
CB547989	Rn. 33084
XM_236376	Rn. 163030
TC524999	-
XM_233526	Rn. 145085
NM_013104	Rn. 6431
NM_021772	Rn. 154405
AF071214	-
XM_215498	Rn. 126604
XM_342750	Rn. 25217
XM_214441	Rn. 103114
XM_214441	Rn. 103114
NM_001008847	Rn. 103146
AA817769	Rn. 1096
BF549735	Rn. 38972
NM_013015	Rn. 11400
XM_237296	Rn. 18155

[0383] Light Touch群と比較してTickling群で1/1.5倍未満の発現を認めた線条体(St)の遺伝子の「Target Accession」及び「UniGene」を下記表65に示す。

[表65]

Target Accession	UniGene
TC525352	-
TC567761	-
L14617	Rn.10062
TC556932	-
XM_220239	-
XM_343674	Rn.145233
TC550302	-
NM_017016	Rn.48653
BQ194469	Rn.161764
NM_012681	Rn.1404
BF398607	Rn.45255
AI010332	Rn.164882
AI044887	Rn.5827
XM_226313	Rn.154585
TC546786	-

[0384] Light Touch群と比較してTickling群で1.5倍超の発現を認めた口腔内細胞(Bc)の遺伝子の「Target Accession」及び「UniGene」を下記表66に示す。

[表66]

Target Accession	UniGene
TC544981	-
TC521714	-
XM_574205	-
XM_217304	Rn. 12843
XM_343674	Rn. 145233
XM_217737	Rn. 41068
XM_573100	Rn. 93735
XM_576895	-
AI072161	Rn. 12102
NM_139082	Rn. 25267
XM_219711	-
XM_224708	-
AW143873	Rn. 17512
AW915718	Rn. 92304
L20996	Rn. 111423
TC560516	-
AI236332	Rn. 107986
XM_222911	Rn. 163233
NM_001012050	Rn. 91689
NM_017100	Rn. 11034
NM_022528	Rn. 161814
TC559298	-
XM_575844	Rn. 13247
AA817782	Rn. 145427
TC546786	-
NM_001014099	Rn. 156585
XM_215924	Rn. 3102
BE110241	-
NM_001012190	Rn. 98217
XM_343727	Rn. 162365
NM_001007006	Rn. 61094
XM_233526	Rn. 145085
BX883052	-
TC567231	-
XM_215264	-
BF522750	Rn. 44913
XM_238588	Rn. 45600
NM_134459	Rn. 20204
TC541222	-
TC526064	-
XM_216797	-
NM_134390	Rn. 26876
XM_232684	Rn. 94436
CB578554	Rn. 179904
AI232517	Rn. 24651
BF543360	Rn. 161307
A_44_P516166	-
TC526529	-
TC538863	-
XM_235691	Rn. 135286
NM_212545	Rn. 106755
M26855	Rn. 91353
NM_001012099	Rn. 13596

Target Accession	UniGene
AI175779	Rn. 153998
NM_017004	Rn. 2549
AW143264	Rn. 96174
NM_031633	Rn. 10665
NM_012949	Rn. 3443
BQ194105	Rn. 125065
NM_001009623	Rn. 19955
XM_224308	Rn. 49950
AW141163	Rn. 18535
XM_342701	Rn. 7449
BI288013	Rn. 40911
TC529338	-
NM_053565	Rn. 127801
NM_001003404	Rn. 13127
TC528927	-
NM_017090	Rn. 1974
NM_019354	Rn. 13333
XM_214130	Rn. 25565
XM_230513	Rn. 17049
XM_342788	Rn. 107176
BC090353	Rn. 119131
XM_226313	Rn. 154585
NM_033099	Rn. 10048
BG709676	Rn. 132980
AI045568	-
NM_012946	Rn. 3091
TC524241	-
NM_019386	Rn. 10
TC544530	-
TC548352	-
XM_216266	-
L04739	-
NM_013113	Rn. 8925
TC557386	-
XM_576716	Rn. 155010
XM_234775	Rn. 154519
XM_221343	Rn. 162055
BQ207842	Rn. 125065
TC561295	-
AY136826	Rn. 14503
XM_236477	Rn. 107533
XM_224509	-
NM_001014166	Rn. 106849
BF289184	Rn. 100732
TC532602	-
NM_021760	Rn. 38654
XM_222849	-
AA924317	Rn. 99891
XM_346173	-
XM_215938	Rn. 161867
NM_001009645	Rn. 8601
NM_013089	Rn. 2906
XM_576774	Rn. 121329

[0385]

Target Accession	UniGene
TC562080	-
XM_230459	Rn. 51673
BF411029	Rn. 10325
XM_345680	-
NM_171991	Rn. 9232
NM_213562	Rn. 48210
BF396295	-
BC087636	Rn. 162186
XM_231469	-
XM_233037	Rn. 38908
U14522	-
AI409900	Rn. 111095
NM_173136	Rn. 23676
NM_001009470	Rn. 6743
TC559262	-
A_44_P337592	-
NM_145671	Rn. 144676
NM_012733	Rn. 902
NM_019370	Rn. 44
NM_133298	Rn. 13778
AW920707	Rn. 25287
AF487544	Rn. 158089
AW919683	Rn. 52238
AW141493	Rn. 4181
TC559522	-
NM_031736	Rn. 3608
NM_019296	Rn. 6934
NM_032063	Rn. 10628
TC519762	-
TC552003	-
NM_012542	Rn. 2063
XM_576656	-
AA955414	-
XM_217515	-
AF473847	Rn. 10346
TC540877	-
BF403977	Rn. 173262
XM_575585	Rn. 43582
XM_343700	Rn. 111036
AI059571	Rn. 22572
NM_138876	Rn. 9794
NM_022391	Rn. 271
XM_343690	Rn. 124726
XM_227391	-
NM_212498	Rn. 136935
XM_224970	Rn. 50526
NM_001008750	Rn. 145402
XM_341592	Rn. 101107
AW917714	Rn. 94179
XM_343688	-
TC518079	-
NM_198752	Rn. 100970
XM_237794	Rn. 46621
BF549558	Rn. 1464
TC557520	-

Target Accession	UniGene
TC539303	-
TC518066	-
CA507680	Rn. 1040
NM_017014	Rn. 625
BQ201045	Rn. 106944
XM_217489	Rn. 65219
AI011505	Rn. 165714
NM_053611	Rn. 11182
NM_017227	Rn. 11155
NM_053976	Rn. 103924
NM_017004	Rn. 2549
A_44_P483274	-
XM_220936	Rn. 110109
XM_215004	-
NM_001013936	Rn. 104973
AI176579	-
BQ191871	Rn. 101608
AB072252	Rn. 112795
XM_343728	-
AW918369	Rn. 44991
AF039218	Rn. 89069
NM_138825	Rn. 79035
XM_227544	-
NM_053570	Rn. 113837
XM_580199	-
XM_232237	Rn. 54266
NM_019363	Rn. 15681
XM_580104	Rn. 162863
NM_017159	Rn. 10037
NM_021595	Rn. 162768
NM_013058	Rn. 2760
NM_001004131	Rn. 61799
NM_031732	Rn. 9937
NM_017013	Rn. 144550
BI278180	Rn. 21549
XM_342494	Rn. 49845
NM_172031	Rn. 19272
BF555532	Rn. 15197
XM_228458	-
TC523524	-
XM_216438	-
CV079334	Rn. 19499
TC560767	-
NM_012614	Rn. 9714
NM_001024257	Rn. 140802
XM_229658	-
NM_012953	Rn. 11306
AA874941	Rn. 101967
BF555796	Rn. 8238
AW143472	Rn. 21549
AW143173	Rn. 22427
AB105879	Rn. 44216
NM_053750	Rn. 10637
NM_153296	Rn. 161874
NM_080892	Rn. 16617

[0386]

Target Accession	UniGene
NM_019311	Rn. 10659
AA925326	Rn. 164908
BF551572	Rn. 18432
TC561304	-
TC550002	-
NM_019257	Rn. 162871
TC530581	-
TC554007	-
XM_214644	-
NM_153737	Rn. 2415
AI029795	Rn. 772
NM_001011915	Rn. 7658
TC557460	-
XM_343686	-
NM_013058	Rn. 2760
XM_343725	-
XM_218002	Rn. 100050
XM_345857	Rn. 127590
AI136348	Rn. 13826
TC560879	-
XM_230758	Rn. 6623
XM_230735	Rn. 161631
NM_001025274	-
AF195789	Rn. 162341
XM_216226	Rn. 162762
NM_017074	Rn. 3881
XM_574957	Rn. 145585
A_44_P414912	-
XM_213891	Rn. 55479
XM_238523	Rn. 18273
TC520137	-
A_44_P215371	-
XM_343674	Rn. 145233
AI412054	Rn. 162966
NM_177421	Rn. 7312
XM_576346	Rn. 162014
NM_030990	Rn. 4550
AW917057	Rn. 263
BQ209315	Rn. 178431
BG376471	Rn. 21359
NM_001025049	Rn. 155689
AI511358	Rn. 168013
TC559950	-
NM_017100	Rn. 11034
XM_216091	Rn. 18101
XM_342828	Rn. 28232
AA893596	Rn. 42579
AW915388	Rn. 162437
XM_342494	Rn. 49845
NM_001009654	Rn. 16268
XM_341649	-
XM_345870	Rn. 52275
AW144441	Rn. 162478
NM_013058	Rn. 2760
AI177507	Rn. 38461

Target Accession	UniGene
NM_153623	Rn. 160166
XM_226381	Rn. 41880
BQ199390	Rn. 144550
BQ200056	Rn. 41038
BG372060	-
NM_031327	Rn. 22129
NM_001008770	Rn. 64439
NM_017013	Rn. 144550
XM_216713	Rn. 82576
TC532286	-
NM_001001071	Rn. 143176
TC536876	-
AA858641	Rn. 16559
XM_216954	Rn. 17241
XM_345284	Rn. 65373
NM_001009920	Rn. 120929
NM_022407	Rn. 6132
U02094	-
XM_220055	Rn. 138477
AA858768	-
NM_031509	Rn. 10460
XM_235687	Rn. 40671
XM_217869	Rn. 144777
XM_345284	Rn. 65373

[0387] Light Touch群と比較してTickling群で1/1.5倍未満の発現を認めた口腔内細胞(Bc)の遺伝子の「Target Accession」及び「UniGene」を下記表67に示す。

[表67]

Target Accession	UniGene
XM_577424	-
TC561220	-
XM_225507	-
XM_341966	-
NM_182735	Rn. 162507
NM_001013853	Rn. 163132
NM_182735	Rn. 162507
NM_198776	Rn. 36966
AI045044	Rn. 166087
XM_225729	Rn. 38235
NM_031776	Rn. 161897
XM_236308	-
TC545218	-
TC523542	-
TC526483	-
XM_213211	Rn. 17380
NM_001012018	Rn. 143976
XM_215372	Rn. 161744
NM_013107	Rn. 40476
XM_215372	Rn. 161744
AW918097	Rn. 16035
NM_013059	Rn. 82764
XM_216925	Rn. 82172
NM_017233	Rn. 3664
NM_031115	Rn. 32256
AI146186	-
BF287585	Rn. 29821
NM_147165	Rn. 9852
XM_238283	Rn. 52060
NM_031678	Rn. 25935
NM_130817	Rn. 81236
XM_575179	Rn. 22639
XM_222985	-
CA511607	Rn. 96943
XM_343604	Rn. 2271
AW915784	Rn. 24783
XM_235687	Rn. 40671
XM_224783	-
AI071797	Rn. 20641
AF159099	-
XM_227567	-
A_44_P898303	-
XM_219201	Rn. 2971
NM_021576	-
NM_012972	Rn. 162789
A_44_P180557	-
XM_221355	Rn. 144723
NM_031677	Rn. 3849
A_44_P163783	-
NM_133303	Rn. 10784
XM_216960	Rn. 19695
A_44_P759962	-
NM_031511	Rn. 118681

Target Accession	UniGene
AA851776	Rn. 103055
NM_031743	Rn. 74242
NM_133392	Rn. 163064
NM_019372	Rn. 31799
TC536649	-
TC541138	-
XM_229433	-
XM_233441	Rn. 95937
XM_340913	Rn. 22469
XM_574938	-
XM_216629	Rn. 2818
TC561906	-
NM_022629	Rn. 162664
BM385414	Rn. 1804
NM_130433	Rn. 3786
TC522018	-
BI289678	Rn. 18034
NM_001012055	Rn. 3478
XM_238649	Rn. 1644
BF545837	Rn. 98481
XM_347166	Rn. 163203
NM_020101	Rn. 48679
XM_342683	Rn. 21291
BM387109	Rn. 11463
BM385378	Rn. 48777
XM_220071	-
BQ195982	Rn. 3192
TC542844	-
XM_216158	Rn. 104463
TC533603	-
TC555895	-
NM_001006997	Rn. 18277
NM_031046	Rn. 89152
XM_216882	Rn. 11
TC537584	-
XM_574002	-
XM_212905	-
XM_574071	Rn. 145501
NM_019349	Rn. 33275
TC557676	-
XM_219201	Rn. 2971
TC538128	-
NM_057119	Rn. 8538
TC539589	-
ENSRNOT00000033438	-
NM_053539	Rn. 10780
AI105127	Rn. 93735
XM_342682	Rn. 27517
XM_577218	Rn. 61952
AA893226	Rn. 6092
XM_342460	Rn. 108023

[0388]

Target Accession	UniGene
A_44_P631361	-
XM_238235	Rn. 83620
NM_134383	Rn. 46942
NM_016999	Rn. 86651
XM_223542	Rn. 137870
NM_001024232	Rn. 178925
NM_001013247	Rn. 16457
XM_342122	-
NM_016998	Rn. 9576
XM_216791	Rn. 34387
XM_215283	Rn. 6581
XM_230305	Rn. 101707
XM_575365	Rn. 13231
XM_576252	Rn. 54812
NM_030997	Rn. 9704
XM_213765	-
BM390993	Rn. 164141
NM_012995	Rn. 9719
TC520894	-
AW918545	Rn. 170325
NM_031552	Rn. 76589
XM_224969	Rn. 163331
NM_001009534	Rn. 108070
AW917512	Rn. 6620
AA924218	Rn. 41412
XM_221711	Rn. 19782
XM_343581	Rn. 163076
NM_017183	Rn. 90347
AW142785	Rn. 32293
XM_213921	Rn. 8051
AA963238	Rn. 37476
TC550601	-
XM_218226	Rn. 162410
BE095847	Rn. 71484
XM_574618	Rn. 112831
TC547982	-
NM_130411	Rn. 6990
U06230	Rn. 2888
XM_224993	Rn. 15556
NM_183053	Rn. 18789
NM_053397	Rn. 154711
TC551486	-
BM387413	Rn. 111901
NM_001025127	Rn. 40877
XM_340847	Rn. 106278
TC519676	-
AI008119	Rn. 2877
A_44_P236378	-
NM_053981	Rn. 10406
NM_031982	Rn. 3073
TC540725	-
ENSRNOT00000048644	-
NM_020082	Rn. 1742
CB544554	Rn. 179710
NM_012529	Rn. 1472

[0389] Light Touch群と比較してTickling群で2.0倍超の発現を認めた末梢血液(BI)の遺伝子のアノテーションを下記表68に示す。

[表68]

表68 #17 T-BI(Cy5) v.s. #17 L-BI(Cy3) :up regulation(Cy5>Cy3)

No	Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Pathway Name	Gene Symbol	Gene Name	Summary	GeneRIF	Homology
26	986.77	383.87	2.57	NM_053687	Sifn3	Rattus norvegicus schlafen 3 (Sifn3), mRNA [NM_053687]	ref|NM_053687|gb|AF1 60795|ens|ENSRNOT000 00012859|tc|TC56950 5	-	-	Sifn3	schlafen 3	regulates cell growth. involved in T cell development [RGD]	-	[Human, Mouse]Ho moloGene :79048
27	2417.59	1069.96	2.26	AA963075	AA963075	AA963075 UI-R-EI-fx-a-09-0-UI.s1 UI-R-EI Rattus norvegicus cDNA clone UI-R-EI-fx-a-09-0-UI 3', mRNA sequence [AA963075]	gb|AA963075	Rn.73451	-	Lactb_predicted	lactamase, beta (predicted)	-	-	[Human, Mouse]Ho moloGene :12755
28	963.10	456.83	2.11	NM_053587	S100a9	Rattus norvegicus S100 calcium binding protein A9 (calgranulin B) (S100a9), mRNA [NM_053587]	ref|NM_053587|gb|AB1 18215|gb|L18948|ens| ENSRNOT00000015351	Rn.6703	-	S100a9	S100 calcium binding protein A9 (calgranulin B)	calcium binding protein that may be associated with acute inflammatory processes [RGD]	Phosphorylation inhibits tubulin polymerization in microtubules.	[Human, Mouse]Ho moloGene :2227

[0390] Light Touch群と比較してTickling群で0.5倍未満の発現を認めた末梢血液(BI)の遺伝子のアノテーションを下記表69に示す。

[表69]

表69 #17 T-Bl(Cy5) v.s. #17 L-Bl(Cy3) :down regulation(Cy5<Cy3)

No	Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Pathway Name	Gene Symbol	Gene Name	Summary	GeneRIF	Homology
29	66.58	133.97	0.50	XM_344917	Bnc1_predicted	PREDICTED: Rattus norvegicus basonuclin 1 (predicted) (Bnc1_predicted), mRNA [XM_344917]	ref|XM_344917|ens|ENSRNOT00000026762	-	-	Bnc1_predicted	basonuclin 1 (predicted)	-	-	[Human, Mouse]Homologene:31048

[0391] Light Touch群と比較してTickling群で2.0倍超の発現を認めた視床下部(Hy)の遺伝子のアノテーションを下記表70に示す。

[表70]

表70 #17 T-Hy(Cy5) v.s. #17 L-Hy(Cy3) :up regulation(Cy5>Cy3)

No	Cy5	Cy3	lrratio	Target Accession	Target Symbol	Target Description	Additional Association	UniGene	Pathway Name	Gene Symbol	Gene Name	Summary	GeneRIF	Homology
30	193.90	65.81	2.95	NM_012694	Slc6a3	Rattus norvegicus solute carrier family 6 (neurotransmitter transporter, dopamine), member 3 (Slc6a3), mRNA [NM_012694]	ref|NM_012694|gb|M60|Rn.10093 570|ens|ENSRNOT00000 024015|tc|TC560830	Rn.10093	-	Slc6a3	solute carrier family 6 (neurotransmitter transporter, dopamine), member 3	acts as a sodium-dependent dopamine transporter and may play a role in regulation of dopamine metabolism and signaling [RGD]	The decrease in DAT cell surface expression in the mPFC may be responsible for decreased DAT function in the mPFC of stimulated compared with undisturbed rats; there is plasticity in the regulatory mechanisms mediating DAT trafficking and function.// the carboxyl terminus regulates dopamine transporter export from endoplasmic reticulum// tyrosine hydroxylase and the dopamine transporter are differentially distributed in the medial- versus the lateral ventral pallidum.// Observed differences in density and distribution of DAT1 sites in Wistar Kyoto rats may lead to altered modulation of synaptic dopamine levels in cell body and mesolimbic regions, contributing to the depression-like behaviors reported in this rat strain.// dopamine transporter constitutively internalizes and recycles in a protein kinase C-regulated manner in stably transfected PC12 cell lines// dopamine membrane transporter (DAT) protein density and mRNA expression is upregulated in restricted-fed adult male rats// (The rest is omitted.)	[Human, Mouse]Homolo geneID :55547
31	1129.52	435.98	2.59	J00757	Cga	Rattus norvegicus glycoprotein hormone alpha subunit precursor mRNA, complete cds. [J00757]	gb|J00757|gb|C656940|Rn.10589 21|gb|D005751|ens|ENSR NOT00000012385	Rn.10589	Neuroactive ligand-receptor interaction, GnRH signaling pathway	Cga	glycoprotein hormones, alpha subunit	alpha subunit of pituitary glycoprotein hormones [RGD]	-	[Human, Mouse]Homolo geneID :587
32	694.24	328.30	2.11	NM_053918	Cga	Rattus norvegicus glycoprotein hormones, alpha subunit (Cga), mRNA [NM_053918]	ref|NM_053918|gb|V01|Rn.10589 253	Rn.10589	Neuroactive ligand-receptor interaction, GnRH signaling pathway	Cga	glycoprotein hormones, alpha subunit	alpha subunit of pituitary glycoprotein hormones [RGD]	-	[Human, Mouse]Homolo geneID :587

[0392] Light Touch群と比較してTickling群で0.5倍未満の発現を認めた視床下部(Hy)の遺伝子のアノテーションを下記表71に示す。

[表71]

表71 #17 T-Hy(Cy5) v.s. #17 L-Hy(Cy3) :down regulation(Cy5<Cy3)

No	Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Pathway Name	Gene Symbol	Gene Name	Summary	GeneRIF	Homology
33	70.49	525.05	0.13	AI044887	AI044887	AI044887 UI-R-C1-kk-a-01-0-UI.s1 UI-R-C1-kk-a-01-0-UI 3', mRNA sequence [AI044887]	gb|AI044887	Rn.5827	Glycerophospholipid metabolism	Pafah1b1	platelet-activating factor acetylhydrolase, isoform 1b, alpha subunit 45kDa	subunit of the brain intracellular platelet-activating factor acetylhydrolase, which is composed of alpha1, alpha2, and beta subunits [RGD]	-	[Human, Mouse]HomoloGene:371
34	96.97	317.21	0.31	BF398607	BF398607	BF398607 UI-R-BS2-beq-g-09-0-UI.s1 UI-R-BS2 Rattus norvegicus cDNA clone UI-R-BS2-beq-g-09-0-UI 3', mRNA sequence [BF398607]	gb|BF398607|gb|BF285611	Rn.46255	-	RGD1564156_predicted	similar to teratocyte-specific carboxylesterase (predicted)	-	-	-

[0393] Light Touch群と比較してTickling群で2.0倍超の発現を認めた線条体(St)の遺伝子のアノテーションを下記表72に示す。

[表72]

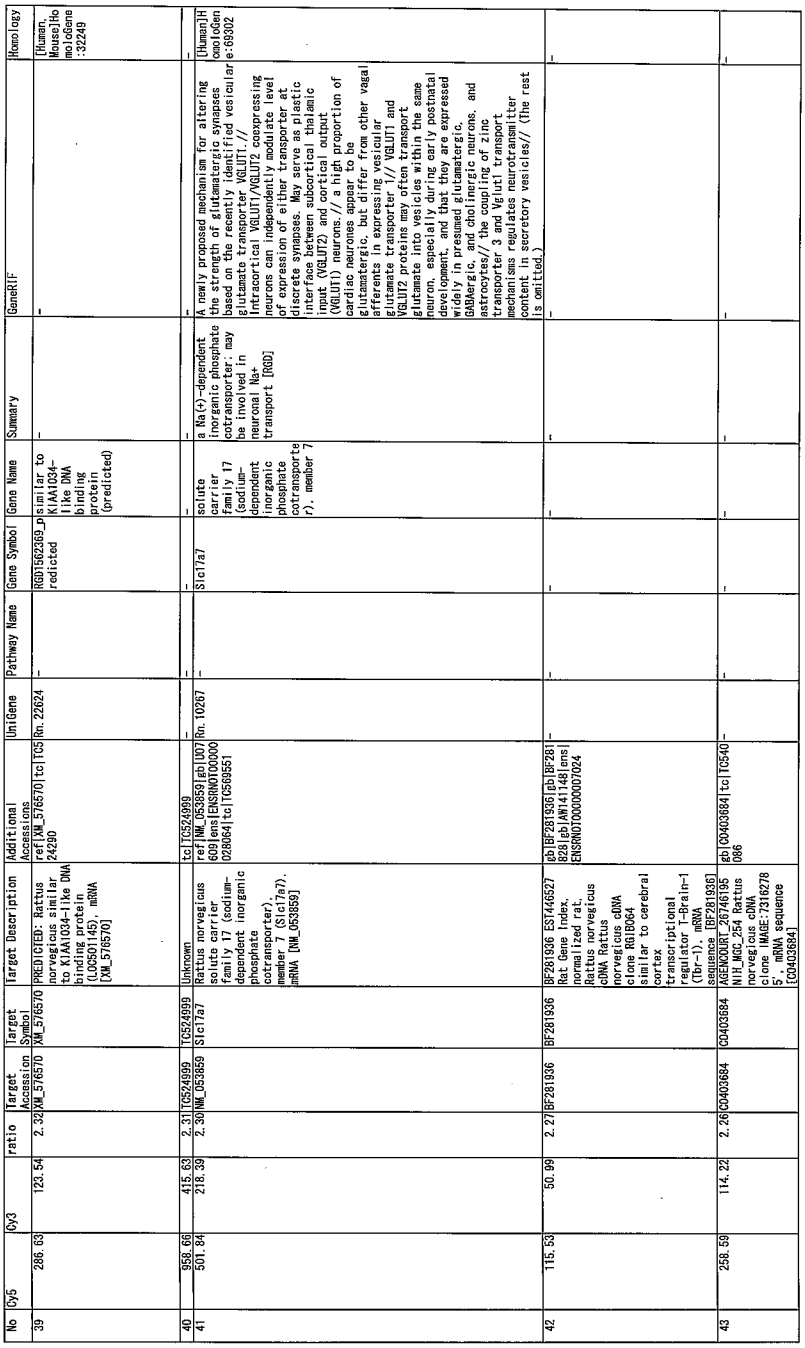
表72 #17 T-St(Cy5) v.s. #17 L-St(Cy3) :up regulation(Cy5>Cy3)

No	Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Pathway Name	Gene Symbol	Gene Name	Summary	GeneRIF	Homology
35	160.27	57.88	2.77	NM_016992	Avp	Rattus norvegicus arginine vasopressin (Avp), mRNA [NM_016992]	ref|NM_016992|gb|M25646|gb|X01637|gb|V01276	Rn.9976	Neuroactive ligand-receptor interaction	Avp	arginine vasopressin	neuropeptide hormone; involved in vasoconstriction to regulate blood pressure and smooth muscle contraction during parturition and lactation [RGD]	These data suggest that testosterone attenuates light-enhanced startle, but not fear-potentiated startle, through a mechanism that may involve AVP.// Both the magnocellular and the parvocellular hypothalamic vasopressin systems are capable of expressing the steroid binding globulin, which is probably subject to axonal transport, along with the peptide hormone.// The A(-1276)G AVP gene SNP plays a role in elevated AVP expression in the paraventricular nucleus of HAB rats. It likely contributes to their anxiety behavior & neuroendocrine phenotype.// AVP acts through V1a receptors and is involved in endogenous central histamine-induced reversal of critical haemorrhagic hypotension in rats// dehydration-induced release of AVP from magnocellular hypothalamic neurons may be responsible for the observed increase in immunoreactive apelin levels within the same neurons// apelin acts as a potent diuretic neuropeptide counteracting AVP actions through inhibition of AVP neuron activity and AVP release.// (The rest is omitted.)	[Human, Mouse]HomoloGene:417
36	146.59	56.31	2.60	NM_019326	Neurod2	Rattus norvegicus neurogenic differentiation 2 (Neurod2), mRNA [NM_019326]	ref|NM_019326|gb|D82868|tc|TC573491	Rn.10724	-	Neurod2	neurogenic differentiation 2	basic helix-loop-helix (bHLH) protein; may have a role in neurogenesis [RGD]	The transduction pathway by which oleic acid induces the expression of genes responsible for neuronal differentiation appears to be mediated by the transcription factor NeuroD2, a regulator of terminal neuronal differentiation	[Human, Mouse]HomoloGene:4489

[0394]

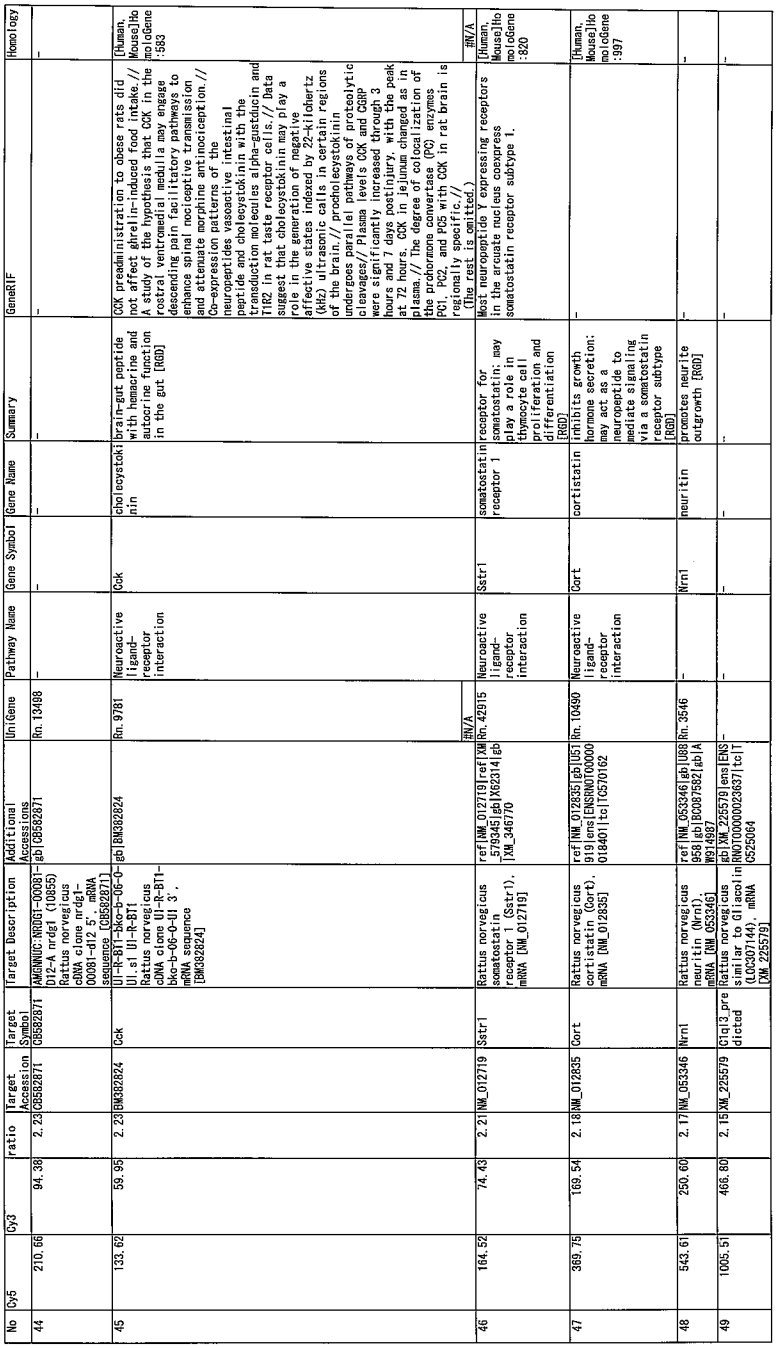
No	Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Pathway Name	Gene Symbol	Gene Name	Summary	GeneRIF	Homology
37	3573.76	1510.08	2.37	AW914894	AW914894	AW914894 EST346198 Normalized rat ovary, Bento Soares Rattus sp. cDNA clone RGIBMO1 5', end, mRNA sequence [AW914894]	gb|AW914894|gb|BF567766|to|TC521958	Rn.10267	-	Slc17a7	solute carrier family 17 (sodium-dependent inorganic phosphate cotransporter), member 7	a Na(+)-dependent inorganic phosphate cotransporter; may be involved in neuronal Na+ transport [RGD]	A newly proposed mechanism for altering the strength of glutamatergic synapses based on the recently identified vesicular glutamate transporter VGLUT1.// Intracortical VGLUT1/VGLUT2 coexpressing neurons can independently modulate level of expression of either transporter at discrete synapses. May serve as plastic interface between subcortical thalamic input (VGLUT2) and cortical output (VGLUT1) neurons.// a high proportion of cardiac neurones appear to be glutamatergic, but differ from other vagal afferents in expressing vesicular glutamate transporter 1// VGLUT1 and VGLUT2 proteins may often transport glutamate into vesicles within the same neuron.// postnatally during early postnatal development and that they are expressed widely in presumed glutamatergic, GABAergic, and cholinergic neurons, and astrocytes// the coupling of zinc transporter 3 and Vglut1 transport mechanisms regulates neurotransmitter content in secretory vesicles// (The rest is omitted.)	[Human]Homologene:63302
38	232.63	99.84	2.33	XM_217838	Vip	PREDICTED: Rattus norvegicus vasoactive intestinal polypeptide (Vip), mRNA [XM_217838]	ref|XM_217838|gb|XM_341|ens|ENSRNOT00000025477|to|TC537816	Rn.18675	Neuroactive ligand-receptor interaction	Vip	vasoactive intestinal polypeptide	peptide that causes vasodilation [RGD]	Vasoactive intestinal polypeptide regulates dynamic changes in astrocyte morphometry: impact on gonadotropin-releasing hormone neurons// Significant changes in NPY and VIP prostate nerve fibers, showing an increase in periurethral ducts at sex maturation.// Co-expression patterns of the neuropeptides vasoactive intestinal peptide and cholecystokinin with the transduction molecules alpha-gustducin and T1R2 in rat taste receptor cells.// VIP had a modulatory action on jejunal potassium absorption when injected into the nucleus tractus solitarius.// VIP can modulate not only immune responses but also hormonal responses during acute inflammation.// The increased nonadrenergic noncholinergic and the decreased effects of VIP in mediating inhibitory nerves may largely relate to the peristaltic abnormalities seen in the isograftedLEW rat jejunum.// Aging reduces vasoactive intestinal peptide (VIP) receptor mRNA and eliminates diurnal expression of VIP mRNA within the suprachiasmatic nucleus of aged male rats.// (The rest is omitted.)	[Human,Mouse]HomoloGene:2539

[0395]



No	Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Pathway Name	Gene Symbol	Gene Name	Summary	GeneRIF	Homology
39	286.63	123.54	2.32	XM_576570	XM_576570	PREDICTED: Rattus norvegicus similar to KIAA1034-like DNA binding protein (LOC501145), mRNA [XM_576570]	ref|XM_576570.1|tc|TC524999	Rn.22624	-	RGD1562369_predicted	similar to KIAA1034-like DNA binding protein (predicted)	-	-	[Human, Mouse]HomoloGene:32249
40	958.66	415.63	2.31	TC524999	TC524999	Unknown	tc|TC524999	-	-	-	-	-	-	-
41	501.84	218.39	2.30	NM_053859	Slc17a7	Rattus norvegicus solute carrier family 17 (sodium-dependent inorganic phosphate cotransporter), member 7 (Slc17a7), mRNA [NM_053859]	ref|NM_053859.1|gb|U07609|ens|ENSRNOT00000028064|tc|TC569561	Rn.10267	-	Slc17a7	solute carrier family 17 (sodium-dependent inorganic phosphate cotransporter), member 7	a Na(+)-dependent inorganic phosphate cotransporter; may be involved in neuronal Na+ transport [RGD]	A newly proposed mechanism for altering the strength of glutamatergic synapses based on the recently identified vesicular glutamate transporter VGLUT1.// Intracortical VGLUT1/VGLUT2 coexpressing neurons can independently modulate level of expression of either transporter at discrete synapses. May serve as plastic interface between subcortical thalamic input (VGLUT2) and cortical output (VGLUT1) neurons.// a high proportion of cardiac neurones appear to be glutamatergic, but differ from other vagal afferents in expressing vesicular glutamate transporter 1// VGLUT1 and VGLUT2 proteins may often transport glutamate into vesicles within the same neuron, especially during early postnatal development, and that they are expressed widely in presumed glutamatergic, GABAergic, and cholinergic neurons. and astrocytes// the coupling of zinc transporter 3 and Vglut1 transport mechanisms regulates neurotransmitter content in secretory vesicles// (the rest is omitted.)	[Human]HomoloGene:69302
42	115.53	50.99	2.27	BF281936	BF281936	BF281936 EST1446527 Rat Gene Index, normalized rat, Rattus norvegicus cDNA Rattus norvegicus cDNA clone RGIB064 similar to cerebral cortex transcriptional regulator T-Brain-1 (Tbr-1), mRNA sequence [BF281936]	gb|BF281936|gb|BF281828|gb|AW141148|ens|ENSRNOT00000007024	-	-	-	-	-	-	-
43	258.59	114.22	2.26	CO403684	CO403684	AGENCOURT_26746195 NIH_MGC_254 Rattus norvegicus cDNA clone IMAGE:7316278 5', mRNA sequence [CO403684]	gb|CO403684|tc|TC540086	-	-	-	-	-	-	-

[0396]

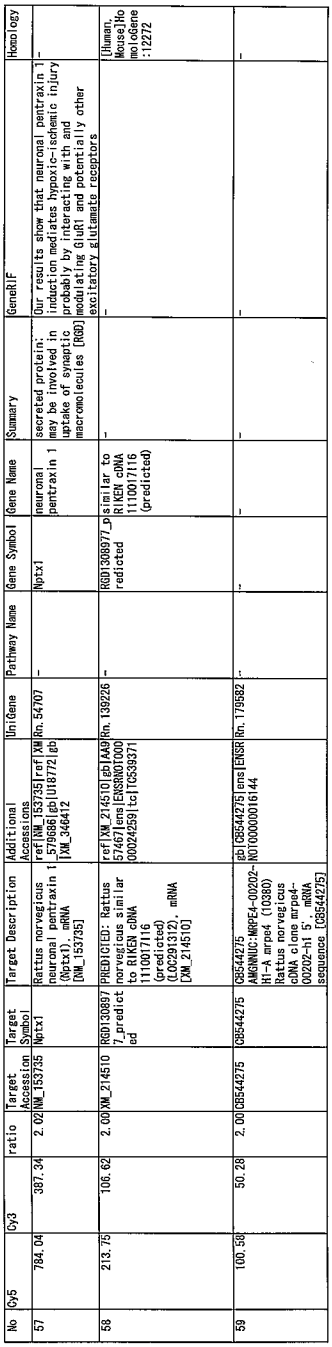


No	Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Pathway Name	Gene Symbol	Gene Name	Summary	GeneRIF	Homology
44	210.66	94.38	2.23	CB582871	CB582871	AMGNWUC-NG051-000981-D12-A nrdg1 (10855) Rattus norvegicus cDNA clone nrdg1-00081-d12 5', mRNA sequence [CB582871]	gb|CB582871	Rn.13498	-	-	-	-	-	-
45	133.62	59.95	2.23	BM382824	Cck	UI-R-BT1-bko-b-06-0-UI.s1 UI-R-BT1 Rattus norvegicus cDNA clone UI-R-BT1-bko-b-06-0-UI 3', mRNA sequence [BM382824]	gb|BM382824	Rn.9761	Neuroactive ligand-receptor interaction	Cck	cholecystokinin	brain-gut peptide with hemacrine and autocrine function in the gut [RGD]	CCK preadministration to obese rats did not affect ghrelin-induced food intake.// A study of the hypothesis that CCK in the rostral ventromedial medulla may engage descending pain facilitatory pathways to enhance spinal nociceptive transmission and attenuate morphine antinociception.// Co-expression patterns of the neuropeptides vasoactive intestinal peptide and cholecystokinin with the transduction molecules alpha-gustducin and T1R2 in rat taste receptor cells.// Data suggest that cholecystokinin may play a role in the generation of negative affective states indexed by 22-kilohertz (kHz) ultrasonic calls in certain regions of the brain.// procholecystokinin undergoes parallel pathways of proteolytic cleavages// Plasma levels CCK and CGRP were significantly increased through 3 hours and 7 days postinjury, with the peak at 72 hours. CCK in jejunum changed as in plasma.// The degree of colocalization of the rodent prohormone convertases (PC) enzymes PC1, PC2, and PC5 with CCK in rat brain is regionally specific.// (The rest is omitted.)	[Human, Mouse]HomoloGene :583
46	164.52	74.43	2.21	NM_012719	Sstr1	Rattus norvegicus somatostatin receptor 1 (Sstr1), mRNA [NM_012719]	ref|NM_012719|ref|XM_579345|gb|X62314|gb|XM_346770	#N/A Rn.42915	Neuroactive ligand-receptor interaction	Sstr1	somatostatin receptor 1	receptor for somatostatin; may play a role in thymocyte cell proliferation and differentiation [RGD]	Most neuropeptide Y expressing receptors in the arcuate nucleus coexpress somatostatin receptor subtype 1.	#N/A [Human, Mouse]HomoloGene :820
47	369.75	169.54	2.18	NM_012835	Cort	Rattus norvegicus cortistatin (Cort), mRNA [NM_012835]	ref|NM_012835|gb|U51918|ens|ENSRNOT00000018401|tc|TC570162	Rn.10490	Neuroactive ligand-receptor interaction	Cort	cortistatin	inhibits growth hormone secretion; may act as a neuropeptide to mediate signaling via a somatostatin receptor subtype [RGD]	-	[Human, Mouse]HomoloGene :997
48	543.61	250.60	2.17	NM_053346	Nrnl	Rattus norvegicus neuritin (Nrnl), mRNA [NM_053346]	ref|NM_053346|gb|U88958|gb|BC087582|gb|AW915977	Rn.3546	-	Nrnl	neuritin	promotes neurite outgrowth [RGD]	-	-
49	1005.51	466.80	2.15	XM_225579	C1ql3_predicted	Rattus norvegicus similar to complement component 1, q subcomponent-like 3 (LOC307144), mRNA [XM_225579]	ref|XM_225579|ens|ENSRNOT00000028637|tc|TC525064	-	-	-	-	-	-	-

[0397]

No	Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Pathway Name	Gene Symbol	Gene Name	Summary	GeneRIF	Homology
50	252.63	121.36	2.08	NM_053504	Prss12	Rattus norvegicus protease, serine, 12 (neurotrypsin, motopsin) (Prss12), mRNA [NM_053504]	ref|NM_053504|gb|AA3 11671|ens|ENSRNOT000 00021116	Rn. 86653	-	Prss12	peptidase, serine, 12 (neurotrypsin, motopsin)	mouse homolog is a serine protease; may be involved in learning and memory [RGD]	-	[Human, Mouse]Homolo gene :7490
51	117.07	56.40	2.08	TC558785	075BU0	075BU0 (075BU0) AGR1810p, partial (3') [TC558785]	tc|TC558785	-	-	-	-	-	-	-
52	178.08	86.09	2.07	TC562720	TC562720	Unknown	tc|TC562720	-	-	-	-	-	-	-
53	449.03	217.09	2.07	TC519964	TC519964	Unknown	tc|TC519964	-	-	-	-	-	-	-
54	707.84	342.26	2.07	NM_030868	Nov	Rattus norvegicus nephroblastoma overexpressed gene (Nov), mRNA [NM_030868]	ref|NM_030868|gb|AF1 71986|gb|BC072548|en s|ENSRNOT00000011904	Rn. 162955	-	Nov	nephroblastoma overexpressed gene	acts as a growth factor for some cells and binds to a specific receptor; may also have growth suppressive effects [RGD]	NOV is expressed during liver fibrogenesis and HSCs may be an important source of hepatic NOV.// Data show that RNA levels of cyr61 and Nov are upregulated in C6 cells transfected with connexin 43.	[Human, Mouse]Homolo gene :1884
55	261.55	126.74	2.06	XM_575489	XM_575489	PREDICTED: Rattus norvegicus similar to NEX-1 (LOC500137), mRNA [XM_575489]	ref|XM_575489|gb|BF5 67707|tc|TC529331	Rn. 162754	-	RGD1562793_p redicted	similar to NEX-1 (predicted)	-	This study provides first evidence of the role of Nex1 in the basic helix-loop-helix transcription factor Nex1/Math-2 of the NeuroD-subfamily promotes an active anti-apoptotic program essential to the survival of neurons.	[Human, Mouse]Homolo gene :7632
56	3103.01	1514.33	2.05	NM_012829	Cck	Rattus norvegicus cholecystokinin (Cck), mRNA [NM_012829]	ref|NM_012829|gb|X01 032|gb|K01259|gb|M25 942	Rn. 9761	Neuroactive ligand-receptor interaction	Cck	cholecystokinin	brain-gut peptide with hemacrine and autocrine function in the gut [RGD]	CCK preadministration to obese rats did not affect ghrelin-induced food intake.// A study of the hypothesis that CCK in the rostral ventromedial medulla may engage descending pain facilitatory pathways to enhance spinal nociceptive transmission and attenuate morphine antinociception.// Co-expression patterns of the neuropeptides vasoactive intestinal peptide and cholecystokinin with the transduction molecules alpha-gustducin and ITR2 in rat taste receptor cells.// Data suggest that cholecystokinin may play a role in the generation of negative affective states indexed by 22-kilohertz (kHz) ultrasonic calls in certain regions of the brain.// prohormone convertase (PC) enzymes underpins parallel pathways of proteolytic cleavage.// Plasma levels CCK and CCK8 were significantly increased through 3 hours and declined similarly after the peak at 72 hours. CCK is secreted in plasma.// The degree of colocalization of the prohormone convertase (PC) enzymes PC1, PC2, and PC5 with CCK in rat brain is regionally specific.// (The rest is omitted.)	[Human, Mouse]Homolo gene :583
								#N/A						#N/A

[0398]



No	Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Pathway Name	Gene Symbol	Gene Name	Summary	GeneRIF	Homology
57	784.04	387.34	2.02	NM_153735	Nptx1	Rattus norvegicus neuronal pentraxin 1 (Nptx1), mRNA [NM_153735]	ref|NM_153735|ref|XM_1579696|gb|U18772|gb|XM_346412	Rn.54707	-	Nptx1	neuronal pentraxin 1	secreted protein: may be involved in uptake of synaptic macromolecules [RGD]	Our results show that neuronal pentraxin 1 induction mediates hypoxic-ischemic injury probably by interacting with AMPA receptors and potentially other excitatory glutamate receptors	-
58	213.75	106.62	2.00	XM_214510	RGD1308897_predicted	PREDICTED: Rattus norvegicus similar to RIKEN cDNA 1110017116 (predicted) (LOC291312), mRNA [XM_214510]	ref|XM_214510|gb|AAG57467|ens|ENSRNOT00000024259|tc|TC6389371	Rn.139226	-	RGD1308897_predicted	similar to RIKEN cDNA 1110017116 (predicted)	-	-	[Human, Mouse]Homologene:12272
59	100.58	50.28	2.00	CB544275	CB544275	CB544275 AMGNMUC:MRPE4-00202-H1-A mrpe4 (10380) Rattus norvegicus cDNA clone mrpe4-00202-h1 5', mRNA sequence (CB544275)	gb|CB544275|ens|ENSRNOT00000016144	Rn.179582	-	-	-	-	-	-

[0399] Light Touch群と比較してTickling群で0.5倍未満の発現を認めた線条体(St)の遺伝子のアノテーションを下記表73に示す。

[表73]

表73 #17 T-St(Cy5) v.s. #17 L-St(Cy3) :down regulation(Cy5<Cy3)

No	Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Pathway Name	GeneSymbol	Gene Name	Summary	GeneRIF	Homology
60	65.85	267.20	0.25	BF398607	BF398607	BF398607 UI-R-RS2-beq-g-09-0-UI.s1 UI-R-RS2 Rattus norvegicus cDNA clone UI-R-RS2-beq-g-09-0-UI 3', mRNA sequence [BF398607]	gb|BF398607|gb|BF285611	Rn.45255	-	RGD1564156_predicted	similar to teratocyte-specific carboxylesterase (predicted)	-	-	-
61	100.50	212.82	0.47	NM_012681	Ttr	Rattus norvegicus transthyretin (Ttr), mRNA [NM_012681]	ref|NM_012681|gb|K02522|gb|AF479660	Rn.1404	-	Ttr	transthyretin	binds thyroxine (T4) and 3,5,3' triiodothyronine (T3); plays a role in thyroid hormone transport in serum [RGD]	Data suggest that monomeric transthyretin may represent an ischemia-specific CSF marker to indicate the sequential changes according to ischemic insults of the brain.// data show the LRI gene is up-regulated following short interval successive partial hepatectomy: it may play an important role in liver regeneration// Amyloid formation in rat transthyretin: effect of oxidative stress// Comparison of binding interactions of dihydroflavonoids with transthyretin// Complex of rat transthyretin with tetraiodothyroacetic acid refined at 2.1 and 1.8 A resolution// Structural basis of negative cooperativity in transthyretin	[Human, Mouse]HomoloGene:317

[0400] Light Touch群と比較してTickling群で2.0倍超の発現を認めた口腔内細胞(Bc)の遺伝子のアノテーションを下記表74に示す。

[表74]

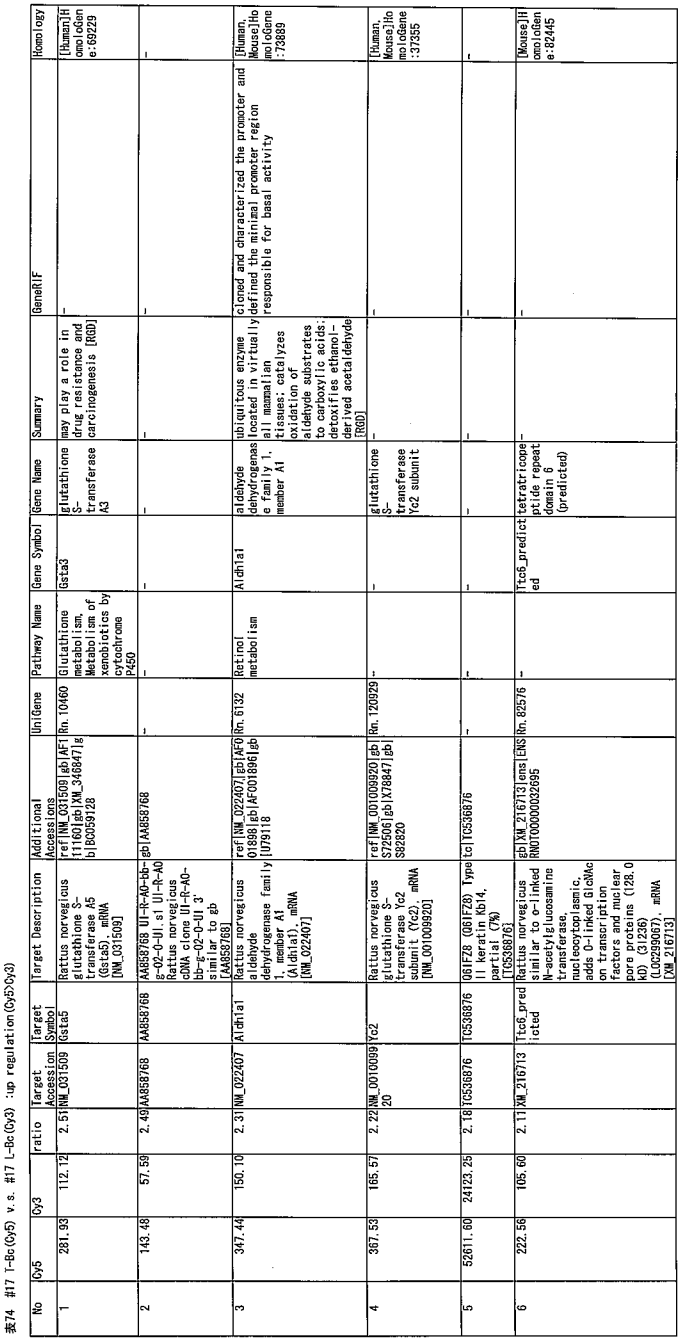


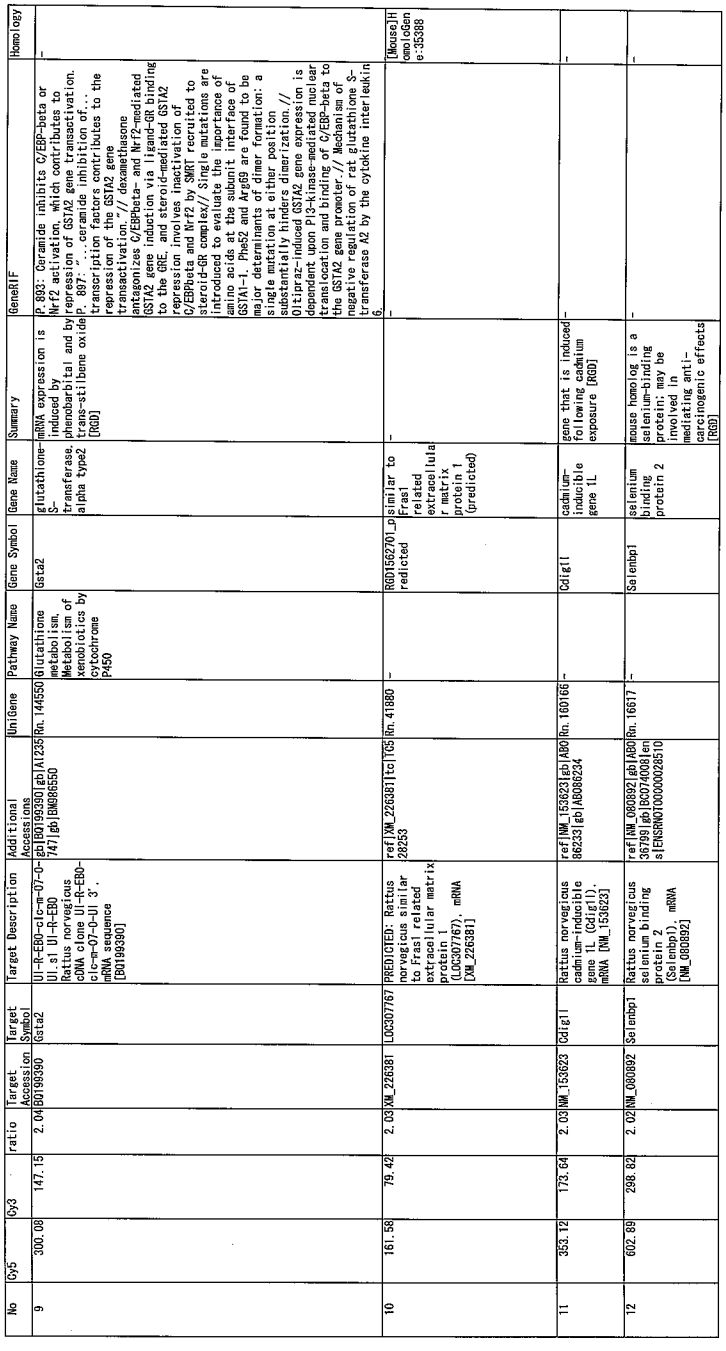
表74 #17 1-Bc(Cy5) v.s. #17 L-Bc(Cy3) :up regulation(Cy5>Cy3)

No	Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Pathway Name	Gene Symbol	Gene Name	Summary	GeneRIF	Homology
1	281.93	112.12	2.51	NM_031509	Gsta5	Rattus norvegicus glutathione S-transferase A5 (Gsta5), mRNA [NM_031509]	ref|NM_031509|gb|AF1116O|gb|XM_346847|gbl|BC059128	Rn.10460	Glutathione metabolism, Metabolism of xenobiotics by cytochrome P450	Gsta3	glutathione S-transferase A3	may play a role in drug resistance and carcinogenesis [RGD]	-	[Human]Homolo Gene.69229
2	143.48	57.59	2.49	AA858768	AA858768	AA858768 UI-R-A0-Bb-g-02-0-Ul.s1 Ul-R-A0 Rattus norvegicus cDNA clone UI-R-A0-bb-g-02-0-Ul 3' similar to gb |AA858768|	gb|AA858768	-	-	-	-	-	-
3	347.44	150.10	2.31	NM_022407	Aldh1a1	Rattus norvegicus aldehyde dehydrogenase family 1, member A1 (Aldh1a1), mRNA [NM_022407]	ref|NM_022407|gb|AF0016898|gb|AF001896|gb|U79118	Rn.6132	Retinol metabolism	Aldh1a1	aldehyde dehydrogenase family 1, member A1	ubiquitous enzyme located in virtually all mammalian tissues; catalyzes oxidation of aldehyde substrates to carboxylic acids; detoxifies ethanol-derived acetaldehyde [RGD]	cloned and characterized the promoter and defined the minimal promoter region responsible for basal activity	[Human, Mouse]Homolodene.73889
4	367.53	165.57	2.22	NM_001009920	Yc2	Rattus norvegicus glutathione S-transferase Yc2 subunit (Yc2), mRNA [NM_001009920]	ref|NM_001009920|gb|S72506|gb|X78847|gb|S82820	Rn.120929	-	-	glutathione S-transferase Yc2 subunit	-	-	[Human, Mouse]Homolodene:37355
5	52611.60	24123.25	2.18	TC536876	TC536876	Q61FZ8 (Q61FZ8) Type II keratin Kb14, partial (7%) [TC536876]	tc|TC536876	-	-	-	-	-	-	-
6	222.56	105.60	2.11	XM_216713	Ttc6_predicted	Rattus norvegicus similar to o-linked N-acetylglucosamine transferase, nucleocytoplasmic, adds O-linked GlcNAc on transcription factors and nuclear pore proteins (728.0 kD) (LOC299067), mRNA [XM_216713]	gb|XM_216713|ens|ENSRNOT00000032695	Rn.82576	-	Ttc6_predicted	tetratricopeptide repeat domain 6 (predicted)	-	-	[Mouse]Homolodene:82445

[0401]

No	Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Pathway Name	Gene Symbol	Gene Name	Summary	GeneRIF	Homology
7	5326.80	2539.25	2.10	NM_017013	Gsta2	Rattus norvegicus glutathione-S-transferase, alpha type2 (Gsta2), mRNA [NM_017013]	ref|NM_017013|gb|M26874|gb|BC078706	Rn.144550	Glutathione metabolism, Metabolism of xenobiotics by cytochrome P450	Gsta2	glutathione-S-transferase, alpha type2	mRNA expression is induced by phenobarbital and by trans-stilbene oxide [RGD]	P.893: Ceramide inhibits C/EBP-beta or Nrf2 activation, which contributes to repression of GSTA2 gene transactivation. P. 897: ...ceramide inhibition of... transcription factors contributes to the repression of the GSTA2 gene transactivation. // dexamethasone antagonizes C/EBPbeta- and Nrf2-mediated GSTA2 gene induction via liganded-GR binding to the GRE, and steroid-mediated GSTA2 repression involves inactivation of C/EBPbeta and Nrf2 by SMRT recruited to steroid-GR complex// Single mutations are introduced to evaluate the importance of amino acids at the dimer interface of GSTA1-1. Phe52 and Arg69 are found to be major determinants of dimer formation. a single mutation at either position substantially hinders dimerization. // Oltipraz-induced GSTA2 gene expression is dependent upon PI3-kinase-mediated nuclear translocation and binding of C/EBP-beta to the GSTA2 gene promoter. // Mechanism of negative regulation of rat glutathione S-transferase A2 by the cytokine interleukin 6.	-
8	197.99	96.99	2.04	BQ200056	BQ200056	BQ200056 UI-R-EA0-clm-i-20-0-UI.s1 UI-R-EA0 Rattus norvegicus cDNA clone UI-R-EA0-clm-i-20-0-UI 3', mRNA sequence [BQ200056]	gb|BQ200056|gb|AI170609	-	-	-	-	-	-	-

[0402]



No	Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Pathway Name	Gene Symbol	Gene Name	Summary	GeneRIF	Homology
9	300.08	147.15	2.04	BG199390	Gsta2	UI-R-EB0-clc-m-07-0-UI.s1 UI-R-EB0 Rattus norvegicus cDNA clone UI-R-EB0-clc-m-07-0-UI 3', mRNA sequence [BG199390]	gb|BG199390|gb|AI235741|gb|BM986550	Rn.144550	Glutathione metabolism Metabolism of xenobiotics by cytochrome P450	Gsta2	glutathione-S-transferase alpha type2 [RGD]	mRNA expression is induced by phenobarbital and by trans-stilbene oxide [RGD]	P. 893: Ceramide inhibits C/EBP-beta or Nrf2 activation, which contributes to repression of GSTA2 gene transactivation. P. 897: ..., ceramide inhibition of... transcription factors contributes to the repression of the GSTA2 gene transactivation."// dexamethasone antagonizes C/EBPbeta- and Nrf2-mediated GSTA2 gene induction via ligand-GR binding to the GRE, and steroid-mediated GSTA2 repression involves inactivation of C/EBPbeta and Nrf2 by SMRT recruited to steroid-GR complex.// Single mutations are introduced to evaluate the importance of amino acids at the subunit interface of GSTA1-1. Phe52 and Arg69 are found to be major determinants of dimer formation: a single mutation at either position substantially hinders dimerization.// Oltipraz-induced GSTA2 gene expression is dependent upon PI3-kinase-mediated nuclear translocation and binding of C/EBP-beta to the GSTA2 gene promoter.// Mechanism of negative regulation of rat glutathione S-transferase A2 by the cytokine interleukin 6.	-
10	161.58	79.42	2.03	XM_226381	LOC307767	PREDICTED: Rattus norvegicus similar to Fras1 related extracellular matrix protein 1 (LOC307767), mRNA [XM_226381]	ref|XM_226381|tc|TC6228253	Rn.41880	-	RGD1562701_predicted	similar to Fras1 related extracellular matrix protein 1 (predicted)	-	-	[Mouse]Homologene:35388
11	353.12	173.64	2.03	NM_153623	Cdigl1	Rattus norvegicus cadmium-inducible gene 1L (Cdigl1), mRNA [NM_153623]	ref|NM_153623|gb|AB086234|gb|AB086234	Rn.160166	-	Cdigl1	cadmium-inducible gene 1L	gene that is induced following cadmium exposure [RGD]	-	-
12	602.89	298.82	2.02	NM_080892	Selenbp1	Rattus norvegicus selenium binding protein 2 (Selenbp2), mRNA [NM_080892]	ref|NM_080892|gb|AB036799|gb|BC074008|ens|ENSRNOT00000028510	Rn.16617	-	Selenbp1	selenium binding protein 2	mouse homolog is a selenium-binding protein; may be involved in mediating anti-carcinogenic effects [RGD]	-	-

[0403] Light Touch群と比較してTickling群で0.5倍未満の発現を認めた口腔内細胞(Bc)の遺伝子のアノテーションを下記表75に示す。

[表75]

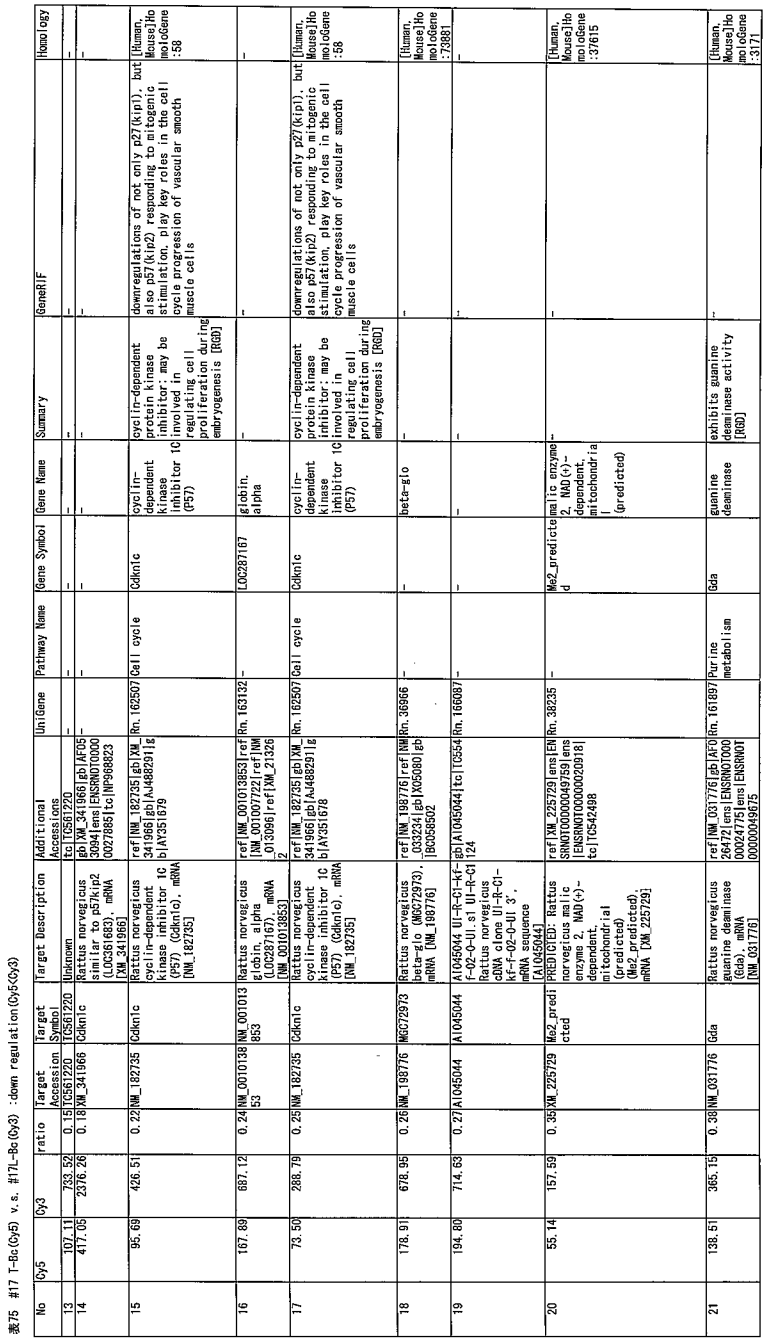
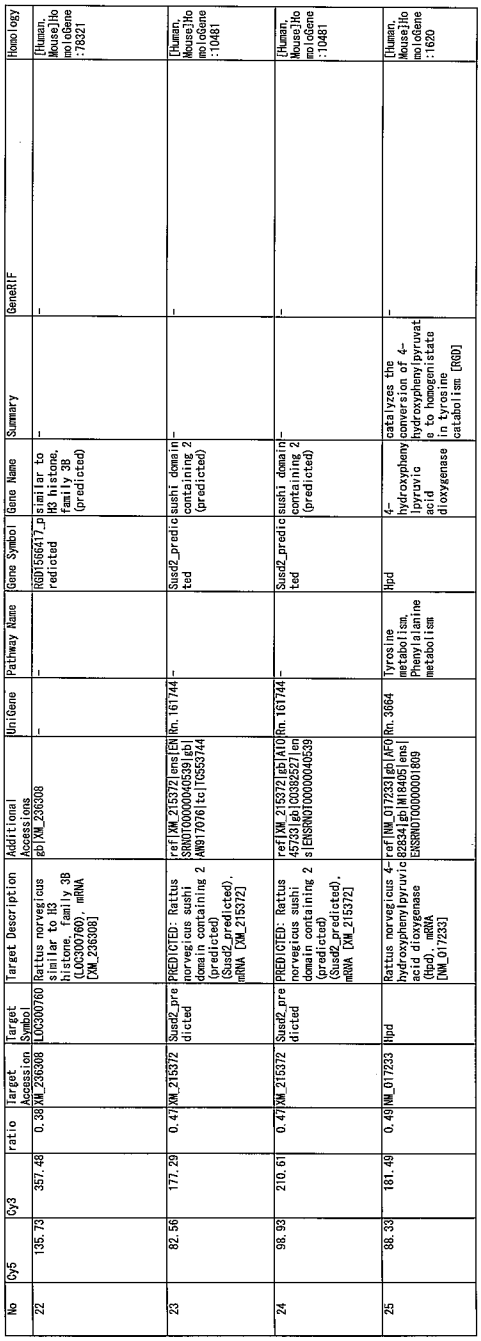


表75 #17 T-Bc(Cy5) v.s. #17L-Bc(Cy3) :down regulation(Cy5<Cy3)

No	Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Pathway Name	Gene Symbol	Gene Name	Summary	GeneRIF	Homology
13	107.11	733.52	0.15	TC561220	TC561220	Unknown	tc|TC561220	–	–	–	–	–	–	–
14	417.05	2376.26	0.18	XM_341966	Cdknlc	Rattus norvegicus similar to p57kip2 (LOC361663), mRNA [XM_341966]	gb|XM_341966|gb|AF05 3094|ens|ENSRNOT0000 0027885|tc|NP968823	–	–	–	–	–	–	–
15	96.69	426.51	0.22	NM_182735	Cdknlc	Rattus norvegicus cyclin-dependent kinase inhibitor 1C (P57) (Cdknlc), mRNA [NM_182735]	ref|NM_182735|gb|XM_ 341966|gb|AJ488291|g b|AY351679	Rn.162507	Cell cycle	Cdknlc	cyclin-dependent kinase inhibitor 1C (P57)	cyclin-dependent protein kinase inhibitor; may be involved in regulating cell proliferation during embryogenesis [RGD]	downregulations of not only p27(kipl), but also p57(kip2) responding to mitogenic stimulation, play key roles in the cell cycle progression of vascular smooth muscle cells	[Human, Mouse]Ho moloGene :58
16	167.89	687.12	0.24	NM_001013853	NM_001013853	Rattus norvegicus globin, alpha (LOC287167), mRNA [NM_001013853]	ref|NM_001013853|ref|Rn. 163132 |NM_001007722|ref|NM _013096|ref|XM_21326 2	–	–	LOC287167	globin, alpha	–	–	–
17	73.50	288.79	0.25	NM_182735	Cdknlc	Rattus norvegicus cyclin-dependent kinase inhibitor 1C (P57) (Cdknlc), mRNA [NM_182735]	ref|NM_182735|gb|XM_ 341966|gb|AJ488291|g b|AY351678	Rn.162507	Cell cycle	Cdknlc	cyclin-dependent kinase inhibitor 1C (P57)	cyclin-dependent protein kinase inhibitor; may be involved in regulating cell proliferation during embryogenesis [RGD]	downregulations of not only p27(kipl), but also p57(kip2) responding to mitogenic stimulation, play key roles in the cell cycle progression of vascular smooth muscle cells	[Human, Mouse]Ho moloGene :58
18	178.91	678.95	0.26	NM_198776	MGC72973	Rattus norvegicus beta-glo (MGC72973), mRNA [NM_198776]	ref|NM_198776|ref|NM _033234|gb|X05080|gb| BG058502	Rn.36966	–	–	beta-glo	–	–	[Human, Mouse]Ho moloGene :73881
19	194.80	714.63	0.27	AI045044	AI045044	AI045044 UI-R-C1-kf-f-02-0-Ul.s1 UI-R-C1-kf-f-02-0-Ul 3', mRNA sequence [AI045044]	gb|AI045044|tc|TC554 124	Rn.166087	–	–	–	–	–	–
20	55.14	157.59	0.35	XM_225729	Me2_predicted	PREDICTED: Rattus norvegicus malic enzyme 2, NAD(+)-dependent, mitochondrial (predicted) (Me2_predicted), mRNA [XM_225729]	ref|XM_225729|ens|EN SRNOT00000049759|ens |ENSRNOT00000020918| tc|TC542498	Rn.38235	–	Me2_predicted	malic enzyme 2, NAD(+)-dependent, mitochondria l (predicted)	–	–	[Human, Mouse]Ho moloGene :37615
21	138.61	365.15	0.38	NM_031776	Gda	Rattus norvegicus guanine deaminase (Gda), mRNA [NM_031776]	ref|NM_031776|gb|AF0 26472|ens|ENSRNOT000 00024775|ens|ENSRNOT 00000049075	Rn.161897	Purine metabolism	Gda	guanine deaminase	exhibits guanine deaminase activity [RGD]	–	[Human, Mouse]Ho molGene :3171

[0404]



No	Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Pathway Name	Gene Symbol	Gene Name	Summary	GeneRIF	Homology
22	135.73	357.48	0.38	XM_236308	LOC300760	Rattus norvegicus similar to H3 histone, family 3B (LOC300760), mRNA [XM_236308]	gb|XM_236308	-	-	RGD1566417_predicted	similar to H3 histone, family 3B (predicted)	-	-	[Human, Mouse]HomoloGene:78321
23	82.56	177.29	0.47	XM_215372	Susd2_predicted	PREDICTED: Rattus norvegicus sushi domain containing 2 (predicted) (Susd2_predicted), mRNA [XM_215372]	ref|XM_215372|ens|ENSRNOT00000040539|gb|AW170761|to|T0553744	Rn.161744	-	Susd2_predicted	sushi domain containing 2 (predicted)	-	-	[Human, Mouse]HomoloGene:10481
24	98.93	210.61	0.47	XM_215372	Susd2_predicted	PREDICTED: Rattus norvegicus sushi domain containing 2 (predicted) (Susd2_predicted), mRNA [XM_215372]	ref|XM_215372|gb|AI107457303|gb|CO382527|ens|ENSRNOT00000040539	Rn.161744	-	Susd2_predicted	sushi domain containing 2 (predicted)	-	-	[Human, Mouse]HomoloGene:10481
25	88.33	181.49	0.49	NM_017233	Hpd	Rattus norvegicus 4-hydroxyphenylpyruvic acid dioxygenase (Hpd), mRNA [NM_017233]	ref|NM_017233|gb|AF028234|gb|AW184405|ens|ENSRNOT00000001809	Rn.3664	Tyrosine metabolism, Phenylalanine metabolism	Hpd	4-hydroxyphenylpyruvic acid dioxygenase	catalyzes the conversion of 4-hydroxyphenylpyruvate to homogenistate in tyrosine catabolism [RGD]	-	[Human, Mouse]HomoloGene:1620

[0405] なお、表68～75中の「No.」は、上記表1中の「No.」に対応している。

[0406] Tickling群の末梢血液で２倍以上の発現を認める遺伝子は３つ、0.5倍以下の発現を認める遺伝子は１つしか存在しなかった。同様に発現差を認める遺伝子をカウントすると、口腔粘膜擦過細胞、視床下部、線条体で２倍以上の発現を認める遺伝子はそれぞれ12、３、25遺伝子存在し、0.5倍以下の発現を認める遺伝子はそれぞれ13、２、２遺伝子存在した。

[0407] 注目すべき遺伝子としては、Ticklingにより口腔粘膜細胞でUp-regulateされたGsta5、Aldh1a1、Yc2、Gsta2、Cdig1l、Selenbp1、Down-regulateされたCdkn1c、Gda、視床下部でUp-regulateされたSlc6a3、線条体でUp-regulateされたAvp、Neurod2、Vip、Slc17a7、Cck、Sstr1、Cort、Nrn1、Prss、Down-regulateされたTtrがある。

[0408] ２－２－４－３．クラスタリング解析

いずれかの解析においてCy3およびCy5の信号強度が50以上あったプローブは24,076遺伝子(トランスクリプトを含む)存在し、これらをクラスタリングした像を図76に示し、また、いずれかの解析において1.5倍以上あるいは1/1.5倍以下の発現差を認めた868プローブのクラスタリング像を図77に、２倍以上あるいは0.5倍以下の発現差を認めた88プローブのクラスタリング像を図78に示した。発現差の程度は、TicklingによりUp-regulateされた遺伝子(トランスクリプトを含む)は赤色、Down-regulateされた遺伝子(トランスクリプトを含む)は緑色の濃さの程度で表した(カラーバーは図中右側に表示)。また、信号強度が低く(50未満)、発現差を表示できない遺伝子(トランスクリプトを含む)は灰色で表示した。血液と口腔粘膜擦過細胞において、双方向(Up-regulationあるいはDown-regulation)に発現変動する遺伝子が顕著であり、特に後者では変動幅が大きい遺伝子(２倍以上あるいは0.5倍以下)を多く含んでいた。視床下部での発現変動は双方向共に鈍いのに対し、線条体ではUp-regulationした遺伝子が多く存在し、その変動幅も２倍以上のものが多かった。

[0409] また、上記のTickling長期（4週間）刺激時のデータも解析対象とし、いずれかの解析において1.5倍以上あるいは1/1.5倍以下の発現差を認めた4,397プローブのクラスタリング像を図79(プローブの並びは長期刺激を基準)と図80(プローブの並びは短期刺激を基準)に、２倍以上あるいは0.5倍以下の発現差を認めた865プローブのクラスタリング像を図81(プローブの並びは長期刺激を基準)と図82(プローブの並びは短期刺激を基準)に示した。長期Tickling刺激負荷を行ったラット血液において双方向(Up-regulationあるいはDown-regulation)に発現変動する遺伝子が多く、その変動幅も２倍以上のものが多かっ

た。長期Tickling負荷を行ったラット脳組織(視床下部、線条体)でも、同様に双方向に発現変動する遺伝子群が存在したが、これらは血液で発現変動する遺伝子とは異なっていた。さらに、血液と線条体では、長期Tickling刺激で発現変動する遺伝子の変化方向と短期Tickling刺激で発現変動する遺伝子の変化方向が逆であることが特徴的であった。

[0410] 2-2-4-4. オントロジー解析

当解析は、Light Touch群と比較してTickling群で1.5倍以上あるいは1/1.5倍以下の発現差を認める遺伝子を対象とし、該条件にて抽出される視床下部、線条体の遺伝子に関し行なった。抽出されたプローブ数と遺伝子数は下記表76に示す。

[表76]

表76 抽出された遺伝子の数

組織	刺激の組み合わせ	Lに対する発現量	プローブ数	遺伝子数	GO Term
視床下部	T-L	UP	21	17	表77
		DOWN	11	6	表78
線条体	T-L	UP	140	98	表79
		DOWN	15	8	表80

[0411] DNAチップ上のプローブと遺伝子(GeneID)との対応付けは、Agilent社の提供する情報とNCBI Entrez(http://www.ncbi.nlm.nih.gov/)の情報に基づいて行なった。GeneIDとGOの対応付けはBiNGO (http://www.psb.ugent.be/cbd/papers/BiNGO/)を用いて行い、GOの階層図はCytoscape (http://www.cytoscape.org/)を用いて描画した。各GO Termについて、Agilent社製Whole Rat Genome Microarray上の全遺伝子中での出現頻度に比べて抽出遺伝子群中での出現頻度が高くなっているかHypergeometric testを用いて有意水準FDR(False Discovery rate)<0.1で検定した。該検定で有意と判定されたGO Termを抽出遺伝子群に特徴的なGOとした。表77から80に、各試料で抽出された遺伝子(表76参照)のGO解析結果を示した。また、有意と判定されたGO Termが存在する解析のそれぞれについてCytoscapeを用いて作図したGO階層図は、図84から図88に示した。尚、図83には色の濃淡とP値の関係を表した。色が濃いほどそのGO

Termに割り当てられる有意性が高く、円の大きさが大きいほど割り当てられる遺伝子数が多いこと示す。

[表77]

表77 視床下部で発現増加した遺伝子のGO解析結果

FDR 0.01 以下
FDR 0.05~0.01
MF: Molecular Function
CC: Cellular Component
BP: Biological Process

分類	GO ID	Description	P値	遺伝子数	
				総数	変動した数
MF	5102	receptor binding	4.31E-02	540	5
CC	5576	extracellular region	4.39E-02	1718	7
MF	5330	dopamine:sodium symporter activity	4.39E-02	1	1
MF	4416	hydroxyacylglutathione hydrolase activity	4.39E-02	1	1
MF	5329	dopamine transporter activity	4.39E-02	1	1
MF	42922	neuromedin U receptor binding	4.39E-02	1	1
MF	1664	G-protein-coupled receptor binding	5.37E-02	61	2
BP	7218	neuropeptide signaling pathway	5.37E-02	63	2
BP	42053	regulation of dopamine metabolism	5.37E-02	2	1
CC	16323	basolateral plasma membrane	5.37E-02	65	2
BP	42069	regulation of catecholamine metabolism	6.13E-02	3	1
CC	5615	extracellular space	6.13E-02	1567	6
BP	15872	dopamine transport	6.13E-02	4	1
MF	5179	hormone activity	6.13E-02	92	2
CC	44421	extracellular region part	6.13E-02	1622	6
BP	42416	dopamine biosynthesis	6.13E-02	5	1
BP	42424	catecholamine catabolism	6.13E-02	5	1
MF	4667	prostaglandin-D synthase activity	6.13E-02	5	1
BP	42420	dopamine catabolism	6.13E-02	5	1
MF	4499	dimethylaniline monooxygenase (N-oxide-forming) activity	6.13E-02	5	1
BP	50802	circadian sleep/wake cycle, sleep	6.13E-02	6	1
MF	8504	monoamine transporter activity	6.13E-02	6	1
BP	15844	monoamine transport	6.13E-02	6	1
BP	45187	regulation of circadian sleep/wake cycle, sleep	6.13E-02	6	1
BP	42749	regulation of circadian sleep/wake cycle	6.13E-02	6	1
CC	42613	MHC class II protein complex	6.13E-02	7	1

[0412]

分類	GO ID	Description	P値	遺伝子数	
				総数	変動した数
MF	5328	neurotransmitter:sodium symporter activity	6.13E-02	7	1
BP	48512	circadian behavior	6.13E-02	7	1
BP	42745	circadian sleep/wake cycle	6.13E-02	7	1
BP	30431	sleep	6.13E-02	7	1
MF	15238	drug transporter activity	6.29E-02	8	1
MF	50750	low-density lipoprotein receptor binding	6.29E-02	8	1
BP	7622	rhythmic behavior	6.29E-02	9	1
CC	5791	rough endoplasmic reticulum	6.29E-02	9	1
BP	1516	prostaglandin biosynthesis	6.29E-02	9	1
BP	46457	prostanoid biosynthesis	6.29E-02	9	1
BP	42135	neurotransmitter catabolism	6.29E-02	10	1
BP	42423	catecholamine biosynthesis	6.29E-02	10	1
MF	15250	water channel activity	6.29E-02	10	1
MF	5372	water transporter activity	6.29E-02	11	1
MF	8013	beta-catenin binding	6.29E-02	11	1
MF	19840	isoprenoid binding	6.29E-02	12	1
MF	5501	retinoid binding	6.29E-02	12	1
BP	6693	prostaglandin metabolism	6.29E-02	12	1
BP	6692	prostanoid metabolism	6.29E-02	12	1
MF	5326	neurotransmitter transporter activity	6.29E-02	12	1
BP	6940	regulation of smooth muscle contraction	6.29E-02	12	1
CC	5902	microvillus	6.29E-02	12	1
BP	6833	water transport	6.29E-02	12	1
BP	42752	regulation of circadian rhythm	6.29E-02	12	1
BP	42136	neurotransmitter biosynthesis	7.05E-02	14	1
BP	42044	fluid transport	7.05E-02	14	1
MF	16709	oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, NAD or NADH as one donor, and incorporation of one atom of oxygen	7.14E-02	15	1
BP	42417	dopamine metabolism	7.14E-02	15	1
BP	42402	biogenic amine catabolism	7.14E-02	15	1
CC	42611	MHC protein complex	7.47E-02	16	1
CC	5886	plasma membrane	7.66E-02	1521	5
BP	42219	amino acid derivative catabolism	7.66E-02	17	1

[0413]

分類	GO ID	Description	P値	遺伝子数	
				総数	変動した数
BP	6584	catecholamine metabolism	8.84E-02	21	1
BP	18958	phenol metabolism	8.84E-02	21	1
CC	5913	cell-cell adherens junction	8.84E-02	21	1
BP	7416	synaptogenesis	8.84E-02	21	1
BP	51260	protein homooligomerization	9.10E-02	22	1
BP	46456	icosanoid biosynthesis	9.37E-02	23	1
BP	50808	synapse organization and biogenesis	9.62E-02	24	1

[表78]

表78　視床下部で発現減少した遺伝子のGO解析結果

分類	GO ID	Description	P値	遺伝子数	
				総数	変動した数
CC	235	astral microtubule	6.92E-03	1	1
BP	51294	establishment of spindle orientation	6.92E-03	1	1
BP	30609	establishment of mitotic spindle orientation	6.92E-03	1	1
CC	5818	aster	7.78E-03	2	1
MF	47179	platelet-activating factor acetyltransferase activity	7.78E-03	3	1
BP	51653	spindle localization	7.78E-03	3	1
BP	51293	establishment of spindle localization	7.78E-03	3	1
BP	30610	establishment of mitotic spindle localization	7.78E-03	3	1
MF	19841	retinol binding	8.30E-03	4	1
MF	15349	thyroid hormone transporter activity	8.30E-03	4	1
MF	45502	dynein binding	9.43E-03	5	1
BP	6590	thyroid hormone generation	1.04E-02	6	1
BP	42403	thyroid hormone metabolism	1.19E-02	8	1
MF	16918	retinal binding	1.19E-02	8	1
BP	51656	establishment of organelle localization	1.38E-02	10	1
MF	19840	isoprenoid binding	1.46E-02	12	1
MF	5501	retinoid binding	1.46E-02	12	1
BP	51640	organelle localization	1.50E-02	13	1
CC	5876	spindle microtubule	1.64E-02	15	1
MF	42562	hormone binding	2.07E-02	20	1
CC	776	kinetochore	2.17E-02	22	1
MF	16407	acetyltransferase activity	3.30E-02	35	1
CC	5938	cell cortex	3.33E-02	37	1
MF	19842	vitamin binding	3.71E-02	43	1
CC	5819	spindle	4.22E-02	52	1
BP	226	microtubule cytoskeleton organization and biogenesis	4.22E-02	53	1

FDR 0.01 以下
FDR 0.05~0.01

MF: Molecular Function
CC: Cellular Component
BP: Biological Process

[0414]

分類	GO ID	Description	P値	遺伝子数	
				総数	変動した数
BP	51301	cell division	4.29E-02	56	1
BP	6576	biogenic amine metabolism	4.36E-02	59	1
CC	5875	microtubule associated complex	5.07E-02	71	1
BP	42445	hormone metabolism	5.14E-02	76	1
MF	8415	acyltransferase activity	5.14E-02	81	1
CC	5874	microtubule	5.14E-02	82	1
MF	16747	transferase activity, transferring groups other than amino-acyl groups	5.14E-02	82	1
MF	16746	transferase activity, transferring acyl groups	5.14E-02	88	1
CC	5635	nuclear envelope	5.14E-02	89	1
BP	6575	amino acid derivative metabolism	5.14E-02	90	1
MF	5179	hormone activity	5.14E-02	92	1
BP	7067	mitosis	5.24E-02	97	1
BP	87	M phase of mitotic cell cycle	5.24E-02	99	1
BP	7017	microtubule-based process	5.37E-02	104	1
MF	15291	porter activity	6.79E-02	141	1
MF	15290	electrochemical potential-driven transporter activity	6.79E-02	142	1
BP	279	M phase	6.79E-02	143	1
CC	8370	obsolete cellular component	6.79E-02	145	1
BP	278	mitotic cell cycle	8.14E-02	181	1
BP	51234	establishment of localization	8.14E-02	1974	2
BP	51179	localization	8.17E-02	1999	2
CC	15630	microtubule cytoskeleton	8.65E-02	202	1
MF	5386	carrier activity	9.14E-02	218	1

[表79]

表79　線条体で発現増加した遺伝子のGO解析結果

	FDR 0.01 以下
	FDR 0.05~0.01
MF:	Molecular Function
CC:	Cellular Component
BP:	Biological Process

分類	GO ID	Description	P値	遺伝子数	
				総数	変動した数
BP	7267	cell-cell signaling	7.17E-07	556	20
MF	5179	hormone activity	5.45E-06	92	9
BP	50880	regulation of blood vessel size	5.45E-06	26	6
MF	5184	neuropeptide hormone activity	3.50E-05	20	5
BP	7268	synaptic transmission	3.50E-05	311	13
BP	19226	transmission of nerve impulse	7.31E-05	337	13
BP	19932	second-messenger-mediated signaling	3.67E-04	222	10
MF	5102	receptor binding	4.23E-04	540	15
CC	5576	extracellular region	6.38E-04	1718	28
CC	5615	extracellular space	3.02E-03	1567	25
BP	19935	cyclic-nucleotide-mediated signaling	3.02E-03	134	7
BP	42310	vasoconstriction	4.14E-03	12	3
CC	44421	extracellular region part	4.14E-03	1622	25
BP	7218	neuropeptide signaling pathway	4.14E-03	63	5
BP	7610	behavior	4.14E-03	258	9
BP	7623	circadian rhythm	6.01E-03	37	4
BP	48511	rhythmic process	6.01E-03	70	5
BP	1978	baroreceptor feedback regulation of blood pressure	6.46E-03	3	2
BP	7187	G-protein signaling, coupled to cyclic nucleotide second messenger	7.38E-03	118	6
BP	7631	feeding behavior	7.51E-03	41	4
BP	8015	circulation	8.76E-03	124	6
BP	48489	synaptic vesicle transport	9.01E-03	44	4
MF	4937	alpha1-adrenergic receptor activity	1.01E-02	4	2
BP	7399	nervous system development	1.12E-02	620	13
BP	7202	phospholipase C activation	1.12E-02	20	3
BP	48168	regulation of neuronal synaptic plasticity	1.42E-02	22	3

[0415]

分類	GO ID	Description	P値	遺伝子数	
				総数	変動した数
MF	4994	somatostatin receptor activity	1.42E-02	5	2
BP	51239	regulation of organismal physiological process	1.49E-02	265	8
BP	48731	system development	1.49E-02	649	13
BP	50802	circadian sleep/wake cycle, sleep	1.74E-02	6	2
BP	1993	norepinephrine-epinephrine regulation of blood pressure	1.74E-02	6	2
BP	45187	regulation of circadian sleep/wake cycle, sleep	1.74E-02	6	2
BP	42749	regulation of circadian sleep/wake cycle	1.74E-02	6	2
BP	19933	cAMP-mediated signaling	1.74E-02	102	5
BP	48512	circadian behavior	2.10E-02	7	2
MF	4936	alpha-adrenergic receptor activity	2.10E-02	7	2
BP	30431	sleep	2.10E-02	7	2
BP	42745	circadian sleep/wake cycle	2.10E-02	7	2
CC	5625	soluble fraction	2.22E-02	166	6
CC	5887	integral to plasma membrane	2.25E-02	886	15
CC	31226	intrinsic to plasma membrane	2.57E-02	900	15
MF	5488	binding	2.78E-02	5647	53
CC	44459	plasma membrane part	2.94E-02	1215	18
BP	7622	rhythmic behavior	3.09E-02	9	2
BP	48167	regulation of synaptic plasticity	3.30E-02	35	3
BP	8371	obsolete biological process	3.44E-02	76	4
CC	267	cell fraction	3.77E-02	757	13
BP	7154	cell communication	3.83E-02	3245	35
MF	4871	signal transducer activity	4.08E-02	2634	30
MF	30594	neurotransmitter receptor activity	4.36E-02	83	4
BP	1990	regulation of blood pressure by hormones	4.50E-02	12	2
BP	42752	regulation of circadian rhythm	4.50E-02	12	2
BP	1976	fast regulation of arterial pressure	4.50E-02	12	2
BP	50804	regulation of synaptic transmission	4.50E-02	42	3
BP	31644	regulation of neurophysiological process	4.50E-02	42	3
BP	51969	regulation of transmission of nerve impulse	4.50E-02	42	3
CC	5886	plasma membrane	4.84E-02	1521	20
BP	7188	G-protein signaling, coupled to cAMP nucleotide second messenger	4.84E-02	89	4
BP	50886	endocrine physiological process	4.87E-02	13	2
MF	42165	neurotransmitter binding	4.87E-02	90	4
BP	7275	development	4.98E-02	1869	23

[0416]

分類	GO ID	Description	P値	遺伝子数	
				総数	変動した数
BP	50803	regulation of synapse structure and function	5.22E-02	46	3
BP	6874	calcium ion homeostasis	5.22E-02	93	4
BP	50874	organismal physiological process	5.44E-02	2739	30
BP	7204	elevation of cytosolic calcium ion concentration	5.44E-02	49	3
BP	8217	blood pressure regulation	5.44E-02	49	3
BP	8285	negative regulation of cell proliferation	5.44E-02	158	5
BP	51480	cytosolic calcium ion homeostasis	5.44E-02	50	3
BP	50768	negative regulation of neurogenesis	5.44E-02	16	2
BP	1505	regulation of neurotransmitter levels	5.44E-02	101	4
MF	8083	growth factor activity	5.44E-02	103	4
MF	8528	peptide receptor activity, G-protein coupled	5.44E-02	103	4
MF	42923	neuropeptide binding	5.44E-02	53	3
BP	7200	G-protein signaling, coupled to IP3 second messenger (phospholipase C activating)	5.44E-02	53	3
MF	8188	neuropeptide receptor activity	5.44E-02	53	3
MF	1653	peptide receptor activity	5.44E-02	104	4
MF	4935	adrenoceptor activity	5.44E-02	18	2
BP	31335	regulation of sulfur amino acid metabolism	5.44E-02	1	1
BP	1986	decreased strength of heart contraction during baroreceptor response to increased blood pressure	5.44E-02	1	1
BP	1982	baroreceptor response to lowering of blood pressure	5.44E-02	1	1
MF	47150	betaine-homocysteine S-methyltransferase activity	5.44E-02	1	1
BP	45818	negative regulation of glycogen catabolism	5.44E-02	1	1
MF	1864	pentraxin binding	5.44E-02	1	1
MF	5167	neurotrophin TRK receptor binding	5.44E-02	1	1
BP	31331	positive regulation of cellular catabolism	5.44E-02	1	1
BP	43279	response to alkaloid	5.44E-02	1	1
BP	45819	positive regulation of glycogen catabolism	5.44E-02	1	1
MF	8029	pentraxin receptor activity	5.44E-02	1	1
BP	1987	vasoconstriction of artery during baroreceptor response to lowering of blood pressure	5.44E-02	1	1
BP	5981	regulation of glycogen catabolism	5.44E-02	1	1
BP	31330	negative regulation of cellular catabolism	5.44E-02	1	1
BP	42137	sequestering of neurotransmitter	5.44E-02	1	1
MF	15319	sodium:inorganic phosphate symporter activity	5.44E-02	1	1
BP	42220	response to cocaine	5.44E-02	1	1

[0417]

分類	GO ID	Description	P値	遺伝子数	
				総数	変動した数
MF	30354	melanin-concentrating hormone activity	5.44E-02	1	1
BP	50666	regulation of homocysteine metabolism	5.44E-02	1	1
BP	43278	response to morphine	5.44E-02	1	1
BP	31329	regulation of cellular catabolism	5.44E-02	1	1
MF	5169	neurotrophin TRKB receptor binding	5.44E-02	1	1
BP	48148	behavioral response to cocaine	5.44E-02	1	1
MF	8898	homocysteine S-methyltransferase activity	5.44E-02	1	1
MF	15054	gastrin receptor activity	5.44E-02	1	1
BP	9956	radial pattern formation	5.44E-02	1	1
MF	5515	protein binding	6.37E-02	3356	34
BP	48519	negative regulation of biological process	6.98E-02	795	12
BP	30005	di-, tri-valent inorganic cation homeostasis	7.36E-02	119	4
BP	6875	metal ion homeostasis	9.01E-02	127	4
BP	42127	regulation of cell proliferation	9.01E-02	359	7
BP	16079	synaptic vesicle exocytosis	9.01E-02	25	2
BP	48172	regulation of short-term neuronal synaptic plasticity	9.01E-02	2	1
BP	1975	response to amphetamine	9.01E-02	2	1
MF	31995	insulin-like growth factor II binding	9.01E-02	2	1
BP	1994	norepinephrine-epinephrine vasoconstriction during regulation of blood pressure	9.01E-02	2	1
BP	7406	negative regulation of neuroblast proliferation	9.01E-02	2	1
BP	50891	body fluid osmoregulation	9.01E-02	2	1
MF	30215	semaphorin receptor binding	9.01E-02	2	1
BP	45822	negative regulation of heart contraction	9.01E-02	2	1
BP	42053	regulation of dopamine metabolism	9.01E-02	2	1
BP	1983	baroreceptor response to increased blood pressure	9.01E-02	2	1
MF	4951	cholecystokinin receptor activity	9.01E-02	2	1
MF	1847	opsonin receptor activity	9.01E-02	2	1
BP	45912	negative regulation of carbohydrate metabolism	9.01E-02	2	1
CC	137	Golgi cis cisterna	9.01E-02	2	1
MF	46935	phosphatidylinositol 3-kinase regulator activity	9.01E-02	2	1
BP	8283	cell proliferation	9.54E-02	552	9
BP	50791	regulation of physiological process	9.54E-02	2092	23
BP	48015	phosphoinositide-mediated signaling	9.54E-02	74	3
BP	30003	cation homeostasis	9.57E-02	136	4
BP	43118	negative regulation of physiological process	9.93E-02	655	10

[0418]

分類	GO ID	Description	P値	遺伝子数	
				総数	変動した数
BP	17035	response to drug	9.98E-02	28	2
BP	19722	calcium-mediated signaling	9.98E-02	28	2
MF	42277	peptide binding	9.98E-02	139	4

[表80]

表80 線条体で発現減少した遺伝子のGO解析結果

	FDR 0.01 以下
	FDR 0.05~0.01
MF:	Molecular Function
CC:	Cellular Component
BP:	Biological Process

分類	GO ID	Description	P値	遺伝子数	
				総数	変動した数
BP	6576	biogenic amine metabolism	1.08E-02	59	2
CC	235	astral microtubule	1.08E-02	1	1
BP	51294	establishment of spindle orientation	1.08E-02	1	1
MF	4398	histidine decarboxylase activity	1.08E-02	1	1
BP	30609	establishment of mitotic spindle orientation	1.08E-02	1	1
MF	4948	calcitonin receptor activity	1.08E-02	1	1
BP	6575	amino acid derivative metabolism	1.08E-02	90	2
CC	5818	aster	1.71E-02	2	1
MF	47179	platelet-activating factor acetyltransferase activity	1.71E-02	3	1
BP	51653	spindle localization	1.71E-02	3	1
BP	51293	establishment of spindle localization	1.71E-02	3	1
BP	30610	establishment of mitotic spindle localization	1.71E-02	3	1
MF	19841	retinol binding	1.71E-02	4	1
MF	15349	thyroid hormone transporter activity	1.71E-02	4	1
BP	9075	histidine family amino acid metabolism	1.71E-02	4	1
BP	6547	histidine metabolism	1.71E-02	4	1
MF	45502	dynein binding	2.02E-02	5	1
BP	6590	thyroid hormone generation	2.28E-02	6	1
BP	42403	thyroid hormone metabolism	2.74E-02	8	1
MF	16918	retinal binding	2.74E-02	8	1
BP	6519	amino acid and derivative metabolism	2.87E-02	256	2
BP	42423	catecholamine biosynthesis	2.98E-02	10	1
BP	51656	establishment of organelle localization	2.98E-02	10	1
BP	9308	amine metabolism	3.16E-02	293	2
MF	19840	isoprenoid binding	3.16E-02	12	1
MF	5501	retinoid binding	3.16E-02	12	1

[0419]

分類	GO ID	Description	P値	遺伝子数	
				総数	変動した数
BP	51640	organelle localization	3.22E-02	13	1
BP	6807	nitrogen compound metabolism	3.22E-02	314	2
CC	5876	spindle microtubule	3.53E-02	15	1
MF	4434	inositol or phosphatidylinositol phosphodiesterase activity	3.53E-02	16	1
MF	4435	phosphoinositide phospholipase C activity	3.53E-02	16	1
MF	16831	carboxy-lyase activity	3.78E-02	19	1
MF	42562	hormone binding	3.78E-02	20	1
BP	7202	phospholipase C activation	3.78E-02	20	1
MF	42298	phospholipase C activity	3.78E-02	20	1
BP	6584	catecholamine metabolism	3.78E-02	21	1
BP	18958	phenol metabolism	3.78E-02	21	1
MF	1633	secretin-like receptor activity	3.78E-02	21	1
CC	776	kinetochore	3.86E-02	22	1
MF	16830	carbon-carbon lyase activity	4.04E-02	24	1
BP	45762	positive regulation of adenylate cyclase activity	4.04E-02	26	1
BP	7190	adenylate cyclase activation	4.04E-02	26	1
BP	31281	positive regulation of cyclase activity	4.04E-02	26	1
BP	51349	positive regulation of lyase activity	4.04E-02	26	1
BP	42401	biogenic amine biosynthesis	4.10E-02	27	1
BP	42398	amino acid derivative biosynthesis	4.90E-02	33	1
MF	16407	acetyltransferase activity	5.08E-02	35	1
CC	5938	cell cortex	5.26E-02	37	1
BP	45761	regulation of adenylate cyclase activity	5.43E-02	39	1
BP	31279	regulation of cyclase activity	5.48E-02	41	1
BP	51339	regulation of lyase activity	5.48E-02	41	1
MF	19842	vitamin binding	5.64E-02	43	1
BP	7189	G-protein signaling, adenylate cyclase activating pathway	6.04E-02	47	1
MF	4620	phospholipase activity	6.33E-02	52	1
CC	5819	spindle	6.33E-02	52	1
BP	226	microtubule cytoskeleton organization and biogenesis	6.33E-02	53	1
BP	7200	G-protein signaling, coupled to IP3 second messenger (phospholipase C activating)	6.33E-02	53	1
BP	51301	cell division	6.57E-02	56	1
BP	9309	amine biosynthesis	6.58E-02	58	1
BP	44271	nitrogen compound biosynthesis	6.58E-02	58	1
MF	16792	phosphoric diester hydrolase activity	6.80E-02	61	1

[0420]

分類	GO ID	Description	P値	遺伝子数	
				総数	変動した数
MF	16298	lipase activity	6.80E-02	62	1
CC	5875	microtubule associated complex	7.65E-02	71	1
BP	48015	phosphoinositide-mediated signaling	7.85E-02	74	1
BP	42445	hormone metabolism	7.93E-02	76	1
MF	8415	acyltransferase activity	8.18E-02	81	1
CC	5874	microtubule	8.18E-02	82	1
MF	16747	transferase activity, transferring groups other than amino-acyl groups	8.18E-02	82	1
MF	16746	transferase activity, transferring acyl groups	8.37E-02	88	1
BP	7188	G-protein signaling, coupled to cAMP nucleotide second messenger	8.37E-02	89	1
CC	5635	nuclear envelope	8.37E-02	89	1
MF	16789	carboxylic ester hydrolase activity	8.37E-02	89	1
MF	5179	hormone activity	8.51E-02	92	1
BP	6725	aromatic compound metabolism	8.51E-02	93	1
BP	7067	mitosis	8.75E-02	97	1
BP	87	M phase of mitotic cell cycle	8.81E-02	99	1
BP	19933	cAMP-mediated signaling	8.96E-02	102	1
BP	7017	microtubule-based process	8.98E-02	104	1
MF	16829	lyase activity	8.98E-02	105	1
BP	7187	G-protein signaling, coupled to cyclic nucleotide second messenger	9.95E-02	118	1

[0421] 線条体でUp-regulateされる遺伝子のGO解析では、健康増進遺伝子探索のための候補遺伝子を特定できた。機能上GOID:5184に割り当てられる神経ペプチドホルモン活性に関する遺伝子(表81)、生物学的経路としてGOID：50880、42310、8015、1978に割り当てられる血圧調節に関する遺伝子(表82)、GOID:7631に割り当てられる食行動に関する遺伝子(表83)、GOID：7623、48511に割り当てられる生体リズムに関する遺伝子(表84)は注目に値する。

[表81]

表81 線条体で発現増加した注目遺伝子
神経ペプチドホルモン活性 (GO ID: 5184)

Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Gene Symbol	Gene Name	Summary	GeneRIF	Pathway	Homology
106.09	45.98	2.31	NM_133570	Grp	Rattus norvegicus gastrin releasing peptide (Grp), mRNA [NM_133570]	ref|NM_133570|gb|M31176|ens|ENSRNOT00000002384|tc|TC5569979	Rn.10930	Grp	gastrin releasing peptide	increases 5-HT neuronal activity in the hypothalamus PVN; inhibits feeding behavior [RGD]	GRP mRNA was detected in rat kidney from embryonic day 19 to postnatal day 30 by RT-PCR// GRP in the central part of the amygdala inhibits feeding, may decrease the efficiency of eating, and may act as a satiety signal.// the increase in gastrin releasing	KEGG pathway: Neuroactive ligand-receptor interaction	[Human, Mouse]HomoloGene:1580
133.62	59.95	2.23	BM382824	Cck	UI-R-BT1-bko-b-06-0-UI.s1 UI-R-BT1 Rattus norvegicus cDNA clone UI-R-BT1-bko-b-06-0-UI 3', mRNA sequence [BM382824]	gb|BM382824	Rn.9781	Cck	cholecystokinin	brain-gut peptide with hemaorine and autocrine function in the gut [RGD]	CCK preadministration to obese rats did not affect ghrelin-induced food intake.// A study of the hypothesis that CCK in the rostral ventromedial medulla may engage descending pain facilitatory pathways to enhance spinal nociceptive transmission and attenu	KEGG pathway: Neuroactive ligand-receptor interaction	[Human, Mouse]HomoloGene:583
369.75	169.54	2.18	NM_012835	Cort	Rattus norvegicus cortistatin (Cort), mRNA [NM_012835]	ref|NM_012835|gb|U51919|ens|ENSRNOT00000001840|tc|TC570162	Rn.10490	Cort	cortistatin	inhibits growth hormone secretion; may act as a neuropeptide to mediate signaling via a somatostatin receptor subtype [RGD]	-	KEGG pathway: Neuroactive ligand-receptor interaction	[Human, Mouse]HomoloGene:997
52.29	27.34	1.91	NM_016989	Adcyap1	Rattus norvegicus adenylate cyclase activating polypeptide 1 (Adcyap1), mRNA [NM_016989]	ref|NM_016989|ref|XM_579383|gb|M63006|gb|XM_346860	Rn.37400	Adcyap1	adenylate cyclase activating polypeptide 1	regulatory protein that stimulates cell proliferation, induces differentiation, modulates neurotransmitter release, vasodilation, bronchodilation, and hormone release, and suppresses inflammatory responses [RGD]	These results indicate that a large number of PACAP neurons and a small number of BDNF neurons of the VMH project to the MCG.// The specificity of PAC1 receptor participation in pituitary adenylate cyclase-activating polypeptide (PACAP)-facilitated sex be	KEGG pathway: Neuroactive ligand-receptor interaction	[Human, Mouse]HomoloGene:869

[0422]

Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Gene Symbol	Gene Name	Summary	GeneRIF	Pathway	Homology
136.42	79.32	1.72	NM_053750	Nppc	Rattus norvegicus natriuretic peptide precursor type C (Nppc), mRNA [NM_053750]	ref|NM_053750|gb|D90219|ens|ENSRNOT00000025582	Rn.10637	Nppc	natriuretic peptide precursor type C	binds natriuretic peptide receptor: involved in inhibition of growth and proliferation in vascular smooth muscle cells [RGD]	Endothelium-derived CNP is involved in the regulation of the coronary circulation, and underlies the vasorelaxant activity of this peptide. Moreover, this newly defined pathway represents a protective mechanism against I/R injury.// endot	-	[Human, Mouse]HomoloGene:7867

[表82]

表82 線条体で発現増加した注目遺伝子
血圧調節関連 (GO ID: 5088

Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Gene Symbol	Gene Name	Summary	GeneRIF	Pathway	Homology
72.06	24.25	2.97	NM_024483	Adra1d	Rattus norvegicus adrenergic receptor, alpha 1d (Adra1d), mRNA [NM_024483]	ref|NM_024483|gb|L31771|gb|M60654|ensembl|ENSRNOT00000028877	Rn.11314	Adra1d	adrenergic receptor, alpha 1d	adrenergic receptor showing high affinity for the antagonist WB4101 and agonists phenylephrine and methoxamine [RGD]	three subpopulations of alpha1-adrenoceptor binding sites exist in the rat lung (alpha1A, alpha1B and alpha1D)// cell surface expression of alpha1D-adrenergic receptors is controlled by heterodimerization with alpha1B-adrenergic receptors	KEGG pathway: Calcium signaling pathway	[Human, Mouse]Homolo Gene:551
160.27	57.88	18:27	NM_016992	Avp	Rattus norvegicus arginine vasopressin (Avp), mRNA [NM_016992]	ref|NM_016992|gb|M25546|gb|X01637|gb|V01276	Rn.9976	Avp	arginine vasopressin	neuropeptide hormone: involved in vasoconstriction to regulate blood pressure and smooth muscle contraction during parturition and lactation [RGD]	These data suggest that testosterone attenuates light-enhanced startle, but not fear-potentiated startle, through a mechanism that may involve AVP.// Both the magnocellular and the parvocellular hypothalamic vasopressin systems are capable of expressing t	KEGG pathway: Neuroactive ligand-receptor interaction	[Human, Mouse]Homolo Gene:417

[0423]

Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Gene Symbol	Gene Name	Summary	GeneRIF	Pathway	Homology
232.63	99.84	2.33	XM_217838	Vip	PREDICTED: Rattus norvegicus vasoactive intestinal polypeptide (Vip), mRNA [XM_217838]	ref|XM_217838.3|gb|XQ2341|ens|ENSRNOT00000025477|tc|TCG37816	Rn.18675	Vip	vasoactive intestinal polypeptide	peptide that causes vasodilation [RGD]	Vasoactive intestinal polypeptide regulates dynamic changes in astrocyte morphometry: impact on gonadotropin-releasing hormone neurons// Significant changes in NPY and VIP prostate nerve fibers, showing an increase in periurethral ducts at sex maturation.// Co-expression patterns of the neuropeptides vasoactive intestinal peptide and cholecystokinin with the transduction molecules alpha-gustducin and T1R2 in rat taste receptor cells.// VIP had a modulatory action on jejunal potassium absorption when injected into the nucleus tractus solitarius.// VIP can modulate not only immune responses but also hormonal responses during acute inflammation.// The increased nonadrenergic noncholinergic and the decreased effects of VIP in mediating inhibitory nerves may largely relate to the peristaltic abnormalities seen in the isografted LEW rat Aging reduces vasoactive intestinal peptide (VIP) receptor mRNA and eliminates diurnal expression of VIP mRNA within the suprachiasmatic nucleus of aged male rats.// (The rest is omitted.)	KEGG pathway: Neuroactive ligand-receptor interaction	[Human, Mouse]Homolo Gene:2539
53.01	25.47	2.08	NM_012612	Nppa	Rattus norvegicus natriuretic peptide precursor type A (Nppa), mRNA [NM_012612]	ref|NM_012612.2|gb|X00665|gb|M27498|ens|ENSRNOT00000011005	Rn.2004	Nppa	natriuretic peptide precursor type A	peptide involved in the control of fluid volume and vascular function [RGD]	The downregulation of ANP and NPRC in retinas of diabetic rats suggests a role for this peptide in experimental diabetic retinopathy.// The ANP might play a role on the synthesis of the oxytocin since ANP and its mRNA appear earlier than oxytocin.// SERCA	-	[Human, Mouse]Homolo Gene:4498

[0424]

Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Gene Symbol	Gene Name	Summary	GeneRIF	Pathway	Homology
136.42	79.32	1.72	NM_053750	Nppc	Rattus norvegicus natriuretic peptide precursor type C (Nppc), mRNA [NM_053750]	ref|NM_053750|gb|D90219|ens|ENSRNOT00000025582	Rn.10637	Nppc	natriuretic peptide precursor type C	binds natriuretic peptide receptor; involved in inhibition of growth and proliferation in vascular smooth muscle cells [RGD]	Endothelium-derived CNP is involved in the regulation of the coronary circulation, and NPR-C activation underlies the vasorelaxant activity of this peptide. Moreover, this newly defined pathway represents a protective mechanism against I/R injury.// endot	-	[Human, Mouse]Homolo Gene:7867
29.03	18.19	1.60	NM_016991	Adra1b	Rattus norvegicus adrenergic receptor, alpha 1b (Adra1b), mRNA [NM_016991]	ref|NM_016991|gb|M60655|gb|AM_346399|gb|X61885	Rn.10032	Adra1b	adrenergic receptor, alpha 1b	couples with G alpha(h) (transglutaminase II) to activate phospholipase C; facilitates Ca2+ release and capacitative Ca2+ entry [RGD]	three subpopulations of alpha1-adrenoceptor binding sites exist in the rat lung (alpha1A, alpha1B and alpha1D)// The rat ovary contains alpha(1)-AR (probably alpha(1B)-subtype), which suggests that this receptor mediates some of the activities of noradren	KEGG pathway: Calcium signaling pathway// KEGG pathway: Neuroactive ligand-receptor interaction	[Human, Mouse]Homolo Gene:55477

[表83]

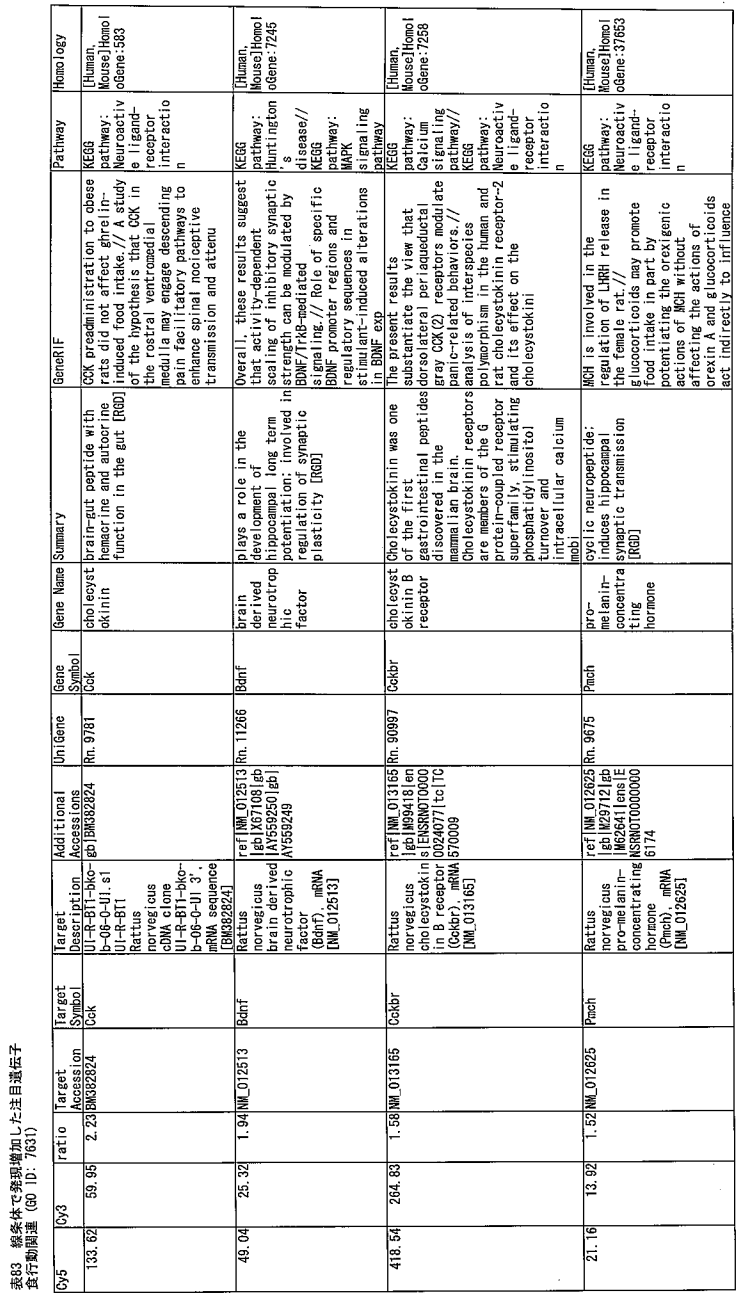


表83 絨条体で発現増加した注目遺伝子
食行動関連 (GO ID: 7631)

Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Gene Symbol	Gene Name	Summary	GeneRIF	Pathway	Homology
133.62	59.95	2.23	BM382824	Cck	UI-R-BT1-bko-b-06-0-UI.s1 UI-R-BT1 Rattus norvegicus cDNA clone UI-R-BT1-bko-b-06-0-UI 3', mRNA sequence [BM382824]	gb|BM382824	Rn.9781	Cck	cholecystokinin	brain-gut peptide with hemacrine and autocrine function in the gut [RGD]	CCK preadministration to obese rats did not affect ghrelin-induced food intake.// A study of the hypothesis that CCK in the rostral ventromedial medulla may engage descending pain facilitatory pathways to enhance spinal nociceptive transmission and attenu	KEGG pathway: Neuroactive ligand-receptor interaction	[Human, Mouse]Homol oGene:583
49.04	25.32	1.94	NM_012513	Bdnf	Rattus norvegicus brain derived neurotrophic factor (Bdnf), mRNA [NM_012513]	ref|NM_012513|gb|X67108|gb|AY559250|gb|AY559249	Rn.11266	Bdnf	brain derived neurotrophic factor	plays a role in the development of hippocampal long term potentiation; involved in regulation of synaptic plasticity [RGD]	Overall, these results suggest that activity-dependent sealing of inhibitory synaptic strength can be modulated by BDNF/TrkB-mediated signaling.// Role of specific BDNF promoter regions and regulatory sequences in stimulant-induced alterations in BDNF exp	KEGG pathway: Huntington's disease// KEGG pathway: MAPK signaling pathway	[Human, Mouse]Homol oGene:7245
418.54	264.83	1.58	NM_013165	Cckbr	Rattus norvegicus cholecystokinin B receptor (Cckbr), mRNA [NM_013165]	ref|NM_013165|gb|M99418|ensembl|ENSRNOT00000024077|tc|TC570009	Rn.90997	Cckbr	cholecystokinin B receptor	Cholecystokinin was one of the first gastrointestinal peptides discovered in the mammalian brain. Cholecystokinin receptors are members of the G protein-coupled receptor superfamily, stimulating phosphatidylinositol turnover and intracellular calcium mobi	The present results substantiate the view that dorsolateral periaqueductal gray CCK(2) receptors modulate panic-related behaviors.// analysis of interspecies polymorphism in the human and rat cholecystokinin receptor-2 and its effect on the cholecystokini	KEGG pathway: Calcium signaling pathway// KEGG pathway: Neuroactive ligand-receptor interaction	[Human, Mouse]Homol oGene:7258
21.16	13.92	1.52	NM_012625	Pmch	Rattus norvegicus pro-melanin-concentrating hormone (Pmch), mRNA [NM_012625]	ref|NM_012625|gb|M29712|gb|M62641|ensembl|ENSRNOT00000006174	Rn.9675	Pmch	pro-melanin-concentrating hormone	cyclic neuropeptide: induces hippocampal synaptic transmission [RGD]	MCH is involved in the regulation of LHRH release in the female rat.// glucocorticoids may promote food intake in part by potentiating the orexigenic actions of MCH without affecting the actions of orexin A and glucocorticoids act indirectly to influence	KEGG pathway: Neuroactive ligand-receptor interaction	[Human, Mouse]Homol oGene:37653

[表84]

表84 線条体で変現増加した注目遺伝子
生体リズム関連 (GO ID: 7623.48511)

Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Gene Symbol	Gene Name	Summary	GeneRIF	Pathway	Homology
369.75	169.54	2.18	NM_012835	Cort	Rattus norvegicus cortistatin (Cort), mRNA [NM_012835]	ref|NM_012835|gb|U51919|ens|ENSRNOT00000018401|ctg570162	Rn.10490	Cort	cortistatin	inhibits growth hormone secretion; may act as a neuropeptide to mediate signaling via a somatostatin receptor subtype [RGD]	-	KEGG pathway: Neuroactive ligand-receptor interaction	[Human, Mouse]HomoloGene:997
1131.31	583.92	1.94	NM_181370	Hs3st2	Rattus norvegicus heparan sulfate (glucosamine) 3-O-sulfotransferase 2 (Hs3st2), mRNA [NM_181370]	ref|NM_181370|gb|AY240870|ens|ENSRNOT00000023733|ctg570569483	Rn.49010	Hs3st2	heparan sulfate (glucosamine) 3-O-sulfotransferase 2	catalyzes the transfer of sulfate groups onto the 3-OH site of glucosamine groups in heparan sulfate proteoglycans [RGD]	3-O sulfation catalyzed by HS 3-O-sulfotransferase (3-OST2) is predominantly restricted to daytime pineal glands in rats	-	[Human, Mouse]HomoloGene:21220
140.87	77.66	1.81	NM_013104	Igfbp6	Rattus norvegicus insulin-like growth factor binding protein 6 (Igfbp6), mRNA [NM_013104]	ref|NM_013104|gb|M69055|gb|BG673588|ens|ENSRNOT00000014807	Rn.6431	Igfbp6	insulin-like growth factor binding protein 6	high-affinity IGF binding ptotein with substantially greater affinity for insulin-like growth factor-II (IGF-II) than IGF-I [RGD]	IGFBP-6, a new negative effector of oligodendrocyte survival and differentiation, is expressed and localized to the Golgi complex in rat oligodendrocyte precursor (O2A) cells.// IGFBP6 Has a role in binding to endothelial cells and in transendothelial tra	-	[Human, Mouse]HomoloGene:1641
111.82	66.27	1.69	XM_345102	Atoh7_predicted	PREDICTED: Rattus norvegicus atonal homolog 7 (Drosophila) (predicted) (Atoh7_predicted), mRNA [XM_345102]	ref|XM_345102|ens|ENSRNOT00000000432	Rn.133599	Atoh7_predicted	atonal homolog 7 (Drosophila) (predicted)	-	-	-	[Human, Mouse]HomoloGene:32338
11976.21	7334.77	1.63	NM_013015	Ptgds	Rattus norvegicus prostaglandin D2 synthase (Ptgds), mRNA [NM_013015]	ref|NM_013015|gb|J04488|gb|M94134|ens|ENSRNOT00000020926	Rn.11400	Ptgds	prostaglandin D2 synthase	catalyzes conversion of prostaglandin H2 to prostaglandin D2, a major prostaglandin that mediates sleep, body temperature, hormone release, and odor responses [RGD]	Gene expression is regulated by Hes-1 through E-box and interleukin-1 beta via two NF-kappa B elements in rat leptomeningeal cells.	KEGG pathway: Arachidonic acid metabolism	[Human, Mouse]HomoloGene:737

[0425] 2-2-4-5. 長期Tickling刺激時と短期Tickling刺激時とで共通して発現変化した遺伝子

長期Tickling刺激時と短期Tickling刺激時に血液、視床下部、線条体において1.5倍以上あるいは1/1.5倍以下に発現量が変化した遺伝子に関し、共通性を解析した結果を表85に示す。

[表85]

表85 長期刺激時と短期刺激時とで共通して発現変化した遺伝子
(1.5倍以上、1/1.5倍以下)

A: 発現変化の方向が順方向である遺伝子

血液	#14UP	#17UP	#14DOWN	#17DOWN
	292	71	349	77
	1		2	
	Unknown		Phospholipid transfer protein	
			Chymase 1	
視床下部	#14UP	#17UP	#14DOWN	#17DOWN
	136	21	185	11
	3		2	
	Hydroxyacyl glutathione hydrolase		Transthyretin	
	LanC-like1		Teratocyte-specific carboxyesterase	
	Dopamine transporter			
線条体	#14UP	#17UP	#14DOWN	#17DOWN
	15	140	44	15
	1		1	
	LanC-like1		Teratocyte-specific carboxyesterase	

B: 発現変化の方向が逆方向である遺伝子

血液	#14DOWN	#17UP	#14UP	#17DOWN
	349	71	292	77
	32		2	
	別紙に記載		Protein tyrosine phosphatase, receptor type	
			Delta-interacting protein A	
視床下部	#14DOWN	#17UP	#14UP	#17DOWN
	185	21	136	11
	0		1	
			Wilms tumor 1-associateing protein	
線条体	#14DOWN	#17UP	#14UP	#17DOWN
	44	140	15	15
	28		1	
	別紙に記載		Wilms tumor 1-associateing protein	

[0426] 血液と視床下部では発現増加した遺伝子、発現減少した遺伝子は共に長期Tickling刺激時に多く、発現変化(増加あるいは減少)した遺伝子はそれぞれ641、321存在し、短期Tickling刺激時の148、32遺伝子を大きく上回った。一方、線条体では短期Tickling刺激時に発現増加した遺伝子が多かった(140遺伝子)のが特徴的であった。しかしながら、長短期間で順方向に発現変化する共通遺伝子はいずれの部位においても1～３程度であったのに対し、血液と線条

体では逆方向に発現変化する遺伝子が多く、短期Tickling刺激ではUp-regulateされるが長期Tickling刺激ではDown-regulateされる遺伝子がそれぞれ32、28存在した。それぞれの遺伝子名については、表86と表87に示す。

[表86]

表86 発現変化の方向が逆方向である血液の32遺伝子

（長期刺激でDOWN＋短期刺激でUP）

1	lactamase, beta (predicted)
2	synaptic vesicle glycoprotein 2b
3	similar to RIKEN cDNA 4921531G14 (predicted)
4	RGD1565641 (predicted)
5	mago-nashi homolog, proliferation-associated (Drosophila) (predicted)
6	ribosomal protein L26
7	polymerase (RNA) II (DNA directed) polypeptide K (predicted)
8	mago-nashi homolog, proliferation-associated (Drosophila) (predicted)
9	mago-nashi homolog, proliferation-associated (Drosophila) (predicted)
10	mago-nashi homolog, proliferation-associated (Drosophila) (predicted)
11	mago-nashi homolog, proliferation-associated (Drosophila) (predicted)
12	mago-nashi homolog, proliferation-associated (Drosophila) (predicted)
13	Unknown
14	mago-nashi homolog, proliferation-associated (Drosophila) (predicted)
15	Unknown
16	mago-nashi homolog, proliferation-associated (Drosophila) (predicted)
17	mago-nashi homolog, proliferation-associated (Drosophila) (predicted)
18	ribosomal protein L23
19	mago-nashi homolog, proliferation-associated (Drosophila) (predicted)
20	Rho-associated coiled-coil forming kinase 1
21	LSM8 homolog, U6 small nuclear RNA associated (S. cerevisiae) (predicted)
22	Unknown
23	SUB1 homolog (S. cerevisiae)
24	Unknown
25	mago-nashi homolog, proliferation-associated (Drosophila) (predicted)
26	similar to RIKEN cDNA 3110001N18 (predicted)
27	Unknown
28	heat shock protein 1, alpha
29	mitogen-activated protein kinase kinase kinase 8
30	zinc finger CCCH type containing 7 A (predicted)
31	matrin 3
32	tubulin cofactor a

[表87]

表87 発現変化の方向が逆方向である線条体の28遺伝子
（長期刺激でDOWN＋短期刺激でUP）

1	neuronal pentraxin receptor
2	somatostatin receptor 3
3	Unknown
4	nephroblastoma overexpressed gene
5	similar to KIAA1034-like DNA binding protein (predicted)
6	nuclear receptor subfamily 4, group A, member 2
7	Unknown
8	peptidase, serine, 12 (neurotrypsin, motopsin)
9	similar to KIAA1034-like DNA binding protein (predicted)
10	similar to NEX-1 (predicted)
11	brain and kidney protein
12	vasoactive intestinal polypeptide
13	similar to hypothetical protein MGC33926
14	heparan sulfate (glucosamine) 3-O-sulfotransferase 2
15	natriuretic peptide precursor type C
16	neuronal pentraxin 1
17	Unknown
18	amyloid beta (A4) precursor protein-binding, family A, member 1 binding protein (predicted)
19	solute carrier family 17 (sodium-dependent inorganic phosphate cotransporter), member 7
20	cholecystokinin
21	neuritin
22	Unknown
23	cholecystokinin
24	Unknown
25	Unknown
26	neurogenic differentiation 2
27	solute carrier family 17 (sodium-dependent inorganic phosphate cotransporter), member 7
28	cortistatin

[0427] 2-2-5. 考察・結論

血液と視床下部ではTicklingによる長期の繰り返し刺激がラットの体質を変化させ、これに伴う遺伝子の発現変化が顕著であるが、これらの組織でのTicklingの短期効果は遺伝子の発現変化としては現れづらかった。一方、線条体では逆に短期刺激で発現増加する遺伝子が多く、外界からの刺激入路がこの部位を経由し、刺激への対応遺伝子を発現させるものと考えられた。長短期Tickling刺激間で共通して発現変化した遺伝子に注目すると、順方向に発現変動する共通遺伝子は極めて少なく、機能面から見ても視床下部での「陽性」刺激の伝達に関わるドーパミントランスポータが長短期を問わず発現増加していることと、血液肥満細胞における過剰免疫への関与が示唆されるキ

マーゼ遺伝子が長短共に発現減少していることのみがTicklingの陽性刺激の効果であった。一方、逆方向に発現変動する共通遺伝子は、血液と線条体で認められるが、血液における共通遺伝子は推定遺伝子が多く注目に値する遺伝子は存在しなかった。線条体では後述の注目遺伝子を相当数含んでいた。

[0428] 個々の組織において発現変化した遺伝子で、健康増進遺伝子候補として位置づけられる可能性を有している注目遺伝子としては、口腔粘膜擦過細胞で発現増加したGsta5、Aldh1a1、Yc2、Gsta2、Cdig1l、Selenbp1があり、前５者は口腔内の解毒に関わる酵素等をコードしており、Selenbp1は味覚に関与するセレン担体をコード化する遺伝子である。一方、発現減少した遺伝子としては、外界からの刺激による細胞ダメージに反応して細胞周期を調節するCDK阻害因子をコードするCdkn1c、アミノ酸代謝を調節する酵素をコードするHpd、肝障害指標であるグアニンデアミナーゼをコードするGdaがあるが、その発現変化が何を意味しているかは現時点では不明である。

[0429] 視床下部では、「陽性」刺激の伝達に関与するドーパミントランスポータをコードするSlc6a3が長期Tickling刺激時と同じく発現増加しており、Tickling刺激の極初期から継続して発現レベルが高くなっていると考えられた。その他Cga遺伝子の発現が増えているが、この遺伝子が雌性に関わるホルモン産生を調整していることを鑑みると、雄性ラットで増える意義についてはマクロでの考察を要する。

[0430] 線条体では、発現増加した遺伝子が最も多く、血圧調節に関与するAvp、Vip、神経成長や分化に関与するNeurod2、Nrn１、神経伝達に関与するSlc17a7、摂食調節に関与するCck、アルツハイマー病に関係するβアミロイド蛋白のレベルを下げ記憶力の改善に関与するSstr1、Cort、精神薄弱の原因遺伝子ともいわれ学習と記憶に関与するPrssの各遺伝子が健康増進遺伝子の候補としてリストアップできた。一方、βアミロイド蛋白の繊維形成を阻害するTtrが線条体でなぜ発現低下するかは不明であるが、Ttr本体の機能(プレアルブミンとしての担体機能)との関係があるのかも知れない。

[0431] GO解析結果からは、線条体での発現増加した遺伝子群での解析以外は各GO

Termに割り当てられる遺伝子が少なく有効な情報が得られなかった。線条体でUp-regulateされた遺伝子が有意に割り当てられたGO Termとしては、シグナル伝達関連、神経ペプチドホルモン活性、血圧調節関連、食行動関連、生体リズム関連のTermがあるが、健康増進遺伝子候補として注目すべきは、後４者のTermに割り当てられる遺伝子である。神経ペプチドホルモン活性に割り当てられる遺伝子としては、上記遺伝子の他にGrp、Adcyap1、Nppcがあるが、Nppcは血圧調節関連のTermに割り当てられるNppa、Avp、Vipと共に血液循環機能を調節する健康増進遺伝子候補となり得る。また、血圧調節関連のTermにはアドレナリン受容体遺伝子も割り当てられている。食行動に関連するTermには長期Tickling刺激実験でのGO解析で抽出されたCck、Pmch以外にBdnfが抽出されたことはストレスとの関連で注目に値する。その他、生体リズム関連のGO Termに有意に遺伝子が割り当てられたことも、Ticklingの短期刺激効果として注目すべきであり、特に睡眠との関係が示唆されているPtgds遺伝子は、動物の「やる気」に関する行動を規定するものとして、健康増進に繋がる可能性が秘められている。

[0432] ２－２－６．総括

ラットを用いて陽性刺激に応じて発現変化する中枢神経系ほかの遺伝子（群）を探索するモデル実験系を作製したが、その刺激期間としてまず４週間を採用し、刺激効果の確実化を図った。その結果、視床下部や唾液腺等において発現変動する遺伝子を特定できたが、長期の繰り返し刺激はラットの体質変化を伴った。４週齢のラットにTickling刺激を与えると、ラットは刺激初日から50 KHz近傍の音声を発し、その音声のピークが２週間であったことから、刺激の受容過程の把握には短期の方が有利と考えられた。短期間（2日間）刺激では、予想した通り、線条体における遺伝子の発現変化が主に観察された。陽性刺激の受容がこの部位を経由するという仮説を支持するものである。健康増進が外界からの刺激に対する心身の適応能力の向上との立場に立てば、短～長期にわたり持続的に活性化される遺伝子は、健康増進遺伝子の候補の一つに挙げることができる。

[0433] [実施例３]

DNAチップデータの精度の検証

上記DNAチップを用いた実験は、一般的には「一次スクリーニングのための手法」、すなわち「DNAチップ上の遺伝子の中から更なる機能解析に用いる遺伝子を選び出す手法」と考えられている。そのため、次のステップとして、得られたDNAチップデータが遺伝子発現状態を正しく反映しているか否かを、定量性の高い方法で確認する必要がある。そこで、DNAチップに比べ1000倍程度感度が良いリアルタイムPCR解析方法を用いて、選抜した遺伝子の発現定量解析を行い、DNAチップデータの検証を行った。

[0434] 本実施例では、陽性刺激を4週間負荷したラットで発現変動することが認められた遺伝子群(上記実施例2参照)の中から、視床下部の食行動に関与する6遺伝子、ドーパミントランスポータ(Slc6a3)、及びコレシストキニン（Cck）遺伝子を選別し、遺伝子発現定量解析を実施した。

[0435] 3-1. 方法

本実施例における遺伝子発現解析実験の流れは図89に示される。

[0436] 3-1-1. 供試材料

本実施例では、4週令(離乳直後[3週令]から個別飼育)から陽性刺激を4週間負荷したラット(Tickling 4個体、Light Touch 2個体)の視床下部から、上記(2-2-2)と同様にして調製したTotal RNAを用いた。

[0437] 3-1-2.Total RNA純度と無傷度の検定

個体毎(Total RNA標品混合前)に、Total RNAの濃度とA260/280比を求めた。

[0438] 3-1-3. 逆転写反応

DNAチップ解析では、Tickling群とLight Touch群の2群での比較を行う。そのため、Tickling 4個体、Light Touch 2個体については、各群の個体のTotal RNAを等量混合し、Tickling群とLight Touch群の2群を逆転写に用いるRNAサンプルとした。

[0439] 逆転写反応には、High Capacity cDNA Reverse Transcription Kit with R

Nase IH(アプライドバイオシステムズ社製)を用いて行った。反応液組成については、Total RNA量を5μg、その他の反応液については説明書に記載の量を加え、トータルボリュームを100μlとした。逆転写反応は、製品説明書に記載の時間と温度で実施した。

[0440] 3-1-4. リアルタイムPCRによる遺伝子の発現定量解析

3-1-4-1. リアルタイムPCR

リアルタイムPCRには、TaqMan アッセイを選択し、7300リアルタイムPCRシステム(アプライドバイオシステムズ社製)を用いて行った。反応は、TaqMan Gene Expression Assaysを用いて、製品説明書に記載の方法に従った。定量方法にはΔΔCt法を用い、相対定量実験を行った。定量結果が得られた後、ΔΔCt法の解析方法により、Light Touchに対するTicklingでの遺伝子発現量の相対値を算出した。

[0441] 3-1-4-2. 解析対象遺伝子

下記表88の8遺伝子について、発現定量を行った。また、初期RNA量の補正のための内在性コントロール遺伝子には、actin, beta遺伝子、およびribosomal protein, large P2遺伝子を使用した（表89）。

[表88]

表 88 ターゲット遺伝子

No.	Assay ID	Availability	Gene Symbol	Gene Name
1	Rn00575275_m1	Inventoried	Galp	NM_022633.1
2	Rn00595020_m1	Inventoried	Pomc	NM_139326.2
3	Rn00561766_g1	Inventoried	Pmch	NM_012625.1
4	Rn01431703_g1	Made to order	Agrp	XM_574228.2
5	Rn00565995_m1	Inventoried	Hcrt	NM_013179.1
6	Rn01410145_m1	Inventoried	Npy	NM_012614.1
7	Rn00562224_m1	Inventoried	Slc6a3	NM_012694.1
8	Rn00563215_m1	Inventoried	Cck	NM_012829.1

[表89]

表 89 内在性コントロール遺伝子

No.	Assay ID	Availability	Gene Symbol	Gene Name
1	Rn00667869_m1	Inventoried	Actb	NM_031144.2
2	Rn01479927_g1	Inventoried	Rplp2	NM_001030021.1

[0442] 3-1-4-3. Unknown Sample

3-1-3で、Total RNAを等量混合したTickling群、Light Touch群の2群について、Total RNAから逆転写反応によって合成したcDNAをUnknown Sampleとした。

[0443] 3-2. 結果

3-2-1. 全RNA純度と無傷度の検定

Tickling群、Light Touch群の各個体のTotal RNA濃度、およびA260/280比を表90に示す。

[表90]

表 90 Tickling 群、Light Touch 群の各個体の Total RNA 濃度、および A260/280 比

	チューブ番号	"全 RNA 濃度 (ng/μl)"	"全RNA A260/280"
Ticling	#14 T1	210.0	2.10
	#14 T2	189.3	2.07
	#14 T3	256.5	2.07
	#14 T4	283.5	2.09
Light touch	#14 L1	264.5	2.09
	#14 L2	239.0	2.09

[0444] 上記の結果、調製した各個体毎のTotal RNAは、純度、無傷度について問題のないレベルの品質であると判断した。

[0445] 3-2-2. リアルタイムPCRによる遺伝子の発現定量解析

3-1-4のリアルタイムPCRによる遺伝子の発現定量解析を実施した。定量結果をもとに、ΔΔCt法の解析方法により算出した相対値を表91に示す。

[表91]

表 91 リアルタイム PCR による遺伝子の発現定量解析

No.	Gene Symbol	遺伝子発現量の相対値	
		内在性コントロール遺伝子 Actin β	内在性コントロール遺伝子 Ribosomal protein, large P2
1	Galp	2.09	2.02
2	Pomc	1.86	1.82
3	Pmch	1.72	1.68
4	Agrp	2.00	1.96
5	Hcrt	1.93	1.87
6	Npy	1.44	1.40
7	Slc6a3	2.80	2.72
8	Cck	0.50	0.49

表の数値は、Light Touch に対する Tickling での遺伝子発現量の相対値を示す。

[0446] 3-2-3. DNAチップ解析結果と、リアルタイムPCR解析結果との比較

3-1-1の供試材料のDNAチップ解析における発現データを表92に示す。

[表92]

表92 DNAチップ解析(#14)における発現データ

Gene Symbol	Gene Name		Feature	Row	Col	Cy5	Cy3	ratio	Probe ID	Target Accession	Target Symbol
Actb	actin, beta	10907	11735	55	125	156.75	164.91	0.95	A_44_P205509	AI179012	AI179012
Actb	actin, beta	24346	26054	122	39	29506.55	32743.71	0.90	A_44_P423803	NM_031144	Actb
Actb	actin, beta	36484	39045	182	130	33016.84	33465.18	0.99	A_44_P423810	NM_031144	Actb
B2m	beta-2 microglobulin	4358	4687	22	172	9776.55	9383.13	1.04	A_43_P11442	NM_012512	B2m
B2m	beta-2 microglobulin	8845	9499	45	39	15530.73	14663.39	1.06	A_44_P214040	NM_012512	B2m
B2m	beta-2 microglobulin	17300	18534	87	44	109.53	99.39	1.10	A_44_P542998	AI172570	AI172570
B2m	beta-2 microglobulin	21993	23519	110	84	8347.27	7798.57	1.07	A_44_P535612	CF111193	B2m
B2m	beta-2 microglobulin	33073	35433	165	173	3030.52	3047.08	0.99	A_44_P122632	CF111193	B2m
Gapdh	glyceraldehyde-3-phosphate dehydrogenase	21782	23304	109	84	40927.02	41614.25	0.98	A_44_P363377	NM_017008	Gapd
Gapdhs	glyceraldehyde-3-phosphate dehydrogenase, spermatogen	26221	28101	131	151	-	-	-	A_44_P116261	NM_023964	Gapds
Gapdh	glyceraldehyde-3-phosphate dehydrogenase	38420	41108	192	43	58397.52	68114.80	0.86	A_44_P193181	NM_017008	Gapd
Gapdh	glyceraldehyde-3-phosphate dehydrogenase	40638	43509	203	79	83.32	79.02	1.05	A_44_P741307	AA818541	AA818541
Rplp2	ribosomal protein, large P2	410	463	3	33	8853.77	9538.63	0.93	A_44_P531848	NM_001030021	NM_001030021
Galp	galanin-like peptide precursor	10825	11649	55	39	153.08	71.65	2.14	A_44_P543334	NM_022633	Galp
Pomc	pro-opiomelanocortin	35938	38433	179	163	4327.77	2030.83	2.13	A_43_P13381	NM_139326	Pomc2
Pmch	pro-melanin-concentrating hormone	37626	40265	188	60	37511.36	20083.44	1.87	A_42_P527961	NM_012625	Pmch
Agrp	agouti related protein homolog (mouse)	25580	27403	128	98	793.72	441.05	1.80	A_44_P257522	XM_574228	XM_574228
Hcrt	hypocretin	12488	13394	63	64	2730.85	1705.40	1.60	A_42_P500675	NM_013179	HcRt
Npy	neuropeptide Y	37659	40301	188	96	2412.90	1515.85	1.59	A_42_P771373	NM_012614	Npy
Slc6a3	solute carrier family 6 (neurotransmitter transpo	29275	31324	146	149	275.61	111.83	2.46	A_44_P314969	NM_012694	Slc6a3
Cck	cholecystokinin	4233	4562	22	47	1739.05	3385.39	0.51	A_44_P119019	NM_012829	Cck
Cck	cholecystokinin	35306	37787	176	162	76.24	151.53	0.50	A_44_P735401	BM382824	Cck

[0447] 解析対象8遺伝子の相対発現量について、リアルタイムPCR解析結果と比較するため、DNAチップ解析の発現データについて、内在性コントロール遺伝子を用いて補正を行い、算出された相対値を表93に示す。

[表93]

表 93 内在性コントロール遺伝子で補正した相対値

No	Gene Symbol	ratio	Light Touch に対する Tickling での遺伝子発現量の相対値		
			内在性コントロール遺伝子 Actb		内在性コントロール遺伝子 Rplp2
			Probe ID:A_44_P423803	Probe ID:A_44_P423810	Probe ID:A_44_P531848
1	Galp	2.14	2.37	2.16	2.30
2	Pomc	2.13	2.37	2.15	2.29
3	Pmch	1.87	2.08	1.89	2.01
4	Agrp	1.80	2.00	1.82	1.94
5	Hcrt	1.60	1.78	1.62	1.72
6	Npy	1.59	1.77	1.61	1.71
7	Slc6a3	2.46	2.74	2.49	2.65
8	Cck	0.51(T v.s. C では、1.94)	0.57	0.52	0.55

[0448] リアルタイムPCR解析とDNAチップ解析とを比較したところ、ともにNo.1～No.7の遺伝子については1.5～2倍以上、No.8の遺伝子については約0.5倍の相対値であり、両者の遺伝子発現の定量値は、ほぼ同程度の値を示した。

[0449] 3-3. 結論

8つの特定遺伝子において、DNAチップ解析およびリアルタイムPCR解析で同程度の遺伝子発現量という結果となり、DNAチップデータが遺伝子発現状態を正しく反映していることを検証できた。

[0450] [実施例４]

本実施例では、ラットを用いたモデル実験の結果を踏まえて、ヒトに陽性刺激（笑い）を負荷し、血液で発現変動する遺伝子を解析することにより、健康に関与する遺伝子の探索と同定に関する研究を行った。

[0451] 4-1. ヒト末梢血白血球細胞において、陽性刺激としての笑いにより発現変動する健康増進遺伝子候補（群）の特定

研究イベント「笑いと健康Part4：歯周病を合併した糖尿病患者における陽性ストレス負荷後の遺伝子発現の変化に関する研究」として実施した。本実験はヒト・ゲノム遺伝子解析研究に関する倫理指針に準じ、筑波大学医の倫理委員会の承認を得た後、被験者の同意を得て行った。

[0452] 4-1-1. 被験者

糖尿病患者はFair ControlがHbA1c値6.5～7.9%領域の患者を対象とした。

対象被験者の募集は、糖尿病患者は糖尿病専門医に依頼し行い、健常被験者は新聞等の公募により行った。

[0453] 4-1-1-1. 歯周病指標

1)歯周病の指標として、WHO基準のCommunity Periodontal Index of Treatment Needs (CPITN)法を用いた（表94）。所定数の歯を測定し、その中で最大の値を示すCPITN値を被験者ごとのCPITN値とした。CPITN値が3以上を示した被験者群を歯周病を有する群(歯周病罹病者群)、2以下を示した被験者群を歯周病を有しない群(歯周病非罹病者群)とした。

[表94]

表 94 CPITN 基準

	評価基準	治療の必要度
code 0	健康な歯肉	治療の必要なし
code 1	プロービング時に出血が認められる	口腔清掃指導
code 2	歯肉縁上･縁下歯石がある 不適合修復物辺縁がある	口腔清掃指導とスケーリング
code 3	4～5mm のポケットがある	口腔清掃指導とスケーリング
code 4	6mm 以上のポケットがある	口腔清掃指導、スケーリングに加えて ポケット掻爬、外科治療などが必要

[0454] 2)各被験者の歯周病の自覚症状の程度は歯科医師作成の問診表を使用し、「はい」の数を数値化して表した。

[0455] 4-1-1-2. 糖尿病指標

糖尿病患者の血糖コントロール指標としてHbA1C値を用いた。測定には、下記(4-1-2)の時程図に示すC1時にサンプリングした血液を用いた。

[0456] 4-1-1-3. 被験者プロフィール

被験者プロフィールを表95に示した。糖尿病患者群のHbA1C値とCPITN値は、それぞれ7.2 ± 0.6%、3.4 ± 0.7、健常者群は5.1 ± 0.3%、2.7 ± 0.6であり、糖尿病患者群のCPITN値は健常者群に比較して有意($p<0.05$)に高かった。このことは、糖尿病患者は歯周病疾患に罹りやすいという臨床上の傾向を検証する結果となった。

[表95]

表 95 被験者プロフィール

	患者群		健常者群	
	2 型糖尿病 (インスリン療法なし)			
被験者数	N=17(M10;、F;7)		N=17(M5;、F;12)	
年齢(yr)	61.0±4.1		56.9±5.6	
BMI(Kg/m^2)	23.7±3.9		22.1±2.7	
HbA_{1C}(%)	7.2±0.6		5.1±0.3	
歯科問診(はいの数)	4.8±2.6		3.3±1.8	
CPITN 値	3.4±0.7	2 以下;N=2	2.7±0.6	2 以下;N=7
		3 以上;N=15		3 以上;N=10

[0457] 4-1-2. 実験方法（実験デザイン）

実験は2日間に渡って行った。被験者に両日とも500Kcalの昼食をとって頂き、昼食後1日目(対照)は単調な講義を45分間聴講してもらった。2日目は、コントを生ステージ鑑賞（45分間）して笑いを体験してもらった。鑑賞（あるいは聴講）前後において、心理テスト、唾液の採取と採血、口腔内観察を行った。口腔内観察は歯科医師(茨城県歯科医師会に協力を得た）が行った。図90に実験時程図を示す。

[0458] 4-1-3. 心理・生理・生化学指標の解析

4-1-3-1. 実験方法（心理・生理・生化学指標の測定）

上記4-1-2の時程図C1、C2、T1、T2時に心理・生理・生化学指標を測定した。測定項目は次の通りである：

心理テスト；POMS、STAI-S

血液；血糖値、白血球数、白血球分画(好中球比、リンパ球比)、NK細胞活性、コルチゾール、C反応性蛋白、HbA1C値（C1のみ）

唾液；量、緩衝能、酸化還元電位、アミラーゼ活性、コルチゾール、s-IgA

統計解析；解析ソフトはエクセルのアドインソフトの「エクセルStatcelQC（S_QC)」を使用した。P値はウィルコクソン符号付順位和検定を用い、危険率5%でP値(両側確率)を算出した。

[0459] 4-1-3-2. 結果・考察

4-1-3-2-1. 糖尿病非罹病かつ歯周病非罹病者群(以下、A群と称する)の解析

解析結果を表96に示す。食後2時間血糖値上昇は講義でもコントでも共に有意差が見られなかった。s-IgA(唾液中の分泌型免疫グロブリンA)は講義後に減少したが、コント後では増加した。感染や炎症時に増加するC反応性蛋白は、講義前後で有意差が見られなかったが、コント後では減少した。

[表96]

表96 「笑いと健康Part4」心理・生理・生化学指標解析データ(糖尿病非罹病かつ歯周病非罹病者群)

糖尿病患者群

	講義前	講義後	P	コント前	コント後	P	P(差間)
TMD	6.1 ± 7.7	4.9 ± 11.8	0.31	-2.3 ± 5.8	-3.1 ± 4.9	0.50	0.50
STAI	35.0 ± 8.7	35.0 ± 5.3	0.83	41.0 ± 7.0	41.7 ± 9.1	0.93	0.75
Amylase活性(KU/L)	36.1 ± 31.2	108.9 ± 128.1	0.13	67.3 ± 65.1	86.4 ± 109.5	0.46	0.20
ORP(mV)	69.7 ± 22.5	26.0 ± 34.2	0.03	49.7 ± 25.4	26.3 ± 42.3	0.13	0.50
Volume(mL)	4.2 ± 0.9	4.1 ± 1.5	0.74	4.8 ± 1.8	4.8 ± 1.8	0.89	0.61
pH	6.2 ± 0.3	5.9 ± 0.5	0.14	6.3 ± 0.5	5.9 ± 0.3	0.08	0.75
s-IgA(μg/mL)	364.4 ± 160.8	354.5 ± 155.3	0.74	227.3 ± 96.6	342.7 ± 201.5	0.06	0.18
唾液CORT(μg/dL)	0.4 ± 0.1	0.3 ± 0.0	0.18	0.4 ± 0.2	0.4 ± 0.1	0.31	0.03
BG(mg/dL)	93.1 ± 12.3	109.7 ± 12.1	0.03	97.6 ± 13.4	123.3 ± 20.4	0.03	0.31
WBC	5600.0 ± 1188.8	6300.0 ± 1134.3	0.09	4928.6 ± 834.1	5700.0 ± 1044.0	0.03	0.55
Neutro(%)	61.7 ± 4.5	63.3 ± 5.8	0.45	60.9 ± 6.7	63.3 ± 6.7	0.31	0.87
Lympho(%)	31.9 ± 4.7	31.3 ± 5.9	0.75	32.3 ± 6.0	31.0 ± 6.4	0.35	0.75
NK活性(%)	51.4 ± 18.2	48.9 ± 14.4	0.61	44.4 ± 16.2	43.0 ± 16.5	0.46	0.55
血液CORT(μg/dL)	11.9 ± 5.4	10.9 ± 3.2	0.50	11.6 ± 6.0	12.1 ± 3.1	0.50	0.18
CRP(μg/dL)	70.9 ± 129.9	65.0 ± 116.5	0.20	44.6 ± 66.1	40.4 ± 60.0	0.07	0.50
PPBG増加(mg/dL)	16.6 ± 14.2			25.7 ± 17.1	P=0.31		

[0460] これらの結果より、A群では、コント鑑賞により、s-IgAの増加から免疫機能が活性化され、またC反応性蛋白の減少から感染・炎症が鎮静しているときの状態になったといえ、コント鑑賞による健康維持・増進が認められた。

[0461] 4-1-3-2-2. 糖尿病非罹病かつ歯周病罹病者群(以下、B群と称する）の解析

解析結果を表97に示す。食後2時間血糖値上昇は講義でもコントでも共に有意差が見られなかった。TMD値（総合感情障害度）は講義聴講前後では差を示さなかったが、コント鑑賞後有意($p<0.05$)に減少した。s-IgAは講義聴講前後では有意差を示さなかったが、コント後では増加した。また、白血球数はコント後に有意($p<0.05$)に増加した。

[表97]

表97「笑いと健康Part4」心理・生理・生化学指標解析データ(糖尿病非罹病かつ歯周病罹病者群)

糖尿病患者群

	講義前	講義後	P	コント前	コント後	P	P(差間)
TMD	4.6 ± 9.8	7.9 ± 15.0	0.84	4.4 ± 9.0	-1.6 ± 8.4	0.007	0.17
STAI	40.8 ± 7.3	40.9 ± 8.0	0.51	38.2 ± 6.9	40.6 ± 8.3	0.14	0.36
Amylase活性(KU/L)	84.2 ± 76.1	51.0 ± 61.7	0.17	75.4 ± 59.6	76.2 ± 69.3	0.65	0.33
ORP(mV)	52.7 ± 28.4	7.2 ± 23.7	0.01	39.1 ± 30.1	30.0 ± 24.0	0.14	0.05
Volume(mL)	5.6 ± 2.0	5.9 ± 2.2	0.59	5.6 ± 2.4	6.2 ± 1.8	0.78	0.88
pH	6.3 ± 0.5	6.2 ± 0.3	0.50	6.3 ± 0.2	6.3 ± 0.2	0.22	1.00
s-IgA(μg/mL)	172.9 ± 63.6	177.5 ± 54.6	0.44	168.3 ± 62.4	194.4 ± 57.1	0.09	0.02
唾液CORT(μg/dL)	0.3 ± 0.1	0.3 ± 0.0	0.20	0.4 ± 0.2	0.3 ± 0.1	0.41	0.51
BG(mg/dL)	90.9 ± 4.4	116.2 ± 21.9	0.009	98.3 ± 12.5	113.4 ± 13.8	0.04	0.68
WBC	5130.0 ± 1079.1	5630.0 ± 1649.3	0.11	4630.0 ± 1496.7	5620.0 ± 1842.0	0.02	0.14
Neutro(%)	54.9 ± 10.8	56.0 ± 9.4	0.51	56.0 ± 9.9	56.6 ± 11.7	0.88	0.91
Lympho(%)	35.5 ± 11.0	35.3 ± 8.7	0.89	35.2 ± 9.9	34.6 ± 10.7	0.78	0.96
NK活性(%)	40.9 ± 19.5	43.5 ± 19.6	0.19	37.7 ± 18.9	39.1 ± 18.1	0.37	0.64
血液CORT(μg/dL)	9.2 ± 2.9	8.0 ± 1.3	0.24	9.6 ± 4.6	9.1 ± 2.9	0.72	0.33
CRP(μg/dL)	30.5 ± 18.5	28.7 ± 17.3	0.05	23.8 ± 13.4	23.8 ± 16.0	0.28	0.24
PPBG増加(mg/dL)	25.3 ± 21.1			15.1 ± 21.4	P=0.68		

[0462] これらの結果より、B群では、コント鑑賞により、s-IgAの増加から免疫機能が活性化されたと推測でき、コント鑑賞による健康維持・増進が認められた。

[0463] 4-1-3-2-3. 糖尿病罹病かつ歯周病非罹病者群(以下、C群と称する)の解析

解析結果を表98に示す。食後2時間血糖値は講義では145.5 ±12.0mg/dL、

コントでは94.0 ±1.4 mg/dLと上昇し、コント鑑賞により上昇が51.5mg/dLと著しく抑制された。ストレスの指標となる唾液中アミラーゼ活性は、講義後に減少し、コント後では著しく減少した。白血球数は、講義聴講前後では差を示さなかったが、コント後に増加した。免疫指標であるリンパ球比は、講義後に減少したが、コント後に増加した。ストレス指標である好中球比は、講義聴講前後では差を示さなかったが、コント後に減少した。感染や炎症時に増加するC反応性蛋白は、講義前後で差が見られなかったが、コント後では減少した。

[表98]

表98 「笑いと健康Part4」心理・生理・生化学指標解析データ(糖尿病罹病かつ歯周病非罹病者群)

糖尿病患者群

	講義前	講義後	P	コント前	コント後	P	P(差間)
TMD	6.0 ± 5.7	10.5 ± 9.2	-	9.5 ± 7.8	8.0 ± 9.9	-	-
STAI	39.0 ± 8.5	40.0 ± 8.5	-	36.0 ± 8.5	36.0 ± 7.1	-	-
Amylase活性(KU/L)	160.0 ± 181.0	88.0 ± 70.7	-	119.0 ± 135.8	20.0 ± 17.0	-	-
ORP(mV)	66.5 ± 7.8	19.0 ± 15.6	-	0.0 ± 33.9	40.0 ± 11.3	-	-
Volume(mL)	3.5 ± 0.7	3.3 ± 0.4	-	3.8 ± 1.1	3.3 ± 0.4	-	-
pH	5.8 ± 0.0	5.8 ± 0.4	-	5.7 ± 0.2	5.5 ± 0.4	-	-
s-IgA(μg/mL)	283.7 ± 47.3	325.5 ± 74.3	-	338.9 ± 107.1	290.1 ± 107.5	-	-
唾液CORT(μg/dL)	0.3 ± 0.1	0.3 ± 0.1	-	0.2 ± 0.02	0.3 ± 0.04	-	-
BG(mg/dL)	114.5 ± 36.1	260.0 ± 48.1	-	127.5 ± 0.7	221.5 ± 0.7	-	-
WBC	6400.0 ± 424.3	6450.0 ± 919.2	-	5800.0 ± 282.8	6250.0 ± 353.6	-	-
Neutro(%)	50.5 ± 3.5	51.5 ± 3.5	-	52.0 ± 8.5	49.5 ± 2.1	-	-
Lympho(%)	44.0 ± 1.4	42.0 ± 1.4	-	41.0 ± 9.9	44.0 ± 2.8	-	-
NK活性(%)	44.5 ± 26.2	42.0 ± 17.0	-	41.0 ± 22.6	36.0 ± 11.3	-	-
血液CORT(μg/dL)	7.3 ± 4.0	8.5 ± 4.7	-	5.3 ± 0.6	7.1 ± 2.1	-	-
CRP(μg/dL)	92.0 ± 32.5	90.9 ± 31.3	-	92.7 ± 40.1	85.3 ± 40.7	-	-
PPBG増加(mg/dL)	145.5 ± 12.0		-	94.0 ± 1.4	-	-	-

＊サンプル数が少なかったため(N=2)、統計処理は行っていない

[0464] これらの結果をまとめると、C群では、コント鑑賞により、食後2時間血糖値上昇が著しく抑制され、ストレス指標である唾液中アミラーゼ活性、好中球比が減少し、免疫指標であるリンパ球比は増加し、C反応性蛋白が減少した。コント鑑賞により、ストレスが減り、免疫機能が活性化し、食後2時間血糖値上昇の抑制効果が認められた。

[0465] 4-1-3-2-4. 糖尿病罹病かつ歯周病罹病者群(以下、D群と称する）の解析

解析結果を表99に示す。食後2時間血糖値は講義では147.0 ±55.3mg/dL、コントでは135.9 ±58.0 mg/dLと上昇し、コント鑑賞により上昇が11.1mg/dL抑制された。TMD値（総合感情障害度）は講義聴講前後では差を示さなかったが、コント鑑賞後有意($p<0.05$)に減少した。s-IgA(唾液中の分泌型免疫グロブリンA)は講義後、コント後とも増加した。感染や炎症時に増加するC反応性蛋白は、講義後、コント後とも減少した。

[表99]

表99 「笑いと健康Part4」心理・生理・生化学指標解析データ(糖尿病罹病かつ歯周病罹病者群)

糖尿病患者群

	講義前	講義後	P	コント前	コント後	P	P(差間)
TMD	13.2 ± 16.3	11.3 ± 16.4	0.20	4.7 ± 10.7	-3.5 ± 7.9	0.003	0.12
STAI	39.3 ± 8.5	37.7 ± 7.4	0.36	37.9 ± 7.1	41.5 ± 7.3	0.08	0.10
Amylase活性(KU/L)	75.0 ± 49.2	52.9 ± 26.1	0.03	58.4 ± 30.9	78.0 ± 63.8	0.08	0.02
ORP(mV)	49.5 ± 28.0	33.2 ± 25.2	0.05	59.3 ± 30.5	50.1 ± 26.7	0.19	0.39
Volume(mL)	5.5 ± 2.1	5.2 ± 2.1	0.36	5.8 ± 1.9	5.1 ± 1.6	0.01	0.08
pH	6.1 ± 0.5	6.0 ± 0.5	0.31	6.0 ± 0.6	5.8 ± 0.5	0.02	0.27
s-IgA(μg/mL)	231.4 ± 186.6	243.3 ± 118.8	0.19	201.6 ± 77.2	215.5 ± 96.4	0.65	0.46
唾液CORT(μg/dL)	0.5 ± 0.2	0.4 ± 0.1	0.14	0.4 ± 0.1	0.5 ± 0.2	0.08	0.01
BG(mg/dL)	142.3 ± 35.1	289.3 ± 52.5	0.001	148.1 ± 31.4	284.0 ± 52.3	0.001	0.38
WBC	5880.0 ± 1183.9	6280.0 ± 1249.7	0.02	5406.7 ± 1223.3	5786.7 ± 1273.8	0.01	0.71
Neutro(%)	58.1 ± 6.7	61.4 ± 6.1	0.16	57.7 ± 5.4	60.1 ± 5.4	0.04	0.97
Lympho(%)	33.3 ± 6.9	30.5 ± 6.1	0.23	33.6 ± 5.7	32.3 ± 6.3	0.08	0.92
NK活性(%)	43.2 ± 13.9	46.5 ± 13.3	0.14	39.3 ± 12.6	39.5 ± 12.6	0.95	0.29
血液CORT(μg/dL)	13.8 ± 6.0	10.9 ± 2.7	0.16	11.9 ± 3.8	13.0 ± 2.5	0.43	0.03
CRP(μg/dL)	102.4 ± 123.0	94.9 ± 110.2	0.02	83.2 ± 86.1	80.1 ± 81.0	0.09	0.17
PPBG増加(mg/dL)	147.0 ± 55.3			135.9 ± 58.0	P=0.38		

[0466] これらの結果をまとめると、糖尿病罹病かつ歯周病罹病者群では、コント鑑賞により、食後2時間血糖値上昇が抑制され、TMD値（総合感情障害度）が有意に減少した。コント鑑賞により、感情障害が改善され、食後2時間血糖値上昇の抑制効果が認められた。

[0467] 4-1-3-3-1. 糖尿病罹病者群／糖尿病非罹病者群(C＋D群/A＋B群)間の解析

採取した心理・生理・生化学データを糖尿病罹病者群／糖尿病非罹病者群間で比較解析した。講義前後、コント前後の心理・生理・生化学データをプロットした図を図91～106に示し、各群の解析結果を表100、101に示す。

[表100]

表100「笑いと健康Part4」心理・生理・生化学指標解析データ(糖尿病罹病者群)

糖尿病罹病者群

	講義前	講義後	P	コント前	コント後	P	P(差間)
TMD	12.4 ± 15.5	11.2 ± 15.5	0.26	5.2 ± 10.3	-2.1 ± 8.7	0.001	0.10
STAI	39.3 ± 8.2	38.0 ± 7.3	0.21	37.6 ± 7.0	40.9 ± 7.3	0.04	0.11
Amylase活性(KU/L)	85.0 ± 70.4	57.1 ± 32.3	0.01	65.5 ± 48.9	71.2 ± 62.8	0.18	0.06
ORP(mV)	51.5 ± 26.9	31.5 ± 24.4	0.01	52.3 ± 35.6	48.9 ± 25.4	0.28	0.14
Volume(mL)	5.2 ± 2.1	5.0 ± 2.1	0.15	5.6 ± 1.9	4.9 ± 1.6	0.003	0.06
pH	6.04 ± 0.5	5.99 ± 0.5	0.06	5.94 ± 0.6	5.79 ± 0.5	0.005	0.25
s-IgA(μg/mL)	244.6 ± 167.3	261.2 ± 113.7	0.05	231.0 ± 97.5	233.1 ± 96.4	0.91	0.21
唾液CORT(μg/dL)	0.5 ± 0.3	0.4 ± 0.1	0.45	0.45 ± 0.2	0.50 ± 0.2	0.07	0.00
BG(mg/dL)	139.1 ± 36.4	282.1 ± 50.7	0.0004	152.1 ± 48.7	276.7 ± 51.3	0.0004	0.14
WBC	5926.3 ± 1310.1	6363.2 ± 1412.3	0.019	5468.4 ± 1434.1	5989.5 ± 1566.6	0.004	1.00
Neutro(%)	57.5 ± 7.8	60.5 ± 7.7	0.12	58.3 ± 7.7	59.8 ± 9.0	0.08	0.86
Lympho(%)	34.5 ± 7.9	31.7 ± 7.5	0.15	33.5 ± 7.7	32.8 ± 8.9	0.20	0.73
NK活性(%)	43.9 ± 14.3	46.3 ± 12.9	0.22	40.3 ± 13.3	39.6 ± 12.1	0.85	0.20
血液CORT(μg/dL)	12.8 ± 5.8	10.4 ± 2.8	0.27	11.8 ± 5.0	12.4 ± 2.9	0.33	0.02
CRP(μg/dL)	94.9 ± 110.9	89.0 ± 99.4	0.01	111.9 ± 159.7	127.9 ± 235.3	0.05	0.03
PPBG増加(mg/dL)	146.8 ± 51.8			130.9 ± 56.0	P=0.14		

[表101]

表101 「笑いと健康Part4」心理・生理・生化学指標解析データ(糖尿病非罹病者群)

糖尿病非罹病者群

	講義前	講義後	P	コント前	コント後	P	P(差間)
TMD	5.2 ± 8.8	6.6 ± 13.4	0.26	1.6 ± 8.4	-2.2 ± 7.0	0.01	0.43
STAI	38.4 ± 8.2	38.5 ± 7.5	0.21	39.4 ± 6.9	41.1 ± 8.4	0.17	0.34
Amylase活性(KU/L)	64.4 ± 64.9	74.8 ± 95.7	0.01	72.1 ± 60.0	80.4 ± 85.0	0.23	1.00
ORP(mV)	59.7 ± 26.8	14.9 ± 29.1	0.01	43.5 ± 27.9	28.5 ± 31.6	0.01	0.03
Volume(mL)	5.0 ± 1.7	5.1 ± 2.1	0.15	5.2 ± 2.1	5.6 ± 1.9	0.19	1.00
pH	6.24 ± 0.4	6.09 ± 0.4	0.06	6.31 ± 0.3	6.12 ± 0.3	0.02	0.84
s-IgA(μg/mL)	242.2 ± 142.4	249.8 ± 135.9	0.05	193.5 ± 78.5	248.2 ± 141.6	0.01	0.02
唾液CORT(μg/dL)	0.37 ± 0.1	0.31 ± 0.1	0.45	0.37 ± 0.2	0.38 ± 0.1	0.49	0.03
BG(mg/dL)	90.9 ± 8.2	111.8 ± 20.0	0.0004	95.7 ± 12.8	116.1 ± 16.0	0.0011	0.76
WBC	5360.0 ± 1267.2	5890.0 ± 1458.2	0.02	4690.0 ± 1220.8	5585.0 ± 1505.2	0.0007	0.18
Neutro(%)	58.7 ± 9.1	60.1 ± 8.7	0.12	58.2 ± 8.3	60.0 ± 9.7	0.21	0.96
Lympho(%)	33.5 ± 8.6	32.7 ± 7.9	0.15	33.9 ± 7.8	32.7 ± 8.6	0.24	0.86
NK活性(%)	44.6 ± 19.1	45.1 ± 18.4	0.22	40.1 ± 17.3	40.3 ± 17.1	0.35	0.94
血液CORT(μg/dL)	10.5 ± 4.2	9.6 ± 2.8	0.27	10.4 ± 4.8	10.4 ± 3.1	0.45	0.11
CRP(μg/dL)	115.3 ± 321.2	111.1 ± 315.8	0.01	94.8 ± 284.2	92.3 ± 279.7	0.03	0.62
PPBG増加(mg/dL)	19.7 ± 20.0			19.8 ± 19.3	P=0.56		

[0468] 糖尿病罹病者群においては、食後2時間値血糖値は講義では146.8 ±51.8mg/dL、コントでは130.9 ±56.0 mg/dLと上昇し、コント鑑賞により上昇が15.9 mg/dL抑制された。POMSの6感情指標より算出したTMD値（総合感情障害度）は講義聴講前後では有意差を示さなかったが、コント鑑賞後有意($p<0.05$)に減少した。唾液中の酸化還元電位は講義後もコント後も減少した。白血球数は

講義後もコント後も有意(p<0.05)に増加した。

[0469] これらの結果をまとめると、糖尿病罹病者群では、コント鑑賞により、食後2時間血糖値上昇が抑制され、TMD値（総合感情障害度）が有意に減少した。コント鑑賞により、感情障害が改善され、食後2時間血糖値上昇の抑制効果が認められた。

[0470] 糖尿病非罹病者群においては、食後2時間血糖値上昇は講義でもコントでも共に有意差が見られなかった。TMD値は講義聴講前後では有意差を示さなかったが、コント鑑賞後有意(p<0.05)に減少した。白血球数は講義後もコント後も有意(p<0.05)に増加した。s-IgAは講義前後では有意差がなかったが、コント後有意(p<0.05)に増加した。唾液量は、コント後に増加した。唾液中の酸化還元電位は講義後もコント後も有意(p<0.05)に減少した。C反応性蛋白は講義前後でもコント前後でも共に有意(p<0.05)に減少した。

[0471] これらの結果より、糖尿病非罹病者群では、コント鑑賞により、TMD値（総合感情障害度）が有意に減少し、唾液量が増加し、s-IgAの増加から免疫機能が活性化され、コント鑑賞による健康維持・増進が認められた。

[0472] 4-1-3-3-2. 歯周病罹病者群／歯周病非罹病者群(B＋D群/A＋C群)間の解析

それぞれの群の講義聴講前後、コント鑑賞前後で心理・生理・生化学データの比較解析を行った。歯周病罹病者群に健常被験者が含まれる割合と、歯周病非罹病者群に糖尿病被験者が含まれる割合は同様であった。講義前後、コント前後の各心理・生理・生化学データをプロットした図を図107～122に示し、各群の解析結果を表102、103に示す。

[表102]

表102 「笑いと健康Part4」心理・生理・生化学指標解析データ(歯周病罹病者群)

歯周病罹病者群

	講義前	講義後	P	コント前	コント後	P	P(差間)
TMD	9.8 ± 14.5	9.9 ± 15.6	0.51	4.6 ± 9.9	-2.7 ± 8.0	0.00009	0.02
STAI	39.9 ± 7.9	39.0 ± 7.6	0.83	38.0 ± 6.9	41.2 ± 7.6	0.02	0.03
Amylase活性(KU/L)	78.7 ± 60.0	52.2 ± 42.7	0.02	65.2 ± 44.3	77.3 ± 64.6	0.17	0.01
ORP(mV)	50.8 ± 27.6	22.8 ± 27.4	0.0003	51.2 ± 31.3	42.1 ± 27.1	0.02	0.02
Volume(mL)	5.5 ± 2.0	5.5 ± 2.1	0.39	5.7 ± 2.1	5.5 ± 1.7	0.14	0.11
pH	6.16 ± 0.5	6.09 ± 0.5	0.24	6.12 ± 0.5	6.00 ± 0.4	0.01	0.20
s-IgA(μg/mL)	208.0 ± 150.6	216.9 ± 102.1	0.10	188.3 ± 72.2	207.0 ± 82.2	0.14	0.04
唾液CORT(μg/dL)	0.4 ± 0.2	0.3 ± 0.1	0.04	0.40 ± 0.2	0.43 ± 0.2	0.32	0.003
BG(mg/dL)	121.7 ± 37.2	220.0 ± 96.3	0.00002	128.2 ± 35.4	215.8 ± 94.6	0.00003	0.11
WBC	5580.0 ± 1181.1	6020.0 ± 1427.1	0.005	5096.0 ± 1365.2	5720.0 ± 1491.9	0.001	0.15
Neutro(%)	56.8 ± 8.5	59.2 ± 7.9	0.15	57.0 ± 7.4	58.7 ± 8.5	0.11	0.44
Lympho(%)	34.2 ± 8.6	32.4 ± 7.5	0.32	34.2 ± 7.5	33.2 ± 8.2	0.20	0.49
NK活性(%)	42.3 ± 16.0	45.3 ± 15.8	0.05	38.7 ± 15.1	39.4 ± 14.7	0.54	0.12
血液CORT(μg/dL)	11.9 ± 5.4	9.8 ± 2.6	0.08	11.0 ± 4.2	11.5 ± 3.3	0.70	0.01
CRP(μg/dL)	73.7 ± 101.2	68.4 ± 91.0	0.002	59.5 ± 72.6	57.6 ± 68.7	0.053	0.05
PPBG増加(mg/dL)	98.3 ± 75.2			87.6 ± 76.0	P=0.11		

[表103]

表103「笑いと健康Part4」心理・生理・生化学指標解析データ(歯周病非罹病者群)

歯周病非罹病者群

	講義前	講義後	P	コント前	コント後	P	P(差間)
TMD	6.1 ± 7.0	6.1 ± 11.0	0.59	0.3 ± 7.7	-0.7 ± 7.4	0.36	0.30
STAI	35.9 ± 8.3	36.1 ± 5.9	0.94	39.9 ± 7.1	40.4 ± 8.6	1.00	0.43
Amylase活性(KU/L)	63.7 ± 88.4	104.2 ± 114.1	0.26	78.8 ± 77.5	71.7 ± 99.5	0.78	0.05
ORP(mV)	69.0 ± 19.7	24.4 ± 30.3	0.01	38.7 ± 33.3	29.3 ± 37.3	0.51	0.07
Volume(mL)	4.1 ± 0.8	3.9 ± 1.4	0.62	4.6 ± 1.7	4.4 ± 1.7	0.53	0.39
pH	6.09 ± 0.3	5.90 ± 0.4	0.11	6.13 ± 0.5	5.84 ± 0.4	0.05	0.31
s-IgA(μg/mL)	346.4 ± 144.7	348.1 ± 137.6	0.37	252.1 ± 104.2	331.0 ± 180.1	0.31	0.11
唾液CORT(μg/dL)	0.39 ± 0.2	0.32 ± 0.1	0.37	0.35 ± 0.2	0.40 ± 0.1	0.21	0.01
BG(mg/dL)	97.9 ± 19.1	143.1 ± 69.2	0.01	104.2 ± 17.6	145.1 ± 46.8	0.01	0.43
WBC	5777.8 ± 1098.6	6333.3 ± 1036.8	0.09	5122.2 ± 824.3	5822.2 ± 944.4	0.01	0.16
Neutro(%)	59.2 ± 6.4	60.7 ± 7.3	0.34	58.9 ± 7.6	60.2 ± 8.5	0.51	0.41
Lympho(%)	34.6 ± 6.8	33.7 ± 7.0	0.48	34.2 ± 7.3	33.9 ± 8.1	0.58	0.37
NK活性(%)	49.9 ± 18.5	47.3 ± 14.2	0.51	43.7 ± 16.2	41.4 ± 15.2	0.33	0.38
血液CORT(μg/dL)	10.9 ± 5.3	10.4 ± 3.4	0.95	10.2 ± 5.9	11.0 ± 3.6	0.37	0.07
CRP(μg/dL)	75.6 ± 113.4	70.7 ± 102.2	0.10	55.3 ± 62.6	50.3 ± 57.4	0.03	0.11
PPBG増加(mg/dL)	45.2 ± 58.3			40.9 ± 33.6	P=0.86		

[0473] 歯周病罹病者群では、TMD値は講義前後では有意差を示さなかったが、コント後有意($p<0.05$)に減少した。唾液中の酸化還元電位は講義後もコント後も共に有意($p<0.05$)に減少した。白血球数は講義後もコント後も共に有意($p<0.05$)に増加した。s-IgAは講義後もコント後も増加した。NK細胞活性は講義後もコント後も増加した。C反応性蛋白は講義後もコント後も減少した。

[0474] 歯周病非罹患者群では、TMD値は講義前後では有意差を示さなかったが、コント後に減少した。s-IgAは講義後は減少したが、コント後に増加した。唾液アミラーゼ活性は、コント後に減少した。唾液中の酸化還元電位は講義後もコント後も減少した。白血球数は講義前後では有意差がなかったが、コント後有意($p<0.05$)に増加した。C反応性蛋白は講義前後では有意差がなかったが、コント後有意($p<0.05$)に減少した。

[0475] これらの結果より、歯周病非罹患者群では、コント鑑賞により、TMD値（総合感情障害度）が減少し、ストレス指標である唾液中アミラーゼ活性が減少し、s-IgAの増加から免疫機能が活性化され、またC反応性蛋白の減少から感染・炎症が鎮静しているときの状態になったといえ、コント鑑賞による健康維持・増進が認められた。

[0476] 4-1-4. 遺伝子発現解析実験

糖尿病罹病者群（C＋D群）と糖尿病非罹病者群（A＋B群）で、笑い体験、講義聴講による遺伝子発現変化をDNAチップ法により解析した。糖尿病非罹病かつ歯周病非罹病者群(A群)、糖尿病非罹病かつ歯周病罹病者群(B群)、糖尿病罹病かつ歯周病非罹病者群（C群）、糖尿病罹病かつ歯周病罹病者群（D群）、歯周病非罹病者群（A＋C群）、歯周病罹病者群（B＋D群）の組合せでは、笑い体験時のみの遺伝子発現変化解析を行なった。DNAチップ解析の組合せを表104に示す。

[表104]

表 104 解析の組み合わせ

解析 No	Cy3	⇔	Cy5
解析 2	N-3	⇔	N-4
解析 4	D-3	⇔	D-4
解析 5	NP1-3	⇔	NP1-4
解析 6	NP2-3	⇔	NP2-4
解析 7	DP1-3	⇔	DP1-4
解析 8	DP2-3	⇔	DP2-4
解析 9	P1-3	⇔	P1-4
解析 10	P2-3	⇔	P2-4

凡例は以下の通り:
N:A+B 群
D:C+D 群
NP1:A 群
NP2:B 群
DP1:C 群
DP2:D 群
P1:A+C 群
P2:B+D 群
-1:講義前(刺激時程図の C1)
-2:講義後(刺激時程図の C3)
-3:コント前(刺激時程図の T1)
-4:コント後(刺激時程図の T3)

[0477] 4-1-4-1. 実験方法

4-1-4-1-1. 解析対象サンプルの採取

血液の採取

PAXgene専用採血管に採取を行ない、室温で4時間、4℃で1晩放置後、-30℃で保存した。

[0478] 4-1-4-1-2. 解析対象サンプルからのRNA調製・検定

1) 血液試料からの全RNA調製

PAXgene Blood RNA Kit (QIAGEN社製)を用いて全RNA標品を調製した。

[0479] 2) 全RNA純度と無傷度の検定

被験者試料毎(全RNA標品混合前)に、全RNA標品の濃度とA260/280比、A230/260比、28S/18S rRNA比を求めた。28S/18S rRNA比は、マイクロチップ型電気

泳動システム(日立コスモアイ、SV1210)により検定・算出した。

[0480] 4-1-4-1-3. DNAチップ解析法

上記(4-1-4-1-1)の血液試料から得られた全RNA標品を出発材料として、T7RNA Polymerase Promoter配列を付加したOligo(dT)24をプライマーとしてcDNA合成し、さらにT7 RNA ポリメラーゼによりmRNAの増幅を行った。この時の増幅反応の基質として、Cyanine [Cy]3-CTP（講義前あるいはコント前）、Cy5-CTP（講義後あるいはコント後）を用いることにより、蛍光標識したcRNAを得、DNAチップ解析に供した。DNAチップ解析は以下の通り行った。各Cyanine色素で蛍光標識したRNA標品を等量混合し、DNAチップ〔Agilent社製(約41,000オリゴDNA搭載)、Whole Human Genome DNA Microarray 4×44K〕上で65℃、17時間ハイブリダイゼーション反応を行い(未反応分子はハイブリダイゼーション反応後洗浄除去)、共焦点レーザースキャナー(Agilent社製、G2565)で各色素に由来する蛍光強度を測定した。バックグランド補正とグローバル正規化の後、Cy5/Cy3比を遺伝子の発現変化として求めた。

[0481] 4-1-4-1-4. リアルタイム定量PCR解析法

上記DNAチップ解析結果より、歯周病罹患者群（解析10）で発現変動した遺伝子群で免疫・炎症・生体防御に関連する4つの遺伝子CTSA(cathepsin A)、CTSB(cathepsin B)、IL8RB(interleukin 8 receptor, beta)、TLR7(toll-like receptor 7)について、リアルタイム定量PCR解析を実施した。内部標準はDNAチップ解析で発現変動の少なかったGUSB(glucuronidase, beta)を用いた。使用するリアルタイム定量PCRのプライマー・プローブはDNAチップ解析で使用したAgilentのプローブIDと配列位置が近いものを使用した。

[0482] 解析を実施したサンプルは、糖尿病罹患者群で歯周病スコア(CPITN値)が高い被験者と低い被験者(上位3名、下位2名)、糖尿病非罹患者群で歯周病スコア(CPITN値)が高い被験者と低い被験者(上位3名、下位3名)、合計11名の被験者を対象とした。検量線を用いた相対定量を行うために、3種類のcDNA反応溶液（被験者サンプル ： 被験者サンプルのtotal RNA から逆転写反応で合成したcDNA サンプル。Standard ： 検量線作成用として被験者番号114の笑い後の

cDNAサンプル「114 P2-3」の希釈系列。Negative Control : cDNA の代わりに水を加えたサンプル) を使用した。PCR 反応溶液はTaqMan プローブとプライマーがセットになった反応液とcDNA反応溶液をTaqMan Universal PCR Master Mix に加えて調製した。測定には各サンプルにつき3 wells使用し、その内蛍光シグナルを観察できた2 wells以上の平均(Replicate) をとることでデータ解析の信頼性を高めた。PCRの条件は、50° Cで2分間(dUを含むPCR産物からの再PCR増幅を防止する為のUNG[AmpErase uracil-N-glycosylase]の活性化)、95° Cで10分間(AmpliTaq Gold(登録商標) DNA polymerase の活性化)の前反応の後、95° Cで15秒(cDNAの変性)と60° Cで1分間(プライマーとプローブのアニーリング、伸長反応)のサイクルを40回繰り返して行った。上述の検量線作成用のサンプル「114 P2-3」の希釈系列(total RNA 換算 ; 50 ng、10 ng、2 ng、0.4 ng、0.08 ng、0.016 ng、0.0032 ng)を用い、各遺伝子の検量線を以下の方法で作成し、各サンプルの定量値を得た。検量線は、PCR反応のサイクル数に対して、増幅されたPCR産物に相当する蛍光シグナル(ΔRn)をプロットした増幅曲線を作成し、増殖曲線が指数関数的に増幅されている領域にベースラインを引きThresholdとし、各増幅曲線上でこのThresholdの値に相当するサイクル数をThreshold Cycle (CT)値とし、既知の濃度と対応するCT値をプロットして作成した。ま

た、各遺伝子の発現データの補正は、被験者サンプルの内在性コントロール定量値のサンプル「114 P2-3」の定量値に対する比を乗じて行った。リアルタイム定量PCR 反応の操作、および解析は、ABI PRISM(登録商標)7900HT Sequence Detection System と付属のソフトウェアであるSDS 2.2 を用いて行った。

[0483] 4-1-4-2. 結果

末梢血白血球細胞を対象に遺伝子発現解析を行った。なお、本結果で用いる「プローブ」と「遺伝子(トランスクリプトを含む)」の用語は同義である。

[0484] 4-1-4-2-1. 発現変化を認めた遺伝子

解析2、4～10において1.5倍以上あるいは1/1.5倍以下の発現変化を認めた遺伝子の数を示した結果を表105に示した。

[表105]

表105 講義・笑いで発現変動した遺伝子
(≧1.5-fold,≦1/1.5)

	群	前後	Flagの除去 (genes/41,000)	1.5倍以上 Up (genes)	1/1.5倍以下 Down (genes)
解析2	A＋B群	笑い	24,273	969	867
解析4	C＋D群	笑い	23,130	204	416
解析5	A群	笑い	22,294	197	615
解析6	B群	笑い	18,429	922	1,027
解析7	C群	笑い	21,878	174	634
解析8	D群	笑い	23,469	634	1,137
解析9	A＋C群	笑い	24,078	157	415
解析10	B＋D群	笑い	22,441	1,998	2,592

[0485] A＋B群で講義聴講によりUp-regulateされた遺伝子は149、Down-regulateされた遺伝子は369あった。C＋D群では講義聴講によりUp-regulateされた遺伝子は553、Down-regulateされた遺伝子は673あった。A＋B群で笑いにより発現変化した遺伝子は多く、Up-regulateされた遺伝子は969、Down-regulateされ

た遺伝子は867あった。

[0486] C＋D群では、A＋B群より発現変化した遺伝子は少なくUp-regulateされた遺伝子は204、Down-regulateされた遺伝子は416であった。歯周病の有無による解析では、B＋D群で発現変化した遺伝子は群間比較中で最も多く、Up-regulateされた遺伝子は1,998、Down-regulateされた遺伝子は2,592であった。これに対しA＋C群では発現変化した遺伝子群は少なくUp-regulateされた遺伝子は157、Down-regulateされた遺伝子は415であった。この傾向は糖尿病罹病者群、糖尿病非罹病者群の中での歯周病の有無においても同様であり、D群で発現変化した遺伝子が1,771、B群で1,949であるのに対し、C群は808、A群では812であった。

[0487] 4-1-4-2-2. ヒストグラム、ベン図

解析2、4～10において、1.5倍以上あるいは1/1.5倍以下の発現変化を認める遺伝子のヒストグラムを図123に示した。縦軸に発現変化倍数のLog2値を表し、横軸にサンプル名を表した。歯周病罹病者群の解析、すなわち解析6(B群の笑い前後)、解析8(D群の笑い前後)、解析10(B＋D群の笑い前後)では、発現変化幅の大きい遺伝子が多い。また、対応する解析ごとの発現変化の相対差を図124に比較して示した。縦軸に発現変化倍数のLog2値を表し、横軸に解析組合せを表した。糖尿病非罹病者群では講義前後と笑い前後では各遺伝子の発現変化の差が大きいが、糖尿病罹病者群では比較的小さい。また、A＋C群とB＋D群間では発現変化の差が大きく、A群とB群でも大きかった。また、C群とD群間の比較では、発現が減少した遺伝子の変化幅が比較的大きかった。

[0488] 次に、笑いにより発現変化を認めた各群の遺伝子の数をベン図に表した。A＋B群とC＋D群で1.5倍以上の発現変化を認めた遺伝子のベン図を図125に示す。A＋B群のみでUp-regulateした遺伝子は928、C＋D群のみでは163、両群共通では41あった。1/1.5倍以下の発現変化を認めた遺伝子のベン図を図126に示す。A＋B群のみでDown-regulateした遺伝子は804、C＋D群のみでは353、両群共通では63あった。同様にA群とB群で1.5倍以上の発現変化を認めた遺伝子のベン図を図127に示す。A群のみでUp-regulateした遺伝子は161、B群のみでは

886、両群共通では36あった。1/1.5倍以下の発現変化を認めた遺伝子のベン図を図128に示す。A群のみでDown-regulateした遺伝子は577、B群のみでは989、両群共通では38あった。A群とC群で1.5倍以上の発現変化を認めた遺伝子のベン図を図129に示す。A群のみでUp-regulateした遺伝子は176、C群のみでは153、両群共通では21あった。1/1.5倍以下の発現変化を認めた遺伝子のベン図を図130に示す。A群のみでDown-regulateした遺伝子は564、C群のみでは583、両群共通では51あった。B群とD群で1.5倍以上の発現変化を認めた遺伝子のベン図を図131に示す。B群のみでUp-regulateした遺伝子は819、D群のみでは531、両群共通では103あった。1/1.5倍以下の発現変化を認めた遺伝子のベン図を図132に示す。B群のみでDown-regulateした遺伝子は771、D群のみでは881、両群共通では256あった。C群とD群で1.5倍以上の発現変化を認めた遺伝子のベン図を図133に示す。C群のみでUp-regulateした遺伝子は129、D群のみでは589、両群共通では45あった。1/1.5倍以下の発現変化を認めた遺伝子のベン図を図134に示す。C群のみでDown-regulateした遺伝子は481、D群のみでは984、両群共通では153あった。A＋C群とB＋D群で1.5倍以上の発現変化を認めた遺伝子のベン図を図135に示す。A＋C群のみでUp-regulateした遺伝子は361、B＋D群のみでは2,538、両群共通では54あった。1/1.5倍以下の発現変化を認めた遺伝子のベン図を図136に示す。A＋C群のみでDown-regulateした遺伝子は103、B＋D群のみでは1,944、両群共通では54あった。

[0489] 解析の結果、A＋C群とB＋D群では、1.5倍以上、1.5倍以下発現変動した遺伝子数が多いにも関わらず、共通で発現変動した遺伝子数は少なかった。また、D群／B群間では共通で発現変動した遺伝子数は比較的多かった。

[0490] 4-1-4-2-3. オントロジー解析（GO解析）

当解析は、解析2、4～10において、1.5倍以上あるいは1/1.5倍以下の発現変化を認める遺伝子を対象として行った。抽出された遺伝子数（プローブ数）とGO term数は表106、107に示した。

[表106]

表106 抽出された遺伝子が割り当てられたGO Term数

（≧1.5-foldで増加した遺伝子）

	群	前後	Biological Process		Cellular Component		Molecular Function	
			(annotated genes)	GO Term数 (p<0.05)	(annotated genes)	GO Term数 (p<0.05)	(annotated genes)	GO Term数 (p<0.05)
All Genes			20,657		20,710		22,684	
解析2	A+B群	笑い	475	91	501	61	521	157
解析4	C+D群	笑い	120	40	123	21	128	67
解析5	A群	笑い	95	43	91	20	100	51
解析6	B群	笑い	507	142	515	63	560	71
解析7	C群	笑い	93	70	93	11	96	76
解析8	D群	笑い	337	138	338	29	371	75
解析9	A+C群	笑い	68	29	80	10	86	23
解析10	B+D群	笑い	1,033	204	1,067	67	1,152	77

[表107]

表107 抽出された遺伝子が割り当てられたGO Term数
（≦1／1.5-foldで減少した遺伝子）

群		前後	Biological Process		Cellular Component		Molecular Function	
			(annotated genes)	GO Term数 (p<0.05)	(annotated genes)	GO Term数 (p<0.05)	(annotated genes)	GO Term数 (p<0.05)
All Genes			20,657		20,710		22,684	
解析2	A+B群	笑い	417	80	424	80	462	72
解析4	C+D群	笑い	196	42	189	26	207	61
解析5	A群	笑い	302	81	304	29	331	75
解析6	B群	笑い	517	141	534	15	580	61
解析7	C群	笑い	270	70	289	12	295	68
解析8	D群	笑い	502	98	513	26	551	82
解析9	A+C群	笑い	196	50	188	9	217	48
解析10	B+D群	笑い	1,451	159	1,433	50	1,579	140

[0491] DNAチップ上のプローブとGO termとの対応付けは、Agilent社の提供するプローブ情報とNCBI Entrez(http://www.ncbi.nlm.nih.gov/)のGeneID情報に基づいて行い、Gene IDとGOの対応付けはBiNGO (http://www.psb.ugent.be/cbd/papers/BiNGO/)を用いて行った。各GO termに割り当てられる遺伝子の出現頻度が、抽出遺伝子の方がDNAチップ搭載遺伝子より有意に大きいか、フィッ

シャーの正確確率検定により求め、有意水準p-Value<0.05で検定した。該検定で有意と判定されたGO termを抽出遺伝子群に特徴的なGOとした。p-Value<0.01で有意と判定されたGO termを表108から表123に示す。

[表108]

表108 糖尿病非罹病者群で笑いにより発現増加した遺伝子のGO解析結果

p-Value 0.01 以下
MF: Molecular Function
CC: Cellular Component
BP: Biological Process

解析2 UP N-3_N-4

分類	BP Category	Genes in Category	% of Genes in Category	Genes in List in Category	% of Genes in List in Category	p-Value
BP	GO:6412: protein biosynthesis	1146	5.548	118	24.84	3.60E-45
	GO:9059: macromolecule biosynthesis	1264	6.119	119	25.05	1.43E-41
	GO:44249: cellular biosynthesis	1852	8.965	127	26.74	2.30E-30
	GO:9058: biosynthesis	2087	10.1	132	27.79	3.53E-28
	GO:44267: cellular protein metabolism	5228	25.31	203	42.74	4.30E-17
	GO:19538: protein metabolism	5269	25.51	203	42.74	1.05E-16
	GO:44260: cellular macromolecule metabolism	5303	25.67	203	42.74	2.19E-16
	GO:43170: macromolecule metabolism	7147	34.6	240	50.53	4.12E-13
	GO:44237: cellular metabolism	11725	56.76	335	70.53	2.90E-10
	GO:44238: primary metabolism	11279	54.6	323	68	1.19E-09
	GO:8152: metabolism	12357	59.82	341	71.79	2.54E-08
	GO:50875: cellular physiological process	16318	79	411	86.53	1.25E-05
	GO:6448: regulation of translational elongation	4	0.0194	3	0.632	4.75E-05
	GO:45900: negative regulation of translational elongation	4	0.0194	3	0.632	4.75E-05
	GO:6413: translational initiation	111	0.537	9	1.895	0.00106
	GO:16478: negative regulation of translation	11	0.0533	3	0.632	0.00174
	GO:50854: regulation of antigen receptor mediated signaling pathway	12	0.0581	3	0.632	0.00228
	GO:42026: protein refolding	4	0.0194	2	0.421	0.00307
	GO:6119: oxidative phosphorylation	139	0.673	9	1.895	0.00491
	GO:50857: positive regulation of antigen receptor mediated signaling pathway	5	0.0242	2	0.421	0.00504
	GO:7582: physiological process	17839	86.36	429	90.32	0.00511
	GO:9987: cellular process	18835	91.18	448	94.32	0.00668
	GO:15701: bicarbonate transport	6	0.029	2	0.421	0.00744
	GO:6610: ribosomal protein import into	6	0.029	2	0.421	0.00744
MF	GO:3684: damaged DNA binding	58	0.256	5	1.992	0.000453
	GO:4840: ubiquitin conjugating enzyme activity	4	0.0176	2	0.797	0.000721
	GO:50051: leukotriene-B4 20-monooxygenase activity	4	0.0176	2	0.797	0.000721
	GO:3677: DNA binding	3253	14.34	54	21.51	0.00129
	GO:16563: transcriptional activator activity	474	2.089	13	5.179	0.00253
	GO:3702: RNA polymerase II transcription factor activity	366	1.613	11	4.382	0.00267
	GO:30528: transcription regulator activity	2089	9.209	37	14.74	0.00288
	GO:8717: D-alanyl-D-alanine endopeptidase activity	11	0.0485	2	0.797	0.00628
	GO:8639: small protein conjugating enzyme activity	12	0.0529	2	0.797	0.00748
	GO:5245: voltage-gated calcium channel	38	0.168	3	1.195	0.00849
CC	GO:16581: NuRD complex	12	0.0579	4	1.681	7.83E-06
	GO:1940: male pronucleus	4	0.0193	2	0.84	0.000777
	GO:5700: polytene chromosome	4	0.0193	2	0.84	0.000777
	GO:5701: polytene chromosome chromocenter	4	0.0193	2	0.84	0.000777
	GO:5654: nucleoplasm	573	2.767	16	6.723	0.00102
	GO:1939: female pronucleus	5	0.0241	2	0.84	0.00129
	GO:5721: centric heterochromatin	5	0.0241	2	0.84	0.00129
	GO:45120: pronucleus	6	0.029	2	0.84	0.00191

[0492]

解析2_UP_N-3_N-4

分類	BP Category	Genes in Category	% of Genes in Category	Genes in List in Category	% of Genes in List in Category	p-Value
CC	GO:5720: nuclear heterochromatin	22	0.106	3	1.261	0.00196
	GO:118: histone deacetylase complex	49	0.237	4	1.681	0.0024
	GO:792: heterochromatin	29	0.14	3	1.261	0.00439
	GO:5891: voltage-gated calcium channel complex	31	0.15	3	1.261	0.00531
	GO:10008: endosome membrane	10	0.0483	2	0.84	0.00557
	GO:228: nuclear chromosome	102	0.493	5	2.101	0.00649
	GO:5667: transcription factor complex	239	1.154	8	3.361	0.00658
	GO:790: nuclear chromatin	34	0.164	3	1.261	0.0069
	GO:5625: soluble fraction	304	1.468	9	3.782	0.0088

[表109]

表109 糖尿病非罹病者群で笑いにより発現減少した遺伝子のGO解析結果

p-Value 0.01 以下
MF: Molecular Function
CC: Cellular Component
BP: Biological Process

解析2_N-3_N-4_Down

分類	BP Category	Genes in Category	% of Genes in Category	Genes in List in Category	% of Genes in List in Category	p-Value
BP	GO:30309: poly-N-acetyllactosamine	3	0.0145	2	0.48	0.0012
	GO:8643: carbohydrate transport	82	0.397	7	1.679	0.00134
	GO:7015: actin filament organization	61	0.295	6	1.439	0.00142
	GO:15758: glucose transport	47	0.228	5	1.199	0.0025
	GO:15749: monosaccharide transport	49	0.237	5	1.199	0.00301
	GO:8645: hexose transport	49	0.237	5	1.199	0.00301
	GO:8104: protein localization	1151	5.572	37	8.873	0.00363
	GO:30036: actin cytoskeleton organization and biogenesis	312	1.51	14	3.357	0.00466
	GO:42157: lipoprotein metabolism	107	0.518	7	1.679	0.00602
	GO:6903: vesicle targeting	19	0.092	3	0.719	0.00622
	GO:6888: ER to Golgi transport	138	0.668	8	1.918	0.00702
	GO:15031: protein transport	1049	5.078	33	7.914	0.00802
	GO:6885: regulation of pH	40	0.194	4	0.959	0.00843
	GO:30029: actin filament-based process	338	1.636	14	3.357	0.00916
	GO:9799: determination of symmetry	22	0.107	3	0.719	0.00946
	GO:9855: determination of bilateral symmetry	22	0.107	3	0.719	0.00946
	GO:7368: determination of left/right symmetry	22	0.107	3	0.719	0.00946
	GO:9719: response to endogenous stimulus	481	2.329	18	5.07	0.00179
MF	GO:50576: 3-keto-steroid reductase activity	2	0.00882	2	0.433	0.000414
	GO:30601: aminopeptidase B activity	2	0.00882	2	0.433	0.000414
	GO:1727: lipid kinase activity	42	0.185	5	1.082	0.00157
	GO:35004: phosphoinositide 3-kinase activity	14	0.0617	3	0.649	0.00258
	GO:16303: phosphatidylinositol 3-kinase	14	0.0617	3	0.649	0.00258
	GO:5484: SNAP receptor activity	14	0.0617	3	0.649	0.00258
	GO:5048: signal sequence binding	32	0.141	4	0.866	0.00389
	GO:4792: thiosulfate sulfurtransferase activity	5	0.022	2	0.433	0.00397
	GO:4463: leukotriene-A4 hydrolase activity	5	0.022	2	0.433	0.00397
	GO:4301: epoxide hydrolase activity	5	0.022	2	0.433	0.00397
	GO:16813: hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds, in linear amidines	18	0.0793	3	0.649	0.00545
	GO:47485: protein N-terminus binding	18	0.0793	3	0.649	0.00545
	GO:46934: phosphatidylinositol-4,5-bisphosphate 3-kinase activity	6	0.0264	2	0.433	0.00588
	GO:4428: inositol or phosphatidylinositol kinase activity	58	0.256	5	1.082	0.00648
	GO:15291: porter activity	322	1.419	14	3.03	0.00662
	GO:15297: antiporter activity	83	0.366	6	1.299	0.00697
	GO:15290: electrochemical potential-driven transporter activity	327	1.441	14	3.03	0.00753
	GO:16783: sulfurtransferase activity	7	0.0309	2	0.433	0.00812
	GO:8133: collagenase activity	7	0.0309	2	0.433	0.00812
	GO:16803: ether hydrolase activity	7	0.0309	2	0.433	0.00812
	GO:4668: protein-arginine deiminase activity	7	0.0309	2	0.433	0.00812
CC	GO:42612: MHC class I protein complex	62	0.299	7	1.651	0.000267
	GO:42611: MHC protein complex	94	0.454	7	1.651	0.00319

[表110]

表110 糖尿病罹病者群で笑いにより発現増加した遺伝子のGO解析結果

p-Value 0.01 以下
MF: Molecular Function
CC: Cellular Component
BP: Biological Process

解析4 UP D-3_D-4

分類	BP Category	Genes in Category	% of Genes in Category	Genes in List in Category	% of Genes in List in Category	p-Value
BP	GO:6627: mitochondrial protein processing	1	0.00484	1	0.833	0.00581
	GO:15888: thiamin transport	1	0.00484	1	0.833	0.00581
	GO:6821: chloride transport	68	0.329	3	2.5	0.00728
MF	GO:4569: glycoprotein endo-alpha-1,2-mannosidase activity	3	0.0132	2	1.562	9.44E-05
	GO:4221: ubiquitin thiolesterase activity	105	0.463	5	3.906	0.000325
	GO:4843: ubiquitin-specific protease activity	109	0.48	5	3.906	0.000387
	GO:16790: thiolester hydrolase activity	131	0.577	5	3.906	0.000892
	GO:51184: cofactor transporter activity	13	0.0573	2	1.562	0.00237
	GO:16717: oxidoreductase activity, acting on paired donors, with oxidation of a pair of donors resulting in the reduction of molecular oxygen to two molecules of water	14	0.0617	2	1.562	0.00275
	GO:4559: alpha-mannosidase activity	15	0.0661	2	1.562	0.00316
	GO:5543: phospholipid binding	358	1.578	7	5.469	0.00426
	GO:4133: glycogen debranching enzyme	1	0.00441	1	0.781	0.00564
	GO:4134: 4-alpha-glucanotransferase activity	1	0.00441	1	0.781	0.00564
	GO:4135: amylo-alpha-1,6-glucosidase activity	1	0.00441	1	0.781	0.00564
	GO:8497: beta-galactosyl-N-acetylglucosaminylgalactosylglucosyl-ceramide beta-1,3-acetylglucosaminyltransferase activity	1	0.00441	1	0.781	0.00564
	GO:4243: mitochondrial intermediate peptidase activity	1	0.00441	1	0.781	0.00564
	GO:42392: sphingosine-1-phosphate phosphatase activity	1	0.00441	1	0.781	0.00564
	GO:156: two-component response regulator activity	1	0.00441	1	0.781	0.00564
	GO:15234: thiamin transporter activity	1	0.00441	1	0.781	0.00564
	GO:51185: coenzyme transporter activity	1	0.00441	1	0.781	0.00564
	GO:8521: acetyl-CoA transporter activity	1	0.00441	1	0.781	0.00564
	GO:5519: cytoskeletal regulatory protein	1	0.00441	1	0.781	0.00564
	GO:5344: oxygen transporter activity	25	0.11	2	1.562	0.00871
	GO:8233: peptidase activity	864	3.809	11	8.594	0.00983
CC	GO:16020: membrane	8391	40.52	65	52.85	0.00371
	GO:43033: isoamylase complex	1	0.00483	1	0.813	0.00594
	GO:5833: hemoglobin complex	20	0.0966	2	1.626	0.0062

[表111]

表111 糖尿病罹病者群で笑いにより発現減少した遺伝子のGO解析結果

p-Value 0.01 以下
MF: Molecular Function
CC: Cellular Component
BP: Biological Process

解析4 D-3_D-4 Down

分類	BP Category	Genes in Category	% of Genes in Category	Genes in List in Category	% of Genes in List in Category	p-Value
BP	GO:6412: protein biosynthesis	1146	5.548	33	16.84	1.06E-08
	GO:9059: macromolecule biosynthesis	1264	6.119	33	16.84	1.09E-07
	GO:44249: cellular biosynthesis	1852	8.965	36	18.37	2.62E-05
	GO:9058: biosynthesis	2087	10.1	37	18.88	0.000138
	GO:6413: translational initiation	111	0.537	6	3.061	0.00067
	GO:6917: induction of apoptosis	277	1.341	8	4.082	0.00507
	GO:12502: induction of programmed cell death	280	1.355	8	4.082	0.00541
	GO:44260: cellular macromolecule metabolism	5303	25.67	66	33.67	0.00741
	GO:44267: cellular protein metabolism	5228	25.31	65	33.16	0.00817
	GO:31581: hemidesmosome assembly	1	0.00484	1	0.51	0.00949
	GO:43037: translation	248	1.201	7	3.571	0.00964
	GO:19538: protein metabolism	5269	25.51	65	33.16	0.00976
MF	GO:3735: structural constituent of ribosome	462	2.037	29	14.01	2.85E-16
	GO:5198: structural molecule activity	1255	5.532	39	18.84	1.43E-11
	GO:3723: RNA binding	1203	5.303	30	14.49	5.49E-07
	GO:4617: phosphoglycerate dehydrogenase activity	1	0.00441	1	0.483	0.00912
	GO:4168: dolichol kinase activity	1	0.00441	1	0.483	0.00912
	GO:16: lactase activity	1	0.00441	1	0.483	0.00912
	GO:17042: glycosylceramidase activity	1	0.00441	1	0.483	0.00912
	GO:15245: fatty acid transporter activity	1	0.00441	1	0.483	0.00912
	GO:17025: TATA-binding protein binding	1	0.00441	1	0.483	0.00912
CC	GO:3677: DNA binding	3253	14.34	70	21.15	0.00046
	GO:8170: N-methyltransferase activity	72	0.317	6	1.813	0.000642
	GO:8276: protein methyltransferase activity	74	0.326	6	1.813	0.000742
	GO:3779: actin binding	464	2.045	16	4.834	0.0014
	GO:42054: histone methyltransferase activity	58	0.256	5	1.511	0.00156
	GO:8469: histone-arginine N-methyltransferase activity	5	0.022	2	0.604	0.00206
	GO:8092: cytoskeletal protein binding	673	2.967	20	6.042	0.00224
	GO:3676: nucleic acid binding	5048	22.25	96	29	0.00232
	GO:5840: ribosome	475	2.294	29	15.34	5.07E-16
	GO:5843: cytosolic small ribosomal subunit (sensu Eukaryota)	89	0.43	14	7.407	7.18E-14
	GO:16283: eukaryotic 48S initiation complex	89	0.43	14	7.407	7.18E-14
	GO:5830: cytosolic ribosome (sensu	212	1.024	19	10.05	8.68E-14
	GO:16282: eukaryotic 43S preinitiation	112	0.541	14	7.407	1.88E-12
	GO:15935: small ribosomal subunit	126	0.608	14	7.407	9.67E-12
	GO:30529: ribonucleoprotein complex	860	4.153	30	15.87	2.60E-10
	GO:5829: cytosol	789	3.81	28	14.81	7.53E-10
	GO:5737: cytoplasm	6440	31.1	87	46.03	1.09E-05
	GO:15934: large ribosomal subunit	157	0.758	8	4.233	9.96E-05
	GO:43232: intracellular non-membrane-bound organelle	2651	12.8	43	22.75	0.000107
	GO:43228: non-membrane-bound organelle	2651	12.8	43	22.75	0.000107
	GO:5842: cytosolic large ribosomal subunit (sensu Eukaryota)	118	0.57	5	2.646	0.00458

[表112]

表112 糖尿病非罹病・歯周病非罹病者群で笑いにより発現増加した遺伝子のGO解析結果

p-Value 0.01 以下
MF: Molecular Function
CC: Cellular Component
BP: Biological Process

解析5 UP NP1-3_NP1-4

分類	BP Category	Genes in Category	% of Genes in Category	Genes in List in Category	% of Genes in List in Category	p-Value
BP	GO:6837: serotonin transport	1	0.00484	1	1.053	0.0046
	GO:15888: thiamin transport	1	0.00484	1	1.053	0.0046
	GO:15671: oxygen transport	27	0.131	2	2.105	0.00682
	GO:15669: gas transport	30	0.145	2	2.105	0.00837
	GO:18200: peptidyl-glutamic acid modification	2	0.00968	1	1.053	0.00918
	GO:17187: peptidyl-glutamic acid	2	0.00968	1	1.053	0.00918
	GO:18214: protein amino acid carboxylation	2	0.00968	1	1.053	0.00918
	GO:6667: sphinganine metabolism	2	0.00968	1	1.053	0.00918
	GO:6668: sphinganine-1-phosphate	2	0.00968	1	1.053	0.00918
MF	GO:46914: transition metal ion binding	4006	17.66	29	29	0.00352
	GO:42392: sphingosine-1-phosphate phosphatase activity	1	0.00441	1	1	0.00441
	GO:15222: serotonin transporter activity	1	0.00441	1	1	0.00441
	GO:5335: serotonin:sodium symporter activity	1	0.00441	1	1	0.00441
	GO:15234: thiamin transporter activity	1	0.00441	1	1	0.00441
	GO:5344: oxygen transporter activity	25	0.11	2	2	0.0054
	GO:5489: electron transporter activity	266	1.173	5	5	0.00651
	GO:5386: carrier activity	775	3.416	9	9	0.00724
	GO:15399: primary active transporter activity	285	1.256	5	5	0.00863
	GO:248: C-5 sterol desaturase activity	2	0.00882	1	1	0.0088
	GO:4164: diphthine synthase activity	2	0.00882	1	1	0.0088
	GO:8488: gamma-glutamyl carboxylase activity	2	0.00882	1	1	0.0088
CC	GO:5833: hemoglobin complex	20	0.0966	2	2.198	0.00345
	GO:31090: organelle membrane	991	4.785	11	12.09	0.00407
	GO:5795: Golgi stack	74	0.357	3	3.297	0.00425
	GO:43231: intracellular membrane-bound organelle	9668	46.68	55	60.44	0.00569
	GO:43227: membrane-bound organelle	9668	46.68	55	60.44	0.00569
	GO:5789: endoplasmic reticulum membrane	182	0.879	4	4.396	0.00852

[表113]

表113 糖尿病非罹病・歯周病非罹病者群で笑いにより発現減少した遺伝子のGO解析結果

p-Value 0.01 以下
MF: Molecular Function
CC: Cellular Component
BP: Biological Process

解析5 Down NP1-3_NP1-4

分類	BP Category	Genes in Category	% of Genes in Category	Genes in List in Category	% of Genes in List in Category	p-Value
BP	GO:6996: organelle organization and biogenesis	1675	8.109	41	13.58	0.000782
	GO:6325: establishment and/or maintenance of chromatin architecture	503	2.435	17	5.629	0.00125
	GO:6323: DNA packaging	511	2.474	17	5.629	0.00148
	GO:7001: chromosome organization and biogenesis (sensu Eukaryota)	563	2.725	18	5.96	0.00169
	GO:18216: peptidyl-arginine methylation	5	0.0242	2	0.662	0.00207
	GO:18195: peptidyl-arginine modification	5	0.0242	2	0.662	0.00207
	GO:48268: clathrin cage assembly	5	0.0242	2	0.662	0.00207
	GO:7030: Golgi organization and biogenesis	19	0.092	3	0.993	0.00252
	GO:16043: cell organization and biogenesis	2946	14.26	61	20.2	0.00279
	GO:8213: protein amino acid alkylation	41	0.198	4	1.325	0.00296
	GO:6479: protein amino acid methylation	41	0.198	4	1.325	0.00296
	GO:16568: chromatin modification	324	1.568	12	3.974	0.00307
	GO:51276: chromosome organization and biogenesis	601	2.909	18	5.96	0.00339
	GO:16570: histone modification	77	0.373	5	1.656	0.00541
	GO:16569: covalent chromatin modification	78	0.378	5	1.656	0.00572
	GO:46209: nitric oxide metabolism	27	0.131	3	0.993	0.00698
	GO:6809: nitric oxide biosynthesis	27	0.131	3	0.993	0.00698
	GO:31056: regulation of histone modification	9	0.0436	2	0.662	0.00717
	GO:6337: nucleosome disassembly	10	0.0484	2	0.662	0.00887
	GO:31498: chromatin disassembly	10	0.0484	2	0.662	0.00887
MF	GO:50576: 3-keto-steroid reductase activity	2	0.00882	2	0.604	0.000212
	GO:3677: DNA binding	3253	14.34	70	21.15	0.00046
	GO:8170: N-methyltransferase activity	72	0.317	6	1.813	0.000642
	GO:8276: protein methyltransferase activity	74	0.326	6	1.813	0.000742
	GO:3779: actin binding	464	2.045	16	4.834	0.0014
	GO:42054: histone methyltransferase activity	58	0.256	5	1.511	0.00156
	GO:8469: histone-arginine N-methyltransferase activity	5	0.022	2	0.604	0.00206
	GO:8092: cytoskeletal protein binding	673	2.967	20	6.042	0.00224
	GO:3676: nucleic acid binding	5048	22.25	96	29	0.00232
	GO:4803: transposase activity	6	0.0264	2	0.604	0.00306
	GO:16273: arginine N-methyltransferase	6	0.0264	2	0.604	0.00306
	GO:16274: protein-arginine N-methyltransferase activity	6	0.0264	2	0.604	0.00306
	GO:8270: zinc ion binding	3334	14.7	67	20.24	0.00359
	GO:5488: binding	17386	76.64	274	82.78	0.00381
	GO:42393: histone binding	22	0.097	3	0.906	0.00386
	GO:46914: transition metal ion binding	4006	17.66	77	23.26	0.00549
	GO:30911: TPR domain binding	8	0.0353	2	0.604	0.00561
	GO:3704: specific RNA polymerase II transcription factor activity	56	0.247	4	1.208	0.00901
	GO:8168: methyltransferase activity	244	1.076	9	2.719	0.00993
CC	GO:1940: male pronucleus	4	0.0193	2	0.658	0.00126
	GO:5700: polytene chromosome	4	0.0193	2	0.658	0.00126
	GO:5701: polytene chromosome chromocenter	4	0.0193	2	0.658	0.00126
	GO:1939: female pronucleus	5	0.0241	2	0.658	0.00209
	GO:5721: centric heterochromatin	5	0.0241	2	0.658	0.00209
	GO:45120: pronucleus	6	0.029	2	0.658	0.0031
	GO:228: nuclear chromosome	102	0.493	6	1.974	0.00395
	GO:5634: nucleus	6618	31.96	119	39.14	0.00455

[表114]

表114 糖尿病非罹病・歯周病罹病者群で笑いにより発現増加した遺伝子のGO解析結果

p-Value 0.01 以下
MF: Molecular Function
CC: Cellular Component
BP: Biological Process

解析6 UP NP2-3_NP2-4

分類	BP Category	Genes in Category	% of Genes in Category	Genes in List in Category	% of Genes in List in Category	p-Value
BP	GO:6412: protein biosynthesis	1146	5.548	147	28.99	5.08E-66
	GO:9059: macromolecule biosynthesis	1264	6.119	150	29.59	7.50E-63
	GO:44249: cellular biosynthesis	1852	8.965	162	31.95	1.13E-49
	GO:9058: biosynthesis	2087	10.1	166	32.74	2.03E-45
	GO:44267: cellular protein metabolism	5228	25.31	239	47.14	5.42E-27
	GO:44260: cellular macromolecule metabolism	5303	25.67	240	47.34	1.78E-26
	GO:19538: protein metabolism	5269	25.51	239	47.14	1.79E-26
	GO:43170: macromolecule metabolism	7147	34.6	279	55.03	1.38E-21
	GO:44237: cellular metabolism	11725	56.76	372	73.37	3.29E-15
	GO:44238: primary metabolism	11279	54.6	356	70.22	2.36E-13
	GO:8152: metabolism	12357	59.82	379	74.75	6.30E-13
	GO:50875: cellular physiological process	16318	79	449	88.56	7.77E-09
	GO:43037: translation	248	1.201	22	4.339	2.30E-07
	GO:6448: regulation of translational elongation	4	0.0194	4	0.789	3.59E-07
	GO:45900: negative regulation of translational elongation	4	0.0194	4	0.789	3.59E-07
	GO:6414: translational elongation	52	0.252	10	1.972	4.55E-07
	GO:7582: physiological process	17839	86.36	470	92.7	4.04E-06
	GO:6413: translational initiation	111	0.537	11	2.17	9.07E-05
	GO:16478: negative regulation of translation	11	0.0533	4	0.789	0.000103
	GO:51103: DNA ligation during DNA repair	5	0.0242	3	0.592	0.000142
	GO:6288: base-excision repair, DNA ligation	5	0.0242	3	0.592	0.000142
	GO:48134: germ-line cyst formation	2	0.00968	2	0.394	0.000601
	GO:48136: male germ-line cyst formation	2	0.00968	2	0.394	0.000601
	GO:48137: spermatocyte division	2	0.00968	2	0.394	0.000601
	GO:6445: regulation of translation	108	0.523	9	1.775	0.00137
	GO:6266: DNA ligation	10	0.0484	3	0.592	0.00155
	GO:42254: ribosome biogenesis and assembly	133	0.644	10	1.972	0.00166
	GO:6754: ATP biosynthesis	71	0.344	7	1.381	0.00177
	GO:6753: nucleoside phosphate metabolism	71	0.344	7	1.381	0.00177
	GO:1919: regulation of receptor recycling	3	0.0145	2	0.394	0.00177
	GO:6511: ubiquitin-dependent protein	259	1.254	15	2.959	0.00195
	GO:19941: modification-dependent protein catabolism	260	1.259	15	2.959	0.00202
	GO:6119: oxidative phosphorylation	139	0.673	10	1.972	0.0023
	GO:9987: cellular process	18835	91.18	479	94.48	0.00333
	GO:17055: negative regulation of transcriptional preinitiation complex formation	4	0.0194	2	0.394	0.00349
	GO:46034: ATP metabolism	81	0.392	7	1.381	0.00375
	GO:6268: DNA unwinding during replication	14	0.0678	3	0.592	0.00437
	GO:6752: group transfer coenzyme metabolism	107	0.518	8	1.578	0.00487
	GO:45047: protein targeting to ER	29	0.14	4	0.789	0.00523
	GO:6916: anti-apoptosis	262	1.268	14	2.761	0.00553
	GO:35269: protein amino acid O-linked mannosylation	5	0.0242	2	0.394	0.00572
	GO:18103: protein amino acid C-linked glycosylation	5	0.0242	2	0.394	0.00572
	GO:18317: protein amino acid C-linked glycosylation via tryptophan	5	0.0242	2	0.394	0.00572

[0493]

解析6 UP NP2-3_NP2-4

分類	BP Category	Genes in Category	% of Genes in Category	Genes in List in Category	% of Genes in List in Category	p-Value
BP	GO:18406: protein amino acid C-linked glycosylation via 2'-alpha-mannosyl-L-tryptophan	5	0.0242	2	0.394	0.00572
	GO:35268: protein amino acid mannosylation	5	0.0242	2	0.394	0.00572
	GO:18211: peptidyl-tryptophan modification	5	0.0242	2	0.394	0.00572
	GO:1881: receptor recycling	5	0.0242	2	0.394	0.00572
	GO:15992: proton transport	110	0.533	8	1.578	0.00575
	GO:6818: hydrogen transport	112	0.542	8	1.578	0.0064
	GO:9145: purine nucleoside triphosphate biosynthesis	90	0.436	7	1.381	0.00667
	GO:9206: purine ribonucleoside triphosphate biosynthesis	90	0.436	7	1.381	0.00667
	GO:6396: RNA processing	690	3.34	28	5.523	0.00675
	GO:9201: ribonucleoside triphosphate biosynthesis	91	0.441	7	1.381	0.00708
	GO:7028: cytoplasm organization and	163	0.789	10	1.972	0.0071
	GO:9142: nucleoside triphosphate biosynthesis	93	0.45	7	1.381	0.00795
	GO:7379: segment specification	6	0.029	2	0.394	0.00845
	GO:6610: ribosomal protein import into	6	0.029	2	0.394	0.00845
	GO:16070: RNA metabolism	834	4.037	32	6.312	0.00874
	GO:46489: phosphoinositide biosynthesis	52	0.252	5	0.986	0.00879
	GO:245: spliceosome assembly	52	0.252	5	0.986	0.00879
	GO:6886: intracellular protein transport	614	2.972	25	4.931	0.00976
MF	GO:3735: structural constituent of ribosome	462	2.037	125	22.32	4.02E-95
	GO:5198: structural molecule activity	1255	5.532	132	23.57	1.08E-47
	GO:3723: RNA binding	1203	5.303	121	21.61	1.81E-41
	GO:3676: nucleic acid binding	5048	22.25	196	35	2.18E-12
	GO:43021: ribonucleoprotein binding	25	0.11	7	1.25	1.76E-06
	GO:15077: monovalent inorganic cation transporter activity	236	1.04	20	3.571	1.85E-06
	GO:15078: hydrogen ion transporter activity	218	0.961	19	3.393	2.21E-06
	GO:5047: signal recognition particle binding	8	0.0353	4	0.714	2.38E-05
	GO:8312: 7S RNA binding	4	0.0176	3	0.536	5.88E-05
	GO:15399: primary active transporter activity	285	1.256	19	3.393	9.49E-05
	GO:16656: monodehydroascorbate reductase (NADH) activity	2	0.00882	2	0.357	0.000608
	GO:8097: 5S rRNA binding	2	0.00882	2	0.357	0.000608
	GO:19843: rRNA binding	32	0.141	5	0.893	0.00104
	GO:43498: cell surface binding	3	0.0132	2	0.357	0.0018
	GO:43499: eukaryotic cell surface binding	3	0.0132	2	0.357	0.0018
	GO:19834: phospholipase A2 inhibitor activity	3	0.0132	2	0.357	0.0018
	GO:4298: threonine endopeptidase activity	22	0.097	4	0.714	0.00189
	GO:43022: ribosome binding	12	0.0529	3	0.536	0.00279
	GO:17070: U6 snRNA binding	4	0.0176	2	0.357	0.00353
	GO:15002: heme-copper terminal oxidase activity	42	0.185	5	0.893	0.0036
	GO:4129: cytochrome-c oxidase activity	42	0.185	5	0.893	0.0036
	GO:16675: oxidoreductase activity, acting on heme group of donors	42	0.185	5	0.893	0.0036
	GO:16676: oxidoreductase activity, acting on heme group of donors, oxygen as acceptor	42	0.185	5	0.893	0.0036
	GO:15036: disulfide oxidoreductase activity	29	0.128	4	0.714	0.00535
	GO:4765: shikimate kinase activity	5	0.022	2	0.357	0.00579
	GO:5386: carrier activity	775	3.416	31	5.536	0.00607

[0494]

解析6 UP NP2-3_NP2-4

分類	BP Category	Genes in Category	% of Genes in Category	Genes in List in Category	% of Genes in List in Category	p-Value
MF	GO:16655: oxidoreductase activity, acting on NADH or NADPH, quinone or similar compound as acceptor	72	0.317	6	1.071	0.0087
	GO:8301: DNA bending activity	18	0.0793	3	0.536	0.00926
	GO:1608: nucleotide receptor activity, G-protein coupled	34	0.15	4	0.714	0.00948
	GO:45028: purinergic nucleotide receptor activity, G-protein coupled	34	0.15	4	0.714	0.00948
	GO:16502: nucleotide receptor activity	34	0.15	4	0.714	0.00948
	GO:1614: purinergic nucleotide receptor	34	0.15	4	0.714	0.00948
CC	GO:5840: ribosome	475	2.294	125	24.27	1.21E-93
	GO:30529: ribonucleoprotein complex	860	4.153	150	29.13	8.25E-86
	GO:5830: cytosolic ribosome (sensu	212	1.024	77	14.95	5.80E-69
	GO:43234: protein complex	3428	16.55	233	45.24	6.34E-54
	GO:15934: large ribosomal subunit	157	0.758	53	10.29	1.64E-45
	GO:5829: cytosol	789	3.81	96	18.64	1.81E-39
	GO:5842: cytosolic large ribosomal subunit (sensu Eukaryota)	118	0.57	43	8.35	1.01E-38
	GO:15935: small ribosomal subunit	126	0.608	40	7.767	2.50E-33
	GO:5843: cytosolic small ribosomal subunit (sensu Eukaryota)	89	0.43	35	6.796	4.47E-33
	GO:16283: eukaryotic 48S initiation complex	89	0.43	35	6.796	4.47E-33
	GO:16282: eukaryotic 43S preinitiation	112	0.541	38	7.379	5.84E-33
	GO:43232: intracellular non-membrane-bound organelle	2651	12.8	164	31.84	2.85E-30
	GO:43228: non-membrane-bound organelle	2651	12.8	164	31.84	2.85E-30
	GO:5737: cytoplasm	6440	31.1	280	54.37	1.41E-28
	GO:5622: intracellular	13693	66.12	427	82.91	5.21E-18
	GO:43229: intracellular organelle	11143	53.8	366	71.07	3.69E-16
	GO:43226: organelle	11143	53.8	366	71.07	3.69E-16
	GO:45263: proton-transporting ATP synthase complex, coupling factor F(o)	14	0.0676	7	1.359	1.67E-08
	GO:48500: signal recognition particle	23	0.111	7	1.359	9.80E-07
	GO:5786: signal recognition particle (sensu Eukaryota)	23	0.111	7	1.359	9.80E-07
	GO:45259: proton-transporting ATP synthase complex	23	0.111	7	1.359	9.80E-07
	GO:5785: signal recognition particle receptor complex	8	0.0386	4	0.777	2.44E-05
	GO:5761: mitochondrial ribosome	68	0.328	9	1.748	4.54E-05
	GO:313: organellar ribosome	68	0.328	9	1.748	4.54E-05
	GO:5623: cell	19120	92.32	497	96.5	5.38E-05
	GO:502: proteasome complex (sensu	70	0.338	9	1.748	5.73E-05
	GO:5739: mitochondrion	1235	5.963	53	10.29	7.73E-05
	GO:45298: tubulin	5	0.0241	3	0.583	0.000147
	GO:5730: nucleolus	222	1.072	15	2.913	0.000468
	GO:5771: multivesicular body	7	0.0338	3	0.583	0.000497
	GO:30867: rough endoplasmic reticulum membrane	16	0.0773	4	0.777	0.000542
	GO:31090: organelle membrane	991	4.785	42	8.155	0.00056
	GO:5789: endoplasmic reticulum membrane	182	0.879	13	2.524	0.000655
	GO:42175: nuclear envelope-endoplasmic reticulum network	193	0.932	13	2.524	0.00113
	GO:5732: small nucleolar ribonucleoprotein complex	20	0.0966	4	0.777	0.00133
	GO:5763: mitochondrial small ribosomal	20	0.0966	4	0.777	0.00133

[0495]

解析6 UP NP2-3_NP2-4

分類	BP Category	Genes in Category	% of Genes in Category	Genes in List in Category	% of Genes in List in Category	p-Value
CC	GO:314: organellar small ribosomal subunit	20	0.0966	4	0.777	0.00133
	GO:5759: mitochondrial matrix	130	0.628	10	1.942	0.00154
	GO:5791: rough endoplasmic reticulum	21	0.101	4	0.777	0.00162
	GO:8180: signalosome complex	11	0.0531	3	0.583	0.00217
	GO:5839: proteasome core complex (sensu Eukaryota)	23	0.111	4	0.777	0.0023
	GO:16272: prefoldin complex	13	0.0628	3	0.583	0.00363
	GO:16469: proton-transporting two-sector ATPase complex	60	0.29	6	1.165	0.00369
	GO:5740: mitochondrial membrane	400	1.931	19	3.689	0.00567
	GO:31501: mannosyltransferase complex	5	0.0241	2	0.388	0.00587
	GO:5743: mitochondrial inner membrane	328	1.584	16	3.107	0.00836
	GO:5746: mitochondrial electron transport	94	0.454	7	1.359	0.00901

[表115]

表115 糖尿病非罹病・歯周病罹病者群で笑いにより発現減少した遺伝子のGO解析結果

p-Value 0.01 以下
MF: Molecular Function
CC: Cellular Component
BP: Biological Process

解析6 Down NP2-3_NP2-4

分類	BP Category	Genes in Category	% of Genes in Category	Genes in List in Category	% of Genes in List in Category	p-Value
BP	GO:31293: membrane protein intracellular domain proteolysis	2	0.00968	2	0.387	0.000625
	GO:30029: actin filament-based process	338	1.636	19	3.675	0.000937
	GO:6509: membrane protein ectodomain proteolysis	19	0.092	4	0.774	0.00111
	GO:9613: response to pest, pathogen or	667	3.229	30	5.803	0.00153
	GO:43207: response to external biotic stimulus	729	3.529	32	6.19	0.0016
	GO:7220: Notch receptor processing	11	0.0533	3	0.58	0.00221
	GO:30036: actin cytoskeleton organization and biogenesis	312	1.51	17	3.288	0.00236
	GO:19221: cytokine and chemokine mediated signaling pathway	58	0.281	6	1.161	0.00321
	GO:7259: JAK-STAT cascade	59	0.286	6	1.161	0.0035
	GO:42159: lipoprotein catabolism	4	0.0194	2	0.387	0.00363
	GO:45192: low-density lipoprotein catabolism	4	0.0194	2	0.387	0.00363
	GO:6869: lipid transport	148	0.716	10	1.934	0.00416
	GO:19318: hexose metabolism	223	1.08	13	2.515	0.00422
	GO:8643: carbohydrate transport	82	0.397	7	1.354	0.00446
	GO:5996: monosaccharide metabolism	228	1.104	13	2.515	0.00508
	GO:8286: insulin receptor signaling pathway	65	0.315	6	1.161	0.00566
	GO:45408: regulation of interleukin-6 biosynthesis	15	0.0726	3	0.58	0.00567
	GO:30157: pancreatic juice secretion	5	0.0242	2	0.387	0.00595
	GO:6916: anti-apoptosis	262	1.268	14	2.708	0.00652
	GO:42987: amyloid precursor protein	16	0.0775	3	0.58	0.00685
	GO:6643: membrane lipid metabolism	266	1.288	14	2.708	0.00742
	GO:42226: interleukin-6 biosynthesis	17	0.0823	3	0.58	0.00816
	GO:51248: negative regulation of protein metabolism	115	0.557	8	1.547	0.00836
	GO:9607: response to biotic stimulus	1414	6.845	50	9.671	0.00858
	GO:46627: negative regulation of insulin receptor signaling pathway	6	0.029	2	0.387	0.00877
	GO:6468: protein amino acid phosphorylation	949	4.594	36	6.963	0.00893
	GO:7586: digestion	95	0.46	7	1.354	0.00984
MF	GO:16772: transferase activity, transferring phosphorus-containing groups	1500	6.612	57	9.828	0.00181
	GO:4098: cerebroside-sulfatase activity	3	0.0132	2	0.345	0.00192
	GO:4557: alpha-galactosidase activity	3	0.0132	2	0.345	0.00192
	GO:3779: actin binding	464	2.045	23	3.966	0.00208
	GO:16301: kinase activity	1299	5.726	50	8.621	0.00265
	GO:4428: inositol or phosphatidylinositol kinase activity	58	0.256	6	1.034	0.00357
	GO:16511: endothelin-converting enzyme activity	4	0.0176	2	0.345	0.00378
	GO:4336: galactosylceramidase activity	4	0.0176	2	0.345	0.00378
	GO:1727: lipid kinase activity	42	0.185	5	0.862	0.00418
	GO:8092: cytoskeletal protein binding	673	2.967	29	5	0.00461
	GO:35004: phosphoinositide 3-kinase activity	14	0.0617	3	0.517	0.0049
	GO:16303: phosphatidylinositol 3-kinase	14	0.0617	3	0.517	0.0049

[0496]

解析6 Down NP2-3_NP2-4

分類	BP Category	Genes in Category	% of Genes in Category	Genes in List in Category	% of Genes in List in Category	p-Value
MF	GO:5484: SNAP receptor activity	14	0.0617	3	0.517	0.0049
	GO:16811: hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds, in	84	0.37	7	1.207	0.00572
	GO:4348: glucosylceramidase activity	5	0.022	2	0.345	0.0062
	GO:16773: phosphotransferase activity, alcohol group as acceptor	1103	4.862	42	7.241	0.00679
	GO:46934: phosphatidylinositol-4,5-bisphosphate 3-kinase activity	6	0.0264	2	0.345	0.00914
	GO:16810: hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds	164	0.723	10	1.724	0.00973
CC	GO:5623: cell	19120	92.32	515	96.44	5.20E-05
	GO:16020: membrane	8391	40.52	246	46.07	0.00481

[表116]

表116 糖尿病罹病・歯周病非罹病者群で笑いにより発現増加した遺伝子のGO解析結果

p-Value 0.01 以下
MF: Molecular Function
CC: Cellular Component
BP: Biological Process

解析7 UP DP1-3_DP1-4

分類	BP Category	Genes in Category	% of Genes in Category	Genes in List in Category	% of Genes in List in Category	p-Value
BP	GO:15671: oxygen transport	27	0.131	3	3.226	0.000239
	GO:15669: gas transport	30	0.145	3	3.226	0.000328
	GO:9086: methionine biosynthesis	13	0.0629	2	2.151	0.00151
	GO:6470: protein amino acid	211	1.021	5	5.376	0.00266
	GO:6555: methionine metabolism	18	0.0871	2	2.151	0.00293
	GO:9067: aspartate family amino acid biosynthesis	18	0.0871	2	2.151	0.00293
	GO:97: sulfur amino acid biosynthesis	22	0.107	2	2.151	0.00437
	GO:16311: dephosphorylation	237	1.147	5	5.376	0.00437
	GO:48178: negative regulation of hepatocyte growth factor biosynthesis	1	0.00484	1	1.075	0.0045
	GO:48176: regulation of hepatocyte growth factor biosynthesis	1	0.00484	1	1.075	0.0045
	GO:48175: hepatocyte growth factor biosynthesis	1	0.00484	1	1.075	0.0045
	GO:6591: ornithine metabolism	2	0.00968	1	1.075	0.00898
	GO:19794: nonprotein amino acid metabolism	2	0.00968	1	1.075	0.00898
	GO:6667: sphinganine metabolism	2	0.00968	1	1.075	0.00898
	GO:6668: sphinganine-1-phosphate	2	0.00968	1	1.075	0.00898
	GO:42997: negative regulation of Golgi to plasma membrane protein transport	2	0.00968	1	1.075	0.00898
	GO:43002: negative regulation of Golgi to plasma membrane CFTR protein transport	2	0.00968	1	1.075	0.00898
	GO:43004: cytoplasmic sequestering of CFTR protein	2	0.00968	1	1.075	0.00898
	GO:42996: regulation of Golgi to plasma membrane protein transport	2	0.00968	1	1.075	0.00898
	GO:42999: regulation of Golgi to plasma membrane CFTR protein transport	2	0.00968	1	1.075	0.00898
	GO:43000: Golgi to plasma membrane CFTR protein transport	2	0.00968	1	1.075	0.00898
	GO:9066: aspartate family amino acid	32	0.155	2	2.151	0.00911
MF	GO:4912: interleukin-3 receptor activity	3	0.0132	2	2.083	5.30E-05
	GO:19978: interleukin-3 binding	3	0.0132	2	2.083	5.30E-05
	GO:5344: oxygen transporter activity	25	0.11	3	3.125	0.000158
	GO:16791: phosphoric monoester hydrolase activity	375	1.653	8	8.333	0.000194
	GO:5001: transmembrane receptor protein tyrosine phosphatase activity	31	0.137	3	3.125	0.000303
	GO:19198: transmembrane receptor protein phosphatase activity	31	0.137	3	3.125	0.000303
	GO:46906: tetrapyrrole binding	158	0.696	5	5.208	0.000565
	GO:20037: heme binding	158	0.696	5	5.208	0.000565
	GO:16788: hydrolase activity, acting on ester bonds	975	4.298	12	12.5	0.000836
	GO:4221: ubiquitin thiolesterase activity	105	0.463	4	4.167	0.00104
	GO:4843: ubiquitin-specific protease activity	109	0.48	4	4.167	0.00119
	GO:42578: phosphoric ester hydrolase activity	495	2.182	8	8.333	0.0012
	GO:19825: oxygen binding	56	0.247	3	3.125	0.00173

[0497]

解析7 UP DP1-3_DP1-4

分類	BP Category	Genes in Category	% of Genes in Category	Genes in List in Category	% of Genes in List in Category	p-Value
MF	GO:16790: thiolester hydrolase activity	131	0.577	4	4.167	0.00234
	GO:4133: glycogen debranching enzyme	1	0.00441	1	1.042	0.00423
	GO:4134: 4-alpha-glucanotransferase activity	1	0.00441	1	1.042	0.00423
	GO:4135: amylo-alpha-1,6-glucosidase activity	1	0.00441	1	1.042	0.00423
	GO:4587: ornithine-oxo-acid transaminase activity	1	0.00441	1	1.042	0.00423
	GO:4484: mRNA guanylyltransferase activity	1	0.00441	1	1.042	0.00423
	GO:4261: cathepsin G activity	1	0.00441	1	1.042	0.00423
	GO:4651: polynucleotide 5'-phosphatase	1	0.00441	1	1.042	0.00423
	GO:42392: sphingosine-1-phosphate phosphatase activity	1	0.00441	1	1.042	0.00423
	GO:4398: histidine decarboxylase activity	1	0.00441	1	1.042	0.00423
	GO:46789: host cell surface receptor binding	1	0.00441	1	1.042	0.00423
	GO:51185: coenzyme transporter activity	1	0.00441	1	1.042	0.00423
	GO:8521: acetyl-CoA transporter activity	1	0.00441	1	1.042	0.00423
	GO:46812: host cell surface binding	1	0.00441	1	1.042	0.00423
	GO:8321: Ral guanyl-nucleotide exchange factor activity	1	0.00441	1	1.042	0.00423
	GO:4721: phosphoprotein phosphatase activity	261	1.151	5	5.208	0.00507
	GO:5506: iron ion binding	413	1.821	6	6.25	0.00823
	GO:8705: methionine synthase activity	2	0.00882	1	1.042	0.00845
	GO:42084: 5-methyltetrahydrofolate-dependent methyltransferase activity	2	0.00882	1	1.042	0.00845
	GO:4156: dihydropteroate synthase activity	2	0.00882	1	1.042	0.00845
	GO:47493: ceramide cholinephosphotransferase activity	2	0.00882	1	1.042	0.00845
	GO:19204: nucleotide phosphatase activity	2	0.00882	1	1.042	0.00845
	GO:50430: syntaxin-6 binding	2	0.00882	1	1.042	0.00845
	GO:42980: cystic fibrosis transmembrane conductance regulator binding	2	0.00882	1	1.042	0.00845
CC	GO:5833: hemoglobin complex	20	0.0966	3	3.226	9.46E-05
	GO:43033: isoamylase complex	1	0.00483	1	1.075	0.00449
	GO:46821: extrachromosomal DNA	1	0.00483	1	1.075	0.00449
	GO:5727: extrachromosomal circular DNA	1	0.00483	1	1.075	0.00449

[表117]

表117 糖尿病罹病・歯周病非罹病者群で笑いにより発現減少した遺伝子のGO解析結果

p-Value 0.01 以下
MF: Molecular Function
CC: Cellular Component
BP: Biological Process

解析7 Down DP1-3_DP1-4

分類	BP Category	Genes in Category	% of Genes in Category	Genes in List in Category	% of Genes in List in Category	p-Value
BP	GO:17000: antibiotic biosynthesis	7	0.0339	2	0.741	0.00342
	GO:16999: antibiotic metabolism	8	0.0387	2	0.741	0.00452
	GO:6526: arginine biosynthesis	9	0.0436	2	0.741	0.00577
	GO:19627: urea metabolism	10	0.0484	2	0.741	0.00715
	GO:50: urea cycle	10	0.0484	2	0.741	0.00715
	GO:30098: lymphocyte differentiation	92	0.445	5	1.852	0.00718
	GO:17144: drug metabolism	11	0.0533	2	0.741	0.00866
MF	GO:3823: antigen binding	81	0.357	8	2.712	1.05E-05
	GO:3677: DNA binding	3253	14.34	60	20.34	0.00291
	GO:8451: X-Pro aminopeptidase activity	7	0.0309	2	0.678	0.00339
	GO:3704: specific RNA polymerase II transcription factor activity	56	0.247	4	1.356	0.00605
	GO:8235: metalloexopeptidase activity	96	0.423	5	1.695	0.0084
	GO:3702: RNA polymerase II transcription factor activity	366	1.613	11	3.729	0.00879
CC	GO:42612: MHC class I protein complex	62	0.299	9	3.114	1.88E-07
	GO:42611: MHC protein complex	94	0.454	9	3.114	6.68E-06
	GO:1772: immunological synapse	118	0.57	9	3.114	4.20E-05

[表118]

表118 糖尿病罹病・歯周病罹病者群で笑いにより発現増加した遺伝子のGO解析結果

p-Value 0.01 以下
MF: Molecular Function
CC: Cellular Component
BP: Biological Process

解析8_UP_DP2-3_DP2-4

分類	BP Category	Genes in Category	% of Genes in Category	Genes in List in Category	% of Genes in List in Category	p-Value
BP	GO:19371: cyclooxygenase pathway	2	0.00968	2	0.593	0.000265
	GO:15031: protein transport	1049	5.078	32	9.496	0.000524
	GO:45184: establishment of protein	1102	5.335	33	9.792	0.00059
	GO:8104: protein localization	1151	5.572	34	10.09	0.000619
	GO:51607: defense response to virus	12	0.0581	3	0.89	0.000849
	GO:6448: regulation of translational elongation	4	0.0194	2	0.593	0.00156
	GO:45900: negative regulation of translational elongation	4	0.0194	2	0.593	0.00156
	GO:43496: regulation of protein homodimerization	4	0.0194	2	0.593	0.00156
	GO:43497: regulation of protein heterodimerization	4	0.0194	2	0.593	0.00156
	GO:45356: positive regulation of interferon-alpha biosynthesis	5	0.0242	2	0.593	0.00257
	GO:45359: positive regulation of interferon-beta biosynthesis	5	0.0242	2	0.593	0.00257
	GO:45357: regulation of interferon-beta biosynthesis	5	0.0242	2	0.593	0.00257
	GO:45350: interferon-beta biosynthesis	5	0.0242	2	0.593	0.00257
	GO:6605: protein targeting	364	1.762	14	4.154	0.00277
	GO:1836: release of cytochrome c from mitochondria	18	0.0871	3	0.89	0.00293
	GO:45354: regulation of interferon-alpha biosynthesis	6	0.029	2	0.593	0.00381
	GO:45349: interferon-alpha biosynthesis	6	0.029	2	0.593	0.00381
	GO:16050: vesicle organization and biogenesis	6	0.029	2	0.593	0.00381
	GO:6352: transcription initiation	94	0.455	6	1.78	0.00441
	GO:19722: calcium-mediated signaling	43	0.208	4	1.187	0.0052
	GO:42640: anagen	7	0.0339	2	0.593	0.00528
	GO:45416: positive regulation of interleukin-8 biosynthesis	7	0.0339	2	0.593	0.00528
	GO:46902: regulation of mitochondrial membrane permeability	7	0.0339	2	0.593	0.00528
	GO:6886: intracellular protein transport	614	2.972	19	5.638	0.00605
	GO:7006: mitochondrial membrane organization and biogenesis	24	0.116	3	0.89	0.00676
	GO:46839: phospholipid dephosphorylation	25	0.121	3	0.89	0.00759
	GO:6464: protein modification	2702	13.08	60	17.8	0.00769
	GO:8637: apoptotic mitochondrial changes	26	0.126	3	0.89	0.00847
	GO:1943: hair follicle maturation	9	0.0436	2	0.593	0.00886
	GO:45414: regulation of interleukin-8 biosynthesis	9	0.0436	2	0.593	0.00886
	GO:45351: interferon type I biosynthesis	9	0.0436	2	0.593	0.00886
	GO:43393: regulation of protein binding	9	0.0436	2	0.593	0.00886
	GO:43412: biopolymer modification	2779	13.45	61	18.1	0.00915
MF	GO:5544: calcium-dependent phospholipid binding	35	0.154	5	1.348	0.000247
	GO:16986: transcription initiation factor	11	0.0485	3	0.809	0.000649

[0498]

解析8_UP_DP2-3_DP2-4

分類	BP Category	Genes in Category	% of Genes in Category	Genes in List in Category	% of Genes in List in Category	p-Value
MF	GO:4569: glycoprotein endo-alpha-1,2-mannosidase activity	3	0.0132	2	0.539	0.000792
	GO:51400: BH domain binding	3	0.0132	2	0.539	0.000792
	GO:51434: BH3 domain binding	3	0.0132	2	0.539	0.000792
	GO:46872: metal ion binding	5847	25.77	123	33.15	0.000842
	GO:43167: ion binding	5954	26.25	124	33.42	0.00118
	GO:4666: prostaglandin-endoperoxide synthase activity	4	0.0176	2	0.539	0.00157
	GO:5543: phospholipid binding	358	1.578	14	3.774	0.00246
	GO:3727: single-stranded RNA binding	35	0.154	4	1.078	0.00247
	GO:43169: cation binding	5392	23.77	111	29.92	0.00363
	GO:19863: IgE binding	6	0.0264	2	0.539	0.00383
	GO:46914: transition metal ion binding	4006	17.66	85	22.91	0.00565
	GO:5047: signal recognition particle binding	8	0.0353	2	0.539	0.007
	GO:4221: ubiquitin thiolesterase activity	105	0.463	6	1.617	0.00762
	GO:4843: ubiquitin-specific protease activity	109	0.48	6	1.617	0.00909
	GO:3676: nucleic acid binding	5048	22.25	102	27.49	0.00972
CC	GO:12505: endomembrane system	587	2.834	25	7.396	1.36E-05
	GO:5635: nuclear membrane	203	0.98	11	3.254	0.000529
	GO:5667: transcription factor complex	239	1.154	11	3.254	0.00199
	GO:5789: endoplasmic reticulum membrane	182	0.879	9	2.663	0.0031
	GO:5794: Golgi apparatus	535	2.583	18	5.325	0.0032
	GO:42175: nuclear envelope-endoplasmic reticulum network	193	0.932	9	2.663	0.00456
	GO:31090: organelle membrane	991	4.785	27	7.988	0.00663
	GO:5785: signal recognition particle receptor complex	8	0.0386	2	0.592	0.00697

[表119]

表119 糖尿病罹病・歯周病罹病者群で笑いにより発現減少した遺伝子のGO解析結果

p-Value 0.01 以下
MF: Molecular Function
CC: Cellular Component
BP: Biological Process

解析8 Down DP2-3_DP2-4

分類	BP Category	Genes in Category	% of Genes in Category	Genes in List in Category	% of Genes in List in Category	p-Value
BP	GO:6412: protein biosynthesis	1146	5.548	53	10.56	5.40E-06
	GO:9058: biosynthesis	2087	10.1	81	16.14	1.47E-05
	GO:9059: macromolecule biosynthesis	1264	6.119	55	10.96	2.04E-05
	GO:44249: cellular biosynthesis	1852	8.965	72	14.34	4.48E-05
	GO:6413: translational initiation	111	0.537	10	1.992	0.000378
	GO:43037: translation	248	1.201	15	2.988	0.00115
	GO:15788: UDP-N-acetylglucosamine	5	0.0242	2	0.398	0.00561
	GO:6733: oxidoreduction coenzyme	50	0.242	5	0.996	0.00716
	GO:6098: pentose-phosphate shunt	17	0.0823	3	0.598	0.00753
	GO:6740: NADPH regeneration	17	0.0823	3	0.598	0.00753
	GO:19216: regulation of lipid metabolism	33	0.16	4	0.797	0.00807
	GO:6769: nicotinamide metabolism	33	0.16	4	0.797	0.00807
	GO:50810: regulation of steroid biosynthesis	6	0.029	2	0.398	0.00829
	GO:7252: I-kappaB phosphorylation	6	0.029	2	0.398	0.00829
MF	GO:3735: structural constituent of ribosome	462	2.037	32	5.808	1.27E-07
	GO:50576: 3-keto-steroid reductase activity	2	0.00882	2	0.363	0.000589
	GO:5155: epidermal growth factor receptor activating ligand activity	2	0.00882	2	0.363	0.000589
	GO:8168: methyltransferase activity	244	1.076	15	2.722	0.000981
	GO:16741: transferase activity, transferring one-carbon groups	247	1.089	15	2.722	0.00111
	GO:3723: RNA binding	1203	5.303	45	8.167	0.0028
	GO:5154: epidermal growth factor receptor binding	13	0.0573	3	0.544	0.0034
	GO:43522: leucine zipper domain binding	4	0.0176	2	0.363	0.00342
	GO:45735: nutrient reservoir activity	4	0.0176	2	0.363	0.00342
	GO:5351: sugar porter activity	65	0.287	6	1.089	0.00491
	GO:17057: 6-phosphogluconolactonase	5	0.022	2	0.363	0.00561
	GO:5462: UDP-N-acetylglucosamine transporter activity	5	0.022	2	0.363	0.00561
	GO:3746: translation elongation factor activity	49	0.216	5	0.907	0.00657
	GO:51119: sugar transporter activity	69	0.304	6	1.089	0.00658
	GO:15144: carbohydrate transporter activity	70	0.309	6	1.089	0.00705
	GO:16614: oxidoreductase activity, acting on CH-OH group of donors	166	0.732	10	1.815	0.00752
	GO:8170: N-methyltransferase activity	72	0.317	6	1.089	0.00807
	GO:30275: LRR domain binding	6	0.0264	2	0.363	0.00828
	GO:8135: translation factor activity, nucleic acid binding	195	0.86	11	1.996	0.00836
	GO:5198: structural molecule activity	1255	5.532	44	7.985	0.00954
CC	GO:5830: cytosolic ribosome (sensu	212	1.024	22	4.288	1.65E-08
	GO:5843: cytosolic small ribosomal subunit (sensu Eukaryota)	89	0.43	13	2.534	2.87E-07
	GO:16283: eukaryotic 48S initiation complex	89	0.43	13	2.534	2.87E-07
	GO:5840: ribosome	475	2.294	32	6.238	3.54E-07
	GO:15935: small ribosomal subunit	126	0.608	15	2.924	5.46E-07
	GO:16282: eukaryotic 43S preinitiation	112	0.541	14	2.729	7.15E-07
	GO:5737: cytoplasm	6440	31.1	198	38.6	0.000155
	GO:30529: ribonucleoprotein complex	860	4.153	39	7.602	0.00022

[0499]

解析8 Down DP2-3_DP2-4

分類	BP Category	Genes in Category	% of Genes in Category	Genes in List in Category	% of Genes in List in Category	p-Value
CC	GO:5829: cytosol	789	3.81	36	7.018	0.000341
	GO:5853: eukaryotic translation elongation factor 1 complex	20	0.0966	4	0.78	0.00131
	GO:5902: microvillus	23	0.111	4	0.78	0.00227
	GO:5622: intracellular	13693	66.12	369	71.93	0.00251
	GO:5842: cytosolic large ribosomal subunit (sensu Eukaryota)	118	0.57	9	1.754	0.00269
	GO:15934: large ribosomal subunit	157	0.758	10	1.949	0.00585

[表120]

表120 歯周病非罹病者群で笑いにより発現増加した遺伝子のGO解析結果

p-Value 0.01 以下
MF: Molecular Function
CC: Cellular Component
BP: Biological Process

解析9 UP P1-3_P1-4

分類	BP Category	Genes in Category	% of Genes in Category	Genes in List in Category	% of Genes in List in Category	p-Value
BP	GO:6627: mitochondrial protein processing	1	0.00484	1	1.471	0.00329
	GO:15888: thiamin transport	1	0.00484	1	1.471	0.00329
	GO:41: transition metal ion transport	95	0.46	3	4.412	0.0038
	GO:6565: L-serine catabolism	3	0.0145	1	1.471	0.00984
	GO:16078: tRNA catabolism	3	0.0145	1	1.471	0.00984
	GO:1682: tRNA 5'-leader removal	3	0.0145	1	1.471	0.00984
MF	GO:4243: mitochondrial intermediate peptidase activity	1	0.00441	1	1.163	0.00379
	GO:15234: thiamin transporter activity	1	0.00441	1	1.163	0.00379
	GO:16620: oxidoreductase activity, acting on the aldehyde or oxo group of donors, NAD or NADP as acceptor	34	0.15	2	2.326	0.00737
	GO:4102: choline O-acetyltransferase activity	2	0.00882	1	1.163	0.00757
CC	GO:48179: activin receptor complex	2	0.00966	1	1.25	0.00771

[表121]

表121 歯周病非罹病者群で笑いより発現減少した遺伝子のGO解析結果

p-Value 0.01 以下
MF: Molecular Function
CC: Cellular Component
BP: Biological Process

解析9 Down P1-3_P1-4

分類	BP Category	Genes in Category	% of Genes in Category	Genes in List in Category	% of Genes in List in Category	p-Value
BP	GO:6584: catecholamine metabolism	22	0.107	3	1.531	0.00113
	GO:1838: embryonic epithelial tube formation	23	0.111	3	1.531	0.0013
	GO:1841: neural tube formation	23	0.111	3	1.531	0.0013
	GO:1839: neural plate morphogenesis	23	0.111	3	1.531	0.0013
	GO:18958: phenol metabolism	24	0.116	3	1.531	0.00147
	GO:16331: morphogenesis of embryonic epithelium	28	0.136	3	1.531	0.00231
	GO:18106: peptidyl-histidine phosphorylation	8	0.0387	2	1.02	0.00242
	GO:35239: tube morphogenesis	63	0.305	4	2.041	0.00303
	GO:18202: peptidyl-histidine modification	12	0.0581	2	1.02	0.00555
	GO:1947: heart looping	13	0.0629	2	1.02	0.00652
	GO:42733: embryonic digit morphogenesis	15	0.0726	2	1.02	0.00867
	GO:46676: negative regulation of insulin secretion	1	0.00484	1	0.51	0.00949
MF	GO:8131: amine oxidase activity	6	0.0264	2	0.922	0.00133
	GO:15036: disulfide oxidoreductase activity	29	0.128	3	1.382	0.00263
	GO:4645: phosphorylase activity	9	0.0397	2	0.922	0.00314
	GO:8581: ubiquitin-specific protease 5 activity	1	0.00441	1	0.461	0.00957
	GO:15245: fatty acid transporter activity	1	0.00441	1	0.461	0.00957

[表122]

表122 歯周病罹病者群で笑いにより発現増加した遺伝子のGO解析結果

p-Value 0.01 以下
MF: Molecular Function
CC: Cellular Component
BP: Biological Process

解析10 UP P2-3_P2-4

分類	BP Category	Genes in Category	% of Genes in Category	Genes in List in Category	% of Genes in List in Category	p-Value
BP	GO:50875: cellular physiological process	16318	79	912	88.29	8.16E-16
	GO:44237: cellular metabolism	11725	56.76	700	67.76	7.23E-14
	GO:8152: metabolism	12357	59.82	723	69.99	2.21E-12
	GO:44238: primary metabolism	11279	54.6	665	64.38	4.07E-11
	GO:7582: physiological process	17839	86.36	953	92.26	9.26E-10
	GO:6397: mRNA processing	407	1.97	48	4.647	3.20E-08
	GO:16071: mRNA metabolism	478	2.314	53	5.131	4.95E-08
	GO:8380: RNA splicing	362	1.752	41	3.969	9.34E-07
	GO:43170: macromolecule metabolism	7147	34.6	428	41.43	1.68E-06
	GO:9058: biosynthesis	2087	10.1	151	14.62	1.72E-06
	GO:44249: cellular biosynthesis	1852	8.965	136	13.17	2.82E-06
	GO:15031: protein transport	1049	5.078	86	8.325	4.08E-06
	GO:45184: establishment of protein	1102	5.335	89	8.616	5.02E-06
	GO:6448: regulation of translational elongation	4	0.0194	4	0.387	6.22E-06
	GO:45900: negative regulation of translational elongation	4	0.0194	4	0.387	6.22E-06
	GO:6139: nucleobase, nucleoside, nucleotide and nucleic acid metabolism	5441	26.34	333	32.24	8.73E-06
	GO:8104: protein localization	1151	5.572	91	8.809	9.15E-06
	GO:43283: biopolymer metabolism	4614	22.34	288	27.88	1.07E-05
	GO:6412: protein biosynthesis	1146	5.548	90	8.712	1.33E-05
	GO:16070: RNA metabolism	834	4.037	70	6.776	1.53E-05
	GO:9059: macromolecule biosynthesis	1264	6.119	97	9.39	1.55E-05
	GO:6396: RNA processing	690	3.34	60	5.808	2.24E-05
	GO:19722: calcium-mediated signaling	43	0.208	10	0.968	3.97E-05
	GO:6888: ER to Golgi transport	138	0.668	19	1.839	5.84E-05
	GO:46907: intracellular transport	1069	5.175	81	7.841	0.000121
	GO:9987: cellular process	18835	91.18	973	94.19	0.000144
	GO:51649: establishment of cellular	1082	5.238	81	7.841	0.000179
	GO:398: nuclear mRNA splicing, via	127	0.615	17	1.646	0.000199
	GO:375: RNA splicing, via transesterification reactions	127	0.615	17	1.646	0.000199
	GO:377: RNA splicing, via transesterification reactions with bulged adenosine as nucleophile	127	0.615	17	1.646	0.000199
	GO:51641: cellular localization	1104	5.344	82	7.938	0.00021
	GO:6511: ubiquitin-dependent protein	259	1.254	27	2.614	0.000259
	GO:19941: modification-dependent protein catabolism	260	1.259	27	2.614	0.000276
	GO:48193: Golgi vesicle transport	194	0.939	22	2.13	0.000293
	GO:7005: mitochondrion organization and biogenesis	38	0.184	8	0.774	0.000487
	GO:45045: secretory pathway	370	1.791	34	3.291	0.00049
	GO:44260: cellular macromolecule metabolism	5303	25.67	310	30.01	0.000707
	GO:6886: intracellular protein transport	614	2.972	49	4.743	0.000879
	GO:44267: cellular protein metabolism	5228	25.31	305	29.53	0.000914
	GO:7049: cell cycle	1295	6.269	90	8.712	0.000917
	GO:7006: mitochondrial membrane organization and biogenesis	24	0.116	6	0.581	0.000954
	GO:245: spliceosome assembly	52	0.252	9	0.871	0.000997

[0500]

解析10 UP P2-3_P2-4

分類	BP Category	Genes in Category	% of Genes in Category	Genes in List in Category	% of Genes in List in Category	p-Value
BP	GO:51103: DNA ligation during DNA repair	5	0.0242	3	0.29	0.00116
	GO:6288: base-excision repair, DNA ligation	5	0.0242	3	0.29	0.00116
	GO:46903: secretion	485	2.348	40	3.872	0.00138
	GO:19538: protein metabolism	5269	25.51	305	29.53	0.00152
	GO:16478: negative regulation of translation	11	0.0533	4	0.387	0.00155
	GO:46831: regulation of RNA export from nucleus	11	0.0533	4	0.387	0.00155
	GO:50791: regulation of physiological process	5732	27.75	329	31.85	0.00159
	GO:50657: nucleic acid transport	114	0.552	14	1.355	0.00166
	GO:50658: RNA transport	114	0.552	14	1.355	0.00166
	GO:51236: establishment of RNA localization	114	0.552	14	1.355	0.00166
	GO:51244: regulation of cellular physiological process	5526	26.75	318	30.78	0.00168
	GO:6643: membrane lipid metabolism	266	1.288	25	2.42	0.0019
	GO:51301: cell division	341	1.651	30	2.904	0.00201
	GO:46467: membrane lipid biosynthesis	130	0.629	15	1.452	0.00216
	GO:6403: RNA localization	118	0.571	14	1.355	0.0023
	GO:19371: cyclooxygenase pathway	2	0.00968	2	0.194	0.0025
	GO:9231: riboflavin biosynthesis	2	0.00968	2	0.194	0.0025
	GO:42726: riboflavin and derivative metabolism	2	0.00968	2	0.194	0.0025
	GO:6771: riboflavin metabolism	2	0.00968	2	0.194	0.0025
	GO:42727: riboflavin and derivative	2	0.00968	2	0.194	0.0025
	GO:42997: negative regulation of Golgi to plasma membrane protein transport	2	0.00968	2	0.194	0.0025
	GO:43002: negative regulation of Golgi to plasma membrane CFTR protein transport	2	0.00968	2	0.194	0.0025
	GO:43004: cytoplasmic sequestering of CFTR protein	2	0.00968	2	0.194	0.0025
	GO:42996: regulation of Golgi to plasma membrane protein transport	2	0.00968	2	0.194	0.0025
	GO:42999: regulation of Golgi to plasma membrane CFTR protein transport	2	0.00968	2	0.194	0.0025
	GO:15782: CMP-sialic acid transport	2	0.00968	2	0.194	0.0025
	GO:43000: Golgi to plasma membrane CFTR protein transport	2	0.00968	2	0.194	0.0025
	GO:6605: protein targeting	364	1.762	31	3.001	0.00281
	GO:9117: nucleotide metabolism	304	1.472	27	2.614	0.00288
	GO:9165: nucleotide biosynthesis	206	0.997	20	1.936	0.00357
	GO:6413: translational initiation	111	0.537	13	1.258	0.00363
	GO:44257: cellular protein catabolism	325	1.573	28	2.711	0.00373
	GO:51603: proteolysis during cellular protein catabolism	325	1.573	28	2.711	0.00373
	GO:8535: cytochrome c oxidase complex assembly	14	0.0678	4	0.387	0.00416
	GO:15931: nucleobase, nucleoside, nucleotide and nucleic acid transport	127	0.615	14	1.355	0.00452
	GO:50789: regulation of biological process	6505	31.49	364	35.24	0.0046
	GO:50794: regulation of cellular process	6023	29.16	339	32.82	0.00471
	GO:46488: phosphatidylinositol metabolism	23	0.111	5	0.484	0.0049
	GO:8333: endosome to lysosome transport	8	0.0387	3	0.29	0.00578
	GO:9892: negative regulation of metabolism	576	2.788	43	4.163	0.00589
	GO:8654: phospholipid biosynthesis	105	0.508	12	1.162	0.00619
	GO:9130: pyrimidine nucleoside monophosphate biosynthesis	3	0.0145	2	0.194	0.00725
	GO:1919: regulation of receptor recycling	3	0.0145	2	0.194	0.00725

[0501]

解析10 UP P2-3_P2-4

分類	BP Category	Genes in Category	% of Genes in Category	Genes in List in Category	% of Genes in List in Category	p-Value
BP	GO:9129: pyrimidine nucleoside monophosphate metabolism	3	0.0145	2	0.194	0.00725
	GO:6926: programmed cell death, virus-infected cells	3	0.0145	2	0.194	0.00725
	GO:43001: Golgi to plasma membrane protein transport	3	0.0145	2	0.194	0.00725
	GO:9116: nucleoside metabolism	36	0.174	6	0.581	0.00828
	GO:51028: mRNA transport	96	0.465	11	1.065	0.00841
	GO:6512: ubiquitin cycle	882	4.27	60	5.808	0.00967
	GO:19222: regulation of metabolism	4061	19.66	233	22.56	0.00985
	GO:7162: negative regulation of cell adhesion	27	0.131	5	0.484	0.00998
MF	GO:3723: RNA binding	1203	5.303	120	10.42	7.12E-13
	GO:3676: nucleic acid binding	5048	22.25	337	29.25	7.78E-09
	GO:3735: structural constituent of ribosome	462	2.037	53	4.601	2.74E-08
	GO:5047: signal recognition particle binding	8	0.0353	4	0.347	0.000393
	GO:15399: primary active transporter activity	285	1.256	28	2.431	0.000677
	GO:15078: hydrogen ion transporter activity	218	0.961	23	1.997	0.000754
	GO:4221: ubiquitin thiolesterase activity	105	0.463	14	1.215	0.000857
	GO:15077: monovalent inorganic cation transporter activity	236	1.04	24	2.083	0.000985
	GO:15002: heme-copper terminal oxidase activity	42	0.185	8	0.694	0.00109
	GO:4129: cytochrome-c oxidase activity	42	0.185	8	0.694	0.00109
	GO:16675: oxidoreductase activity, acting on heme group of donors	42	0.185	8	0.694	0.00109
	GO:16676: oxidoreductase activity, acting on heme group of donors, oxygen as acceptor	42	0.185	8	0.694	0.00109
	GO:3691: double-stranded telomeric DNA binding	5	0.022	3	0.26	0.00121
	GO:4843: ubiquitin-specific protease activity	109	0.48	14	1.215	0.00124
	GO:46914: transition metal ion binding	4006	17.66	242	21.01	0.00153
	GO:8486: diphosphoinositol-polyphosphate diphosphatase activity	11	0.0485	4	0.347	0.00164
	GO:8270: zinc ion binding	3334	14.7	205	17.8	0.00164
	GO:5094: Rho GDP-dissociation inhibitor	6	0.0264	3	0.26	0.00233
	GO:8531: riboflavin kinase activity	2	0.00882	2	0.174	0.00258
	GO:4137: deoxycytidine kinase activity	2	0.00882	2	0.174	0.00258
	GO:5456: CMP-sialic acid transporter activity	2	0.00882	2	0.174	0.00258
	GO:50430: syntaxin-6 binding	2	0.00882	2	0.174	0.00258
	GO:5517: calmodulin inhibitor activity	2	0.00882	2	0.174	0.00258
	GO:42980: cystic fibrosis transmembrane conductance regulator binding	2	0.00882	2	0.174	0.00258
	GO:16790: thiolester hydrolase activity	131	0.577	15	1.302	0.0027
	GO:8234: cysteine-type peptidase activity	233	1.027	22	1.91	0.00393
	GO:16563: transcriptional activator activity	474	2.089	37	3.212	0.00653
	GO:30338: CMP-N-acetylneuraminate monooxygenase activity	3	0.0132	2	0.174	0.00747
	GO:8897: phosphopantetheinyltransferase activity	3	0.0132	2	0.174	0.00747
	GO:1509: legumain activity	3	0.0132	2	0.174	0.00747
	GO:8934: inositol-1(or 4)-monophosphatase activity	3	0.0132	2	0.174	0.00747
	GO:4357: glutamate-cysteine ligase activity	3	0.0132	2	0.174	0.00747
	GO:16780: phosphotransferase activity, for other substituted phosphate groups	25	0.11	5	0.434	0.0076
	GO:43021: ribonucleoprotein binding	25	0.11	5	0.434	0.0076
	GO:4722: protein serine/threonine phosphatase activity	69	0.304	9	0.781	0.00796

[0502]

解析10 UP P2-3_P2-4

分類	BP Category	Genes in Category	% of Genes in Category	Genes in List in Category	% of Genes in List in Category	p-Value
MF	GO:5092: GDP-dissociation inhibitor activity	9	0.0397	3	0.26	0.00871
	GO:4197: cysteine-type endopeptidase	122	0.538	13	1.128	0.00912
	GO:46982: protein heterodimerization activity	136	0.6	14	1.215	0.00936
CC	GO:5622: intracellular	13693	66.12	843	79.01	1.67E-21
	GO:43229: intracellular organelle	11143	53.8	700	65.6	6.87E-16
	GO:43226: organelle	11143	53.8	700	65.6	6.87E-16
	GO:43231: intracellular membrane-bound organelle	9668	46.68	620	58.11	1.05E-14
	GO:43227: membrane-bound organelle	9668	46.68	620	58.11	1.05E-14
	GO:30529: ribonucleoprotein complex	860	4.153	100	9.372	1.38E-14
	GO:5840: ribosome	475	2.294	57	5.342	2.54E-09
	GO:43234: protein complex	3428	16.55	249	23.34	2.88E-09
	GO:5737: cytoplasm	6440	31.1	414	38.8	2.51E-08
	GO:5634: nucleus	6618	31.96	422	39.55	4.64E-08
	GO:5623: cell	19120	92.32	1024	95.97	4.49E-07
	GO:15934: large ribosomal subunit	157	0.758	23	2.156	5.78E-06
	GO:12505: endomembrane system	587	2.834	56	5.248	6.90E-06
	GO:5829: cytosol	789	3.81	68	6.373	2.25E-05
	GO:5830: cytosolic ribosome (sensu	212	1.024	26	2.437	3.74E-05
	GO:31090: organelle membrane	991	4.785	78	7.31	0.000125
	GO:5654: nucleoplasm	573	2.767	50	4.686	0.0002
	GO:5785: signal recognition particle receptor complex	8	0.0386	4	0.375	0.000415
	GO:5791: rough endoplasmic reticulum	21	0.101	6	0.562	0.000513
	GO:5635: nuclear membrane	203	0.98	22	2.062	0.000816
	GO:48500: signal recognition particle	23	0.111	6	0.562	0.000873
	GO:5786: signal recognition particle (sensu Eukaryota)	23	0.111	6	0.562	0.000873
	GO:30867: rough endoplasmic reticulum membrane	16	0.0773	5	0.469	0.000975
	GO:30133: transport vesicle	73	0.352	11	1.031	0.00122
	GO:30140: trans-Golgi network transport	43	0.208	8	0.75	0.0014
	GO:5681: spliceosome complex	217	1.048	22	2.062	0.00194
	GO:5843: cytosolic small ribosomal subunit (sensu Eukaryota)	89	0.43	12	1.125	0.002
	GO:16283: eukaryotic 48S initiation complex	89	0.43	12	1.125	0.002
	GO:15935: small ribosomal subunit	126	0.608	15	1.406	0.00211
	GO:5783: endoplasmic reticulum	1096	5.292	78	7.31	0.00234
	GO:5955: calcineurin complex	6	0.029	3	0.281	0.00243
	GO:5842: cytosolic large ribosomal subunit (sensu Eukaryota)	118	0.57	14	1.312	0.00301
	GO:5667: transcription factor complex	239	1.154	23	2.156	0.00303
	GO:5798: Golgi vesicle	59	0.285	9	0.843	0.00304
	GO:8290: F-actin capping protein complex	13	0.0628	4	0.375	0.00345
	GO:5794: Golgi apparatus	535	2.583	42	3.936	0.00454
	GO:30121: AP-1 adaptor complex	14	0.0676	4	0.375	0.00463
	GO:16282: eukaryotic 43S preinitiation	112	0.541	13	1.218	0.00504
	GO:42175: nuclear envelope-endoplasmic reticulum network	193	0.932	19	1.781	0.00523
	GO:5789: endoplasmic reticulum membrane	182	0.879	18	1.687	0.00616
	GO:5768: endosome	171	0.826	17	1.593	0.00726
	GO:8287: protein serine/threonine phosphatase complex	56	0.27	8	0.75	0.00762
	GO:17109: glutamate-cysteine ligase complex	3	0.0145	2	0.187	0.00768
	GO:5637: nuclear inner membrane	17	0.0821	4	0.375	0.00973

[表123]

表123 歯周病罹病者群で笑いにより発現減少した遺伝子のGO解析結果

p-Value 0.01 以下
MF: Molecular Function
CC: Cellular Component
BP: Biological Process

解析10 P2-3_P2-4 Down

分類	Category	Genes in Category	% of Genes in Category	Genes in List in Category	% of Genes in List in Category	p-Value
BP	GO:19882: antigen presentation	71	0.344	16	1.103	2.58E-05
	GO:15991: ATP hydrolysis coupled proton transport	10	0.0484	5	0.345	0.000317
	GO:6665: sphingolipid metabolism	87	0.421	16	1.103	0.000329
	GO:43122: regulation of I-kappaB kinase/NF-kappaB cascade	176	0.852	25	1.723	0.000595
	GO:19915: sequestering of lipid	17	0.0823	6	0.414	0.000749
	GO:30218: erythrocyte differentiation	38	0.184	9	0.62	0.00103
	GO:43123: positive regulation of I-kappaB kinase/NF-kappaB cascade	163	0.789	23	1.585	0.00106
	GO:8104: protein localization	1151	5.572	108	7.443	0.00117
	GO:1553: luteinization	4	0.0194	3	0.207	0.00131
	GO:46543: development of secondary female sexual characteristics	4	0.0194	3	0.207	0.00131
	GO:46544: development of secondary male sexual characteristics	4	0.0194	3	0.207	0.00131
	GO:1779: natural killer cell differentiation	4	0.0194	3	0.207	0.00131
	GO:15988: energy coupled proton transport, against electrochemical gradient	13	0.0629	5	0.345	0.00136
	GO:15031: protein transport	1049	5.078	99	6.823	0.00154
	GO:6672: ceramide metabolism	49	0.237	10	0.689	0.00187
	GO:30641: hydrogen ion homeostasis	20	0.0968	6	0.414	0.00196
	GO:30004: monovalent inorganic cation homeostasis	27	0.131	7	0.482	0.00212
	GO:7264: small GTPase mediated signal transduction	634	3.069	64	4.411	0.00218
	GO:6092: main pathways of carbohydrate metabolism	163	0.789	22	1.516	0.00239
	GO:45184: establishment of protein	1102	5.335	102	7.03	0.00243
	GO:6897: endocytosis	291	1.409	34	2.343	0.00246
	GO:6687: glycosphingolipid metabolism	35	0.169	8	0.551	0.00247
	GO:46907: intracellular transport	1069	5.175	99	6.823	0.00275
	GO:51649: establishment of cellular	1082	5.238	100	6.892	0.00279
	GO:6563: L-serine metabolism	15	0.0726	5	0.345	0.00281
	GO:46519: sphingoid metabolism	52	0.252	10	0.689	0.00297
	GO:43283: biopolymer metabolism	4614	22.34	367	25.29	0.00308
	GO:45136: development of secondary sexual characteristics	5	0.0242	3	0.207	0.00311
	GO:51641: cellular localization	1104	5.344	101	6.961	0.00361
	GO:15937: coenzyme A biosynthesis	10	0.0484	4	0.276	0.00361
	GO:48255: mRNA stabilization	10	0.0484	4	0.276	0.00361
	GO:43489: RNA stabilization	10	0.0484	4	0.276	0.00361
	GO:43170: macromolecule metabolism	7147	34.6	548	37.77	0.00481
	GO:16486: peptide hormone processing	11	0.0533	4	0.276	0.00536
	GO:9607: response to biotic stimulus	1414	6.845	124	8.546	0.00559
	GO:45647: negative regulation of erythrocyte differentiation	6	0.029	3	0.207	0.00589
	GO:8216: spermidine metabolism	6	0.029	3	0.207	0.00589
	GO:45931: positive regulation of mitotic cell cycle	6	0.029	3	0.207	0.00589

[0503]

解析10 P2-3_P2-4 Down

分類	Category	Genes in Category	% of Genes in Category	Genes in List in Category	% of Genes in List in Category	p-Value
BP	GO:45010: actin nucleation	6	0.029	3	0.207	0.00589
	GO:9966: regulation of signal transduction	654	3.166	63	4.342	0.00668
	GO:43038: amino acid activation	58	0.281	10	0.689	0.00668
	GO:43039: tRNA aminoacylation	58	0.281	10	0.689	0.00668
	GO:6418: tRNA aminoacylation for protein translation	58	0.281	10	0.689	0.00668
	GO:15936: coenzyme A metabolism	12	0.0581	4	0.276	0.0076
	GO:51056: regulation of small GTPase mediated signal transduction	224	1.084	26	1.792	0.00806
	GO:6081: aldehyde metabolism	19	0.092	5	0.345	0.0086
	GO:7249: I-kappaB kinase/NF-kappaB	226	1.094	26	1.792	0.00901
	GO:6664: glycolipid metabolism	43	0.208	8	0.551	0.00926
	GO:9967: positive regulation of signal transduction	216	1.046	25	1.723	0.00957
	GO:45579: positive regulation of B cell differentiation	7	0.0339	3	0.207	0.00977
	GO:43029: T cell homeostasis	7	0.0339	3	0.207	0.00977
	GO:185: activation of MAPKKK activity	7	0.0339	3	0.207	0.00977
MF	GO:166: nucleotide binding	3221	14.2	305	19.32	3.95E-09
	GO:17076: purine nucleotide binding	2752	12.13	263	16.66	2.71E-08
	GO:3824: catalytic activity	7780	34.3	626	39.65	2.43E-06
	GO:30554: adenyl nucleotide binding	2194	9.672	205	12.98	5.56E-06
	GO:5524: ATP binding	2067	9.112	193	12.22	1.13E-05
	GO:8168: methyltransferase activity	244	1.076	35	2.217	3.70E-05
	GO:30106: MHC class I receptor activity	38	0.168	11	0.697	3.73E-05
	GO:16741: transferase activity, transferring one-carbon groups	247	1.089	35	2.217	4.78E-05
	GO:16874: ligase activity	582	2.566	66	4.18	6.20E-05
	GO:16810: hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds	164	0.723	26	1.647	6.73E-05
	GO:4348: glucosylceramidase activity	5	0.022	4	0.253	0.00011
	GO:5085: guanyl-nucleotide exchange factor activity	263	1.159	35	2.217	0.000171
	GO:49: tRNA binding	20	0.0882	7	0.443	0.00027
	GO:8494: translation activator activity	10	0.0441	5	0.317	0.000304
	GO:4250: aminopeptidase I activity	3	0.0132	3	0.19	0.000337
	GO:5083: small GTPase regulator activity	437	1.926	50	3.167	0.000374
	GO:16772: transferase activity, transferring phosphorus-containing groups	1500	6.612	136	8.613	0.000808
	GO:16886: ligase activity, forming phosphoric ester bonds	69	0.304	13	0.823	0.000844
	GO:16740: transferase activity	2634	11.61	223	14.12	0.000922
	GO:30695: GTPase regulator activity	621	2.737	64	4.053	0.00107
	GO:5515: protein binding	9867	43.5	745	47.18	0.00122
	GO:16773: phosphotransferase activity, alcohol group as acceptor	1103	4.862	103	6.523	0.00135
	GO:4289: subtilase activity	19	0.0838	6	0.38	0.00139
	GO:5525: GTP binding	587	2.588	60	3.8	0.00182
	GO:16811: hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds, in	84	0.37	14	0.887	0.00188
	GO:3678: DNA helicase activity	42	0.185	9	0.57	0.00205
	GO:16875: ligase activity, forming carbon-oxygen bonds	60	0.264	11	0.697	0.00259
	GO:16876: ligase activity, forming aminoacyl-tRNA and related compounds	60	0.264	11	0.697	0.00259
	GO:4812: tRNA ligase activity	60	0.264	11	0.697	0.00259
	GO:8452: RNA ligase activity	60	0.264	11	0.697	0.00259

[0504]

解析10 P2-3_P2-4 Down

分類	Category	Genes in Category	% of Genes in Category	Genes in List in Category	% of Genes in List in Category	p-Value
MF	GO:17111: nucleoside-triphosphatase activity	904	3.985	85	5.383	0.00283
	GO:19001: guanyl nucleotide binding	600	2.645	60	3.8	0.003
	GO:17057: 6-phosphogluconolactonase	5	0.022	3	0.19	0.00303
	GO:4634: phosphopyruvate hydratase activity	5	0.022	3	0.19	0.00303
	GO:5391: sodium:potassium-exchanging ATPase activity	16	0.0705	5	0.317	0.00371
	GO:8465: glycerate dehydrogenase activity	2	0.00882	2	0.127	0.00484
	GO:16618: hydroxypyruvate reductase activity	2	0.00882	2	0.127	0.00484
	GO:30267: glyoxylate reductase (NADP)	2	0.00882	2	0.127	0.00484
	GO:50576: 3-keto-steroid reductase activity	2	0.00882	2	0.127	0.00484
	GO:4218: cathepsin S activity	2	0.00882	2	0.127	0.00484
	GO:30601: aminopeptidase B activity	2	0.00882	2	0.127	0.00484
	GO:42576: aspartyl aminopeptidase activity	2	0.00882	2	0.127	0.00484
	GO:1611: A2A adenosine receptor activity, G-protein coupled	2	0.00882	2	0.127	0.00484
	GO:16462: pyrophosphatase activity	948	4.179	87	5.51	0.00491
	GO:4767: sphingomyelin phosphodiesterase activity	11	0.0485	4	0.253	0.00519
	GO:163: protein phosphatase type 1 activity	6	0.0264	3	0.19	0.00574
	GO:16301: kinase activity	1299	5.726	114	7.22	0.00588
	GO:16818: hydrolase activity, acting on acid anhydrides, in phosphorus-containing	956	4.214	87	5.51	0.00611
	GO:16813: hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds, in linear amidines	18	0.0793	5	0.317	0.00647
	GO:16817: hydrolase activity, acting on acid anhydrides	959	4.227	87	5.51	0.00662
	GO:5070: SH3/SH2 adaptor activity	77	0.339	12	0.76	0.00671
	GO:30674: protein binding, bridging	137	0.604	18	1.14	0.00684
	GO:5488: binding	17386	76.64	1250	79.16	0.00714
	GO:30234: enzyme regulator activity	1205	5.312	106	6.713	0.00725
	GO:17040: ceramidase activity	12	0.0529	4	0.253	0.00736
	GO:1727: lipid kinase activity	42	0.185	8	0.507	0.00761
	GO:16798: hydrolase activity, acting on glycosyl bonds	192	0.846	23	1.457	0.00767
	GO:3924: GTPase activity	329	1.45	35	2.217	0.00825
	GO:4674: protein serine/threonine kinase activity	669	2.949	63	3.99	0.00897
	GO:4668: protein-arginine deiminase activity	7	0.0309	3	0.19	0.00952
	GO:15207: adenine transporter activity	7	0.0309	3	0.19	0.00952
	GO:3779: actin binding	464	2.045	46	2.913	0.00994
CC	GO:42612: MHC class I protein complex	62	0.299	20	1.396	3.08E-09
	GO:42611: MHC protein complex	94	0.454	21	1.465	1.36E-06
	GO:1772: immunological synapse	118	0.57	23	1.605	5.25E-06
	GO:5622: intracellular	13693	66.12	1011	70.55	0.000115
	GO:5773: vacuole	260	1.255	34	2.373	0.00026
	GO:10008: endosome membrane	10	0.0483	5	0.349	0.000296
	GO:5623: cell	19120	92.32	1355	94.56	0.000364
	GO:5798: Golgi vesicle	59	0.285	12	0.837	0.000614
	GO:323: lytic vacuole	230	1.111	29	2.024	0.00127
	GO:5764: lysosome	230	1.111	29	2.024	0.00127
	GO:30128: clathrin coat of endocytic vesicle	8	0.0386	4	0.279	0.00127
	GO:30122: AP-2 adaptor complex	8	0.0386	4	0.279	0.00127
	GO:30132: clathrin coat of coated pit	9	0.0435	4	0.279	0.00217
	GO:5737: cytoplasm	6440	31.1	493	34.4	0.00295
	GO:15: phosphopyruvate hydratase complex	5	0.0241	3	0.209	0.00297
	GO:43229: intracellular organelle	11143	53.8	819	57.15	0.00451

[0505]

解析10 P2-3_P2-4 Down

分類	Category	Genes in Category	% of Genes in Category	Genes in List in Category	% of Genes in List in Category	p-Value
CC	GO:43226: organelle	11143	53.8	819	57.15	0.00451
	GO:30130: clathrin coat of trans-Golgi network vesicle	31	0.15	7	0.488	0.00452
	GO:45334: clathrin-coated endocytic vesicle	12	0.0579	4	0.279	0.0072
	GO:5884: actin filament	26	0.126	6	0.419	0.00752
	GO:5793: ER-Golgi intermediate compartment	60	0.29	10	0.698	0.00768
	GO:5856: cytoskeleton	1506	7.272	128	8.932	0.00826
	GO:30140: trans-Golgi network transport	43	0.208	8	0.558	0.00849
	GO:5890: sodium:potassium-exchanging ATPase complex	13	0.0628	4	0.279	0.00984

[0506] 生物学的経路で注目されるTermとしては、糖尿病非罹病者群(A+B群)で笑いによりUp-regulateされる遺伝子の解析において、抗原受容体シグナル伝達経路関連(GO ID: 50854、50857)に割り当てられる3遺伝子(表124)、Down-regulateされる遺伝子の解析において、グルコース輸送(GO ID: 15758)に割り当てられる5遺伝子(表125)、リポ蛋白質代謝(GO ID: 42157)に割り当てられる5遺伝子(表126)、pH調整(GO ID: 6885)に割り当てられる4遺伝子(表127)があった。糖尿病罹病者群 (C+D群) では、笑いによりDown-regulateされる遺伝子の解析において、プログラムされた細胞死の制御(GO ID: 12502)に割り当てられる8遺伝子(表128)があった。

[表124]

表124 糖尿病非罹病者群で笑いにより発現増加した 注目遺伝子
抗原受容体シグナル伝達経路制御関連 (GO ID: 50854または50857)

#	Gene Symbol	-fold change	Gene Name
1	PTPRC	2.52	Protein tyrosine phosphatase, receptor type, C
2	PAWR	2.03	PRKC, apoptosis, WT1, regulator
3	TRAT1	1.56	T cell receptor associated transmembrane adaptor 1

[表125]

表125 糖尿病非罹病者群で笑いにより発現減少した 注目遺伝子
グルコース輸送 (GO ID: 15758)

#	Gene Symbol	-fold change	Gene Name
1	STXBP4	0.56	syntaxin binding protein 4
2	SLC2A5	0.57	solute carrier family 2 (facilitated glucose/fructose transporter), member 5
3	SLC2A3	0.61	solute carrier family 2 (facilitated glucose transporter), member 3
4	SORBS1	0.65	sorbin and SH3 domain containing 1
5	AKT1	0.67	V-akt murine thymoma viral oncogene homolog 1

[表126]

表126 糖尿病非罹病者群で笑いにより発現減少した 注目遺伝子
リポ蛋白質代謝 (GO ID: 42157)

#	Gene Symbol	-fold change	Gene Name
1	APOL6	0.41	apolipoprotein L, 6
2	APOL6	0.49	apolipoprotein L, 6
3	ATG10	0.54	ATG10 autophagy related 10 homolog (S. cerevisiae)
4	SNX17	0.56	Sorting nexin 17
5	APOL6	0.62	apolipoprotein L, 6
6	PIGS	0.63	Phosphatidylinositol glycan anchor biosynthesis, class S
7	FNTB	0.65	Farnesyltransferase, CAAX box, beta

[表127]

表127 糖尿病非罹病者群で笑いにより発現減少した 注目遺伝子
pH調整 (GO ID: 6885)

#	Gene Symbol	-fold change	Gene Name
1	SLC9A5	0.43	solute carrier family 9 (sodium/hydrogen exchanger), member 5
2	LOC133308	0.59	hypothetical protein BC009732
3	CLN5	0.65	ceroid-lipofuscinosis, neuronal 5
4	CLN3	0.66	ceroid-lipofuscinosis, neuronal 3, juvenile (Batten, Spielmeyer-Vogt disease)

[表128]

表128 糖尿病罹病者群で笑いにより発現減少した 注目遺伝子
プログラムされた細胞死(アポトーシス)の制御 (GO ID: 12502)

#	Gene Symbol	-fold change	Gene Name
1	RPS3A	0.49	Ribosomal protein S3A
2	RPS3A	0.49	Ribosomal protein S3A
3	RPS3A	0.50	Ribosomal protein S3A
4	RPS3A	0.50	Ribosomal protein S3A
5	RPS3A	0.50	Ribosomal protein S3A
6	NM_138622	0.57	Homo sapiens BCL2-like 11 (apoptosis facilitator) (BCL2L11), transcript variant 2, mRNA [NM_138622]
7	PPP1R13B	0.57	Protein phosphatase 1, regulatory (inhibitor) subunit 13B
8	RPS3A	0.61	Ribosomal protein S3A

[0507] A群（糖尿病非罹病かつ歯周病非罹病者群）では、笑いよりUp-regulateさ

れる遺伝子の解析において、抗細胞死（GO ID:0006916）に割り当てられる1遺伝子（遺伝子セット１No.3）、IgE受容体活性（GO ID:0019767）に割り当てられる1遺伝子（遺伝子セット１No.4）、レスポンス防御GO:0006952(defense response)に割り当てられる1遺伝子（遺伝子セット１No.5）、セロトニン輸送関連(GO ID: 6837または15222または5335)に割り当てられる1遺伝子（遺伝子セット１No.7）、γグルタミン酸カルボキシラーゼ活性（GOID:0008488）に割り当てられる1遺伝子（遺伝子セット１No.8）、酸素輸送（GOID:0015671）に割り当てられる1遺伝子（遺伝子セット１No.9）、Down-regulateされる遺伝子の解析において、癌関連の7遺伝子（遺伝子セット１No.11-17）、自然免疫反応（GOID:0045087）に割り当てられる2遺伝子（遺伝子セット１No.18-19）、免疫反応（GOID:0006955）に割り当てられる1遺伝子（遺伝子セット1No.20）、レスポンス防御（GO:0006952）に割り当てられる1遺伝子（遺伝子セット１No.22）、転写因子（GOIID:0003700）に割り当てられる1遺伝子（遺伝子セット１No.25）、細胞死（GOID:0006915）に割り当てられる1遺伝子（遺伝子セット１No.27）があった。なお、遺伝子セット1については下記表164を参照のこと。

[0508] B群(糖尿病非罹病・歯周病罹病者群)では、笑いによりDown-regulateされる遺伝子の解析において、サイトカイン・ケモカインシグナル伝達(GO ID: 19221)に割り当てられる6遺伝子(表129)、リポ蛋白質異化(GO ID: 42159、45192)に割り当てられる2遺伝子(表130)、脂質輸送(GO ID: 6869)に割り当てられる10遺伝子(表131)、インスリン受容体シグナル伝達関連(GO ID: 8286または46627)に割り当てられる6遺伝子(表132)、インターロイキン6生合成関連(GO ID: 45408、42226)に割り当てられる3遺伝子(表133)があった。C群(糖尿病罹病・歯周病なし群)で笑いによりDown-regulateされる遺伝子の解析において、抗生物質生合成・代謝(GO ID: 17000、16999)に割り当てられる2遺伝子(表134)、アルギニン合成(GO ID: 6526)や尿酸回路・代謝(GO ID: 19627、50)に割り当てられる2遺伝子(表135)、リンパ球分化(GO ID: 30098)に割り当てられる5遺伝子(表136)があった。D群(糖尿病罹病・歯周病罹病者群)で笑いに

よりUp-regulateされる遺伝子の解析において、ウイルスレスポンス防御(GO ID: 51607)に割り当てられる3遺伝子(表137)、インターフェロン生合成関連(GO ID: 45356、45359、45357、45350、45351)、インターロイキン8生合成(GO ID: 45354、45414、45416)に割り当てられる2遺伝子(表138)、Down-regulateされる遺伝子の解析において、脂質代謝制御(GO ID: 19216)に割り当てられる4遺伝子(表139)、I-kappaBリン酸基転移(GO ID: 7252)に割り当てられる2遺伝子(表140)があった。A+C群(歯周病非罹病者群)で笑いによりDown-regulateされる遺伝子の解析において、カテコールアミン代謝(GO ID:6584)に割り当てられる3遺伝子(表141)、インスリン制御(GO ID: 46676)として割り当てられる1遺伝子(表142)があった。B+D群(歯周病罹病者群)で笑いによってUp-regulateされる遺伝子の解析において、抗原授与(GO ID: 19882)に割り当てられる16遺伝子(表143)、NF-KappaB関連(GO ID: 43122、43123、7249)に割り当てられる27遺伝子(表144)、脂質分泌(GO ID: 19915)に割り当てられる6遺伝子(表145)、NK細胞分化(GO ID; 1779)、B細胞分化(GO ID: 45579)、T細胞恒常性(GO ID: 43029)に割り当てられる3遺伝子(表146)、糖脂質代謝(GO ID: 6664)として割り当てられる8遺伝子(表147)があった。

[表129]

表129 糖尿病非罹病・歯周病罹病者群で笑いにより発現減少した 注目遺伝子
サイトカイン・ケモカインシグナル伝達 (GO ID: 19221)

#	Gene Symbol	-fold change	Gene Name
1	SOCS1	0.40	suppressor of cytokine signaling 1
2	CCR1	0.45	chemokine (C-C motif) receptor 1
3	CSF2RB	0.53	colony stimulating factor 2 receptor, beta, low-affinity (granulocyte-macrophage)
4	STAT5A	0.60	Signal transducer and activator of transcription 5A
5	STAT3	0.64	signal transducer and activator of transcription 3 (acute-phase response factor)
6	TNFRSF1B	0.65	tumor necrosis factor receptor superfamily, member 1B

[表130]

表130 糖尿病非罹病・歯周病罹病者群で笑いにより発現減少した 注目遺伝子
リポ蛋白質異化 (GO ID: 42159、45192)

#	Gene Symbol	-fold change	Gene Name
1	SNX17	0.63	Sorting nexin 17
2	SCARF1	0.65	Scavenger receptor class F, member 1

[表131]

表131 糖尿病非罹病・歯周病罹病者群で笑いにより発現減少した 注目遺伝子
脂質輸送 (GO ID: 6869)

#	Gene Symbol	-fold change	Gene Name
1	LDLR	0.41	low density lipoprotein receptor (familial hypercholesterolemia)
2	STARD3	0.47	START domain containing 3
3	CLN8	0.54	ceroid-lipofuscinosis, neuronal 8 (epilepsy, progressive with mental retardation)
4	APOL1	0.55	apolipoprotein L, 1
5	ATP10A	0.59	ATPase, Class V, type 10A
6	PSAP	0.62	prosaposin (variant Gaucher disease and variant metachromatic leukodystrophy)
7	OSBP2	0.62	oxysterol binding protein 2
8	PSAP	0.63	prosaposin (variant Gaucher disease and variant metachromatic leukodystrophy)
9	SLC27A1	0.63	solute carrier family 27 (fatty acid transporter), member 1
10	APOL6	0.64	apolipoprotein L, 6

[表132]

表132 糖尿病非罹病・歯周病罹病者群で笑いにより発現減少した 注目遺伝子
インスリン受容体シグナル伝達経路関連(GO ID: 8286、または(GO ID: 46627)

#	Gene Symbol	-fold change	Gene Name
1	SOCS1	0.40	Suppressor of cytokine signaling 1
2	STXBP4	0.40	syntaxin binding protein 4
3	SOCS3	0.59	Suppressor of cytokine signaling 3
4	AKT1	0.61	V-akt murine thymoma viral oncogene homolog 1
5	MLLT7	0.61	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 7
6	INSIGF; pp9974; C11orf43; FLJ22066; FLJ44734	0.65	insulin-like growth factor 2 (somatomedin A)

[表133]

表133 糖尿病非罹病・歯周病罹病者群で笑いにより発現減少した 注目遺伝子
インターロイキン6生合成関連 (GO ID: 45408、42226)

#	Gene Symbol	-fold change	Gene Name
1	CEBPB	0.54	CCAAT/enhancer binding protein (C/EBP), beta
2	CEBPB	0.66	CCAAT/enhancer binding protein (C/EBP), beta
3	NLRP12	0.66	NLR family, pyrin domain containing 12

[表134]

表134 糖尿病罹病・歯周病非罹病者群で笑いにより発現減少した 注目遺伝子
抗生物質生合成・代謝 (GO ID: 17000, 16999)

#	Gene Symbol	-fold change	Gene Name
1	APBA2BP	0.58	amyloid beta (A4) precursor protein-binding, family A, member 2 binding protein
2	EFCBP2	0.59	EF-hand calcium binding protein 2

[表135]

表135 糖尿病罹病・歯周病非罹病者群で笑いにより発現減少した 注目遺伝子
アルギニン合成 (GO ID: 6526)、尿酸回路・代謝 (GO ID: 19627,50)

#	Gene Symbol	-fold change	Gene Name
1	ASS1	0.62	argininosuccinate synthetase 1
2	NAGS	0.66	N-acetylglutamate synthase

[表136]

表136 糖尿病罹病・歯周病非罹病者群で笑いにより発現減少した 注目遺伝子
リンパ球分化 (GO ID: 30098)

#	Gene Symbol	-fold change	Gene Name
1	IL6	0.41	Interleukin 6 (interferon, beta 2)
2	FLT3	0.49	Fms-related tyrosine kinase 3
3	IL4	0.52	Interleukin 4
4	U51869	0.59	Human proto-oncogene Bcd orf1 and orf2 mRNA, complete cds. [U51869]
5	CD1D	0.65	CD1d molecule

[表137]

表137 糖尿病罹病・歯周病罹病者群で笑いにより発現増加した 注目遺伝子
ウイルスレスポンス防御 (GO ID: 51607)

#	Gene Symbol	-fold change	Gene Name
1	TLR7	1.74	toll-like receptor 7
2	BCL2	1.52	B-cell CLL/lymphoma 2
3	TLR8	1.51	toll-like receptor 8

[表138]

表138 糖尿病罹病・歯周病罹病者群で笑いにより発現増加した 注目遺伝子
インターフェロン生合成制御、(GO ID: 45356,45359,45357,45350,45351)
インターロイキン8生合成 (GO ID: 45354,45414,45416)

#	Gene Symbol	-fold change	Gene Name
1	TLR7	1.74	toll-like receptor 7
2	TLR8	1.51	toll-like receptor 8

[表139]

表139 糖尿病罹病・歯周病罹病者群で笑いにより発現減少した 注目遺伝子
脂質代謝制御 (GO ID: 19216)

#	Gene Symbol	-fold change	Gene Name
1	SPF; TAP; TAP1; C22orf6; KIAA1186; KIAA1658; MGC65053	0.30	SEC14-like 2 (S. cerevisiae)
2	PPARA	0.46	Peroxisome proliferator-activated receptor alpha
3	NR5A1	0.49	Nuclear receptor subfamily 5, group A, member 1
4	C1QTNF2	0.57	C1q and tumor necrosis factor related protein 2

[表140]

表140 糖尿病罹病・歯周病罹病者群で笑いにより発現減少した 注目遺伝子
I-kappaBリン酸基転移 (GO ID: 7252)

#	Gene Symbol	-fold change	Gene Name
1	ERC1	0.50	ELKS/RAB6-interacting/CAST family member 1
2	ERC1	0.64	ELKS/RAB6-interacting/CAST family member 1

[表141]

表141 歯周病非罹病者群で笑いにより発現減少した 注目遺伝子
カテコールアミン代謝 (GO ID: 6584)

#	Gene Symbol	-fold change	Gene Name
1	MOXD1	0.52	monooxygenase, DBH-like 1
2	AOC2	0.55	amine oxidase, copper containing 2 (retina-specific)
3	NR4A2	0.65	Nuclear receptor subfamily 4, group A, member 2

[表142]

表142 歯周病非罹病者群で笑いによって発現減少した 注目遺伝子
インスリン制御 (GO ID: 46676)

#	Gene Symbol	-fold change	Gene Name
1	FAM3D	0.61	family with sequence similarity 3, member D

[表143]

表143 歯周病罹病者群で笑いにより発現減少した 注目遺伝子
抗原提示 (GO ID: 19882)

#	Gene Symbol	-fold change	Gene Name
1	HLA-C	0.47	major histocompatibility complex, class I, C
2	HLA-H	0.47	major histocompatibility complex, class I, H (pseudogene)
3	ENST00000355804	0.47	GB|M80470.1|AAA66955.1 MHC class I HLA-J antigen [NP111779]
4	HLA-A	0.47	major histocompatibility complex, class I, A
5	IGHG1	0.51	Immunoglobulin heavy constant gamma 1 (G1m marker)
6	HLA-E	0.52	major histocompatibility complex, class I, E
7	HLA-B	0.53	major histocompatibility complex, class I, B
8	CD1D	0.54	CD1d molecule
9	FLJ45422	0.55	FLJ45422 protein
10	HLA-F	0.59	major histocompatibility complex, class I, F
11	LOC649853	0.59	similar to HLA class I histocompatibility antigen, A-29 alpha chain precursor (MHC class I antigen A*29) (Aw-19)
12	HLA-B	0.59	major histocompatibility complex, class I, B
13	CD74	0.61	CD74 molecule, major histocompatibility complex, class II invariant chain
14	HLA-E	0.61	major histocompatibility complex, class I, E
15	HLA-A	0.64	major histocompatibility complex, class I, A
16	AP3B1	0.64	Adaptor-related protein complex 3, beta 1 subunit

[表144]

表144 歯周病罹病者群で笑いにより発現減少した 注目遺伝子
NF-KappaB制御関連 (GO ID: 43122または43123または7249)

#	Gene Symbol	-fold change	Gene Name
1	VISA	0.40	Virus-induced signaling adapter
2	CASP8	0.49	Caspase 8, apoptosis-related cysteine peptidase
3	NDFIP1	0.51	Nedd4 family interacting protein 1
4	CFLAR	0.52	CASP8 and FADD-like apoptosis regulator
5	SECTM1	0.54	Secreted and transmembrane 1
6	APOL3	0.54	Apolipoprotein L, 3
7	LTBR	0.55	Lymphotoxin beta receptor (TNFR superfamily, member 3)
8	C1orf166	0.55	Chromosome 1 open reading frame 166
9	MYD88	0.57	Myeloid differentiation primary response gene (88)
10	TRIM38	0.58	Tripartite motif-containing 38
11	CANT1	0.58	Calcium activated nucleotidase 1
12	SLC20A1	0.59	Solute carrier family 20 (phosphate transporter), member 1
13	NDFIP1	0.59	Nedd4 family interacting protein 1
14	REL	0.60	V-rel reticuloendotheliosis viral oncogene homolog (avian)
15	NLRP12	0.61	NLR family, pyrin domain containing 12
16	LGALS9	0.62	Lectin, galactoside-binding, soluble, 9 (galectin 9)
17	MIER1	0.62	Mesoderm induction early response 1 homolog (Xenopus laevis)
18	SCOTIN	0.62	Scotin
19	NM_014261	0.62	Homo sapiens toll-like receptor adaptor molecule 1 (TICAM1), transcript variant 1, mRNA [NM_014261]
20	TICAM1	0.62	toll-like receptor adaptor molecule 1
21	CXXC5	0.64	CXXC finger 5
22	SQSTM1	0.64	sequestosome 1
23	TRIM38	0.64	Tripartite motif-containing 38
24	IKBKE	0.65	Inhibitor of kappa light polypeptide gene enhancer in B-cells, kinase epsilon
25	FKBP1A	0.65	FK506 binding protein 1A, 12kDa
26	FLNA	0.66	Filamin A, alpha (actin binding protein 280)
27	EDARADD	0.66	EDAR-associated death domain

[表145]

表145 歯周病罹病者群で笑いにより発現減少した 注目遺伝子
脂質分泌 (GO ID: 19915)

#	Gene Symbol	-fold change	Gene Name
1	STAT5A	0.56	Signal transducer and activator of transcription 5A
2	STAT5B	0.58	Signal transducer and activator of transcription 5B
3	STAT5B	0.63	Signal transducer and activator of transcription 5B
4	GM2A	0.63	GM2 ganglioside activator
5	HEXA	0.66	hexosaminidase A (alpha polypeptide)
6	GM2A	0.67	GM2 ganglioside activator

[表146]

表146 歯周病罹病者群で笑いにより発現減少した 注目遺伝子
NK細胞活性分化 (GO ID: 1779)、B細胞分化(GO ID:45579)、
T細胞恒常性(GO ID:43029)

#	Gene Symbol	-fold change	Gene Name
1	STAT5A	0.56	Signal transducer and activator of transcription 5A
2	STAT5B	0.58	Signal transducer and activator of transcription 5B
3	STAT5B	0.63	Signal transducer and activator of transcription 5B

[表147]

表147 歯周病罹病者群で笑いにより発現減少した 注目遺伝子
糖脂質代謝 (GO ID: 6664)

#	Gene Symbol	-fold change	Gene Name
1	LARGE	0.45	Like-glycosyltransferase
2	PSAP	0.48	Prosaposin (variant Gaucher disease and variant metachromatic leukodystrophy)
3	PSAP	0.50	Prosaposin (variant Gaucher disease and variant metachromatic leukodystrophy)
4	CLN3	0.57	Ceroid-lipofuscinosis, neuronal 3, juvenile (Batten, Spielmeyer-Vogt disease)
5	CLN3	0.62	Ceroid-lipofuscinosis, neuronal 3, juvenile (Batten, Spielmeyer-Vogt disease)
6	GM2A	0.63	GM2 ganglioside activator
7	TSD; MGC99608	0.66	hexosaminidase A (alpha polypeptide)
8	GM2A	0.67	GM2 ganglioside activator

[0509] 4-1-4-2-4. リアルタイム定量PCR解析

被験者ごとの各遺伝子の笑い体験前のPCR定量値に対する笑い体験後の定量値の比を表148に示す。今回の結果ではDNAチップ解析結果とリアルタイムPCR解析結果では、対象被験者により不一致が見られ、確実な相関は得られなかった。

[表148]

表148 歯周病罹病者群(P2)で笑い前後の発現変動が大きかった4遺伝子の各被験者ごとの発現比(リアルタイム定量PCR解析)

	Sample Name	Gene Name			
		CTSA	CTSB	IL8RB	TLR7
糖尿病罹病・歯周病非罹病者群	003 P1	1.09	1.19	0.96	1.07
	006 P1	1.16	1.12	1.31	1.08
糖尿病非罹病・歯周病非罹病者群	105 P1	0.62	0.62	0.94	0.44
	110 P1	0.92	1.02	1.37	0.89
	119 P1	1.27	1.13	1.24	0.86
糖尿病罹病・歯周病罹病者群	053 P2	0.89	0.77	0.96	1.70
	060 P2	0.83	0.79	1.21	0.85
	066 P2	0.94	1.06	0.72	1.28
糖尿病非罹病・歯周病罹病者群	106 P2	0.85	0.92	0.68	1.64
	107 P2	1.00	1.16	1.03	1.33
	114 P2	0.81	0.89	1.46	1.39
DNAチップ解析データ	P1	0.84	0.90	0.89	1.24
	P2	0.49	0.50	0.46	1.94

[0510] 4-1-4-3. 考察・結論

今回の実験について、以下の2つの観点から考察した。

[0511] (1) 健康な状態の人において、笑い刺激により発現変動する遺伝子群

(2) 歯周病罹病者において、笑い刺激により発現変動する遺伝子群

(1) 健康な状態の人において、笑い刺激により発現変動する遺伝子群

A群では、免疫系を始め、生体防御、抗細胞死など様々な機能の遺伝子が発現変化し、B群、A+B群においても同様に免疫系を始めとする多くの遺伝子の発現変化がみられた。A群、B群、A+B群においては、笑いによりs-IgA(唾液中の分泌型免疫グロブリンA)の増加が認められた。

[0512] このことは、健康な状態の人において、笑い刺激により、肺への酸素取り込みや、筋肉への酸素運搬量が増加し、様々な生体機能の活性化が起こり、免疫系や生体防御などの健康維持・増進を担う多くの遺伝子の発現変化が起こったのではないかと示唆される。具体的な遺伝子については以下に示す。

[0513] A群において、Up-regulateされる遺伝子としては、GO解析において抗細胞死（GO ID:0006916）に割り当てられる遺伝子PROK2（遺伝子セット１No.3）があり、IgE受容体活性（GO ID:0019767）に割り当てられる遺伝子FCER1A（遺伝子セット１No.4）、レスポンス防御GO:0006952(defense response)に割り当てられる遺伝子CD69（遺伝子セット１No.5）、セロトニン輸送関連（GO ID: 6837または15222または5335）に割り当てられる遺伝子SLC6A4（遺伝子セット１No.7）、γグルタミン酸カルボキシラーゼ活性（GOID:0008488）に割り当てられる遺伝子GGCX（遺伝子セット１No.8）、酸素輸送（GOID:0015671）に割り当てられる遺伝子HBA2（遺伝子セット１No.9）、アルコール脱水素酵素活性（GOID :0004022）に割り当てられる遺伝子ADH5があった。逆にDown-regulateされる遺伝子としては、癌関連の遺伝子JUN、TP53、RAB5B、RAB8A、RAB12、RAB20、RAB30（遺伝子セット１No.11-17）、自然免疫反応（GOID:0045087）に割り当てられる遺伝子VISA、CD55（遺伝子セット１No.18-19）、免疫反応（GOID:0006955）に割り当てられる遺伝子IGHG1（遺伝子セット１No.20）、レスポンス防御（GO:0006952）に割り当てられる遺伝子CD84（遺伝子セット１No.22）、転写因子（GOIID:0003700）に割り当てられる遺伝子NFAT5（遺伝子セット１No.25）、細胞死（GOID:0006915）に割り当てられる遺伝子TNFAIP3（遺伝子セット１No.27）があった。

[0514] B群では、笑いによりDown-regulateされる遺伝子の解析において、サイトカイン・ケモカインシグナル伝達(GO ID: 19221)に割り当てられる遺伝子SOCS1、CCR1、CSF2RB、STAT5A、
STAT3、TNFRSF1B (表129)、リポ蛋白質異化(GO ID: 42159、45192)に割り当てられる遺伝子SNX17、SCARF1 (表130)、脂質輸送(GO ID: 6869)に割り当てられる脂質輸送(GO ID: 6869)に割り当てられるLDLR、STARD3、CLN8、APOL1、ATP10A、PSAP、OSBP2、SLC27A1、APOL6(表131)、インスリン受容体シグナル伝達関連(GO ID: 8286または46627)に割り当てられるSOCS1、STXBP4、SOCS3、AKT1、MLLT7、INSIGF(表132)、インターロイキン6生合成関連(GO ID: 45408、42226)に割り当てられる遺伝子CEBPB、NLRP12 (表133)があった。

[0515] A+B群においては、Up-regulateされる遺伝子の解析において、抗原受容体シグナル伝達経路関連(GO ID: 50854、50857)に割り当てられる3遺伝子PTPRC、PAWR、TRAT1 (表124)、Down-regulateされる遺伝子の解析において、グルコース輸送(GO ID: 15758)に割り当てられる5遺伝子STXBP4、SLC2A5、SLC2A3、SORBS1、AKT1 (表126)、リポ蛋白質代謝(GO ID: 42157)に割り当てられる遺伝子APOL6、ATG10、SNX17、PIGS、FNTB (表126)、pH調整(GO ID: 6885)に割り当てられる遺伝子SLC9A5、LOC133308、CLN5、CLN3 (表127)があった。

[0516] (2) 歯周病罹病者において、笑い刺激により発現変動する遺伝子群

B+D群(歯周病罹病者群)において、笑いにより多くの遺伝子発現変化が認められた。この結果は、C群とD群との比較でも、A群のB群の比較でも同様であった。このことは、歯周病が慢性炎症疾患であり、常に細菌などの刺激にさらされ、免疫系を始めとする様々な機能が活性された状態であるため、笑いという刺激が多くの遺伝子の発現変化を引き起こす要因となったのではないかと示唆される。

[0517] 歯周病は糖尿病の第6の合併症といわれ、糖尿病による末梢血管の脆弱性の亢進は歯周病発症や増悪の原因となり、また、慢性炎症疾患である歯周病では腫瘍壊死因子(TNF-α)などのサイトカインが産生されることによりインスリン抵抗性が増し、糖尿病の増悪因子となることが報告されている。更に、

糖尿病と歯周病の相関は、近年多くのことがわかってきており、糖尿病患者の歯周炎の組織では、多形核白血球機能（走化能、貪食能、殺菌能）の低下、歯周結合組織のコラーゲン代謝異常、終末糖化産物(AGE;advanced endproduct)の歯肉組織への蓄積による炎症、創傷治癒の遅延などが認められる。

[0518] 今回の研究では、歯周病罹病者群(B＋D群)が歯周病非罹病者群(A＋C群)に比較して多くの遺伝子の発現変化がみられ、これらの遺伝子が多くのGO termに割り当てられた。Up-regulateされる遺伝子としてはGOカテゴリー上比較的上位である代謝や生合成に関するGO termに割り当てられ、特異的な下位のGO termには割り当てられなかった。逆にDown-regulateされる遺伝子としてはGOカテゴリー上、特異的な下位のGO termにも割り与えられた。これらのGO termに含まれる遺伝子としてはHLA-A 、HLA-B、HLA-C、HLA-E、HLA-H、CD1D、CD74、VISA、CASP8、CFLAR、APOL、LTBR、CTSA、CTSB、LOC391803、KRTAP3-3、SESN2など免疫・炎症・自己防衛などに関わる遺伝子やSTAT5A、STAT5Bなど脂質分泌に関わる遺伝子、FFAR2など脂質代謝に関わる遺伝子があった。

[0519] また、D群(糖尿病罹病・歯周病罹病者群)では、笑いによりUp-regulateされた遺伝子としては、GO解析においてウイルスレスポンス防御(GO ID: 51607)、インターフェロン生合成関連(GO ID: 45356、45359、45357、45350、45351)、インターロイキン8生合成(GO ID: 45354、45414、45416)に割り当てられる遺伝子TLR7、TLR8、BCL2があり、Down-regulateされた遺伝子としては、GO解析において脂質代謝制御(GO ID: 19216)に割り当てられるPPARA、NR5A1、C1QTNF、I-kappaB、リン酸基転移(GO ID:7252)割り当てられるERC1があった。

[0520] 同様に、B群(糖尿病非罹病・歯周病罹病者群)では、Up-regulate された遺伝子としては、特異的な機能を有するGOtermは少なく、Down-regulateされた遺伝子としては、GO解析においてサイトカイン・ケモカインシグナル伝達 (GO ID: 19221)に割り当てられるSOCS1、CCR1、CFS2RB、STAT5A、STAT3、TINFRSF1B、リポ蛋白質異化(GO ID: 42159)に割り当てられるSNX17、SCARF1、脂質輸送(GO ID: 6869)に割り当てられるLDLR、STARD3、CLN8、APOL1、ATP10A、PSAP、SLC27A1、APOL6、インスリン受容体シグナル伝達関連(GO ID: 8286また

は46627)に割り当てられるSOCS1、STXBP4、SOCS3、AKT1、MLLT7、INSIGFがあった。

[0521] B＋D群(歯周病罹病者群)と、D群(糖尿病患者・歯周病罹病者群)で発現変化した遺伝子のオントロジー解析では、主に免疫・炎症・生体防御に関するGOtermに割り当てられた。B群(糖尿病非罹病・歯周病罹病者群)ではこれらTermに割り当てられる遺伝子は少なかった。糖尿病と歯周病との相関には免疫・炎症・生体防御が深く関与しているとされているが、これらに関連する遺伝子の発現が笑いにより変化することが、末梢血白血球の遺伝子発現の網羅的解析で検証される結果となった。

[0522] 4-1-5. 特定された遺伝子

上記解析2で笑いにより遺伝子発現の変動が認められた遺伝子のうち、機能面で注目すべき遺伝子、及び特に発現変動の大きかった上位15遺伝子を表149～154に示し、これらを要約した表155を遺伝子セット5の表として示す。

[表149]

表149 遺伝子セット5(No.1-17:複数面で注目する遺伝子)

No	Cy5	Cy3	ratio	RefSeq Accession	Genbank Accession	Entrez Gene ID	Gene Symbol	Gene Name	Ensembl ID	TIGR ID	GO	Description	Genomic Coordinates
1	141.70	56.17	2.52	NM_080923	NM_080923	5788	PTPRC	protein tyrosine phosphatase, receptor type, C	ENST00000367364	THC2479594	GO:0001915(negative regulation of T cell mediated cytotoxicity)|GO:0001960(negative regulation of cytokine and chemokine mediated signaling pathway)|GO:0004725(protein tyrosine phosphatase activity)|GO:0004872(receptor activity)|GO:0005001(transmembrane r	Homo sapiens protein tyrosine phosphatase, receptor type, C (PTPRC), transcript variant 4, mRNA [NM_080923]	chr1:196922886 3-196928922
2	85.90	42.37	2.03	NM_002583	NM_002583	5074	PAWR	PRKC, apoptosis, WT1, regulator	ENST00000328827	NP083946	GO:0000122(negative regulation of transcription from RNA polymerase II promoter)|GO:0003714(transcription corepressor activity)|GO:0005634(nucleus)|GO:0005737(cytoplasm)|GO:0006350(transcription)|GO:0006355(regulation of transcription, DNA-dependent)|GO:0	Homo sapiens PRKC, apoptosis, WT1, regulator (PAWR), mRNA [NM_002583]	chr12:78514551 0-78514491
3	341.12	218.23	1.56	NM_016388	NM_016388	50852	TRAT1	T cell receptor associated transmembrane adaptor 1	ENST00000295756	NP174928	GO:0001920(negative regulation of receptor recycling)|GO:0005068(transmembrane receptor protein tyrosine kinase adaptor protein activity)|GO:0005886(plasma membrane)|GO:0005887(integral to plasma membrane)|GO:0006955(immune response)|GO:0006968(cellular d	Homo sapiens T cell receptor associated transmembrane adaptor 1 (TRAT1), mRNA [NM_016388]	chr3:111005543 8-111055497

[表150]

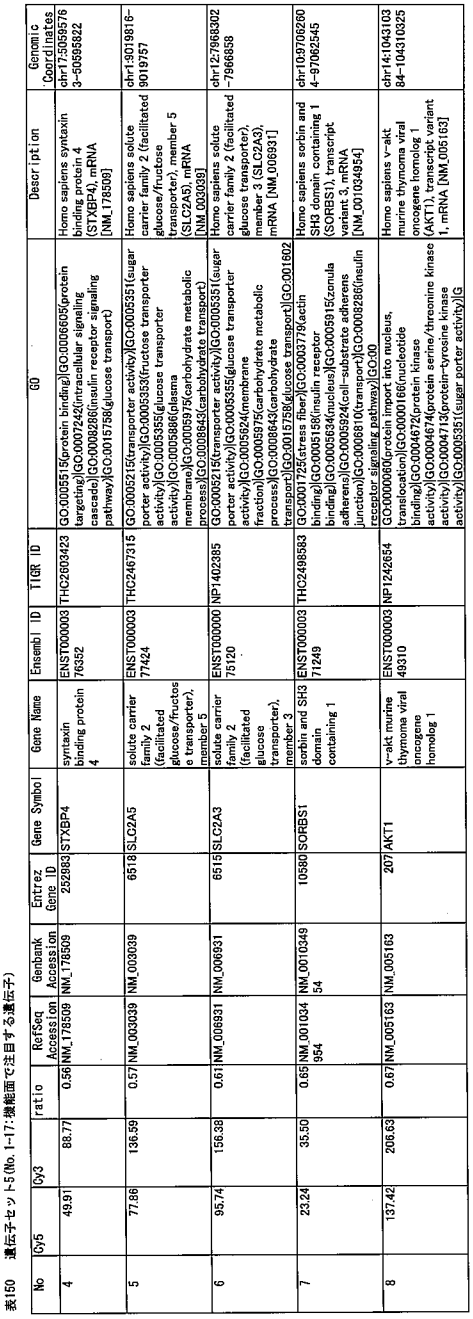


表150 遺伝子セット5(No. 1-17:機能面で注目する遺伝子)

No	Cy5	Cy3	ratio	RefSeq Accession	Genbank Accession	Entrez Gene ID	Gene Symbol	Gene Name	Ensembl ID	TIGR ID	GO	Description	Genomic Coordinates
4	49.91	88.77	0.56	NM_178509	NM_178509	252983	STXBP4	syntaxin binding protein 4	ENST00000376352	THC2603423	GO:0005515(protein binding)|GO:0006605(protein targeting)|GO:0007242(intracellular signaling cascade)|GO:0008286(insulin receptor signaling pathway)|GO:0015758(glucose transport)	Homo sapiens syntaxin binding protein 4 (STXBP4), mRNA [NM_178509]	chr17:3595576 3-30395822
5	77.86	136.59	0.57	NM_003039	NM_003039	6518	SLC2A5	solute carrier family 2 (facilitated glucose/fructose transporter), member 5	ENST00000377424	THC2467315	GO:0005215(transporter activity)|GO:0005351(sugar porter activity)|GO:0005353(fructose transporter activity)|GO:0005355(glucose transporter activity)|GO:0005986(disaccharide metabolic process)|GO:0005975(carbohydrate metabolic process)|GO:0009643(carbohydrate transport)	Homo sapiens solute carrier family 2 (facilitated glucose/fructose transporter), member 5 (SLC2A5), mRNA [NM_003039]	chr1:9019816-9019757
6	95.74	156.38	0.61	NM_006931	NM_006931	6515	SLC2A3	solute carrier family 2 (facilitated glucose transporter), member 3	ENST00000375120	NP1402385	GO:0005215(transporter activity)|GO:0005351(sugar porter activity)|GO:0005355(glucose transporter activity)|GO:0005624(membrane fraction)|GO:0005975(carbohydrate metabolic process)|GO:0008645(carbohydrate transport)|GO:0015758(glucose transport)|GO:0016021	Homo sapiens solute carrier family 2 (facilitated glucose transporter), member 3 (SLC2A3), mRNA [NM_006931]	chr12:7968302 -7966858
7	23.24	35.50	0.65	NM_001034954	NM_001034954	10580	SORBS1	sorbin and SH3 domain containing 1	ENST00000371249	THC2498583	GO:0001725(stress fiber)|GO:0003779(actin binding)|GO:0005198(insulin receptor binding)|GO:0005634(nucleus)|GO:0005915(zonula adherens)|GO:0009924(cell-substrate adherens junction)|GO:0008810(transporter)|GO:0008286(insulin receptor signaling pathway)|GO:00	Homo sapiens sorbin and SH3 domain containing 1 (SORBS1), transcript variant 3, mRNA [NM_001034954]	chr10:9706260 4-97062345
8	137.42	206.63	0.67	NM_005163	NM_005163	207	AKT1	v-akt murine thymoma viral oncogene homolog 1	ENST00000349310	NP1242654	GO:0000060(protein import into nucleus, translocation)|GO:0000166(nucleotide binding)|GO:0004672(protein kinase activity)|GO:0004674(protein serine/threonine kinase activity)|GO:0004713(protein-tyrosine kinase activity)|G	Homo sapiens v-akt murine thymoma viral oncogene homolog 1 (AKT1), transcript variant 1, mRNA [NM_005163]	chr14:1043103 84-104310825

[表151]

表151 遺伝子セット5(No. 1-17:機能面で注目する遺伝子)

No	Cy5	Cy3	ratio	RefSeq Accession	Genbank Accession	Entrez Gene ID	Gene Symbol	Gene Name	Ensembl ID	TIGR ID	GO	Description	Genomic Coordinates
9	3497.72	8575.59	0.41	NM_030641	NM_030641	80830	APOL6	apolipoprotein L, 6	0	THC2464922	GO:0003700(transcription factor activity)|GO:0005319(lipid transporter activity)|GO:0005576(extracellular region)|GO:0005737(cytoplasm)|GO:0008355(regulation of transcription, DNA-dependent)|GO:0006869(lipid transport)|GO:0008289(lipid binding)|GO:0042157	Homo sapiens apolipoprotein L, 6 (APOL6), mRNA [NM_030641]	chr22:34438706 4-34387123
10	36.58	68.24	0.54	NM_031482	NM_031482	83734	ATG10	ATG10 autophagy related 10 homolog (S. cerevisiae)	ENST0000003 80170	THC2567425	GO:0005515(protein binding)|GO:0005622(intracellular)|GO:0006497(protein amino acid lipidation)|GO:0006512(ubiquitin cycle)|GO:0006914(autophagy)|GO:0015031(protein transport)|GO:0031401(positive regulation of protein modification)	Homo sapiens ATG10 autophagy related 10 homolog (S. cerevisiae) (ATG10), mRNA [NM_031482]	chr5:81390072 -81390131
11	245.59	436.69	0.56	NM_014748	NM_014748	9784	SNX17	sorting nexin 17	ENST0000003 79967	THC2505892	GO:0005102(receptor binding)|GO:0005737(cytoplasm)|GO:0005769(early endosome)|GO:0005794(Golgi apparatus)|GO:0006886(intracellular protein transport)|GO:0006898(receptor-mediated endocytosis)|GO:0007165(signal transduction)|GO:0008022(protein C-terminus b	Homo sapiens sorting nexin 17 (SNX17), mRNA [NM_014748]	chr2:27450515 -27450744
12	147.10	231.66	0.63	NM_033198	NM_033198	94005	PIGS	phosphatidylinositol glycan anchor biosynthesis, class S	ENST0000003 08360	THC2595819	GO:0000329(GPI-anchor transamidase activity)|GO:0005515(protein binding)|GO:0005783(endoplasmic reticulum)|GO:0016020(membrane)|GO:0016021(integral to membrane)|GO:0016255(attachment of GPI anchor to protein)|GO:0042765(GPI-anchor transamidase complex)	Homo sapiens phosphatidylinositol glycan anchor biosynthesis, class S (PIGS), mRNA [NM_033198]	chr17:2390617 8-2390619
13	69.31	107.36	0.65	NM_002028	NM_002028	2342	FNTB	farnesyltransferase, CAAX box, alpha beta	ENST0000002 46166	THC2548627	GO:0004311(farnesyltransferase activity)|GO:0004660(protein farnesyltransferase activity)|GO:0005515(protein binding)|GO:0005737(cytoplasm)|GO:0008270(zinc ion binding)|GO:0008285(negative regulation of cell proliferation)|GO:0016740(transferase acti	Homo sapiens farnesyltransferase, CAAX box, beta (FNTB), mRNA [NM_002028]	chr14:8459772 1-64597780

[表152]

表152 遺伝子セット5(No.1-17:横断面で注目する遺伝子)

No	Cy5	Cy3	ratio	RefSeq Accession	Genbank Accession	Entrez Gene ID	Gene Symbol	Gene Name	Ensembl ID	TIGR ID	GO	Description	Genomic Coordinates
14	52.03	121.89	0.43	NM_004594	NM_004594	6558	SLC9A5	solute carrier family 9 (sodium/hydrogen exchanger), member 5	ENST00000299798	THC2602449	GO:0006811(ion transport)|GO:0006814(sodium ion transport)|GO:0006885(regulation of pH)|GO:0015297(antiporter activity)|GO:0015298(solute:hydrogen antiporter activity)|GO:0015385(sodium:hydrogen antiporter activity)|GO:0016020(membrane)|GO:0016021(integra	Homo sapiens solute carrier family 9 (sodium/hydrogen exchanger), member 5 (SLC9A5), mRNA [NM_004594]	chr16:65586351 -65863575
15	23.47	39.57	0.59	NM_178833	NM_178833	133308	LOC133308	hypothetical protein BC009732	ENST00000362026	THC2625365	GO:0006810(transport)|GO:0006885(regulation of pH)|GO:0015299(solute:hydrogen antiporter activity)|GO:0016021(integral to membrane)	Homo sapiens hypothetical protein BC009732 (LOC133308), mRNA [NM_178833]	chr4:104418391 -104172373
16	25.76	39.33	0.65	NM_006493	NM_006493	1203	CLN5	ceroid-lipofuscinosis, neuronal 5	ENST00000377453	THC2467058	GO:0005515(protein binding)|GO:0005615(extracellular space)|GO:0005765(lysosomal membrane)|GO:0005775(vacuolar lumen)|GO:0005783(endoplasmic reticulum)|GO:0005794(Golgi apparatus)|GO:0007042(lysosomal lumen acidification)|GO:0007420(brain development)|GO:	Homo sapiens ceroid-lipofuscinosis, neuronal 5 (CLN5), mRNA [NM_006493]	chr13:76474211 -76474270
17	382.33	578.56	0.66	NM_001042432	NM_001042432	1201	CLN3	ceroid-lipofuscinosis, neuronal 3, juvenile (Batten, Spielmeyer-Vogt disease)	ENST00000360019	NP072643	GO:0000139(Golgi membrane)|GO:0001575(globoside metabolic process)|GO:0005624(membrane fraction)|GO:0005634(nucleus)|GO:0005737(cytoplasm)|GO:0005739(mitochondrion)|GO:0005764(lysosome)|GO:0005769(early endosome)|GO:0005783(endoplasmic reticulum)|GO:00057	Homo sapiens ceroid-lipofuscinosis, neuronal 3, juvenile (Batten, Spielmeyer-Vogt disease) (CLN3), transcript variant 1, mRNA [NM_001042432]	chr16:28401132 -28401170

[表153]

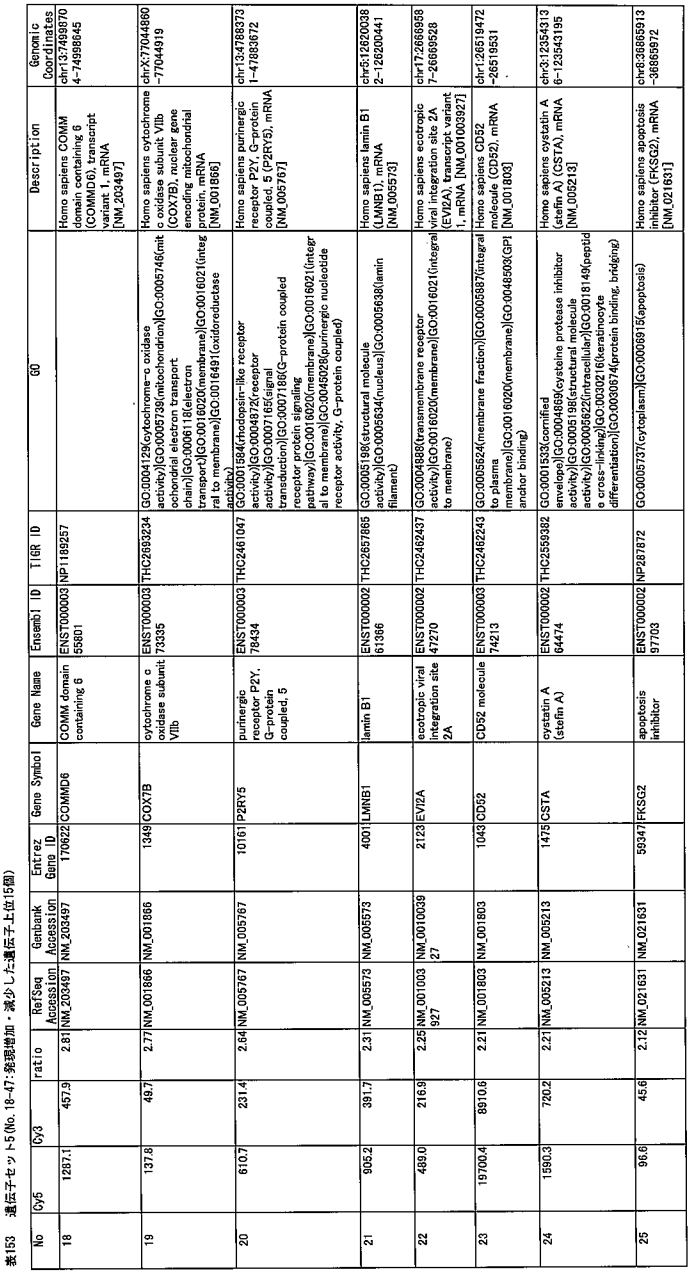


表153 遺伝子セット5(No.18-47:発現増加・減少した遺伝子上位15個)

No	Cy5	Cy3	ratio	RefSeq Accession	Genbank Accession	Entrez Gene ID	Gene Symbol	Gene Name	Ensembl ID	T16R ID	GO	Description	Genomic Coordinates
18	1287.1	457.9	2.81	NM_203497	NM_203497	170622	COMMD6	COMM domain containing 6	ENST00000355801	NP1189257		Homo sapiens COMM domain containing 6 (COMMD6), transcript variant 1, mRNA [NM_203497]	chr13:74998670-74998645
19	137.8	49.7	2.77	NM_001866	NM_001866	1349	COX7B	cytochrome c oxidase subunit VIIb	ENST00000373335	THC2693234	GO:0004129(cytochrome-c oxidase activity)|GO:0005739(mitochondrion)|GO:0005746(mitochondrial electron transport chain)|GO:0006118(electron transport)|GO:0016020(membrane)|GO:0016021(integral to membrane)|GO:0016491(oxidoreductase activity)	Homo sapiens cytochrome c oxidase subunit VIIb (COX7B), nuclear gene encoding mitochondrial protein, mRNA [NM_001866]	chrX:77044860-77044919
20	610.7	231.4	2.64	NM_005767	NM_005767	10161	P2RY5	purinergic receptor P2Y, G-protein coupled, 5	ENST00000378434	THC2461047	GO:0001584(rhodopsin-like receptor activity)|GO:0004872(receptor activity)|GO:0007165(signal transduction)|GO:0007186(G-protein coupled receptor protein signaling pathway)|GO:0016020(membrane)|GO:0016021(integral to membrane)|GO:0045028(purinergic nucleotide receptor activity, G-protein coupled)	Homo sapiens purinergic receptor P2Y, G-protein coupled, 5 (P2RY5), mRNA [NM_005767]	chr13:47883733-47883672
21	905.2	391.7	2.31	NM_005573	NM_005573	4001	LMNB1	lamin B1	ENST00000261366	THC2657865	GO:0005198(structural molecule activity)|GO:0005634(nucleus)|GO:0005638(lamin filament)	Homo sapiens lamin B1 (LMNB1), mRNA [NM_005573]	chr5:132620038-132620441
22	489.0	216.9	2.25	NM_001003927	NM_001003927	2123	EVI2A	ecotropic viral integration site 2A	ENST00000247270	THC2462437	GO:0004888(transmembrane receptor activity)|GO:0016020(membrane)|GO:0016021(integral to membrane)	Homo sapiens ecotropic viral integration site 2A (EVI2A), transcript variant 1, mRNA [NM_001003927]	chr17:26669868-26669526
23	19700.4	8910.6	2.21	NM_001803	NM_001803	1043	CD52	CD52 molecule	ENST00000374213	THC2462243	GO:0005624(membrane fraction)|GO:0005887(integral to plasma membrane)|GO:0016020(membrane)|GO:0048503(GPI anchor binding)	Homo sapiens CD52 molecule (CD52), mRNA [NM_001803]	chr1:26519472-26519531
24	1590.3	720.2	2.21	NM_005213	NM_005213	1475	CSTA	cystatin A (stefin A)	ENST00000264474	THC2559382	GO:0001533(cornified envelope)|GO:0004869(cysteine protease inhibitor activity)|GO:0005198(structural molecule activity)|GO:0005622(intracellular)|GO:0018149(peptide cross-linking)|GO:0030216(keratinocyte differentiation)|GO:0030674(protein binding, bridging)	Homo sapiens cystatin A (stefin A) (CSTA), mRNA [NM_005213]	chr3:123543313-123543195
25	96.6	45.6	2.12	NM_021631	NM_021631	58347	FKSG2	apoptosis inhibitor	ENST00000297703	NP287872	GO:0005737(cytoplasm)|GO:0006915(apoptosis)	Homo sapiens apoptosis inhibitor (FKSG2), mRNA [NM_021631]	chr6:38665913-38665972

[0523]

表153　遺伝子セット5(No.18-47:発現増加・減少した遺伝子上位15個)

No	Cy5	Cy3	ratio	RefSeq Accession	Genbank Accession	Entrez Gene ID	Gene Symbol	Gene Name	Ensembl ID	TIGR ID	GO	Description	Genomic Coordinates
26	84.1	39.7	2.12	NM_004280	NM_004280	9521	EEF1E1	eukaryotic translation elongation factor 1 epsilon 1	ENST00000379715	THC2708665	GO:0000074(regulation of progression through cell cycle)|GO:0005515(protein binding)|GO:0005634(nucleus)|GO:0005737(cytoplasm)|GO:0006281(DNA repair)|GO:0006412(translation)|GO:0008285(negative regulation of cell proliferation)|GO:0009790(embryonic development)|GO:0017101(aminoacyl-tRNA synthetase multienzyme complex)|GO:0043065(positive regulation of apoptosis)|GO:0043517(positive regulation of DNA	Homo sapiens eukaryotic translation elongation factor 1 epsilon 1 (EEF1E1), mRNA [NM_004280]	chr6:8042590-8042531
27	97.9	46.3	2.11	NM_000484	NM_000484	351	APP	amyloid beta (A4) precursor protein (peptidase nexin-II, Alzheimer disease)	ENST00000346798	NP922631	GO:0000085(G2 phase of mitotic cell cycle)|GO:0001967(suckling behavior)|GO:0004867(serine-type endopeptidase inhibitor activity)|GO:0005488(binding)|GO:0005506(iron ion binding)|GO:0005507(copper ion binding)|GO:0005515(protein binding)|GO:0005576(extrac	Homo sapiens amyloid beta (A4) precursor protein (peptidase nexin-II, Alzheimer disease) (APP), transcript variant 1, mRNA [NM_000484]	chr21:26191816-26191757
28	124.3	58.9	2.11	NM_002351	NM_002351	4068	SH2D1A	SH2 domain protein 1A, Duncan's disease (lymphoproliferative syndrome)	ENST00000371139	THC2471348	GO:0005070(SH3/SH2 adaptor activity)|GO:0005737(cytoplasm)|GO:0006959(humoral immune response)|GO:0006968(cellular defense response)|GO:0007242(intracellular signaling cascade)|GO:0007267(cell-cell signaling)	Homo sapiens SH2 domain protein 1A, Duncan's disease (lymphoproliferative syndrome) (SH2D1A), mRNA [NM_002351]	chrX:123333021-123333080
29	165.0	79.6	2.07	NM_015387	NM_015387	25843	PREI3	preimplantation protein 3	ENST00000323303	THC2499735	GO:0006810(transport)|GO:0008270(zinc ion binding)|GO:0016020(membrane)|GO:0046872(metal ion binding)	Homo sapiens preimplantation protein 3 (PREI3), transcript variant 1, mRNA [NM_015387]	chr2:198123278-198123337
30	63.6	32.0	1.99	NM_021914	NM_021914	1073	CFL2	cofilin 2 (muscle)	ENST00000298159	THC2485744	GO:0003779(actin binding)|GO:0005515(protein binding)|GO:0005622(intracellular)|GO:0005634(nucleus)|GO:0005856(cytoskeleton)	Homo sapiens cofilin 2 (muscle) (CFL2), transcript variant 1, mRNA [NM_021914]	chr14:34249492-34249433
31	291.4	146.5	1.99	NM_207038	NM_207038	6938	TCF12	transcription factor 12 (HTF4, helix-loop-helix transcription factors 4)	ENST00000333725	THC2579430	GO:0003677(DNA binding)|GO:0003702(RNA polymerase II transcription factor activity)|GO:0005634(nucleus)|GO:0006357(regulation of transcription from RNA polymerase II promoter)|GO:0006955(immune response)|GO:0007275(multicellular organismal development)|GO:0007517(muscle development)|GO:0030528(transcription regulator activity)|GO:0045449(regulation of transcription)	Homo sapiens transcription factor 12 (HTF4, helix-loop-helix transcription factors 4) (TCF12), transcript variant 4, mRNA [NM_207038]	chr15:55352693-55352752
32	745.9	378.8	1.97	NM_015364	NM_015364	23643	LY96	lymphocyte antigen 96	ENST00000284818	THC2477637	GO:0005615(extracellular space)|GO:0005886(plasma membrane)|GO:0006954(inflammatory response)|GO:0006955(immune response)|GO:0006968(cellular defense response)|GO:0007166(cell surface receptor linked signal transduction)|GO:0015026(coreceptor activity)|GO:0019733(antibacterial humoral response (sensu the Vertebrata research community))	Homo sapiens lymphocyte antigen 96 (LY96), mRNA [NM_015364]	chr8:75103765-75103824

[表154]

表154 遺伝子セット5(No.18-47:発現増加・減少した遺伝子上位15個)

No	Cy5	Cy3	ratio	RefSeq Accession	Genbank Accession	Entrez Gene ID	Gene Symbol	Gene Name	Ensembl ID	TIGR ID	GO	Description	Genomic Coordinates
33	106.0	682.0	0.16	NM_007110	NM_007110	7011	TEP1	telomerase-associated protein 1	ENST00000262715	NP1473063	GO:0000166(nucleotide binding)|GO:0000722(telomere maintenance via recombination)|GO:0000781(chromosome, telomeric region)|GO:0000720(telomerase activity)|GO:0003723(RNA binding)|GO:0005524(ATP binding)|GO:0005635(soluble fraction)|GO:0005634(nucleus)|GO:0005694(chromosome)|GO:0005697(telomerase holoenzyme complex)|GO:0005737(cytoplasm)|GO:0007004(telomere maintenance via telomerase)|GO:0016363(nuclear matrix)	Homo sapiens telomerase-associated protein 1 (TEP1), mRNA [NM_007110]	chr14:1990599 8-19805939
34	230.2	1451.3	0.16	NM_015071	NM_015071	23092	ARHGAP26	Rho GTPase activating protein 26	ENST00000378013	THC2495953	GO:0005096(GTPase activator activity)|GO:0005100(Rho GTPase activator activity)|GO:0005575(cellular_component)|GO:0005622(intracellular)|GO:0007165(signal transduction)|GO:0007399(nervous system development)|GO:0030036(actin cytoskeleton organization and biogenesis)	Homo sapiens Rho GTPase activating protein 26 (ARHGAP26), mRNA [NM_015071]	chr5:142456582 7-142863886
35	30.4	160.0	0.19	NM_153634	NM_153634	144402	CPNE8	copine VIII	ENST00000331366	NP1161985		Homo sapiens copine VIII (CPNE8), mRNA [NM_153634]	chr12:3735581 3-37350840
36	23.7	88.7	0.27	NM_080662	NM_080662	92960	PEX11G	peroxisomal biogenesis factor 11 gamma	ENST00000221480	THC2767751	GO:0005777(peroxisome)|GO:0005778(peroxisomal membrane)|GO:0016020(membrane)|GO:0016021(integral to membrane)|GO:0016559(peroxisome fission)	Homo sapiens peroxisomal biogenesis factor 11 gamma (PEX11G), mRNA [NM_080662]	chr19:7456798 -7456739
37	48.2	178.7	0.27	NM_180989	NM_180989	160897	GPR180	G protein-coupled receptor 180	ENST00000376998	THC2684760	GO:0005615(extracellular space)|GO:0016020(membrane)|GO:0016021(integral to membrane)	Homo sapiens G protein-coupled receptor 180 (GPR180), mRNA [NM_180989]	chr13:94073437 0-94073489
38	22.4	74.7	0.30	NM_000846	NM_000846	2939	GSTA2	glutathione S-transferase A2	ENST00000334575	THC2627372	GO:0004364(glutathione transferase activity)|GO:0008152(metabolic process)|GO:0016740(transferase activity)	Homo sapiens glutathione S-transferase A2 (GSTA2), mRNA [NM_000846]	chr6:52730647 -52729037
39	28.4	93.0	0.31	NM_033663	NM_033663	1814	DRD3	dopamine receptor D3	ENST00000383673	NP518117	GO:0001584(rhodopsin-like receptor activity)|GO:0004872(receptor activity)|GO:0004952(dopamine receptor activity)|GO:0005886(plasma membrane)|GO:0005887(integral to plasma membrane)|GO:0007165(signal transduction)|GO:0007212(dopamine receptor signaling pathway)|GO:0007268(synaptic transmission)|GO:0007610(behavior)	Homo sapiens dopamine receptor D3 (DRD3), transcript variant e, mRNA [NM_033663]	chr3:111537328 4-115361370

[0524]

表154 遺伝子セット5(No. 18-47:発現増加・減少した遺伝子上位15個)

No	Cy5	Cy3	ratio	RefSeq Accession	Genbank Accession	Entrez Gene ID	Gene Symbol	Gene Name	Ensembl ID	TIGR ID	GO	Description	Genomic Coordinates
40	31.9	103.1	0.31		AK022408	23637	RABGAP1	RAB GTPase activating protein 1	ENST00000317419	THC2484522	GO:0005096(GTPase activator activity)|GO:0005813(centrosome)|GO:0005829(cytosol)|GO:0005875(microtubule associated complex)|GO:0007049(cell cycle)|GO:0015631(tubulin binding)	Homo sapiens cDNA FLJ12346 fis, clone MAMMA1002297, highly similar to Homo sapiens mRNA for Rab6 GTPase activating protein. [AK022408]	chr9:124792250-124792565
41	54.2	167.4	0.32	NM_004285	NM_004285	9563	H6PD	hexose-6-phosphate dehydrogenase (glucose 1-dehydrogenase)	ENST00000377403	THC2531319	GO:0004345(glucose-6-phosphate 1-dehydrogenase activity)|GO:0005783(endoplasmic reticulum)|GO:0005792(microsoma)|GO:0005975(carbohydrate metabolic process)|GO:0006006(glucose metabolic process)|GO:0006098(pentose-phosphate shunt)|GO:0016491(oxidoreductase activity)|GO:0016787(hydrolase activity)|GO:0017057(6-phosphogluconolactonase activity)|GO:0047936(glucose 1-dehydrogenase activity)	Homo sapiens hexose-6-phosphate dehydrogenase (glucose 1-dehydrogenase) (H6PD), mRNA [NM_004285]	chr1:9252938-9252997
42	95.2	290.2	0.33	NM_144503	NM_144503	50848	F11R	F11 receptor	ENST00000368027	THC2747714	GO:0004792(thiosulfate sulfurtransferase activity)|GO:0005515(protein binding)|GO:0005737(cytoplasm)|GO:0005886(plasma membrane)|GO:0005923(tight junction)|GO:0006928(cell motility)|GO:0006954(inflammatory response)|GO:0007155(cell adhesion)|GO:0016021(integral to membrane)|GO:0016740(transferase activity)|GO:0030855(epithelial cell differentiation)	Homo sapiens F11 receptor (F11R), transcript variant 4, mRNA [NM_144503]	chr1:159233336-159233305
43	107.5	316.8	0.34	NM_000051	NM_000051	472	ATM	ataxia telangiectasia mutated (includes complementation groups A, C and D)	ENST00000389512	THC2482213	GO:0003677(DNA binding)|GO:0004674(protein serine/threonine kinase activity)|GO:0005634(nucleus)|GO:0006281(DNA repair)|GO:0007049(cell cycle)|GO:0007094(mitotic spindle checkpoint)|GO:0007131(meiotic recombination)|GO:0007165(signal transduction)|GO:0010212(response to ionizing radiation)|GO:0016303(phosphatidylinositol 3-kinase activity)|GO:0016740(transferase activity)|GO:0016773(phosphotransferase activity, alcohol group as acceptor)|GO:0045786(negative regulation of progression through cell cycle)|GO:0044255(protein N-terminus binding)	Homo sapiens ataxia telangiectasia mutated (includes complementation groups A, C and D) (ATM), transcript variant 1, mRNA [NM_000051]	chr11:107741295-107741354
44	31.2	89.8	0.35	NM_033448	NM_033448	112802	KRT71	keratin 71	ENST00000267119	THC2478222		Homo sapiens keratin 71 (KRT71), mRNA [NM_033448]	chr12:51224230-51224171

[0525]

表154　遺伝子セット5(No. 18-47:発現増加・減少した遺伝子上位15個)

No	Cy5	Cy3	ratio	RefSeq Accession	Genbank Accession	Entrez Gene ID	Gene Symbol	Gene Name	Ensembl ID	TIGR ID	GO	Description	Genomic Coordinates
45	32.6	88.7	0.37		AF351612	7430	VIL2	villin 2 (ezrin)		THC2481886	GO:0001726(ruffle)|GO:0005198(structural molecule activity)|GO:0005488(binding)|GO:0005737(cytoplasm)|GO:0005829(cytosol)|GO:0005856(cytoskeleton)|GO:0005884(actin filament)|GO:0005902(microvillus)|GO:0007016(cytoskeletal anchoring)|GO:0008092(cytoskeletal protein binding)|GO:0008360(regulation of cell shape)|GO:0016020(membrane)|GO:0019898(extrinsic to membrane)|GO:0030863(cortical cytoskeleton)|GO:0043621(protein self-association)|GO:0051015(actin filament binding)|GO:0051017(actin filament bundle formation)	Homo sapiens UG0651E06 mRNA, complete cds. [AF351612]	chr3:95287753-95287812
46	3497.7	8575.6	0.41	NM_030641	NM_030641	80830	APOL6	apolipoprotein L, 6		THC2464922	GO:0003700(transcription factor activity)|GO:0005319(lipid transporter activity)|GO:0005576(extracellular region)|GO:0005737(cytoplasm)|GO:0006355(regulation of transcription, DNA-dependent)|GO:0006869(lipid transport)|GO:0008289(lipid binding)|GO:0042157(lipoprotein metabolic process)	Homo sapiens apolipoprotein L, 6 (APOL6), mRNA [NM_030641]	chr22:34387064-34387123
47	17.7	41.7	0.43	NM_020552	NM_020552	27004	TCL6	T-cell leukemia/lymphoma 6		THC2481759	GO:0003674(molecular_function)|GO:0005575(cellular_component)|GO:0008150(biological_process)	Homo sapiens T-cell leukemia/lymphoma 6 (TCL6), transcript variant TCL6b1, mRNA [NM_020552]	chr14:95209256-95209315

[表155]

表155 遺伝子セット5(No.1-17:機能面で注目する遺伝子,No.18-47:発現増加・減少した遺伝子上位15個)

No	Target(Gene)Symbol	Target Accession	UniGene	Up/Down	被験者群	配列番号
1	PTPRC	NM_080923	Hs.192039	Up	A+B	162
2	PAWR	NM_002583	Hs.643130	Up	A+B	163
3	TRAT1	NM_016388	Hs.138701	Up	A+B	164
4	STXBP4	NM_178509	Hs.35199	Down	A+B	69
5	SLC2A5	NM_003039	Hs.530003	Down	A+B	165
6	SLC2A3	NM_006931	Hs.419240	Down	A+B	166
7	SORBS1	NM_001034954	Hs.38621	Down	A+B	167
8	AKT1	NM_005163	Hs.525622	Down	A+B	71
9	APOL6	NM_030641	Hs.257352	Down	A+B	68
10	ATG10	NM_031482	Hs.651173	Down	A+B	168
11	SNX17	NM_014748	Hs.278569	Down	A+B	59
12	PIGS	NM_033198	Hs.462550	Down	A+B	169
13	FNTB	NM_002028	Hs.632345	Down	A+B	170
14	SLC9A5	NM_004594	Hs.439650	Down	A+B	171
15	LOC133308	NM_178833	Hs.546482	Down	A+B	172
16	CLN5	NM_006493	Hs.30213	Down	A+B	173
17	CLN3	NM_001042432	Hs.628393	Down	A+B	174
18	COMMD6	NM_203497	Hs.508266	Up	A+B	75
19	COX7B	NM_001866	Hs.522699	Up	A+B	175
20	P2RY5	NM_005767	Hs.123464	Up	A+B	76
21	LMNB1	NM_005573	Hs.89497	Up	A+B	139
22	EVI2A	NM_001003927	Hs.591198	Up	A+B	74
23	CD52	NM_001803	Hs.276770	Up	A+B	78
24	CSTA	NM_005213	Hs.518198	Up	A+B	81
25	FKSG2	NM_021631	Hs.651853	Up	A+B	176
26	EEF1E1	NM_004280	Hs.631818	Up	A+B	177
27	APP	NM_000484	Hs.651215	Up	A+B	178
28	SH2D1A	NM_002351	Hs.349094	Up	A+B	179
29	PREI3	NM_015387	Hs.645458	Up	A+B	-
30	CFL2	NM_021914	Hs.180141	Up	A+B	180
31	TCF12	NM_207038	Hs.511504	Up	A+B	181
32	LY96	NM_015364	Hs.69328	Up	A+B	82
33	TEP1	NM_007110	Hs.508835	Down	A+B	91
34	ARHGAP26	NM_015071	Hs.293593	Down	A+B	93
35	CPNE8	NM_153634	Hs.40910	Down	A+B	182
36	PEX11G	NM_080662	Hs.515100	Down	A+B	183
37	GPR180	NM_180989	Hs.439363	Down	A+B	184
38	GSTA2	NM_000846	Hs.94107	Down	A+B	185
39	DRD3	NM_033663	Hs.121478	Down	A+B	186
40	RABGAP1		Hs.271341	Down	A+B	-
41	H6PD	NM_004285	Hs.463511	Down	A+B	187
42	F11R	NM_144503	Hs.517293	Down	A+B	188
43	ATM	NM_000051	Hs.367437	Down	A+B	189
44	KRT71	NM_033448	Hs.433845	Down	A+B	190
45	VIL2		Hs.642735	Down	A+B	-
46	APOL6	NM_030641	Hs.257352	Down	A+B	68
47	TCL6	NM_020552	Hs.510368	Down	A+B	191

[0526] 上記解析4で笑いにより遺伝子発現の変動が認められた遺伝子のうち、機能面で注目すべき遺伝子、及び特に発現変動の大きかった上位15遺伝子を表156～158に示し、これらを要約した表159を遺伝子セット6の表として示す。

[表156]

表156　遺伝子セット6(No.1-2:機能面で注目する遺伝子)

No	Cy5	Cy3	ratio	RefSeq Accession	Genbank Accession	Entrez Gene ID	Gene Symbol	Gene Name	Ensembl ID	TIGR ID	GO	Description	Genomic Coordinates
1	1021.67	2094.29	0.49	NM_001006	NM_001006	6189.00	RPS3A	ribosomal protein S3A	ENST00000274085	TIGR25598600	GO:0003723(RNA binding)|GO:0003735(structural constituent of ribosome)|GO:0005515(protein binding)|GO:0005622(intracellular)|GO:0005634(nucleus)|GO:0005829(cytosol)|GO:0005840(ribosome)|GO:0005843(cytosolic small ribosomal subunit (sensu the Eukaryota res	Homo sapiens ribosomal protein S3A (RPS3A), mRNA [NM_001006]	chr4:152243533 6-152243595
2	30.28	52.75	0.57	NM_015316	NM_015316	23368.00	PPP1R13B	protein phosphatase 1, regulatory (inhibitor) subunit 13B	ENST00000302556	NP1151875	GO:0005515(protein binding)|GO:0005634(nucleus)|GO:0005737(cytoplasm)|GO:0006915(apoptosis)|GO:0006917(induction of apoptosis)|GO:0008952(defense responses)|GO:0045786(negative regulation of progression through cell cycle)	Homo sapiens protein phosphatase 1, regulatory (inhibitor) subunit 13B (PPP1R13B), mRNA [NM_015316]	chr14:1032711 47-103271088

[表157]

表157 遺伝子セット6(No.3-32:発現増加・減少した遺伝子上位15個)

No	Cy5	Cy3	ratio	RefSeq Accession	Genbank Accession	Entrez Gene_ID	Gene Symbol	Gene Name	Ensembl ID	TIGR ID	GO	Description	Genomic Coordinates
3		147.5	33.1	4.45 NM_006568	NM_006568	10668	CGRRF1	cell growth regulator with ring finger domain 1	ENST00000216420	THC2629888	GO:0005515(protein binding)|GO:0006950(response to stress)|GO:0007049(cell cycle)|GO:0007050(cell cycle arrest)|GO:0008270(zinc ion binding)|GO:0008285(negative regulation of cell proliferation)|GO:0046872(metal ion binding)	Homo sapiens cell growth regulator with ring finger domain 1 (CGRRF1), mRNA [NM_006568]	chr14:5406741 0-54067469
4		197.0	48.5	4.06 NM_176798	NM_176798	5031	P2RY6	pyrimidinergic receptor P2Y, G-protein coupled, 6	ENST00000349767	THC2603885	GO:0001584(rhodopsin-like receptor activity)|GO:0004872(receptor activity)|GO:0005887(integral to plasma membrane)|GO:0007165(signal transduction)|GO:0007200(G-protein signaling, coupled to IP3 second messenger (phospholipase C activating))|GO:0016020(membrane)|GO:0019103(pyrimidine nucleotide binding)|GO:0030321(transepithelial chloride transport)|GO:0045028(purinergic nucleotide receptor activity, G-protein coupled)|GO:0045028(UDP-activated nucleotide receptor activity)	Homo sapiens pyrimidinergic receptor P2Y, G-protein coupled, 6 (P2RY6), transcript variant 2, mRNA [NM_176798]	chr11:7288827 3-72686332
5		105.8	45.2	2.34 NM_016205	NM_016205	56034	PDGFC	platelet derived growth factor C	ENST00000274071	THC2601312	GO:0000074(regulation of progression through cell cycle)|GO:0005576(extracellular region)|GO:0007417(central nervous system development)|GO:0008083(growth factor activity)|GO:0008283(cell proliferation)|GO:0016020(membrane)	Homo sapiens platelet derived growth factor C (PDGFC), mRNA [NM_016205]	chr4:157902402 49-157902349
6		66.9	30.2	2.22 NM_020870	NM_020870	57630	SH3RF1	SH3 domain containing ring finger 1	ENST00000284837	THC2462298	GO:0005515(protein binding)|GO:0008270(zinc ion binding)	Homo sapiens SH3 domain containing ring finger 1 (SH3RF1), mRNA [NM_020870]	chr4:170252132 09-170252080
7		83.6	38.3	2.18 NM_005932	NM_005932	4285	MIPEP	mitochondrial intermediate peptidase	ENST00000382172	THC2461260	GO:0000287(magnesium ion binding)|GO:0004243(mitochondrial intermediate peptidase activity)|GO:0005506(iron ion binding)|GO:0005509(calcium ion binding)|GO:0005739(mitochondrion)|GO:0006508(proteolysis)|GO:0006627(mitochondrial protein processing)|GO:0008270(zinc ion binding)|GO:0030145(manganese ion binding)|GO:0050897(cobalt ion binding)	Homo sapiens mitochondrial intermediate peptidase (MIPEP), nuclear gene encoding mitochondrial protein, mRNA [NM_005932]	chr13:23309575 7-23309698
8		117.3	65.0	1.80 NM_001017403	NM_001017403	59352	LGR6	leucine-rich repeat-containing G protein-coupled receptor 6	ENST00000355432	THC2473026	GO:0004872(receptor activity)|GO:0005515(protein binding)|GO:0007165(signal transduction)|GO:0007186(G-protein coupled receptor protein signaling pathway)|GO:0016020(membrane)|GO:0016021(integral to membrane)|GO:0016500(protein-hormone receptor activity)	Homo sapiens leucine-rich repeat-containing G protein-coupled receptor 6 (LGR6), transcript variant 1, mRNA [NM_001017403]	chr1:200555542 6-200555485

[0527]

表157 遺伝子セット6(No. 3-32:発現増加・減少した遺伝子上位15個)

No	Cy5	Cy3	ratio	RefSeq Accession	Genbank Accession	Entrez Gene ID	Gene Symbol	Gene Name	Ensembl ID	TIGR ID	GO	Description	Genomic Coordinates
9	171.7	95.5	1.80	NM_032047	NM_032047	84002	B3GNT5	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 5	ENST00000326505	THC2462855	GO:0005622(intracellular)|GO:0006486(protein amino acid glycosylation)|GO:0007417(central nervous system development)|GO:0008378(galactosyltransferase activity)|GO:0008457(beta-galactosyl-N-acetylglucosaminylgalactosylglucosyl-ceramide beta-1,3-acetylglucosaminyltransferase activity)|GO:0009247(glycolipid biosynthetic process)|GO:0016020(membrane)|GO:0016757(transferase activity, transferring glycosyl groups)	Homo sapiens UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 5 (B3GNT5), mRNA [NM_032047]	chr3:184473692-184473886
10	337.0	191.6	1.76	NM_147156	NM_147156	259230	TMEM23	transmembrane protein 23	ENST00000361781	THC2461642	GO:0000138(Golgi trans cisterna)|GO:0006629(lipid metabolic process)|GO:0006665(sphingolipid metabolic process)|GO:0006686(sphingomyelin biosynthetic process)|GO:0016020(membrane)|GO:0016021(integral to membrane)|GO:0016301(kinase activity)|GO:0016740(transferase activity)|GO:0030173(integral to Golgi membrane)|GO:0047493(ceramide cholinephosphotransferase activity)	Homo sapiens transmembrane protein 23 (TMEM23), mRNA [NM_147156]	chr10:5173562-51735866
11	79.5	45.6	1.74	NM_033050	NM_033050	56670	SUCNR1	succinate receptor 1		THC2480670	GO:0001584(rhodopsin-like receptor activity)|GO:0004872(receptor activity)|GO:0007165(signal transduction)|GO:0007186(G-protein coupled receptor protein signaling pathway)|GO:0008150(biological_process)|GO:0016020(membrane)|GO:0016021(integral to membrane)|GO:0045028(purinergic nucleotide receptor activity, G-protein coupled)	Homo sapiens succinate receptor 1 (SUCNR1), mRNA [NM_033050]	chr3:153082100-153082159
12	449.6	258.1	1.74	NM_005139	NM_005139	306	ANXA3	annexin A3	ENST00000264908	THC2770714	GO:0005509(calcium ion binding)|GO:0005544(calcium-dependent phospholipid binding)|GO:0005737(cytoplasm)|GO:0007165(signal transduction)|GO:0008486(diphosphoinositol-polyphosphate diphosphatase activity)|GO:0019834(phospholipase A2 inhibitor activity)	Homo sapiens annexin A3 (ANXA3), mRNA [NM_005139]	chr4:79744519-79750234
13	106.8	61.7	1.73	NM_005725	NM_005725	10100	TSPAN2	tetraspanin 2	ENST00000369516	THC2470727	GO:0006928(cell motility)|GO:0007155(cell adhesion)|GO:0008283(cell proliferation)|GO:0016020(membrane)|GO:0016021(integral to membrane)	Homo sapiens tetraspanin 2 (TSPAN2), mRNA [NM_005725]	chr1:115392595-115392531

[0528]

表157 遺伝子セット6(No. 3-32:発現増加・減少した遺伝子上位15個)

No	Cy5	Cy3	ratio	RefSeq Accession	Genbank Accession	Entrez Gene ID	Gene Symbol	Gene Name	Ensembl ID	TIGR ID	GO	Description	Genomic Coordinates
14	53.1	30.8	1.73	NM_003719	NM_003719	8622	PDE8B	phosphodiesterase 8B	ENST00000380403	THC2657683	GO:0000156(two-component response regulator activity)|GO:0000160(two-component signal transduction system (phosphorelay))|GO:0000287(magnesium ion binding)|GO:0004114(3',5'-cyclic-nucleotide phosphodiesterase activity)|GO:0005575(cellular_componentt)|GO:0006355(regulation of transcription, DNA-dependent)|GO:0009187(cyclic nucleotide metabolic process)|GO:0016787(hydrolase activity)|GO:0030145(manganese ion binding)	Homo sapiens phosphodiesterase 8B (PDE8B), transcript variant 1, mRNA [NM_003719]	chr5:76758549 -76758608
15	70.5	40.8	1.73	NM_030791	NM_030791	81537	SGPP1	sphingosine-1-phosphate phosphatase 1	ENST00000241225	THC2463640	GO:0003993(acid phosphatase activity)|GO:0005624(membrane fraction)|GO:0005739(mitochondrion)|GO:0005783(endoplasmic reticulum)|GO:0005794(Golgi apparatus)|GO:0006665(sphingolipid metabolic process)|GO:0006688(sphingosine-1-phosphate metabolic process)|GO:0006670(sphingosine metabolic process)|GO:0006915(apoptosis)|GO:0015629(actin cytoskeleton)|GO:0016020(membrane)|GO:0016021(integral to membrane)|GO:0016787(hydrolase activity)|GO:0042392(sphingosine-1-phosphate phosphatase activity)	Homo sapiens sphingosine-1-phosphate phosphatase 1 (SGPP1), mRNA [NM_030791]	chr1:46322186 -46321802
16	18830.3	9251.6	1.71	NM_021935	NM_021935	60675	PROK2	prokineticin 2	ENST00000353065	THC2479819	GO:0000187(activation of MAPK activity)|GO:0001525(angiogenesis)|GO:0001664(G-protein-coupled receptor binding)|GO:0005576(extracellular region)|GO:0005615(extracellular space)|GO:0006916(anti-apoptosis)|GO:0006935(chemotaxis)|GO:0006954(inflammatory response)|GO:0007204(elevation of cytosolic calcium ion concentration)|GO:0007218(neuropeptide signaling pathway)|GO:0007283(spermatogenesis)|GO:0007623(circadian rhythm)|GO:0008283(cell proliferation)|GO:0019233(sensory perception of pain)|GO:0045987(positive regulation of smooth muscle contraction)	Homo sapiens prokineticin 2 (PROK2), mRNA [NM_021935]	chr3:71903651 -71903592

[0529]

表157　遺伝子セット6(No.3-32:発現増加・減少した遺伝子上位15個)

No	Cy5	Cy3	ratio	RefSeq Accession	Genbank Accession	Entrez Gene ID	Gene Symbol	Gene Name	Ensembl ID	TIGR ID	GO	Description	Genomic Coordinates
17	60.1	35.4	1.70	NM_002840	NM_002840	5792	PTPRF	protein tyrosine phosphatase, receptor type, F	ENST00000359947	THC2617582	GO:0004725(protein tyrosine phosphatase activity)|GO:0004872(receptor activity)|GO:0005001(transmembrane receptor protein tyrosine phosphatase activity)|GO:0005515(protein binding)|GO:0005887(integral to plasma membrane)|GO:0006470(protein amino acid dephosphorylation)|GO:0007155(cell adhesion)|GO:0007185(transmembrane receptor protein tyrosine phosphatase signaling pathway)|GO:0016020(membrane)|GO:0016787(hydrolase activity)	Homo sapiens protein tyrosine phosphatase, receptor type, F (PTPRF), transcript variant 1, mRNA [NM_002840]	chr1:43861770-43861829

[表158]

表158 遺伝子セット6(No.3-32:発現増加・減少した遺伝子上位15個)

No	Cy5	Cy3	ratio	RefSeq Accession	Genbank Accession	Entrez Gene ID	Gene Symbol	Gene Name	Ensembl ID	TIGR ID	GO	Description	Genomic Coordinates
18	30.4	176.4	0.17	NM_144773	NM_144773	128674	PROKR2	prokineticin receptor 2	ENST00000217270	THC2482644	GO:0001584(rhodopsin-like receptor activity)|GO:0004872(receptor activity)|GO:0004983(neuropeptide Y receptor activity)|GO:0007165(signal transduction)|GO:0007186(G-protein coupled receptor protein signaling pathway)|GO:0007623(circadian rhythm)|GO:0016020(membrane)|GO:0016021(integral to membrane)	Homo sapiens prokineticin receptor 2 (PROKR2), mRNA [NM_144773]	chr20:5233 1328 -5231289
19	21.4	115.0	0.19	NM_145865	NM_145865	257629	ANKS4B	ankyrin repeat and sterile alpha motif domain containing 4B		THC2479942	GO:0005515(protein binding)|GO:0005886(plasma membrane)	Homo sapiens ankyrin repeat and sterile alpha motif domain containing 4B (ANKS4B), mRNA [NM_145865]	chr16:2117037 4-21170433
20	25.8	137.4	0.19	NM_002885	NM_002885	5909	RAP1GAP	RAP1 GTPase activating protein	ENST00000317967	THC2604954	GO:0003924(GTPase activity)|GO:0005096(GTPase activator activity)|GO:0005622(intracellular)|GO:0005624(membrane fraction)|GO:0005829(cytosol)|GO:0007165(signal transduction)|GO:0016020(membrane)|GO:0051056(re	Homo sapiens RAP1 GTPase activating protein (RAP1GAP), mRNA [NM_002885]	chr1:21800821 -21798696
21	22.3	71.6	0.31	NM_001441	NM_001441	2166	FAAH	fatty acid amide hydrolase	ENST00000243167	THC2776169	GO:0004040(amidase activity)|GO:0005102(receptor binding)|GO:0005615(extracellular space)|GO:0005624(membrane fraction)|GO:0005626(insoluble fraction)|GO:0006631(fatty acid metabolic process)|GO:0016020(membrane)|GO:0016021(integral to membrane)|GO:0016787(hydrolase activity)	Homo sapiens fatty acid amide hydrolase (FAAH), mRNA [NM_001441]	chr1:46849078 -46649894
22	15.3	42.0	0.37	NM_002299	NM_002299	3938	LCT	lactase	ENST00000264162	THC2477016	GO:0000016(lactase activity)|GO:0005624(membrane fraction)|GO:0005887(integral to plasma membrane)|GO:0005975(carbohydrate metabolic process)|GO:0008152(metabolic process)|GO:0015926(glucosidase activity)|GO:0016020(membrane)|GO:0017042(glycosylceramidase activity)|GO:0043169(cation binding)	Homo sapiens lactase (LCT), mRNA [NM_002299]	chr2:13626241 6-136262357
23	19.4	52.8	0.37	NM_198229	NM_198229	6002	RGS12	regulator of G-protein signalling 12	ENST00000344733	THC2486480	GO:0000794(condensed nuclear chromosome)|GO:0005057(receptor signaling protein activity)|GO:0005096(GTPase activator activity)|GO:0005515(protein binding)|GO:0005634(nucleus)|GO:0007165(signal transduction)|GO:0008277(regulation of G-protein coupled receptor protein signaling pathway)|GO:0009968(negative regulation of signal transduction)	Homo sapiens regulator of G-protein signalling 12 (RGS12), transcript variant 1, mRNA [NM_198229]	chr4:3314508-3314567

[0530]

表158 遺伝子セット6(No.3-32:発現増加・減少した遺伝子上位15個)

No	Cy5	Cy3	ratio	RefSeq Accession	Genbank Accession	Entrez Gene ID	Gene Symbol	Gene Name	Ensembl ID	TIGR ID	GO	Description	Genomic Coordinates
24	37.5	98.3	0.38	NM_001933	NM_001933	1743	DLST	dihydrolipoamide S-succinyltransferase (E2 component of 2-oxo-glutarate complex)	ENST00000334220	THC2574190	GO:0004149(dihydrolipoyllysine-residue succinyltransferase activity)|GO:0005739(mitochondrion)|GO:0006091(generation of precursor metabolites and energy)|GO:0006099(tricarboxylic acid cycle)|GO:0008152(metabolic process)|GO:0008415(acyltransferase activity)|GO:0016740(transferase activity)|GO:0031405(lipoic acid binding)|GO:0045252(oxoglutarate dehydrogenase complex)	Homo sapiens dihydrolipoamide S-succinyltransferase (E2 component of 2-oxo-glutarate complex) (DLST), mRNA [NM_001933]	chr14:74436761-74436820
25	23.3	60.6	0.38	NM_001001976	NM_001001976	11101	ATE1	arginyltransferase 1	ENST00000224652	THC2471323	GO:0004057(arginyltransferase activity)|GO:0005634(nucleus)|GO:0005737(cytoplasm)|GO:0006512(ubiquitin cycle)|GO:0008415(acyltransferase activity)|GO:0016598(protein arginylation)|GO:0016740(transferase activity)|GO:0042176(regulation of protein catabolic process)	Homo sapiens arginyltransferase 1 (ATE1), transcript variant 1, mRNA [NM_001001976]	chr10:123492764-123492705
26	15.6	36.2	0.43	NM_001761	NM_001761	899	CCNF	cyclin F	ENST00000293968	THC2463529	GO:0000320(re-entry into mitotic cell cycle)|GO:0001880(placenta development)|GO:0005634(nucleus)|GO:0007049(cell cycle)|GO:0007067(mitosis)|GO:0051301(cell division)	Homo sapiens cyclin F (CCNF), mRNA [NM_001761]	chr16:2447223-2447282
27	24.1	49.4	0.49	NM_001631	NM_001631	248	ALPI	alkaline phosphatase, intestinal	ENST00000295463	THC2475142	GO:0000287(magnesium ion binding)|GO:0004035(alkaline phosphatase activity)|GO:0008152(metabolic process)|GO:0008270(zinc ion binding)|GO:0016020(membrane)|GO:0016021(integral to membrane)|GO:0016310(phosphorylation)|GO:0016787(hydrolase activity)|GO:0046503(GPI anchor binding)	Homo sapiens alkaline phosphatase, intestinal (ALPI), mRNA [NM_001631]	chr2:233032177-233032236
28	53.8	108.8	0.49	NM_001890	NM_001890	1446	CSN1S1	casein alpha s1	ENST00000246891	THC2759870	GO:0005215(transporter activity)|GO:0005576(extracellular region)|GO:0006810(transport)|GO:0007586(digestion)	Homo sapiens casein alpha s1 (CSN1S1), transcript variant 1, mRNA [NM_001890]	chr4:70845191-70845250
29	47.8	95.6	0.50	NM_024749	NM_024749	78805	VASH2	vasohibin 2	ENST00000271776	THC2482158		Homo sapiens vasohibin 2 (VASH2), mRNA [NM_024749]	chr1:211229951-211230010
30	30.9	61.0	0.51	NM_005769	NM_005769	10164	CHST4	carbohydrate (N-acetylglucosamine 6-O) sulfotransferase 4	ENST00000338482	THC2476272	GO:0001517(N-acetylglucosamine 6-O-sulfotransferase activity)|GO:0000802(Golgi transface)|GO:0005975(carbohydrate metabolic process)|GO:0008044(N-acetylglucosamine metabolic process)|GO:0008477(protein amino acid sulfation)|GO:0006790(sulfur metabolic process)|GO:0006928(cell motility)|GO:0006954(inflammatory response)|GO:0006955(immune response)|GO:0007155(cell adhesion)|GO:0007267(cell-cell signaling)|GO:0016020(membrane)|GO:0016021(integral to membrane)|GO:0016740(transferase activity)|GO:0031228(intrinsic to Golgi membrane)	Homo sapiens carbohydrate (N-acetylglucosamine 6-O) sulfotransferase 4 (CHST4), mRNA [NM_005769]	chr16:70129779-70129838

[0531]

表158　遺伝子セット6(No. 3-32:発現増加・減少した遺伝子上位15個)

No	Cy5	Cy3	ratio	RefSeq Accession	Genbank Accession	Entrez Gene ID	Gene Symbol	Gene Name	Ensembl ID	TIGR ID	GO	Description	Genomic Coordinates
31	16.7	32.8	0.51	NM_000353	NM_000353	6898	TAT	tyrosine aminotransferase	ENST00000355962	THC2471329	GO:0004838(tyrosine transaminase activity)|GO:0005575(cellular_component)|GO:0005739(mitochondrion)|GO:0006519(amino acid and derivative metabolic process)|GO:0006559(L-phenylalanine catabolic process)|GO:0006572(tyrosine catabolic process)|GO:0009058(biosynthetic process)|GO:0009074(aromatic amino acid family catabolic process)|GO:0016847(1-aminocyclopropane-1-carboxylate synthase	Homo sapiens tyrosine aminotransferase (TAT), nuclear gene encoding mitochondrial protein, mRNA [NM_000353]	chr16:70158971-70158911
32	24.0	47.1	0.51	NM_001004019	NM_001004019	2199	FBLN2	fibulin 2	ENST00000295761	NP1157898	GO:0005201(extracellular matrix structural constituent)|GO:0005509(calcium ion binding)|GO:0005576(extracellular region)|GO:0005578(extracellular matrix (sensu the Metazoa research community))	Homo sapiens fibulin 2 (FBLN2), transcript variant 1, mRNA [NM_001004019]	chr3:13654467-13654526

[表159]

表159 遺伝子セット6(No.1-2:機能面で注目する遺伝子,No.3-32:発現増加・減少した遺伝子上位15個)

No	Target(Gene)Symbol	Target Accession	UniGene	Up/Down	被験者群	配列番号
1	RPS3A	NM_001006	Hs.356572	Down	C+D	192
2	PPP1R13B	NM_015316	Hs.436113	Down	C+D	193
3	CGRRF1	NM_006568	Hs.59106	Up	C+D	194
4	P2RY6	NM_176798	Hs.16362	Up	C+D	195
5	PDGFC	NM_016205	Hs.570855	Up	C+D	38
6	SH3RF1	NM_020870	Hs.301804	Up	C+D	196
7	MIPEP	NM_005932	Hs.507498	Up	C+D	197
8	LGR6	NM_001017403	Hs.497402	Up	C+D	198
9	B3GNT5	NM_032047	Hs.208267	Up	C+D	148
10	TMEM23	NM_147156	Hs.386215	Up	C+D	-
11	SUCNR1	NM_033050	Hs.279575	Up	C+D	199
12	ANXA3	NM_005139	Hs.480042	Up	C+D	200
13	TSPAN2	NM_005725	Hs.310458	Up	C+D	201
14	PDE8B	NM_003719	Hs.584830	Up	C+D	202
15	SGPP1	NM_030791	Hs.24678	Up	C+D	116
16	PROK2	NM_021935	Hs.528665	Up	C+D	203
17	PTPRF	NM_002840	Hs.272062	Up	C+D	204
18	PROKR2	NM_144773	Hs.375029	Down	C+D	205
19	ANKS4B	NM_145865	Hs.115959	Down	C+D	206
20	RAP1GAP	NM_002885	Hs.148178	Down	C+D	207
21	FAAH	NM_001441	Hs.528334	Down	C+D	208
22	LCT	NM_002299	Hs.551506	Down	C+D	209
23	RGS12	NM_198229	Hs.527061	Down	C+D	210
24	DLST	NM_001933	Hs.525459	Down	C+D	211
25	ATE1	NM_001001976	Hs.632080	Down	C+D	212
26	CCNF	NM_001761	Hs.1973	Down	C+D	213
27	ALPI	NM_001631	Hs.37009	Down	C+D	214
28	CSN1S1	NM_001890	Hs.3155	Down	C+D	215
29	VASH2	NM_024749	Hs.96885	Down	C+D	216
30	CHST4	NM_005769	Hs.251383	Down	C+D	217
31	TAT	NM_000353	Hs.161640	Down	C+D	-
32	FBLN2	NM_001004019	Hs.198862	Down	C+D	218

[0532] 上記解析5で笑いにより遺伝子発現の変動が認められた遺伝子のうち、機能面で注目すべき遺伝子、及び特に発現変動の大きかった上位15遺伝子を表160～163に示し、これらを要約した表164を遺伝子セット1の表として示す。

[表160]

表160 遺伝子セット1(No.1-31:機能面で注目する遺伝子)

No	Cy5	Cy3	ratio	RefSeq Accession	Genbank Accession	Entrez Gene ID	Gene Symbol	Gene Name	Ensembl ID	TIGR ID	GO	Description	Genomic Coordinates
1	239.9	151.4	1.58	NM_007045	NM_007045	11116	FGFR1OP	FGFR1 oncogene partner	ENST00000349556	THC2500822	GO:0008284(positive regulation of cell proliferation)	Homo sapiens FGFR1 oncogene partner (FGFR1OP), transcript variant 1, mRNA [NM_007045]	chr6:167373714-167373773
2	170.8	103.4	1.65	NM_012115	NM_012115	9994	CASP8AP2	CASP8 associated protein 2		THC2493448	GO:0003714(transcription corepressor activity)|GO:0005125(death receptor binding)|GO:0005634(nucleus)|GO:0005737(cytoplasm)|GO:0006350(transcription)|GO:0008355(regulation of transcription, DNA-dependent)|GO:0006915(apoptosis)|GO:0006919(caspase activatio	Homo sapiens CASP8 associated protein 2 (CASP8AP2), mRNA [NM_012115]	chr6:90640368-90640427
3	14897.3	9705.0	1.54	NM_021935	NM_021935	60675	PROK2	prokineticin 2	ENST00000353065	THC2478819	GO:0001187(activation of MAPK activity)|GO:0001525(angiogenesis)|GO:0001664(G-protein-coupled receptor binding)|GO:0005576(extracellular region)|GO:0005615(extracellular space)|GO:0006916(anti-apoptosis)|GO:0006935(chemotaxis)|GO:0006954(inflammatory resp	Homo sapiens prokineticin 2 (PROK2), mRNA [NM_021935]	chr3:71903651-71903592
4	697.6	416.1	1.68	NM_002001	NM_002001	2205	FCER1A	Fc fragment of IgE, high affinity I, receptor for; alpha polypeptide	ENST00000317818	THC2611062	GO:0001812(positive regulation of type I hypersensitivity)|GO:0001820(serotonin secretion)|GO:0004872(receptor activity)|GO:0005057(receptor signaling protein activity)|GO:0005886(plasma membrane)|GO:0005887(integral to plasma membrane)|GO:0006955(immune	Homo sapiens Fc fragment of IgE, high affinity I, receptor for; alpha polypeptide (FCER1A), mRNA [NM_002001]	chr1:157542658-157544219
5	91.5	60.6	1.51	NM_001781	NM_001781	969	CD69	CD69 molecule	ENST00000228434	THC2461288	GO:0004888(transmembrane receptor activity)|GO:0005529(sugar binding)|GO:0005887(integral to plasma membrane)|GO:0006952(defense response)|GO:0007166(cell surface receptor linked signal transduction)|GO:0009897(external side of plasma membrane)|GO:0016020(membrane)	Homo sapiens CD69 molecule (CD69), mRNA [NM_001781]	chr12:9796587-9796528
6	196.2	125.6	1.56	NM_001040202	NM_001040202	152559	PAQR3	progestin and adipoQ receptor family member III		THC2601844	GO:0004872(receptor activity)|GO:0016020(membrane)|GO:0016021(integral to membrane)	Homo sapiens progestin and adipoQ receptor family member III (PAQR3), mRNA [NM_001040202]	chr4:80058589-80058530

[0533]

表160　遺伝子セット1(No. 1-31：機能面で注目する遺伝子)

No	Cy5	Cy3	ratio	RefSeq Accession	Genbank Accession	Entrez Gene ID	Gene Symbol	Gene Name	Ensembl ID	TIGR ID	GO	Description	Genomic Coordinates
7	55.4	35.3	1.57	NM_001045	NM_001045	6532	SLC6A4	solute carrier family 6 (neurotransmitter transporter, serotonin), member 4	ENST00000261707	THC2477611	GO:0001504(neurotransmitter uptake)|GO:0005335(serotonin:sodium symporter activity)|GO:0005515(protein binding)|GO:0005887(integral to plasma membrane)|GO:0006837(serotonin transport)|GO:0008504(monoamine transporter activity)|GO:0015222(serotonin transpo	Homo sapiens solute carrier family 6 (neurotransmitter transporter, serotonin), member 4 (SLC6A4), mRNA [NM_001045]	chr17:25549128-25549069
8	53.9	34.6	1.56	NM_000821	NM_000821	2677	GGCX	gamma-glutamyl carboxylase	ENST00000233838	THC2515894	GO:0003676(nucleic acid binding)|GO:0005624(membrane fraction)|GO:0005783(endoplasmic reticulum)|GO:0006464(protein modification)|GO:0007596(blood coagulation)|GO:0008488(gamma-glutamyl carboxylase activity)|GO:0016020(membrane)|GO:0016021(integral to membrane)|GO:0016874(ligase activity)|GO:0017187(peptidyl-glutamic acid carboxylation)	Homo sapiens gamma-glutamyl carboxylase (GGCX), mRNA [NM_000821]	chr2:85629656-85629637
9	516916.3	334429.6	1.55	NM_000517	NM_000517	3040	HBA2	hemoglobin, alpha 2	ENST00000251595	THC2564653	GO:0005344(oxygen transporter activity)|GO:0005506(iron ion binding)|GO:0005515(protein binding)|GO:0005833(hemoglobin complex)|GO:0006810(transport)|GO:0015671(oxygen transport)|GO:0019825(oxygen binding)|GO:0020037(heme binding)|GO:0046872(metal ion binding)	Homo sapiens hemoglobin, alpha 2 (HBA2), mRNA [NM_000517]	chr16:163560-163619
10	84.0	54.3	1.55	NM_000671	NM_000671	128	ADH5	alcohol dehydrogenase 5 (class III), chi polypeptide		THC2465499	GO:0004022(alcohol dehydrogenase activity)|GO:0004327(formaldehyde dehydrogenase (glutathione) activity)|GO:0005504(fatty acid binding)|GO:0006069(ethanol oxidation)|GO:0008270(zinc ion binding)|GO:0009055(electron carrier activity)|GO:0046872(metal ion b	Homo sapiens alcohol dehydrogenase 5 (class III), chi polypeptide (ADH5), mRNA [NM_000671]	chr4:100211833-100211774

[表161]

表161 遺伝子セット1(No.1-31:機能面で注目する遺伝子)

No	Cy5	Cy3	ratio	RefSeq Accession	Genbank Accession	Entrez Gene ID	Gene Symbol	Gene Name	Ensembl ID	TIGR ID	GO	Description	Genomic Coordinates
11	668.8	1086.6	0.62	NM_002228	NM_002228	3725	JUN	jun oncogene	ENST00000371222	THC2537886	GO:0000074(regulation of progression through cell cycle)|GO:0000228(nuclear chromosome)|GO:0003700(transcription factor activity)|GO:0003702(RNA polymerase II transcription factor activity)|GO:0005634(nucleus)|GO:0005667(transcription factor complex)|GO:0	Homo sapiens jun oncogene (JUN), mRNA [NM_002228]	chr1:59020376-59020317
12	26.4	61.3	0.43	NM_000546	NM_000546	7157	TP53	tumor protein p53 (Li-Fraumeni syndrome)	ENST00000269305	NP1459124	GO:0000060(protein import into nucleus, translocation)|GO:0000739(DNA strand annealing activity)|GO:0003700(transcription factor activity)|GO:0004518(nuclease activity)|GO:0005507(copper ion	Homo sapiens tumor protein p53 (Li-Fraumeni syndrome) (TP53), mRNA [NM_000546]	chr17:7513416-7513357
13	27.1	45.3	0.60		X54871	5869	RAB5B	RAB5B, member RAS oncogene family		THC2543024	GO:0000166(nucleotide binding)|GO:0003924(GTPase activity)|GO:0005525(GTP binding)|GO:0005622(intracellular)|GO:0005624(membrane fraction)|GO:0005768(endosome)|GO:0005886(plasma	H.sapiens mRNA for ras-related protein Rab5b. [X54871]	chr12:54673057-54673117
14	222.8	348.4	0.64	NM_005370	NM_005370	4218	RAB8A	RAB8A, member RAS oncogene family	ENST00000309935	THC2518923	GO:0000160(two-component signal transduction system (phosphorelay))|GO:0000166(nucleotide binding)|GO:0003677(DNA binding)|GO:0005515(protein binding)|GO:0005525(GTP	Homo sapiens RAB8A, member RAS oncogene family (RAB8A), mRNA [NM_005370]	chr19:1609274-16089333
15	52.9	88.8	0.60	NM_001025300	NM_001025300	201475	RAB12	RAB12, member RAS oncogene family		THC2510066	0	Homo sapiens RAB12, member RAS oncogene family (RAB12), mRNA [NM_001025300]	chr18:8625551-8625610
16	81.8	142.9	0.57	NM_017817	NM_017817	55647	RAB20	RAB20, member RAS oncogene family	ENST00000367328	THC2471982	GO:0000166(nucleotide binding)|GO:0005525(GTP binding)|GO:0007264(small GTPase mediated signal transduction)|GO:0015031(protein transport)	Homo sapiens RAB20, member RAS oncogene family (RAB20), mRNA [NM_017817]	chr13:109974079-109974020
17	22.6	47.8	0.47	NM_014488	NM_014488	27314	RAB30	RAB30, member RAS oncogene family	ENST00000360056	THC2476006	GO:0000166(nucleotide binding)|GO:0003924(GTPase activity)|GO:0005525(GTP binding)|GO:0005795(Golgi stack)|GO:0006886(intracellular protein transport)|GO:0007264(small GTPase mediated signal transduction)|GO:0016020(membrane)	Homo sapiens RAB30, member RAS oncogene family (RAB30), mRNA [NM_014488]	chr1:9237098-9237109

[0534]

表161 遺伝子セット1(No. 1-31:機能面で注目する遺伝子)

No	Cy5	Cy3	ratio	RefSeq Accession	Genbank Accession	Entrez Gene ID	Gene Symbol	Gene Name	Ensembl ID	TIGR ID	GO	Description	Genomic Coordinates
18	39.0	76.7	0.51		AX775775	57506	VISA	virus-induced signaling adapter	ENST00000379563	THC2461420	GO:0004871(signal transducer activity)|GO:0005515(protein binding)|GO:0005739(mitochondrion)|GO:0009615(response to virus)|GO:0016020(membrane)|GO:0016021(integral to membrane)|GO:0019867(outer membrane)|GO:0043123(positive regulation of I-kappaB kinase/N	Mitochondrial antiviral signaling protein (Interferon-beta promoter stimulator protein 1) (IPS-1) (Virus-induced signaling adapter) (CARD adapter inducing interferon-beta) (Cardif) (Putative NF-kappa-B- activating protein)	chr20:3796310-3796369
19	91.0	146.8	0.62		AB240569	1604	CD55	CD55 molecule, decay accelerating factor for complement (Cromer blood		NP437598	GO:0005625(soluble fraction)|GO:0005887(integral to plasma membrane)|GO:0006958(complement activation, classical pathway)|GO:0016020(membrane)|GO:0045087(innate immune response)|GO:0048503(GPI anchor binding)	Homo sapiens DAF mRNA for decay-accelerating factor splicing variant 4, complete cds. [AB240569]	chr1:205576959-205577018
20	87.0	132.5	0.66		BC092518	3500	IGHG1	immunoglobulin heavy constant gamma 1 (G1m marker)		NP1161370	GO:0002474(antigen processing and presentation of peptide antigen via MHC class I)|GO:0003823(antigen binding)|GO:0005515(protein binding)|GO:0005824(membrane fraction)|GO:0006955(immune response)|GO:0042612(MHC class I protein complex)	Homo sapiens immunoglobulin heavy constant gamma 1 (G1m marker), mRNA (cDNA clone MGC:105004 IMAGE:3056327), complete cds. [BC092518]	chr14:105997722-105997661
21	21.0	34.2	0.61	NM_020163	NM_020163	56920	SEMA3G	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin)	ENST00000231721	THC2600994	GO:0004872(receptor activity)|GO:0007275(multicellular organismal development)|GO:0016020(membrane)	Homo sapiens sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3G (SEMA3G), mRNA [NM_020163]	chr3:52443241-52443182
22	33.9	58.3	0.58	NM_003874	NM_003874	8832	CD84	CD84 molecule	ENST00000368054	NP164805	GO:0004872(receptor activity)|GO:0005515(protein binding)|GO:0005886(plasma membrane)|GO:0005887(integral to plasma membrane)|GO:0006952(defense response)|GO:0007155(cell adhesion)|GO:0007156(homophilic cell adhesion)	Homo sapiens CD84 molecule (CD84), mRNA [NM_003874]	chr1:158801964-158801905

[0535]

表161 遺伝子セット1(No.1-31:横軸面で注目する遺伝子)

No	Cy5	Cy3	ratio	RefSeq Accession	Genbank Accession	Entrez Gene ID	Gene Symbol	Gene Name	Ensembl ID	TIGR ID	GO	Description	Genomic Coordinates
23	2256.5	3712.2	0.61	NM_000073	NM_000073	917	CD3G	CD3g molecule, gamma (CD3-TCR complex)	ENST00000292144	NP1454348	GO:0004888(transmembrane receptor activity)|GO:0005515(protein binding)|GO:0005887(integral to plasma membrane)|GO:0006461(protein complex assembly)|GO:0007163(establishment and/or maintenance of cell polarity)|GO:0007166(cell surface receptor linked sign	Homo sapiens CD3g molecule, gamma (CD3-TCR complex) (CD3G), mRNA [NM_000073]	chr11:117729200 41-117729200
24	27.3	42.1	0.65	NM_020406	NM_020406	57126	CD177	CD177 molecule		THC2896197	GO:0016020(membrane)|GO:0046503(GPI anchor binding)	Homo sapiens CD177 molecule (CD177), mRNA [NM_020406]	chr19:48557159-48557218
25	179.5	286.1	0.63	NM_173215	NM_173215	10725	NFAT5	nuclear factor of activated T-cells 5, tonicity-responsive	ENST00000349945	THC2495056	GO:0001816(cytokine production)|GO:0003700(transcription factor activity)|GO:0003702(RNA polymerase II transcription factor activity)|GO:0005515(protein binding)|GO:0005634(nucleus)|GO:0005737(cytoplasm)|GO:0006355(regulation of transcription, DNA-depende	Homo sapiens nuclear factor of activated T-cells 5, tonicity-responsive (NFAT5), transcript variant 5, mRNA [NM_173215]	chr16:68828669-68286756
26	3258.3	4987.8	0.65	NM_004494	NM_004494	3068	HDGF	hepatoma-derived growth factor (high-mobility group protein 1-like)	ENST00000357325	NP417915	GO:0005615(extracellular space)|GO:0005737(cytoplasm)|GO:0007165(signal transduction)|GO:0008083(growth factor activity)|GO:0008201(heparin binding)|GO:0008283(cell proliferation)	Homo sapiens hepatoma-derived growth factor (high-mobility group protein 1-like) (HDGF), mRNA [NM_004494]	chr1:154437923-154479173
27	33.8	58.7	0.58	NM_006290	NM_006290	7128	TNFAIP3	tumor necrosis factor, alpha-induced protein 3	ENST00000372289	THC2466354	GO:0000677(DNA binding)|GO:0005515(protein binding)|GO:0005634(nucleus)|GO:0005737(cytoplasm)|GO:0006512(ubiquitin cycle)|GO:0006915(apoptosis)|GO:0006916(anti-apoptosis)|GO:0008234(cysteine-type peptidase activity)|GO:0008270(zinc ion binding)|GO:0043124	Homo sapiens tumor necrosis factor, alpha-induced protein 3 (TNFAIP3), mRNA [NM_006290]	chr6:138243000-138243062

[0536]

表161 遺伝子セット1(No. 1-31:濃能面で注目する遺伝子)

No	Cy5	Cy3	ratio	RefSeq Accession	Genbank Accession	Entrez Gene ID	Gene Symbol	Gene Name	Ensembl ID	TIGR ID	GO	Description	Genomic Coordinates
28	17.4	38.4	0.44	NM_004248	NM_004248	2834	PRLHR	prolactin releasing hormone receptor	ENST00000369169	THC2479782	GO:0001584(rhodopsin-like receptor activity)|GO:0004872(receptor activity)|GO:0004983(neuropeptide Y receptor activity)|GO:0005887(integral to plasma membrane)|GO:0007165(signal transduction)|GO:0007186(G-protein coupled receptor protein signaling pathway	Homo sapiens prolactin releasing hormone receptor (PRLHR), mRNA [NM_004248]	chr10:1203443 21-120344262
29	35.5	53.2	0.67	NM_177402	NM_177402	127833	SYT2	synaptotagmin II	ENST00000367268	THC2571904	GO:0005215(transporter activity)|GO:0005509(calcium ion binding)|GO:0005515(protein binding)|GO:0005544(calcium-dependent phospholipid binding)|GO:0005886(plasma membrane)|GO:0006810(transport)|GO:0008021(syna	Homo sapiens synaptotagmin II (SYT2), mRNA [NM_177402]	chr1:200832522 -200832462
30	92.9	185.0	0.50	NM_014478	NM_014478	27297	RCP9	calcitonin gene-related peptide-receptor component	ENST00000338592	THC2476920	GO:0001669(acrosomal)|GO:0004948(calcitonin receptor activity)|GO:0005575(cellular_component)|GO:0007218(neuropeptide signaling pathway)|GO:0007340(acrosome reaction)	Homo sapiens calcitonin gene-related peptide-receptor component protein (RCP9), transcript variant 1, mRNA	chr7:85255342 -85255401
31	34.3	65.5	0.52	NM_172312	NM_172312	26206	SPAG8	sperm associated antigen 8	ENST00000378035	THC2474024	GO:0003674(molecular_function)|GO:0008150(biological_process)|GO:0016020(membrane)	Homo sapiens sperm associated antigen 8 (SPAG8), transcript variant 2, mRNA	chr9:35798128 -35798069

[表162]

表162 遺伝子セット1(No.32-61:発現増加・減少した遺伝子上位15個)

No	Cy5	Cy3	ratio	RefSeq Accession	Genbank Accession	Entrez Gene ID	Gene Symbol	Gene Name	Ensembl ID	TIGR ID	GO	Description	Genomic Coordinates
32	74.0	40.4	1.83	NM_005536	NM_005536	3612	IMPA1	inositol(myo)-1(or 4)-monophosphatase 1	ENST00000256108	THC2615788	GO:0000287(magnesium ion binding)|GO:0005975(carbohydrate metabolic process)|GO:0006020(myo-inositol metabolic process)|GO:0006661(phosphatidylinositol biosynthetic process)|GO:0006796(phosphate metabolic process)|GO:0007165(signal transduction)|GO:0008934(inositol-1(or 4)-monophosphatase activity)|GO:0016787(hydrolase activity)|GO:0031403(lithium ion binding)|GO:0042578(phosphoric ester hydrolase activity)	Homo sapiens inositol(myo)-1(or 4)-monophosphatase 1 (IMPA1), mRNA [NM_005536]	chr8:82735352-82734244
33	82.6	45.3	1.82		AK023131	9213	XPR1	xenotropic and polytropic retrovirus receptor	ENST00000367590	THC2492481	GO:0004930(G-protein coupled receptor activity)|GO:0005886(plasma membrane)|GO:0005887(integral to plasma membrane)|GO:0007186(G-protein coupled receptor protein signaling pathway)	xenotropic and polytropic retrovirus receptor [Source:RefSeq_peptide;AccNP_004727] [ENST00000367590]	chr1:179126842-179125901
34	66.0	36.3	1.82	NM_006577	NM_006577	10678	B3GNT2	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 2	ENST00000301998	THC2463386	GO:0006486(protein amino acid glycosylation)|GO:0007411(axon guidance)|GO:0007606(sensory perception of smell)|GO:0008150(biological_process)|GO:0008378(galactosyltransferase activity)|GO:0008499(UDP-galactose:beta-N-acetylglucosamine beta-1,3-galactosyltransferase activity)|GO:0016020(membrane)|GO:0016021(integral to membrane)|GO:0016757(transferase activity, transferring glycosyl groups)|GO:0030145(manganese ion binding)	Homo sapiens UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 2 (B3GNT2), mRNA [NM_006577]	chr2:62304735-62304794
35	142.5	79.7	1.79	NM_014739	NM_014739	9774	BCLAF1	BCL2-associated transcription factor 1		THC2503556	GO:0003677(DNA binding)|GO:0005515(protein binding)|GO:0005634(nucleus)|GO:0006350(transcription)|GO:0006355(regulation of transcription, DNA-dependent)|GO:0006917(induction of apoptosis)|GO:0016481(negative regulation of transcription)|GO:0016564(transcriptional repressor activity)	Homo sapiens BCL2-associated transcription factor 1 (BCLAF1), transcript variant 1, mRNA [NM_014739]	chr6:136620254-136620195
36	138.5	79.7	1.74	NM_021144	NM_021144	11168	PSIP1	PC4 and SFRS1 interacting protein 1	ENST00000380716	THC2479222	GO:0003677(DNA binding)|GO:0005634(nucleus)|GO:0006350(transcription)|GO:0006355(regulation of transcription, DNA-dependent)	Homo sapiens PC4 and SFRS1 interacting protein 1 (PSIP1), transcript variant 1, mRNA [NM_021144]	chr9:15460911-15460852
37	128.7	74.2	1.73	NM_006499	NM_006499	3964	LGALS8	lectin, galactoside-binding, soluble, 8 (galectin 8)	ENST00000352231	THC2540379	GO:0005529(sugar binding)|GO:0005615(extracellular space)	Homo sapiens lectin, galactoside-binding, soluble, 8 (galectin 8) (LGALS8), transcript variant 1, mRNA [NM_006499]	chr1:234777936-234777995

[0537]

表162 遺伝子セット1(No.32-61:発現増加・減少した遺伝子上位15個)

No	Cy5	Cy3	ratio	RefSeq Accession	Genbank Accession	Entrez Gene ID	Gene Symbol	Gene Name	Ensembl ID	T1GR ID	GO	Description	Genomic Coordinates
38	196.0	116.2	1.69	NM_021982	NM_021982	10802	SEC24A	SEC24 related gene family, member A (S. cerevisiae)	ENST00000265341	THC2493017	GO:0003674(molecular_function)|GO:0005515(protein binding)|GO:0005783(endoplasmic reticulum)|GO:0006886(intracellular protein transport)|GO:0006888(ER to Golgi vesicle-mediated transport)|GO:0006270(zinc ion binding)|GO:0030127(COPII vesicle coat)	Homo sapiens SEC24 related gene family, member A (S. cerevisiae) (SEC24A), mRNA [NM_021982]	chr2:134091112 2-134091181
39	150.8	87.4	1.72	NM_001007189	NM_001007189	492311	LOC492311	similar to bovine IgA regulatory protein	ENST00000333305	THC2472605		Homo sapiens similar to bovine IgA regulatory protein (LOC492311), mRNA [NM_001007189]	chr5:139468822 5-139468284
40	172.9	103.2	1.68	NM_016467	NM_016467	94101	ORMDL1	ORM1-like 1 (S. cerevisiae)	ENST00000325795	THC2468861	GO:0005783(endoplasmic reticulum)|GO:0005789(endoplasmic reticulum membrane)|GO:0006695(protein targeting)|GO:0016020(membrane)|GO:0016021(integral to membrane)	Homo sapiens ORM1-like 1 (S. cerevisiae) (ORMDL1), mRNA [NM_016467]	chr2:190343501 0-190343441
41	150.6	88.6	1.70	NM_133330	NM_133330	7468	WHSC1	Wolf-Hirschhorn syndrome candidate 1	ENST00000312087	THC2865202	GO:0003677(DNA binding)|GO:0005515(protein binding)|GO:0005634(nucleus)|GO:0006350(transcription)|GO:0006355(regulation of transcription, DNA-dependent)|GO:0008168(methyltransferase activity)|GO:0008270(zinc ion binding)|GO:0009653(anatomical structure morphogenesis)|GO:0016568(chromatin modification)|GO:0016740(transferase activity)|GO:0018024(histone-lysine N-methyltransferase activity)|GO:0046872(metal ion binding)	Homo sapiens Wolf-Hirschhorn syndrome candidate 1 (WHSC1), transcript variant 1, mRNA [NM_133330]	chr4:1953344-1953403
42	91.0	54.4	1.67	NM_005432	NM_005432	7517	XRCC3	X-ray repair complementing defective repair in Chinese hamster cells 3	ENST00000352127	THC2510767	GO:0000166(nucleotide binding)|GO:0003677(DNA binding)|GO:0005524(ATP binding)|GO:0005634(nucleus)|GO:0006281(DNA repair)|GO:0006310(DNA recombination)|GO:0008094(DNA-dependent ATPase activity)	Homo sapiens X-ray repair complementing defective repair in Chinese hamster cells 3 (XRCC3), mRNA [NM_005432]	chr14:103235093-103235034
43	164.2	101.0	1.62	NM_174909	NM_174909	153339	TMEM167	transmembrane protein 167	ENST00000308489	THC2523245	GO:0016020(membrane)|GO:0016021(integral to membrane)	Homo sapiens transmembrane protein 167 (TMEM167), mRNA [NM_174909]	chr5:82388449-82388391
44	201.8	124.2	1.62	NM_015387	NM_015387	25843	PREI3	preimplantation protein 3	ENST00000323303	THC2467915	GO:0006810(transport)|GO:0008270(zinc ion binding)|GO:0016020(membrane)|GO:0046872(metal ion binding)	Homo sapiens preimplantation protein 3 (PREI3), transcript variant 1, mRNA [NM_015387]	chr2:198112539 3-198125452

[0538]

表162 遺伝子セット1(No.32-61:発現増加・減少した遺伝子上位15個)

No	Cy5	Cy3	ratio	RefSeq Accession	Genbank Accession	Entrez Gene ID	Gene Symbol	Gene Name	Ensembl ID	TIGR ID	GO	Description	Genomic Coordinates
45	125.2	77.5	1.62	NM_006896	NM_006896	10560	SLC19A2	solute carrier family 19 (thiamine transporter), member 2	ENST00000236137	THC2485904	GO:0001584(rhodopsin-like receptor activity)|GO:0005542(folic acid binding)|GO:0005886(plasma membrane)|GO:0006810(transport)|GO:0007186(G-protein coupled receptor protein signaling pathway)|GO:0007605(sensory perception of sound)|GO:0008517(folic acid transporter activity)|GO:0008518(reduced folate carrier activity)|GO:0015234(thiamin transporter activity)|GO:0015888(thiamin transport)|GO:0016020(membrane)|GO:0016021(integral to membrane)	Homo sapiens solute carrier family 19 (thiamine transporter), member 2 (SLC19A2), mRNA [NM_006896]	chr1:167889894-167899886
46	101.7	63.7	1.60	NM_016205	NM_016205	56034	PDGFC	platelet derived growth factor C	ENST00000274071	THC2601312	GO:0000074(regulation of progression through cell cycle)|GO:0005576(extracellular region)|GO:0007417(central nervous system development)|GO:0008083(growth factor activity)|GO:0008283(cell proliferation)|GO:0016020(membrane)	Homo sapiens platelet derived growth factor C (PDGFC), mRNA [NM_016205]	chr4:157902408-157902349

[表163]

表163 遺伝子セット1 (No. 32-61:発現増加・減少した遺伝子上位15個)

No	Cy5	Cy3	ratio	RefSeq Accession	Genbank Accession	Entrez Gene ID	Gene Symbol	Gene Name	Ensembl ID	TIGR ID	GO	Description	Genomic Coordinates
47	26.0	160.3	0.16	NM_005236	NM_005236	2072	ERCC4	excision repair cross-complementing rodent repair deficiency, complementation group 4	ENST00000389138	THC2577227	GO:0000109(nucleotide-excision repair complex)|GO:0000287(magnesium ion binding)|GO:0003677(DNA binding)|GO:0004520(endodeoxyribonuclease activity)|GO:0005634(nucleus)|GO:0006289(nucleotide-excision repair)|GO:0016787(hydrolase activity)	Homo sapiens excision repair cross-complementing rodent repair deficiency, complementation group 4 (ERCC4), mRNA [NM_005236]	chr16:13936865-13936913
48	15.0	86.3	0.17	NM_001017995	NM_001017995	285590	SH3PXD2B	SH3 and PX domains 2B	ENST00000311601	THC2491704		Homo sapiens SH3 and PX domains 2B (SH3PXD2B), mRNA [NM_001017995]	chr5:171697513-171697454
49	28.5	117.3	0.24	NM_012147	NM_012147	26583	DUX2	double homeobox, 2		THC2487011	GO:0003700(transcription factor activity)|GO:0005634(nucleus)|GO:0006355(regulation of transcription, DNA-dependent)|GO:0043565(sequence-specific DNA binding)	Homo sapiens double homeobox, 2 (DUX2), mRNA [NM_012147]	chr3:075800826-075800884
50	17.6	70.7	0.25	NM_001283	NM_001283	1174	AP1S1	adaptor-related protein complex 1, sigma 1 subunit	ENST00000337619	THC2464757	GO:0005515(protein binding)|GO:0005802(Golgi trans face)|GO:0005905(coated pit)|GO:0006886(intracellular protein transport)|GO:0006898(receptor-mediated endocytosis)|GO:0008565(protein transporter activity)|GO:0030121(AP-1 adaptor complex)|GO:0030662(coated vesicle membrane)	Homo sapiens adaptor-related protein complex 1, sigma 1 subunit (AP1S1), transcript variant 1, mRNA [NM_001283]	chr7:100567431-100589063
51	29.7	110.0	0.27	NM_032638	NM_032638	2624	GATA2	GATA binding protein 2	ENST00000341105	NP099465	GO:0003700(transcription factor activity)|GO:0005634(nucleus)|GO:0006350(transcription)|GO:0006355(regulation of transcription, DNA-dependent)|GO:0006366(transcription from RNA polymerase II promoter)|GO:0008909(phagocytosis)|GO:0008270(zinc ion binding)|GO:0030182(neuron differentiation)|GO:0043565(sequence-specific DNA binding)|GO:0046872(metal ion binding)|GO:0090766(positive regulation of phagocytosis)	Homo sapiens GATA binding protein 2 (GATA2), mRNA [NM_032638]	chr3:129868335-129682795
52	23.6	85.6	0.28	XR_015273	XR_015273	728371	LOC728371	similar to ankyrin repeat domain 20A		THC2740861		PREDICTED: Homo sapiens similar to ankyrin repeat domain 20A (LOC728371), mRNA [XR_015273]	chr4:49210459-49219400

[0539]

表163 遺伝子セット1(No.32-61:発現増加・減少した遺伝子上位15個)

No	Cy5	Cy3	ratio	RefSeq Accession	Genbank Accession	Entrez Gene ID	Gene Symbol	Gene Name	Ensembl ID	TIGR ID	GO	Description	Genomic Coordinates
53	105.7	383.4	0.28	NM_004566	NM_004566	5208	PFKFB3	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 3	ENST00000379775	THC2677305	GO:0000166(nucleotide binding)|GO:0003824(catalytic activity)|GO:0004331(fructose-2,6-bisphosphate 2-phosphatase activity)|GO:0005524(ATP binding)|GO:0005575(cellular_component)|GO:0006003(fructose 2,6-bisphosphate metabolic process)|GO:0008152(metabolic process)|GO:0016301(kinase activity)|GO:0016740(transferase activity)|GO:0016787(hydrolase activity)|GO:0042802(identical protein binding)	Homo sapiens 6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 3 (PFKFB3), mRNA [NM_004566]	chr10:6314902-6314961
54	51.4	172.6	0.30	NM_006623	NM_006623	26227	PHGDH	phosphoglycerate dehydrogenase	ENST00000369409	THC2565900	GO:0004617(phosphoglycerate dehydrogenase activity)|GO:0005215(transporter activity)|GO:0005576(extracellular region)|GO:0006564(L-serine biosynthetic process)|GO:0006810(transport)|GO:0007420(brain development)|GO:0008152(metabolic process)|GO:0008652(amino acid biosynthetic process)|GO:0009055(electron carrier activity)|GO:0016491(oxidoreductase activity)|GO:0016616(oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor)|GO:0051287(NAD binding)	Homo sapiens phosphoglycerate dehydrogenase (PHGDH), mRNA [NM_006623]	chr1:120087057-120087111
55	23.6	75.2	0.31		AK094300	401541	CENPP	centromere protein P	ENST00000375587	THC2601773	GO:0000775(chromosome, pericentric region)|GO:0005634(nucleus)|GO:0005694(chromosome)	Centromere protein P (CENP-P), [Source:Uniprot/SWISSPROT;Acc:Q68PU0] [ENST00000375587]	chr3:84422069-84422126
56	17.7	55.3	0.32	NM_001004728	NM_001004728	219982	OR5A1	olfactory receptor, family 5, subfamily A, member 1	ENST00000302030	THC2611945	GO:0004872(receptor activity)|GO:0004984(olfactory receptor activity)|GO:0007165(signal transduction)|GO:0007186(G-protein coupled receptor protein signaling pathway)|GO:0007608(sensory perception of smell)|GO:0016020(membrane)|GO:0016021(integral to membrane)|GO:0050896(response to stimulus)	Homo sapiens olfactory receptor, family 5, subfamily A, member 1 (OR5A1), mRNA [NM_001004728]	chr11:58867427-58867486
57	47.9	148.2	0.32	NM_020421	NM_020421	57143	ADCK1	aarF domain containing kinase 1	ENST00000238561	THC2464727	GO:0000166(nucleotide binding)|GO:0004672(protein kinase activity)|GO:0005524(ATP binding)|GO:0006468(protein amino acid phosphorylation)|GO:0016740(transferase activity)	Homo sapiens aarF domain containing kinase 1 (ADCK1), mRNA [NM_020421]	chr14:77467803-77468370
58	24.4	71.2	0.34	NM_012252	NM_012252	22797	TFEC	transcription factor EC	ENST00000265440	THC2602661	GO:0003700(transcription factor activity)|GO:0003713(transcription coactivator activity)|GO:0003714(transcription corepressor activity)|GO:0005634(nucleus)|GO:0030528(transcription regulator activity)|GO:0045449(regulation of transcription)	Homo sapiens transcription factor EC (TFEC), transcript variant 1, mRNA [NM_012252]	chr7:115382779-115382733

[0540]

表163　遺伝子セット1(No. 32-61:発現増加・減少した遺伝子上位15個)

No	Cy5	Cy3	ratio	RefSeq Accession	Genbank Accession	Entrez Gene ID	Gene Symbol	Gene Name	Ensembl ID	TIGR ID	GO	Description	Genomic Coordinates
59	61.6	179.5	0.34	NM_006583	NM_006583	10692	RRH	retinal pigment epithelium-derived rhodopsin homolog	ENST00000317735	THC2483909	GO:0001584(rhodopsin-like receptor activity)|GO:0004872(receptor activity)|GO:0005887(integral to plasma membrane)|GO:0007165(signal transduction)|GO:0007186(G-protein coupled receptor protein signaling pathway)|GO:0007601(visual perception)|GO:0016020(membrane)|GO:0018298(protein-chromophore linkage)	Homo sapiens retinal pigment epithelium-derived rhodopsin homolog (RRH), mRNA [NM_006583]	chr4:110985039-110985098
60	117.2	328.8	0.36	NM_152721	NM_152721	220164	DOK6	docking protein 6	ENST00000382713	NP362987	GO:0005158(insulin receptor binding)	Homo sapiens docking protein 6 (DOK6), mRNA [NM_152721]	chr18:65660237-65660296
61	13.1	36.7	0.36	NM_182610	NM_182610	344658	SAMD7	sterile alpha motif domain containing 7	ENST00000335556	THC2485083		Homo sapiens sterile alpha motif domain containing 7 (SAMD7), mRNA [NM_182610]	chr3:171138886-171138945

[表164]

表164 遺伝子セット1(No. 1-31:機能面で注目する遺伝子, No. 32-61:発現増加・減少した遺伝子上位15個)

No	Target(Gene)Symbol	Target Accession	UniGene	Up/Down	被験者群	配列番号
1	FGFR1OP	NM_007045	Hs.487175	Up	A	1
2	CASP8AP2	NM_012115	Hs.558218	Up	A	2
3	PROK2	NM_021935	Hs.528665	Up	A	3
4	FCER1A	NM_002001	Hs.897	Up	A	4
5	CD69	NM_001781	Hs.208854	Up	A	5
6	PAQR3	NM_001040202	Hs.632591	Up	A	6
7	SLC6A4	NM_001045	Hs.591192	Up	A	7
8	GGCX	NM_000821	Hs.77719	Up	A	8
9	HBA2	NM_000517	Hs.449630	Up	A	9
10	ADH5	NM_000671	Hs.78989	Up	A	10
11	JUN	NM_002228	Hs.525704	Down	A	11
12	TP53	NM_000546	Hs.408312	Down	A	12
13	RAB5B		Hs.567328	Down	A	-
14	RAB8A	NM_005370	Hs.642874	Down	A	13
15	RAB12	NM_001025300	Hs.270074	Down	A	14
16	RAB20	NM_017817	Hs.508720	Down	A	15
17	RAB30	NM_014488	Hs.40758	Down	A	16
18	VISA		Hs.646283	Down	A	-
19	CD55		Hs.527653	Down	A	-
20	IGHG1	BC092518	Hs.510635	Down	A	-
21	SEMA3G	NM_020163	Hs.59729	Down	A	17
22	CD84	NM_003874	Hs.398093	Down	A	-
23	CD3G	NM_000073	Hs.2259	Down	A	18
24	CD177	NM_020406	Hs.232165	Down	A	19
25	NFAT5	NM_173215	Hs.371987	Down	A	20
26	HDGF	NM_004494	Hs.506748	Down	A	21
27	TNFAIP3	NM_006290	Hs.591338	Down	A	22
28	PRLHR	NM_004248	Hs.248119	Down	A	23
29	SYT2	NM_177402	Hs.585015	Down	A	24
30	RCP9	NM_014478	Hs.300684	Down	A	25
31	SPAG8	NM_172312	Hs.256747	Down	A	26
32	IMPA1	NM_005536	Hs.555086	Up	A	27
33	XPR1		Hs.648372	Up	A	-
34	B3GNT2	NM_006577	Hs.173203	Up	A	28
35	BCLAF1	NM_014739		Up	A	29
36	PSIP1	NM_021144	Hs.493516	Up	A	30
37	LGALS8	NM_006499	Hs.4082	Up	A	31
38	SEC24A	NM_021982	Hs.595540	Up	A	32
39	LOC492311	NM_001007189	Hs.200938	Up	A	-
40	ORMDL1	NM_016467	Hs.651259	Up	A	33
41	WHSC1	NM_133330	Hs.113876	Up	A	34
42	XRCC3	NM_005432	Hs.592325	Up	A	35
43	TMEM167	NM_174909	Hs.355606	Up	A	36
44	PREI3	NM_015387	Hs.645458	Up	A	-
45	SLC19A2	NM_006996	Hs.30246	Up	A	37
46	PDGFC	NM_016205	Hs.570855	Up	A	38
47	ERCC4	NM_005236	Hs.567265	Down	A	39
48	SH3PXD2B	NM_001017995	Hs.285666	Down	A	40
49	DUX2	NM_012147		Down	A	41
50	AP1S1	NM_001283	Hs.563509	Down	A	42
51	GATA2	NM_032638	Hs.367725	Down	A	43
52	LOC728371	XR_015273	Hs.558795	Down	A	44
53	PFKFB3	NM_004566	Hs.195471	Down	A	45
54	PHGDH	NM_006623	Hs.487296	Down	A	46
55	CENPP		Hs.459896	Down	A	-
56	OR5A1	NM_001004728	Hs.553649	Down	A	47
57	ADCK1	NM_020421	Hs.413208	Down	A	48
58	TFEC	NM_012252	Hs.125962	Down	A	49
59	RRH	NM_006583	Hs.352262	Down	A	50
60	DOK6	NM_152721	Hs.569915	Down	A	51
61	SAMD7	NM_182610	Hs.439922	Down	A	52

[0541] 上記解析6で笑いにより遺伝子発現の変動が認められた遺伝子のうち、機能面で注目すべき遺伝子、及び特に発現変動の大きかった上位15遺伝子を表165～171に示し、これらを要約した表172を遺伝子セット2の表として示す。

[表165]

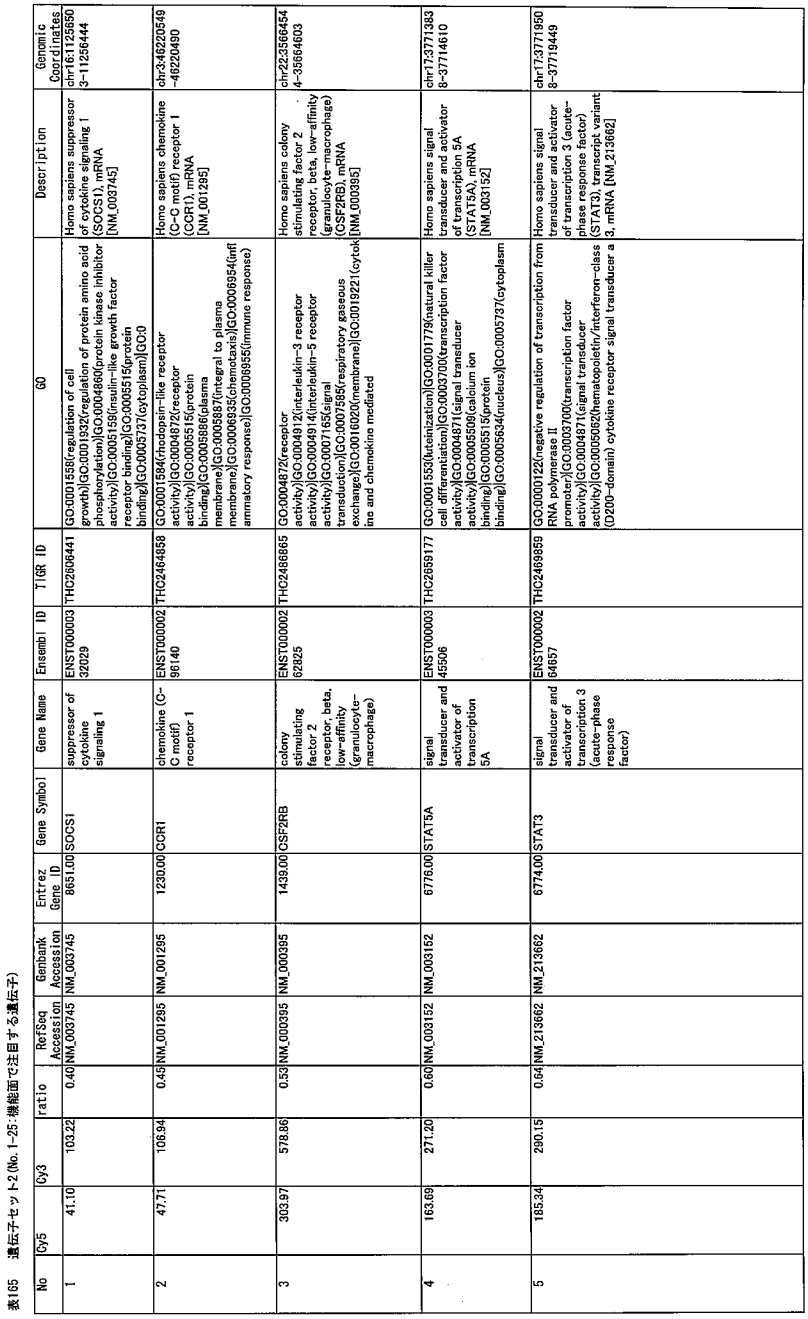


表165 遺伝子セット2(No. 1-25:機能面で注目する遺伝子)

No	Cy5	Cy3	ratio	RefSeq Accession	Genbank Accession	Entrez Gene ID	Gene Symbol	Gene Name	Ensembl ID	TIGR ID	GO	Description	Genomic Coordinates
1	41.10	103.22	0.40	NM_003745	NM_003745	8651.00	SOCS1	suppressor of cytokine signaling 1	ENST00000329029	THC2606441	GO:0001556(regulation of cell growth)|GO:0001932(regulation of protein amino acid phosphorylation)|GO:0004860(protein kinase inhibitor activity)|GO:0005159(insulin-like growth factor receptor binding)|GO:0005515(protein binding)|GO:0005737(cytoplasm)|GO:0	Homo sapiens suppressor of cytokine signaling 1 (SOCS1), mRNA [NM_003745]	chr16:11235690-11236444
2	47.71	106.94	0.45	NM_001295	NM_001295	1230.00	CCR1	chemokine (C-C motif) receptor 1	ENST00000296140	THC2464858	GO:0001594(rhodopsin-like receptor activity)|GO:0004872(receptor activity)|GO:0005515(protein binding)|GO:0005886(plasma membrane)|GO:0005887(integral to plasma membrane)|GO:0006935(chemotaxis)|GO:0006954(inflammatory response)|GO:0009595(immune response)	Homo sapiens chemokine (C-C motif) receptor 1 (CCR1), mRNA [NM_001295]	chr3:46220549-46220490
3	303.97	578.86	0.53	NM_000395	NM_000395	1439.00	CSF2RB	colony stimulating factor 2 receptor, beta, low-affinity (granulocyte-macrophage)	ENST00000262825	THC2486865	GO:0004872(receptor activity)|GO:0004912(interleukin-3 receptor activity)|GO:0004914(interleukin-5 receptor activity)|GO:0007165(signal transduction)|GO:0007595(respiratory gaseous exchange)|GO:0016020(membrane)|GO:0019221(cytokine and chemokine mediated	Homo sapiens colony stimulating factor 2 receptor, beta, low-affinity (granulocyte-macrophage) (CSF2RB), mRNA [NM_000395]	chr22:35664544-35664603
4	163.69	271.20	0.60	NM_003152	NM_003152	6776.00	STAT5A	signal transducer and activator of transcription 5A	ENST00000345506	THC2659177	GO:0001553(luteinization)|GO:0001779(natural killer cell differentiation)|GO:0003700(transcription factor activity)|GO:0004871(signal transducer activity)|GO:0005509(calcium ion binding)|GO:0005515(protein binding)|GO:0005634(nucleus)|GO:0005737(cytoplasm	Homo sapiens signal transducer and activator of transcription 5A (STAT5A), mRNA [NM_003152]	chr17:37713838-37714610
5	185.34	290.15	0.64	NM_213662	NM_213662	6774.00	STAT3	signal transducer and activator of transcription 3 (acute-phase response factor)	ENST00000364657	THC2469859	GO:0000122(negative regulation of transcription from RNA polymerase II promoter)|GO:0003700(transcription factor activity)|GO:0004871(signal transducer activity)|GO:0005062(hematopoietin/interferon-class (D200-domain) cytokine receptor signal transducer a	Homo sapiens signal transducer and activator of transcription 3 (acute-phase response factor) (STAT3), transcript variant 3, mRNA [NM_213662]	chr17:37713950-37719449

[0542]

表165 遺伝子セット2(No. 1-25:機能面で注目する遺伝子)

No	Cy5	Cy3	ratio	RefSeq Accession	Genbank Accession	Entrez Gene ID	Gene Symbol	Gene Name	Ensembl ID	TIGR ID	GO	Description	Genomic Coordinates
6	1136.06	1747.16	0.65	NM_001066	NM_001066	7133.00	TNFRSF1B	tumor necrosis factor receptor superfamily, member 1B	ENST00000039239	TIGR2461304	GO:0004872(receptor activity)|GO:0005031(tumor necrosis factor receptor activity)|GO:0005515(protein binding)|GO:0005615(extracellular space)|GO:0006915(apoptosis)|GO:0006954(inflammatory response)|GO:0008219(cell death)|GO:0008283(cell proliferation)|GO:	Homo sapiens tumor necrosis factor receptor superfamily, member 1B (TNFRSF1B), mRNA [NM_001066]	chr1:12190862 -12190921

[表166]

表166 遺伝子セット2(No. 1-25:機能面で注目する遺伝子)

No	Cy5	Cy3	ratio	RefSeq Accession	Genbank Accession	Entrez Gene ID	Gene Symbol	Gene Name	Ensembl ID	TIGR ID	GO	Description	Genomic Coordinates
7	215.67	341.54	0.63	NM_014748	NM_014748	9784.00	SNX17	sorting nexin 17	ENST00000379967	THC2505892	GO:0005102(receptor binding)|GO:0005737(cytoplasm)|GO:0005769(early endosome)|GO:0005794(Golgi apparatus)|GO:0006886(intracellular protein transport)|GO:0006898(receptor-mediated endocytosis)|GO:0007165(signal transduction)|GO:0008022(protein C-terminus b	Homo sapiens sorting nexin 17 (SNX17), mRNA [NM_014748]	chr2:27450515 -27450744
8	298.35	457.34	0.65	NM_145351	NM_145351	8578.00	SCARF1	scavenger receptor class F, member 1	ENST00000348987	NP494816	GO:0004888(transmembrane receptor activity)|GO:0005515(protein binding)|GO:0006898(receptor-mediated endocytosis)|GO:0007155(cell adhesion)|GO:0016020(membrane)|GO:0016021(integral to membrane)|GO:0016358(dendrite development)|GO:0030169(low-density lipop	Homo sapiens scavenger receptor class F, member 1 (SCARF1), transcript variant 4, mRNA [NM_145351]	chr17:1484562 -1484503

[表167]

表167 遺伝子セット2(No.1-25:機能面で注目する遺伝子)

No	Cy5	Cy3	ratio	RefSeq Accession	Genbank Accession	Entrez Gene ID	Gene Symbol	Gene Name	Ensembl ID	TIGR ID	GO	Description	Genomic Coordinates
9	91.42	220.37	0.41	0.00	M28219	3949.00	LDLR	low density lipoprotein receptor (familial hypercholesterolemia)	0.00	NP097371	GO:0004872(receptor activity)|GO:0004888(transmembrane receptor activity)|GO:0005041(low-density lipoprotein receptor activity)|GO:0005319(lipid transporter activity)|GO:0005509(calcium ion binding)|GO:0005615(extracellular space)|GO:0005768(endosome)|GO:	Homo sapiens low density lipoprotein receptor (FH 10 mutant causing familial hypercholesterolemia) mRNA, 3' end. [M28219]	chr19:1109507 -11095134
10	96.94	206.04	0.47	NM_006804	NM_006804	10948.00	STARD3	START domain containing 3	ENST00000336308	THC2509314	GO:0005737(cytoplasm)|GO:0005770(late endosome)|GO:0006629(lipid metabolic process)|GO:0006694(steroid biosynthetic process)|GO:0006706(C21-steroid hormone biosynthetic process)|GO:0006839(mitochondrial transport)|GO:0006869(lipid transport)|GO:0008203(ch	Homo sapiens START domain containing 3 (STARD3), mRNA [NM_006804]	chr17:3506930 9-35070024
11	78.45	145.91	0.54	NM_018941	NM_018941	2055.00	CLN8	ceroid-lipofuscinosis, neuronal 8 (epilepsy, progressive with mental retardation)	ENST00000382811	THC2556584	GO:0005783(endoplasmic reticulum)|GO:0005793(ER-Golgi intermediate compartment)|GO:0006644(phospholipid metabolic process)|GO:0006869(lipid transport)|GO:0007399(nervous system development)|GO:0008203(cholesterol metabolic process)|GO:0008610(lipid biosyn	Homo sapiens ceroid-lipofuscinosis, neuronal 8 (epilepsy, progressive with mental retardation) (CLN8), mRNA [NM_018941]	chr8:1719283-1719362
12	58.22	106.48	0.55	NM_145343	NM_145343	8542.00	APOL1	apolipoprotein L, 1	ENST00000319136	NP1212023	GO:0005319(lipid transporter activity)|GO:0005576(extracellular region)|GO:0005615(extracellular space)|GO:0006629(lipid metabolic process)|GO:0006869(lipid transport)|GO:0008202(steroid metabolic process)|GO:0008203(cholesterol metabolic process)|GO:0008	Homo sapiens apolipoprotein L, 1 (APOL1), transcript variant 2, mRNA [NM_145343]	chr22:3499155 0-34991609

[0543]

表167　遺伝子セット2(No. 1-25:機能面で注目する遺伝子)

No	Cy5	Cy3	ratio	RefSeq Accession	Genbank Accession	Entrez Gene ID	Gene Symbol	Gene Name	Ensembl ID	TIGR ID	GO	Description	Genomic Coordinates
13	105.55	178.59	0.59	NM_024490	NM_024490	57194.00	ATP10A	ATPase, Class V, type 10A	ENST00000389966	THC2473865	GO:0000166(nucleotide binding)|GO:0000287(magnesium ion binding)|GO:0004012(phospholipid-translocating ATPase activity)|GO:0005524(ATP binding)|GO:0006810(transport)|GO:0006812(cation transport)|GO:0008360(regulation of cell shape)|GO:0015662(ATPase activ	Homo sapiens ATPase, Class V, type 10A (ATP10A), mRNA [NM_024490]	chr15:23476185-23476126
14	4207.61	6770.80	0.62	NM_001042465	NM_001042465	5660.00	PSAP	prosaposin (variant Gaucher disease and variant metachromatic leukodystrophy)	ENST00000357471	THC2569349	GO:0004098(cerebroside-sulfatase activity)|GO:0004336(galactosylceramidase activity)|GO:0004348(glucosylceramidase activity)|GO:0004557(alpha-galactosidase activity)|GO:0004565(beta-galactosidase activity)|GO:0004767(sphingomyelin phosphodiesterase activi	Homo sapiens prosaposin (variant Gaucher disease and variant metachromatic leukodystrophy) (PSAP), transcript variant 2, mRNA [NM_001042465]	chr10:73249266-73248854
15	152.26	243.88	0.62	NM_030758	NM_030758	23762.00	OSBP2	oxysterol binding protein 2	ENST00000332585	THC2731705	GO:0006869(lipid transport)|GO:0008202(steroid metabolic process)|GO:0016020(membrane)	Homo sapiens oxysterol binding protein 2 (OSBP2), transcript variant 1, mRNA [NM_030758]	chr22:29632848-29632907
16	1111.61	1757.75	0.63	NM_198580	NM_198580	376497.00	SLC27A1	solute carrier family 27 (fatty acid transporter), member 1	ENST00000252595	NP390220	GO:0000166(nucleotide binding)|GO:0003824(catalytic activity)|GO:0006629(lipid metabolic process)|GO:0006631(fatty acid metabolic process)|GO:0006869(lipid transport)|GO:0008152(metabolic process)|GO:0016020(membrane)|GO:0016021(integral to membrane)|GO:0	Homo sapiens solute carrier family 27 (fatty acid transporter), member 1 (SLC27A1), mRNA [NM_198580]	chr19:17476894-17476953
17	134.83	211.84	0.64	NM_030641	NM_030641	80830.00	APOL6	apolipoprotein L, 6	ENST00000306062	THC2475727	GO:0003700(transcription factor activity)|GO:0005319(lipid transporter activity)|GO:0005576(extracellular region)|GO:0005737(cytoplasm)|GO:0006355(regulation of transcription, DNA-dependent)|GO:0006869(lipid transport)|GO:0008289(lipid binding)|GO:0042157	Homo sapiens apolipoprotein L, 6 (APOL6), mRNA [NM_030641]	chr22:34385572-34385631

[表168]

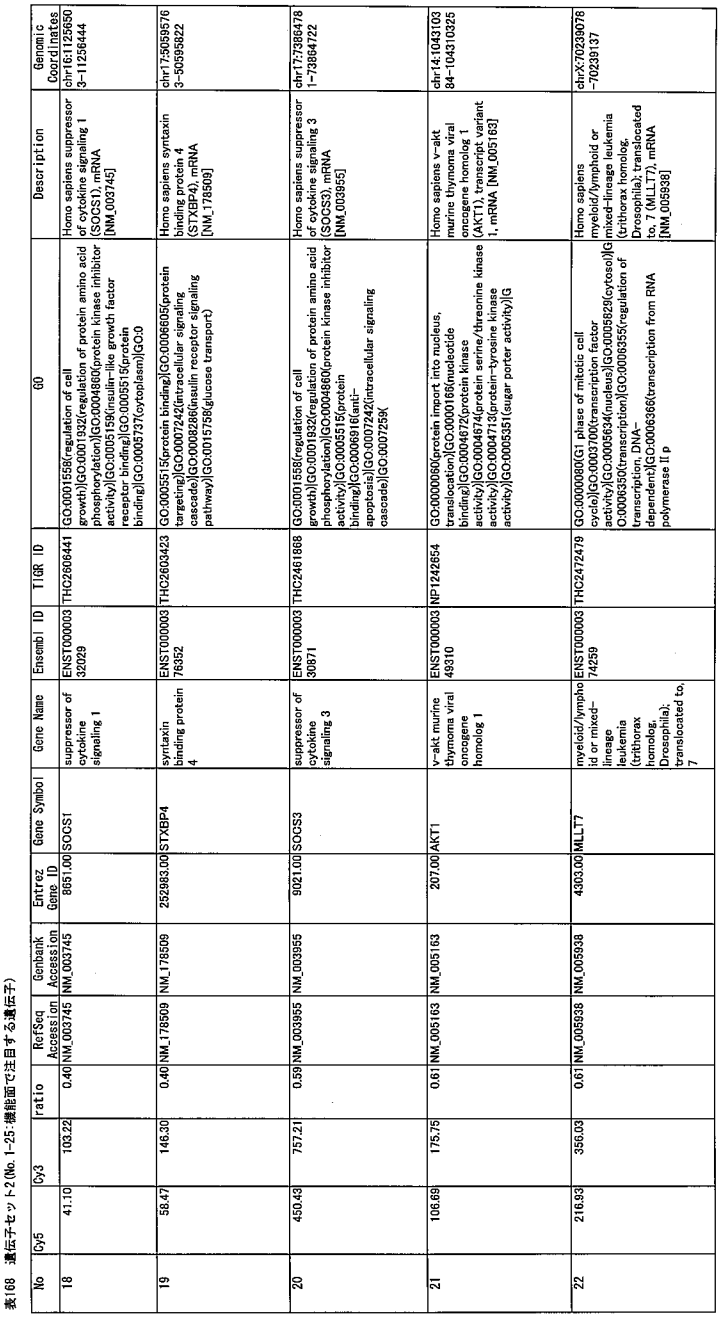


表168 遺伝子セット2(No.1-25:機能面で注目する遺伝子)

No	Cy5	Cy3	ratio	RefSeq Accession	Genbank Accession	Entrez Gene ID	Gene Symbol	Gene Name	Ensembl ID	TIGR ID	GO	Description	Genomic Coordinates
18	41.10	103.22	0.40	NM_003745	NM_003745	8651.00	SOCS1	suppressor of cytokine signaling 1	ENST00000332029	THC2606441	GO:0001558(regulation of cell growth)|GO:0001932(regulation of protein amino acid phosphorylation)|GO:0004860(protein kinase inhibitor activity)|GO:0005159(insulin-like growth factor receptor binding)|GO:0005515(protein binding)|GO:0005737(cytoplasm)|GO:0	Homo sapiens suppressor of cytokine signaling 1 (SOCS1), mRNA [NM_003745]	chr16:11256503-11256444
19	58.47	146.30	0.40	NM_178509	NM_178509	252983.00	STXBP4	syntaxin binding protein 4	ENST00000376352	THC2603423	GO:0005515(protein binding)|GO:0006605(protein targeting)|GO:0007242(intracellular signaling cascade)|GO:0008286(insulin receptor signaling pathway)|GO:0015758(glucose transport)|	Homo sapiens syntaxin binding protein 4 (STXBP4), mRNA [NM_178509]	chr17:5059576-50595822
20	450.43	757.21	0.59	NM_003955	NM_003955	9021.00	SOCS3	suppressor of cytokine signaling 3	ENST00000330871	THC2461868	GO:0001558(regulation of cell growth)|GO:0001932(regulation of protein amino acid phosphorylation)|GO:0004860(protein kinase inhibitor activity)|GO:0005515(protein binding)|GO:0006916(anti-apoptosis)|GO:0007242(intracellular signaling cascade)|GO:0007259(J	Homo sapiens suppressor of cytokine signaling 3 (SOCS3), mRNA [NM_003955]	chr17:73864478-73864722
21	106.69	175.75	0.61	NM_005163	NM_005163	207.00	AKT1	v-akt murine thymoma viral oncogene homolog 1	ENST00000349310	NP1242654	GO:0000060(protein import into nucleus, translocation)|GO:0000166(nucleotide binding)|GO:0004672(protein kinase activity)|GO:0004674(protein serine/threonine kinase activity)|GO:0004713(protein-tyrosine kinase activity)|GO:0005351(sugar porter activity)|G	Homo sapiens v-akt murine thymoma viral oncogene homolog 1 (AKT1), transcript variant 1, mRNA [NM_005163]	chr14:104310384-104310325
22	216.83	356.03	0.61	NM_005938	NM_005938	4303.00	MLLT7	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 7	ENST00000374259	THC2472479	GO:0000080(G1 phase of mitotic cell cycle)|GO:0003700(transcription factor activity)|GO:0005634(nucleus)|GO:0005829(cytosol)|GO:0006350(transcription)|GO:0006355(regulation of transcription, DNA-dependent)|GO:0006366(transcription from RNA polymerase II p	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 7 (MLLT7), mRNA [NM_005938]	chrX:70239078-70239137

[表169]

表169 遺伝子セット2(No. 1-25:機能面で注目する遺伝子)

No	Cy5	Cy3	ratio	RefSeq Accession	Genbank Accession	Entrez Gene ID	Gene Symbol	Gene Name	Ensembl ID	T1GR ID	GO	Description	Genomic Coordinates
23	568.54	1049.21	0.54	NM_005194	NM_005194	1051.00	CEBPB	CCAAT/enhancer binding protein (C/EBP), beta	ENST00000371644	THC2575878	GO:0001892(embryonic placenta development)|GO:0003700(transcription factor activity)|GO:0005634(nucleus)|GO:0005737(cytoplasm)|GO:0006350(transcription)|GO:0006355(regulation of transcription, DNA-dependent)|GO:0006366(transcription from RNA polymerase II	Homo sapiens CCAAT/enhancer binding protein (C/EBP), beta (CEBPB), mRNA [NM_005194]	chr20:48244132 0-48241379
24	25639.21	39168.75	0.66	NM_005194	NM_005194	1051.00	CEBPB	CCAAT/enhancer binding protein (C/EBP), beta	ENST00000371644	THC2511538	GO:0001892(embryonic placenta development)|GO:0003700(transcription factor activity)|GO:0005634(nucleus)|GO:0005737(cytoplasm)|GO:0006350(transcription)|GO:0006355(regulation of transcription, DNA-dependent)|GO:0006366(transcription from RNA polymerase II	Homo sapiens CCAAT/enhancer binding protein (C/EBP), beta (CEBPB), mRNA [NM_005194]	chr20:48244239 6-48242455
25	815.23	1229.46	0.66	NM_033297	NM_033297	91662.00	NLRP12	NLR family, pyrin domain containing 12	ENST00000358661	NP496202	GO:0000166(nucleotide binding)|GO:0005515(protein binding)|GO:0005524(ATP binding)|GO:0005737(cytoplasm)|GO:0006919(caspase activation)|GO:0007165(signal transduction)|GO:0008588(release of cytoplasmic sequestered NF-kappaB)|GO:0008656(caspase activator a	Homo sapiens NLR family, pyrin domain containing 12 (NLRP12), transcript variant 1, mRNA [NM_033297]	chr19:58999910 0-58999041

[表170]

表170 遺伝子セット2(No.26-55:発現増加・減少した遺伝子上位15個)

No	Cy5	Cy3	ratio	RefSeq Accession	Genbank Accession	Entrez Gene ID	Gene Symbol	Gene Name	Ensembl ID	TIGR ID	GO	Description	Genomic Coordinates
26	527	103	5	NM_001003927	NM_001003927	2123	EVI2A	ecotropic viral integration site 2A	ENST00000247270	THC2462437	GO:0004888(transmembrane receptor activity)[GO:0016020(membrane)|GO:0016021(integral to membrane)	Homo sapiens ecotropic viral integration site 2A (EVI2A), transcript variant 1, mRNA [NM_001003927]	chr17:26869587-26869528
27	1246	251	5	NM_203497	NM_203497	170622	COMMD6	COMM domain containing 6	ENST00000355801	NP1189257		Homo sapiens COMM domain containing 6 (COMMD6), transcript variant 1, mRNA [NM_203497]	chr13:74998704-74998645
28	527	123	4	NM_005767	NM_005767	10161	P2RY5	purinergic receptor P2Y, G-protein coupled, 5	ENST00000378434	THC2461047	GO:0001584(rhodopsin-like receptor activity)[GO:0004872(receptor activity)[GO:0007165(signal transduction)[GO:0007186(G-protein coupled receptor protein signaling pathway)[GO:0016020(membrane)|GO:0016021(integral to membrane)|GO:0045028(purinergic nucleotide receptor activity, G-protein coupled)	Homo sapiens purinergic receptor P2Y, G-protein coupled, 5 (P2RY5), mRNA [NM_005767]	chr13:47883837-47883672
29	618	158	4	NM_017845	NM_017845	54951	COMMD8	COMM domain containing 8	ENST00000306948	THC2602334		Homo sapiens COMM domain containing 8 (COMMD8), mRNA [NM_017845]	chr4:47147723-47147778
30	17969	5423	3	NM_001803	NM_001803	1043	CD52	CD52 molecule	ENST00000374213	THC2462243	GO:0005624(membrane fraction)[GO:0005887(integral to plasma membrane)[GO:0016020(membrane)[GO:0048503(GPI anchor binding)	Homo sapiens CD52 molecule (CD52), mRNA [NM_001803]	chr1:26519531-26519941
31	7057	2149	3	NM_005980	NM_005980	6286	S100P	S100 calcium binding protein P	ENST00000296370	THC2461598	GO:0000287(magnesium ion binding)[GO:0005509(calcium ion binding)[GO:0005634(nucleus)[GO:0005737(cytoplasm)[GO:0043542(endothelial cell migration)[GO:0048306(calcium-dependent protein binding)	Homo sapiens S100 calcium binding protein P (S100P), mRNA [NM_005980]	chr4:6749720-6749779
32	2548	822	3	NM_001867	NM_001867	1350	COX7C	cytochrome c oxidase subunit VIIc	ENST00000380124	THC2470074	GO:0004129(cytochrome-c oxidase activity)[GO:0005739(mitochondrion)[GO:0006118(electron transport)[GO:0016020(membrane)|GO:0016021(integral to membrane)[GO:0016491(oxidoreductase activity)	Homo sapiens cytochrome c oxidase subunit VIIc (COX7C), nuclear gene encoding mitochondrial protein, mRNA [NM_001867]	chr5:85952268-85962325
33	1435	485	3	NM_005213	NM_005213	1475	CSTA	cystatin A (stefin A)	ENST00000264474	THC2559382	GO:0001533(cornified envelope)[GO:0004869(cysteine protease inhibitor activity)[GO:0005198(structural molecule activity)[GO:0005622(intracellular)[GO:0018149(peptide cross-linking)[GO:0030216(keratinocyte differentiation)[GO:0030674(protein binding, bridging)	Homo sapiens cystatin A (stefin A) (CSTA), mRNA [NM_005213]	chr3:123543136-123543195

[0544]

表170 遺伝子セット2(No.26-55:発現増加・減少した遺伝子上位15個)

No	Cy5	Cy3	ratio	RefSeq Accession	Genbank Accession	Entrez Gene ID	Gene Symbol	Gene Name	Ensembl ID	TIGR ID	GO	Description	Genomic Coordinates
34	687	236	3	NM_015364	NM_015364	23643	LY96	lymphocyte antigen 96	ENST00000028 4318	THG2477637	GO:0005615(extracellular space)|GO:0005886(plasma membrane)|GO:0006954(inflammatory response)|GO:0006955(immune response)|GO:0006968(cellular defense response)|GO:0007166(cell surface receptor linked signal transduction)|GO:0015026(coreceptor activity)|GO:0019733(antibacterial humoral response (sensu tho Vertebrata research community))	Homo sapiens lymphocyte antigen 96 (LY96), mRNA [NM_015364]	chr8:75103824 5-75103824
35	29074	10992	3	NM_002964	NM_002964	6279	S100A8	S100 calcium binding protein A8	ENST00000036 8733	THG2550959	GO:0005509(calcium ion binding)|GO:0005615(extracellular space)|GO:0006954(inflammatory response)	Homo sapiens S100 calcium binding protein A8 (S100A8), mRNA [NM_002964]	chr1:1516282 31-151629172
36	243	94	3	NM_003615	NM_003615	9497	SLC4A7	solute carrier family 4, sodium bicarbonate cotransporter, member 7	ENST00000034 9751	THG2464309	GO:0005452(inorganic anion exchanger activity)|GO:0006814(sodium ion transport)|GO:0006820(anion transport)|GO:0008510(sodium:bicarbonate symporter activity)|GO:0015293(symporter activity)|GO:0015701(bicarbonate transport)|GO:0016020(membrane)|GO:0016021(integral to membrane)|GO:0031402(sodium ion binding)	Homo sapiens solute carrier family 4, sodium bicarbonate cotransporter, member 7 (SLC4A7), mRNA [NM_003615]	chr3:2738964 8-27389589
37	226	94	2	NM_032458	NM_032458	84295	PHF6	PHD finger protein 6	ENST00000037 0803	THG2498119	GO:0005515(protein binding)|GO:0005634(nucleus)|GO:0006350(transcription)|GO:0006355(regulation of transcription, DNA-dependent)|GO:0008270(zinc ion binding)|GO:0046872(metal ion binding)	Homo sapiens PHD finger protein 6 (PHF6), transcript variant 2, mRNA [NM_032458]	chrX:1333903 96-133390455
38	198	83	2	NM_174909	NM_174909	153339	TMEM167	transmembrane protein 167	ENST00000030 8489	THG2523245	GO:0016020(membrane)|GO:0016021(integral to membrane)	Homo sapiens transmembrane protein 167 (TMEM167), mRNA [NM_174909]	chr5:82388844 9-82388391
39	569	244	2	NM_001412	NM_001412	1964	EIF1AX	eukaryotic translation initiation factor 1A, X-linked	ENST00000037 9607	THG2559655	GO:0003723(RNA binding)|GO:0003743(translation initiation factor activity)|GO:0006412(translation)|GO:0006413(translational initiation)|GO:0016281(eukaryotic translation initiation factor 4F complex)	Homo sapiens eukaryotic translation initiation factor 1A, X-linked (EIF1AX), mRNA [NM_001412]	chrX:2005293 9-20052880

[0545]

表170　遺伝子セット2(No.26-55:発現増加・減少した遺伝子上位15個)

No	Cy5	Cy3	ratio	RefSeq Accession	Genbank Accession	Entrez Gene ID	Gene Symbol	Gene Name	Ensembl ID	TIGR ID	GO	Description	Genomic Coordinates
40	162	73	2	NM_019604	NM_019604	56253	CRTAM	cytotoxic and regulatory T cell molecule	ENST00000022 7348	TH022475044	GO:0001913(T cell mediated cytotoxicity)|GO:0002355(detection of tumor cell)|GO:0002860(positive regulation of natural killer cell mediated cytotoxicity directed against tumor cell target)|GO:0005102(receptor binding)|GO:0005886(plasma membrane)|GO:0008037(cell recognition)|GO:0050715(positive regulation of cytokine secretion)|GO:0050798(activated T cell proliferation)|GO:0051606(detection of stimulus)	Homo sapiens cytotoxic and regulatory T cell molecule (CRTAM), mRNA |NM_019604|	chr11:122248374-122249433

[表171]

表171 遺伝子セット2(No.26-55:発現増加・減少した遺伝子上位15個)

No	Cy5	Cy3	ratio	RefSeq Accession	Genbank Accession	Entrez Gene ID	Gene Symbol	Gene Name	Ensembl ID	TIGR ID	GO	Description	Genomic Coordinates
41	16.0	274.5	0.06	NM_003557	NM_003557	8394	PIP5K1A	phosphatidylinositol-4-phosphate 5-kinase, type I, alpha	ENST00000349792	THC2484066	GO:0005575(cellular_component)|GO:0006650(glycerophospholipid metabolic process)|GO:0007165(signal transduction)|GO:0016020(membrane)|GO:0016301(kinase activity)|GO:0016308(1-phosphatidylinositol-4-phosphate 5-kinase activity)|GO:0016310(phosphorylation)|GO:0016740(transferase activity)	Homo sapiens phosphatidylinositol-4-phosphate 5-kinase, type I, alpha (PIP5K1A), mRNA [NM_003557]	chr1:149448166-149486974
42	12.8	127.9	0.10	NM_001005802	NM_001005862	2064	ERBB2	v-erb-b2 erythroblastic leukemia viral oncogene homolog 2, neuro/glioblastoma derived oncogene homolog (avian)	ENST00000302930	NP238108	GO:0000166(nucleotide binding)|GO:0004674(protein serine/threonine kinase activity)|GO:0004713(protein-tyrosine kinase activity)|GO:0004715(non-membrane spanning protein tyrosine kinase activity)|GO:0004716(receptor signaling protein tyrosine kinase activity	Homo sapiens v-erb-b2 erythroblastic leukemia viral oncogene homolog 2, neuro/glioblastoma derived oncogene homolog (avian) (ERBB2), transcript variant 2, mRNA [NM_004448]	chr17:35120177-35120235
43	15.5	130.0	0.12	NM_198721	NM_198721	84570	COL25A1	collagen, type XXV, alpha 1	ENST00000367373	THC2482673	GO:0001540(beta-amyloid binding)|GO:0005615(extracellular space)|GO:0005737(cytoplasm)|GO:0008817(phosphatase activity)|GO:0008201(heparin binding)|GO:0016020(membrane)|GO:0016021(integral to membrane)	Homo sapiens collagen, type XXV, alpha 1 (COL25A1), transcript variant 1, mRNA [NM_198721]	chr4:110000033-110000278
44	90.7	672.7	0.13	NM_007110	NM_007110	7011	TEP1	telomerase-associated protein 1	ENST00000262715	NP1473063	GO:0000166(nucleotide binding)|GO:0000722(telomere maintenance via recombination)|GO:0000781(chromosome, telomeric region)|GO:0003720(telomerase activity)|GO:0003723(RNA binding)|GO:0005524(ATP binding)|GO:0005634(nucleus)|GO:0005694(chromosome)|GO:0005697(telomerase holoenzyme complex)|GO:0005737(cytoplasm)|GO:0007004(telomere maintenance via telomerase)|GO:0016363(nuclear matrix)	Homo sapiens telomerase-associated protein 1 (TEP1), mRNA [NM_007110]	chr14:19905699-19905939
45	13.2	94.2	0.14	NM_138295	NM_138295	168507	PKD1L1	polycystic kidney disease 1 like 1	ENST00000296672	THC2486581	GO:0003674(molecular_function)|GO:0016020(membrane)|GO:0016021(integral to membrane)|GO:0016337(cell-cell adhesion)	Homo sapiens polycystic kidney disease 1 like 1 (PKD1L1), mRNA [NM_138295]	chr7:47820117-47920058
46	210.7	1324.3	0.16	NM_015071	NM_015071	23092	ARHGAP26	Rho GTPase activating protein 26	ENST00000378013	THC2495953	GO:0005096(GTPase activator activity)|GO:0005100(Rho GTPase activator activity)|GO:0005575(cellular_component)|GO:0005622(intracellular)|GO:0007165(signal transduction)|GO:0007399(nervous system development)|GO:0030036(actin cytoskeleton organization and biogenesis)	Homo sapiens Rho GTPase activating protein 26 (ARHGAP26), mRNA [NM_015071]	chr5:142585882-142585886

[0546]

表171 遺伝子セット2(No.26-55:発現増加・減少した遺伝子上位15個)

No	Cy5	Cy3	ratio	RefSeq Accession	Genbank Accession	Entrez Gene ID	Gene Symbol	Gene Name	Ensembl ID	TIGR ID	GO	Description	Genomic Coordinates
47	31.4	195.1	0.16	NM_002870	NM_002870	5872	RAB13	RAB13, member RAS oncogene family	ENST00000368575	THC2663743	GO:0000166(nucleotide binding)|GO:0003924(GTPase activity)|GO:0005525(GTP binding)|GO:0005923(tight junction)|GO:0007155(cell adhesion)|GO:0007264(small GTPase mediated signal transduction)|GO:0015031(protein transport)|GO:0016192(vesicle-mediated transport)	Homo sapiens RAB13, member RAS oncogene family (RAB13), mRNA [NM_002870]	chr1:152222237 -152221906
48	15.7	93.2	0.17	NM_004732	NM_004732	9196	KCNAB3	potassium voltage-gated channel, shaker-related subfamily, beta member 3	ENST00000380304	THC2493066	GO:0005249(voltage-gated potassium channel activity)|GO:0005737(cytoplasm)|GO:0006811(ion transport)|GO:0006813(potassium ion transport)|GO:0015459(potassium channel regulator activity)|GO:0016021(integral to membrane)|GO:0016491(oxidoreductase activity)|GO:0030955(potassium ion binding)	Homo sapiens potassium voltage-gated channel, shaker-related subfamily, beta member 3 (KCNAB3), mRNA [NM_004732]	chr17:7766814 -7766755
49	18.1	104.5	0.17	NM_001025616	NM_001025616	83478	ARHGAP24	Rho GTPase activating protein 24	ENST00000264343	THC2476510	GO:0005096(GTPase activator activity)|GO:0005515(protein binding)|GO:0005622(intracellular)|GO:0005886(plasma membrane)|GO:0007165(signal transduction)	Homo sapiens Rho GTPase activating protein 24 (ARHGAP24), transcript variant 1, mRNA [NM_001025616]	chr4:87135414 -87135473
50	21.9	121.9	0.18	NM_012137	NM_012137	23576	DDAH1	dimethylarginine dimethylaminohydrolase 1	ENST00000284031	THC2743592	GO:0006527(arginine catabolic process)|GO:0007263(nitric oxide mediated signal transduction)|GO:0008270(zinc ion binding)|GO:0016403(dimethylarginine activity)|GO:0018787(hydrolase activity)|GO:0046872(metal ion binding)	Homo sapiens dimethylarginine dimethylaminohydrolase 1 (DDAH1), mRNA [NM_012137]	chr1:85557121 -85557062
51	14.5	76.5	0.19	NM_020812	NM_020812	57572	DOCK6	dedicator of cytokinesis 6	ENST00000319667	THC2491633	GO:0005085(guanyl-nucleotide exchange factor activity)|GO:0005525(GTP binding)|GO:0051020(GTPase binding)	Homo sapiens dedicator of cytokinesis 6 (DOCK6), mRNA [NM_020812]	chr19:1117240 5-111172100
52	15.3	80.2	0.19	NM_001040442	NM_001040442	2172	FABP6	fatty acid binding protein 6, ileal (gastrotropin)	ENST00000310650	THC2473525	GO:0005504(fatty acid binding)|GO:0005737(cytoplasm)|GO:0006629(lipid metabolic process)|GO:0006810(transport)|GO:0008206(bile acid metabolic process)|GO:0008285(negative regulation of cell proliferation)|GO:0008289(lipid binding)	Homo sapiens fatty acid binding protein 6, ileal (gastrotropin) (FABP6), transcript variant 1, mRNA [NM_001040442]	chr5:159591816 -159594421
53	20.2	103.8	0.19	NM_021808	NM_021808	50614	GALNT9	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 9 (GalNAc-T9)	ENST00000289577	THC2602095	GO:0004656(polypeptide N-acetylgalactosaminyltransferase activity)|GO:0005509(calcium ion binding)|GO:0005529(sugar binding)|GO:0006486(protein amino acid O-linked glycosylation)|GO:0016020(membrane)|GO:0016021(integral to membrane)|GO:0016757(transferase activity, transferring glycosyl groups)|GO:0030145(manganese ion binding)	Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 9 (GalNAc-T9) (GALNT9), mRNA [NM_021808]	chr12:13124767 9-131247620

[0547]

表171 遺伝子セット2(No. 26-55:発現増加・減少した遺伝子上位15個)

No	Cy5	Cy3	ratio	RefSeq Accession	Genbank Accession	Entrez Gene ID	Gene Symbol	Gene Name	Ensembl ID	TIGR ID	GO	Description	Genomic Coordinates
54	16.5	78.7	0.21	NM_005755		10148	EBI3	Epstein-Barr virus induced gene 3	ENST00000221847	THC2737205	GO:0004896(hematopoietin/interferon-class (D200-domain) cytokine receptor activity)|GO:0005515(protein binding)|GO:0005615(extracellular space)|GO:0005886(plasma membrane)|GO:0006959(humoral immune response)|GO:0019965(interleukin binding)|GO:0042088(T-helper 1 type immune response)|GO:0045078(positive regulation of interferon-gamma biosynthetic process)|GO:0045523(interleukin-27 receptor binding)|GO:0046641(positive regulation of alpha-beta T cell proliferation)	Homo sapiens Epstein-Barr virus induced gene 3 (EBI3), mRNA [NM_005755]	chr19:4188260 -4188319
55	23.5	108.1	0.22	NM_001703		576	BAI2	brain-specific angiogenesis inhibitor 2	ENST00000257070	THC2462908	GO:0004872(receptor activity)|GO:0004930(G-protein coupled receptor activity)|GO:0007165(signal transduction)|GO:0007216(neuropeptide signaling pathway)|GO:0016020(membrane)|GO:0001021(integral to membrane)|GO:0016527(brain-specific angiogenesis inhibitor activity)	Homo sapiens brain-specific angiogenesis inhibitor 2 (BAI2), mRNA [NM_001703]	chr1:31965577 -31965518

[表172]

表172 遺伝子セット2(No. 1-25:機能面で注目する遺伝子, No. 26-55:発現増加・減少した遺伝子上位15個)

No	Target(Gene)Symbol	Target Accession	UniGene	Up/Down	被験者群	配列番号
1	SOCS1	NM_003745	Hs. 50640	Down	B	53
2	CCR1	NM_001295	Hs. 301921	Down	B	54
3	CSF2RB	NM_000395	Hs. 592192	Down	B	55
4	STAT5A	NM_003152	Hs. 437058	Down	B	56
5	STAT3	NM_213662	Hs. 463059	Down	B	57
6	TNFRSF1B	NM_001066	Hs. 256278	Down	B	58
7	SNX17	NM_014748	Hs. 278569	Down	B	59
8	SCARF1	NM_145351	Hs. 647430	Down	B	60
9	LDLR		Hs. 213289	Down	B	-
10	STARD3	NM_006804	Hs. 77628	Down	B	61
11	CLN8	NM_018941	Hs. 127675	Down	B	62
12	APOL1	NM_145343	Hs. 114309	Down	B	63
13	ATP10A	NM_024490	Hs. 128041	Down	B	64
14	PSAP	NM_001042465	Hs. 523004	Down	B	65
15	OSBP2	NM_030758	Hs. 517546	Down	B	66
16	SLC27A1	NM_198580	Hs. 363138	Down	B	67
17	APOL6	NM_030641	Hs. 257352	Down	B	68
18	SOCS1	NM_003745	Hs. 50640	Down	B	53
19	STXBP4	NM_178509	Hs. 35199	Down	B	69
20	SOCS3	NM_003955	Hs. 527973	Down	B	70
21	AKT1	NM_005163	Hs. 525622	Down	B	71
22	MLLT7	NM_005938	Hs. 584654	Down	B	-
23	CEBPB	NM_005194	Hs. 642680	Down	B	72
24	CEBPB	NM_005194	Hs. 642680	Down	B	72
25	NLRP12	NM_033297	Hs. 631573	Down	B	73
26	EVI2A	NM_001003927	Hs.591198	Up	B	74
27	COMMD6	NM_203497	Hs.508266	Up	B	75
28	P2RY5	NM_005767	Hs.123464	Up	B	76
29	COMMD8	NM_017845	Hs.23956	Up	B	77
30	CD52	NM_001803	Hs.276770	Up	B	78
31	S100P	NM_005980	Hs.2962	Up	B	79
32	COX7C	NM_001867	Hs.430075	Up	B	80
33	CSTA	NM_005213	Hs.518198	Up	B	81
34	LY96	NM_015364	Hs.69328	Up	B	82
35	S100A8	NM_002964	Hs.416073	Up	B	83
36	SLC4A7	NM_003615	Hs.250072	Up	B	84
37	PHF6	NM_032458	Hs.356501	Up	B	85
38	TMEM167	NM_174909	Hs.355606	Up	B	36
39	EIF1AX	NM_001412	Hs.522590	Up	B	86
40	CRTAM	NM_019604	Hs.159523	Up	B	87
41	PIP5K1A	NM_003557	Hs.546316	Down	B	88
42	ERBB2	NM_001005862	Hs.446352	Down	B	89
43	COL25A1	NM_198721	Hs.112925	Down	B	90
44	TEP1	NM_007110	Hs.508835	Down	B	91
45	PKD1L1	NM_138295	Hs.195979	Down	B	92
46	ARHGAP26	NM_015071	Hs.293593	Down	B	93
47	RAB13	NM_002870	Hs.151536	Down	B	94
48	KCNAB3	NM_004732	Hs.435074	Down	B	95
49	ARHGAP24	NM_001025616	Hs.444229	Down	B	96
50	DDAH1	NM_012137	Hs.379858	Down	B	97
51	DOCK6	NM_020812	Hs.591002	Down	B	98
52	FABP6	NM_001040442	Hs.519719	Down	B	99
53	GALNT9	NM_021808	Hs.301062	Down	B	100
54	EBI3	NM_005755	Hs.501452	Down	B	101
55	BAI2	NM_001703	Hs.524138	Down	B	102

[0548] 上記解析7で笑いにより遺伝子発現の変動が認められた遺伝子のうち、機能面で注目すべき遺伝子、及び特に発現変動の大きかった上位15遺伝子を表173～177に示し、これらを要約した表178を遺伝子セット3の表として示す。

[表173]

表173 遺伝子セット3

No	Cy5	Cy3	ratio	RefSeq Accession	Genbank Accession	Entrez Gene_ID	Gene Symbol	Gene Name	Ensembl ID	TIGR ID	GO	Description	Genomic Coordinates
1	60.69	104.07	0.58	NM_031232	NM_031232	63941.00	APBA2BP	amyloid beta (A4) precursor protein-binding, family A, member 2 binding protein	ENST00000246190	NP707928	GO:0000137(Golgi cis cisterna)|GO:0005509(calcium ion binding)|GO:0005515(protein binding)|GO:0005615(extracellular space)|GO:0005634(nucleus)|GO:0005737(cytoplasm)|GO:0005783(endoplasmic reticulum)|GO:0005789(endoplasmic reticulum membrane)|GO:0009306(pr	Homo sapiens amyloid beta (A4) precursor protein-binding, family A, member 2 binding protein (APBA2BP), transcript variant 2, mRNA [NM_031232]	chr20:31709184-31709125
2	28.99	49.20	0.59	NM_019065	NM_019065	54550.00	EFCBP2	EF-hand calcium binding protein 2	ENST00000305202	THC2476304	GO:0005509(calcium ion binding)|GO:0005737(cytoplasm)|GO:0016491(oxidoreductase activity)|GO:0017000(antibiotic biosynthetic process)	Homo sapiens EF-hand calcium binding protein 2 (EFCBP2), mRNA [NM_019065]	chr16:82593351-82583574

[表174]

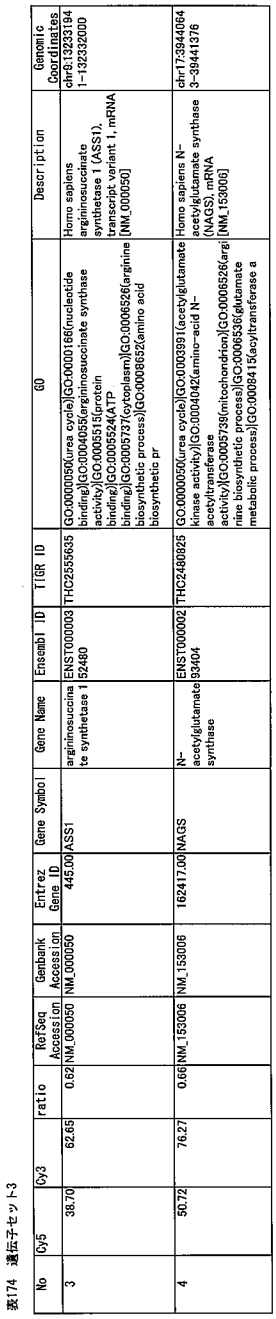


表174 遺伝子セット3

No	Cy5	Cy3	ratio	RefSeq Accession	Genbank Accession	Entrez Gene ID	Gene Symbol	Gene Name	Ensembl ID	TIGR ID	GO	Description	Genomic Coordinates
3	38.70	62.65	0.62	NM_000050	NM_000050	445.00	ASS1	argininosuccinate synthetase 1	ENST00000352480	THC2555635	GO:0000050(urea cycle)|GO:0000166(nucleotide binding)|GO:0004055(argininosuccinate synthase activity)|GO:0005515(protein binding)|GO:0005524(ATP binding)|GO:0005737(cytoplasm)|GO:0006526(arginine biosynthetic process)|GO:0008652(amino acid biosynthetic pr	Homo sapiens argininosuccinate synthetase 1 (ASS1), transcript variant 1, mRNA [NM_000050]	chr9:130233194 1-132332000
4	50.72	76.27	0.66	NM_153006	NM_153006	162417.00	NAGS	N-acetylglutamate synthase	ENST00000293404	THC2480825	GO:0000050(urea cycle)|GO:0003991(acetylglutamate kinase activity)|GO:0004042(amino-acid N-acetyltransferase activity)|GO:0005739(mitochondrion)|GO:0006526(arginine biosynthetic process)|GO:0006536(glutamate metabolic process)|GO:0008415(acyltransferase a	Homo sapiens N-acetylglutamate synthase (NAGS), mRNA [NM_153006]	chr17:39440464 3-39441376

[表175]

表175 遺伝子セット3

No	Cy5	Cy3	ratio	RefSeq Accession	Genbank Accession	Entrez Gene ID	Gene Symbol	Gene Name	Ensembl ID	TIGR ID	GO	Description	Genomic Coordinates
5	18.93	46.02	0.41	NM_000600	NM_000600	3569.00	IL6	interleukin 6 (interferon, beta 2)	ENST00000259743	THC2603924	GO:0001781(neutrophil apoptosis)|GO:0005125(cytokine activity)|GO:0005138(interleukin-6 receptor binding)|GO:0005515(protein binding)|GO:0005576(extracellular region)|GO:0005615(extracellular space)|GO:0006953(acute-phase response)|GO:0009595(humoral immu	Homo sapiens interleukin 6 (interferon, beta 2) (IL6), mRNA [NM_000600]	chr7:22737732 -22737791
6	40.90	84.31	0.49	NM_004119	NM_004119	2322.00	FLT3	fms-related tyrosine kinase 3	ENST00000380982	THC2478480	GO:0000166(nucleotide binding)|GO:0004872(receptor activity)|GO:0005021(vascular endothelial growth factor receptor activity)|GO:0005524(ATP binding)|GO:0005887(integral to plasma membrane)|GO:0006468(protein amino acid phosphorylation)|GO:0007169(transme	Homo sapiens fms-related tyrosine kinase 3 (FLT3), mRNA [NM_004119]	chr13:27477605 2-27475993
7	23.40	45.08	0.52	NM_000589	NM_000589	3565.00	IL4	interleukin 4	ENST00000231449	THC2476876	GO:0005136(interleukin-4 receptor binding)|GO:0005515(protein binding)|GO:0005576(extracellular region)|GO:0005615(extracellular space)|GO:0006935(chemotaxis)|GO:0006968(cellular defense response)|GO:0008203(cholesterol metabolic process)|GO:0030183(B cel	Homo sapiens interleukin 4 (IL4), transcript variant 1, mRNA [NM_000589]	chr5:132043513 -132043572
8	113.30	173.16	0.65	NM_001766	NM_001766	912.00	CD1D	CD1d molecule	ENST00000368171	THC2781332	GO:0004872(receptor activity)|GO:0005887(integral to plasma membrane)|GO:0016020(membrane)|GO:0019045(detection of bacterium)|GO:0030881(beta-2-microglobulin binding)|GO:0030884(exogenous lipid antigen binding)|GO:0045058(T cell selection)|GO:0045089(posi	Homo sapiens CD1d molecule (CD1D), mRNA [NM_001766]	chr1:156418495 -156418554

[表176]

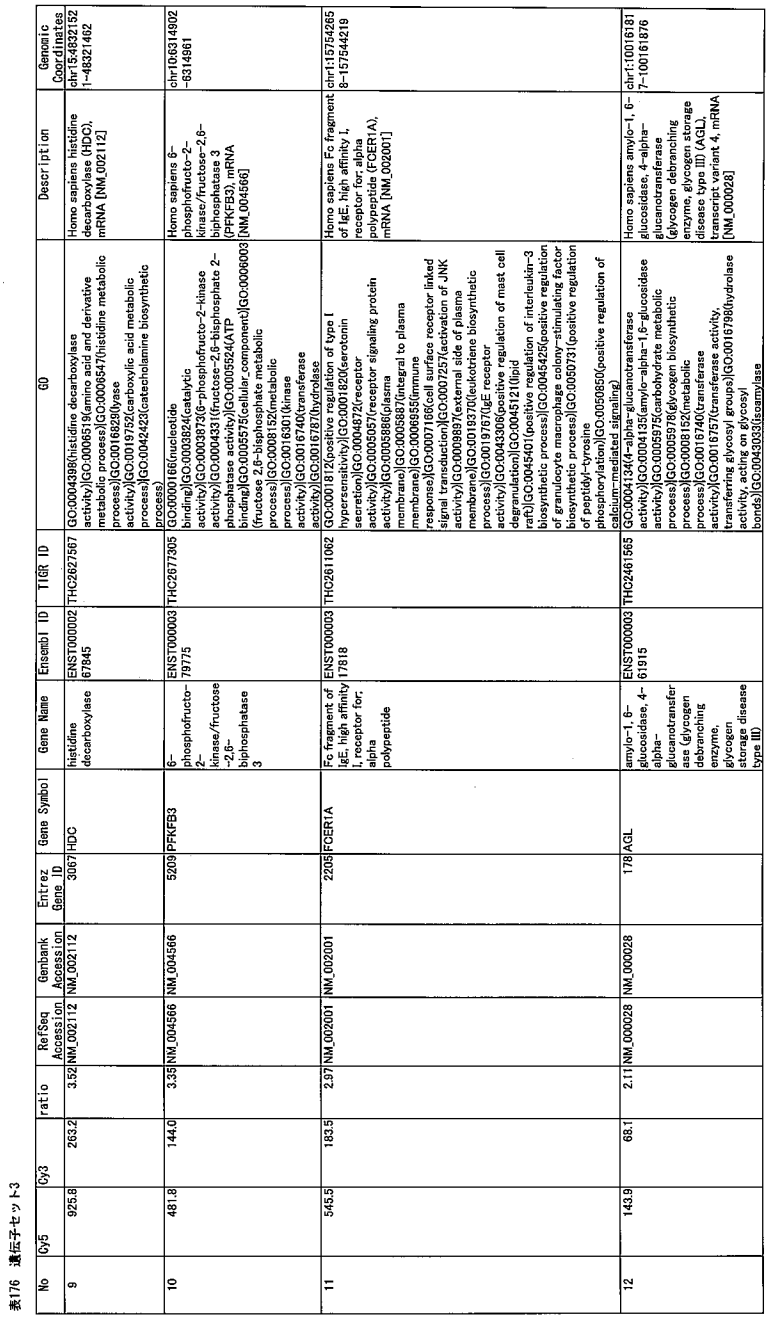


表176 遺伝子セット3

No	Cy5	Cy3	ratio	RefSeq Accession	Genbank Accession	Entrez Gene ID	Gene Symbol	Gene Name	Ensembl ID	T16R ID	GO	Description	Genomic Coordinates
9	925.8	263.2	3.52	NM_002112	NM_002112	3067	HDC	histidine decarboxylase	ENST00000267845	THC2627567	GO:0004398(histidine decarboxylase activity)|GO:0006519(amino acid and derivative metabolic process)|GO:0006547(histidine metabolic process)|GO:0016829(lyase activity)|GO:0019752(carboxylic acid metabolic process)|GO:0042423(catecholamine biosynthetic process)	Homo sapiens histidine decarboxylase (HDC), mRNA [NM_002112]	chr15:48321521-48321402
10	481.8	144.0	3.35	NM_004566	NM_004566	5209	PFKFB3	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 3	ENST00000379775	THC2677305	GO:0000166(nucleotide binding)|GO:0003824(catalytic activity)|GO:0003873(6-phosphofructo-2-kinase activity)|GO:0004331(fructose-2,6-bisphosphate 2-phosphatase activity)|GO:0005524(ATP binding)|GO:0005575(cellular_component)|GO:0006003(fructose 2,6-bisphosphate metabolic process)|GO:0008152(metabolic process)|GO:0016301(kinase activity)|GO:0016740(transferase activity)|GO:0016787(hydrolase activity)	Homo sapiens 6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 3 (PFKFB3), mRNA [NM_004566]	chr10:6314902-6314861
11	545.5	183.5	2.97	NM_002001	NM_002001	2205	FCER1A	Fc fragment of IgE, high affinity I, receptor for; alpha polypeptide	ENST00000317818	THC2611062	GO:0001812(positive regulation of type I hypersensitivity)|GO:0001820(serotonin secretion)|GO:0004872(receptor activity)|GO:0005057(receptor signaling protein activity)|GO:0005886(plasma membrane)|GO:0005887(integral to plasma membrane)|GO:0006955(immune response)|GO:0007166(cell surface receptor linked signal transduction)|GO:0007257(activation of JNK activity)|GO:0009897(external side of plasma membrane)|GO:0019370(leukotriene biosynthetic process)|GO:0019767(IgE receptor activity)|GO:0043306(positive regulation of mast cell degranulation)|GO:0045121(lipid raft)|GO:0045401(positive regulation of interleukin-3 biosynthetic process)|GO:0045425(positive regulation of granulocyte macrophage colony-stimulating factor biosynthetic process)|GO:0050731(positive regulation of peptidyl-tyrosine phosphorylation)|GO:0050850(positive regulation of calcium-mediated signaling)	Homo sapiens Fc fragment of IgE, high affinity I, receptor for; alpha polypeptide (FCER1A), mRNA [NM_002001]	chr1:157542658-157544219
12	143.9	68.1	2.11	NM_000028	NM_000028	178	AGL	amylo-1, 6-glucosidase, 4-alpha-glucanotransferase (glycogen debranching enzyme, glycogen storage disease type III)	ENST00000361915	THC2461565	GO:0004134(4-alpha-glucanotransferase activity)|GO:0004135(amylo-alpha-1,6-glucosidase activity)|GO:0005975(carbohydrate metabolic process)|GO:0005978(glycogen biosynthetic process)|GO:0008152(metabolic process)|GO:0016740(transferase activity)|GO:0016757(transferase activity, transferring glycosyl groups)|GO:0016798(hydrolase activity, acting on glycosyl bonds)|GO:0043037(isoamylase	Homo sapiens amylo-1, 6-glucosidase, 4-alpha-glucanotransferase (glycogen debranching enzyme, glycogen storage disease type III) (AGL), transcript variant 4, mRNA [NM_000028]	chr1:100161817-100161876

[0549]

表176 遺伝子セット3

No	Cy5	Cy3	ratio	RefSeq Accession	Genbank Accession	Entrez Gene ID	Gene Symbol	Gene Name	Ensembl ID	T16R ID	GO	Description	Genomic Coordinates
13	835.5	430.2	1.94	NM_002343	NM_002343	4057	LTF	lactotransferrin	ENST0000002 31751	THC2485813	GO:0004252(serine-type endopeptidase activity)|GO:0005576(extracellular region)|GO:0005615(extracellular space)|GO:0006811(ion transport)|GO:0006826(iron ion transport)|GO:0006878(iron ion homeostasis)|GO:0006959(humoral immune response)|GO:0008199(ferric iron binding)|GO:0008233(peptidase activity)|GO:0042742(defense response to bacterium)|GO:0046872(metal ion binding)	Homo sapiens lactotransferrin (LTF), mRNA [NM_002343]	chr3:46454483 -46452724
14	432371.0	235238.1	1.84	NM_000558	NM_000558	3039	HBA1	hemoglobin, alpha 1	ENST0000003 20868	THC2587597		Homo sapiens hemoglobin, alpha 1 (HBA1), mRNA [NM_000558]	chr16:167382-167441
15	80.0	53.0	1.51	NM_000608	NM_000608	5005	ORM2	orosomucoid 2	ENST0000003 74100	THC2562815	GO:0005488(binding)|GO:0005615(extracellular space)|GO:0006953(acute-phase response)	Homo sapiens orosomucoid 2 (ORM2), mRNA [NM_000608]	chr9:116133372 6-116133936
16	1842.7	1017.6	1.81	NM_002183	NM_002183	3563	IL3RA	interleukin 3 receptor, alpha (low affinity)	ENST0000003 31035	THC2474356	GO:0004872(receptor activity)|GO:0004896(hematopoietin/interferon-class (D200-domain) cytokine receptor activity)|GO:0004912(interleukin-3 receptor activity)|GO:0005057(receptor signaling protein activity)|GO:0005615(extracellular space)|GO:0005468(protein amino acid phosphorylation)|GO:0007275(multicellular organismal development)|GO:0016020(membrane)|GO:0016021(integral to membrane)	Homo sapiens interleukin 3 receptor, alpha (low affinity) (IL3RA), mRNA [NM_002183]	chrY:1461487-1461546
17	142.2	78.8	1.80	NM_006948	NM_006948	6782	STCH	stress 70 protein chaperone, microsome-associated, 60kDa	ENST0000002 85667	THC2469197	GO:0000166(nucleotide binding)|GO:0005524(ATP binding)|GO:0005615(extracellular space)|GO:0005783(endoplasmic reticulum)|GO:0005792(microsome)	Homo sapiens stress 70 protein chaperone, microsome-associated, 60kDa (STCH), mRNA [NM_006948]	chr21:1466550 6-14665447
18	519005.0	301571.2	1.72	NM_000517	NM_000517	3040	HBA2	hemoglobin, alpha 2	ENST0000002 51595	THC2564653	GO:0005344(oxygen transporter activity)|GO:0005506(iron ion binding)|GO:0005515(protein binding)|GO:0005833(hemoglobin complex)|GO:0006810(transport)|GO:0015671(oxygen transport)|GO:0019825(oxygen binding)|GO:0020037(heme binding)|GO:0046872(metal ion binding)	Homo sapiens hemoglobin, alpha 2 (HBA2), mRNA [NM_000517]	chr16:163560-163619
19	74.4	43.3	1.72	NM_030791	NM_030791	81537	SGPP1	sphingosine-1-phosphate phosphatase 1	ENST0000002 47225	THC2463640	GO:0003993(acid phosphatase activity)|GO:0005624(membrane fraction)|GO:0005739(mitochondrion)|GO:0005783(endoplasmic reticulum)|GO:0005794(Golgi apparatus)|GO:0006665(sphingolipid metabolic process)|GO:0006668(sphinganine-1-phosphate metabolic process)|GO:0006670(sphingosine metabolic process)|GO:0006915(apoptosis)|GO:0015629(actin cytoskeleton)|GO:0016020(membrane)|GO:0016021(integral to membrane)|GO:0016787(hydrolase activity)|GO:0042392(sphingosine-1-phosphate	Homo sapiens sphingosine-1-phosphate phosphatase 1 (SGPP1), mRNA [NM_030791]	chr14:63221861-63221802

[0550]

表176 遺伝子セット3

No	Cy5	Cy3	ratio	RefSeq Accession	Genbank Accession	Entrez Gene ID	Gene Symbol	Gene Name	Ensembl ID	TIGR ID	GO	Description	Genomic Coordinates
20	78.5	46.3	1.69	NM_002845	NM_002845	5797	PTPRM	protein tyrosine phosphatase, receptor type, M		THC2604867	GO:0004725(protein tyrosine phosphatase activity)|GO:0004872(receptor activity)|GO:0005001(transmembrane receptor protein tyrosine phosphatase activity)|GO:0005615(extracellular space)|GO:0005887(integral to plasma membrane)|GO:0006470(protein amino acid dephosphorylation)|GO:0016020(membrane)|GO:0016	Homo sapiens protein tyrosine phosphatase, receptor type, M (PTPRM), mRNA [NM_002845]	chr18:8396388 -8396457
21	114.8	68.3	1.68	NM_032918	NM_032918	85004	RERG	RAS-like, estrogen-regulated, growth inhibitor	ENST000002 56953	THC2462986	GO:0000166(nucleotide binding)|GO:0003924(GTPase activity)|GO:0005525(GTP binding)|GO:0005622(intracellular)|GO:0005634(nucleus)|GO:0005829(cytosol)|GO:0007264(small GTPase mediated signal transduction)|GO:0008285(negative regulation of cell proliferation)|GO:0009725(response to hormone stimulus)|GO:0019003(GDP binding)|GO:0030308(negative regulation of cell growth)|GO:0030331(estrogen receptor binding)	Homo sapiens RAS-like, estrogen-regulated, growth inhibitor (RERG), mRNA [NM_032918]	chr12:1515223 7-15152178
22	85.9	51.4	1.67	NM_014739	NM_014739	9774	BCLAF1	BCL2-associated transcription factor 1		THC2503556	GO:0003677(DNA binding)|GO:0005515(protein binding)|GO:0005634(nucleus)|GO:0006350(transcription)|GO:0006355(regulation of transcription, DNA-dependent)|GO:0006917(induction of apoptosis)|GO:0016481(negative regulation of transcription)|GO:0016564(transcriptional repressor activity)	Homo sapiens BCL2-associated transcription factor 1 (BCLAF1), transcript variant 1, mRNA [NM_014739]	chr6:136620254-136620195
23	301.9	180.9	1.67	NM_021204	NM_021204	58478	MASA	E-1 enzyme	ENST000002 73920	THC2501913	GO:0000287(magnesium ion binding)|GO:0008152(metabolic process)|GO:0008652(amino acid biosynthetic process)|GO:0008967(phosphoglycolate phosphatase activity)|GO:0009086(methionine biosynthetic process)|GO:0016787(hydrolase activity)	Homo sapiens E-1 enzyme (MASA), mRNA [NM_021204]	chr4:83600862 -83600921

[表177]

表177 遺伝子セット3

No	Cy5	Cy3	ratio	RefSeq Accession	Genbank Accession	Entrez Gene_ID	Gene Symbol	Gene Name	Ensembl ID	TIGR ID	GO	Description	Genomic Coordinates
24	14.1	103.7	0.14	NM_032134	NM_032134	84074	QRICH2	glutamine rich 2	ENST00000301613	NP404683		Homo sapiens glutamine rich 2 (QRICH2), mRNA [NM_032134]	chr17:71778808-71788025
25	19.7	107.4	0.18	NM_182832	NM_182832	191585	PLAC4	placenta-specific 4		THC2461986		Homo sapiens placenta-specific 4 (PLAC4), mRNA [NM_182832]	chr21:41470685-41474074
26	16.1	87.3	0.18	NM_004425	NM_004425	1893	EOM1	extracellular matrix protein 1	ENST00000314869	THC2802786	GO:0004871(signal transducer activity)|GO:0005386(carrier activity)|GO:0005578(extracellular matrix (sensu the Metazoa research community))|GO:0005615(extracellular space)|GO:0006810(transport)|GO:0043123(positive regulation of I-kappaB kinase/NF-kappaB cascade)	Homo sapiens extracellular matrix protein 1 (ECM1), transcript variant 1, mRNA [NM_004425]	chr1:148752421-148752480
27	22.7	122.1	0.19	NM_007109	NM_007109	6941	TCF19	transcription factor 19 (SC1)	ENST00000376257	NP1161356	GO:0000074(regulation of progression through cell cycle)|GO:0003700(transcription factor activity)|GO:0005515(protein binding)|GO:0005634(nucleus)|GO:0006350(transcription)|GO:0006357(regulation of transcription from RNA polymerase II promoter)|GO:0008270(zinc ion binding)|GO:0008283(cell proliferation)|GO:0046872(metal ion binding)	Homo sapiens transcription factor 19 (SC1) (TCF19), transcript variant 1, mRNA [NM_007109]	chr6:31237628-31237688
28	35.6	184.0	0.19	NM_001868	NM_001868	1357	CPA1	carboxypeptidase A1 (pancreatic)	ENST00000311292	THC2481187	GO:0004180(carboxypeptidase activity)|GO:0004182(carboxypeptidase A activity)|GO:0005615(extracellular space)|GO:0006508(proteolysis)|GO:0008237(metallopeptidase activity)|GO:0008270(zinc ion binding)|GO:0046872(metal ion binding)	Homo sapiens carboxypeptidase A1 (pancreatic) (CPA1), mRNA [NM_001868]	chr7:129812972-129814931
29	30.5	140.7	0.22	NM_031435	NM_031435	83591	THAP2	THAP domain containing, apoptosis associated protein 2	ENST00000290086	THC2525470	GO:0003677(DNA binding)|GO:0005730(nucleolus)|GO:0008270(zinc ion binding)|GO:0046872(metal ion binding)	Homo sapiens THAP domain containing, apoptosis associated protein 2 (THAP2), mRNA [NM_031435]	chr12:70360278-70380337
30	35.5	162.9	0.22	AF130075	AF130075	11341	SORG1	sorcin responsive protein 1			GO:0005615(extracellular space)|GO:0007399(nervous system development)	Homo sapiens clone FLB9413 PRO2532 mRNA, complete cds. [AF130075]	chr4:174625701-174625847
31	22.3	98.0	0.23	NM_004932	NM_004932	1004	CDH6	cadherin 6, type 2, K-cadherin (fetal kidney)	ENST00000265071	THC2464544	GO:0005509(calcium ion binding)|GO:0005515(protein binding)|GO:0005615(extracellular space)|GO:0005886(plasma membrane)|GO:0007155(cell adhesion)|GO:0007156(homophilic cell adhesion)|GO:0016021(integral to membrane)	Homo sapiens cadherin 6, type 2, K-cadherin (fetal kidney) (CDH6), mRNA [NM_004932]	chr5:31359964-31360023

[0551]

表177 遺伝子セット3

No	Cy5	Cy3	ratio	RefSeq Accession	Genbank Accession	Entrez Gene ID	Gene Symbol	Gene Name	Ensembl ID	TIGR ID	GO	Description	Genomic Coordinates
32	29.5	129.1	0.23	NM_004473	NM_004473	2304	FOXE1	forkhead box E1 (thyroid transcription factor 2)	ENST00000375123	NP0081541	GO:0000122(negative regulation of transcription from RNA polymerase II promoter)GO:0003700(transcription factor activity)GO:0003702(RNA polymerase II transcription factor activity)GO:0005634(nucleus)GO:0006350(transcription)GO:0006355(regulation of transcription, DNA-dependent)GO:0009653(anatomical structure morphogenesis)GO:0030878(thyroid gland development)GO:0043565(sequence-specific DNA binding)GO:0045893(positive regulation of transcription, DNA-dependent)	Homo sapiens forkhead box E1 (thyroid transcription factor 2) (FOXE1), mRNA [NM_004473]	chr9:99657469-99657528
33	21.9	86.6	0.25	NM_006838	NM_006838	10988	METAP2	methionyl aminopeptidase 2		THC2521081	GO:0004239(methionyl aminopeptidase activity)GO:0005515(protein binding)GO:0005737(cytoplasm)GO:0008464(protein modification)GO:0006508(proteolysis)GO:0008233(peptidase activity)GO:0018206(peptidyl-methionine modification)GO:0031365(N-terminal protein amino acid modification)GO:0046872(metal ion binding)GO:0050897(cobalt ion binding)	Homo sapiens methionyl aminopeptidase 2 (METAP2), mRNA [NM_006838]	chr12:9443319-94433253
34	20.0	79.0	0.25	NM_012324	NM_012324	23542	MAPK8IP2	mitogen-activated protein kinase 8 interacting protein 2	ENST00000329492	THC2559123	GO:0001540(beta-amyloid binding)GO:0005078(MAP-kinase scaffold activity)GO:0005198(structural molecule activity)GO:0005737(cytoplasm)GO:0007172(signal complex formation)GO:0019894(kinesin binding)GO:0019901(protein kinase binding)GO:0046328(positive regulation of JNK cascade)	Homo sapiens mitogen-activated protein kinase 8 interacting protein 2 (MAPK8IP2), transcript variant 1, mRNA [NM_012324]	chr22:49396366-49398425
35	14.8	54.2	0.27	NM_033036	NM_033036	89792	GAL3ST3	galactose-3-O-sulfotransferase 3	ENST00000312006	THC2474626	GO:0000287(magnesium ion binding)GO:0001733(galactosylceramide sulfotransferase activity)GO:0005794(Golgi apparatus)GO:0005986(monosaccharide metabolic process)GO:0006790(sulfur metabolic process)GO:0009058(biosynthetic process)GO:0009311(oligosaccharide metabolic process)GO:0016020(membrane)GO:0016021(integral to membrane)GO:0016749(transferase activity)GO:0030166(proteoglycan biosynthetic process)GO:0030246(carbohydrate binding)GO:0030309(poly-N-acetyllactosamine metabolic process)GO:0050656(3'-phosphoadenosine 5'-phosphosulfate binding)GO:0050698(proteoglycan sulfotransferase activity)	Homo sapiens galactose-3-O-sulfotransferase 3 (GAL3ST3), mRNA [NM_033036]	chr11:65567095-65567036

[0552]

表177 遺伝子セット3

No	Cy5	Cy3	ratio	RefSeq Accession	Genbank Accession	Entrez Gene ID	Gene Symbol	Gene Name	Ensembl ID	TIGR ID	GO	Description	Genomic Coordinates
36	75.7	276.3	0.27	NM_002002	NM_002002	2208	FCER2	Fc fragment of IgE, low affinity II, receptor for (CD23)	ENST00003 46664	THC2607080	GO:0004872(receptor activity)|GO:0005057(receptor signaling protein activity)|GO:0005178(integrin binding)|GO:0005529(sugar binding)|GO:0005887(integral to plasma membrane)|GO:0009897(external side of plasma membrane)|GO:0016020(membrane)|GO:0019863(IgE binding)	Homo sapiens Fc fragment of IgE, low affinity II, receptor for (CD23) (FCER2), mRNA [NM_002002]	chr19:7667956 -7667799
37	12.0	43.6	0.28	NM_021049	NM_021049	4104	MAGEA5	melanoma antigen family A, 5	ENST00003 45830	THC2484685	GO:0003674(molecular_function)|GO:0005575(cellular_component)|GO:0008150(biological_process)	Homo sapiens melanoma antigen family A, 5 (MAGEA5), mRNA [NM_021049]	chrX:151034447-151034383
38	66.1	234.0	0.28	NM_001042723	NM_00104272 3	6261	RYR1	ryanodine receptor 1 (skeletal)	ENST00003 89232	THC2490181	GO:0004872(receptor activity)|GO:0005216(ion channel activity)|GO:0005219(ryanodine-sensitive calcium-release channel activity)|GO:0005509(calcium ion binding)|GO:0005790(smooth endoplasmic reticulum)|GO:0005887(integral to plasma membrane)|GO:0006811(ion transport)|GO:0006816(calcium ion transport)|GO:0006874(calcium ion homeostasis)|GO:0006936(muscle contraction)|GO:0015278(calcium-release channel activity)|GO:0016020(membrane)	Homo sapiens ryanodine receptor 1 (skeletal) (RYR1), transcript variant 2, mRNA [NM_001042723]	chr19:43682266-43682411

[表178]

表178 遺伝子セット3(No. 1-8:機能面で注目する遺伝子, No. 9-38:発現増加・減少した遺伝子上位15個)

No	Target(Gene)Symbol	Target Accession	UniGene	Up/Down	被験者群	配列番号
1	APBA2BP	NM_031232	Hs. 516986	Down	C	-
2	EFCBP2	NM_019065	Hs. 140950	Down	C	-
3	ASS1	NM_000050	Hs. 160786	Down	C	103
4	NAGS	NM_153006	Hs. 8876	Down	C	104
5	IL6	NM_000600	Hs. 512234	Down	C	105
6	FLT3	NM_004119	Hs. 507590	Down	C	106
7	IL4	NM_000589	Hs. 73917	Down	C	107
8	CD1D	NM_001766	Hs. 1799	Down	C	108
9	HDC	NM_002112	Hs.1481	Up	C	109
10	PFKFB3	NM_004566	Hs.195471	Up	C	45
11	FCER1A	NM_002001	Hs.897	Up	C	110
12	AGL	NM_000028	Hs.904	Up	C	111
13	LTF	NM_002343	Hs.529517	Up	C	112
14	HBA1	NM_000558	Hs.449630	Up	C	113
15	ORM2	NM_000608	Hs.522356	Up	C	114
16	IL3RA	NM_002183	Hs.632790	Up	C	115
17	STCH	NM_006948	Hs.352341	Up	C	-
18	HBA2	NM_000517	Hs.449630	Up	C	9
19	SGPP1	NM_030791	Hs.24678	Up	C	116
20	PTPRM	NM_002845	Hs.49774	Up	C	117
21	RERG	NM_032918	Hs.199487	Up	C	118
22	BCLAF1	NM_014739		Up	C	29
23	MASA	NM_021204	Hs.18442	Up	C	-
24	QRICH2	NM_032134	Hs.252739	Down	C	119
25	PLAC4	NM_182832	Hs.472492	Down	C	120
26	ECM1	NM_004425	Hs.81071	Down	C	121
27	TCF19	NM_007109	Hs.584807	Down	C	122
28	CPA1	NM_001868	Hs.2879	Down	C	123
29	THAP2	NM_031435	Hs.245798	Down	C	124
30	SCRG1		Hs.7122	Down	C	-
31	CDH6	NM_004932	Hs.171054	Down	C	125
32	FOXE1	NM_004473	Hs.159234	Down	C	126
33	METAP2	NM_006838	Hs.591005	Down	C	127
34	MAPK8IP2	NM_012324	Hs.558180	Down	C	128
35	GAL3ST3	NM_033036	Hs.208343	Down	C	129
36	FCER2	NM_002002	Hs.465778	Down	C	130
37	MAGEA5	NM_021049	Hs.18048	Down	C	131
38	RYR1	NM_001042723	Hs.466664	Down	C	132

[0553] 上記解析8で笑いにより遺伝子発現の変動が認められた遺伝子のうち、機能面で注目すべき遺伝子、及び特に発現変動の大きかった上位15遺伝子を表179～184に示し、これらを要約した表185を遺伝子セット4の表として示す。

[表179]

表179 遺伝子セット4(No.1-7:機能面で注目する遺伝子)

No	Cy5	Cy3	ratio	RefSeq Accession	Genbank Accession	Entrez Gene ID	Gene Symbol	Gene Name	Ensembl ID	TIGR ID	GO	Description	Genomic Coordinates
1	400.76	230.32	1.74	NM_016562	NM_016562	51284.00	TLR7	toll-like receptor 7	ENST00000380659	THC2475229	GO:0003725(double-stranded RNA binding)|GO:0003727(single-stranded RNA binding)|GO:0004888(transmembrane receptor activity)|GO:0005515(protein binding)|GO:0005615(extracellular space)|GO:0006954(inflammatory response)|GO:0006955(immune response)|GO:0016020	Homo sapiens toll-like receptor 7 (TLR7), mRNA [NM_016562]	chrX:12818181-12818240
2	955.30	627.15	1.52	NM_000633	NM_000633	596.00	BCL2	B-cell CLL/lymphoma 2	ENST00000333681	THC2614996	GO:0000074(regulation of progression through cell cycle)|GO:0001836(release of cytochrome c from mitochondria)|GO:0005634(nucleus)|GO:0005739(mitochondrion)|GO:0005741(mitochondrial outer membrane)|GO:0005783(endoplasmic reticulum)|GO:0005829(cytosol)|GO:	Homo sapiens B-cell CLL/lymphoma 2 (BCL2), nuclear gene encoding mitochondrial protein, transcript variant alpha, mRNA [NM_000633]	chr18:58941762-58941703

[表180]

表180 遺伝子セット4(No.1-7:横断面で注目する遺伝子)

No	Cy5	Cy3	ratio	RefSeq Accession	Genbank Accession	Entrez Gene ID	Gene Symbol	Gene Name	Ensembl ID	TIGR ID	GO	Description	Genomic Coordinates
3	658.49	437.34	1.51	NM_016610	NM_016610	51311.00	TLR8	toll-like receptor 8	ENST00000031912	THC2474479	GO:0000677(DNA binding)|GO:0003725(double-stranded RNA binding)|GO:0003727(single-stranded RNA binding)|GO:0004888(transmembrane receptor activity)|GO:0005121(Toll binding)|GO:0005515(protein binding)|GO:0006954(inflammatory response)|GO:0007249(I-kappaB	Homo sapiens toll-like receptor 8 (TLR8), transcript variant 1, mRNA [NM_016610]	chrX:12850183-12850242

[表181]

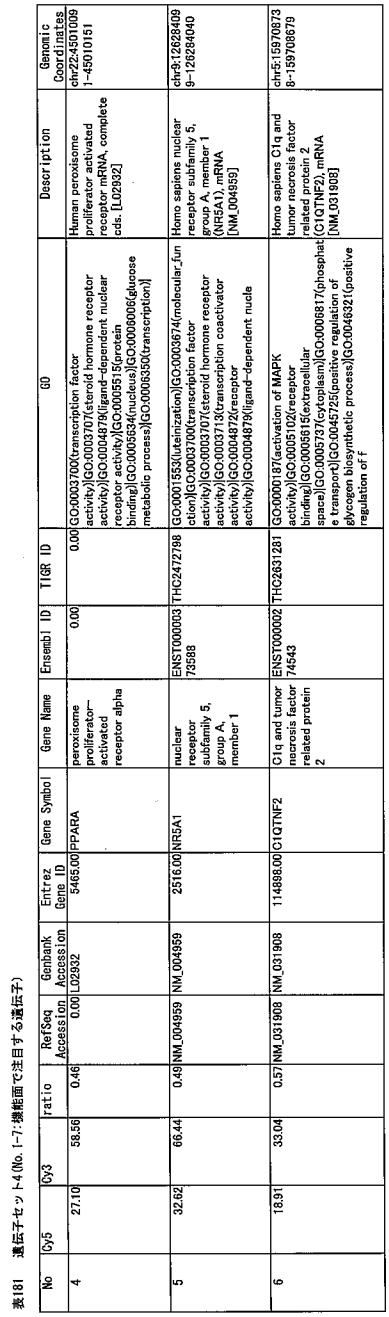


表181 遺伝子セット4(No. 1-7:機能面で注目する遺伝子)

No	Cy5	Cy3	ratio	RefSeq Accession	Genbank Accession	Entrez Gene ID	Gene Symbol	Gene Name	Ensembl ID	TIGR ID	GO	Description	Genomic Coordinates
4	27.10	58.56	0.46	0.00	L02932	5465.00	PPARA	peroxisome proliferator-activated receptor alpha	0.00	0.00	GO:0003700(transcription factor activity)|GO:0003707(steroid hormone receptor activity)|GO:0004879(ligand-dependent nuclear receptor activity)|GO:0005515(protein binding)|GO:0005634(nucleus)|GO:0006006(glucose metabolic process)|GO:0006350(transcription)|	Human peroxisome proliferator activated receptor mRNA, complete cds. [L02932]	chr22:45010099-45010161
5	32.62	66.44	0.49	NM_004959	NM_004959	2516.00	NR5A1	nuclear receptor subfamily 5, group A, member 1	ENST00000373588	THC2472788	GO:0001553(luteinization)|GO:0003674(molecular_function)|GO:0003700(transcription factor activity)|GO:0003707(steroid hormone receptor activity)|GO:0003713(transcription coactivator activity)|GO:0004872(receptor activity)|GO:0004879(ligand-dependent nucle	Homo sapiens nuclear receptor subfamily 5, group A, member 1 (NR5A1), mRNA [NM_004959]	chr9:126284099-126284040
6	18.91	33.04	0.57	NM_031908	NM_031908	114898.00	C1QTNF2	C1q and tumor necrosis factor related protein 2	ENST00000274543	THC2631281	GO:0000187(activation of MAPK activity)|GO:0005102(receptor binding)|GO:0005615(extracellular space)|GO:0005737(cytoplasm)|GO:0006817(phosphate transport)|GO:0045725(positive regulation of glycogen biosynthetic process)|GO:0046321(positive regulation of f	Homo sapiens C1q and tumor necrosis factor related protein 2 (C1QTNF2), mRNA [NM_031908]	chr5:159708738-159708679

[表182]

表182 遺伝子セット4(No. 1-7:横断面で注目する遺伝子)

No	Cy5	Cy3	ratio	RefSeq Accession	Genbank Accession	Entrez Gene ID	Gene Symbol	Gene Name	Ensembl ID	TIGR ID	GO	Description	Genomic Coordinates
7	26.31	52.31	0.50	NM_178037	NM_178037	23085.00	ERC1	ELKS/RAB6-interacting/CAST family member 1	ENST00000360905	NP500066	GO:0005515(protein binding)|GO:0005737(cytoplasm)|GO:0006355(regulation of transcription, DNA-dependent)|GO:0007252(I-kappaB phosphorylation)|GO:0007275(multicellular organismal development)|GO:0008385(IkappaB kinase complex)|GO:0015031(protein transport)	Homo sapiens ELKS/RAB6-interacting/CAST family member 1 (ERC1), transcript variant beta, mRNA [NM_178037]	chr12:1470388-1470447
7	29.24	45.86	0.64	NM_178037	NM_178037	23085.00	ERC1	ELKS/RAB6-interacting/CAST family member 1	ENST00000360905	THC2475234	GO:0005515(protein binding)|GO:0005737(cytoplasm)|GO:0006355(regulation of transcription, DNA-dependent)|GO:0007252(I-kappaB phosphorylation)|GO:0007275(multicellular organismal development)|GO:0008385(IkappaB kinase complex)|GO:0015031(protein transport)	Homo sapiens ELKS/RAB6-interacting/CAST family member 1 (ERC1), transcript variant beta, mRNA [NM_178037]	chr12:1472584-1472643

[表183]

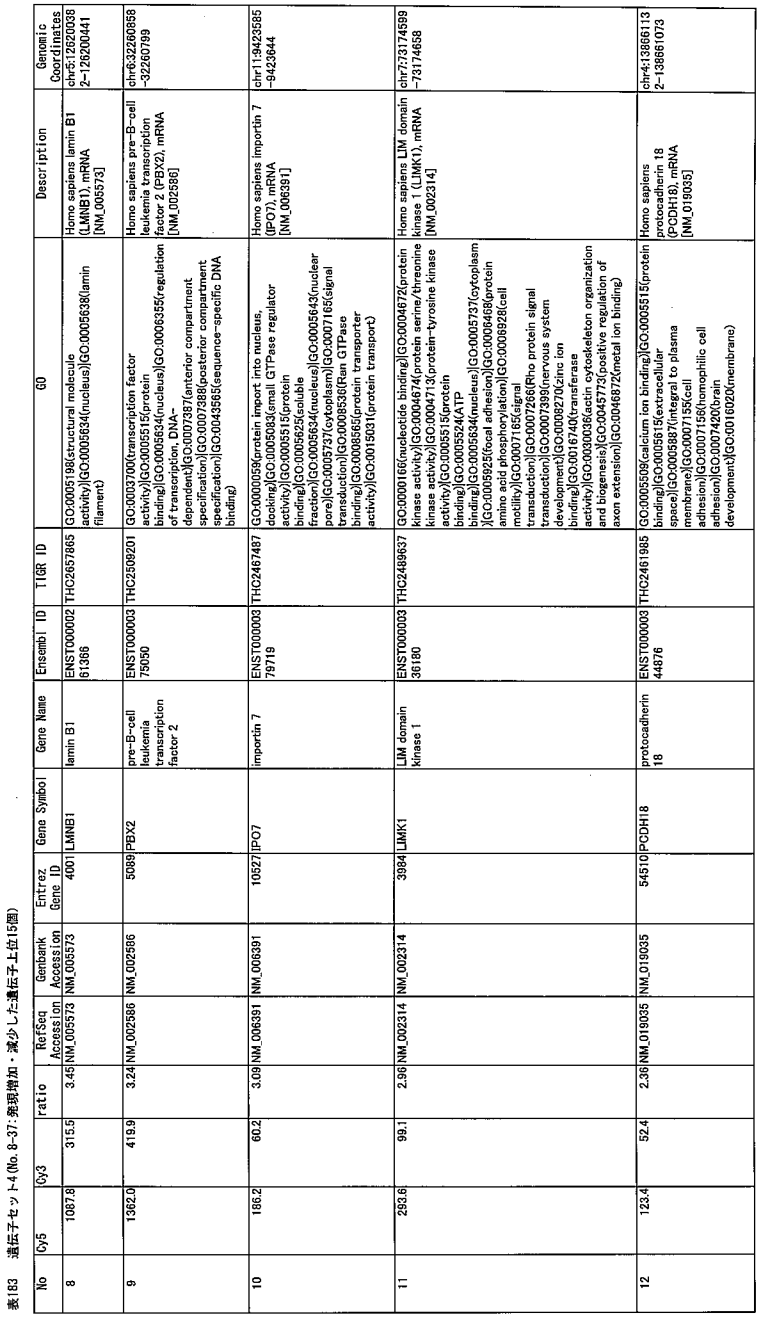


表183 遺伝子セット4(No.8-37:発現増加・減少した遺伝子上位15個)

No	Cy5	Cy3	ratio	RefSeq Accession	Genbank Accession	Entrez Gene ID	Gene Symbol	Gene Name	Ensembl ID	TIGR ID	GO	Description	Genomic Coordinates
8	1087.8	315.5	3.45	NM_005573	NM_005573	4001	LMNB1	lamin B1	ENST00000026161386	THC2657865	GO:0005198(structural molecule activity)|GO:0005634(nucleus)|GO:0005638(lamin filament)	Homo sapiens lamin B1 (LMNB1), mRNA [NM_005573]	chr5:126200382-126200441
9	1362.0	419.9	3.24	NM_002586	NM_002586	5089	PBX2	pre-B-cell leukemia transcription factor 2	ENST00000037375060	THC2509201	GO:0003700(transcription factor activity)|GO:0005515(protein binding)|GO:0005634(nucleus)|GO:0006355(regulation of transcription, DNA-dependent)|GO:0007387(anterior compartment specification)|GO:0007388(posterior compartment specification)|GO:0043565(sequence-specific DNA binding)	Homo sapiens pre-B-cell leukemia transcription factor 2 (PBX2), mRNA [NM_002586]	chr6:32260858-32260799
10	186.2	60.2	3.09	NM_006391	NM_006391	10527	IPO7	importin 7	ENST00000037979719	THC2467487	GO:0000059(protein import into nucleus, docking)|GO:0005083(small GTPase regulator activity)|GO:0005515(protein binding)|GO:0005625(soluble fraction)|GO:0005634(nucleus)|GO:0005643(nuclear pore)|GO:0005737(cytoplasm)|GO:0007165(signal transduction)|GO:0008536(Ran GTPase binding)|GO:0008565(protein transporter activity)|GO:0015031(protein transport)	Homo sapiens importin 7 (IPO7), mRNA [NM_006391]	chr11:9423585-9423644
11	293.6	99.1	2.96	NM_002314	NM_002314	3984	LIMK1	LIM domain kinase 1	ENST00000033636180	THC2489637	GO:0000166(nucleotide binding)|GO:0004672(protein kinase activity)|GO:0004674(protein serine/threonine kinase activity)|GO:0004713(protein-tyrosine kinase activity)|GO:0005515(protein binding)|GO:0005524(ATP binding)|GO:0005634(nucleus)|GO:0005737(cytoplasm)|GO:0005925(focal adhesion)|GO:0006468(protein amino acid phosphorylation)|GO:0008928(cell motility)|GO:0007165(signal transduction)|GO:0007266(Rho protein signal transduction)|GO:0007399(nervous system development)|GO:0008270(zinc ion binding)|GO:0016740(transferase activity)|GO:0030036(actin cytoskeleton organization and biogenesis)|GO:0045773(positive regulation of axon extension)|GO:0046872(metal ion binding)	Homo sapiens LIM domain kinase 1 (LIMK1), mRNA [NM_002314]	chr7:73174599-73174658
12	123.4	52.4	2.36	NM_019035	NM_019035	54510	PCDH18	protocadherin 18	ENST00000034944876	THC2461985	GO:0005509(calcium ion binding)|GO:0005515(protein binding)|GO:0005615(extracellular space)|GO:0005887(integral to plasma membrane)|GO:0007156(cell adhesion)|GO:0007420(brain development)|GO:0016020(membrane)	Homo sapiens protocadherin 18 (PCDH18), mRNA [NM_019035]	chr4:138661132-138661073

[0554]

表163 遺伝子セット4(No.8-37:発現増加・減少した遺伝子上位15個)

No	Cy5	Cy3	ratio	RefSeq Accession	Genbank Accession	Entrez Gene ID	Gene Symbol	Gene Name	Ensembl ID	TIGR ID	GO	Description	Genomic Coordinates
13	134.3	57.6	2.33	NM_001040694	NM_0010406 94	3619	INCENP	inner centromere protein antigens 135/155kDa		THC2640910	GO:0000801(central element)|GO:0000910(cytokinesis)|GO:0005515(protein n binding)|GO:0005634(nucleus)|GO:0005721(centric heterochromatin)|GO:0005819(spindle)|GO:0005874(microtubule)|GO:0007049(cell cycle)|GO:0007059(chromosome segregation)|GO:0007067(mitosis)|GO:0030496(midbody)|GO:0043234(protein complex)	Homo sapiens inner centromere protein antigens 135/155kDa (INCENP), transcript variant 1, mRNA [NM_001040694]	chr11:61167831 8-61676377
14	1916.3	855.8	2.24	NM_001336	NM_001336	1522	CTSZ	cathepsin Z	ENST0000002 17131	THC2466332	GO:0004197(cysteine-type endopeptidase activity)|GO:0005615(extracellular space)|GO:0005764(lysosome)|GO:0005783(endoplasmic reticulum)|GO:0006508(proteolysis)|GO:0008234(cysteine-type peptidase activity)	Homo sapiens cathepsin Z (CTSZ), mRNA [NM_001336]	chr20:5700381 5-57003756
15	80.0	37.2	2.15	NM_016577	NM_016577	51560	RAB6B	RAB6B, member RAS oncogene family	ENST0000002 85208	THC2464609	GO:0000166(nucleotide binding)|GO:0003924(GTPase activity)|GO:0005525(GTP binding)|GO:0005794(Golgi apparatus)|GO:0006886(intracellular protein transport)|GO:0006888(ER to Golgi vesicle-mediated transport)|GO:0006890(retrograde vesicle-mediated transport, Golgi to ER)|GO:0007264(small GTPase mediated signal transduction)|GO:0008565(protein transporter activity)	Homo sapiens RAB6B, member RAS oncogene family (RAB6B), mRNA [NM_016577]	chr3:13503025 3-135030194
16	158.4	75.4	2.10	NM_000028	NM_000028	178	AGL	amylo-1, 6-glucosidase, 4-alpha-glucanotransferase (glycogen debranching enzyme, glycogen storage disease type III)	ENST0000003 61915	THC2461565	GO:0004134(4-alpha-glucanotransferase activity)|GO:0004135(amylo-alpha-1,6-glucosidase activity)|GO:0005975(carbohydrate metabolic process)|GO:0005978(glycogen biosynthetic process)|GO:0008152(metabolic process)|GO:0016740(transferase activity)|GO:0016757(transferase activity, transferring glycosyl groups)|GO:0016798(hydrolase activity, acting on glycosyl bonds)|GO:0043033(isoamylase complex)|GO:0043169(cation binding)	Homo sapiens amylo-1, 6-glucosidase, 4-alpha-glucanotransferase (glycogen debranching enzyme, glycogen storage disease type III) (AGL), transcript variant 4, mRNA [NM_000028]	chr1:10016181 7-100161876
17	1266.8	612.2	2.07	NM_007124	NM_007124	7402	UTRN	utrophin	ENST0000003 67545	THC2586966	GO:0003779(actin binding)|GO:0004888(transmembrane receptor activity)|GO:0005198(structural molecule activity)|GO:0005509(calcium ion binding)|GO:0005515(protein binding)|GO:0005624(membrane fraction)|GO:0005856(cytoskeleton)|GO:0005886(plasma membrane)|GO:0006935(chemotaxis)|GO:0006936(muscle contraction)|GO:0007165(signal transduction)|GO:0007517(muscle development)|GO:0007527(adult somatic muscle development)|GO:0008270(zinc ion binding)|GO:0030054(cell	Homo sapiens utrophin (UTRN), mRNA [NM_007124]	chr6:145215631 -145215690

[0555]

表183 遺伝子セット4(No.8-37:発現増加・減少した遺伝子上位15個)

No	Cy5	Cy3	ratio	RefSeq Accession	Genbank Accession	Entrez Gene ID	Gene Symbol	Gene Name	Ensembl ID	TIGR ID	GO	Description	Genomic Coordinates
18	166.6	83.9	1.98	NM_032047	NM_032047	84002	B3GNT5	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 5	ENST00000326505	THC2462855	GO:0005622(intracellular)|GO:0006486(protein amino acid glycosylation)|GO:0007417(central nervous system development)|GO:0008378(galactosyltransferase activity)|GO:0008457(beta-galactosyl-N-acetylglucosaminylgalactosylglucosyl-ceramide beta-1,3-acetylglucosaminyltransferase activity)|GO:0009247(glycolipid biosynthetic process)|GO:0016020(membrane)|GO:0016757(transferase activity, transferring glycosyl groups)	Homo sapiens UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 5 (B3GNT5), mRNA [NM_032047]	chr3:184473362-184473686
19	125.8	64.9	1.94	NM_000963	NM_000963	5743	PTGS2	prostaglandin-endoperoxide synthase 2 (prostaglandin G/H synthase and cyclooxygenase)	ENST00000367468	NP097723	GO:0001516(prostaglandin biosynthetic process)|GO:0004601(peroxidase activity)|GO:0005506(iron ion binding)|GO:0005615(extracellular space)|GO:0005634(nucleus)|GO:0005737(cytoplasm)|GO:0006633(fatty acid biosynthetic process)|GO:0006928(cell motility)|GO:0008217(blood pressure regulation)|GO:0016020(membrane)|GO:0016491(oxidoreductase activity)|GO:0016702(oxidoreductase activity, acting on single donors with incorporation of molecular oxygen, incorporation of two atoms of oxygen)|GO:0019371(cyclooxygenase pathway)|GO:0030216(keratinocyte differentiation)|GO:0042640(anagen)|GO:0046872(metal ion binding)|GO:0050727(regulation of inflammatory response)	Homo sapiens prostaglandin-endoperoxide synthase 2 (prostaglandin G/H synthase and cyclooxygenase) (PTGS2), mRNA [NM_000963]	chr1:184909978-184909731
20	283.4	147.5	1.92	NM_003566	NM_003566	8411	EEA1	early endosome antigen 1, 162kD		THC2471292	GO:0003676(nucleic acid binding)|GO:0005516(calmodulin binding)|GO:0005545(phosphatidylinositol binding)|GO:0005622(intracellular)|GO:0005624(membrane fraction)|GO:0005737(cytoplasm)|GO:0005769(early endosome)|GO:0005829(cytosol)|GO:0006906(vesicle fusion)|GO:0008270(zinc ion binding)|GO:0016188(synaptic vesicle to endosome fusion)|GO:0019897(extrinsic to plasma membrane)|GO:0030742(GTP-dependent protein binding)|GO:0042803(protein homodimerization activity)|GO:0045022(early endosome to late endosome transport)|GO:0046872(metal ion binding)	Homo sapiens early endosome antigen 1, 162kD (EEA1), mRNA [NM_003566]	chr12:91690065-91690593

[0556]

表183　遺伝子セット4(No. 8-37:発現増加・減少した遺伝子上位15個)

No	Cy5	Cy3	ratio	RefSeq Accession	Genbank Accession	Entrez Gene ID	Gene Symbol	Gene Name	Ensembl ID	TIGR ID	GO	Description	Genomic Coordinates
21	78.2	40.9	1.91	NM_000139	NM_000139	2206	MS4A2	membrane-spanning 4-domains, subfamily A, member 2 (Fc fragment of IgE, high affinity I, receptor for; beta	ENST00000278888		GO:0004872(receptor activity)|GO:0005262(calcium channel activity)|GO:0005887(integral to plasma membrane)|GO:0006959(humoral immune response)|GO:0007186(G-protein coupled receptor protein signaling pathway)|GO:0008283(cell proliferation)|GO:0009897(external side of plasma membrane)|GO:0016020(membrane)|GO:0019863(IgE binding)|GO:0045121(lipid raft)	Homo sapiens membrane-spanning 4-domains, subfamily A, member 2 (Fc fragment of IgE, high affinity I, receptor for; beta polypeptide) (MS4A2), mRNA [NM_000139]	chr11:59622332-59622391
22	154.2	80.6	1.91	NM_031296	NM_031296	83452	RAB33B	RAB33B, member RAS oncogene family	ENST00000305626	THC2501558	GO:0000166(nucleotide binding)|GO:0005525(GTP binding)|GO:0005794(Golgi apparatus)|GO:0007264(small GTPase mediated signal transduction)|GO:0015031(protein transport)	Homo sapiens RAB33B, member RAS oncogene family (RAB33B), mRNA [NM_031296]	chr4:140616362-140616421

[表184]

表184 遺伝子セット4(No.8-37:発現増加・減少した遺伝子上位15個)

No	Cy5	Cy3	ratio	RefSeq Accession	Genbank Accession	Entrez Gene ID	Gene Symbol	Gene Name	Ensembl ID	TIGR ID	GO	Description	Genomic Coordinates
23	57.2	809.7	0.07	NM_007110	NM_007110	7011	TEP1	telomerase-associated protein 1	ENST00000262715	NP1473063	GO:0000166(nucleotide binding)|GO:0000722(telomere maintenance via recombination)|GO:0000781(chromosome, telomeric region)|GO:0003720(telomerase activity)|GO:0003723(RNA binding)|GO:0005524(ATP binding)|GO:0005625(soluble fraction)|GO:0005634(nucleus)|GO:0005694(chromosome)|GO:0005697(telomerase holoenzyme complex)|GO:0005737(cytoplasm)|GO:0007004(telomere maintenance via telomerase)|GO:0016363(nuclear matrix)	Homo sapiens telomerase-associated protein 1 (TEP1), mRNA [NM_007110]	chr14:19905939 8-19905939
24	17.7	166.2	0.11		BC020707	6898	TAT	tyrosine aminotransferase		THC2811148	GO:0004838(tyrosine transaminase activity)|GO:0005576(cellular_component)|GO:0005739(mitochondrion)|GO:0006519(amino acid and derivative metabolic process)|GO:0006559(L-phenylalanine catabolic process)|GO:0006572(tyrosine catabolic process)|GO:0009058(biosynthetic process)|GO:0009074(aromatic amino acid family catabolic process)|GO:0016847(1-aminocyclopropane-1-carboxylate synthase activity)|GO:0030170(pyridoxal phosphate binding)	Homo sapiens tyrosine aminotransferase, mRNA (cDNA clone IMAGE:4710626), complete cds. [BC020707]	chr16:70167228 5-70167228
25	30.0	251.4	0.12	NM_002987	NM_002987	6361	CCL17	chemokine (C-C motif) ligand 17	ENST00000262715	THC2484250	GO:0005576(extracellular region)|GO:0005615(extracellular space)|GO:0006935(chemotaxis)|GO:0006954(inflammatory response)|GO:0009395(immune response)|GO:0009968(cellular defense response)|GO:0007165(signal transduction)|GO:0007186(G-protein coupled receptor protein signaling pathway)|GO:0007267(cell-cell signaling)|GO:0007275(multicellular organismal development)|GO:0008009(chemokine activity)	Homo sapiens chemokine (C-C motif) ligand 17 (CCL17), mRNA [NM_002987]	chr16:5600738 9-58007446
26	19.9	158.4	0.13	NM_001007529	NM_0010075 29	124871	FLJ40194	FLJ40194 protein	ENST00000322227	THC2687540		Homo sapiens FLJ40194 protein (FLJ40194), mRNA [NM_001007529]	chr17:4468492 2-44684981
27	22.3	162.5	0.14	NM_005142	NM_005142	2694	GIF	gastric intrinsic factor (vitamin B synthesis)	ENST00000257248	THC2474702	GO:0005488(binding)|GO:0005615(extracellular space)|GO:0006811(ion transport)|GO:0006824(cobalt ion transport)|GO:0015087(cobalt ion transporter activity)|GO:0050897(cobalt ion binding)	Homo sapiens gastric intrinsic factor (vitamin B synthesis) (GIF), mRNA [NM_005142]	chr11:5935993 8-58359879
28	180.5	1267.3	0.14	NM_015071	NM_015071	23092	ARHGAP26	Rho GTPase activating protein 26	ENST00000378013	THC2495953	GO:0005096(GTPase activator activity)|GO:0005100(Rho GTPase activator activity)|GO:0005575(cellular_component)|GO:0005622(intracellular)|GO:0007165(signal transduction)|GO:0007399(nervous system development)|GO:0030036(actin cytoskeleton organization and biogenesis)	Homo sapiens Rho GTPase activating protein 26 (ARHGAP26), mRNA [NM_015071]	chr5:142458582 7-142585886

[0557]

表184 遺伝子セット4(No.8-37:発現増加・減少した遺伝子上位15個)

No	Cy5	Cy3	ratio	RefSeq Accession	Genbank Accession	Entrez Gene ID	Gene Symbol	Gene Name	Ensembl ID	TIGR ID	GO	Description	Genomic Coordinates
29	62.3	394.8	0.16	NM_002511	NM_002511	4829	NMBR	neuromedin B receptor	ENST00000028042	THC2477505	GO:0001584(rhodopsin-like receptor activity)|GO:0004872(receptor activity)|GO:0004946(bombesin receptor activity)|GO:0004983(neuropeptide Y receptor activity)|GO:0005886(plasma membrane)|GO:0005887(integral to plasma membrane)|GO:0007165(signal transduction)|GO:0007200(G-protein signaling, coupled to IP3 second messenger (phospholipase C activating))	Homo sapiens neuromedin B receptor (NMBR), mRNA [NM_002511]	chr8:142441145-142441399
30	21.5	135.0	0.16	NM_004093	NM_004093	1948	EFNB2	ephrin-B2	ENST00000243323	THC2732430	GO:0001945(lymph vessel development)|GO:0005515(protein binding)|GO:0005886(plasma membrane)|GO:0005887(integral to plasma membrane)|GO:0007267(cell-cell signaling)|GO:0007399(nervous system development)|GO:0009887(organ morphogenesis)|GO:0016020(membrane)|GO:0030154(cell differentiation)|GO:0046875(ephrin receptor binding)	Homo sapiens ephrin-B2 (EFNB2), mRNA [NM_004093]	chr13:105940737-106940737
31	25.1	151.5	0.17		AK022408	23637	RABGAP1	RAB GTPase activating protein 1	ENST00000317419	THG2484822	GO:0005096(GTPase activator activity)|GO:0005813(centrosome)|GO:0005829(cytosol)|GO:0005875(microtubule associated complex)|GO:0007049(cell cycle)|GO:0015631(tubulin binding)	Homo sapiens cDNA FLJ12346 fis, clone MAMMA1002297, highly similar to Homo sapiens mRNA for Rab6 GTPase activating protein. [AK022408]	chr9:124792565-124792565
32	20.7	118.9	0.17		S69023	3216	HOXB6	homeobox B6			GO:0003700(transcription factor activity)|GO:0005634(nucleus)|GO:0006355(regulation of transcription, DNA-dependent)|GO:0007275(multicellular organismal development)|GO:0008595(determination of anterior/posterior axis, embryo)|GO:0043565(sequence-specific DNA binding)	HOX B6=class I homeobox [fragment M2, homeodomain] [human, MCF7 cells, mRNA Partial, 1117 nt]. [S69023]	chr17:20440289-20440289
33	111.1	605.5	0.18	NM_001040214	NM_001040214	154215	TCBA1	T-cell lymphoma breakpoint associated target 1	ENST00000368417	THC2472544		Homo sapiens T-cell lymphoma breakpoint associated target 1 (TCBA1), mRNA [NM_001040214]	chr6:125168827-125188336

[0558]

表184　遺伝子セット4(No. 8-37:発現増加・減少した遺伝子上位15個)

No	Cy5	Cy3	ratio	RefSeq Accession	Genbank Accession	Entrez Gene ID	Gene Symbol	Gene Name	Ensembl ID	TIGR ID	GO	Description	Genomic Coordinates
34	40.6	219.2	0.19	NM_001963	NM_001963	1950	EGF	epidermal growth factor (beta-urogastrone)	ENST00000265171	THC2732656	GO:0000187(activation of MAPK activity)|GO:0005155(epidermal growth factor receptor activating ligand activity)|GO:0005509(calcium ion binding)|GO:0005515(protein binding)|GO:0005576(extracellular region)|GO:0005615(extracellular space)|GO:0005634(nucleus)|GO:0005886(plasma membrane)|GO:0006260(DNA replication)|GO:0007001(chromosome organization and biogenesis (sensu the Eukaryota research community))|GO:0007173(epidermal growth factor receptor signaling pathway)|GO:0008083(growth factor activity)|GO:0008284(positive regulation of cell proliferation)|GO:0016021(integral to membrane)|GO:0048754(branching morphogenesis of a tube)|GO:0050730(regulation of peptidyl-tyrosine phosphorylation)	Homo sapiens epidermal growth factor (beta-urogastrone) (EGF), mRNA [NM_001963]	chr4:111152138-111152197
35	16.7	83.0	0.20	NM_002662	NM_002662	5337	PLD1	phospholipase D1, phosphatidylcholine-specific	ENST00000351298	THC2495260	GO:0004630(phospholipase D activity)|GO:0005515(protein binding)|GO:0005768(endosome)|GO:0005783(endoplasmic reticulum)|GO:0005794(Golgi apparatus)|GO:0006644(phospholipid metabolic process)|GO:0006935(chemotaxis)|GO:0007154(cell communication)|GO:0007265(Ras protein signal transduction)|GO:0008152(metabolic process)|GO:0016020(membrane)|GO:0016042(lipid catabolic process)|GO:0016787(hydrolase activity)|GO:0035091(phosphoinositide binding)	Homo sapiens phospholipase D1, phosphatidylcholine-specific (PLD1), mRNA [NM_002662]	chr3:172803006-172802947
36	75.6	360.7	0.21	NM_033328	NM_033328	93661	CAPZA3	capping protein (actin filament) muscle Z-line, alpha 3	ENST00000317658	THC2477121	GO:0003779(actin binding)|GO:0008290(F-actin capping protein complex)|GO:0030036(actin cytoskeleton organization and biogenesis)|GO:0051016(barbed-end actin filament capping)	Homo sapiens capping protein (actin filament) muscle Z-line, alpha 3 (CAPZA3), mRNA [NM_033328]	chr12:187829233-18782982
37	124.1	553.0	0.22	NM_207585	NM_207585	3455	IFNAR2	interferon (alpha, beta and omega) receptor 2	ENST00000318433	THC2464141	GO:0004872(receptor activity)|GO:0004896(hematopoietin/interferon-class (D200-domain) cytokine receptor activity)|GO:0004905(interferon-alpha/beta receptor activity)|GO:0005515(protein binding)|GO:0005576(extracellular region)|GO:0005615(extracellular space)|GO:0005886(plasma membrane)|GO:0005887(integral to plasma membrane)|GO:0006357(regulation of transcription from RNA polymerase II promoter)|GO:0007166(cell surface receptor linked signal transduction)|GO:0007259(JAK-STAT cascade)|GO:0008283(cell proliferation)|GO:0009615(response to virus)	Homo sapiens interferon (alpha, beta and omega) receptor 2 (IFNAR2), transcript variant 1, mRNA [NM_207585]	chr21:33557839-33557898

[表185]

表185 遺伝子セット4(No.1-7:機能面で注目する遺伝子,No.8-37:発現増加・減少した遺伝子上位15個)

No	Target(Gene)Symbol	Target Accession	UniGene	Up/Down	被験者群	配列番号
1	TLR7	NM_016562	Hs.443036	Up	D	133
2	BCL2	NM_000633	Hs.150749	Up	D	134
3	TLR8	NM_016610	Hs.272410	Up	D	135
4	PPARA		Hs.103110	Down	D	-
5	NR5A1	NM_004959	Hs.495108	Down	D	136
6	C1QTNF2	NM_031908	Hs.110062	Down	D	137
7	ERC1	NM_178037	Hs.400431	Down	D	138
8	LMNB1	NM_005573	Hs.89497	Up	D	139
9	PBX2	NM_002586	Hs.509545	Up	D	140
10	IPO7	NM_006391	Hs.643522	Up	D	141
11	LIMK1	NM_002314	Hs.647035	Up	D	142
12	PCDH18	NM_019035	Hs.591691	Up	D	143
13	INCENP	NM_001040694	Hs.142179	Up	D	144
14	CTSZ	NM_001336	Hs.252549	Up	D	145
15	RAB6B	NM_016577	Hs.12152	Up	D	146
16	AGL	NM_000028	Hs.904	Up	D	111
17	UTRN	NM_007124	Hs.133135	Up	D	147
18	B3GNT5	NM_032047	Hs.208267	Up	D	148
19	PTGS2	NM_000963	Hs.196384	Up	D	149
20	EEA1	NM_003566	Hs.567367	Up	D	150
21	MS4A2	NM_000139	Hs.386748	Up	D	151
22	RAB33B	NM_031296	Hs.591679	Up	D	152
23	TEP1	NM_007110	Hs.508835	Down	D	91
24	TAT		Hs.161640	Down	D	-
25	CCL17	NM_002987	Hs.546294	Down	D	153
26	FLJ40194	NM_001007529	Hs.446890	Down	D	154
27	GIF	NM_005142	Hs.110014	Down	D	155
28	ARHGAP26	NM_015071	Hs.293593	Down	D	93
29	NMBR	NM_002511	Hs.552106	Down	D	156
30	EFNB2	NM_004093	Hs.149239	Down	D	157
31	RABGAP1		Hs.271341	Down	D	-
32	HOXB6		Hs.98428	Down	D	-
33	TCBA1	NM_001040214	Hs.269722	Down	D	-
34	EGF	NM_001963	Hs.419815	Down	D	158
35	PLD1	NM_002662	Hs.382865	Down	D	159
36	CAPZA3	NM_033328	Hs.131288	Down	D	160
37	IFNAR2	NM_207585	Hs.642682	Down	D	161

[0559] 上記解析9で笑いにより遺伝子発現の変動が認められた遺伝子のうち、機能面で注目すべき遺伝子、及び特に発現変動の大きかった上位15遺伝子を表186～189に示し、これらを要約した表190を遺伝子セット7の表として示す。

[表186]

表186 遺伝子セット7(No.1-4:膵癌面で注目する遺伝子)

No	Cy5	Cy3	ratio	RefSeq Accession	Genbank Accession	Entrez Gene ID	Gene Symbol	Gene Name	Ensembl ID	TIGR ID	GO	Description	Genomic Coordinates
1	23.46	45.08	0.52	NM_015529	NM_015529	26002.00	MOXD1	monooxygenase, DBH-like 1	ENST00000336749	THC2463188	GO:0004497(monooxygenase activity)|GO:0004500(dopamine beta-monooxygenase activity)|GO:0005507(copper ion binding)|GO:0006548(histidine catabolic process)|GO:0006584(catecholamine metabolic process)	Homo sapiens monooxygenase, DBH-like 1 (MOXD1), transcript variant 2, mRNA [NM_015529]	chr6:132659133-132659079
2	19.09	34.65	0.55	NM_001158	NM_001158	314.00	AOC2	amine oxidase, copper containing 2 (retina-specific)	ENST00000253799	THC2497172	GO:0005507(copper ion binding)|GO:0005509(calcium ion binding)|GO:0006584(catecholamine metabolic process)|GO:0007601(visual perception)|GO:0008131(amine oxidase activity)|GO:0009055(electron carrier activity)	Homo sapiens amine oxidase, copper containing 2 (retina-specific) (AOC2), transcript variant 1, mRNA [NM_001158]	chr17:38251617-38251676
3	21.71	33.24	0.65	NM_006186	NM_006186	4929.00	NR4A2	nuclear receptor subfamily 4, group A, member 2	ENST00000339562	THC2466693	GO:0003700(transcription factor activity)|GO:0003707(steroid hormone receptor activity)|GO:0005515(protein binding)|GO:0005634(nucleus)|GO:0006350(transcription)|GO:0006355(regulation of transcription, DNA-dependent)|GO:0007165(signal transduction)|GO:000	Homo sapiens nuclear receptor subfamily 4, group A, member 2 (NR4A2), transcript variant 1, mRNA [NM_006186]	chr2:156869003-156868973

[表187]

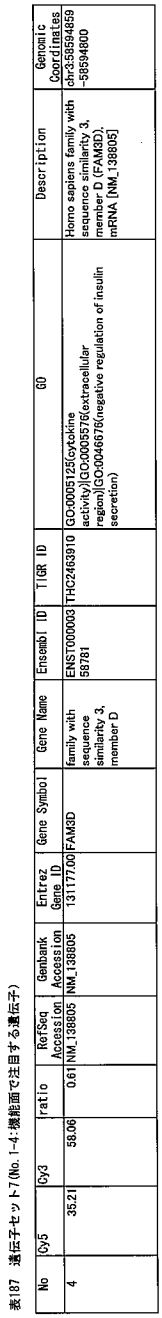


表187 遺伝子セット7(No.1-4:機能面で注目する遺伝子)

No	Cy5	Cy3	ratio	RefSeq Accession	Genbank Accession	Entrez Gene ID	Gene Symbol	Gene Name	Ensembl ID	TIGR ID	GO	Description	Genomic Coordinates
4	35.21	58.06	0.61	NM_138805	NM_138805	131177.00	FAM3D	family with sequence similarity 3, member D	ENST0000003 58781	TIHC2463910	GO:0005125(cytokine activity)|GO:0005576(extracellular region)|GO:0046676(negative regulation of insulin secretion)	Homo sapiens family with sequence similarity 3, member D (FAM3D), mRNA [NM_138805]	chr3:58594859 -58594800

[表188]

表188 遺伝子セット7(No. 5-34:発現増加・減少した遺伝子上位15個)

No	Cy5	Cy3	ratio	RefSeq Accession	Genbank Accession	Entrez Gene ID	Gene Symbol	Gene Name	Ensembl ID	TIGR ID	GO	Description	Genomic Coordinates
5	63.2	33.3	1.90	NM_001076682	NM_001076682	4684	NCAM1	neural cell adhesion molecule 1	ENST00000316851	THC2481779	GO:0005515(protein binding)|GO:0005886(plasma membrane)|GO:0007155(cell adhesion)|GO:0007267(cell-cell signaling)|GO:0007268(synaptic transmission)|GO:0016020(membrane)|GO:0016021(integral to membrane)|GO:0048503(GPI anchor binding)	Homo sapiens neural cell adhesion molecule 1 (NCAM1), transcript variant 3, mRNA [NM_001076682]	chr11:112608654-112608713
6	84.4	47.1	1.79	NM_144717	NM_144717	53833	IL20RB	interleukin 20 receptor beta	ENST00000329582	THC2473132	GO:0004872(receptor activity)|GO:0016020(membrane)|GO:0016021(integral to membrane)	Homo sapiens interleukin 20 receptor beta (IL20RB), mRNA [NM_144717]	chr3:138212488-138212547
7	58.9	34.2	1.72	CR605792	CR605792	8997	KALRN	kalirin, RhoGEF kinase		THC2473179	GO:0000166(nucleotide binding)|GO:0004674(protein serine/threonine kinase activity)|GO:0005085(guanyl-nucleotide exchange factor activity)|GO:0005089(Rho guanyl-nucleotide exchange factor activity)|GO:0005515(protein binding)|GO:0005524(ATP binding)|GO:0005622(intracellular)|GO:0006468(protein amino acid phosphorylation)|GO:0007165(signal transduction)|GO:0007242(intracellular signaling cascade)|GO:0007399(nervous system development)|GO:0015629(actin cytoskeleton)|GO:0016192(vesicle-mediated transport)|GO:0016740(transferase activity)|GO:0035023(regulation of Rho protein signal transduction)	full-length cDNA clone CS0DF007YD09 of Fetal brain of Homo sapiens (human). [CR605792]	chr3:125876765-125876828
8	62.9	37.4	1.68	NM_014917	NM_014917	22854	NTNG1	netrin G1	ENST00000376004	THC2473043	GO:0005515(protein binding)|GO:0005576(extracellular matrix (sensu the Metazoa research community))|GO:0007399(nervous system development)|GO:0007409(axonogenesis)|GO:0016020(membrane)|GO:0030154(cell differentiation)|GO:0046658(anchored to plasma membrane)|GO:0048306(GPI anchor binding)	Homo sapiens netrin G1 (NTNG1), mRNA [NM_014917]	chr1:107739446-107824762
9	41.0	24.5	1.67	NM_005262	NM_005262	2671	GFER	growth factor, augmenter of liver regeneration (ERV1 homolog, S. cerevisiae)	ENST00000248114	THC2463654	GO:0005515(protein binding)|GO:0005575(cellular_component)|GO:0005739(mitochondrion)|GO:0007283(spermatogenesis)|GO:0008283(cell proliferation)	Homo sapiens growth factor, augmenter of liver regeneration (ERV1 homolog, S. cerevisiae) (GFER), mRNA [NM_005262]	chr16:1976686-1976745
10	52.7	31.6	1.67	NM_001627	NM_001627	214	ALCAM	activated leukocyte cell adhesion molecule	ENST00000389926	THC2511276	GO:0005102(receptor binding)|GO:0005624(membrane fraction)|GO:0005887(integral to plasma membrane)|GO:0007155(cell adhesion)|GO:0007165(signal transduction)|GO:0016020(membrane)|GO:0019735(antimicrobial humoral response (sensu the Vertebrata research community))	Homo sapiens activated leukocyte cell adhesion molecule (ALCAM), mRNA [NM_001627]	chr3:105675407-105773400

[0560]

表188 遺伝子セット7(No.5-34:発現増加・減少した遺伝子上位15個)

No	Cy5	Cy3	ratio	RefSeq Accession	Genbank Accession	Entrez Gene ID	Gene Symbol	Gene Name	Ensembl ID	TIGR ID	GO	Description	Genomic Coordinates
11	54.3	33.1	1.64	NM_001063	NM_001063	7018	TF	transferrin	ENST00000264998	THC2512885	GO:0005576(extracellular region)|GO:0005615(extracellular space)|GO:0005768(endosome)|GO:0008811(ion transport)|GO:0008828(iron ion transport)|GO:0008879(iron ion homeostasis)|GO:0008198(ferric iron binding)|GO:0030139(endocytic vesicle)|GO:0046872(metal ion binding)	Homo sapiens transferrin (TF), mRNA [NM_001063]	chr3:134980239-134980298
12	602.0	370.9	1.62	NM_002001	NM_002001	2205	FCER1A	Fc fragment of IgE, high affinity I, receptor for; alpha polypeptide	ENST00000317818	THC2611062	GO:0001812(positive regulation of type I hypersensitivity)|GO:0001820(serotonin secretion)|GO:0004972(receptor activity)|GO:0005057(receptor signaling protein activity)|GO:0005886(plasma membrane)|GO:0005887(integral to plasma membrane)|GO:0006955(immune response)|GO:0007166(cell surface receptor linked signal transduction)|GO:0007257(activation of JNK activity)|GO:0009897(external side of plasma membrane)|GO:0019370(leukotriene biosynthetic process)|GO:0019767(IgE receptor activity)|GO:0043306(positive regulation of mast cell degranulation)|GO:0045121(lipid raft)|GO:0045401(positive regulation of interleukin-3 biosynthetic process)|GO:0045425(positive regulation of granulocyte macrophage colony-stimulating factor biosynthetic process)|GO:0050731(positive regulation of peptidyl-tyrosine phosphorylation)|GO:0050850(positive regulation of calcium-mediated signaling)	Homo sapiens Fc fragment of IgE, high affinity I, receptor for; alpha polypeptide (FCER1A), mRNA [NM_002001]	chr1:157542659-157544219
13	65.6	41.2	1.59	NM_005536	NM_005536	3612	IMPA1	inositol(myo)-1(or 4)-monophosphatase 1	ENST00000256108	THC2615788	GO:0000287(magnesium ion binding)|GO:0005975(carbohydrate metabolic process)|GO:0006020(inyo-inositol metabolic process)|GO:0006661(phosphatidylinositol biosynthetic process)|GO:0006796(phosphate metabolic process)|GO:0007165(signal transduction)|GO:0008934(inositol-1(or 4)-monophosphatase activity)|GO:0016787(hydrolase activity)|GO:0031420(lithium ion binding)|GO:0042578(phosphoric ester hydrolase activity)	Homo sapiens inositol(myo)-1(or 4)-monophosphatase 1 (IMPA1), mRNA [NM_005536]	chr8:82735352-82734244
14	101.4	64.0	1.58	NM_012395	NM_012395	5218	PFTK1	PFTAIRE protein kinase 1	ENST00000265741	THC2626613	GO:0000166(nucleotide binding)|GO:0004674(protein serine/threonine kinase activity)|GO:0004713(protein-tyrosine kinase activity)|GO:0005524(ATP binding)|GO:0005634(nucleus)|GO:0005737(cytoplasm)|GO:0006468(protein amino acid phosphorylation)|GO:0016740(transferase activity)	Homo sapiens PFTAIRE protein kinase 1 (PFTK1), mRNA [NM_012395]	chr7:90677200-90677259

[0561]

表188　遺伝子セット7(No. 5-34:発現増加・減少した遺伝子上位15個)

No	Cy5	Cy3	ratio	RefSeq Accession	Genbank Accession	Entrez Gene ID	Gene Symbol	Gene Name	Ensembl ID	TIGR ID	GO	Description	Genomic Coordinates
15	79.4	50.2	1.58	NM_001037131	NM_001037131	116987	CENTG2	centaurin, gamma 2		THC2465129		Homo sapiens centaurin, gamma 2 (CENTG2), transcript variant 1, mRNA [NM_001037131]	chr2:236698003-236698062
16	55.0	35.1	1.57	NM_014780	NM_014780	9820	CUL7	cullin 7	ENST00000265348	NP1184858	GO:0001570(vasculogenesis)|GO:0005515(protein binding)|GO:0005622(intracellular)|GO:0005680(anaphase-promoting complex)|GO:0005743(mitochondrial inner membrane)|GO:0006508(proteolysis)|GO:0006512(ubiquitin cycle)|GO:0006810(transport)|GO:0007049(cell cycle)|GO:0030071(regulation of mitotic metaphase/anaphase transition)|GO:0042981(regulation of apoptosis)|GO:0045601(regulation of endothelial cell differentiation)	Homo sapiens cullin 7 (CUL7), mRNA [NM_014780]	chr6:43114632-43114573
17	73.7	47.6	1.55	NM_024583	NM_024583	79634	SCRN3	secernin 3	ENST00000272732	THC2526517		Homo sapiens secernin 3 (SCRN3), mRNA [NM_024583]	chr2:175000852-175000911
18	73.6	47.7	1.54	NM_153634	NM_153634	144402	CPNE8	copine VIII	ENST00000331366	NP1161985		Homo sapiens copine VIII (CPNE8), mRNA [NM_153634]	chr12:37332921-37332862
19	48.3	31.4	1.54	NM_004475	NM_004475	2319	FLOT2	flotillin 2	ENST00000335362	THC2468986	GO:0005515(protein binding)|GO:0005886(plasma membrane)|GO:0007155(cell adhesion)|GO:0008544(epidermis development)|GO:0009986(cell surface)|GO:0016021(integral to membrane)|GO:0016600(flotillin complex)|GO:0045121(lipid raft)	Homo sapiens flotillin 2 (FLOT2), mRNA [NM_004475]	chr17:24233332-24233273

[表189]

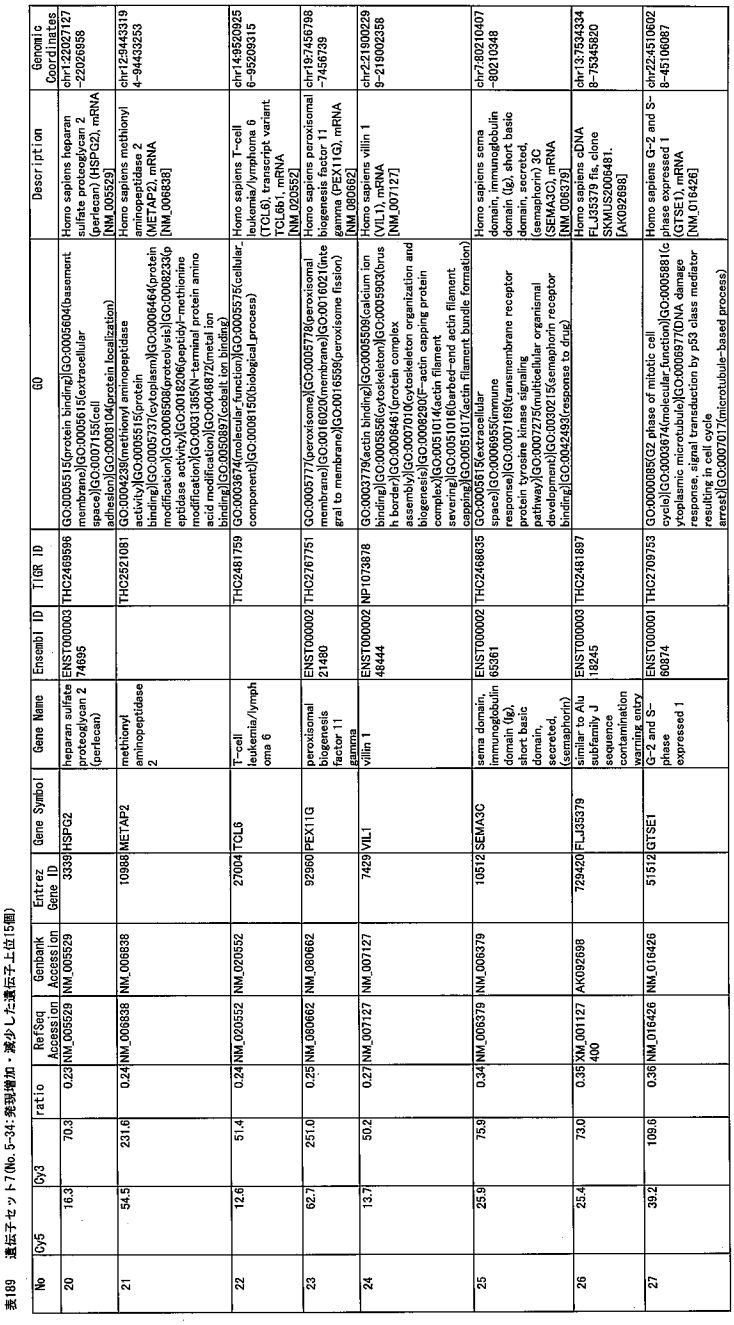


表189 遺伝子セット7(No.5-34:発現増加・減少した遺伝子上位15個)

No	Cy5	Cy3	ratio	RefSeq Accession	Genbank Accession	Entrez Gene ID	Gene Symbol	Gene Name	Ensembl ID	TIGR ID	GO	Description	Genomic Coordinates
20	16.3	70.3	0.23	NM_005529	NM_005529	3339	HSPG2	heparan sulfate proteoglycan 2 (perlecan)	ENST00000374695	THC2469596	GO:0005515(protein binding)|GO:0005604(basement membrane)|GO:0005615(extracellular space)|GO:0007155(cell adhesion)|GO:0008104(protein localization)	Homo sapiens heparan sulfate proteoglycan 2 (perlecan) (HSPG2), mRNA [NM_005529]	chr1:22027127 -22026958
21	54.5	231.6	0.24	NM_006838	NM_006838	10988	METAP2	methionyl aminopeptidase 2		THC2521081	GO:0004238(methionyl aminopeptidase activity)|GO:0005515(protein binding)|GO:0005737(cytoplasm)|GO:0006464(protein modification)|GO:0006508(proteolysis)|GO:0008233(peptidase activity)|GO:0018206(peptidyl-methionine modification)|GO:0031365(N-terminal protein amino acid modification)|GO:0046872(metal ion binding)|GO:0050897(cobalt ion binding)	Homo sapiens methionyl aminopeptidase 2 (METAP2), mRNA [NM_006838]	chr12:94453319 4-94443253
22	12.6	51.4	0.24	NM_020552	NM_020552	27004	TGL6	T-cell leukemia/lymphoma 6		THC2481759	GO:0003674(molecular_function)|GO:0005575(cellular_component)|GO:0008150(biological_process)	Homo sapiens T-cell leukemia/lymphoma 6 (TGL6), transcript variant TGL6b1, mRNA [NM_020552]	chr14:9520925 6-95208315
23	62.7	251.0	0.25	NM_080662	NM_080662	92960	PEX11G	peroxisomal biogenesis factor 11 gamma	ENST00000221480	THC2767751	GO:0005777(peroxisome)|GO:0005778(peroxisomal membrane)|GO:0016020(membrane)|GO:0016021(integral to membrane)|GO:0016559(peroxisome fission)	Homo sapiens peroxisomal biogenesis factor 11 gamma (PEX11G), mRNA [NM_080662]	chr19:7456798 -7456739
24	13.7	50.2	0.27	NM_007127	NM_007127	7429	VIL1	villin 1	ENST00000248444	NP1073878	GO:0003779(actin binding)|GO:0005509(calcium ion binding)|GO:0005856(cytoskeleton)|GO:0005903(brush border)|GO:0008461(protein complex assembly)|GO:0007010(cytoskeleton organization and biogenesis)|GO:0008290(F-actin capping protein complex)|GO:0051014(actin filament severing)|GO:0051016(barbed-end actin filament capping)|GO:0051017(actin filament bundle formation)	Homo sapiens villin 1 (VIL1), mRNA [NM_007127]	chr2:219002229 9-219002358
25	25.9	75.9	0.34	NM_006379	NM_006379	10512	SEMA3C	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin)	ENST00000265361	THC2468635	GO:0005615(extracellular space)|GO:0006955(immune response)|GO:0007169(transmembrane receptor protein tyrosine kinase signaling pathway)|GO:0007275(multicellular organismal development)|GO:0030215(semaphorin receptor binding)|GO:0042493(response to drug)	Homo sapiens sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3C (SEMA3C), mRNA [NM_006379]	chr7:80210407 -80210348
26	25.4	730	0.35	XM_001127400	AK092698	729420	FLJ35379	similar to Alu subfamily J sequence contamination warning entry	ENST00000318245	THC2481897		Homo sapiens cDNA FLJ35379 fis, clone SKMUS2006481. [AK092698]	chr13:7534334 8-75345820
27	39.2	108.6	0.36	NM_016426	NM_016426	51512	GTSE1	G-2 and S-phase expressed 1	ENST00000360874	THC2709753	GO:0000085(G2 phase of mitotic cell cycle)|GO:0003674(molecular_function)|GO:0005881(cytoplasmic microtubule)|GO:0006977(DNA damage response, signal transduction by p53 class mediator resulting in cell cycle arrest)|GO:0007017(microtubule-based process)	Homo sapiens G-2 and S-phase expressed 1 (GTSE1), mRNA [NM_016426]	chr22:4510602 8-45106087

[0562]

表189 遺伝子セット7(No.5-34:発現増加・減少した遺伝子上位15個)

No	Cy5	Cy3	ratio	RefSeq Accession	Genbank Accession	Entrez Gene ID	Gene Symbol	Gene Name	Ensembl ID	TIGR ID	GO	Description	Genomic Coordinates
28	12.4	31.2	0.40	NM_000461	NM_000461	7068	THRB	thyroid hormone receptor, beta (erythroblastic leukemia viral (v-erb-a) oncogene homolog 2, avian)	ENST00000356447	THC2479277	GO:0003700(transcription factor activity)|GO:0003707(steroid hormone receptor activity)|GO:0003714(transcription corepressor activity)|GO:0004872(receptor activity)|GO:0004887(thyroid hormone receptor activity)|GO:0005515(protein binding)|GO:0005634(nucleus)|GO:0006350(transcription)|GO:0008355(regulation of transcription, DNA-dependent)|GO:0007605(sensory perception of sound)|GO:0008016(regulation of heart contraction)|GO:0008270(zinc ion binding)|GO:0009887(organ morphogenesis)|GO:0016481(negative regulation of transcription)|GO:0043565(sequence-specific DNA binding)|GO:0046872(metal ion binding)	Homo sapiens thyroid hormone receptor, beta (erythroblastic leukemia viral (v-erb-a) oncogene homolog 2, avian) (THRB), mRNA [NM_000461]	chr3:24139552 -24139493
29	29.3	70.0	0.42	NM_001235	NM_001235	871	SERPINH1	serpin peptidase inhibitor, clade H (heat shock protein 47), member 1, (collagen binding protein	ENST00000358171	NP094444	GO:0004867(serine-type endopeptidase inhibitor activity)|GO:0005518(collagen binding)|GO:0005615(extracellular space)|GO:0005783(endoplasmic reticulum)|GO:0005793(ER-Golgi intermediate compartment)|GO:0006457(protein folding)|GO:0008986(response to unfolded protein)|GO:0051082(unfolded protein binding)	Homo sapiens serpin peptidase inhibitor, clade H (heat shock protein 47), member 1, (collagen binding protein 1) (SERPINH1), mRNA [NM_001235]	chr11:7495749 0-74957658
30	12.8	30.2	0.42	NM_052968	NM_052968	116519	APOA5	apolipoprotein A-V	ENST00000375063	THC2477063	GO:0005319(lipid transporter activity)|GO:0005576(extracellular region)|GO:0005783(endoplasmic reticulum)|GO:0006869(lipid transport)|GO:0017129(triglyceride binding)|GO:0042157(lipoprotein metabolic process)|GO:0044246(cellular response)|GO:0046627(chylomicron)|GO:0046890(regulation of lipid biosynthetic process)	Homo sapiens apolipoprotein A-V (APOA5), mRNA [NM_052968]	chr1:161654 75-161654 16
31	18.3	41.4	0.44	NM_017637	NM_017637	54796	BNC2	basonuclin 2	ENST00000317612	THC2491095	GO:0003677(DNA binding)|GO:0005622(intracellular)|GO:0005634(nucleus)|GO:0006350(transcription)|GO:0006355(regulation of transcription, DNA-dependent)|GO:0008270(zinc ion binding)|GO:0046872(metal ion binding)	Homo sapiens basonuclin 2 (BNC2), mRNA [NM_017637]	chr9:16406908 -16408949
32	14.5	29.1	0.50	NM_002225	NM_002225	3712	IVD	isovaleryl Coenzyme A dehydrogenase	ENST00000249760	THC2527630	GO:0003995(acyl-CoA dehydrogenase activity)|GO:0005739(mitochondrion)|GO:0005759(mitochondrial matrix)|GO:0006118(electron transport)|GO:0008152(metabolic process)|GO:0008470(isovaleryl-CoA dehydrogenase activity)|GO:0050660(FAD binding)	Homo sapiens isovaleryl Coenzyme A dehydrogenase (IVD), nuclear gene encoding mitochondrial protein, mRNA [NM_002225]	chr15:3849081 5-38491075

[0563]

表189 遺伝子セット7(No. 5-34:発現増加・減少した遺伝子上位15個)

No	Cy5	Cy3	ratio	RefSeq Accession	Genbank Accession	Entrez Gene ID	Gene Symbol	Gene Name	Ensembl ID	TIGR ID	GO	Description	Genomic Coordinates
33	15.7	23.6	0.53	NM_000798	NM_000798	1816	DRD5	dopamine receptor D5	ENST00000382465	THC2475950	GO:0001584(rhodopsin-like receptor activity)GO:0004872(receptor activity)GO:0004935(adrenoceptor activity)GO:0004952(dopamine receptor activity)GO:0005887(integral to plasma membrane)GO:0007165(signal transduction)GO:0007186(G-protein coupled receptor protein signaling pathway)GO:0007191(dopamine receptor adenylate cyclase activating pathway)GO:0007268(synaptic transmission)GO:0016020(membrane)	Homo sapiens dopamine receptor D5 (DRD5), mRNA [NM_000798]	chr4:9394324-9394383
34	36.0	66.6	0.54	NM_003567	NM_003567	8412	BCAR3	breast cancer anti-estrogen resistance 3	ENST00000370244	THC2624185	GO:0000074(regulation of progression through cell cycle)GO:0005085(guanyl-nucleotide exchange factor activity)GO:0005622(intracellular)GO:0007264(small GTPase mediated signal	Homo sapiens breast cancer anti-estrogen resistance 3 (BCAR3), mRNA [NM_003567]	chr1:93800386-93800327

[表190]

表190 遺伝子セット7(No. 1-4:機能面で注目する遺伝子, No. 5-34:発現増加・減少した遺伝子上位15個)

No	Target(Gene)Symbol	Target Accession	UniGene	Up/Down	被験者群	配列番号
1	MOXD1	NM_015529	Hs. 6909	Down	A+C	219
2	AOC2	NM_001158	Hs. 143102	Down	A+C	220
3	NR4A2	NM_006186	Hs. 563344	Down	A+C	221
4	FAM3D	NM_138805	Hs. 61265	Down	A+C	222
5	NCAM1	NM_001076682	Hs.503878	Up	A+C	223
6	IL20RB	NM_144717	Hs.61232	Up	A+C	224
7	KALRN		Hs.8004	Up	A+C	-
8	NTNG1	NM_014917	Hs.143707	Up	A+C	225
9	GFER	NM_005262	Hs.27184	Up	A+C	226
10	ALCAM	NM_001627	Hs.591293	Up	A+C	227
11	TF	NM_001063	Hs.518267	Up	A+C	228
12	FCER1A	NM_002001	Hs.897	Up	A+C	110
13	IMPA1	NM_005536	Hs.555086	Up	A+C	27
14	PFTK1	NM_012395	Hs.430742	Up	A+C	229
15	CENTG2	NM_001037131	Hs.435039	Up	A+C	-
16	CUL7	NM_014780	Hs.520136	Up	A+C	230
17	SCRN3	NM_024583	Hs.470679	Up	A+C	231
18	CPNE8	NM_153634	Hs.40910	Up	A+C	182
19	FLOT2	NM_004475	Hs.514038	Up	A+C	232
20	HSPG2	NM_005529	Hs.651231	Down	A+C	233
21	METAP2	NM_006838	Hs.591005	Down	A+C	127
22	TCL6	NM_020552	Hs.510368	Down	A+C	191
23	PEX11G	NM_080662	Hs.515100	Down	A+C	183
24	VIL1	NM_007127	Hs.647885	Down	A+C	234
25	SEMA3C	NM_006379	Hs.269109	Down	A+C	235
26	FLJ35379	XM_001127400	Hs.586820	Down	A+C	236
27	GTSE1	NM_016426	Hs.386189	Down	A+C	237
28	THRB	NM_000461	Hs.187861	Down	A+C	238
29	SERPINH1	NM_001235	Hs.596449	Down	A+C	239
30	APOA5	NM_052968	Hs.283923	Down	A+C	240
31	BNC2	NM_017637	Hs.435309	Down	A+C	241
32	IVD	NM_002225	Hs.513646	Down	A+C	242
33	DRD5	NM_000798	Hs.380681	Down	A+C	243
34	BCAR3	NM_003567	Hs.36958	Down	A+C	244

[0564] 上記解析10で笑いにより遺伝子発現の変動が認められた遺伝子のうち、機能面で注目すべき遺伝子、及び特に発現変動の大きかった上位15遺伝子を表191～197に示し、これらを要約した表198を遺伝子セット8の表として示す。

[表191]

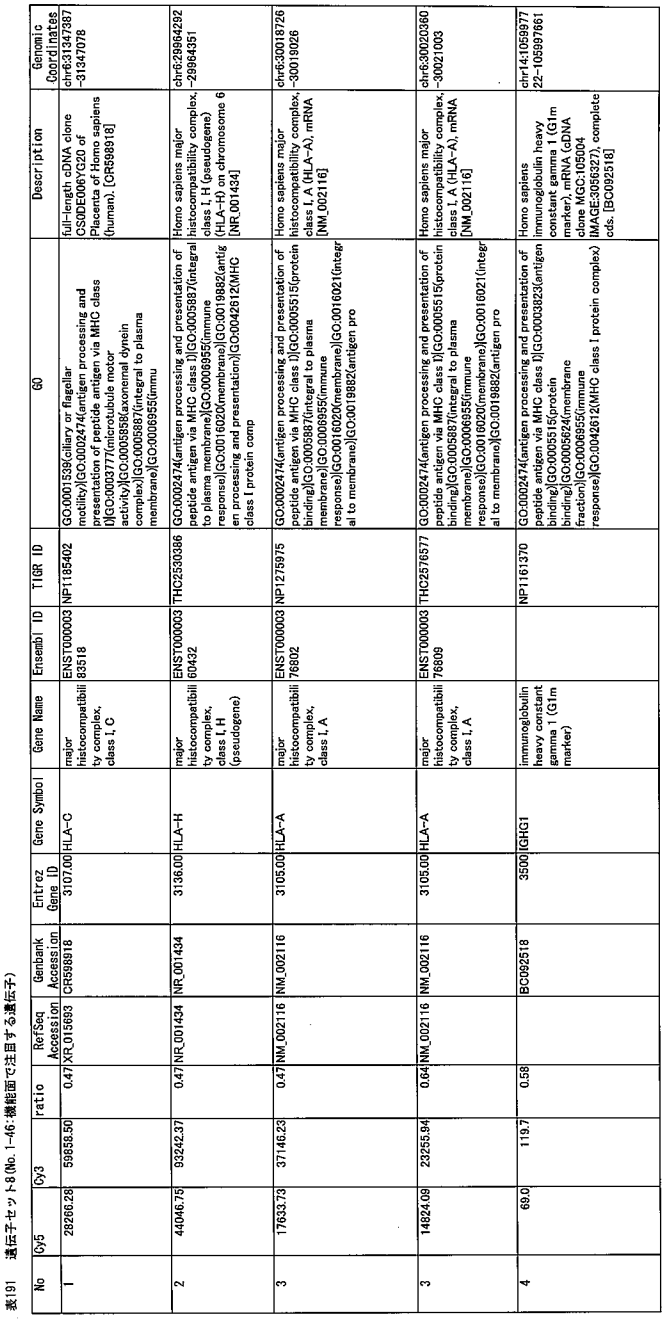


表191 遺伝子セット8(No.1-46:機能面で注目する遺伝子)

No	Cy5	Cy3	ratio	RefSeq Accession	Genbank Accession	Entrez Gene_ID	Gene Symbol	Gene Name	Ensembl ID	TIGR ID	GO	Description	Genomic Coordinates
1	28266.28	59858.50	0.47	XR_015693	CR598918	3107.00	HLA-C	major histocompatibility complex, class I, C	ENST00000383518	NP1185402	GO:0001539(ciliary or flagellar motility)|GO:0002474(antigen processing and presentation of peptide antigen via MHC class I)|GO:0003777(microtubule motor activity)|GO:0005858(axonemal dynein complex)|GO:0005887(integral to plasma membrane)|GO:0006955(immu	full-length cDNA clone CS0DE006YG20 of Placenta of Homo sapiens (human). [CR598918]	chr6:31347387 -31347078
2	44046.75	93242.37	0.47	NR_001434	NR_001434	3136.00	HLA-H	major histocompatibility complex, class I, H (pseudogene)	ENST00000360432	THC2530386	GO:0002474(antigen processing and presentation of peptide antigen via MHC class I)|GO:0005887(integral to plasma membrane)|GO:0006955(immune response)|GO:0016020(membrane)|GO:0019882(antigen processing and presentation)|GO:0042612(MHC class I protein comp	Homo sapiens major histocompatibility complex, class I, H (pseudogene) (HLA-H) on chromosome 6 [NR_001434]	chr6:29964292 -29964351
3	17633.73	37146.23	0.47	NM_002116	NM_002116	3105.00	HLA-A	major histocompatibility complex, class I, A	ENST00000376802	NP1275975	GO:0002474(antigen processing and presentation of peptide antigen via MHC class I)|GO:0005515(protein binding)|GO:0005887(integral to plasma membrane)|GO:0006955(immune response)|GO:0016020(membrane)|GO:0016021(integral to membrane)|GO:0019882(antigen pro	Homo sapiens major histocompatibility complex, class I, A (HLA-A), mRNA [NM_002116]	chr6:30018726 -30019026
3	14824.09	23255.94	0.64	NM_002116	NM_002116	3105.00	HLA-A	major histocompatibility complex, class I, A	ENST00000376809	THC2576577	GO:0002474(antigen processing and presentation of peptide antigen via MHC class I)|GO:0005515(protein binding)|GO:0005887(integral to plasma membrane)|GO:0006955(immune response)|GO:0016020(membrane)|GO:0016021(integral to membrane)|GO:0019882(antigen pro	Homo sapiens major histocompatibility complex, class I, A (HLA-A), mRNA [NM_002116]	chr6:30020380 -30021003
4	69.0	119.7	0.58		BC092518	3500	IGHG1	immunoglobulin heavy constant gamma 1 (G1m marker)		NP1161370	GO:0002474(antigen processing and presentation of peptide antigen via MHC class I)|GO:0003823(antigen binding)|GO:0005515(protein binding)|GO:0005624(membrane fraction)|GO:0006955(immune response)|GO:0042612(MHC class I protein complex)	Homo sapiens immunoglobulin heavy constant gamma 1 (G1m marker), mRNA (cDNA clone MGC:105004 IMAGE:30563227), complete cds. [BC092518]	chr14:1059977 22-105997661

[0565]

表191 遺伝子セット8(No. 1-46:膜表面で注目する遺伝子)

No	0y5	0y3	ratio	RefSeq Accession	Genbank Accession	Entrez Gene ID	Gene Symbol	Gene Name	Ensembl ID	TIGR ID	GO	Description	Genomic Coordinates
5	25227.26	48725.44	0.52	NM_005516	NM_005516	3133.00	HLA-E	major histocompatibility complex, class I, E	ENST00000376628	THC2589494	GO:0002474(antigen processing and presentation of peptide antigen via MHC class I)|GO:0006955(immune response)|GO:0016020(membrane)|GO:0016021(integral to membrane)|GO:0019882(antigen processing and presentation)|GO:0042612(MHC class I protein complex)	Homo sapiens major histocompatibility complex, class I, E (HLA-E), mRNA [NM_005516]	chr6:30569046 -30566105
5	83998.52	137800.10	0.61	NM_005516	NM_005516	3133.00	HLA-E	major histocompatibility complex, class I, E	ENST00000376628	THC2580019	GO:0002474(antigen processing and presentation of peptide antigen via MHC class I)|GO:0006955(immune response)|GO:0016020(membrane)|GO:0016021(integral to membrane)|GO:0019882(antigen processing and presentation)|GO:0042612(MHC class I protein complex)	Homo sapiens major histocompatibility complex, class I, E (HLA-E), mRNA [NM_005516]	chr6:30567339 -30567398
6	45799.67	87136.41	0.53	0.00	CR608347	3106.00	HLA-B	major histocompatibility complex, class I, B	ENST00000376683326	THC2578374	GO:0002474(antigen processing and presentation of peptide antigen via MHC class I)|GO:0003674(molecular_function)|GO:0005575(cellular_component)|GO:0005624(membrane fraction)|GO:0005887(integral to plasma membrane)|GO:0006952(defense response)|GO:0006955(	full-length cDNA clone CS0DJG002YJ10 of B cells (Ramos cell line) of Homo sapiens (human). [CR608347]	chr6:31431988 -31431929
7	111.94	205.40	0.54	NM_001766	NM_001766	912.00	CD1D	CD1d molecule	ENST00000376868171	THC2781332	GO:0004872(receptor activity)|GO:0005887(integral to plasma membrane)|GO:0016020(membrane)|GO:0016045(detection of bacterium)|GO:0030881(beta-2-microglobulin binding)|GO:0030884(exogenous lipid antigen binding)|GO:0045058(T cell selection)|GO:0045089(posi	Homo sapiens CD1d molecule (CD1D), mRNA [NM_001766]	chr1:156418495-156418554
8	675.53	1236.17	0.55	NM_001004349	NM_001004349	441140.00	FLJ45422	FLJ45422 protein	ENST00000376868668	THC2510082	GO:0002474(antigen processing and presentation of peptide antigen via MHC class I)|GO:0019882(antigen processing and presentation)|GO:0042612(MHC class I protein complex)	Homo sapiens FLJ45422 protein (FLJ45422), mRNA [NM_001004349]	chr6:30336266 -30336327
9	44709.03	76219.79	0.59	NM_018950	NM_018950	3134.00	HLA-F	major histocompatibility complex, class I, F	ENST00000376842322	THC2467503	GO:0002474(antigen processing and presentation of peptide antigen via MHC class I)|GO:0006955(immune response)|GO:0016020(membrane)|GO:0016021(integral to membrane)|GO:0019882(antigen processing and presentation)|GO:0042612(MHC class I protein complex)	Homo sapiens major histocompatibility complex, class I, F (HLA-F), mRNA [NM_018950]	chr6:29800992 -29801051

[0566]

表191　遺伝子セット8(No. 1-46:機能面で注目する遺伝子)

No	Cy5	Cy3	ratio	RefSeq Accession	Genbank Accession	Entrez Gene ID	Gene Symbol	Gene Name	Ensembl ID	TIGR ID	GO	Description	Genomic Coordinates
10	11719.04	19814.93	0.59	0.00	M64260	649853.00	LOC649853	similar to HLA class I histocompatibility antigen, A-29 alpha chain precursor (MHC class I antigen A*29)	ENST00000376802	NP097277	GO:0019882(antigen processing and presentation)|GO:0042612(MHC class I protein complex)	HLA class I histocompatibility antigen, alpha chain G precursor (HLA G antigen). [Source:Uniprot/SWISSPROT;Acc:P17693] [ENST00000376802]	chr6:30020138-30021000
11	109678.80	185030.50	0.59	NM_005514	NM_005514	3106.00	HLA-B	major histocompatibility complex, class I, B	ENST00000359635	THC2556153	GO:0002474(antigen processing and presentation of peptide antigen via MHC class I)|GO:0003674(molecular_function)|GO:0005575(cellular_component)|GO:0005624(membrane fraction)|GO:0005887(integral to plasma membrane)|GO:0006952(defense response)|GO:0006955(	Homo sapiens major histocompatibility complex, class I, B (HLA-B), mRNA [NM_005514]	chr6:31431138-31431079
12	1197.35	1971.49	0.61	NM_001025158	NM_001025158	972.00	CD74	CD74 molecule, major histocompatibility complex, class II invariant chain	ENST00000353334	THC2590686	GO:0001516(prostaglandin biosynthetic process)|GO:0005622(intracellular)|GO:0005764(lysosome)|GO:0005771(multivesicular body)|GO:0005783(endoplasmic reticulum)|GO:0005794(Golgi apparatus)|GO:0005887(integral to plasma membrane)|GO:0006457(protein folding)	Homo sapiens CD74 molecule, major histocompatibility complex, class II invariant chain (CD74), transcript variant 3, mRNA [NM_001025158]	chr5:149772474-149772415
13	684.72	1062.72	0.64	NM_003664	NM_003664	8546.00	AP3B1	adaptor-related protein complex 3, beta 1 subunit	ENST00000380357	THC2466221	GO:0005488(binding)|GO:0005794(Golgi apparatus)|GO:0005802(Golgi trans face)|GO:0005905(coated pit)|GO:0006622(protein targeting to lysosome)|GO:0006886(intracellular protein transport)|GO:0006897(endocytosis)|GO:0048007(anti	Homo sapiens adaptor-related protein complex 3, beta 1 subunit (AP3B1), mRNA [NM_003664]	chr5:77334267-77334208

[表192]

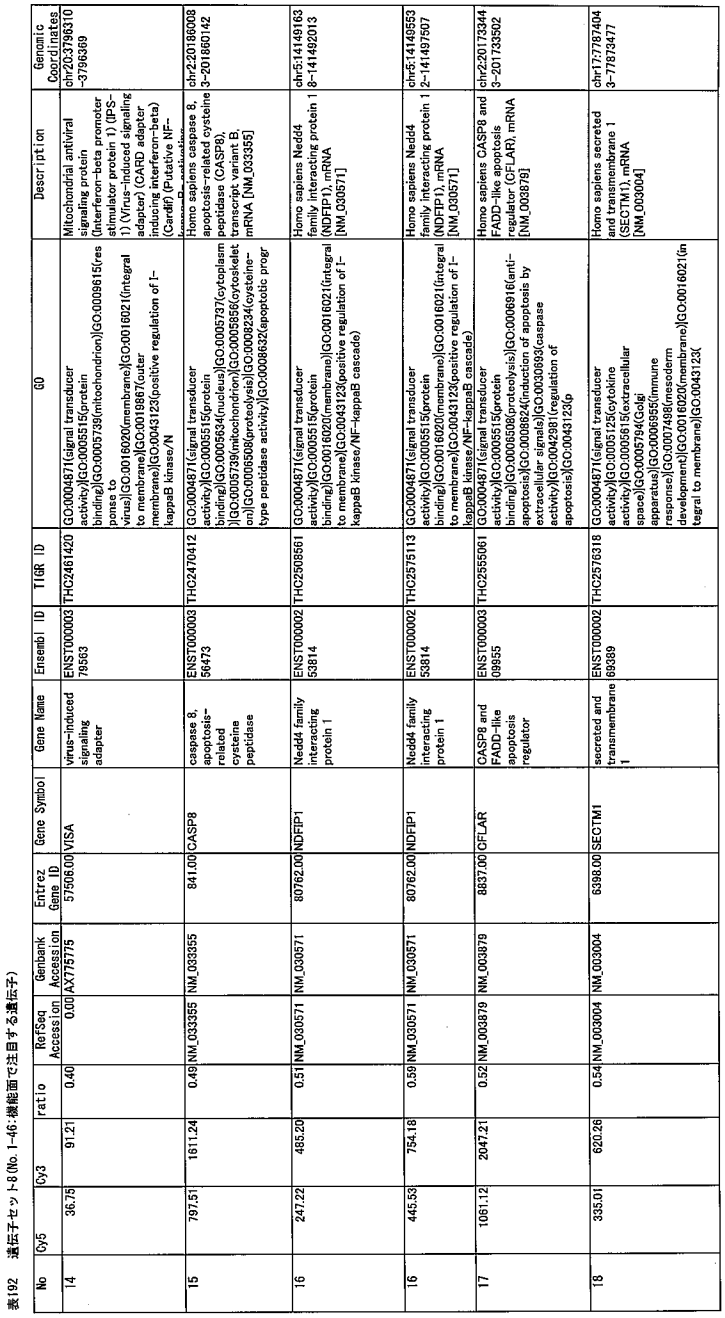


表192 遺伝子セット8(No. 1-46:機能面で注目する遺伝子)

No	Cy5	Cy3	ratio	RefSeq Accession	Genbank Accession	Entrez Gene ID	Gene Symbol	Gene Name	Ensembl ID	T1&R ID	GO	Description	Genomic Coordinates
14	36.75	91.21	0.40	0.00	AX776775	57506.00	VISA	virus-induced signaling adapter	ENST00000378563	THC2461420	GO:0004871(signal transducer activity)|GO:0005515(protein binding)|GO:0005738(mitochondrion)|GO:0009615(response to virus)|GO:0016020(membrane)|GO:0016021(integral to membrane)|GO:0019887(outer membrane)|GO:0043123(positive regulation of I-kappaB kinase/N	Mitochondrial antiviral signaling protein (Interferon-beta promoter stimulator protein 1) (IPS-1) (Virus-induced signaling adapter) (CARD adapter inducing interferon-beta) (Cardif) (Putative NF-	chr20:3796310-3796369
15	797.51	1611.24	0.49	NM_033355	NM_033355	841.00	CASP8	caspase 8, apoptosis-related cysteine peptidase	ENST00000356473	THC2470412	GO:0004871(signal transducer activity)|GO:0005515(protein binding)|GO:0005634(nucleus)|GO:0005737(cytoplasm)|GO:0005739(mitochondrion)|GO:0005856(cytoskeleton)|GO:0006508(proteolysis)|GO:0008234(cysteine-type peptidase activity)|GO:0008632(apoptotic progr	Homo sapiens caspase 8, apoptosis-related cysteine peptidase (CASP8), transcript variant B, mRNA [NM_033355]	chr2:201860008-201860142
16	247.22	485.20	0.51	NM_030571	NM_030571	80762.00	NDFIP1	Nedd4 family interacting protein 1	ENST00000253814	THC2508561	GO:0004871(signal transducer activity)|GO:0005515(protein binding)|GO:0016020(membrane)|GO:0016021(integral to membrane)|GO:0043123(positive regulation of I-kappaB kinase/NF-kappaB cascade)	Homo sapiens Nedd4 family interacting protein 1 (NDFIP1), mRNA [NM_030571]	chr5:141491638-141492013
16	445.53	754.18	0.59	NM_030571	NM_030571	80762.00	NDFIP1	Nedd4 family interacting protein 1	ENST00000253814	THC2575113	GO:0004871(signal transducer activity)|GO:0005515(protein binding)|GO:0016020(membrane)|GO:0016021(integral to membrane)|GO:0043123(positive regulation of I-kappaB kinase/NF-kappaB cascade)	Homo sapiens Nedd4 family interacting protein 1 (NDFIP1), mRNA [NM_030571]	chr5:141491553-141497507
17	1061.12	2047.21	0.52	NM_003879	NM_003879	8837.00	CFLAR	CASP8 and FADD-like apoptosis regulator	ENST00000309955	THC2555061	GO:0004871(signal transducer activity)|GO:0005515(protein binding)|GO:0006508(proteolysis)|GO:0006916(anti-apoptosis)|GO:0008824(induction of apoptosis by extracellular signals)|GO:0030693(caspase activity)|GO:0042981(regulation of apoptosis)|GO:0043123(p	Homo sapiens CASP8 and FADD-like apoptosis regulator (CFLAR), mRNA [NM_003879]	chr2:201733344-201733502
18	335.01	620.26	0.54	NM_003004	NM_003004	6398.00	SECTM1	secreted and transmembrane 1	ENST00000269389	THC2576318	GO:0004871(signal transducer activity)|GO:0005125(cytokine activity)|GO:0005615(extracellular space)|GO:0005794(Golgi apparatus)|GO:0006955(immune response)|GO:0007498(mesoderm development)|GO:0016020(membrane)|GO:0016021(integral to membrane)|GO:0043123(	Homo sapiens secreted and transmembrane 1 (SECTM1), mRNA [NM_003004]	chr17:77874047-77873477

[0567]

表192 遺伝子セット8(No.1-46:横軸面で注目する遺伝子)

No	Cy5	Cy3	ratio	RefSeq Accession	Genbank Accession	Entrez Gene ID	Gene Symbol	Gene Name	Ensembl ID	TIGR ID	GO	Description	Genomic Coordinates
19	80.25	147.81	0.54	NM_145641	NM_145641	80833.00	APOL3	apolipoprotein L, 3	ENST00000361710	THC2494358	GO:0004871(signal transducer activity)|GO:0005319(lipid transporter activity)|GO:0005576(extracellular region)|GO:0006869(lipid transport)|GO:0006954(inflammatory response)|GO:0008289(lipid binding)|GO:0042157(lipoprotein metabolic process)|GO:0043123(pos	Homo sapiens apolipoprotein L, 3 (APOL3), transcript variant beta/a, mRNA [NM_145641]	chr22:34866894 I-34866882
20	436.07	792.72	0.55	NM_002342	NM_002342	4055.00	LTBR	lymphotoxin beta receptor (TNFR superfamily, member 3)	ENST00000228918	THC2468834	GO:0004888(transmembrane receptor activity)|GO:0005515(protein binding)|GO:0005615(extracellular space)|GO:0006915(apoptosis)|GO:0006955(immune response)|GO:0007165(signal transduction)|GO:0016020(membrane)|GO:0016021(integral to membrane)|GO:0043123(positi	Homo sapiens lymphotoxin beta receptor (TNFR superfamily, member 3) (LTBR), mRNA [NM_002342]	chr12:6370331 -6370390
21	460.92	833.74	0.55	NM_024544	NM_024544	79594.00	C1orf166	chromosome 1 open reading frame 166	ENST00000264198	THC2469447	GO:0004871(signal transducer activity)|GO:0005515(protein binding)|GO:0005739(mitochondrion)|GO:0008270(zinc ion binding)|GO:0043123(positive regulation of I-kappaB kinase/NF-kappaB cascade)|GO:0046872(metal ion binding)	Homo sapiens chromosome 1 open reading frame 166 (C1orf166), mRNA [NM_024544]	chr1:20698567 -20998530
22	291.85	515.27	0.57	NM_002468	NM_002468	4615.00	MYD88	myeloid differentiation primary response gene (88)	ENST00000318044	THC2511648	GO:0004871(signal transducer activity)|GO:0004888(transmembrane receptor activity)|GO:0005123(death receptor binding)|GO:0005515(protein binding)|GO:0005737(cytoplasm)|GO:0006954(inflammatory response)|GO:0007166(cell surface r	Homo sapiens myeloid differentiation primary response gene (88) (MYD88), mRNA [NM_002468]	chr3:38157022 -38157269
23	660.80	1149.11	0.58	NM_006355	NM_006355	10475.00	TRIM38	tripartite motif-containing 38	ENST00000349458	THC2466904	GO:0004871(signal transducer activity)|GO:0005515(protein binding)|GO:0005576(cellular_component)|GO:0005622(intracellular)|GO:0008270(zinc ion binding)|GO:0043123(positive regulation of I-kappaB kinase/NF-kappaB cascade)|GO:0046872(metal ion binding)	Homo sapiens tripartite motif-containing 38 (TRIM38), mRNA [NM_006355]	chr6:26092676 -26092735

[0568]

表192 遺伝子セット8(No.1-46:機能面で注目する遺伝子)

No	Cy5	Cy3	ratio	RefSeq Accession	Genbank Accession	Entrez Gene ID	Gene Symbol	Gene Name	Ensembl ID	TIGR ID	GO	Description	Genomic Coordinates
24	150.26	258.28	0.58	NM_138793	NM_138783	124583.00	CANT1	calcium activated nucleotidase 1	ENST00000302345	THC2787861	GO:0004871(signal transducer activity)|GO:0005509(calcium ion binding)|GO:0005783(endoplasmic reticulum)|GO:0009191(ribonucleoside diphosphate catabolic process)|GO:0016020(membrane)|GO:0016021(integral to membrane)|GO:0016787(hydrolase activity)|GO:00171	Homo sapiens calcium activated nucleotidase 1 (CANT1), mRNA (NM_138793)	chr17:7450034 8-74500289
25	133.29	226.30	0.59	NM_005415	NM_005415	6574.00	SLC20A1	solute carrier family 20 (phosphate transporter), member 1	ENST00000272542	THC2468844	GO:0004872(receptor activity)|GO:0005315(inorganic phosphate transporter activity)|GO:0005436(sodium:phosphate symporter activity)|GO:0005615(extracellular space)|GO:0005887(integral to plasma membrane)|GO:0006796(phosphate metabolic process)|GO:0006810(t	Homo sapiens solute carrier family 20 (phosphate transporter), member 1 (SLC20A1), mRNA (NM_005415)	chr2:113134477 4-113134533
26	282.25	470.23	0.60	NM_002908	NM_002908	5966.00	REL	v-rel reticuloendotheliosis viral oncogene homolog (avian)	ENST00000295025	THC2474586	GO:0001816(cytokine production)|GO:0003700(transcription factor activity)|GO:0004871(signal transducer activity)|GO:0005515(protein binding)|GO:0005634(nucleus)|GO:0006366(transcription from RNA polymerase II promoter)|GO:0043123(positive regulation of I-	Homo sapiens v-rel reticuloendotheliosis viral oncogene homolog (avian) (REL), mRNA (NM_002908)	chr2:61003100 -61003159
27	629.56	1028.17	0.61	NM_033297	NM_033297	91662.00	NLRP12	NLR family, pyrin domain containing 12	ENST00000358661	NP496202	GO:0000166(nucleotide binding)|GO:0005515(protein binding)|GO:0005524(ATP binding)|GO:0005737(cytoplasm)|GO:0006919(caspase activation)|GO:0007165(signal transduction)|GO:0008588(release of cytoplasmic sequestered NF-kappaB)|GO:0008656(caspase activator a	Homo sapiens NLR family, pyrin domain containing 12 (NLRP12), transcript variant 1, mRNA (NM_033297)	chr19:58999810 0-58999041
28	256.50	420.08	0.62	NM_009587	NM_009587	3965.00	LGALS9	lectin, galactoside-binding, soluble, 9 (galectin 9)	ENST00000313648	THC2621267	GO:0004871(signal transducer activity)|GO:0005529(sugar binding)|GO:0005534(galactose binding)|GO:0043123(positive regulation of I-kappaB kinase/NF-kappaB cascade)	Homo sapiens lectin, galactoside-binding, soluble, 9 (galectin 9) (LGALS9), transcript variant long, mRNA	chr17:2299858 5-23000047
29	289.33	469.44	0.62	NM_001077702	NM_0010777 02	57708.00	MIER1	mesoderm induction early response 1 homolog (Xenopus laevis)	ENST00000371016	NP1277585	GO:0003677(DNA binding)|GO:0004871(signal transducer activity)|GO:0005634(nucleus)|GO:0006350(transcription)|GO:0006355(regulation of transcription, DNA-dependent)|GO:0043123(positive regulation of I-kappaB kinase/NF-kappaB cascade)	Homo sapiens mesoderm induction early response 1 homolog (Xenopus laevis) (MIER1), transcript variant 4, mRNA (NM_001077702)	chr1:67197213 -67197967
30	1300.50	2109.32	0.62	NM_016479	NM_016479	51246.00	SCOTIN	scotin	ENST00000296444	NP11190917	GO:0003677(DNA binding)|GO:0004871(signal transducer activity)|GO:0043123(positive regulation of I-kappaB kinase/NF-kappaB cascade)	Homo sapiens scotin (SCOTIN), mRNA (NM_016479)	chr3:48485290 -48485231
31	74.21	119.05	0.62	NM_182919	NM_182919	148022.00	TICAM1	toll-like receptor adaptor molecule 1	ENST00000246244	THC2640280	GO:0004871(signal transducer activity)|GO:0004888(transmembrane receptor activity)|GO:0016020(membrane)|GO:0043123(positive regulation of I-kappaB kinase/NF-kappaB cascade)	Homo sapiens toll-like receptor adaptor molecule 1 (TICAM1), transcript variant 2, mRNA	chr19:4767695 -4767636
32	514.95	804.61	0.64	NM_016463	NM_016463	51523.00	CXXC5	CXXC finger 5	ENST00000328708	THC2507968	GO:0003677(DNA binding)|GO:0004871(signal transducer activity)|GO:0008270(zinc ion binding)|GO:0043123(positive regulation of I-kappaB kinase/NF-kappaB cascade)	Homo sapiens CXXC finger 5 (CXXC5), mRNA (NM_016463)	chr5:139040892 7-139040986

[0569]

表192　遺伝子セット8(No. 1-46:機能面で注目する遺伝子)

No	Cy5	Cy3	ratio	RefSeq Accession	Genbank Accession	Entrez Gene ID	Gene Symbol	Gene Name	Ensembl ID	TIGR ID	GO	Description	Genomic Coordinates
33	2398.17	3742.62	0.64	NM_003900	NM_003900	8878.00	SQSTM1	sequestosome 1	0.00	THC2565333	GO:0005515(protein binding)|GO:0005634(nucleus)|GO:0005829(cytosol)|GO:0006511(ubiquitin-dependent protein catabolic process)|GO:0006915(apoptosis)|GO:0006950(response to stress)|GO:0006955(immune response)|GO:0007242(intracellular signaling cascade)|GO:0	Homo sapiens sequestosome 1 (SQSTM1), mRNA [NM_003900]	chr5:179196315-179196374
34	113.62	176.39	0.64	NM_006355	NM_006355	10475.00	TRIM38	tripartite motif-containing 38	ENST00000349458	THC2493487	GO:0004871(signal transducer activity)|GO:0005515(protein binding)|GO:0005575(cellular_component)|GO:0005622(intracellular)|GO:0008270(zinc ion binding)|GO:0043123(positive regulation of I-kappaB kinase/NF-kappaB cascade)|GO:0046872(metal ion binding)	Homo sapiens tripartite motif-containing 38 (TRIM38), mRNA [NM_006355]	chr6:26081447-26091384
35	105.46	161.60	0.65	NM_014002	NM_014002	9641.00	IKBKE	inhibitor of kappa light polypeptide gene enhancer in B-cells, kinase epsilon	ENST00000367120	THC2462762	GO:0000166(nucleotide binding)|GO:0004704(NF-kappaB-inducing kinase activity)|GO:0004713(protein-tyrosine kinase activity)|GO:0004871(signal transducer activity)|GO:0005515(protein binding)|GO:0005524(ATP	Homo sapiens inhibitor of kappa light polypeptide gene enhancer in B-cells, kinase epsilon (IKBKE), mRNA [NM_014002]	chr1:204730783-204731631
36	721.02	1103.78	0.65	NM_000801	NM_000801	2280.00	FKBP1A	FK506 binding protein 1A, 12kDa	ENST00000381742	NP1401859	GO:0003755(peptidyl-prolyl cis-trans isomerase activity)|GO:0004872(receptor activity)|GO:0005515(protein binding)|GO:0006457(protein folding)|GO:0016853(isomerase activity)|GO:0043123(positive regulation of I-kappaB kinase/NF-kappaB cascade)	Homo sapiens FK506 binding protein 1A, 12kDa (FKBP1A), transcript variant 12B, mRNA [NM_000801]	chr20:1298146-1298087
37	1040.80	1579.76	0.66	NM_001456	NM_001456	2316.00	FLNA	filamin A, alpha (actin binding protein 280)	ENST00000344736	THC2570847	GO:0003779(actin binding)|GO:0004871(signal transducer activity)|GO:0005634(nucleus)|GO:0005737(cytoplasm)|GO:0006928(cell motility)|GO:0007166(cell surface receptor linked signal transduction)|GO:0007399(nervous system development)|GO:0008134(transcripti	Homo sapiens filamin A, alpha (actin binding protein 280) (FLNA), mRNA [NM_001456]	chrX:153231748-153231689
38	1808.56	2741.64	0.66	NM_080738	NM_080738	128178.00	EDARADD	EDAR-associated death domain	ENST00000334232	THC2477869	GO:0005123(death receptor binding)|GO:0005515(protein binding)|GO:0005737(cytoplasm)|GO:0007165(signal transduction)|GO:0007249(I-kappaB kinase/NF-kappaB cascade)|GO:0030154(cell differentiation)	Homo sapiens EDAR-associated death domain (EDARADD), transcript variant B, mRNA [NM_080738]	chr1:234714174-234714233

[表193]

表193 遺伝子セット8(No.1~46:機能面で注目する遺伝子)

No	Cy5	Cy3	ratio	RefSeq Accession	Genbank Accession	Entrez Gene ID	Gene Symbol	Gene Name	Ensembl ID	TIGR ID	GO	Description	Genomic Coordinates
39	31.19	49.49	0.63	NM_000405	NM_000405	2760.00	GM2A	GM2 ganglioside activator	ENST00000357164	THC2469568	GO:0004563|beta-N-acetylhexosaminidase activity|GO:0005615|extracellular space|GO:0005739|mitochondrion|GO:0005764|lysosome|GO:0006687|glycosphingolipid metabolic process|GO:0006689|ganglioside catabolic process|GO:0007611|learning and/or memory|GO	Homo sapiens GM2 ganglioside activator (GM2A), mRNA [NM_000405]	chr5:150627644-150627699
39	52.97	79.62	0.67	NM_000405	NM_000405	2760.00	GM2A	GM2 ganglioside activator	ENST00000357164	THC2560254	GO:0004563|beta-N-acetylhexosaminidase activity|GO:0005615|extracellular space|GO:0005739|mitochondrion|GO:0005764|lysosome|GO:0006687|glycosphingolipid metabolic process|GO:0006689|ganglioside catabolic process|GO:0007611|learning and/or memory|GO	Homo sapiens GM2 ganglioside activator (GM2A), mRNA [NM_000405]	chr5:150627462-150627527
40	479.29	730.95	0.66	S76980	S76980	3073.00	HEXA	hexosaminidase A (alpha polypeptide)	0.00	0.00	GO:0001501|skeletal development|GO:0004563|beta-N-acetylhexosaminidase activity|GO:0005764|lysosome|GO:0005975|carbohydrate metabolic process|GO:0006687|glycosphingolipid metabolic process|GO:0006689|ganglioside catabolic	HEXA [HEXA4bpDeltaA mutation, exon 11] [human, Tay-Sachs disease patient, mRNA Partial Mutant, 78 nt]. [S76980]	chr15:70704259-70725923

[表194]

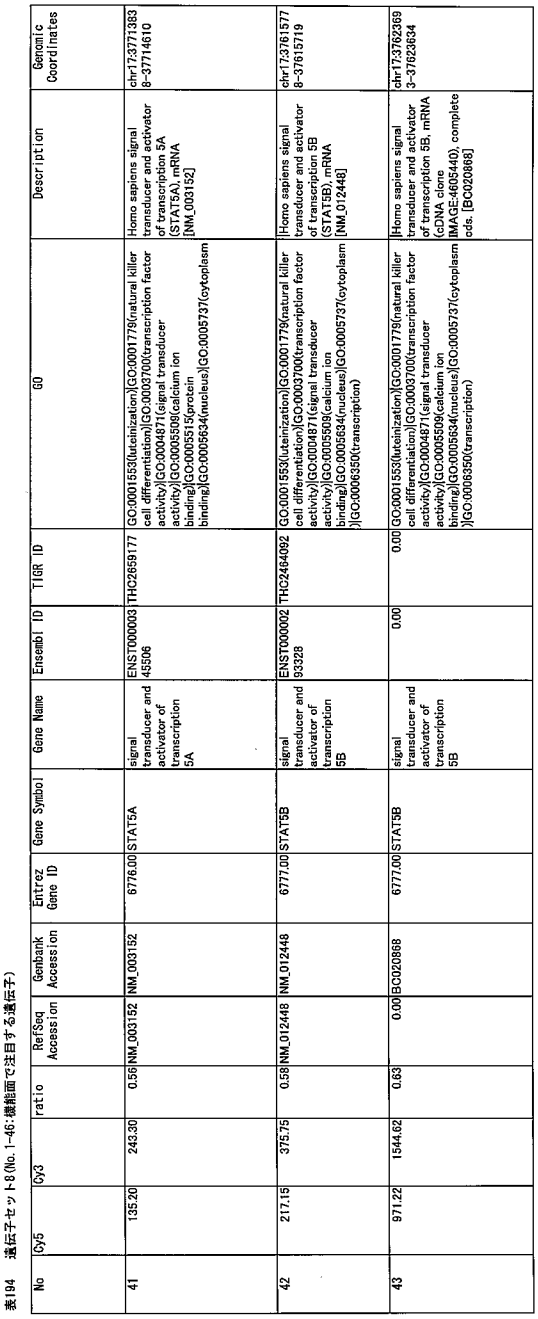


表194 遺伝子セット8(No.1~46:濃縮面で注目する遺伝子)

No	Cy5	Cy3	ratio	RefSeq Accession	Genbank Accession	Entrez Gene ID	Gene Symbol	Gene Name	Ensembl ID	TIGR ID	GO	Description	Genomic Coordinates
41	135.20	243.30	0.56	NM_003152	NM_003152	6776.00	STAT5A	signal transducer and activator of transcription 5A	ENST00000346506	THC2659177	GO:0001553(luteinization)|GO:0001779(natural killer cell differentiation)|GO:0003700(transcription factor activity)|GO:0004871(signal transducer activity)|GO:0005509(calcium ion binding)|GO:0005515(protein binding)|GO:0005634(nucleus)|GO:0005737(cytoplasm	Homo sapiens signal transducer and activator of transcription 5A (STAT5A), mRNA [NM_003152]	chr17:37713838-37714610
42	217.15	375.75	0.58	NM_012448	NM_012448	6777.00	STAT5B	signal transducer and activator of transcription 5B	ENST00000293328	THC2464092	GO:0001553(luteinization)|GO:0001779(natural killer cell differentiation)|GO:0003700(transcription factor activity)|GO:0004871(signal transducer activity)|GO:0005509(calcium ion binding)|GO:0005634(nucleus)|GO:0005737(cytoplasm)|GO:0006350(transcription)	Homo sapiens signal transducer and activator of transcription 5B (STAT5B), mRNA [NM_012448]	chr17:37615771-37615719
43	971.22	1544.62	0.63	0.00	BC020868	6777.00	STAT5B	signal transducer and activator of transcription 5B	0.00	0.00	GO:0001553(luteinization)|GO:0001779(natural killer cell differentiation)|GO:0003700(transcription factor activity)|GO:0004871(signal transducer activity)|GO:0005509(calcium ion binding)|GO:0005634(nucleus)|GO:0005737(cytoplasm)|GO:0006350(transcription)	Homo sapiens signal transducer and activator of transcription 5B, mRNA (cDNA clone IMAGE:4605440), complete cds. [BC020868]	chr17:37762369-37823634

[表195]

表195 遺伝子セット8(No.1-46:横断面で注目する遺伝子)

No	Cy5	Cy3	ratio	RefSeq Accession	Genbank Accession	Entrez Gene ID	Gene Symbol	Gene Name	Ensembl ID	TIGR ID	GO	Description	Genomic Coordinates
44	71.10	158.28	0.45	NM_004737	NM_004737	9215.00	LARGE	like-glycosyltransferase	ENST00000354992	NP1400257	GO:0006044(N-acetylglucosamine metabolic process)|GO:0006486(protein amino acid glycosylation)|GO:0006688(glycosphingolipid biosynthetic process)|GO:0007268(synaptic transmission)|GO:0007605(sensory perception of sound)|GO:0008375(acetylglucosaminyltransf	Homo sapiens like-glycosyltransferase (LARGE), transcript variant 1, mRNA [NM_004737]	chr22:31998391-31999332
45	2691.21	5633.48	0.48	NM_001042465	NM_001042465	5660.00	PSAP	prosaposin (variant Gaucher disease and variant metachromatic leukodystrophy)	ENST00000357471	THC2569349	GO:0004098(cerebroside-sulfatase activity)|GO:0004336(galactosylceramidase activity)|GO:0004348(glucosylceramidase activity)|GO:0004557(alpha-galactosidase activity)|GO:0004565(beta-galactosidase activity)|GO:0004767(sphingomyelin phosphodiesterase activi	Homo sapiens prosaposin (variant Gaucher disease and variant metachromatic leukodystrophy) (PSAP), transcript variant 2, mRNA [NM_001042465]	chr10:73248926-73248854
45	9261.22	18426.84	0.50	NM_001042465	NM_001042465	5660.00	PSAP	prosaposin (variant Gaucher disease and variant metachromatic leukodystrophy)	ENST00000357471	THC2557296	GO:0004098(cerebroside-sulfatase activity)|GO:0004336(galactosylceramidase activity)|GO:0004348(glucosylceramidase activity)|GO:0004557(alpha-galactosidase activity)|GO:0004565(beta-galactosidase activity)|GO:0004767(sphingomyelin phosphodiesterase activi	Homo sapiens prosaposin (variant Gaucher disease and variant metachromatic leukodystrophy) (PSAP), transcript variant 2, mRNA [NM_001042465]	chr10:73247703-73246977
46	314.21	547.93	0.57	NM_001042432	NM_001042432	1201.00	CLN3	ceroid-lipofuscinosis, neuronal 3, juvenile (Batten, Spielmeyer-Vogt disease)	ENST00000360019	NP079302	GO:0000139(Golgi membrane)|GO:0001575(globoside metabolic process)|GO:0005624(membrane fraction)|GO:0005634(nucleus)|GO:0005737(cytoplasm)|GO:0005739(mitochondrion)|GO:0005764(lysosome)|GO:0005769(early endosome)|GO:0005783(endoplasmic reticulum)|GO:00057	Homo sapiens ceroid-lipofuscinosis, neuronal 3, juvenile (Batten, Spielmeyer-Vogt disease) (CLN3), transcript variant 1, mRNA [NM_001042432]	chr16:28406834-28406286
46	305.49	493.20	0.62	NM_001042432	NM_001042432	1201.00	CLN3	ceroid-lipofuscinosis, neuronal 3, juvenile (Batten, Spielmeyer-Vogt disease)	ENST00000360019	NP072643	GO:0000139(Golgi membrane)|GO:0001575(globoside metabolic process)|GO:0005624(membrane fraction)|GO:0005634(nucleus)|GO:0005737(cytoplasm)|GO:0005739(mitochondrion)|GO:0005764(lysosome)|GO:0005769(early endosome)|GO:0005783(endoplasmic reticulum)|GO:00057	Homo sapiens ceroid-lipofuscinosis, neuronal 3, juvenile (Batten, Spielmeyer-Vogt disease) (CLN3), transcript variant 1, mRNA [NM_001042432]	chr16:28401132-28401170

[表196]

表196 遺伝子セット8(No.47-76:発現増加・減少した遺伝子上位15個)

No	Cy5	Cy3	ratio	RefSeq Accession	Genbank Accession	Entrez Gene ID	Gene Symbol	Gene Name	Ensembl ID	TIGR ID	GO	Description	Genomic Coordinates
47	4048.0	1052.1	3.85	NM_001336	NM_001336	1522	CTSZ	cathepsin Z	ENST00000217131	THC2466332	GO:0004197(cysteine-type endopeptidase activity)|GO:0005615(extracellular space)|GO:0005764(lysosome)|GO:0005783(endoplasmic reticulum)|GO:0006508(proteolysis)|GO:0008234(cysteine-type peptidase activity)	Homo sapiens cathepsin Z (CTSZ), mRNA [NM_001336]	chr20:5700381 5-57003756
48	381.9	80.8	4.72	NM_017590	NM_017590	23264	ZC3H7B	zinc finger CCCH-type containing 7B	ENST00000352645	THC2465043	GO:0003676(nucleic acid binding)|GO:0005622(intracellular)|GO:0005634(nucleus)|GO:0008270(zinc ion binding)|GO:0046872(metal ion binding)	Homo sapiens zinc finger CCCH-type containing 7B (ZC3H7B), mRNA [NM_017590]	chr22:4008590 3-40085962
49	231.6	79.5	2.91	NM_021970	NM_021970	8649	MAP2K1IP1	mitogen-activated protein kinase kinase 1 interacting	ENST00000226522	THC2809212	GO:0005515(protein binding)|GO:0016020(membrane)	Homo sapiens mitogen-activated protein kinase kinase 1 interacting protein 1 (MAP2K1IP1), mRNA [NM_021970]	chr4:101022201 1-101022142
50	114.1	41.8	2.73	NM_020666	NM_020666	57396	CLK4	CDC-like kinase 4	ENST00000316308	THC2494262	GO:0000166(nucleotide binding)|GO:0004674(protein serine/threonine kinase activity)|GO:0004713(protein-tyrosine kinase activity)|GO:0005524(ATP binding)|GO:0005634(nucleus)|GO:0016740(transferase activity)|GO:0018108(peptidyl-tyrosine phosphorylation)|GO:0046777(protein amino acid autophosphorylation)	Homo sapiens CDC-like kinase 4 (CLK4), mRNA [NM_020666]	chr5:177972140-177972081
51	152.3	56.7	2.69	NM_001192	NM_001192	608	TNFRSF17	tumor necrosis factor receptor superfamily, member 17	ENST00000349243	NP093457	GO:0003674(molecular_function)|GO:0004872(receptor activity)|GO:0005515(protein binding)|GO:0005575(cellular_component)|GO:0005886(plasma membrane)|GO:0006955(immune response)|GO:0007165(signal transduction)|GO:0007275(multicellular organismal development)|GO:0008150(biological_process)|GO:0008283(cell proliferation)|GO:0016021(integral to membrane)|GO:0019735(antimicrobial humoral response (sensu the Vertebrata research community))	Homo sapiens tumor necrosis factor receptor superfamily, member 17 (TNFRSF17), mRNA [NM_001192]	chr16:1196926 9-11969328
52	233.2	90.0	2.59	NM_031296	NM_031296	83452	RAB33B	RAB33B, member RAS oncogene family	ENST00000305805	THC2501558	GO:0000166(nucleotide binding)|GO:0005525(GTP binding)|GO:0005794(Golgi apparatus)|GO:0007264(small GTPase mediated signal transduction)|GO:0015031(protein transport)	Homo sapiens RAB33B, member RAS oncogene family (RAB33B), mRNA [NM_031296]	chr4:140616382-140616421
53	721.7	280.0	2.58	NM_005573	NM_005573	4001	LMNB1	lamin B1	ENST00000261361	THC2657885	GO:0005198(structural molecule activity)|GO:0005634(nucleus)|GO:0005638(lamin filament)	Homo sapiens lamin B1 (LMNB1), mRNA [NM_005573]	chr5:126200382-126200441

[0570]

表196 遺伝子セット8(No.47-76:発現増加・減少した遺伝子上位15個)

No	Cy5	Cy3	ratio	RefSeq Accession	Genbank Accession	Entrez Gene ID	Gene Symbol	Gene Name	Ensembl ID	TIGR ID	GO	Description	Genomic Coordinates
54	369.1	144.9	2.55	NM_003566	NM_003566	8411	EEA1	early endosome antigen 1, 162kD		THC2471292	GO:0003676(nucleic acid binding)|GO:0005516(calmodulin binding)|GO:0005545(phosphatidylinositol binding)|GO:0005622(intracellular)|GO:0005524(membrane fraction)|GO:0005737(cytoplasm)|GO:0005769(early endosome)|GO:0005829(cytosol)|GO:0006906(vesicle fusion)|GO:0008270(zinc ion binding)|GO:0016189(synaptic vesicle to endosome fusion)|GO:0018897(extrinsic to plasma membrane)|GO:0030742(GTP-dependent protein binding)|GO:0042803(protein homodimerization activity)|GO:0045022(early endosome to late endosome transport)|GO:0046872(metal ion binding)	Homo sapiens early endosome antigen 1, 162kD (EEA1), mRNA [NM_003566]	chr1:29169065 2-91690593
55	178.4	72.9	2.45	NM_015387	NM_015387	25843	PREI3	preimplantation protein 3	ENST00000323303	THC2499735	GO:0006810(transport)|GO:0008270(zinc ion binding)|GO:0016020(membrane)|GO:0046872(metal ion binding)	Homo sapiens preimplantation protein 3 (PREI3), transcript variant 1, mRNA [NM_015387]	chr2:198123278 -198123337
56	150.4	61.8	2.43	NM_014739	NM_014739	9774	BCLAF1	BCL2-associated transcription factor 1		THC2503556	GO:0003677(DNA binding)|GO:0005515(protein binding)|GO:0005634(nucleus)|GO:0006350(transcription)|GO:0006355(regulation of transcription, DNA-dependent)|GO:0006917(induction of apoptosis)|GO:0016481(negative regulation of transcription)|GO:0016564(transcriptional repressor activity)	Homo sapiens BCL2-associated transcription factor 1 (BCLAF1), transcript variant 1, mRNA [NM_014739]	chr6:136620254 -136620195
57	194.4	80.0	2.43	NM_006948	NM_006948	6782	STCH	stress 70 protein chaperone, microsome-associated, 60kDa	ENST00000285667	THC2469197	GO:0000166(nucleotide binding)|GO:0005524(ATP binding)|GO:0005615(extracellular space)|GO:0005783(endoplasmic reticulum)|GO:0005792(microsome)	Homo sapiens stress 70 protein chaperone, microsome-associated, 60kDa (STCH), mRNA [NM_006948]	chr21:14665502 -14665447
58	98.8	41.0	2.41		QR603697	6921	TCEB1	transcription elongation factor B (SIII), polypeptide 1 (15kDa, elongin C)	ENST00000284811	THC2513033	GO:0003711(transcriptional elongation regulator activity)|GO:0005515(protein binding)|GO:0005634(nucleus)|GO:0006350(transcription)|GO:0006357(regulation of transcription from RNA polymerase II promoter)|GO:0006512(ubiquitin cycle)	Transcription elongation factor B polypeptide 1 (RNA polymerase II transcription factor SIII subunit C) (SIII p15) (Elongin-C) (EloC) (Elongin 15 kDa subunit). [Source:Uniprot/SWISSPROT;Acc:Q15369] OT:Acc:Q15369] [ENST00000284811]	chr8:75020713 -75020654

[0571]

表196　遺伝子セット8(No. 47-76:発現増加・減少した遺伝子上位15個)

No	Cy5	Cy3	ratio	RefSeq Accession	Genbank Accession	Entrez Gene ID	Gene Symbol	Gene Name	Ensembl ID	TIGR ID	GO	Description	Genomic Coordinates
59	2471.9	1061.4	2.33	NM_003111	NM_003111	6670	SP3	Sp3 transcription factor	ENST00000310015	THC2466406	GO:0001779(natural killer cell differentiation)|GO:0003676(nucleic acid binding)|GO:0003682(chromatin binding)|GO:0003690(double-stranded DNA binding)|GO:0003700(transcription factor activity)|GO:0005515(protein binding)|GO:0005622(intracellular)|GO:0005634(nucleus)|GO:0006350(transcription)|GO:0006355(regulation of transcription, DNA-dependent)|GO:0008270(zinc ion binding)|GO:0016563(transcriptional activator activity)|GO:0016564(transcriptional repressor activity)|GO:0030183(B cell differentiation)|GO:0030217(T cell differentiation)|GO:0030218(erythrocyte differentiation)|GO:0030224(monocyte differentiation)|GO:0030851(granulocyte differentiation)|GO:0046872(metal ion binding)	Homo sapiens Sp3 transcription factor (SP3), transcript variant 1, mRNA [NM_003111]	chr2:174481596-174481537
60	166.0	71.4	2.32	NM_000963	NM_000963	5743	PTGS2	prostaglandin-endoperoxide synthase 2 (prostaglandin G/H synthase and cyclooxygenase)	ENST00000367468	NP097723	GO:0001516(prostaglandin biosynthetic process)|GO:0004601(peroxidase activity)|GO:0004666(prostaglandin-endoperoxide synthase activity)|GO:0005506(iron ion binding)|GO:0005615(extracellular space)|GO:0005634(nucleus)|GO:0005737(cytoplasm)|GO:0006633(fatty acid biosynthetic process)|GO:0006928(cell motility)|GO:0008217(blood pressure regulation)|GO:0016020(membrane)|GO:0016491(oxidoreductase activity)|GO:0016702(oxidoreductase activity, acting on single donors with incorporation of molecular oxygen, incorporation of two atoms of oxygen)|GO:0019371(cyclooxygenase pathway)|GO:0030216(keratinocyte differentiation)|GO:0042640(anagen)|GO:0046872(metal ion binding)|GO:0050727(regulation of inflammatory response)	Homo sapiens prostaglandin-endoperoxide synthase 2 (prostaglandin G/H synthase and cyclooxygenase) (PTGS2), mRNA [NM_000963]	chr1:184909789-184909731
61	233.0	102.1	2.28	NM_021252	NM_021252	22931	RAB18	RAB18, member RAS oncogene family	ENST00000356940	THC2778145	GO:0000166(nucleotide binding)|GO:0003924(GTPase activity)|GO:0005524(ATP binding)|GO:0005525(GTP binding)|GO:0005575(cellular_component)|GO:0005622(intracellular)|GO:0006355(regulation of transcription, DNA-dependent)|GO:0006897(endocytosis)|GO:0007264(small GTPase mediated signal transduction)|GO:0008134(transcription factor binding)|GO:0015031(protein transport)|GO:0016020(membrane)	Homo sapiens RAB18, member RAS oncogene family (RAB18), mRNA [NM_021252]	chr10:27868390-27868439

[表197]

表197 遺伝子セット8(No. 47-76:発現増加・減少した遺伝子上位15個)

No	Cy5	Cy3	ratio	RefSeq Accession	Genbank Accession	Entrez Gene ID	Gene Symbol	Gene Name	Ensembl ID	TIGR ID	GO	Description	Genomic Coordinates
62	29.0	698.3	0.04	NM_178569	NM_178569	153571	CEI	coordinated expression to IRXA2 homeobox gene	ENST00000334000	THC2484018	GO:0003677(DNA binding)	Homo sapiens coordinated expression to IRXA2 homeobox gene (CEI), mRNA [NM_178569]	chr5:2805741-2805800
63	56.7	529.2	0.11	NM_007110	NM_007110	7011	TEP1	telomerase-associated protein 1	ENST00000282715	NP1473063	GO:0000166(nucleotide binding)|GO:0000722(telomere maintenance via recombination)|GO:0000781(chromosome, telomeric region)|GO:0003720(telomerase activity)|GO:0003723(RNA binding)|GO:0005524(ATP binding)|GO:0005625(soluble fraction)|GO:0005634(nucleus)|GO:0005694(chromosome)|GO:0005697(telomerase holoenzyme complex)|GO:0005737(cytoplasm)|GO:0007004(telomere maintenance via telomerase)|GO:0016363(nuclear matrix)	Homo sapiens telomerase-associated protein 1 (TEP1), mRNA [NM_007110]	chr14:1990599 8-19905939
64	92.1	549.8	0.17	NM_207585	NM_207585	3455	IFNAR2	interferon (alpha, beta and omega) receptor 2	ENST00000318433	THC2464141	GO:0004872(receptor activity)|GO:0004896(hematopoietin/interferon-class (D200-domain) cytokine receptor activity)|GO:0004905(interferon-alpha/beta receptor activity)|GO:0005515(protein binding)|GO:0005576(extracellular region)|GO:0005615(extracellular space)|GO:0005886(plasma membrane)|GO:0008285(cell proliferation)|GO:0008283(cell surface receptor linked signal transduction)|GO:0007259(JAK-STAT cascade)|GO:0019221(cytokine mediated signaling pathway)|GO:0019079(viral genome replication)|GO:0042742(defense response to bacterium)|GO:0045087(innate immune response)|GO:0046596(regulation of viral entry into host cell)|GO:0050688(regulation of viral reproduction)|GO:0050727(regulation of inflammatory response)|GO:0050776(regulation of immune response)|GO:0050830(defense response to gram-positive bacterium)|GO:0051607(defense response to virus)	Homo sapiens interferon (alpha, beta and omega) receptor 2 (IFNAR2), transcript variant 1, mRNA [NM_207585]	chr21:3355783 9-33557898
65	43.0	253.6	0.17	NM_001322	NM_001322	1470	CST2	cystatin SA	ENST00000304725	THC2477714	GO:0004869(cysteine protease inhibitor activity)	Homo sapiens cystatin SA (CST2), mRNA [NM_001322]	chr20:2375516 2-23755103
66	161.9	951.6	0.17	NM_015071	NM_015071	23092	ARHGAP26	Rho GTPase activating protein 26	ENST00000378013	THC2495953	GO:0005096(GTPase activator activity)|GO:0005100(Rho GTPase activator activity)|GO:0005575(cellular_component)|GO:0005622(intracellular)|GO:0007165(signal transduction)|GO:0007399(nervous system development)|GO:0030036(actin cytoskeleton organization and biogenesis)	Homo sapiens Rho GTPase activating protein 26 (ARHGAP26), mRNA [NM_015071]	chr5:142565827-142565886
67	28.2	165.6	0.17	NM_001703	NM_001703	576	BAI2	brain-specific angiogenesis inhibitor 2	ENST00000357070	THC2462908	GO:0004872(receptor activity)|GO:0004930(G-protein coupled receptor activity)|GO:0007165(signal transduction)|GO:0007216(neuropeptide signaling pathway)|GO:0016020(membrane)|GO:0016021(integral to membrane)|GO:0016527(brain-specific angiogenesis inhibitor activity)	Homo sapiens brain-specific angiogenesis inhibitor 2 (BAI2), mRNA [NM_001703]	chr1:319655777-31965518

[0572]

表197 遺伝子セット8(No. 47-76:発現増加・減少した遺伝子上位15個)

No	Cy5	Cy3	ratio	RefSeq Accession	Genbank Accession	Entrez Gene ID	Gene Symbol	Gene Name	Ensembl ID	TIGR ID	GO	Description	Genomic Coordinates
68	193.9	864.7	0.22	NM_006505	NM_006505	5817	PVR	poliovirus receptor	ENST00000187830	THC2731504	GO:0004872(receptor activity)|GO:0005515(protein binding)|GO:0005615(extracellular space)|GO:0005737(cytoplasm)|GO:0016020(membrane)|GO:0016021(integral to membrane)|GO:0016337(cell-cell adhesion)|GO:0016477(cell migration)	Homo sapiens poliovirus receptor (PVR), mRNA [NM_006505]	chr19:4985393 8-49853997
69	18.0	73.9	0.24		AK027509	9329	GTF3C4	general transcription factor IIIC, polypeptide 4, 90kDa	ENST00000372146	THC2502425	GO:0000127(transcription factor TFIIIC complex)|GO:0003677(DNA binding)|GO:0003709(RNA polymerase III transcription factor activity)|GO:0004402(H3/H4 histone acetyltransferase activity)|GO:0005634(nucleus)|GO:0006350(transcription)|GO:0006384(transcription initiation from RNA polymerase III promoter)|GO:0008047(enzyme activator activity)|GO:0008415(acyltransferase activity)|GO:0016740(transferase activity)	General transcription factor IIIC (Transcription factor IIIC subunit delta) (TF3C-delta) (TFIIIC 90 kDa subunit) (TFIIIC 90). [Source:Uniprot/SWISSPROT:Acc:Q9UKN8] [ENST00000372146]	chr9:134554478 9-134554648
70	32.7	133.9	0.24	NM_018534	NM_018534	8828	NRP2	neuropilin 2	ENST00000272849	THC2488330	GO:0001525(angiogenesis)|GO:0004872(receptor activity)|GO:0005021(vascular endothelial growth factor receptor activity)|GO:0005515(protein binding)|GO:0005615(extracellular space)|GO:0005624(membrane fraction)|GO:0005886(plasma membrane)|GO:0007155(cell adhesion)|GO:0007399(nervous system development)|GO:0007411(axon guidance)|GO:0007507(heart development)|GO:0008095(electron carrier activity)|GO:0015035(protein disulfide oxidoreductase activity)|GO:0016020(membrane)|GO:0016021(integral to membrane)|GO:0017154(semaphorin receptor activity)|GO:0030154(cell differentiation)|GO:0045454(cell redox homeostasis)	Homo sapiens neuropilin 2 (NRP2), transcript variant 4, mRNA [NM_018534]	chr2:206949967 6-206349735
71	516.6	2099.7	0.25	NR_002819	NR_002819	378338	MALAT1	metastasis associated lung adenocarcinoma transcript 1 (non-coding RNA)		THC2590215		Homo sapiens metastasis associated lung adenocarcinoma transcript 1 (non-coding RNA) (MALAT1) on chromosome 11 [NR_002819]	chr11:65029944 9-65029508
72	29.8	119.7	0.25	NM_001541	NM_001541	3316	HSPB2	heat shock 27kDa protein 2	ENST00000304298	THC2649717	GO:0005515(protein binding)|GO:0005625(soluble fraction)|GO:0005829(cytosol)|GO:0006457(protein folding)|GO:0006986(response to unfolded protein)|GO:0007525(somatic muscle development)|GO:0008047(enzyme activator activity)	Homo sapiens heat shock 27kDa protein 2 (HSPB2), mRNA [NM_001541]	chr11:111128991 51-111129010
73	25.9	96.7	0.27	NR_001458	NR_001458	114614	BIC	BIC transcript		THC2733832		Homo sapiens BIC transcript (BIC) on chromosome 21 [NR_001458]	chr21:25868822 1-25868280

[0573]

表197 遺伝子セット8(No. 47-76:発現増加・減少した遺伝子上位15個)

No	Cy5	Cy3	ratio	RefSeq Accession	Genbank Accession	Entrez Gene ID	Gene Symbol	Gene Name	Ensembl ID	TIGR ID	GO	Description	Genomic Coordinates
74	562.9	1146.1	0.49	NM_000308	NM_000308	5476	CTSA	cathepsin A	ENST00000354880	THC2535850	GO:0004185(serine carboxypeptidase activity)|GO:0004186(carboxypeptidase C activity)|GO:0005478(intracellular transporter activity)|GO:0005615(protein binding)|GO:0005739(mitochondrion)|GO:0005764(lysosome)|GO:0005783(endoplasmic reticulum)|GO:0006508(proteolysis)|GO:0006886(intracellular protein transport)|GO:0008047(enzyme activator activity)|GO:0008233(peptidase activity)	Homo sapiens cathepsin A (CTSA), mRNA [NM_000308]	chr20:43959763-43959822
75	1521.1	3033.7	0.50	NM_147780	NM_147780	1508	CTSB	cathepsin B	ENST00000353047	THC2501660	GO:0004197(cysteine-type endopeptidase activity)|GO:0004213(cathepsin B activity)|GO:0004601(peroxidase activity)|GO:0005515(protein binding)|GO:0005622(intracellular)|GO:0005739(mitochondrion)|GO:0005764(lysosome)|GO:0006508(proteolysis)|GO:0006979(response to oxidative stress)|GO:0042981(regulation of apoptosis)|GO:0050790(regulation of catalytic activity)	Homo sapiens cathepsin B (CTSB), transcript variant 2, mRNA [NM_147780]	chr8:11742632-11742063
76	359.7	787.9	0.46	NM_001557	NM_001557	3579	IL8RB	interleukin 8 receptor, beta	ENST00000318507	NP096327	GO:0001584(rhodopsin-like receptor activity)|GO:0004872(receptor activity)|GO:0004918(interleukin-8 receptor activity)|GO:0005622(intracellular)|GO:0005887(integral to plasma membrane)|GO:0006935(chemotaxis)|GO:0006954(inflammatory response)|GO:0006968(cellular defense response)|GO:0007200(G-protein signaling, coupled to IP3 second messenger (phospholipase C activating))|GO:0009284(positive regulation of cell proliferation)|GO:0009986(cell surface)|GO:0016020(membrane)|GO:0030593(neutrophil chemotaxis)|GO:0042119(neutrophil activation)|GO:0042629(mast cell granule)	Homo sapiens interleukin 8 receptor, beta (IL8RB), mRNA [NM_001557]	chr2:218707757-218707814

[表198]

表198　遺伝子セット8(No.1-46:機能面で注目する遺伝子,No.47-76:発現増加・減少した遺伝子上位15個)

No	Target(Gene)Symbol	Target Accession	UniGene	Up/Down	被験者群	配列番号
1	HLA-C	XR_015693	Hs.77961	Down	B+D	-
2	HLA-H	NR_001434	Hs.181244	Down	B+D	245
3	HLA-A	NM_002116	Hs.181244	Down	B+D	246
4	IGHG1	BC092518	Hs.510635	Down	B+D	-
5	HLA-E	NM_005516	Hs.118354	Down	B+D	247
6	HLA-B	CR608347	Hs.77961	Down	B+D	-
7	CD1D	NM_001766	Hs.1799	Down	B+D	108
8	FLJ45422	NM_001004349	Hs.591791	Down	B+D	248
9	HLA-F	NM_018950	Hs.519972	Down	B+D	249
10	LOC649853	0	Hs.181244	Down	B+D	-
11	HLA-B	NM_005514	Hs.77961	Down	B+D	250
12	CD74	NM_001025158	Hs.436568	Down	B+D	251
13	AP3B1	NM_003664	Hs.532091	Down	B+D	252
14	VISA		Hs.646283	Down	B+D	-
15	CASP8	NM_033355	Hs.591630	Down	B+D	253
16	NDFIP1	NM_030571	Hs.9788	Down	B+D	254
17	CFLAR	NM_003879	Hs.390736	Down	B+D	255
18	SECTM1	NM_003004	Hs.558009	Down	B+D	256
19	APOL3	NM_145641	Hs.474737	Down	B+D	257
20	LTBR	NM_002342	Hs.1116	Down	B+D	258
21	C1orf166	NM_024544	Hs.10101	Down	B+D	-
22	MYD88	NM_002468	Hs.82116	Down	B+D	259
23	TRIM38	NM_006355	Hs.584851	Down	B+D	260
24	CANT1	NM_138793	Hs.8859	Down	B+D	261
25	SLC20A1	NM_005415	Hs.187946	Down	B+D	262
26	REL	NM_002908	Hs.631886	Down	B+D	263
27	NLRP12	NM_033297	Hs.631573	Down	B+D	73
28	LGALS9	NM_009587	Hs.81337	Down	B+D	264
29	MIER1	NM_001077702	Hs.651300	Down	B+D	265
30	SCOTIN	NM_016479	Hs.414579	Down	B+D	-
31	TICAM1	NM_182919	Hs.29344	Down	B+D	266
32	CXXC5	NM_016463	Hs.189119	Down	B+D	267
33	SQSTM1	NM_003900	Hs.437277	Down	B+D	268
34	TRIM38	NM_006355	Hs.584851	Down	B+D	260
35	IKBKE	NM_014002	Hs.321045	Down	B+D	269
36	FKBP1A	NM_000801	Hs.471933	Down	B+D	270
37	FLNA	NM_001456	Hs.195464	Down	B+D	271
38	EDARADD	NM_080738	Hs.352224	Down	B+D	272
39	GM2A	NM_000405	Hs.483873	Down	B+D	273
40	HEXA	S76980		Down	B+D	-
41	STAT5A	NM_003152	Hs.437058	Down	B+D	56
42	STAT5B	NM_012448	Hs.632256	Down	B+D	274
43	STAT5B	BC020868	Hs.632256	Down	B+D	-
44	LARGE	NM_004737	Hs.474667	Down	B+D	275
45	PSAP	NM_001042465	Hs.523004	Down	B+D	65
46	CLN3	NM_001042432	Hs.628393	Down	B+D	174
47	CTSZ	NM_001336	Hs.252549	Up	B+D	145
48	ZC3H7B	NM_017590	Hs.592188	Up	B+D	276
49	MAP2K1IP1	NM_021970	Hs.647988	Up	B+D	-
50	CLK4	NM_020666	Hs.406557	Up	B+D	277
51	TNFRSF17	NM_001192	Hs.2556	Up	B+D	278
52	RAB33B	NM_031296	Hs.591679	Up	B+D	152
53	LMNB1	NM_005573	Hs.89497	Up	B+D	139
54	EEA1	NM_003566	Hs.567367	Up	B+D	150
55	PREI3	NM_015387	Hs.645458	Up	B+D	-
56	BCLAF1	NM_014739		Up	B+D	29
57	STCH	NM_006948	Hs.352341	Up	B+D	-
58	TCEB1		Hs.554594	Up	B+D	-
59	SP3	NM_003111	Hs.531587	Up	B+D	279
60	PTGS2	NM_000963	Hs.196384	Up	B+D	149

[0574]

表198　遺伝子セット8(No.1-46:機能面で注目する遺伝子,No.47-76:発現増加・減少した遺伝子上位15個)

No	Target(Gene)Symbol	Target Accession	UniGene	Up/Down	被験者群	配列番号
61	RAB18	NM_021252	Hs.406799	Up	B+D	280
62	CEI	NM_178569	Hs.148486	Down	B+D	-
63	TEP1	NM_007110	Hs.508835	Down	B+D	91
64	IFNAR2	NM_207585	Hs.642682	Down	B+D	161
65	CST2	NM_001322	Hs.123114	Down	B+D	281
66	ARHGAP26	NM_015071	Hs.293593	Down	B+D	93
67	BAI2	NM_001703	Hs.524138	Down	B+D	102
68	PVR	NM_006505	Hs.171844	Down	B+D	282
69	GTF3C4		Hs.22302	Down	B+D	-
70	NRP2	NM_018534	Hs.471200	Down	B+D	283
71	MALAT1	NR_002819	Hs.621695	Down	B+D	284
72	HSPB2	NM_001541	Hs.78846	Down	B+D	285
73	BIC	NR_001458	Hs.388313	Down	B+D	-
74	CTSA	NM_000308	Hs.517076	Down	B+D	286
75	CTSB	NM_147780	Hs.520898	Down	B+D	287
76	IL8RB	NM_001557	Hs.846	Down	B+D	288

[0575] 4-2. 陽性刺激で発現変化するラット／ヒト間で共通する遺伝子（群）の特定

4-2-1. 解析法

ラットを対象とした陽性刺激モデル実験・短期刺激(上記2-2)時と、ヒトを対象とした「笑いと健康Part4」の末梢血液における遺伝子発現解析で得られたデータの比較解析を行った。

[0576] 4-2-2. 結果・考察

解析2、4～10において、ラット短期陽性刺激(Tickling刺激)負荷時と同方向に発現変化した遺伝子（1.5倍以上、1/1.5倍以下）、逆方向に発現変化した遺伝子（1.5倍以上、1/1.5倍以下）を表199に示す。

[表199]

表199　陽性感情で発現変動するラット/ヒト間で共通する遺伝子

	ヒトGene Symbol	N-2	N-1	ratio	Rat Gene Symbol	cy5	cy3	ratio
解析2up	RPL23	16386.30	5506.08	2.98	Rpl23	129.42	79.43	1.63
	ARID4B	471.51	301.76	1.56	Arid4b	27.58	16.12	1.71
	S100A8	30075.0	18294.3	1.64	S100a8	786.71	409.73	1.92
	IFI44	2745.4	1761.1	1.56	Ifi44	265.55	166.09	1.60
	SUB1	799.0	353.8	2.26	Sub1	1700.59	1069.50	1.59
	ROCK1	98.2	50.8	1.93	Rock1	904.30	559.77	1.62
	RPL26	6683.7	2329.7	2.87	Rpl26	16552.66	9435.60	1.75
	RPL23	6103.5	1873.3	3.26	Rpl23	23600.16	13156.17	1.79
	ECHDC1	1809.0	1152.3	1.57	Echdc1	46.40	29.76	1.56
	IFIT2	1078.0	662.2	1.63	Ifit2	69.01	37.15	1.86
解析2down	MAOA	20.1	39.2	0.51	Maoa	9.45	15.83	0.60
	C1S	43.1	66.2	0.65	C1s	20.86	33.68	0.62
	MUC5AC	55.0	90.3	0.61	Muc5ac	29.62	50.22	0.59
	STX11	1314.4	2090.7	0.63	Stx11	9.63	17.22	0.56
	FUS	1774.8	2681.0	0.66	Fus	20.85	13.91	1.50
	DGAT2	1288.8	2062.8	0.62	Dgat2	37.74	23.83	1.58
	PHC2	1484.1	2805.7	0.53	Phc2	20.34	30.73	0.66
	AP2A2	107.6	181.0	0.59	Ap2a2	9.27	14.15	0.66
解析4up	CPA3	107.0	70.0	1.53	Cpa3	29.69	59.29	0.50
	PTPRO	87.2	51.0	1.71	Ptpro	80.06	49.51	1.62
解析4down	MAS1	21.1	227.5	0.09	Mas1	11.34	18.09	0.63
	CCR1	47.7	86.9	0.55	Ccr1	23.79	13.91	1.71
解析5down	CLCC1	27.0	53.0	0.51	Clcc1	28.92	18.99	1.52
	MAOA	23.8	42.5	0.56	Maoa	9.45	15.83	0.60
	RNF138	21.6	48.9	0.44	Rnf138	8.80	14.47	0.61
	ROCK1	63.3	100.4	0.63	Rock1	904.30	559.77	1.62
	PLK1	20.6	47.5	0.43	Plk1	63.56	98.86	0.64
	ELK1	24.6	49.4	0.50	Elk1	10.17	17.33	0.59
解析6up	RPL23	5485.4	1150.9	4.77	Rpl23	23600.16	13156.17	1.79
	ARID4B	344.5	186.6	1.85	Arid4b	27.58	16.12	1.71
	S100A8	29074.0	10991.9	2.65	S100a8	786.71	409.73	1.92
	IFI44	3120.6	1927.2	1.62	Ifi44	265.55	166.09	1.60
	ANXA1	3990.1	2469.5	1.62	Anxa1	748.06	429.08	1.74
	SUB1	552.4	163.8	3.37	Sub1	1700.59	1069.50	1.59
	RPL26	7532.1	1972.9	3.82	Rpl26	16552.66	9435.60	1.75
	ECHDC1	1495.5	866.3	1.73	Echdc1	46.40	29.76	1.56
	MATR3	364.7	203.2	1.79	Matr3	841.99	556.05	1.51
	RNF138	702.7	425.7	1.65	Rnf138	8.80	14.47	0.61
解析6down	CCR1	47.7	106.9	0.45	Ccr1	23.79	13.91	1.71
	PHC2	1127.6	2155.8	0.52	Phc2	20.34	30.73	0.66
	PSEN1	169.4	276.5	0.61	Psen1	14.18	26.54	0.53
	PTPRO	25.7	117.0	0.22	Ptpro	80.06	49.51	1.62
	QTRT1	152.5	261.9	0.58	Qtrt1	49.18	74.73	0.66
	ROCK1	62.1	113.9	0.55	Rock1	904.30	559.77	1.62
	STX11	1198.9	2004.5	0.60	Stx11	9.63	17.22	0.56
解析7up	PRSS21	64.6	42.0	1.54	Prss21	35.98	55.91	0.64
	PTPRO	76.1	49.5	1.54	Ptpro	80.06	49.51	1.62
	RNF138	687.8	457.4	1.50	Rnf138	8.80	14.47	0.61
解析7down	PHC2	1121.5	1856.5	0.60	Phc2	20.34	30.73	0.66
	ST6GALNAC3	29.1	46.7	0.62	St6galnac3	13.43	24.22	0.55
解析8up	ARID4B	311.3	202.0	1.54	Arid4b	27.58	16.12	1.71
	BHLHB3	50.0	31.8	1.57	Bhlhb3	13.83	21.98	0.63
	PTPRO	92.5	52.3	1.77	Ptpro	80.06	49.51	1.62
	RNF138	649.9	402.0	1.62	Rnf138	8.80	14.47	0.61
	SYNCRIP	121.1	75.4	1.61	Syncrip	24.19	15.64	1.55
解析8down	C1QTNF5	34.0	51.3	0.66	C1qtnf5	31.68	46.98	0.67
	CCR1	44.5	73.4	0.61	Ccr1	23.79	13.91	1.71
	DGAT2	1176.4	1845.4	0.64	Dgat2	37.74	23.83	1.58
	ELK1	33.3	54.3	0.61	Elk1	10.17	17.33	0.59
	LTBP1	45.9	69.4	0.66	Ltbp1	22.24	32.99	0.67
	PHC2	1460.4	2574.6	0.57	Phc2	20.34	30.73	0.66
	RLN3	21.6	34.8	0.62	Rln3	8.88	14.49	0.61

[0577]

	ヒトGene Symbol	N-2	N-1	ratio	Rat Gene Symbol	cy5	cy3	ratio
解析9up	SHMT1	65.9	43.3	1.52	Shmt1	35.93	20.07	1.79
	SLC30A2	57.5	37.9	1.52	Slc30a2	11.43	19.57	0.58
解析9down	C1S	42.6	71.2	0.60	C1s	20.86	33.68	0.62
解析10up	ANGPT1	121.7	65.3	1.86	Angpt1	11.21	19.59	0.57
	ARID4B	448.1	202.5	2.21	Arid4b	27.58	16.12	1.71
	CLK1	233.9	145.0	1.61	Clk1	1093.65	682.73	1.60
	ECHDC1	1643.8	856.3	1.92	Echdc1	46.40	29.76	1.56
	IFI44	1915.1	1161.4	1.65	Ifi44	265.55	166.09	1.60
	MATR3	448.5	212.9	2.11	Matr3	841.99	556.05	1.51
	MXRA8	91.9	53.2	1.73	Mxra8	9.55	18.88	0.51
	PTPRO	111.3	45.4	2.45	Ptpro	80.06	49.51	1.62
	RAB27B	94.0	56.8	1.66	Rab27b	18.22	28.79	0.63
	RNF138	874.1	442.1	1.98	Rnf138	8.80	14.47	0.61
	ROCK1	494.8	263.7	1.88	Rock1	904.30	559.77	1.62
	RPL23	5157.4	2629.0	1.96	Rpl23	23600.16	13156.17	1.79
	RPL26	4721.0	2472.5	1.91	Rpl26	16552.66	9435.60	1.75
	S100A8	31390.9	17120.2	1.83	S100a8	786.71	409.73	1.92
	SHMT1	122.8	75.9	1.62	Shmt1	35.93	20.07	1.79
	SLC40A1	1549.2	1025.1	1.51	Slc40a1	39.51	62.01	0.64
	SUB1	245.3	102.6	2.39	Sub1	1700.59	1069.50	1.59
	SYNCRIP	116.4	74.8	1.56	Syncrip	24.19	15.64	1.55
	ZNF291	115.9	54.4	2.13	Znf291	36.76	23.79	1.55
解析10down	AP2A2	419.0	702.5	0.60	Ap2a2	9.27	14.15	0.66
	BTBD9	24.2	58.8	0.41	Btbd9	13.20	25.88	0.51
	C1QA	62.8	126.2	0.50	C1qa	32.15	52.74	0.61
	CCR1	49.2	81.3	0.61	Ccr1	23.79	13.91	1.71
	COMT	801.2	1237.1	0.65	Comt	12.47	24.51	0.51
	DGAT2	741.4	1551.3	0.48	Dgat2	37.74	23.83	1.58
	FUS	1111.0	2096.9	0.53	Fus	20.85	13.91	1.50
	GMPR	1190.6	2129.0	0.56	Gmpr	51.10	82.49	0.62
	GNB1	1232.6	2072.7	0.59	Gnb1	11.12	17.83	0.62
	HYOU1	66.9	101.5	0.66	Hyou1	26.28	42.33	0.62
	IFIT3	1034.1	1695.9	0.61	Ifit3	48.65	23.81	2.04
	PHC2	1176.8	2549.9	0.46	Phc2	20.34	30.73	0.66
	QTRT1	46.2	145.4	0.32	Qtrt1	49.18	74.73	0.66
	RND2	67.4	187.8	0.36	Rnd2	72.62	116.09	0.63
	SFRS5	6593.9	10624.4	0.62	Sfrs5	311.64	195.57	1.59
	SHMT1	19.3	48.9	0.39	Shmt1	35.93	20.07	1.79
	STX11	948.7	1697.8	0.56	Stx11	9.63	17.22	0.56
	TMEM39A	119.0	229.9	0.52	Tmem39a	10.91	17.40	0.63

[0578] また表200及び201には、ラット短期陽性刺激(Tickling刺激)負荷時と同方向に発現変化したヒト遺伝子(ヒト共通遺伝子)40種のアノテーションを示し、表202にはその要約を示す。

[表200]

表200

No	Cy5	Cy3	ratio	RefSeq Accession	Genbank Accession	Entrez Gene ID	Gene Symbol	Gene Name	Ensembl ID	TIGR ID	GO	Description	Genomic Coordinates
1	3990.11	2469.51	1.62	NM_000700	NM_000700	301.00	ANXA1	annexin A1	ENST00000257497	THC2563662	GO:0001533(cornified envelope)|GO:0004858(phospholipase inhibitor activity)|GO:0005102(receptor binding)|GO:0005198(structural molecule activity)|GO:0005509(calcium ion binding)|GO:0005544(calcium-dependent phospholipid binding)|GO:0005737(cytoplasm)|GO:0	Homo sapiens annexin A1 (ANXA1), mRNA [NM_000700]	chr9:74974822 -74974881
2	448.10	202.50	2.21	NM_016374	NM_016374	51742.00	ARID4B	AT rich interactive domain 4B (RBP1-like)	ENST00000264183	THC2779546	GO:0000785(chromatin)|GO:0003674(molecular_function)|GO:0003676(nucleic acid binding)|GO:0003677(DNA binding)|GO:0003682(chromatin binding)|GO:0005575(cellular_component)|GO:0005622(intracellular)|GO:0005634(nucleus)|GO:0006333(chromatin assembly or diss	Homo sapiens AT rich interactive domain 4B (RBP1-like) (ARID4B), transcript variant 1, mRNA [NM_016374]	chr1:23339703 2-233396973
3	233.90	144.97	1.61	NM_004071	NM_004071	1195.00	CLK1	CDC-like kinase 1	ENST00000321356	NP1179542	GO:0000074(regulation of progression through cell cycle)|GO:0000166(nucleotide binding)|GO:0004674(protein serine/threonine kinase activity)|GO:0004715(non-membrane spanning protein tyrosine kinase activity)|GO:0005524(ATP binding)|GO:0005634(nucleus)|GO:	Homo sapiens CDC-like kinase 1 (CLK1), transcript variant 1, mRNA [NM_004071]	chr2:201143070 3-201429912
4	1643.79	856.31	1.92	NM_018479	NM_018479	55862.00	ECHDC1	enoyl Coenzyme A hydratase domain containing 1	ENST00000368293	THC2467942	GO:0003824(catalytic activity)|GO:0008152(metabolic process)	Homo sapiens enoyl Coenzyme A hydratase domain containing 1 (ECHDC1), mRNA [NM_018479]	chr6:12765164 7-127651588
5	1915.09	1161.41	1.65	NM_006417	NM_006417	10561.00	IFI44	interferon-induced protein 44	ENST00000370747	THC2515948	GO:0005737(cytoplasm)|GO:0009615(response to virus)	Homo sapiens interferon-induced protein 44 (IFI44), mRNA [NM_006417]	chr1:78901067 -78901126
6	1077.98	662.17	1.63	NM_001547	NM_001547	3433.00	IFIT2	interferon-induced protein with tetratricopeptide repeats 2	ENST00000371826	THC2463173	GO:0005488(binding)|GO:0005575(cellular_component)|GO:0006955(immune response)|GO:0008150(biological_process)	Homo sapiens interferon-induced protein with tetratricopeptide repeats 2 (IFIT2), mRNA [NM_001547]	chr10:91056593-91056652
7	448.54	212.90	2.11	NM_199189	NM_199189	9782.00	MATR3	matrin 3	ENST00000361059	THC2522130	GO:0000166(nucleotide binding)|GO:0003676(nucleic acid binding)|GO:0003723(RNA binding)|GO:0005198(structural molecule activity)|GO:0005622(intracellular)|GO:0005634(nucleus)|GO:0005637(nuclear inner membrane)|GO:0008270(zinc ion binding)|GO:0046872(metal	Homo sapiens matrin 3 (MATR3), transcript variant 1, mRNA [NM_199189]	chr5:138693199-138693258

[0579]

表200

No	Cy5	Cy3	ratio	RefSeq Accession	Genbank Accession	Entrez Gene ID	Gene Symbol	Gene Name	Ensembl ID	TIGR ID	GO	Description	Genomic Coordinates
8	92.54	52.33	1.77	NM_030667	NM_030667	5800.00	PTPRO	protein tyrosine phosphatase, receptor type, O	ENST00000281171	THC2479375	GO:0004725(protein tyrosine phosphatase activity)|GO:0004872(receptor activity)|GO:0005001(transmembrane receptor protein tyrosine phosphatase activity)|GO:0005887(integral to plasma membrane)|GO:0006470(protein amino acid dephosphorylation)|GO:0016020(me	Homo sapiens protein tyrosine phosphatase, receptor type, O (PTPRO), transcript variant 1, mRNA [NM_030667]	chr12:1564095 5-15641014
9	494.80	263.69	1.88	NM_005406	NM_005406	6093.00	ROCK1	Rho-associated, coiled-coil containing protein kinase 1	0.00	THC2555942	GO:0000166(nucleotide binding)|GO:0004674(protein serine/threonine kinase activity)|GO:0004713(protein-tyrosine kinase activity)|GO:0005198(structural molecule activity)|GO:0005524(ATP binding)|GO:0005622(intracellular)|GO:0005856(cytoskeleton)|GO:0006974	Homo sapiens Rho-associated, coiled-coil containing protein kinase 1 (ROCK1), mRNA [NM_005406]	chr18:1678428 9-16784230
10	5485.43	1150.91	4.77	NM_000978	NM_000978	9349.00	RPL23	ribosomal protein L23	ENST00000246857	THC2496402	GO:0003735(structural constituent of ribosome)|GO:0005622(intracellular)|GO:0005840(ribosome)|GO:0006412(translation)|GO:0006610(ribosomal protein import into nucleus)	Homo sapiens ribosomal protein L23 (RPL23), mRNA [NM_000978]	chr17:3426022 9-34260170
11	7532.08	1972.89	3.82	NM_000987	NM_000987	6154.00	RPL26	ribosomal protein L26	ENST00000293842	THC2550597	GO:0003723(RNA binding)|GO:0003735(structural constituent of ribosome)|GO:0005622(intracellular)|GO:0005842(cytosolic large ribosomal subunit (sensu_the Eukaryota research community))|GO:0006412(translation)|GO:0015934(large ribosomal subunit)	Homo sapiens ribosomal protein L26 (RPL26), mRNA [NM_000987]	chr17:8226187 -8223922
12	29074.04	10991.90	2.65	NM_002964	NM_002964	6279.00	S100A8	S100 calcium binding protein A8	ENST00000316893	THC2550959	GO:0005509(calcium ion binding)|GO:0005615(extracellular space)|GO:0006954(inflammatory response)	Homo sapiens S100 calcium binding protein A8 (S100A8), mRNA [NM_002964]	chr1:15162923 1-151629172
13	122.84	75.94	1.62	NM_004169	NM_004169	6470.00	SHMT1	serine hydroxymethyltransferase 1 (soluble)	ENST00000316894	THC2468055	GO:0004372(glycine hydroxymethyltransferase activity)|GO:0005739(mitochondrion)|GO:0005829(cytosol)|GO:0006544(glycine metabolic process)|GO:0006563(L-serine metabolic process)|GO:0006565(L-serine catabolic process)|GO:0006730(one-carbon compound metaboli	Homo sapiens serine hydroxymethyltransferase 1 (soluble) (SHMT1), transcript variant 1, mRNA [NM_004169]	chr17:1817231 0-18172251
14	552.45	163.82	3.37	NM_006713	NM_006713	10923.00	SUB1	SUB1 homolog (S. cerevisiae)	ENST00000265073	THC2553325	GO:0003677(DNA binding)|GO:0003697(single-stranded DNA binding)|GO:0003713(transcription coactivator activity)|GO:0005515(protein binding)|GO:0005634(nucleus)|GO:0005667(transcription factor complex)|GO:0006350(transcription)|GO:0006357(regulation of tran	Homo sapiens SUB1 homolog (S. cerevisiae) (SUB1), mRNA [NM_006713]	chr5:32634922 -32636916

212

[0580]

表200

No	Cy5	Cy3	ratio	RefSeq Accession	Genbank Accession	Entrez Gene ID	Gene Symbol	Gene Name	Ensembl ID	TIGR ID	GO	Description	Genomic Coordinates
15	121.10	75.39	1.61		BC032643	10492.00	SYNCRIP	synaptotagmin binding, cytoplasmic RNA interacting protein	ENST00000257768	THC2544830	GO:0000166(nucleotide binding)|GO:0003723(RNA binding)|GO:0005515(protein binding)|GO:0005634(nucleus)|GO:0005681(spliceosome)|GO:0005737(cytoplasm)|GO:0005783(endoplasmic reticulum)|GO:0006397(mRNA processing)|GO:0008143(poly(A) binding)|GO:0008380(RNA s	Homo sapiens synaptotagmin binding, cytoplasmic RNA interacting protein, mRNA (cDNA clone MGC:45213 IMAGE:5495201), complete cds. [BC032643]	chr6:86378429 -86378370
16	115.86	54.39	2.13	NM_020843	NM_020843	49855.00	ZNF291	zinc finger protein 291	ENST00000324767	NP1161245	GO:0003676(nucleic acid binding)|GO:0005622(intracellular)|GO:0008270(zinc ion binding)|GO:0046872(metal ion binding)	Homo sapiens zinc finger protein 291 (ZNF291), mRNA [NM_020843]	chr15:74427796 -74427905

[表201]

表201 ヒト共通遺伝子 (Down)

No	Cy5	Cy3	ratio	RefSeq Accession	Genbank Accession	Entrez Gene ID	Gene Symbol	Gene Name	Ensembl ID	TIGR ID	GO	Description	Genomic Coordinates
17	107.57	181.00	107.57	NM_012305	NM_012305	161.00	AP2A2	adaptor-related protein complex 2, alpha 2 subunit	ENST0000003 32231	THC2579138	GO:0005198(structural molecule activity)|GO:0005488(binding)|GO:0005905(coated pit)|GO:0006461(protein complex assembly)|GO:0006886(intracellular protein transport)|GO:0006897(endocytosis)|GO:0008289(lipid binding)|GO:0015031(protein transport)|GO:0030117	Homo sapiens adaptor-related protein complex 2, alpha 2 subunit (AP2A2), mRNA [NM_012305]	chr11:996537-998596
18	24.2	58.8	0.41	NM_152733	NM_152733	114781	BTBD9	BTB (POZ) domain containing 9	ENST0000003 28403	NP1460172	GO:0005515(protein binding)|GO:0007155(cell adhesion)	Homo sapiens BTB (POZ) domain containing 9 (BTBD9), mRNA [NM_152733]	chr6:38653420-38653361
19	62.8	126.2	0.50	NM_015991	NM_015991	712	C1QA	complement component 1, q subcomponent, A chain	ENST0000003 74842	THC2691241	GO:0005602(complement component C1q complex)|GO:0005737(cytoplasm)|GO:0006817(phosphate transport)|GO:0006958(complement activation, classical pathway)|GO:0007267(cell-cell signaling)|GO:0045087(innate immune response)	Homo sapiens complement component 1, q subcomponent, A chain (C1QA), mRNA [NM_015991]	chr1:22838382-22838441
20	34.02	51.29	0.66	NM_015645	NM_015645	114902.00	C1QTNF5	C1q and tumor necrosis factor related protein 5	ENST0000003 10588	THC2464395	GO:0005737(cytoplasm)|GO:0006817(phosphate transport)	Homo sapiens C1q and tumor necrosis factor related protein 5 (C1QTNF5), mRNA [NM_015645]	chr11:1187151 64-118715105
21	42.59	71.19	0.60	NM_001734	NM_001734	716.00	C1S	complement component 1, s subcomponent	ENST0000003 28916	THC2553139	GO:0001584(rhodopsin-like receptor activity)|GO:0003674(molecular_function)|GO:0003816(complement component C1s activity)|GO:0004263(chymotrypsin activity)|GO:0004295(trypsin activity)|GO:0005509(calcium ion binding)|GO:0005575(cellular_component)|GO:0005	Homo sapiens complement component 1, s subcomponent (C1S), transcript variant 1, mRNA [NM_001734]	chr12:7048354-7048413
22	801.20	1237.06	0.65	NM_000754	NM_000754	1312.00	COMT	catechol-O-methyltransferase	ENST0000002 07636	THC2555559	GO:0000287(magnesium ion binding)|GO:0005515(protein binding)|GO:0005615(extracellular space)|GO:0005625(soluble fraction)|GO:0005792(microsome)|GO:0006584(catec	Homo sapiens catechol-O-methyltransferase (COMT), transcript variant MB-COMT, mRNA [NM_000754]	chr22:18331771-18331771
23	33.32	54.30	0.61	NM_005229	NM_005229	2002.00	ELK1	ELK1, member of ETS oncogene family	ENST0000002 47161	THC2565271	GO:0003700(transcription factor activity)|GO:0005515(protein binding)|GO:0005634(nucleus)|GO:0006350(transcription)|GO:0006355(regulation of transcription, DNA-dependent)|GO:0043565(sequence-specific DNA binding)|GO:0045944(positive regulation of transcri	Homo sapiens ELK1, member of ETS oncogene family (ELK1), mRNA [NM_005229]	chrX:47380828-47380769

[0581]

表201 ヒト共通遺伝子 (Down)

No	Cy5	Cy3	ratio	RefSeq Accession	Genbank Accession	Entrez Gene ID	Gene Symbol	Gene Name	Ensembl ID	TIGR ID	GO	Description	Genomic Coordinates
24	1190.60	2128.97	0.56	NM_006877	NM_006877	2766.00	GMPR	guanosine monophosphate reductase	ENST00000259727	THC2640768	GO:0003920(GMP reductase activity)|GO:0008152(metabolic process)|GO:0009117(nucleotide metabolic process)|GO:0009408(response to cold)|GO:0016491(oxidoreductase activity)|GO:0030955(potassium ion binding)|GO:0046872(metal ion binding)	Homo sapiens guanosine monophosphate reductase (GMPR), mRNA [NM_006877]	chr6:16398745 -16388804
25	1232.61	2072.72	0.59	NM_002074	NM_002074	2782.00	GNB1	guanine nucleotide binding protein (G protein), beta polypeptide 1	ENST00000378609	THC2587663	GO:0003924(GTPase activity)|GO:0004871(signal transducer activity)|GO:0005834(heterotrimeric G-protein complex)|GO:0007165(signal transduction)|GO:0007200(G-protein signaling, coupled to IP3 second messenger (phospholipase C activating))|GO:0007213(acetyl	Homo sapiens guanine nucleotide binding protein (G protein), beta polypeptide 1 (GNB1), mRNA [NM_002074]	chr1:1711836-1711777
26	66.9	101.5	0.66	NM_006389	NM_006389	10525	HYOU1	hypoxia up-regulated 1	ENST00000353883	THC2764863	GO:0000166(nucleotide binding)|GO:0005524(ATP binding)|GO:0005515(extracellular space)|GO:0005783(endoplasmic reticulum)|GO:0006457(protein folding)|GO:0009790(response to stress)	Homo sapiens hypoxia up-regulated 1 (HYOU1), mRNA [NM_006389]	chr11:11842106-11842107
27	45.93	69.36	0.66	NM_206943	NM_206943	Hs.49787	LTBP1	latent transforming growth factor beta binding protein 1	ENST00000354476	THC2465969	GO:0005024(transforming growth factor beta receptor activity)|GO:0005509(calcium ion binding)|GO:0005578(extracellular matrix (sensu the Metazoa research community))|GO:0008150(biological_process)|GO:0019838(growth factor binding)	Homo sapiens latent transforming growth factor beta binding protein 1 (LTBP1), transcript variant 1, mRNA [NM_206943]	chr2:33477340-33477399
28	23.77	42.52	0.56	NM_000240	NM_000240	4128.00	MAOA	monoamine oxidase A	ENST00000378702	THC2786684	GO:0005215(transporter activity)|GO:0005739(mitochondrion)|GO:0006118(electron transport)|GO:0006584(catecholamine metabolic process)|GO:0006810(transport)|GO:0007610(behavior)|GO:0008131(amine oxidase activity)|GO:0016020(membrane)|GO:0016021(integral	Homo sapiens monoamine oxidase A (MAOA), nuclear gene encoding mitochondrial protein, mRNA [NM_000240]	chrX:43488621-43488680
29	21.05	227.48	0.09	NM_002377	NM_002377	4142.00	MAS1	MAS1 oncogene	ENST00000252660	THC2480075	GO:0001584(rhodopsin-like receptor activity)|GO:0004872(receptor activity)|GO:0004945(angiotensin type II receptor activity)|GO:0005887(integral to plasma membrane)|GO:0007165(signal transduction)|GO:0007186(G-protein coupled receptor protein signaling pa	Homo sapiens MAS1 oncogene (MAS1), mRNA [NM_002377]	chr6:160246881-160246873
30	55.02	90.28	55.02	XM_001130382	AF015521	4586.00	MUC5AC	mucin 5AC, oligomeric mucus/gel-forming		THC2601022	GO:0003674(molecular_function)|GO:0005201(extracellular matrix structural constituent)|GO:0005575(cellular_component)|GO:0007155(cell adhesion)|GO:0008150(biological_process)|GO:0043205(fibril)|GO:0043206(fibril organization and biogenesis)	Homo sapiens mucin (MUC5AC) mRNA, partial cds. [AF015521]	

[0582]

表201 ヒト共通遺伝子 (Down)

No	Cy5	Cy3	ratio	RefSeq Accession	Genbank Accession	Entrez Gene ID	Gene Symbol	Gene Name	Ensembl ID	TIGR ID	GO	Description	Genomic Coordinates
31	1176.8	2549.9	0.46	NM_198040	NM_198040	1912	PHC2	polyhomeotic homolog 2 (Drosophila)	ENST00000257118	THC2745707	GO:0003677(DNA binding)|GO:0005515(protein binding)|GO:0005634(nucleus)|GO:0007275(multicellular organismal development)|GO:0008270(zinc ion binding)|GO:0046872(metal ion binding)	Homo sapiens polyhomeotic homolog 2 (Drosophila) (PHC2), transcript variant 1, mRNA [NM_198040]	chr1:33567141 -33567082
32	20.60	47.46	0.43	NM_005030	NM_005030	5347.00	PLK1	polo-like kinase 1 (Drosophila)	ENST00000300093	THC2501829	GO:0000074(regulation of progression through cell cycle)|GO:0000166(nucleotide binding)|GO:0004674(protein serine/threonine kinase activity)|GO:0004713(protein-tyrosine kinase activity)|GO:0005515(protein binding)|GO:0005524(ATP binding)|GO:0005634(nucleu	Homo sapiens polo-like kinase 1 (Drosophila) (PLK1), mRNA [NM_005030]	chr16:23609847 1-23608713
33	169.41	276.54	0.61	0.00	AJ008005	5663.00	PSEN1	presenilin 1 (Alzheimer disease 3)	0.00	THC2485339	GO:0000776(kinetochore)|GO:0001568(blood vessel development)|GO:0001708(cell fate specification)|GO:0001764(neuron migration)|GO:0004175(endopeptidase activity)|GO:0005515(protein binding)|GO:0005624(membrane fraction)|GO:0005634(nucleus)|GO:0005639(integ	Homo sapiens PSN1 gene, alternative transcript. [AJ008005]	chr14:72710128 9-72710188
34	152.53	261.92	0.58	NM_031209	NM_031209	81690.00	QTRT1	queuine tRNA-ribosyltransferase 1 (tRNA-guanine transglycosylase)	ENST00000250237	THC2668931	GO:0005840(ribosome)|GO:0008033(tRNA processing)|GO:0008270(zinc ion binding)|GO:0008479(queuine tRNA-ribosyltransferase activity)|GO:0008616(queuosine biosynthetic process)|GO:0016757(transferase activity, transferring glycosyl groups)|GO:0046872(metal i	Homo sapiens queuine tRNA-ribosyltransferase 1 (tRNA-guanine transglycosylase) (QTRT1), mRNA [NM_031209]	chr19:1068393 9-10684251
35	21.59	34.80	0.62	NM_080864	NM_080864	Hs.352155	RLN3	relaxin 3	ENST00000306822	THC2487082	GO:0005179(hormone activity)|GO:0005576(extracellular region)	Homo sapiens relaxin 3 (RLN3), mRNA [NM_080864]	chr19:14002678-14002737
36	67.4	187.8	0.36	NM_005440	NM_005440	8153	RND2	Rho family GTPase 2	ENST00000225973	THC2471564	GO:0000166(nucleotide binding)|GO:0003924(GTPase activity)|GO:0005515(protein binding)|GO:0005525(GTP binding)|GO:0005622(intracellular)|GO:0007165(signal transduction)|GO:0007264(small GTPase mediated signal transduction)|GO:0016020(membrane)	Homo sapiens Rho family GTPase 2 (RND2), mRNA [NM_005440]	chr17:3843157 4-38432768
37	21.62	48.92	0.44	NM_016271	NM_016271	51444.00	RNF138	ring finger protein 138	ENST00000261593	THC2644024	GO:0003676(nucleic acid binding)|GO:0005515(protein binding)|GO:0005622(intracellular)|GO:0006512(ubiquitin cycle)|GO:0008270(zinc ion binding)|GO:0016874(ligase activity)|GO:0046872(metal ion binding)	Homo sapiens ring finger protein 138 (RNF138), transcript variant 1, mRNA [NM_016271]	chr18:2794774 3-27947802

[0583]

表201 ヒト共通遺伝子 (Down)

No	Cy5	Cy3	ratio	RefSeq Accession	Genbank Accession	Entrez Gene ID	Gene Symbol	Gene Name	Ensembl ID	TIGR ID	GO	Description	Genomic Coordinates
38	28.10	46.73	0.62	NM_152996	NM_152996	256435.00	ST6GALNAC3	ST6 (alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1,3)-N-acetylgalactosaminide alpha-2,6-sialyltransferase 3	ENST00000328299	THC2471836	GO:0005615(extracellular space)|GO:0006486(protein amino acid glycosylation)|GO:0008373(sialyltransferase activity)|GO:0016020(membrane)|GO:0016021(integral to membrane)|GO:0030173(integral to Golgi membrane)	Homo sapiens ST6 (alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1,3)-N-acetylgalactosaminide alpha-2,6-sialyltransferase 3 (ST6GALNAC3), mRNA [NM_152996]	chr1:76869131-76869190
39	948.7	1697.8	0.56	NM_003764	NM_003764	8676	STX11	syntaxin 11	ENST00000367568	THC2472207	GO:0005484(SNAP receptor activity)|GO:0005515(protein binding)|GO:0006886(intracellular protein transport)|GO:0006944(membrane fusion)|GO:0008565(protein transporter activity)|GO:0016020(membrane)	Homo sapiens syntaxin 11 (STX11), mRNA [NM_003764]	chr6:144550391-144550460
40	119.0	229.9	0.52	NM_018266	NM_018266	55254	TMEM39A	transmembrane protein 39A	ENST00000319172	THC2461947	GO:0016021(integral to membrane)	Homo sapiens transmembrane protein 39A (TMEM39A), mRNA [NM_018266]	chr3:120632642-120632583

[表202]

表202 ヒト共通遺伝子

No	Target(Gene)Symbol	Target Accession	UniGene	Up/Down	被験者群	配列番号
1	ANXA1	NM_000700	Hs.494173	Up	B	289
2	ARID4B	NM_016374	Hs.575782	Up	A+B, B, D, B+D	290
3	CLK1	NM_004071	Hs.433732	Up	B+D	291
4	ECHDC1	NM_018479	Hs.486410	Up	A+B, B, B+D	292
5	IFI44	NM_006417	Hs.82316	Up	A+B, B, B+D	293
6	IFIT2	NM_001547	Hs.437609	Up	A+B	294
7	MATR3	NM_199189	Hs.268939	Up	B+D	295
8	PTPRO	NM_030667	Hs.160871	Up	C+D, A+C, D, B+D	296
9	ROCK1	NM_005406	Hs.306307	Up	A+B, B+D	297
10	RPL23	NM_000978	Hs.406300	Up	A+B, B, B+D	298
11	RPL26	NM_000987	Hs.645380	Up	A+B, B, B+D	299
12	S100A8	NM_002964	Hs.416073	Up	A+B, B, B+D	83
13	SHMT1	NM_004169	Hs.513987	Up	A+C, B+D	300
14	SUB1	NM_006713	Hs.229641	Up	A+B, B, B+D	301
15	SYNCRIP	BC032643	Hs.571177	Up	D, B+D	-
16	ZNF291	NM_020843	Hs.458986	Up	B+D	-
17	AP2A2	NM_012305	Hs.19121	Down	A+B, B+D	302
18	BTBD9	NM_152733	Hs.116233	Down	B+D	303
19	C1QA	NM_015991	Hs.632379	Down	B+D	304
20	C1QTNF5	NM_015645	Hs.632102	Down	D	305
21	C1S	NM_001734	Hs.458355	Down	A+B, A+C	306
22	COMT	NM_000754	Hs.370408	Down	B+D	307
23	ELK1	NM_005229	Hs.181128	Down	A, D	308
24	GMPR	NM_006877	Hs.484741	Down	B+D	309
25	GNB1	NM_002074	Hs.430425	Down	B+D	310
26	HYOU1	NM_006389	Hs.277704	Down	B+D	311
27	LTBP1	NM_206943	Hs.49787	Down	D	312
28	MAOA	NM_000240	Hs.183109	Down	A+B, A	313
29	MAS1	NM_002377	Hs.99900	Down	C+D	314
30	MUC5AC	XM_001130382	Hs.558950	Down	A+B	-
31	PHC2	NM_198040	Hs.524271	Down	A+B, B, C, D, B+D	315
32	PLK1	NM_005030	Hs.592049	Down	A	316
33	PSEN1	AJ008005	Hs.592324	Down	B	-
34	QTRT1	NM_031209	Hs.631638	Down	B, B+D	317
35	RLN3	NM_080864	Hs.352155	Down	D	318
36	RND2	NM_005440	Hs.603111	Down	B+D	319
37	RNF138	NM_016271	Hs.302408	Down	A	320
38	ST6GALNAC3	NM_152996	Hs.337040	Down	C	321
39	STX11	NM_003764	Hs.118958	Down	A+B, B, B+D	322
40	TMEM39A	NM_018266	Hs.434927	Down	B+D	323

[0584] また表203及び204には、ヒトの笑いにより発現変動した遺伝子と同方向に発現変化した短期陽性刺激(Tickling刺激)負荷ラットの遺伝子(ラット共通遺伝子)40種のアノテーションを示し、表205にはその要約を示す。

[表203]

表203 ラット共通遺伝子

No	Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	Pathway Name	Gene Symbol	Gene Name	Summary	GeneRIF
1	748.06	429.08	1.74	NM_012904	Anxa1	Rattus norvegicus annexin A1 (Anxa1), mRNA [NM_012904]	ref|NM_012904|gb|Y00446|gb|M19967|gb|BC061710	-	Anxa1	annexin A1	plays a role in regulation of insulin secretion; may inhibit phospholipase A2 [RGD]	Study reveals increased expression of the annexin 1 isoform at the mRNA level following moderate contusive spinal cord injury.// Annexin 1 mediates the disruption of normal cell morphology and inhibits cyclin D1 expression, therefore reducing cell prolife
2	27.58	16.12	1.71	AA955478	AA955478	AA955478 UI-R-A1-ax-f-02-0-UI.s1 UI-R-A1 Rattus norvegicus cDNA clone UI-R-A1-ax-f-02-0-UI 3', similar to gi [AA955478]	gb|AA955478	-	Arid4b	AT rich interactive domain 4B (Rbp1 like)	-	-
3	1093.65	682.73	1.60	XM_217405	Clk1_predicted	PREDICTED: Rattus norvegicus CDC-like kinase 1 (predicted) (Clk1_predicted), mRNA [XM_217405]	ref|XM_217405|ens|ENSRNOT00000030934|gb|BC081942|gb|BC097451	-	Clk1	CDC-like kinase 1	-	-
4	46.40	29.76	1.56	NM_001007734	Echdc1	Rattus norvegicus enoyl Coenzyme A hydratase domain containing 1 (Echdc1), mRNA [NM_001007734]	ref|NM_001007734|ens|ENSRNOT00000016358|gb|BC079052|gb|AW915152	-	Echdc1	enoyl Coenzyme A hydratase domain containing 1	-	-

[0585]

表203 ラット共通遺伝子

No	Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	Pathway Name	Gene Symbol	Gene Name	Summary	GeneRIF
5	265.55	166.09	1.60	XM_227821	Ifi44_predicted	PREDICTED: Rattus norvegicus interferon-induced protein 44 (predicted) (Ifi44_predicted), mRNA [XM_227821]	ref|XM_227821|gb|BG088420|gb|AI548270|tc|TC555800	-	Ifi44	interferon-induced protein 44	-	-
6	69.01	37.15	1.86	NM_001024753	NM_001024753	Rattus norvegicus interferon-induced protein with tetratricopeptide repeats 2 (predicted) (Ifit2_predicted), mRNA [NM_001024753]	ref|NM_001024753|gb|BC097384|gb|AA799298|gb|BF564940	-	Ifit2	interferon-induced protein with tetratricopeptide repeats 2	-	-
7	841.99	556.05	1.51	NM_019149	Matr3	Rattus norvegicus matrin 3 (Matr3), mRNA [NM_019149]	ref|NM_019149|ref|XM_574923|gb|NM63465|gb|XM_212889	-	Matr3	matrin 3	an internal nuclear matrix protein [RGD]	-
8	80.06	49.51	1.62	NM_017336	Ptpro	Rattus norvegicus protein tyrosine phosphatase, receptor type, O (Ptpro), mRNA [NM_017336]	ref|NM_017336|gb|U28938|ens|ENSRNOT00000040576|tc|TC572663	-	Ptpro	protein tyrosine phosphatase, receptor type, O	may regulate glomerular epithelial cell function; may play a role in neural cell development [RGD]	Results suggest that GLEPP1 (Ptpro) expression reflects podocyte injury induced by puromycin aminonucleoside.

[0586]

表203 ラット共通遺伝子

No	Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	Pathway Name	Gene Symbol	Gene Name	Summary	GeneRIF
9	904.30	559.77	1.62	NM_031098	Rock1	Rattus norvegicus Rho-associated coiled-coil forming kinase 1 (Rock1), mRNA [NM_031098]	ref|NM_031098|gb|AY3 25220|gb|U61266|ens| ENSRNOT00000040922	KEGG pathway: Axon guidance// KEGG pathway: Focal adhesion// KEGG pathway: Leukocyte transendothelial migration// KEGG pathway: Regulation of actin cytoskeleton// KEGG pathway: TGF-beta signaling pathway// KEGG pathway: Wnt signaling pathway	Rock1	Rho-associated coiled-coil forming kinase 1	protein serine/threonine kinase involved in intracellular signaling [RGD]	Results suggest that ethanol-exposed astrocytes undergo apoptosis by amoikis and also that the RhoA/ROCK-1/MLC pathway participates in this process.// results suggest Rho kinase-mediated sustained vasoconstriction plays an important role in established pu
10	23600.16	13156.17	1.79	NM_0010075 99	Rp123	Rattus norvegicus ribosomal protein L23 (Rpl23), mRNA [NM_001007599]	ref|NM_001007599|gb| BC058500|gb|XM_21344 8|ens|ENSRNOT0000000 5471	-	Rpl23	ribosomal protein L23	ribosomal protein L23 [RGD]	-
11	16552.66	9435.60	1.76	XM_213346	Rpl26_pre dicted	PREDICTED: Rattus norvegicus ribosomal protein L26 (predicted) (Rpl26_predicted), mRNA [XM_213346]	ref|XM_213346|ref|XM _574290|gb|CB545144| ens|ENSRNOT0000000055 88	-	Rpl26	ribosomal protein L26	-	-
12	786.71	409.73	1.92	NM_053822	S100a8	Rattus norvegicus S100 calcium binding protein A8 (calgranulin A) (S100a8), mRNA [NM_053822]	ref|NM_053822|gb|L18 891|ens|ENSRNOT00000 0154731|tc|TC567929	-	S100a8	S100 calcium binding protein A8 (calgranulin A)	S100 calcium may play a role in inflammatory response [RGD]	-

[0587]

表203　ラット共通遺伝子

No	Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	Pathway Name	Gene Symbol	Gene Name	Summary	GeneRIF
13	35.93	20.07	1.79	AI010087	AI010087	AI010087 EST204538 Normalized rat lung, Bento Soares Rattus sp. cDNA clone RLUBT56 3' end, mRNA sequence [AI010087]	gb|AI010087|gb|AI137077|gb|AI105184	-	Shmt1	serine hydroxymethyl transferase 1 (soluble)	-	Vitamin B 6 intake affects level of serine hydroxymethyltransferase in rat liver cytosol and mitochondria.// The low activity of SHMT in the human and rat placenta suggests that, unlike in the sheep, placental conversion of serine to glycine is not a majo
14	1700.59	1069.50	1.59	NM_0010096 18	Rpo2tc1	Rattus norvegicus RNA polymerase II transcriptional coactivator (Rpo2tc1), mRNA [NM_001009618]	ref|NM_001009618|gb|K02816|gb|XM_342200|gb|CB605675	-	Sub1	SUB1 homolog (S. cerevisiae)	expressed in 12 day embryo and in a chemically induced pancreatic B-cell tumor; not expressed in normal differentiated cells [RGD]	-
15	24.19	15.64	1.55	XM_343446	Syncrip_predicted	PREDICTED: Rattus norvegicus synaptotagmin binding, cytoplasmic RNA interacting protein (predicted) (Syncrip_predicted), mRNA [XM_343446]	ref|XM_343446|ens|ENSRNOT00000000222|gb|AI548569|tc|TC539251	-	Syncrip	synaptotagmin binding, cytoplasmic RNA interacting protein	-	SYNCRIP is transported within the dendrite as a component of mRNA granules
16	36.76	23.79	1.55	XM_343394	Znf291	PREDICTED: Rattus norvegicus zinc finger protein 291 (Znf291), mRNA [XM_343394]	ref|XM_343394|gb|XM_217161|gb|AI071787|ens|ENSRNOT00000009169	-	Znf291	zinc finger protein 291	-	-

[表204]

表204 ラット共通遺伝子

No	Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	Pathway Name	Gene Symbol	Gene Name	Summary	GeneRIF
17	9.27	14.15	0.66	BF414152	BF414152	BF414152 UI-R-BJ2-bom-h-11-0-UI.s1 UI-R-BJ2 Rattus norvegicus cDNA clone UI-R-BJ2-bom-h-11-0-UI 3', mRNA sequence [BF414152]	gb|BF414152|gb|B1285640|gb|AI072063|gb|BE113110	-	Ap2a2	adaptor protein complex AP-2, alpha 2 subunit	alpha c large chain of the clathrin associated protein complex [RGD]	AP-2 binds to unique sites on the C-terminus of NMDA receptor subunit NR2B and has an antagonistic functional consequence that is independent of the ability of PSD-95 to cluster receptors on the plasma membrane.
18	13.20	25.88	0.51	BF401614	BF401614	BF401614 UI-R-CA0-bgm-f-08-0-UI.s1 UI-R-CA0 Rattus norvegicus cDNA clone UI-R-CA0-bgm-f-08-0-UI 3', mRNA sequence [BF401614]	gb|BF401614	-	Btbd9	BTB (POZ) domain containing 9	-	-
19	32.15	52.74	0.61	NM_0010085 15	C1qa_predicted	Rattus norvegicus complement component 1, q subcomponent, alpha polypeptide (predicted) (C1qa_predicted), mRNA [NM_0010085]	ref|NM_0010085 15|gb|XM_216554|gb|BC086605|ens|ENSRNOT00000017385	-	C1qa	complement component 1, q subcomponent, alpha polypeptide	-	-
20	31.68	46.98	0.67	NM_001012123	C1qtnf5_predicted	Rattus norvegicus C1q and tumor necrosis factor related protein 5 (predicted) (C1qtnf5_predicted), mRNA [NM_001012123]	ref|NM_001012123|ref|XM_576395|gb|XM_236180|ens|ENSRNOT00000010127	-	C1qtnf5	C1q and tumor necrosis factor related protein 5	-	-
21	20.86	33.68	0.62	NM_138900	C1s	Rattus norvegicus complement component 1, s subcomponent (C1s), mRNA [NM_138900]	ref|NM_138900|ref|XM_575664|gb|D88226|gb|BC006204|2	KEGG pathway: Complement and coagulation cascades	C1s	complement component 1, s subcomponent	a secreted enzyme; may have a role in glial cell differentiation [RGD]	These results suggest that r-Gsp protein could not induce glial differentiation alone, and suggest that r-Gsp protein was secreted as a proenzyme and processed in culture medium [rGsp protein].

[0588]

表204 ラット共通遺伝子

No	Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	Pathway Name	Gene Symbol	Gene Name	Summary	GeneRIF
22	12.47	24.51	0.51	AA858639	AA858639	AA858639 UI-R-E0-bg-d-07-0-UI.s1 UI-R-E0 Rattus norvegicus cDNA clone UI-R-E0-bg-d-07-0-UI 3' similar to emb [AA858639]	gb|AA858639	KEGG pathway: Tyrosine metabolism	Comt	catechol-O-methyltransferase	catalyzes the conversion of S-adenosyl-L-methionine and catechol to S-adenosyl-L-homocysteine and guaiacol [RGD]	Crystals diffract to 1.6 A resolution on a synchrotron-radiation source and belong to the monoclinic space group P2(1).// Strong COMT mRNA expression was observed in the suprachiasmatic nucleus throughout its rostrocaudal extent at postnatal day 1 (P1) an
23	10.17	17.33	0.59	BF558309	BF558309	BF558309 UI-R-E0-dk-c-07-0-UI.r1 UI-R-E0 Rattus norvegicus cDNA clone UI-R-E0-dk-c-07-0-UI 5', mRNA sequence [BF558309]	gb|BF558309|tc|TC6565912	-	Elk1	ELK1, member of ETS oncogene family	-	-
24	51.10	82.49	0.62	NM_057188	Gmpr	Rattus norvegicus guanosine monophosphate reductase (Gmpr), mRNA [NM_057188]	ref|NM_057188|gb|AF01 90867|ens|ENSRNOT000 00022613|tc|TC568850	KEGG pathway: Purine metabolism	Gmpr	guanosine monophosphate reductase	may convert guanine nucleotides to IMP and facilitate uncoupling protein-1 function in response to cold exposure [RGD]	-

[0589]

表204 ラット共通遺伝子

No	Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	Pathway Name	Gene Symbol	Gene Name	Summary	GeneRIF
25	11.12	17.83	0.62	NM_030987	Gnb1	Rattus norvegicus guanine nucleotide binding protein, beta 1 (Gnb1), mRNA [NM_030987]	ref|NM_030987|gb|U88324|gb|AI008284|ens|ENSRNOT00000022649		Gnb1	guanine nucleotide binding protein, beta 1	component of heterotrimeric G-proteins; mediates activity of effector molecules and contributes to the specificity of G-protein receptor interaction; mat confer preferential receptor specificity to the voltage-sensitive calcium channel [RGD]	G betagamma binds HDAC5 and inhibits its transcriptional co-repression activity
26	26.28	42.33	0.62	NM_138867	Hyoul	Rattus norvegicus hypoxia up-regulated 1 (hyoul), mRNA [NM_138867]	ref|NM_138867|gb|U41653|ens|ENSRNOT00000044613		Hyoul	hypoxia up-regulated 1	a stress protein induced by hypoxia [RGD]	role for the protein both in preventing cardiomyocyte death and in preserving contractile function after ischemic damage
27	22.24	32.99	0.67	NM_021587	Ltbp1	Rattus norvegicus latent transforming growth factor beta binding protein 1 (Ltbp1), mRNA [NM_021587]	ref|NM_021587|gb|M554 31|tc|TC569105	KEGG pathway: TGF-beta signaling pathway	Ltbp1	latent transforming growth factor beta binding protein 1	large subunit component of masking protein; neutralizes the activity of TGF-beta 1 [RGD]	Mesangial expression of LTBP-1 and fibrillin-1 is induced early in experimental nephritis and LTBP-1 and fibrillin-1 are partially colocalized in the nephritic glomerulus.// fibronectin has a role in LTBP1 assembly in the ECM and in regulation of TGF beta via LTBP1 interactions.// LTBP-1 but not TGF-beta1 is induced by PDGF-BB and TGF-beta1 autoinduction does not affect the expression of LTBP-beta1// observations suggest that latent transforming growth factor-beta binding protein-1 plays a critical role in intimal thickening of diabetic artery through the acceleration of smooth muscle cell migration via integrin-beta(3)

[0590]

表204 ラット共通遺伝子

No	Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	Pathway Name	Gene Symbol	Gene Name	Summary	GeneRIF
28	9.45	15.83	0.60	AI105223	AI105223	AI105223 EST214512 Normalized rat Kidney, Bento Soares Rattus sp. cDNA clone RKIDH26 3' end, mRNA sequence [AI105223]	gb|AI105223	-	Maoa	monoamine oxidase A	enzyme involved in the oxidative deamination of biogenic and xenobiotic amines [RGD]	oxidative stress induced by MAO is responsible for receptor-independent apoptotic effects of 5-HT in cardiomyocytes and postischemic myocardial injury//important component of the active site structure of hMAO A is the loop conformation of residues 210-21
29	11.34	18.09	0.63	NM_012757	Mas1	Rattus norvegicus MAS1 oncogene (Mas1), mRNA [NM_012757]	ref|NM_012757|gb|BC060100|tc|TC543216	-	Mas1	MAS1 oncogene	oncogene: may be involved in function or development of neural tissues [RGD]	-
30	29.62	50.22	0.59	U83139	Muc5ac	Rattus norvegicus mucin (MUC5AC) mRNA, partial cds [U83139]	gb|U83139|tc|TC56990_2	-	Muc5ac	mucin 5, subtypes A and C, tracheobronchial/gastric	a secretory mucin expressed in the airway:expression is associated with mucous cell differentiation [RGD]	The effect of geranylgeranylacetone on the expression of MUC1, MUC5AC, and MUC6 in ethanol-treated rats is reported.// Mapping of two new epitopes on the apomucin encoded by MUC5AC gene: expression in normal GI tract and colon tumors.

[0591]

表204 ラット共通遺伝子

No	Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	Pathway Name	Gene Symbol	Gene Name	Summary	GeneRIF
31	20.34	30.73	0.66	NM_232751	Phc2_predicted	PREDICTED: Rattus norvegicus polyhomeotic-like 2 (Drosophila) (predicted) (Phc2_predicted), mRNA [XM_232751]	ref|XM_232751|gb|BG090339|ens|ENSRNOT00000008550|tc|TC053059	-	Phc2	polyhomeotic-like 2 (Drosophila)	-	-
32	63.56	98.86	0.64	NM_017100	Plk1	Rattus norvegicus polo-like kinase 1 (Drosophila) (Plk1), mRNA [NM_017100]	ref|NM_017100|gb|U10188|gb|BC083926|gb|AW914279	KEGG pathway: A Cell cycle	Plk1	polo-like kinase 1 (Drosophila)	human homolog catalyzes the phosphorylation of a Golgi reassembly stacking protein (GRASP65); may play a role in Golgi apparatus fragmentation and reorganization during mitosis [RGD]	may be a multifunctional kinase that plays pivotal regulatory roles in microtubule assembly during rat oocyte meiotic maturation, fertilization, and early embryonic mitosis
33	14.18	26.54	0.53	NM_019163	Psen1	Rattus norvegicus presenilin 1 (Psen1), mRNA [NM_019163]	ref|NM_019163|gb|BC070877|ens|ENSRNOT00000012495|tc|TC072323	KEGG pathway: Alzheimer's disease// KEGG pathway: Neurodegenerative Disorders// KEGG pathway: Notch signaling pathway// KEGG pathway: Wnt signaling pathway	Psen1	presenilin 1	multitransmembrane protein; human homolog mutated in most cases of early onset familial Alzheimer's disease; may mediate retinal lamination and pattern formation [RGD]	amyloid precursor protein and presenilin 1 packaging into coat protein complex II vesicles is normally uncoupled// N-toastrin, presenilin, APH-1, and PEN-2 form active gamma-secretase complexes in mitochondria// experiments establish amyloid precursor prot

[0592]

表204 ラット共通遺伝子

No	Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	Pathway Name	Gene Symbol	Gene Name	Summary	GeneRIF
34	49.18	74.73	0.66	NM_022250	Qtrtl	Rattus norvegicus queuine tRNA-ribosyltransferase 1 (Qtrtl), mRNA [NM_022250]	ref|NM_022250|gb|AB034634|gb|BC097321|ens|ENSRNOT00000010030	-	Qtrtl	queuine tRNA-ribosyltransferase 1	catalyzes exchange of queuine (the base of queuosine, Q) in tRNA queuosine biosynthesis [RGD]	-
35	8.88	14.49	0.61	NM_170667	Rln3	Rattus norvegicus relaxin 3 (Rln3), mRNA [NM_170667]	ref|NM_170667|gb|AY127241|gb|AW521175|ens|ENSRNOT00000007775	-	Rln3	relaxin 3	-	Results suggest that relaxin could be an endogenous cardioprotective factor in ischemic heart diseases.// Relaxin 3 produced in the nucleus incertus is released from nerve endings and is involved in the regulation of the stress response.// relaxin regulat
36	72.62	116.09	0.63	NM_00101010953	Rohm_predicted	Rattus norvegicus ras homolog gene family, member N (predicted) (Rohm_predicted), mRNA [NM_00101010953]	ref|NM_00101010953|gb|XM_220993|gb|CB547935|ens|ENSRNOT00000028089	-	Rnd2	Rho family GTPase 2	-	-
37	8.80	14.47	0.61	NM_053588	Rnf138	Rattus norvegicus ring finger protein 138 (Rnf138), mRNA [NM_053588]	ref|NM_053588|gb|BC061821|gb|AF315468|ens|ENSRNOT00000021061	-	Rnf138	ring finger protein 138	-	-

[0593]

表204　ラット共通遺伝子

No	Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	Pathway Name	Gene Symbol	Gene Name	Summary	GeneRIF
38	13.43	24.22	0.55	NM_019123	St7o	Rattus norvegicus sialyltransferase 7c (St7c), mRNA [NM_019123]	ref|NM_019123|gb|L29554|gb|BC072501|gb|AW141837	KEGG pathway: Ganglioside biosynthesis	St6galnac3	ST6 (alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1,3)-N-acetylgalactosamide alpha-2,6-sialyltransferase 3	GalNAc alpha-2,6-sialyltransferase that forms a ganglioside GD1(alpha) from GM1b). [RGD]	-
39	9.63	17.22	0.56	XM_218092	Stx11_predicted	Rattus norvegicus similar to Syntaxin 11 (LOC292483), mRNA [XM_218092]	gb|XM_218092|ens|ENSRNOT00000019983	-	Stx11	syntaxin 11	-	-
40	10.91	17.40	0.63	NM_001013865	NM_001013865	Rattus norvegicus similar to RIKEN cDNA 2610033C09 (predicted) (RGD1306421_predicted), mRNA [NM_001013865]	ref|NM_001013865|gb|XM_213608|gb|BI554814|ens|ENSRNOT00000004116	-	Tmem39a	transmembrane protein 39a	-	-

[表205]

表205 ラット共通遺伝子

No	Target(Gene)Symbol	Target Accession	UniGene	Up/Down	生体由来試料	配列番号
1	Anxa1	NM_012904	Rn.1792	Up	BI	324
2	Arid4b	AA955478	Rn.47249	Up	BI	-
3	Clk1	XM_217405	Rn.36770	Up	BI	325
4	Echdc1	NM_001007734	Rn.4220	Up	BI	326
5	Ifi44	XM_227821	Rn.43876	Up	BI	327
6	Ifit2	NM_001024753	Rn.6175	Up	BI	328
7	Matr3	NM_019149	Rn.29774	Up	BI	329
8	Ptpro	NM_017336	Rn.10163	Up	BI	330
9	Rock1	NM_031098	Rn.89756	Up	BI	-
10	Rpl23	NM_001007599	Rn.103172	Up	BI	331
11	Rpl26	XM_213346	Rn.144702	Up	BI	332
12	S100a8	NM_053822	Rn.31839	Up	BI	333
13	Shmt1	AI010087	Rn.3684	Up	BI	-
14	Sub1	NM_001009618	Rn.8706	Up	BI	-
15	Syncrip	XM_343446	Rn.25065	Up	BI	334
16	Znf291	XM_343394	Rn.163002	Up	BI	335
17	Ap2a2	BF414152	Rn.34928	Down	BI	336
18	Btbd9	BF401614	Rn.48897	Down	BI	337
19	C1qa	NM_001008515	Rn.105647	Down	BI	338
20	C1qtnf5	NM_001012123	Rn.99884	Down	BI	339
21	C1s	NM_138900	Rn.4037	Down	BI	340
22	Comt	AA858639	Rn.220	Down	BI	341
23	Elk1	BF558309	Rn.1714	Down	BI	342
24	Gmpr	NM_057188	Rn.3862	Down	BI	343
25	Gnb1	NM_030987	Rn.126047	Down	BI	344
26	Hyou1	NM_138867	Rn.10542	Down	BI	345
27	Ltbp1	NM_021587	Rn.40942	Down	BI	346
28	Maoa	AI105223	Rn.163443	Down	BI	347
29	Mas1	NM_012757	Rn.21943	Down	BI	348
30	Muc5ac	U83139	Rn.10789	Down	BI	349
31	Phc2	XM_232751	Rn.2428	Down	BI	350
32	Plk1	NM_017100	Rn.11034	Down	BI	351
33	Psen1	NM_019163	Rn.44440	Down	BI	352
34	Qtrt1	NM_022250	Rn.53858	Down	BI	353
35	Rln3	NM_170667	Rn.45123	Down	BI	354
36	Rnd2	NM_001010953	Rn.22162	Down	BI	355
37	Rnf138	NM_053588	Rn.6814	Down	BI	356
38	St6galnac3	NM_019123	Rn.88072	Down	BI	357
39	Stx11	XM_218092	-	Down	BI	358
40	Tmem39a	NM_001013865	Rn.13663	Down	BI	359

[0594] 4-3. 総括

陽性感情で活性化される健康増進遺伝子の特定のために、糖尿病の第6の合併症である歯周病に注目して、笑いによる遺伝子の発現変化を解析した。末梢血白血球による網羅的な遺伝子発現解析を実施し、笑いにより特異的に発現変化する遺伝子群を抽出することができた。また、ラットの短期陽性刺激（Tickling刺激）と、ヒトの「笑い」体験により、共通に発現変化した遺伝子を特定できた。

[0595] 本明細書で引用した全ての刊行物、特許および特許出願をそのまま参考として本明細書にとり入れるものとする。

請求の範囲

[請求項1] ラットに評価対象である刺激を負荷する第1のステップと、

下記の表1に示す遺伝子群から選択される少なくとも1種の遺伝子の発現量を指定の生体由来試料において測定する第2のステップと、

測定した前記遺伝子の発現量に基づいて、対象刺激が陽性刺激であるか否かを評価する第3のステップと

を含む、所与の刺激がラットに対する陽性刺激であるか否かを評価する方法。

[表1]

表１

No	Target(Gene)Symbol	Target Accession	UniGene	Up/Down	生体由来試料
1	Gsta5	NM_031509	Rn.10460	Up	Bc
2	-	AA858768	-	Up	Bc
3	Aldh1a1	NM_022407	Rn.6132	Up	Bc
4	Yc2	NM_001009920	Rn.120929	Up	Bc
5	-	TC536876	-	Up	Bc
6	Ttc6_predicted	XM_216713	Rn.82576	Up	Bc
7	Gsta2	NM_017013	Rn.144550	Up	Bc
8	-	BQ200056	-	Up	Bc
9	Gsta2	BQ199390	Rn.144550	Up	Bc
10	LOC307767	XM_226381	Rn.41880	Up	Bc
11	Cdigll	NM_153623	Rn.160166	Up	Bc
12	Selenbp1	NM_080892	Rn.16617	Up	Bc
13	-	TC561220	-	Down	Bc
14	Cdkn1c	XM_341966	-	Down	Bc
15	Cdkn1c	NM_182735	Rn.162507	Down	Bc
16	-	NM_001013853	Rn.163132	Down	Bc
17	Cdkn1c	NM_182735	Rn.162507	Down	Bc
18	MGC72973	NM_198776	Rn.36966	Down	Bc
19	-	AI045044	Rn.166087	Down	Bc
20	Me2_predicted	XM_225729	Rn.38235	Down	Bc
21	Gda	NM_031776	Rn.161897	Down	Bc
22	LOC300760	XM_236308	-	Down	Bc
23	Susd2_predicted	XM_215372	Rn.161744	Down	Bc
24	Susd2_predicted	XM_215372	Rn.161744	Down	Bc
25	Hpd	NM_017233	Rn.3664	Down	Bc
26	Slfn3	NM_053687	-	Up	Bl
27	-	AA963075	Rn.73451	Up	Bl
28	S100a9	NM_053587	Rn.6703	Up	Bl
29	Bnc1_predicted	XM_344917	-	Down	Bl
30	Slc6a3	NM_012694	Rn.10093	Up	Hy
31	Cga	J00757	Rn.10589	Up	Hy
32	Cga	NM_053918	Rn.10589	Up	Hy
33	-	AI044887	Rn.5827	Down	Hy
34	-	BF398607	Rn.45255	Down	Hy
35	Avp	NM_016992	Rn.9976	Up	St
36	Neurod2	NM_019326	Rn.10724	Up	St
37	-	AW914894	Rn.10267	Up	St
38	Vip	XM_217838	Rn.18675	Up	St
39	-	XM_576570	Rn.22624	Up	St
40	-	TC524999	-	Up	St
41	Slc17a7	NM_053859	Rn.10267	Up	St
42	-	BF281936	-	Up	St
43	-	CO403684	-	Up	St
44	-	CB582871	Rn.13498	Up	St
45	Cck	BM382824	Rn.9781	Up	St
46	Sstr1	NM_012719	#N/A	Up	St
47	Cort	NM_012835	Rn.42915	Up	St
48	Nrn1	NM_053346	Rn.10490	Up	St
49	C1ql3_predicted	XM_225579	Rn.3546	Up	St
50	Prss12	NM_053504	-	Up	St
51	-	TC558785	Rn.86653	Up	St
52	-	TC562720	-	Up	St
53	-	TC519964	-	Up	St

No	Target(Gene)Symbol	Target Accession	UniGene	Up/Down	生体由来試料
54	Nov	NM_030868	-	Up	St
55	-	XM_575489	Rn.162955	Up	St
56	Cck	NM_012829	Rn.162754	Up	St
57	Nptx1	NM_153735	Rn.9781	Up	St
58	RGD1308977_predicted	XM_214510	Rn.139226	Up	St
59	-	CB544275	Rn.54707	Up	St
60	-	BF398607	Rn.45255	Down	St
61	Ttr	NM_012681	Rn.1404	Down	St

[表中、

Bcは口腔内細胞であり；Blは血液であり；Hyは視床下部であり；Stは線条体である。]

[請求項2] ラットに評価対象である刺激を負荷する第1のステップと、

神経ペプチドホルモン活性を有する表81に示す遺伝子群、血圧調節に関連する表82に示す遺伝子群、食行動に関連する表83に示す遺伝子群、生体リズムに関連する表84に示す遺伝子群、からなる群から選択される少なくとも1種の遺伝子の発現量を指定の生体由来試料において測定する第2のステップと、

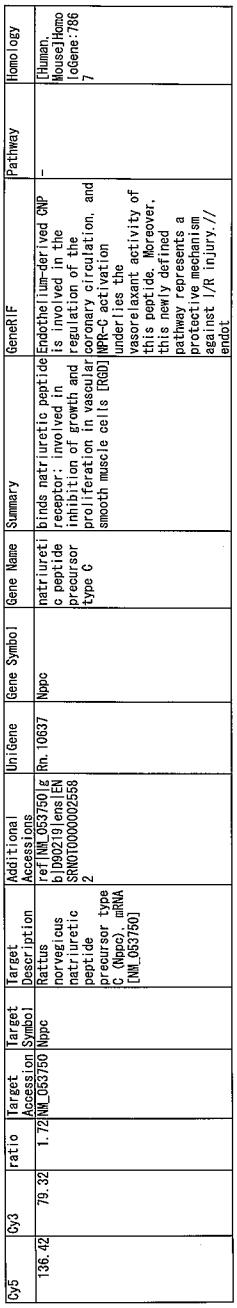
測定した前記遺伝子の発現量に基づいて、対象刺激が陽性刺激であるか否かを評価する第3のステップと

を含む、所与の刺激がラットに対する陽性刺激であるか否かを評価する方法。

[表2]

表81 線条体で発現増加した注目遺伝子
神経ペプチドホルモン活性 (GO ID: 5184)

Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Gene Symbol	Gene Name	Summary	GeneRIF	Pathway	Homology
106.09	45.98	2.31	NM_133570	Grp	Rattus norvegicus gastrin releasing peptide (Grp), mRNA [NM_133570]	ref|NM_133570|gb|M31176|ens|ENSRNOT00000022845|tc|TC569979	Rn.10930	Grp	gastrin releasing peptide	increases 5-HT neuronal activity in the hypothalamus PVN; inhibits feeding behavior	GRP mRNA was detected in rat kidney from embryonic day 19 to postnatal day 30 by RT-PCR// GRP in the central part of the amygdala inhibits feeding, may decrease the efficiency of eating, and may act as a satiety signal.// the increase in gastrin releasing	KEGG pathway: Neuroactive ligand-receptor interaction	[Human, Mouse]HomoloGene:1580
133.62	59.95	2.23	BM382824	Cck	UI-R-BT1-bko-b-06-0-UI.s1 UI-R-BT1 Rattus norvegicus cDNA clone UI-R-BT1-bko-b-06-0-UI 3', mRNA sequence [BM382824]	gb|BM382824	Rn.9781	Cck	cholecystokinin	brain-gut peptide with hemacrine and autocrine function in the gut [RGD]	CCK preadministration to obese rats did not affect ghrelin-induced food intake.// A study of the hypothesis that CCK in the rostral ventromedial medulla may engage descending pain facilitatory pathways to enhance spinal nociceptive transmission and attenu	KEGG pathway: Neuroactive ligand-receptor interaction	[Human, Mouse]HomoloGene:583
369.75	169.54	2.18	NM_012835	Cort	Rattus norvegicus cortistatin (Cort), mRNA [NM_012835]	ref|NM_012835|gb|U51919|ens|ENSRNOT00000018401|tc|TC570162	Rn.10490	Cort	cortistatin	inhibits growth hormone secretion; may act as a neuropeptide to mediate signaling via a somatostatin receptor subtype [RGD]	-	KEGG pathway: Neuroactive ligand-receptor interaction	[Human, Mouse]HomoloGene:997
52.29	27.34	1.91	NM_016989	Adcyap1	Rattus norvegicus adenylate cyclase activating polypeptide 1 (Adcyap1), mRNA [NM_016989]	ref|NM_016989|ref|XM_579383|gb|M63006|gb|XM_346860	Rn.37400	Adcyap1	adenylate cyclase activating polypeptide 1	regulatory protein that stimulates cell proliferation, induces differentiation, modulates neurotransmitter release, vasodilation, bronchodilation, and hormone release, and suppresses inflammatory responses [RGD]	These results indicate that a large number of PACAP neurons and a small number of BDNF neurons of the VMH project to the MCG.// The specificity of PAC1 receptor participation in pituitary adenylate cyclase-activating polypeptide (PACAP)-facilitated sex be	KEGG pathway: Neuroactive ligand-receptor interaction	[Human, Mouse]HomoloGene:869



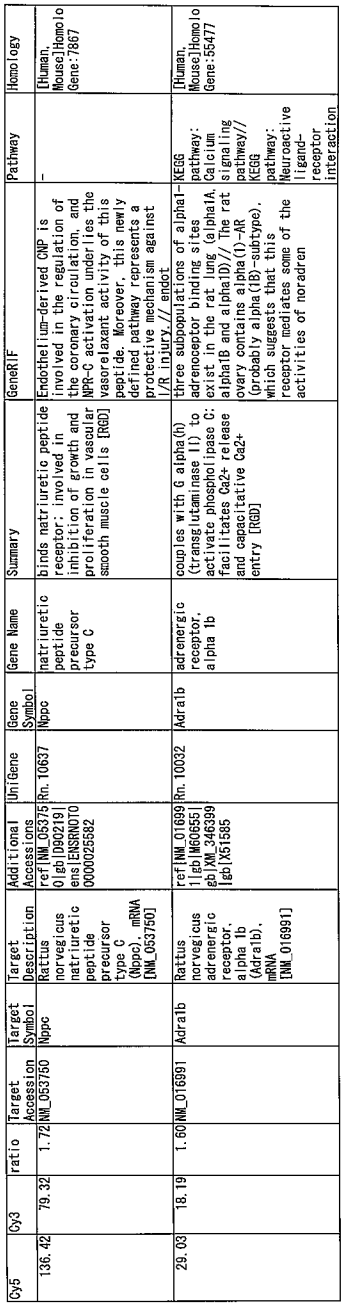
Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Gene Symbol	Gene Name	Summary	GeneRIF	Pathway	Homology
136.42	79.32	1.72	NM_053750	Nppc	Rattus norvegicus natriuretic peptide precursor type C (Nppc), mRNA [NM_053750]	ref|NM_053750|gb|D90219|ensEMBL|ENSRNOT00000002558|2	Rn.10637	Nppc	natriuretic peptide precursor type C	binds natriuretic peptide receptor; involved in inhibition of growth and proliferation in vascular smooth muscle cells [RGD]	Endothelium-derived CNP is involved in the regulation of the coronary circulation, and NPR-C activation underlies the vasorelaxant activity of this peptide. Moreover, this newly defined pathway represents a protective mechanism against I/R injury.// endot	-	[Human, Mouse]Homologene:7867

[表3]

表62 線条体で発現増加した注目遺伝子
血圧調節関連 (GO ID: 5088

Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Gene Symbol	Gene Name	Summary	GeneRIF	Pathway	Homology
72.06	24.25	2.97	NM_024483	Adra1d	Rattus norvegicus adrenergic receptor, alpha 1d (Adra1d), mRNA [NM_024483]	ref|NM_024483.2|gb|L31771|gb|M60654|ens|ENSRNOT00000028877	Rn.11314	Adra1d	adrenergic receptor, alpha 1d	adrenergic receptor showing high affinity for the antagonist WB4101 and agonists phenylephrine and methoxamine [RGD]	three subpopulations of alpha1-adrenoceptor binding sites exist in the rat lung (alpha1A, alpha1B and alpha1D)// cell surface expression of alpha1D-adrenergic receptors is controlled by heterodimerization with alpha1B-adrenergic receptors	KEGG pathway: Calcium signaling pathway	[Human, Mouse]Homolo Gene:551
160.27	57.88	18.27	NM_016992	Avp	Rattus norvegicus arginine vasopressin (Avp), mRNA [NM_016992]	ref|NM_016992.2|gb|M25646|gb|X01637|gb|V01276	Rn.9976	Avp	arginine vasopressin	neuropeptide hormone: involved in vasoconstriction to regulate blood pressure and smooth muscle contraction during parturition and lactation [RGD]	These data suggest that testosterone attenuates light-enhanced startle, but not fear-potentiated startle, through a mechanism that may involve AVP.// Both the magnocellular and the parvocellular hypothalamic vasopressin systems are capable of expressing t	KEGG pathway: Neuroactive ligand-receptor interaction	[Human, Mouse]Homolo Gene:417

Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Gene Symbol	Gene Name	Summary	GeneRIF	Pathway	Homology
232.63	99.84	2.33	XM_217838	Vip	PREDICTED: Rattus norvegicus vasoactive intestinal polypeptide (Vip), mRNA [XM_217838]	ref|XM_217838|gb|X02341|ens|ENSRNOT00000025477|tc|TC537816	Rn.18675	Vip	vasoactive intestinal polypeptide	peptide that causes vasodilation [RGD]	Vasoactive intestinal polypeptide regulates dynamic changes in astrocyte morphometry: impact on gonadotropin-releasing hormone neurons// Significant changes in NPY and VIP prostate nerve fibers, showing an increase in periurethral ducts at sex maturation.// Co-expression patterns of the neuropeptides vasoactive intestinal peptide and cholecystokinin with the transduction molecules alpha-gustducin and T1R2 in rat taste receptor cells.// VIP had a modulatory action on jejunal potassium absorption when injected into the nucleus tractus solitarius.// VIP can modulate not only immune responses but also hormonal responses during acute inflammation.// The increased noradrenergic noncholinergic and the decreased effects of VIP in mediating inhibitory nerves may largely relate to the peristaltic abnormalities seen in the isografted LEW rat // Aging reduces vasoactive intestinal peptide (VIP) receptor mRNA and eliminates diurnal expression of VIP mRNA within the suprachiasmatic nucleus of aged male rats.// (The rest is omitted.)	KEGG pathway: Neuroactive ligand-receptor interaction	[Human, Mouse]Homolo Gene:2539
53.01	25.47	2.08	NM_012612	Nppa	Rattus norvegicus natriuretic peptide precursor type A (Nppa), mRNA [NM_012612]	ref|NM_012612|gb|X00665|gb|M27498|ens|ENSRNOT00000011005	Rn.2004	Nppa	natriuretic peptide precursor type A	peptide involved in the control of fluid volume and vascular function [RGD]	The downregulation of ANP and NPRC in retinas of diabetic rats suggests a role for this peptide in experimental diabetic retinopathy.// The ANP might play a role on the synthesis of the oxytocin since ANP and its mRNA appear earlier than oxytocin.// SERCA	-	[Human, Mouse]Homolo Gene:4498



Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Gene Symbol	Gene Name	Summary	GeneRIF	Pathway	Homology
136.42	79.32	1.72	NM_053750	Nppc	Rattus norvegicus natriuretic peptide precursor type C (Nppc), mRNA [NM_053750]	ref|NM_053750.1|Ogb|D90219|ens|ENSRNOT00000025582	Rn.10637	Nppc	natriuretic peptide precursor type C	binds natriuretic peptide receptor; involved in inhibition of growth and proliferation in vascular smooth muscle cells [RGD]	Endothelium-derived CNP is involved in the regulation of the coronary circulation, and NPR-C activation underlies the vasorelaxant activity of this peptide. Moreover, this newly defined pathway represents a protective mechanism against I/R injury.// endot	-	[Human, Mouse]Homolo Gene:7867
29.03	18.19	1.60	NM_016991	Adra1b	Rattus norvegicus adrenergic receptor, alpha 1b (Adra1b), mRNA [NM_016991]	ref|NM_016991.1|gb|M60655|gb|XM_346399|gb|X51585	Rn.10032	Adra1b	adrenergic receptor, alpha 1b	couples with G alpha(h) (transglutaminase II) to activate phospholipase C; facilitates Ca2+ release and capacitative Ca2+ entry [RGD]	three subpopulations of alpha1-adrenoceptor binding sites exist in the rat lung (alpha1A, alpha1B and alpha1D)// The rat ovary contains alpha(1)-AR (probably alpha(1B)-subtype), which suggests that this receptor mediates some of the activities of noradren	KEGG pathway: Calcium signaling pathway// KEGG pathway: Neuroactive ligand-receptor interaction	[Human, Mouse]Homolo Gene:55477

[表4]

表83 線条体で発現増加した注目遺伝子
食行動関連 (GO ID: 7631)

Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Gene Symbol	Gene Name	Summary	GeneRIF	Pathway	Homology
133.62	59.95	2.23	BM382824	Cck	UI-R-BT1-bko-b-06-0-UI.s1 UI-R-BT1 Rattus norvegicus cDNA clone UI-R-BT1-bko-b-06-0-UI 3', mRNA sequence [BM382824]	gb|BM382824	Rn.9781	Cck	cholecystokinin	brain-gut peptide with hemaorine and autoorine function in the gut [RGD]	CCK preadministration to obese rats did not affect ghrelin-induced food intake.// A study of the hypothesis that CCK in the rostral ventromedial medulla may engage descending pain facilitatory pathways to enhance spinal nociceptive transmission and attenu	KEGG pathway: Neuroactive ligand-receptor interaction	[Human, Mouse]HomoloGene:583
49.04	25.32	1.94	NM_012513	Bdnf	Rattus norvegicus brain derived neurotrophic factor (Bdnf), mRNA [NM_012513]	ref|NM_012513 |gb|X67108|gb |AY559250|gb |AY559249	Rn.11266	Bdnf	brain derived neurotrophic factor	plays a role in the development of hippocampal long term potentiation: involved in regulation of synaptic plasticity [RGD]	Overall, these results suggest that activity-dependent scaling of inhibitory synaptic strength can be modulated by BDNF/TrkB-mediated signaling.// Role of specific BDNF promoter regions and regulatory sequences in stimulant-induced alterations in BDNF exp	KEGG pathway: Huntington's disease// KEGG pathway: MAPK signaling pathway	[Human, Mouse]HomoloGene:7245
418.54	264.83	1.58	NM_013165	Cckbr	Rattus norvegicus cholecystokinin B receptor (Cckbr), mRNA [NM_013165]	ref|NM_013165 |gb|M99418|en s|ENSRNOT0000 00240771|tc|TC 570009	Rn.90997	Cckbr	cholecystokinin B receptor	Cholecystokinin was one of the first gastrointestinal peptides discovered in the mammalian brain. Cholecystokinin receptors are members of the G protein-coupled receptor superfamily, stimulating phosphatidylinositol turnover and intracellular calcium mobi	The present results substantiate the view that dorsolateral periaqueductal gray CCK(2) receptors modulate panic-related behaviors.// analysis of interspecies polymorphism in the human and rat cholecystokinin receptor-2 and its effect on the cholecystokini	KEGG pathway: Calcium signaling pathway// KEGG pathway: Neuroactive ligand-receptor interaction	[Human, Mouse]HomoloGene:7258
21.16	13.92	1.52	NM_012625	Pmch	Rattus norvegicus pro-melanin-concentrating hormone (Pmch), mRNA [NM_012625]	ref|NM_012625 |gb|M29712|gb |M62641|ens|E NSRNOT0000000 6174	Rn.9675	Pmch	pro-melanin-concentrating hormone	cyclic neuropeptide: induces hippocampal synaptic transmission [RGD]	MCH is involved in the regulation of LHRH release in the female rat.// glucocorticoids may promote food intake in part by potentiating the orexigenic actions of MCH without affecting the actions of orexin A and glucocorticoids act indirectly to influence	KEGG pathway: Neuroactive ligand-receptor interaction	[Human, Mouse]HomoloGene:37653

[表5]

表84 線条体で発現増加した注目遺伝子
生体リズム関連 (GO ID: 7623,48511)

Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Gene Symbol	Gene Name	Summary	GeneRIF	Pathway	Homology
369.75	169.54	2.18	NM_012835	Cort	Rattus norvegicus cortistatin (Cort), mRNA [NM_012835]	ref|NM_012835|gb|U51919|ens|ENSRNOT00000018401|tc|TC570162	Rn.10490	Cort	cortistatin	inhibits growth hormone secretion; may act as a neuropeptide to mediate signaling via a somatostatin receptor subtype [RGD]	-	KEGG pathway: Neuroactive ligand-receptor interaction	[Human, Mouse]Homologene:997
1131.31	583.92	1.94	NM_181370	Hs3st2	Rattus norvegicus heparan sulfate (glucosamine) 3-O-sulfotransferase 2 (Hs3st2), mRNA [NM_181370]	ref|NM_181370|gb|AY424087|ens|ENSRNOT00000023773|tc|TC569483	Rn.49010	Hs3st2	heparan sulfate (glucosamine) 3-O-sulfotransferase 2	catalyzes the transfer of sulfate groups onto the 3-OH site of glucosamine groups in heparan sulfate proteoglycans [RGD]	3-O sulfation catalyzed by HS 3-O-sulfotransferase (3-OST2) is predominantly restricted to daytime pineal glands in rats	-	[Human, Mouse]Homologene:21220
140.87	77.66	1.81	NM_013104	Igfbp6	Rattus norvegicus insulin-like growth factor binding protein 6 (Igfbp6). mRNA [NM_013104]	ref|NM_013104|gb|M69055|gb|BG673588|ens|ENSRNOT00000014807	Rn.6431	Igfbp6	insulin-like growth factor binding protein 6	high-affinity IGF binding protein with substantially greater affinity for insulin-like growth factor-II (IGF-II) than IGF-I [RGD]	IGFBP-6, a new negative effector of oligodendrocyte survival and differentiation, is expressed and localized to the Golgi complex in rat oligodendrocyte precursor (O2A) cells.// IGFBP6 has a role in binding to endothelial cells and in transendothelial tra	-	[Human, Mouse]Homologene:1641
111.82	86.27	1.69	XM_345102	Atoh7_predicted	PREDICTED: Rattus norvegicus atonal homolog 7 (Drosophila) (predicted) (Atoh7_predicted), mRNA [XM_345102]	ref|XM_345102|ens|ENSRNOT00000000432	Rn.133599	Atoh7_predicted	atonal homolog 7 (Drosophila) (predicted)	-	-	-	[Human, Mouse]Homologene:32338
11976.21	7334.77	1.63	NM_013015	Ptgds	Rattus norvegicus prostaglandin D2 synthase (Ptgds), mRNA [NM_013015]	ref|NM_013015|gb|JU04488|gb|M94134|ens|ENSRNOT00000020926	Rn.11400	Ptgds	prostaglandin D2 synthase	catalyzes conversion of prostaglandin H2 to prostaglandin D2, a major mediates sleep, body temperature, hormone release, and odor responses [RGD]	Gene expression is regulated by Hes-1 through E-box and interleukin-1 beta via two NF-Kappa B elements in rat leptomeningeal cells.	KEGG pathway: Arachidonic acid metabolism	[Human, Mouse]Homologene:737

[請求項3] ラットに評価対象である刺激を負荷する第1のステップと、

下記の表2に示す遺伝子群から選択される少なくとも1種の遺伝子の発現量を指定の生体由来試料において測定する第2のステップと、

測定した前記遺伝子の発現量に基づいて、対象刺激が陽性刺激であるか否かを評価する第3のステップと

を含む、所与の刺激がラットに対する陽性刺激であるか否かを評価する方法。

[表6]

表２

No	Target(Gene)Symbol	Target Accession	UniGene	Up/Down	生体由来試料
62	-	NM_001013853	Rn.163132	Up	BI
63	RGD1308591_predicted	XM_230631	Rn.22314	Up	BI
64	-	TC545861	-	Up	BI
65	-	TC559380	-	Up	BI
66	-	TC551459	-	Up	BI
67	-	TC560203	-	Up	BI
68	RGD1309846_predicted	XM_231625	-	Up	BI
69	-	TC532273	-	Up	BI
70	-	TC568188	-	Up	BI
71	-	XM_343940	-	Up	BI
72	-	TC549515	-	Up	BI
73	-	TC555328	-	Up	BI
74	MGC72973	NM_198776	Rn.36966	Up	BI
75	-	TC549495	-	Up	BI
76	-	CB544341	Rn.6526	Up	BI
77	Gabrd	NM_017289	Rn.10927	Up	BI
78	-	TC542956	-	Up	BI
79	Olr1572_predicted	XM_221921	-	Up	BI
80	-	TC525431	-	Up	BI
81	Strn4_predicted	XM_218432	Rn.137083	Up	BI
82	-	A_44_P337592	-	Up	BI
83	-	AW143701	Rn.17098	Up	BI
84	Rnf40	NM_153471	Rn.162466	Up	BI
85	-	TC544981	-	Up	BI
86	Bst2	NM_198134	Rn.32168	Up	BI
87	LOC361100	XM_341386	Rn.104585	Up	BI
88	-	BQ211845	Rn.165621	Up	BI
89	-	AA900394	Rn.165621	Up	BI
90	Olr1234_predicted	NM_001000446	Rn.143535	Up	BI
91	-	AW918996	Rn.7470	Up	BI
92	RGD1307160_predicted	XM_219953	Rn.61235	Up	BI
93	-	BI395434	-	Up	BI
94	-	XM_215067	-	Up	BI
95	-	TC561947	-	Up	BI
96	-	A_44_P426640	-	Up	BI
97	-	A_44_P368450	-	Up	BI
98	Cox6a2	NM_012812	Rn.5119	Up	BI
99	-	AA925776	Rn.11283	Up	BI
100	-	TC528645	Rn.14945	Up	BI
101	Ltap_predicted	XM_222896	Rn.19850	Up	BI
102	-	XM_346943	Rn.22985	Up	BI
103	-	AA900371	Rn.161752	Down	BI
104	-	AA900000	Rn.103172	Down	BI
105	-	AA899215	-	Down	BI
106	-	TC555778	-	Down	BI
107	Jund	NM_138875	Rn.46225	Down	BI
108	-	AI556201	Rn.48701	Down	BI
109	-	BI302367	Rn.94935	Down	BI
110	-	BI277534	Rn.122326	Down	BI
111	-	BF416864	Rn.161752	Down	BI
112	RGD1311005_predicted	XM_341099	Rn.65800	Down	BI
113	-	XM_575687	Rn.162772	Down	BI
114	-	BI277534	Rn.122326	Down	BI
115	-	BI277534	Rn.122326	Down	BI
116	Rpl26_predicted	XM_213346	Rn.144702	Down	BI
117	-	BI277534	Rn.122326	Down	BI
118	Mrps18c_predicted	XM_214003	Rn.105741	Down	BI
119	Plp	NM_030990	Rn.4550	Down	BI

No	Target(Gene)Symbol	Target Accession	UniGene	Up/Down	生体由来試料
120	-	BI277534	Rn.7999	Down	BI
121	Polr2k_predicted	XM_219604	-	Down	BI
122	-	BI277534	-	Down	BI
123	-	BI277534	-	Down	BI
124	-	NM_001014207	Rn.137575	Down	BI
125	-	TC559328	-	Down	BI
126	-	BI277534	Rn.122326	Down	BI
127	Cma1	NM_013092	Rn.10182	Down	BI
128	Rpl37	BI277661	Rn.129486	Down	BI
129	-	TC559328	Rn.122326	Down	BI
130	-	BE098803	Rn.122326	Down	BI
131	-	BI277534	Rn.122326	Down	BI
132	-	AI231572	Rn.1180	Down	BI
133	Slpi	NM_053372	Rn.18560	Up	BI
134	Slpi	NM_053372	Rn.18560	Up	BI
135	LOC296356	XM_215940	Rn.144851	Up	BI
136	Fn1	NM_019143	Rn.1604	Up	BI
137	-	NM_001013853	Rn.163132	Up	BI
138	-	TC551459	-	Up	BI
139	Adn	XM_343169	Rn.16172	Up	BI
140	Timp2	NM_021989	Rn.10161	Up	BI
141	-	NM_001013110	Rn.91296	Up	BI
142	Ptpn11	NM_013088	Rn.98209	Up	BI
143	LOC298270	XM_233230	Rn.162076	Down	BI
144	LOC292088	XM_238058	-	Down	BI
145	Slc6a3	NM_012694	Rn.10093	Up	Hy
146	-	TC543527	-	Up	Hy
147	-	BE108176	Rn.3464	Up	Hy
148	Galp	NM_022633	Rn.48754	Up	Hy
149	Pomc2	NM_139326	Rn.108195	Up	Hy
150	-	BF398607	Rn.45255	Down	Hy
151	Chrna3	NM_052805	Rn.10996	Down	Hy
152	-	AW914894	Rn.10267	Down	Hy
153	Shox2	NM_013028	Rn.11258	Down	Hy
154	LOC289633	XM_223426	Rn.123835	Down	Hy
155	Prpf31_predicted	XM_218173	Rn.99310	Down	Hy
156	-	TC530743	-	Down	Hy
157	Slc5a7	NM_053521	Rn.44872	Down	Hy
158	Ttr	NM_012681	Rn.1404	Down	Hy
159	Lhx9	NM_181367	Rn.75111	Down	Hy
160	-	AW527509	Rn.41179	Down	Hy
161	Shox2	NM_013028	Rn.11258	Down	Hy
162	Grifin	NM_057187	Rn.26894	Down	Hy
163	-	TC556932	-	Down	Hy
164	Zic1	NM_022677	Rn.161923	Down	Hy
165	Prkcd	NM_133307	Rn.98279	Down	Hy
166	Slc18a3	NM_031663	Rn.9987	Down	Hy
167	Cpne4_predicted	XM_345977	Rn.124862	Down	Hy
168	-	TC519964	-	Down	Hy
169	RGD1311951_predicted	XM_237334	Rn.70007	Down	Hy
170	-	AI178665	Rn.58356	Down	Hy
171	-	BC092605	Rn.22271	Down	Hy
172	-	TC543142	-	Down	Hy
173	-	TC567761	-	Down	Hy
174	Ramp3	NM_020100	Rn.48672	Down	Hy
175	Lef1	NM_130429	Rn.21926	Down	Hy
176	Irx5_predicted	XM_225077	-	Down	Hy
177	MGC95205	NM_001005540	Rn.12833	Down	Hy
178	-	BE126741	-	Down	Hy
179	-	TC551026	-	Down	Hy

No	Target(Gene)Symbol	Target Accession	UniGene	Up/Down	生体由来試料
180	Cga	J00757	Rn.10589	Up	Hy
181	Cga	NM_053918	Rn.10589	Up	Hy
182	Shox2	NM_013028	Rn.11258	Up	Hy
183	-	BC092605	Rn.22271	Up	Hy
184	-	BE108176	Rn.3464	Up	Hy
185	Prkcd	NM_133307	Rn.98279	Up	Hy
186	-	TC543263	-	Up	Hy
187	Vip	XM_217838	Rn.18675	Up	Hy
188	Grifin	NM_057187	Rn.26894	Up	Hy
189	-	TC530743	-	Up	Hy
190	Nexn	NM_139230	Rn.107975	Up	Hy
191	Ramp3	NM_020100	Rn.48672	Up	Hy
192	-	XM_575030	Rn.7078	Up	Hy
193	Ttr	NM_012681	Rn.1404	Down	Hy
194	-	BF398607	Rn.45255	Down	Hy
195	Gnrh1	NM_012767	Rn.59459	Down	Hy
196	Foxg1	NM_012560	Rn.9864	Down	Hy
197	Prpf31_predicted	XM_218173	Rn.99310	Down	Hy
198	Slc18a3	NM_031663	Rn.9987	Down	Hy
199	Ngfr	NM_012610	Rn.10980	Down	Hy
200	Zfyve9_predicted	XM_233341	Rn.23612	Down	Hy
201	Avp	NM_016992	Rn.9976	Down	Hy
202	-	AI013718	-	Down	Hy
203	Slc5a7	NM_053521	Rn.44872	Down	Hy
204	-	BQ194469	Rn.161764	Up	St
205	LOC290372	XM_237952	Rn.19611	Up	St
206	-	BG672648	-	Up	St
207	-	BF398607	Rn.45255	Down	St
208	Prpf31_predicted	XM_218173	Rn.99310	Down	St
209	Vip	XM_217838	Rn.18675	Down	St
210	Slc17a7	NM_053859	Rn.10267	Down	St
211	Cck	BM382824	Rn.9781	Down	St
212	-	AW914894	#N/A	Down	St
213	Homer1	U92079	Rn.10267	Down	St
214	Cck	NM_012829	-	Down	St
215	Tjp1_predicted	XM_218747	Rn.101871	Up	St
216	Tjp1_predicted	XM_218747	Rn.101871	Up	St
217	Tjp1_predicted	XM_218747	Rn.101871	Up	St
218	-	AW144721	Rn.3039	Up	St
219	-	AA963075	Rn.73451	Up	St
220	Sv2b	NM_057207	Rn.58137	Up	St
221	-	BG672648	-	Up	St
222	Avp	NM_016992	Rn.9976	Up	St
223	-	BF398607	Rn.45255	Down	St
224	Prpf31_predicted	XM_218173	Rn.99310	Down	St
225	-	TC560395	-	Down	St
226	RGD:1303100	NM_001003929	Rn.55036	Down	St
227	Slc17a7	NM_053859	Rn.10267	Down	St
228	-	A_44_P302611	-	Down	St
229	-	BF546193	Rn.174580	Down	St
230	RGD1309846_predicted	XM_231625	-	Down	St
231	Bhlhb3	NM_133303	Rn.10784	Down	St
232	Cck	NM_012829	Rn.9781	Down	St
233	-	AW914894	Rn.10267	Down	St
234	Homer1	U92079	-	Down	St
235	Crisp1	NM_022859	Rn.10102	Up	Sg
236	-	ENSRNOT00000040037	-	Up	Sg
237	Prpg2	NM_172065	Rn.29950	Up	Sg
238	Psp	NM_052808	Rn.9766	Up	Sg
239	-	BF415117	Rn.2635	Up	Sg

No	Target(Gene)Symbol	Target Accession	UniGene	Up/Down	生体由来試料
240	Mgat3	NM_019239	Rn.9803	Up	Sg
241	-	TC519989	-	Up	Sg
242	-	XM_341973	-	Up	Sg
243	Scgb2a1	NM_080770	Rn.144559	Up	Sg
244	-	A_44_P875993	-	Up	Sg
245	-	M87788	Rn.118336	Up	Sg
246	Amy2_predicted	XM_345278	Rn.67070	Up	Sg
247	Amy1	NM_001010970	Rn.116361	Up	Sg
248	-	XM_342323	-	Up	Sg
249	-	CB545830	Rn.157214	Up	Sg
250	RGD1311424_predicted	XM_343001	Rn.57800	Up	Sg
251	-	BI288013	Rn.40911	Up	Sg
252	Mycl1	XM_233490	Rn.41400	Up	Sg
253	-	NM_001013941	Rn.161900	Up	Sg
254	Dusp1	NM_053769	Rn.98260	Up	Sg
255	LOC366764	XM_345751	-	Up	Sg
256	-	L07402	Rn.119901	Down	Sg
257	LOC314509	XM_234661	Rn.110660	Down	Sg
258	-	Z93368	Rn.110663	Down	Sg
259	LOC299469	XM_234749	-	Down	Sg
260	LOC366769	XM_345756	Rn.126669	Down	Sg
261	-	Z93350	Rn.10956	Down	Sg
262	-	ENSRNOT00000043097	-	Down	Sg
263	-	XM_575540	Rn.117940	Down	Sg
264	LOC299551	XM_234830	-	Down	Sg
265	LOC366758	XM_345745	Rn.112181	Down	Sg
266	-	XM_345746	-	Down	Sg
267	Prpf31_predicted	XM_218173	Rn.99310	Down	Sg
268	-	NM_001014264	Rn.102149	Down	Sg
269	-	BE098883	Rn.15951	Down	Sg
270	LOC314512	XM_234676	Rn.110661	Down	Sg
271	LOC297260	XM_231999	-	Down	Sg
272	Fetub	NM_053348	Rn.2464	Down	Sg
273	-	BC092624	Rn.163825	Down	Sg
274	LOC366758	XM_345745	Rn.112181	Down	Sg
275	-	XM_234741	-	Down	Sg
276	Igkv28	L17078	Rn.92371	Down	Sg
277	-	BF560128	Rn.28431	Down	Sg
278	-	XM_345749	-	Up	Sg
279	Klk1c10	XM_214947	Rn.136578	Up	Sg
280	Klks3	NM_175759	Rn.34527	Up	Sg
281	Ton	NM_012677	Rn.9882	Up	Sg
282	Vcsa1	NM_012684	Rn.9927	Up	Sg
283	RGD:619853	NM_022709	Rn.162774	Up	Sg
284	Klk12	NM_001005382	Rn.141980	Up	Sg
285	Olr1223_predicted	NM_001000441	Rn.143544	Up	Sg
286	RGD:735032	XM_214931	Rn.107068	Up	Sg
287	-	XM_341973	-	Up	Sg
288	Vcsa1	NM_012684	Rn.9927	Up	Sg
289	Acaca	NM_022193	Rn.44372	Up	Sg
290	-	NM_001013067	Rn.79264	Up	Sg
291	Egf	NM_012842	Rn.6075	Up	Sg
292	RGD:735160	NM_198685	Rn.79319	Up	Sg
293	Svs6_predicted	XM_342575	Rn.145207	Up	Sg
294	-	CB545830	Rn.157214	Up	Sg
295	Klk7	NM_012593	Rn.144553	Up	Sg
296	Pip	NM_022708	Rn.78367	Up	Sg
297	RGD:735032	XM_214931	Rn.107068	Up	Sg
298	Muc10	NM_133513	Rn.10113	Up	Sg
299	RGD:1303220	NM_001003977	Rn.141979	Up	Sg

No	Target(Gene)Symbol	Target Accession	UniGene	Up/Down	生体由来試料
300	Grpca	NM_181440	Rn.10942	Up	Sg
301	-	TC524810	-	Up	Sg
302	-	AA963004	Rn.24539	Up	Sg
303	Scgb2a1	NM_080770	Rn.144559	Up	Sg
304	Ngfg	NM_031523	Rn.11331	Up	Sg
305	-	ENSRNOT00000042436	-	Up	Sg
306	RGD:735228	XM_214939	Rn.21391	Up	Sg
307	Gpr83	NM_080411	Rn.63075	Up	Sg
308	-	NM_001013941	Rn.161900	Up	Sg
309	Tgfb2	NM_031131	Rn.24539	Up	Sg
310	Prpg2	NM_172065	Rn.29950	Up	Sg
311	Mpv17l_predicted	XM_340739	Rn.22842	Up	Sg
312	Npas3_predicted	XM_234124	Rn.135138	Up	Sg
313	LOC290262	XM_224224	-	Up	Sg
314	LOC287803	XM_221081	Rn.163171	Up	Sg
315	LOC362603	XM_347064	Rn.91410	Up	Sg
316	Oxt	NM_012996	Rn.48915	Up	Sg
317	Vgll2_predicted	XM_228170	Rn.17643	Up	Sg
318	Th	NM_012740	Rn.11082	Up	Sg
319	RGD1309050_predicted	XM_240734	Rn.6819	Up	Sg
320	B4galt6	NM_031740	-	Up	Sg
321	LOC361702	XM_341985	Rn.61872	Up	Sg
322	-	AA956502	-	Up	Sg
323	-	CK595775	Rn.125806	Up	Sg
324	Rbp3	XM_341400	Rn.41214	Up	Sg
325	Lrrc27_predicted	XM_341954	Rn.162479	Up	Sg
326	RGD1308967_predicted	XM_232748	Rn.143980	Up	Sg
327	Fmo5	NM_144739	Rn.7038	Up	Sg
328	LOC361340	XM_341623	Rn.132740	Up	Sg
329	Tbx5_predicted	NM_001009964	Rn.6327	Up	Sg
330	-	X89700	-	Up	Sg
331	Kif23_predicted	XM_236313	Rn.63734	Up	Sg
332	-	ENSRNOT00000016430	-	Up	Sg
333	LOC309745	XM_228133	Rn.84956	Up	Sg
334	Riok3_predicted	XM_341578	Rn.4181	Up	Sg
335	Lyl1	NM_001007677	Rn.17352	Up	Sg
336	Zfp393_predicted	XM_233437	Rn.159750	Up	Sg
337	Mxi1	NM_013160	Rn.37510	Up	Sg
338	Gdf5	AB087404	Rn.127822	Up	Sg
339	-	AW917276	Rn.7332	Up	Sg
340	B4galt6	NM_031740	-	Up	Sg
341	LOC313633	XM_233574	Rn.27233	Up	Sg
342	-	TC541862	-	Up	Sg
343	-	NM_001024751	Rn.76073	Up	Sg
344	Erabp	NM_024136	Rn.10362	Up	Sg
345	-	XM_345742	-	Up	Sg
346	Limd1_predicted	XM_236734	Rn.161977	Up	Sg
347	RGD1309038_predicted	XM_225887	Rn.24687	Up	Sg
348	-	TC562194	-	Up	Sg
349	Actn3	NM_133424	Rn.17592	Up	Sg
350	-	CB547130	Rn.179696	Up	Sg
351	Cart1	NM_012921	Rn.9282	Up	Sg
352	RGD1311019_predicted	XM_238442	Rn.18688	Up	Sg
353	Znf507_predicted	XM_218515	Rn.141981	Up	Sg
354	LOC310631	XM_227403	Rn.104095	Up	Sg
355	-	AI045861	Rn.10526	Up	Sg
356	Ccl17	NM_057151	Rn.46679	Up	Sg
357	Arl12_predicted	XM_220907	Rn.18110	Up	Sg
358	-	TC559056	Rn.147866	Up	Sg
359	Mobp	NM_012720	Rn.91185	Up	Sg

No	Target(Gene)Symbol	Target Accession	UniGene	Up/Down	生体由来試料
360	Golph2_predicted	XM_225147	Rn.1545	Up	Sg
361	-	ENSRNOT00000038788	-	Up	Sg
362	-	AA800803	Rn.102152	Up	Sg
363	Mospd4_predicted	BF400026	Rn.63770	Up	Sg
364	-	XM_578308	-	Up	Sg
365	Rasgrp4	NM_130824	Rn.81227	Up	Sg
366	-	NM_001024273	Rn.14280	Up	Sg
367	-	A_44_P882921	-	Up	Sg
368	-	A_44_P729420	-	Up	Sg
369	Hsf4_predicted	XM_214668	Rn.163399	Up	Sg
370	Znf297	NM_001009172	Rn.17135	Up	Sg
371	-	TC540693	-	Up	Sg
372	LOC301121	XM_236777	Rn.35756	Up	Sg
373	Spata18	NM_199374	Rn.27773	Up	Sg
374	LOC367391	XM_346122	Rn.83054	Up	Sg
375	P2rx2	NM_053656	Rn.88799	Up	Sg
376	-	TC545251	-	Up	Sg
377	-	A_44_P278941	-	Up	Sg
378	Andpro	NM_012718	Rn.9977	Up	Sg
379	Sult1a2	NM_031732	Rn.9937	Up	Sg
380	-	NM_001014232	Rn.8173	Up	Sg
381	Sprr3_predicted	XM_227339	Rn.19820	Up	Sg
382	Mgat4a_predicted	NM_001012225	Rn.145359	Up	Sg
383	Hapln1	NM_019189	Rn.50531	Up	Sg
384	-	BM388083	Rn.41133	Up	Sg
385	-	BG380409	Rn.143966	Up	Sg
386	Sds	NM_053962	Rn.9918	Up	Sg
387	Cngb1	AJ224680	Rn.10733	Up	Sg
388	-	NM_001024983	Rn.152074	Up	Sg
389	LOC365807	XM_345218	Rn.111884	Up	Sg
390	RGD:628846	NM_031605	Rn.10034	Up	Sg
391	-	BF567941	Rn.169222	Up	Sg
392	RGD:727806	NM_001001508	Rn.58355	Up	Sg
393	Pex11a	NM_053487	Rn.14519	Up	Sg
394	-	AA963232	Rn.1053	Up	Sg
395	-	AW142782	Rn.43391	Up	Sg
396	-	A_44_P260574	Rn.43391	Up	Sg
397	Adcyap1	NM_016989	Rn.37400	Up	Sg
398	Nr4a1	NM_024388	Rn.10000	Up	Sg
399	Spt2_predicted	XM_238528	-	Up	Sg
400	-	TC538568	-	Up	Sg
401	-	BF290953	Rn.24673	Up	Sg
402	LOC296782	XM_216075	-	Up	Sg
403	-	XM_343522	-	Up	Sg
404	Akr1cl1_predicted	XM_341550	Rn.132469	Up	Sg
405	-	A_44_P304740	-	Up	Sg
406	-	AW142587	Rn.9491	Up	Sg
407	Itm2c_predicted	NM_001009674	Rn.8450	Up	Sg
408	-	AW916070	Rn.167735	Up	Sg
409	-	TC531872	Rn.167735	Up	Sg
410	LOC300150	XM_235563	-	Up	Sg
411	-	ENSRNOT00000049913	-	Up	Sg
412	Nr1d1	NM_145775	Rn.29848	Up	Sg
413	RGD1308684_predicted	XM_341641	Rn.41567	Up	Sg
414	LOC365316	XM_344926	-	Up	Sg
415	Scnn1g	NM_017046	Rn.10360	Up	Sg
416	Gpx6	NM_147165	Rn.9852	Up	Sg
417	Lrp2	NM_030827	Rn.26430	Up	Sg
418	-	TC566080	-	Up	Sg
419	-	NM_001017383	Rn.22468	Up	Sg

No	Target(Gene)Symbol	Target Accession	UniGene	Up/Down	生体由来試料
420	-	BI279326	Rn. 48786	Up	Sg
421	LOC297757	XM_216317	Rn. 144410	Up	Sg
422	Pex11a	BC061835	Rn. 14519	Up	Sg
423	Cdh11	XM_341639	Rn. 8900	Up	Sg
424	RGD1306750_predicted	XM_347055	Rn. 48786	Up	Sg
425	LOC313589	XM_233520	Rn. 162826	Up	Sg
426	-	AA875449	Rn. 2923	Up	Sg
427	Duox2	NM_024141	Rn. 55542	Up	Sg
428	LOC474169	NM_001007015	Rn. 87496	Up	Sg
429	-	BC091324	Rn. 13679	Up	Sg
430	RGD:708361	NM_138547	Rn. 10021	Up	Sg
431	-	X55180	Rn. 117936	Up	Sg
432	LOC288979	XM_222564	Rn. 24014	Up	Sg
433	-	AW918545	Rn. 13679	Up	Sg
434	-	TC542673	Rn. 13679	Up	Sg
435	-	BG672648	-	Up	Sg
436	RGD:735199	NM_198734	Rn. 154471	Up	Sg
437	RGD1309403_predicted	XM_227140	Rn. 38949	Up	Sg
438	-	CO556754	Rn. 15953	Up	Sg
439	Muc19_predicted	XM_235593	Rn. 162964	Down	Sg
440	Smgb	NM_080775	Rn. 9925	Down	Sg
441	Rasl12_predicted	XM_236351	Rn. 147874	Down	Sg
442	Cdh22	NM_019161	Rn. 145674	Down	Sg
443	LOC314509	XM_234661	Rn. 110660	Down	Sg
444	RGD:708577	NM_133622	Rn. 9752	Down	Sg
445	Lman1l_predicted	XM_217166	-	Down	Sg
446	-	XM_214055	-	Down	Sg
447	Bpil1_predicted	XM_215892	Rn. 162713	Down	Sg
448	LOC362442	XM_342764	Rn. 77935	Down	Sg
449	LOC362442	XM_342764	Rn. 77935	Down	Sg
450	RGD:1303308	NM_001004236	Rn. 33830	Down	Sg
451	LOC292801	XM_218497	-	Down	Sg
452	-	A_44_P950925	-	Down	Sg
453	RGD1311224_predicted	XM_215767	Rn. 47550	Down	Sg
454	Kcne1	NM_012973	Rn. 9734	Down	Sg
455	Kntc1_predicted	XM_222157	Rn. 47918	Down	Sg
456	Mme	NM_012608	Rn. 33598	Down	Sg
457	Fetub	NM_053348	Rn. 2464	Down	Sg
458	Galnt12_predicted	XM_223905	-	Down	Sg
459	-	XM_344059	-	Down	Sg
460	-	NM_001013180	Rn. 30648	Down	Sg
461	Cox4i2	NM_053472	Rn. 7214	Down	Sg
462	Gnas	L10326	Rn. 31	Down	Sg
463	Runx3	NM_130425	Rn. 34220	Down	Sg
464	Olr1654_predicted	NM_021860	Rn. 138118	Down	Sg
465	Serpina1	NM_022519	Rn. 1419	Down	Sg
466	Igkv28	L17078	Rn. 92371	Down	Sg
467	Dlk1	NM_053744	Rn. 14547	Down	Sg
468	LOC299434	XM_234680	Rn. 134951	Down	Sg
469	LOC366769	XM_345756	Rn. 126669	Down	Sg
470	-	TC527103	Rn. 107412	Down	Sg
471	Creb3l4	XM_227391	Rn. 107412	Down	Sg
472	-	TC539429	Rn. 107412	Down	Sg
473	Galnt7	NM_022926	Rn. 144577	Down	Sg
474	Oit1_predicted	XM_214143	Rn. 38497	Down	Sg
475	-	L07410	-	Down	Sg
476	RGD1311701_predicted	XM_230278	Rn. 34843	Down	Sg
477	-	AF217591	Rn. 134336	Down	Sg
478	-	AW144181	-	Down	Sg
479	-	TC539049	-	Down	Sg

No	Target(Gene)Symbol	Target Accession	UniGene	Up/Down	生体由来試料
480	RGD:1303068	NM_203337	Rn.24125	Down	Sg
481	-	Z93368	Rn.167718	Down	Sg
482	-	AW144454	Rn.167718	Down	Sg
483	-	NM_001014264	Rn.102149	Down	Sg
484	RGD:620649	CA509211	Rn.3517	Down	Sg
485	-	XM_573320	Rn.163185	Down	Sg
486	Dnajc10_predicted	XM_215751	Rn.8642	Down	Sg
487	-	NM_001025041	Rn.162656	Down	Sg
488	-	M84148	Rn.134335	Down	Sg
489	Ces3	NM_133295	Rn.2549	Down	Sg
490	Dnajc10_predicted	XM_215751	Rn.8642	Down	Sg
491	Cdh22	NM_019161	Rn.145674	Down	Sg
492	-	L07402	-	Down	Sg
493	RGD:1303167	NM_212541	Rn.27480	Down	Sg
494	Ca3	NM_019292	Rn.1647	Down	Sg
495	Cyp2f2	NM_019303	Rn.10817	Down	Sg
496	LOC299469	XM_234749	-	Down	Sg
497	Sectm1	NM_199082	-	Down	Sg
498	-	NM_001013219	Rn.104514	Down	Sg
499	RGD:708486	NM_020091	Rn.48676	Down	Sg
500	-	XM_575093	Rn.116833	Down	Sg
501	Fam3b_predicted	XM_221623	Rn.162007	Down	Sg
502	Gm1012	XM_342493	Rn.44656	Down	Sg
503	-	XM_234741	-	Down	Sg
504	LOC314512	XM_234676	Rn.110661	Down	Sg
505	Acdc	NM_144744	Rn.24299	Down	Sg
506	Bf	NM_212466	Rn.109148	Down	Sg
507	Olr197_predicted	NM_001000188	Rn.141814	Down	Sg
508	LOC299551	XM_234830	-	Down	Sg
509	-	Z93354	Rn.179369	Down	Sg
510	Sec23b_predicted	XM_342531	Rn.8735	Down	Sg
511	Amy1	NM_001010970	Rn.116361	Down	Sg
512	Cxadrl1	NM_199406	Rn.162547	Down	Sg
513	Galnt5	NM_031796	Rn.30048	Down	Sg
514	-	XM_344373	-	Down	Sg
515	-	TC525800	-	Down	Sg
516	-	XM_575540	Rn.117940	Down	Sg
517	C1ql3_predicted	BF391573	Rn.39092	Down	Sg
518	Igfbp2	NM_013122	Rn.6813	Down	Sg
519	Cnnm4_predicted	XM_343554	Rn.857	Down	Sg
520	RGD:1303241	NM_001002802	Rn.38581	Down	Sg
521	-	BC091425	-	Down	Sg
522	Creb3l1	NM_001005562	Rn.24541	Down	Sg
523	-	U75411	-	Down	Sg
524	LOC366733	XM_345725	Rn.8473	Down	Sg
525	Galnt12_predicted	XM_223905	-	Down	Sg
526	-	XM_342323	-	Down	Sg
527	Akr1b8	NM_173136	Rn.23676	Down	Sg
528	-	XM_575775	Rn.23267	Down	Sg
529	Dnase1	NM_013097	Rn.6077	Down	Sg
530	Tgoln2	NM_138840	Rn.11349	Down	Sg
531	Prpf31_predicted	XM_218173	Rn.99310	Down	Sg
532	-	XM_234755	-	Down	Sg
533	Cd14	NM_021744	-	Down	Sg
534	F3	NM_013057	Rn.9980	Down	Sg
535	-	XM_575534	-	Down	Sg
536	-	TC554663	-	Down	Sg
537	Tgoln2	NM_138840	Rn.11349	Down	Sg
538	-	NM_001025683	Rn.16921	Down	Sg
539	Hcn3	NM_053685	Rn.48801	Down	Sg

No	Target(Gene)Symbol	Target Accession	UniGene	Up/Down	生体由来試料
540	-	NM_001025683	Rn.16921	Down	Sg
541	-	AF468681	-	Down	Sg
542	-	BF524215	-	Down	Sg
543	Ddc	NM_012545	Rn.11064	Down	Sg
544	-	TC538655	-	Down	Sg
545	Cnn1	NM_031747	Rn.31788	Down	Sg
546	LOC366765	XM_345752	Rn.112186	Down	Sg
547	-	BQ200884	Rn.11349	Down	Sg
548	Amy2_predicted	XM_345278	Rn.67070	Down	Sg
549	-	BE103448	Rn.165522	Down	Sg
550	RGD:1303221	NM_001004215	Rn.144176	Down	Sg
551	-	L07408	Rn.117930	Down	Sg
552	Pcsk3	NM_019331	Rn.3220	Down	Sg
553	LOC301711	XM_237538	-	Down	Sg
554	LOC363618	XM_343911	Rn.72525	Down	Sg
555	Mapt	NM_017212	Rn.2455	Down	Sg
556	-	TC555084	-	Down	Sg
557	Retn	NM_144741	Rn.16746	Down	Sg
558	LOC310429	XM_227167	-	Down	Sg
559	RGD1304977_predicted	XM_238325	Rn.101794	Down	Sg
560	Srebf1	XM_213329	Rn.801	Down	Sg
561	-	AW520826	-	Down	Sg
562	LOC307231	XM_225713	Rn.148475	Down	Sg
563	LOC366733	XM_345725	Rn.8473	Down	Sg
564	Arg2	NM_019168	Rn.11055	Down	Sg
565	Cd14	NM_021744	-	Down	Sg
566	Gpx2	NM_183403	Rn.3503	Down	Sg
567	Frmpd1_predicted	XM_233002	Rn.37934	Down	Sg
568	-	TC555358	-	Down	Sg
569	Acsl1	NM_012820	Rn.6215	Down	Sg
570	RGD:1303180	NR_002149	-	Down	Sg
571	LOC362348	XM_342669	Rn.91492	Down	Sg
572	-	BE110753	Rn.8285	Down	Sg
573	-	TC540316	Rn.8285	Down	Sg
574	-	AW917167	Rn.18668	Down	Sg
575	Nid67	NM_173126	Rn.8865	Down	Sg
576	Rhoc_predicted	XM_215659	Rn.162614	Down	Sg
577	Acsl1	NM_012820	Rn.6215	Down	Sg
578	Lama5	XM_215963	Rn.62616	Down	Sg
579	Gpr2_predicted	XM_343968	Rn.49607	Down	Sg
580	Scn11a	NM_019265	Rn.30023	Down	Sg
581	-	NM_001013232	Rn.111376	Down	Sg

[表中、

Sgは唾液腺であり；Blは血液であり；Hyは視床下部であり；Stは線条体である。]

[請求項4] ラットに評価対象である刺激を負荷する第1のステップと、

MAPキナーゼ脱リン酸化酵素活性を有する表45に示す遺伝子群、組織カリクレイン活性を有する表46に示す遺伝子群、細胞外成分である表47および表51に示す遺伝子群、脂質代謝に関連する表48に示す遺伝子群、ドーパミン合成に関連する表49に示す遺伝子群、アクチン結合に関連する表50に示す遺伝子群、核酸構成糖の代謝に関連する表52に示す遺伝子群、ホルモン活性を有する表53に示す遺伝子群、モノアミントランスポーターに関連する表54に示す遺伝子群、受容体結合に関

連する表55に示す遺伝子群、食行動に関連する表56に示す遺伝子群、生体アミン合成に関連する表57に示す遺伝子群、生体アミン代謝に関連する表58に示す遺伝子群、陽イオン結合に関連する表59に示す遺伝子群からなる群から選択される少なくとも1種の遺伝子の発現量を指定の生体由来試料において測定する第2のステップと、

測定した前記遺伝子の発現量に基づいて、対象刺激が陽性刺激であるか否かを評価する第3のステップと

を含む、所与の刺激がラットに対する陽性刺激であるか否かを評価する方法。

[表7]

表45 Cに対してで発現増加した唾液腺の注目遺伝子
MAPキナーゼ脱リン酸化酵素活性 (GO ID: 17017)

Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Gene Symbol	Gene Name	Summary	GeneRIF	Pathway	Homology
593.12	329.46	1.80	NM_053769	Dusp1	Rattus norvegicus dual specificity phosphatase 1 (Dusp1), mRNA [NM_053769]	ref|NM_053769 |gb|X94004|gb |S74351|ens|E NSRNOT0000000 5383	Rn.98260	Dusp1	dual specificity phosphatase 1	catalyzes the phosphorylation and inactivation of MAP kinase; may be involved in insulin mediated signaling [RGD]	Anandamide-induced rapid MKP-1 expression switches off MAPK signal transduction in microglial cells activated by stimulation of pattern recognition receptors.// findings suggest the involvement of MKP-1 in the regulation of the nocturnal AA-NAT signal// i	KEGG pathway: MAPK signaling pathway	[Human, Mouse]Homologene:3254
31.66	18.38	1.72	NM_022199	Dusp4	Rattus norvegicus dual specificity phosphatase 4 (Dusp4), mRNA [NM_022199]	ref|NM_022199 |gb|U23438|en s|ENSRNOT0000 0016328	Rn.44407	Dusp4	dual specificity phosphatase 4	exhibits vanadate-sensitive phosphatase activity for MAP kinase; inhibits transcription of MAP kinase-dependent genes [RGD]	The 1(1)-imidazoline receptor in PC12 pheochromocytoma cells induces MKP-2 phosphatase.	KEGG pathway: MAPK signaling pathway	[Human, Mouse]Homologene:1065
26.05	15.22	1.71	AA924847	AA92484 7	AA924847 UI-R-A1-eb-a-04-0-UI.s1 UI-R-A1 Rattus norvegicus cDNA clone UI-R-A1-eb-a-04-0-UI.3' similar to gi [AA924847]	gb|AA924847|g b|AA963216|gb |AA963233|gb| BF417479	Rn.9470	Dhcr24	24-dehydrocholesterol reductase	-	identification, using a direct genetic screen, Seladin-1 (also known as Dhcr24) as a key mediator of Ras-induced senescence	-	[Human, Mouse]Homologene:8850
1298.38	861.58	1.51	NM_133578	Dusp5	Rattus norvegicus dual specificity phosphatase 5 (Dusp5), mRNA [NM_133578]	ref|NM_133578 |gb|AF013144| gb|XM_346588| ens|ENSRNOT00 000018889	Rn.10877	Dusp5	dual specificity phosphatase 5	inactivates MAP kinase; may be involved in long term potentiation [RGD]	-	KEGG pathway: MAPK signaling pathway	[Human, Mouse]Homologene:3256

[表8]

表46 Cに対して発現増加した唾液腺の注目遺伝子
組織カリクレイン活性 (GO ID: 4293)

Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Gene Symbol	Gene Name	Summary	GeneRIF	Pathway	Homology
32731.46	2472.09	13.24	NM_175759	Klks3	Rattus norvegicus kallikrein, submaxillary gland S3 (Klks3), mRNA [NM_175759]	ref|NM_175759 |gb|M11566|gb |BC061771|ens |ENSRNOT00000 025723	Rn.34627	Klks3	kallikrein, submaxillary gland S3	a kallikrein-related serine protease: first isolated from the rat submaxillary gland: acts as a potent enzymatic vasoconstrictor [RGD]	-	-	-
70828.46	5776.93	12.26	NM_012677	Ton	Rattus norvegicus tonin (Ton), mRNA [NM_012677]	ref|NM_012677 |gb|M11565|gb |M23878|ens|E NSRNOT0000002 5701	Rn.9882	Ton	tonin	serine protease involved in generating the octapeptide angiotensin II from precursors [RGD]	tonin may play a role in the process of heart hypertrophy// expression in the rat brain and mediation of the central production of angiotensin II	-	-
1543.60	182.10	8.48	NM_0010053 82	Klk12	Rattus norvegicus glandular kallikrein 12, submandibular/renal (Klk12), mRNA [NM_0010053822]	ref|NM_001005 382|gb|XM_218 567|gb|M19648 |ens|ENSRNOT0 0000025631	Rn.141980	Klk12	glandular kallikrein 12, submandibular/renal	-	-	-	[Human, Mouse]HomoloGene:81694
88887.34	13877.73	6.41	XM_214931	RGD:735 032	PREDICTED: Rattus norvegicus kallikrein (LOC292872), mRNA [XM_214931]	ref|XM_214931 |gb|L33840|gb |M11564|ens|E NSRNOT0000002 5777	Rn.107068	-	kallikrein	a putative kallikrein-related serine protease first isolated from the rat submaxillary gland [RGD]	-	-	-

Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Gene Symbol	Gene Name	Summary	GeneRIF	Pathway	Homology
124036.40	40026.25	3.10	NM_031523	Ngfg	Rattus norvegicus nerve growth factor, gamma (Ngfg), mRNA [NM_0315231]	ref|NM_031523 |gb|M11563|gb |X03560|gb|BC 078784	Rn.11331	Ngfg	nerve growth factor, gamma	a putative pancreatic kallikrein [RGD]	the the kallikrein-kinin system has roles in intramyocardial inflammation, endothelial dysfunction and oxidative stress in diabetic cardiomyopathy // PKA phosphorylation of Src mediates Rap1 activation in NGF and cAMP signaling		[Mouse]Homologene-83259

[表9]

表47 Gに対して発現増加した唾液腺の注目遺伝子
細胞外成分 (GO ID: 5576, 44421, 5615)

Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Gene Symbol	Gene Name	Summary	GeneRIF	Pathway	Homology
42529.56	9583.96	4.44	NM_001013067	NM_001013067	Rattus norvegicus kallikrein 6 (predicted) (Klk6_predicted), mRNA [NM_001013067]	ref|NM_001013067|gb|AAH85932|gb|AAI24932|gb|EDM27217|ensembl|ENSRNOT00000025715	Rn.79264	Klk6_predicted	kallikrein 6 (predicted)	–	–	–	[Mouse]HomoloGene:83265
6218.28	1414.59	4.40	NM_012842	Egf	Rattus norvegicus epidermal growth factor (Egf), mRNA [NM_012842]	ref|NM_012842|gb|AAH85942|gb|BC003021|gb|AAH14030|gb|AAI14863	Rn.6075	Egf	epidermal growth factor	binds tha epidermal growth factor receptor; may play a role in MAP kinase mediated signaling pathways [RGD]	EGF-based signaling cascades phosphorylate Cavl and have roles in caveolae assembly// ERK1/2 mediates EGF-induced rapid Rb phosphorylation at Ser780 and Ser795// Neo-natal rats with intestinal injury have significantly lower levels of ileum EGF.// Linear	KEGG pathway: Cytokine-cytokine receptor interaction// KEGG pathway: Focal adhesion// KEGG pathway: Gap junction// KEGG pathway: MAPK signaling pathway// KEGG pathway: Regulation of actin cytoskeleton	[Human, Mouse]HomoloGene:1483
2022.83	528.42	3.83	XM_342575	Svs6_predicted	PREDICTED: Rattus norvegicus seminal vesicle secretion 6 (predicted) (Svs6_predicted), mRNA [XM_342575]	ref|XM_342575|ENSRNOP00000018975|tc|TC51018976|tc|TC51018977|tc|TC51018976	Rn.14520	Svs6_predicted	seminal vesicle secretion 6 (predicted)	–	–	–	[Mouse]HomoloGene:49347
165383.40	45178.89	3.66	NM_022708	Pip	Rattus norvegicus prolactin induced protein (Pip), mRNA [NM_022708]	ref|NM_022708|gb|AF054008|gb|AAF27054|ENSEMBL|ENSRNOP00000027015|tc|TC51041374	Rn.78367	Pip	prolactin induced protein	secretory protein localized to acinar cells of neonatal and adult submandibular and parotid glands, also expressed in sublingual glands [RGD]	–	–	[Human, Mouse]HomoloGene:1990

Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Gene Symbol	Gene Name	Summary	GeneRIF	Pathway	Homology
213570.10	61274.66	3.49	NM_133513	Muc10	Rattus norvegicus mucin 10, submandibular gland salivary mucin (Muc10), mRNA [NM_133513]	ref|NM_133513|gb|U03407|gb|U03442|ens|ENSRNOT00000032459	Rn.10113	Muc10	mucin 10, submandibular gland salivary mucin	a submandibular gland apomucin [RGD]	-	-	[Mouse]HomoloGene:69025
267.70	82.81	3.23	AA963004	AA96300 4	Rattus norvegicus cDNA clone UI-R-E1-gd-d-04-0-UI.s1 UI-R-E1 Rattus norvegicus cDNA clone UI-R-E1-gd-d-04-0-UI 3', mRNA sequence [AA963004]	gb|AA963004|tc|TC55441	Rn.24539	Tgfb2	transforming growth factor, beta 2	binds the transforming growth factor-beta receptor: plays a role in regulation of cell growth and proliferation: may be involved in mesenchymal-epithelial cell interactions during development [RGD]	the pro-inflammatory cytokine MIF can shift the cytokine balance from the immunosuppressive state towards an inflammatory reaction, potentially through the inhibition of TGF-beta2 secretion by testicular peritubular cells.// TGF-beta2 mRNA and protein exp	KEGG pathway: Cell cycle// KEGG pathway: MAPK signaling pathway// KEGG pathway: TGF-beta signaling pathway	[Human, Mouse]HomoloGene:2432
277.61	92.00	3.02	NM_080411	Gpr83	Rattus norvegicus G protein-coupled receptor 83 (Gpr83), mRNA [NM_080411]	ref|NM_080411|ref|XM_579605|gb|AY029071|gb|XM_346815	Rn.63075	Gpr83	G protein-coupled receptor 83	glucocorticoid-induced receptor found in brain and may be involved in behavioral sensitization [RGD]	-	KEGG pathway: Neuroactive ligand-receptor interaction	-
42529.56	9583.96	4.44	NM_001013067	NM_0010 13067	Rattus norvegicus kallikrein 6 (predicted) (Klk6_predicted), mRNA [NM_001013067]	ref|NM_001013067|gb|XM_214932|gb|M27217|ens|ENSRNOT00000025715	Rn.79264	Klk6_predicted	kallikrein 6 (predicted)	-	-	-	[Mouse]HomoloGene:83265
164227.44	57850.42	2.84	NM_172065	Prpg2	Rattus norvegicus proline-rich proteoglycan 2 (Prpg2), mRNA [NM_172065]	ref|NM_172065|gb|M11891|gb|L17318|ens|ENSRNOT00000013943	Rn.29950	Prpg2	proline-rich proteoglycan 2	member of a family of proline rich proteins that are induced in salivary gland by isoproterenol treatment and by feeding tannins [RGD]	-	-	-

Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Gene Symbol	Gene Name	Summary	GeneRIF	Pathway	Homology
144.02	53.99	2.67	NM_012996	Oxt	Rattus norvegicus oxytocin (Oxt), mRNA [NM_012996]	ref|NM_0129961|gb|M25647|ens|ENSRNOT00000002881|tc|TC57290	Rn.48915	Oxt	oxytocin	hormone involved in contraction of smooth muscle during parturition and lactation; gene encodes two proteins, oxytocin and neurophysin I [RGD]	oxytocin has a role in gonadal steroid modulation of stress-induced hypothalamo-pituitary-adrenal activity and anxiety behavior// Oxytocin may strengthen mother-infant bond formation partly by acting through brain areas involved in regulating olfactory di	KEGG pathway: Neuroactive ligand-receptor interaction	[Human, Mouse]HomoloGene: 55494
80.76	31.28	2.58	NM_053738	Wif1	Rattus norvegicus Wnt inhibitory factor 1 (Wif1), mRNA [NM_053738]	ref|NM_053738|gb|AY030278|gb|BC072473|ens|ENSRNOT00000006426	Rn.74256	Wif1	Wnt inhibitory factor 1	human homolog has decreased mRNA expression in some prostate cancers and other cancers; may act as a secreted inhibitor of the Wnt signaling pathway [RGD]	GLT mRNA was translated in Wnt-1-expressing G6 cells when the GLT mRNA required no splicing before translation occurred	KEGG pathway: Wnt signaling pathway	[Human, Mouse]HomoloGene: 31430
8361.31	3258.64	2.57	XM_341400	Rbp3	PREDICTED: Rattus norvegicus retinol binding protein 3, interstitial (Rbp3), mRNA [XM_341400]	ref|XM_341400|gb|X56150|gb|X69523|ens|ENSRNOT00000027446	Rn.41214	Rbp3	retinol binding protein 3, interstitial	may play a role in vision [RGD]	-	-	[Human, Mouse]HomoloGene: 9261
4805.70	1924.09	2.50	AB087404	Gdf5	Rattus norvegicus gdf-5 gene for growth and differentiation factor-5, partial cds [AB087404]	gb|AB087404|tc|NP495152	Rn.12782	Gdf5	growth differentiation factor 5	member of the bone morphogenetic protein (BMP) family and the TGF-beta superfamily; regulates cell growth and differentiation; involved with tendon and ligament formation [RGD]	Expression of GDF-5 in developing rat ventral mesencephalon (VM) was found to begin at embryonic day (E) 12 and peak on E14. In the adult rat was found in heart and brain, being expressed in many areas of the brain, including striatum and midbrain.// invol	-	-

Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Gene Symbol	Gene Name	Summary	GeneRIF	Pathway	Homology
2733.04	1114.24	2.45	NM_024136	Erabp	Rattus norvegicus epididymal retinoic acid-binding protein (Erabp), mRNA [NM_024136]	ref|NM_0241 36|gb|AY5983 21|gb|M12790 |tc|TC56991 4	Rn. 10362	Erabp	epididymal retinoic acid-binding protein	has a low galactosyltransferase modifying activity in vitro: however, this activity is predicted to be too low for physiological significance [RGD]	-	-	[Mouse]HomoloGene :7305
781.76	327.17	2.39	NM_057151	Ccl17	Rattus norvegicus small inducible cytokine subfamily A (Cys-Cys), member 17 (Ccl17), mRNA [NM_057151]	ref|NM_0571 51|gb|AF312 687|ens|ENS RNOT0000002 1842|tc|TC5 61888	Rn. 46679	Ccl17	chemokine (C-C motif) ligand 17	a thymus and activation-regulated chemokine [RGD]	Our data indicate that instead of Th2 cells, airway epithelial cells expressing CCR4 might be the principal targets for MDC and TARC released from alveolar macrophages during cigarette smoke-induced airway inflammation.	-	[Human, Mouse]HomoloGene: 2246
200.79	88.11	2.28	NM_019189	Hapln1	Rattus norvegicus hyaluronan and proteoglycan link protein 1 (Hapln1), mRNA [NM_019189]	ref|NM_0191 89|ens|ENSR NOT0000042 958|ens|ENS RNOT0000004 3196|gb|M22 340	Rn. 50531	Hapln1	hyaluronan and proteoglycan link protein 1	stabilizs cartilage proteoglycan/hyaluronic acid aggregates by binding to each component [RGD]	study represents the first report that follicle stimulating hormone amplifies insulin-like growth factor-1-mediated cartilage link protein Crtl1 production, possibly via phosphatidylinositol 3-kinase-Akt sigmaling cascades in rat granulosa cells	-	[Human, Mouse]HomoloGene: 1420
395.11	173.49	2.28	BM388083	BM38808 3	BM388083 UI-R-DM1-cjz-d-11-0-UI.s1 UI-R-DM1 Rattus norvegicus cDNA clone UI-R-DM1-cjz-d-11-0-UI 3', mRNA sequence [BM388083]	gb|BM388083 |gb|BF41687 7	Rn. 41133	Sorcs2_predicted	sortilin-related VPS10 domain containing receptor 2 (predicted)	-	-	-	[Mouse]HomoloGene :75305

Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Gene Symbol	Gene Name	Summary	GeneRIF	Pathway	Homology
44.00	19.81	2.22	NM_053504	Prss12	Rattus norvegicus protease, serine, 12 (Prss12), mRNA [NM_053504]	ref|NM_053504|gb|AAJ31104|ens|ENSRNOT00000021116	Rn.86653	Prss12	peptidase, serine, 12 (neurotrypsin, motopsin)	mouse homolog is a serine protease; may be involved in learning and memory [RGD]	-	-	[Human, Mouse]HomoloGene: 7490
			NM_016989	Adcyap1	Rattus norvegicus adenylate cyclase activating polypeptide 1 (Adcyap1), mRNA [NM_016989]	ref|NM_016989|ref|XM_579383|gb|M63006|gb|AAL346860	Rn.37400	Adcyap1	adenylate cyclase activating polypeptide 1	regulatory protein that stimulates cell proliferation, induces differentiation, modulates neurotransmitter release, vasodilation, bronchodilation, and hormone release, and suppresses inflammatory responses [RGD]	These results indicate that a large number of PACAP neurons and a small number of BDNF neurons of the VMH project to the MPG.// The specificity of PAC1 receptor participation in pituitary adenylate cyclase-activating polypeptide (PACAP)-facilitated sex be	KEGG pathway: Neuroactive ligand-receptor interaction	[Human, Mouse]HomoloGene: 869
			NM_031736	Slc27a2	Rattus norvegicus solute carrier family 27 (fatty acid transporter), member 2 (Slc27a2), mRNA [NM_031736]	ref|NM_031736|ref|XM_579526|gb|D85100|gb|AAL346669	Rn.3608	Slc27a2	solute carrier family 27 (fatty acid transporter), member 2	has very long-chain acyl-CoA synthetase activity; may play a role in fatty acid metabolism [RGD]	in response to an increase of cellular cholesterol. fatty acid transporter is translocated from cytosol to membranes of type II pneumocytes.	KEGG pathway: Alkaloid biosynthesis II// KEGG pathway: Caprolactam degradation// KEGG pathway: Ethylbenzene degradation// KEGG pathway: Limonene and pinene degradation// KEGG pathway: Propanoate metabolism	-
			NM_147165	Gpx6	Rattus norvegicus glutathione peroxidase 6 (Gpx6), mRNA [NM_147165]	ref|NM_147165|gb|AW767365	Rn.9852	Gpx6	glutathione peroxidase 6	a lipophilic molecule carrier in olfactory mucosa [RGD]	-	KEGG pathway: Arachidonic acid metabolism// KEGG pathway: Glutathione metabolism	[Human, Mouse]HomoloGene: 25418

Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Gene Symbol	Gene Name	Summary	GeneRIF	Pathway	Homology
			AA875449	AA875449	AA875449 UI-R-E0-op-b-02-0-UI.s1 UI-R-E0 Rattus norvegicus cDNA clone UI-R-E0-op-b-02-0-UI 3' similar to gi [AA875449]	gb|AA875449	Rn. 2923	Ppif	peptidylprolyl isomerase F (cyclophilin F)	mitochondrial isozyme of peptidyl-prolyl cis-trans-isomerase; enzyme activity is inhibited by cyclosporin A [RGD]	The present study examines the effects of cyclophilin-D on mitochondrial permeability transition and lethal cell injury.	-	[Human, Mouse]HomoloGene: 38696
			BE111679	BE111679	BE111679 UI-R-BJ1-avv-e-09-0-5 UI.s1 UI-R-BJ1 Rattus norvegicus cDNA clone UI-R-BJ1-avv-e-09-0-UI 3', mRNA sequence [BE111679]	gb|BE111679 |gb|AA892395 |gb|AI44098	Rn. 13642	Slc20a2	solute carrier family 20, member 2	cellular receptor which mediates virus entry [RGD]	PiT-1 (Slc20a1) and PiT-2 (Slc20a2) were detected at the basolateral membrane of hepatocytes.// mRNA expression level of Glvr-2 was increased by the addition of inorganic phosphate (Pi) in bone marrow stromal cells	-	[Human, Mouse]HomoloGene: 68531
			NM_013107	Bmp6	Rattus norvegicus bone morphogenetic protein 6 (Bmp6), mRNA [NM_013107]	ref|NM_013107 |gb|AY184240 |gb|X58830 |gb|XM_341514	Rn. 40476	Bmp6	bone morphogenetic protein 6	plays a role in induction of osteogenesis; may be involved in liver growth and differentiation in response to injury [RGD]	Expression of BMP-6 by tibial marrow megakaryocytes in 5-week-old rats suggests a mechanism by which megakaryocyte-derived BMPs may promote bone growth and repair	KEGG pathway: Hedgehog signaling pathway// KEGG pathway: TGF-beta signaling pathway	[Human, Mouse]HomoloGene: 1300
			XM_213416	Spaca3_predicted	PREDICTED: Rattus norvegicus sperm acrosome associated 3 (predicted) (Spaca3_predicted), mRNA [XM_213416]	ref|XM_213416 |ens|ENSRNOT00000009172 |tc|TC527499	Rn. 47764	Spaca3_predicted	sperm acrosome associated 3 (predicted)	-	-	-	[Human, Mouse]HomoloGene: 18365

Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Gene Symbol	Gene Name	Summary	GeneRIF	Pathway	Homology
			NM_138902	Ear11	Rattus norvegicus eosinophil-associated, ribonuclease A family, member 11 (Ear11), mRNA [NM_138902]	ref|NM_138902|gb|AF475093|tc|TC0573	Rn. 10626	Ear11	eosinophil-associated, ribonuclease A family, member 11	cationic protein with similarity to human ECP; also has similarity to human eosinophil-derived neurotoxin and human ribonuclease k6 [RGD]	-	-	-
			AF475093	AF47509 3	Rattus norvegicus liver regeneration-related protein 1 (Lrrp1) mRNA, complete cds. [AF475093]	gb|AF475093|tc|NRP59824	Rn. 3040	Sdhd	succinate dehydrogenase complex, subunit D, integral membrane protein	human homolog is a subunit of succinate-ubiquinone oxidoreductase, which plays a role in mitochondrial electron transport [RGD]	-	KEGG pathway: Citrate cycle (TCA cycle)// KEGG pathway: Oxidative phosphorylation	[Human, Mouse]HomoloGene: 37718
			NM_023962	Pdgfd	Rattus norvegicus platelet-derived growth factor, D polypeptide (Pdgfd), mRNA [NM_023962]	ref|NM_023962|gb|AB062170|tc|TC571827	Rn. 64493	Pdgfd	platelet-derived growth factor, D polypeptide	a growth factor with mitogenic activity in the central nervous system [RGD]	analysis of expression of PDGF-A, -B, -C and -D and the PDGF-receptors alpha and beta in activated rat hepatic stellate cells// These results support the fact that PDGF-D is involved in the formation of neointimal hyperplasia induced by balloon catheter i	KEGG pathway: Focal adhesion// KEGG pathway: Gap junction	[Human, Mouse]HomoloGene: 11875
			BE112231	Fcna	UI-R-BJ1-avl-c-05-0-UI.s1 UI-R-BJ1 Rattus norvegicus cDNA clone UI-R-BJ1-avl-c-05-0-UI 3', mRNA sequence. [BE112231]	gb|BE112231|gb|AI10459|gb|AI10720	Rn. 20051	Fcna	ficolin A	mouse homolog is a plasma protein that binds elastin and GlcNAc [RGD]	-	-	[Mouse]HomoloGene :74880

Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Gene Symbol	Gene Name	Summary	GeneRIF	Pathway	Homology
			NM_021698	F13a	Rattus norvegicus coagulation factor XIII, A1 subunit (F13a), mRNA [NM_021698]	ref|NM_0216 98|gb|Y1250 2|gb|AW9190 18|ens|ENSR NOT00000021 568	Rn. 42925	F13a1	coagulation factor XIII, A1 subunit	enhances gastric mucosa healing; reduces endothelial permeability [RGD]	-	KEGG pathway: Complement and coagulation cascades	[Human, Mouse]HomoloGene: 20077
			NM_080394	Reln	Rattus norvegicus reelin (Reln), mRNA [NM_080394]	ref|NM_0803 94|gb|AB062 680|gb|AW14 0590|tc|TC5 72679	Rn. 16177	Reln	reelin	regulates neuronal cell migration during development; plays a role in locomotor behavior [RGD]	reelin, which is expressed along the route of the migrating GnRH neurons, has an inhibitory role in guiding GnRH neurons to the basal forebrain// differentiation factor for radial glial cells of dentate gyrus and as a positional cue for radial fiber orien	KEGG pathway: Cell Communication// KEGG pathway: ECM-receptor interaction// KEGG pathway: Focal adhesion	[Human, Mouse]HomoloGene: 3699
			AA891661	AA89166 1	AA891661 EST195464 Normalized rat kidney, Bento Soares Rattus sp. cDNA clone RKIAF23 3' end, mRNA sequence [AA891661]	gb|AA891661	Rn. 1618	Aqp1	aquaporin 1	integral membrane protein that is a major water transport molecule in the kidney proximal tubule and red blood cells [RGD]	data indicate that the ar/R constriction is a major checkpoint for solute permeability, and that the exquisite electrostatic proton barrier in AQPs comprises both the NPA constriction as well as the ar/R constriction// AQP1 and AQP6, and the heterotrimeri	-	[Human, Mouse]HomoloGene: 68051
			XM_225585	Mrc1_pr edicted	PREDICTED: Rattus norvegicus mannose receptor, C type 1 (Mrc1_predicted), mRNA [XM_225585]	ref|XM_2255 85|gb|CB544 854|ens|ENS RNOT00000002 6736|tc|TC5 55463	Rn. 9197	Mrc1_predicted	mannose receptor, C type 1 (predicted)	-	-	-	-

Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Gene Symbol	Gene Name	Summary	GeneRIF	Pathway	Homology
			X61479	X61479	RRCSF1 Rat mRNA for CSF-1 receptor [X61479]	gb|X61479	-	Csf1r	colony stimulating factor 1 receptor	may modiate normal and neoplastic growth of muscular cells [RGD]	the CSF1R mutation of Asp-802 to Val confers resistance to kinase inhibitor imatinib	-	[Human, Mouse]HomoloGene: 3817
			XM_573463	XM_573463	PREDICTED: Rattus norvegicus similar to complement component factor h (LOC498240), mRNA [XM_573463]	ref|XM_573463.1|gb|BC089231|gb|BC089231|ENSRNOT00000084502|Ensembl|ENSRNOT00000092834|Ensembl|ENSRNOT00000029294	Rn.13761	Cfh	complement component factor H	regulator of complement cascade activation [RGD]	Glomerular epithelial cells(GEC) and glomeruli express factor H mRNA and protein. Up-regulated in membranous nephropathy. Likely direct response of GEC to complement attack and may represent protective response.// Complement Factor H is highly expressed i	KEGG pathway: Complement and coagulation cascades	[Human, Mouse]HomoloGene: 20086
			NM_021682	Negr1	Rattus norvegicus neuronal growth regulator 1 (Negr1), mRNA [NM_021682]	ref|NM_021682.1|gb|AB017139|tc|TC572970	Rn.42884	Negr1	neuronal growth regulator 1	glycosylphosphatidylinositol-anchored cell adhesion protein [RGD]	-	KEGG pathway: Cell adhesion molecules (CAMs)	[Human, Mouse]HomoloGene: 41447
			NM_031590	Wisp2	Rattus norvegicus WNT1 inducible signaling pathway protein 2 (Wisp2), mRNA [NM_031590]	ref|NM_031590.1|gb|AF259981|gb|BC091870|Ensembl|ENSRNOT00000014346	Rn.53991	Wisp2	WNT1 inducible signaling pathway protein 2	involved in negative regulation of cell growth: mRNA expression is lost upon cell transformation induced by activated H-ras oncogene and inactivated p53 tumor supressor [RGD]	data indicate that CCN5 protein is positively regulated by estrogen in the rat uterus and suggests that this gene may play an important role in maintaining normal uterine physiology	-	[Human, Mouse]HomoloGene: 2982

Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Gene Symbol	Gene Name	Summary	GeneRIF	Pathway	Homology
			NM_053856	Scg3	Rattus norvegicus secretogranin III (Scg3), mRNA [NM_053856]	ref|NM_053856|gb|U00298|tc|TC5688 16	Rn.11093	Scg3	secretogranin III	component of intracellular dense core vesicles [RGD]	SgIII and CPE form the separate functional sorting complex by anchoring to cholesterol-rich SG membranes, and POMC-derived peptides are transferred from CPE to SgIII, and subsequently to CgA.// SgIII is closely associated with the secretory granule membra	-	[Human, Mouse]HomoloGene: 7526
			AA924847	AA924847 /7	AA924847 UI-R-A1-eb-a-04-0-UI.s1 UI-R-A1 Rattus norvegicus cDNA clone UI-R-A1-eb-a-04-0-UI 3' similar to gi [AA924847]	gb|AA924847|gb|AA96321|gb|AA9632|gb|BF417 479	Rn.9470	Dhcr24	24-dehydrocholesterol reductase	-	identification. using a direct genetic screen, Seladin-1 (also known as Dhcr24) as a key mediator of Ras-induced senescence	-	[Human, Mouse]HomoloGene: 8650
			B6664056	B6664056	B6664056 DRAACD11 Rat DRG Library Rattus norvegicus cDNA clone DRAACD11 5', mRNA sequence [BG664056]	gb|B6664056|tc|TC55234 1	Rn.10796	Ndufa9	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 9	-	-	-	-
			XM_343373	RGD1310 431_predicted	PREDICTED: Rattus norvegicus similar to sialic-acid O-acetylesterase (predicted) (LOC363045), mRNA [XM_343373]	ref|XM_343373|gb|CB546 057|Ens|ENSRNOT00000004 4293|tc|TC5 59384	Rn.21775	Siae_predicted	sialic acid acetylesterase (predicted)	-	-	-	[Human, Mouse]HomoloGene: 8001

Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Gene Symbol	Gene Name	Summary	GeneRIF	Pathway	Homology
			L14933	Posk5	Rattus norvegicus convertase PC5 mRNA, partial cds [L14933]	gb|L14933|g b|XM_342032 |ens|ENSRNO T0000001616 4|tc|TC5711 52	Rn. 10400 2	Posk5	proprotein convertase subtilisin/ kexin type 5	may play a role in peptide processing and maturation [RGD]	Data suggest that inhibition of furin and PC5 and resulting inhibition of insulin-like growth factor 1 receptor (IGF-1R) activation can inhibit IGF-I-induced membrane-type 1 matrix metalloproteinase activity in vascular smooth muscle cells.// Activation o	-	[Human, Mouse]HomoloGene: 21244
			NM_133538	Il13ra2	Rattus norvegicus interleukin 13 receptor, alpha 2 (Il13ra2), mRNA [NM_133538]	ref|NM_1335 38|ref|XM_5 79624|gb|AF 448818|gb|X M_346867	Rn. 16230 8	Il13ra2	interleukin 13 receptor, alpha 2	used as a target for immunotherapeutic approaches for treating brain tumors [RGD]	gene sequence and tissue distribution of IL-13Ralpha2 in the rat	KEGG pathway: Jak-STAT signaling pathway	[Human, Mouse]HomoloGene: 534
			NM_00100340 4	Il22ra2	Rattus norvegicus interleukin 22 receptor, alpha 2 (Il22ra2), mRNA [NM_0010034 04]	ref|NM_0010 03404|gb|AJ 565485|gb|X M_344797|en s|ENSRNOT00 000016354	Rn. 13127	Il22ra2	interleukin 22 receptor, alpha 2	-	-	-	[Human, Mouse]HomoloGene: 18657
			NM_00101304 5	NM_0010 13045	Rattus norvegicus chemokine (C-C motif) ligand 24 (predicted) (Ccl24_pred icted), mRNA [NM_0010130 45]	ref|NM_0010 13045|ref|X M_573388|gb |XM_213743| ens|ENSRNOT 00000001963	Rn. 13882 2	Ccl24	chemokine (C-C motif) ligand 24	-	-	-	[Mouse]HomoloGene :83177

Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Gene Symbol	Gene Name	Summary	GeneRIF	Pathway	Homology
			NM_019192	Sepp1	Rattus norvegicus selenoprotein P, plasma, 1 (Sepp1), mRNA [NM_019192]	ref|NM_0191 92|gb|M6357 4|tc|TC6166 88	Rn. 1451	Sepp1	selenoprotein P, plasma, 1	plasma glycoprotein that contains ten selenocysteine residues; may play a role in response to oxidative stress [RGD]	selenenylsulfide linkages Sec304-Cys314 and Cys306-Sec316 were present: selenoprotein P contains these two selenenylsulfide bonds// mass spectrometric characterization of full-length protein and three isoforms shortened at the C terminus	-	-
			NM_024358	Notch2	Rattus norvegicus notch gene homolog 2 (Drosophila) (Notch2), mRNA [NM_024358]	ref|NM_0243 58|gb|M9366 1|ens|ENSRN OT0000002257 |ens|ENSR NOT0000000045 062	Rn. 65930	Notch2	notch gene homolog 2 (Drosophila)	transmembrane protein that may be involved in cellular interactions that specify cell fate [RGD]	-	KEGG pathway: Dorso-ventral axis formation// KEGG pathway: Notch signaling pathway	[Human, Mouse]HomoloGene: 7865
			NM_053289	Pap	Rattus norvegicus pancreatitis-associated protein (Pap), mRNA [NM_053289]	ref|NM_0532 89|gb|S77741 3|gb|S43715 |ens|ENSRNO T0000000821 2	Rn. 9727	Pap	pancreatitis-associated protein	lectin-related secretory protein: may be involved in stress response to control bacterial proliferation during acute pancreatitis [RGD]	These results suggest that Reg family members would be new mediators among injured neurons and glial cells, and may play pivotal roles during nerve regeneration.// Sepsis resulted in an up-regulation of PAP-1 gene expression and increase in its protein le	-	[Human, Mouse]HomoloGene: 49257

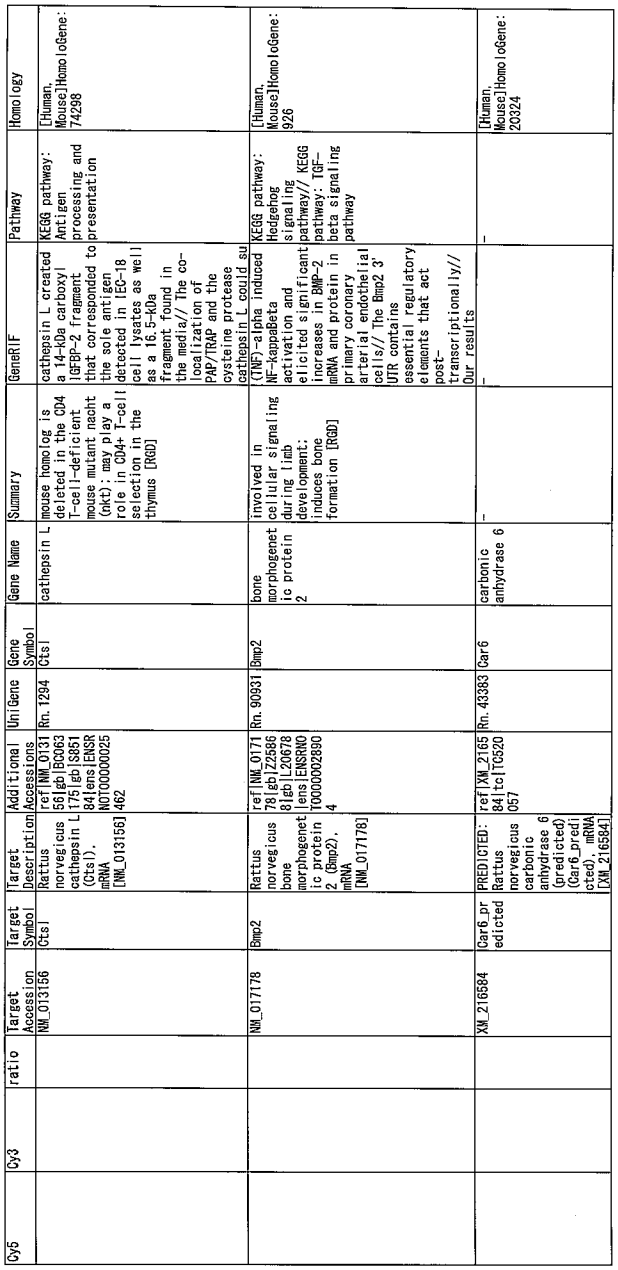
Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Gene Symbol	Gene Name	Summary	GeneRIF	Pathway	Homology
			XM_346464	Slit2	PREDICTED: Rattus norvegicus slit homolog 2 (Drosophila) (Slit2), mRNA [XM_346464]	ref|XM_346464.4|ENSR NOT00000007005 4771|tc|TC557626	Rn.46211	Slit2	slit homolog 2 (Drosophila)	acts as a ligand for glypican-1, a heparan sulfate proteoglycan; may play a role in neurogenesis and midline development [RGD]	Slit2 inhibits vascular smooth muscle cell migration by suppressing small GTPase Rac1 activation.// disruption of the continuity of basal lamina tubes induces the expression of slit2 in Schwann cells during peripheral nerve regeneration// Slit-2 inhibited	-	[Human, Mouse]HomoloGene: 3516
			NM_172328	Tac4	Rattus norvegicus tachykinin 4 (Tac4), mRNA [NM_172328]	ref|NM_172328.1|BC091561|gb|AY471575|ens|ENSRNOG00000035023	Rn.91139	Tac4	tachykinin 4	human and mouse homologs are processed to form hemokinin-1 (HK-1), a substance P-like peptide that displays high affinity binding to the neurokinin 1 (NK-1) receptor [RGD]	-	KEGG pathway: Neuroactive ligand-receptor interaction	[Mouse]HomoloGene :50484
			NM_017024	Lcat	Rattus norvegicus lecithin cholesterol acyltransferase (Lcat), mRNA [NM_017024]	ref|NM_017024.2|BC086241|gb|U62803|ens|ENSRNOT00000026685	Rn.10481	Lcat	lecithin cholesterol acyltransferase	enzyme involved in the metabolism of plasma lipoproteins [RGD]	-	KEGG pathway: Glycerophospholipid metabolism	[Human, Mouse]HomoloGene: 68042
			XM_573983	Tgfbi	PREDICTED: Rattus norvegicus transforming growth factor, beta induced, 68 kDa (Tgfbi), mRNA [XM_573983]	ref|XM_573983.2|BC083141|AW141699|tc|TC516884	Rn.1046	Tgfbi	transforming growth factor, beta induced	mouse homolog is an extracellular matrix protein; human homolog is associated with hereditary corneal dystrophies [RGD]	These results suggest that mechanical strain negatively regulates the terminal differentiation of chondrocytes through the signal pathway of TGF-ss with the induction of RGD-CAP.// Pravastatin significantly inhibited beta1g-h3 mRNA production and gene exp	-	[Human, Mouse]HomoloGene: 37294

Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Gene Symbol	Gene Name	Summary	GeneRIF	Pathway	Homology
			NM_053595	Pgf	Rattus norvegicus placental growth factor (Pgf), mRNA [NM_053595]	ref|NM_0535 95|gb|L4003 01|gb|BC0870 06|ens|ENSR NOT00000007 790	Rn. 6960	Pgf	placental growth factor	forms a heterodimer with VEGF: may play a role in vascular endothelial cell proliferation [RGD]	vascular endothelial growth factor and placental growth factor-2 effects in dorsal root ganglion neurons are mediated via neuropilin-1 and cyclooxygenase-derived prostanoid production	KEGG pathway: Focal adhesion	[Human, Mouse]HomoloGene: 1978
			NM_001001970	RGD:1303064	Rattus norvegicus lymphocyte antigen 6 complex, locus G6D (Ly6g6d), mRNA [NM_001001970]	ref|NM_0010 01970|gb|XM1 _227992|ens |ENSRNOT000 00001120|tc |NP1090614	Rn. 14539	-	lymphocyte antigen 6 complex, locus G6D	putative member of the Ly-6 superfamily, a group of GPI-anchored cell surface proteins; mouse human and rat homologs all localized to the MHC class III region [RGD]	-	--	[Human, Mouse]HomoloGene: 76442
			NM_022177	Cxcl12	Rattus norvegicus chemokine (C-X-C motif) ligand 12 (Cxcl12), mRNA [NM_022177]	ref|NM_0221 77|gb|AF209 976|gb|BC007 87|gb|AW9 16737	Rn. 54439	Cxcl12	chemokine (C-X-C motif) ligand 12	a chemoattractant molecule: involved in cell migration [RGD]	Our results show that SDF-1alpha induces, via presynaptic mechanisms, alterations in the excitability of DA neurones as confirmed by current-clamp experiments.// Myocardial SDF-1 expression was increased only in the early phase post myocardial infarct.// S	KEGG pathway: Axon guidance// KEGG pathway: Cytokine-cytokine receptor interaction// KEGG pathway: Leukocyte transendothelial migration	[Human, Mouse]HomoloGene: 507

Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Gene Symbol	Gene Name	Summary	GeneRIF	Pathway	Homology
			NM_001012459	Sogf	Rattus norvegicus stem cell growth factor (Sogf), mRNA [NM_001012459]	ref|NM_001012459|gb|XM_344888|gb|BC090344|ensembl|ENSRNOT00000025949	Rn.16242	Clec11a	C-type lectin domain family 11, member a	growth factor for primitive hematopoietic progenitor cells [RGD]	Dramatic increase in c-kit expression observed in the rat carotid artery after balloon injury suggests SCF/c-kit signaling may affect smooth muscle cell function via an autocrine pathway.// negative feedback with kit ligand (Sogf) and oocyte BNP15 regulat	-	[Human, Mouse]HomoloGene: 2236
			NM_031701	Cldn5	Rattus norvegicus claudin 5 (Cldn5), mRNA [NM_031701]	ref|NM_031701|gb|AF241260|gb|AW_344038|gb|BC082073	Rn.17420	Cldn5	claudin 5	a component of tight junctions in myelinating Schwann cells [RGD]	Induction of wild-type claudin-5 is sufficient to reconstitute the paracellular barrier against inulin (5 kDa), but not mannitol (182 Da), in leaky rat lung epithelial cells// MUPP1 and claudin-5 colocalized in the incisures, and the COOH-terminal region	KEGG pathway: Cell adhesion molecules (CAMs)// KEGG pathway: Leukocyte transendothelial migration// KEGG pathway: Tight junction	[Human, Mouse]HomoloGene: 2459
			NM_022005	Fxyd6	Rattus norvegicus FXYD domain-containing ion transport regulator 6 (Fxyd6), mRNA [NM_022005]	ref|NM_022005|gb|AB030908|gb|BC027328|gb|AF142439	Rn.839	Fxyd6	FXYD domain-containing ion transport regulator 6	(The rest is omitted.)	findings suggest that Php may play an important role in the excitability of neurons in the central nervous system during postnatal development, as well as those in the adult brain	-	[Human, Mouse]HomoloGene: 11090

Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Gene Symbol	Gene Name	Summary	GeneRIF	Pathway	Homology
			NM_017081	Hsd11b2	Rattus norvegicus hydroxysteroid 11-beta dehydrogenase 2 (Hsd11b2), mRNA [NM_017081]	ref|NM_017081|gb|U12422|gb|BC087023|ens|ENSRNOT00000023130	Rn.10186	Hsd11b2	hydroxysteroid 11-beta dehydrogenase 2	catalyzes the conversion of cortiosterone to 11-dehydrocorticosterone [RGD]	increased apical targeting of ENaC subunits combined with diminished abundance of 11betaHSD2 may contribute to sodium retention associated with HgCl(2)-induced nephrotic syndrome.// Increased apical targeting of epithelial channel subunits subunits combin	KEGG pathway: Androgen and estrogen metabolism// KEGG pathway: C21-Steroid hormone metabolism	[Human, Mouse]HomoloGene: 20088
			XM_017066	Ptn	Rattus norvegicus pleiotrophin (Ptn), mRNA [NM_017066]	ref|NM_017066|gb|M65606|gb|BC006208|ens|ENSRNOT00000016088	Rn.1653	Ptn	pleiotrophin	binds heparin: may act as a growth factor; may play a role in liver regeneration and fibrinogenesis [RGD]	PTN-immunolabeled neurons contained nitric oxide synthase or somatostatin and expressed the vesicular acetylcholine transporter, supporting that they were GABAergic nitric oxide synthase/somatostatin-containing and cholinergic interneurons// thrombospondi	-	[Human, Mouse]HomoloGene: 2117
			XM_230608	Sn_predicted	PREDICTED: Rattus norvegicus sialoadhesin (predicted) (Sn_predicted), mRNA [XM_230608]	ref|XM_230608|ens|ENSRNOT00000046830|ens|ENSRNOT00000051301|ens|ENSRNOT00000028855	Rn.80962	Sigleol_predicted	sialic acid binding Ig-like lectin 1, sialoadhesin (predicted)	-	Sialoadhesin is a macrophage-restricted adhesion molecule that recognizes N-acetylneuraminylalpha2-3galactose structure. Macrophages in lymph nodes express high levels of unmasked sialoadhesin.	KEGG pathway: Cell adhesion molecules (CAMs)	[Human, Mouse]HomoloGene: 7947

Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Gene Symbol	Gene Name	Summary	GeneRIF	Pathway	Homology
			NM_021653	Dio1	Rattus norvegicus deiodinase, iodothyronine, type I (Dio1), mRNA (NM_021653)	ref|NM_0216 53|gb|X5799 9|ens|ENSRN OT00000044 66|ens|ENSR NOT00000044 375	Rn. 87549	Dio1	deiodinase, iodothyroni ne, type I	This gene belongs to the iodothyronine deiodinase family. It encodes a selenoprotein that deiodinates prohormone thyroxine (T4, 3,5,3',5'- tetraiodothyronine) to bioactive T3 (3,3',5- triiodothyronine). Selenocysteine (aa 126), which is encoded by UGA (usua	D1 3'UTR may play an important role in regulating the stability and translational efficiency of the D1 mRNA// Mammary gland carcinoma-related increase of type I iodothyronine 5'- deiodinase activity in Sprague-Dawley rats.	-	[Human, Mouse]HomoloGene: 620
			NM_012643	Ret	Rattus norvegicus ret proto-oncogene (Ret), mRNA [NM_012643]	ref|NM_0126 43|gb|AJ299 016|gb|XM_2 16254|ens|E NSRNOT00000 047685	Rn. 93200	Ret	ret proto-oncogene	may play a role in exoretory system and enteric nervous system development: human homolog is associated with Hirschsprung disease and Multiple Endocrine Neoplasia type 2 [RGD]	Ability of 17-allylamino-17-demethoxygeldanamycin (17-AAG) to increase radioiodide accumulation is not restricted to thyroid cells expressing RET/PTC1.// Shp-1 and Shp-2 are recruited on cell membrane in two distinct molecular complexes including Ret onco	-	[Human, Mouse]HomoloGene: 7517
			NM_138843	Mpst	Rattus norvegicus mercaptopyruvate sulfurtransferase (Mpst), mRNA [NM_138843]	ref|NM_1388 43|ref|XM_5 79654|gb|D5 0564|gb|XM_ 346800	Rn. 32263	Mpst	mercaptopyruvate sulfurtransferase	catalyzes the formation of thiocyanide and pyruvate [RGD]	the redox state regulates MST activity at the enzymatic level, and MST controls redox to maintain cellular redox homeostasis	KEGG pathway: Cysteine metabolism	[Human, Mouse]HomoloGene: 31942



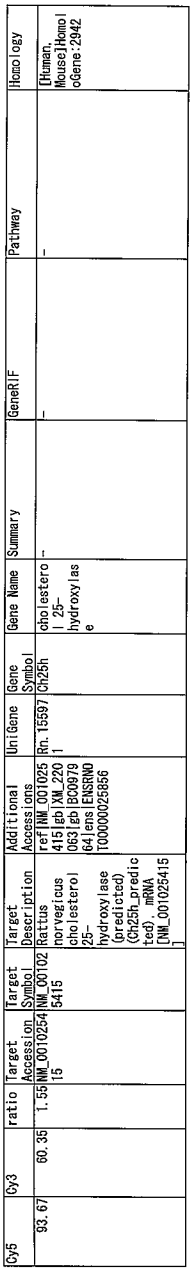
Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Gene Symbol	Gene Name	Summary	GeneRIF	Pathway	Homology
			NM_013156	Ctsl	Rattus norvegicus cathepsin L (Ctsl), mRNA [NM_013156]	ref|NM_0131 56|gb|BG063 175|gb|S851 84|ens|ENSR NOT00000025 462	Rn. 1294	Ctsl	cathepsin L	mouse homolog is deleted in the CD4 T-cell-deficient mouse mutant nacht (nkt); may play a role in CD4+ T-cell selection in the thymus [RGD]	cathepsin L created a 14-kDa carboxyl |GFBP-2 fragment that corresponded to the sole antigen detected in IEC-18 cell lysates as well as a 16.5-kDa fragment found in the media// The co-localization of PAP/TRAP and the cysteine protease cathepsin L could su	KEGG pathway: Antigen processing and presentation	[Human, Mouse]HomoloGene: 74298
			NM_017178	Bmp2	Rattus norvegicus bone morphogenetic protein 2 (Bmp2), mRNA [NM_017178]	ref|NM_0171 78|gb|Z25886 81|gb|L20678 |ens|ENSRNO T00000002890 4	Rn. 90931	Bmp2	bone morphogenetic protein 2	involved in cellular signaling during limb development; induces bone formation [RGD]	(TNF)-alpha induced NF-kappaBeta activation and elicited significant increases in BMP-2 mRNA and protein in primary coronary arterial endothelial cells// The Bmp2 3' UTR contains essential regulatory elements that act post-transcriptionally// Our results	KEGG pathway: Hedgehog signaling pathway// KEGG pathway: TGF-beta signaling pathway	[Human, Mouse]HomoloGene: 926
			XM_216584	Car6_predicted	PREDICTED: Rattus norvegicus carbonic anhydrase 6 (predicted) (Car6_predicted), mRNA [XM_216584]	ref|XM_2165 84|to|TC620 057	Rn. 43383	Car6	carbonic anhydrase 6	-	-	-	[Human, Mouse]HomoloGene: 20324

[表10]

表48 Cに対して発現増加した唾液腺の注目遺伝子
脂質代謝 (GO ID: 6629, 44255)

Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Gene Symbol	Gene Name	Summary	GeneRIF	Pathway	Homology
8361.31	3259.64	2.57	XM_341400	Rbp3	PREDICTED: Rattus norvegicus retinol binding protein 3, interstitial (Rbp3), mRNA [XM_341400]	ref|XM_341400 |gb|X56159|gb |X69523|ens|E NSRNOT0000002 7446	Rn. 41214	Rbp3	retinol binding protein 3, interstitial	may play a role in vision [RGD]	-	-	[Human, Mouse]Homol oGene:9261
61.95	24.36	2.54	NM_019169	Snca	Rattus norvegicus synuclein, alpha (Snca), mRNA [NM_019169]	ref|NM_019169 |gb|AF007758| gb|AY550005|g b|AY550006	Rn. 1827	Snca	synuclein, alpha	may play a role in regulation of synaptic vesicle biogenesis and organization; may be involved in neurotransmission [RGD]	we were able to modulate tyrosine hydroxylase-positive neuronal cell death by silencing alpha-synuclein expression, suggesting that down-regulation of alpha-synuclein is important in neuronal cell death of Parkinson's disease// DJ-1 up-regulates glutathio	KEGG pathway: Alzheimer's disease// KEGG pathway: Neurodegenerative Disorders// KEGG pathway: Parkinson's disease	[Human, Mouse]Homol oGene:293
40.56	19.56	2.07	NM_031736	Slc27a2	Rattus norvegicus solute carrier family 27 (fatty acid transporter), member 2 (Slc27a2), mRNA [NM_031736]	ref|NM_031736 |ref|XM_57952 6|gb|D85100|g b|XM_346669	Rn. 3608	Slc27a2	solute carrier family 27 (fatty acid transporter), member 2	has very long-chain acyl-CoA synthetase activity; may play a role in fatty acid metabolism [RGD]	in response to an increase of cellular cholesterol, fatty acid transporter is translocated from cytosol to membranes of type II pneumocytes.	KEGG pathway: Alkaloid biosynthesis II// KEGG pathway: Caprolactam degradation// KEGG pathway: Ethylbenzene degradation// KEGG pathway: Limonene and pinene degradation// KEGG pathway: Propanoate metabolism	-
182.19	88.28	2.06	NM_030827	Lrp2	Rattus norvegicus low density lipoprotein receptor-related protein 2 (Lrp2), mRNA [NM_030827]	ref|NM_030827 |ref|XM_57949 3|gb|L34049|g b|XM_346656	Rn. 26430	Lrp2	low density lipoprotein receptor-related protein 2	receptor for low density lipoprotein and a major kidney glomerular antigen for rat Heymann nephritis [RGD]	Megalin mediates IGF-I-induced clearance of Abeta and is involved in IGF-I transport into brain. Attenuated IGF-I/megalin input may contribute to increased risk of neurodegeneration, including late-onset Alzheimer's disease.// These data suggest that ligh	KEGG pathway: Hedgehog signaling pathway	-

Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Gene Symbol	Gene Name	Summary	GeneRIF	Pathway	Homology
716.84	423.92	1.69	NM_031561	Cd36	Rattus norvegicus cd36 antigen (Cd36), mRNA [NM_031561]	ref|NM_031561|ref|XM_57533 8|ref|NM_57539 4|gb|AF11391 4	Rn.10241	Cd36	cd36 antigen	fatty acid translocase; involved in long-chain fatty acid (LCFA) transport; important in fatty acid metabolism and insulin function [RGD]	Up-regulation of CD36 may have a role in increasing oxidative stress in cultured microvascular endothelial cells and the heart in chronic diabetes.// the subcellular distribution of fatty acid binding protein plasma membrane, as well as FAT/CD36, is acute	KEGG pathway: Adipocytokine signaling pathway// KEGG pathway: ECM-receptor interaction// KEGG pathway: Hematopoietic cell lineage	-
1541.69	985.71	1.56	NM_024396	Abca2	Rattus norvegicus ATP-binding cassette, sub-family A (ABC1), member 2 (Abca2), mRNA [NM_024396]	ref|NM_024396|gb|ABC37937|ens|ENSRNOT00000020339|ens|ENSRNOT00000036243	Rn.13115	Abca2	ATP-binding cassette, sub-family A (ABC1), member 2	glycosylated ABC transporter that binds ATP in the presence of magnesium: may play an important role in brain function [RGD]	ABCA2 protein is expressed predominantly in oligodendrocytes, and the expression of the protein is upregulated in the brain during maturation, especially between postnatal days 6 and 19.// ATP-binding cassette transporter ABCA2 (ABC2) expression in the de	KEGG pathway: ABC transporters - General	[Human, Mouse]Homol oGene:55590
139.55	89.53	1.56	NM_080778	Nr2f2	Rattus norvegicus nuclear receptor subfamily 2, group F, member 2 (Nr2f2), mRNA [NM_080778]	ref|NM_080778|gb|AF003944|ens|ENSRNOT00000014152|tc|TC57269 3	Rn.17815	Nr2f2	nuclear receptor subfamily 2, group F, member 2	transcriptional activator or repressor; involved in determining the metabolic phenotype of hepatic cells [RGD]	ARP-1/COUP-TFII acts as both a transcriptional repressor of microsomal triglyceride transfer protein and as a transcription activator of CYP7A1.	-	[Human, Mouse]Homol oGene:7628
1085.12	697.07	1.56	NM_053674	Phyh	Rattus norvegicus phytanoyl-CoA hydroxylase (Phyh), mRNA [NM_053674]	ref|NM_053674|gb|AF121345|gb|BC086573|ens|ENSRNOT00000024362	Rn.7279	Phyh	phytanoyl-CoA hydroxylase	catalyzes the conversion of phytanoyl-CoA to 2-hydroxyphytanoyl-CoA: plays a role in phytanic acid alpha-oxidation [RGD]	-	-	[Human, Mouse]Homol oGene:4530



Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Gene Symbol	Gene Name	Summary	GeneRIF	Pathway	Homology
93.67	60.35	1.55	NM_001025415	NM_001025415	Rattus norvegicus cholesterol 25-hydroxylase (predicted) (Ch25h_predicted), mRNA [NM_001025415]	ref|NM_001025415|gb|XM_220063|gb|BC009796|ens|ENSRNOG00000025656	Rn.155971	Ch25h	cholesterol 25-hydroxylase	-	-	-	[Human, Mouse]Homologene:2942

[表11]

表49 Gに対して発現増加した唾液腺の注目遺伝子
ドーパミン合成 (GO ID: 42416)

Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Gene Symbol	Gene Name	Summary	GeneRIF	Pathway	Homology
267.70	82.81	3.23	AA963004	AA963004	AA963004 UI-R-E1-gd-d-04-0-UI.s1 UI-R-E1 Rattus norvegicus cDNA clone UI-R-E1-gd-d-04-0-UI 3', mRNA sequence [AA963004]	gb|AA963004|CK04ltc1T C3544413	Rn.24539	Tgfb2	transforming growth factor, beta 2	binds the transforming growth factor-beta receptor: plays a role in regulation of cell growth and proliferation: may be involved in mesenchymal-epithelial cell interactions during development [RGD]	the pro-inflammatory cytokine MIF can shift the cytokine balance from the immunosuppressive state towards an inflammatory reaction, potentially through the inhibition of TGF-beta2 secretion by testicular peritubular cells.// TGF-beta2 mRNA and protein exp	KEGG pathway: Cell cycle// KEGG pathway: MAPK signaling pathway// KEGG pathway: TGF-beta signaling pathway	[Human, Mouse]Homolo Gene:2432
218.08	82.41	2.65	NM_012740	Th	Rattus norvegicus tyrosine hydroxylase (Th), mRNA [NM_012740]	ref|NM_012740|gb|L22651|gb|M10241|ens|ENSRNOT00000027682	Rn.11082	Th	tyrosine hydroxylase	catalyzes the rate limiting step in catecholamine biosynthesis; may be involved in response to hypoxia [RGD]	The kinetics of reduction of ferric TyrH by several reductants were determined by anaerobic stopped-flow spectroscopy. phosphorylation does not directly regulate the interconversion of the ferric and ferrous forms// The results indicate that the NGF/NGF	KEGG pathway: Parkinson's disease// KEGG pathway: Tyrosine metabolism	[Human, Mouse]Homolo Gene:307
61.95	24.38	2.54	NM_019169	Snca	Rattus norvegicus synuclein, alpha (Snca), mRNA [NM_019169]	ref|NM_019169|gb|AF007758|gb|AY550056|gb|AY550006	Rn.1827	Snca	synuclein, alpha	may play a role in regulation of synaptic vesicle biogenesis and organization: may be involved in neurotransmission [RGD]	we were able to modulate tyrosine hydroxylase-positive neuronal cell death by silencing alpha-synuclein expression, suggesting that down-regulation of alpha-synuclein is important in neuronal cell death of Parkinson's disease// DJ-1 up-regulates glutathio	KEGG pathway: Alzheimer's disease// KEGG pathway: Neurodegenerative Disorders// KEGG pathway: Parkinson's disease	[Human, Mouse]Homolo Gene:293

[表12]

表60 0に対しLで発現減少した唾液腺の注目遺伝子
アクセッション結合 (60 ID: 3779)

Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Gene Symbol	Gene Name	Summary	GeneRIF	Pathway	Homology
16509.25	39439.68	0.42	NM_013097	Dnase1	Rattus norvegicus deoxyribonuclease I (Dnase1), mRNA [NM_013097]	ref|NM_0130970|gb|X56060|gb|AF39710|gb|AF397150	Rn.6077	Dnase1	deoxyribonuclease I	glycoprotein that cleaves DNA endonucleolytically to yield 5(alpha)-phosphodinucleotide and oligonucleotide end products; facilitates DNA hydrolysis in alimentary duct and other digestive tissues [RGD]	A comparison of the expression and transport of DNAse1 from rats and DNAse1L3 from mice is reported.// results show that the chief cells of the stomach produce DNase I	-	[Human, Mouse]Homolo Gene:3826
115.15	257.92	0.45	NM_031747	Cnn1	Rattus norvegicus calponin 1 (Cnn1), mRNA [NM_031747]	ref|NM_031747|gb|D14437|gb|X71071|gb|BC006180|g	Rn.31788	Cnn1	calponin 1	binds actin stress fibers; involved in actin bundling [RGD]	Calponin increased in the molecular layer of the dentate gyrus, the site of mossy fiber sprouting, and neo-synaptogenesis, at 1 and 2 weeks after pilocarpine injection, when the reorganization was taking place.// CNN1 plays a role as tumor suppressor in S	-	[Human, Mouse]Homolo Gene:995
122.47	253.42	0.48	AW917167	AW917167	AW917167 EST348471 Rat gene index, normalized rat, norvegicus, Bento Soares Rattus norvegicus cDNA clone RGIEA09 5' end, mRNA sequence [AW917167]	gb|AW917167|tc|TC55565|g	Rn.18668	Plsl_predicted	plastin 1 (I isoform) (predicted)	-	-	-	[Human, Mouse]Homolo Gene:68270
1910.91	3729.09	0.51	NM_00102434545	NM_00102	Rattus norvegicus similar to tropomyosin 1, embryonic fibroblast - rat (MGC109519), mRNA [NM_001024345]	ref|NM_001024345|gb|BC090009|gb|IL00382|tc|TC518644	Rn.17680	--	similar to tropomyosin 1, embryonic fibroblast - rat	-	-	-	[Human, Mouse]Homolo Gene:55509

Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Gene Symbol	Gene Name	Summary	GeneRIF	Pathway	Homology
40.70	72.05	0.56	XM_234332	Plekhh1_predicted	PREDICTED: Rattus norvegicus pleckstrin homology domain containing, family H (with MyTH4 domain) member 1 (predicted) (Plekhh1_predicted), mRNA [XM_234332]	ref|XM_234332|Ensembl|ENSRNOT00000014257	Rn.35024	Plekhh1_predicted	pleckstrin homology domain containing, family H (with MyTH4 domain) member 1 (predicted)	-	-	-	[Human, Mouse]Homologene:24741
209.62	361.03	0.58	NM_019131	Tpm1	Rattus norvegicus tropomyosin 1, alpha (Tpm1), mRNA [NM_019131]	ref|NM_019131|gb|AF372217|gb|AF372215|gb|M60668	Rn.87540	Tpm1	tropomyosin 1, alpha	This gene is a member of the tropomyosin family and encodes a protein that heterodimerizes with a beta subunit, binding actin in both muscle and nonmuscle cells. In both smooth and striated musole cells, it plays a role in calcium dependent-regulation of	analysis of tropomyosin binding and binding sites for actin// The stability and energetics of the tropomyosin coiled coil are important for actin affinity.// A splicing silencer that regulates smooth muscle specific alternative splicing is active in multi	-	-
441.61	756.18	0.58	XM_573030	Myh11	PREDICTED: Rattus norvegicus myosin heavy chain 11 (Myh11), mRNA [XM_573030]	ref|XM_573030|gb|X16261|gb|XM_239866	Rn.94969	Myh11	myosin, heavy polypeptide 11, smooth muscle	transcription decreases following transformation with mutant p53 [RGD]	-	-	-
91.13	155.56	0.59	NM_182844	Myrip	Rattus norvegicus myosin VIIA and Rab interacting protein (Myrip), mRNA [NM_182844]	ref|NM_182844|gb|AY331984|gb|AW919575|tc|TC536770	Rn.16197	Myrip	myosin VIIA and Rab interacting protein	human and mouse homologs form a complex with Rab27A and Myosin VIIa; involved in melanosome trafficking to the actin cytoskeleton [RGD]	the Rab27B-Slac2-c complex is an important constituent of secretory granule exocytosis in parotid acinar cells	-	[Human, Mouse]Homologene:9150

Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Gene Symbol	Gene Name	Summary	GeneRIF	Pathway	Homology
45.87	78.08	0.59	XM_233196	Hook1_predicted	PREDICTED: Rattus norvegicus hook homolog 1 (Drosophila) (predicted) (Hook1_predicted), mRNA [XM_233196]	ref|XM_233196|TC544207	Rn.96284	Hook1_predicted	hook homolog 1 (Drosophila) (predicted)	-	-	-	[Human, Mouse]Homolo Gene:9289
57.95	95.57	0.61	NM_031520	Myh10	Rattus norvegicus myosin heavy chain 10, non-muscle (Myh10), mRNA [NM_031520]	ref|NM_031520|AF139055|ens|ENSRNOTG0000003983|tc|TC570280	Rn.98166	Myh10	myosin, heavy polypeptide 10, non-muscle	nonmuscle myosin II heavy chain: produces motor activity with actin filaments; isoform B2 may play a role in neuronal cell motility [RGD]	non-muscle myosin II and myosin light chain kinase are downstream targets for vasopressin signaling in the renal collecting duct// These results suggest that the mesangial expression of SMemb is related to glomerular matrix accumulation and that angiotens	KEGG pathway: Regulation of actin cytoskeleton// KEGG pathway: Tight junction	[Human, Mouse]Homolo Gene:55941
44.47	71.65	0.62	XM_226874	Myo10_predicted	PREDICTED: Rattus norvegicus myosin X (predicted) (Myo10_predicted), mRNA [XM_226874]	ref|XM_226874|ENSRNOT0000001422	Rn.20775	Myo10_predicted	myosin X (predicted)	-	-	-	[Human, Mouse]Homolo Gene:36328
184.78	282.04	0.66	NM_030873	Pfn2	Rattus norvegicus profilin 2 (Pfn2), mRNA [NM_030873]	ref|NM_030873|AY004289|gb|BC087013|gb|AI556217	Rn.17153	Pfn2	profilin 2	binds actin; regulates the rate of actin polymerization [RGD]	Following hypophysectomy, the actin cytoskeleton of the Sertoli cell shifts to a predominantly depolymerized state, perhaps in part because of decreases in profilin II and espin gene products.// RhoA/ROCK/PIIa-mediated regulation of actin stability, shown	KEGG pathway: Regulation of actin cytoskeleton	[Human, Mouse]Homolo Gene:1974

Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Gene Symbol	Gene Name	Summary	GeneRIF	Pathway	Homology
			XM_240417	Mtmr7_predicted	PREDICTED: Rattus norvegicus myotubularin related protein 7 (predicted) (Mtmr7_predicted), mRNA [XM_240417]	ref|XM_240417|gb|AA998777|ens|ENSRNOT00000015625|tc|TC538804	Rn.12785	Mtmr7_predicted	myotubularin related protein 7 (predicted)	-	-	-	[Human]HomoloGene:56848

[表13]

表51 Ciに対して発現減少した唾液腺の注目遺伝子
細胞外成分 (GO ID: 5576, 44421, 5615)

Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Gene Symbol	Gene Name	Summary	GeneRIF	Pathway	Homology
66.53	1235.35	0.05	NM_019161	Cdh22	Rattus norvegicus cadherin 22 (Cdh22), mRNA [NM_019161]	ref|NM_019161|gb|D63349|tc|T C588625	Rn.145674	Cdh22	cadherin 22	mediates Ca2+ dependent cell adhesion: may play a role in brain and neuroendocrine organ morphogenesis [RGD]	PB-cadherin promotes survival of spermatocytes and activates Jak2 and Stat3 signaling.	-	[Human, Mouse]HomoloGene:23148
30527.51	498133.39	0.06	NM_133622	RGD:708577	Rattus norvegicus common salivary protein 1 (LOC171161), mRNA [NM_133622]	ref|NM_133622|gb|U00964|tc|T C568908|tc|T05 71345	Rn.9752	-	common salivary protein 1	precursor appears to undergo post-translational modification to form a family of related salivary proteins [RGD]	-	-	-
25.47	367.35	0.07	NM_139087	Cgref1	Rattus norvegicus cell growth regulator with EF hand domain 1 (Cgref1), mRNA [NM_139087]	ref|NM_139087|gb|U66470|gb|A W913954|ens|EN SRNOT00000010 586	Rn.31842	Cgref1	cell growth regulator with EF hand domain 1	inhibits cell growth [RGD]	CGR11 appears to be a primary response gene expressed to moderate levels in functional p53 cells.	-	[Human, Mouse]HomoloGene:4790
37.00	247.55	0.15	NM_001100772	Pf4	Rattus norvegicus platelet factor 4 (Pf4), mRNA [NM_001100772 9]	ref|NM_001100772 9|gb|XM_34119 2|gb|AW915663| ens|ENSRNOT000 00033406	Rn.6800	Cxcl4	chemokine (C-X-C motif) ligand 4	member of low-molecular weight chemokines superfamily; may mediate inflammation and immune response [RGD]	this study identified a novel regulatory element, TME(tandem repeat of MEIS1 binding element)in the PF4 promoter and demonstrated that MEIS1/PBX complexes bind to the TME// A carboxyl-terminal fragment of this protein effects a rapid histamine release from	KEGG pathway: Leukocyte transendothelial migration	[Mouse]HomoloGene:69289
204.73	1204.31	0.17	NM_053348	Fetub	Rattus norvegicus fetuin beta (Fetub), mRNA [NM_053348]	ref|NM_053348|gb|AJ242926|gb [BC070508|ens| ENSRNOT00000004 6199	Rn.2464	Fetub	fetuin beta	inhibits insulin receptor tyrosine kinase activity, protease inhibitory activities; developmentally regulates calcium metabolism and osteogenesis [RGD]	-	-	[Human, Mouse]HomoloGene:8660

Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Gene Symbol	Gene Name	Summary	GeneRIF	Pathway	Homology
136.51	775.96	0.18	NM_001013180	NM_001013180	Rattus norvegicus secretoglobin, family 3A, member 1 (Scgb3a1), mRNA [NM_001013180]	ref|NM_001013180|gb|AF436841|gb|XM_340791|gb|BK000202	Rn.30648	Scgb3a1	secretoglobin, family 3A, member 1	secretoglobin: may have a role in airway function [RGD]	-	-	[Mouse]Homolo Gene:14160
54.55	254.82	0.21	NM_053744	Dlk1	Rattus norvegicus delta-like 1 homolog (Drosophila) (Dlk1), mRNA [NM_053744]	ref|NM_053744|ref|XM_579575|gb|D84336|gb|XM_346776	Rn.14547	Dlk1	delta-like 1 homolog (Drosophila)	involved in maintaining the undifferentiated status of the preadipocyte [RGD]	localisation in rat was in the medulla and the zona glomerulosa of the cortex of the adrenal glands, in the pars distalis of the adenohypophysis, and in the ovarian granulosa lutein cells but no staining was found in the pancreas	-	[Human, Mouse]HomoloGene:2846
154.13	608.12	0.25	XM_214143	Oit1_predicted	PREDICTED: Rattus norvegicus oncoprotein induced transcript 1 (predicted) (Oit1_predicted), mRNA [XM_214143]	ref|XM_214143|ens|ENSRNOT00000055554	Rn.38497	Oit1_predicted	oncoprotein induced transcript 1 homolog (mouse) (predicted)	-	-	-	[Human, Mouse]HomoloGene:16354
103.38	383.73	0.27	NM_203337	RGD:1303068	Rattus norvegicus alpha-2,3-sialyltransferase ST3Gal IV (siat4c), mRNA [NM_203337]	ref|NM_203337|gb|AJ626923|gb|BC089057|ens|ENSRNOT00000013243	Rn.24125	St3gal4	ST3 beta-galactoside alpha-2,3-sialyltransferase 4	plasma membrane-specific alpha 2,3- sialic acid transporter: may be important for protein amino acid glycosylation [RGD]	-	-	[Human, Mouse]HomoloGene:46572
75.56	262.31	0.29	NM_133295	Ces3	Rattus norvegicus carboxylesterase 3 (Ces3), mRNA [NM_133295]	ref|NM_133295|ref|NM_001013889|ref|XM_579616|gb|X51974	Rn.2549	Ces3	carboxylesterase 3	enzyme that hydrolizes long-chain fatty acids and thioesters; may play a role in lipid metabolism and/or the elimination of toxic substances [RGD]	-	KEGG pathway: Alkaloid biosynthesis II	-

Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Gene Symbol	Gene Name	Summary	GeneRIF	Pathway	Homology
331.89	1058.38	0.31	XM_019303	Cyp2f2	Rattus norvegicus cytochrome P450, family 2, subfamily f, polypeptide 2 (Cyp2f2), mRNA [NM_019303]	ref|NM_019303|gb|AF017393|gb|BC007939|tc|TC571084	Rn.10817	Cyp2f2	cytochrome P450, family 2, subfamily f, polypeptide 2	member of the p450 2F subfamily; forms styrene glycol from styrene in liver and lung microsomes [RGD]	-	KEGG pathway: Metabolism of xenobiotics by cytochrome P450	[Human, Mouse]Homolo Gene:73898
83.84	264.21	0.32	XM_199082	Sectm1	Rattus norvegicus secreted and transmembrane 1 (Sectm1), mRNA [NM_199082]	ref|NM_199082|gb|BC061794|gb|XM_213545|tc|TC569738	-	Sectm1	secreted and transmembrane 1	human homolog is a Golgi-associated protein; may have a role in hematopoietic and/or immune system processes [RGD]	-	-	[Human, Mouse]Homolo Gene:48157
171.07	532.76	0.32	NM_00101321 9	NM_001013 219	Rattus norvegicus sialyltransferase 4A (beta-galactoside alpha-2,3-sialytransferase) (predicted) (Siat4a_predicted), mRNA [NM_00101321 9]	ref|NM_00101321 9|gb|XM_343254|gb|AJ748840|ens|ENSRNOT00000010980	Rn.104514	St3gal1	ST3 beta-galactoside alpha-2,3-sialyltransferase 1	-	-	-	[Human, Mouse]Homolo Gene:7540
337.06	1003.53	0.34	XM_221623	Fam3b_predicted	PREDICTED: Rattus norvegicus family with sequence similarity 3, member B (predicted) (Fam3b_predicted), mRNA [XM_221623]	ref|XM_221623|ens|ENSRNOT00000002683|ens|ENSRNOT00000005116|ens|ENSRNOT00000042012	Rn.162007	RGD1311662_predicted	similar to open reading frame 9	-	-	-	[Human, Mouse]Homolo Gene:10766

Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Gene Symbol	Gene Name	Summary	GeneRIF	Pathway	Homology
557.00	1547.24	0.36	NM_001010970	Amy1	Rattus norvegicus amylase 1, salivary (Amy1), mRNA [NM_001010970]	ref|NM_001010970|gb|AB057450|gb|BC088228|ens|ENSRNOT00000022496	Rn.116361	Amy1	amylase 1, salivary	-	the HCO3-anion participates in the secretory sequence at sites distal to the identification of secretagogues in both endocrine and exocrine cells, the absence of extracellular bicarbonate is shown to decrease by about 50% basal alpha-amylase secretion	KEGG pathway: Starch and sucrose metabolism	-
26.73	72.15	0.37	NM_013080	Ptprz1	Rattus norvegicus protein tyrosine phosphatase, receptor-type, Z polypeptide 1 (Ptprz1), mRNA [NM_013080]	ref|NM_013080|ref|XM_579367|gb|U09357|gb|X M_346695	Rn.10088	Ptprz1	protein tyrosine phosphatase, receptor-type, Z polypeptide 1	alternative splicing product phosphocan inhibits neural cell adhesion and neurite outgrowth [RGD]	RPTPzeta/beta is localized mainly at the postsynaptic membrane of pyramidal neurons in adult cerebral cortex and hippocampus// findings suggest that PTN-PTPzeta signaling regulates the morphogenesis of Purkinje cell dendrites and that the mechanisms under	-	-
18.96	50.49	0.38	NM_057201	Gpr37	Rattus norvegicus G protein-coupled receptor 37 (Gpr37), mRNA [NM_057201]	ref|NM_057201|gb|AF087946|gb|BC087728|ens|ENSRNOT00000003593	Rn.28035	Gpr37	G protein-coupled receptor 37	an orphan G protein-coupled receptor that may have an important role in the central nervous system [RGD]	expression of Pael-R genes in the nigro-striatal pathway may have significant implication for pathophysiology and treatment of parkinson disease.	KEGG pathway: Parkinson's disease	[Human, Mouse]Homolo Gene:3875
38.43	101.49	0.38	NM_012870	Tnfrsf11b	Rattus norvegicus tumor necrosis factor receptor superfamily, member 11b (osteoprotegerin) (Tnfrsf11b), mRNA [NM_012870]	ref|NM_012870|gb|U94330|gb|BC081830|ens|ENSRNOT00000011344	-	Tnfrsf11b	tumor necrosis factor receptor superfamily, member 11b (osteoprotegerin)	plays a role in the negative regulation of bone resorption by inhibiting formation of osteoclasts [RGD]	Regulation of OPG production by the dental follicle likely affects the alveolar bone resorption needed for tooth eruption.// Detection of osteoprotegerin mRNA and protein in bone cells,// reduces osteoclast numbers and prevents bone erosion in collagen-in	KEGG pathway: Cytokine-cytokine receptor interaction	[Human, Mouse]Homolo Gene:1912

Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Gene Symbol	Gene Name	Summary	GeneRIF	Pathway	Homology
83.39	216.00	0.39	NM_013122	Igfbp2	Rattus norvegicus insulin-like growth factor binding protein 2 (Igfbp2). mRNA [NM_013122]	ref|NM_013122|gb|J04486|gb|M31672|ens|ENSRNOT00000023068	Rn. 6813	Igfbp2	insulin-like growth factor binding protein 2	protein that binds to Igf-I and Igf-II [RGD]	Growth inhibition, which was supported by the strong induction of p21CIP1/WAF1, was correlated with increased secretion of IGFBP-2 and, unexpectedly, with its increased localization in the nucleus and particularly in the cytoplasm.// retinoic acid modulat	-	[Human, Mouse]Homolog ene:499
276.12	681.07	0.41	NM_001002802	RGD:1303241	Rattus norvegicus beta-site APP-cleaving enzyme 2 (Bace2). mRNA [NM_001002802]	ref|NM_001002802|ref|XM_579078|gb|XM_213642|gb|BM000318	Rn. 38581	Bace2	beta-site APP-cleaving enzyme 2	-	-	KEGG pathway: Alzheimer's disease	[Human, Mouse]Homolog ene:22696
18.53	45.46	0.41	NM_031697	Siat6	Rattus norvegicus sialyltransferase 6 (N-acetyllacosaminide alpha 2,3-sialyltransferase) (Siat6), mRNA [NM_031697]	ref|NM_031697|gb|M97754|ens|ENSRNOT00000026990|tc|TC54369595	Rn. 44390	St3gal3	ST3 beta-galactoside alpha-2,3-sialyltransferase 3	plays a role in the formation of terminal carbohydrate groups of glycolipids and glycoproteins [RGD]	-	KEGG pathway: Blood group glycolipid biosynthesis - lactoseries// KEGG pathway: Keratan sulfate biosynthesis	[Human, Mouse]Homolog ene:7539
16509.25	39439.68	0.42	NM_013097	Dnase1	Rattus norvegicus deoxyribonuclease I (Dnase1). mRNA [NM_013097]	ref|NM_013097|gb|X56060|gb|AF397151|gb|AF397150	Rn. 6077	Dnase1	deoxyribonuclease I	glycoprotein that cleaves DNA endonucleolytically to yield 5(alpha)-phosphodinucleotide and oligonucleotide end products: facilitates DNA hydrolysis in alimentary duct and other digestive tissues [RGD]	A comparison of the expression and transport of DNAse1 from rats and DNAse1L3 from mice is reported.// results show that the chief cells of the stomach produce DNase I	-	[Human, Mouse]Homolog ene:3826

Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Gene Symbol	Gene Name	Summary	GeneRIF	Pathway	Homology
38.32	89.20	0.43	NM_012596	Lepr	Rattus norvegicus leptin receptor (Lepr), mRNA [NM_012596]	ref|NM_012596|gb|U52966|gb|D84125|gb|D84126	Rn. 9891	Lepr	leptin receptor	receptor for leptin; may have a role in body weight maintainence [RGD]	Results suggest that changes in leptin level and its receptor expression may influence the energy homeostasis during pregnancy. // Shedding of OsRa membrane-anchored receptors, rather than OsRe expression, might preferentially contribute to generation of i	KEGG pathway: Adipocytokine signaling pathway// KEGG pathway: Cytokine-cytokine receptor interaction// KEGG pathway: Jak-STAT signaling pathway// KEGG pathway: Neuroactive ligand-receptor interaction	[Human, Mouse]Homolo gene:1731
307.85	715.76	0.43	NM_021744	Cd14	Rattus norvegicus CD14 antigen (Cd14), mRNA [NM_021744]	ref|NM_021744|gb|U51804|gb|BC061733|ens|ENSRNOT00000023977	-	Cd14	CD14 antigen	component of the lipopolysaccharide receptor complex: mediates LPS-induced neuroinflammation and inflammatory response [RGD]	CD14 glycoprotein is present on the cell membranes of vascular smooth muscle cells of rat aorta, where it acts as a lipopolysaccharide receptor. // in kupffer cells, increase of TLR4, CD14 expression may be induced by LPS within 1-3 hours, and further incr	KEGG pathway: Hematopoietic cell lineage// KEGG pathway: MAPK signaling pathway// KEGG pathway: Regulation of actin cytoskeleton// KEGG pathway: Toll-like receptor signaling pathway	[Human, Mouse]Homolo gene:493
24.27	55.83	0.43	NM_017131	Casq2	Rattus norvegicus calsequestrin 2 (Casq2), mRNA [NM_017131]	ref|NM_017131|gb|U33287|gb|AF001334|gb|BC072547	Rn. 10111	Casq2	calsequestrin 2	binds activated epsilon protein kinase C holoenzyme; human homolog serves as a calcium resevoir in cardiac myocytes [RGD]	The role of CASQ2 in calcium (Ca2+) handling in cardiac myocytes can be attributed to its action as a Ca2+ buffer in the lumen of the sarcoplasmic reticulum.	-	[Human, Mouse]Homolo gene:20330
54.73	124.73	0.44	NM_001102568	NM_001025683	Rattus norvegicus similiar to RIKEN cDNA 1810055G02 (predicted) (RGD1311946_predicted), mRNA [NM_001025683]	ref|NM_001025683|gb|XM_219679|gb|BC096053|ens|ENSRNOT00000034240	Rn. 16921	RGD1311946	similar to RIKEN cDNA 1810055G02	-	-	-	[Human, Mouse]Homolo gene:11174

Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Gene Symbol	Gene Name	Summary	GeneRIF	Pathway	Homology
54.73	124.73	0.44	NM_001025683	Rattus norvegicus similar to RIKEN cDNA 1810055G02 (predicted) (RGD1311946_predicted), mRNA [NM_001025683]	ref|NM_001025683|gb|XM_217969|gb|BC096053|ens|ENSRNOT00000034240	Rn.16921	RGD1311946	similar to RIKEN cDNA 1810055G02	-	-	-	[Human, Mouse]HomoloGene:11174
481.18	1069.10	0.45	XM_345278	Amy2_predicted	Rattus norvegicus similar to amylase 1; amylase 1, salivary (LOC365914), mRNA [XM_345278]	gb|XM_345278|ens|ENSRNOT00000049844|ens|ENSRNOT00000090693	Rn.67070	Amy2_predicted	amylase 2, pancreatic (predicted)	-	-	-	-
56.10	123.83	0.45	NM_001004215	RGD:1303221	Rattus norvegicus peptidylprolyl isomerase C (Ppic), mRNA [NM_001004215]	ref|NM_001004215|gb|XM_214534|gb|BC078949|ens|ENSRNOT00000023485	Rn.144176	Ppic	peptidylprolyl isomerase C	-	-	-	[Human, Mouse]HomoloGene:727
3503.77	7655.60	0.46	NM_019331	Posk3	Rattus norvegicus proprotein convertase subtilisin/kexin type3 (Posk3), mRNA [NM_019331]	ref|NM_019331|ref|XM_579432|gb|X65660|gb|M_346546	Rn.3220	Posk3	proprotein convertase subtilisin/kexin type3	may be one of several enzymes involved in the proteolytic processing of extracellular superoxide dismutase (EC-SOD) [RGD]	CDX2 regulates furin expression in intestinal epithelial cells// Data suggest that inhibition of furin and PC5 and resulting inhibition of insulin-like growth factor 1 receptor (IGF-1R) activation can inhibit IGF-1-induced membrane-type 1 matrix metallopr	-	-
23.20	49.85	0.47	NM_031565	RGD:621508	Rattus norvegicus carboxylesterase 1 (Ces1), mRNA [NM_031565]	ref|NM_031565|gb|X81395|ens|ENSRNOT00000020775|Tc|Tc05672	Rn.161717	-	carboxylesterase 1	enzyme that hydrolyzes long-chain fatty acids: necessary for cholesterol esterification: may be important for detoxification of certain drugs [RGD]	results demonstrate elevation of FC and depletion of cholesteryl esters by over-expression of hncCEH, which were resistant to compensatory responses by other enzymes of cholesterol homeostasis	KEGG pathway: Alkaloid biosynthesis II	[Mouse]HomoloGene:75318

Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Gene Symbol	Gene Name	Summary	GeneRIF	Pathway	Homology
71.61	143.96	0.50	NM_001013232	NM_001013232	Rattus norvegicus ribonuclease, RNase A family, 1 (pancreatic) (predicted) (Rnase1_predicted), mRNA [NM_001013232]	ref|NM_001013232|ens|ENSRNOT00000033809|tc|TC519040	Rn.111376	Rnase1_predicted	ribonuclease, RNase A family, 1 (pancreatic) (predicted)	-	-	-	-
70.95	141.83	0.50	NM_001012018	B4galt4_predicted	Rattus norvegicus UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 4 (predicted) (B4galt4_predicted), mRNA [NM_001012018]	ref|NM_001012018|ref|XM_573289|gb|XM_221439|gb|BC081866	Rn.143976	B4galt4	UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 4	-	-	-	[Human, Mouse]Homolog ene:37848
1570.81	2982.75	0.53	NM_001024240	NM_001024240	Rattus norvegicus similar to RIKEN cDNA 2010001M09 (predicted) (RGD1310251_predicted), mRNA [NM_001024240]	ref|NM_001024240|gb|XM_214585|gb|BC093397|ens|ENSRNOT00000036301	Rn.19595	RGD1310251	similar to RIKEN cDNA 2010001M09	-	-	-	[Mouse]Homolo Gene:12333
22.76	42.13	0.54	NM_172333	Cthrc1	Rattus norvegicus collagen triple helix repeat containing 1 (Cthrc1), mRNA [NM_172333]	ref|NM_172333|gb|AY136824|ens|ENSRNOT00000061421|tc|TC569980	Rn.9468	Cthrc1	collagen triple helix repeat containing 1	-	CTHRC1 is transiently expressed in the arterial wall in response to injury where it may contribute to vascular remodeling by limiting collagen matrix deposition and promoting cell migration.	-	[Human, Mouse]Homolog ene:16320

Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Gene Symbol	Gene Name	Summary	GeneRIF	Pathway	Homology
92.73	169.69	0.55	XM_215963	Lama5	PREDICTED: Rattus norvegicus laminin, alpha 5 (Lama5), mRNA [XM_215963]	ref|XM_215963|ens|ENSRNOT0000009811ens|ENSRNOT00000005139711tc|TC51890 6	Rn. 62816	Lama5	laminin, alpha 5	an extracellular matrix glycoprotein involved in cell migration and differentiation [RGD]	Data suggest that the early arrest of tumor cells in the pulmonary vasculature through interaction of alpha3beta1 integrin with laminin-5 in exposed basement membrane provides a basis for cell arrest during pulmonary metastasis.// laminin 6 and 5 have dis	KEGG pathway: Cell Communication// KEGG pathway: ECM-receptor interaction// KEGG pathway: Focal adhesion	[Human, Mouse]Homolo Gene:4060
59.27	107.57	0.55	XM_235478	Kdelr3_predicted	PREDICTED: Rattus norvegicus KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 3 (predicted) (Kdelr3_predicted), mRNA [XM_235478]	ref|XM_235478|ens|ENSRNOT00000181741|tc|TC545855	Rn. 161994	Kdelr3_predicted	KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 3 (predicted)	-	-	-	[Human, Mouse]Homolo Gene:68533
120.04	217.05	0.55	NM_012729	Prss2	Rattus norvegicus protease, serine, 2 (Prss2), mRNA [NM_012729]	ref|NM_012729|ref|XM_342669|gb|V01274|ens|ENSRNOT00000018852	Rn. 1584	Prss2	protease, serine, 2	catalyzes the cleavage of Arg-Xaa, Lys-Xaa [RGD]	-	-	-
72.00	130.17	0.55	NM_134432	Agt	Rattus norvegicus angiotensinogen (Agt), mRNA [NM_134432]	ref|NM_134432|gb|BC078741|gb|L00094|ens|ENSRNOT00000024917	Rn. 6319	Agt	angiotensinogen (serpin peptidase inhibitor, clade A, member 8)	plays a role in regulation of blood pressure [RGD]	modification of the critical balance between ANG II and ET-1 systems through variant Dear contributes to hypertension susceptibility in female F2(RxS) intercross rats// the mechanism by which Ang II stimulates IGF-IR expression in VSMCs involves NF-kappaB	-	[Human, Mouse]Homolo Gene:14

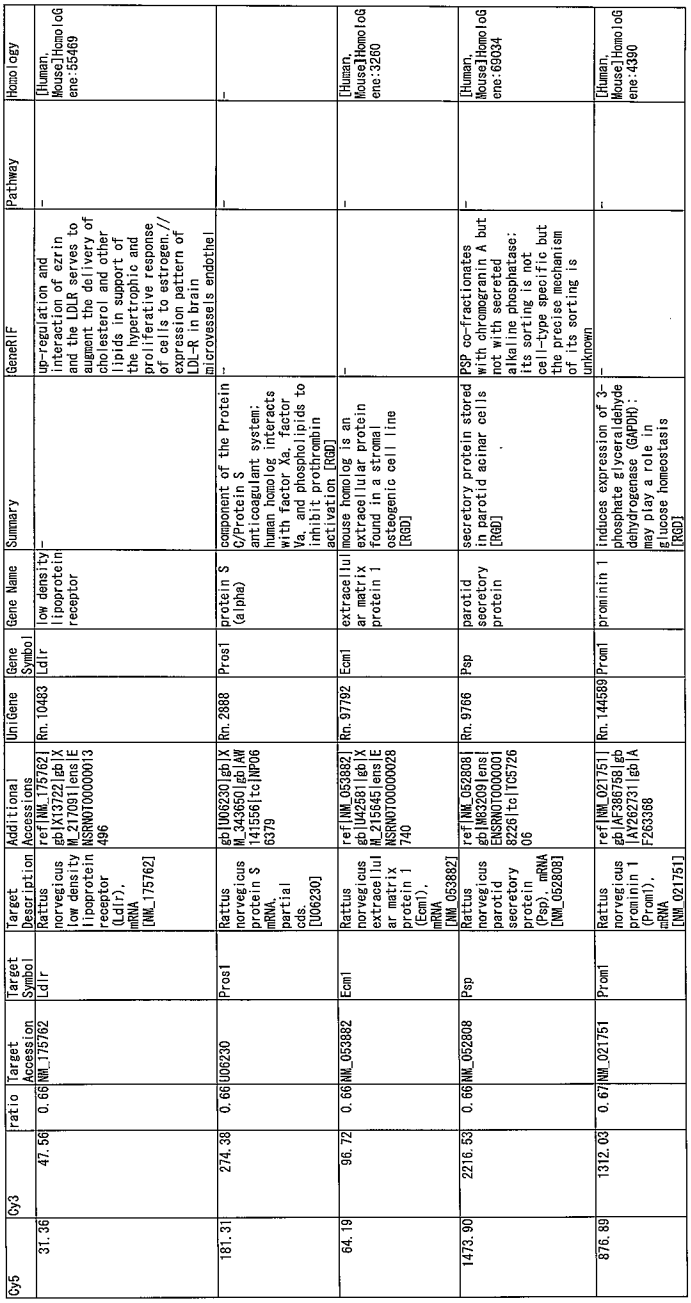
Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Gene Symbol	Gene Name	Summary	GeneRIF	Pathway	Homology
812.47	1464.83	0.55	NM_00100833 4	RGD1307423_predicted	Rattus norvegicus similar to RIKEN cDNA 1810014L12 (predicted) (RGD1307423_predicted), mRNA [NM_00100833 4]	ref|NM_00100083 4|gb|XM_22074 1|gb|BC065344| gb|BF546446	Rn.20057	Tmem97	transmembrane protein 97	-	-	-	[Human, Mouse]Homolo gene:6443
61.64	110.31	0.56	XM_342668	Prss3_predicted	PREDICTED: Rattus norvegicus protease, serine, 3 (mesotrypsin) (predicted) (Prss3_predicted), mRNA [XM_342668]	ref|XM_342668| ens|ENSRNOT000 00041100	Rn.154705	Prss3_predicted	protease, serine, 3 (mesotrypsin) (predicted)	-	-	-	-
47.51	84.12	0.56	NM_176074	C6	Rattus norvegicus complement component 6 (C6), mRNA [NM_176074]	ref|NM_176074| gb|AY230250|en s|ENSRNOT00000 033112|tc|TC56 9389	Rn.16145	C6	complement component 6	component of the complement cascade for immune response; may be a component of the membrane attack complex [RGD]	Lung allografts from C6-deficient donors to C6(-) recipients survive 13-17 days, whereas allografts from C6-sufficient donors to C6(+) recipients are rejected with intense vasoular infiltration and diffuse alveolar hemorrhage 7 days posttransplant.// The	KEGG pathway: Complement and coagulation cascades	[Human, Mouse]Homolo gene:47
547.92	965.78	0.57	XM_340999	Tfrc	PREDICTED: Rattus norvegicus Transferrin receptor (Tfrc), mRNA [XM_340999]	ref|XM_340999| ens|ENSRNOT000 00002407|ens|E NSRNOT00000004 868|ens|ENSRNO T00000041968	Rn.98672	Tfrc	transferrin receptor	receptor for transferrin: involved in regulating stellate cell activation [RGD]	a region of the TfR that can potentially interact with hsc70// These data suggest that alveolar type II (but not type I) cells express functional transferrin receptor in adult rat alveolar epithelium.// MPP(+)-dependent aconitase inactivation, Tf-iron upt	KEGG pathway: Hematopoietic cell lineage	[Human, Mouse]Homolo gene:2429

Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Gene Symbol	Gene Name	Summary	GeneRIF	Pathway	Homology
169.47	293.25	0.58	NM_173114	Cipar1	Rattus norvegicus castration induced prostatic apoptosis-related protein 1 (Cipar1), mRNA [NM_173114]	ref|NM_173114|gb|AJ010750|gb|BC060539|ens|ENSRNOT00000003472	Rn.127830	Cipar1	castration induced prostatic apoptosis-related protein 1	displays increased expression in ventral prostate after castration; expression in prostate is associated with apoptosis [RGD]	-	-	[Human, Mouse]Homolo Gene:41036
198.39	339.18	0.58	NM_001013137	Rattus norvegicus chemokine (C-X-C motif) ligand 14 (predicted) (Cxcl14_predicted), mRNA [NM_001013137]	ref|NM_001013137|gb|AI043862|tc|TC655043	Rn.3130	Cxcl14	chemokine (C-X-C motif) ligand 14	-	-	-	-
54.48	92.88	0.59	NM_021664	Dlad	Rattus norvegicus DNaseII-like acid DNase (Dlad), mRNA [NM_021664]	ref|NM_021664|gb|AF178974|ens|ENSRNOT00000021861|tc|TC571381	Rn.41640	Dnase2b	deoxyribonuclease II beta	catalyzes the divalent cation-independent hydrolysis of DNA into oligonucleotides [RGD]	-	-	[Human, Mouse]Homolo Gene:1052
86.98	146.18	0.60	NM_138533	Spon2	Rattus norvegicus spondin 2, extracellular matrix protein (Spon2), mRNA [NM_138533]	ref|NM_138533|gb|AF155196|gb|BC078734|tc|TC569008	Rn.6699	Spon2	spondin 2, extracellular matrix protein	promotes cell adhesion and outgrowth of embryonic hippocampal neurons [RGD]	F-spondin can alter cell differentiation in multiple ways, depending upon its concentration and distribution between substrate-attached and soluble forms.// F-spondin may be an endogenous regulator of APP cleavage.	-	-

Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Gene Symbol	Gene Name	Summary	GeneRIF	Pathway	Homology
16.93	28.09	0.60	XM_342055	Sema4g_predicted	PREDICTED: Rattus norvegicus sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4G (predicted) (Sema4g_predicted), mRNA [XM_342055]	ref|XM_342055|gb|AW914054|gb|BG088250|tc|TC535808	Rn.1645	Sema4g_predicted	sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4G (predicted)	-	-	KEGG pathway: Axon guidance	[Human, Mouse]HomoloGene:22682
27.72	45.98	0.60	XM_231381	Sema3c_predicted	Rattus norvegicus similar to semaphorin 3C: semaphorin E (LOC296787), mRNA [XM_231381]	gb|XM_231381|ens|ENSRNOT00000009132|tc|TC569331	Rn.136960	Sema3c_predicted	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3C (predicted)	-	-	KEGG pathway: Axon guidance	[Human, Mouse]HomoloGene:36201
78.96	128.23	0.62	NM_053591	Dpep1	Rattus norvegicus dipeptidase 1 (renal) (Dpep1), mRNA [NM_053591]	ref|NM_053591|gb|LO7315|ens|ENSRNOT00000021397|tc|TC5770770	Rn.6051	Dpep1	dipeptidase 1 (renal)	renal enzyme that cleaves proteins [RGD]	carboxypeptidase A, dipeptidase and Na+/K+ ATPase levels in the rat intestine change when exposed to different doses of cadmium	-	[Human, Mouse]HomoloGene:80192
107.57	174.23	0.62	XM_224987	Sfrp1	PREDICTED: Rattus norvegicus secreted frizzled-related protein 1 (Sfrp1), mRNA [XM_224987]	ref|XM_224987|gb|AF167308|ens|ENSRNOT00000024128|tc|TC537124	Rn.163333	Sfrp1	secreted frizzled-related protein 1	a secreted protein involved in binding Wnt and antagonizing Wnt signaling [RGD]	Sfrp1 gene was identified and characterized by using bioinformatics, consisting of three exons, a signal peptide (codon 1-31), Frizzled domain with ten conserved Cys residues (codon 49-168), and Netrin (NTR) domain with six conserved Cys residues.// findi	KEGG pathway: Wnt signaling pathway	[Human, Mouse]HomoloGene:2266

Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Gene Symbol	Gene Name	Summary	GeneRIF	Pathway	Homology
160.89	258.31	0.62	AI009597	AI009597	AI009597 EST204048 Normalized rat lung, Bento Soares Rattus sp. cDNA clone RLUBG14.3' end, mRNA sequence [AI009597]	gb|AI009597	Rn.3896	Fxyd3	FXYD domain-containing ion transport regulator 3	This gene encodes a member of a family of small membrane proteins that share a 35-amino acid signature sequence domain, beginning with the sequence PFXYD and containing 7 invariant and 6 highly conserved amino acids. The approved human gene nomenclature f	-	-	[Mouse]Homolo Gene:4356
23.22	37.03	0.63	U70050	Jag2	Rattus norvegicus jagged2 precursor, mRNA, partial cds. [U70050]	gb|U70050|tc|T C537474	Rn.22469	Jag2	Jagged 2	may function as a ligand for Notch and may be involved in limb development [RGD]	-	KEGG pathway: Notch signaling pathway	[Human, Mouse]Homolo Gene:1677
54.99	87.55	0.63	NM_031598	Pla2g2a	Rattus norvegicus phospholipase A2, group IIA (platelets, synovial fluid) (Pla2g2a), mRNA [NM_031598]	ref|NM_031598| gb|AF363363|gb |U00523|gb|M37 127	Rn.11346	Pla2g2a	phospholipase A2, group IIA (platelets, synovial fluid)	hydrolyzes acyl group at the sn-2 position of phospholipids, forming non-esterified fatty acids and lysophospholipids: plays a critical role in inflammation: induces proliferation of smooth muscle cells [RGD]	These results indicate that phospholipase A(2)-IIA is coexpressed with SNAP-25 in mature taste receptor cells that possess exocytotic machinery.// new autocrine and paracrine pathways activating sPLA2-IIA gene expression in rat and human vascular smooth m	KEGG pathway: Arachidonic acid metabolism// KEGG pathway: Glycerophospholipid metabolism// KEGG pathway: Linoleic acid metabolism// KEGG pathway: MAPK signaling pathway	[Human]Homolo Gene:254
291.74	463.56	0.63	NM_080698	Fmod	Rattus norvegicus fibromodulin (Fmod), mRNA [NM_080698]	ref|NM_080698| gb|AB2132|ens| ENSRNOT0000000 4382|tc|TC5685 92	Rn.8778	Fmod	fibromodulin	-	-	-	[Human, Mouse]HomoloG ene:1530
692.47	1079.99	0.64	NM_001012 5	NM_001014 125	Rattus norvegicus protein disulfide isomerase-associated 5 (Pdia5), mRNA [NM_0010141 25]	ref|NM_0010141 25|gb|XM_34099 4|gb|BC088305| gb|AW916891	Rn.162053	Pdia5	protein disulfide isomerase-associated 5	-	-	-	[Human, Mouse]HomoloG ene:4957

Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Gene Symbol	Gene Name	Summary	GeneRIF	Pathway	Homology
143.16	222.55	0.64	XM_213313	Mfap4_predicted	PREDICTED: Rattus norvegicus microfibrillar-associated protein 4 (predicted) (Mfap4_predicted), mRNA [XM_213313]	ref|XM_213313|gb|AA851092|ens|ENSRNOT00000003268|tc|TC535408	-	Mfap4	microfibrillar-associated protein 4	-	-	-	[Human, Mouse]HomoloGene:36098
227.09	352.24	0.64	XM_340798	P4ha2_predicted	Rattus norvegicus similar to Prolyl 4-hydroxylase alpha IIa subunit (LOC360526), mRNA [XM_340798]	gb|XM_340798|ens|ENSRNOT00000042144|tc|TC536079	Rn.79891	P4ha2_predicted	procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), alpha II polypeptide (predicted)	-	-	-	[Human, Mouse]HomoloGene:55806
111.67	172.97	0.65	NM_022284	Guca2b	Rattus norvegicus guanylate cyclase activator 2b (Guca2b), mRNA [NM_022284]	ref|NM_022284|ref|XM_579455|gb|U75186|gb|X|M_346750	Rn.97693	Guca2b	guanylate cyclase activator 2b	member of the guanylin peptide family; regulates water and electrolyte balance in the intestine [RGD]	-	-	[Human, Mouse]HomoloGene:5150
39.06	60.06	0.65	NM_012774	Gpc3	Rattus norvegicus glypican 3 (Gpc3), mRNA [NM_012774]	ref|NM_012774|gb|M22400|ens|ENSRNOT00000030995|ens|ENSRNOT00000040122	Rn.9717	Gpc3	glypican 3	heparan sulfate cell surface proteoglycan, may be involved in development of mesodermal tissues, may modulate IgF2 function [RGD]	-	-	[Human, Mouse]HomoloGene:20944
32.89	49.94	0.66	NM_031022	Gspg4	Rattus norvegicus chondroitin sulfate proteoglycan 4 (Gspg4), mRNA [NM_031022]	ref|NM_031022|gb|X56541|ens|ENSRNOT00000023326|tc|TC56927	Rn.10381	Gspg4	chondroitin sulfate proteoglycan 4	extracellular matrix protein secreted by many cell types; member of the large chondroitin sulfate proteoglycan (CSPG) family; may be involved with angiogenesis-dependent processes such as wound healing or tumor growth [RGD]	While most glia in the NG2 lineage preserve a certain amount of voltage-gated ion conductances, mature GLAST(+) astrocytes are electrophysiologically passive.// NG2 is expressed by all perivascular cells along arterioles, and its absence denotes a venule-	-	[Human, Mouse]HomoloGene:20445



Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Gene Symbol	Gene Name	Summary	GeneRIF	Pathway	Homology
31.36	47.56	0.66	NM_175762	Ldlr	Rattus norvegicus low density lipoprotein receptor (Ldlr), mRNA [NM_175762]	ref|NM_175762| gb|X13722|gb|X M_217091|ensIE NSRNOT00000013 496	Rn.10483	Ldlr	low density lipoprotein receptor	-	up-regulation and interaction of ezrin and the LDLR serves to augment the delivery of cholesterol and other lipids in support of the hypertrophic and proliferative response of cells to estrogen.// expression pattern of LDL-R in brain microvessels endothel	-	[Human, Mouse]HomoloG ene:55469
181.31	274.38	0.66	U06230	Prost	Rattus norvegicus protein S mRNA, partial cds. [U06230]	gb|U06230|gb|X M_343650|gb|AW 1415556|tc|NP06 6379	Rn.2888	Prost	protein S (alpha)	component of the Protein C/Protein S anticoagulant system: human homolog interacts with factor Xa, factor Va, and phospholipids to inhibit prothrombin activation [RGD]	-	-	-
64.19	96.72	0.66	NM_053882	Ecm1	Rattus norvegicus extracellul ar matrix protein 1 (Ecm1), mRNA [NM_053882]	ref|NM_053882| gb|U42581|gb|X M_215645|ensIE NSRNOT00000028 740	Rn.97792	Ecm1	extracellul ar matrix protein 1	mouse homolog is an extracellular protein found in a stromal osteogenic cell line [RGD]	-	-	[Human, Mouse]HomoloG ene:3260
1473.90	2216.53	0.66	NM_052808	Psp	Rattus norvegicus parotid secretory protein (Psp), mRNA [NM_052808]	ref|NM_052808| gb|M83209|ens| ENSRNOT0000001 8226|tc|TC5726 06	Rn.9766	Psp	parotid secretory protein	secretory protein stored in parotid acinar cells [RGD]	PSP co-fractionates with chromogranin A but not with secreted alkaline phosphatase: its sorting is not cell-type specific but the precise mechanism of its sorting is unknown	-	[Human, Mouse]HomoloG ene:69034
876.89	1312.03	0.67	NM_021751	Prom1	Rattus norvegicus prominin 1 (Prom1), mRNA [NM_021751]	ref|NM_021751| gb|AF386768|gb |AY262731|gb|A F263368	Rn.144589	Prom1	prominin 1	induces expression of 3-phosphate glyceraldehyde dehydrogenase (GAPDH): may play a role in glucose homeostasis [RGD]	-	-	[Human, Mouse]HomoloG ene:4390

[表14]

表62 Cに対して発現減少した唾液腺の注目遺伝子
核酸構成糖の代謝 (GO ID: 9225)

Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Gene Symbol	Gene Name	Summary	GeneRIF	Pathway	Homology
451.09	837.57	0.54	NM_080783	Gale	Rattus norvegicus galactose-4-epimerase, UDP (Gale), mRNA [NM_080783]	ref|NM_080783|gb|X53949|gb|BC097293|ens|ENSRNOT00000001 3322	Rn. 29908	Gale	galactose-4-epimerase, UDP	enzyme with galactose-4 epimerase activity [RGD]	-	KEGG pathway: Galactose metabolism// KEGG pathway: Nucleotide sugars metabolism	[Human, Mouse]Homol oGene:347
552.35	846.24	0.65	XM_216968	Tsta3_predicted	PREDICTED: Rattus norvegicus tissue specific transplantation antigen P35B (predicted) (Tsta3_predicted), mRNA [XM_216968]	ref|XM_216968|ens|ENSRNOT00000012306|gb|BF289545|gb|AW917281	Rn. 6606	Tsta3_predicted	tissue specific transplantation antigen P35B (predicted)	-	-	-	[Human, Mouse]Homol oGene:2484

[表15]

表53 Liに対して発現増加した視床下部の注目遺伝子
ホルモン活性 (GO ID: 5184, 5179)

Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Gene Symbol	Gene Name	Summary	GeneRIF	Pathway	Homology
37511.36	20083.44	1.87	NM_012625	Pmch	Rattus norvegicus pro-melanin-concentrating hormone (Pmch), mRNA [NM_012625]	ref|NM_012625|gb|M29712|gb|M62641|ensIENSRNOT00000006174	Rn.9675	Pmch	pro-melanin-concentrating hormone	cyclic neuropeptide: induces hippocampal synaptic transmission [RGD]	MCH is involved in the regulation of LHRH release in the female rat.// glucocorticoids may promote food intake in part by potentiating the orexigenic actions of MCH without affecting the actions of orexin A and glucocorticoids act indirectly to influence	KEGG pathway: Neuroactive ligand-receptor interaction	[Human, Mouse]HomoloGene:37653
793.72	441.05	1.80	XM_574228	XM_574228	PREDICTED: Rattus norvegicus agouti related protein homolog (mouse) (Agrp), mRNA [XM_574228]	ref|XM_574228|gb|AF206017|gb|XM_214672|ens|ENSRNOT00000023606	Rn.13759	Agrp	agouti related protein homolog (mouse)	may interact with melanocortin receptors: may play a role in appetite stimulation [RGD]	Because AGRP is cleaved before secretion, syndecan-3 must influence food intake independently of the MC4-R.// conclude that leptin requires phosphatidylinositol 3-OH-kinase (PI3K) signaling both to inhibit hypothalamic neuropeptide Y and agouti-related pe	-	[Human, Mouse]HomoloGene:7184

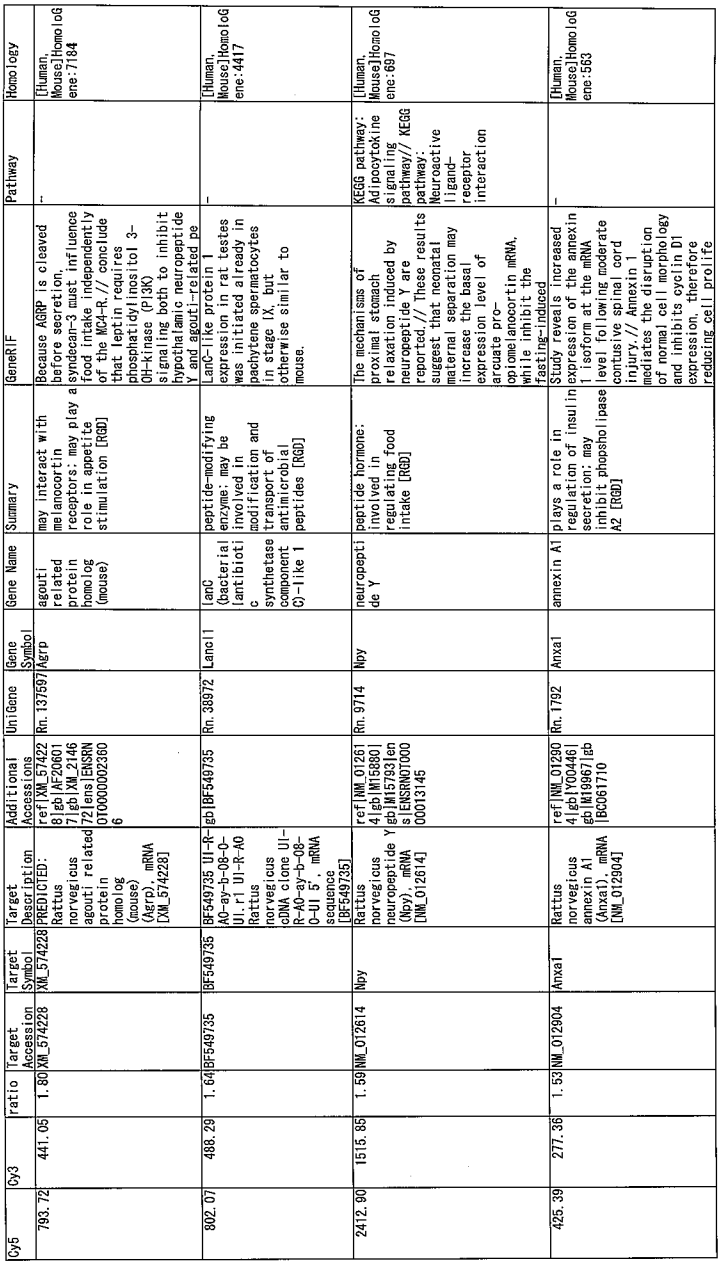
[表16]

表54 Liに対して発現増加した視床下部の注目遺伝子
モノアミントランスポーター (GO ID:

Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Gene Symbol	Gene Name	Summary	GeneRIF	Pathway	Homology
276.61	111.83	2.46	NM_012694	Slc6a3	Rattus norvegicus solute carrier family 6 (neurotransmitter transporter, dopamine), member 3 (Slc6a3), mRNA [NM_012694]	ref|NM_012694|gb|M80241|ens|ENSRNOT00000024015|tc|TC569830	Rn.10093	Slc6a3	solute carrier family 6 (neurotransmitter transporter, dopamine), member 3	acts as a sodium-dependent dopamine transporter; may play a role in regulation of dopamine metabolism and signaling [RGD]	The decrease in DAT cell surface expression in the mPFC may be responsible for decreased DAT function in the mPFC of stimulated compared with deprived rats: there is plasticity in the regulatory mechanisms mediating DAT trafficking and function.// the car	-	[Human, Mouse]HomoloGene:55547
336.96	195.16	1.73	NM_013031	Slc18a2	Rattus norvegicus solute carrier family 18 (vesicular monoamine), member 2 (Slc18a2), mRNA [NM_013031]	ref|NM_013031|gb|L00603|ens|ENSRNOT00000011983	Rn.9686	Slc18a2	solute carrier family 18 (vesicular monoamine), member 2	transports N-methyl-4-phenylpyridinium (MPP+), a neurotoxin metabolite associated with Parkinson's disease [RGD]	VMAT2 defines a population of secretory vesicles that mediate the activity-dependent somatodendritic release of multiple retrograde signals involved in synaptic function, growth, and plasticity.// Down-regulation of VMAT2 in the nucleus accumbens and stri	-	[Human, Mouse]HomoloGene:2298
1180.13	750.06	1.57	NM_019374	Pdyn	Rattus norvegicus prodynorphin (Pdyn), mRNA [NM_019374]	ref|NM_019374|gb|M32784|ens|ENSRNOT00000037576	Rn.44471	Pdyn	prodynorphin	expression in hippocampus increases in response to traumatic brain injury; may play a role in regulatio of neurotransmitter release [RGD]	dynorphin can signal information to the cell interior through neuropeptide translocation across the plasma membrane// The increased enkephalin mRNA and prodynorphin mRNA gene expressions in rat hippocampus were involved in chronic stress.// Fluoxetine was	-	[Human, Mouse]HomoloGene:10321

[表17]

表55 Liに対して発現増加した視床下部の注目遺伝子
受容体結合 (GO ID: 5102)

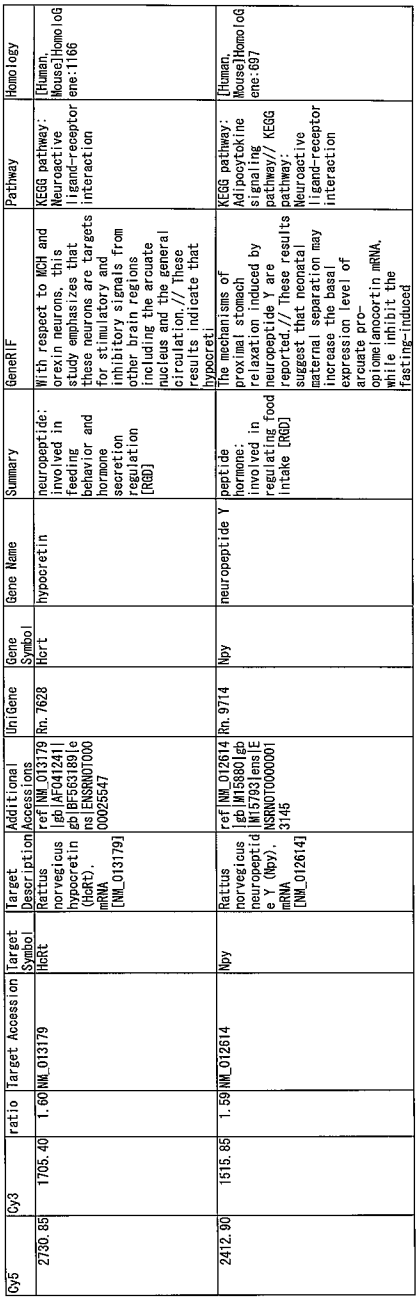


Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Gene Symbol	Gene Name	Summary	GeneRIF	Pathway	Homology
793.72	441.05	1.80	XM_574228	XM_574228	PREDICTED: Rattus norvegicus agouti related protein homolog (mouse) (Agrp), mRNA [XM_574228]	ref|XM_574228.1|gb|AF20601.1|AF20601|XM_2146721|ENSRNOT00000002360.6	Rn.137597	Agrp	agouti related protein homolog (mouse)	may interact with melanocortin receptors; may play a role in appetite stimulation [RGD]	Because AGRP is cleaved before secretion, syndecan-3 must influence food intake independently of the MC4-R.// conclude that leptin requires phosphatidylinositol 3-OH-kinase (PI3K) signaling both to inhibit hypothalamic neuropeptide Y and agouti-related pe	-	[Human, Mouse]HomoloGene:7184
802.07	488.29	1.64	BF549735	BF549735	BF549735 UI-R-A0-ay-b-08-0-UI.r1 UI-R-A0 Rattus norvegicus cDNA clone UI-R-A0-ay-b-08-0-UI 5', mRNA sequence [BF549735]	gb|BF549735.1	Rn.38972	Lancl1	lanC (bacterial lantibiotic synthetase component C)-like 1	peptide-modifying enzyme; may be involved in modification and transport of antimicrobial peptides [RGD]	lanC-like protein 1 expression in rat testes was initiated already in pachytene spermatocytes in stage IX, but otherwise similar to mouse.	-	[Human, Mouse]HomoloGene:4417
2412.90	1515.85	1.59	NM_012614	Npy	Rattus norvegicus neuropeptide Y (Npy), mRNA [NM_012614]	ref|NM_012614.4|gb|M15880.1|RATNPYGB|gb|M15793.1|ens|ENSRNOT00000013145	Rn.9714	Npy	neuropeptide Y	peptide hormone: involved in regulating food intake [RGD]	The mechanisms of proximal stomach relaxation induced by neuropeptide Y are reported.// These results suggest that neonatal maternal separation may increase the basal expression level of arcuate pro-opiomelanocortin mRNA, while inhibit the fasting-induced	KEGG pathway: Adipocytokine signaling pathway// KEGG pathway: Neuroactive ligand-receptor interaction	[Human, Mouse]HomoloGene:697
425.39	277.36	1.53	NM_012904	Anxa1	Rattus norvegicus annexin A1 (Anxa1), mRNA [NM_012904]	ref|NM_012904.1|gb|Y00446.1|RATLIPOCOR|gb|M19967.1|RATANXA1|gb|BC061710.1	Rn.1792	Anxa1	annexin A1	plays a role in regulation of insulin secretion; may inhibit phospholipase A2 [RGD]	Study reveals increased expression of the annexin 1 isoform at the mRNA level following moderate contusive spinal cord injury.// Annexin 1 mediates the disruption of normal cell morphology and inhibits cyclin D1 expression, therefore reducing cell prolife	-	[Human, Mouse]HomoloGene:563

[表18]

表56 Lに対して発現増加した視床下部の注目遺伝子
食行動 (GO ID: 7631)

Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Gene Symbol	Gene Name	Summary	GeneRIF	Pathway	Homology
153.08	71.65	2.14	NM_022633	Galp	Rattus norvegicus galanin-like peptide precursor (Galp), mRNA [NM_022633]	ref|NM_022633 |gb|AF188491| ens|ENSRNOT00 000034854|tc| NP999873	Rn.48754	Galp	galanin-like peptide precursor	-	observations demonstrate that endogenous Galanin-like peptide (GALP)provides trophic support to the neuroendocrine reproductive axis, including sexual behavior// adaptive responses in GALP signaling might occur during chronic overfeeding// GALP gene expre	-	[Human, Mouse]HomoloG ene:11217
4327.77	2030.83	2.13	NM_139326	Pomc2	Rattus norvegicus proopiomelanocortin, beta (endorphin, beta) (Pomc2), mRNA [NM_139326]	ref|NM_139326 |gb|BC058443| gb|AF510391|g b|J00759	Rn.108195	Pomc	pro-opiomelanocortin	-	POMC expression decreased progressively during eye movement sleep deprivation of rats. // Enhanced insulin sensitivity via exercise training might be mediated by endogenous beta-endorphin that leads to improved glucose disposal in obese Zucker rats.// die	KEGG pathway: Adipocytokine signaling pathway// KEGG pathway: Neuroactive ligand-receptor interaction	[Human, Mouse]HomoloG ene:723
37511.36	20083.44	1.87	NM_012625	Pmch	Rattus norvegicus pro-melanin-concentrating hormone (Pmch), mRNA [NM_012625]	ref|NM_012625 |gb|M29712|gb |M62641|ens|E NSRNOT0000000 6174	Rn.9675	Pmch	pro-melanin-concentrating hormone	cyclic neuropeptide; induces hippocampal synaptic transmission [RGD]	MCH is involved in the regulation of LHRH release in the female rat.// glucocorticoids may promote food intake in part by potentiating the orexigenic actions of MCH without affecting the actions of orexin A and glucocorticoids act indirectly to influence	KEGG pathway: Neuroactive ligand-receptor interaction	[Human, Mouse]HomoloG ene:37653
793.72	441.05	1.80	XM_574228	XM_574228	PREDICTED: Rattus norvegicus agouti related protein homolog (mouse) (Agrp), mRNA [XM_574228]	ref|XM_574228 |gb|AF206017| gb|XM_214672| ens|ENSRNOT00 000023606	Rn.137597	Agrp	agouti related protein homolog (mouse)	may interact with melanocortin receptors; may play a role in appetite stimulation [RGD]	Because AGRP is cleaved before secretion, syndecan-3 must influence food intake independently of the MC4-R.// conclude that leptin requires phosphatidylinositol 3-OH-kinase (PI3K) signaling both to inhibit hypothalamic neuropeptide Y and agouti-related pe	-	[Human, Mouse]HomoloG ene:7184



Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Gene Symbol	Gene Name	Summary	GeneRIF	Pathway	Homology
2730.85	1705.40	1.60	NM_013179	Hcrt	Rattus norvegicus hypocretin (Hcrt), mRNA [NM_013179]	ref|NM_013179|gb|AF041241|gb|BF563189|ens|ENSRNOT00000025547	Rn.7628	Hcrt	hypocretin	neuropeptide: involved in feeding behavior and hormone secretion regulation [RGD]	With respect to MCH and orexin neurons, this study emphasizes that these neurons are targets for stimulatory and inhibitory signals from other brain regions including the arcuate nucleus and the general circulation.// These results indicate that hypocreti	KEGG pathway: Neuroactive ligand-receptor interaction	[Human, Mouse]HomoloGene:1166
2412.90	1515.85	1.59	NM_012614	Npy	Rattus norvegicus neuropeptide Y (Npy), mRNA [NM_012614]	ref|NM_012614|gb|M15880|gb|M15793|ens|ENSRNOT00000013145	Rn.9714	Npy	neuropeptide Y	peptide hormone: involved in regulating food intake [RGD]	The mechanisms of proximal stomach relaxation induced by neuropeptide Y are reported.// These results suggest that neonatal maternal separation may increase the basal expression level of arcuate pro-opiomelanocortin mRNA, while inhibit the fasting-induced	KEGG pathway: Adipocytokine signaling pathway// KEGG pathway: Neuroactive ligand-receptor interaction	[Human, Mouse]HomoloGene:697

[表19]

表57 LIに対して発現増加した視床下部の注目遺伝子
生体アミン合成 (GO ID: 42401, 42423, 42416, 9309)

Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Gene Symbol	Gene Name	Summary	GeneRIF	Pathway	Homology
275.61	111.83	2.46	NM_012694	Slc6a3	Rattus norvegicus solute carrier family 6 (neurotransmitter transporter, dopamine), member 3 (Slc6a3), mRNA [NM_012694]	ref|NM_01269 4|gb|M80670| ens|ENSRNOT O0000024015|t cITC669830	Rn. 10093	Slc6a3	solute carrier family 6 (neurotransmitter transporter, dopamine), member 3	acts as a sodium-dependent dopamine transporter; may play a role in regulation of dopamine metabolism and signaling [RGD]	The decrease in DAT cell surface expression in the mPFC may be responsible for decreased DAT function in the mPFC of stimulated compared with deprived rats; there is plasticity in the regulatory mechanisms mediating DAT trafficking and function.// the car	-	[Human, Mouse]Homolo Gene:55547
1270.69	704.13	1.80	NM_017016	Hdc	Rattus norvegicus histidine decarboxylase (Hdc), mRNA [NM_017016]	ref|NM_01701 6|gb|M38759| gb|XM_346674 |gb|M29591	Rn. 48653	Hdc	histidine decarboxyla se	involved in the formation of histamine from its precursor histidine [RGD]	histidine decarboxylase mRNA and protein are found in rat aorta and more specifically in cultured rat aortic smooth muscle, indicative of their capability to synthesize histamine// Identification of catalytically important residues in L-histidine decarbox	KEGG pathway: Histidine metabolism	[Human, Mouse]Homolo Gene:20490
888.26	560.95	1.58	NM_012740	Th	Rattus norvegicus tyrosine hydroxylase (Th), mRNA [NM_012740]	ref|NM_01274 0|gb|L22651| gb|M10244|en s|ENSRNOT000 00027682	Rn. 11082	Th	tyrosine hydroxylase	catalyzes the rate limiting step in catecholamine biosynthesis; may be involved in response to hypoxia [RGD]	The kinetics of reduction of ferric TyrH by several reductants were determined by anaerobic stopped-flow spectroscopy. phosphorylation does not directly regulate the interconversion of the ferric and ferrous forms// The results indicate that the NGF/NGF	KEGG pathway: Parkinson's disease// KEGG pathway: Tyrosine metabolism	[Human, Mouse]Homolo Gene:307

[表20]

表58 Lに対して発現増加した視床下部の注目遺伝子
生体アミン代謝 (GO ID: 9308, 6584, 6576)

Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Gene Symbol	Gene Name	Summary	GeneRIF	Pathway	Homology
275.61	111.83	2.46	NM_012694	Slc6a3	Rattus norvegicus solute carrier family 6 (neurotransmitter transporter, dopamine), member 3 (Slc6a3), mRNA [NM_012694]	ref|NM_0126 94|gb|M8057 0|ens|ENSRN OT0000002400 15|tc|TC569 830	Rn.10093	Slc6a3	solute carrier family 6 (neurotransmitter transporter, dopamine), member 3	acts as a sodium-dependent dopamine transporter; may play a role in regulation of dopamine metabolism and signaling [RGD]	The decrease in DAT cell surface expression in the mPFC may be responsible for decreased DAT function in the mPFC of stimulated compared with deprived rats: there is plasticity in the regulatory mechanisms mediating DAT trafficking and function.// the car	-	[Human, Mouse]Homo logene:555 47

[表21]

表59 Liに対して発現減少した根床下部の注目遺伝子
陽イオン結合 (GO ID: 5509, 43169)

Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Gene Symbol	Gene Name	Summary	GeneRIF	Pathway	Homology
192.09	296.29	0.65	NM_172224	Impa2	Rattus norvegicus inositol (myo)-1(or 4)-monophosphatase 2 (Impa2), mRNA [NM_172224]	ref|NM_172224|gb|AY160191|gb|BC008354|ens|ENSRNOT00000025147	Rn.856	Impa2	inositol (myo)-1(or 4)-monophosphatase 2	mouse homolog is an enzyme that catalyzes the synthesis of free myo-inositol from various myo-inositol monophosphates [RGD]	-	KEGG pathway: Inositol phosphate metabolism// KEGG pathway: Phosphatidylinositol signaling system// KEGG pathway: Streptomycin biosynthesis	[Human, Mouse]Homolog ene:22799
390.79	588.19	0.66	NM_133415	Efcbp2	Rattus norvegicus neuronal calcium binding 2 (Efcbp2), mRNA [NM_133415]	ref|NM_133415|gb|AF193751|ens|ENSRNOT00000020341	Rn.62703	Efcbp2	EF hand calcium binding protein 2	may mediate calcium signaling and play a role in neuronal function [RGD]	-	-	[Human, Mouse]Homolog ene:62200

Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Gene Symbol	Gene Name	Summary	GeneRIF	Pathway	Homology
115.10	188.76	0.61	NM_031828	Kcnma1	Rattus norvegicus potassium large conductance calcium-activated channel, subfamily M, alpha member 1 (Kcnma1), mRNA [NM_031828]	ref|NM_031828|ref|XM_579539|gb|AF083342|gb|AJ617197	Rn. 30616	Kcnma1	potassium large conductance calcium-activated channel, subfamily M, alpha member 1	large-conductance Ca(2+)-activated K(+) channel; may be involved in the shortened duration of action potential in hippocampal CA1 pyramidal neurons and in channel activity in carotid body chemoreceptor cells [RGD]	Data suggest that the regulation of STREX splicing directed by estrogen and Pg provides a mechanism for Slo's PKA-related phenotypic alteration with pregnancy.// there is a novel interaction between the C-terminal tail of the BKCa channel and the light chain of MAP1A, which enables channel association with and modulation by the cytoskeleton// Slo gene-encoded BK potassium channels alternative splicing variants are found with and without the 'STREX' exon. In the adrenal medulla, castration increased STREX transcripts slightly and decreased STREX representation in the pituitary.// cAMP-dependent vasodilators activate BK(Ca) channels in PASMC of rats via PKG-dependent and PKA-independent signaling pathways. which suggests cross-activation between cyclic nucleotide-dependent protein kinases in pulmonary arterial smooth muscle// Steady-state and closed-state inactivation properties// Nitric oxide enhances Ca(2+)-dependent K(+) channel activity in rat carotid body cells.// (The rest is omitted.)	-	[Human, Mouse]Homolo gene:1693

Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Gene Symbol	Gene Name	Summary	GeneRIF	Pathway	Homology
44.48	71.33	0.62	NM_019292	Ca3	Rattus norvegicus carbonic anhydrase 3 (Ca3), mRNA [NM_019292]	ref|NM_019292|gb|AB003082|gb|AB003083|gb|BC006198|0	Rn.1647	Ca3	carbonic anhydrase 3	catalyzes hydration of carbon dioxide; may be involved in cellular response to oxidative stress [RGD]	conformational changes provide a mechanistic basis for modulation of the susceptibility of carbonic anhydrase 3 to glutathionylation.// Dorzolamide, a CA3 inhibitor, caused a decrease in dexamethasone and insulin-induced leptin secretion in epididymal adipocytes tissue.// leptin decreased CA III expression while insulin increased it which suggests that the decrease in CA III expression observed in obesity in rat adipose tissue may be related to hyperleptinemia// Major soluble protein in rat liver and muscle. Function probably to protect proteins of these tissues from oxidation catalyzed by iron-containing degradation products of haemoglobin and myoglobin.// Androgen-linked control of carbonic anhydrase III expression occurs in rat perivenous hepatocytes	KEGG pathway: Nitrogen metabolism	[Human, Mouse]HomoloGene:31298
27.69	42.90	0.65	AA800765	AA800765	AA800765 EST190262 Normalized rat lung, Bento Soares Rattus sp. cDNA clone RLUAL20_3' end, mRNA sequence [AA800765]	gb|AA800765|gb|AA892549	Rn.3576	Manla_predicted	mannosidase 1, alpha (predicted)	-	-	-	[Human, Mouse]HomoloGene:4316

Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Gene Symbol	Gene Name	Summary	GeneRIF	Pathway	Homology
246.07	372.76	0.66	U90444	U90444	Rattus norvegicus double stranded RNA specific deaminase RED1 mRNA, partial cds. [U90444]	gb|U90444|Rc|TC560724	Rn.89675	Adarb1	adenosine deaminase, RNA-specific, B1	catalyzes the deamination of adenosine in double stranded mRNA: required for pre-mRNA editing of brain glutamate receptor RNAs [RGD]	RNA structure-dependent recognition by the two double-stranded RNA binding motifs of rat ADAR2.// the nucleolar localization of ADAR2 represents an important mechanism by which RNA editing can be modulated by the sequestration of enzymatic activity from potential RNA substrates in the nucleoplasm// interaction with RNA transcripts containing selective and nonselective editing sites// both sequence and structural elements are required to define adenosine moieties targeted for specific ADAR2-mediated deamination	-	[Human, Mouse]Homolo gene:8280
133.95	204.57	0.65	NM_019211	Rasgrp1	Rattus norvegicus RAS guanyl releasing protein 1 (Rasgrp1). mRNA [NM_019211]	ref|NM_019211|Rc|BI281195|gb|AF068081|ens|ENSRNOT00000007687	Rn.16268	Rasgrp1	RAS guanyl releasing protein 1	putative guanine nucleotide exchange factor with Ca2+ and diacylglycerol binding domains: may activate Rap protein mediated inhibition of Ras signaling pathways [RGD]	contribution of these two lipid pools to PLC-dependent Ras activation in response to TCR. triggering// RasGRP1 is a diacylglycerol/phorbol ester receptor in epidermal keratinocytes	KEGG pathway: MAPK signaling pathway// KEGG pathway: T cell receptor signaling pathway	[Human, Mouse]Homolo gene:4195
54.73	82.84	0.66	NM_021698	F13a	Rattus norvegicus coagulation factor XIII, A1 subunit (F13a), mRNA [NM_021698]	ref|NM_021698|gb|Y12502|gb|AW690181|ens|ENSRNOT00000021568	Rn.42925	F13a1	coagulation factor XIII, A1 subunit	enhances gastric mucosa healing; reduces endothelial permeability [RGD]	-	KEGG pathway: Complement and coagulation cascades	[Human, Mouse]Homolo gene:20077

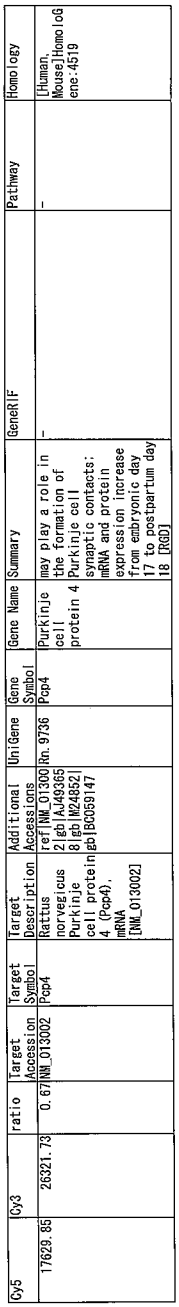
Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Gene Symbol	Gene Name	Summary	GeneRIF	Pathway	Homology
2578.08	5839.26	0.44	NM_133307	Prkcd	Rattus norvegicus protein kinase C, delta (Prkcd), mRNA [NM_133307]	ref|NM_133307|gb|AF219629|gb|BC076505|gb|AJ230633	Rn.98279	Prkcd	protein kinase C, delta	mediates mitochondrial-dependent apoptosis [RGD]	Tetradecanoylphorbol acetate, endothelin-1, and pdgf regulate the gene expression of Pkcd.// Data suggest that proteolytic activation of the proapoptotic protein kinase Cdelta (PKCdelta) by caspase 3 is a key step in 6-hydroxydopamine-induced cell death.// These results suggest that in RBA-1 cells, bradykinin-induced cytosolic phospholipase A2 expression is sequentially mediated through activation of PKC-delta, p42/p44 MAPK, and NF-kappaB.// The present data show that lovastatin may induce neuroblast apoptosis by both caspase-dependent and independent pathways.// Results demonstrate that wild-type alpha-synuclein interacts with the pro-apoptotic molecules BAD and protein kinase C delta to protect dopaminergic neuronal cells against neurotoxic insults.// vascular smooth muscle cell apoptosis proceeds through a pathway that involves PKCdelta, the intermediary p38 MAPK, and the downstream target tumor suppressor p53// (The rest is omitted.)	KEGG pathway: Tight junction// KEGG pathway: Type II diabetes mellitus	[Human, Mouse]Homolo Gene:55963
284.05	474.89	0.60	NM_022302	Efcbp1	Rattus norvegicus EF hand calcium binding protein 1 (Efcbp1), mRNA	ref|NM_022302|gb|AF193755|ens|ENSRNOT00000009718|tc|NP399992	Rn.64485	Efcbp1	EF hand calcium binding protein 1	may play a role in neuronal Ca(2+)-signalling [RGD]	Determines domain structure of the Necab 1 protein that expressed in the brain.	--	[Human, Mouse]Homolo Gene:11172

Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Gene Symbol	Gene Name	Summary	GeneRIF	Pathway	Homology
1112.96	1765.21	0.63	NM_019372	Ppm2c	Rattus norvegicus protein phosphatase 2C, magnesium-dependent, catalytic subunit (Ppm2c), mRNA	ref|NM_019372.2|gb|AF062743.1|gb|AW920770.1|ens|ENSRNOT00000021642	Rn.31799	Ppm2c	protein phosphatase 2C, magnesium dependent, catalytic subunit	catalytic subunit of the mitochondrial matrix phosphatase; involved in reactivation of the pyruvate dehydrogenase complex [RGD]	role of PP2C and AMPK in the derangements of cardiac lipid metabolism in obesity// Asp445 might be involved in the control of interactions between PDP1c and the protein substrate pyruvate dehydrogenase	-	[Human, Mouse]HomoloGene:31928
292.12	457.72	0.64	XM_221901	Nptx2_predicted	PREDICTED: Rattus norvegicus neuronal pentraxin II (predicted) (Nptx2_predicted), mRNA [XM_221901]	ref|XM_221901.1|gb|BI282491.1|ens|ENSRNOT00000049444|ens|ENSRNOT00000001331	-	Nptx2	neuronal pentraxin II	-	-	-	[Human, Mouse]HomoloGene:1892
33.11	53.97	0.61	NM_031590	Wisp2	Rattus norvegicus WNT1 inducible signaling pathway protein 2 (Wisp2), mRNA [NM_031590]	ref|NM_031590.1|gb|AF259980.1|gb|BG089180.1|ens|ENSRNOT00000014346	Rn.53991	Wisp2	WNT1 inducible signaling pathway protein 2	involved in negative regulation of cell growth; mRNA expression is lost upon cell transformation induced by activated H-ras oncogene and inactivated p53 tumor supressor [RGD]	data indicate that CCN5 protein is positively regulated by estrogen in the rat uterus and suggests that this gene may play an important role in maintaining normal uterine physiology	-	[Human, Mouse]HomoloGene:2882

Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Gene Symbol	Gene Name	Summary	GeneRIF	Pathway	Homology
224.81	377.95	0.59	NM_053981	Kcnj12	Rattus norvegicus potassium inwardly-rectifying channel, subfamily J, member 12 (Kcnj12), mRNA [NM_053981]	ref|NM_053981|gb|X78461|ens|ENSRNOT00000003138|tc|TC5700004	Rn.10406	Kcnj12	potassium inwardly-rectifying channel, subfamily J, member 12	inward rectifier potassium channel [RGD]	preferential Golgi export of Kir2.1 controls the stoichiometry of Kir2.x heteromers expressed on the cell surface.// There was a strong correlation between the transcript levels of Kir2.1 and Ki-induced relaxation.// In PCR analyses using isolated juxtaglomerular cells, the mRNA for Kir2.1 (Kcnj2) and Kir2.2 (Kcnj12) was detected. Kir2.1 is the dominant component of the channel.// Myo15 and Kcnj12 can be regarded as candidate genes for the deafblind phenotype of the LEW-ci2 rat.// a complex composed of SAP97, CASK, Veli, and Mint1 associates with Kir2 channels via the C-terminal PDZ-binding motif: SAP97, Veli-1, or Veli-3 binds directly to the Kir2.2 C terminus and recruits CASK// candidate gene for the deafblind phenotype of the LEW-ci2 rat	-	[Human, Mouse]Homolog ene:7793
203.20	319.64	0.64	NM_053324	Syt9	Rattus norvegicus synaptotagmin 9 (Syt9), mRNA [NM_053324]	ref|NM_053324|AF375464|gb|U20108|ens|ENSRNOT00000026607	Rn.10194	Syt9	synaptotagmin IX	member of a family of membrane proteins characterized by one transmembrane region and two C2 domains [RGD]	Data suggest that synaptotagmin 9 may act as Ca(2+) sensor for beta-cell secretion.	-	[Human, Mouse]Homolog ene:11062
207.97	356.58	0.58	NM_139217	Kcnc2	Rattus norvegicus potassium voltage gated channel, Shaw-related subfamily, member 2, (Kcnc2), transcript variant b, mRNA	ref|NM_139217|gb|M59323|gb|M84203|ens|ENSRNOT00000005773	Rn.9733	Kcnc2	potassium voltage gated channel, Shaw-related subfamily, member 2	a voltage-gated K+ channel; functions as a delayed rectifier-type K+ channel activated by large membrane depolarizations [RGD]	Kv3-like currents may be important for maintaining spike width and calcium influx within acceptable limits during repetitive firing.// strong, selective localization of Kv3.2 to basket cell axons of cerebellum.	-	[Human, Mouse]Homolog ene:71199

Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Gene Symbol	Gene Name	Summary	GeneRIF	Pathway	Homology
481.00	905.44	0.53	XM_230761	Abba2bp_predicted	PREDICTED: Rattus norvegicus amyloid beta (A4) precursor protein-binding, family A, member 1 binding protein (predicted) (Abba2bp_predicted). mRNA	ref|XM_230761.1|ens|ENSRNOT00000022115 |ens|ENSRNOT00000047894|ens|ENSRNOT00000043456	Rn.14505	Abba2bp_predicted	amyloid beta (A4) precursor protein-binding, family A, member 1 binding protein (predicted)	-	-	-	[Human, Mouse]Homologene:10992
24.31	39.73	0.61	XM_342172	Thbs4	PREDICTED: Rattus norvegicus thrombospondin 4 (Thbs4). mRNA [XM_342172]	ref|XM_342172.2|gb|X89963|gb|AW916235|ens|ENSRNOT00000017078	Rn.11207	Thbs4	thrombospondin 4	extracellular matrix protein. involved in neuronal development [RGD]	-	KEGG pathway: Cell Communication// KEGG pathway: ECM-receptor interaction// KEGG pathway: Focal adhesion// KEGG pathway: TGF-beta signaling pathway	[Human, Mouse]Homologene:20691

Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Gene Symbol	Gene Name	Summary	GeneRIF	Pathway	Homology
338.67	553.40	0.61	NM_021771	Trpc3	Rattus norvegicus transient receptor potential cation channel, subfamily C, member 3 (Trpc3), mRNA [NM_021771]	ref|NM_021771|gb|AB022233|ens|ENSRNO T00000021948|tc|TC569878	Rn. 45385	Trpc3	transient receptor potential cation channel, subfamily C, member 3	a calcium-activated cation channel [RGD]	Study shows, for the first time, increased TRPC3 channel expression and increased TRPC3-related calcium influx in spontaneously hypertensive rats.// prostate smooth muscle PS1 cells express TRPC3 and TRPC6 proteins which function as receptor- and store-operated Ca(2+) entry pathways.// TRPC3 mediates UTP-induced depolarization of arterial smooth muscle cells// TRPC3/TRPC6 channels are localized to the apical region of polarized epithelial cells, which in salivary gland ducts could contribute to the regulation of salivary [Ca2+] and secretion// TRPC3a gave rise to Ca2+-entry channels that are not only activated by the Gq-phospholipase C beta pathway// siRNA specific for TRPC1 and TRPC3 in proliferating cells inhibited approximately the same amount of Store operated calcium entry.// Data suggest that VAMP2-dependent exocytosis regulates plasma membrane insertion of TRPC3 channels and contributes to carbachol-stimulation of Ca2+ influx.// (The rest is omitted.)	-	[Human, Mouse]HomoloGene:20708
123.77	323.37	0.38	NM_053521	Slc5a7	Rattus norvegicus solute carrier family 5 (choline transporter), member 7 (Slc5a7), mRNA [NM_053521]	ref|NM_053521|gb|AB030947|ens|ENSRNOT00000014548	Rn. 44872	Slc5a7	solute carrier family 5 (choline transporter), member 7	high-affinity choline transporter: give choline to nuerons for the synthesis of acetylcholine [RGD]	This protein is expressed in the rat trachea.// close apposition of CHT1 to reported sites of localization of choline acetyltransferase in these cells is strongly in favour of ACh synthesis being fuelled by choline uptake via CHT1 in these epithelia// high-affinity choline transporter, choline transporter 1, in nerve fibers and epithelial cells in the human and rat skin supporting the pivotal role of this transporter in both the neuronal and non-neuronal cholinergic system of the skin.	-	[Human, Mouse]HomoloGene:32516



Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Gene Symbol	Gene Name	Summary	GeneRIF	Pathway	Homology
17629.85	26321.73	0.67	NM_013002	Pcp4	Rattus norvegicus Purkinje cell protein 4 (Pcp4), mRNA [NM_013002]	ref|NM_013002|Rn.9736 2|gb|AJ49365 8|gb|M24852| gb|BC059147		Pcp4	Purkinje cell protein 4	may play a role in the formation of Purkinje cell synaptic contacts; mRNA and protein expression increase from embryonic day 17 to postpartum day 18 [RGD]	-	-	[Human, Mouse]Homolo Gene:4519

[請求項5] 第1のステップにおいて、評価対象である刺激を断続的に2分以上、又は一日当たり断続的に5分以上の刺激を1日以上で負荷することを特徴とする請求項1～4のいずれか1項記載の方法。

[請求項6] 前記第2のステップでは、測定対象の遺伝子の塩基配列の少なくとも一部を含む核酸を固定化した支持体を用いて、当該遺伝子の発現量を測定することを特徴とする請求項1～5のいずれか1項記載の方法。

[請求項7] 下記の表1に示す遺伝子の塩基配列の少なくとも一部を含む核酸か

らなる群から選ばれる少なくとも1種の核酸、又は下記の表1に示す遺伝子によってコードされるタンパク質に対して特異的に結合する分子からなる群から選択される少なくとも1種の分子を含む、ラットの陽性感情を評価するための検査キット。

[表22]

表１

No	Target(Gene)Symbol	Target Accession	UniGene	Up/Down	生体由来試料
1	Gsta5	NM_031509	Rn.10460	Up	Bc
2	-	AA858768	-	Up	Bc
3	Aldh1a1	NM_022407	Rn.6132	Up	Bc
4	Yc2	NM_001009920	Rn.120929	Up	Bc
5	-	TC536876	-	Up	Bc
6	Ttc6_predicted	XM_216713	Rn.82576	Up	Bc
7	Gsta2	NM_017013	Rn.144550	Up	Bc
8	-	BQ200056	-	Up	Bc
9	Gsta2	BQ199390	Rn.144550	Up	Bc
10	LOC307767	XM_226381	Rn.41880	Up	Bc
11	Cdigll	NM_153623	Rn.160166	Up	Bc
12	Selenbp1	NM_080892	Rn.16617	Up	Bc
13	-	TC561220	-	Down	Bc
14	Cdkn1c	XM_341966	-	Down	Bc
15	Cdkn1c	NM_182735	Rn.162507	Down	Bc
16	-	NM_001013853	Rn.163132	Down	Bc
17	Cdkn1c	NM_182735	Rn.162507	Down	Bc
18	MGC72973	NM_198776	Rn.36966	Down	Bc
19	-	AI045044	Rn.166087	Down	Bc
20	Me2_predicted	XM_225729	Rn.38235	Down	Bc
21	Gda	NM_031776	Rn.161897	Down	Bc
22	LOC300760	XM_236308	-	Down	Bc
23	Susd2_predicted	XM_215372	Rn.161744	Down	Bc
24	Susd2_predicted	XM_215372	Rn.161744	Down	Bc
25	Hpd	NM_017233	Rn.3664	Down	Bc
26	Slfn3	NM_053687	-	Up	Bl
27	-	AA963075	Rn.73451	Up	Bl
28	S100a9	NM_053587	Rn.6703	Up	Bl
29	Bnc1_predicted	XM_344917	-	Down	Bl
30	Slc6a3	NM_012694	Rn.10093	Up	Hy
31	Cga	J00757	Rn.10589	Up	Hy
32	Cga	NM_053918	Rn.10589	Up	Hy
33	-	AI044887	Rn.5827	Down	Hy
34	-	BF398607	Rn.45255	Down	Hy
35	Avp	NM_016992	Rn.9976	Up	St
36	Neurod2	NM_019326	Rn.10724	Up	St
37	-	AW914894	Rn.10267	Up	St
38	Vip	XM_217838	Rn.18675	Up	St
39	-	XM_576570	Rn.22624	Up	St
40	-	TC524999	-	Up	St
41	Slc17a7	NM_053859	Rn.10267	Up	St
42	-	BF281936	-	Up	St
43	-	CO403684	-	Up	St
44	-	CB582871	Rn.13498	Up	St
45	Cck	BM382824	Rn.9781	Up	St
46	Sstr1	NM_012719	#N/A	Up	St
47	Cort	NM_012835	Rn.42915	Up	St
48	Nrn1	NM_053346	Rn.10490	Up	St
49	C1ql3_predicted	XM_225579	Rn.3546	Up	St
50	Prss12	NM_053504	-	Up	St
51	-	TC558785	Rn.86653	Up	St
52	-	TC562720	-	Up	St
53	-	TC519964	-	Up	St

No	Target(Gene)Symbol	Target Accession	UniGene	Up/Down	生体由来試料
54	Nov	NM_030868	-	Up	St
55	-	XM_575489	Rn.162955	Up	St
56	Cck	NM_012829	Rn.162754	Up	St
57	Nptx1	NM_153735	Rn.9781	Up	St
58	RGD1308977_predicted	XM_214510	Rn.139226	Up	St
59	-	CB544275	Rn.54707	Up	St
60	-	BF398607	Rn.45255	Down	St
61	Ttr	NM_012681	Rn.1404	Down	St

[表中、

Bcは口腔内細胞であり；Blは血液であり；Hyは視床下部であり；Stは線条体である。]

[請求項8] 下記の表2に示す遺伝子の塩基配列の少なくとも一部を含む核酸からなる群から選ばれる少なくとも1種の核酸、又は下記の表2に示す遺伝子によってコードされるタンパク質に対して特異的に結合する分子からなる群から選択される少なくとも1種の分子を含む、ラットの陽性感情を評価するための検査キット。

[表23]

表２

No	Target(Gene)Symbol	Target Accession	UniGene	Up/Down	生体由来試料
62	-	NM_001013853	Rn.163132	Up	BI
63	RGD1308591_predicted	XM_230631	Rn.22314	Up	BI
64	-	TC545861	-	Up	BI
65	-	TC559380	-	Up	BI
66	-	TC551459	-	Up	BI
67	-	TC560203	-	Up	BI
68	RGD1309846_predicted	XM_231625	-	Up	BI
69	-	TC532273	-	Up	BI
70	-	TC568188	-	Up	BI
71	-	XM_343940	-	Up	BI
72	-	TC549515	-	Up	BI
73	-	TC555328	-	Up	BI
74	MGC72973	NM_198776	Rn.36966	Up	BI
75	-	TC549495	-	Up	BI
76	-	CB544341	Rn.6526	Up	BI
77	Gabrd	NM_017289	Rn.10927	Up	BI
78	-	TC542956	-	Up	BI
79	Olr1572_predicted	XM_221921	-	Up	BI
80	-	TC525431	-	Up	BI
81	Strn4_predicted	XM_218432	Rn.137083	Up	BI
82	-	A_44_P337592	-	Up	BI
83	-	AW143701	Rn.17098	Up	BI
84	Rnf40	NM_153471	Rn.162466	Up	BI
85	-	TC544981	-	Up	BI
86	Bst2	NM_198134	Rn.32168	Up	BI
87	LOC361100	XM_341386	Rn.104585	Up	BI
88	-	BQ211845	Rn.165621	Up	BI
89	-	AA900394	Rn.165621	Up	BI
90	Olr1234_predicted	NM_001000446	Rn.143535	Up	BI
91	-	AW918996	Rn.7470	Up	BI
92	RGD1307160_predicted	XM_219953	Rn.61235	Up	BI
93	-	BI395434	-	Up	BI
94	-	XM_215067	-	Up	BI
95	-	TC561947	-	Up	BI
96	-	A_44_P426640	-	Up	BI
97	-	A_44_P368450	-	Up	BI
98	Cox6a2	NM_012812	Rn.5119	Up	BI
99	-	AA925776	Rn.11283	Up	BI
100	-	TC528645	Rn.14945	Up	BI
101	Ltap_predicted	XM_222896	Rn.19850	Up	BI
102	-	XM_346943	Rn.22985	Up	BI
103	-	AA900371	Rn.161752	Down	BI
104	-	AA900000	Rn.103172	Down	BI
105	-	AA899215	-	Down	BI
106	-	TC555778	-	Down	BI
107	Jund	NM_138875	Rn.46225	Down	BI
108	-	AI556201	Rn.48701	Down	BI
109	-	BI302367	Rn.94935	Down	BI
110	-	BI277534	Rn.122326	Down	BI
111	-	BF416864	Rn.161752	Down	BI
112	RGD1311005_predicted	XM_341099	Rn.65800	Down	BI
113	-	XM_575687	Rn.162772	Down	BI
114	-	BI277534	Rn.122326	Down	BI
115	-	BI277534	Rn.122326	Down	BI
116	Rpl26_predicted	XM_213346	Rn.144702	Down	BI
117	-	BI277534	Rn.122326	Down	BI
118	Mrps18c_predicted	XM_214003	Rn.105741	Down	BI
119	Plp	NM_030990	Rn.4550	Down	BI

No	Target(Gene)Symbol	Target Accession	UniGene	Up/Down	生体由来試料
120	-	BI277534	Rn.7999	Down	BI
121	Polr2k_predicted	XM_219604	-	Down	BI
122	-	BI277534	-	Down	BI
123	-	BI277534	-	Down	BI
124	-	NM_001014207	Rn.137575	Down	BI
125	-	TC559328	-	Down	BI
126	-	BI277534	Rn.122326	Down	BI
127	Cma1	NM_013092	Rn.10182	Down	BI
128	Rpl37	BI277661	Rn.129486	Down	BI
129	-	TC559328	Rn.122326	Down	BI
130	-	BE098803	Rn.122326	Down	BI
131	-	BI277534	Rn.122326	Down	BI
132	-	AI231572	Rn.1180	Down	BI
133	Slpi	NM_053372	Rn.18560	Up	BI
134	Slpi	NM_053372	Rn.18560	Up	BI
135	LOC296356	XM_215940	Rn.144851	Up	BI
136	Fn1	NM_019143	Rn.1604	Up	BI
137	-	NM_001013853	Rn.163132	Up	BI
138	-	TC551459	-	Up	BI
139	Adn	XM_343169	Rn.16172	Up	BI
140	Timp2	NM_021989	Rn.10161	Up	BI
141	-	NM_001013110	Rn.91296	Up	BI
142	Ptpn11	NM_013088	Rn.98209	Up	BI
143	LOC298270	XM_233230	Rn.162076	Down	BI
144	LOC292088	XM_238058	-	Down	BI
145	Slc6a3	NM_012694	Rn.10093	Up	Hy
146	-	TC543527	-	Up	Hy
147	-	BE108176	Rn.3464	Up	Hy
148	Galp	NM_022633	Rn.48754	Up	Hy
149	Pomc2	NM_139326	Rn.108195	Up	Hy
150	-	BF398607	Rn.45255	Down	Hy
151	Chrna3	NM_052805	Rn.10996	Down	Hy
152	-	AW914894	Rn.10267	Down	Hy
153	Shox2	NM_013028	Rn.11258	Down	Hy
154	LOC289633	XM_223426	Rn.123835	Down	Hy
155	Prpf31_predicted	XM_218173	Rn.99310	Down	Hy
156	-	TC530743	-	Down	Hy
157	Slc5a7	NM_053521	Rn.44872	Down	Hy
158	Ttr	NM_012681	Rn.1404	Down	Hy
159	Lhx9	NM_181367	Rn.75111	Down	Hy
160	-	AW527509	Rn.41179	Down	Hy
161	Shox2	NM_013028	Rn.11258	Down	Hy
162	Grifin	NM_057187	Rn.26894	Down	Hy
163	-	TC556932	-	Down	Hy
164	Zic1	NM_022677	Rn.161923	Down	Hy
165	Prkcd	NM_133307	Rn.98279	Down	Hy
166	Slc18a3	NM_031663	Rn.9987	Down	Hy
167	Cpne4_predicted	XM_345977	Rn.124862	Down	Hy
168	-	TC519964	-	Down	Hy
169	RGD1311951_predicted	XM_237334	Rn.70007	Down	Hy
170	-	AI178665	Rn.58356	Down	Hy
171	-	BC092605	Rn.22271	Down	Hy
172	-	TC543142	-	Down	Hy
173	-	TC567761	-	Down	Hy
174	Ramp3	NM_020100	Rn.48672	Down	Hy
175	Lef1	NM_130429	Rn.21926	Down	Hy
176	Irx5_predicted	XM_225077	-	Down	Hy
177	MGC95205	NM_001005540	Rn.12833	Down	Hy
178	-	BE126741	-	Down	Hy
179	-	TC551026	-	Down	Hy

No	Target(Gene)Symbol	Target Accession	UniGene	Up/Down	生体由来試料
180	Cga	J00757	Rn.10589	Up	Hy
181	Cga	NM_053918	Rn.10589	Up	Hy
182	Shox2	NM_013028	Rn.11258	Up	Hy
183	-	BC092605	Rn.22271	Up	Hy
184	-	BE108176	Rn.3464	Up	Hy
185	Prkcd	NM_133307	Rn.98279	Up	Hy
186	-	TC543263	-	Up	Hy
187	Vip	XM_217838	Rn.18675	Up	Hy
188	Grifin	NM_057187	Rn.26894	Up	Hy
189	-	TC530743	-	Up	Hy
190	Nexn	NM_139230	Rn.107975	Up	Hy
191	Ramp3	NM_020100	Rn.48672	Up	Hy
192	-	XM_575030	Rn.7078	Up	Hy
193	Ttr	NM_012681	Rn.1404	Down	Hy
194	-	BF398607	Rn.45255	Down	Hy
195	Gnrh1	NM_012767	Rn.59459	Down	Hy
196	Foxg1	NM_012560	Rn.9864	Down	Hy
197	Prpf31_predicted	XM_218173	Rn.99310	Down	Hy
198	Slc18a3	NM_031663	Rn.9987	Down	Hy
199	Ngfr	NM_012610	Rn.10980	Down	Hy
200	Zfyve9_predicted	XM_233341	Rn.23612	Down	Hy
201	Avp	NM_016992	Rn.9976	Down	Hy
202	-	AI013718	-	Down	Hy
203	Slc5a7	NM_053521	Rn.44872	Down	Hy
204	-	BQ194469	Rn.161764	Up	St
205	LOC290372	XM_237952	Rn.19611	Up	St
206	-	BG672648	-	Up	St
207	-	BF398607	Rn.45255	Down	St
208	Prpf31_predicted	XM_218173	Rn.99310	Down	St
209	Vip	XM_217838	Rn.18675	Down	St
210	Slc17a7	NM_053859	Rn.10267	Down	St
211	Cck	BM382824	Rn.9781	Down	St
212	-	AW914894	#N/A	Down	St
213	Homer1	U92079	Rn.10267	Down	St
214	Cck	NM_012829	-	Down	St
215	Tjp1_predicted	XM_218747	Rn.101871	Up	St
216	Tjp1_predicted	XM_218747	Rn.101871	Up	St
217	Tjp1_predicted	XM_218747	Rn.101871	Up	St
218	-	AW144721	Rn.3039	Up	St
219	-	AA963075	Rn.73451	Up	St
220	Sv2b	NM_057207	Rn.58137	Up	St
221	-	BG672648	-	Up	St
222	Avp	NM_016992	Rn.9976	Up	St
223	-	BF398607	Rn.45255	Down	St
224	Prpf31_predicted	XM_218173	Rn.99310	Down	St
225	-	TC560395	-	Down	St
226	RGD:1303100	NM_001003929	Rn.55036	Down	St
227	Slc17a7	NM_053859	Rn.10267	Down	St
228	-	A_44_P302611	-	Down	St
229	-	BF546193	Rn.174580	Down	St
230	RGD1309846_predicted	XM_231625	-	Down	St
231	Bhlhb3	NM_133303	Rn.10784	Down	St
232	Cck	NM_012829	Rn.9781	Down	St
233	-	AW914894	Rn.10267	Down	St
234	Homer1	U92079	-	Down	St
235	Crisp1	NM_022859	Rn.10102	Up	Sg
236	-	ENSRNOT00000040037	-	Up	Sg
237	Prpg2	NM_172065	Rn.29950	Up	Sg
238	Psp	NM_052808	Rn.9766	Up	Sg
239	-	BF415117	Rn.2635	Up	Sg

No	Target(Gene)Symbol	Target Accession	UniGene	Up/Down	生体由来試料
240	Mgat3	NM_019239	Rn.9803	Up	Sg
241	-	TC519989	-	Up	Sg
242	-	XM_341973	-	Up	Sg
243	Scgb2a1	NM_080770	Rn.144559	Up	Sg
244	-	A_44_P875993	-	Up	Sg
245	-	M87788	Rn.118336	Up	Sg
246	Amy2_predicted	XM_345278	Rn.67070	Up	Sg
247	Amy1	NM_001010970	Rn.116361	Up	Sg
248	-	XM_342323	-	Up	Sg
249	-	CB545830	Rn.157214	Up	Sg
250	RGD1311424_predicted	XM_343001	Rn.57800	Up	Sg
251	-	BI288013	Rn.40911	Up	Sg
252	Mycl1	XM_233490	Rn.41400	Up	Sg
253	-	NM_001013941	Rn.161900	Up	Sg
254	Dusp1	NM_053769	Rn.98260	Up	Sg
255	LOC366764	XM_345751	-	Up	Sg
256	-	L07402	Rn.119901	Down	Sg
257	LOC314509	XM_234661	Rn.110660	Down	Sg
258	-	Z93368	Rn.110663	Down	Sg
259	LOC299469	XM_234749	-	Down	Sg
260	LOC366769	XM_345756	Rn.126669	Down	Sg
261	-	Z93350	Rn.10956	Down	Sg
262	-	ENSRNOT00000043097	-	Down	Sg
263	-	XM_575540	Rn.117940	Down	Sg
264	LOC299551	XM_234830	-	Down	Sg
265	LOC366758	XM_345745	Rn.112181	Down	Sg
266	-	XM_345746	-	Down	Sg
267	Prpf31_predicted	XM_218173	Rn.99310	Down	Sg
268	-	NM_001014264	Rn.102149	Down	Sg
269	-	BE098883	Rn.15951	Down	Sg
270	LOC314512	XM_234676	Rn.110661	Down	Sg
271	LOC297260	XM_231999	-	Down	Sg
272	Fetub	NM_053348	Rn.2464	Down	Sg
273	-	BC092624	Rn.163825	Down	Sg
274	LOC366758	XM_345745	Rn.112181	Down	Sg
275	-	XM_234741	-	Down	Sg
276	Igkv28	L17078	Rn.92371	Down	Sg
277	-	BF560128	Rn.28431	Down	Sg
278	-	XM_345749	-	Up	Sg
279	Klk1c10	XM_214947	Rn.136578	Up	Sg
280	Klks3	NM_175759	Rn.34527	Up	Sg
281	Ton	NM_012677	Rn.9882	Up	Sg
282	Vcsa1	NM_012684	Rn.9927	Up	Sg
283	RGD:619853	NM_022709	Rn.162774	Up	Sg
284	Klk12	NM_001005382	Rn.141980	Up	Sg
285	Olr1223_predicted	NM_001000441	Rn.143544	Up	Sg
286	RGD:735032	XM_214931	Rn.107068	Up	Sg
287	-	XM_341973	-	Up	Sg
288	Vcsa1	NM_012684	Rn.9927	Up	Sg
289	Acaca	NM_022193	Rn.44372	Up	Sg
290	-	NM_001013067	Rn.79264	Up	Sg
291	Egf	NM_012842	Rn.6075	Up	Sg
292	RGD:735160	NM_198685	Rn.79319	Up	Sg
293	Svs6_predicted	XM_342575	Rn.145207	Up	Sg
294	-	CB545830	Rn.157214	Up	Sg
295	Klk7	NM_012593	Rn.144553	Up	Sg
296	Pip	NM_022708	Rn.78367	Up	Sg
297	RGD:735032	XM_214931	Rn.107068	Up	Sg
298	Muc10	NM_133513	Rn.10113	Up	Sg
299	RGD:1303220	NM_001003977	Rn.141979	Up	Sg

No	Target(Gene)Symbol	Target Accession	UniGene	Up/Down	生体由来試料
300	Grpca	NM_181440	Rn.10942	Up	Sg
301	-	TC524810	-	Up	Sg
302	-	AA963004	Rn.24539	Up	Sg
303	Scgb2a1	NM_080770	Rn.144559	Up	Sg
304	Ngfg	NM_031523	Rn.11331	Up	Sg
305	-	ENSRNOT00000042436	-	Up	Sg
306	RGD:735228	XM_214939	Rn.21391	Up	Sg
307	Gpr83	NM_080411	Rn.63075	Up	Sg
308	-	NM_001013941	Rn.161900	Up	Sg
309	Tgfb2	NM_031131	Rn.24539	Up	Sg
310	Prpg2	NM_172065	Rn.29950	Up	Sg
311	Mpv17l_predicted	XM_340739	Rn.22842	Up	Sg
312	Npas3_predicted	XM_234124	Rn.135138	Up	Sg
313	LOC290262	XM_224224	-	Up	Sg
314	LOC287803	XM_221081	Rn.163171	Up	Sg
315	LOC362603	XM_347064	Rn.91410	Up	Sg
316	Oxt	NM_012996	Rn.48915	Up	Sg
317	Vgll2_predicted	XM_228170	Rn.17643	Up	Sg
318	Th	NM_012740	Rn.11082	Up	Sg
319	RGD1309050_predicted	XM_240734	Rn.6819	Up	Sg
320	B4galt6	NM_031740	-	Up	Sg
321	LOC361702	XM_341985	Rn.61872	Up	Sg
322	-	AA956502	-	Up	Sg
323	-	CK595775	Rn.125806	Up	Sg
324	Rbp3	XM_341400	Rn.41214	Up	Sg
325	Lrrc27_predicted	XM_341954	Rn.162479	Up	Sg
326	RGD1308967_predicted	XM_232748	Rn.143980	Up	Sg
327	Fmo5	NM_144739	Rn.7038	Up	Sg
328	LOC361340	XM_341623	Rn.132740	Up	Sg
329	Tbx5_predicted	NM_001009964	Rn.6327	Up	Sg
330	-	X89700	-	Up	Sg
331	Kif23_predicted	XM_236313	Rn.63734	Up	Sg
332	-	ENSRNOT00000016430	-	Up	Sg
333	LOC309745	XM_228133	Rn.84956	Up	Sg
334	Riok3_predicted	XM_341578	Rn.4181	Up	Sg
335	Lyl1	NM_001007677	Rn.17352	Up	Sg
336	Zfp393_predicted	XM_233437	Rn.159750	Up	Sg
337	Mxi1	NM_013160	Rn.37510	Up	Sg
338	Gdf5	AB087404	Rn.127822	Up	Sg
339	-	AW917276	Rn.7332	Up	Sg
340	B4galt6	NM_031740	-	Up	Sg
341	LOC313633	XM_233574	Rn.27233	Up	Sg
342	-	TC541862	-	Up	Sg
343	-	NM_001024751	Rn.76073	Up	Sg
344	Erabp	NM_024136	Rn.10362	Up	Sg
345	-	XM_345742	-	Up	Sg
346	Limd1_predicted	XM_236734	Rn.161977	Up	Sg
347	RGD1309038_predicted	XM_225887	Rn.24687	Up	Sg
348	-	TC562194	-	Up	Sg
349	Actn3	NM_133424	Rn.17592	Up	Sg
350	-	CB547130	Rn.179696	Up	Sg
351	Cart1	NM_012921	Rn.9282	Up	Sg
352	RGD1311019_predicted	XM_238442	Rn.18688	Up	Sg
353	Znf507_predicted	XM_218515	Rn.141981	Up	Sg
354	LOC310631	XM_227403	Rn.104095	Up	Sg
355	-	AI045861	Rn.10526	Up	Sg
356	Ccl17	NM_057151	Rn.46679	Up	Sg
357	Arl12_predicted	XM_220907	Rn.18110	Up	Sg
358	-	TC559056	Rn.147866	Up	Sg
359	Mobp	NM_012720	Rn.91185	Up	Sg

No	Target(Gene)Symbol	Target Accession	UniGene	Up/Down	生体由来試料
360	Golph2_predicted	XM_225147	Rn.1545	Up	Sg
361	-	ENSRNOT00000038788	-	Up	Sg
362	-	AA800803	Rn.102152	Up	Sg
363	Mospd4_predicted	BF400026	Rn.63770	Up	Sg
364	-	XM_578308	-	Up	Sg
365	Rasgrp4	NM_130824	Rn.81227	Up	Sg
366	-	NM_001024273	Rn.14280	Up	Sg
367	-	A_44_P882921	-	Up	Sg
368	-	A_44_P729420	-	Up	Sg
369	Hsf4_predicted	XM_214668	Rn.163399	Up	Sg
370	Znf297	NM_001009172	Rn.17135	Up	Sg
371	-	TC540693	-	Up	Sg
372	LOC301121	XM_236777	Rn.35756	Up	Sg
373	Spata18	NM_199374	Rn.27773	Up	Sg
374	LOC367391	XM_346122	Rn.83054	Up	Sg
375	P2rx2	NM_053656	Rn.88799	Up	Sg
376	-	TC545251	-	Up	Sg
377	-	A_44_P278941	-	Up	Sg
378	Andpro	NM_012718	Rn.9977	Up	Sg
379	Sult1a2	NM_031732	Rn.9937	Up	Sg
380	-	NM_001014232	Rn.8173	Up	Sg
381	Sprr3_predicted	XM_227339	Rn.19820	Up	Sg
382	Mgat4a_predicted	NM_001012225	Rn.145359	Up	Sg
383	Hapln1	NM_019189	Rn.50531	Up	Sg
384	-	BM388083	Rn.41133	Up	Sg
385	-	BG380409	Rn.143966	Up	Sg
386	Sds	NM_053962	Rn.9918	Up	Sg
387	Cngb1	AJ224680	Rn.10733	Up	Sg
388	-	NM_001024983	Rn.152074	Up	Sg
389	LOC365807	XM_345218	Rn.111884	Up	Sg
390	RGD:628846	NM_031605	Rn.10034	Up	Sg
391	-	BF567941	Rn.169222	Up	Sg
392	RGD:727806	NM_001001508	Rn.58355	Up	Sg
393	Pex11a	NM_053487	Rn.14519	Up	Sg
394	-	AA963232	Rn.1053	Up	Sg
395	-	AW142782	Rn.43391	Up	Sg
396	-	A_44_P260574	Rn.43391	Up	Sg
397	Adcyap1	NM_016989	Rn.37400	Up	Sg
398	Nr4a1	NM_024388	Rn.10000	Up	Sg
399	Spt2_predicted	XM_238528	-	Up	Sg
400	-	TC538568	-	Up	Sg
401	-	BF290953	Rn.24673	Up	Sg
402	LOC296782	XM_216075	-	Up	Sg
403	-	XM_343522	-	Up	Sg
404	Akr1cl1_predicted	XM_341550	Rn.132469	Up	Sg
405	-	A_44_P304740	-	Up	Sg
406	-	AW142587	Rn.9491	Up	Sg
407	Itm2c_predicted	NM_001009674	Rn.8450	Up	Sg
408	-	AW916070	Rn.167735	Up	Sg
409	-	TC531872	Rn.167735	Up	Sg
410	LOC300150	XM_235563	-	Up	Sg
411	-	ENSRNOT00000049913	-	Up	Sg
412	Nr1d1	NM_145775	Rn.29848	Up	Sg
413	RGD1308684_predicted	XM_341641	Rn.41567	Up	Sg
414	LOC365316	XM_344926	-	Up	Sg
415	Scnn1g	NM_017046	Rn.10360	Up	Sg
416	Gpx6	NM_147165	Rn.9852	Up	Sg
417	Lrp2	NM_030827	Rn.26430	Up	Sg
418	-	TC566080	-	Up	Sg
419	-	NM_001017383	Rn.22468	Up	Sg

No	Target(Gene)Symbol	Target Accession	UniGene	Up/Down	生体由来試料
420	-	BI279326	Rn. 48786	Up	Sg
421	LOC297757	XM_216317	Rn. 144410	Up	Sg
422	Pex11a	BC061835	Rn. 14519	Up	Sg
423	Cdh11	XM_341639	Rn. 8900	Up	Sg
424	RGD1306750_predicted	XM_347055	Rn. 48786	Up	Sg
425	LOC313589	XM_233520	Rn. 162826	Up	Sg
426	-	AA875449	Rn. 2923	Up	Sg
427	Duox2	NM_024141	Rn. 55542	Up	Sg
428	LOC474169	NM_001007015	Rn. 87496	Up	Sg
429	-	BC091324	Rn. 13679	Up	Sg
430	RGD:708361	NM_138547	Rn. 10021	Up	Sg
431	-	X55180	Rn. 117936	Up	Sg
432	LOC288979	XM_222564	Rn. 24014	Up	Sg
433	-	AW918545	Rn. 13679	Up	Sg
434	-	TC542673	Rn. 13679	Up	Sg
435	-	BG672648	-	Up	Sg
436	RGD:735199	NM_198734	Rn. 154471	Up	Sg
437	RGD1309403_predicted	XM_227140	Rn. 38949	Up	Sg
438	-	CO556754	Rn. 15953	Up	Sg
439	Muc19_predicted	XM_235593	Rn. 162964	Down	Sg
440	Smgb	NM_080775	Rn. 9925	Down	Sg
441	Rasl12_predicted	XM_236351	Rn. 147874	Down	Sg
442	Cdh22	NM_019161	Rn. 145674	Down	Sg
443	LOC314509	XM_234661	Rn. 110660	Down	Sg
444	RGD:708577	NM_133622	Rn. 9752	Down	Sg
445	Lman1l_predicted	XM_217166	-	Down	Sg
446	-	XM_214055	-	Down	Sg
447	Bpil1_predicted	XM_215892	Rn. 162713	Down	Sg
448	LOC362442	XM_342764	Rn. 77935	Down	Sg
449	LOC362442	XM_342764	Rn. 77935	Down	Sg
450	RGD:1303308	NM_001004236	Rn. 33830	Down	Sg
451	LOC292801	XM_218497	-	Down	Sg
452	-	A_44_P950925	-	Down	Sg
453	RGD1311224_predicted	XM_215767	Rn. 47550	Down	Sg
454	Kcne1	NM_012973	Rn. 9734	Down	Sg
455	Kntc1_predicted	XM_222157	Rn. 47918	Down	Sg
456	Mme	NM_012608	Rn. 33598	Down	Sg
457	Fetub	NM_053348	Rn. 2464	Down	Sg
458	Galnt12_predicted	XM_223905	-	Down	Sg
459	-	XM_344059	-	Down	Sg
460	-	NM_001013180	Rn. 30648	Down	Sg
461	Cox4i2	NM_053472	Rn. 7214	Down	Sg
462	Gnas	L10326	Rn. 31	Down	Sg
463	Runx3	NM_130425	Rn. 34220	Down	Sg
464	Olr1654_predicted	NM_021860	Rn. 138118	Down	Sg
465	Serpina1	NM_022519	Rn. 1419	Down	Sg
466	Igkv28	L17078	Rn. 92371	Down	Sg
467	Dlk1	NM_053744	Rn. 14547	Down	Sg
468	LOC299434	XM_234680	Rn. 134951	Down	Sg
469	LOC366769	XM_345756	Rn. 126669	Down	Sg
470	-	TC527103	Rn. 107412	Down	Sg
471	Creb3l4	XM_227391	Rn. 107412	Down	Sg
472	-	TC539429	Rn. 107412	Down	Sg
473	Galnt7	NM_022926	Rn. 144577	Down	Sg
474	Oit1_predicted	XM_214143	Rn. 38497	Down	Sg
475	-	L07410	-	Down	Sg
476	RGD1311701_predicted	XM_230278	Rn. 34843	Down	Sg
477	-	AF217591	Rn. 134336	Down	Sg
478	-	AW144181	-	Down	Sg
479	-	TC539049	-	Down	Sg

No	Target(Gene)Symbol	Target Accession	UniGene	Up/Down	生体由来試料
480	RGD:1303068	NM_203337	Rn.24125	Down	Sg
481	-	Z93368	Rn.167718	Down	Sg
482	-	AW144454	Rn.167718	Down	Sg
483	-	NM_001014264	Rn.102149	Down	Sg
484	RGD:620649	CA509211	Rn.3517	Down	Sg
485	-	XM_573320	Rn.163185	Down	Sg
486	Dnajc10_predicted	XM_215751	Rn.8642	Down	Sg
487	-	NM_001025041	Rn.162656	Down	Sg
488	-	M84148	Rn.134335	Down	Sg
489	Ces3	NM_133295	Rn.2549	Down	Sg
490	Dnajc10_predicted	XM_215751	Rn.8642	Down	Sg
491	Cdh22	NM_019161	Rn.145674	Down	Sg
492	-	L07402	-	Down	Sg
493	RGD:1303167	NM_212541	Rn.27480	Down	Sg
494	Ca3	NM_019292	Rn.1647	Down	Sg
495	Cyp2f2	NM_019303	Rn.10817	Down	Sg
496	LOC299469	XM_234749	-	Down	Sg
497	Sectm1	NM_199082	-	Down	Sg
498	-	NM_001013219	Rn.104514	Down	Sg
499	RGD:708486	NM_020091	Rn.48676	Down	Sg
500	-	XM_575093	Rn.116833	Down	Sg
501	Fam3b_predicted	XM_221623	Rn.162007	Down	Sg
502	Gm1012	XM_342493	Rn.44656	Down	Sg
503	-	XM_234741	-	Down	Sg
504	LOC314512	XM_234676	Rn.110661	Down	Sg
505	Acdc	NM_144744	Rn.24299	Down	Sg
506	Bf	NM_212466	Rn.109148	Down	Sg
507	Olr197_predicted	NM_001000188	Rn.141814	Down	Sg
508	LOC299551	XM_234830	-	Down	Sg
509	-	Z93354	Rn.179369	Down	Sg
510	Sec23b_predicted	XM_342531	Rn.8735	Down	Sg
511	Amy1	NM_001010970	Rn.116361	Down	Sg
512	Cxadrl1	NM_199406	Rn.162547	Down	Sg
513	Galnt5	NM_031796	Rn.30048	Down	Sg
514	-	XM_344373	-	Down	Sg
515	-	TC525800	-	Down	Sg
516	-	XM_575540	Rn.117940	Down	Sg
517	C1ql3_predicted	BF391573	Rn.39092	Down	Sg
518	Igfbp2	NM_013122	Rn.6813	Down	Sg
519	Cnnm4_predicted	XM_343554	Rn.857	Down	Sg
520	RGD:1303241	NM_001002802	Rn.38581	Down	Sg
521	-	BC091425	-	Down	Sg
522	Creb3l1	NM_001005562	Rn.24541	Down	Sg
523	-	U75411	-	Down	Sg
524	LOC366733	XM_345725	Rn.8473	Down	Sg
525	Galnt12_predicted	XM_223905	-	Down	Sg
526	-	XM_342323	-	Down	Sg
527	Akr1b8	NM_173136	Rn.23676	Down	Sg
528	-	XM_575775	Rn.23267	Down	Sg
529	Dnase1	NM_013097	Rn.6077	Down	Sg
530	Tgoln2	NM_138840	Rn.11349	Down	Sg
531	Prpf31_predicted	XM_218173	Rn.99310	Down	Sg
532	-	XM_234755	-	Down	Sg
533	Cd14	NM_021744	-	Down	Sg
534	F3	NM_013057	Rn.9980	Down	Sg
535	-	XM_575534	-	Down	Sg
536	-	TC554663	-	Down	Sg
537	Tgoln2	NM_138840	Rn.11349	Down	Sg
538	-	NM_001025683	Rn.16921	Down	Sg
539	Hcn3	NM_053685	Rn.48801	Down	Sg

No	Target(Gene)Symbol	Target Accession	UniGene	Up/Down	生体由来試料
540	-	NM_001025683	Rn.16921	Down	Sg
541	-	AF468681	-	Down	Sg
542	-	BF524215	-	Down	Sg
543	Ddc	NM_012545	Rn.11064	Down	Sg
544	-	TC538655	-	Down	Sg
545	Cnn1	NM_031747	Rn.31788	Down	Sg
546	LOC366765	XM_345752	Rn.112186	Down	Sg
547	-	BQ200884	Rn.11349	Down	Sg
548	Amy2_predicted	XM_345278	Rn.67070	Down	Sg
549	-	BE103448	Rn.165522	Down	Sg
550	RGD:1303221	NM_001004215	Rn.144176	Down	Sg
551	-	L07408	Rn.117930	Down	Sg
552	Pcsk3	NM_019331	Rn.3220	Down	Sg
553	LOC301711	XM_237538	-	Down	Sg
554	LOC363618	XM_343911	Rn.72525	Down	Sg
555	Mapt	NM_017212	Rn.2455	Down	Sg
556	-	TC555084	-	Down	Sg
557	Retn	NM_144741	Rn.16746	Down	Sg
558	LOC310429	XM_227167	-	Down	Sg
559	RGD1304977_predicted	XM_238325	Rn.101794	Down	Sg
560	Srebf1	XM_213329	Rn.801	Down	Sg
561	-	AW520826	-	Down	Sg
562	LOC307231	XM_225713	Rn.148475	Down	Sg
563	LOC366733	XM_345725	Rn.8473	Down	Sg
564	Arg2	NM_019168	Rn.11055	Down	Sg
565	Cd14	NM_021744	-	Down	Sg
566	Gpx2	NM_183403	Rn.3503	Down	Sg
567	Frmpd1_predicted	XM_233002	Rn.37934	Down	Sg
568	-	TC555358	-	Down	Sg
569	Acsl1	NM_012820	Rn.6215	Down	Sg
570	RGD:1303180	NR_002149	-	Down	Sg
571	LOC362348	XM_342669	Rn.91492	Down	Sg
572	-	BE110753	Rn.8285	Down	Sg
573	-	TC540316	Rn.8285	Down	Sg
574	-	AW917167	Rn.18668	Down	Sg
575	Nid67	NM_173126	Rn.8865	Down	Sg
576	Rhoc_predicted	XM_215659	Rn.162614	Down	Sg
577	Acsl1	NM_012820	Rn.6215	Down	Sg
578	Lama5	XM_215963	Rn.62616	Down	Sg
579	Gpr2_predicted	XM_343968	Rn.49607	Down	Sg
580	Scn11a	NM_019265	Rn.30023	Down	Sg
581	-	NM_001013232	Rn.111376	Down	Sg

[表中、

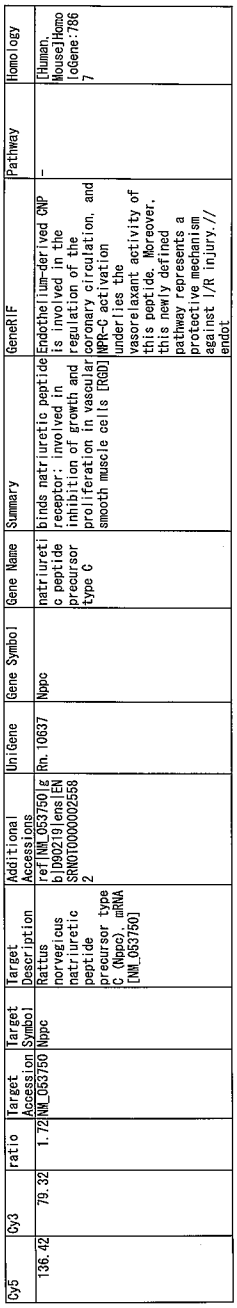
Sgは唾液腺であり；Blは血液であり；Hyは視床下部であり；Stは線条体である。]

[請求項9] 下記の表81～84に示す遺伝子の塩基配列の少なくとも一部を含む核酸からなる群から選ばれる少なくとも1種の核酸、又は下記の表1に示す遺伝子によってコードされるタンパク質に対して特異的に結合する分子からなる群から選択される少なくとも1種の分子を含む、ラットの陽性感情を評価するための検査キット。

[表24]

表81 線条体で発現増加した注目遺伝子
神経ペプチドホルモン活性 (GO ID: 5184)

Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Gene Symbol	Gene Name	Summary	GeneRIF	Pathway	Homology
106.09	45.98	2.31	NM_133570	Grp	Rattus norvegicus gastrin releasing peptide (Grp), mRNA [NM_133570]	ref|NM_133570|gb|M31176|ens|ENSRNOT00000022845|tc|TC569979	Rn.10930	Grp	gastrin releasing peptide	increases 5-HT neuronal activity in the hypothalamus PVN; inhibits feeding behavior	GRP mRNA was detected in rat kidney from embryonic day 19 to postnatal day 30 by RT-PCR// GRP in the central part of the amygdala inhibits feeding, may decrease the efficiency of eating, and may act as a satiety signal.// the increase in gastrin releasing	KEGG pathway: Neuroactive ligand-receptor interaction	[Human, Mouse]HomoloGene:1580
133.62	59.95	2.23	BM382824	Cck	UI-R-BT1-bko-b-06-0-UI.s1 UI-R-BT1 Rattus norvegicus cDNA clone UI-R-BT1-bko-b-06-0-UI 3', mRNA sequence [BM382824]	gb|BM382824	Rn.9781	Cck	cholecystokinin	brain-gut peptide with hemacrine and autocrine function in the gut [RGD]	CCK preadministration to obese rats did not affect ghrelin-induced food intake.// A study of the hypothesis that CCK in the rostral ventromedial medulla may engage descending pain facilitatory pathways to enhance spinal nociceptive transmission and attenu	KEGG pathway: Neuroactive ligand-receptor interaction	[Human, Mouse]HomoloGene:583
369.75	169.54	2.18	NM_012835	Cort	Rattus norvegicus cortistatin (Cort), mRNA [NM_012835]	ref|NM_012835|gb|U51919|ens|ENSRNOT00000018401|tc|TC570162	Rn.10490	Cort	cortistatin	inhibits growth hormone secretion; may act as a neuropeptide to mediate signaling via a somatostatin receptor subtype [RGD]	-	KEGG pathway: Neuroactive ligand-receptor interaction	[Human, Mouse]HomoloGene:997
52.29	27.34	1.91	NM_016989	Adcyap1	Rattus norvegicus adenylate cyclase activating polypeptide 1 (Adcyap1), mRNA [NM_016989]	ref|NM_016989|ref|XM_579383|gb|M63006|gb|AW146860	Rn.37400	Adcyap1	adenylate cyclase activating polypeptide 1	regulatory protein that stimulates cell proliferation, induces proliferation, modulates neurotransmitter release, vasodilation, bronchodilation, and hormone release, and suppresses inflammatory responses [RGD]	These results indicate that a large number of PACAP neurons and a small number of BDNF neurons of the VMH project to the MCG.// The specificity of PAC1 receptor participation in pituitary adenylate cyclase-activating polypeptide (PACAP)-facilitated sex be	KEGG pathway: Neuroactive ligand-receptor interaction	[Human, Mouse]HomoloGene:869



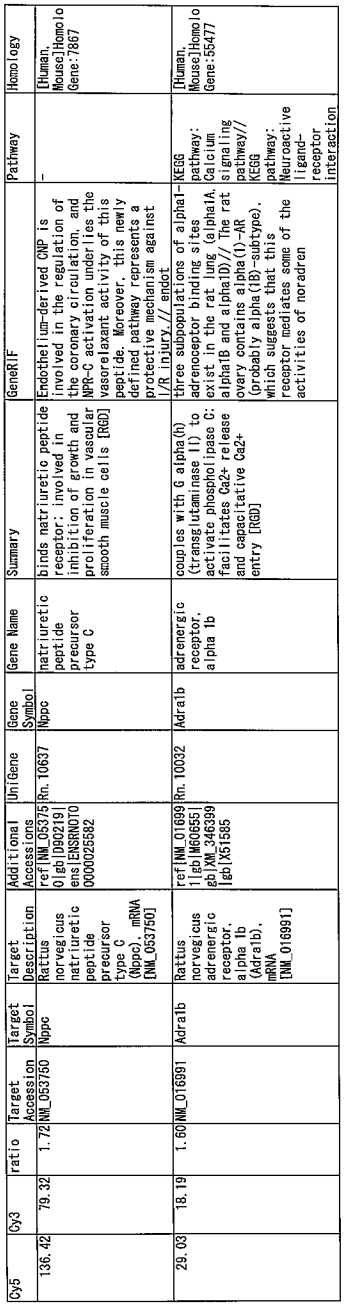
Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Gene Symbol	Gene Name	Summary	GeneRIF	Pathway	Homology
136.42	79.32	1.72	NM_053750	Nppc	Rattus norvegicus natriuretic peptide precursor type C (Nppc), mRNA [NM_053750]	ref|NM_053750|gb|D90219|ensEMBL|ENSRNOT00000002558|2	Rn.10637	Nppc	natriuretic peptide precursor type C	binds natriuretic peptide receptor; involved in inhibition of growth and proliferation in vascular smooth muscle cells [RGD]	Endothelium-derived CNP is involved in the regulation of the coronary circulation, and NPR-C activation underlies the vasorelaxant activity of this peptide. Moreover, this newly defined pathway represents a protective mechanism against I/R injury.// endot	-	[Human, Mouse]Homologene:7867

[表25]

表62 線条体で発現増加した注目遺伝子
血圧調節関連 (GO ID: 5088

Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Gene Symbol	Gene Name	Summary	GeneRIF	Pathway	Homology
72.06	24.25	2.97	NM_024483	Adra1d	Rattus norvegicus adrenergic receptor, alpha 1d (Adra1d), mRNA [NM_024483]	ref|NM_024483.1|gb|L31771|gb|M60654|ens|ENSRNOT00000028877	Rn.11314	Adra1d	adrenergic receptor, alpha 1d	adrenergic receptor showing high affinity for the antagonist WB4101 and agonists phenylephrine and methoxamine [RGD]	three subpopulations of alpha1-adrenoceptor binding sites exist in the rat lung (alpha1A, alpha1B and alpha1D)// cell surface expression of alpha1D-adrenergic receptors is controlled by heterodimerization with alpha1B-adrenergic receptors	KEGG pathway: Calcium signaling pathway	[Human, Mouse]Homolo Gene:551
160.27	57.88	18.27	NM_016992	Avp	Rattus norvegicus arginine vasopressin (Avp), mRNA [NM_016992]	ref|NM_016992.2|gb|M25646|gb|X01637|gb|V01276	Rn.9976	Avp	arginine vasopressin	neuropeptide hormone: involved in vasoconstriction to regulate blood pressure and smooth muscle contraction during parturition and lactation [RGD]	These data suggest that testosterone attenuates light-enhanced startle, but not fear-potentiated startle, through a mechanism that may involve AVP.// Both the magnocellular and the parvocellular hypothalamic vasopressin systems are capable of expressing t	KEGG pathway: Neuroactive ligand-receptor interaction	[Human, Mouse]Homolo Gene:417

Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Gene Symbol	Gene Name	Summary	GeneRIF	Pathway	Homology
232.63	99.84	2.33	XM_217838	Vip	PREDICTED: Rattus norvegicus vasoactive intestinal polypeptide (Vip), mRNA [XM_217838]	ref|XM_217838|gb|X02341|ens|ENSRNOT00000025477|tc|TC537816	Rn.18675	Vip	vasoactive intestinal polypeptide	peptide that causes vasodilation [RGD]	Vasoactive intestinal polypeptide regulates dynamic changes in astrocyte morphometry: impact on gonadotropin-releasing hormone neurons// Significant changes in NPY and VIP prostate nerve fibers, showing an increase in periurethral ducts at sex maturation.// Co-expression patterns of the neuropeptides vasoactive intestinal peptide and cholecystokinin with the transduction molecules alpha-gustducin and T1R2 in rat taste receptor cells.// VIP had a modulatory action on jejunal potassium absorption when injected into the nucleus tractus solitarius.// VIP can modulate not only immune responses but also hormonal responses during acute inflammation.// The increased noradrenergic noncholinergic and the decreased effects of VIP in mediating inhibitory nerves may largely relate to the peristaltic abnormalities seen in the isografted LEW rat // Aging reduces vasoactive intestinal peptide (VIP) receptor mRNA and eliminates diurnal expression of VIP mRNA within the suprachiasmatic nucleus of aged male rats.// (The rest is omitted.)	KEGG pathway: Neuroactive ligand-receptor interaction	[Human, Mouse]Homolo Gene:2539
53.01	25.47	2.08	NM_012612	Nppa	Rattus norvegicus natriuretic peptide precursor type A (Nppa), mRNA [NM_012612]	ref|NM_012612|gb|X06665|gb|M27498|ens|ENSRNOT00000011005	Rn.2004	Nppa	natriuretic peptide precursor type A	peptide involved in the control of fluid volume and vascular function [RGD]	The downregulation of ANP and NPRC in retinas of diabetic rats suggests a role for this peptide in experimental diabetic retinopathy.// The ANP might play a role on the synthesis of the oxytocin since ANP and its mRNA appear earlier than oxytocin.// SERCA	-	[Human, Mouse]Homolo Gene:4498



Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Gene Symbol	Gene Name	Summary	GeneRIF	Pathway	Homology
136.42	79.32	1.72	NM_053750	Nppc	Rattus norvegicus natriuretic peptide precursor type C (Nppc), mRNA [NM_053750]	ref|NM_053750.1|Ol go|D90219|ens|ENSRNOT00000025582	Rn.10637	Nppc	natriuretic peptide precursor type C	binds natriuretic peptide receptor; involved in inhibition of growth and proliferation in vascular smooth muscle cells [RGD]	Endothelium-derived CNP is involved in the regulation of the coronary circulation, and NPR-C activation underlies the vasorelaxant activity of this peptide. Moreover, this newly defined pathway represents a protective mechanism against I/R injury.// endot	-	[Human, Mouse]Homolo Gene:7867
29.03	18.19	1.60	NM_016991	Adra1b	Rattus norvegicus adrenergic receptor, alpha 1b (Adra1b), mRNA [NM_016991]	ref|NM_016991.1|gb|M60655|gb|XM_346399|gb|X51585	Rn.10032	Adra1b	adrenergic receptor, alpha 1b	couples with G alpha(h) (transglutaminase II) to activate phospholipase C; facilitates Ca2+ release and capacitative Ca2+ entry [RGD]	three subpopulations of alpha1-adrenoceptor binding sites exist in the rat lung (alpha1A, alpha1B and alpha1D)// The rat ovary contains alpha(1)-AR (probably alpha(1B)-subtype), which suggests that this receptor mediates some of the activities of noradren	KEGG pathway: Calcium signaling pathway// KEGG pathway: Neuroactive ligand-receptor interaction	[Human, Mouse]Homolo Gene:55477

[表26]

表83 絶条体で発現増加した注目遺伝子
食行動関連 (GO ID: 7631)

Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Gene Symbol	Gene Name	Summary	GeneRIF	Pathway	Homology
133.62	59.95	2.23	BM382824	Cck	UI-R-BT1-bko-b-06-0-UI.s1 UI-R-BT1 Rattus norvegicus cDNA clone UI-R-BT1-bko-b-06-0-UI 3', mRNA sequence [BM382824]	gb|BM382824	Rn.9781	Cck	cholecystokinin	brain-gut peptide with hemaorine and autocrine function in the gut [RGD]	CCK preadministration to obese rats did not affect ghrelin-induced food intake.// A study of the hypothesis that CCK in the rostral ventromedial medulla may engage descending pain facilitatory pathways to enhance spinal nociceptive transmission and attenu	KEGG pathway: Neuroactive ligand-receptor interaction	[Human, Mouse]HomoloGene:583
49.04	25.32	1.94	NM_012513	Bdnf	Rattus norvegicus brain derived neurotrophic factor (Bdnf), mRNA [NM_012513]	ref|NM_012513 |gb|X67108|gb |AY559250|gb |AY559249	Rn.11266	Bdnf	brain derived neurotrophic factor	plays a role in the development of hippocampal long term potentiation; involved in regulation of synaptic plasticity [RGD]	Overall, these results suggest that activity-dependent scaling of inhibitory synaptic strength can be modulated by BDNF/TrkB-mediated signaling.// Role of specific BDNF promoter regions and regulatory sequences in stimulant-induced alterations in BDNF exp	KEGG pathway: Huntington's disease// KEGG pathway: MAPK signaling pathway	[Human, Mouse]HomoloGene:7245
418.54	264.83	1.58	NM_013165	Cckbr	Rattus norvegicus cholecystokinin B receptor (Cckbr), mRNA [NM_013165]	ref|NM_013165 |gb|M99418|en s|ENSRNOT0000 00240771|tc|TC 570009	Rn.90997	Cckbr	cholecystokinin B receptor	Cholecystokinin was one of the first gastrointestinal peptides discovered in the mammalian brain. Cholecystokinin receptors are members of the G protein-coupled receptor superfamily, stimulating phosphatidylinositol turnover and intracellular calcium mobi	The present results substantiate the view that dorsolateral periaqueductal gray CCK(2) receptors modulate panic-related behaviors.// analysis of interspecies polymorphism in the human and rat cholecystokinin receptor-2 and its effect on the cholecystokini	KEGG pathway: Calcium signaling pathway// KEGG pathway: Neuroactive ligand-receptor interaction	[Human, Mouse]HomoloGene:7258
21.16	13.92	1.52	NM_012625	Pmch	Rattus norvegicus pro-melanin-concentrating hormone (Pmch), mRNA [NM_012625]	ref|NM_012625 |gb|M29712|gb |M62641|ens|E NSRNOT0000000 6174	Rn.9675	Pmch	pro-melanin-concentrating hormone	cyclic neuropeptide; induces hippocampal synaptic transmission [RGD]	MCH is involved in the regulation of LHRH release in the female rat.// glucocorticoids may promote food intake in part by potentiating the orexigenic actions of MCH without affecting the actions of orexin A and glucocorticoids act indirectly to influence	KEGG pathway: Neuroactive ligand-receptor interaction	[Human, Mouse]HomoloGene:37653

[表27]

表84 線条体で発現増加した注目遺伝子
生体リズム関連 (GO ID: 7623,48511)

Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Gene Symbol	Gene Name	Summary	GeneRIF	Pathway	Homology
369.75	169.54	2.18	NM_012835	Cort	Rattus norvegicus cortistatin (Cort), mRNA [NM_012835]	ref|NM_012835|Rn.10490 5|gb|U51919|ens|ENSRNOT00000018401|tc|TC670162	Rn.10490	Cort	cortistatin	inhibits growth hormone secretion; may act as a neuropeptide to mediate signaling via a somatostatin receptor subtype [RGD]	-	KEGG pathway: Neuroactive ligand-receptor interaction	[Human, Mouse]Homologene:997
1131.31	583.92	1.94	NM_181370	Hs3st2	Rattus norvegicus heparan sulfate (glucosamine) 3-O-sulfotransferase 2 (Hs3st2), mRNA [NM_181370]	ref|NM_181370|Rn.49010 0|gb|AY424087|ens|ENSRNOT00000023773|tc|TC669483	Rn.49010	Hs3st2	heparan sulfate (glucosamine) 3-O-sulfotransferase 2	catalyzes the transfer of sulfate groups onto the 3-OH site of glucosamine groups in heparan sulfate proteoglycans [RGD]	3-O sulfation catalyzed by HS 3-O-sulfotransferase (3-OST2) is predominantly restricted to daytime pineal glands in rats	-	[Human, Mouse]Homologene:21220
140.87	77.66	1.81	NM_013104	Igfbp6	Rattus norvegicus insulin-like growth factor binding protein 6 (Igfbp6). mRNA [NM_013104]	ref|NM_013104|Rn.6431 4|gb|M69055|gb|BG673588|ens|ENSRNOT00000014807	Rn.6431	Igfbp6	insulin-like growth factor binding protein 6	high-affinity IGF binding ptotein with substantially greater affinity for insulin-like growth factor-II (IGF-II) than IGF-I [RGD]	IGFBP-6, a new negative effector of oligodendrocyte survival and differentiation, is expressed and localized to the Golgi complex in rat oligodendrocyte precursor (O2A) cells.// IGFBP6 has a role in binding to endothelial cells and in transendothelial tra	-	[Human, Mouse]Homologene:1641
111.82	86.27	1.69	XM_345102	Atoh7_predicted	PREDICTED: Rattus norvegicus atonal homolog 7 (Drosophila) (predicted) (Atoh7_predicted), mRNA [XM_345102]	ref|XM_345102|Rn.133599 2|ens|ENSRNOT00000000432	Rn.133599	Atoh7_predicted	atonal homolog 7 (Drosophila) (predicted)	-	-	-	[Human, Mouse]Homologene:32338
11976.21	7334.77	1.63	NM_013015	Ptgds	Rattus norvegicus prostaglandin D2 synthase (Ptgds), mRNA [NM_013015]	ref|NM_013015|Rn.11400 5|gb|J04488|gb|M94134|ens|ENSRNOT00000020926	Rn.11400	Ptgds	prostaglandin D2 synthase	catalyzes conversion of prostaglandin H2 to prostaglandin D2, a major prostaglandin that mediates sleep, body temperature, hormone release, and odor responses [RGD]	Gene expression is regulated by Hes-1 through E-box and interleukin-1 beta via two NF-Kappa B elements in rat leptomeningeal cells.	KEGG pathway: Arachidonic acid metabolism	[Human, Mouse]Homologene:737

[請求項10] 下記の表45～59に示す遺伝子の塩基配列の少なくとも一部を含む核酸からなる群から選ばれる少なくとも1種の核酸、又は下記の表1に示す遺伝子によってコードされるタンパク質に対して特異的に結合する分子からなる群から選択される少なくとも1種の分子を含む、ラットの陽性感情を評価するための検査キット。

[表28]

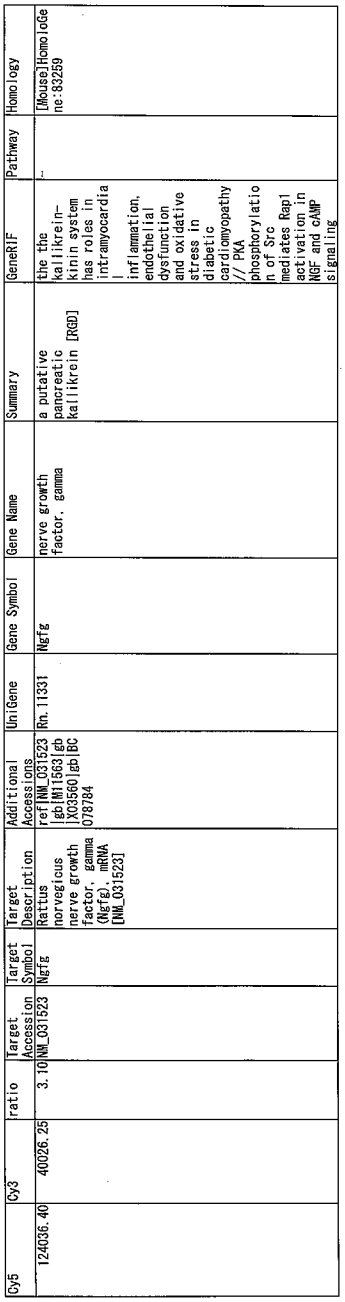
表45 Cに対してで発現増加した唾液腺の注目遺伝子
MAPキナーゼ脱リン酸化酵素活性 (GO ID: 17017)

Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Gene Symbol	Gene Name	Summary	GeneRIF	Pathway	Homology
593.12	329.46	1.80	NM_053769	Dusp1	Rattus norvegicus dual specificity phosphatase 1 (Dusp1), mRNA [NM_053769]	ref|NM_053769|gb|X94004|gb|S74351|ens|ENSRNOT00000005383	Rn.98260	Dusp1	dual specificity phosphatase 1	catalyzes the phosphorylation and inactivation of MAP kinase; may be involved in insulin mediated signaling [RGD]	Anandamide-induced rapid MKP-1 expression switches off MAPK signal transduction in microglial cells activated by stimulation of pattern recognition receptors.// findings suggest the involvement of MKP-1 in the regulation of the nocturnal AA-NAT signal//i	KEGG pathway: MAPK signaling pathway	[Human, Mouse]Homologene:3254
31.66	18.38	1.72	NM_022199	Dusp4	Rattus norvegicus dual specificity phosphatase 4 (Dusp4), mRNA [NM_022199]	ref|NM_022199|gb|U23438|ens|ENSRNOT00000016328	Rn.44407	Dusp4	dual specificity phosphatase 4	exhibits vanadate-sensitive phosphatase activity for MAP kinase; inhibits transcription of MAP kinase-dependent genes [RGD]	The 1(1)-imidazoline receptor in PC12 pheochromocytoma cells induces MKP-2 phosphatase.	KEGG pathway: MAPK signaling pathway	[Human, Mouse]Homologene:1065
26.05	15.22	1.71	AA924847	AA92484 7	AA924847 UI-R-A1-eb-a-04-0-UI.s1 UI-R-A1 Rattus norvegicus cDNA clone UI-R-A1-eb-a-04-0-UI.3' similar to gi [AA924847]	gb|AA924847|gb|AA963216|gb|AA963233|gb|BF417479	Rn.9470	Dhcr24	24-dehydrocholesterol reductase	-	identification, using a direct genetic screen, Seladin-1 (also known as Dhcr24) as a key mediator of Ras-induced senescence	-	[Human, Mouse]Homologene:8850
1298.38	861.58	1.51	NM_133578	Dusp5	Rattus norvegicus dual specificity phosphatase 5 (Dusp5), mRNA [NM_133578]	ref|NM_133578|gb|AF013144|gb|XM_346588|ens|ENSRNOT00000018889	Rn.10877	Dusp5	dual specificity phosphatase 5	inactivates MAP kinase; may be involved in long term potentiation [RGD]	-	KEGG pathway: MAPK signaling pathway	[Human, Mouse]Homologene:3256

[表29]

表46 Cに対して発現増加した唾液腺の注目遺伝子
組織カリクレイン活性 (GO ID: 4293)

Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Gene Symbol	Gene Name	Summary	GeneRIF	Pathway	Homology
32731.46	2472.09	13.24	NM_175759	Klks3	Rattus norvegicus kallikrein, submaxillary gland S3 (Klks3), mRNA [NM_175759]	ref|NM_175759 |gb|M11566|gb |BC061771|ens |ENSRNOT00000 025723	Rn.34627	Klks3	kallikrein, submaxillary gland S3	a kallikrein-related serine protease: first isolated from the rat submaxillary gland: acts as a potent enzymatic vasoconstrictor [RGD]	-	-	-
70828.46	5776.93	12.26	NM_012677	Ton	Rattus norvegicus tonin (Ton), mRNA [NM_012677]	ref|NM_012677 |gb|M11565|gb |M23878|ens|E NSRNOT0000002 5701	Rn.9882	Ton	tonin	serine protease involved in generating the octapeptide angiotensin II from precursors [RGD]	tonin may play a role in the process of heart hypertrophy// expression in the rat brain and mediation of the central production of angiotensin II	-	-
1543.60	182.10	8.48	NM_0010053 82	Klk12	Rattus norvegicus glandular kallikrein 12, submandibular/renal (Klk12), mRNA [NM_0010053822]	ref|NM_001005 382|gb|XM_218 567|gb|M19648 |ens|ENSRNOT0 0000025631	Rn.141980	Klk12	glandular kallikrein 12, submandibular/renal	-	-	-	[Human, Mouse]HomoloGene:81694
88887.34	13877.73	6.41	XM_214931	RGD:735 032	PREDICTED: Rattus norvegicus kallikrein (LOC292872), mRNA [XM_214931]	ref|XM_214931 |gb|L33840|gb |M11564|ens|E NSRNOT0000002 5777	Rn.107068	-	kallikrein	a putative kallikrein-related serine protease first isolated from the rat submaxillary gland [RGD]	-	-	-



Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Gene Symbol	Gene Name	Summary	GeneRIF	Pathway	Homology
124036.40	40026.25	3.10	NM_031523	Ngfg	Rattus norvegicus nerve growth factor, gamma (Ngfg), mRNA [NM_031523]	ref|NM_031523 |gb|M11563|gb |X03560|gb|BC 078784	Rn.11331	Ngfg	nerve growth factor, gamma	a putative pancreatic kallikrein [RGD]	the the kallikrein-kinin system has roles in intramyocardial inflammation, endothelial dysfunction and oxidative stress in diabetic cardiomyopathy // PKA phosphorylation of Src mediates Rap1 activation in NGF and cAMP signaling		[Mouse]Homologene-83259

[表30]

表47 Gに対して発現増加した唾液腺の注目遺伝子
細胞外成分 (GO ID: 5576, 44421, 5615)

Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Gene Symbol	Gene Name	Summary	GeneRIF	Pathway	Homology
42529.56	9583.96	4.44	NM_001013067	NM_001013067	Rattus norvegicus kallikrein 6 (predicted) (Klk6_predicted), mRNA [NM_001013067]	ref|NM_001013067|gb|AAH85932|gb|AAI24932|gb|EDM27217|ensembl|ENSRNOT00000025715	Rn.79264	Klk6_predicted	kallikrein 6 (predicted)	–	–	–	[Mouse]HomoloGene:83265
6218.28	1414.59	4.40	NM_012842	Egf	Rattus norvegicus epidermal growth factor (Egf), mRNA [NM_012842]	ref|NM_012842|gb|AAA41128|gb|AAH60484|gb|BC003621|gb|AAI14030|gb|AAI14063	Rn.6075	Egf	epidermal growth factor	binds tha epidermal growth factor receptor; may play a role in MAP kinase mediated signaling pathways [RGD]	EGF-based signaling cascades phosphorylate Cavl and have roles in caveolae assembly// ERK1/2 mediates EGF-induced rapid Rb phosphorylation at Ser780 and Ser795// Neo-natal rats with intestinal injury have significantly lower levels of ileum EGF.// Linear	KEGG pathway: Cytokine-cytokine receptor interaction// KEGG pathway: Focal adhesion// KEGG pathway: Gap junction// KEGG pathway: MAPK signaling pathway// KEGG pathway: Regulation of actin cytoskeleton	[Human, Mouse]HomoloGene:1483
2022.83	528.42	3.83	XM_342575	Svs6_predicted	PREDICTED: Rattus norvegicus seminal vesicle secretion 6 (predicted) (Svs6_predicted), mRNA [XM_342575]	ref|XM_342575|ens|ENSRNOT00000018510|tc|TC51897|tc|TC518976	Rn.14520	Svs6_predicted	seminal vesicle secretion 6 (predicted)	–	–	–	[Mouse]HomoloGene:49347
165383.40	45178.89	3.66	NM_022708	Pip	Rattus norvegicus prolactin induced protein (Pip), mRNA [NM_022708]	ref|NM_022708|gb|AF054008|gb|AF054270|ens|ENSRNOT00000021576|tc|TC541374	Rn.78367	Pip	prolactin induced protein	secretory protein localized to acinar cells of neonatal and adult submandibular and parotid glands, also expressed in sublingual glands [RGD]	–	–	[Human, Mouse]HomoloGene:1990

Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Gene Symbol	Gene Name	Summary	GeneRIF	Pathway	Homology
213570.10	61274.66	3.49	NM_133513	Muc10	Rattus norvegicus mucin 10, submandibular gland salivary mucin (Muc10), mRNA [NM_133513]	ref|NM_133513|gb|U03407|gb|U03442|ens|ENSRNOT00000032459	Rn.10113	Muc10	mucin 10, submandibular gland salivary mucin	a submandibular gland apomucin [RGD]	-	-	[Mouse]HomoloGene:69025
267.70	82.81	3.23	AA963004	AA96300 4	Rattus norvegicus UI-R-E1-gd-d-04-0-UI.s1 UI-R-E1 Rattus norvegicus cDNA clone UI-R-E1-gd-d-04-0-UI 3', mRNA sequence [AA963004]	gb|AA963004|tc|TC55441 3	Rn.24539	Tgfb2	transforming growth factor, beta 2	binds the transforming growth factor-beta receptor: plays a role in regulation of cell growth and proliferation: may be involved in mesenchymal-epithelial cell interactions during development [RGD]	the pro-inflammatory cytokine MIF can shift the cytokine balance from the immunosuppressive state towards an inflammatory reaction, potentially through the inhibition of TGF-beta2 secretion by testicular peritubular cells.// TGF-beta2 mRNA and protein exp	KEGG pathway: Cell cycle// KEGG pathway: MAPK signaling pathway// KEGG pathway: TGF-beta signaling pathway	[Human, Mouse]HomoloGene:2432
277.61	92.00	3.02	NM_080411	Gpr83	Rattus norvegicus G protein-coupled receptor 83 (Gpr83), mRNA [NM_080411]	ref|NM_080411|ref|XM_579605|gb|AY029071|gb|X|M_346815	Rn.63075	Gpr83	G protein-coupled receptor 83	glucocorticoid-induced receptor found in brain and may be involved in behavioral sensitization [RGD]	-	KEGG pathway: Neuroactive ligand-receptor interaction	-
42529.56	9583.96	4.44	NM_001013067	NM_0010 13067	Rattus norvegicus kallikrein 6 (predicted) (Klk6_predicted), mRNA [NM_001013067]	ref|NM_001013067|gb|XM_214932|gb|M27217|ens|ENSRNOT00000025715	Rn.79264	Klk6_predicted	kallikrein 6 (predicted)	-	-	-	[Mouse]HomoloGene:83265
164227.44	57850.42	2.84	NM_172065	Prpg2	Rattus norvegicus proline-rich proteoglycan 2 (Prpg2), mRNA [NM_172065]	ref|NM_172065|gb|M11891|gb|L17318|ens|ENSRNOT00000013943	Rn.29950	Prpg2	proline-rich proteoglycan 2	member of a family of proline rich proteins that are induced in salivary gland by isoproterenol treatment and by feeding tannins [RGD]	-	-	-

Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Gene Symbol	Gene Name	Summary	GeneRIF	Pathway	Homology
144.02	53.99	2.67	NM_012996	Oxt	Rattus norvegicus oxytocin (Oxt), mRNA [NM_012996]	ref|NM_0129961|gb|M25647|ens|ENSRNOT00000002887|tc|TC57290	Rn.48915	Oxt	oxytocin	hormone involved in contraction of smooth muscle during parturition and lactation; gene encodes two proteins, oxytocin and neurophysin I [RGD]	oxytocin has a role in gonadal steroid modulation of stress-induced hypothalamo-pituitary-adrenal activity and anxiety behavior// Oxytocin may strengthen mother-infant bond formation partly by acting through brain areas involved in regulating olfactory di	KEGG pathway: Neuroactive ligand-receptor interaction	[Human, Mouse]HomoloGene: 55494
80.76	31.28	2.58	NM_053738	Wif1	Rattus norvegicus Wnt inhibitory factor 1 (Wif1), mRNA [NM_053738]	ref|NM_053738|gb|AY030278|gb|BC072473|ens|ENSRNOT00000006426	Rn.74256	Wif1	Wnt inhibitory factor 1	human homolog has decreased mRNA expression in some prostate cancers and other cancers; may act as a secreted inhibitor of the Wnt signaling pathway [RGD]	GLT mRNA was translated in Wnt-1-expressing G6 cells when the GLT mRNA required no splicing before translation occurred	KEGG pathway: Wnt signaling pathway	[Human, Mouse]HomoloGene: 31430
8361.31	3258.64	2.57	XM_341400	Rbp3	PREDICTED: Rattus norvegicus retinol binding protein 3, interstitial (Rbp3), mRNA [XM_341400]	ref|XM_341400|gb|X56150|gb|X69523|ens|ENSRNOT00000027446	Rn.41214	Rbp3	retinol binding protein 3, interstitial	may play a role in vision [RGD]	-	-	[Human, Mouse]HomoloGene: 9261
4805.70	1924.09	2.50	AB087404	Gdf5	Rattus norvegicus gdf-5 gene for growth and differentiation factor-5, partial cds [AB087404]	gb|AB087404|tc|NP495152	Rn.12782	Gdf5	growth differentiation factor 5	member of the bone morphogenetic protein (BMP) family and the TGF-beta superfamily; regulates cell growth and differentiation; involved with tendon and ligament formation [RGD]	Expression of GDF-5 in developing rat ventral mesencephalon (VM) was found to begin at embryonic day (E) 12 and peak on E14. In the adult rat was found in heart and brain, being expressed in many areas of the brain, including striatum and midbrain.// invol	-	-

Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Gene Symbol	Gene Name	Summary	GeneRIF	Pathway	Homology
2733.04	1114.24	2.45	NM_024136	Erabp	Rattus norvegicus epididymal retinoic acid-binding protein (Erabp), mRNA [NM_024136]	ref|NM_0241 36|gb|X5983 2|gb|M12790 |tc|TC56991 4	Rn. 10362	Erabp	epididymal retinoic acid-binding protein	has a low galactosyltransferase modifying activity in vitro: however, this activity is predicted to be too low for physiological significance [RGD]	-	-	[Mouse]HomoloGene :7305
781.76	327.17	2.39	NM_057151	Ccl17	Rattus norvegicus small inducible cytokine subfamily A (Cys-Cys), member 17 (Ccl17), mRNA [NM_057151]	ref|NM_0571 68|ens|ENS RNOT0000002 1842|tc|TC5 61888	Rn. 46679	Ccl17	chemokine (C-C motif) ligand 17	a thymus and activation-regulated chemokine [RGD]	Our data indicate that instead of Th2 cells, airway epithelial cells expressing CCR4 might be the principal targets for MDC and TARC released from alveolar macrophages during cigarette smoke-induced airway inflammation.	-	[Human, Mouse]HomoloGene: 2246
200.79	88.11	2.28	NM_019189	Hapln1	Rattus norvegicus hyaluronan and proteoglycan link protein 1 (Hapln1), mRNA [NM_019189]	ref|NM_0191 89|ens|ENSR NOT0000042 958|ens|ENS RNOT0000004 3196|gb|M22 340	Rn. 50531	Hapln1	hyaluronan and proteoglycan link protein 1	stabilizs cartilage proteoglycan/hyaluronic acid aggregates by binding to each component [RGD]	study represents the first report that follicle stimulating hormone amplifies insulin-like growth factor-1-mediated cartilage link protein Crtl1 production, possibly via phosphatidylinositol 3-kinase-Akt sigmaling cascades in rat granulosa cells	-	[Human, Mouse]HomoloGene: 1420
395.11	173.49	2.28	BM388083	BM38808 3	BM388083 UI-R-DM1-cjz-d-11-0-UI.s1 UI-R-DM1 Rattus norvegicus cDNA clone UI-R-DM1-cjz-d-11-0-UI 3', mRNA sequence [BM388083]	gb|BM388083 |gb|BF41687 7	Rn. 41133	Sorcs2_predicted	sortilin-related VPS10 domain containing receptor 2 (predicted)	-	-	-	[Mouse]HomoloGene :75305

Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Gene Symbol	Gene Name	Summary	GeneRIF	Pathway	Homology
44.00	19.81	2.22	NM_053504	Prss12	Rattus norvegicus protease, serine, 12 (Prss12), mRNA [NM_053504]	ref|NM_053504|gb|AAJ31104|ens|ENSRNOT00000021116	Rn.86653	Prss12	peptidase, serine, 12 (neurotrypsin, motopsin)	mouse homolog is a serine protease: may be involved in learning and memory [RGD]	-	-	[Human, Mouse]HomoloGene: 7490
			NM_016989	Adcyap1	Rattus norvegicus adenylate cyclase activating polypeptide 1 (Adcyap1), mRNA [NM_016989]	ref|NM_016989|ref|XM_579383|gb|M63006|gb|AAL346860	Rn.37400	Adcyap1	adenylate cyclase activating polypeptide 1	regulatory protein that stimulates cell proliferation, induces differentiation, modulates neurotransmitter release, vasodilation, bronchodilation, and hormone release, and suppresses inflammatory responses [RGD]	These results indicate that a large number of PACAP neurons and a small number of BDNF neurons of the VMH project to the MPG.// The specificity of PAC1 receptor participation in pituitary adenylate cyclase-activating polypeptide (PACAP)-facilitated sex be	KEGG pathway: Neuroactive ligand-receptor interaction	[Human, Mouse]HomoloGene: 869
			NM_031736	Slc27a2	Rattus norvegicus solute carrier family 27 (fatty acid transporter), member 2 (Slc27a2), mRNA [NM_031736]	ref|NM_031736|ref|XM_579526|gb|D85100|gb|AAL346669	Rn.3608	Slc27a2	solute carrier family 27 (fatty acid transporter), member 2	has very long-chain acyl-CoA synthetase activity; may play a role in fatty acid metabolism [RGD]	in response to an increase of cellular cholesterol, fatty acid transporter is translocated from cytosol to membranes of type II pneumocytes.	KEGG pathway: Alkaloid biosynthesis II// KEGG pathway: Caprolactam degradation// KEGG pathway: Ethylbenzene degradation// KEGG pathway: Limonene and pinene degradation// KEGG pathway: Propanoate metabolism	-
			NM_147165	Gpx6	Rattus norvegicus glutathione peroxidase 6 (Gpx6), mRNA [NM_147165]	ref|NM_147165|gb|AA799363	Rn.9852	Gpx6	glutathione peroxidase 6	a lipophilic molecule carrier in olfactory mucosa [RGD]	-	KEGG pathway: Arachidonic acid metabolism// KEGG pathway: Glutathione metabolism	[Human, Mouse]HomoloGene: 25418

Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Gene Symbol	Gene Name	Summary	GeneRIF	Pathway	Homology
			AA875449	AA875449	AA875449 UI-R-E0-op-b-02-0-UI.s1 UI-R-E0 Rattus norvegicus cDNA clone UI-R-E0-op-b-02-0-UI 3' similar to gi [AA875449]	gb|AA875449	Rn. 2923	Ppif	peptidylprolyl isomerase F (cyclophilin F)	mitochondrial isozyme of peptidyl-prolyl cis-trans-isomerase; enzyme activity is inhibited by cyclosporin A [RGD]	The present study examines the effects of cyclophilin-D on mitochondrial permeability transition and lethal cell injury.	-	[Human, Mouse]HomoloGene: 38696
			BE111679	BE111679	BE111679 UI-R-BJ1-avv-e-09-0-5 UI.s1 UI-R-BJ1 Rattus norvegicus cDNA clone UI-R-BJ1-avv-e-09-0-UI 3', mRNA sequence [BE111679]	gb|BE111679 |gb|AA892395 |gb|AI44098	Rn. 13642	Slc20a2	solute carrier family 20, member 2	cellular receptor which mediates virus entry [RGD]	PiT-1 (Slc20a1) and PiT-2 (Slc20a2) were detected at the basolateral membrane of hepatocytes.// mRNA expression level of Glvr-2 was increased by the addition of inorganic phosphate (Pi) in bone marrow stromal cells	-	[Human, Mouse]HomoloGene: 68531
			NM_013107	Bmp6	Rattus norvegicus bone morphogenetic protein 6 (Bmp6), mRNA [NM_013107]	ref|NM_0131 07|gb|AY184 240|gb|X588 30|gb|XM_34 1514	Rn. 40476	Bmp6	bone morphogenetic protein 6	plays a role in induction of osteogenesis: may be involved in liver growth and differentiation in response to injury [RGD]	Expression of BMP-6 by tibial marrow megakaryocytes in 5-week-old rats suggests a mechanism by which megakaryocyte-derived BMPs may promote bone growth and repair	KEGG pathway: Hedgehog signaling pathway// KEGG pathway: TGF-beta signaling pathway	[Human, Mouse]HomoloGene: 1300
			XM_213416	Spaca3_predicted	PREDICTED: Rattus norvegicus sperm acrosome associated 3 (predicted) (Spaca3_predicted), mRNA [XM_213416]	ref|XM_2134 16|ens|ENSR NOT00000009 172|tc|TC52 7499	Rn. 47764	Spaca3_predicted	sperm acrosome associated 3 (predicted)	-	-	-	[Human, Mouse]HomoloGene: 18365

Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Gene Symbol	Gene Name	Summary	GeneRIF	Pathway	Homology
			NM_138902	Ear11	Rattus norvegicus eosinophil-associated, ribonuclease A family, member 11 (Ear11), mRNA [NM_138902]	ref|NM_138902|gb|D88581|ens|ENSRNOG00000008571|tc|TC6573	Rn. 10626	Ear11	eosinophil-associated, ribonuclease A family, member 11	cationic protein with similarity to human ECP; also has similarity to human eosinophil-derived neurotoxin and human ribonuclease k6 [RGD]	-	-	-
			AF475093	AF47509 3	Rattus norvegicus liver regeneration-related protein 1 (Lrrp1) mRNA, complete cds. [AF475093]	gb|AF475093|tc|NRP59247	Rn. 3040	Sdhd	succinate dehydrogenase complex, subunit D, integral membrane protein	human homolog is a subunit of succinate-ubiquinone oxidoreductase, which plays a role in mitochondrial electron transport [RGD]	-	KEGG pathway: Citrate cycle (TCA cycle)// KEGG pathway: Oxidative phosphorylation	[Human, Mouse]HomoloGene: 37718
			NM_023962	Pdgfd	Rattus norvegicus platelet-derived growth factor, D polypeptide (Pdgfd), mRNA [NM_023962]	ref|NM_023962|gb|AB062170|tc|TC571827	Rn. 64403	Pdgfd	platelet-derived growth factor, D polypeptide	a growth factor with mitogenic activity in the central nervous system [RGD]	analysis of expression of PDGF-A, -B, -C and -D and the PDGF-receptors alpha and beta in activated rat hepatic stellate cells// These results support the fact that PDGF-D is involved in the formation of neointimal hyperplasia induced by balloon catheter i	KEGG pathway: Focal adhesion// KEGG pathway: Gap junction	[Human, Mouse]HomoloGene: 11875
			BE112231	Fcna	UI-R-BJ1-avl-c-05-0-UI.s1 UI-R-BJ1 Rattus norvegicus cDNA clone UI-R-BJ1-avl-c-05-0-UI 3', mRNA sequence. [BE112231]	gb|BE112231|gb|AI10459 3|gb|AI10720 87	Rn. 20051	Fcna	ficolin A	mouse homolog is a plasma protein that binds elastin and GlcNAc [RGD]	-	-	[Mouse]HomoloGene :74880

Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Gene Symbol	Gene Name	Summary	GeneRIF	Pathway	Homology
			NM_021698	F13a	Rattus norvegicus coagulation factor XIII, A1 subunit (F13a), mRNA [NM_021698]	ref|NM_0216 98|gb|Y1250 2|gb|AW9190 18|ens|ENSR NOT00000021 568	Rn. 42925	F13a1	coagulation factor XIII, A1 subunit	enhances gastric mucosa healing; reduces endothelial permeability [RGD]	-	KEGG pathway: Complement and coagulation cascades	[Human, Mouse]HomoloGene: 20077
			NM_080394	Reln	Rattus norvegicus reelin (Reln), mRNA [NM_080394]	ref|NM_0803 94|gb|AB062 680|gb|AW14 0590|tc|TC5 72679	Rn. 16177	Reln	reelin	regulates neuronal cell migration during development; plays a role in locomotor behavior [RGD]	reelin, which is expressed along the route of the migrating GnRH neurons, has an inhibitory role in guiding GnRH neurons to the basal forebrain// differentiation factor for radial glial cells of dentate gyrus and as a positional cue for radial fiber orien	KEGG pathway: Cell Communication// KEGG pathway: ECM-receptor interaction// KEGG pathway: Focal adhesion	[Human, Mouse]HomoloGene: 3699
			AA891661	AA89166 1	AA891661 EST195464 Normalized rat kidney, Bento Soares Rattus sp. cDNA clone RK1AF23 3' end, mRNA sequence [AA891661]	gb|AA891661	Rn. 1618	Aqp1	aquaporin 1	integral membrane protein that is a major water transport molecule in the kidney proximal tubule and red blood cells [RGD]	data indicate that the ar/R constriction is a major checkpoint for solute permeability, and that the exquisite electrostatic proton barrier in AQPs comprises both the NPA constriction as well as the ar/R constriction// AQP1 and AQP6, and the heterotrimeri	-	[Human, Mouse]HomoloGene: 68051
			XM_225585	Mrc1_pr edicted	PREDICTED: Rattus norvegicus mannose receptor, C type 1 (predicted) (Mrc1_predicted), mRNA [XM_225585]	ref|XM_2255 85|gb|CB544 854|ens|ENS RNOT00000002 6736|tc|TC5 55463	Rn. 9197	Mrc1_predicted	mannose receptor, C type 1 (predicted)	-	-	-	-

Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Gene Symbol	Gene Name	Summary	GeneRIF	Pathway	Homology
			X61479	X61479	RRCSF1 Rat mRNA for CSF-1 receptor [X61479]	gb|X61479	-	Csf1r	colony stimulating factor 1 receptor	may modiate normal and neoplastic growth of muscular cells [RGD]	the CSF1R mutation of Asp-802 to Val confers resistance to kinase inhibitor imatinib	-	[Human, Mouse]HomoloGene: 3817
			XM_573463	XM_573463	PREDICTED: Rattus norvegicus similar to complement component factor h (LOC498240), mRNA [XM_573463]	ref|XM_573463.1|gb|BC089845|ENSRNOT00000029294|ENSRNOT00000029294	Rn.13761	Cfh	complement component factor H	regulator of complement cascade activation [RGD]	Glomerular epithelial cells(GEC) and glomeruli express factor H mRNA and protein. Up-regulated in membranous nephropathy. Likely direct response of GEC to complement attack and may represent protective response.// Complement Factor H is highly expressed i	KEGG pathway: Complement and coagulation cascades	[Human, Mouse]HomoloGene: 20086
			NM_021682	Negr1	Rattus norvegicus neuronal growth regulator 1 (Negr1), mRNA [NM_021682]	ref|NM_021682.1|gb|AB017139|TC572970	Rn.42884	Negr1	neuronal growth regulator 1	glycosylphosphatidylinositol-anchored cell adhesion protein [RGD]	--	KEGG pathway: Cell adhesion molecules (CAMs)	[Human, Mouse]HomoloGene: 41447
			NM_031590	Wisp2	Rattus norvegicus WNT1 inducible signaling pathway protein 2 (Wisp2), mRNA [NM_031590]	ref|NM_031590.1|gb|AF259981|gb|BC091814|ENSRNOT00000014346	Rn.53991	Wisp2	WNT1 inducible signaling pathway protein 2	involved in negative regulation of cell growth: mRNA expression is lost upon cell transformation induced by activated H-ras oncogene and inactivated p53 tumor supressor [RGD]	data indicate that CCN5 protein is positively regulated by estrogen in the rat uterus and suggests that this gene may play an important role in maintaining normal uterine physiology	-	[Human, Mouse]HomoloGene: 2982

Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Gene Symbol	Gene Name	Summary	GeneRIF	Pathway	Homology
			NM_053856	Scg3	Rattus norvegicus secretogranin III (Scg3), mRNA [NM_053856]	ref|NM_053856|gb|U00298|tc|TC5688|6	Rn.11093	Scg3	secretogranin III	component of intracellular dense core vesicles [RGD]	SgIII and CPE form the separate functional sorting complex by anchoring to cholesterol-rich SG membranes, and POMC-derived peptides are transferred from CPE to SgIII, and subsequently to CgA.// SgIII is closely associated with the secretory granule membra	-	[Human, Mouse]HomoloGene: 7526
			AA924847	AA924847	AA924847 UI-R-A1-eb-a-04-0-UI.s1 UI-R-A1 Rattus norvegicus cDNA clone UI-R-A1-eb-a-04-0-UI 3' similar to gi [AA924847]	gb|AA924847|gb|AA96321|gb|AA9632|gb|BF417479	Rn.9470	Dhcr24	24-dehydrocholesterol reductase	-	identification. using a direct genetic screen, Seladin-1 (also known as Dhcr24) as a key mediator of Ras-induced senescence	-	[Human, Mouse]HomoloGene: 8850
			B6664056	B6664056	B6664056 DRAACD11 Rat DRG Library Rattus norvegicus cDNA clone DRAACD11 5', mRNA sequence [BG664056]	gb|B6664056|tc|TC55234|3	Rn.10796	Ndufa9	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 9	-	-	-	-
			XM_343373	RGD1310431_predicted	PREDICTED: Rattus norvegicus similar to sialic-acid 4290 0-acetylesterase (predicted) (LOC363045), mRNA [XM_343373]	ref|XM_343373|gb|CB546057|Ens|ENSRNOT00000044290|tc|TC559384	Rn.21775	Siae_predicted	sialic acid acetylesterase (predicted)	-	-	-	[Human, Mouse]HomoloGene: 8001

Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Gene Symbol	Gene Name	Summary	GeneRIF	Pathway	Homology
			L14933	Pcsk5	Rattus norvegicus convertase PC5 mRNA, partial cds [L14933]	gb|L14933|g b|XM_342032 |ens|ENSRNO T0000001616 4|tc|TC5711 52	Rn. 10400 2	Pcsk5	proprotein convertase subtilisin/ kexin type 5	may play a role in peptide processing and maturation [RGD]	Data suggest that inhibition of furin and PC5 and resulting inhibition of insulin-like growth factor 1 receptor (IGF-1R) activation can inhibit IGF-I-induced membrane-type 1 matrix metalloproteinase activity in vascular smooth muscle cells.// Activation o	-	[Human, Mouse]HomoloGene: 21244
			NM_133538	Il13ra2	Rattus norvegicus interleukin 13 receptor, alpha 2 (Il13ra2), mRNA [NM_133538]	ref|NM_1335 38|ref|XM_5 79624|gb|AF 448818|gb|X M_346867	Rn. 16230 8	Il13ra2	interleukin 13 receptor, alpha 2	used as a target for immunotherapeutic approaches for treating brain tumors [RGD]	gene sequence and tissue distribution of IL-13Ralpha2 in the rat	KEGG pathway: Jak-STAT signaling pathway	[Human, Mouse]HomoloGene: 534
			NM_00100340 4	Il22ra2	Rattus norvegicus interleukin 22 receptor, alpha 2 (Il22ra2), mRNA [NM_0010034 04]	ref|NM_0010 03404|gb|AJ 565485|gb|X M_344797|en s|ENSRNOT00 000016354	Rn. 13127	Il22ra2	interleukin 22 receptor, alpha 2	-	-	-	[Human, Mouse]HomoloGene: 18657
			NM_00101304 5	NM_0010 13045	Rattus norvegicus chemokine (C-C motif) ligand 24 (predicted) (Ccl24_pred icted), mRNA [NM_0010130 45]	ref|NM_0010 13045|ref|X M_573388|gb |XM_213743| ens|ENSRNOT 00000001963	Rn. 13882 2	Ccl24	chemokine (C-C motif) ligand 24	-	-	-	[Mouse]HomoloGene :83177

Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Gene Symbol	Gene Name	Summary	GeneRIF	Pathway	Homology
			NM_019192	Sepp1	Rattus norvegicus selenoprotein P, plasma, 1 (Sepp1), mRNA [NM_019192]	ref|NM_0191 92|gb|M6357 4|tc|TC6166 88	Rn. 1451	Sepp1	selenoprotein P, plasma, 1	plasma glycoprotein that contains ten selenocysteine residues; may play a role in response to oxidative stress [RGD]	selenenylsulfide linkages Sec304-Cys314 and Cys306-Sec316 were present: selenoprotein P contains these two selenenylsulfide bonds// mass spectrometric characterization of full-length protein and three isoforms shortened at the C terminus	-	[Human, Mouse]HomoloGene: 49257
			NM_024358	Notch2	Rattus norvegicus notch gene homolog 2 (Drosophila) (Notch2), mRNA [NM_024358]	ref|NM_0243 58|gb|M9366 1|ens|ENSRN OT0000002257 |ens|ENSR NOT0000000045 062	Rn. 65930	Notch2	notch gene homolog 2 (Drosophila)	transmembrane protein that may be involved in cellular interactions that specify cell fate [RGD]	-	KEGG pathway: Dorso-ventral axis formation// KEGG pathway: Notch signaling pathway	[Human, Mouse]HomoloGene: 7865
			NM_053289	Pap	Rattus norvegicus pancreatitis-associated protein (Pap), mRNA [NM_053289]	ref|NM_0532 89|gb|S77741 3|gb|S43715 |ens|ENSRNO T0000000821 2	Rn. 9727	Pap	pancreatitis-associated protein	lectin-related secretory protein: may be involved in stress response to control bacterial proliferation during acute pancreatitis [RGD]	These results suggest that Reg family members would be new mediators among injured neurons and glial cells, and may play pivotal roles during nerve regeneration.// Sepsis resulted in an up-regulation of PAP-1 gene expression and increase in its protein le	-	[Human, Mouse]HomoloGene: 49257

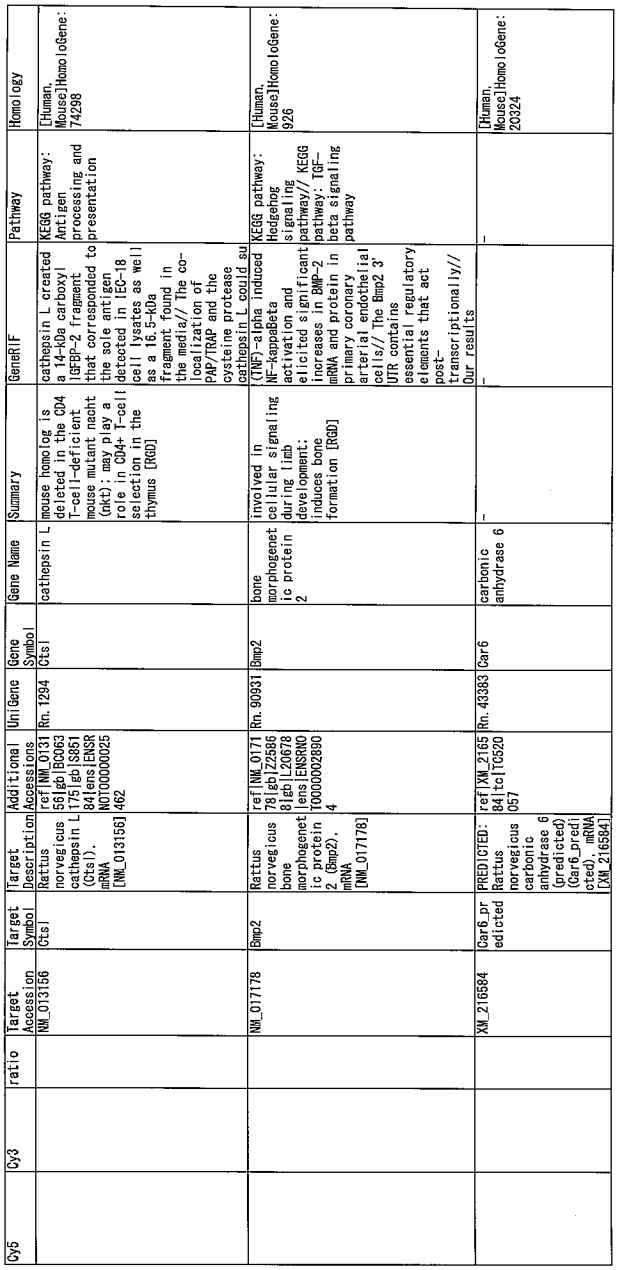
Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Gene Symbol	Gene Name	Summary	GeneRIF	Pathway	Homology
			XM_346464	Slit2	PREDICTED: Rattus norvegicus slit homolog 2 (Drosophila) (Slit2), mRNA [XM_346464]	ref|XM_3464 64|ens|ENSR NOT00000005 477|tc|TC55 7526	Rn. 46211	Slit2	slit homolog 2 (Drosophila)	acts as a ligand for glypican-1, a heparan sulfate proteoglycan; may play a role in neurogenesis and midline development [RGD]	Slit2 inhibits vascular smooth muscle cell migration by suppressing small GTPase Rac1 activation.// disruption of the continuity of basal lamina tubes induces the expression of slit2 in Schwann cells during peripheral nerve regeneration// Slit-2 inhibited	-	[Human, Mouse]HomoloGene: 3516
			NM_172328	Tac4	Rattus norvegicus tachykinin 4 (Tac4), mRNA [NM_172328]	ref|NM_1723 28|gb|AF521 561|gb|AY47 1575|ens|EN SRNOT000000 35023	Rn. 91139	Tac4	tachykinin 4	human and mouse homologs are processed to form hemokinin-1 (HK-1), a substance P-like peptide that displays high affinity binding to the neurokinin 1 (NK-1) receptor [RGD]	-	KEGG pathway: Neuroactive ligand-receptor interaction	[Mouse]HomoloGene :50484
			NM_017024	Lcat	Rattus norvegicus lecithin cholesterol acyltransfe rase (Lcat), mRNA [NM_017024]	ref|NM_0170 24|gb|X5409 6|gb|U62803 |ens|ENSRNO T0000002668 5	Rn. 10481	Lcat	lecithin cholesterol acyltransfe rase	enzyme involved in the metabolism of plasma lipoproteins [RGD]	-	KEGG pathway: Glycerophosphol ipid metabolism	[Human, Mouse]HomoloGene: 68042
			XM_573983	Tgfbi	PREDICTED: Rattus norvegicus transforming growth factor, beta induced, 68 kDa (Tgfbi), mRNA [XM_573983]	ref|XM_5739 83|gb|AW141 699|tc|TC51 8684	Rn. 1046	Tgfbi	transforming growth factor, beta induced	mouse homolog is an extracellular matrix protein; human homolog is associated with hereditary corneal dystrophies [RGD]	These results suggest that mechanical strain negatively regulates the terminal differentiation of chondrocytes through the signal pathway of TGF-ss with the induction of RGD-CAP.// Pravastatin significantly inhibited beta-h3 mRNA production and gene exp	-	[Human, Mouse]HomoloGene: 37294

Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Gene Symbol	Gene Name	Summary	GeneRIF	Pathway	Homology
			NM_053595	Pgf	Rattus norvegicus placental growth factor (Pgf), mRNA [NM_053595]	ref|NM_0535 95|gb|L4003 01|gb|BC0870 06|ens|ENSR NOT00000007 790	Rn. 6960	Pgf	placental growth factor	forms a heterodimer with VEGF: may play a role in vascular endothelial cell proliferation [RGD]	vascular endothelial growth factor and placental growth factor-2 effects in dorsal root ganglion neurons are mediated via neuropilin-1 and cyclooxygenase-derived prostanoid production	KEGG pathway: Focal adhesion	[Human, Mouse]HomoloGene: 1978
			NM_001001970	RGD:1303064	Rattus norvegicus lymphocyte antigen 6 complex, locus G6D (Ly6g6d), mRNA [NM_001001970]	ref|NM_0010 01970|gb|XM_ 227992|ens |ENSRNOT000 00001120|tc |NP1090614	Rn. 14639	-	lymphocyte antigen 6 complex, locus G6D	putative member of the Ly-6 superfamily, a group of GPI-anchored cell surface proteins; mouse human and rat homologs all localized to the MHC class III region [RGD]	-	--	[Human, Mouse]HomoloGene: 76442
			NM_022177	Cxcl12	Rattus norvegicus chemokine (C-X-C motif) ligand 12 (Cxcl12), mRNA [NM_022177]	ref|NM_0221 77|gb|AF209 976|gb|BC007 873|gb|AW9 16737	Rn. 54439	Cxcl12	chemokine (C-X-C motif) ligand 12	a chemoattractant molecule: involved in cell migration [RGD]	Our results show that SDF-1alpha induces, via presynaptic mechanisms, alterations in the excitability of DA neurones as confirmed by current-clamp experiments.// Myocardial SDF-1 expression was increased only in the early phase post myocardial infarct.// S	KEGG pathway: Axon guidance// KEGG pathway: Cytokine-cytokine receptor interaction// KEGG pathway: Leukocyte transendothelial migration	[Human, Mouse]HomoloGene: 507

Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Gene Symbol	Gene Name	Summary	GeneRIF	Pathway	Homology
			NM_001012459	Sogf	Rattus norvegicus stem cell growth factor (Sogf), mRNA [NM_001012459]	ref|NM_001012459.1|gb|XM_344888.3|gb|BC090344.1|ens|ENSRNOT00000025949	Rn.16242	Clec11a	C-type lectin domain family 11, member a	growth factor for primitive hematopoietic progenitor cells [RGD]	Dramatic increase in c-kit expression observed in the rat carotid artery after balloon injury suggests SCF/c-kit signaling may affect smooth muscle cell function via an autocrine pathway.// negative feedback with kit ligand (Sogf) and oocyte BNP15 regulat	-	[Human, Mouse]HomoloGene: 2236
			NM_031701	Cldn5	Rattus norvegicus claudin 5 (Cldn5), mRNA [NM_031701]	ref|NM_031701.1|gb|AF241260.1|gb|AW_344038.1|gb|BC082073	Rn.17420	Cldn5	claudin 5	a component of tight junctions in myelinating Schwann cells [RGD]	Induction of wild-type claudin-5 is sufficient to reconstitute the paracellular barrier against inulin (5 kDa), but not mannitol (182 Da), in leaky rat lung epithelial cells// MUPP1 and claudin-5 colocalized in the incisures, and the COOH-terminal region	KEGG pathway: Cell adhesion molecules (CAMs)// KEGG pathway: Leukocyte transendothelial migration// KEGG pathway: Tight junction	[Human, Mouse]HomoloGene: 2459
			NM_022005	Fxyd6	Rattus norvegicus FXYD domain-containing ion transport regulator 6 (Fxyd6), mRNA [NM_022005]	ref|NM_022005.1|gb|AB030905.1|gb|BC027328.1|AF142439	Rn.839	Fxyd6	FXYD domain-containing ion transport regulator 6	(The rest is omitted.)	findings suggest that Php may play an important role in the excitability of neurons in the central nervous system during postnatal development, as well as those in the adult brain	-	[Human, Mouse]HomoloGene: 11090

Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Gene Symbol	Gene Name	Summary	GeneRIF	Pathway	Homology
			NM_017081	Hsd11b2	Rattus norvegicus hydroxysteroid 11-beta dehydrogenase 2 (Hsd11b2), mRNA [NM_017081]	ref|NM_017081|gb|U12242|gb|BC087023|ens|ENSRNOT00000023130	Rn.10186	Hsd11b2	hydroxysteroid 11-beta dehydrogenase 2	catalyzes the conversion of cortiosterone to 11-dehydrocorticosterone [RGD]	increased apical targeting of ENaC subunits combined with diminished abundance of 11betaHSD2 may contribute to sodium retention associated with HgCl(2)-induced nephrotic syndrome.// Increased apical targeting of epithelial channel subunits subunits combin	KEGG pathway: Androgen and estrogen metabolism// KEGG pathway: C21-Steroid hormone metabolism	[Human, Mouse]HomoloGene: 20088
			XM_017066	Ptn	Rattus norvegicus pleiotrophin (Ptn), mRNA [NM_017066]	ref|NM_017066|gb|M65601|gb|BC006201|ens|ENSRNOT00000016088	Rn.1653	Ptn	pleiotrophin	binds heparin: may act as a growth factor; may play a role in liver regeneration and fibrinogenesis [RGD]	PTN-immunolabeled neurons contained nitric oxide synthase or somatostatin and expressed the vesicular acetylcholine transporter, supporting that they were GABAergic nitric oxide synthase/somatostatin-containing and cholinergic interneurons// thrombospondi	-	[Human, Mouse]HomoloGene: 2117
			XM_230608	Sn_predicted	PREDICTED: Rattus norvegicus sialoadhesin (predicted) (Sn_predicted), mRNA [XM_230608]	ref|XM_230608|ens|ENSRNOT00000004683|ens|ENSRNOT00000005130|ens|ENSRNOT00000028855	Rn.80962	Sigleol_predicted	sialic acid binding Ig-like lectin 1, sialoadhesin (predicted)	-	Sialoadhesin is a macrophage-restricted adhesion molecule that recognizes N-acetylneuraminylalpha2-3galactose structure. Macrophages in lymph nodes express high levels of unmasked sialoadhesin.	KEGG pathway: Cell adhesion molecules (CAMs)	[Human, Mouse]HomoloGene: 7947

Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Gene Symbol	Gene Name	Summary	GeneRIF	Pathway	Homology
			NM_021653	Dio1	Rattus norvegicus deiodinase, iodothyronine, type I (Dio1), mRNA [NM_021653]	ref|NM_0216 53|gb|X5799 9|ens|ENSRN OT00000044 66|ens|ENSR NOT00000044 375	Rn. 87549	Dio1	deiodinase, iodothyroni ne, type I	This gene belongs to the iodothyronine deiodinase family. It encodes a selenoprotein that deiodinates prohormone thyroxine (T4, 3,5,3',5'- tetraiodothyronine) to bioactive T3 (3,3',5- triiodothyronine). Selenocysteine (aa 126), which is encoded by UGA (usua	D1 3'UTR may play an important role in regulating the stability and translational efficiency of the D1 mRNA// Mammary gland carcinoma-related increase of type I iodothyronine 5'- deiodinase activity in Sprague-Dawley rats.	-	[Human, Mouse]HomoloGene: 620
			NM_012643	Ret	Rattus norvegicus ret proto- oncogene (Ret), mRNA [NM_012643]	ref|NM_0126 43|gb|AJ299 016|gb|XM_2 16254|ens|E NSRNOT00000 047685	Rn. 93200	Ret	ret proto- oncogene	may play a role in exoretory system and enteric nervous system development: human homolog is associated with Hirschsprung disease and Multiple Endocrine Neoplasia type 2 [RGD]	Ability of 17- allylamino-17- demethoxygeldanamycin (17-AAG) to increase radioiodide accumulation is not restricted to thyroid cells expressing RET/PTC1.// Shp-1 and Shp-2 are recruited on cell membrane in two distinct molecular complexes including Ret onco	-	[Human, Mouse]HomoloGene: 7517
			NM_138843	Mpst	Rattus norvegicus mercaptopyruvate sulfurtransferase (Mpst), mRNA [NM_138843]	ref|NM_1388 43|ref|XM_5 79654|gb|D5 0564|gb|XM_ 346800	Rn. 32263	Mpst	mercaptopyruvate sulfurtransferase	catalyzes the formation of thiocyanide and pyruvate [RGD]	the redox state regulates MST activity at the enzymatic level, and MST controls redox to maintain cellular redox homeostasis	KEGG pathway: Cysteine metabolism	[Human, Mouse]HomoloGene: 31942



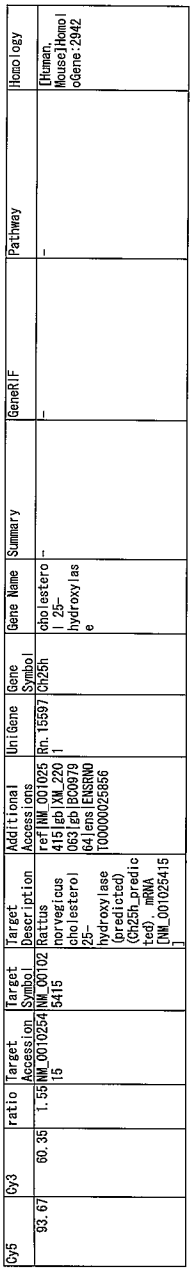
Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Gene Symbol	Gene Name	Summary	GeneRIF	Pathway	Homology
			NM_013156	Ctsl	Rattus norvegicus cathepsin L (Ctsl), mRNA [NM_013156]	ref|NM_0131 56|gb|BG063 175|gb|S851 84|ens|ENSR NOT00000025 462	Rn. 1294	Ctsl	cathepsin L	mouse homolog is deleted in the CD4 T-cell-deficient mouse mutant nacht (nkt); may play a role in CD4+ T-cell selection in the thymus [RGD]	cathepsin L created a 14-kDa carboxyl |GFBP-2 fragment that corresponded to the sole antigen detected in IEC-18 cell lysates as well as a 16.5-kDa fragment found in the media// The co-localization of PAP/TRAP and the cysteine protease cathepsin L could su	KEGG pathway: Antigen processing and presentation	[Human, Mouse]HomoloGene: 74298
			NM_017178	Bmp2	Rattus norvegicus bone morphogenetic protein 2 (Bmp2), mRNA [NM_017178]	ref|NM_0171 78|gb|Z26886 81|gb|L20678 |ens|ENSRNO T00000002890 4	Rn. 90931	Bmp2	bone morphogenetic protein 2	involved in cellular signaling during limb development; induces bone formation [RGD]	NF-kappaBeta activation and elicited significant increases in BMP-2 mRNA and protein in primary coronary arterial endothelial cells// The Bmp2 3' UTR contains essential regulatory elements that act post-transcriptionally// Our results	KEGG pathway: Hedgehog signaling pathway// KEGG pathway: TGF-beta signaling pathway	[Human, Mouse]HomoloGene: 926
			XM_216584	Car6_predicted	PREDICTED: Rattus norvegicus carbonic anhydrase 6 (predicted) (Car6_predicted), mRNA [XM_216584]	ref|XM_2165 84|tc|TC620 057	Rn. 43383	Car6	carbonic anhydrase 6	-	-	[Human, Mouse]HomoloGene: 20324

[表31]

表48 Cに対してで発現増加した唾液腺の注目遺伝子
脂質代謝 (GO ID: 6629, 44255)

Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Gene Symbol	Gene Name	Summary	GeneRIF	Pathway	Homology
8361.31	3259.64	2.57	XM_341400	Rbp3	PREDICTED: Rattus norvegicus retinol binding protein 3, interstitial (Rbp3), mRNA [XM_341400]	ref|XM_341400|gb|X56159|gb|X69523|ens|ENSRNOT00000027446	Rn.41214	Rbp3	retinol binding protein 3, interstitial	may play a role in vision [RGD]	-	-	[Human, Mouse]HomoloGene:9261
61.95	24.38	2.54	NM_019169	Snca	Rattus norvegicus synuclein, alpha (Snca), mRNA [NM_019169]	ref|NM_019169|gb|AF007758|gb|AY550005|gb|AY550006	Rn.1827	Snca	synuclein, alpha	may play a role in regulation of synaptic vesicle biogenesis and organization; may be involved in neurotransmission [RGD]	we were able to modulate tyrosine hydroxylase-positive neuronal cell death by silencing alpha-synuclein expression, suggesting that down-regulation of alpha-synuclein is important in neuronal cell death of Parkinson's disease// DJ-1 up-regulates glutathio	KEGG pathway: Alzheimer's disease// KEGG pathway: Neurodegenerative Disorders// KEGG pathway: Parkinson's disease	[Human, Mouse]HomoloGene:293
40.56	19.56	2.07	NM_031736	Slc27a2	Rattus norvegicus solute carrier family 27 (fatty acid transporter), member 2 (Slc27a2), mRNA [NM_031736]	ref|NM_031736|ref|XM_579526|gb|D85100|gb|XM_346669	Rn.3608	Slc27a2	solute carrier family 27 (fatty acid transporter), member 2	has very long-chain acyl-CoA synthetase activity; may play a role in fatty acid metabolism [RGD]	In response to an increase of cellular cholesterol, fatty acid transporter is translocated from cytosol to membranes of type II pneumocytes.	KEGG pathway: Alkaloid biosynthesis II// KEGG pathway: Caprolactam degradation// KEGG pathway: Ethylbenzene degradation// KEGG pathway: Limonene and pinene degradation// KEGG pathway: Propanoate metabolism	-
182.19	88.28	2.06	NM_030827	Lrp2	Rattus norvegicus low density lipoprotein receptor-related protein 2 (Lrp2), mRNA [NM_030827]	ref|NM_030827|ref|XM_579493|gb|L34049|gb|XM_346656	Rn.26430	Lrp2	low density lipoprotein receptor-related protein 2	receptor for low density lipoprotein and a major kidney glomerular antigen for rat Heymann nephritis [RGD]	Megalin mediates IGF-I-induced clearance of Abeta and is involved in IGF-I transport into brain. Attenuated IGF-I/megalin input may contribute to increased risk of neurodegeneration, including late-onset Alzheimer's disease.// These data suggest that ligh	KEGG pathway: Hedgehog signaling pathway	-

Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Gene Symbol	Gene Name	Summary	GeneRIF	Pathway	Homology
716.84	423.92	1.69	NM_031561	Cd36	Rattus norvegicus cd36 antigen (Cd36), mRNA [NM_031561]	ref|NM_031561|ref|XM_57533 8|ref|NM_57539 4|gb|AF11391 4	Rn.10241	Cd36	cd36 antigen	fatty acid translocase; involved in long-chain fatty acid (LCFA) transport; important in fatty acid metabolism and insulin function [RGD]	Up-regulation of CD36 may have a role in increasing oxidative stress in cultured microvascular endothelial cells and the heart in chronic diabetes.// the subcellular distribution of fatty acid binding protein plasma membrane, as well as FAT/CD36, is acute	KEGG pathway: Adipocytokine signaling pathway// KEGG pathway: ECM-receptor interaction// KEGG pathway: Hematopoietic cell lineage	-
1541.69	985.71	1.56	NM_024396	Abca2	Rattus norvegicus ATP-binding cassette, sub-family A (ABC1), member 2 (Abca2), mRNA [NM_024396]	ref|NM_024396|gb|ABC37937|ens|ENSRNOT00000020339|ens|ENSRNOT00000036243	Rn.13115	Abca2	ATP-binding cassette, sub-family A (ABC1), member 2	glycosylated ABC transporter that binds ATP in the presence of magnesium: may play an important role in brain function [RGD]	ABCA2 protein is expressed predominantly in oligodendrocytes, and the expression of the protein is upregulated in the brain during maturation, especially between postnatal days 6 and 19.// ATP-binding cassette transporter ABCA2 (ABC2) expression in the de	KEGG pathway: ABC transporters - General	[Human, Mouse]Homol oGene:55590
139.55	89.53	1.56	NM_080778	Nr2f2	Rattus norvegicus nuclear receptor subfamily 2, group F, member 2 (Nr2f2), mRNA [NM_080778]	ref|NM_080778|gb|AF003944|ens|ENSRNOT00000014152|tc|TC57269 3	Rn.17815	Nr2f2	nuclear receptor subfamily 2, group F, member 2	transcriptional activator or repressor; involved in determining the metabolic phenotype of hepatic cells [RGD]	ARP-1/COUP-TFII acts as both a transcriptional repressor of microsomal triglyceride transfer protein and as a transcription activator of CYP7A1.	-	[Human, Mouse]Homol oGene:7628
1085.12	697.07	1.56	NM_053674	Phyh	Rattus norvegicus phytanoyl-CoA hydroxylase (Phyh), mRNA [NM_053674]	ref|NM_053674|gb|AF121345|gb|BC086573|ens|ENSRNOT00000024362	Rn.7279	Phyh	phytanoyl-CoA hydroxylase	catalyzes the conversion of phytanoyl-CoA to 2-hydroxyphytanoyl-CoA: plays a role in phytanic acid alpha-oxidation [RGD]	-	-	[Human, Mouse]Homol oGene:4530



Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Gene Symbol	Gene Name	Summary	GeneRIF	Pathway	Homology
93.67	60.35	1.55	NM_001025415	NM_001025415	Rattus norvegicus cholesterol 25-hydroxylase (predicted) (Ch25h_predicted), mRNA [NM_001025415]	ref|NM_001025415|gb|XM_220063|gb|BC009796|ens|ENSRNOT00000025656	Rn.155971	Ch25h	cholesterol 25-hydroxylase	-	-	-	[Human, Mouse]Homologene:2942

[表32]

表49 Gに対して発現増加した唾液腺の注目遺伝子
ドーパミン合成 (GO ID: 42416)

Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Addition al Accessio ns	UniGene	Gene Symbol	Gene Name	Summary	GeneRIF	Pathway	Homology
267.70	82.81	3.23	AA963004	AA963004	AA963004 UI-R-E1-gd-d-04-0-UI.s1 UI-R-E1 Rattus norvegicus cDNA clone UI-R-E1-gd-d-04-0-UI 3', mRNA sequence [AA963004]	gb|AA963004|UI-R-E1-gd-d-04-0-UI.s1|UI-R-E1|G3544413	Rn.24539	Tgfb2	transforming growth factor, beta 2	binds the transforming growth factor-beta receptor; plays a role in regulation of cell growth and proliferation; may be involved in mesenchymal-epithelial cell interactions during development [RGD]	the pro-inflammatory cytokine MIF can shift the cytokine balance from the immunosuppressive state towards an inflammatory reaction, potentially through the inhibition of TGF-beta2 secretion by testicular peritubular cells.// TGF-beta2 mRNA and protein exp	KEGG pathway: Cell cycle// KEGG pathway: MAPK signaling pathway// KEGG pathway: TGF-beta signaling pathway	[Human, Mouse]Homolo Gene:2432
218.08	82.41	2.65	NM_012740	Th	Rattus norvegicus tyrosine hydroxylase (Th), mRNA [NM_012740]	ref|NM_012740|gb|L22651|gb|M10241|ens|ENSRNOT00000027682	Rn.11082	Th	tyrosine hydroxylase	catalyzes the rate limiting step in catecholamine biosynthesis; may be involved in response to hypoxia [RGD]	The kinetics of reduction of ferric TyrH by several reductants were determined by anaerobic stopped-flow spectroscopy. phosphorylation does not directly regulate the interconversion of the ferric and ferrous forms// The results indicate that the NGF/NGF	KEGG pathway: Parkinson's disease// KEGG pathway: Tyrosine metabolism	[Human, Mouse]Homolo Gene:307
61.95	24.38	2.54	NM_019169	Snca	Rattus norvegicus synuclein, alpha (Snca), mRNA [NM_019169]	ref|NM_019169|gb|AF007581|gb|AY550006|AY550006	Rn.1827	Snca	synuclein, alpha	may play a role in regulation of synaptic vesicle biogenesis and organization; may be involved in neurotransmission [RGD]	we were able to modulate tyrosine hydroxylase-positive neuronal cell death by silencing alpha-synuclein expression, suggesting that down-regulation of alpha-synuclein is important in neuronal cell death of Parkinson's disease// DJ-1 up-regulates glutathio	KEGG pathway: Alzheimer's disease// KEGG pathway: Neurodegenerative Disorders// KEGG pathway: Parkinson's disease	[Human, Mouse]Homolo Gene:293

[表33]

表60 0に対しLで発現減少した唾液腺の注目遺伝子
アクセッション結合 (60 ID: 3779)

Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Gene Symbol	Gene Name	Summary	GeneRIF	Pathway	Homology
16509.25	39439.68	0.42	NM_013097	Dnase1	Rattus norvegicus deoxyribonuclease I (Dnase1), mRNA [NM_013097]	ref|NM_0130970|gb|X56060|gb|AF39710|gb|AF397150	Rn.6077	Dnase1	deoxyribonuclease I	glycoprotein that cleaves DNA endonucleolytically to yield 5(alpha)-phosphodinucleotide and oligonucleotide end products; facilitates DNA hydrolysis in alimentary duct and other digestive tissues [RGD]	A comparison of the expression and transport of DNAse1 from rats and DNAse1L3 from mice is reported.// results show that the chief cells of the stomach produce DNase I	-	[Human, Mouse]Homolo Gene:3826
115.15	257.92	0.45	NM_031747	Cnn1	Rattus norvegicus calponin 1 (Cnn1), mRNA [NM_031747]	ref|NM_031747|gb|D14437|gb|X71071|gb|BC006180|g	Rn.31788	Cnn1	calponin 1	binds actin stress fibers; involved in actin bundling [RGD]	Calponin increased in the molecular layer of the dentate gyrus, the site of mossy fiber sprouting, and neo-synaptogenesis, at 1 and 2 weeks after pilocarpine injection, when the reorganization was taking place.// CNN1 plays a role as tumor suppressor in S	-	[Human, Mouse]Homolo Gene:995
122.47	253.42	0.48	AW917167	AW917167	AW917167 EST348471 Rat gene index, normalized rat, norvegicus, Bento Soares Rattus norvegicus cDNA clone RGIEA09 5' end, mRNA sequence [AW917167]	gb|AW917167|tc|TC55565|g	Rn.18668	Plsl_predicted	plastin 1 (I isoform) (predicted)	-	-	-	[Human, Mouse]Homolo Gene:68270
1910.91	3729.09	0.51	NM_00102434245	NM_00102	Rattus norvegicus similar to tropomyosin 1, embryonic fibroblast - rat (MGC109519), mRNA [NM_001024345]	ref|NM_001024345|gb|BC090009|gb|IL00382|tc|TC518644	Rn.17680	--	similar to tropomyosin 1, embryonic fibroblast - rat	-	-	-	[Human, Mouse]Homolo Gene:55509

Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Gene Symbol	Gene Name	Summary	GeneRIF	Pathway	Homology
40.70	72.05	0.56	XM_234332	Plekhh1_predicted	PREDICTED: Rattus norvegicus pleckstrin homology domain containing, family H (with MyTH4 domain) member 1 (predicted) (Plekhh1_predicted), mRNA [XM_234332]	ref|XM_234332|Ensembl|ENSRNOT00000014257	Rn.35024	Plekhh1_predicted	pleckstrin homology domain containing, family H (with MyTH4 domain) member 1 (predicted)	-	-	-	[Human, Mouse]Homologene:24741
209.62	361.03	0.58	NM_019131	Tpm1	Rattus norvegicus tropomyosin 1, alpha (Tpm1), mRNA [NM_019131]	ref|NM_019131|gb|AF372217|gb|AF372215|gb|M60668	Rn.87540	Tpm1	tropomyosin 1, alpha	This gene is a member of the tropomyosin family and encodes a protein that heterodimerizes with a beta subunit, binding actin in both muscle and nonmuscle cells. In both smooth and striated musole cells, it plays a role in calcium dependent-regulation of	analysis of tropomyosin binding and binding sites for actin// The stability and energetics of the tropomyosin coiled coil are important for actin affinity.// A splicing silencer that regulates smooth muscle specific alternative splicing is active in multi	-	-
441.61	756.18	0.58	XM_573030	Myh11	PREDICTED: Rattus norvegicus myosin heavy chain 11 (Myh11), mRNA [XM_573030]	ref|XM_573030|gb|X16262|gb|X16261|gb|XM_239866	Rn.94969	Myh11	myosin, heavy polypeptide 11, smooth muscle	transcription decreases following transformation with mutant p53 [RGD]	-	-	-
91.13	155.56	0.59	NM_182844	Myrip	Rattus norvegicus myosin VIIA and Rab interacting protein (Myrip), mRNA [NM_182844]	ref|NM_182844|gb|AY331344|gb|AW919849575|tc|TC536770	Rn.16197	Myrip	myosin VIIA and Rab interacting protein	human and mouse homologs form a complex with Rab27A and Myosin VIIa; involved in melanosome trafficking to the actin cytoskeleton [RGD]	the Rab27B-Slac2-c complex is an important constituent of secretory granule exocytosis in parotid acinar cells	-	[Human, Mouse]Homologene:9150

Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Gene Symbol	Gene Name	Summary	GeneRIF	Pathway	Homology
45.87	78.08	0.59	XM_233196	Hook1_predicted	PREDICTED: Rattus norvegicus hook homolog 1 (Drosophila) (predicted) (Hook1_predicted), mRNA [XM_233196]	ref|XM_233196|TC544207	Rn.96284	Hook1_predicted	hook homolog 1 (Drosophila) (predicted)	-	-	-	[Human, Mouse]Homolo Gene:9289
57.95	95.57	0.61	NM_031520	Myh10	Rattus norvegicus myosin heavy chain 10, non-muscle (Myh10), mRNA [NM_031520]	ref|NM_031520|AF139055|ens|ENSRNOTG0000003983|tc|TC570280	Rn.98166	Myh10	myosin, heavy polypeptide 10, non-muscle	nonmuscle myosin II heavy chain: produces motor activity with actin filaments; isoform B2 may play a role in neuronal cell motility [RGD]	non-muscle myosin II and myosin light chain kinase are downstream targets for vasopressin signaling in the renal collecting duct// These results suggest that the mesangial expression of SMemb is related to glomerular matrix accumulation and that angiotens	KEGG pathway: Regulation of actin cytoskeleton// KEGG pathway: Tight junction	[Human, Mouse]Homolo Gene:55941
44.47	71.65	0.62	XM_226874	Myo10_predicted	PREDICTED: Rattus norvegicus myosin X (predicted) (Myo10_predicted), mRNA [XM_226874]	ref|XM_226874|ens|ENSRNOT0000001402 2	Rn.20775	Myo10_predicted	myosin X (predicted)	-	-	-	[Human, Mouse]Homolo Gene:36328
184.78	282.04	0.66	NM_030873	Pfn2	Rattus norvegicus profilin 2 (Pfn2), mRNA [NM_030873]	ref|NM_030873|AY004289|gb|BC087013|gb|AI556217	Rn.17153	Pfn2	profilin 2	binds actin; regulates the rate of actin polymerization [RGD]	Following hypophysectomy, the actin cytoskeleton of the Sertoli cell shifts to a predominantly depolymerized state, perhaps in part because of decreases in profilin II and espin gene products.// RhoA/ROCK/PIIa-mediated regulation of actin stability, shown	KEGG pathway: Regulation of actin cytoskeleton	[Human, Mouse]Homolo Gene:1974

Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Gene Symbol	Gene Name	Summary	GeneRIF	Pathway	Homology
			XM_240417	Mtmr7_predicted	PREDICTED: Rattus norvegicus myotubularin related protein 7 (predicted) (Mtmr7_predicted), mRNA [XM_240417]	ref|XM_240417|gb|AA998777|ens|ENSRNOT00000015625|tc|TC538804	Rn.12785	Mtmr7_predicted	myotubularin related protein 7 (predicted)	-	-	-	[Human]HomoloGene:56848

[表34]

表51 Cに対して発現減少した唾液腺の注目遺伝子
細胞外成分 (GO ID: 5576, 44421, 5615)

Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Gene Symbol	Gene Name	Summary	GeneRIF	Pathway	Homology
66.53	1235.35	0.05	NM_019161	Cdh22	Rattus norvegicus cadherin 22 (Cdh22), mRNA [NM_019161]	ref|NM_019161|gb|D63349|tc|T C588625	Rn.145674	Cdh22	cadherin 22	mediates Ca2+ dependent cell adhesion: may play a role in brain and neuroendocrine organ morphogenesis [RGD]	PB-cadherin promotes survival of spermatocytes and activates Jak2 and Stat3 signaling.	-	[Human, Mouse]Homolo gene:23148
30527.51	498133.39	0.06	NM_133622	RGD:708577	Rattus norvegicus common salivary protein 1 (LOC171161), mRNA [NM_133622]	ref|NM_133622|gb|U00964|tc|T C568908|tc|T05 71345	Rn.9752	-	common salivary protein 1	precursor appears to undergo post-translational modification to form a family of related salivary proteins [RGD]	-	-	-
25.47	367.35	0.07	NM_139087	Cgref1	Rattus norvegicus cell growth regulator with EF hand domain 1 (Cgref1), mRNA [NM_139087]	ref|NM_139087|gb|U66470|gb|A W913954|ens|EN SRNOT00000010 586	Rn.31842	Cgref1	cell growth regulator with EF hand domain 1	inhibits cell growth [RGD]	CGR11 appears to be a primary response gene expressed to moderate levels in functional p53 cells.	-	[Human, Mouse]Homolo gene:4790
37.00	247.55	0.15	NM_001100772	Pf4	Rattus norvegicus platelet factor 4 (Pf4), mRNA [NM_001100772 9]	ref|NM_001100772 9|gb|XM_34119 2|gb|AW915663| ens|ENSRNOT000 00033406	Rn.6800	Cxcl4	chemokine (C-X-C motif) ligand 4	member of low-molecular weight chemokines superfamily; may mediate inflammation and immune response [RGD]	this study identified a novel regulatory element, TME(tandem repeat of MEIS1 binding element)in the PF4 promoter and demonstrated that MEIS1/PBX complexes bind to the TME// A carboxyl-terminal fragment of this protein effects a rapid histamine release from	KEGG pathway: Leukocyte transendothelia l migration	[Mouse]Homolo Gene:69289
204.73	1204.31	0.17	NM_053348	Fetub	Rattus norvegicus fetuin beta (Fetub), mRNA [NM_053348]	ref|NM_053348|gb|AJ242926|gb [BC070508|ens| ENSRNOT00000004 6199	Rn.2464	Fetub	fetuin beta	inhibits insulin receptor tyrosine kinase activity, protease inhibitory activities; developmentally regulates calcium metabolism and osteogenesis [RGD]	-	-	[Human, Mouse]Homolo gene:8660

Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Gene Symbol	Gene Name	Summary	GeneRIF	Pathway	Homology
136.51	775.96	0.18	NM_001013180	NM_001013180	Rattus norvegicus secretoglobin, family 3A, member 1 (Scgb3a1), mRNA [NM_001013180]	ref|NM_001013180|gb|AF436841|gb|AAL34079|gb|BK000202	Rn.30648	Scgb3a1	secretoglobin, family 3A, member 1	secretoglobin: may have a role in airway function [RGD]	-	-	[Mouse]Homolo Gene:14160
54.55	254.82	0.21	NM_053744	Dlk1	Rattus norvegicus delta-like 1 homolog (Drosophila) (Dlk1), mRNA [NM_053744]	ref|NM_053744|ref|XM_579575|gb|D84336|gb|X M_346776	Rn.14547	Dlk1	delta-like 1 homolog (Drosophila)	involved in maintaining the undifferentiated status of the preadipocyte [RGD]	localisation in rat was in the medulla and the zona glomerulosa of the cortex of the adrenal glands, in the pars distalis of the adenohypophysis, and in the ovarian granulosa lutein cells but no staining was found in the pancreas	-	[Human, Mouse]HomoloG ene:2846
154.13	608.12	0.25	XM_214143	Oit1_predicted	PREDICTED: Rattus norvegicus oncoprotein induced transcript 1 (predicted) (Oit1_predicted), mRNA [XM_214143]	ref|XM_214143|ens|ENSRNOT0000055554|tc|TC	Rn.38497	Oit1_predicted	oncoprotein induced transcript 1 homolog (mouse) (predicted)	-	-	-	[Human, Mouse]HomoloG ene:16354
103.38	383.73	0.27	NM_203337	RGD:1303068	Rattus norvegicus alpha-2,3-sialyltransferase ST3Gal IV (siat4c), mRNA [NM_203337]	ref|NM_203337|gb|AJ626923|gb|BC089057|ens|ENSRNOT00000013243	Rn.24125	St3gal4	ST3 beta-galactoside alpha-2,3-sialyltransferase 4	plasma membrane-specific alpha 2,3-sialic acid transporter; may be important for protein amino acid glycosylation [RGD]	-	-	[Human, Mouse]HomoloG ene:46572
75.56	262.31	0.29	NM_133295	Ces3	Rattus norvegicus carboxylesterase 3 (Ces3), mRNA [NM_133295]	ref|NM_133295|ref|NM_001013889|ref|XM_579616|gb|X51974	Rn.2549	Ces3	carboxylesterase 3	enzyme that hydrolizes long-chain fatty acids and thioesters; may play a role in lipid metabolism and/or the elimination of toxic substances [RGD]	-	KEGG pathway: Alkaloid biosynthesis II	-

Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Gene Symbol	Gene Name	Summary	GeneRIF	Pathway	Homology
331.89	1058.38	0.31	NM_019303	Cyp2f2	Rattus norvegicus cytochrome P450, family 2, subfamily f, polypeptide 2 (Cyp2f2), mRNA [NM_019303]	ref|NM_019303|gb|AF017393|gb|BC007939|tc|TC571084	Rn.10817	Cyp2f2	cytochrome P450, family 2, subfamily f, polypeptide 2	member of the p450 2F subfamily; forms styrene glycol from styrene in liver and lung microsomes [RGD]	-	KEGG pathway: Metabolism of xenobiotics by cytochrome P450	[Human, Mouse]Homolog ene:73898
83.84	264.21	0.32	NM_199082	Sectm1	Rattus norvegicus secreted and transmembrane 1 (Sectm1), mRNA [NM_199082]	ref|NM_199082|gb|BC061794|gb|XM_213545|tc|TC569738	-	Sectm1	secreted and transmembrane 1	human homolog is a Golgi-associated protein; may have a role in hematopoietic and/or immune system processes [RGD]	-	-	[Human, Mouse]Homolog ene:48157
171.07	532.76	0.32	NM_001013219	NM_001013219	Rattus norvegicus sialyltransferase 4A (beta-galactoside alpha-2,3-sialytransferase) (predicted) (Siat4a_predicted), mRNA [NM_001013219]	ref|NM_001013219|gb|XM_343254|gb|AJ748840|ens|ENSRNOT00000010980	Rn.104514	St3gal1	ST3 beta-galactoside alpha-2,3-sialyltransferase 1	-	-	-	[Human, Mouse]Homolog ene:7540
337.06	1003.53	0.34	XM_221623	Fam3b_predicted	PREDICTED: Rattus norvegicus family with sequence similarity 3, member B (predicted) (Fam3b_predicted), mRNA [XM_221623]	ref|XM_221623|ens|ENSRNOT00000002683|ens|ENSRNOT00000005116|ens|ENSRNOT00000042012	Rn.162007	RGD1311662_predicted	similar to open reading frame 9	-	-	-	[Human, Mouse]Homolog ene:10766

Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Gene Symbol	Gene Name	Summary	GeneRIF	Pathway	Homology
557.00	1547.24	0.36	NM_001010970	Amy1	Rattus norvegicus amylase 1, salivary (Amy1), mRNA [NM_001010970]	ref|NM_001010970|gb|AB057450|gb|BC088228|ens|ENSRNOT00000022496	Rn.116361	Amy1	amylase 1, salivary	-	the HCO3-anion participates in the secretory sequence at sites distal to the identification of secretagogues in both endocrine and exocrine cells, the absence of extracellular bicarbonate is shown to decrease by about 50% basal alpha-amylase secretion	KEGG pathway: Starch and sucrose metabolism	-
26.73	72.15	0.37	NM_013080	Ptprz1	Rattus norvegicus protein tyrosine phosphatase, receptor-type, Z polypeptide 1 (Ptprz1), mRNA [NM_013080]	ref|NM_013080|ref|XM_579367|gb|U09357|gb|X M_346695	Rn.10088	Ptprz1	protein tyrosine phosphatase, receptor-type, Z polypeptide 1	alternative splicing product phosphocan inhibits neural cell adhesion and neurite outgrowth [RGD]	RPTPzeta/beta is localized mainly at the postsynaptic membrane of pyramidal neurons in adult cerebral cortex and hippocampus// findings suggest that PTN-PTPzeta signaling regulates the morphogenesis of Purkinje cell dendrites and that the mechanisms under	-	-
18.96	50.49	0.38	NM_057201	Gpr37	Rattus norvegicus G protein-coupled receptor 37 (Gpr37), mRNA [NM_057201]	ref|NM_057201|gb|AF087946|gb|BC087728|ens|ENSRNOT00000003593	Rn.28035	Gpr37	G protein-coupled receptor 37	an orphan G protein-coupled receptor that may have an important role in the central nervous system [RGD]	expression of Pael-R genes in the nigro-striatal pathway may have significant implication for pathophysiology and treatment of parkinson disease.	KEGG pathway: Parkinson's disease	[Human, Mouse]Homolo Gene:3875
38.43	101.49	0.38	NM_012870	Tnfrsf11b	Rattus norvegicus tumor necrosis factor receptor superfamily, member 11b (osteoprotegerin) (Tnfrsf11b), mRNA [NM_012870]	ref|NM_012870|gb|U94330|gb|BC081830|ens|ENSRNOT00000011344	-	Tnfrsf11b	tumor necrosis factor receptor superfamily, member 11b (osteoprotegerin)	plays a role in the negative regulation of bone resorption by inhibiting formation of osteoclasts [RGD]	Regulation of OPG production by the dental follicle likely affects the alveolar bone resorption needed for tooth eruption.// Detection of osteoprotegerin mRNA and protein in bone cells,// reduces osteoclast numbers and prevents bone erosion in collagen-in	KEGG pathway: Cytokine-cytokine receptor interaction	[Human, Mouse]Homolo Gene:1912

Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Gene Symbol	Gene Name	Summary	GeneRIF	Pathway	Homology
83.39	216.00	0.39	NM_013122	Igfbp2	Rattus norvegicus insulin-like growth factor binding protein 2 (Igfbp2), mRNA [NM_013122]	ref|NM_013122|gb|J04486|gb|M31672|ens|ENSRNOT00000023068	Rn. 6813	Igfbp2	insulin-like growth factor binding protein 2	protein that binds to Igf-I and Igf-II [RGD]	Growth inhibition, which was supported by the strong induction of p21CIP1/WAF1, was correlated with increased secretion of IGFBP-2 and, unexpectedly, with its increased localization in the nucleus and particularly in the cytoplasm.// retinoic acid modulat	-	[Human, Mouse]Homolog ene:499
276.12	681.07	0.41	NM_001002802	RGD:1303241	Rattus norvegicus beta-site APP-cleaving enzyme 2 (Bace2), mRNA [NM_001002802]	ref|NM_001002802|ref|XM_579078|gb|XM_213642|gb|BM000318	Rn. 38581	Bace2	beta-site APP-cleaving enzyme 2	-	-	KEGG pathway: Alzheimer's disease	[Human, Mouse]Homolog ene:22696
18.53	45.46	0.41	NM_031697	Siat6	Rattus norvegicus sialyltransferase 6 (N-acetyllacosaminide alpha 2,3-sialyltransferase) (Siat6), mRNA [NM_031697]	ref|NM_031697|gb|M97754|ens|ENSRNOT00000026990|tc|TC54369595	Rn. 44390	St3gal3	ST3 beta-galactoside alpha-2,3-sialyltransferase 3	plays a role in the formation of terminal carbohydrate groups of glycolipids and glycoproteins [RGD]	-	KEGG pathway: Blood group glycolipid biosynthesis - lactoseries// KEGG pathway: Keratan sulfate biosynthesis	[Human, Mouse]Homolog ene:7539
16509.25	39439.68	0.42	NM_013097	Dnase1	Rattus norvegicus deoxyribonuclease I (Dnase1), mRNA [NM_013097]	ref|NM_013097|gb|X56060|gb|AF397151|gb|AF397150	Rn. 6077	Dnase1	deoxyribonuclease I	glycoprotein that cleaves DNA endonucleolytically to yield 5(alpha)-phosphodinucleotide and oligonucleotide end products: facilitates DNA hydrolysis in alimentary duct and other digestive tissues [RGD]	A comparison of the expression and transport of DNAse1 from rats and DNAse1L3 from mice is reported.// results show that the chief cells of the stomach produce DNase I	-	[Human, Mouse]Homolog ene:3826

Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Gene Symbol	Gene Name	Summary	GeneRIF	Pathway	Homology
38.32	89.20	0.43	NM_012596	Lepr	Rattus norvegicus leptin receptor (Lepr), mRNA [NM_012596]	ref|NM_012596|gb|U52966|gb|D84125|gb|D84126	Rn. 9891	Lepr	leptin receptor	receptor for leptin; may have a role in body weight maintainence [RGD]	Results suggest that changes in leptin level and its receptor expression may influence the energy homeostasis during pregnancy. // Shedding of DbRa membrane-anchored receptors, rather than DbRe expression, might preferentially contribute to generation of i	KEGG pathway: Adipocytokine signaling pathway// KEGG pathway: Cytokine-cytokine receptor interaction// KEGG pathway: Jak-STAT signaling pathway// KEGG pathway: Neuroactive ligand-receptor interaction	[Human, Mouse]Homolo Gene:1731
307.85	715.76	0.43	NM_021744	Cd14	Rattus norvegicus CD14 antigen (Cd14), mRNA [NM_021744]	ref|NM_021744|gb|U51804|gb|BC061733|ens|ENSRNOT00000000239|SRNOT00000000277	-	Cd14	CD14 antigen	component of the lipopolysaccharide receptor complex; mediates LPS-induced neuroinflammation and inflammatory response [RGD]	CD14 glycoprotein is present on the cell membranes of vascular smooth muscle cells of rat aorta, where it acts as a lipopolysaccharide receptor.// in kupffer cells, increase of TLR4, CD14 expression may be induced by LPS within 1-3 hours, and further incr	KEGG pathway: Hematopoietic cell lineage// KEGG pathway: MAPK signaling pathway// KEGG pathway: Regulation of actin cytoskeleton// KEGG pathway: Toll-like receptor signaling pathway	[Human, Mouse]Homolo Gene:493
24.27	55.83	0.43	NM_017131	Casq2	Rattus norvegicus calsequestrin 2 (Casq2), mRNA [NM_017131]	ref|NM_017131|gb|U33287|gb|AF001334|gb|BC072547	Rn. 10111	Casq2	calsequestrin 2	binds activated epsilon protein kinase C holoenzyme; human homolog serves as a calcium resevoir in cardiac myocytes [RGD]	The role of CASQ2 in calcium (Ca2+) handling in cardiac myocytes can be attributed to its action as a Ca2+ buffer in the lumen of the sarcoplasmic reticulum.	-	[Human, Mouse]Homolo Gene:20330
54.73	124.73	0.44	NM_001102568	NM_001025683	Rattus norvegicus similiar to RIKEN cDNA 1810055G02 (predicted) (RGD1311946_predicted), mRNA [NM_001025683]	ref|NM_001025683|gb|XM_219679|gb|BC096053|ens|ENSRNOT00000034240	Rn. 16921	RGD1311946	similar to RIKEN cDNA 1810055G02	-	-	-	[Human, Mouse]Homolo Gene:11174

Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Gene Symbol	Gene Name	Summary	GeneRIF	Pathway	Homology
54.73	124.73	0.44	NM_001025683	Rattus norvegicus similar to RIKEN cDNA 1810055G02 (predicted) (RGD1311946_predicted), mRNA [NM_001025683]	ref|NM_001025683|gb|XM_217967|gb|BC096053|ens|ENSRNOT00000034240	Rn.16921	RGD1311946	similar to RIKEN cDNA 1810055G02	-	-	-	[Human, Mouse]HomoloGene:11174
481.18	1069.10	0.45	XM_345278	Amy2_predicted	Rattus norvegicus similar to amylase 1; amylase 1, salivary (LOC365914), mRNA [XM_345278]	gb|XM_345278|ens|ENSRNOT00000049844|ens|ENSRNOT00000090693	Rn.67070	Amy2_predicted	amylase 2, pancreatic (predicted)	-	-	-	-
56.10	123.83	0.45	NM_001004215	RGD:1303221	Rattus norvegicus peptidylproly| isomerase C (Ppic), mRNA [NM_001004215]	ref|NM_001004215|gb|XM_214534|gb|BC078949|ens|ENSRNOT00000023485	Rn.144176	Ppic	peptidylprolyl isomerase C	-	-	-	[Human, Mouse]HomoloGene:727
3503.77	7655.60	0.46	NM_019331	Posk3	Rattus norvegicus proprotein convertase subtilisin/kexin type3 (Posk3), mRNA [NM_019331]	ref|NM_019331|ref|XM_579432|gb|X65660|gb|M_346546	Rn.3220	Posk3	proprotein convertase subtilisin/kexin type3	may be one of several enzymes involved in the proteolytic processing of extracellular superoxide dismutase (EC-SOD) [RGD]	CDX2 regulates furin expression in intestinal epithelial cells// Data suggest that inhibition of furin and PC5 and resulting inhibition of insulin-like growth factor 1 receptor (IGF-1R) activation can inhibit IGF-1-induced membrane-type 1 matrix metallopr	-	-
23.20	49.85	0.47	NM_031565	RGD:62150	Rattus norvegicus carboxylesterase 1 (Ces1), mRNA [NM_031565]	ref|NM_031565|gb|X81395|ens|ENSRNOT00000020775|Tc|Tc05672	Rn.161717	-	carboxylesterase 1	enzyme that hydrolyzes long-chain fatty acids: necessary for cholesterol esterification: may be important for detoxification of certain drugs [RGD]	results demonstrate elevation of FC and depletion of cholesteryl esters by over-expression of hncCEH, which were resistant to compensatory responses by other enzymes of cholesterol homeostasis	KEGG pathway: Alkaloid biosynthesis II	[Mouse]HomoloGene:75318

Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Gene Symbol	Gene Name	Summary	GeneRIF	Pathway	Homology
71.61	143.96	0.50	NM_001013232	NM_001013232	Rattus norvegicus ribonuclease, RNase A family, 1 (pancreatic) (predicted) (Rnase1_predicted), mRNA [NM_001013232]	ref|NM_001013232|ens|ENSRNOT00000033809|tc|TC519040	Rn.111376	Rnase1_predicted	ribonuclease, RNase A family, 1 (pancreatic) (predicted)	-	-	-	-
70.95	141.83	0.50	NM_001012018	B4galt4_predicted	Rattus norvegicus UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 4 (predicted) (B4galt4_predicted), mRNA [NM_001012018]	ref|NM_001012018|ref|XM_573289|gb|XM_221439|gb|BC081866	Rn.143976	B4galt4	UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 4	-	-	-	[Human, Mouse]Homolog ene:37848
1570.81	2982.75	0.53	NM_001024240	NM_001024240	Rattus norvegicus similar to RIKEN cDNA 2010001M09 (predicted) (RGD1310251_predicted), mRNA [NM_001024240]	ref|NM_001024240|gb|XM_214585|gb|BC093397|ens|ENSRNOT00000036301	Rn.19595	RGD1310251	similar to RIKEN cDNA 2010001M09	-	-	-	[Mouse]Homolo Gene:12333
22.76	42.13	0.54	NM_172333	Cthrc1	Rattus norvegicus collagen triple helix repeat containing 1 (Cthrc1), mRNA [NM_172333]	ref|NM_172333|gb|AY136824|ens|ENSRNOT00000061421|tc|TC569980	Rn.9468	Cthrc1	collagen triple helix repeat containing 1	-	CTHRC1 is transiently expressed in the arterial wall in response to injury where it may contribute to vascular remodeling by limiting collagen matrix deposition and promoting cell migration.	-	[Human, Mouse]Homolog ene:16320

Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Gene Symbol	Gene Name	Summary	GeneRIF	Pathway	Homology
92.73	169.69	0.55	XM_215963	Lama5	PREDICTED: Rattus norvegicus laminin, alpha 5 (Lama5), mRNA [XM_215963]	ref|XM_215963|ens|ENSRNOT0000000981|ens|ENSRNOT00000005139|tc|TC51890	Rn. 62816	Lama5	laminin, alpha 5	an extracellular matrix glycoprotein involved in cell migration and differentiation [RGD]	Data suggest that the early arrest of tumor cells in the pulmonary vasculature through interaction of alpha3beta1 integrin with laminin-5 in exposed basement membrane provides a basis for cell arrest during pulmonary metastasis.// laminin 6 and 5 have dis	KEGG pathway: Cell Communication//KEGG pathway: ECM-receptor interaction//KEGG pathway: Focal adhesion	[Human, Mouse]HomoloGene:4060
59.27	107.57	0.55	XM_235478	Kdelr3_predicted	PREDICTED: Rattus norvegicus KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 3 (predicted) (Kdelr3_predicted), mRNA [XM_235478]	ref|XM_235478|ens|ENSRNOT00000018174|tc|TC54885	Rn. 161994	Kdelr3_predicted	KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 3 (predicted)	-	-	-	[Human, Mouse]HomoloGene:68533
120.04	217.05	0.55	NM_012729	Prss2	Rattus norvegicus protease, serine, 2 (Prss2), mRNA [NM_012729]	ref|NM_012729|ref|XM_342669|gb|V01274|ens|ENSRNOT00000018852	Rn. 1584	Prss2	protease, serine, 2	catalyzes the cleavage of Arg-Xaa, Lys-Xaa [RGD]	-	-	-
72.00	130.17	0.55	NM_134432	Agt	Rattus norvegicus angiotensinogen (Agt), mRNA [NM_134432]	ref|NM_134432|gb|BC078741|gb|L00094|ens|ENSRNOT00000024917	Rn. 6319	Agt	angiotensinogen (serpin peptidase inhibitor, clade A, member 8)	plays a role in regulation of blood pressure [RGD]	modification of the critical balance between ANG II and ET-1 systems through variant Dear contributes to hypertension susceptibility in female F2(RxS) intercross rats// the mechanism by which Ang II stimulates IGF-IR expression in VSMCs involves NF-kappaB	-	[Human, Mouse]HomoloGene:14

Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Gene Symbol	Gene Name	Summary	GeneRIF	Pathway	Homology
812.47	1464.83	0.55	NM_00100833 4	RGD1307423_predicted	Rattus norvegicus similar to RIKEN cDNA 1810014L12 (predicted) (RGD1307423_predicted), mRNA [NM_00100833 4]	ref|NM_00100083 4|gb|XM_22074 1|gb|BC065344| gb|BF546446	Rn.20057	Tmem97	transmembrane protein 97	-	-	-	[Human, Mouse]Homolo gene:6443
61.64	110.31	0.56	XM_342668	Prss3_predicted	PREDICTED: Rattus norvegicus protease, serine, 3 (mesotrypsin) (predicted) (Prss3_predicted), mRNA [XM_342668]	ref|XM_342668| ens|ENSRNOT000 00041100	Rn.154705	Prss3_predicted	protease, serine, 3 (mesotrypsin) (predicted)	-	-	-	-
47.51	84.12	0.56	NM_176074	C6	Rattus norvegicus complement component 6 (C6), mRNA [NM_176074]	ref|NM_176074| gb|AY230250|en s|ENSRNOT00000 033112|tc|TC56 9389	Rn.16145	C6	complement component 6	component of the complement cascade for immune response; may be a component of the membrane attack complex [RGD]	Lung allografts from C6-deficient donors to C6(-) recipients survive 13-17 days, whereas allografts from C6-sufficient donors to C6(+) recipients are rejected with intense vasoular infiltration and diffuse alveolar hemorrhage 7 days posttransplant.// The	KEGG pathway: Complement and coagulation cascades	[Human, Mouse]Homolo gene:47
547.92	965.78	0.57	XM_340999	Tfrc	PREDICTED: Rattus norvegicus Transferrin receptor (Tfrc), mRNA [XM_340999]	ref|XM_340999| ens|ENSRNOT000 00002407|ens|E NSRNOT00000004 868|ens|ENSRNO T00000041968	Rn.98672	Tfrc	transferrin receptor	receptor for transferrin: involved in regulating stellate cell activation [RGD]	a region of the TfR that can potentially interact with hsc70// These data suggest that alveolar type II (but not type I) cells express functional transferrin receptor in adult rat alveolar epithelium.// MPP(+)-dependent aconitase inactivation, Tf-iron upt	KEGG pathway: Hematopoietic cell lineage	[Human, Mouse]Homolo gene:2429

Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Gene Symbol	Gene Name	Summary	GeneRIF	Pathway	Homology
169.47	293.25	0.58	NM_173114	Cipar1	Rattus norvegicus castration induced prostatic apoptosis-related protein 1 (Cipar1), mRNA [NM_173114]	ref|NM_173114|gb|AJ010750|gb|BC060539|ens|ENSRNOT00000003472	Rn.127830	Cipar1	castration induced prostatic apoptosis-related protein 1	displays increased expression in ventral prostate after castration; expression in prostate is associated with apoptosis [RGD]	-	-	[Human, Mouse]Homolo Gene:41036
198.39	339.18	0.58	NM_00101313 7	NM_001013 137	Rattus norvegicus chemokine (C-X-C motif) ligand 14 (predicted) (Cxcl14_predicted), mRNA [NM_0010131 37]	ref|NM_0010131 37|gb|AI043862|tc|TC655043	Rn.3130	Cxcl14	chemokine (C-X-C motif) ligand 14	-	-	-	-
54.48	92.88	0.59	NM_021664	Dlad	Rattus norvegicus DNaseII-like acid DNase (Dlad), mRNA [NM_021664]	ref|NM_0216641|gb|AF178974|ens|ENSRNOT00000021861|tc|TC571381	Rn.41640	Dnase2b	deoxyribonuclease II beta	catalyzes the divalent cation-independent hydrolysis of DNA into oligonucleotides [RGD]	-	-	[Human, Mouse]Homolo Gene:1052
86.98	146.18	0.60	NM_138533	Spon2	Rattus norvegicus spondin 2, extracellular matrix protein (Spon2), mRNA [NM_138533]	ref|NM_138533|gb|AF155196|gb|BC078734|tc|TC569008	Rn.6699	Spon2	spondin 2, extracellular matrix protein	promotes cell adhesion and outgrowth of embryonic hippocampal neurons [RGD]	F-spondin can alter cell differentiation in multiple ways, depending upon its concentration and distribution between substrate-attached and soluble forms.// F-spondin may be an endogenous regulator of APP cleavage.	-	-

Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Gene Symbol	Gene Name	Summary	GeneRIF	Pathway	Homology
16.93	28.09	0.60	XM_342055	Sema4g_predicted	PREDICTED: Rattus norvegicus sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4G (predicted) (Sema4g_predicted), mRNA [XM_342055]	ref|XM_342055|gb|AW914054|gb|BG088250|tc|TC535808	Rn.1645	Sema4g_predicted	sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4G (predicted)	-	-	KEGG pathway: Axon guidance	[Human, Mouse]HomoloGene:22682
27.72	45.98	0.60	XM_231381	Sema3c_predicted	Rattus norvegicus similar to semaphorin 3C: semaphorin E (LOC296787), mRNA [XM_231381]	gb|XM_231381|ens|ENSRNOT00000009132|tc|TC569331	Rn.136960	Sema3c_predicted	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3C (predicted)	-	-	KEGG pathway: Axon guidance	[Human, Mouse]HomoloGene:36201
78.96	128.23	0.62	NM_053591	Dpep1	Rattus norvegicus dipeptidase 1 (renal) (Dpep1), mRNA [NM_053591]	ref|NM_053591|gb|LO7315|ens|ENSRNOT00000021397|tc|TC5770770	Rn.6051	Dpep1	dipeptidase 1 (renal)	renal enzyme that cleaves proteins [RGD]	carboxypeptidase A, dipeptidase and Na+/K+ ATPase levels in the rat intestine change when exposed to different doses of cadmium	-	[Human, Mouse]HomoloGene:80192
107.57	174.23	0.62	XM_224987	Sfrp1	PREDICTED: Rattus norvegicus secreted frizzled-related protein 1 (Sfrp1), mRNA [XM_224987]	ref|XM_224987|gb|AF167308|ens|ENSRNOT00000024128|tc|TC537124	Rn.163333	Sfrp1	secreted frizzled-related protein 1	a secreted protein involved in binding Wnt and antagonizing Wnt signaling [RGD]	Sfrp1 gene was identified and characterized by using bioinformatics, consisting of three exons, a signal peptide (codon 1-31), Frizzled domain with ten conserved Cys residues (codon 49-168), and Netrin (NTR) domain with six conserved Cys residues.// findi	KEGG pathway: Wnt signaling pathway	[Human, Mouse]HomoloGene:2266

Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Gene Symbol	Gene Name	Summary	GeneRIF	Pathway	Homology
160.89	258.31	0.62	AI009597	AI009597	AI009597 EST204048 Normalized rat lung, Bento Soares Rattus sp. cDNA clone RLUBG14.3' end, mRNA sequence [AI009597]	gb|AI009597	Rn.3896	Fxyd3	FXYD domain-containing ion transport regulator 3	This gene encodes a member of a family of small membrane proteins that share a 35-amino acid signature sequence domain, beginning with the sequence PFXYD and containing 7 invariant and 6 highly conserved amino acids. The approved human gene nomenclature f	-	-	[Mouse]Homolo Gene:4356
23.22	37.03	0.63	U70050	Jag2	Rattus norvegicus jagged2 precursor, mRNA, partial cds. [U70050]	gb|U70050|tc|T C537474	Rn.22469	Jag2	Jagged 2	may function as a ligand for Notch and may be involved in limb development [RGD]	-	KEGG pathway: Notch signaling pathway	[Human, Mouse]HomoloG ene:1677
54.99	87.55	0.63	NM_031598	Pla2g2a	Rattus norvegicus phospholipase A2, group IIA (platelets, synovial fluid) (Pla2g2a), mRNA [NM_031598]	ref|NM_031598| gb|AF363363|gb |U00523|gb|M37 127	Rn.11346	Pla2g2a	phospholipase A2, group IIA (platelets, synovial fluid)	hydrolyzes acyl group at the sn-2 position of phospholipids, forming non-esterified fatty acids and lysophospholipids: plays a critical role in inflammation: induces proliferation of smooth muscle cells [RGD]	These results indicate that phospholipase A(2)-IIA is coexpressed with SNAP-25 in mature taste receptor cells that possess exocytotic machinery.// new autocrine and paracrine pathways activating sPLA2-IIA gene expression in rat and human vascular smooth m	KEGG pathway: Arachidonic acid metabolism// KEGG pathway: Glycerophospholipid metabolism// KEGG pathway: Linoleic acid metabolism// KEGG pathway: MAPK signaling pathway	[Human]Homolo Gene:254
291.74	463.56	0.63	NM_080698	Fmod	Rattus norvegicus fibromodulin (Fmod), mRNA [NM_080698]	ref|NM_080698| gb|AB2132|ens| ENSRNOT0000000 4382|tc|TC65685 92	Rn.8778	Fmod	fibromodulin	-	-	-	[Human, Mouse]HomoloG ene:1530
692.47	1079.99	0.64	NM_001012 5	NM_001014 125	Rattus norvegicus protein disulfide isomerase-associated 5 (Pdia5), mRNA [NM_0010141 25]	ref|NM_0010141 25|gb|XM_34099 4|gb|BC088305| gb|AW916891	Rn.162053	Pdia5	protein disulfide isomerase-associated 5	-	-	-	[Human, Mouse]HomoloG ene:4957

Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Gene Symbol	Gene Name	Summary	GeneRIF	Pathway	Homology
143.16	222.55	0.64	XM_213313	Mfap4_predicted	PREDICTED: Rattus norvegicus microfibrillar-associated protein 4 (predicted) (Mfap4_predicted), mRNA [XM_213313]	ref|XM_213313|gb|AA851092|ens|ENSRNOT00000003268|tc|TC535408	-	Mfap4	microfibrillar-associated protein 4	-	-	-	[Human, Mouse]HomoloGene:36098
227.09	352.24	0.64	XM_340798	P4ha2_predicted	Rattus norvegicus similar to Prolyl 4-hydroxylase alpha IIa subunit (LOC360526), mRNA [XM_340798]	gb|XM_340798|ens|ENSRNOT00000042144|tc|TC536079	Rn.79891	P4ha2_predicted	procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), alpha II polypeptide (predicted)	-	-	-	[Human, Mouse]HomoloGene:55806
111.67	172.97	0.65	NM_022284	Guca2b	Rattus norvegicus guanylate cyclase activator 2b (Guca2b), mRNA [NM_022284]	ref|NM_022284|ref|XM_579455|gb|U75186|gb|X|M_346750	Rn.97693	Guca2b	guanylate cyclase activator 2b	member of the guanylin peptide family; regulates water and electrolyte balance in the intestine [RGD]	-	-	[Human, Mouse]HomoloGene:5150
39.06	60.06	0.65	NM_012774	Gpc3	Rattus norvegicus glypican 3 (Gpc3), mRNA [NM_012774]	ref|NM_012774|gb|M22400|ens|ENSRNOT00000030995|ens|ENSRNOT00000040122	Rn.9717	Gpc3	glypican 3	heparan sulfate cell surface proteoglycan, may be involved in development of mesodermal tissues, may modulate IgF2 function [RGD]	-	-	[Human, Mouse]HomoloGene:20944
32.89	49.94	0.66	NM_031022	Cspg4	Rattus norvegicus chondroitin sulfate proteoglycan 4 (Cspg4), mRNA [NM_031022]	ref|NM_031022|gb|X56541|ens|ENSRNOT00000023326|tc|TC56927	Rn.10381	Cspg4	chondroitin sulfate proteoglycan 4	extracellular matrix protein secreted by many cell types; member of the large chondroitin sulfate proteoglycan (CSPG) family; may be involved with angiogenesis-dependent processes such as wound healing or tumor growth [RGD]	While most glia in the NG2 lineage preserve a certain amount of voltage-gated ion conductances, mature GLAST(+) astrocytes are electrophysiologically passive.// NG2 is expressed by all perivascular cells along arterioles, and its absence denotes a venule-	-	[Human, Mouse]HomoloGene:20445

Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Gene Symbol	Gene Name	Summary	GeneRIF	Pathway	Homology
31.36	47.56	0.66	NM_175762	Ldlr	Rattus norvegicus low density lipoprotein receptor (Ldlr), mRNA [NM_175762]	ref|NM_175762| gb|X13722|gb|X M_217091|ensIE NSRNOT00000013 496	Rn.10483	Ldlr	low density lipoprotein receptor	-	up-regulation and interaction of ezrin and the LDLR serves to augment the delivery of cholesterol and other lipids in support of the hypertrophic and proliferative response of cells to estrogen.// expression pattern of LDL-R in brain microvessels endothel	-	[Human, Mouse]Homolo gene:55469
181.31	274.38	0.66	U06230	Prost	Rattus norvegicus protein S mRNA, partial cds. [U06230]	gb|U06230|gb|X M_343650|gb|AW 1415556|tc|NP06 6379	Rn.2888	Prost	protein S (alpha)	component of the Protein C/Protein S anticoagulant system; human homolog interacts with factor Xa, factor Va, and phospholipids to inhibit prothrombin activation [RGD]	-	-	-
64.19	96.72	0.66	NM_053882	Ecm1	Rattus norvegicus extracellul ar matrix protein 1 (Ecm1), mRNA [NM_053882]	ref|NM_053882| gb|U42581|gb|X M_215645|ensIE NSRNOT00000028 740	Rn.97792	Ecm1	extracellul ar matrix protein 1	mouse homolog is an extracellular protein found in a stromal osteogenic cell line [RGD]	-	-	[Human, Mouse]Homolo gene:3260
1473.90	2216.53	0.66	NM_052808	Psp	Rattus norvegicus parotid secretory protein (Psp), mRNA [NM_052808]	ref|NM_052808| gb|M83209|ens| ENSRNOT0000001 8226|tc|TC5726 06	Rn.9766	Psp	parotid secretory protein	secretory protein stored in parotid acinar cells [RGD]	PSP co-fractionates with chromogranin A but not with secreted alkaline phosphatase: its sorting is not cell-type specific but the precise mechanism of its sorting is unknown	-	[Human, Mouse]Homolo gene:69034
876.89	1312.03	0.67	NM_021751	Proml	Rattus norvegicus prominin 1 (Proml), mRNA [NM_021751]	ref|NM_021751| gb|AF386768|gb |AY262731|gb|A F263368	Rn.144589	Proml	prominin 1	induces expression of 3-phosphate glyceraldehyde dehydrogenase (GAPDH); may play a role in glucose homeostasis [RGD]	-	-	[Human, Mouse]Homolo gene:4390

[表35]

表62 Cに対して発現減少した唾液腺の注目遺伝子
核酸構成糖の代謝 (GO ID: 9225)

Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Gene Symbol	Gene Name	Summary	GeneRIF	Pathway	Homology
451.09	837.57	0.54	NM_080783	Gale	Rattus norvegicus galactose-4-epimerase, UDP (Gale), mRNA [NM_080783]	ref|NM_080783|gb|X53949|gb|BC097293|ens|ENSRNOT00000001 3322	Rn. 29908	Gale	galactose-4-epimerase, UDP	enzyme with galactose-4 epimerase activity [RGD]	-	KEGG pathway: Galactose metabolism// KEGG pathway: Nucleotide sugars metabolism	[Human, Mouse]Homol oGene:347
552.35	846.24	0.65	XM_216968	Tsta3_predicted	PREDICTED: Rattus norvegicus tissue specific transplantation antigen P35B (predicted) (Tsta3_predicted), mRNA [XM_216968]	ref|XM_216968|ens|ENSRNOT00000012306|gb|BF289545|gb|AW917281	Rn. 6606	Tsta3_predicted	tissue specific transplantation antigen P35B (predicted)	-	-	-	[Human, Mouse]Homol oGene:2484

[表36]

表53 Liに対して発現増加した視床下部の注目遺伝子
ホルモン活性 (GO ID: 5184, 5179)

Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Gene Symbol	Gene Name	Summary	GeneRIF	Pathway	Homology
37511.36	20083.44	1.87	NM_012625	Pmch	Rattus norvegicus pro-melanin-concentrating hormone (Pmch), mRNA [NM_012625]	ref|NM_012625|gb|M29712|gb|M62641|ensIENSRNOT00000006174	Rn.9675	Pmch	pro-melanin-concentrating hormone	cyclic neuropeptide: induces hippocampal synaptic transmission [RGD]	MCH is involved in the regulation of LHRH release in the female rat.// glucocorticoids may promote food intake in part by potentiating the orexigenic actions of MCH without affecting the actions of orexin A and glucocorticoids act indirectly to influence	KEGG pathway: Neuroactive ligand-receptor interaction	[Human, Mouse]HomoloGene:37653
793.72	441.05	1.80	XM_574228	XM_57422 8	PREDICTED: Rattus norvegicus agouti related protein homolog (mouse) (Agrp), mRNA [XM_574228]	ref|XM_574228|gb|AF206017|gb|XM_214672|ensIENSRNOT00000023606	Rn.13759	Agrp	agouti related protein homolog (mouse)	may interact with melanocortin receptors: may play a role in appetite stimulation [RGD]	Because AGRP is cleaved before secretion, syndecan-3 must influence food intake independently of the MC4-R.// conclude that leptin requires phosphatidylinositol 3-OH-kinase (PI3K) signaling both to inhibit hypothalamic neuropeptide Y and agouti-related pe	-	[Human, Mouse]HomoloGene:7184

[表37]

表54 Liに対して発現増加した視床下部の注目遺伝子
モノアミントランスポーター (GO ID:

Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Gene Symbol	Gene Name	Summary	GeneRIF	Pathway	Homology
276.61	111.83	2.46	NM_012694	Slc6a3	Rattus norvegicus solute carrier family 6 (neurotransmitter transporter, dopamine), member 3 (Slc6a3), mRNA [NM_012694]	ref|NM_012694|gb|M80241|ens|ENSRNOT00000024015|tc|TC569830	Rn.10093	Slc6a3	solute carrier family 6 (neurotransmitter transporter, dopamine), member 3	acts as a sodium-dependent dopamine transporter; may play a role in regulation of dopamine metabolism and signaling [RGD]	The decrease in DAT cell surface expression in the mPFC may be responsible for decreased DAT function in the mPFC of stimulated compared with deprived rats: there is plasticity in the regulatory mechanisms mediating DAT trafficking and function.// the car	-	[Human, Mouse]HomoloGene:55547
336.96	195.16	1.73	NM_013031	Slc18a2	Rattus norvegicus solute carrier family 18 (vesicular monoamine), member 2 (Slc18a2), mRNA [NM_013031]	ref|NM_013031|gb|L00603|ens|ENSRNOT00000011983	Rn.9686	Slc18a2	solute carrier family 18 (vesicular monoamine), member 2	transports N-methyl-4-phenylpyridinium (MPP+), a neurotoxin metabolite associated with Parkinson's disease [RGD]	VMAT2 defines a population of secretory vesicles that mediate the activity-dependent somatodendritic release of multiple retrograde signals involved in synaptic function, growth, and plasticity.// Down-regulation of VMAT2 in the nucleus accumbens and stri	-	[Human, Mouse]HomoloGene:2298
1180.13	750.06	1.57	NM_019374	Pdyn	Rattus norvegicus prodynorphin (Pdyn), mRNA [NM_019374]	ref|NM_019374|gb|M32784|ens|ENSRNOT00000037576	Rn.44471	Pdyn	prodynorphin	expression in hippocampus increases in response to traumatic brain injury; may play a role in regulatio of neurotransmitter release [RGD]	dynorphin can signal information to the cell interior through neuropeptide translocation across the plasma membrane// The increased enkephalin mRNA and prodynorphin mRNA gene expressions in rat hippocampus were involved in chronic stress.// Fluoxetine was	-	[Human, Mouse]HomoloGene:10321

[表38]

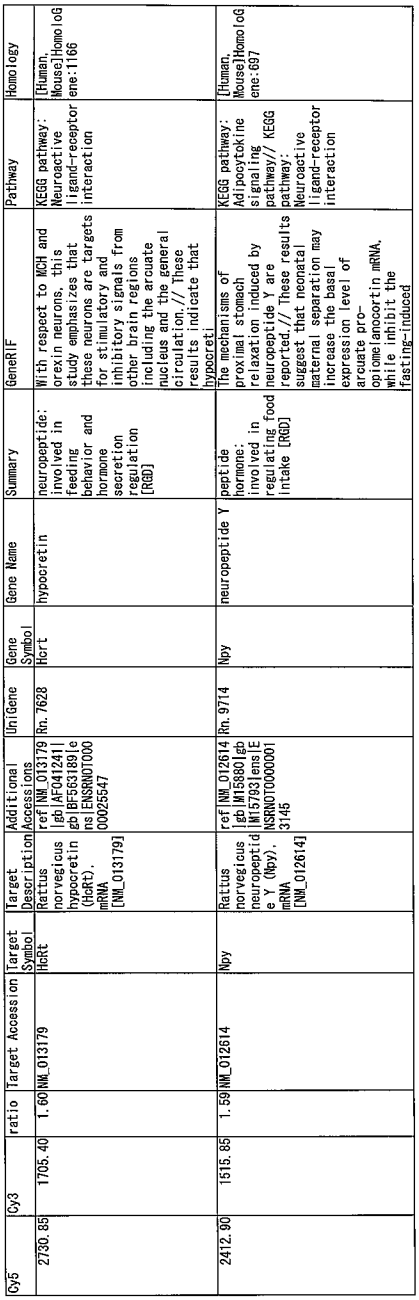
表55 Liに対して発現増加した視床下部の注目遺伝子
受容体結合 (GO ID: 5102)

Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Gene Symbol	Gene Name	Summary	GeneRIF	Pathway	Homology
793.72	441.05	1.80	XM_574228	XM_574228	PREDICTED: Rattus norvegicus agouti related protein homolog (mouse) (Agrp), mRNA [XM_574228]	ref|XM_574228.1|gb|AF20601.1|AF20601|XM_2146721|ENSRNOT00000002360.6	Rn.137597	Agrp	agouti related protein homolog (mouse)	may interact with melanocortin receptors; may play a role in appetite stimulation [RGD]	Because AGRP is cleaved before secretion, syndecan-3 must influence food intake independently of the MC4-R.// conclude that leptin requires phosphatidylinositol 3-OH-kinase (PI3K) signaling both to inhibit hypothalamic neuropeptide Y and agouti-related pe	-	[Human, Mouse]HomoloGene:7184
802.07	488.29	1.64	BF549735	BF549735	BF549735 UI-R-A0-ay-b-08-0-UI.r1 UI-R-A0 Rattus norvegicus cDNA clone UI-R-A0-ay-b-08-0-UI 5', mRNA sequence [BF549735]	gb|BF549735.1	Rn.38972	Lancl1	lanC (bacterial lantibiotic synthetase component C)-like 1	peptide-modifying enzyme; may be involved in modification and transport of antimicrobial peptides [RGD]	lanC-like protein 1 expression in rat testes was initiated already in pachytene spermatocytes in stage IX, but otherwise similar to mouse.	-	[Human, Mouse]HomoloGene:4417
2412.90	1515.85	1.59	NM_012614	Npy	Rattus norvegicus neuropeptide Y (Npy), mRNA [NM_012614]	ref|NM_012614.4|gb|M15880.1|gb|M15793.1|ens|ENSRNOT00000013145	Rn.9714	Npy	neuropeptide Y	peptide hormone: involved in regulating food intake [RGD]	The mechanisms of proximal stomach relaxation induced by neuropeptide Y are reported.// These results suggest that neonatal maternal separation may increase the basal expression level of arcuate pro-opiomelanocortin mRNA, while inhibit the fasting-induced	KEGG pathway: Adipocytokine signaling pathway// KEGG pathway: Neuroactive ligand-receptor interaction	[Human, Mouse]HomoloGene:697
425.39	277.36	1.53	NM_012904	Anxa1	Rattus norvegicus annexin A1 (Anxa1), mRNA [NM_012904]	ref|NM_012904.1|gb|Y00446.1|gb|M19967.1|gb|BC061710.1	Rn.1792	Anxa1	annexin A1	plays a role in regulation of insulin secretion; may inhibit phospholipase A2 [RGD]	Study reveals increased expression of the annexin 1 isoform at the mRNA level following moderate contusive spinal cord injury.// Annexin 1 mediates the disruption of normal cell morphology and inhibits cyclin D1 expression, therefore reducing cell prolife	-	[Human, Mouse]HomoloGene:563

[表39]

表56 Lに対して発現増加した視床下部の注目遺伝子
食行動 (GO ID: 7631)

Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Gene Symbol	Gene Name	Summary	GeneRIF	Pathway	Homology
153.08	71.65	2.14	NM_022633	Galp	Rattus norvegicus galanin-like peptide precursor (Galp), mRNA [NM_022633]	ref|NM_022633|gb|AF188491|ens|ENSRNOT00000034854|tc|NP399873	Rn.48754	Galp	galanin-like peptide precursor	-	observations demonstrate that endogenous Galanin-like peptide (GALP)provides trophic support to the neuroendocrine reproductive axis, including sexual behavior// adaptive responses in GALP signaling might occur during chronic overfeeding// GALP gene expre	-	[Human, Mouse]HomoloGene:11217
4327.77	2030.83	2.13	NM_139326	Pomc2	Rattus norvegicus proopiomelanocortin, beta (endorphin, beta) (Pomc2), mRNA [NM_139326]	ref|NM_139326|gb|BC058443|gb|AF510391|gb|J00759	Rn.108195	Pomc	pro-opiomelanocortin	-	POMC expression decreased progressively during eye movement sleep deprivation of rats. // Enhanced insulin sensitivity via exercise training might be mediated by endogenous beta-endorphin that leads to improved glucose disposal in obese Zucker rats.// die	KEGG pathway: Adipocytokine signaling pathway// KEGG pathway: Neuroactive ligand-receptor interaction	[Human, Mouse]HomoloGene:723
37511.36	20083.44	1.87	NM_012625	Pmch	Rattus norvegicus pro-melanin-concentrating hormone (Pmch), mRNA [NM_012625]	ref|NM_012625|gb|M29712|gb|M62641|ens|ENSRNOT00000006174	Rn.9675	Pmch	pro-melanin-concentrating hormone	cyclic neuropeptide; induces hippocampal synaptic transmission [RGD]	MCH is involved in the regulation of LHRH release in the female rat.// glucocorticoids may promote food intake in part by potentiating the orexigenic actions of MCH without affecting the actions of orexin A and glucocorticoids act indirectly to influence	KEGG pathway: Neuroactive ligand-receptor interaction	[Human, Mouse]HomoloGene:37653
793.72	441.05	1.80	XM_574228	XM_574228	PREDICTED: Rattus norvegicus agouti related protein homolog (mouse) (Agrp), mRNA [XM_574228]	ref|XM_574228|gb|AF206017|gb|XM_214672|ens|ENSRNOT00000023606	Rn.137597	Agrp	agouti related protein homolog (mouse)	may interact with melanocortin receptors; may play a role in appetite stimulation [RGD]	Because AGRP is cleaved before secretion, syndecan-3 must influence food intake independently of the MC4-R.// conclude that leptin requires phosphatidylinositol 3-OH-kinase (PI3K) signaling both to inhibit hypothalamic neuropeptide Y and agouti-related pe	-	[Human, Mouse]HomoloGene:7184



Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Gene Symbol	Gene Name	Summary	GeneRIF	Pathway	Homology
2730.85	1705.40	1.60	NM_013179	Hcrt	Rattus norvegicus hypocretin (Hcrt), mRNA [NM_013179]	ref|NM_013179|gb|AF041241|gb|BF563189|ens|ENSRNOT00000025547	Rn.7628	Hcrt	hypocretin	neuropeptide: involved in feeding behavior and hormone secretion regulation [RGD]	With respect to MCH and orexin neurons, this study emphasizes that these neurons are targets for stimulatory and inhibitory signals from other brain regions including the arcuate nucleus and the general circulation.// These results indicate that hypocreti	KEGG pathway: Neuroactive ligand-receptor interaction	[Human, Mouse]HomoloGene:1166
2412.90	1515.85	1.59	NM_012614	Npy	Rattus norvegicus neuropeptide Y (Npy), mRNA [NM_012614]	ref|NM_012614|gb|M15880|gb|M15793|ens|ENSRNOT00000013145	Rn.9714	Npy	neuropeptide Y	peptide hormone: involved in regulating food intake [RGD]	The mechanisms of proximal stomach relaxation induced by neuropeptide Y are reported.// These results suggest that neonatal maternal separation may increase the basal expression level of arcuate pro-opiomelanocortin mRNA, while inhibit the fasting-induced	KEGG pathway: Adipocytokine signaling pathway// KEGG pathway: Neuroactive ligand-receptor interaction	[Human, Mouse]HomoloGene:697

[表40]

表57 LIに対して発現増加した視床下部の注目遺伝子
生体アミン合成 (GO ID: 42401, 42423, 42416, 9309)

Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Gene Symbol	Gene Name	Summary	GeneRIF	Pathway	Homology
275.61	111.83	2.46	NM_012694	Slc6a3	Rattus norvegicus solute carrier family 6 (neurotransmitter transporter, dopamine), member 3 (Slc6a3), mRNA [NM_012694]	ref|NM_01269 4|gb|M80670| ens|ENSRNOT0 0000024015|t c|TC569830	Rn.10093	Slc6a3	solute carrier family 6 (neurotransmitter transporter, dopamine), member 3	acts as a sodium-dependent dopamine transporter; may play a role in regulation of dopamine metabolism and signaling [RGD]	The decrease in DAT cell surface expression in the mPFC may be responsible for decreased DAT function in the mPFC of stimulated compared with deprived rats; there is plasticity in the regulatory mechanisms mediating DAT trafficking and function.// the car	-	[Human, Mouse]Homolo gene:55547
1270.69	704.13	1.80	NM_017016	Hdc	Rattus norvegicus histidine decarboxylase (Hdc), mRNA [NM_017016]	ref|NM_01701 6|gb|M38759| gb|AW_346674 |gb|M29591	Rn.48653	Hdc	histidine decarboxyla se	involved in the formation of histamine from its precursor histidine [RGD]	histidine decarboxylase mRNA and protein are found in rat aorta and more specifically in cultured rat aortic smooth muscle, indicative of their capability to synthesize histamine// Identification of catalytically important residues in L-histidine decarbox	KEGG pathway: Histidine metabolism	[Human, Mouse]Homolo gene:20490
888.26	560.95	1.58	NM_012740	Th	Rattus norvegicus tyrosine hydroxylase (Th), mRNA [NM_012740]	ref|NM_01274 0|gb|L22651| gb|M10244|en s|ENSRNOT000 00027682	Rn.11082	Th	tyrosine hydroxylase	catalyzes the rate limiting step in catecholamine biosynthesis; may be involved in response to hypoxia [RGD]	The kinetics of reduction of ferric TyrH by several reductants were determined by anaerobic stopped-flow spectroscopy. phosphorylation does not directly regulate the interconversion of the ferric and ferrous forms// The results indicate that the NGF/NGF	KEGG pathway: Parkinson's disease// KEGG pathway: Tyrosine metabolism	[Human, Mouse]Homolo gene:307

[表41]

表58 Lに対して発現増加した視床下部の注目遺伝子
生体アミン代謝 (GO ID: 9308, 6584, 6576)

Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Gene Symbol	Gene Name	Summary	GeneRIF	Pathway	Homology
275.61	111.83	2.46	NM_012694	Slc6a3	Rattus norvegicus solute carrier family 6 (neurotransmitter transporter, dopamine), member 3 (Slc6a3), mRNA [NM_012694]	ref|NM_0126 94|gb|M8057 0|ens|ENSRN OT0000002401 5|tc|TC569 830	Rn.10093	Slc6a3	solute carrier family 6 (neurotransmitter transporter, dopamine), member 3	acts as a sodium-dependent dopamine transporter; may play a role in regulation of dopamine metabolism and signaling [RGD]	The decrease in DAT cell surface expression in the mPFC may be responsible for decreased DAT function in the mPFC of stimulated compared with deprived rats: there is plasticity in the regulatory mechanisms mediating DAT trafficking and function.// the car	-	[Human, Mouse]Homo logene:555 47

[表42]

表59 Liに対して発現減少した根床下部の注目遺伝子
陽イオン結合 (GO ID: 5509, 43169)

Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Gene Symbol	Gene Name	Summary	GeneRIF	Pathway	Homology
192.09	296.29	0.65	NM_172224	Impa2	Rattus norvegicus inositol (myo)-1(or 4)-monophosphatase 2 (Impa2), mRNA [NM_172224]	ref|NM_172224|gb|AY160191|gb|BC008354|ens|ENSRNOT00000025147	Rn.856	Impa2	inositol (myo)-1(or 4)-monophosphatase 2	mouse homolog is an enzyme that catalyzes the synthesis of free myo-inositol from various myo-inositol monophosphates [RGD]	-	KEGG pathway: Inositol phosphate metabolism// KEGG pathway: Phosphatidylinositol signaling system// KEGG pathway: Streptomycin biosynthesis	[Human, Mouse]Homolog ene:22799
390.79	588.19	0.66	NM_133415	Efcbp2	Rattus norvegicus neuronal calcium binding 2 (Efcbp2), mRNA [NM_133415]	ref|NM_133415|gb|AF193751|ens|ENSRNOT00000020341	Rn.62703	Efcbp2	EF hand calcium binding protein 2	may mediate calcium signaling and play a role in neuronal function [RGD]	-	-	[Human, Mouse]Homolog ene:62200

Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Gene Symbol	Gene Name	Summary	GeneRIF	Pathway	Homology
115.10	188.76	0.61	NM_031828	Kcnma1	Rattus norvegicus potassium large conductance calcium-activated channel, subfamily M, alpha member 1 (Kcnma1), mRNA [NM_031828]	ref|NM_031828|Rn.30616 8|ref|XM_579539|gb|AF083342|gb|AJ617197	Rn.30616	Kcnma1	potassium large conductance calcium-activated channel, subfamily M, alpha member 1	large-conductance Ca(2+)-activated K(+) channel; may be involved in the shortened duration of action potential in hippocampal CA1 pyramidal neurons and in channel activity in carotid body chemoreceptor cells [RGD]	Data suggest that the regulation of STREX splicing directed by estrogen and Pg provides a mechanism for Slo's PKA-related phenotypic alteration with pregnancy.// there is a novel interaction between the C-terminal tail of the BKCa channel and the light chain of MAP1A, which enables channel association with and modulation by the cytoskeleton// Slo gene-encoded BK potassium channels alternative splicing variants are found with and without the 'STREX' exon. In the adrenal medulla, castration increased STREX transcripts slightly and decreased STREX representation in the pituitary.// cAMP-dependent vasodilators activate BK(Ca) channels in PASMC of rats via PKG-dependent and PKA-independent signaling pathways, which suggests cross-activation between cyclic nucleotide-dependent protein kinases in pulmonary arterial smooth muscle// Steady-state and closed-state inactivation properties// Nitric oxide enhances Ca(2+)-dependent K(+) channel activity in rat carotid body cells.// (The rest is omitted.)	-	[Human, Mouse]Homolo gene:1693

Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Gene Symbol	Gene Name	Summary	GeneRIF	Pathway	Homology
44.48	71.33	0.62	NM_019292	Ca3	Rattus norvegicus carbonic anhydrase 3 (Ca3), mRNA [NM_019292]	ref|NM_019292|gb|AB003082|gb|AB003083|gb|BC006198|0	Rn.1647	Ca3	carbonic anhydrase 3	catalyzes hydration of carbon dioxide; may be involved in cellular response to oxidative stress [RGD]	conformational changes provide a mechanistic basis for modulation of the susceptibility of carbonic anhydrase 3 to glutathionylation.// Dorzolamide, a CA3 inhibitor, caused a decrease in dexamethasone and insulin-induced leptin secretion in epididymal adipocytes tissue.// leptin decreased CA III expression while insulin increased it which suggests that the decrease in CA III expression observed in obesity in rat adipose tissue may be related to hyperleptinemia// Major soluble protein in rat liver and muscle. Function probably to protect proteins of these tissues from oxidation catalyzed by iron-containing degradation products of haemoglobin and myoglobin.// Androgen-linked control of carbonic anhydrase III expression occurs in rat perivenous hepatocytes	KEGG pathway: Nitrogen metabolism	[Human, Mouse]HomoloGene:31298
27.69	42.90	0.65	AA800765	AA800765	AA800765 EST190262 Normalized rat lung, Bento Soares Rattus sp. cDNA clone RLUAL20 3' end, mRNA sequence [AA800765]	gb|AA800765|gb|AA892549	Rn.3576	Manla_predicted	mannosidase 1, alpha (predicted)	-	-	-	[Human, Mouse]HomoloGene:4316

Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Gene Symbol	Gene Name	Summary	GeneRIF	Pathway	Homology
246.07	372.76	0.66	U90444	U90444	Rattus norvegicus double stranded RNA specific deaminase RED1 mRNA, partial cds. [U90444]	gb|U90444|TC|TC560724	Rn.89675	Adarb1	adenosine deaminase, RNA-specific, B1	catalyzes the deamination of adenosine in double stranded mRNA: required for pre-mRNA editing of brain glutamate receptor RNAs [RGD]	RNA structure-dependent recognition by the two double-stranded RNA binding motifs of rat ADAR2.// the nucleolar localization of ADAR2 represents an important mechanism by which RNA editing can be modulated by the sequestration of enzymatic activity from potential RNA substrates in the nucleoplasm// interaction with RNA transcripts containing selective and nonselective editing sites// both sequence and structural elements are required to define adenosine moieties targeted for specific ADAR2-mediated deamination	-	[Human, Mouse]Homolo gene:8280
133.95	204.57	0.65	NM_019211	Rasgrp1	Rattus norvegicus RAS guanyl releasing protein 1 (Rasgrp1). mRNA [NM_019211]	ref|NM_019211|gb|AF081195|gb|AF060881|ens|ENSRNO00000007687	Rn.16268	Rasgrp1	RAS guanyl releasing protein 1	putative guanine nucleotide exchange factor with Ca2+ and diacylglycerol binding domains; may activate Rap protein mediated inhibition of Ras signaling pathways [RGD]	contribution of these two lipid pools to PLC-dependent Ras activation in response to TCR. triggering// RasGRP1 is a diacylglycerol/phorbol ester receptor in epidermal keratinocytes	KEGG pathway: MAPK signaling pathway// KEGG pathway: T cell receptor signaling pathway	[Human, Mouse]Homolo gene:4195
54.73	82.84	0.66	NM_021698	F13a	Rattus norvegicus coagulation factor XIII, A1 subunit (F13a), mRNA [NM_021698]	ref|NM_021698|gb|Y12502|gb|AW619018|ens|ENSRNOT00000021568	Rn.42925	F13a1	coagulation factor XIII, A1 subunit	enhances gastric mucosa healing; reduces endothelial permeability [RGD]	-	KEGG pathway: Complement and coagulation cascades	[Human, Mouse]Homolo gene:20077

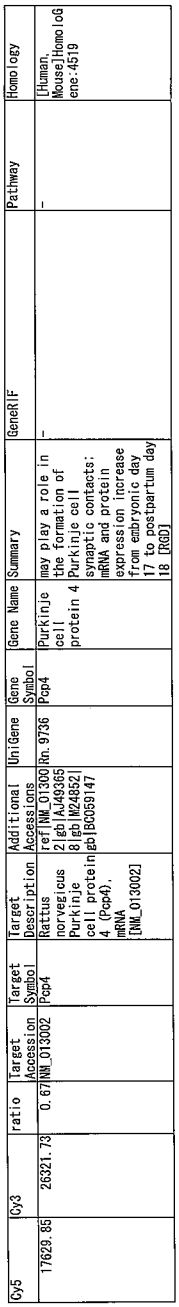
Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Gene Symbol	Gene Name	Summary	GeneRIF	Pathway	Homology
2578.08	5839.26	0.44	NM_133307	Prkcd	Rattus norvegicus protein kinase C, delta (Prkcd), mRNA [NM_133307]	ref|NM_133307|gb|AF219629|gb|BC076505|gb|AJ230633	Rn.98279	Prkcd	protein kinase C, delta	mediates mitochondrial-dependent apoptosis [RGD]	Tetradecanoylphorbol acetate, endothelin-1, and pdgf regulate the gene expression of Pkcd.// Data suggest that proteolytic activation of the proapoptotic protein kinase Cdelta (PKCdelta) by caspase 3 is a key step in 6-hydroxydopamine-induced cell death.// These results suggest that in RBA-1 cells, bradykinin-induced cytosolic phospholipase A2 expression is sequentially mediated through activation of PKC-delta, p42/p44 MAPK, and NF-kappaB.// The present data show that lovastatin may induce neuroblast apoptosis by both caspase-dependent and independent pathways.// Results demonstrate that wild-type alpha-synuclein interacts with the pro-apoptotic molecules BAD and protein kinase C delta to protect dopaminergic neuronal cells against neurotoxic insults.// vascular smooth muscle cell apoptosis proceeds through a pathway that involves PKCdelta, the intermediary p38 MAPK, and the downstream target tumor suppressor p53// (The rest is omitted.)	KEGG pathway: Tight junction// KEGG pathway: Type II diabetes mellitus	[Human, Mouse]HomoloGene:55963
284.05	474.89	0.60	NM_022302	Efcbp1	Rattus norvegicus EF hand calcium binding protein 1 (Efcbp1), mRNA	ref|NM_022302|gb|AF193755|ens|ENSRNOT00000009718|tc|NP399992	Rn.64485	Efcbp1	EF hand calcium binding protein 1	may play a role in neuronal Ca(2+)-signalling [RGD]	Determines domain structure of the Necab 1 protein that expressed in the brain.	--	[Human, Mouse]HomoloGene:11172

Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Gene Symbol	Gene Name	Summary	GeneRIF	Pathway	Homology
1112.96	1765.21	0.63	NM_019372	Ppm2c	Rattus norvegicus protein phosphatase 2C, magnesium-dependent, catalytic subunit (Ppm2c), mRNA	ref|NM_019372.2|gb|AF062743.1|gb|AW920770.1|ens|ENSRNOT00000021642	Rn.31799	Ppm2c	protein phosphatase 2C, magnesium dependent, catalytic subunit	catalytic subunit of the mitochondrial matrix phosphatase; involved in reactivation of the pyruvate dehydrogenase complex [RGD]	role of PP2C and AMPK in the derangements of cardiac lipid metabolism in obesity// Asp445 might be involved in the control of interactions between PDP1c and the protein substrate pyruvate dehydrogenase	-	[Human, Mouse]HomoloGene:31928
292.12	457.72	0.64	XM_221901	Nptx2_predicted	PREDICTED: Rattus norvegicus neuronal pentraxin II (predicted) (Nptx2_predicted), mRNA [XM_221901]	ref|XM_221901.1|gb|BI282491.1|ens|ENSRNOT00000049444|ens|ENSRNOT00000001331	-	Nptx2	neuronal pentraxin II	-	-	-	[Human, Mouse]HomoloGene:1892
33.11	53.97	0.61	NM_031590	Wisp2	Rattus norvegicus WNT1 inducible signaling pathway protein 2 (Wisp2), mRNA [NM_031590]	ref|NM_031590.1|gb|AF259980.1|gb|BG089180.1|ens|ENSRNOT00000014346	Rn.53991	Wisp2	WNT1 inducible signaling pathway protein 2	involved in negative regulation of cell growth; mRNA expression is lost upon cell transformation induced by activated H-ras oncogene and inactivated p53 tumor supressor [RGD]	data indicate that CCN5 protein is positively regulated by estrogen in the rat uterus and suggests that this gene may play an important role in maintaining normal uterine physiology	-	[Human, Mouse]HomoloGene:2882

Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Gene Symbol	Gene Name	Summary	GeneRIF	Pathway	Homology
224.81	377.95	0.59	NM_053981	Kcnj12	Rattus norvegicus potassium inwardly-rectifying channel, subfamily J, member 12 (Kcnj12), mRNA [NM_053981]	ref|NM_053981|gb|X78461|ens|ENSRNOT00000003138|tc|TC5700004	Rn.10406	Kcnj12	potassium inwardly-rectifying channel, subfamily J, member 12	inward rectifier potassium channel [RGD]	preferential Golgi export of Kir2.1 controls the stoichiometry of Kir2.x heteromers expressed on the cell surface.// There was a strong correlation between the transcript levels of Kir2.1 and Kv-induced relaxation.// In PCR analyses using isolated juxtaglomerular cells, the mRNA for Kir2.1 (Kcnj2) and Kir2.2 (Kcnj12) was detected. Kir2.1 is the dominant component of the channel.// Myo15 and Kcnj12 can be regarded as candidate genes for the deafblind phenotype of the LEW-ci2 rat.// a complex composed of SAP97, CASK, Veli, and Mint1 associates with Kir2 channels via the C-terminal PDZ-binding motif: SAP97, Veli-1, or Veli-3 binds directly to the Kir2.2 C terminus and recruits CASK// candidate gene for the deafblind phenotype of the LEW-ci2 rat	-	[Human, Mouse]Homolog ene:7793
203.20	319.64	0.64	NM_053324	Syt9	Rattus norvegicus synaptotagmin 9 (Syt9), mRNA [NM_053324]	ref|NM_053324|AF375464|gb|U20108|ens|ENSRNOT00000026607	Rn.10194	Syt9	synaptotagmin IX	member of a family of membrane proteins characterized by one transmembrane region and two C2 domains [RGD]	Data suggest that synaptotagmin 9 may act as Ca(2+) sensor for beta-cell secretion.	-	[Human, Mouse]Homolog ene:11062
207.97	356.58	0.58	NM_139217	Kcnc2	Rattus norvegicus potassium voltage gated channel, Shaw-related subfamily, member 2, (Kcnc2), transcript variant b, mRNA	ref|NM_139217|gb|M59313|gb|M84203|ens|ENSRNOT00000005773	Rn.9733	Kcnc2	potassium voltage gated channel, Shaw-related subfamily, member 2	a voltage-gated K+ channel; functions as a delayed rectifier-type K+ channel activated by large membrane depolarizations [RGD]	Kv3-like currents may be important for maintaining spike width and calcium influx within acceptable limits during repetitive firing.// strong, selective localization of Kv3.2 to basket cell axons of cerebellum.	-	[Human, Mouse]Homolog ene:71199

Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Gene Symbol	Gene Name	Summary	GeneRIF	Pathway	Homology
481.00	905.44	0.53	XM_230761	Abba2bp_predicted	PREDICTED: Rattus norvegicus amyloid beta (A4) precursor protein-binding, family A, member 1 binding protein (predicted) (Abba2bp_predicted). mRNA	ref|XM_230761.1|ens|ENSRNOT00000022115 |ens|ENSRNOT00000047894|ens|ENSRNOT00000043456	Rn.14505	Abba2bp_predicted	amyloid beta (A4) precursor protein-binding, family A, member 1 binding protein (predicted)	-	-	-	[Human, Mouse]Homolo gene:10092
24.31	39.73	0.61	XM_342172	Thbs4	PREDICTED: Rattus norvegicus thrombospondin 4 (Thbs4). mRNA [XM_342172]	ref|XM_342172.2|gb|X89963|gb|AW916235|ens|ENSRNOT00000017078	Rn.11207	Thbs4	thrombospondin 4	extracellular matrix protein, involved in neuronal development [RGD]	-	KEGG pathway: Cell Communication// KEGG pathway: ECM-receptor interaction// KEGG pathway: Focal adhesion// KEGG pathway: TGF-beta signaling pathway	[Human, Mouse]Homolo gene:20691

Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Gene Symbol	Gene Name	Summary	GeneRIF	Pathway	Homology
338.67	553.40	0.61	NM_021771	Trpc3	Rattus norvegicus transient receptor potential cation channel, subfamily C, member 3 (Trpc3), mRNA [NM_021771]	ref|NM_021771|gb|AB022233|ens|ENSRNO T0000002194 8|tc|TC569878	Rn. 45385	Trpc3	transient receptor potential cation channel, subfamily C, member 3	a calcium-activated cation channel [RGD]	Study shows, for the first time, increased TRPC3 channel expression and increased TRPC3-related calcium influx in spontaneously hypertensive rats.// prostate smooth muscle PS1 cells express TRPC3 and TRPC6 proteins which function as receptor- and store-operated Ca(2+) entry pathways.// TRPC3 mediates UTP-induced depolarization of arterial smooth muscle cells// TRPC3/TRPC6 channels are localized to the apical region of polarized epithelial cells, which in salivary gland ducts could contribute to the regulation of salivary [Ca2+] and secretion// TRPC3a gave rise to Ca2+-entry channels that are not only activated by the Gq-phospholipase C beta pathway// siRNA specific for TRPC1 and TRPC3 in proliferating cells inhibited approximately the same amount of Store operated calcium entry.// Data suggest that VAMP2-dependent exocytosis regulates plasma membrane insertion of TRPC3 channels and contributes to carbachol-stimulation of Ca2+ influx.// (The rest is omitted.)	-	[Human, Mouse]HomoloGene:20708
123.77	323.37	0.38	NM_053521	Slc5a7	Rattus norvegicus solute carrier family 5 (choline transporter), member 7 (Slc5a7), mRNA [NM_053521]	ref|NM_053521|gb|AB030947|ens|ENSRNO T0000001454 8	Rn. 44872	Slc5a7	solute carrier family 5 (choline transporter), member 7	high-affinity choline transporter: give choline to nuerons for the synthesis of acetylcholine [RGD]	This protein is expressed in the rat trachea.// close apposition of CHT1 to reported sites of localization of choline acetyltransferase in these cells is strongly in favour of ACh synthesis being fuelled by choline uptake via CHT1 in these epithelia// high-affinity choline transporter, choline transporter 1, in nerve fibers and epithelial cells in the human and rat skin supporting the pivotal role of this transporter in both the neuronal and non-neuronal cholinergic system of the skin.	-	[Human, Mouse]HomoloGene:32516



Cy5	Cy3	ratio	Target Accession	Target Symbol	Target Description	Additional Accessions	UniGene	Gene Symbol	Gene Name	Summary	GeneRIF	Pathway	Homology
17629.85	26321.73	0.67	NM_013002	Pcp4	Rattus norvegicus Purkinje cell protein 4 (Pcp4), mRNA [NM_013002]	ref|NM_013002|Rn.9736 2|gb|AJ49365 8|gb|M24852| gb|BC059147		Pcp4	Purkinje cell protein 4	may play a role in the formation of Purkinje cell synaptic contacts; mRNA and protein expression increase from embryonic day 17 to postpartum day 18 [RGD]	-	-	[Human, Mouse]Homolo Gene:4519

[請求項11] 前記分子は抗体、リガンドタンパク質又は受容体タンパク質であることを特徴とする請求項7～10のいずれか1項記載の検査キット。

[請求項12] 前記核酸又は分子は支持体に固定されていることを特徴とする請求項7～10のいずれか1項記載の検査キット。

[請求項13] 下記の表155、159、164、172、178、185、190、198又は202に示す遺伝子群中の各遺伝子の発現量をヒト生体由来試料において測定する第1のステップと、

測定した各遺伝子の発現量に基づいて、ヒトの陽性感情又は健康度を評価する第2のステップと

を含む、ヒトの陽性感情又は健康度の評価方法。

[表43]

表155　遺伝子セット5(No.1-17:機能面で注目する遺伝子,No.18-47:発現増加・減少した遺伝子上位15個)

No	Target(Gene)Symbol	Target Accession	UniGene	Up/Down	被験者群	配列番号
1	PTPRC	NM_080923	Hs.192039	Up	A+B	162
2	PAWR	NM_002583	Hs.643130	Up	A+B	163
3	TRAT1	NM_016388	Hs.138701	Up	A+B	164
4	STXBP4	NM_178509	Hs.35199	Down	A+B	69
5	SLC2A5	NM_003039	Hs.530003	Down	A+B	165
6	SLC2A3	NM_006931	Hs.419240	Down	A+B	166
7	SORBS1	NM_001034954	Hs.38621	Down	A+B	167
8	AKT1	NM_005163	Hs.525622	Down	A+B	71
9	APOL6	NM_030641	Hs.257352	Down	A+B	68
10	ATG10	NM_031482	Hs.651173	Down	A+B	168
11	SNX17	NM_014748	Hs.278569	Down	A+B	59
12	PIGS	NM_033198	Hs.462550	Down	A+B	169
13	FNTB	NM_002028	Hs.632345	Down	A+B	170
14	SLC9A5	NM_004594	Hs.439650	Down	A+B	171
15	LOC133308	NM_178833	Hs.546482	Down	A+B	172
16	CLN5	NM_006493	Hs.30213	Down	A+B	173
17	CLN3	NM_001042432	Hs.628393	Down	A+B	174
18	COMMD6	NM_203497	Hs.508266	Up	A+B	75
19	COX7B	NM_001866	Hs.522699	Up	A+B	175
20	P2RY5	NM_005767	Hs.123464	Up	A+B	76
21	LMNB1	NM_005573	Hs.89497	Up	A+B	139
22	EVI2A	NM_001003927	Hs.591198	Up	A+B	74
23	CD52	NM_001803	Hs.276770	Up	A+B	78
24	CSTA	NM_005213	Hs.518198	Up	A+B	81
25	FKSG2	NM_021631	Hs.651853	Up	A+B	176
26	EEF1E1	NM_004280	Hs.631818	Up	A+B	177
27	APP	NM_000484	Hs.651215	Up	A+B	178
28	SH2D1A	NM_002351	Hs.349094	Up	A+B	179
29	PREI3	NM_015387	Hs.645458	Up	A+B	-
30	CFL2	NM_021914	Hs.180141	Up	A+B	180
31	TCF12	NM_207038	Hs.511504	Up	A+B	181
32	LY96	NM_015364	Hs.69328	Up	A+B	82
33	TEP1	NM_007110	Hs.508835	Down	A+B	91
34	ARHGAP26	NM_015071	Hs.293593	Down	A+B	93
35	CPNE8	NM_153634	Hs.40910	Down	A+B	182
36	PEX11G	NM_080662	Hs.515100	Down	A+B	183
37	GPR180	NM_180989	Hs.439363	Down	A+B	184
38	GSTA2	NM_000846	Hs.94107	Down	A+B	185
39	DRD3	NM_033663	Hs.121478	Down	A+B	186
40	RABGAP1		Hs.271341	Down	A+B	-
41	H6PD	NM_004285	Hs.463511	Down	A+B	187
42	F11R	NM_144503	Hs.517293	Down	A+B	188
43	ATM	NM_000051	Hs.367437	Down	A+B	189
44	KRT71	NM_033448	Hs.433845	Down	A+B	190
45	VIL2		Hs.642735	Down	A+B	-
46	APOL6	NM_030641	Hs.257352	Down	A+B	68
47	TCL6	NM_020552	Hs.510368	Down	A+B	191

[表44]

表159　遺伝子セット6(No.1-2:機能面で注目する遺伝子,No.3-32:発現増加・減少した遺伝子上位15個)

No	Target(Gene)Symbol	Target Accession	UniGene	Up/Down	被験者群	配列番号
1	RPS3A	NM_001006	Hs.356572	Down	C+D	192
2	PPP1R13B	NM_015316	Hs.436113	Down	C+D	193
3	CGRRF1	NM_006568	Hs.59106	Up	C+D	194
4	P2RY6	NM_176798	Hs.16362	Up	C+D	195
5	PDGFC	NM_016205	Hs.570855	Up	C+D	38
6	SH3RF1	NM_020870	Hs.301804	Up	C+D	196
7	MIPEP	NM_005932	Hs.507498	Up	C+D	197
8	LGR6	NM_001017403	Hs.497402	Up	C+D	198
9	B3GNT5	NM_032047	Hs.208267	Up	C+D	148
10	TMEM23	NM_147156	Hs.386215	Up	C+D	-
11	SUCNR1	NM_033050	Hs.279575	Up	C+D	199
12	ANXA3	NM_005139	Hs.480042	Up	C+D	200
13	TSPAN2	NM_005725	Hs.310458	Up	C+D	201
14	PDE8B	NM_003719	Hs.584830	Up	C+D	202
15	SGPP1	NM_030791	Hs.24678	Up	C+D	116
16	PROK2	NM_021935	Hs.528665	Up	C+D	203
17	PTPRF	NM_002840	Hs.272062	Up	C+D	204
18	PROKR2	NM_144773	Hs.375029	Down	C+D	205
19	ANKS4B	NM_145865	Hs.115959	Down	C+D	206
20	RAP1GAP	NM_002885	Hs.148178	Down	C+D	207
21	FAAH	NM_001441	Hs.528334	Down	C+D	208
22	LCT	NM_002299	Hs.551506	Down	C+D	209
23	RGS12	NM_198229	Hs.527061	Down	C+D	210
24	DLST	NM_001933	Hs.525459	Down	C+D	211
25	ATE1	NM_001001976	Hs.632080	Down	C+D	212
26	CCNF	NM_001761	Hs.1973	Down	C+D	213
27	ALPI	NM_001631	Hs.37009	Down	C+D	214
28	CSN1S1	NM_001890	Hs.3155	Down	C+D	215
29	VASH2	NM_024749	Hs.96885	Down	C+D	216
30	CHST4	NM_005769	Hs.251383	Down	C+D	217
31	TAT	NM_000353	Hs.161640	Down	C+D	-
32	FBLN2	NM_001004019	Hs.198862	Down	C+D	218

[表45]

表164 遺伝子セット1(No.1-31:機能面で注目する遺伝子,No.32-61:発現増加・減少した遺伝子上位15個)

No	Target(Gene)Symbol	Target Accession	UniGene	Up/Down	被験者群	配列番号
1	FGFR1OP	NM_007045	Hs.487175	Up	A	1
2	CASP8AP2	NM_012115	Hs.558218	Up	A	2
3	PROK2	NM_021935	Hs.528665	Up	A	3
4	FCER1A	NM_002001	Hs.897	Up	A	4
5	CD69	NM_001781	Hs.208854	Up	A	5
6	PAQR3	NM_001040202	Hs.632591	Up	A	6
7	SLC6A4	NM_001045	Hs.591192	Up	A	7
8	GGCX	NM_000821	Hs.77719	Up	A	8
9	HBA2	NM_000517	Hs.449630	Up	A	9
10	ADH5	NM_000671	Hs.78989	Up	A	10
11	JUN	NM_002228	Hs.525704	Down	A	11
12	TP53	NM_000546	Hs.408312	Down	A	12
13	RAB5B		Hs.567328	Down	A	-
14	RAB8A	NM_005370	Hs.642874	Down	A	13
15	RAB12	NM_001025300	Hs.270074	Down	A	14
16	RAB20	NM_017817	Hs.508720	Down	A	15
17	RAB30	NM_014488	Hs.40758	Down	A	16
18	VISA		Hs.646283	Down	A	-
19	CD55		Hs.527653	Down	A	-
20	IGHG1	BC092518	Hs.510635	Down	A	-
21	SEMA3G	NM_020163	Hs.59729	Down	A	17
22	CD84	NM_003874	Hs.398093	Down	A	-
23	CD3G	NM_000073	Hs.2259	Down	A	18
24	CD177	NM_020406	Hs.232165	Down	A	19
25	NFAT5	NM_173215	Hs.371987	Down	A	20
26	HDGF	NM_004494	Hs.506748	Down	A	21
27	TNFAIP3	NM_006290	Hs.591338	Down	A	22
28	PRLHR	NM_004248	Hs.248119	Down	A	23
29	SYT2	NM_177402	Hs.585015	Down	A	24
30	RCP9	NM_014478	Hs.300684	Down	A	25
31	SPAG8	NM_172312	Hs.256747	Down	A	26
32	IMPA1	NM_005536	Hs.555086	Up	A	27
33	XPR1		Hs.648372	Up	A	-
34	B3GNT2	NM_006577	Hs.173203	Up	A	28
35	BCLAF1	NM_014739		Up	A	29
36	PSIP1	NM_021144	Hs.493516	Up	A	30
37	LGALS8	NM_006499	Hs.4082	Up	A	31
38	SEC24A	NM_021982	Hs.595540	Up	A	32
39	LOC492311	NM_001007189	Hs.200938	Up	A	-
40	ORMDL1	NM_016467	Hs.651259	Up	A	33
41	WHSC1	NM_133330	Hs.113876	Up	A	34
42	XRCC3	NM_005432	Hs.592325	Up	A	35
43	TMEM167	NM_174909	Hs.355606	Up	A	36
44	PREI3	NM_015387	Hs.645458	Up	A	-
45	SLC19A2	NM_006996	Hs.30246	Up	A	37
46	PDGFC	NM_016205	Hs.570855	Up	A	38
47	ERCC4	NM_005236	Hs.567265	Down	A	39
48	SH3PXD2B	NM_001017995	Hs.285666	Down	A	40
49	DUX2	NM_012147		Down	A	41
50	AP1S1	NM_001283	Hs.563509	Down	A	42
51	GATA2	NM_032638	Hs.367725	Down	A	43
52	LOC728371	XR_015273	Hs.558795	Down	A	44
53	PFKFB3	NM_004566	Hs.195471	Down	A	45
54	PHGDH	NM_006623	Hs.487296	Down	A	46
55	CENPP		Hs.459896	Down	A	-
56	OR5A1	NM_001004728	Hs.553649	Down	A	47
57	ADCK1	NM_020421	Hs.413208	Down	A	48
58	TFEC	NM_012252	Hs.125962	Down	A	49
59	RRH	NM_006583	Hs.352262	Down	A	50
60	DOK6	NM_152721	Hs.569915	Down	A	51
61	SAMD7	NM_182610	Hs.439922	Down	A	52

[表46]

表172　遺伝子セット2(No. 1-25:機能面で注目する遺伝子, No. 26-55:発現増加・減少した遺伝子上位15個)

No	Target(Gene)Symbol	Target Accession	UniGene	Up/Down	被験者群	配列番号
1	SOCS1	NM_003745	Hs. 50640	Down	B	53
2	CCR1	NM_001295	Hs. 301921	Down	B	54
3	CSF2RB	NM_000395	Hs. 592192	Down	B	55
4	STAT5A	NM_003152	Hs. 437058	Down	B	56
5	STAT3	NM_213662	Hs. 463059	Down	B	57
6	TNFRSF1B	NM_001066	Hs. 256278	Down	B	58
7	SNX17	NM_014748	Hs. 278569	Down	B	59
8	SCARF1	NM_145351	Hs. 647430	Down	B	60
9	LDLR		Hs. 213289	Down	B	-
10	STARD3	NM_006804	Hs. 77628	Down	B	61
11	CLN8	NM_018941	Hs. 127675	Down	B	62
12	APOL1	NM_145343	Hs. 114309	Down	B	63
13	ATP10A	NM_024490	Hs. 128041	Down	B	64
14	PSAP	NM_001042465	Hs. 523004	Down	B	65
15	OSBP2	NM_030758	Hs. 517546	Down	B	66
16	SLC27A1	NM_198580	Hs. 363138	Down	B	67
17	APOL6	NM_030641	Hs. 257352	Down	B	68
18	SOCS1	NM_003745	Hs. 50640	Down	B	53
19	STXBP4	NM_178509	Hs. 35199	Down	B	69
20	SOCS3	NM_003955	Hs. 527973	Down	B	70
21	AKT1	NM_005163	Hs. 525622	Down	B	71
22	MLLT7	NM_005938	Hs. 584654	Down	B	-
23	CEBPB	NM_005194	Hs. 642680	Down	B	72
24	CEBPB	NM_005194	Hs. 642680	Down	B	72
25	NLRP12	NM_033297	Hs. 631573	Down	B	73
26	EVI2A	NM_001003927	Hs.591198	Up	B	74
27	COMMD6	NM_203497	Hs.508266	Up	B	75
28	P2RY5	NM_005767	Hs.123464	Up	B	76
29	COMMD8	NM_017845	Hs.23956	Up	B	77
30	CD52	NM_001803	Hs.276770	Up	B	78
31	S100P	NM_005980	Hs.2962	Up	B	79
32	COX7C	NM_001867	Hs.430075	Up	B	80
33	CSTA	NM_005213	Hs.518198	Up	B	81
34	LY96	NM_015364	Hs.69328	Up	B	82
35	S100A8	NM_002964	Hs.416073	Up	B	83
36	SLC4A7	NM_003615	Hs.250072	Up	B	84
37	PHF6	NM_032458	Hs.356501	Up	B	85
38	TMEM167	NM_174909	Hs.355606	Up	B	36
39	EIF1AX	NM_001412	Hs.522590	Up	B	86
40	CRTAM	NM_019604	Hs.159523	Up	B	87
41	PIP5K1A	NM_003557	Hs.546316	Down	B	88
42	ERBB2	NM_001005862	Hs.446352	Down	B	89
43	COL25A1	NM_198721	Hs.112925	Down	B	90
44	TEP1	NM_007110	Hs.508835	Down	B	91
45	PKD1L1	NM_138295	Hs.195979	Down	B	92
46	ARHGAP26	NM_015071	Hs.293593	Down	B	93
47	RAB13	NM_002870	Hs.151536	Down	B	94
48	KCNAB3	NM_004732	Hs.435074	Down	B	95
49	ARHGAP24	NM_001025616	Hs.444229	Down	B	96
50	DDAH1	NM_012137	Hs.379858	Down	B	97
51	DOCK6	NM_020812	Hs.591002	Down	B	98
52	FABP6	NM_001040442	Hs.519719	Down	B	99
53	GALNT9	NM_021808	Hs.301062	Down	B	100
54	EBI3	NM_005755	Hs.501452	Down	B	101
55	BAI2	NM_001703	Hs.524138	Down	B	102

[表47]

表178　遺伝子セット3(No.1-8:機能面で注目する遺伝子,No.9-38:発現増加・減少した遺伝子上位15個)

No	Target(Gene)Symbol	Target Accession	UniGene	Up/Down	被験者群	配列番号
1	APBA2BP	NM_031232	Hs.516986	Down	C	-
2	EFCBP2	NM_019065	Hs.140950	Down	C	-
3	ASS1	NM_000050	Hs.160786	Down	C	103
4	NAGS	NM_153006	Hs.8876	Down	C	104
5	IL6	NM_000600	Hs.512234	Down	C	105
6	FLT3	NM_004119	Hs.507590	Down	C	106
7	IL4	NM_000589	Hs.73917	Down	C	107
8	CD1D	NM_001766	Hs.1799	Down	C	108
9	HDC	NM_002112	Hs.1481	Up	C	109
10	PFKFB3	NM_004566	Hs.195471	Up	C	45
11	FCER1A	NM_002001	Hs.897	Up	C	110
12	AGL	NM_000028	Hs.904	Up	C	111
13	LTF	NM_002343	Hs.529517	Up	C	112
14	HBA1	NM_000558	Hs.449630	Up	C	113
15	ORM2	NM_000608	Hs.522356	Up	C	114
16	IL3RA	NM_002183	Hs.632790	Up	C	115
17	STCH	NM_006948	Hs.352341	Up	C	-
18	HBA2	NM_000517	Hs.449630	Up	C	9
19	SGPP1	NM_030791	Hs.24678	Up	C	116
20	PTPRM	NM_002845	Hs.49774	Up	C	117
21	RERG	NM_032918	Hs.199487	Up	C	118
22	BCLAF1	NM_014739		Up	C	29
23	MASA	NM_021204	Hs.18442	Up	C	-
24	QRICH2	NM_032134	Hs.252739	Down	C	119
25	PLAC4	NM_182832	Hs.472492	Down	C	120
26	ECM1	NM_004425	Hs.81071	Down	C	121
27	TCF19	NM_007109	Hs.584807	Down	C	122
28	CPA1	NM_001868	Hs.2879	Down	C	123
29	THAP2	NM_031435	Hs.245798	Down	C	124
30	SCRG1		Hs.7122	Down	C	-
31	CDH6	NM_004932	Hs.171054	Down	C	125
32	FOXE1	NM_004473	Hs.159234	Down	C	126
33	METAP2	NM_006838	Hs.591005	Down	C	127
34	MAPK8IP2	NM_012324	Hs.558180	Down	C	128
35	GAL3ST3	NM_033036	Hs.208343	Down	C	129
36	FCER2	NM_002002	Hs.465778	Down	C	130
37	MAGEA5	NM_021049	Hs.18048	Down	C	131
38	RYR1	NM_001042723	Hs.466664	Down	C	132

[表48]

表185　遺伝子セット4(No. 1-7:機能面で注目する遺伝子, No. 8-37:発現増加・減少した遺伝子上位15個)

No	Target(Gene)Symbol	Target Accession	UniGene	Up/Down	被験者群	配列番号
1	TLR7	NM_016562	Hs. 443036	Up	D	133
2	BCL2	NM_000633	Hs. 150749	Up	D	134
3	TLR8	NM_016610	Hs. 272410	Up	D	135
4	PPARA		Hs. 103110	Down	D	-
5	NR5A1	NM_004959	Hs. 495108	Down	D	136
6	C1QTNF2	NM_031908	Hs. 110062	Down	D	137
7	ERC1	NM_178037	Hs. 400431	Down	D	138
8	LMNB1	NM_005573	Hs.89497	Up	D	139
9	PBX2	NM_002586	Hs.509545	Up	D	140
10	IPO7	NM_006391	Hs.643522	Up	D	141
11	LIMK1	NM_002314	Hs.647035	Up	D	142
12	PCDH18	NM_019035	Hs.591691	Up	D	143
13	INCENP	NM_001040694	Hs.142179	Up	D	144
14	CTSZ	NM_001336	Hs.252549	Up	D	145
15	RAB6B	NM_016577	Hs.12152	Up	D	146
16	AGL	NM_000028	Hs.904	Up	D	111
17	UTRN	NM_007124	Hs.133135	Up	D	147
18	B3GNT5	NM_032047	Hs.208267	Up	D	148
19	PTGS2	NM_000963	Hs.196384	Up	D	149
20	EEA1	NM_003566	Hs.567367	Up	D	150
21	MS4A2	NM_000139	Hs.386748	Up	D	151
22	RAB33B	NM_031296	Hs.591679	Up	D	152
23	TEP1	NM_007110	Hs.508835	Down	D	91
24	TAT		Hs.161640	Down	D	-
25	CCL17	NM_002987	Hs.546294	Down	D	153
26	FLJ40194	NM_001007529	Hs.446890	Down	D	154
27	GIF	NM_005142	Hs.110014	Down	D	155
28	ARHGAP26	NM_015071	Hs.293593	Down	D	93
29	NMBR	NM_002511	Hs.552106	Down	D	156
30	EFNB2	NM_004093	Hs.149239	Down	D	157
31	RABGAP1		Hs.271341	Down	D	-
32	HOXB6		Hs.98428	Down	D	-
33	TCBA1	NM_001040214	Hs.269722	Down	D	-
34	EGF	NM_001963	Hs.419815	Down	D	158
35	PLD1	NM_002662	Hs.382865	Down	D	159
36	CAPZA3	NM_033328	Hs.131288	Down	D	160
37	IFNAR2	NM_207585	Hs.642682	Down	D	161

[表49]

表190　遺伝子セット7(No. 1-4:機能面で注目する遺伝子, No. 5-34:発現増加・減少した遺伝子上位15個)

No	Target(Gene)Symbol	Target Accession	UniGene	Up/Down	被験者群	配列番号
1	MOXD1	NM_015529	Hs. 6909	Down	A+C	219
2	AOC2	NM_001158	Hs. 143102	Down	A+C	220
3	NR4A2	NM_006186	Hs. 563344	Down	A+C	221
4	FAM3D	NM_138805	Hs. 61265	Down	A+C	222
5	NCAM1	NM_001076682	Hs.503878	Up	A+C	223
6	IL20RB	NM_144717	Hs.61232	Up	A+C	224
7	KALRN		Hs.8004	Up	A+C	-
8	NTNG1	NM_014917	Hs.143707	Up	A+C	225
9	GFER	NM_005262	Hs.27184	Up	A+C	226
10	ALCAM	NM_001627	Hs.591293	Up	A+C	227
11	TF	NM_001063	Hs.518267	Up	A+C	228
12	FCER1A	NM_002001	Hs.897	Up	A+C	110
13	IMPA1	NM_005536	Hs.555086	Up	A+C	27
14	PFTK1	NM_012395	Hs.430742	Up	A+C	229
15	CENTG2	NM_001037131	Hs.435039	Up	A+C	-
16	CUL7	NM_014780	Hs.520136	Up	A+C	230
17	SCRN3	NM_024583	Hs.470679	Up	A+C	231
18	CPNE8	NM_153634	Hs.40910	Up	A+C	182
19	FLOT2	NM_004475	Hs.514038	Up	A+C	232
20	HSPG2	NM_005529	Hs.651231	Down	A+C	233
21	METAP2	NM_006838	Hs.591005	Down	A+C	127
22	TCL6	NM_020552	Hs.510368	Down	A+C	191
23	PEX11G	NM_080662	Hs.515100	Down	A+C	183
24	VIL1	NM_007127	Hs.647885	Down	A+C	234
25	SEMA3C	NM_006379	Hs.269109	Down	A+C	235
26	FLJ35379	XM_001127400	Hs.586820	Down	A+C	236
27	GTSE1	NM_016426	Hs.386189	Down	A+C	237
28	THRB	NM_000461	Hs.187861	Down	A+C	238
29	SERPINH1	NM_001235	Hs.596449	Down	A+C	239
30	APOA5	NM_052968	Hs.283923	Down	A+C	240
31	BNC2	NM_017637	Hs.435309	Down	A+C	241
32	IVD	NM_002225	Hs.513646	Down	A+C	242
33	DRD5	NM_000798	Hs.380681	Down	A+C	243
34	BCAR3	NM_003567	Hs.36958	Down	A+C	244

[表50]

表198　遺伝子セット8(No.1-46:機能面で注目する遺伝子,No.47-76:発現増加・減少した遺伝子上位15個)

No	Target(Gene)Symbol	Target Accession	UniGene	Up/Down	被験者群	配列番号
1	HLA-C	XR_015693	Hs.77961	Down	B+D	-
2	HLA-H	NR_001434	Hs.181244	Down	B+D	245
3	HLA-A	NM_002116	Hs.181244	Down	B+D	246
4	IGHG1	BC092518	Hs.510635	Down	B+D	-
5	HLA-E	NM_005516	Hs.118354	Down	B+D	247
6	HLA-B	CR608347	Hs.77961	Down	B+D	-
7	CD1D	NM_001766	Hs.1799	Down	B+D	108
8	FLJ45422	NM_001004349	Hs.591791	Down	B+D	248
9	HLA-F	NM_018950	Hs.519972	Down	B+D	249
10	LOC649853	0	Hs.181244	Down	B+D	-
11	HLA-B	NM_005514	Hs.77961	Down	B+D	250
12	CD74	NM_001025158	Hs.436568	Down	B+D	251
13	AP3B1	NM_003664	Hs.532091	Down	B+D	252
14	VISA		Hs.646283	Down	B+D	-
15	CASP8	NM_033355	Hs.591630	Down	B+D	253
16	NDFIP1	NM_030571	Hs.9788	Down	B+D	254
17	CFLAR	NM_003879	Hs.390736	Down	B+D	255
18	SECTM1	NM_003004	Hs.558009	Down	B+D	256
19	APOL3	NM_145641	Hs.474737	Down	B+D	257
20	LTBR	NM_002342	Hs.1116	Down	B+D	258
21	C1orf166	NM_024544	Hs.10101	Down	B+D	-
22	MYD88	NM_002468	Hs.82116	Down	B+D	259
23	TRIM38	NM_006355	Hs.584851	Down	B+D	260
24	CANT1	NM_138793	Hs.8859	Down	B+D	261
25	SLC20A1	NM_005415	Hs.187946	Down	B+D	262
26	REL	NM_002908	Hs.631886	Down	B+D	263
27	NLRP12	NM_033297	Hs.631573	Down	B+D	73
28	LGALS9	NM_009587	Hs.81337	Down	B+D	264
29	MIER1	NM_001077702	Hs.651300	Down	B+D	265
30	SCOTIN	NM_016479	Hs.414579	Down	B+D	-
31	TICAM1	NM_182919	Hs.29344	Down	B+D	266
32	CXXC5	NM_016463	Hs.189119	Down	B+D	267
33	SQSTM1	NM_003900	Hs.437277	Down	B+D	268
34	TRIM38	NM_006355	Hs.584851	Down	B+D	260
35	IKBKE	NM_014002	Hs.321045	Down	B+D	269
36	FKBP1A	NM_000801	Hs.471933	Down	B+D	270
37	FLNA	NM_001456	Hs.195464	Down	B+D	271
38	EDARADD	NM_080738	Hs.352224	Down	B+D	272
39	GM2A	NM_000405	Hs.483873	Down	B+D	273
40	HEXA	S76980		Down	B+D	-
41	STAT5A	NM_003152	Hs.437058	Down	B+D	56
42	STAT5B	NM_012448	Hs.632256	Down	B+D	274
43	STAT5B	BC020868	Hs.632256	Down	B+D	-
44	LARGE	NM_004737	Hs.474667	Down	B+D	275
45	PSAP	NM_001042465	Hs.523004	Down	B+D	65
46	CLN3	NM_001042432	Hs.628393	Down	B+D	174
47	CTSZ	NM_001336	Hs.252549	Up	B+D	145
48	ZC3H7B	NM_017590	Hs.592188	Up	B+D	276
49	MAP2K1IP1	NM_021970	Hs.647988	Up	B+D	-
50	CLK4	NM_020666	Hs.406557	Up	B+D	277
51	TNFRSF17	NM_001192	Hs.2556	Up	B+D	278
52	RAB33B	NM_031296	Hs.591679	Up	B+D	152
53	LMNB1	NM_005573	Hs.89497	Up	B+D	139
54	EEA1	NM_003566	Hs.567367	Up	B+D	150
55	PREI3	NM_015387	Hs.645458	Up	B+D	-
56	BCLAF1	NM_014739		Up	B+D	29
57	STCH	NM_006948	Hs.352341	Up	B+D	-
58	TCEB1		Hs.554594	Up	B+D	-
59	SP3	NM_003111	Hs.531587	Up	B+D	279
60	PTGS2	NM_000963	Hs.196384	Up	B+D	149

表198　遺伝子セット8(No.1-46:機能面で注目する遺伝子,No.47-76:発現増加・減少した遺伝子上位15個)

No	Target(Gene)Symbol	Target Accession	UniGene	Up/Down	被験者群	配列番号
61	RAB18	NM_021252	Hs.406799	Up	B+D	280
62	CEI	NM_178569	Hs.148486	Down	B+D	-
63	TEP1	NM_007110	Hs.508835	Down	B+D	91
64	IFNAR2	NM_207585	Hs.642682	Down	B+D	161
65	CST2	NM_001322	Hs.123114	Down	B+D	281
66	ARHGAP26	NM_015071	Hs.293593	Down	B+D	93
67	BAI2	NM_001703	Hs.524138	Down	B+D	102
68	PVR	NM_006505	Hs.171844	Down	B+D	282
69	GTF3C4		Hs.22302	Down	B+D	-
70	NRP2	NM_018534	Hs.471200	Down	B+D	283
71	MALAT1	NR_002819	Hs.621695	Down	B+D	284
72	HSPB2	NM_001541	Hs.78846	Down	B+D	285
73	BIC	NR_001458	Hs.388313	Down	B+D	-
74	CTSA	NM_000308	Hs.517076	Down	B+D	286
75	CTSB	NM_147780	Hs.520898	Down	B+D	287
76	IL8RB	NM_001557	Hs.846	Down	B+D	288

[表51]

表202　ヒト共通遺伝子

No	Target(Gene)Symbol	Target Accession	UniGene	Up/Down	被験者群	配列番号
1	ANXA1	NM_000700	Hs.494173	Up	B	289
2	ARID4B	NM_016374	Hs.575782	Up	A+B,B,D,B+D	290
3	CLK1	NM_004071	Hs.433732	Up	B+D	291
4	ECHDC1	NM_018479	Hs.486410	Up	A+B,B,B+D	292
5	IFI44	NM_006417	Hs.82316	Up	A+B,B,B+D	293
6	IFIT2	NM_001547	Hs.437609	Up	A+B	294
7	MATR3	NM_199189	Hs.268939	Up	B+D	295
8	PTPRO	NM_030667	Hs.160871	Up	C+D,A+C,D,B+D	296
9	ROCK1	NM_005406	Hs.306307	Up	A+B,B+D	297
10	RPL23	NM_000978	Hs.406300	Up	A+B,B,B+D	298
11	RPL26	NM_000987	Hs.645380	Up	A+B,B,B+D	299
12	S100A8	NM_002964	Hs.416073	Up	A+B,B,B+D	83
13	SHMT1	NM_004169	Hs.513987	Up	A+C,B+D	300
14	SUB1	NM_006713	Hs.229641	Up	A+B,B,B+D	301
15	SYNCRIP	BC032643	Hs.571177	Up	D,B+D	-
16	ZNF291	NM_020843	Hs.458986	Up	B+D	-
17	AP2A2	NM_012305	Hs.19121	Down	A+B,B+D	302
18	BTBD9	NM_152733	Hs.116233	Down	B+D	303
19	C1QA	NM_015991	Hs.632379	Down	B+D	304
20	C1QTNF5	NM_015645	Hs.632102	Down	D	305
21	C1S	NM_001734	Hs.458355	Down	A+B,A+C	306
22	COMT	NM_000754	Hs.370408	Down	B+D	307
23	ELK1	NM_005229	Hs.181128	Down	A,D	308
24	GMPR	NM_006877	Hs.484741	Down	B+D	309
25	GNB1	NM_002074	Hs.430425	Down	B+D	310
26	HYOU1	NM_006389	Hs.277704	Down	B+D	311
27	LTBP1	NM_206943	Hs.49787	Down	D	312
28	MAOA	NM_000240	Hs.183109	Down	A+B,A	313
29	MAS1	NM_002377	Hs.99900	Down	C+D	314
30	MUC5AC	XM_001130382	Hs.558950	Down	A+B	-
31	PHC2	NM_198040	Hs.524271	Down	A+B,B,C,D,B+D	315
32	PLK1	NM_005030	Hs.592049	Down	A	316
33	PSEN1	AJ008005	Hs.592324	Down	B	-
34	QTRT1	NM_031209	Hs.631638	Down	B,B+D	317
35	RLN3	NM_080864	Hs.352155	Down	D	318
36	RND2	NM_005440	Hs.603111	Down	B+D	319
37	RNF138	NM_016271	Hs.302408	Down	A	320
38	ST6GALNAC3	NM_152996	Hs.337040	Down	C	321
39	STX11	NM_003764	Hs.118958	Down	A+B,B,B+D	322
40	TMEM39A	NM_018266	Hs.434927	Down	B+D	323

[請求項14]　ヒト生体由来試料は血液である、請求項13記載の方法。

[請求項15]　前記第1のステップでは、測定対象の遺伝子群中の各遺伝子の塩基配列の少なくとも一部を含む核酸を固定化した支持体を用いて、遺伝子の発現量を測定することを特徴とする請求項13記載の方法。

[請求項16] ヒトに評価対象である刺激を負荷する第1のステップと、

下記の表155、159、164、172、178、185、190、198又は202に示す遺伝子群中の各遺伝子の発現量をヒト生体由来試料において測定する第2のステップと、

測定した各遺伝子の発現量に基づいて、対象刺激が陽性刺激であるか否かを評価する第3のステップと

を含む、所与の刺激がヒトに対する陽性刺激であるか否かを評価する方法。

[表52]

表155 遺伝子セット5(No.1-17:機能面で注目する遺伝子,No.18-47:発現増加・減少した遺伝子上位15個)

No	Target(Gene)Symbol	Target Accession	UniGene	Up/Down	被験者群	配列番号
1	PTPRC	NM_080923	Hs.192039	Up	A+B	162
2	PAWR	NM_002583	Hs.643130	Up	A+B	163
3	TRAT1	NM_016388	Hs.138701	Up	A+B	164
4	STXBP4	NM_178509	Hs.35199	Down	A+B	69
5	SLC2A5	NM_003039	Hs.530003	Down	A+B	165
6	SLC2A3	NM_006931	Hs.419240	Down	A+B	166
7	SORBS1	NM_001034954	Hs.38621	Down	A+B	167
8	AKT1	NM_005163	Hs.525622	Down	A+B	71
9	APOL6	NM_030641	Hs.257352	Down	A+B	68
10	ATG10	NM_031482	Hs.651173	Down	A+B	168
11	SNX17	NM_014748	Hs.278569	Down	A+B	59
12	PIGS	NM_033198	Hs.462550	Down	A+B	169
13	FNTB	NM_002028	Hs.632345	Down	A+B	170
14	SLC9A5	NM_004594	Hs.439650	Down	A+B	171
15	LOC133308	NM_178833	Hs.546482	Down	A+B	172
16	CLN5	NM_006493	Hs.30213	Down	A+B	173
17	CLN3	NM_001042432	Hs.628393	Down	A+B	174
18	COMMD6	NM_203497	Hs.508266	Up	A+B	75
19	COX7B	NM_001866	Hs.522699	Up	A+B	175
20	P2RY5	NM_005767	Hs.123464	Up	A+B	76
21	LMNB1	NM_005573	Hs.89497	Up	A+B	139
22	EVI2A	NM_001003927	Hs.591198	Up	A+B	74
23	CD52	NM_001803	Hs.276770	Up	A+B	78
24	CSTA	NM_005213	Hs.518198	Up	A+B	81
25	FKSG2	NM_021631	Hs.651853	Up	A+B	176
26	EEF1E1	NM_004280	Hs.631818	Up	A+B	177
27	APP	NM_000484	Hs.651215	Up	A+B	178
28	SH2D1A	NM_002351	Hs.349094	Up	A+B	179
29	PREI3	NM_015387	Hs.645458	Up	A+B	-
30	CFL2	NM_021914	Hs.180141	Up	A+B	180
31	TCF12	NM_207038	Hs.511504	Up	A+B	181
32	LY96	NM_015364	Hs.69328	Up	A+B	82
33	TEP1	NM_007110	Hs.508835	Down	A+B	91
34	ARHGAP26	NM_015071	Hs.293593	Down	A+B	93
35	CPNE8	NM_153634	Hs.40910	Down	A+B	182
36	PEX11G	NM_080662	Hs.515100	Down	A+B	183
37	GPR180	NM_180989	Hs.439363	Down	A+B	184
38	GSTA2	NM_000846	Hs.94107	Down	A+B	185
39	DRD3	NM_033663	Hs.121478	Down	A+B	186
40	RABGAP1		Hs.271341	Down	A+B	-
41	H6PD	NM_004285	Hs.463511	Down	A+B	187
42	F11R	NM_144503	Hs.517293	Down	A+B	188
43	ATM	NM_000051	Hs.367437	Down	A+B	189
44	KRT71	NM_033448	Hs.433845	Down	A+B	190
45	VIL2		Hs.642735	Down	A+B	-
46	APOL6	NM_030641	Hs.257352	Down	A+B	68
47	TCL6	NM_020552	Hs.510368	Down	A+B	191

[表53]

表159　遺伝子セット6(No.1-2:機能面で注目する遺伝子,No.3-32:発現増加・減少した遺伝子上位15個)

No	Target(Gene)Symbol	Target Accession	UniGene	Up/Down	被験者群	配列番号
1	RPS3A	NM_001006	Hs.356572	Down	C+D	192
2	PPP1R13B	NM_015316	Hs.436113	Down	C+D	193
3	CGRRF1	NM_006568	Hs.59106	Up	C+D	194
4	P2RY6	NM_176798	Hs.16362	Up	C+D	195
5	PDGFC	NM_016205	Hs.570855	Up	C+D	38
6	SH3RF1	NM_020870	Hs.301804	Up	C+D	196
7	MIPEP	NM_005932	Hs.507498	Up	C+D	197
8	LGR6	NM_001017403	Hs.497402	Up	C+D	198
9	B3GNT5	NM_032047	Hs.208267	Up	C+D	148
10	TMEM23	NM_147156	Hs.386215	Up	C+D	-
11	SUCNR1	NM_033050	Hs.279575	Up	C+D	199
12	ANXA3	NM_005139	Hs.480042	Up	C+D	200
13	TSPAN2	NM_005725	Hs.310458	Up	C+D	201
14	PDE8B	NM_003719	Hs.584830	Up	C+D	202
15	SGPP1	NM_030791	Hs.24678	Up	C+D	116
16	PROK2	NM_021935	Hs.528665	Up	C+D	203
17	PTPRF	NM_002840	Hs.272062	Up	C+D	204
18	PROKR2	NM_144773	Hs.375029	Down	C+D	205
19	ANKS4B	NM_145865	Hs.115959	Down	C+D	206
20	RAP1GAP	NM_002885	Hs.148178	Down	C+D	207
21	FAAH	NM_001441	Hs.528334	Down	C+D	208
22	LCT	NM_002299	Hs.551506	Down	C+D	209
23	RGS12	NM_198229	Hs.527061	Down	C+D	210
24	DLST	NM_001933	Hs.525459	Down	C+D	211
25	ATE1	NM_001001976	Hs.632080	Down	C+D	212
26	CCNF	NM_001761	Hs.1973	Down	C+D	213
27	ALPI	NM_001631	Hs.37009	Down	C+D	214
28	CSN1S1	NM_001890	Hs.3155	Down	C+D	215
29	VASH2	NM_024749	Hs.96885	Down	C+D	216
30	CHST4	NM_005769	Hs.251383	Down	C+D	217
31	TAT	NM_000353	Hs.161640	Down	C+D	-
32	FBLN2	NM_001004019	Hs.198862	Down	C+D	218

[表54]

表164　遺伝子セット1(No.1-31:機能面で注目する遺伝子,No.32-61:発現増加・減少した遺伝子上位15個)

No	Target(Gene)Symbol	Target Accession	UniGene	Up/Down	被験者群	配列番号
1	FGFR1OP	NM_007045	Hs.487175	Up	A	1
2	CASP8AP2	NM_012115	Hs.558218	Up	A	2
3	PROK2	NM_021935	Hs.528665	Up	A	3
4	FCER1A	NM_002001	Hs.897	Up	A	4
5	CD69	NM_001781	Hs.208854	Up	A	5
6	PAQR3	NM_001040202	Hs.632591	Up	A	6
7	SLC6A4	NM_001045	Hs.591192	Up	A	7
8	GGCX	NM_000821	Hs.77719	Up	A	8
9	HBA2	NM_000517	Hs.449630	Up	A	9
10	ADH5	NM_000671	Hs.78989	Up	A	10
11	JUN	NM_002228	Hs.525704	Down	A	11
12	TP53	NM_000546	Hs.408312	Down	A	12
13	RAB5B		Hs.567328	Down	A	-
14	RAB8A	NM_005370	Hs.642874	Down	A	13
15	RAB12	NM_001025300	Hs.270074	Down	A	14
16	RAB20	NM_017817	Hs.508720	Down	A	15
17	RAB30	NM_014488	Hs.40758	Down	A	16
18	VISA		Hs.646283	Down	A	-
19	CD55		Hs.527653	Down	A	-
20	IGHG1	BC092518	Hs.510635	Down	A	-
21	SEMA3G	NM_020163	Hs.59729	Down	A	17
22	CD84	NM_003874	Hs.398093	Down	A	-
23	CD3G	NM_000073	Hs.2259	Down	A	18
24	CD177	NM_020406	Hs.232165	Down	A	19
25	NFAT5	NM_173215	Hs.371987	Down	A	20
26	HDGF	NM_004494	Hs.506748	Down	A	21
27	TNFAIP3	NM_006290	Hs.591338	Down	A	22
28	PRLHR	NM_004248	Hs.248119	Down	A	23
29	SYT2	NM_177402	Hs.585015	Down	A	24
30	RCP9	NM_014478	Hs.300684	Down	A	25
31	SPAG8	NM_172312	Hs.256747	Down	A	26
32	IMPA1	NM_005536	Hs.555086	Up	A	27
33	XPR1		Hs.648372	Up	A	-
34	B3GNT2	NM_006577	Hs.173203	Up	A	28
35	BCLAF1	NM_014739		Up	A	29
36	PSIP1	NM_021144	Hs.493516	Up	A	30
37	LGALS8	NM_006499	Hs.4082	Up	A	31
38	SEC24A	NM_021982	Hs.595540	Up	A	32
39	LOC492311	NM_001007189	Hs.200938	Up	A	-
40	ORMDL1	NM_016467	Hs.651259	Up	A	33
41	WHSC1	NM_133330	Hs.113876	Up	A	34
42	XRCC3	NM_005432	Hs.592325	Up	A	35
43	TMEM167	NM_174909	Hs.355606	Up	A	36
44	PREI3	NM_015387	Hs.645458	Up	A	-
45	SLC19A2	NM_006996	Hs.30246	Up	A	37
46	PDGFC	NM_016205	Hs.570855	Up	A	38
47	ERCC4	NM_005236	Hs.567265	Down	A	39
48	SH3PXD2B	NM_001017995	Hs.285666	Down	A	40
49	DUX2	NM_012147		Down	A	41
50	AP1S1	NM_001283	Hs.563509	Down	A	42
51	GATA2	NM_032638	Hs.367725	Down	A	43
52	LOC728371	XR_015273	Hs.558795	Down	A	44
53	PFKFB3	NM_004566	Hs.195471	Down	A	45
54	PHGDH	NM_006623	Hs.487296	Down	A	46
55	CENPP		Hs.459896	Down	A	-
56	OR5A1	NM_001004728	Hs.553649	Down	A	47
57	ADCK1	NM_020421	Hs.413208	Down	A	48
58	TFEC	NM_012252	Hs.125962	Down	A	49
59	RRH	NM_006583	Hs.352262	Down	A	50
60	DOK6	NM_152721	Hs.569915	Down	A	51
61	SAMD7	NM_182610	Hs.439922	Down	A	52

[表55]

表172　遺伝子セット2(No. 1-25:機能面で注目する遺伝子, No. 26-55:発現増加・減少した遺伝子上位15個)

No	Target(Gene)Symbol	Target Accession	UniGene	Up/Down	被験者群	配列番号
1	SOCS1	NM_003745	Hs. 50640	Down	B	53
2	CCR1	NM_001295	Hs. 301921	Down	B	54
3	CSF2RB	NM_000395	Hs. 592192	Down	B	55
4	STAT5A	NM_003152	Hs. 437058	Down	B	56
5	STAT3	NM_213662	Hs. 463059	Down	B	57
6	TNFRSF1B	NM_001066	Hs. 256278	Down	B	58
7	SNX17	NM_014748	Hs. 278569	Down	B	59
8	SCARF1	NM_145351	Hs. 647430	Down	B	60
9	LDLR		Hs. 213289	Down	B	-
10	STARD3	NM_006804	Hs. 77628	Down	B	61
11	CLN8	NM_018941	Hs. 127675	Down	B	62
12	APOL1	NM_145343	Hs. 114309	Down	B	63
13	ATP10A	NM_024490	Hs. 128041	Down	B	64
14	PSAP	NM_001042465	Hs. 523004	Down	B	65
15	OSBP2	NM_030758	Hs. 517546	Down	B	66
16	SLC27A1	NM_198580	Hs. 363138	Down	B	67
17	APOL6	NM_030641	Hs. 257352	Down	B	68
18	SOCS1	NM_003745	Hs. 50640	Down	B	53
19	STXBP4	NM_178509	Hs. 35199	Down	B	69
20	SOCS3	NM_003955	Hs. 527973	Down	B	70
21	AKT1	NM_005163	Hs. 525622	Down	B	71
22	MLLT7	NM_005938	Hs. 584654	Down	B	-
23	CEBPB	NM_005194	Hs. 642680	Down	B	72
24	CEBPB	NM_005194	Hs. 642680	Down	B	72
25	NLRP12	NM_033297	Hs. 631573	Down	B	73
26	EVI2A	NM_001003927	Hs.591198	Up	B	74
27	COMMD6	NM_203497	Hs.508266	Up	B	75
28	P2RY5	NM_005767	Hs.123464	Up	B	76
29	COMMD8	NM_017845	Hs.23956	Up	B	77
30	CD52	NM_001803	Hs.276770	Up	B	78
31	S100P	NM_005980	Hs.2962	Up	B	79
32	COX7C	NM_001867	Hs.430075	Up	B	80
33	CSTA	NM_005213	Hs.518198	Up	B	81
34	LY96	NM_015364	Hs.69328	Up	B	82
35	S100A8	NM_002964	Hs.416073	Up	B	83
36	SLC4A7	NM_003615	Hs.250072	Up	B	84
37	PHF6	NM_032458	Hs.356501	Up	B	85
38	TMEM167	NM_174909	Hs.355606	Up	B	36
39	EIF1AX	NM_001412	Hs.522590	Up	B	86
40	CRTAM	NM_019604	Hs.159523	Up	B	87
41	PIP5K1A	NM_003557	Hs.546316	Down	B	88
42	ERBB2	NM_001005862	Hs.446352	Down	B	89
43	COL25A1	NM_198721	Hs.112925	Down	B	90
44	TEP1	NM_007110	Hs.508835	Down	B	91
45	PKD1L1	NM_138295	Hs.195979	Down	B	92
46	ARHGAP26	NM_015071	Hs.293593	Down	B	93
47	RAB13	NM_002870	Hs.151536	Down	B	94
48	KCNAB3	NM_004732	Hs.435074	Down	B	95
49	ARHGAP24	NM_001025616	Hs.444229	Down	B	96
50	DDAH1	NM_012137	Hs.379858	Down	B	97
51	DOCK6	NM_020812	Hs.591002	Down	B	98
52	FABP6	NM_001040442	Hs.519719	Down	B	99
53	GALNT9	NM_021808	Hs.301062	Down	B	100
54	EBI3	NM_005755	Hs.501452	Down	B	101
55	BAI2	NM_001703	Hs.524138	Down	B	102

[表56]

表178　遺伝子セット3(No. 1-8:機能面で注目する遺伝子, No. 9-38:発現増加・減少した遺伝子上位15個)

No	Target(Gene)Symbol	Target Accession	UniGene	Up/Down	被験者群	配列番号
1	APBA2BP	NM_031232	Hs. 516986	Down	C	-
2	EFCBP2	NM_019065	Hs. 140950	Down	C	-
3	ASS1	NM_000050	Hs. 160786	Down	C	103
4	NAGS	NM_153006	Hs. 8876	Down	C	104
5	IL6	NM_000600	Hs. 512234	Down	C	105
6	FLT3	NM_004119	Hs. 507590	Down	C	106
7	IL4	NM_000589	Hs. 73917	Down	C	107
8	CD1D	NM_001766	Hs. 1799	Down	C	108
9	HDC	NM_002112	Hs.1481	Up	C	109
10	PFKFB3	NM_004566	Hs.195471	Up	C	45
11	FCER1A	NM_002001	Hs.897	Up	C	110
12	AGL	NM_000028	Hs.904	Up	C	111
13	LTF	NM_002343	Hs.529517	Up	C	112
14	HBA1	NM_000558	Hs.449630	Up	C	113
15	ORM2	NM_000608	Hs.522356	Up	C	114
16	IL3RA	NM_002183	Hs.632790	Up	C	115
17	STCH	NM_006948	Hs.352341	Up	C	-
18	HBA2	NM_000517	Hs.449630	Up	C	9
19	SGPP1	NM_030791	Hs.24678	Up	C	116
20	PTPRM	NM_002845	Hs.49774	Up	C	117
21	RERG	NM_032918	Hs.199487	Up	C	118
22	BCLAF1	NM_014739		Up	C	29
23	MASA	NM_021204	Hs.18442	Up	C	-
24	QRICH2	NM_032134	Hs.252739	Down	C	119
25	PLAC4	NM_182832	Hs.472492	Down	C	120
26	ECM1	NM_004425	Hs.81071	Down	C	121
27	TCF19	NM_007109	Hs.584807	Down	C	122
28	CPA1	NM_001868	Hs.2879	Down	C	123
29	THAP2	NM_031435	Hs.245798	Down	C	124
30	SCRG1		Hs.7122	Down	C	-
31	CDH6	NM_004932	Hs.171054	Down	C	125
32	FOXE1	NM_004473	Hs.159234	Down	C	126
33	METAP2	NM_006838	Hs.591005	Down	C	127
34	MAPK8IP2	NM_012324	Hs.558180	Down	C	128
35	GAL3ST3	NM_033036	Hs.208343	Down	C	129
36	FCER2	NM_002002	Hs.465778	Down	C	130
37	MAGEA5	NM_021049	Hs.18048	Down	C	131
38	RYR1	NM_001042723	Hs.466664	Down	C	132

[表57]

表185　遺伝子セット4(No. 1-7:機能面で注目する遺伝子, No. 8-37:発現増加・減少した遺伝子上位15個)

No	Target(Gene)Symbol	Target Accession	UniGene	Up/Down	被験者群	配列番号
1	TLR7	NM_016562	Hs. 443036	Up	D	133
2	BCL2	NM_000633	Hs. 150749	Up	D	134
3	TLR8	NM_016610	Hs. 272410	Up	D	135
4	PPARA		Hs. 103110	Down	D	-
5	NR5A1	NM_004959	Hs. 495108	Down	D	136
6	C1QTNF2	NM_031908	Hs. 110062	Down	D	137
7	ERC1	NM_178037	Hs. 400431	Down	D	138
8	LMNB1	NM_005573	Hs.89497	Up	D	139
9	PBX2	NM_002586	Hs.509545	Up	D	140
10	IPO7	NM_006391	Hs.643522	Up	D	141
11	LIMK1	NM_002314	Hs.647035	Up	D	142
12	PCDH18	NM_019035	Hs.591691	Up	D	143
13	INCENP	NM_001040694	Hs.142179	Up	D	144
14	CTSZ	NM_001336	Hs.252549	Up	D	145
15	RAB6B	NM_016577	Hs.12152	Up	D	146
16	AGL	NM_000028	Hs.904	Up	D	111
17	UTRN	NM_007124	Hs.133135	Up	D	147
18	B3GNT5	NM_032047	Hs.208267	Up	D	148
19	PTGS2	NM_000963	Hs.196384	Up	D	149
20	EEA1	NM_003566	Hs.567367	Up	D	150
21	MS4A2	NM_000139	Hs.386748	Up	D	151
22	RAB33B	NM_031296	Hs.591679	Up	D	152
23	TEP1	NM_007110	Hs.508835	Down	D	91
24	TAT		Hs.161640	Down	D	-
25	CCL17	NM_002987	Hs.546294	Down	D	153
26	FLJ40194	NM_001007529	Hs.446890	Down	D	154
27	GIF	NM_005142	Hs.110014	Down	D	155
28	ARHGAP26	NM_015071	Hs.293593	Down	D	93
29	NMBR	NM_002511	Hs.552106	Down	D	156
30	EFNB2	NM_004093	Hs.149239	Down	D	157
31	RABGAP1		Hs.271341	Down	D	-
32	HOXB6		Hs.98428	Down	D	-
33	TCBA1	NM_001040214	Hs.269722	Down	D	-
34	EGF	NM_001963	Hs.419815	Down	D	158
35	PLD1	NM_002662	Hs.382865	Down	D	159
36	CAPZA3	NM_033328	Hs.131288	Down	D	160
37	IFNAR2	NM_207585	Hs.642682	Down	D	161

[表58]

表190　遺伝子セット7(No. 1-4:機能面で注目する遺伝子, No. 5-34:発現増加・減少した遺伝子上位15個)

No	Target(Gene)Symbol	Target Accession	UniGene	Up/Down	被験者群	配列番号
1	MOXD1	NM_015529	Hs. 6909	Down	A+C	219
2	AOC2	NM_001158	Hs. 143102	Down	A+C	220
3	NR4A2	NM_006186	Hs. 563344	Down	A+C	221
4	FAM3D	NM_138805	Hs. 61265	Down	A+C	222
5	NCAM1	NM_001076682	Hs.503878	Up	A+C	223
6	IL20RB	NM_144717	Hs.61232	Up	A+C	224
7	KALRN		Hs.8004	Up	A+C	-
8	NTNG1	NM_014917	Hs.143707	Up	A+C	225
9	GFER	NM_005262	Hs.27184	Up	A+C	226
10	ALCAM	NM_001627	Hs.591293	Up	A+C	227
11	TF	NM_001063	Hs.518267	Up	A+C	228
12	FCER1A	NM_002001	Hs.897	Up	A+C	110
13	IMPA1	NM_005536	Hs.555086	Up	A+C	27
14	PFTK1	NM_012395	Hs.430742	Up	A+C	229
15	CENTG2	NM_001037131	Hs.435039	Up	A+C	-
16	CUL7	NM_014780	Hs.520136	Up	A+C	230
17	SCRN3	NM_024583	Hs.470679	Up	A+C	231
18	CPNE8	NM_153634	Hs.40910	Up	A+C	182
19	FLOT2	NM_004475	Hs.514038	Up	A+C	232
20	HSPG2	NM_005529	Hs.651231	Down	A+C	233
21	METAP2	NM_006838	Hs.591005	Down	A+C	127
22	TCL6	NM_020552	Hs.510368	Down	A+C	191
23	PEX11G	NM_080662	Hs.515100	Down	A+C	183
24	VIL1	NM_007127	Hs.647885	Down	A+C	234
25	SEMA3C	NM_006379	Hs.269109	Down	A+C	235
26	FLJ35379	XM_001127400	Hs.586820	Down	A+C	236
27	GTSE1	NM_016426	Hs.386189	Down	A+C	237
28	THRB	NM_000461	Hs.187861	Down	A+C	238
29	SERPINH1	NM_001235	Hs.596449	Down	A+C	239
30	APOA5	NM_052968	Hs.283923	Down	A+C	240
31	BNC2	NM_017637	Hs.435309	Down	A+C	241
32	IVD	NM_002225	Hs.513646	Down	A+C	242
33	DRD5	NM_000798	Hs.380681	Down	A+C	243
34	BCAR3	NM_003567	Hs.36958	Down	A+C	244

[表59]

表198　遺伝子セット8(No.1-46:機能面で注目する遺伝子,No.47-76:発現増加・減少した遺伝子上位15個)

No	Target(Gene)Symbol	Target Accession	UniGene	Up/Down	被験者群	配列番号
1	HLA-C	XR_015693	Hs.77961	Down	B+D	-
2	HLA-H	NR_001434	Hs.181244	Down	B+D	245
3	HLA-A	NM_002116	Hs.181244	Down	B+D	246
4	IGHG1	BC092518	Hs.510635	Down	B+D	-
5	HLA-E	NM_005516	Hs.118354	Down	B+D	247
6	HLA-B	CR608347	Hs.77961	Down	B+D	-
7	CD1D	NM_001766	Hs.1799	Down	B+D	108
8	FLJ45422	NM_001004349	Hs.591791	Down	B+D	248
9	HLA-F	NM_018950	Hs.519972	Down	B+D	249
10	LOC649853	0	Hs.181244	Down	B+D	-
11	HLA-B	NM_005514	Hs.77961	Down	B+D	250
12	CD74	NM_001025158	Hs.436568	Down	B+D	251
13	AP3B1	NM_003664	Hs.532091	Down	B+D	252
14	VISA		Hs.646283	Down	B+D	-
15	CASP8	NM_033355	Hs.591630	Down	B+D	253
16	NDFIP1	NM_030571	Hs.9788	Down	B+D	254
17	CFLAR	NM_003879	Hs.390736	Down	B+D	255
18	SECTM1	NM_003004	Hs.558009	Down	B+D	256
19	APOL3	NM_145641	Hs.474737	Down	B+D	257
20	LTBR	NM_002342	Hs.1116	Down	B+D	258
21	C1orf166	NM_024544	Hs.10101	Down	B+D	-
22	MYD88	NM_002468	Hs.82116	Down	B+D	259
23	TRIM38	NM_006355	Hs.584851	Down	B+D	260
24	CANT1	NM_138793	Hs.8859	Down	B+D	261
25	SLC20A1	NM_005415	Hs.187946	Down	B+D	262
26	REL	NM_002908	Hs.631886	Down	B+D	263
27	NLRP12	NM_033297	Hs.631573	Down	B+D	73
28	LGALS9	NM_009587	Hs.81337	Down	B+D	264
29	MIER1	NM_001077702	Hs.651300	Down	B+D	265
30	SCOTIN	NM_016479	Hs.414579	Down	B+D	-
31	TICAM1	NM_182919	Hs.29344	Down	B+D	266
32	CXXC5	NM_016463	Hs.189119	Down	B+D	267
33	SQSTM1	NM_003900	Hs.437277	Down	B+D	268
34	TRIM38	NM_006355	Hs.584851	Down	B+D	260
35	IKBKE	NM_014002	Hs.321045	Down	B+D	269
36	FKBP1A	NM_000801	Hs.471933	Down	B+D	270
37	FLNA	NM_001456	Hs.195464	Down	B+D	271
38	EDARADD	NM_080738	Hs.352224	Down	B+D	272
39	GM2A	NM_000405	Hs.483873	Down	B+D	273
40	HEXA	S76980		Down	B+D	-
41	STAT5A	NM_003152	Hs.437058	Down	B+D	56
42	STAT5B	NM_012448	Hs.632256	Down	B+D	274
43	STAT5B	BC020868	Hs.632256	Down	B+D	-
44	LARGE	NM_004737	Hs.474667	Down	B+D	275
45	PSAP	NM_001042465	Hs.523004	Down	B+D	65
46	CLN3	NM_001042432	Hs.628393	Down	B+D	174
47	CTSZ	NM_001336	Hs.252549	Up	B+D	145
48	ZC3H7B	NM_017590	Hs.592188	Up	B+D	276
49	MAP2K1IP1	NM_021970	Hs.647988	Up	B+D	-
50	CLK4	NM_020666	Hs.406557	Up	B+D	277
51	TNFRSF17	NM_001192	Hs.2556	Up	B+D	278
52	RAB33B	NM_031296	Hs.591679	Up	B+D	152
53	LMNB1	NM_005573	Hs.89497	Up	B+D	139
54	EEA1	NM_003566	Hs.567367	Up	B+D	150
55	PREI3	NM_015387	Hs.645458	Up	B+D	-
56	BCLAF1	NM_014739		Up	B+D	29
57	STCH	NM_006948	Hs.352341	Up	B+D	-
58	TCEB1		Hs.554594	Up	B+D	-
59	SP3	NM_003111	Hs.531587	Up	B+D	279
60	PTGS2	NM_000963	Hs.196384	Up	B+D	149

表198　遺伝子セット8(No.1-46:機能面で注目する遺伝子,No.47-76:発現増加・減少した遺伝子上位15個)

No	Target(Gene)Symbol	Target Accession	UniGene	Up/Down	被験者群	配列番号
61	RAB18	NM_021252	Hs.406799	Up	B+D	280
62	CEI	NM_178569	Hs.148486	Down	B+D	-
63	TEP1	NM_007110	Hs.508835	Down	B+D	91
64	IFNAR2	NM_207585	Hs.642682	Down	B+D	161
65	CST2	NM_001322	Hs.123114	Down	B+D	281
66	ARHGAP26	NM_015071	Hs.293593	Down	B+D	93
67	BAI2	NM_001703	Hs.524138	Down	B+D	102
68	PVR	NM_006505	Hs.171844	Down	B+D	282
69	GTF3C4		Hs.22302	Down	B+D	-
70	NRP2	NM_018534	Hs.471200	Down	B+D	283
71	MALAT1	NR_002819	Hs.621695	Down	B+D	284
72	HSPB2	NM_001541	Hs.78846	Down	B+D	285
73	BIC	NR_001458	Hs.388313	Down	B+D	-
74	CTSA	NM_000308	Hs.517076	Down	B+D	286
75	CTSB	NM_147780	Hs.520898	Down	B+D	287
76	IL8RB	NM_001557	Hs.846	Down	B+D	288

[表60]

表202　ヒト共通遺伝子

No	Target(Gene)Symbol	Target Accession	UniGene	Up/Down	被験者群	配列番号
1	ANXA1	NM_000700	Hs.494173	Up	B	289
2	ARID4B	NM_016374	Hs.575782	Up	A+B,B,D,B+D	290
3	CLK1	NM_004071	Hs.433732	Up	B+D	291
4	ECHDC1	NM_018479	Hs.486410	Up	A+B,B,B+D	292
5	IFI44	NM_006417	Hs.82316	Up	A+B,B,B+D	293
6	IFIT2	NM_001547	Hs.437609	Up	A+B	294
7	MATR3	NM_199189	Hs.268939	Up	B+D	295
8	PTPRO	NM_030667	Hs.160871	Up	C+D,A+C,D,B+D	296
9	ROCK1	NM_005406	Hs.306307	Up	A+B,B+D	297
10	RPL23	NM_000978	Hs.406300	Up	A+B,B,B+D	298
11	RPL26	NM_000987	Hs.645380	Up	A+B,B,B+D	299
12	S100A8	NM_002964	Hs.416073	Up	A+B,B,B+D	83
13	SHMT1	NM_004169	Hs.513987	Up	A+C,B+D	300
14	SUB1	NM_006713	Hs.229641	Up	A+B,B,B+D	301
15	SYNCRIP	BC032643	Hs.571177	Up	D,B+D	-
16	ZNF291	NM_020843	Hs.458986	Up	B+D	-
17	AP2A2	NM_012305	Hs.19121	Down	A+B,B+D	302
18	BTBD9	NM_152733	Hs.116233	Down	B+D	303
19	C1QA	NM_015991	Hs.632379	Down	B+D	304
20	C1QTNF5	NM_015645	Hs.632102	Down	D	305
21	C1S	NM_001734	Hs.458355	Down	A+B,A+C	306
22	COMT	NM_000754	Hs.370408	Down	B+D	307
23	ELK1	NM_005229	Hs.181128	Down	A,D	308
24	GMPR	NM_006877	Hs.484741	Down	B+D	309
25	GNB1	NM_002074	Hs.430425	Down	B+D	310
26	HYOU1	NM_006389	Hs.277704	Down	B+D	311
27	LTBP1	NM_206943	Hs.49787	Down	D	312
28	MAOA	NM_000240	Hs.183109	Down	A+B,A	313
29	MAS1	NM_002377	Hs.99900	Down	C+D	314
30	MUC5AC	XM_001130382	Hs.558950	Down	A+B	-
31	PHC2	NM_198040	Hs.524271	Down	A+B,B,C,D,B+D	315
32	PLK1	NM_005030	Hs.592049	Down	A	316
33	PSEN1	AJ008005	Hs.592324	Down	B	-
34	QTRT1	NM_031209	Hs.631638	Down	B,B+D	317
35	RLN3	NM_080864	Hs.352155	Down	D	318
36	RND2	NM_005440	Hs.603111	Down	B+D	319
37	RNF138	NM_016271	Hs.302408	Down	A	320
38	ST6GALNAC3	NM_152996	Hs.337040	Down	C	321
39	STX11	NM_003764	Hs.118958	Down	A+B,B,B+D	322
40	TMEM39A	NM_018266	Hs.434927	Down	B+D	323

[請求項17]　ヒト生体由来試料は血液である、請求項16記載の方法。

[請求項18]　ラットに評価対象である刺激を負荷する第1のステップと、

下記の表205に示す遺伝子群中の各遺伝子の発現量を指定の生体由来試料において測定する第2のステップと、

測定した前記遺伝子の発現量に基づいて、対象刺激が陽性刺激であるか否かを評価する第3のステップと、

対象刺激がラットに対する陽性刺激であると評価された場合に、該対象刺激をヒト陽性刺激であると認定する第4のステップと、

を含む、所与の刺激がヒトに対する陽性刺激であるか否かを評価する方法。

[表61]

表205　ラット共通遺伝子

No	Target(Gene)Symbol	Target Accession	UniGene	Up/Down	生体由来試料	配列番号
1	Anxa1	NM_012904	Rn.1792	Up	BI	324
2	Arid4b	AA955478	Rn.47249	Up	BI	-
3	Clk1	XM_217405	Rn.36770	Up	BI	325
4	Echdc1	NM_001007734	Rn.4220	Up	BI	326
5	Ifi44	XM_227821	Rn.43876	Up	BI	327
6	Ifit2	NM_001024753	Rn.6175	Up	BI	328
7	Matr3	NM_019149	Rn.29774	Up	BI	329
8	Ptpro	NM_017336	Rn.10163	Up	BI	330
9	Rock1	NM_031098	Rn.89756	Up	BI	-
10	Rpl23	NM_001007599	Rn.103172	Up	BI	331
11	Rpl26	XM_213346	Rn.144702	Up	BI	332
12	S100a8	NM_053822	Rn.31839	Up	BI	333
13	Shmt1	AI010087	Rn.3684	Up	BI	-
14	Sub1	NM_001009618	Rn.8706	Up	BI	-
15	Syncrip	XM_343446	Rn.25065	Up	BI	334
16	Znf291	XM_343394	Rn.163002	Up	BI	335
17	Ap2a2	BF414152	Rn.34928	Down	BI	336
18	Btbd9	BF401614	Rn.48897	Down	BI	337
19	C1qa	NM_001008515	Rn.105647	Down	BI	338
20	C1qtnf5	NM_001012123	Rn.99884	Down	BI	339
21	C1s	NM_138900	Rn.4037	Down	BI	340
22	Comt	AA858639	Rn.220	Down	BI	341
23	Elk1	BF558309	Rn.1714	Down	BI	342
24	Gmpr	NM_057188	Rn.3862	Down	BI	343
25	Gnb1	NM_030987	Rn.126047	Down	BI	344
26	Hyou1	NM_138867	Rn.10542	Down	BI	345
27	Ltbp1	NM_021587	Rn.40942	Down	BI	346
28	Maoa	AI105223	Rn.163443	Down	BI	347
29	Mas1	NM_012757	Rn.21943	Down	BI	348
30	Muc5ac	U83139	Rn.10789	Down	BI	349
31	Phc2	XM_232751	Rn.2428	Down	BI	350
32	Plk1	NM_017100	Rn.11034	Down	BI	351
33	Psen1	NM_019163	Rn.44440	Down	BI	352
34	Qtrt1	NM_022250	Rn.53858	Down	BI	353
35	Rln3	NM_170667	Rn.45123	Down	BI	354
36	Rnd2	NM_001010953	Rn.22162	Down	BI	355
37	Rnf138	NM_053588	Rn.6814	Down	BI	356
38	St6galnac3	NM_019123	Rn.88072	Down	BI	357
39	Stx11	XM_218092	-	Down	BI	358
40	Tmem39a	NM_001013865	Rn.13663	Down	BI	359

[請求項19]　ラットに評価対象である刺激を負荷する第1のステップと、

下記の表205に示す遺伝子群中の各遺伝子の発現量を指定の生体由来試料において測定する第2のステップと、

測定した前記遺伝子の発現量に基づいて、対象刺激が陽性刺激であるか否かを評価する第3のステップと

を含む、所与の刺激がラットに対する陽性刺激であるか否かを評価す

る方法。

[表62]

表205 ラット共通遺伝子

No	Target(Gene)Symbol	Target Accession	UniGene	Up/Down	生体由来試料	配列番号
1	Anxa1	NM_012904	Rn.1792	Up	BI	324
2	Arid4b	AA955478	Rn.47249	Up	BI	-
3	Clk1	XM_217405	Rn.36770	Up	BI	325
4	Echdc1	NM_001007734	Rn.4220	Up	BI	326
5	Ifi44	XM_227821	Rn.43876	Up	BI	327
6	Ifit2	NM_001024753	Rn.6175	Up	BI	328
7	Matr3	NM_019149	Rn.29774	Up	BI	329
8	Ptpro	NM_017336	Rn.10163	Up	BI	330
9	Rock1	NM_031098	Rn.89756	Up	BI	-
10	Rpl23	NM_001007599	Rn.103172	Up	BI	331
11	Rpl26	XM_213346	Rn.144702	Up	BI	332
12	S100a8	NM_053822	Rn.31839	Up	BI	333
13	Shmt1	AI010087	Rn.3684	Up	BI	-
14	Sub1	NM_001009618	Rn.8706	Up	BI	-
15	Syncrip	XM_343446	Rn.25065	Up	BI	334
16	Znf291	XM_343394	Rn.163002	Up	BI	335
17	Ap2a2	BF414152	Rn.34928	Down	BI	336
18	Btbd9	BF401614	Rn.48897	Down	BI	337
19	C1qa	NM_001008515	Rn.105647	Down	BI	338
20	C1qtnf5	NM_001012123	Rn.99884	Down	BI	339
21	C1s	NM_138900	Rn.4037	Down	BI	340
22	Comt	AA858639	Rn.220	Down	BI	341
23	Elk1	BF558309	Rn.1714	Down	BI	342
24	Gmpr	NM_057188	Rn.3862	Down	BI	343
25	Gnb1	NM_030987	Rn.126047	Down	BI	344
26	Hyou1	NM_138867	Rn.10542	Down	BI	345
27	Ltbp1	NM_021587	Rn.40942	Down	BI	346
28	Maoa	AI105223	Rn.163443	Down	BI	347
29	Mas1	NM_012757	Rn.21943	Down	BI	348
30	Muc5ac	U83139	Rn.10789	Down	BI	349
31	Phc2	XM_232751	Rn.2428	Down	BI	350
32	Plk1	NM_017100	Rn.11034	Down	BI	351
33	Psen1	NM_019163	Rn.44440	Down	BI	352
34	Qtrt1	NM_022250	Rn.53858	Down	BI	353
35	Rln3	NM_170667	Rn.45123	Down	BI	354
36	Rnd2	NM_001010953	Rn.22162	Down	BI	355
37	Rnf138	NM_053588	Rn.6814	Down	BI	356
38	St6galnac3	NM_019123	Rn.88072	Down	BI	357
39	Stx11	XM_218092	-	Down	BI	358
40	Tmem39a	NM_001013865	Rn.13663	Down	BI	359

[請求項20] 前記第2のステップでは、測定対象の遺伝子群中の各遺伝子の塩基配列の少なくとも一部を含む核酸を固定化した支持体を用いて、遺伝子の発現量を測定することを特徴とする請求項16、18又は19記載の方法。

[請求項21] 下記の表155、159、164、172、178、185、190、198又は202に示す遺伝子群中の各遺伝子の塩基配列の少なくとも一部を含む核酸、又は下記の表155、159、164、172、178、185、190、198又は202に示す遺伝子群中の各遺伝子によってコードされるタンパク質に対して特異的に結合する分子を含む、ヒトの陽性感情又は健康度を評価するための検査キット。

[表63]

表155　遺伝子セット5(No.1-17:機能面で注目する遺伝子,No.18-47:発現増加・減少した遺伝子上位15個)

No	Target(Gene)Symbol	Target Accession	UniGene	Up/Down	被験者群	配列番号
1	PTPRC	NM_080923	Hs.192039	Up	A+B	162
2	PAWR	NM_002583	Hs.643130	Up	A+B	163
3	TRAT1	NM_016388	Hs.138701	Up	A+B	164
4	STXBP4	NM_178509	Hs.35199	Down	A+B	69
5	SLC2A5	NM_003039	Hs.530003	Down	A+B	165
6	SLC2A3	NM_006931	Hs.419240	Down	A+B	166
7	SORBS1	NM_001034954	Hs.38621	Down	A+B	167
8	AKT1	NM_005163	Hs.525622	Down	A+B	71
9	APOL6	NM_030641	Hs.257352	Down	A+B	68
10	ATG10	NM_031482	Hs.651173	Down	A+B	168
11	SNX17	NM_014748	Hs.278569	Down	A+B	59
12	PIGS	NM_033198	Hs.462550	Down	A+B	169
13	FNTB	NM_002028	Hs.632345	Down	A+B	170
14	SLC9A5	NM_004594	Hs.439650	Down	A+B	171
15	LOC133308	NM_178833	Hs.546482	Down	A+B	172
16	CLN5	NM_006493	Hs.30213	Down	A+B	173
17	CLN3	NM_001042432	Hs.628393	Down	A+B	174
18	COMMD6	NM_203497	Hs.508266	Up	A+B	75
19	COX7B	NM_001866	Hs.522699	Up	A+B	175
20	P2RY5	NM_005767	Hs.123464	Up	A+B	76
21	LMNB1	NM_005573	Hs.89497	Up	A+B	139
22	EVI2A	NM_001003927	Hs.591198	Up	A+B	74
23	CD52	NM_001803	Hs.276770	Up	A+B	78
24	CSTA	NM_005213	Hs.518198	Up	A+B	81
25	FKSG2	NM_021631	Hs.651853	Up	A+B	176
26	EEF1E1	NM_004280	Hs.631818	Up	A+B	177
27	APP	NM_000484	Hs.651215	Up	A+B	178
28	SH2D1A	NM_002351	Hs.349094	Up	A+B	179
29	PREI3	NM_015387	Hs.645458	Up	A+B	-
30	CFL2	NM_021914	Hs.180141	Up	A+B	180
31	TCF12	NM_207038	Hs.511504	Up	A+B	181
32	LY96	NM_015364	Hs.69328	Up	A+B	82
33	TEP1	NM_007110	Hs.508835	Down	A+B	91
34	ARHGAP26	NM_015071	Hs.293593	Down	A+B	93
35	CPNE8	NM_153634	Hs.40910	Down	A+B	182
36	PEX11G	NM_080662	Hs.515100	Down	A+B	183
37	GPR180	NM_180989	Hs.439363	Down	A+B	184
38	GSTA2	NM_000846	Hs.94107	Down	A+B	185
39	DRD3	NM_033663	Hs.121478	Down	A+B	186
40	RABGAP1		Hs.271341	Down	A+B	-
41	H6PD	NM_004285	Hs.463511	Down	A+B	187
42	F11R	NM_144503	Hs.517293	Down	A+B	188
43	ATM	NM_000051	Hs.367437	Down	A+B	189
44	KRT71	NM_033448	Hs.433845	Down	A+B	190
45	VIL2		Hs.642735	Down	A+B	-
46	APOL6	NM_030641	Hs.257352	Down	A+B	68
47	TCL6	NM_020552	Hs.510368	Down	A+B	191

[表64]

表159　遺伝子セット6(No.1-2:機能面で注目する遺伝子,No.3-32:発現増加・減少した遺伝子上位15個)

No	Target(Gene)Symbol	Target Accession	UniGene	Up/Down	被験者群	配列番号
1	RPS3A	NM_001006	Hs.356572	Down	C+D	192
2	PPP1R13B	NM_015316	Hs.436113	Down	C+D	193
3	CGRRF1	NM_006568	Hs.59106	Up	C+D	194
4	P2RY6	NM_176798	Hs.16362	Up	C+D	195
5	PDGFC	NM_016205	Hs.570855	Up	C+D	38
6	SH3RF1	NM_020870	Hs.301804	Up	C+D	196
7	MIPEP	NM_005932	Hs.507498	Up	C+D	197
8	LGR6	NM_001017403	Hs.497402	Up	C+D	198
9	B3GNT5	NM_032047	Hs.208267	Up	C+D	148
10	TMEM23	NM_147156	Hs.386215	Up	C+D	-
11	SUCNR1	NM_033050	Hs.279575	Up	C+D	199
12	ANXA3	NM_005139	Hs.480042	Up	C+D	200
13	TSPAN2	NM_005725	Hs.310458	Up	C+D	201
14	PDE8B	NM_003719	Hs.584830	Up	C+D	202
15	SGPP1	NM_030791	Hs.24678	Up	C+D	116
16	PROK2	NM_021935	Hs.528665	Up	C+D	203
17	PTPRF	NM_002840	Hs.272062	Up	C+D	204
18	PROKR2	NM_144773	Hs.375029	Down	C+D	205
19	ANKS4B	NM_145865	Hs.115959	Down	C+D	206
20	RAP1GAP	NM_002885	Hs.148178	Down	C+D	207
21	FAAH	NM_001441	Hs.528334	Down	C+D	208
22	LCT	NM_002299	Hs.551506	Down	C+D	209
23	RGS12	NM_198229	Hs.527061	Down	C+D	210
24	DLST	NM_001933	Hs.525459	Down	C+D	211
25	ATE1	NM_001001976	Hs.632080	Down	C+D	212
26	CCNF	NM_001761	Hs.1973	Down	C+D	213
27	ALPI	NM_001631	Hs.37009	Down	C+D	214
28	CSN1S1	NM_001890	Hs.3155	Down	C+D	215
29	VASH2	NM_024749	Hs.96885	Down	C+D	216
30	CHST4	NM_005769	Hs.251383	Down	C+D	217
31	TAT	NM_000353	Hs.161640	Down	C+D	-
32	FBLN2	NM_001004019	Hs.198862	Down	C+D	218

[表65]

表164 遺伝子セット1(No.1-31:機能面で注目する遺伝子,No.32-61:発現増加・減少した遺伝子上位15個)

No	Target(Gene)Symbol	Target Accession	UniGene	Up/Down	被験者群	配列番号
1	FGFR1OP	NM_007045	Hs.487175	Up	A	1
2	CASP8AP2	NM_012115	Hs.558218	Up	A	2
3	PROK2	NM_021935	Hs.528665	Up	A	3
4	FCER1A	NM_002001	Hs.897	Up	A	4
5	CD69	NM_001781	Hs.208854	Up	A	5
6	PAQR3	NM_001040202	Hs.632591	Up	A	6
7	SLC6A4	NM_001045	Hs.591192	Up	A	7
8	GGCX	NM_000821	Hs.77719	Up	A	8
9	HBA2	NM_000517	Hs.449630	Up	A	9
10	ADH5	NM_000671	Hs.78989	Up	A	10
11	JUN	NM_002228	Hs.525704	Down	A	11
12	TP53	NM_000546	Hs.408312	Down	A	12
13	RAB5B		Hs.567328	Down	A	-
14	RAB8A	NM_005370	Hs.642874	Down	A	13
15	RAB12	NM_001025300	Hs.270074	Down	A	14
16	RAB20	NM_017817	Hs.508720	Down	A	15
17	RAB30	NM_014488	Hs.40758	Down	A	16
18	VISA		Hs.646283	Down	A	-
19	CD55		Hs.527653	Down	A	-
20	IGHG1	BC092518	Hs.510635	Down	A	-
21	SEMA3G	NM_020163	Hs.59729	Down	A	17
22	CD84	NM_003874	Hs.398093	Down	A	-
23	CD3G	NM_000073	Hs.2259	Down	A	18
24	CD177	NM_020406	Hs.232165	Down	A	19
25	NFAT5	NM_173215	Hs.371987	Down	A	20
26	HDGF	NM_004494	Hs.506748	Down	A	21
27	TNFAIP3	NM_006290	Hs.591338	Down	A	22
28	PRLHR	NM_004248	Hs.248119	Down	A	23
29	SYT2	NM_177402	Hs.585015	Down	A	24
30	RCP9	NM_014478	Hs.300684	Down	A	25
31	SPAG8	NM_172312	Hs.256747	Down	A	26
32	IMPA1	NM_005536	Hs.555086	Up	A	27
33	XPR1		Hs.648372	Up	A	-
34	B3GNT2	NM_006577	Hs.173203	Up	A	28
35	BCLAF1	NM_014739		Up	A	29
36	PSIP1	NM_021144	Hs.493516	Up	A	30
37	LGALS8	NM_006499	Hs.4082	Up	A	31
38	SEC24A	NM_021982	Hs.595540	Up	A	32
39	LOC492311	NM_001007189	Hs.200938	Up	A	-
40	ORMDL1	NM_016467	Hs.651259	Up	A	33
41	WHSC1	NM_133330	Hs.113876	Up	A	34
42	XRCC3	NM_005432	Hs.592325	Up	A	35
43	TMEM167	NM_174909	Hs.355606	Up	A	36
44	PREI3	NM_015387	Hs.645458	Up	A	-
45	SLC19A2	NM_006996	Hs.30246	Up	A	37
46	PDGFC	NM_016205	Hs.570855	Up	A	38
47	ERCC4	NM_005236	Hs.567265	Down	A	39
48	SH3PXD2B	NM_001017995	Hs.285666	Down	A	40
49	DUX2	NM_012147		Down	A	41
50	AP1S1	NM_001283	Hs.563509	Down	A	42
51	GATA2	NM_032638	Hs.367725	Down	A	43
52	LOC728371	XR_015273	Hs.558795	Down	A	44
53	PFKFB3	NM_004566	Hs.195471	Down	A	45
54	PHGDH	NM_006623	Hs.487296	Down	A	46
55	CENPP		Hs.459896	Down	A	-
56	OR5A1	NM_001004728	Hs.553649	Down	A	47
57	ADCK1	NM_020421	Hs.413208	Down	A	48
58	TFEC	NM_012252	Hs.125962	Down	A	49
59	RRH	NM_006583	Hs.352262	Down	A	50
60	DOK6	NM_152721	Hs.569915	Down	A	51
61	SAMD7	NM_182610	Hs.439922	Down	A	52

[表66]

表172　遺伝子セット2(No. 1-25:機能面で注目する遺伝子, No. 26-55:発現増加・減少した遺伝子上位15個)

No	Target(Gene)Symbol	Target Accession	UniGene	Up/Down	被験者群	配列番号
1	SOCS1	NM_003745	Hs. 50640	Down	B	53
2	CCR1	NM_001295	Hs. 301921	Down	B	54
3	CSF2RB	NM_000395	Hs. 592192	Down	B	55
4	STAT5A	NM_003152	Hs. 437058	Down	B	56
5	STAT3	NM_213662	Hs. 463059	Down	B	57
6	TNFRSF1B	NM_001066	Hs. 256278	Down	B	58
7	SNX17	NM_014748	Hs. 278569	Down	B	59
8	SCARF1	NM_145351	Hs. 647430	Down	B	60
9	LDLR		Hs. 213289	Down	B	-
10	STARD3	NM_006804	Hs. 77628	Down	B	61
11	CLN8	NM_018941	Hs. 127675	Down	B	62
12	APOL1	NM_145343	Hs. 114309	Down	B	63
13	ATP10A	NM_024490	Hs. 128041	Down	B	64
14	PSAP	NM_001042465	Hs. 523004	Down	B	65
15	OSBP2	NM_030758	Hs. 517546	Down	B	66
16	SLC27A1	NM_198580	Hs. 363138	Down	B	67
17	APOL6	NM_030641	Hs. 257352	Down	B	68
18	SOCS1	NM_003745	Hs. 50640	Down	B	53
19	STXBP4	NM_178509	Hs. 35199	Down	B	69
20	SOCS3	NM_003955	Hs. 527973	Down	B	70
21	AKT1	NM_005163	Hs. 525622	Down	B	71
22	MLLT7	NM_005938	Hs. 584654	Down	B	-
23	CEBPB	NM_005194	Hs. 642680	Down	B	72
24	CEBPB	NM_005194	Hs. 642680	Down	B	72
25	NLRP12	NM_033297	Hs. 631573	Down	B	73
26	EVI2A	NM_001003927	Hs.591198	Up	B	74
27	COMMD6	NM_203497	Hs.508266	Up	B	75
28	P2RY5	NM_005767	Hs.123464	Up	B	76
29	COMMD8	NM_017845	Hs.23956	Up	B	77
30	CD52	NM_001803	Hs.276770	Up	B	78
31	S100P	NM_005980	Hs.2962	Up	B	79
32	COX7C	NM_001867	Hs.430075	Up	B	80
33	CSTA	NM_005213	Hs.518198	Up	B	81
34	LY96	NM_015364	Hs.69328	Up	B	82
35	S100A8	NM_002964	Hs.416073	Up	B	83
36	SLC4A7	NM_003615	Hs.250072	Up	B	84
37	PHF6	NM_032458	Hs.356501	Up	B	85
38	TMEM167	NM_174909	Hs.355606	Up	B	36
39	EIF1AX	NM_001412	Hs.522590	Up	B	86
40	CRTAM	NM_019604	Hs.159523	Up	B	87
41	PIP5K1A	NM_003557	Hs.546316	Down	B	88
42	ERBB2	NM_001005862	Hs.446352	Down	B	89
43	COL25A1	NM_198721	Hs.112925	Down	B	90
44	TEP1	NM_007110	Hs.508835	Down	B	91
45	PKD1L1	NM_138295	Hs.195979	Down	B	92
46	ARHGAP26	NM_015071	Hs.293593	Down	B	93
47	RAB13	NM_002870	Hs.151536	Down	B	94
48	KCNAB3	NM_004732	Hs.435074	Down	B	95
49	ARHGAP24	NM_001025616	Hs.444229	Down	B	96
50	DDAH1	NM_012137	Hs.379858	Down	B	97
51	DOCK6	NM_020812	Hs.591002	Down	B	98
52	FABP6	NM_001040442	Hs.519719	Down	B	99
53	GALNT9	NM_021808	Hs.301062	Down	B	100
54	EBI3	NM_005755	Hs.501452	Down	B	101
55	BAI2	NM_001703	Hs.524138	Down	B	102

[表67]

表178　遺伝子セット3(No. 1-8:機能面で注目する遺伝子, No. 9-38:発現増加・減少した遺伝子上位15個)

No	Target(Gene)Symbol	Target Accession	UniGene	Up/Down	被験者群	配列番号
1	APBA2BP	NM_031232	Hs. 516986	Down	C	-
2	EFCBP2	NM_019065	Hs. 140950	Down	C	-
3	ASS1	NM_000050	Hs. 160786	Down	C	103
4	NAGS	NM_153006	Hs. 8876	Down	C	104
5	IL6	NM_000600	Hs. 512234	Down	C	105
6	FLT3	NM_004119	Hs. 507590	Down	C	106
7	IL4	NM_000589	Hs. 73917	Down	C	107
8	CD1D	NM_001766	Hs. 1799	Down	C	108
9	HDC	NM_002112	Hs.1481	Up	C	109
10	PFKFB3	NM_004566	Hs.195471	Up	C	45
11	FCER1A	NM_002001	Hs.897	Up	C	110
12	AGL	NM_000028	Hs.904	Up	C	111
13	LTF	NM_002343	Hs.529517	Up	C	112
14	HBA1	NM_000558	Hs.449630	Up	C	113
15	ORM2	NM_000608	Hs.522356	Up	C	114
16	IL3RA	NM_002183	Hs.632790	Up	C	115
17	STCH	NM_006948	Hs.352341	Up	C	-
18	HBA2	NM_000517	Hs.449630	Up	C	9
19	SGPP1	NM_030791	Hs.24678	Up	C	116
20	PTPRM	NM_002845	Hs.49774	Up	C	117
21	RERG	NM_032918	Hs.199487	Up	C	118
22	BCLAF1	NM_014739		Up	C	29
23	MASA	NM_021204	Hs.18442	Up	C	-
24	QRICH2	NM_032134	Hs.252739	Down	C	119
25	PLAC4	NM_182832	Hs.472492	Down	C	120
26	ECM1	NM_004425	Hs.81071	Down	C	121
27	TCF19	NM_007109	Hs.584807	Down	C	122
28	CPA1	NM_001868	Hs.2879	Down	C	123
29	THAP2	NM_031435	Hs.245798	Down	C	124
30	SCRG1		Hs.7122	Down	C	-
31	CDH6	NM_004932	Hs.171054	Down	C	125
32	FOXE1	NM_004473	Hs.159234	Down	C	126
33	METAP2	NM_006838	Hs.591005	Down	C	127
34	MAPK8IP2	NM_012324	Hs.558180	Down	C	128
35	GAL3ST3	NM_033036	Hs.208343	Down	C	129
36	FCER2	NM_002002	Hs.465778	Down	C	130
37	MAGEA5	NM_021049	Hs.18048	Down	C	131
38	RYR1	NM_001042723	Hs.466664	Down	C	132

[表68]

表185　遺伝子セット4(No. 1-7:機能面で注目する遺伝子, No. 8-37:発現増加・減少した遺伝子上位15個)

No	Target(Gene)Symbol	Target Accession	UniGene	Up/Down	被験者群	配列番号
1	TLR7	NM_016562	Hs. 443036	Up	D	133
2	BCL2	NM_000633	Hs. 150749	Up	D	134
3	TLR8	NM_016610	Hs. 272410	Up	D	135
4	PPARA		Hs. 103110	Down	D	-
5	NR5A1	NM_004959	Hs. 495108	Down	D	136
6	C1QTNF2	NM_031908	Hs. 110062	Down	D	137
7	ERC1	NM_178037	Hs. 400431	Down	D	138
8	LMNB1	NM_005573	Hs.89497	Up	D	139
9	PBX2	NM_002586	Hs.509545	Up	D	140
10	IPO7	NM_006391	Hs.643522	Up	D	141
11	LIMK1	NM_002314	Hs.647035	Up	D	142
12	PCDH18	NM_019035	Hs.591691	Up	D	143
13	INCENP	NM_001040694	Hs.142179	Up	D	144
14	CTSZ	NM_001336	Hs.252549	Up	D	145
15	RAB6B	NM_016577	Hs.12152	Up	D	146
16	AGL	NM_000028	Hs.904	Up	D	111
17	UTRN	NM_007124	Hs.133135	Up	D	147
18	B3GNT5	NM_032047	Hs.208267	Up	D	148
19	PTGS2	NM_000963	Hs.196384	Up	D	149
20	EEA1	NM_003566	Hs.567367	Up	D	150
21	MS4A2	NM_000139	Hs.386748	Up	D	151
22	RAB33B	NM_031296	Hs.591679	Up	D	152
23	TEP1	NM_007110	Hs.508835	Down	D	91
24	TAT		Hs.161640	Down	D	-
25	CCL17	NM_002987	Hs.546294	Down	D	153
26	FLJ40194	NM_001007529	Hs.446890	Down	D	154
27	GIF	NM_005142	Hs.110014	Down	D	155
28	ARHGAP26	NM_015071	Hs.293593	Down	D	93
29	NMBR	NM_002511	Hs.552106	Down	D	156
30	EFNB2	NM_004093	Hs.149239	Down	D	157
31	RABGAP1		Hs.271341	Down	D	-
32	HOXB6		Hs.98428	Down	D	-
33	TCBA1	NM_001040214	Hs.269722	Down	D	-
34	EGF	NM_001963	Hs.419815	Down	D	158
35	PLD1	NM_002662	Hs.382865	Down	D	159
36	CAPZA3	NM_033328	Hs.131288	Down	D	160
37	IFNAR2	NM_207585	Hs.642682	Down	D	161

[表69]

表190　遺伝子セット7(No. 1-4:機能面で注目する遺伝子, No. 5-34:発現増加・減少した遺伝子上位15個)

No	Target(Gene)Symbol	Target Accession	UniGene	Up/Down	被験者群	配列番号
1	MOXD1	NM_015529	Hs. 6909	Down	A+C	219
2	AOC2	NM_001158	Hs. 143102	Down	A+C	220
3	NR4A2	NM_006186	Hs. 563344	Down	A+C	221
4	FAM3D	NM_138805	Hs. 61265	Down	A+C	222
5	NCAM1	NM_001076682	Hs.503878	Up	A+C	223
6	IL20RB	NM_144717	Hs.61232	Up	A+C	224
7	KALRN		Hs.8004	Up	A+C	-
8	NTNG1	NM_014917	Hs.143707	Up	A+C	225
9	GFER	NM_005262	Hs.27184	Up	A+C	226
10	ALCAM	NM_001627	Hs.591293	Up	A+C	227
11	TF	NM_001063	Hs.518267	Up	A+C	228
12	FCER1A	NM_002001	Hs.897	Up	A+C	110
13	IMPA1	NM_005536	Hs.555086	Up	A+C	27
14	PFTK1	NM_012395	Hs.430742	Up	A+C	229
15	CENTG2	NM_001037131	Hs.435039	Up	A+C	-
16	CUL7	NM_014780	Hs.520136	Up	A+C	230
17	SCRN3	NM_024583	Hs.470679	Up	A+C	231
18	CPNE8	NM_153634	Hs.40910	Up	A+C	182
19	FLOT2	NM_004475	Hs.514038	Up	A+C	232
20	HSPG2	NM_005529	Hs.651231	Down	A+C	233
21	METAP2	NM_006838	Hs.591005	Down	A+C	127
22	TCL6	NM_020552	Hs.510368	Down	A+C	191
23	PEX11G	NM_080662	Hs.515100	Down	A+C	183
24	VIL1	NM_007127	Hs.647885	Down	A+C	234
25	SEMA3C	NM_006379	Hs.269109	Down	A+C	235
26	FLJ35379	XM_001127400	Hs.586820	Down	A+C	236
27	GTSE1	NM_016426	Hs.386189	Down	A+C	237
28	THRB	NM_000461	Hs.187861	Down	A+C	238
29	SERPINH1	NM_001235	Hs.596449	Down	A+C	239
30	APOA5	NM_052968	Hs.283923	Down	A+C	240
31	BNC2	NM_017637	Hs.435309	Down	A+C	241
32	IVD	NM_002225	Hs.513646	Down	A+C	242
33	DRD5	NM_000798	Hs.380681	Down	A+C	243
34	BCAR3	NM_003567	Hs.36958	Down	A+C	244

[表70]

表198　遺伝子セット8(No.1-46:機能面で注目する遺伝子,No.47-76:発現増加・減少した遺伝子上位15個)

No	Target(Gene)Symbol	Target Accession	UniGene	Up/Down	被験者群	配列番号
1	HLA-C	XR_015693	Hs.77961	Down	B+D	-
2	HLA-H	NR_001434	Hs.181244	Down	B+D	245
3	HLA-A	NM_002116	Hs.181244	Down	B+D	246
4	IGHG1	BC092518	Hs.510635	Down	B+D	-
5	HLA-E	NM_005516	Hs.118354	Down	B+D	247
6	HLA-B	CR608347	Hs.77961	Down	B+D	-
7	CD1D	NM_001766	Hs.1799	Down	B+D	108
8	FLJ45422	NM_001004349	Hs.591791	Down	B+D	248
9	HLA-F	NM_018950	Hs.519972	Down	B+D	249
10	LOC649853	0	Hs.181244	Down	B+D	-
11	HLA-B	NM_005514	Hs.77961	Down	B+D	250
12	CD74	NM_001025158	Hs.436568	Down	B+D	251
13	AP3B1	NM_003664	Hs.532091	Down	B+D	252
14	VISA		Hs.646283	Down	B+D	-
15	CASP8	NM_033355	Hs.591630	Down	B+D	253
16	NDFIP1	NM_030571	Hs.9788	Down	B+D	254
17	CFLAR	NM_003879	Hs.390736	Down	B+D	255
18	SECTM1	NM_003004	Hs.558009	Down	B+D	256
19	APOL3	NM_145641	Hs.474737	Down	B+D	257
20	LTBR	NM_002342	Hs.1116	Down	B+D	258
21	C1orf166	NM_024544	Hs.10101	Down	B+D	-
22	MYD88	NM_002468	Hs.82116	Down	B+D	259
23	TRIM38	NM_006355	Hs.584851	Down	B+D	260
24	CANT1	NM_138793	Hs.8859	Down	B+D	261
25	SLC20A1	NM_005415	Hs.187946	Down	B+D	262
26	REL	NM_002908	Hs.631886	Down	B+D	263
27	NLRP12	NM_033297	Hs.631573	Down	B+D	73
28	LGALS9	NM_009587	Hs.81337	Down	B+D	264
29	MIER1	NM_001077702	Hs.651300	Down	B+D	265
30	SCOTIN	NM_016479	Hs.414579	Down	B+D	-
31	TICAM1	NM_182919	Hs.29344	Down	B+D	266
32	CXXC5	NM_016463	Hs.189119	Down	B+D	267
33	SQSTM1	NM_003900	Hs.437277	Down	B+D	268
34	TRIM38	NM_006355	Hs.584851	Down	B+D	260
35	IKBKE	NM_014002	Hs.321045	Down	B+D	269
36	FKBP1A	NM_000801	Hs.471933	Down	B+D	270
37	FLNA	NM_001456	Hs.195464	Down	B+D	271
38	EDARADD	NM_080738	Hs.352224	Down	B+D	272
39	GM2A	NM_000405	Hs.483873	Down	B+D	273
40	HEXA	S76980		Down	B+D	-
41	STAT5A	NM_003152	Hs.437058	Down	B+D	56
42	STAT5B	NM_012448	Hs.632256	Down	B+D	274
43	STAT5B	BC020868	Hs.632256	Down	B+D	-
44	LARGE	NM_004737	Hs.474667	Down	B+D	275
45	PSAP	NM_001042465	Hs.523004	Down	B+D	65
46	CLN3	NM_001042432	Hs.628393	Down	B+D	174
47	CTSZ	NM_001336	Hs.252549	Up	B+D	145
48	ZC3H7B	NM_017590	Hs.592188	Up	B+D	276
49	MAP2K1IP1	NM_021970	Hs.647988	Up	B+D	-
50	CLK4	NM_020666	Hs.406557	Up	B+D	277
51	TNFRSF17	NM_001192	Hs.2556	Up	B+D	278
52	RAB33B	NM_031296	Hs.591679	Up	B+D	152
53	LMNB1	NM_005573	Hs.89497	Up	B+D	139
54	EEA1	NM_003566	Hs.567367	Up	B+D	150
55	PREI3	NM_015387	Hs.645458	Up	B+D	-
56	BCLAF1	NM_014739		Up	B+D	29
57	STCH	NM_006948	Hs.352341	Up	B+D	-
58	TCEB1		Hs.554594	Up	B+D	-
59	SP3	NM_003111	Hs.531587	Up	B+D	279
60	PTGS2	NM_000963	Hs.196384	Up	B+D	149

表198　遺伝子セット8(No.1-46:機能面で注目する遺伝子,No.47-76:発現増加・減少した遺伝子上位15個)

No	Target(Gene)Symbol	Target Accession	UniGene	Up/Down	被験者群	配列番号
61	RAB18	NM_021252	Hs.406799	Up	B+D	280
62	CEI	NM_178569	Hs.148486	Down	B+D	-
63	TEP1	NM_007110	Hs.508835	Down	B+D	91
64	IFNAR2	NM_207585	Hs.642682	Down	B+D	161
65	CST2	NM_001322	Hs.123114	Down	B+D	281
66	ARHGAP26	NM_015071	Hs.293593	Down	B+D	93
67	BAI2	NM_001703	Hs.524138	Down	B+D	102
68	PVR	NM_006505	Hs.171844	Down	B+D	282
69	GTF3C4		Hs.22302	Down	B+D	-
70	NRP2	NM_018534	Hs.471200	Down	B+D	283
71	MALAT1	NR_002819	Hs.621695	Down	B+D	284
72	HSPB2	NM_001541	Hs.78846	Down	B+D	285
73	BIC	NR_001458	Hs.388313	Down	B+D	-
74	CTSA	NM_000308	Hs.517076	Down	B+D	286
75	CTSB	NM_147780	Hs.520898	Down	B+D	287
76	IL8RB	NM_001557	Hs.846	Down	B+D	288

[表71]

表202　ヒト共通遺伝子

No	Target(Gene)Symbol	Target Accession	UniGene	Up/Down	被験者群	配列番号
1	ANXA1	NM_000700	Hs.494173	Up	B	289
2	ARID4B	NM_016374	Hs.575782	Up	A+B,B,D,B+D	290
3	CLK1	NM_004071	Hs.433732	Up	B+D	291
4	ECHDC1	NM_018479	Hs.486410	Up	A+B,B,B+D	292
5	IFI44	NM_006417	Hs.82316	Up	A+B,B,B+D	293
6	IFIT2	NM_001547	Hs.437609	Up	A+B	294
7	MATR3	NM_199189	Hs.268939	Up	B+D	295
8	PTPRO	NM_030667	Hs.160871	Up	C+D,A+C,D,B+D	296
9	ROCK1	NM_005406	Hs.306307	Up	A+B,B+D	297
10	RPL23	NM_000978	Hs.406300	Up	A+B,B,B+D	298
11	RPL26	NM_000987	Hs.645380	Up	A+B,B,B+D	299
12	S100A8	NM_002964	Hs.416073	Up	A+B,B,B+D	83
13	SHMT1	NM_004169	Hs.513987	Up	A+C,B+D	300
14	SUB1	NM_006713	Hs.229641	Up	A+B,B,B+D	301
15	SYNCRIP	BC032643	Hs.571177	Up	D,B+D	-
16	ZNF291	NM_020843	Hs.458986	Up	B+D	-
17	AP2A2	NM_012305	Hs.19121	Down	A+B,B+D	302
18	BTBD9	NM_152733	Hs.116233	Down	B+D	303
19	C1QA	NM_015991	Hs.632379	Down	B+D	304
20	C1QTNF5	NM_015645	Hs.632102	Down	D	305
21	C1S	NM_001734	Hs.458355	Down	A+B,A+C	306
22	COMT	NM_000754	Hs.370408	Down	B+D	307
23	ELK1	NM_005229	Hs.181128	Down	A,D	308
24	GMPR	NM_006877	Hs.484741	Down	B+D	309
25	GNB1	NM_002074	Hs.430425	Down	B+D	310
26	HYOU1	NM_006389	Hs.277704	Down	B+D	311
27	LTBP1	NM_206943	Hs.49787	Down	D	312
28	MAOA	NM_000240	Hs.183109	Down	A+B,A	313
29	MAS1	NM_002377	Hs.99900	Down	C+D	314
30	MUC5AC	XM_001130382	Hs.558950	Down	A+B	-
31	PHC2	NM_198040	Hs.524271	Down	A+B,B,C,D,B+D	315
32	PLK1	NM_005030	Hs.592049	Down	A	316
33	PSEN1	AJ008005	Hs.592324	Down	B	-
34	QTRT1	NM_031209	Hs.631638	Down	B,B+D	317
35	RLN3	NM_080864	Hs.352155	Down	D	318
36	RND2	NM_005440	Hs.603111	Down	B+D	319
37	RNF138	NM_016271	Hs.302408	Down	A	320
38	ST6GALNAC3	NM_152996	Hs.337040	Down	C	321
39	STX11	NM_003764	Hs.118958	Down	A+B,B,B+D	322
40	TMEM39A	NM_018266	Hs.434927	Down	B+D	323

[請求項22]　下記の表205に示す遺伝子群中の各遺伝子の塩基配列の少なくとも一部を含む核酸、又は下記の表205に示す遺伝子群中の各遺伝子によってコードされるタンパク質に対して特異的に結合する分子を含む、ラットの陽性感情を評価するための検査キット。

[表72]

表205 ラット共通遺伝子

No	Target(Gene)Symbol	Target Accession	UniGene	Up/Down	生体由来試料	配列番号
1	Anxa1	NM_012904	Rn.1792	Up	BI	324
2	Arid4b	AA955478	Rn.47249	Up	BI	-
3	Clk1	XM_217405	Rn.36770	Up	BI	325
4	Echdc1	NM_001007734	Rn.4220	Up	BI	326
5	Ifi44	XM_227821	Rn.43876	Up	BI	327
6	Ifit2	NM_001024753	Rn.6175	Up	BI	328
7	Matr3	NM_019149	Rn.29774	Up	BI	329
8	Ptpro	NM_017336	Rn.10163	Up	BI	330
9	Rock1	NM_031098	Rn.89756	Up	BI	-
10	Rpl23	NM_001007599	Rn.103172	Up	BI	331
11	Rpl26	XM_213346	Rn.144702	Up	BI	332
12	S100a8	NM_053822	Rn.31839	Up	BI	333
13	Shmt1	AI010087	Rn.3684	Up	BI	-
14	Sub1	NM_001009618	Rn.8706	Up	BI	-
15	Syncrip	XM_343446	Rn.25065	Up	BI	334
16	Znf291	XM_343394	Rn.163002	Up	BI	335
17	Ap2a2	BF414152	Rn.34928	Down	BI	336
18	Btbd9	BF401614	Rn.48897	Down	BI	337
19	C1qa	NM_001008515	Rn.105647	Down	BI	338
20	C1qtnf5	NM_001012123	Rn.99884	Down	BI	339
21	C1s	NM_138900	Rn.4037	Down	BI	340
22	Comt	AA858639	Rn.220	Down	BI	341
23	Elk1	BF558309	Rn.1714	Down	BI	342
24	Gmpr	NM_057188	Rn.3862	Down	BI	343
25	Gnb1	NM_030987	Rn.126047	Down	BI	344
26	Hyou1	NM_138867	Rn.10542	Down	BI	345
27	Ltbp1	NM_021587	Rn.40942	Down	BI	346
28	Maoa	AI105223	Rn.163443	Down	BI	347
29	Mas1	NM_012757	Rn.21943	Down	BI	348
30	Muc5ac	U83139	Rn.10789	Down	BI	349
31	Phc2	XM_232751	Rn.2428	Down	BI	350
32	Plk1	NM_017100	Rn.11034	Down	BI	351
33	Psen1	NM_019163	Rn.44440	Down	BI	352
34	Qtrt1	NM_022250	Rn.53858	Down	BI	353
35	Rln3	NM_170667	Rn.45123	Down	BI	354
36	Rnd2	NM_001010953	Rn.22162	Down	BI	355
37	Rnf138	NM_053588	Rn.6814	Down	BI	356
38	St6galnac3	NM_019123	Rn.88072	Down	BI	357
39	Stx11	XM_218092	-	Down	BI	358
40	Tmem39a	NM_001013865	Rn.13663	Down	BI	359

[請求項23] 前記分子は抗体、リガンドタンパク質又は受容体タンパク質であることを特徴とする請求項21又は22記載の検査キット。

[請求項24] 前記核酸又は分子は支持体に固定されていることを特徴とする請求項21又は22記載の検査キット。

[請求項25] ラットの生体由来試料中の遺伝子発現量を網羅的に測定する第1のステップと、

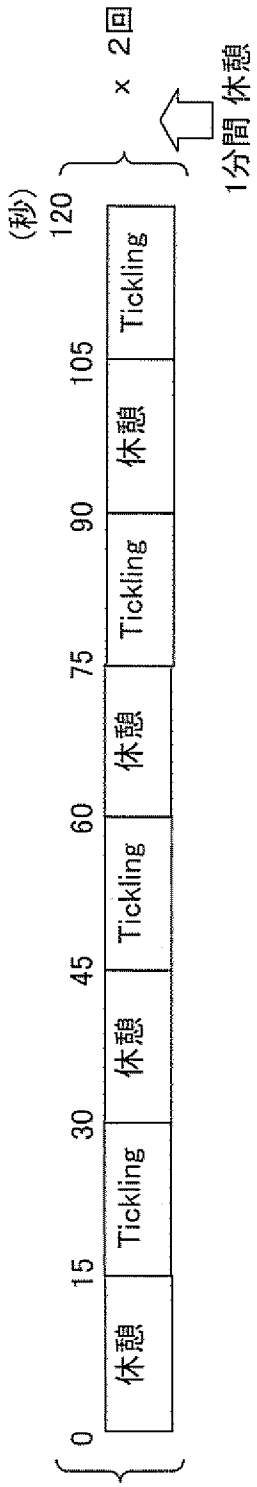
ラットに陽性刺激を負荷した後の生体由来試料中の遺伝子発現量を網羅的に測定する第2のステップと、

第1のステップで測定した結果と第2のステップで測定した結果とを比較し、発現変動が認められた遺伝子を選択する第3のステップと、

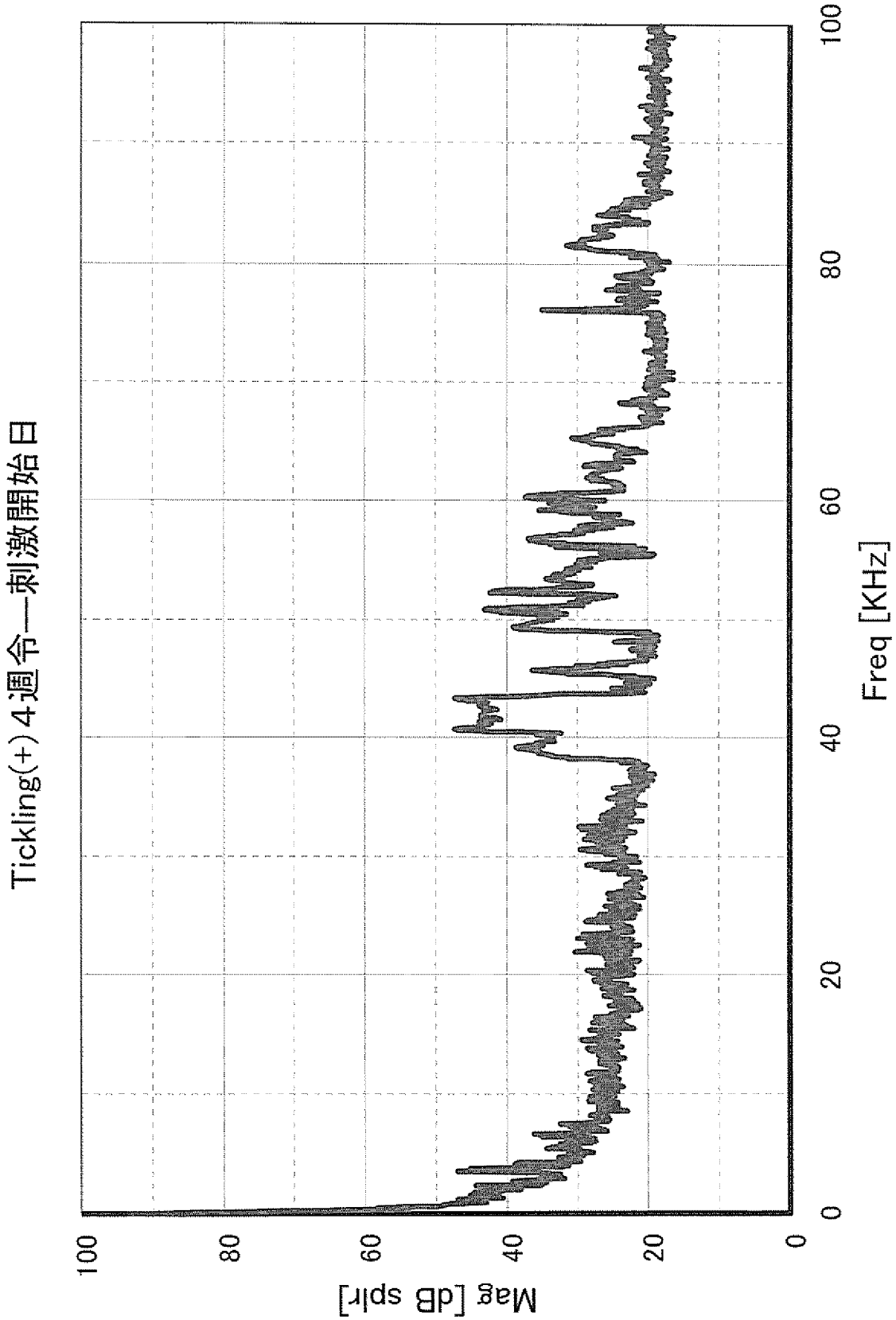
第3のステップで選択された遺伝子のヒトホモログをヒト陽性感情マーカー遺伝子であると特定する第4のステップと

を含む、ヒト陽性感情マーカー遺伝子

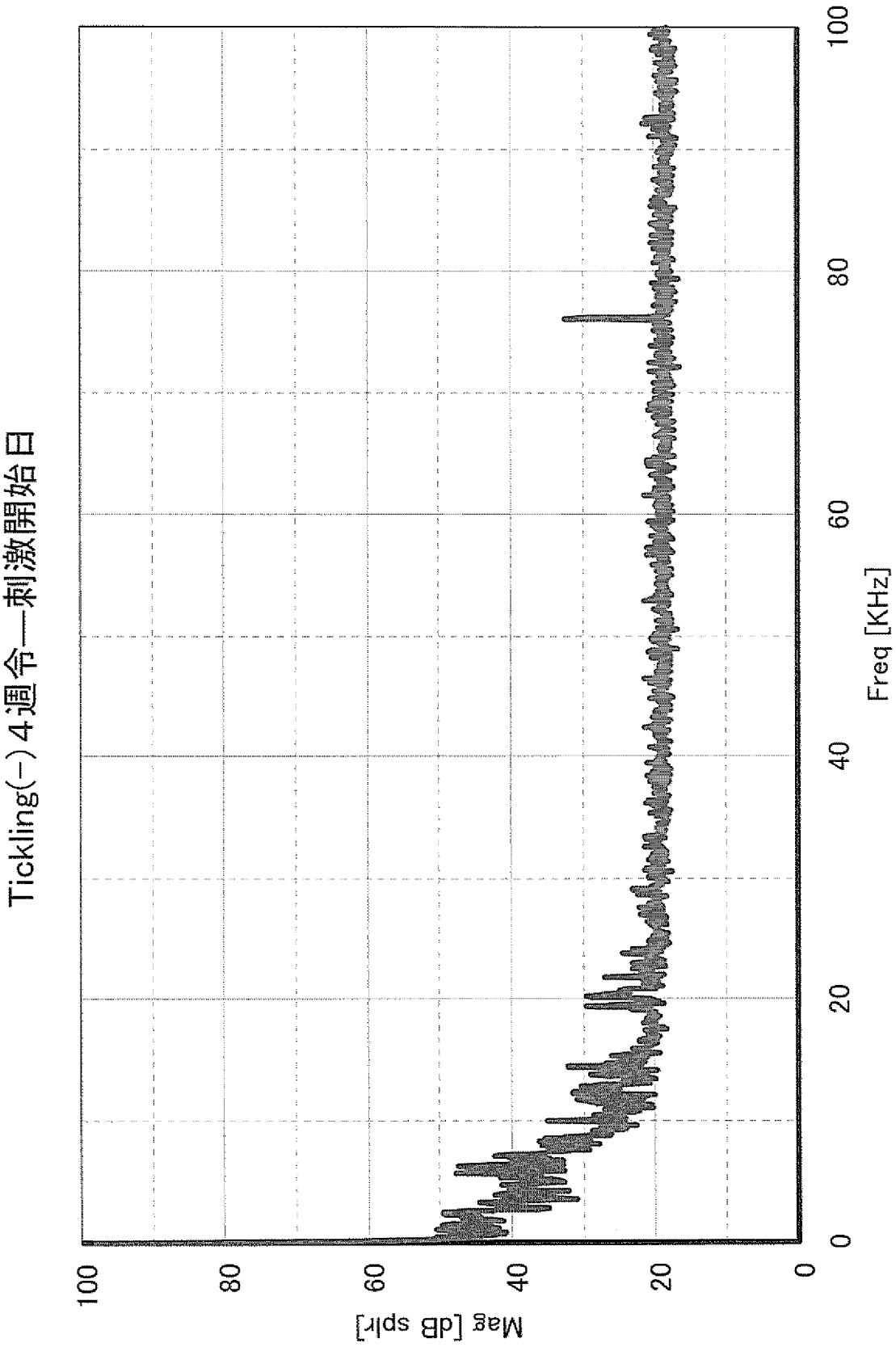
[図1]


(秒)
0
15
30
45
60
75
90
105
120
休憩
Tickling
休憩
Tickling
休憩
Tickling
休憩
Tickling
1分間 休憩
× 2回

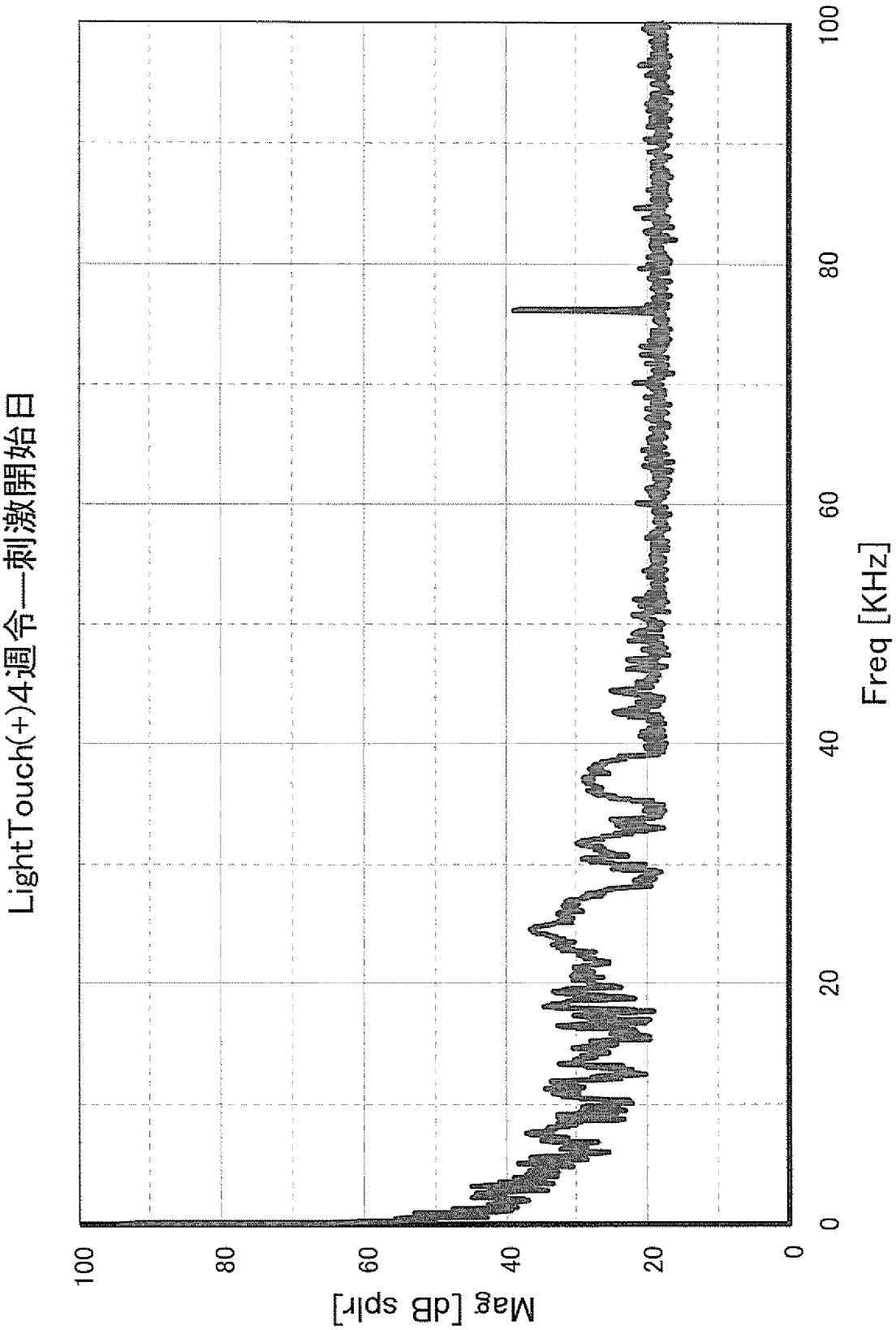
[図2]


Tickling(+) 4週令—刺激開始日
Mag [dB spir]
100
80
60
40
20
0
0
20
40
60
80
100
Freq [KHz]

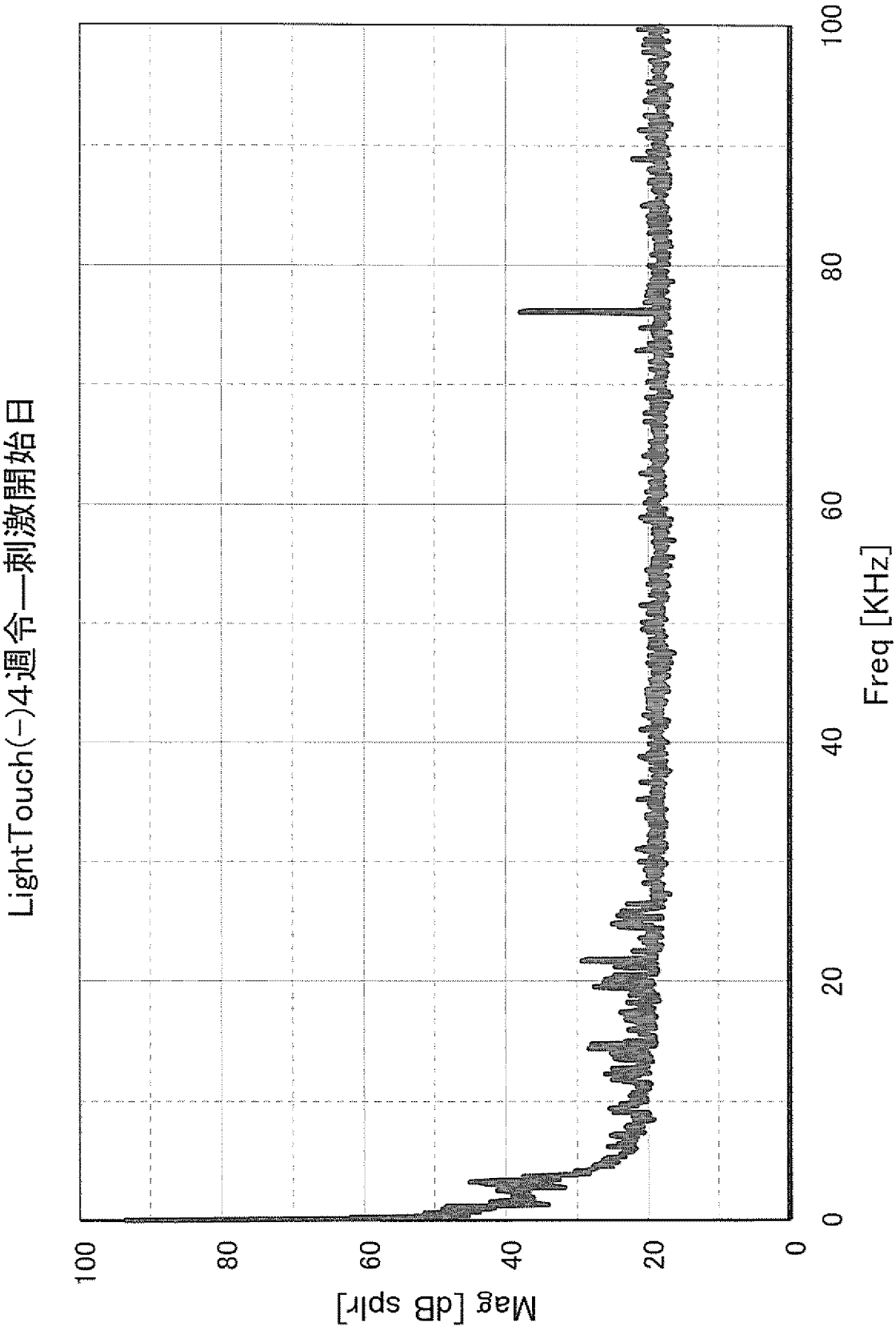
[図3]


Tickling(−) 4週令—刺激開始日
Mag [dB spl]
0
20
40
60
80
100
Freq [KHz]
0
20
40
60
80
100

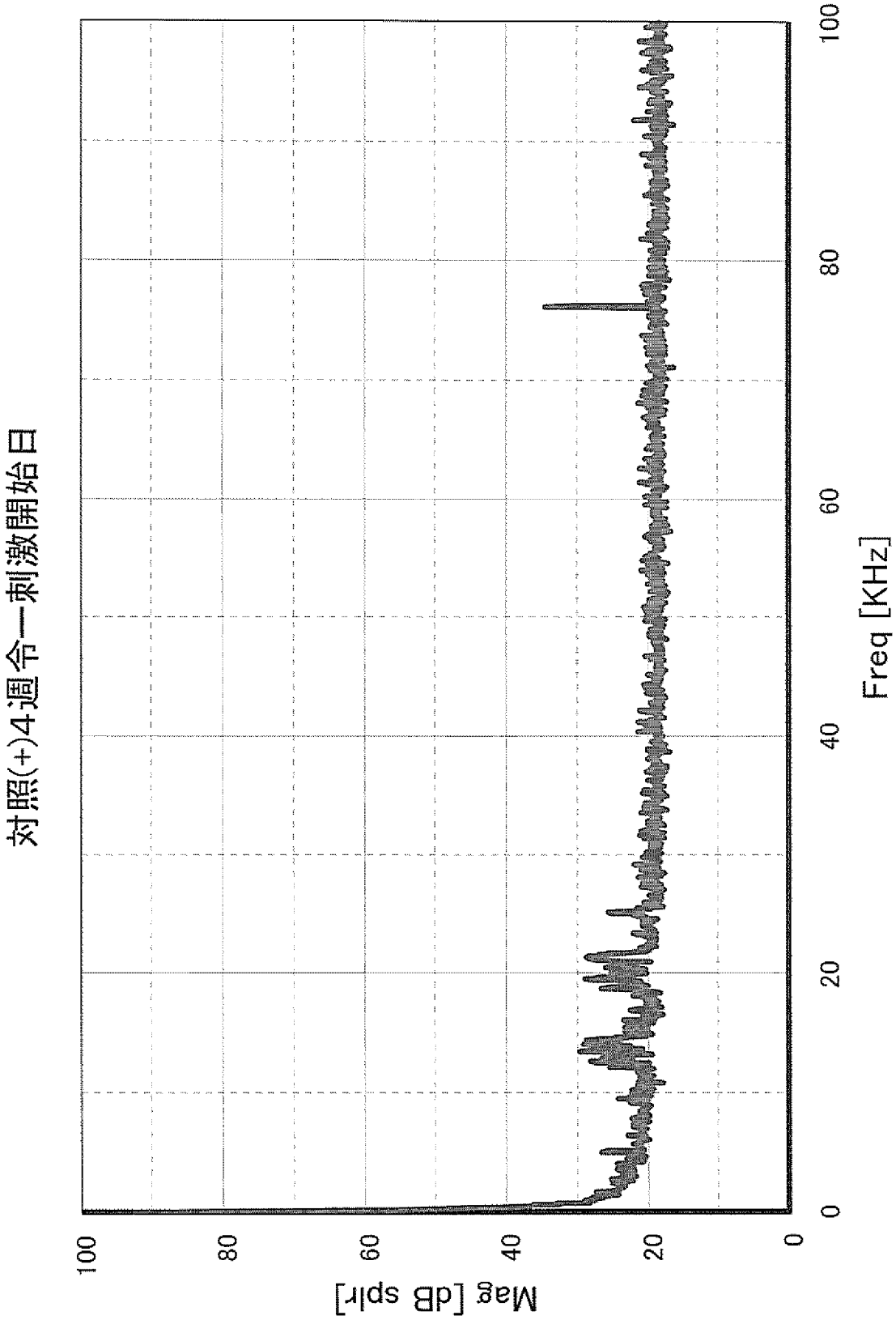
[図4]


LightTouch(+)4週令—刺激開始日
Mag [dB spl]
Freq [KHz]
0
20
40
60
80
100
0
20
40
60
80
100

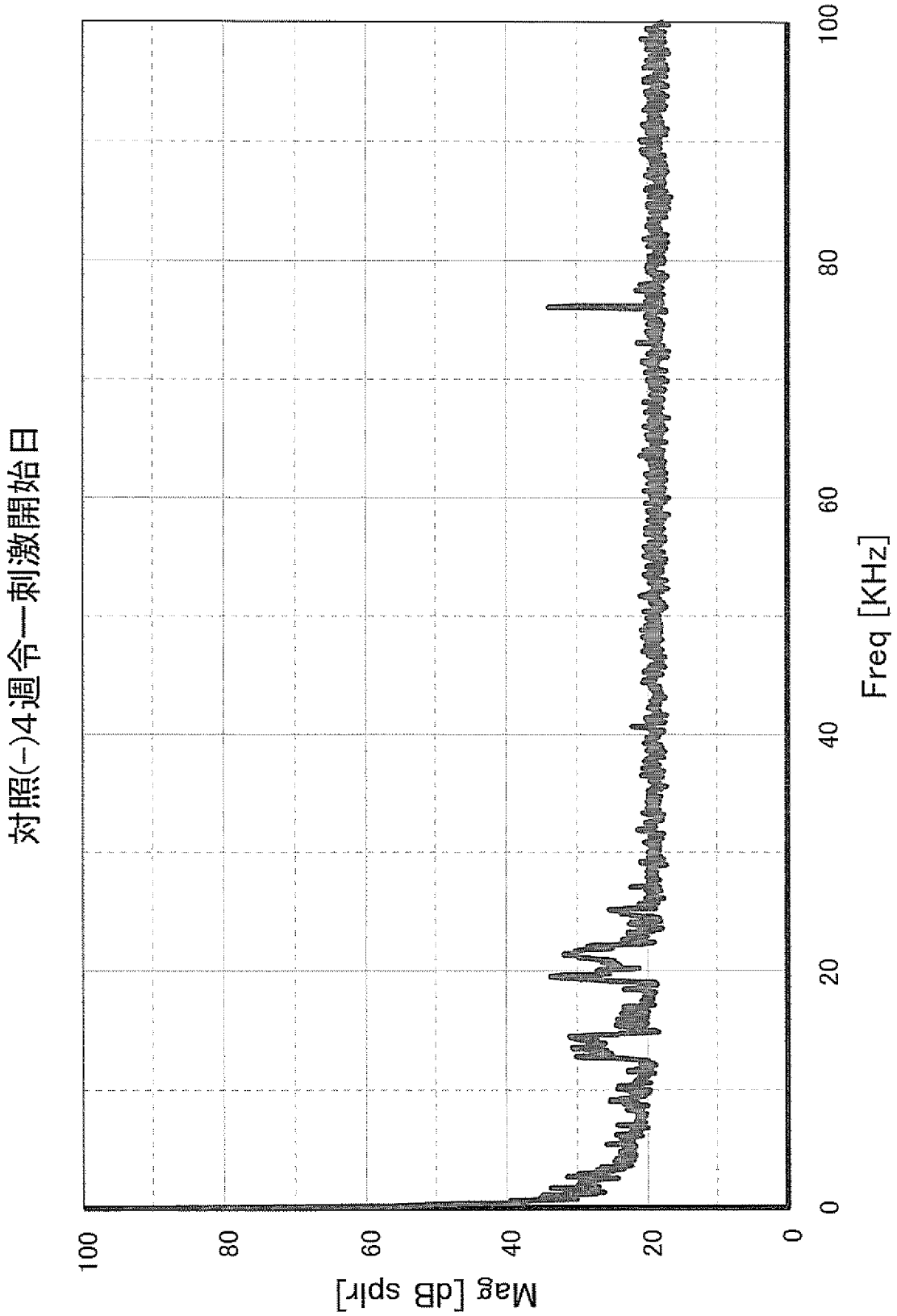
[図5]


LightTouch(−)4週令—刺激開始日
Mag [dB spir]
100
80
60
40
20
0
0
20
40
60
80
100
Freq [KHz]

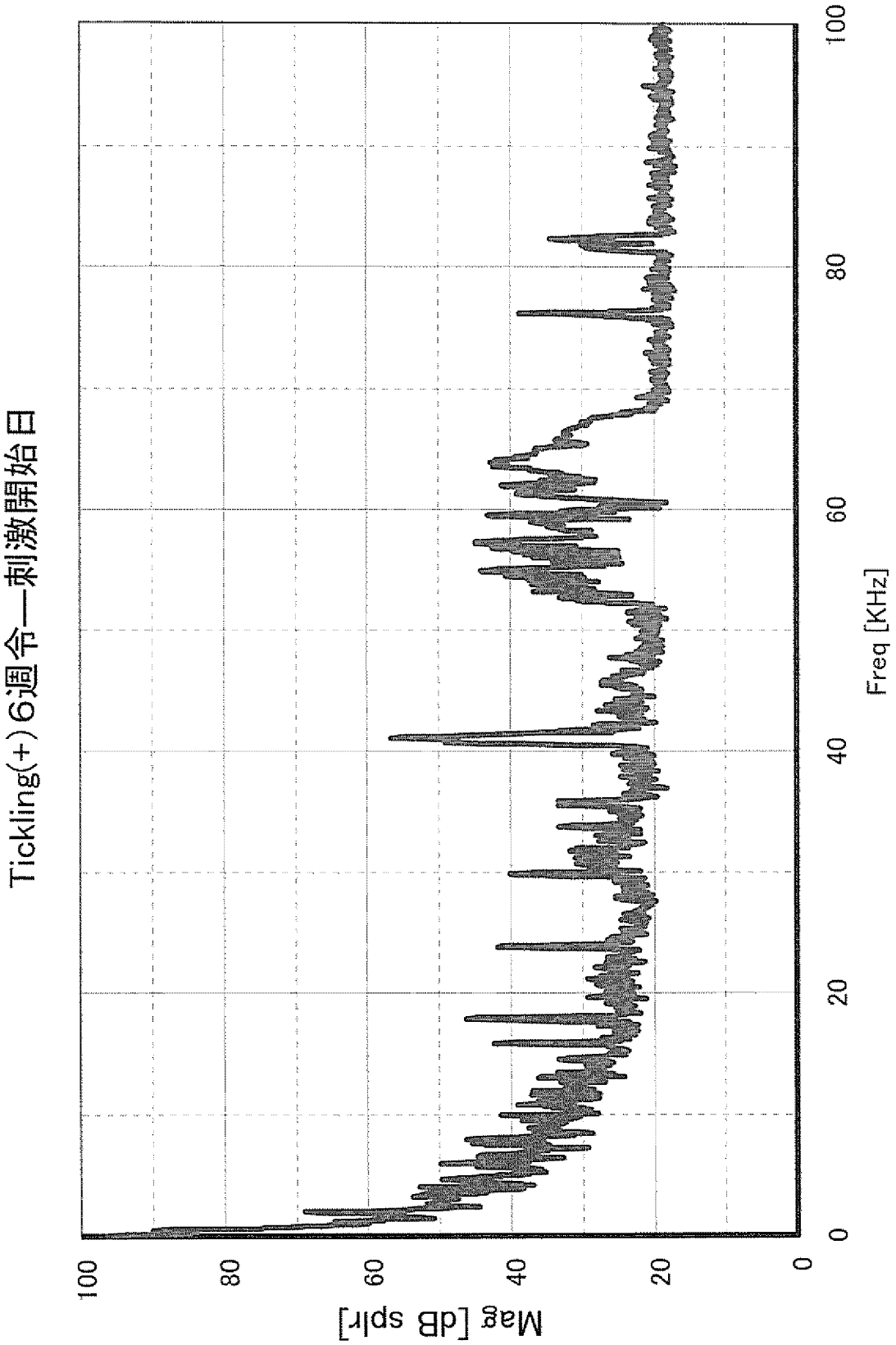
[図6]



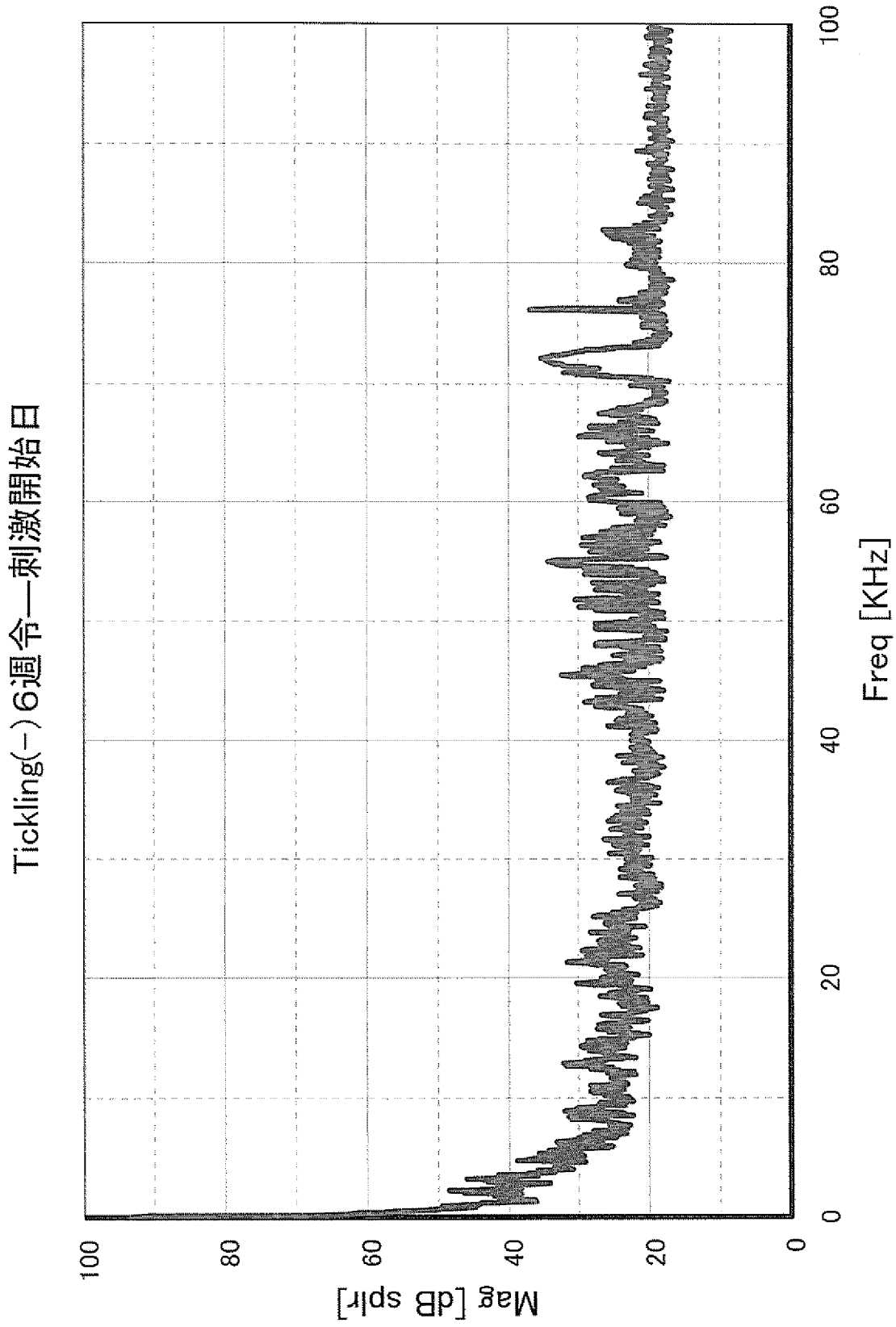
[図7]


対照(−)4週令−刺激開始日
Mag [dB spir]
0
20
40
60
80
100
Freq [KHz]
0
20
40
60
80
100

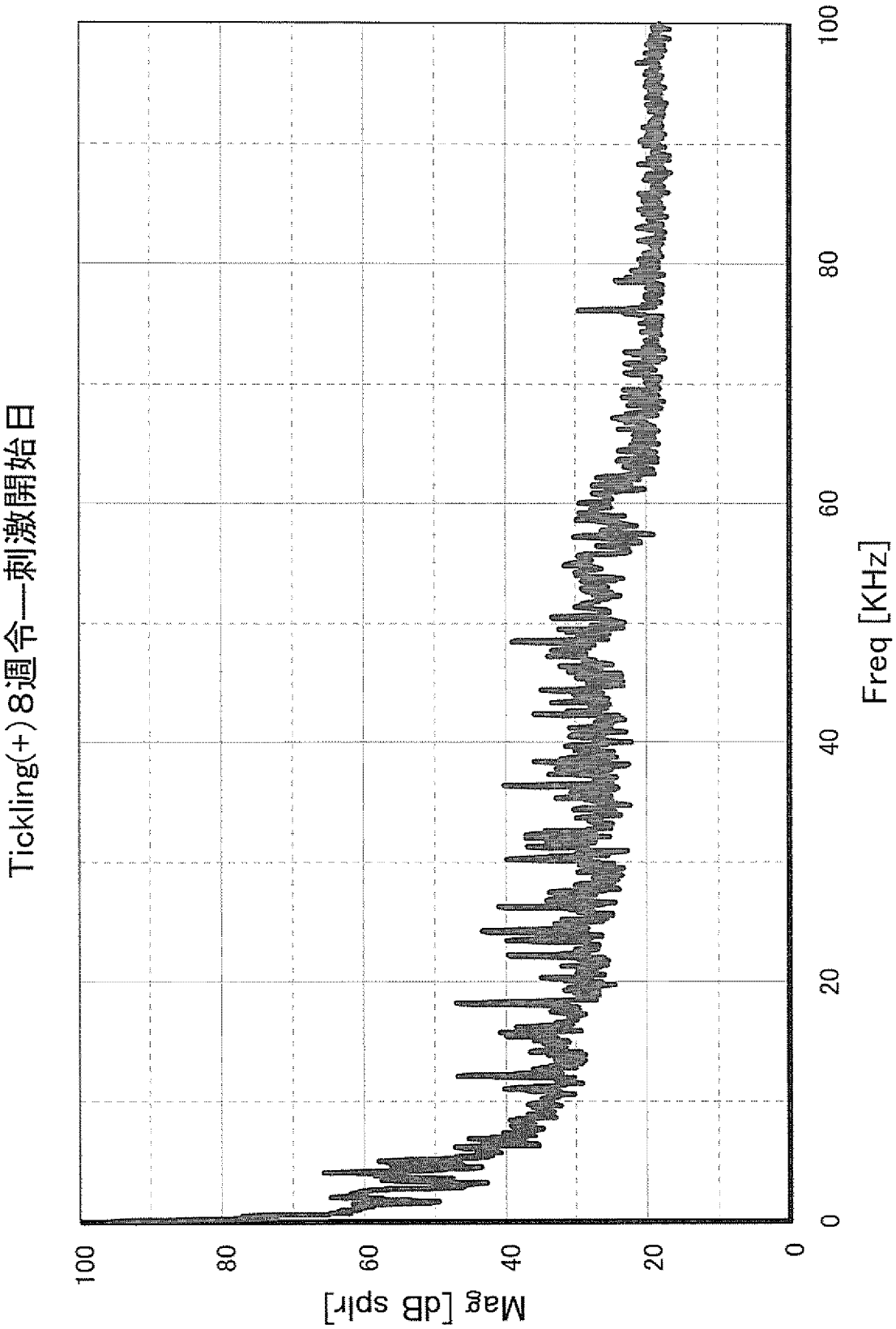
[図8]


Tickling(+)6週令—刺激開始日
Mag [dB spir]
100
80
60
40
20
0
0
20
40
60
80
100
Freq [KHz]

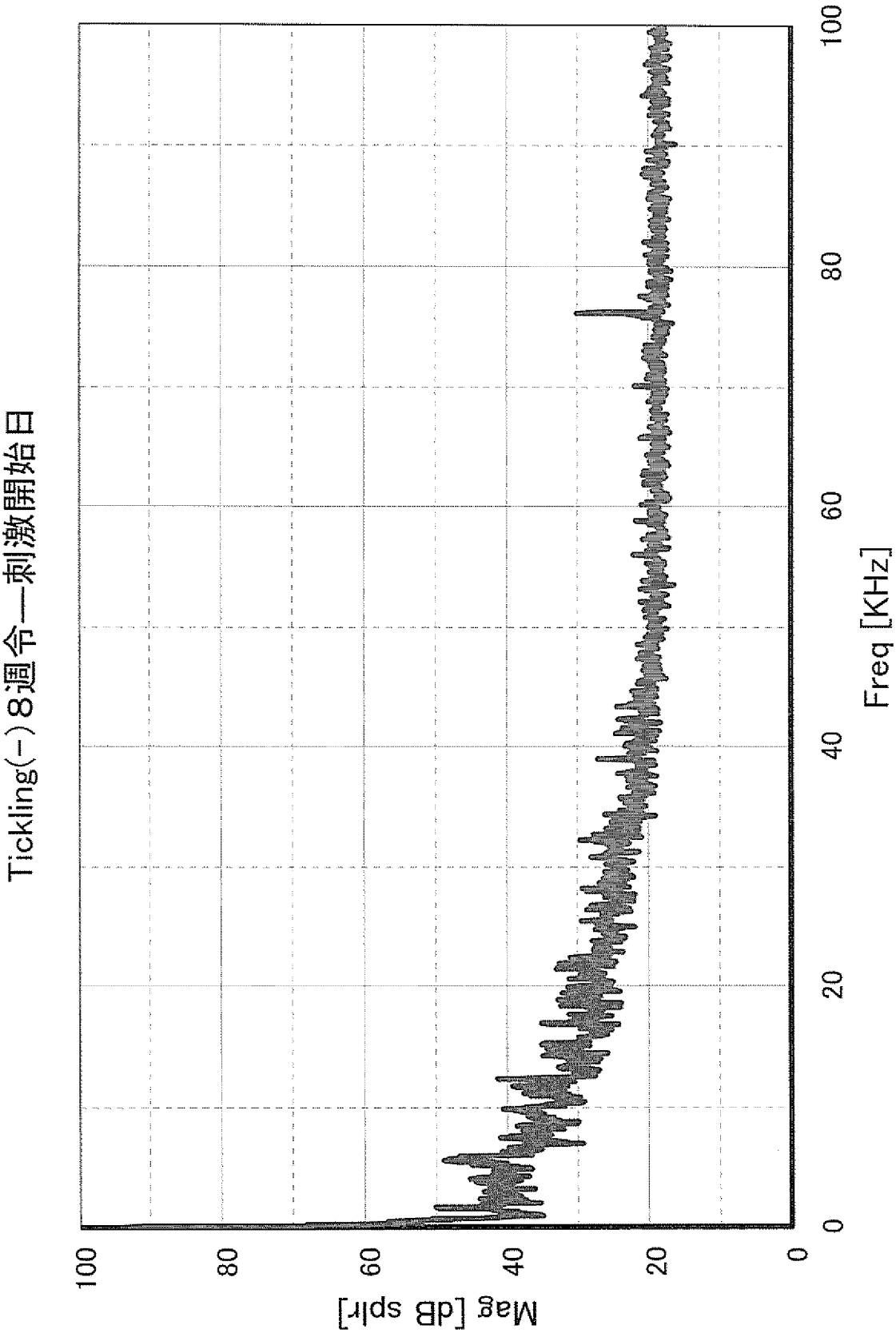
[図9]


Tickling(−)6週令—刺激開始日
Mag [dB spl]
0
20
40
60
80
100
Freq [KHz]
0
20
40
60
80
100

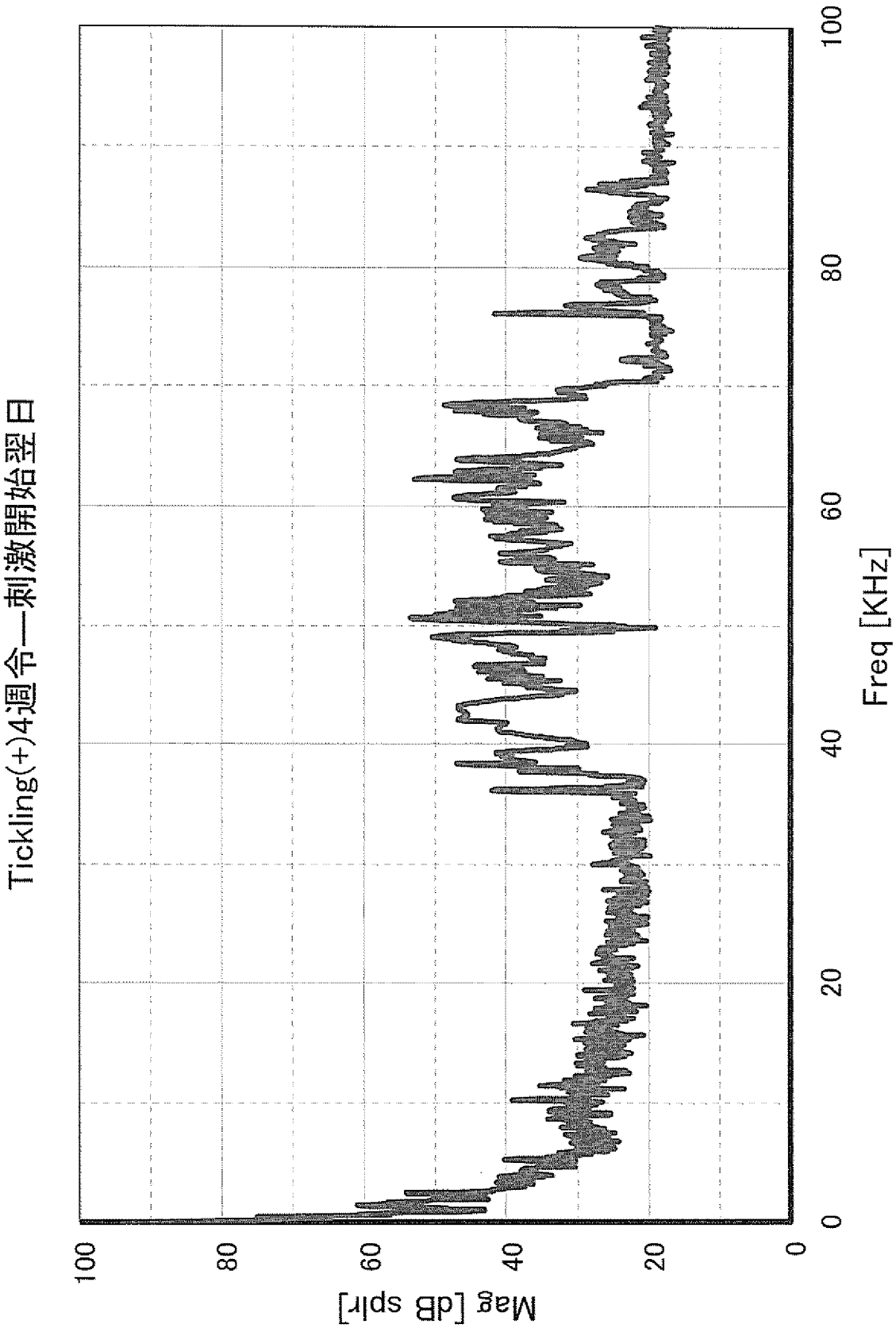
[図10]


Tickling(+)8週令—刺激開始日
Mag [dB spir]
100
80
60
40
20
0
0
20
40
60
80
100
Freq [KHz]

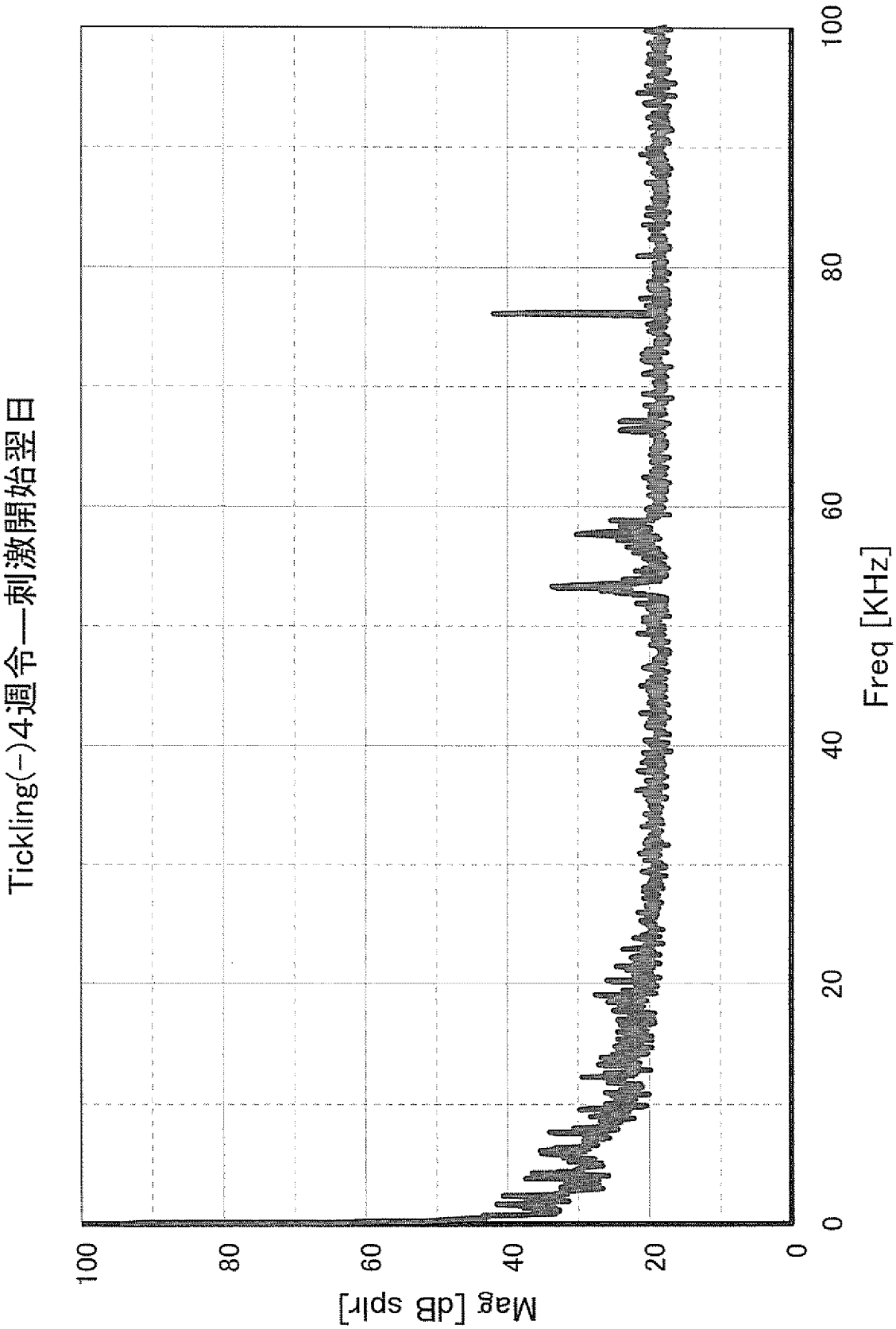
[図11]


Tickling(−)8週令—刺激開始日
Mag [dB spl]
100
80
60
40
20
0
Freq [KHz]
0
20
40
60
80
100

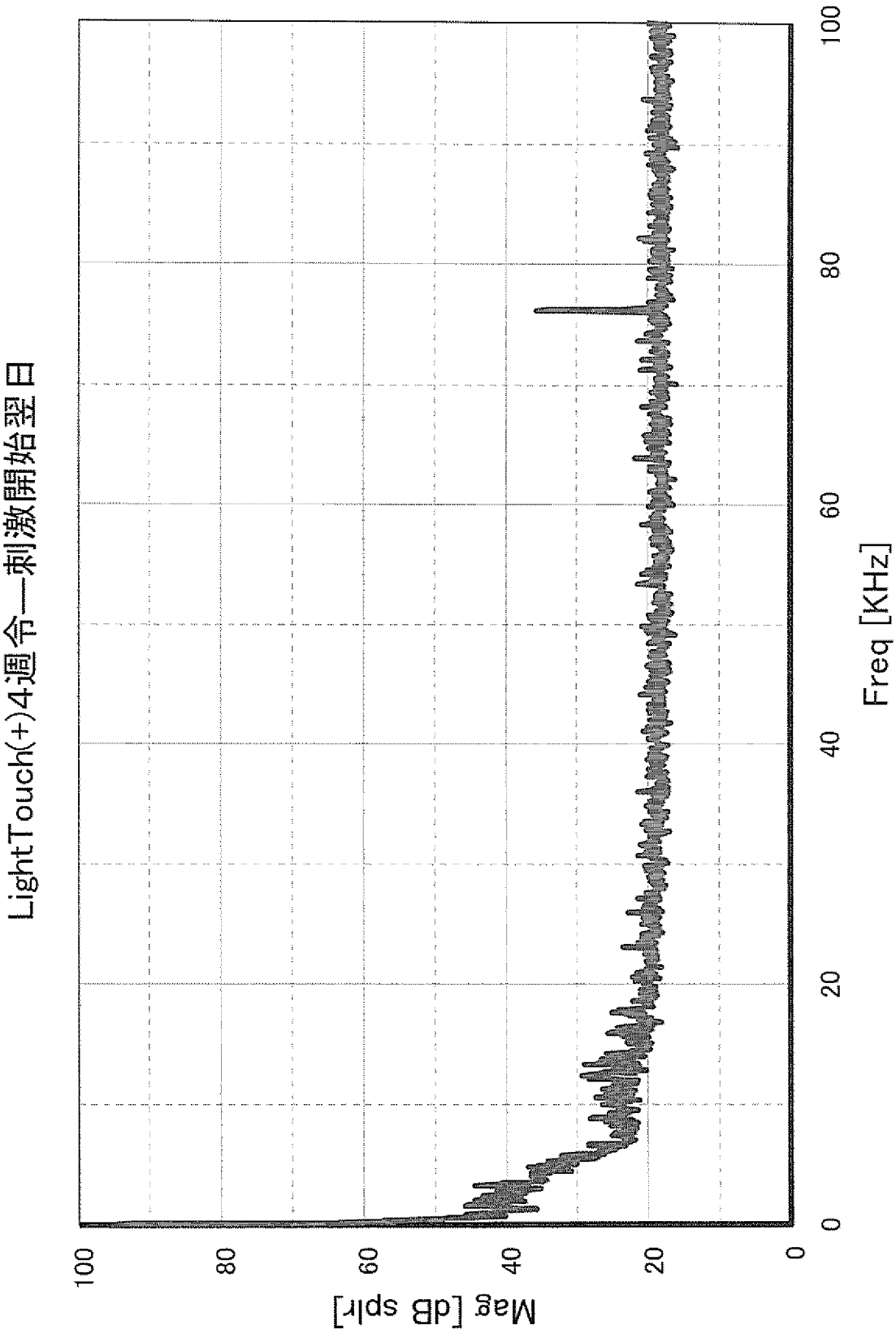
[図12]


Tickling(+)4週令—刺激開始翌日
Mag [dB spir]
100
80
60
40
20
0
0
20
40
60
80
100
Freq [KHz]

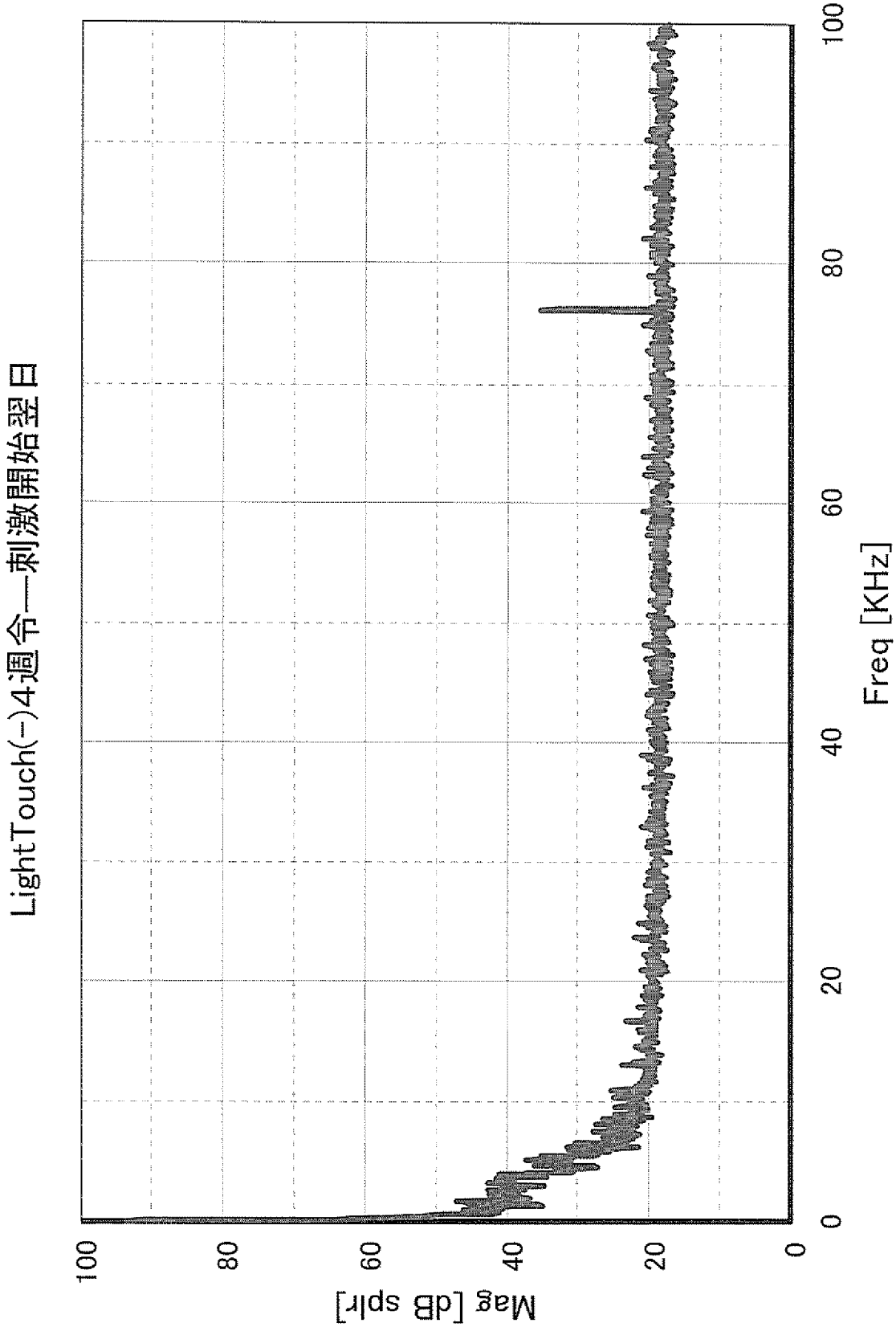
[図13]


Tickling(−)4週令—刺激開始翌日
Mag [dB spl]
100
80
60
40
20
0
0
20
40
60
80
100
Freq [KHz]

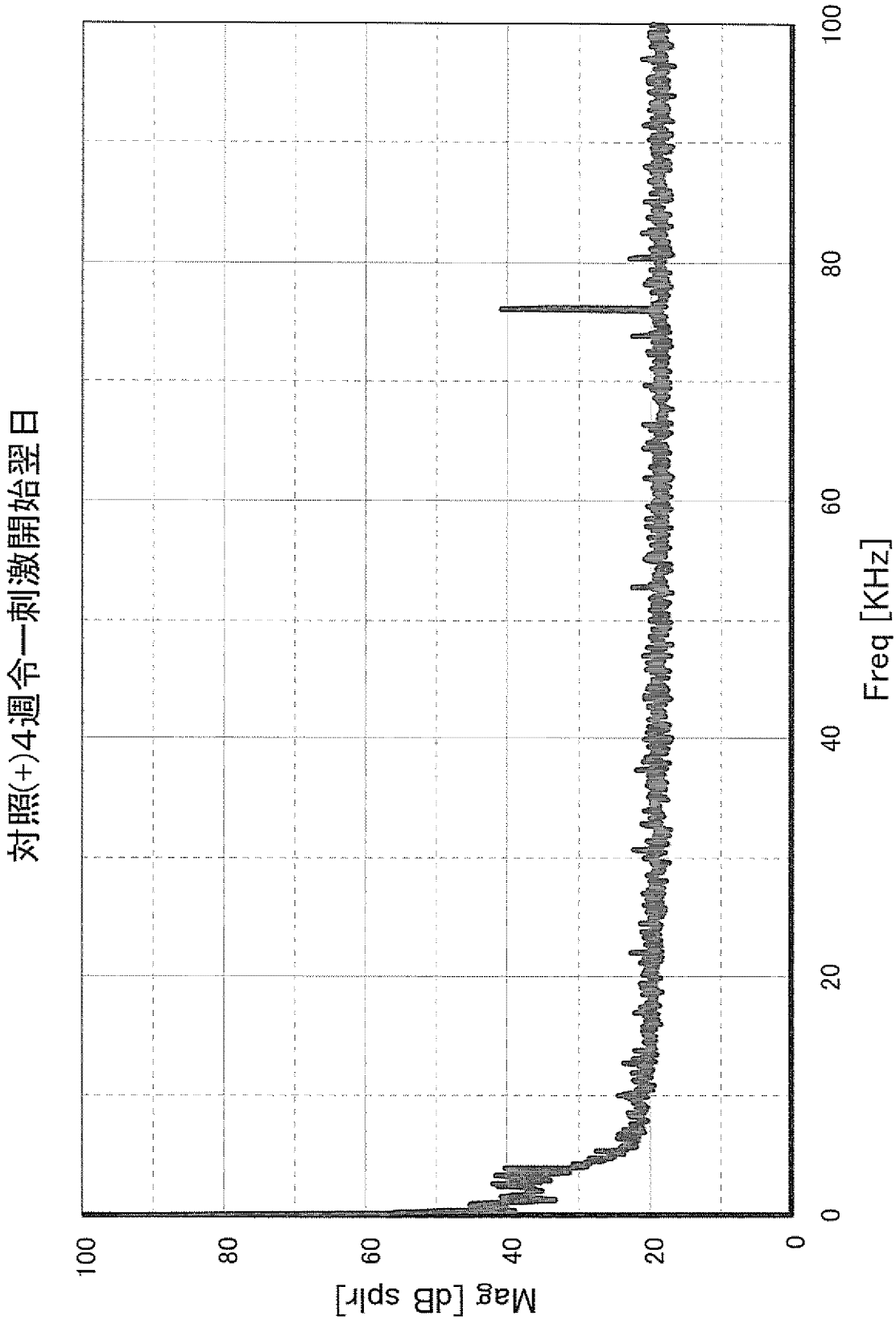
[図14]


LightTouch(+)4週令—刺激開始翌日
Mag [dB spl]
100
80
60
40
20
0
0
20
40
60
80
100
Freq [KHz]

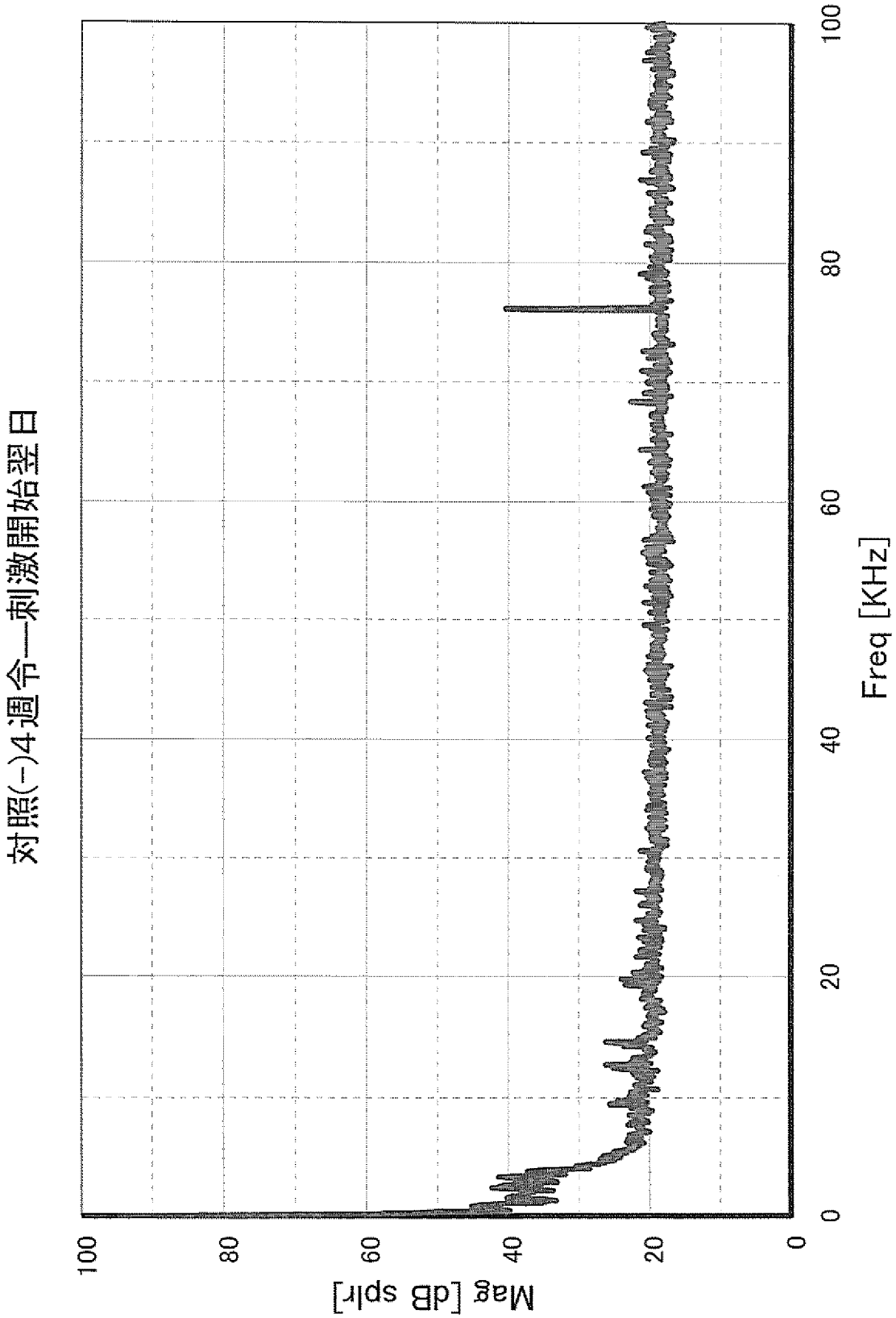
[図15]


LightTouch(−)4週令—刺激開始翌日
Mag [dB spl]
100
80
60
40
20
0
0
20
40
60
80
100
Freq [KHz]

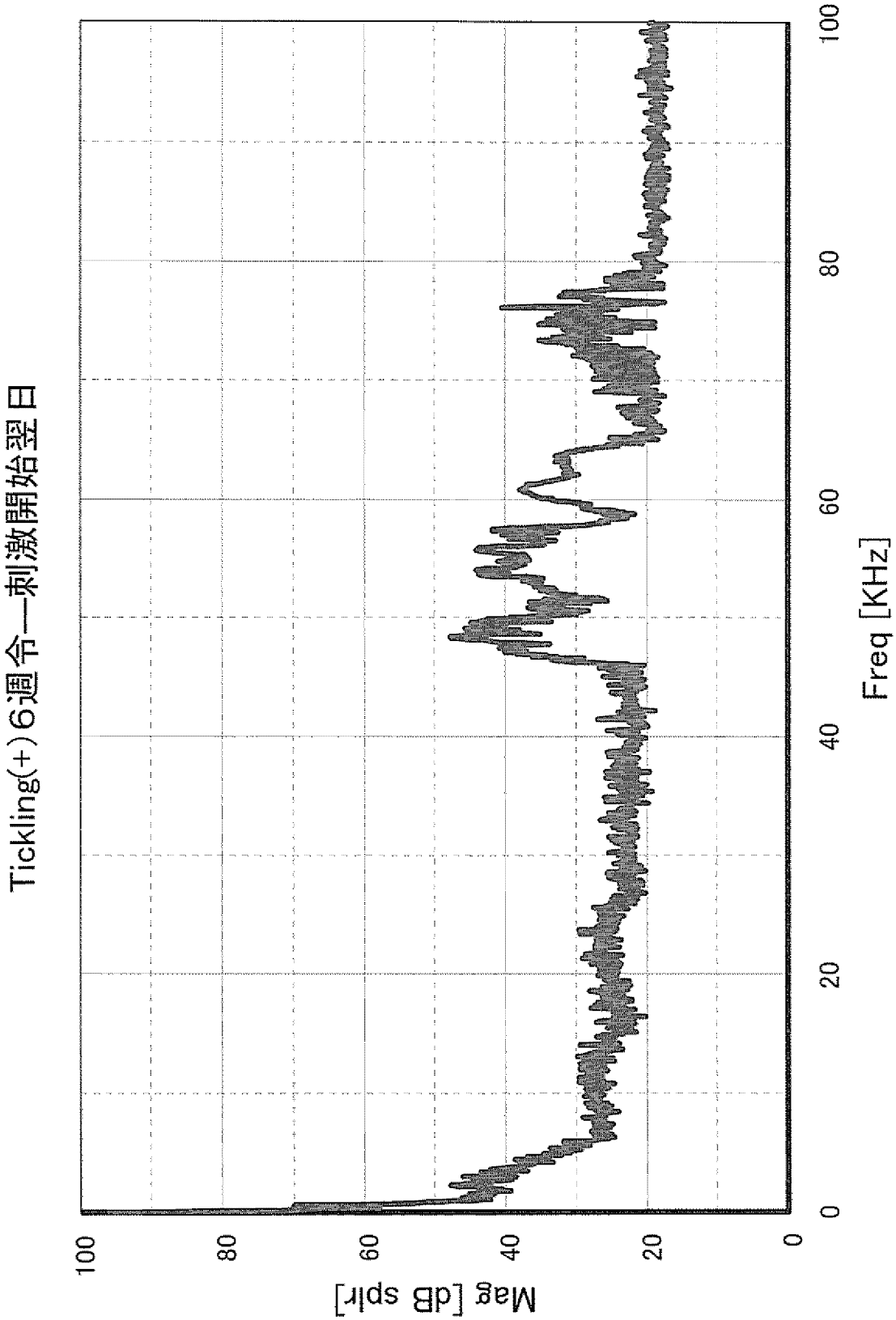
[図16]



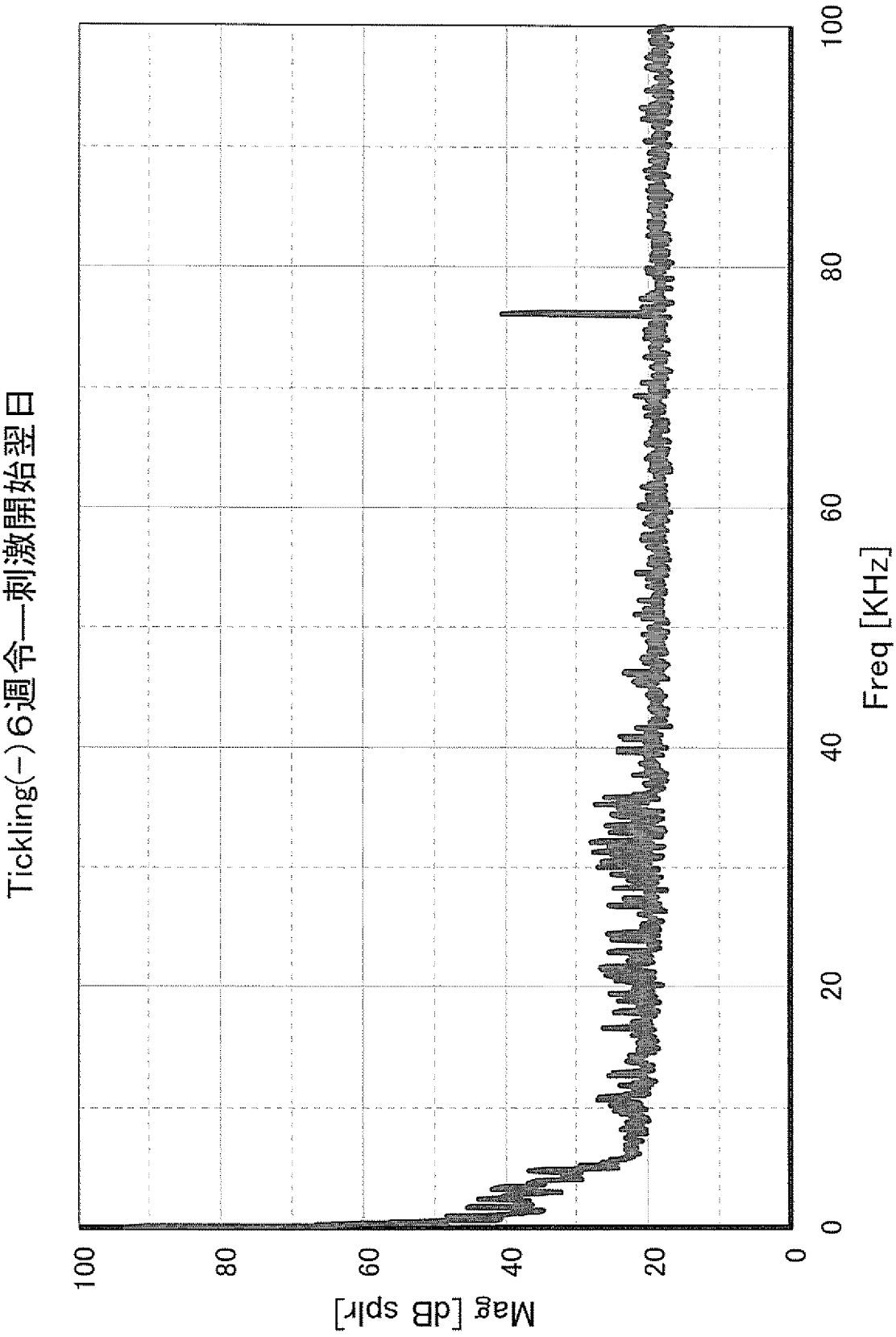
[図17]


対照(−)4週令—刺激開始翌日
Mag [dB spl]
100
80
60
40
20
0
0
20
40
60
80
100
Freq [KHz]

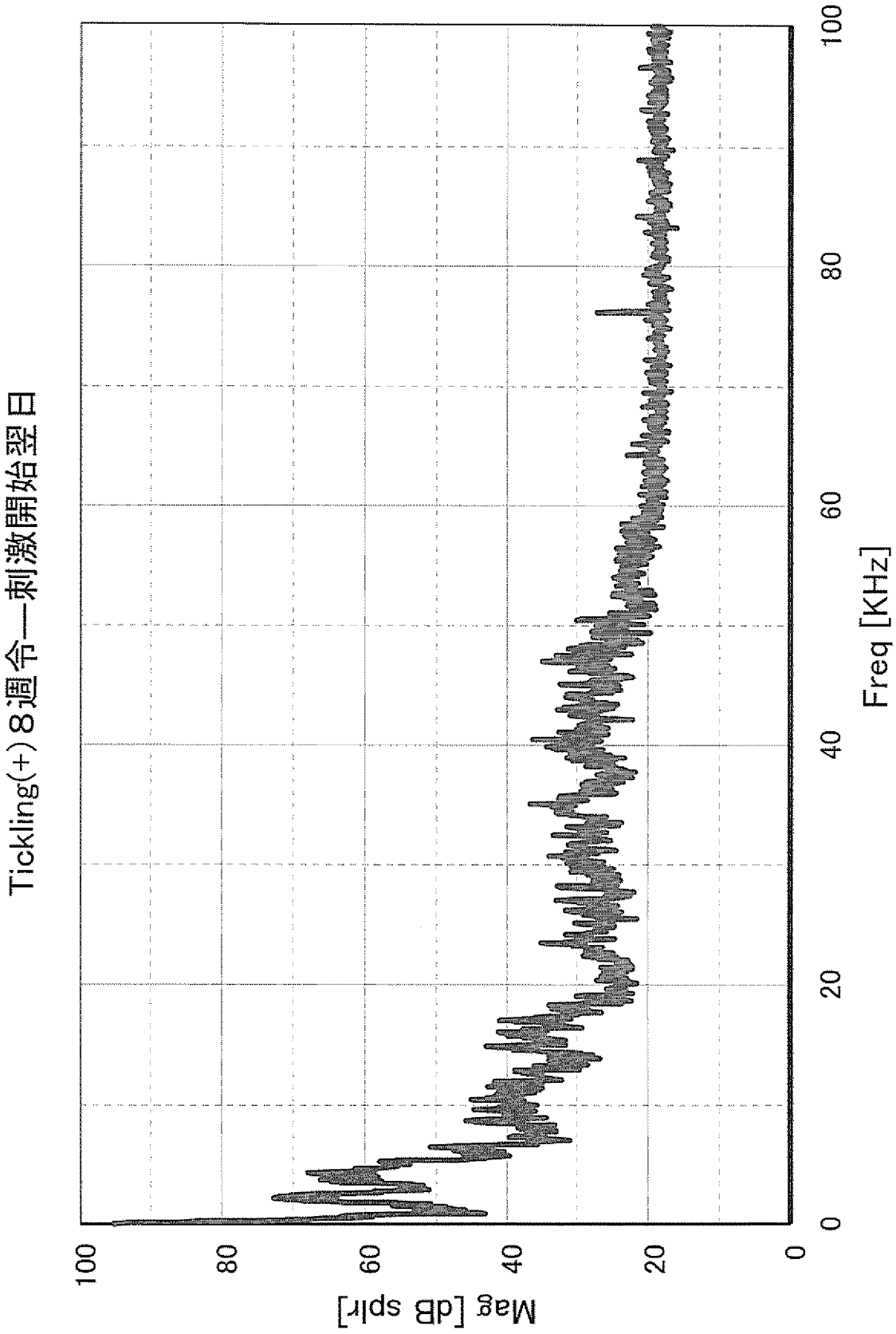
[図18]


Tickling(+)6週令—刺激開始翌日
Mag [dB spir]
0
20
40
60
80
100
Freq [KHz]
0
20
40
60
80
100

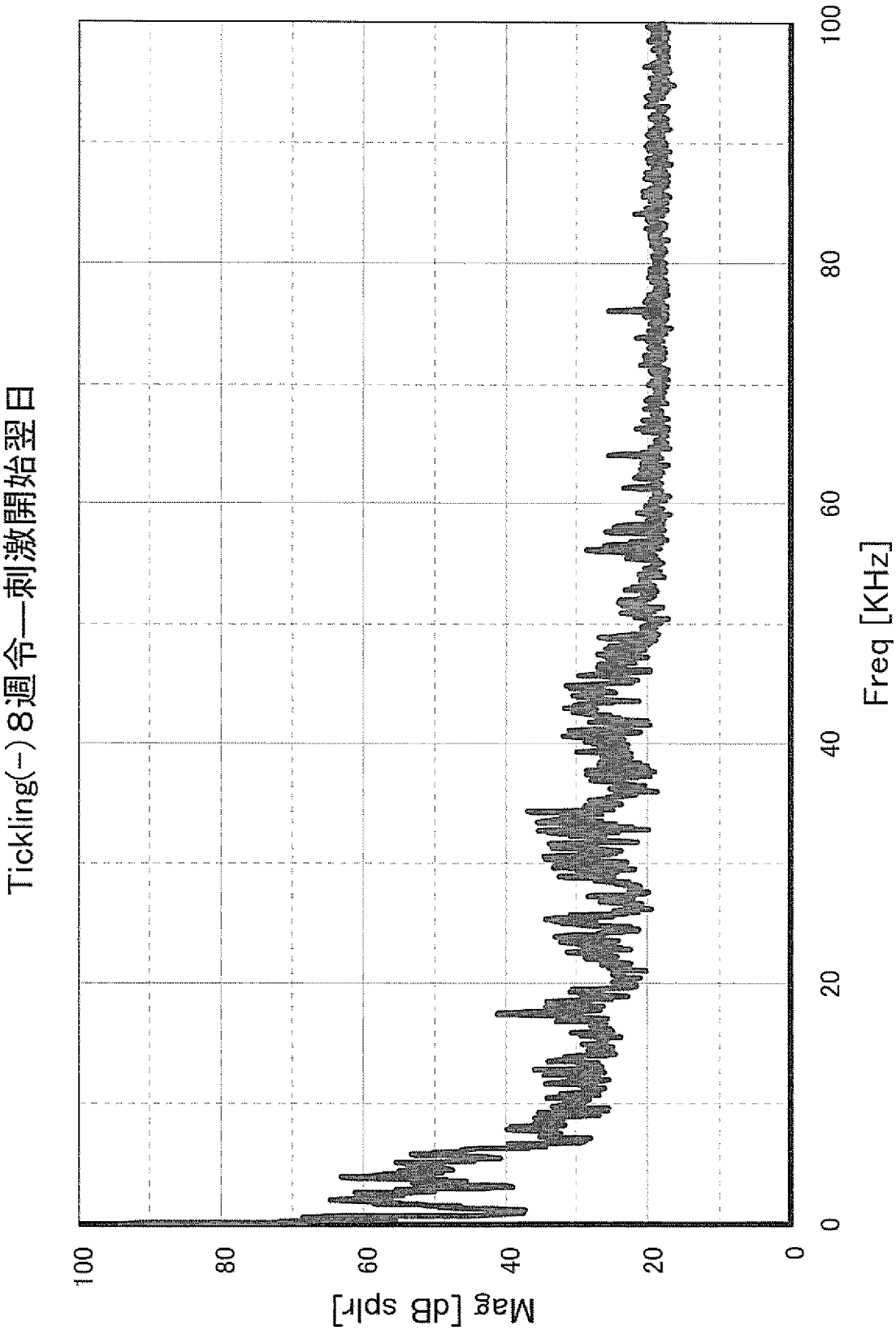
[図19]


Tickling(−)6週令—刺激開始翌日
Mag [dB spir]
100
80
60
40
20
0
0
20
40
60
80
100
Freq [KHz]

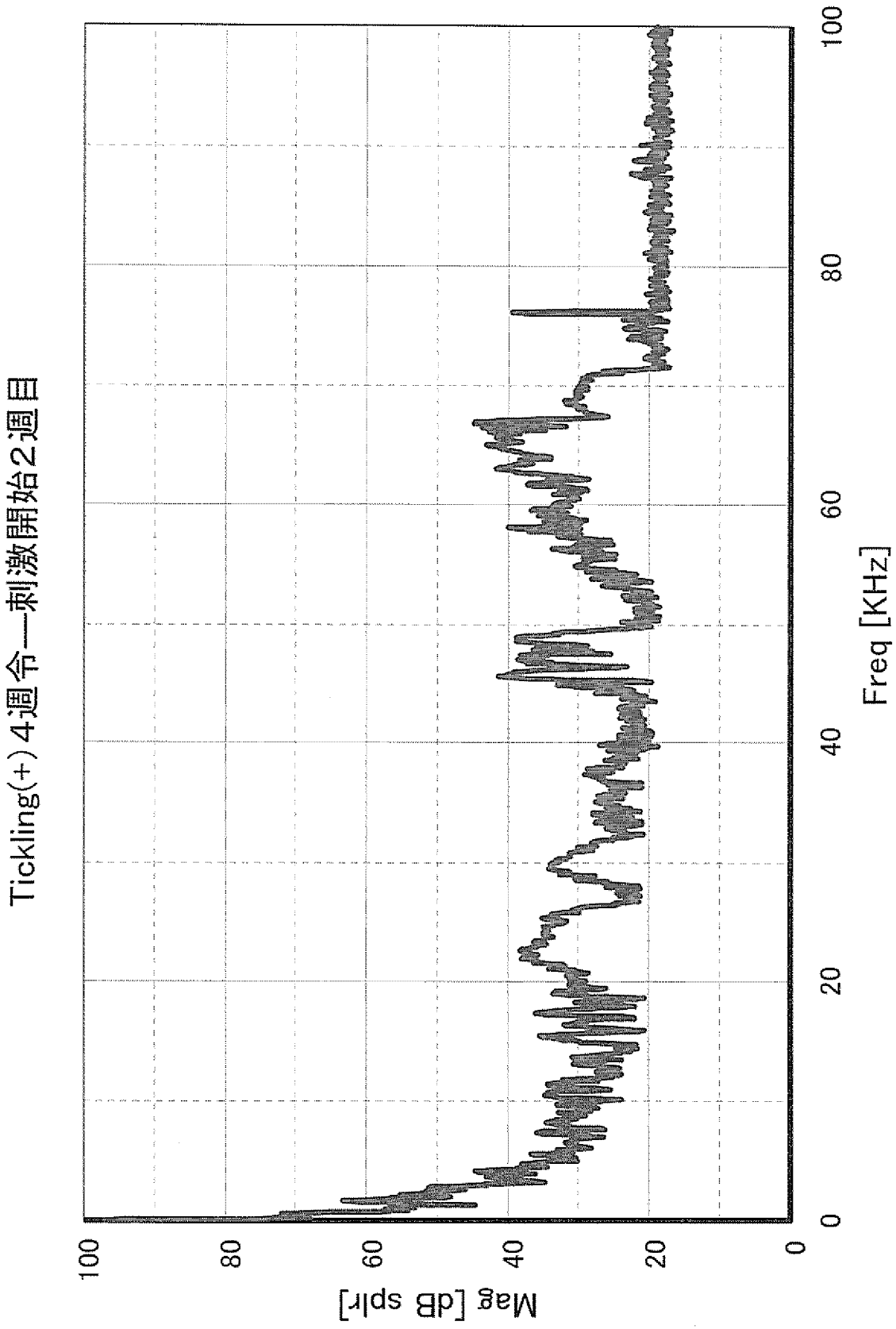
[図20]


Tickling(+)８週令—刺激開始翌日
Mag [dB spl]
100
80
60
40
20
0
0
20
40
60
80
100
Freq [KHz]

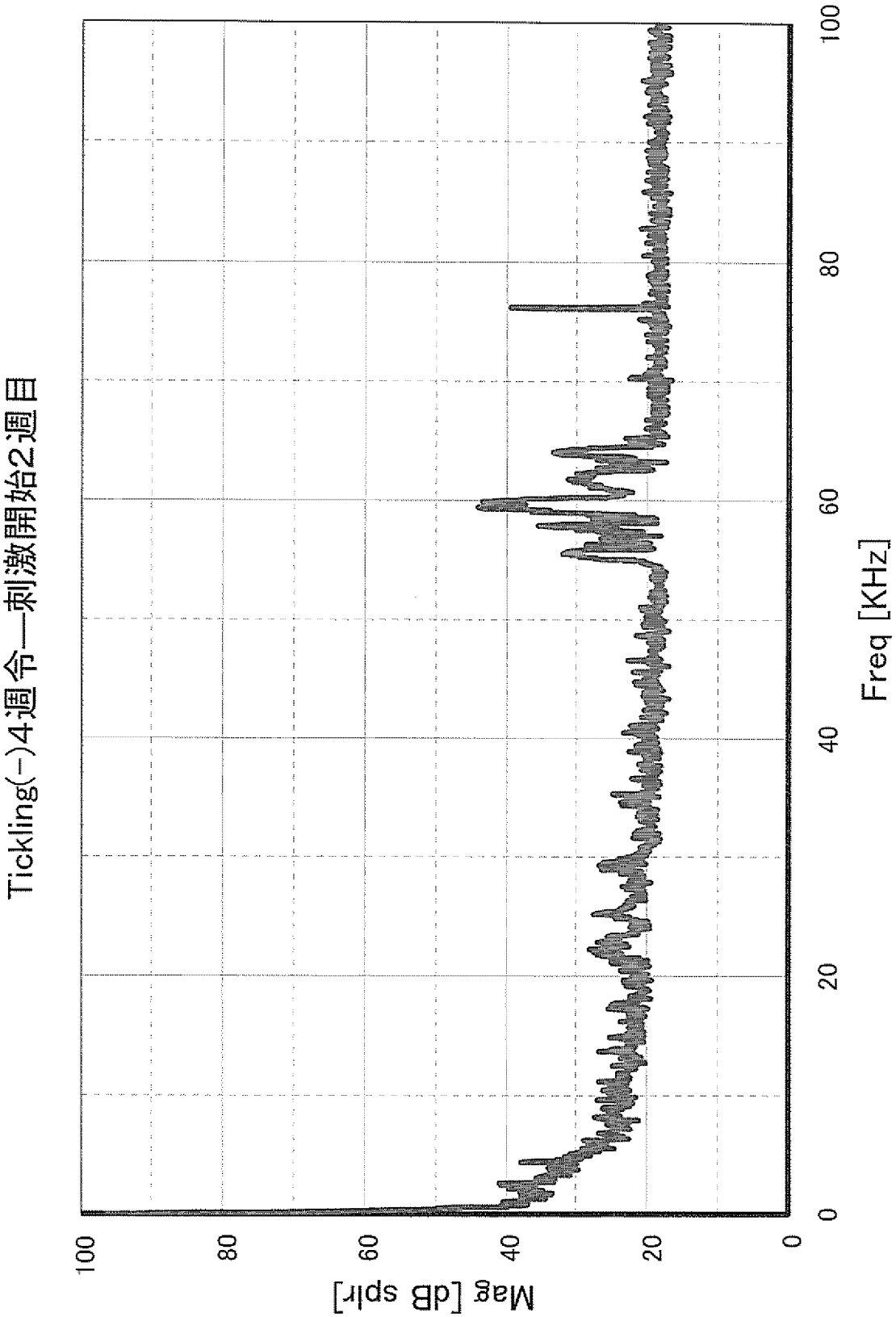
[図21]


Tickling(−) 8週令—刺激開始翌日
Mag [dB spl]
Freq [KHz]
0
20
40
60
80
100
0
20
40
60
80
100

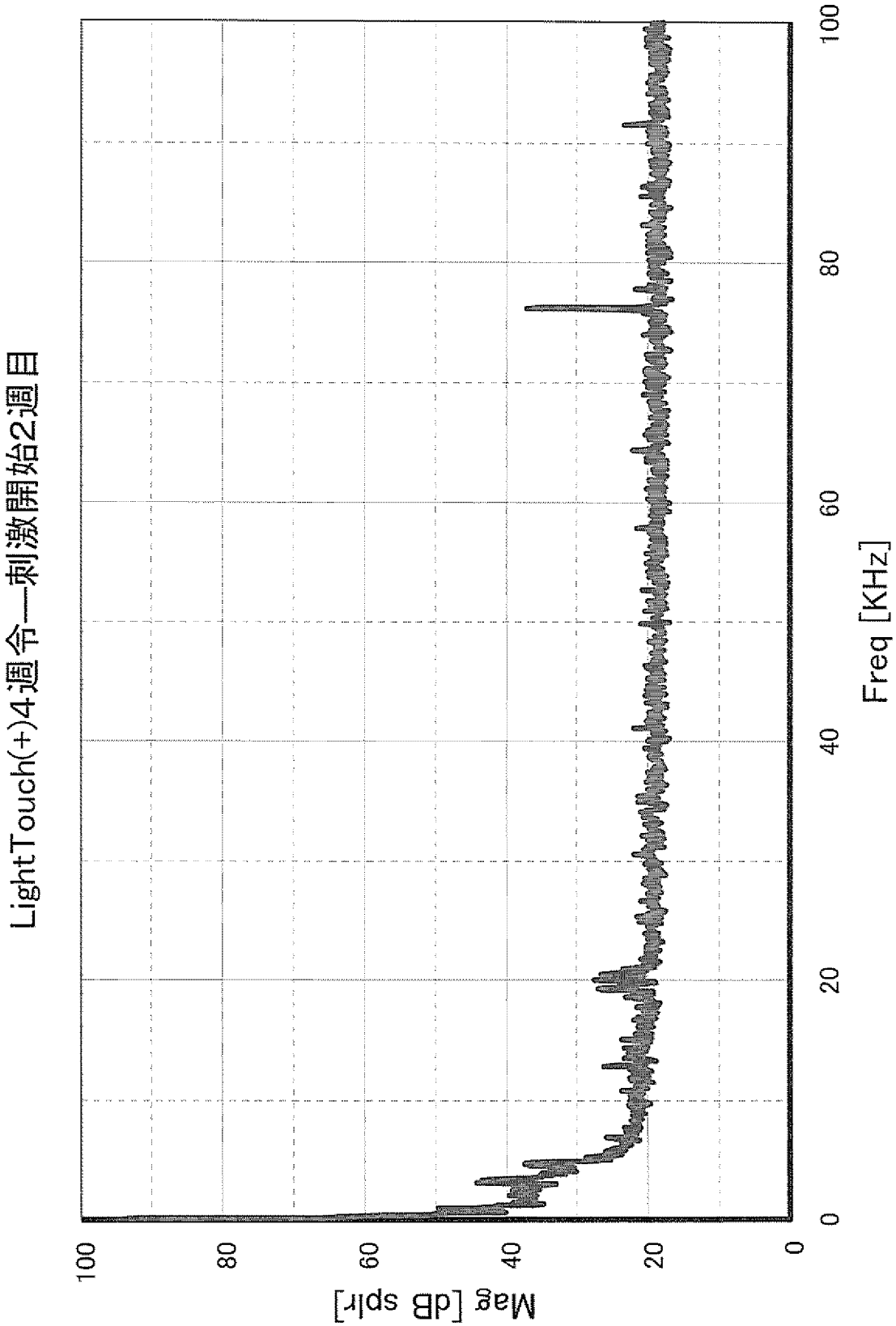
[図22]


Tickling(+) 4週令—刺激開始2週目
Mag [dB spir]
100
80
60
40
20
0
0
20
40
60
80
100
Freq [KHz]

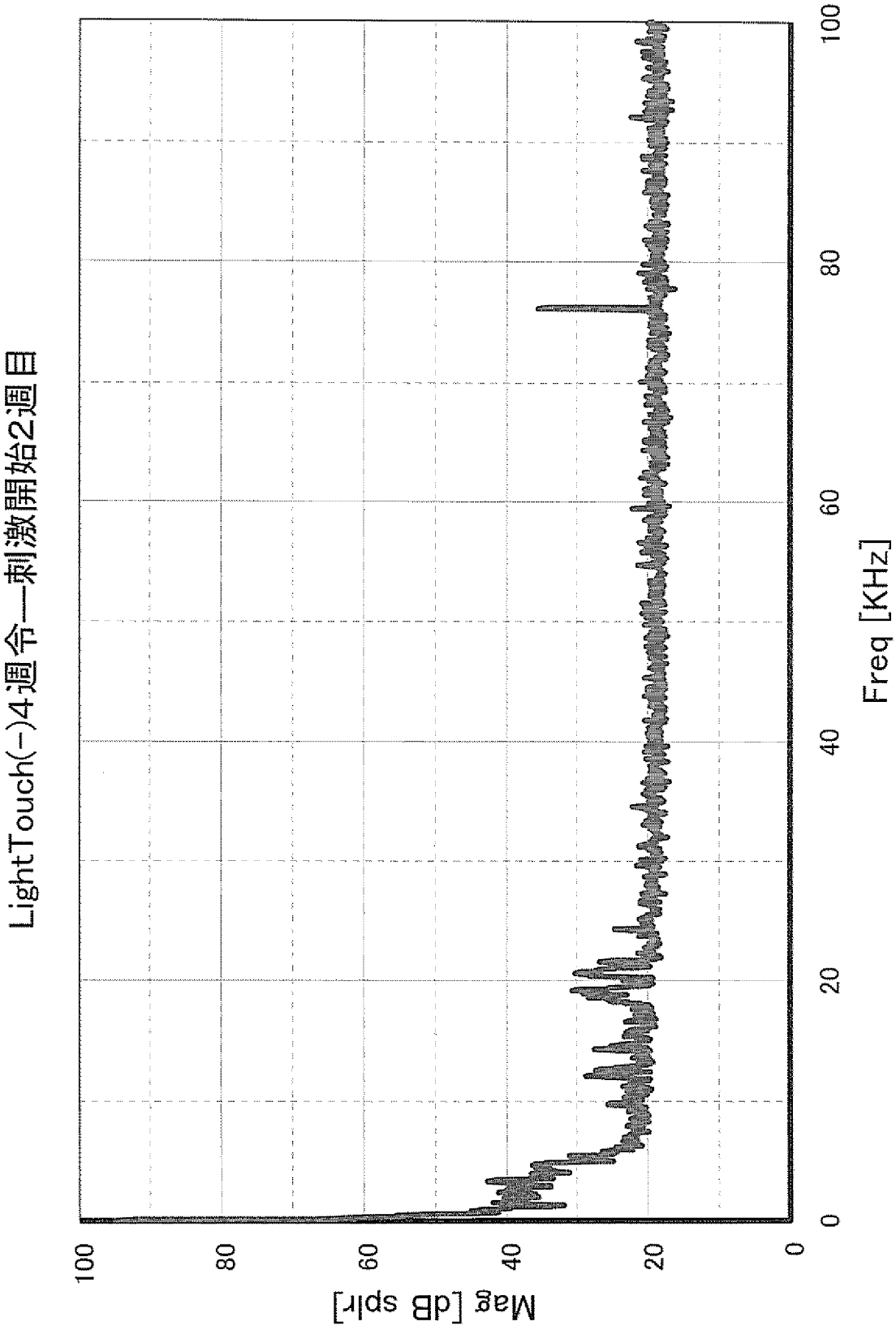
[図23]


Tickling(−)4週令—刺激開始2週目
Mag [dB spl]
100
80
60
40
20
0
0
20
40
60
80
100
Freq [KHz]

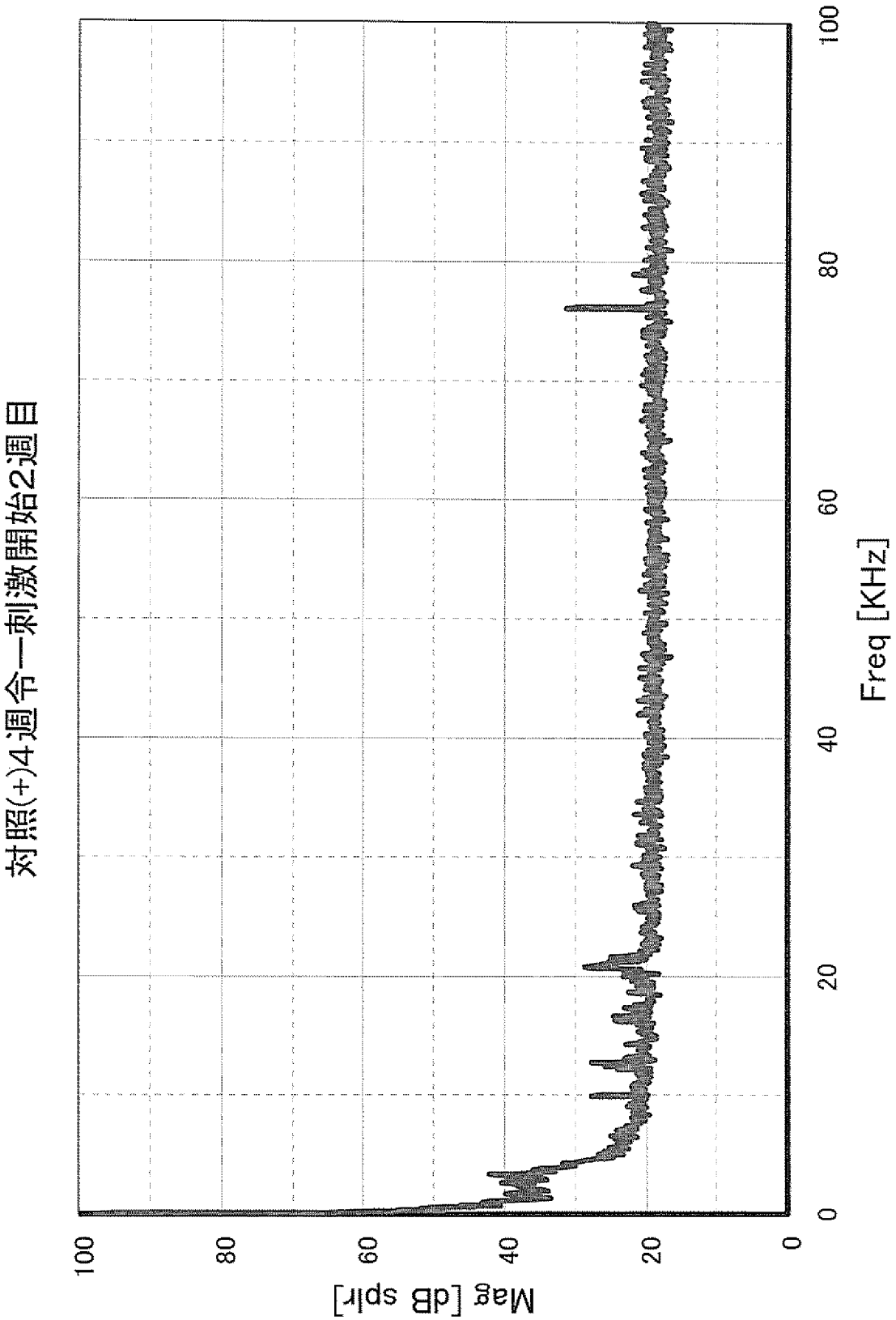
[図24]


LightTouch(+)4週令—刺激開始2週目
Mag [dB spir]
100
80
60
40
20
0
0
20
40
60
80
100
Freq [KHz]

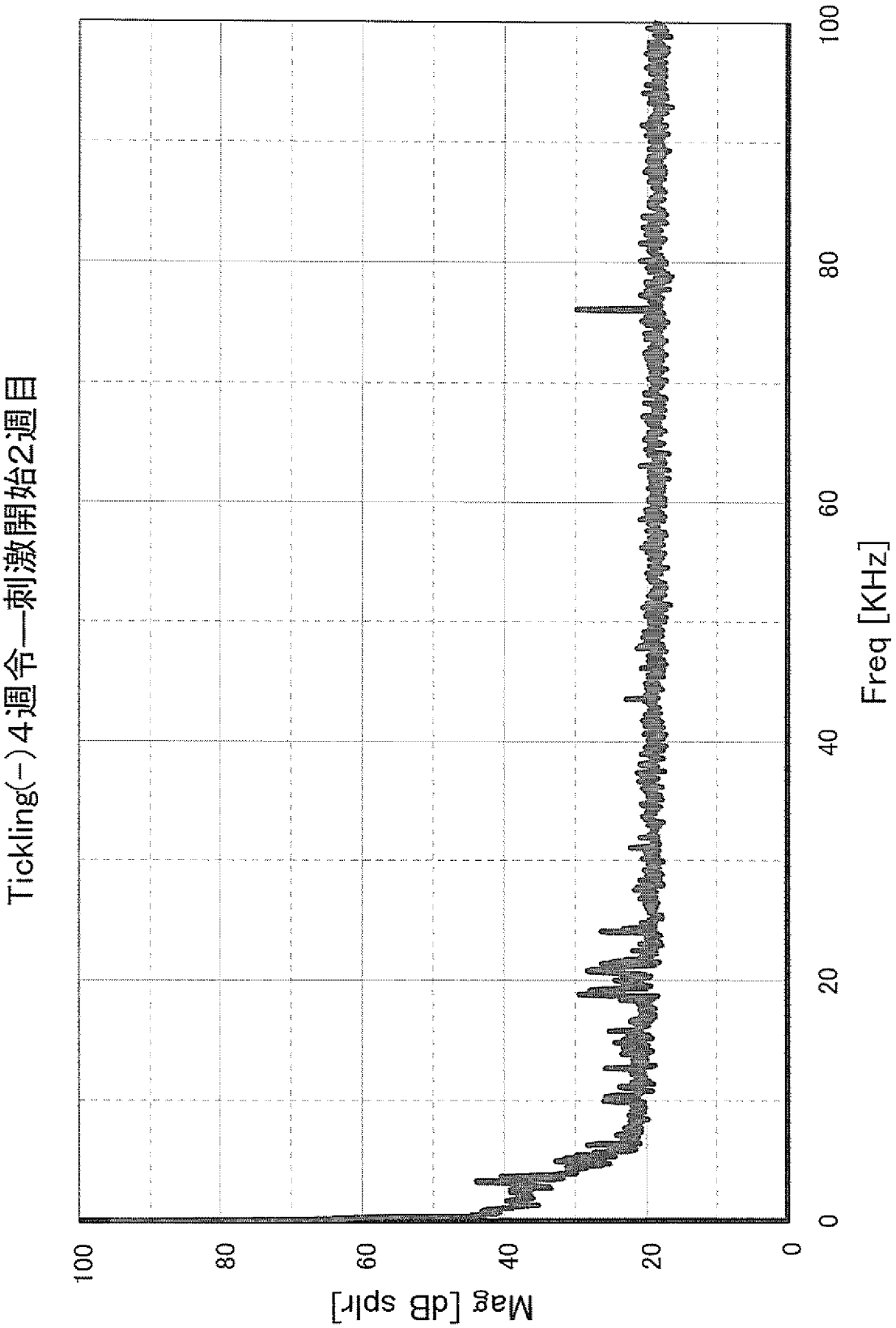
[図25]


LightTouch(−)4週令—刺激開始2週目
Mag [dB spir]
100
80
60
40
20
0
Freq [KHz]
0
20
40
60
80
100

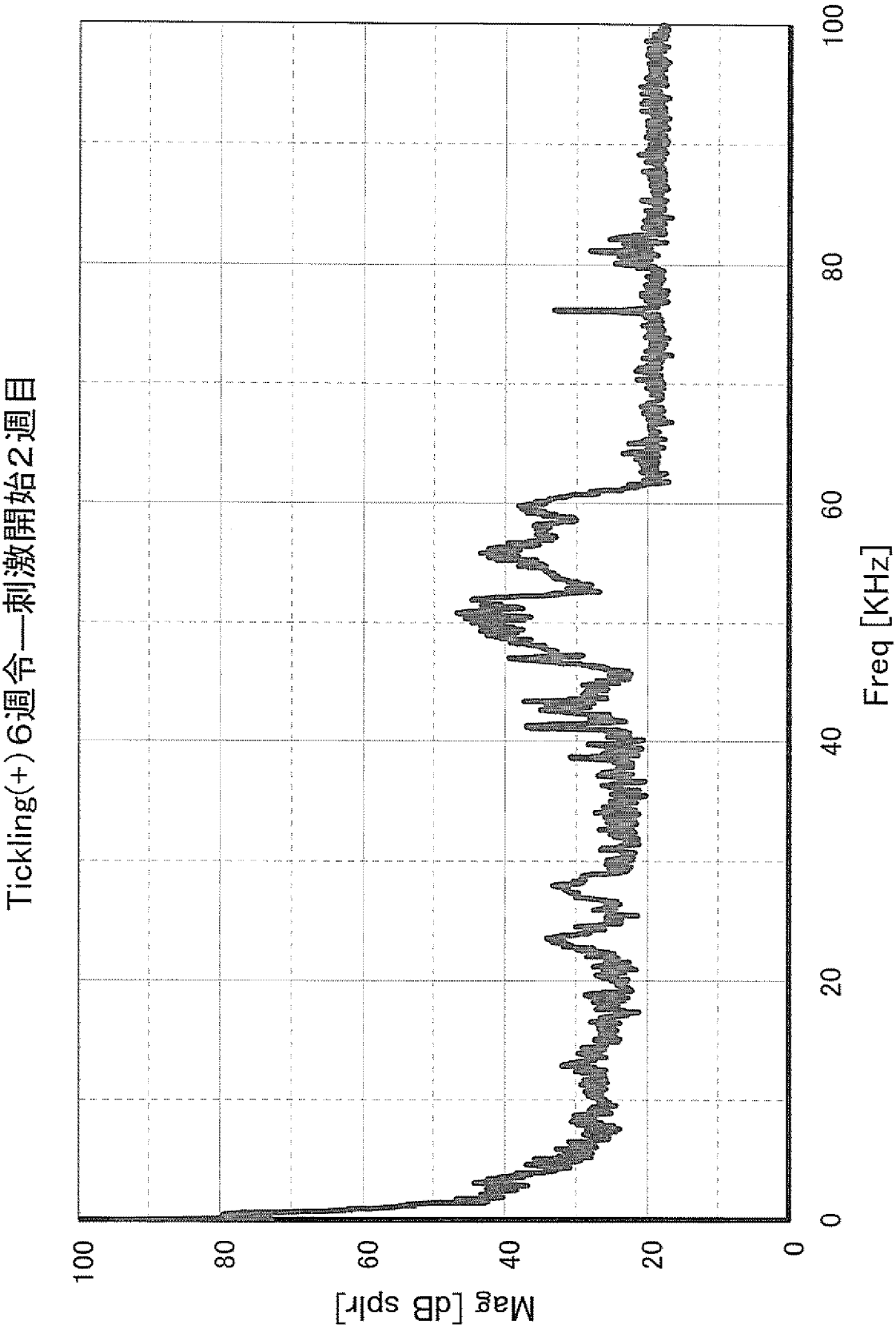
[図26]


対照(+)4週令—刺激開始2週目
Mag [dB spl]
100
80
60
40
20
0
0
20
40
60
80
100
Freq [KHz]

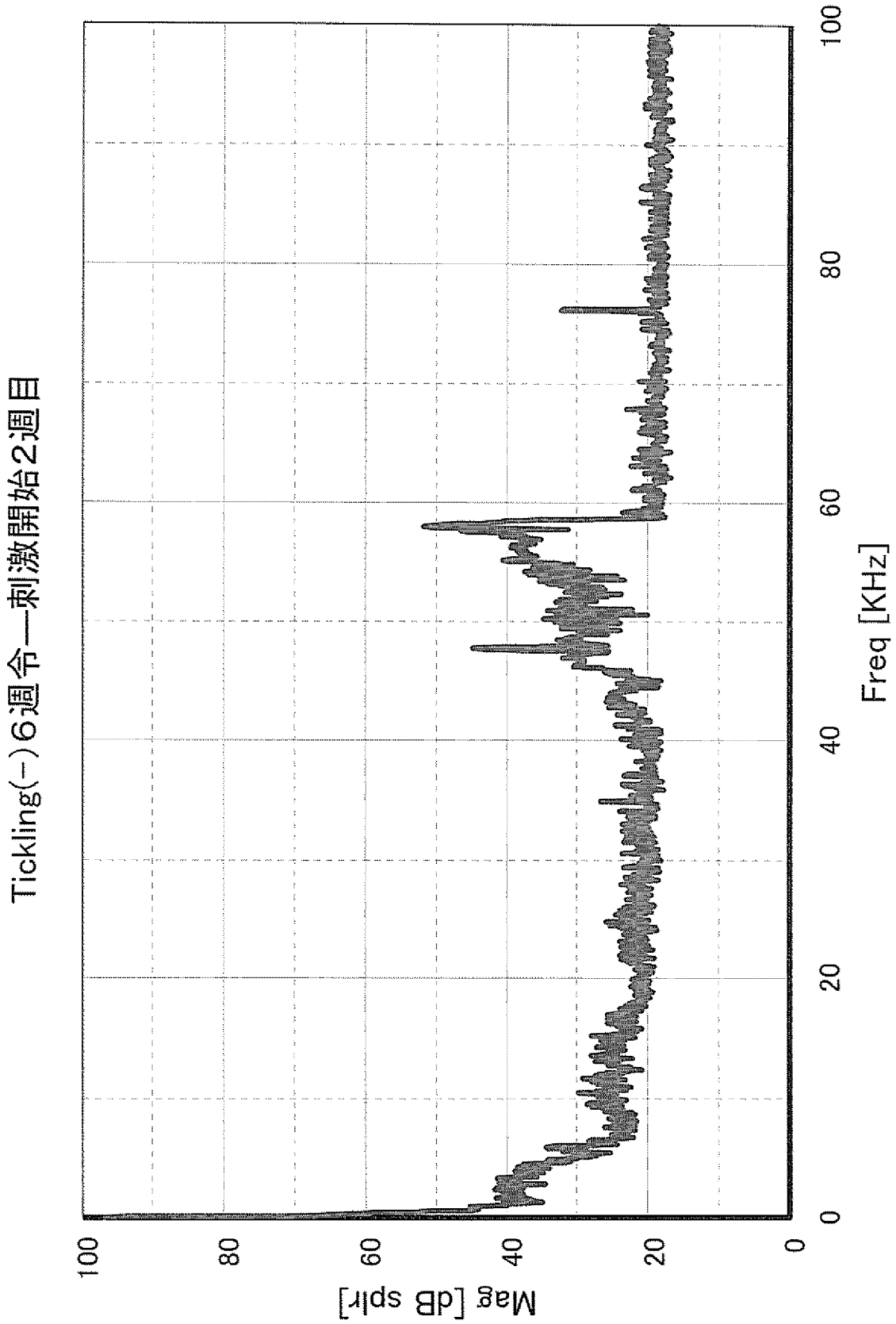
[図27]


Tickling(−)4週令—刺激開始2週目
Mag [dB spir]
100
80
60
40
20
0
0
20
40
60
80
100
Freq [KHz]

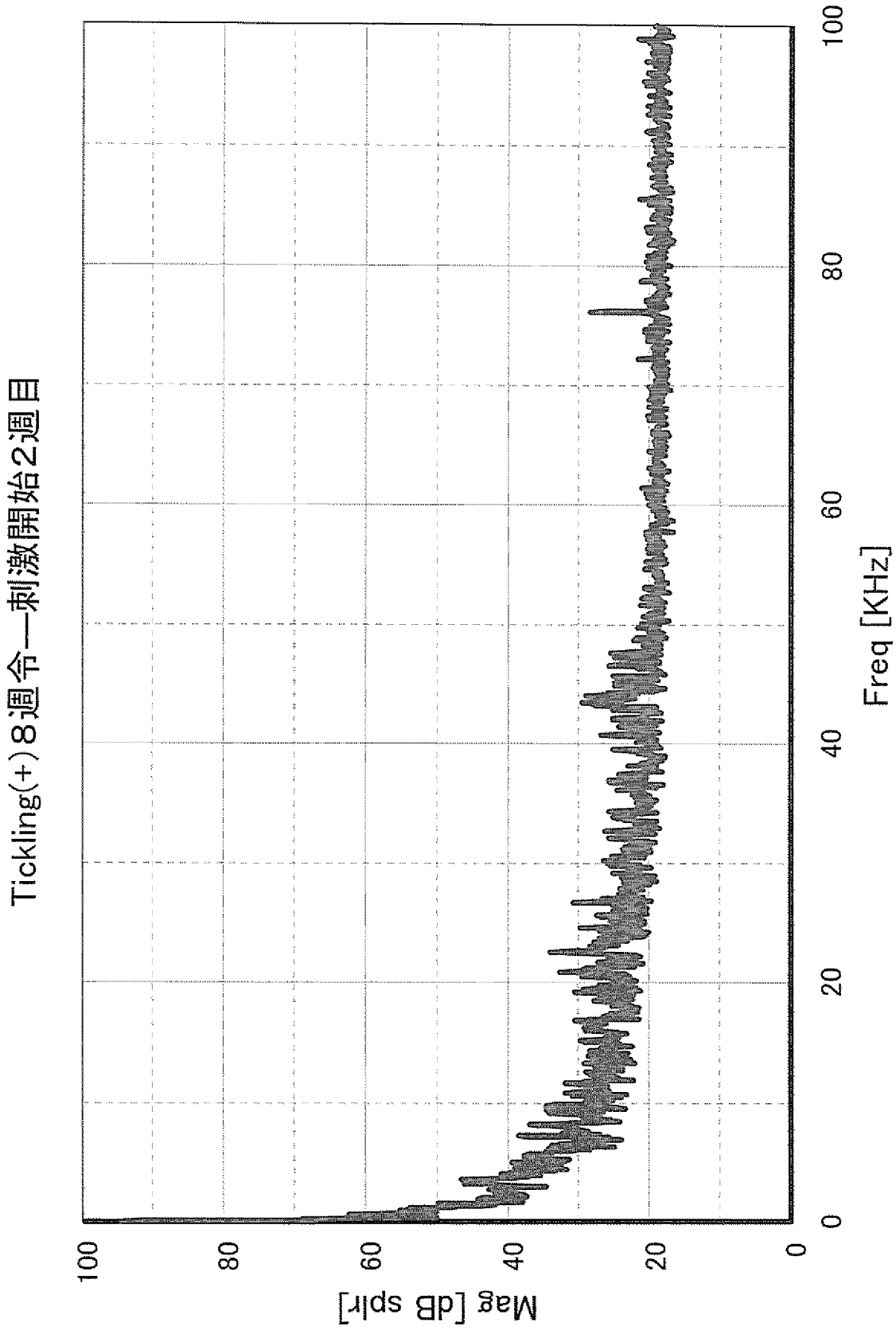
[図28]


Tickling(+) 6週令—刺激開始2週目
Mag [dB spir]
0
20
40
60
80
100
Freq [KHz]
0
20
40
60
80
100

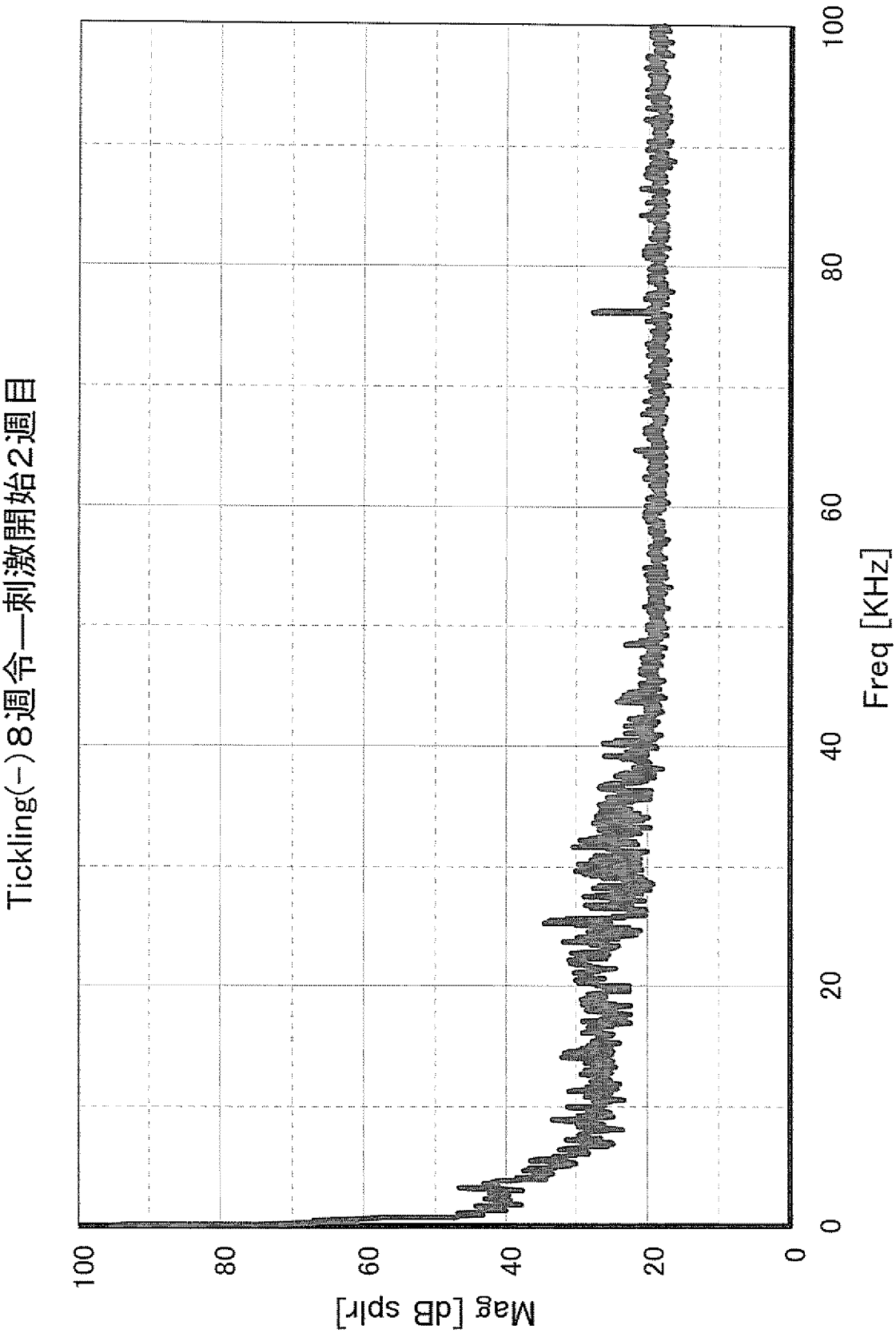
[図29]


Tickling(−)6週令—刺激開始2週目
Mag [dB spir]
100
80
60
40
20
0
0
20
40
60
80
100
Freq [KHz]

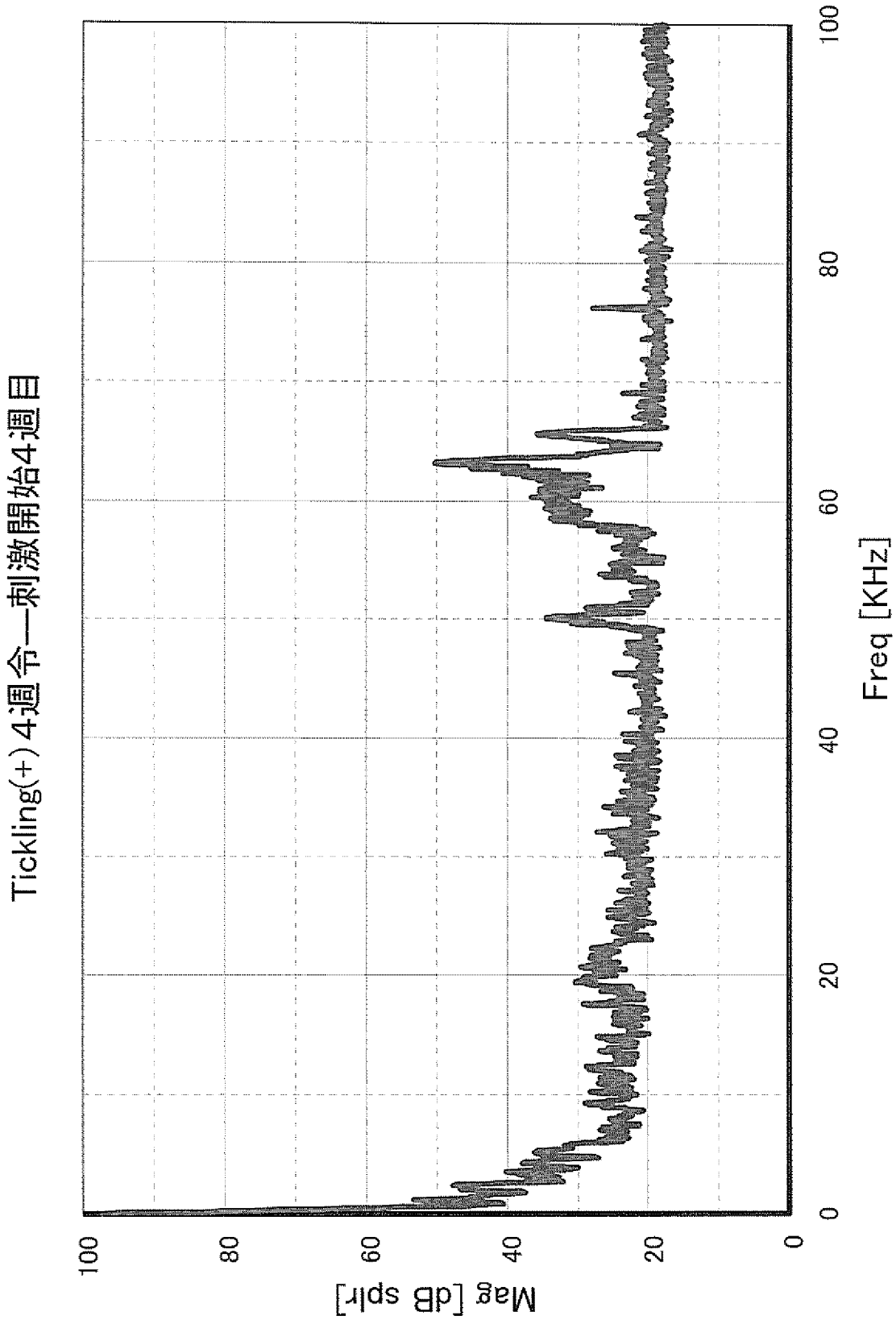
[図30]



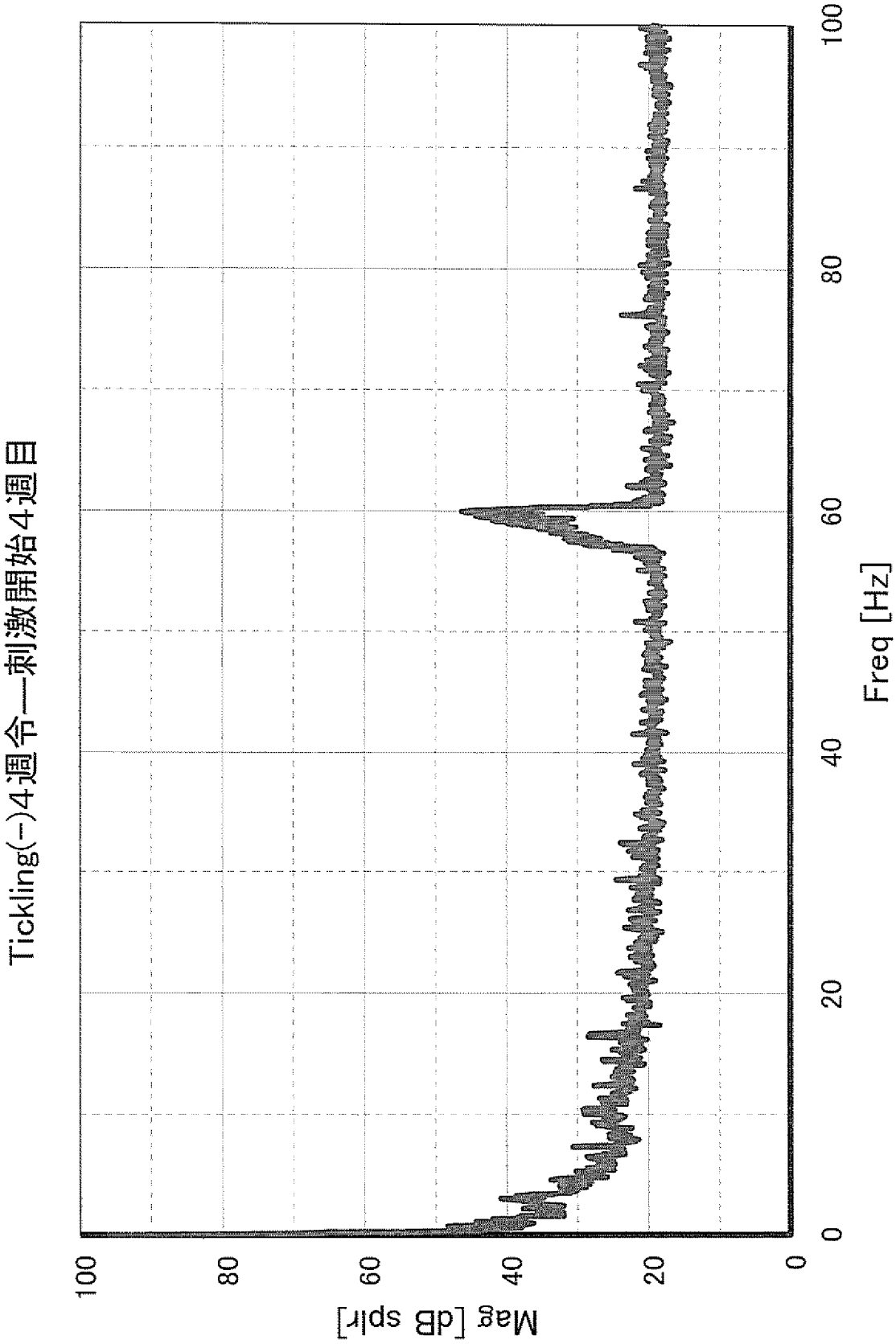
[図31]



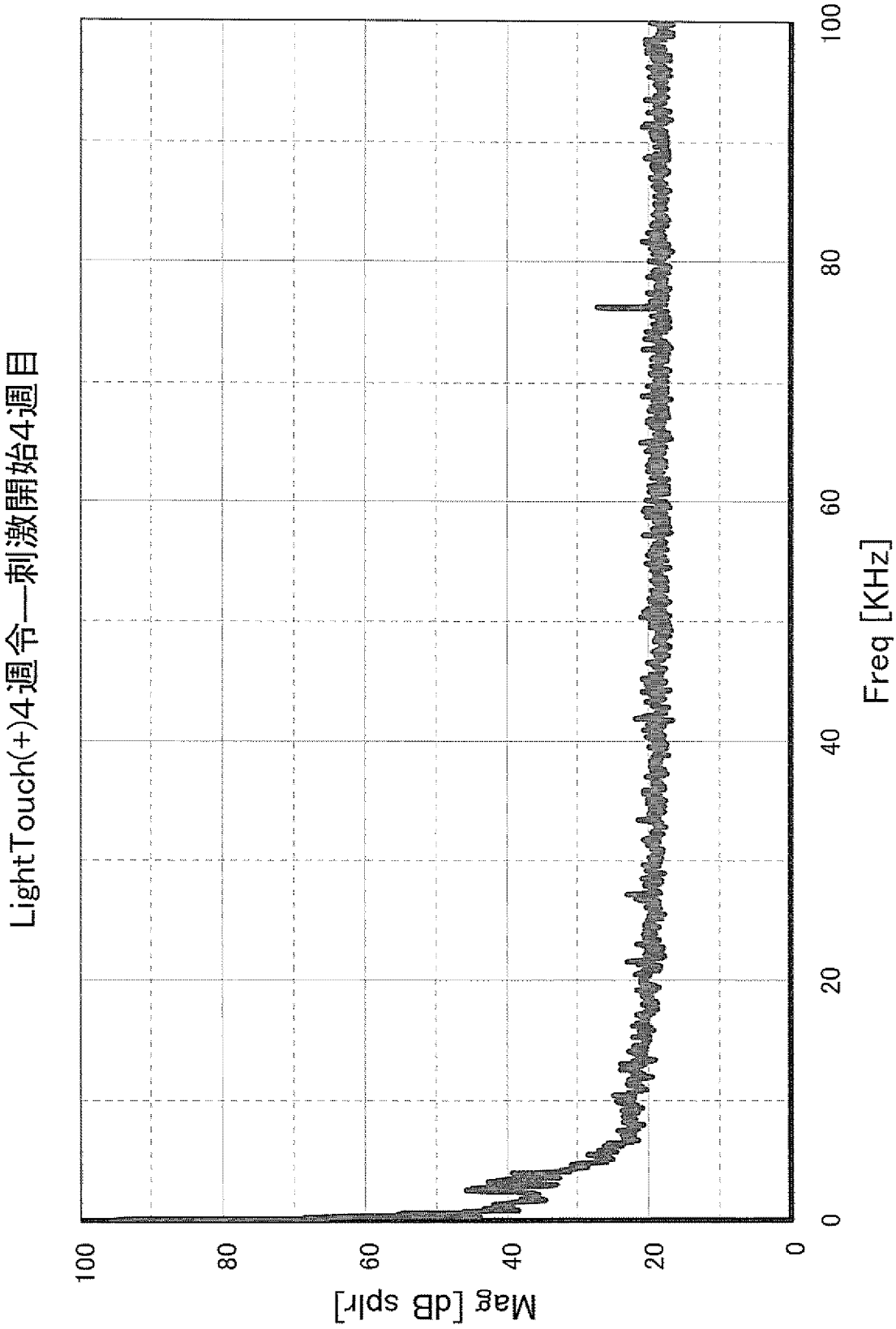
[図32]


Tickling(+) 4週令—刺激開始4週目
Mag [dB spl]
100
80
60
40
20
0
0
20
40
60
80
100
Freq [KHz]

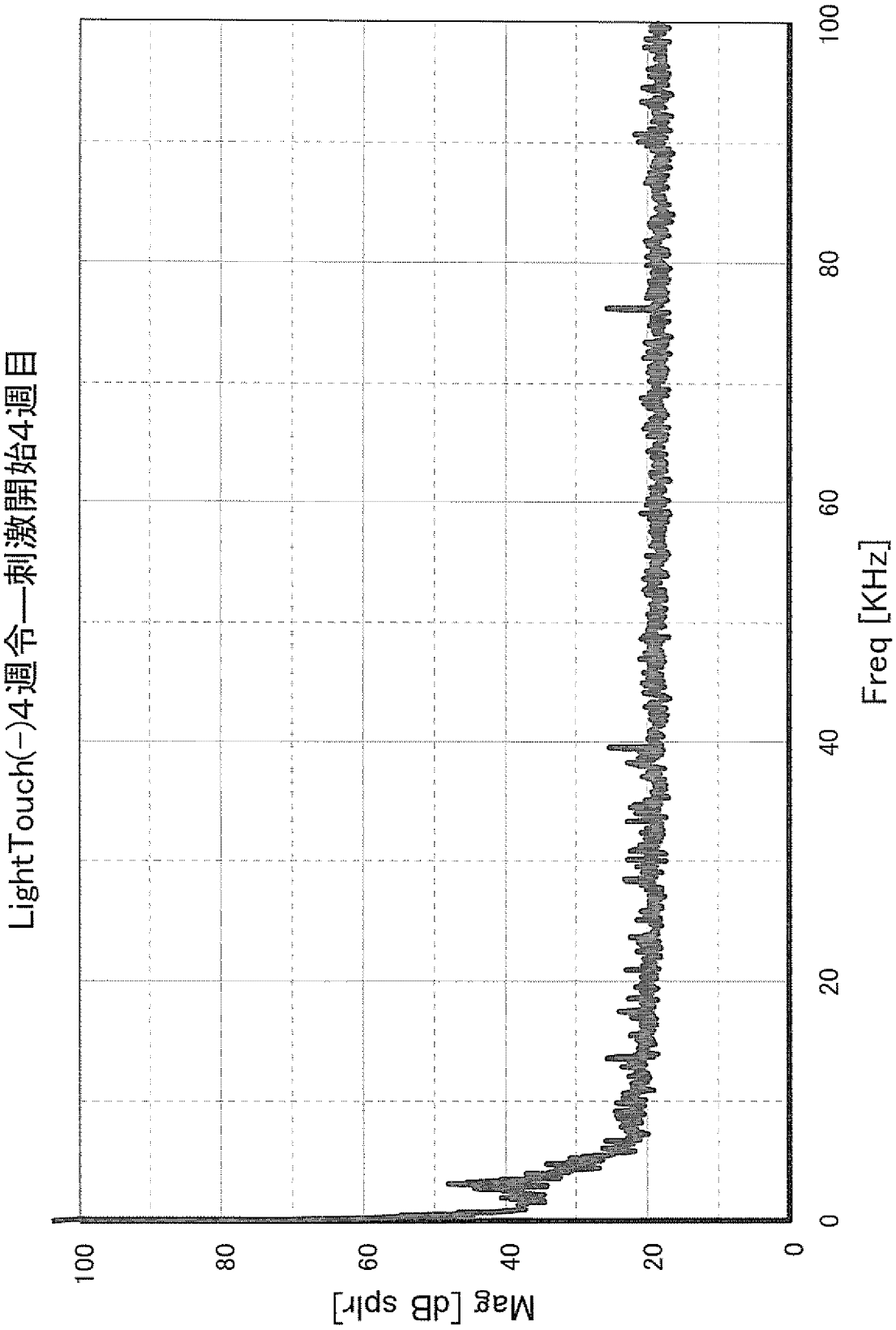
[図33]


Tickling(−)4週令—刺激開始4週目
Mag [dB spl]
0
20
40
60
80
100
Freq [Hz]
0
20
40
60
80
100

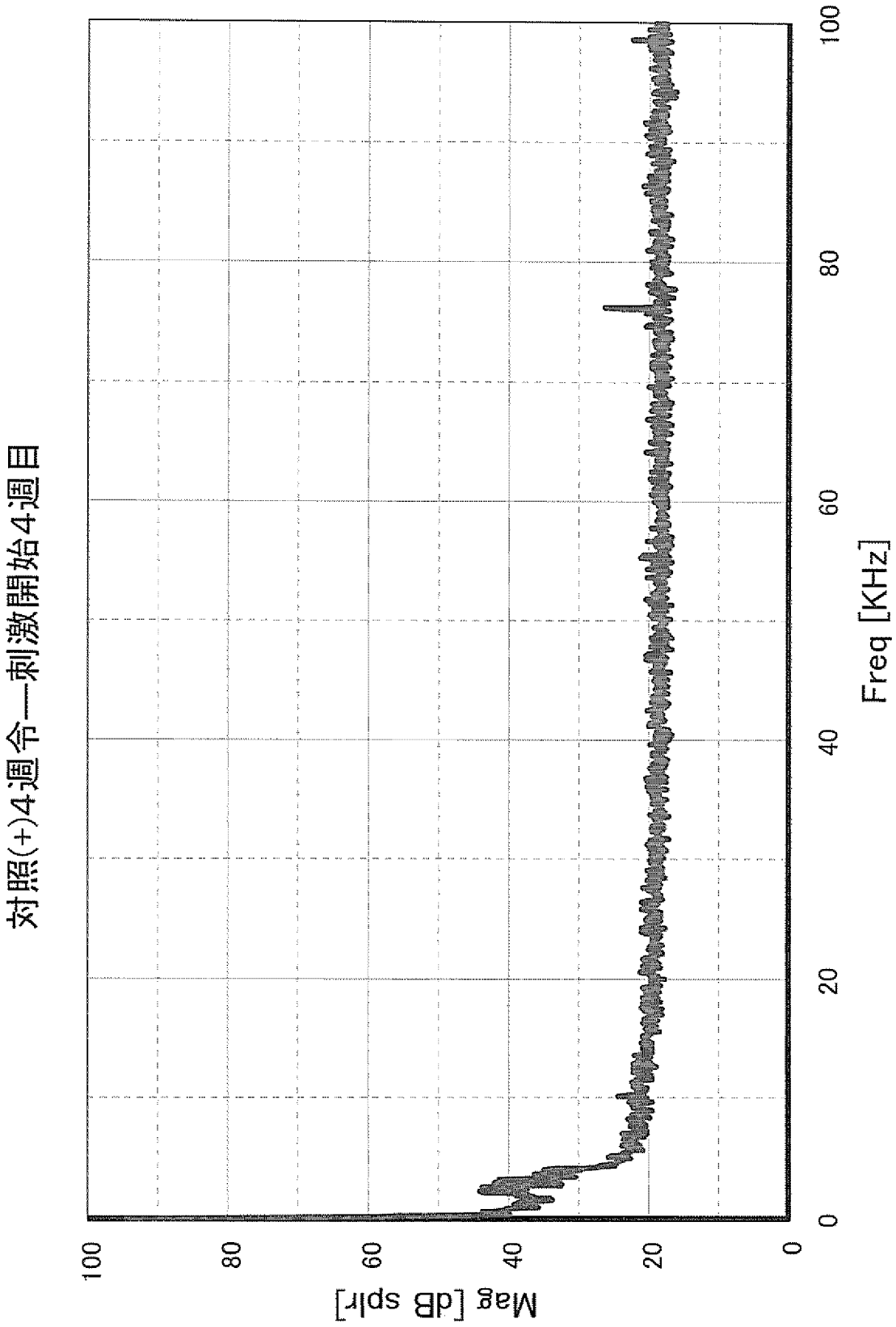
[図34]



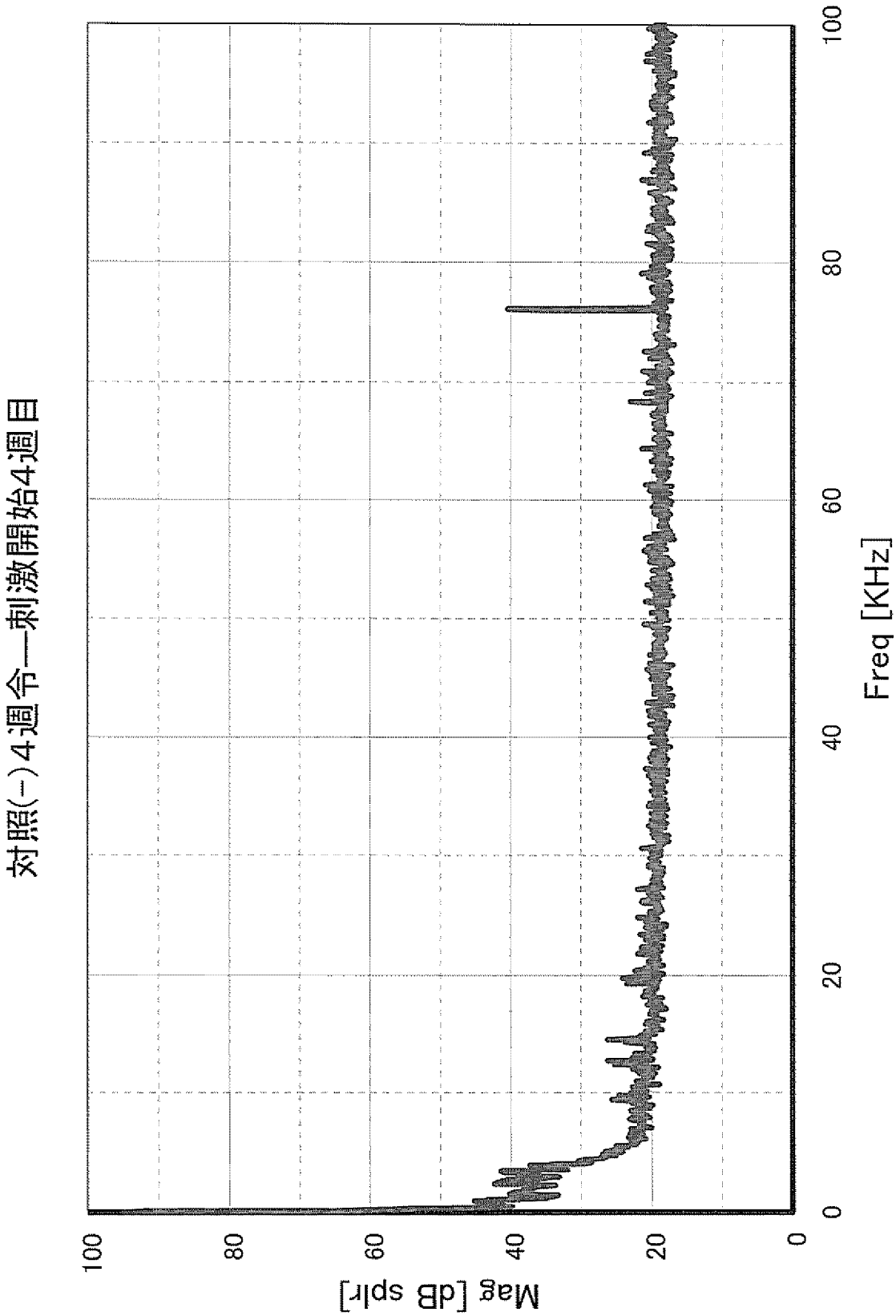
[図35]


LightTouch(−)4週令—刺激開始4週目
Mag [dB spir]
100
80
60
40
20
0
Freq [KHz]
0
20
40
60
80
100

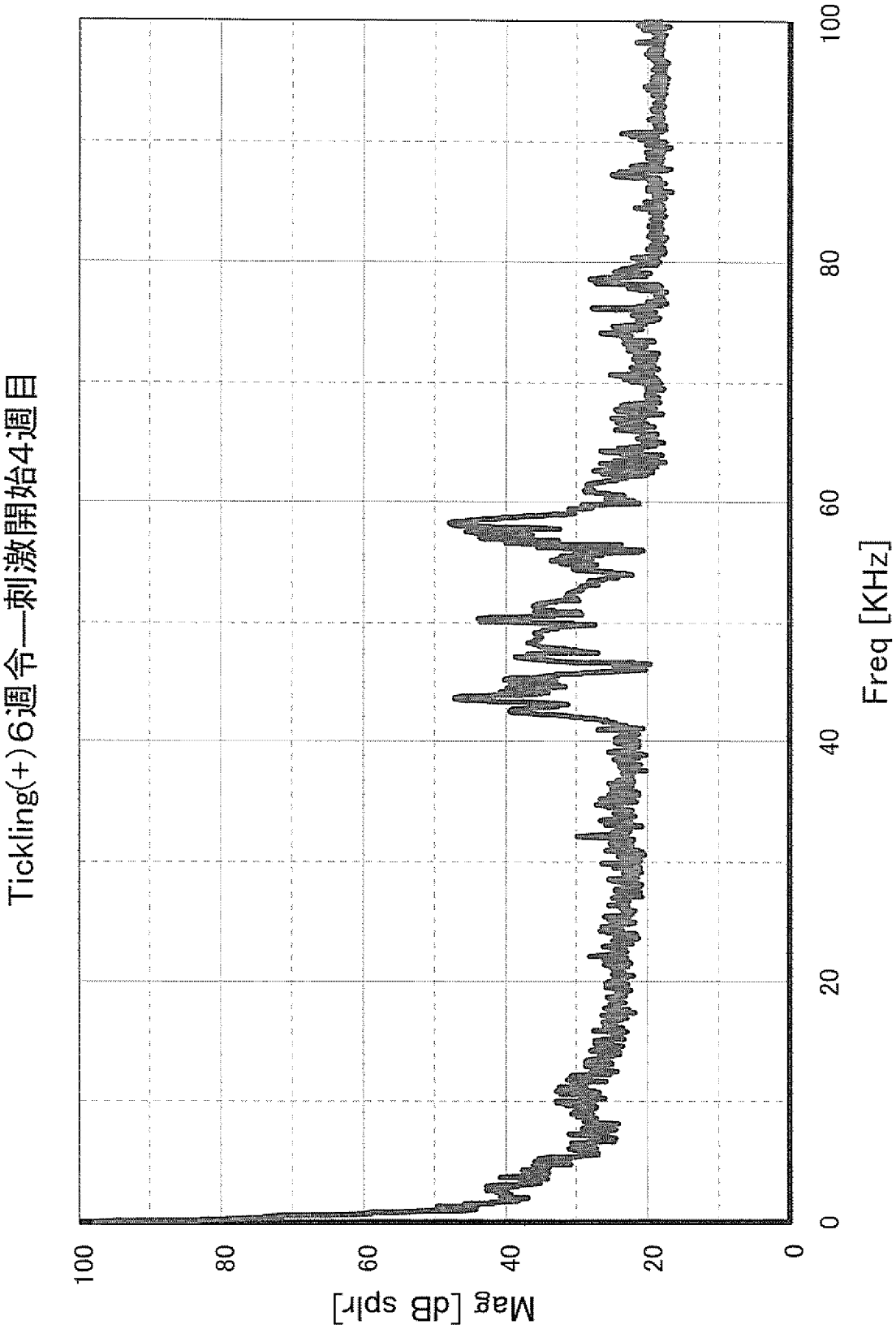
[図36]


対照(+)4週令—刺激開始4週目
Mag [dB spl]
100
80
60
40
20
0
0
20
40
60
80
100
Freq [KHz]

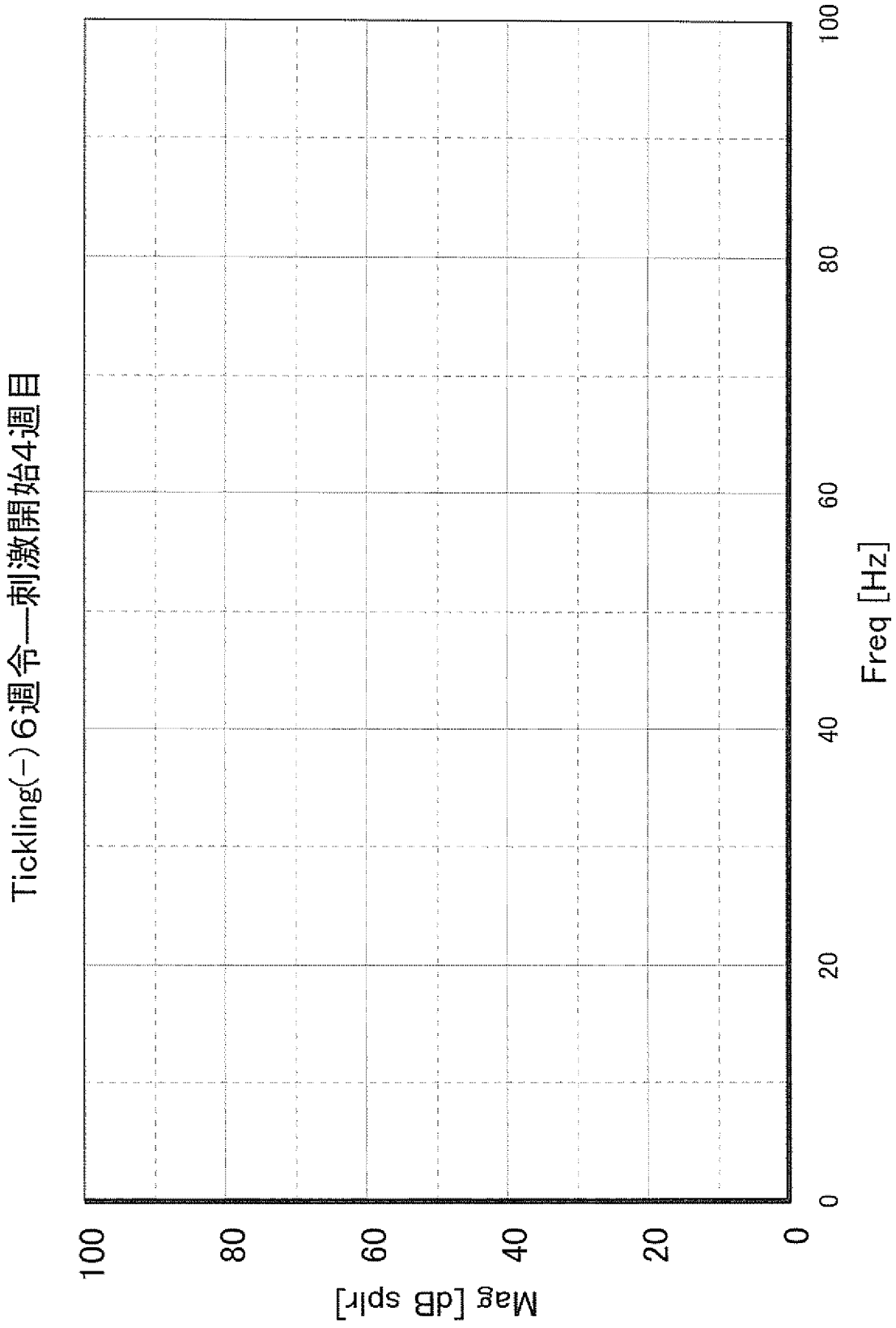
[図37]


対照(−)4週令—刺激開始4週目
Mag [dB spl]
100
80
60
40
20
0
Freq [KHz]
0
20
40
60
80
100

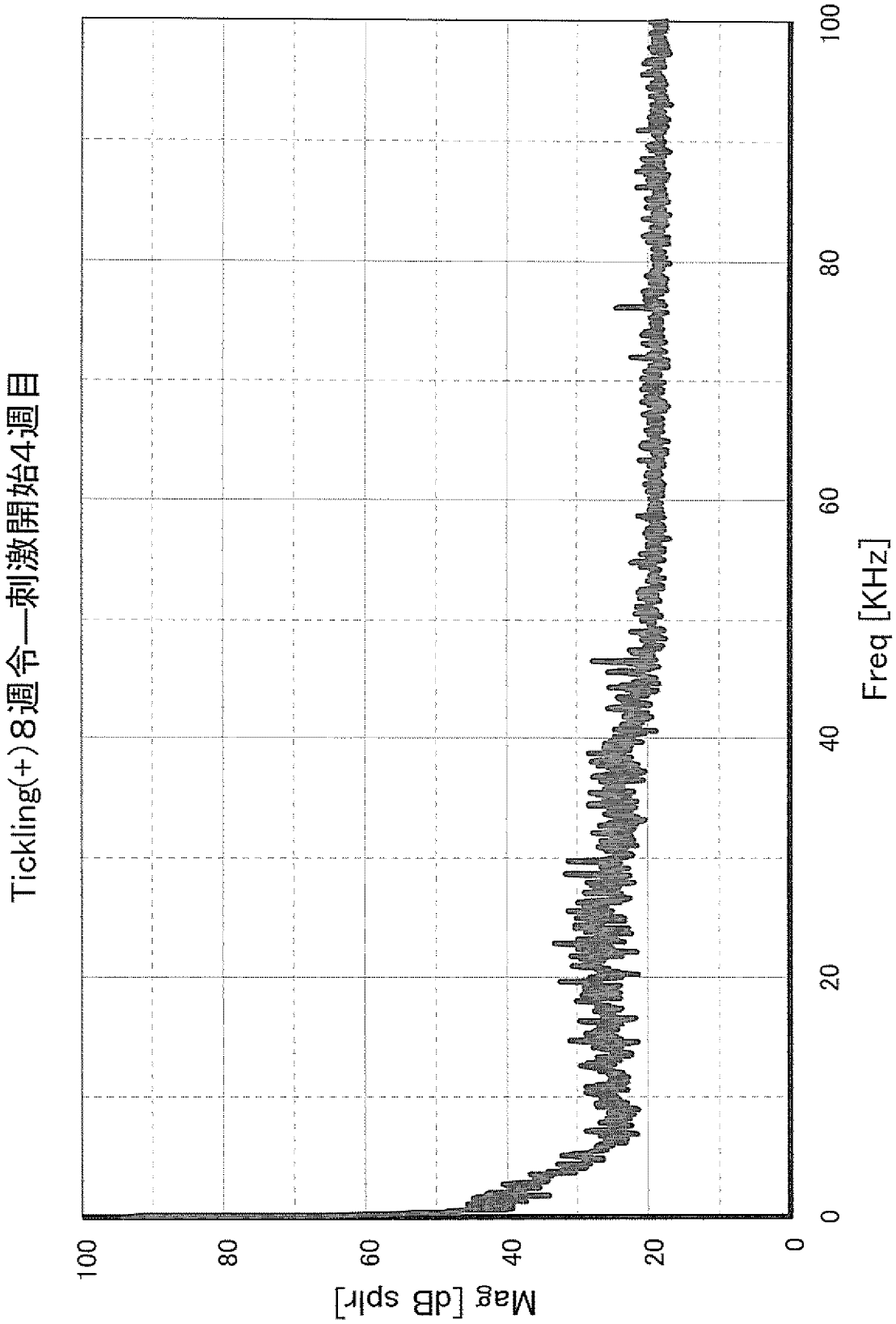
[図38]


Tickling(+)6週令—刺激開始4週目
Mag [dB spl]
Freq [KHz]
0
20
40
60
80
100
0
20
40
60
80
100

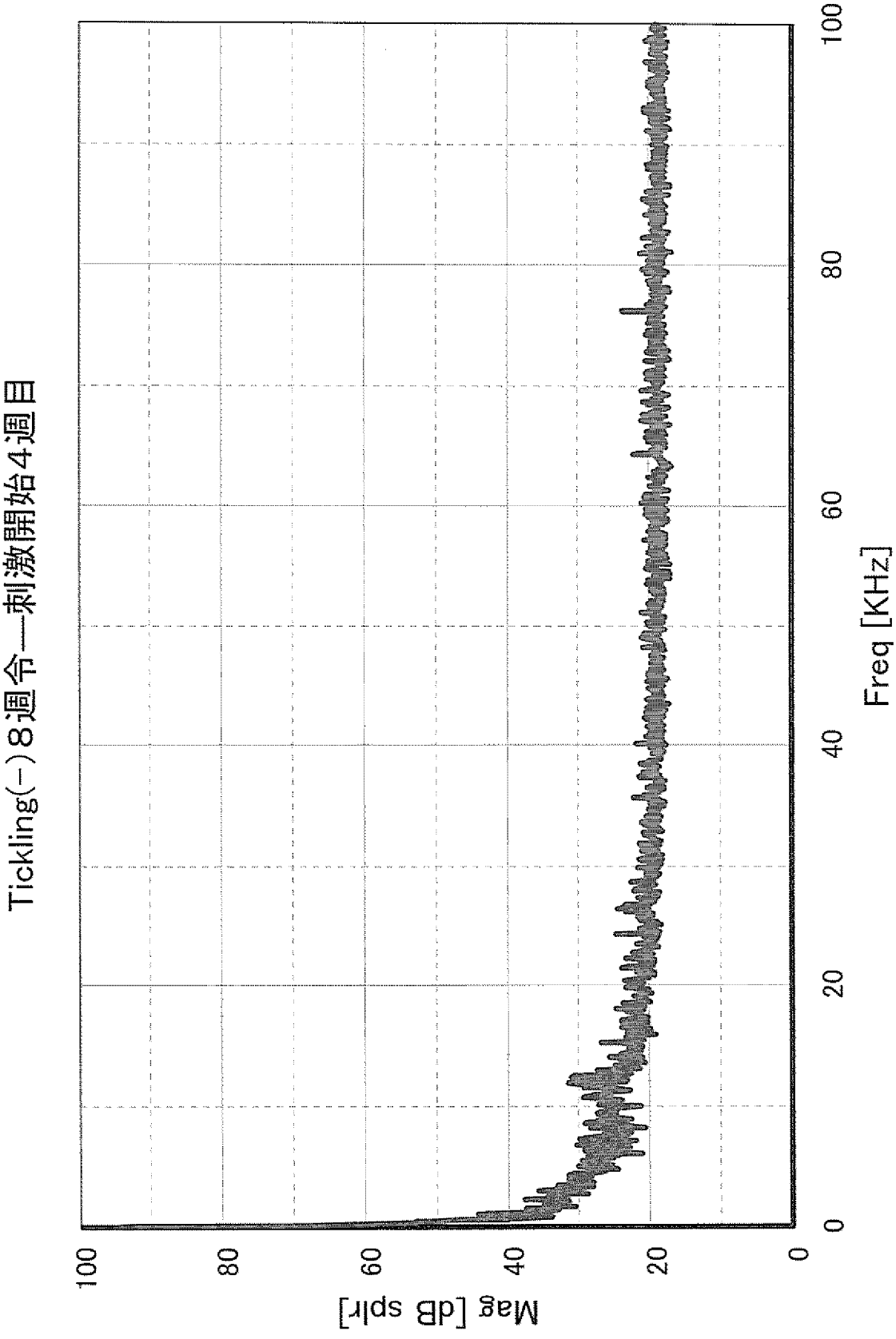
[図39]


Tickling(−)6週令—刺激開始4週目
Mag [dB spl]
100
80
60
40
20
0
0
20
40
60
80
100
Freq [Hz]

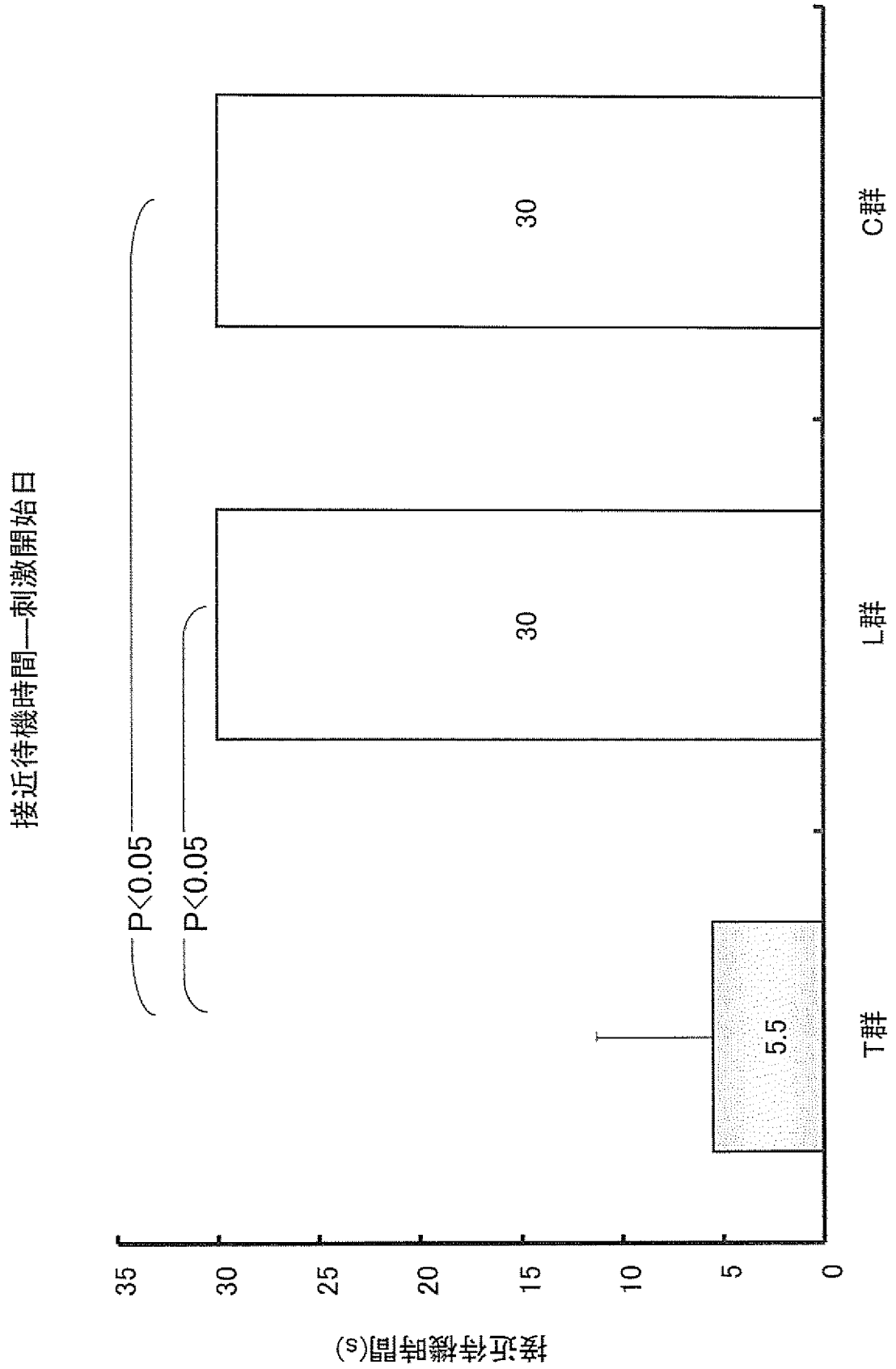
[図40]


Ticklingg(+)8週令—刺激開始4週目
Mag [dB spir]
100
80
60
40
20
0
0
20
40
60
80
100
Freq [KHz]

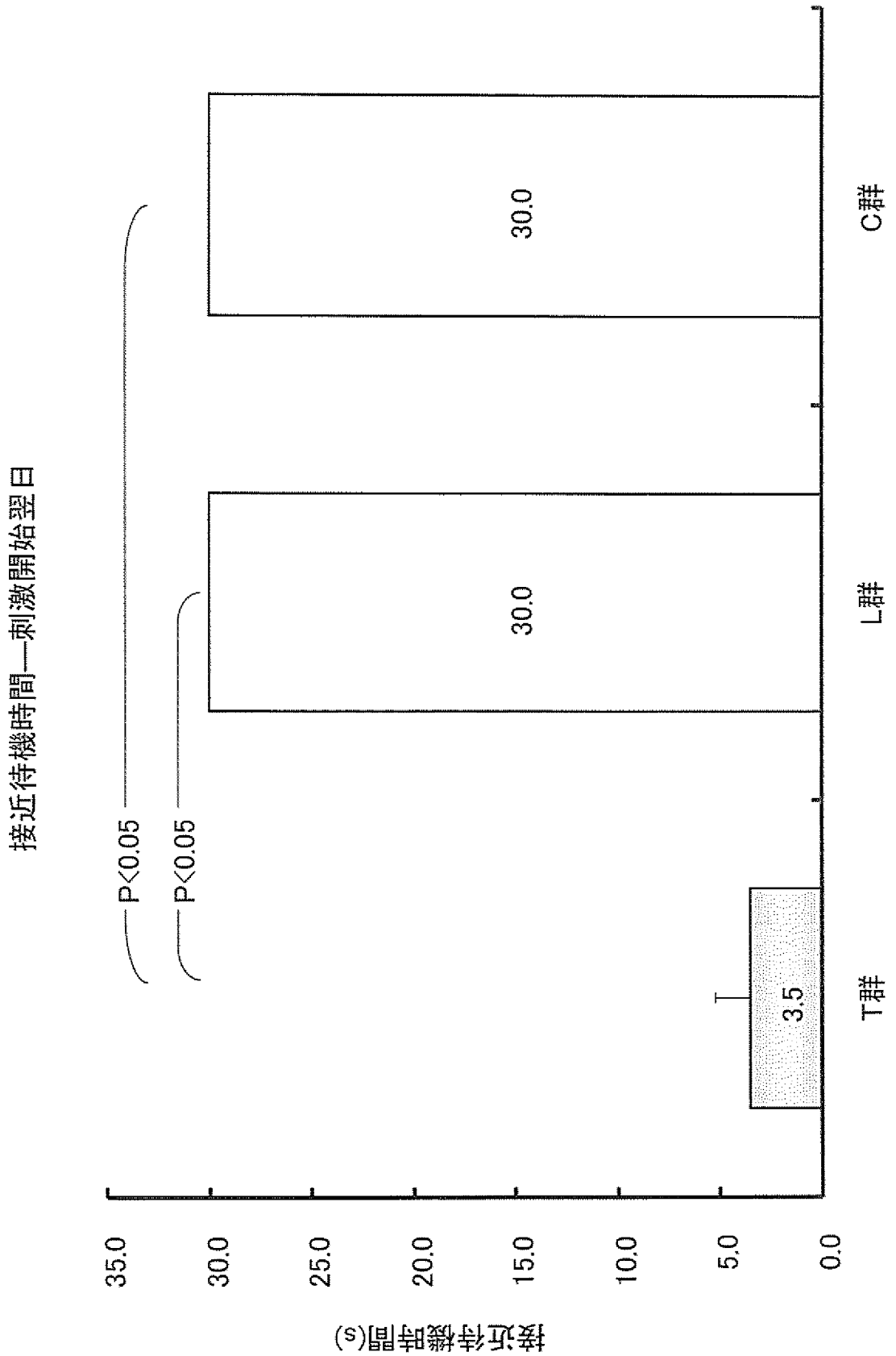
[図41]


Tickling(−)8週令—刺激開始4週目
Mag [dB spl]
100
80
60
40
20
0
Freq [KHz]
0
20
40
60
80
100

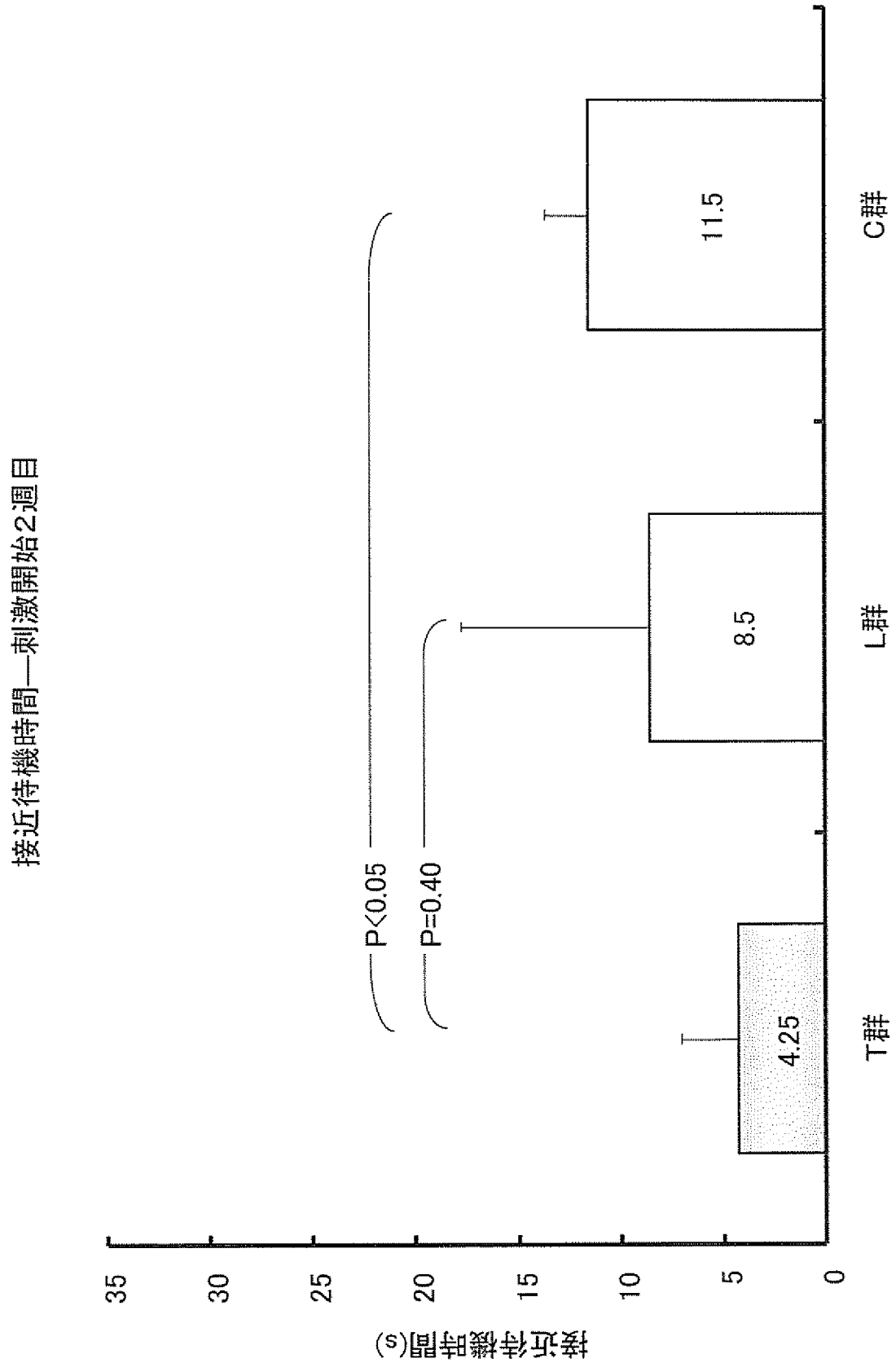
[図42]


接近待機時間—刺激開始日
接近待機時間(s)
0
5
10
15
20
25
30
35
5.5
30
30
P<0.05
P<0.05
T群
L群
C群

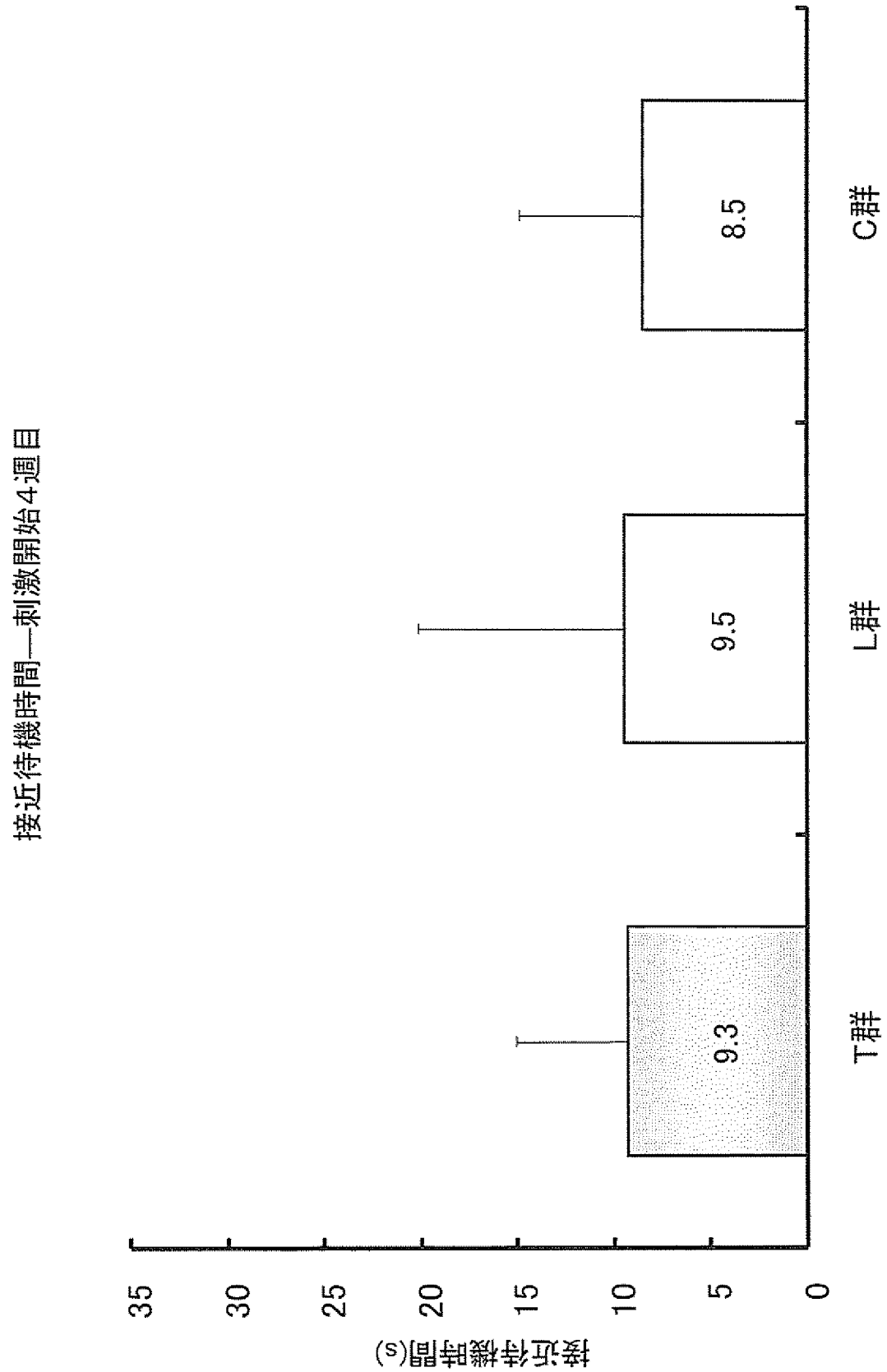
[図43]


接近待機時間—刺激開始翌日
接近待機時間(s)
35.0
30.0
25.0
20.0
15.0
10.0
5.0
0.0
3.5
30.0
30.0
P<0.05
P<0.05
T群
L群
C群

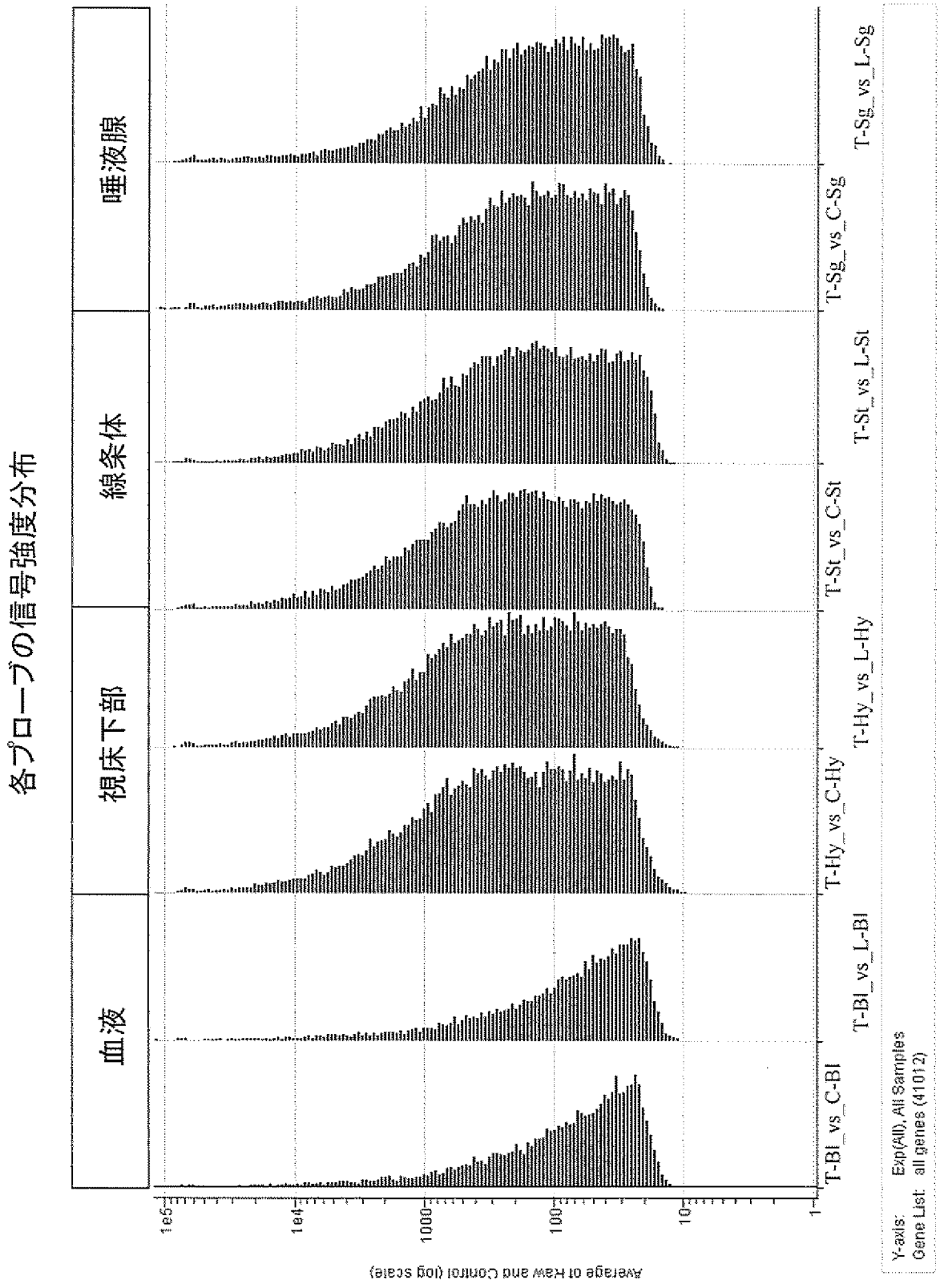
[図44]


接近待機時間—刺激開始2週目
接近待機時間(s)
0
5
10
15
20
25
30
35
4.25
8.5
11.5
T群
L群
C群
P=0.40
P<0.05

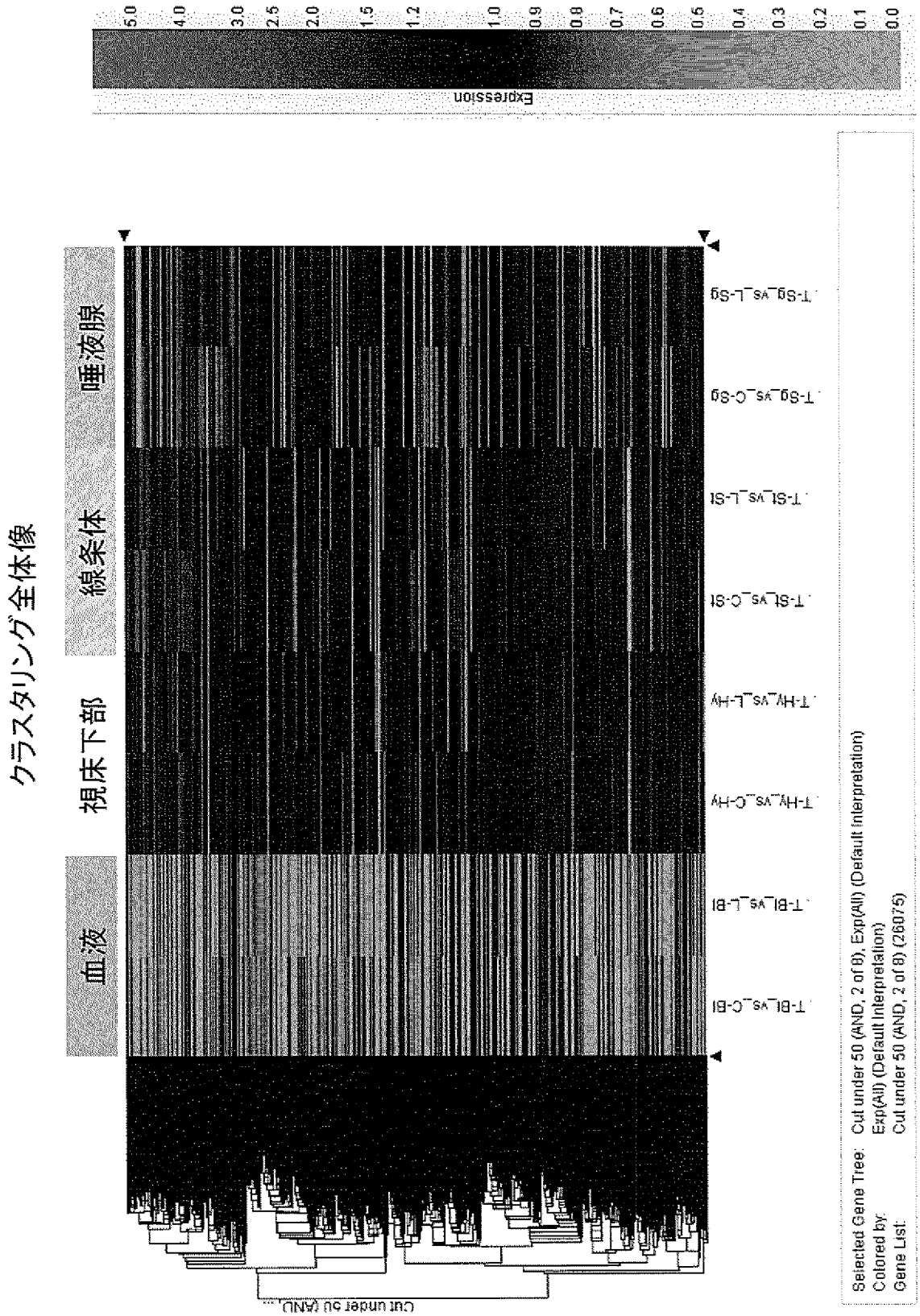
[図45]



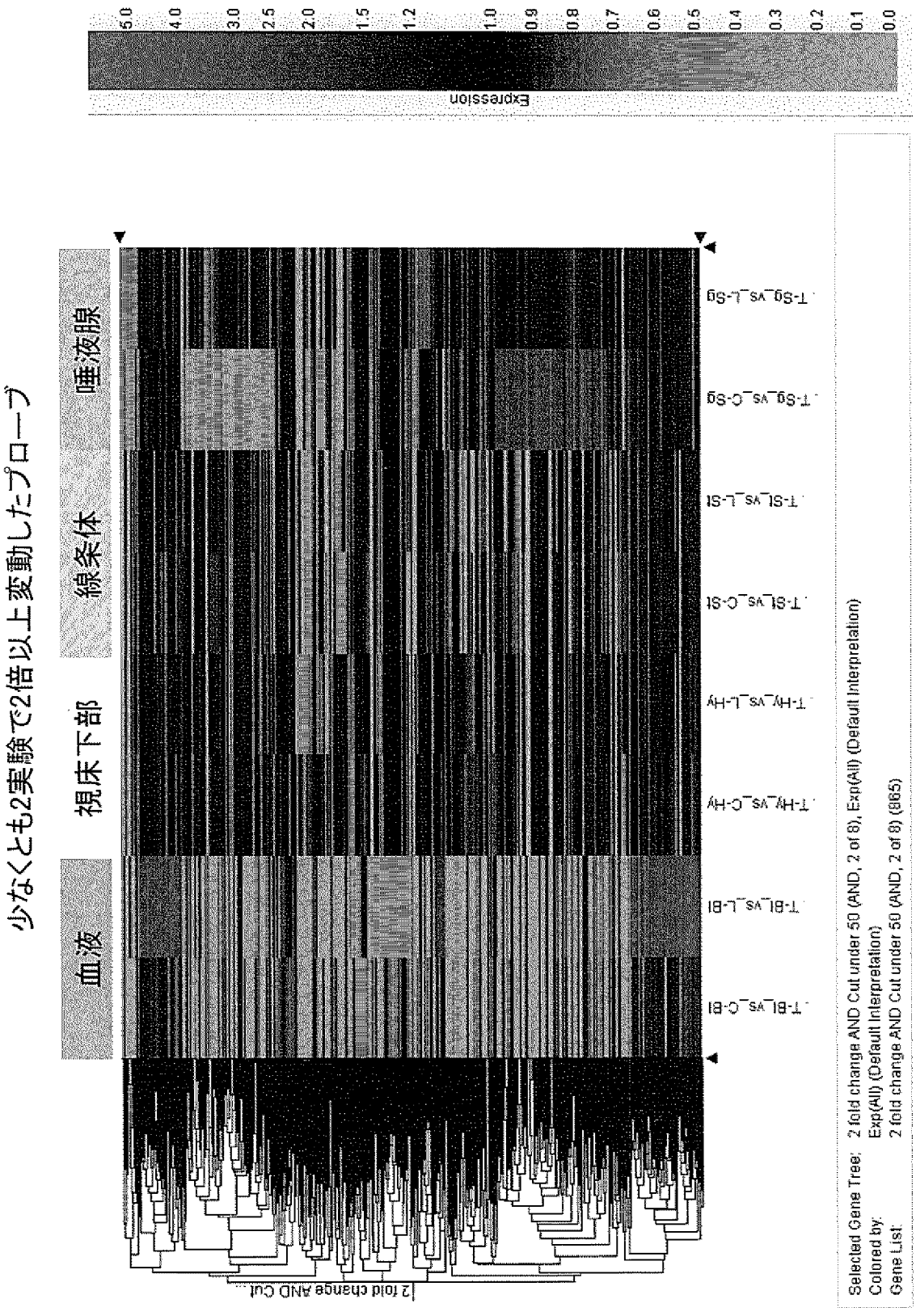
[図46]


各プローブの信号強度分布
血液
視床下部
線条体
唾液腺
T-Bl_vs_C-Bl
T-Bl_vs_L-Bl
T-Hy_vs_C-Hy
T-Hy_vs_L-Hy
T-St_vs_C-St
T-St_vs_L-St
T-Sg_vs_C-Sg
T-Sg_vs_L-Sg
1e5
1e4
1000
100
10
1
Average of Raw and Control (log scale)
Y-axis: Exp(All), All Samples
Gene List: all genes (41012)

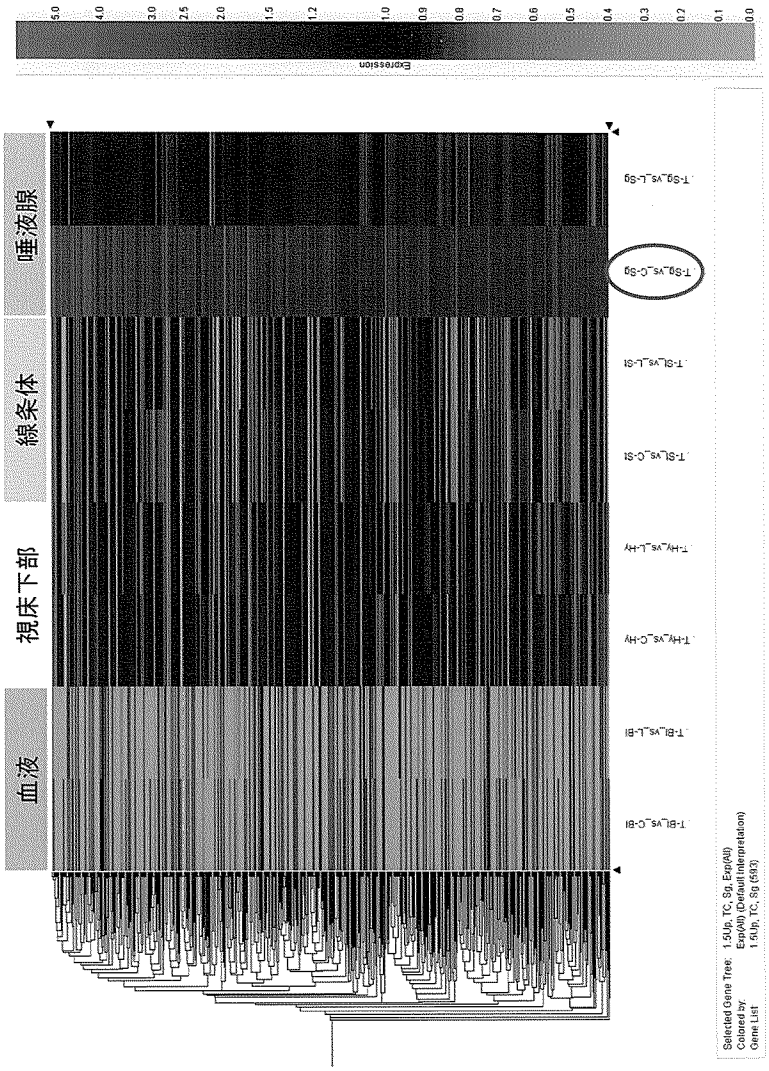
[図47]


クラスタリング全体像
血液
視床下部
線条体
唾液腺
T-Bl_vs_C-Bl
T-Bl_vs_L-Bl
T-Hy_vs_C-Hy
T-Hy_vs_L-Hy
T-Sl_vs_C-Sl
T-Sl_vs_L-Sl
T-Sg_vs_C-Sg
T-Sg_vs_L-Sg
Expression
5.0
4.0
3.0
2.5
2.0
1.5
1.2
1.0
0.9
0.8
0.7
0.6
0.5
0.4
0.3
0.2
0.1
0.0
Selected Gene Tree: Cut under 50 (AND, 2 of 8), Exp(All) (Default Interpretation)
Colored by: Exp(All) (Default Interpretation)
Gene List: Cut under 50 (AND, 2 of 8) (26075)

[図48]

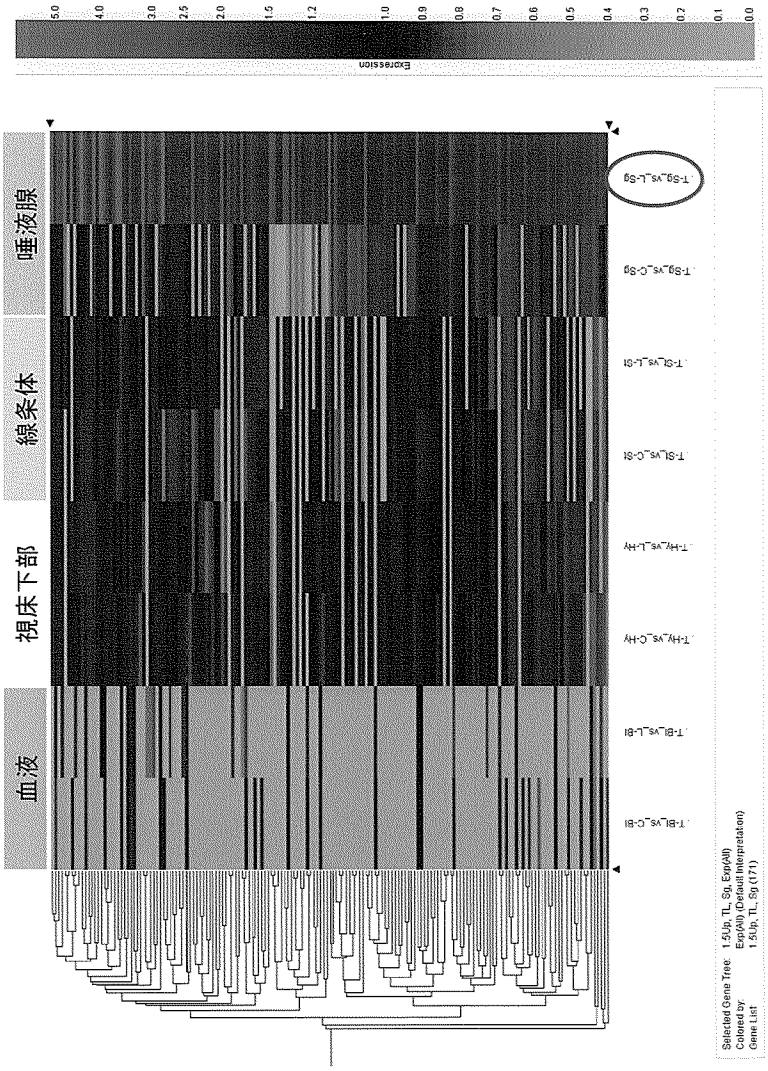

少なくとも2実験で2倍以上変動したプローブ
血液
視床下部
線条体
唾液腺
T-Bl_vs_C-Bl
T-Bl_vs_L-Bl
T-Hy_vs_C-Hy
T-Hy_vs_L-Hy
T-Sl_vs_C-Sl
T-Sl_vs_L-Sl
T-Sg_vs_C-Sg
T-Sg_vs_L-Sg
2 fold change AND Cut
Expression
5.0
4.0
3.0
2.5
2.0
1.5
1.2
1.0
0.9
0.8
0.7
0.6
0.5
0.4
0.3
0.2
0.1
0.0
Selected Gene Tree: 2 fold change AND Cut under 50 (AND, 2 of 8), Exp(All) (Default Interpretation)
Colored by: Exp(All) (Default Interpretation)
Gene List: 2 fold change AND Cut under 50 (AND, 2 of 8) (865)

[図49]



Cに対してTの唾液腺において、
1.5倍超の発現を認めた593プローブによるクラスタリング図

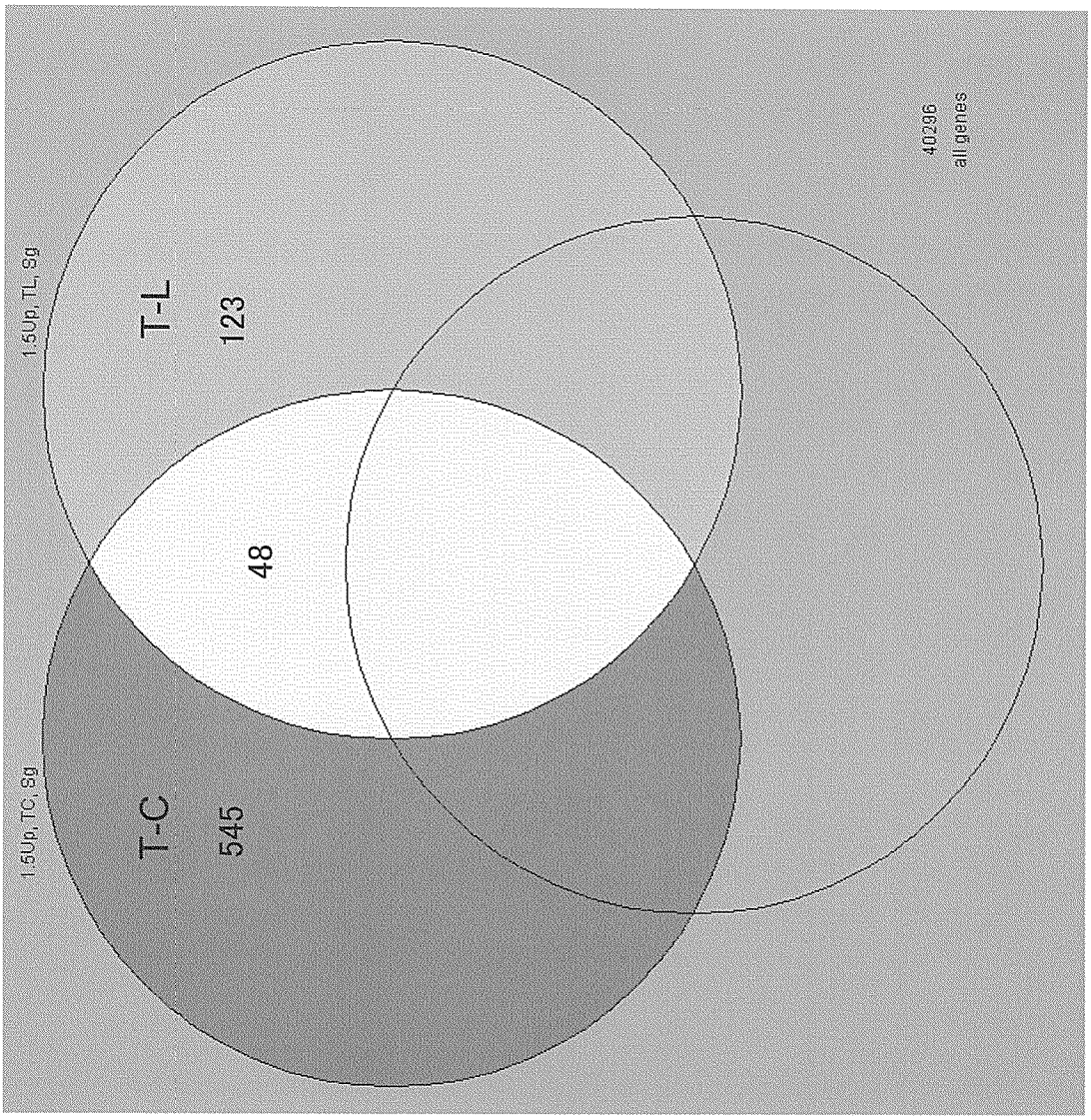
[図50]



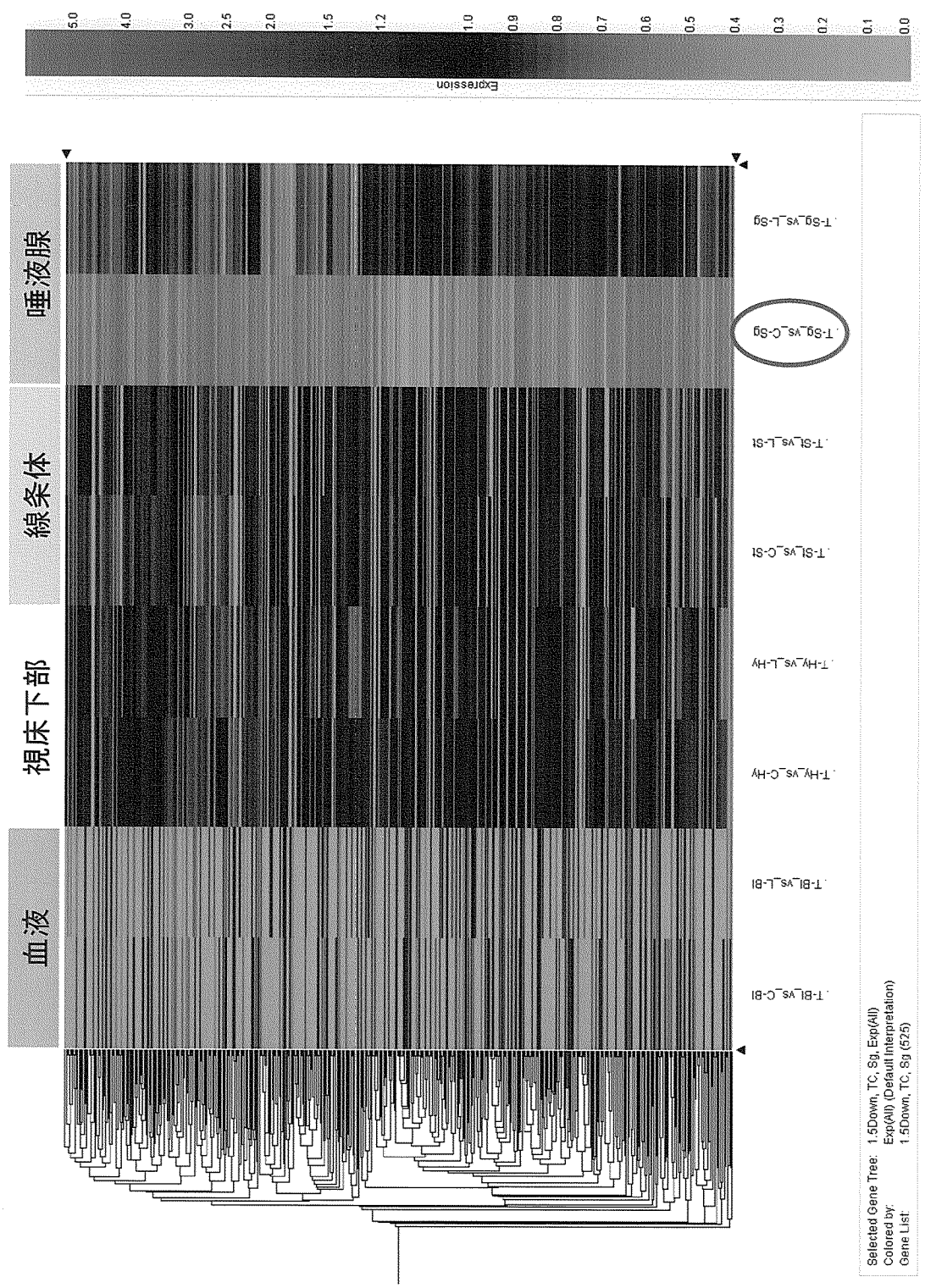
Lに対してTの唾液腺において、
1.5倍超の発現を認めた171プローブによるクラスタリング図

[図51]

Cあるいは Lと比較して Tで1.5倍超の発現差を認めた唾液腺の遺伝子

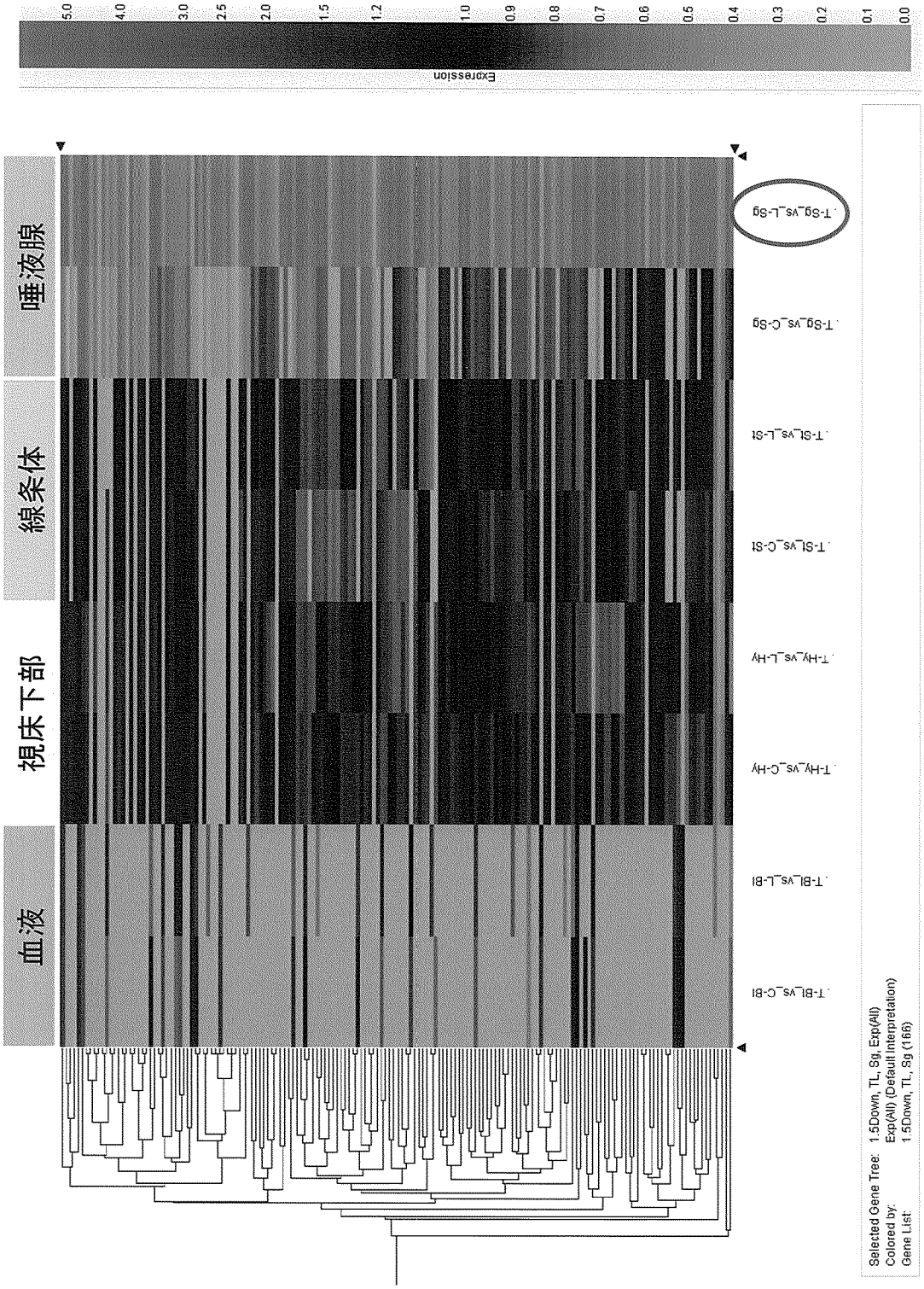


[図52]



Cに対してTの唾液腺において、
1/1.5倍未満の発現を認めた525プローブによるクラスタリング図

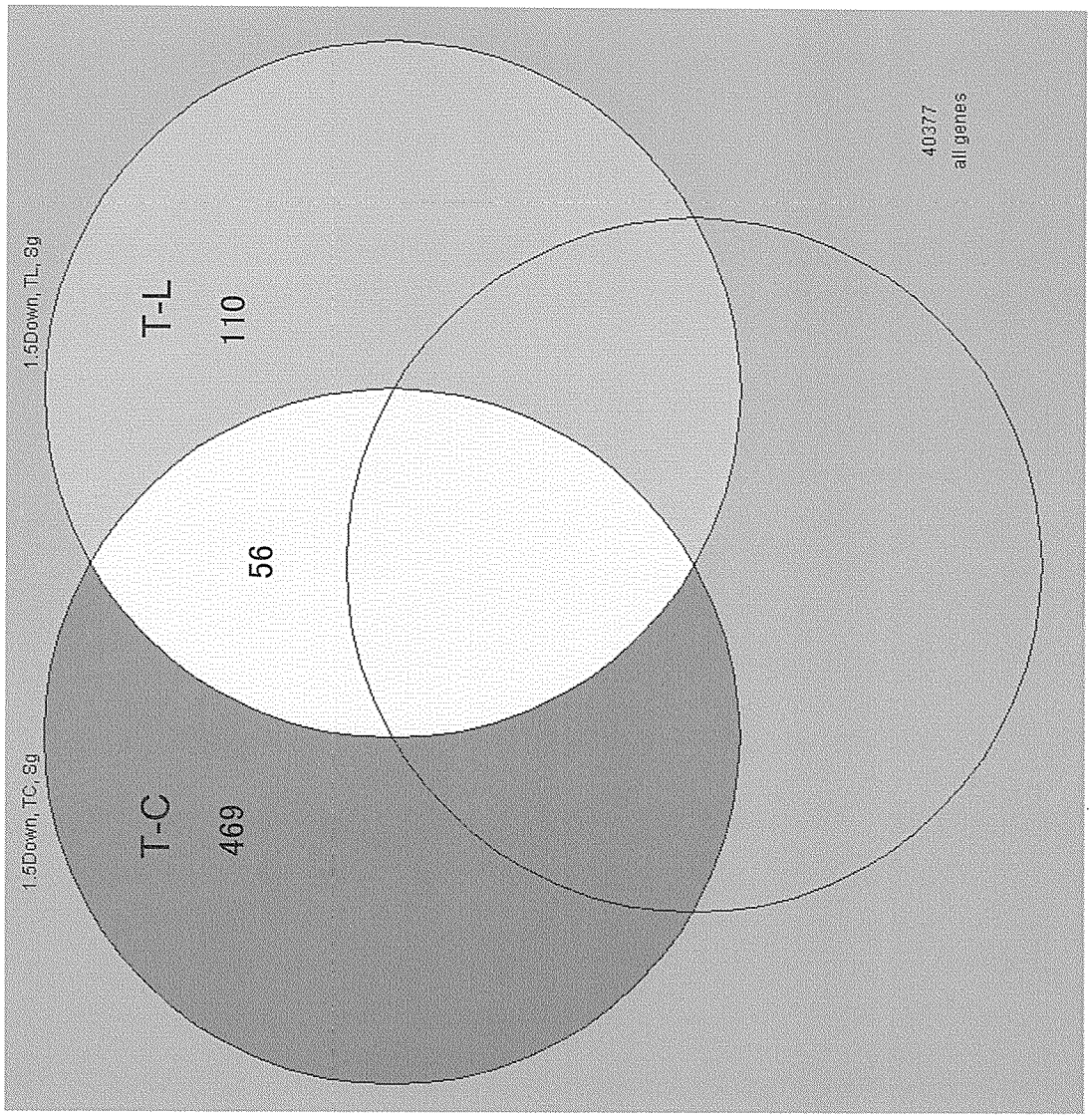
[図53]



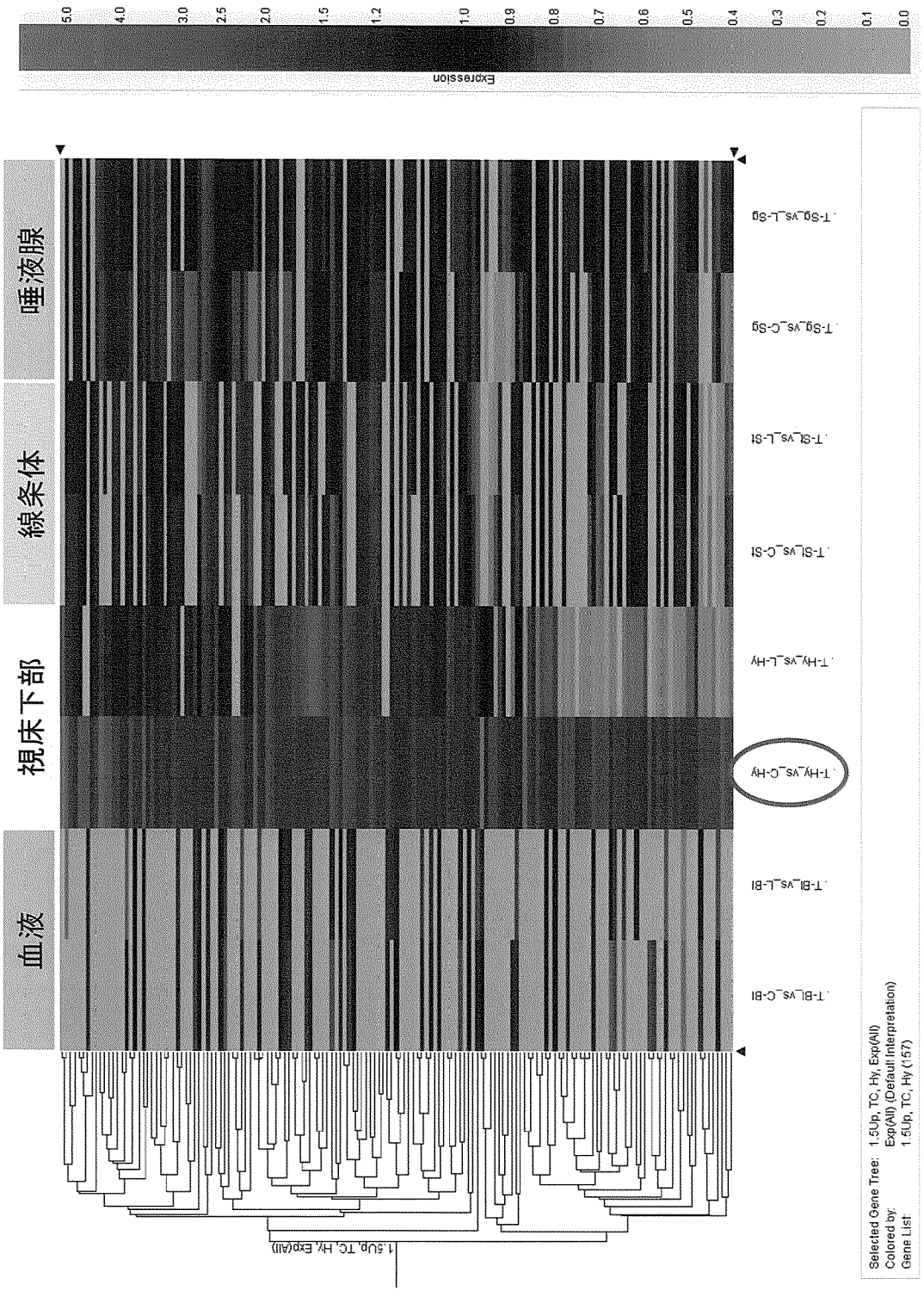
Lに対してTの唾液腺において、
1/1.5倍未満の発現を認めた166プローブによるクラスタリング図

[図54]

Cあるいはしと比較してTで1/1.5倍未満の発現差を認めた唾液腺の遺伝子

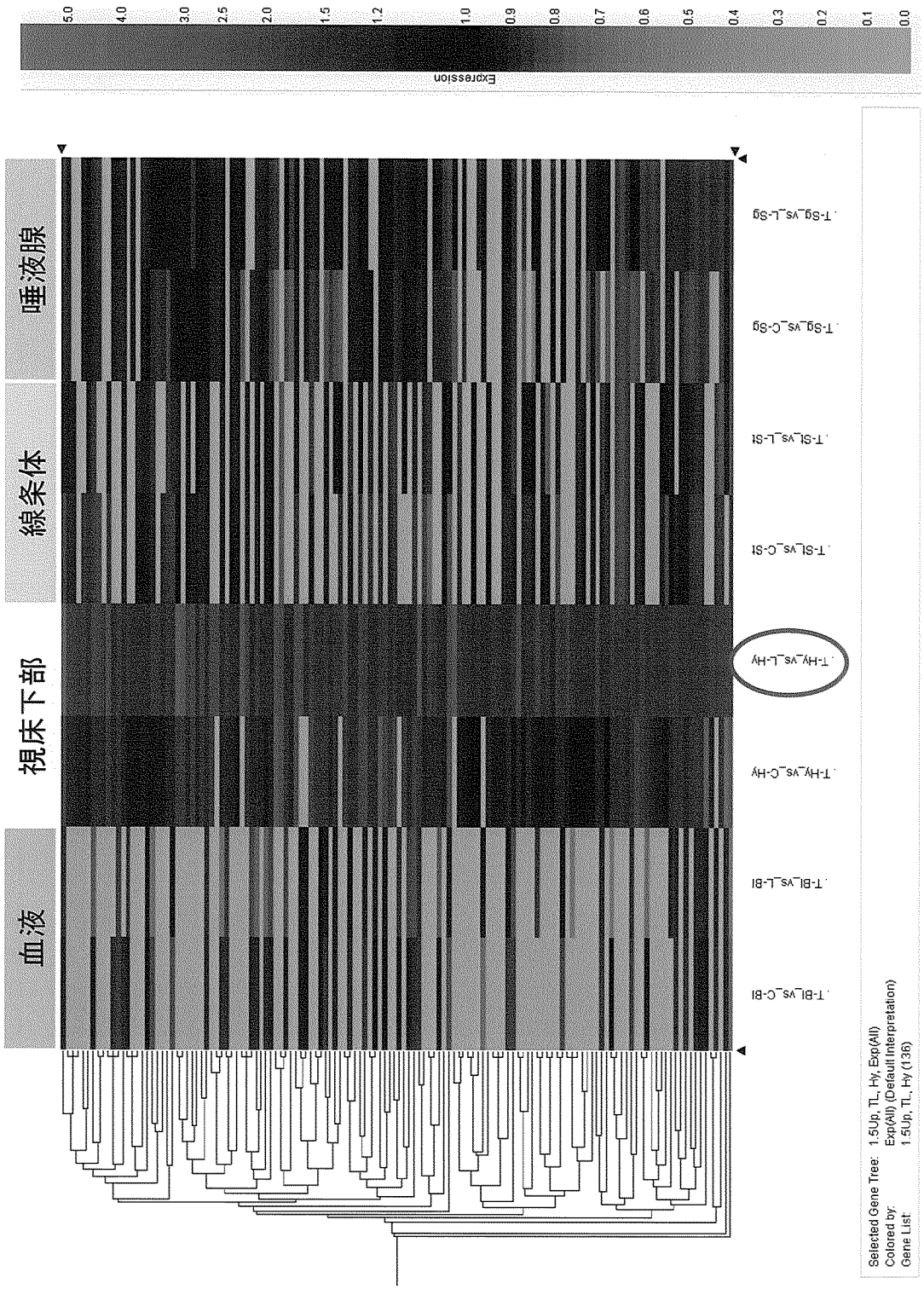


[図55]



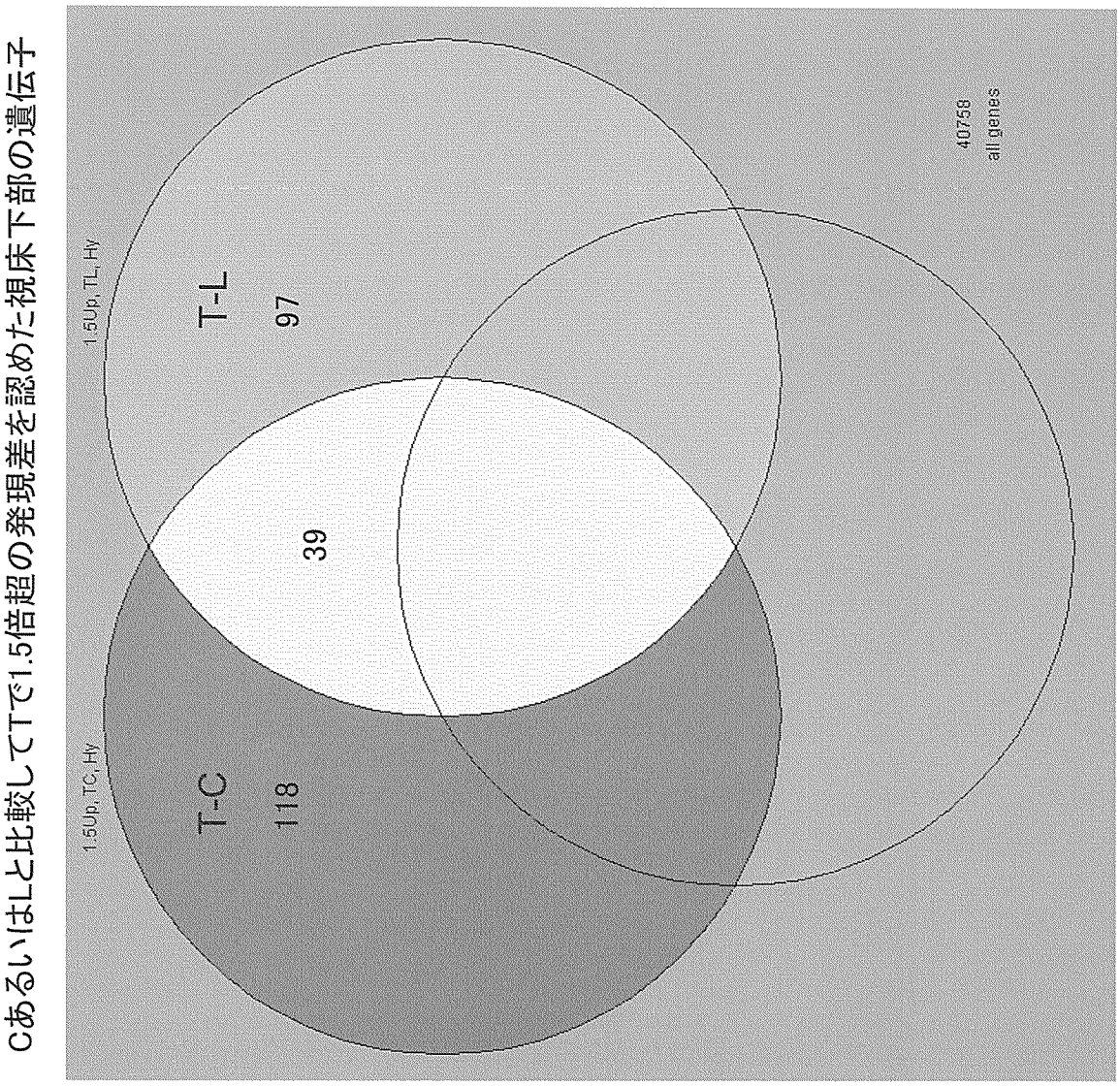
Cに対してTの視床下部において、
1.5倍超の発現を認めた157プローブによるクラスタリング図

[図56]

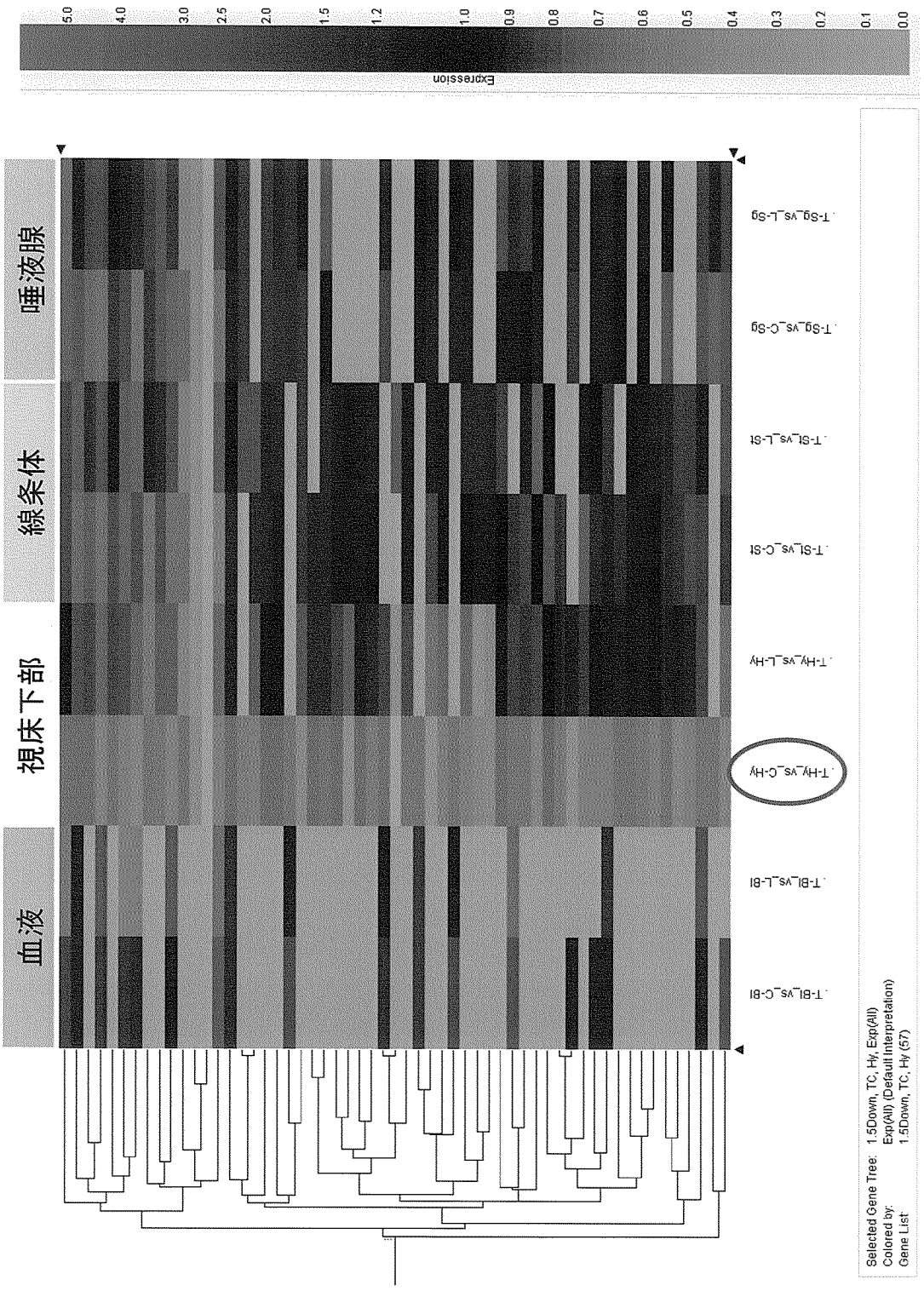


Lに対してTの視床下部において、
1.5倍超の発現を認めた136プローブによるクラスタリング図

[図57]

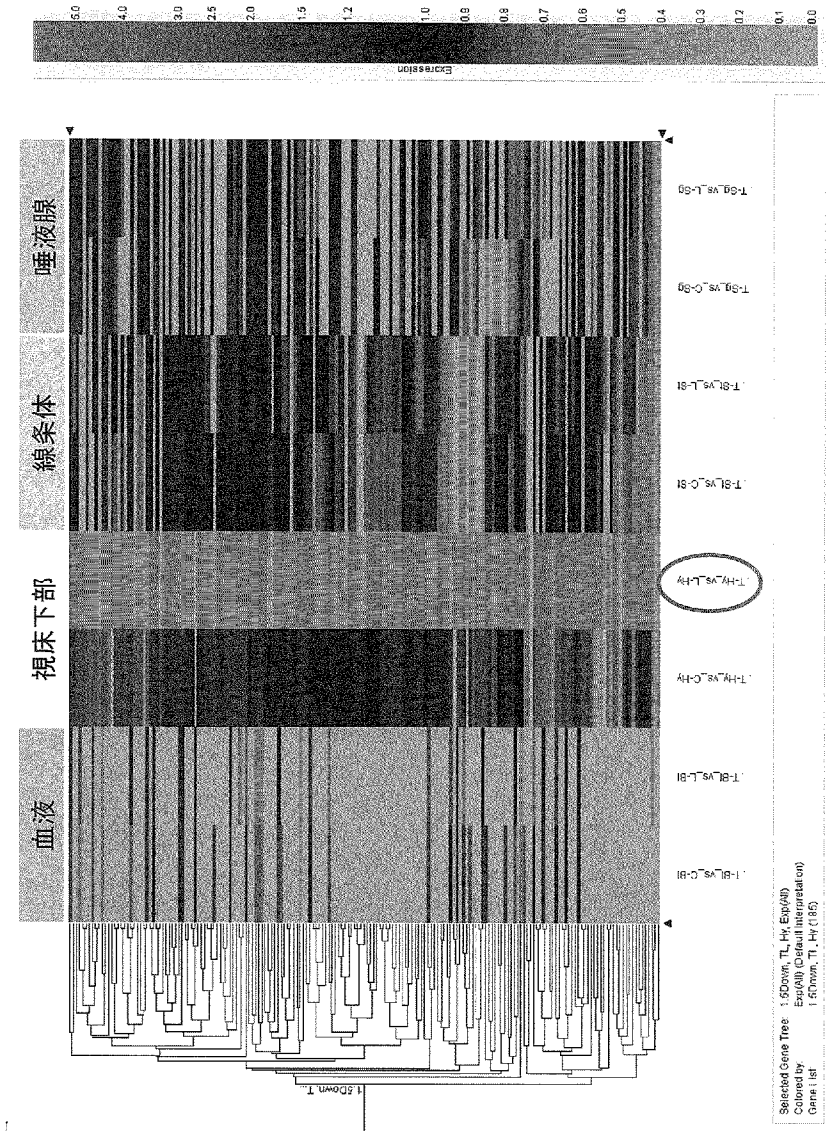

Cあるいは L と比較して T で 1.5 倍超の発現差を認めた視床下部の遺伝子
1.5Up, TC, Hv
1.5Up, TL, Hv
T-C
118
39
T-L
97
all genes
40758

[図58]



Cに対してTの視床下部において、
1/1.5倍未満の発現を認めた57プローブによるクラスタリング図

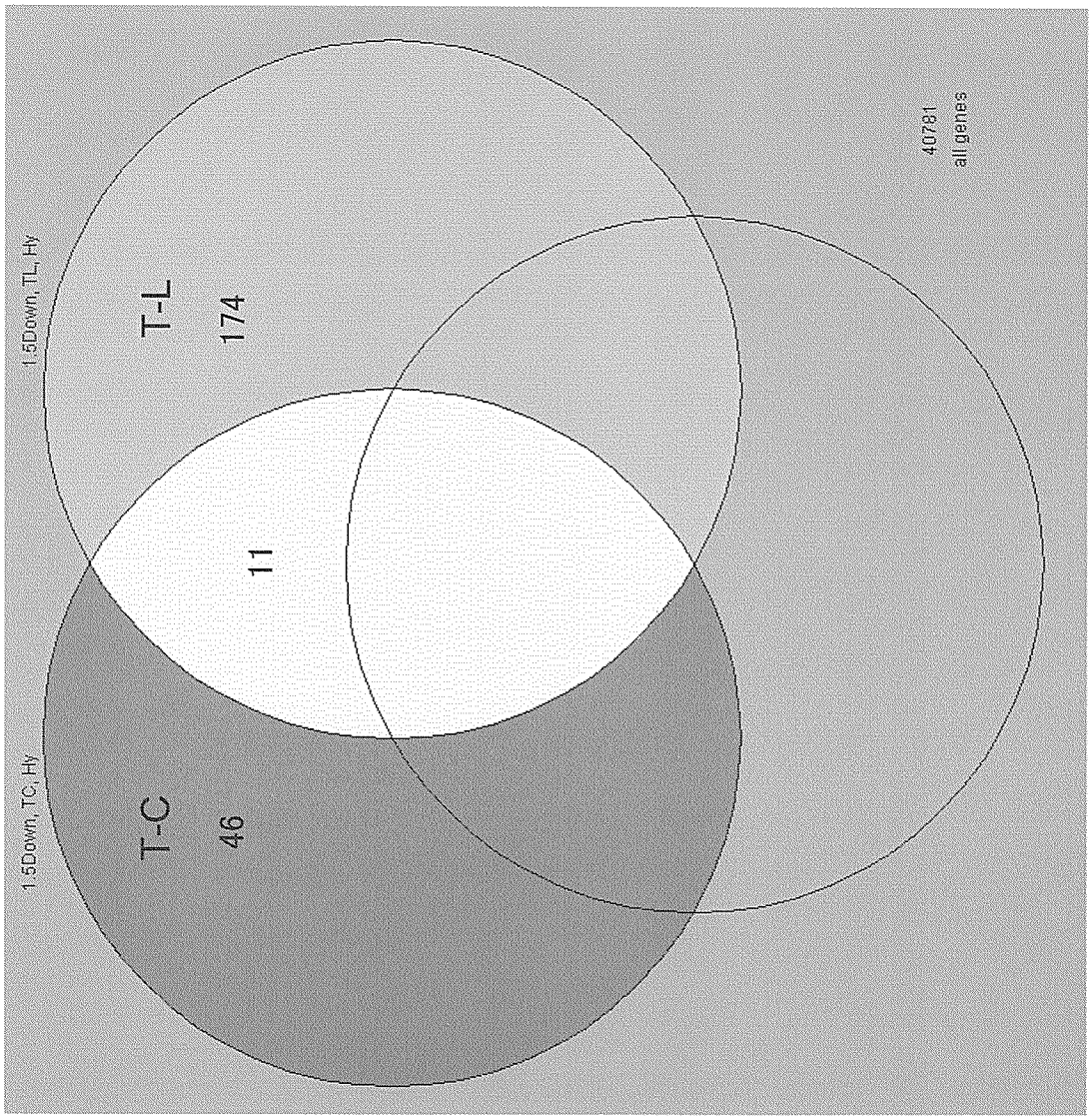
[図59]



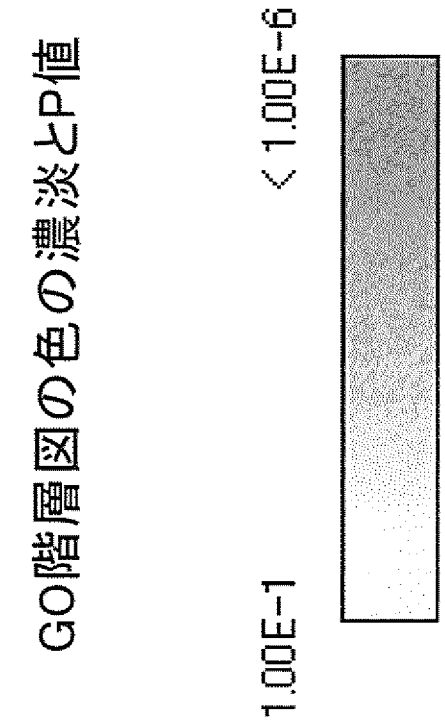
LIに対してTの視床下部において、
1/1.5倍未満の発現を認めた185プローブによるクラスタリング図

[図60]

Cあるいは比較してTで1/1.5倍未満の発現差を認めた視床下部の遺伝子

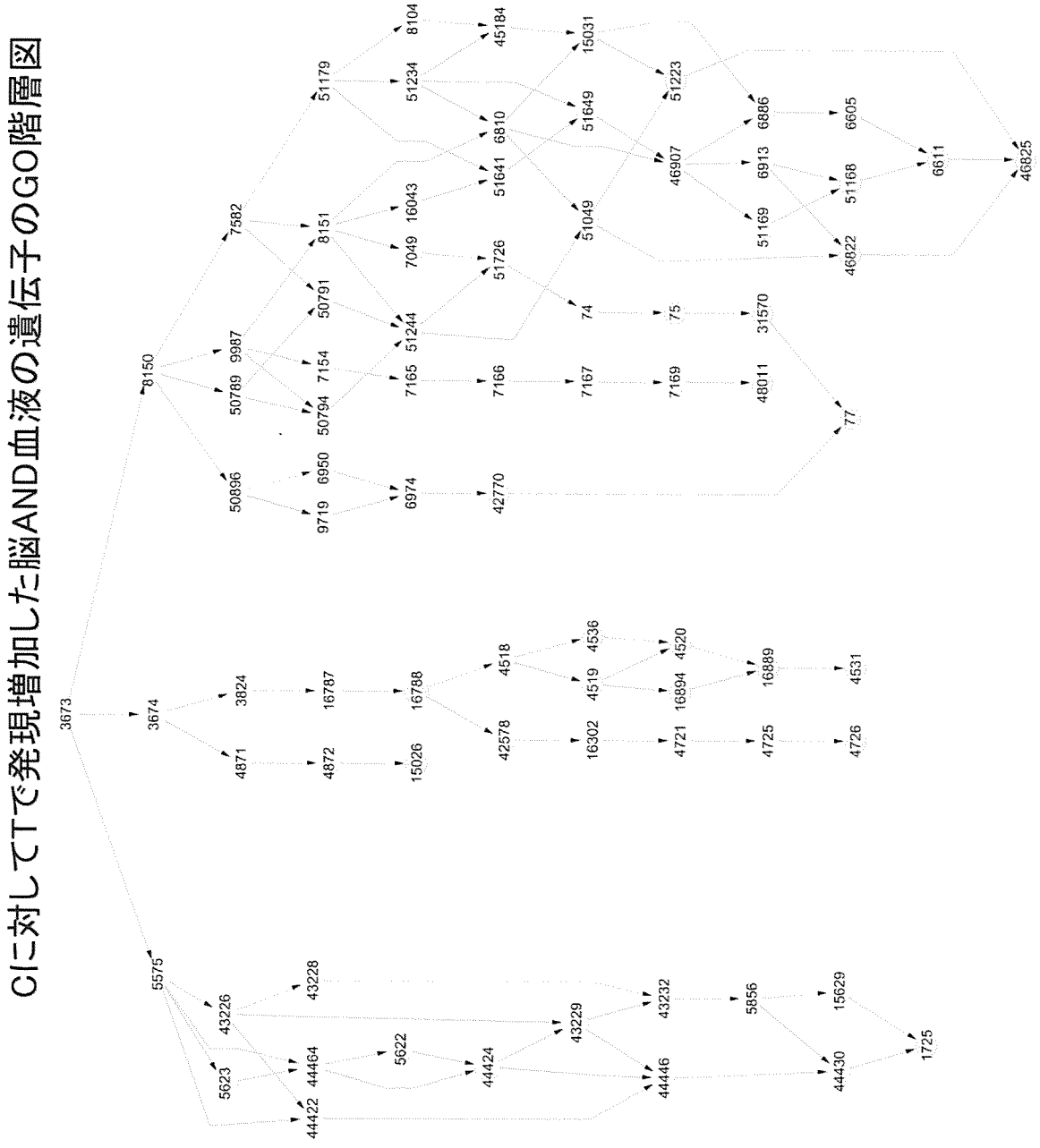


[図61]

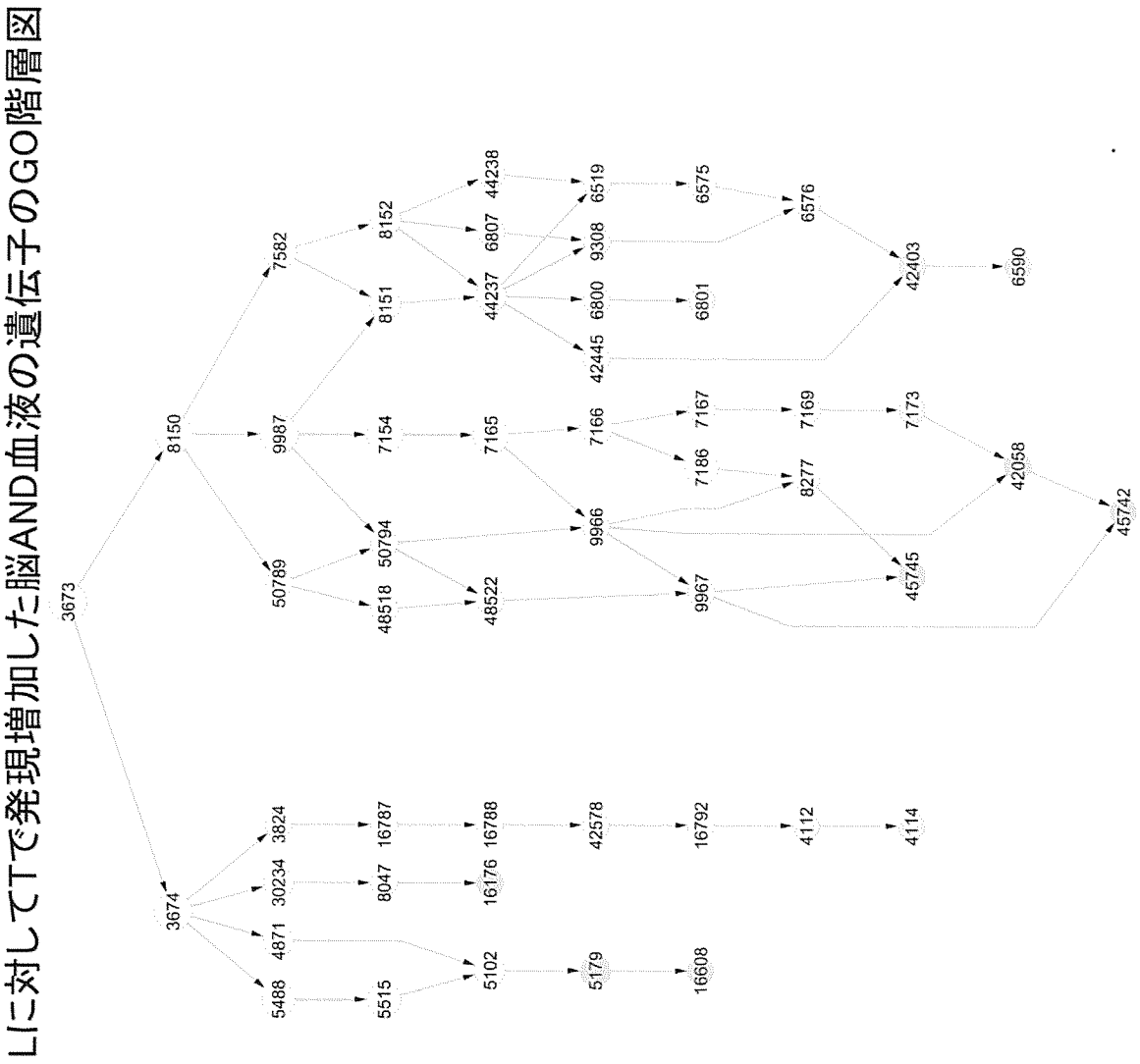


[図62]

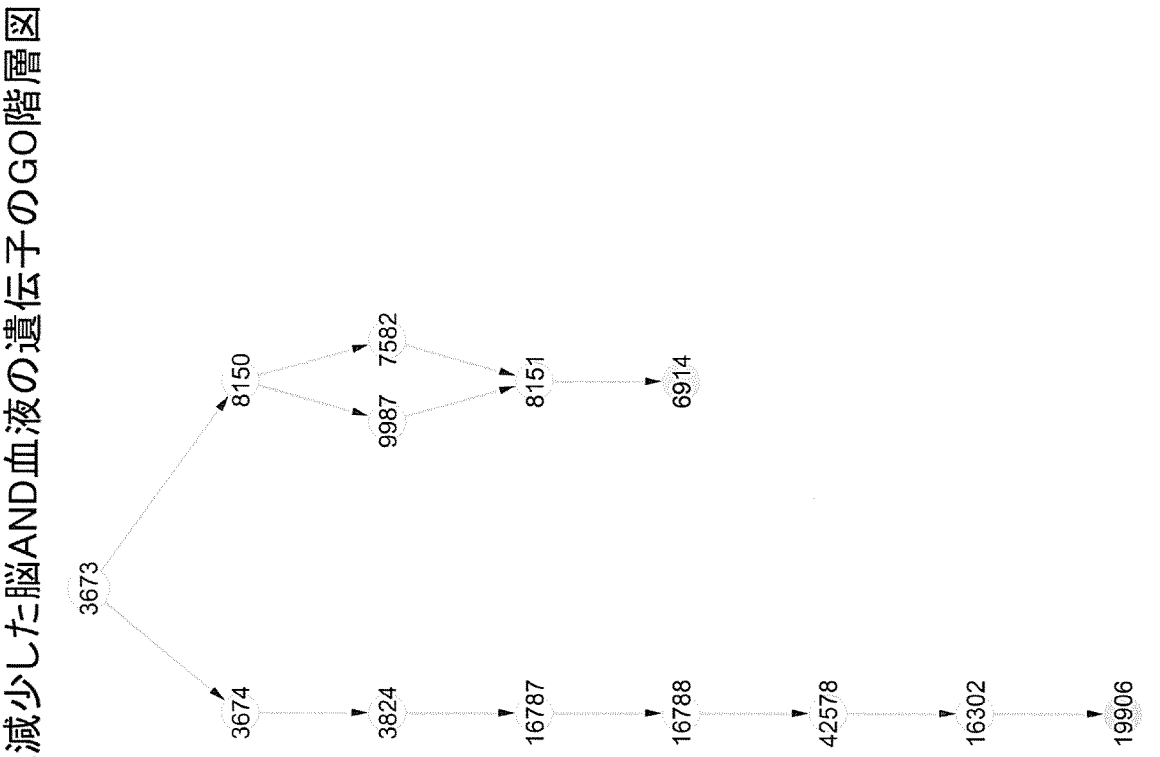
CIに対してTで発現増加した脳AND血液の遺伝子のGO階層図



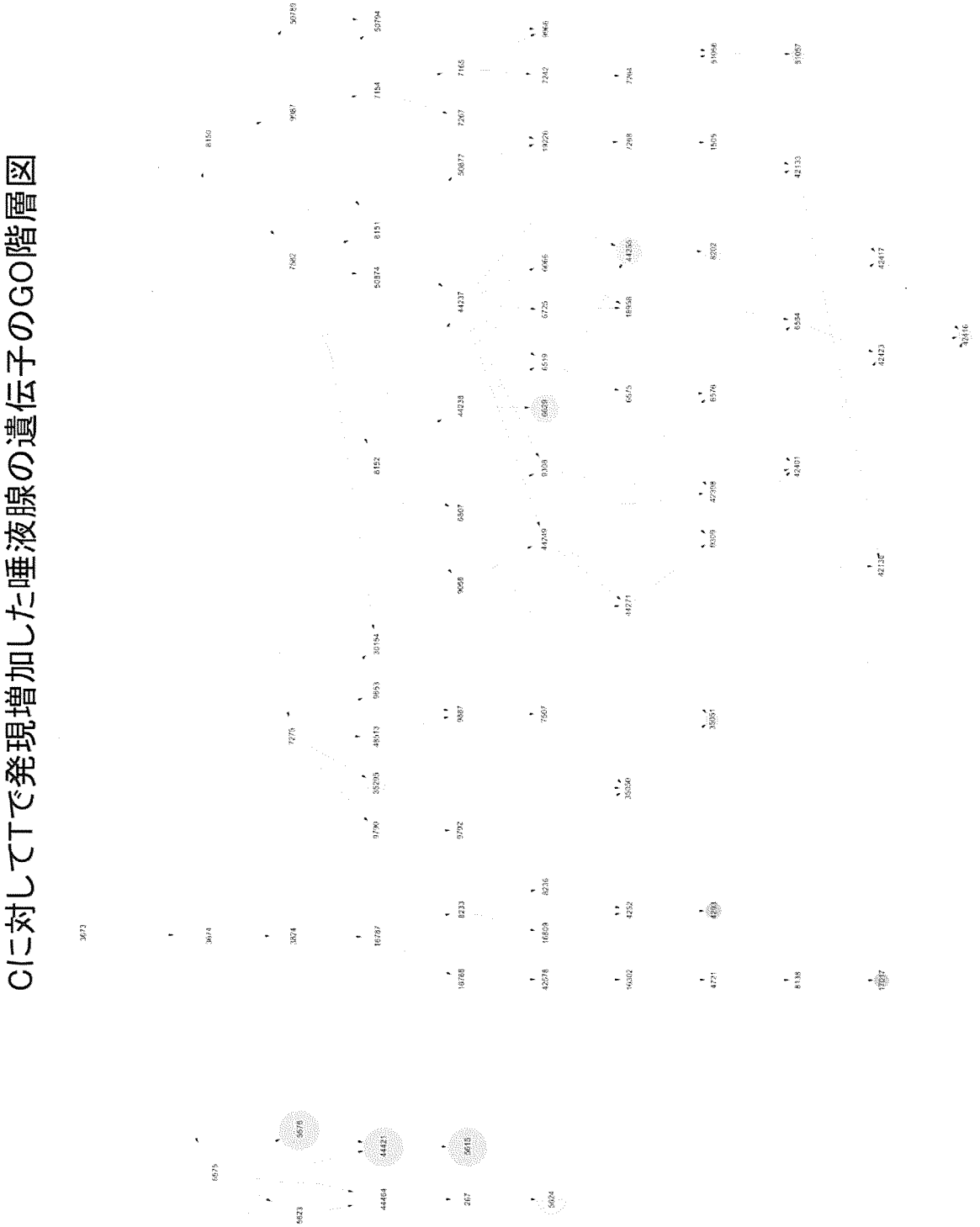
[図63]


Lに対してTで発現増加した脳AND血液の遺伝子のGO階層図
3673
3674
8150
7582
9987
50789
8152
8151
7154
50794
48518
7165
48522
44238
6807
44237
6519
9308
6800
42445
7166
9966
7186
7167
6575
6576
6801
7169
8277
9967
7173
42403
6590
45745
42058
45742
5488
4871
30234
3824
5515
8047
16787
5102
16176
16788
5179
42578
16608
16792
4112
4114

[図64]


Lに対してTで発現減少した脳AND血液の遺伝子のGO階層図
3673
8150
3674
7582
9987
3824
8151
16787
6914
16788
42578
16302
19906

[図65]



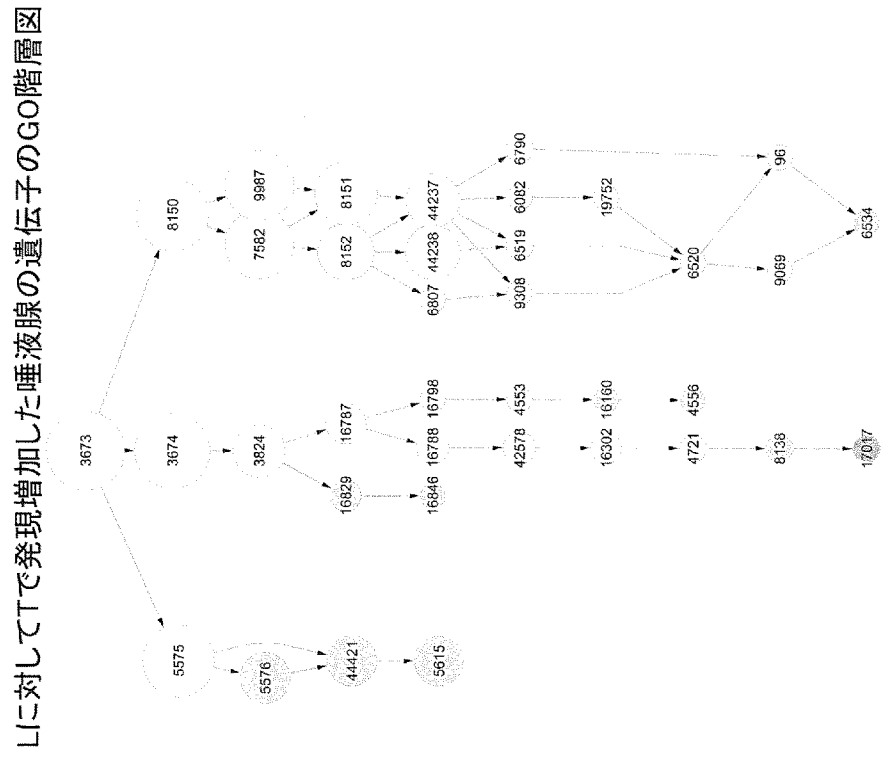
[図66]

Cに対してTで発現減少した唾液腺の遺伝子のGO階層図

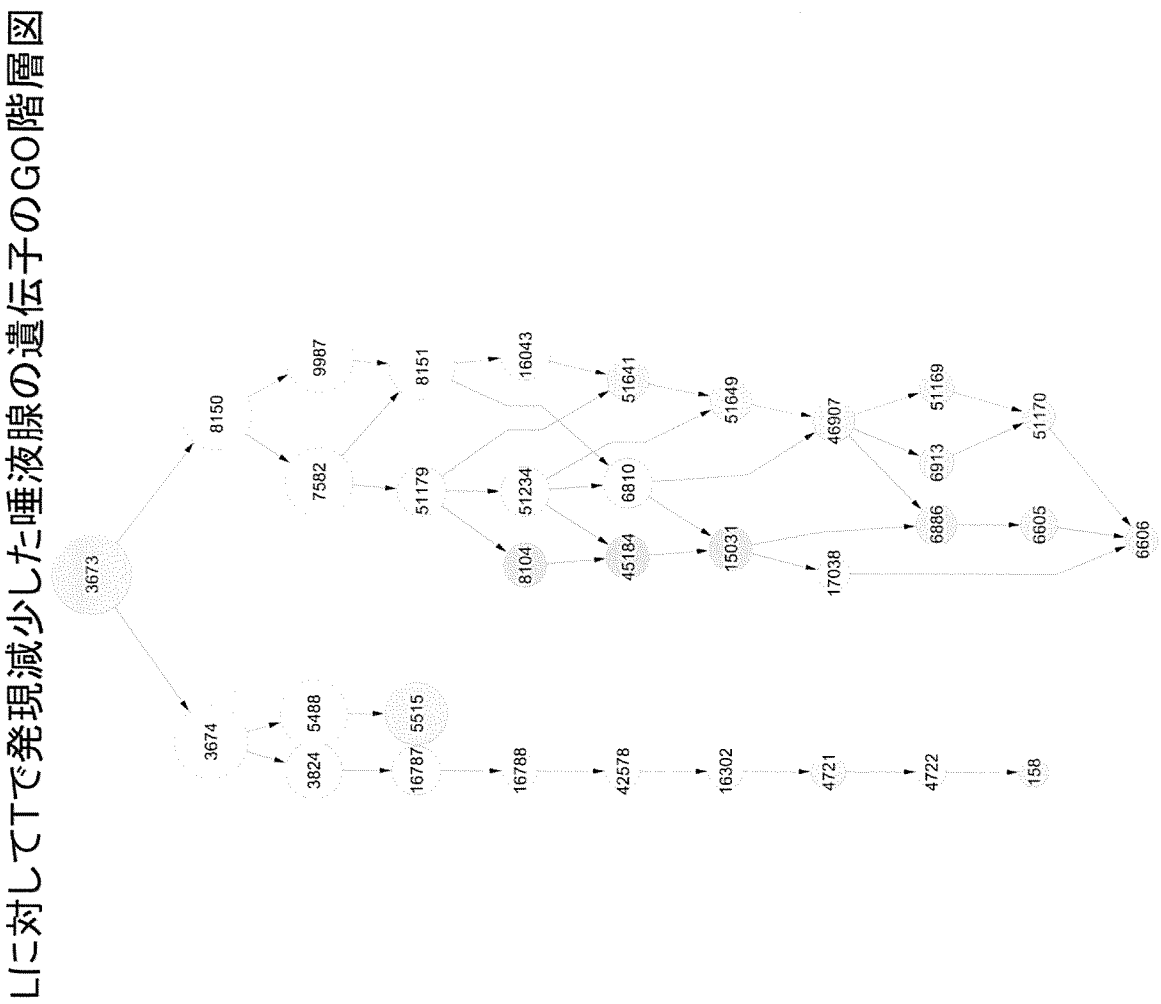


[図67]

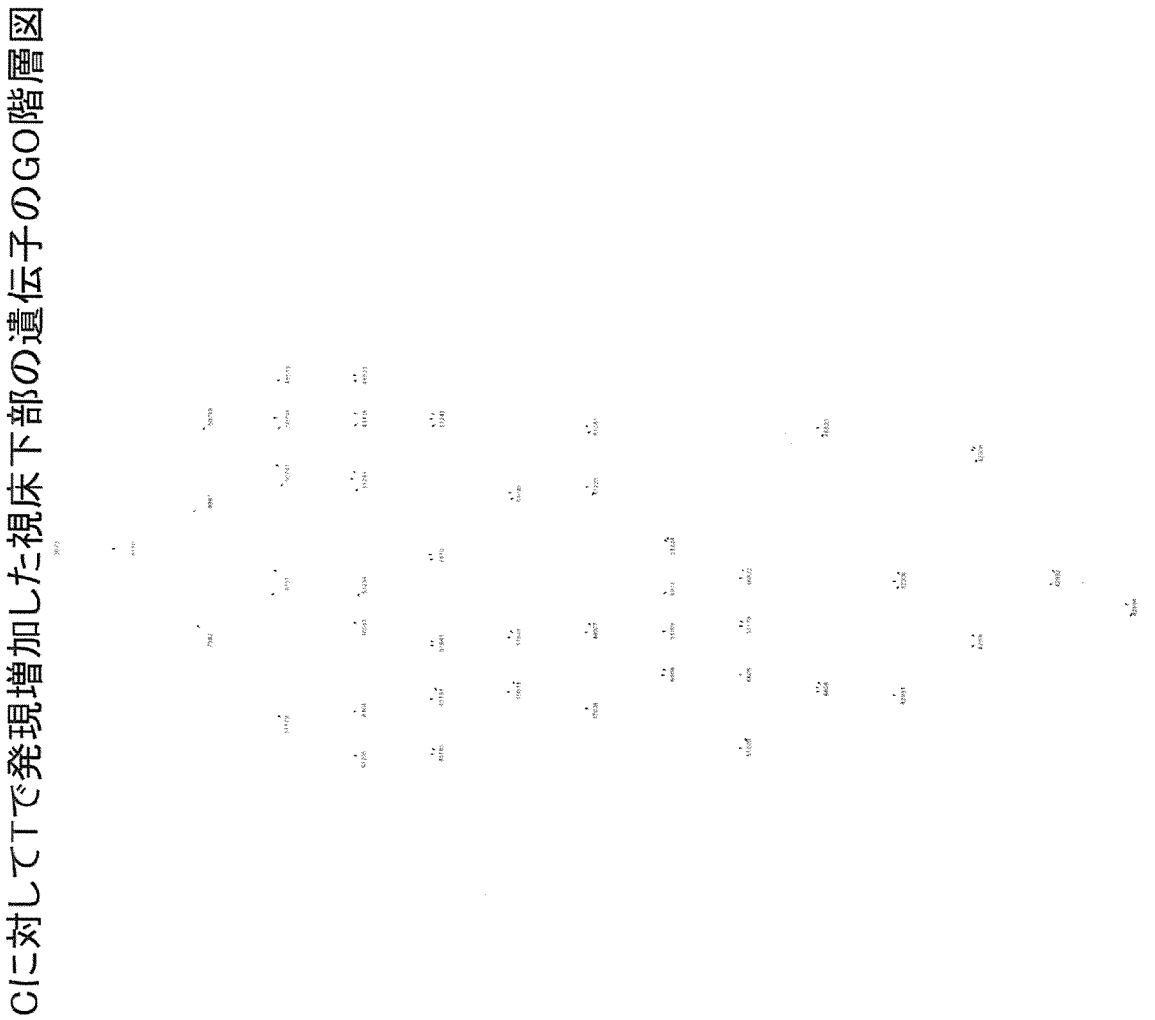
Lに対してTで発現増加した唾液腺の遺伝子のGO階層図



[図68]

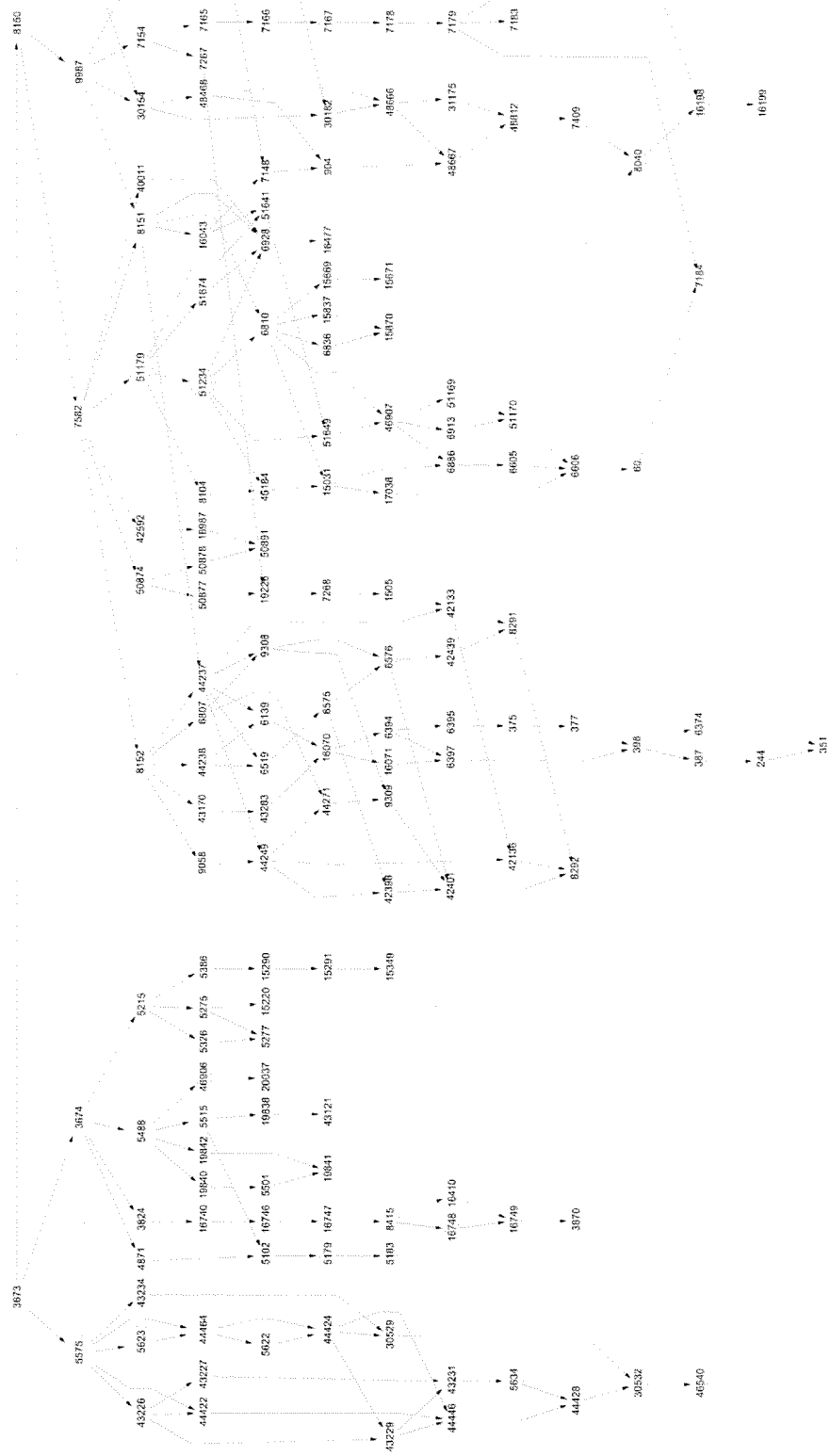

Lに対してTで発現減少した唾液腺の遺伝子のGO階層図
3673
8150
3674
7582
9987
3824
5488
51179
8151
16787
5515
8104
51234
16043
16788
45184
6810
51641
42578
15031
51649
16302
17038
46907
4721
6886
6913
51169
4722
6605
51170
158
6606

[図69]



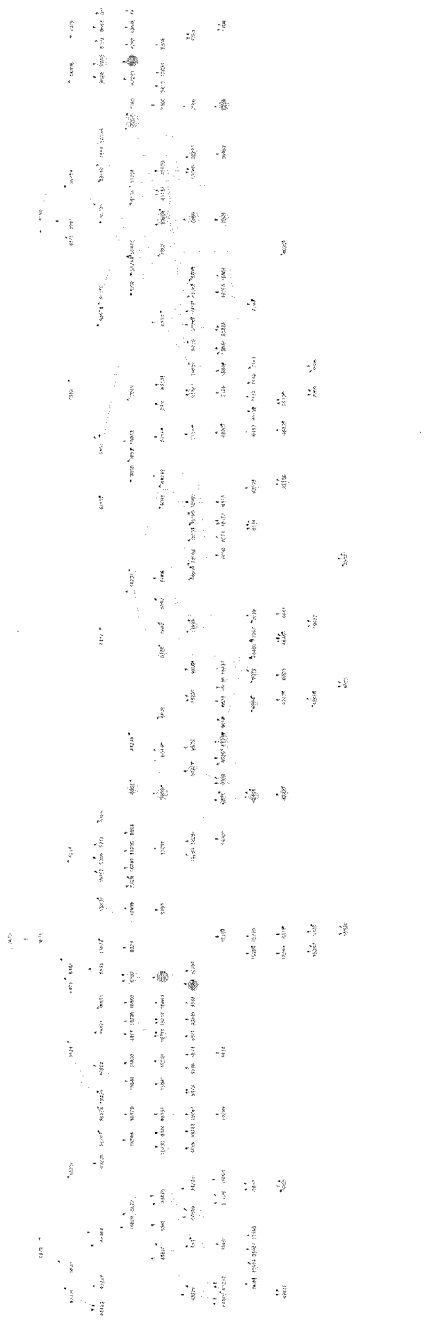
[図70]

CIに対してTで発現減少した視床下部の遺伝子のGO階層図



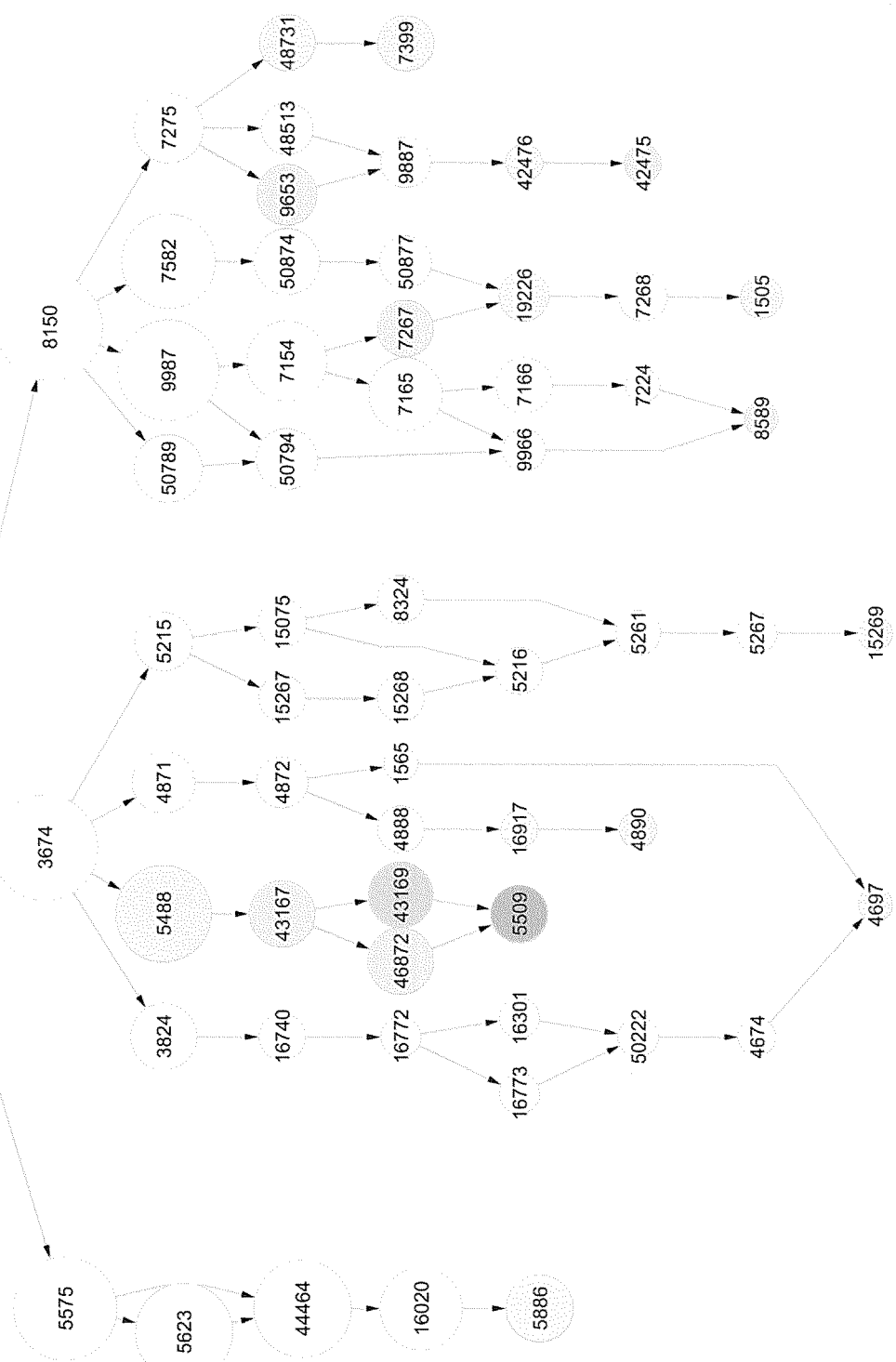
[図71]

LIに対してTで発現増加した視床下部の遺伝子のGO階層図

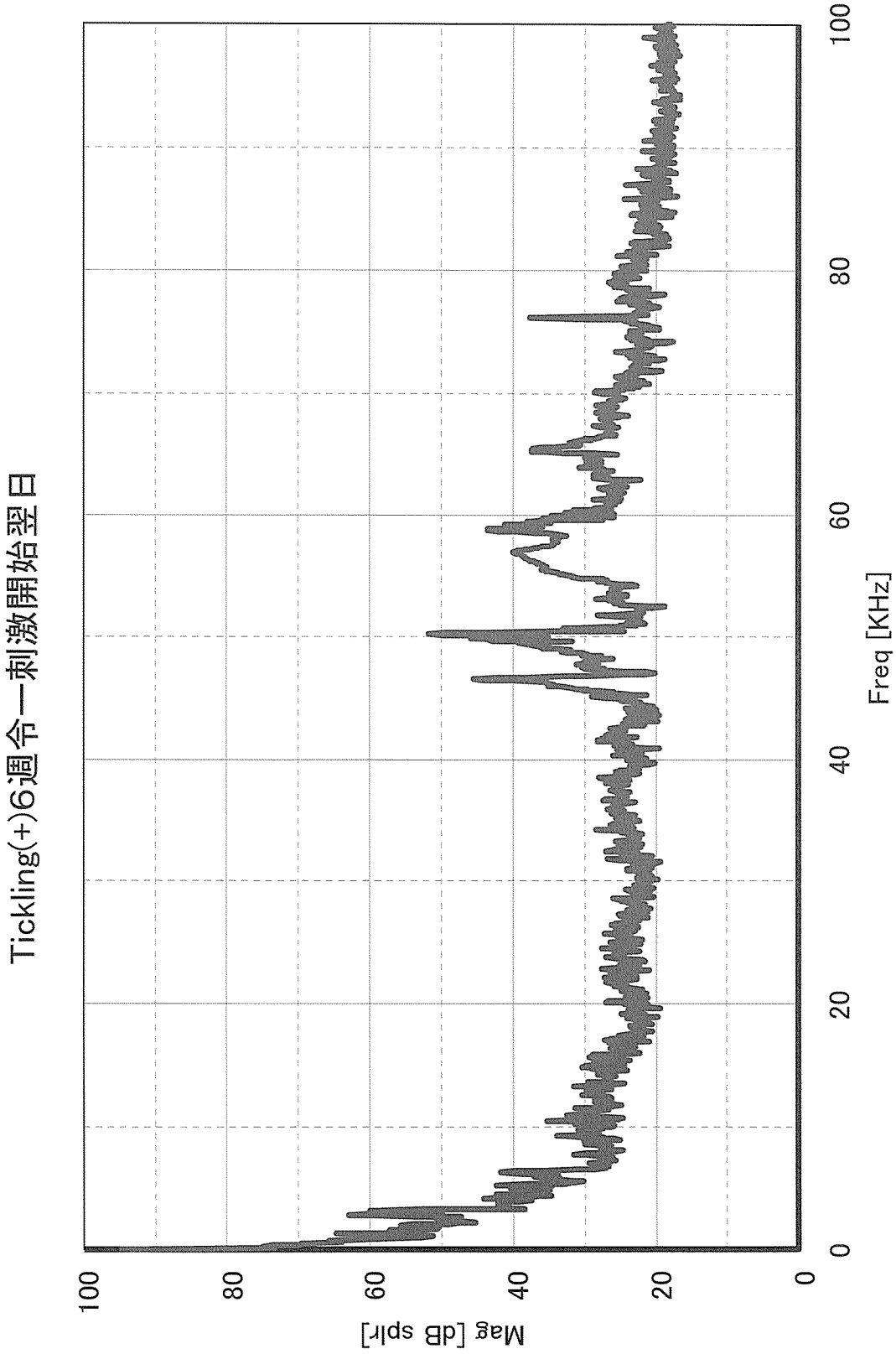


[図72]

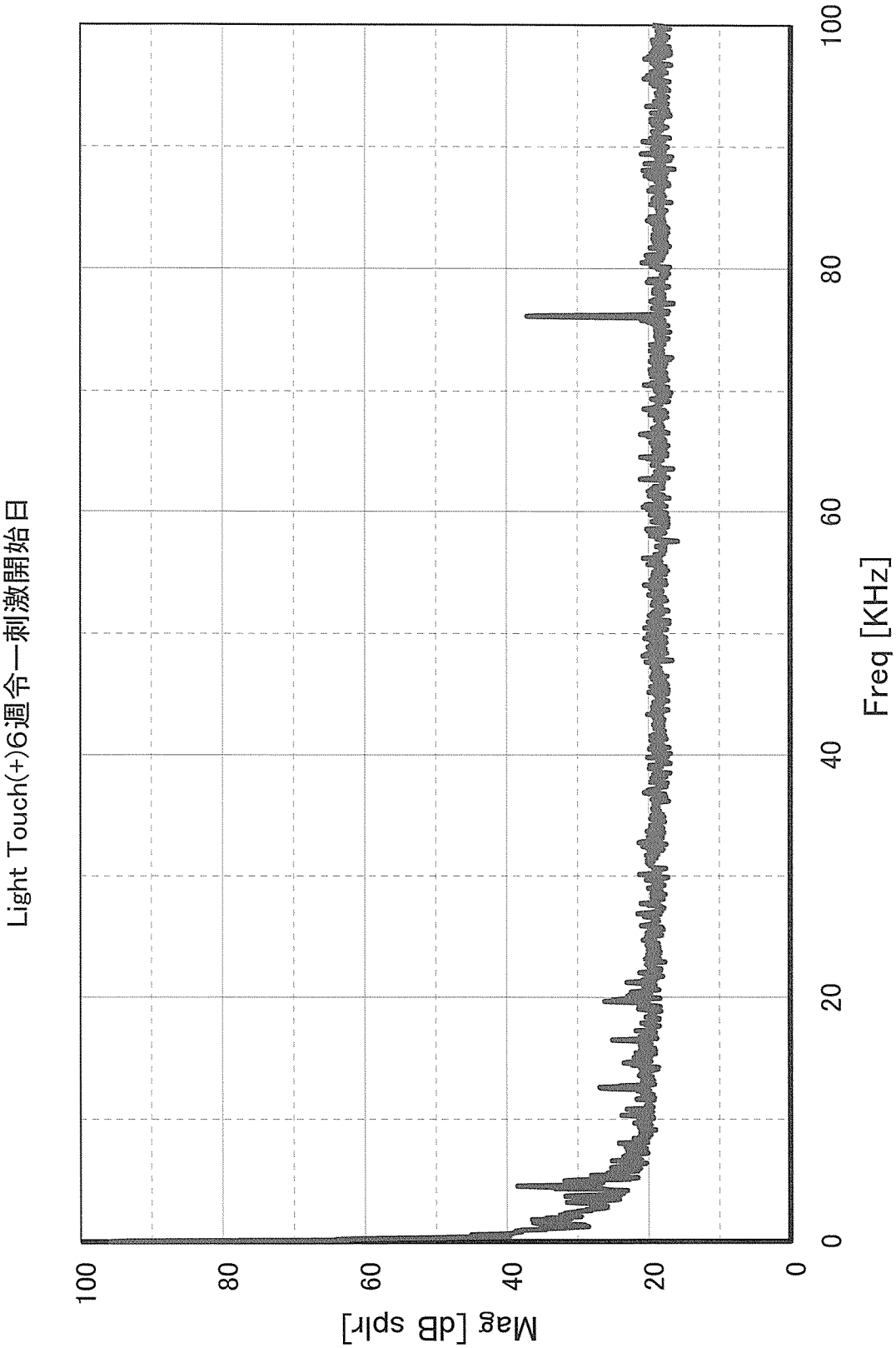
Lに対してTで発現減少した視床下部の遺伝子のGO階層図



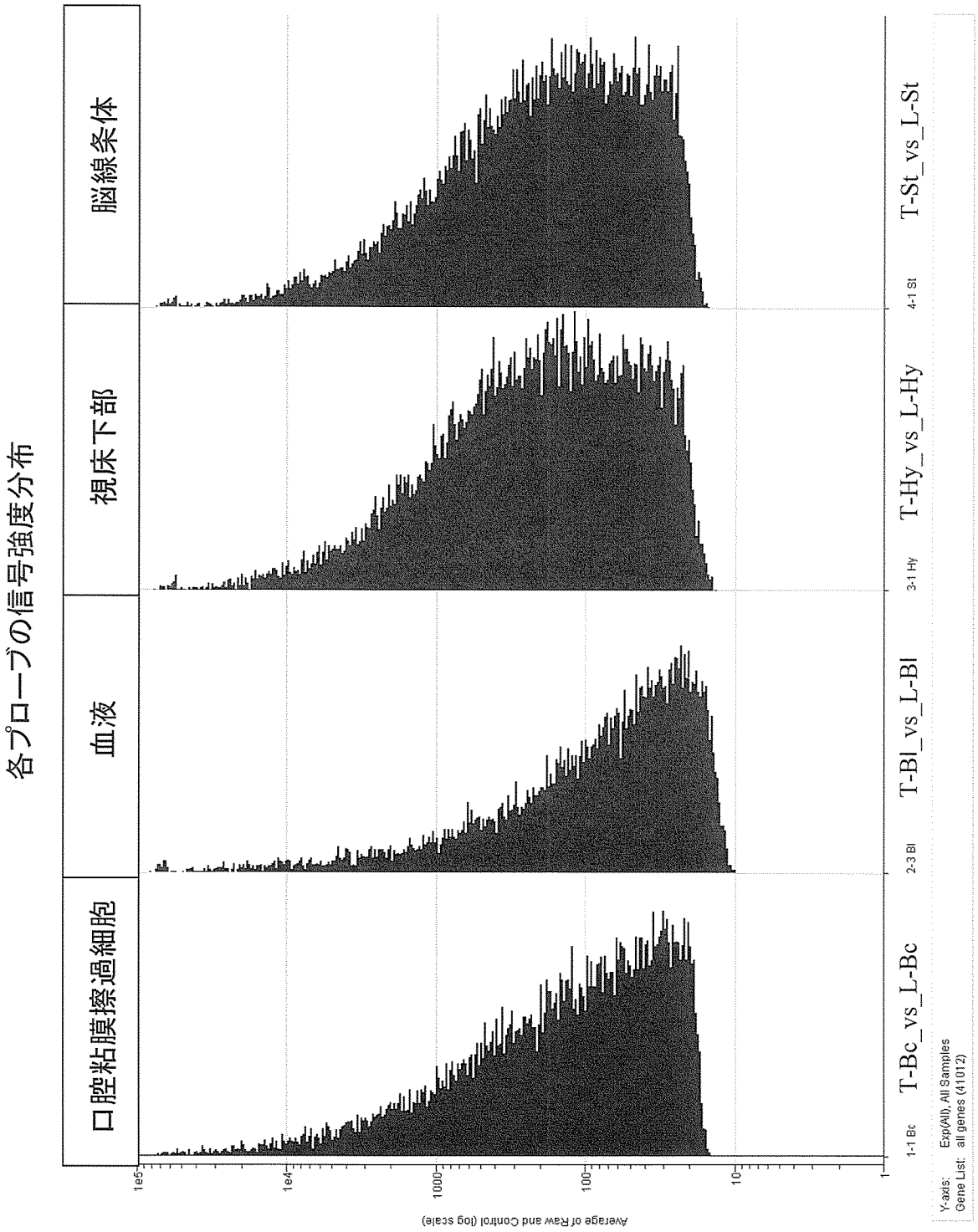
[図73]


Tickling(+)6週令—刺激開始翌日
Mag [dB spir]
100
80
60
40
20
0
0
20
40
60
80
100
Freq [KHz]

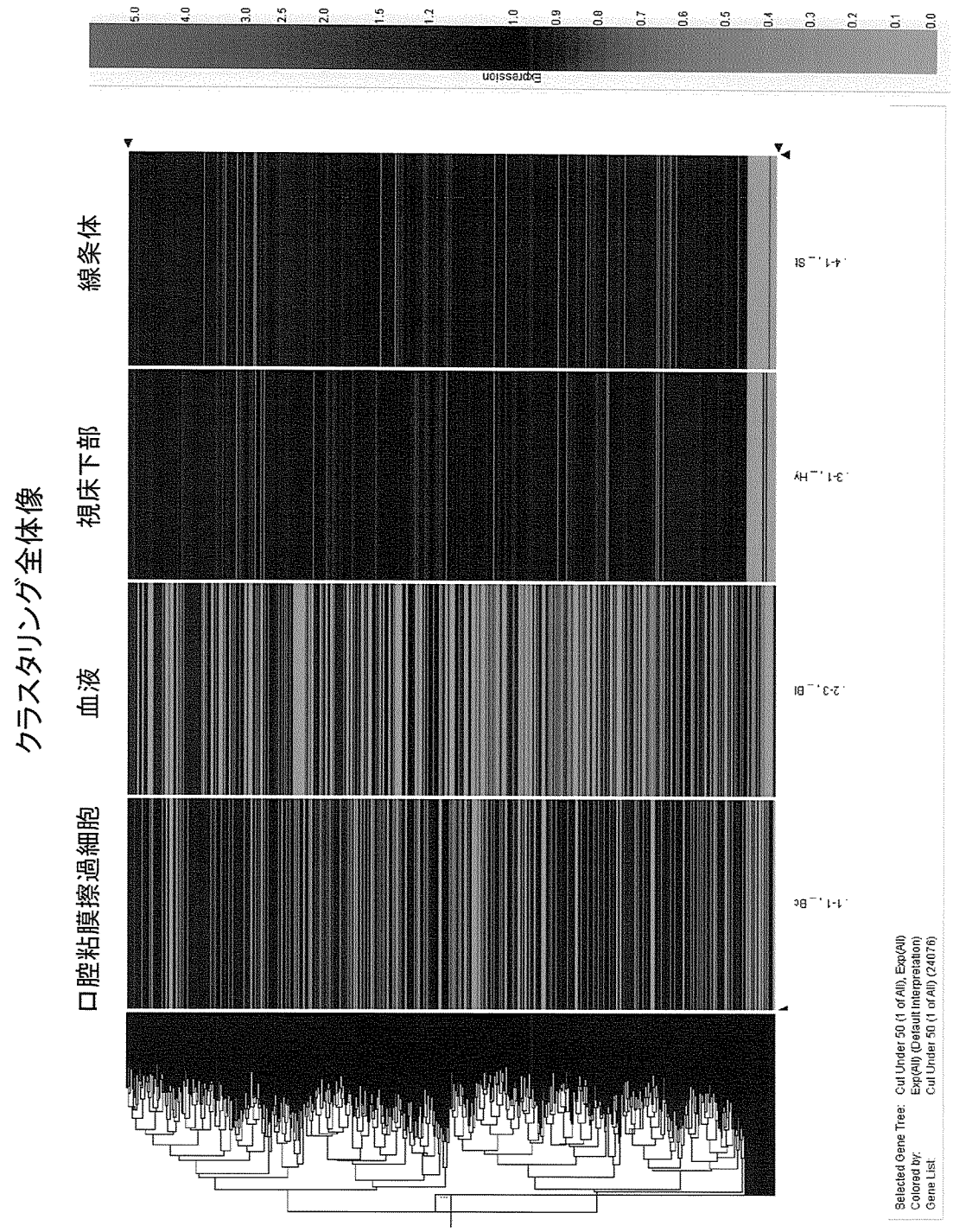
[図74]


Light Touch(+)6週令—刺激開始日
Mag [dB spir]
Freq [KHz]
0
20
40
60
80
100
0
20
40
60
80
100

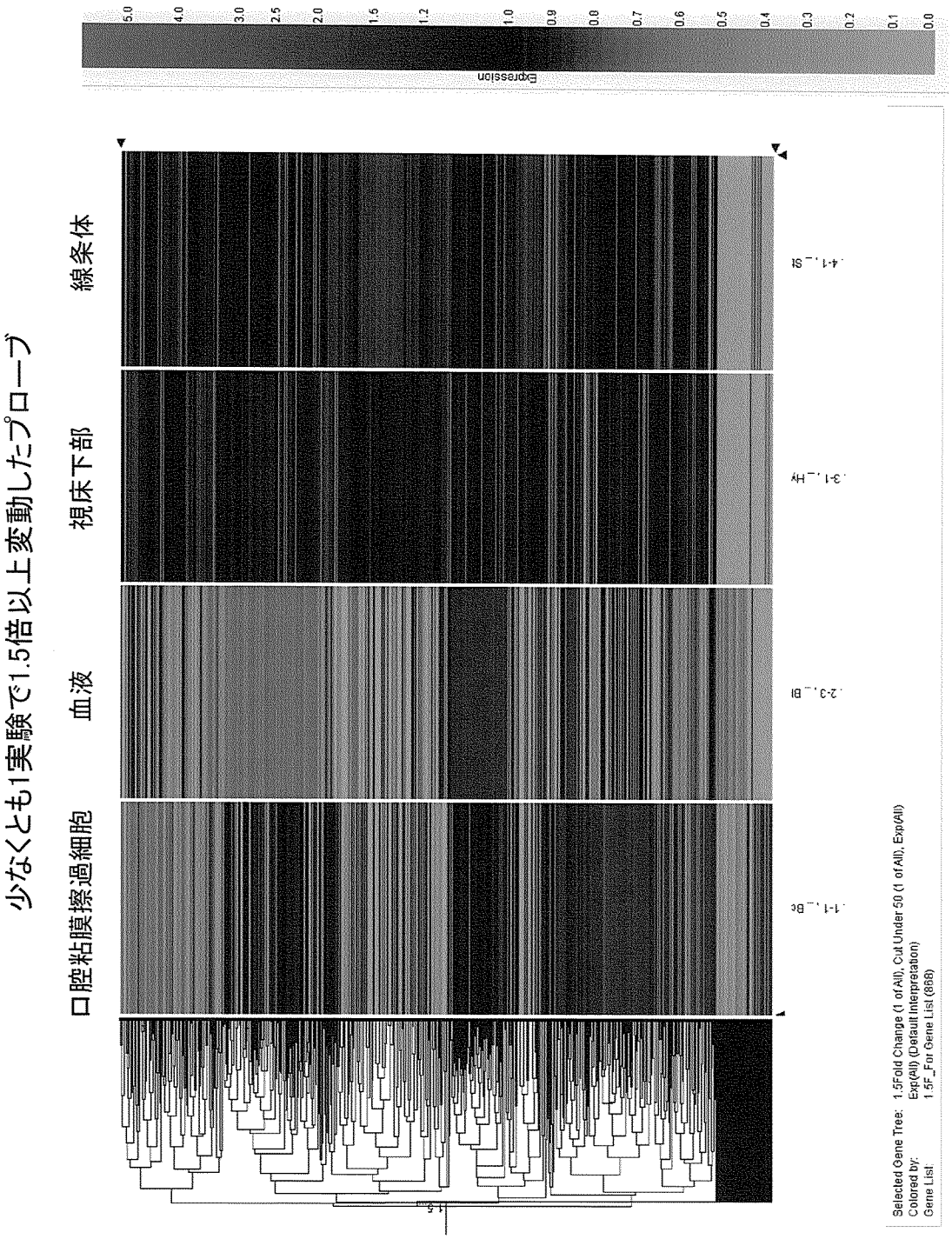
[図75]


各プローブの信号強度分布
口腔粘膜擦過細胞
血液
視床下部
脳線条体
Average of Raw and Control (log scale)
1e5
1e4
1000
100
10
1
1-1 Bc
T-Bc_vs_L-Bc
2-3 Bl
T-Bl_vs_L-Bl
3-1 Hy
T-Hy_vs_L-Hy
4-1 St
T-St_vs_L-St
Y-axis: Exp(All), All Samples
Gene List: all genes (41012)

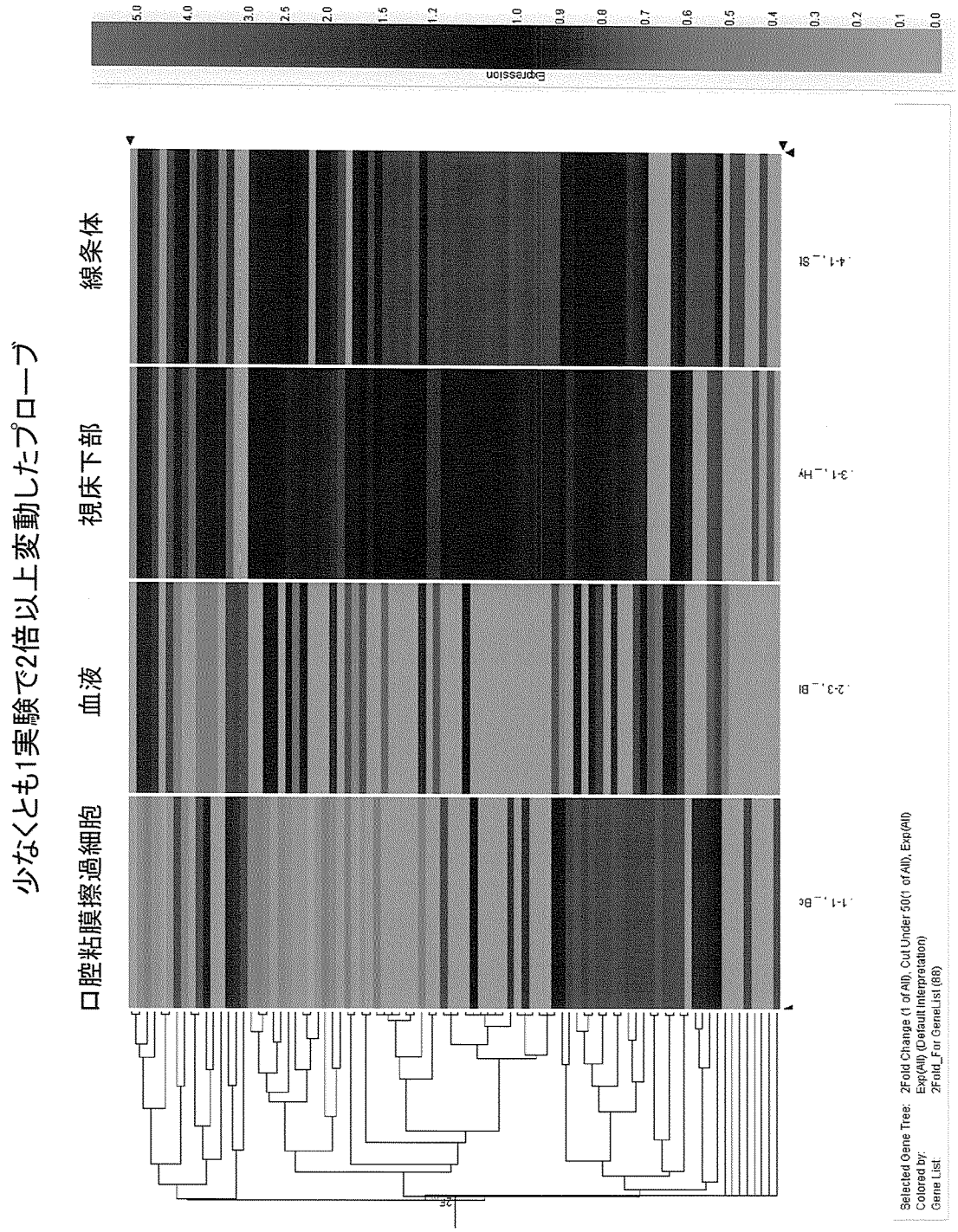
[図76]


クラスタリング全体像
口腔粘膜擦過細胞
血液
視床下部
線条体
Expression
5.0
4.0
3.0
2.5
2.0
1.5
1.2
1.0
0.9
0.8
0.7
0.6
0.5
0.4
0.3
0.2
0.1
0.0
1-1_Bc
2-3_Bl
3-1_Hy
4-1_St
Selected Gene Tree: Cut Under 50 (1 of All), Exp(All)
Colored by: Exp(All) (Default Interpretation)
Gene List: Cut Under 50 (1 of All) (24076)

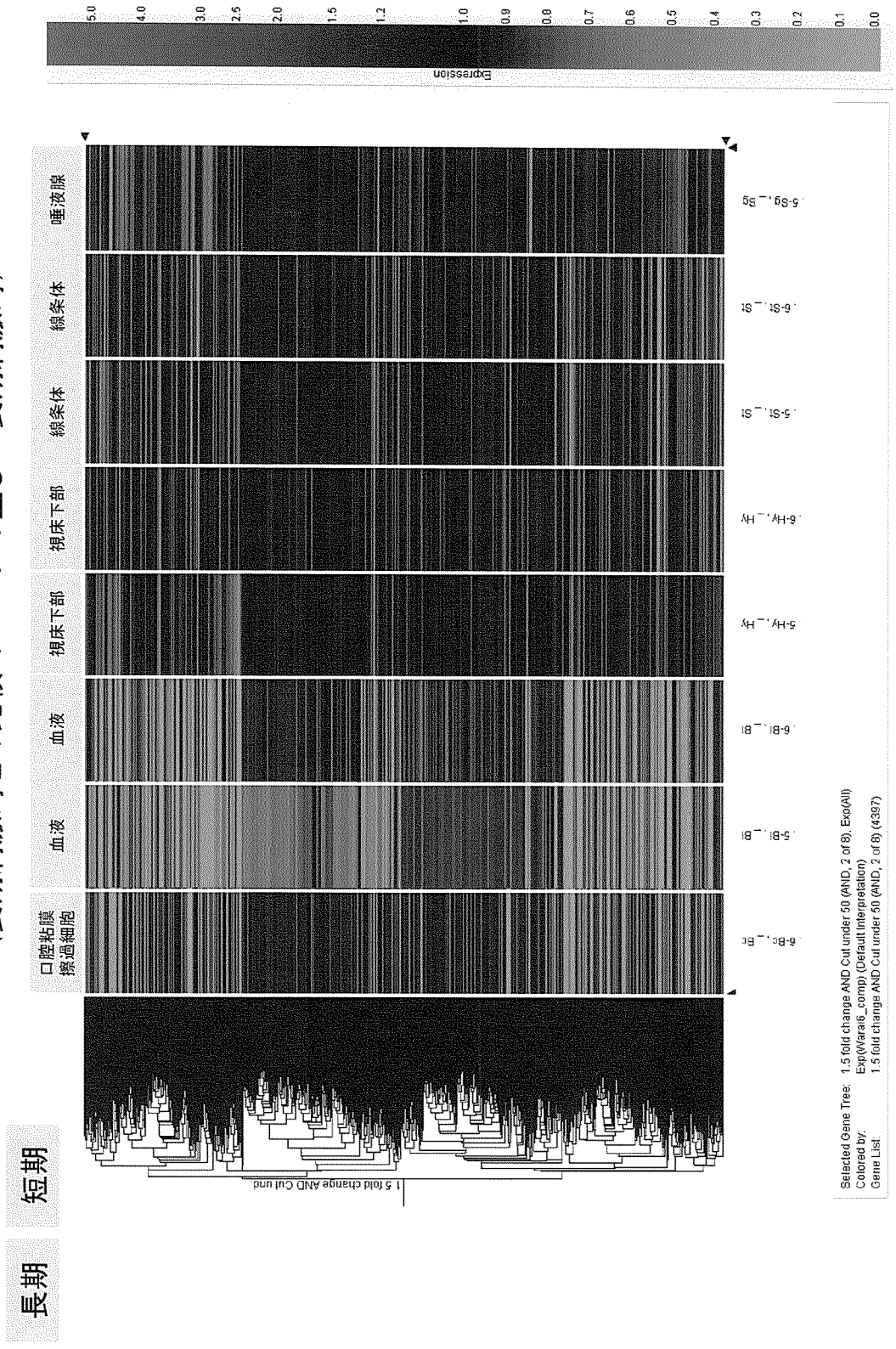
[図77]


少なくとも1実験で1.5倍以上変動したプローブ
口腔粘膜擦過細胞
血液
視床下部
線条体
Expression
5.0
4.0
3.0
2.5
2.0
1.5
1.2
1.0
0.9
0.8
0.7
0.6
0.5
0.4
0.3
0.2
0.1
0.0
1-1_Bc
2-3_Bl
3-1_Hy
4-1_St
Selected Gene Tree: 1.5Fold Change (1 of All), Cut Under 50 (1 of All), Exp(All)
Colored by: Exp(All) (Default Interpretation)
Gene List: 1.5F_For Gene List (868)

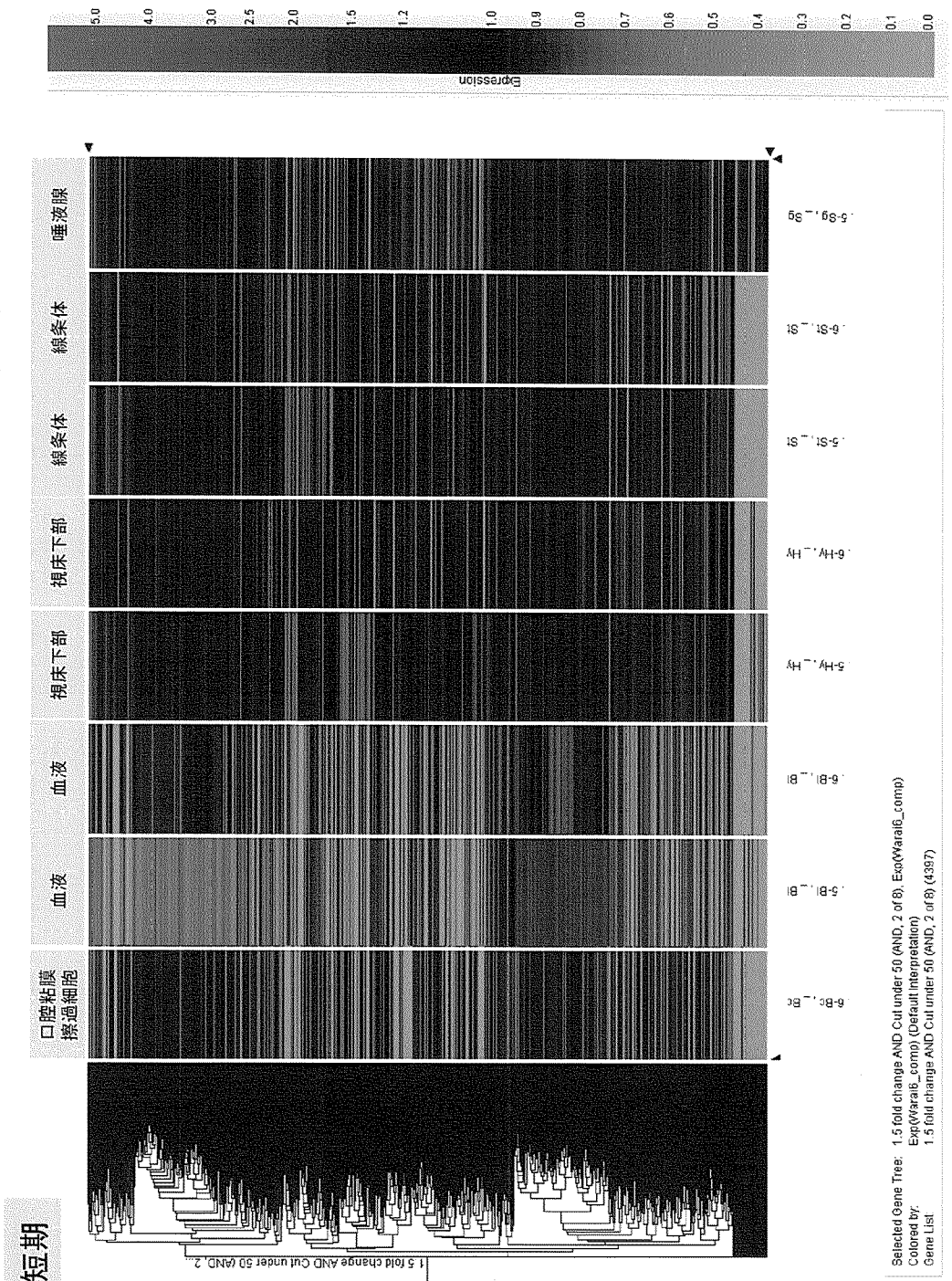
[図78]


少なくとも1実験で2倍以上変動したプローブ
口腔粘膜擦過細胞
血液
視床下部
線条体
Expression
5.0
4.0
3.0
2.5
2.0
1.5
1.2
1.0
0.9
0.8
0.7
0.6
0.5
0.4
0.3
0.2
0.1
0.0
Selected Gene Tree: 2Fold Change (1 of All), Cut Under 50(1 of All), Exp(All)
Colored by: Exp(All) (Default Interpretation)
Gene List: 2Fold_For GeneList (86)

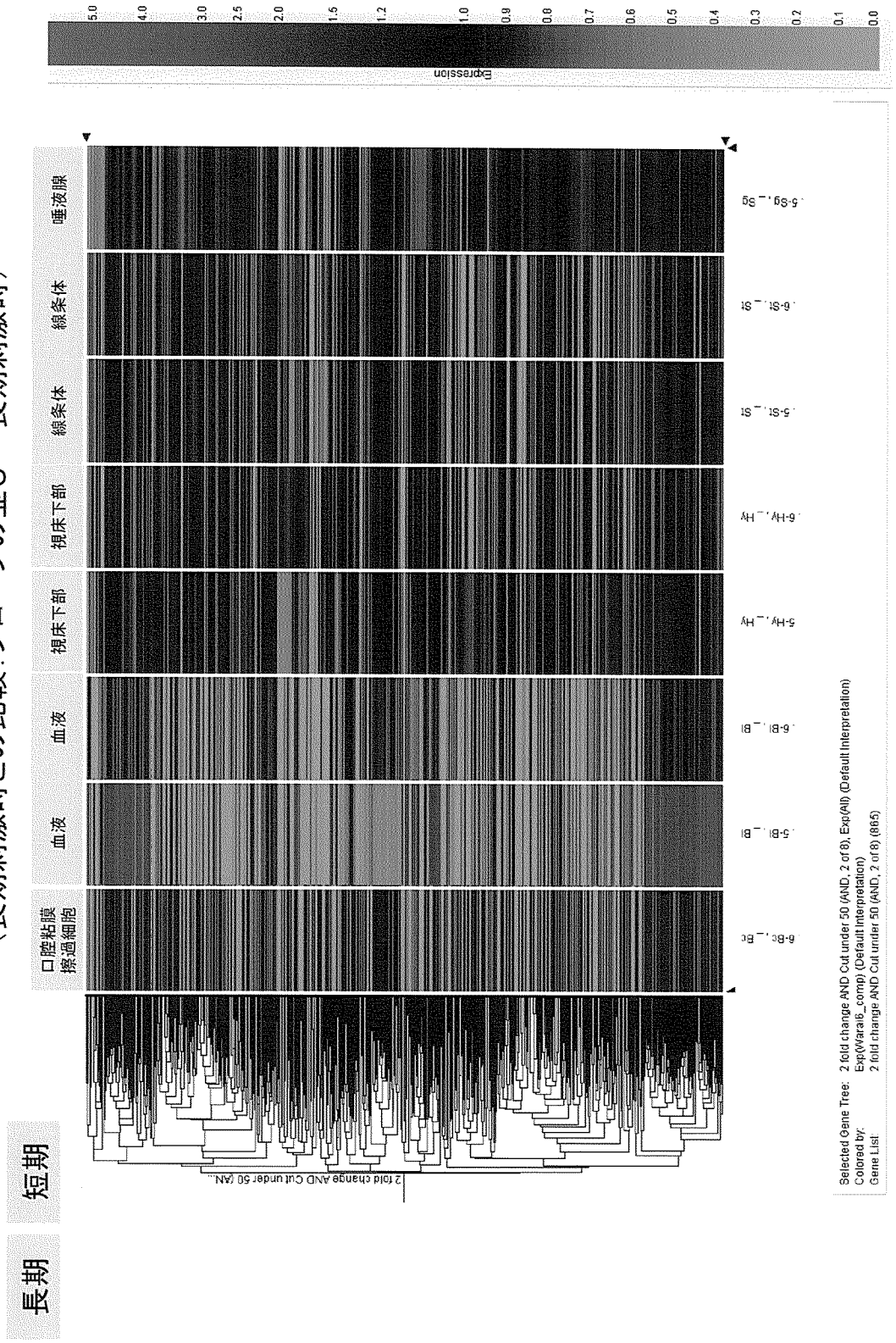
[図79]


少なくとも1実験で1.5倍以上変動したプローブ
（長期刺激時との比較：プローブの並び＝長期刺激時）
長期
短期
口腔粘膜擦過細胞
血液
血液
視床下部
視床下部
線条体
線条体
唾液腺
Expression
5.0
4.0
3.0
2.5
2.0
1.5
1.2
1.0
0.9
0.8
0.7
0.6
0.5
0.4
0.3
0.2
0.1
0.0
1.5 fold change AND Cut und
Selected Gene Tree: 1.5 fold change AND Cut under 50 (AND, 2 of 8), Exp(All)
Colored by: Exp(Warai6_comp) (Default Interpretation)
Gene List: 1.5 fold change AND Cut under 50 (AND, 2 of 8) (4397)

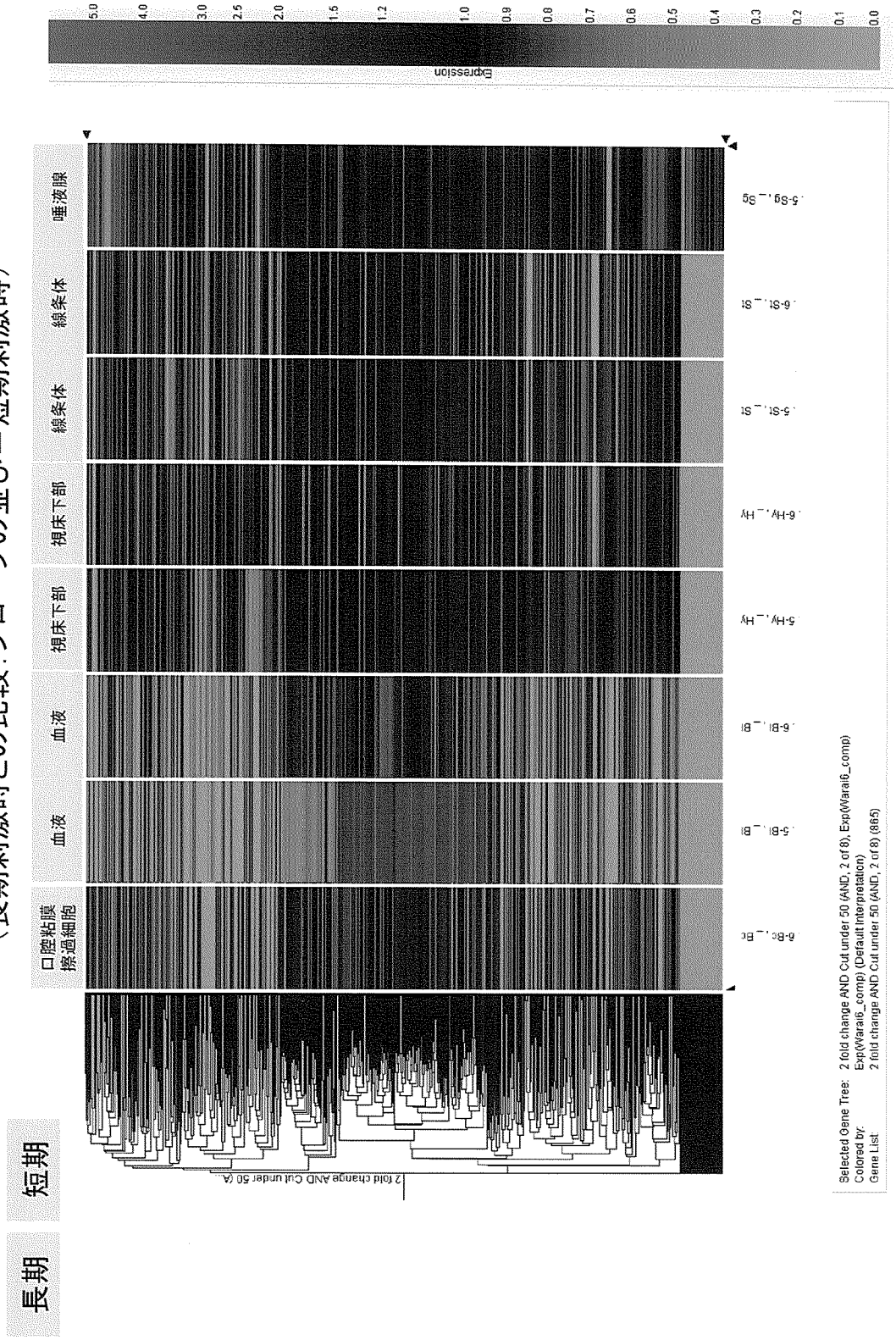
[図80]


少なくとも1実験で1.5倍以上変動したプローブ
（長期刺激時との比較：プローブの並び＝短期刺激時）
長期
短期
口腔粘膜擦過細胞
血液
血液
血液
視床下部
視床下部
視床下部
線条体
線条体
線条体
唾液腺
Expression
5.0
4.0
3.0
2.5
2.0
1.5
1.2
1.0
0.9
0.8
0.7
0.6
0.5
0.4
0.3
0.2
0.1
0.0
1.5 fold change AND Cut under 50 (AND, 2...
Selected Gene Tree: 1.5 fold change AND Cut under 50 (AND, 2 of 8), Exp(WaraI6_comp)
Colored by: Exp(WaraI6_comp) (Default interpretation)
Gene List 1.5 fold change AND Cut under 50 (AND, 2 of 8) (4397)

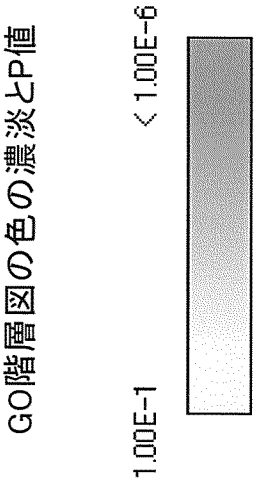
[図81]


少なくとも1実験で2倍以上変動したプローブ
（長期刺激時との比較：プローブの並び＝長期刺激時）
長期
短期
口腔粘膜擦過細胞
血液
血液
血液
視床下部
視床下部
線条体
線条体
線条体
唾液腺
Expression
5.0
4.0
3.0
2.5
2.0
1.5
1.2
1.0
0.9
0.8
0.7
0.6
0.5
0.4
0.3
0.2
0.1
0.0
2 fold change AND Cut under 50 (AN
6-Bc_Bc
5-Bl_Bl
6-Bl_Bl
5-Hy_Hy
6-Hy_Hy
5-St_St
6-St_St
5-Sg_Sg
Selected Gene Tree: 2 fold change AND Cut under 50 (AND, 2 of 8), Exp(All) (Default Interpretation)
Colored by: Exp(Wararib_comp) (Default Interpretation)
Gene List: 2 fold change AND Cut under 50 (AND, 2 of 8) (865)

[図82]

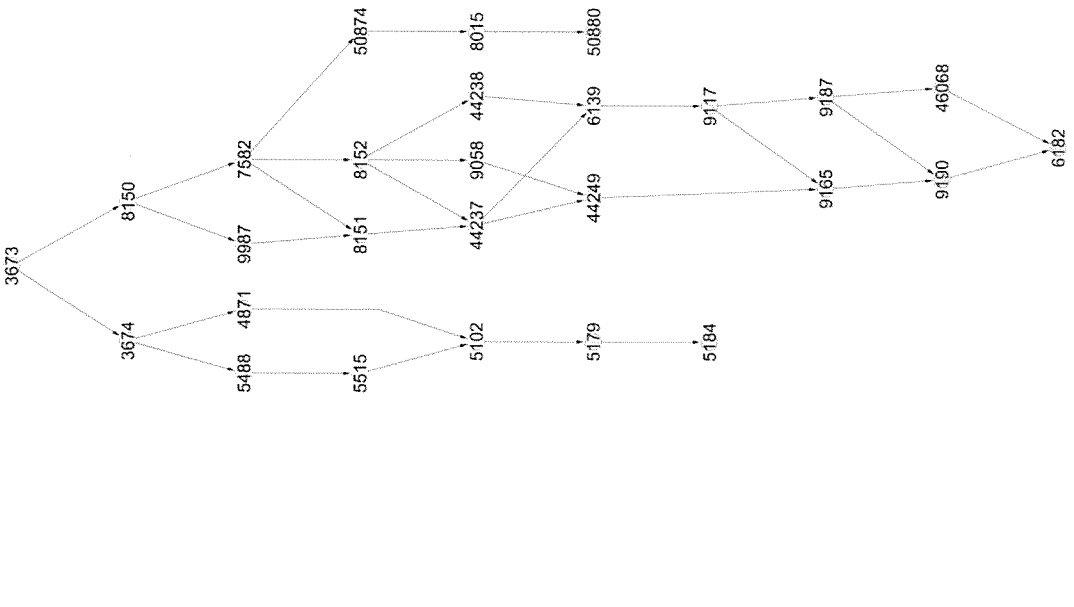

少なくとも1実験で2倍以上変動したプローブ
（長期刺激時とのの比較：プローブの並び＝短期刺激時）
長期
短期
口腔粘膜擦過細胞
血液
血液
血液
視床下部
視床下部
線条体
線条体
線条体
唾液腺
Expression
5.0
4.0
3.0
2.5
2.0
1.5
1.2
1.0
0.9
0.8
0.7
0.6
0.5
0.4
0.3
0.2
0.1
0.0
2 fold change AND Cut under 50 (A
Selected Gene Tree: 2 fold change AND Cut under 50 (AND, 2 of 8), Exp(Warai6_comp)
Colored by: Exp(Warai6_comp) (Default Interpretation)
Gene List 2 fold change AND Cut under 50 (AND, 2 of 8) (865)

[図83]



[図84]

脳と擦過細胞で共通して発現増加した遺伝子のGO階層図



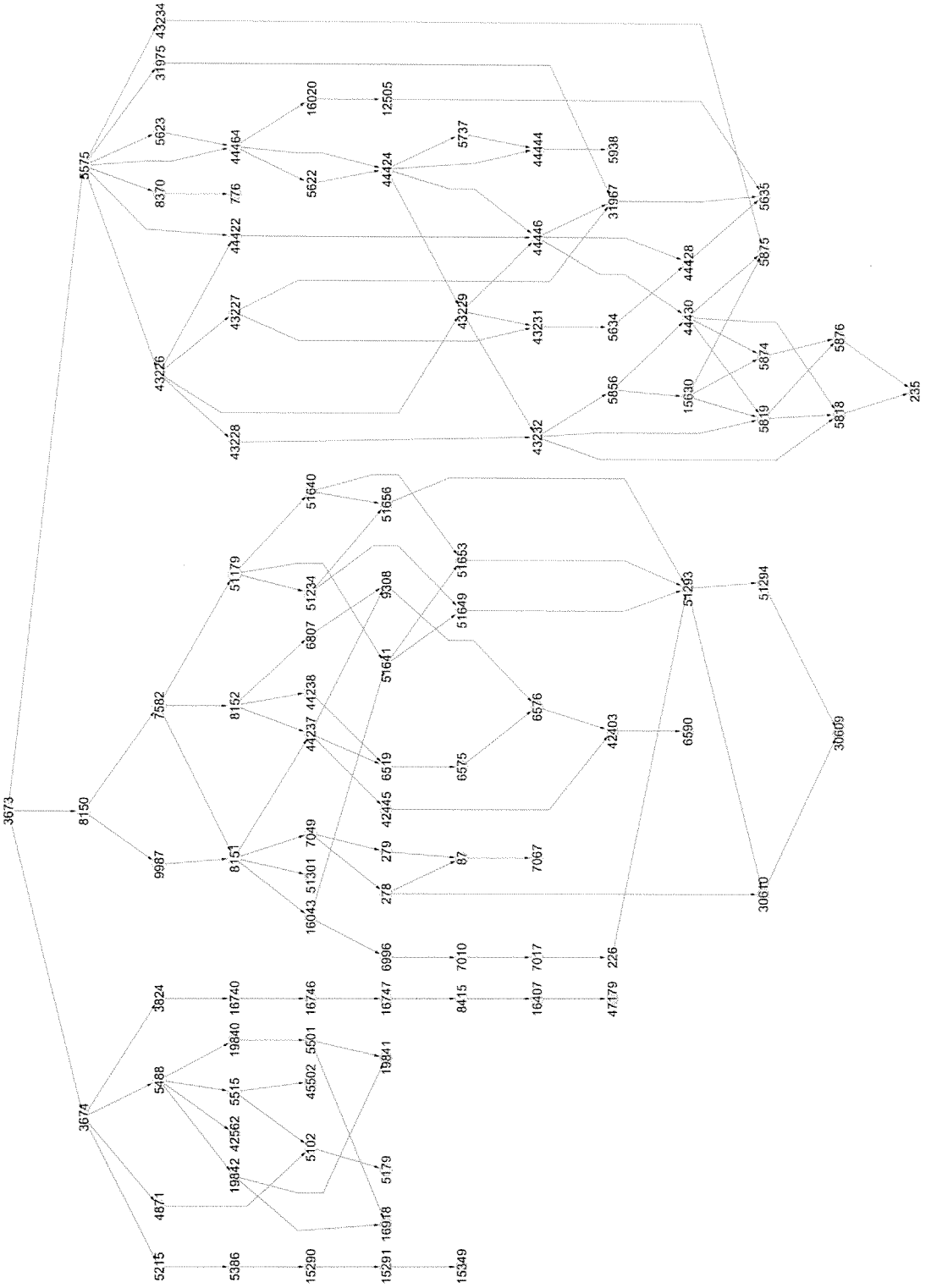
[図85]

視床下部で発現増加した遺伝子のGO階層図



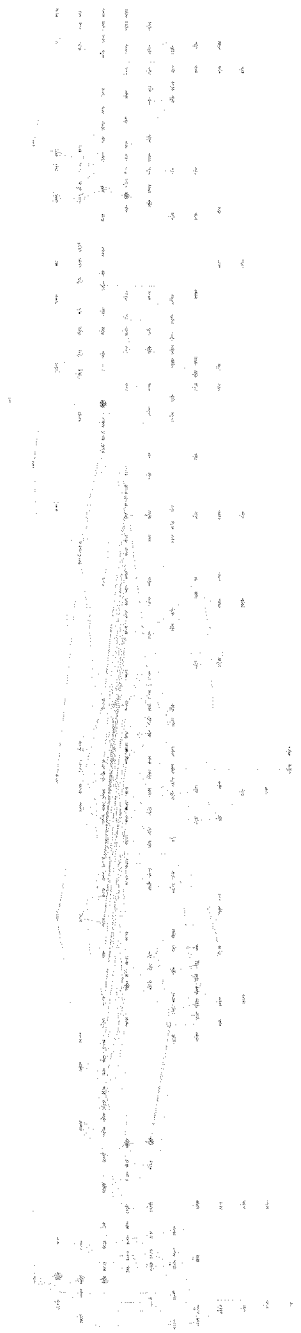
[図86]

視床下部で発現減少した遺伝子のGO階層図



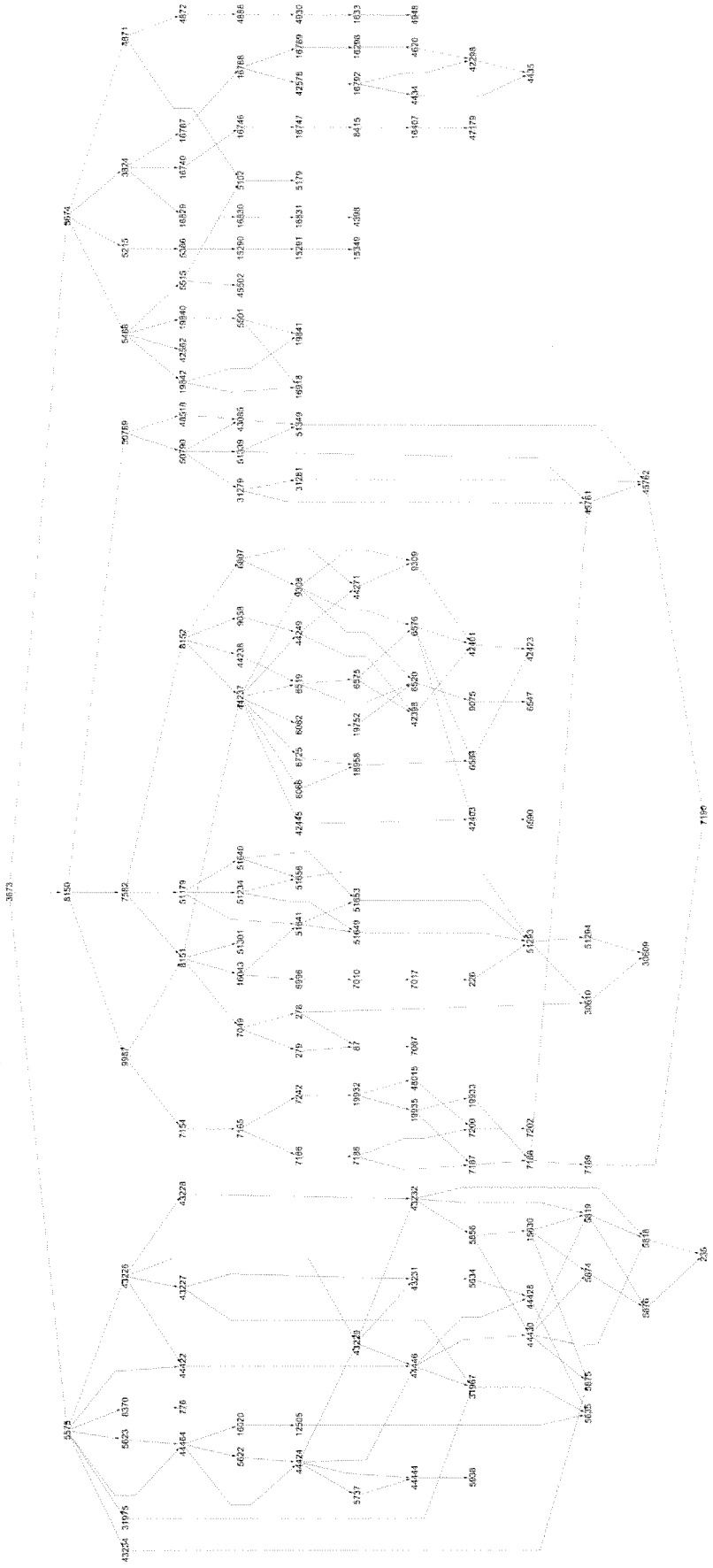
[図87]

線条体で発現増加した遺伝子のGO階層図

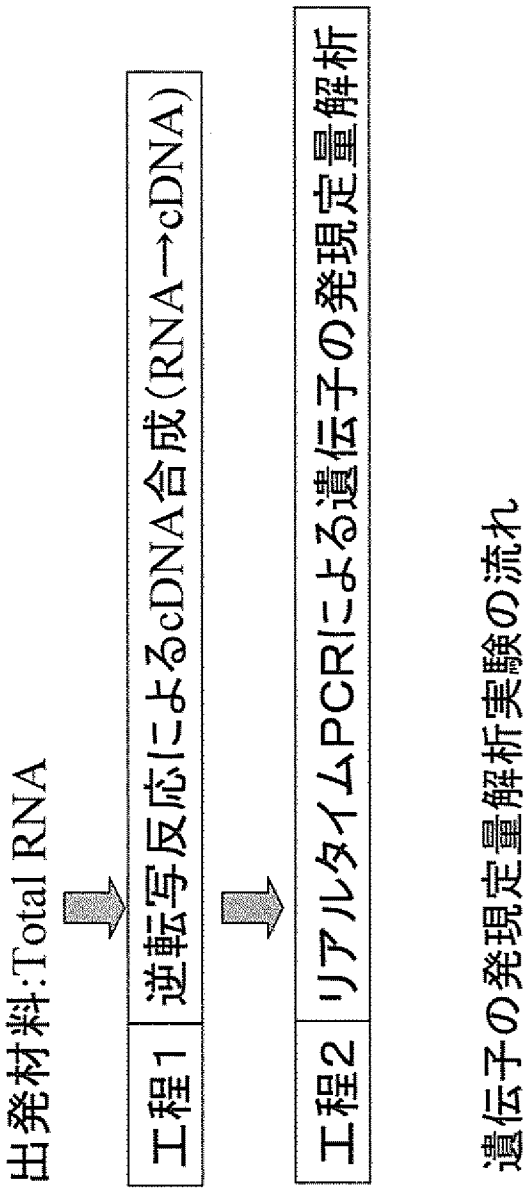


[図88]

線条体で発現減少した遺伝子のGO階層図



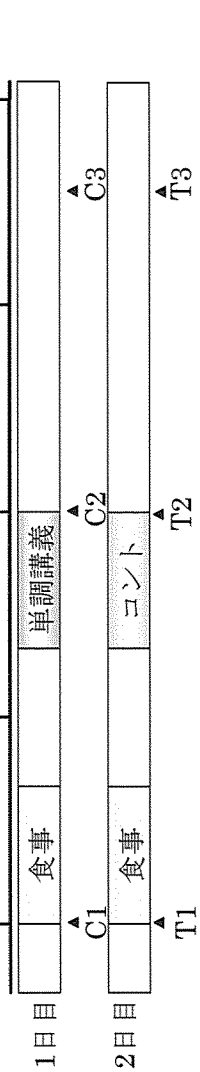
[図89]



遺伝子の発現定量解析実験の流れ

[図90]

図90：実験時程図

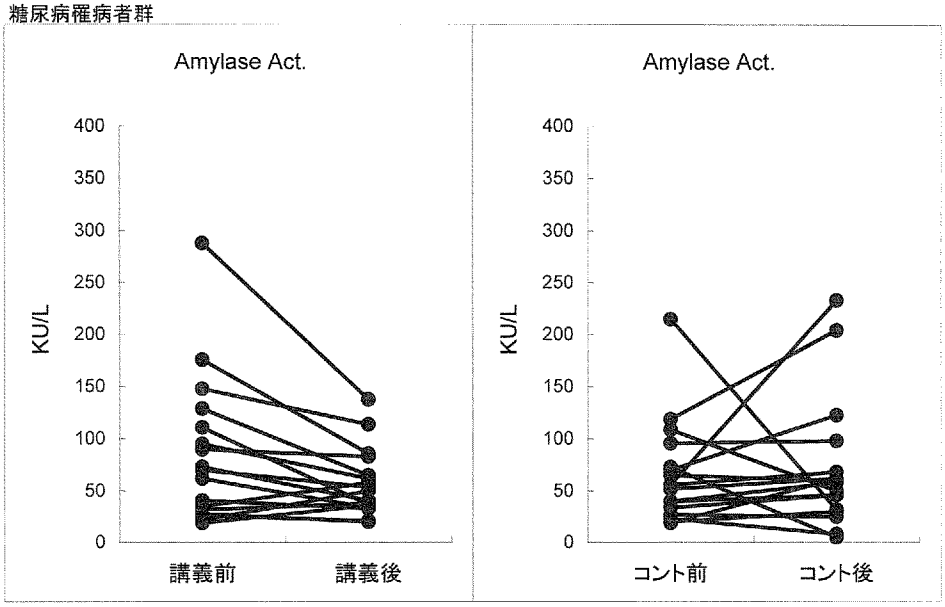


食事：500Kcal
単調講義：大学教官による講義（筑波大学）
コント：ゆーとぴあ（エポカルつくば）
C1～T3：サンプリング時点を示す

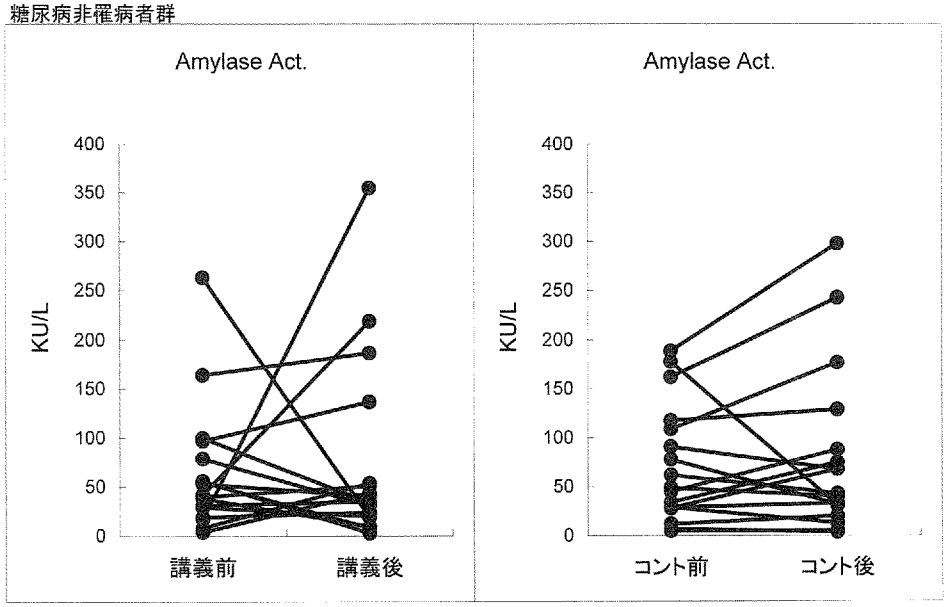
[図91]

図91 唾液中アミラーゼ活性
（糖尿病罹病者群、糖尿病非罹病者群）

糖尿病罹病者群



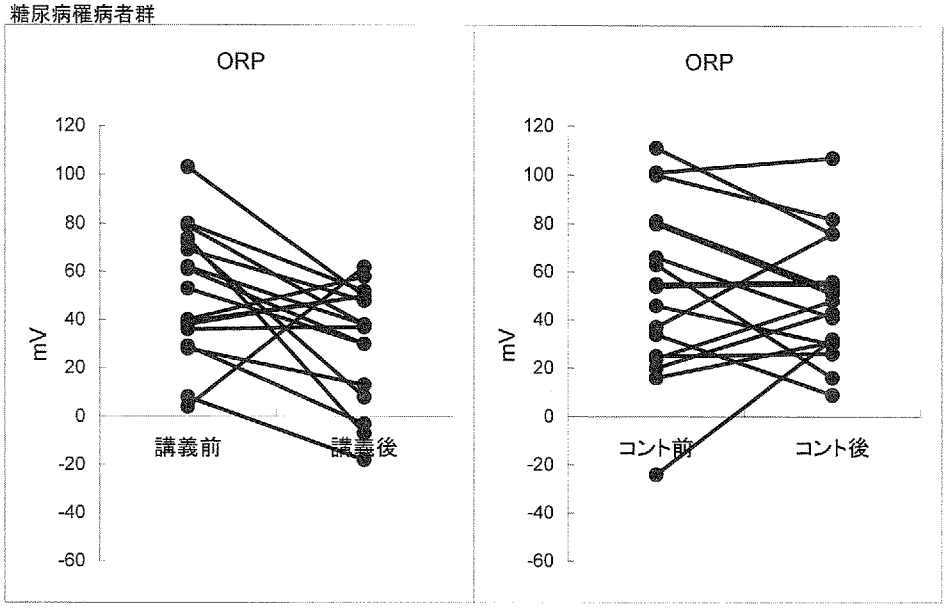
糖尿病非罹病者群



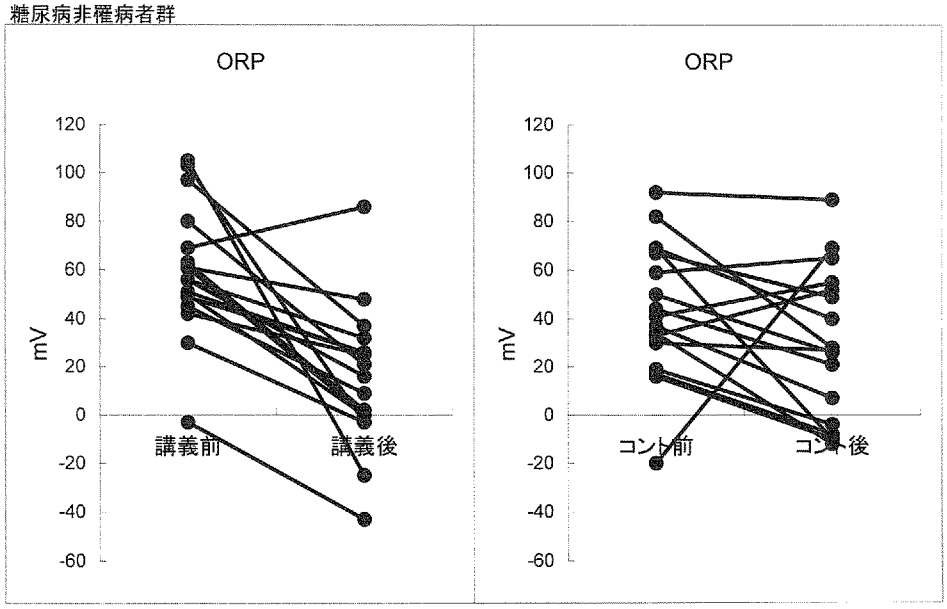
[図92]

図92 唾液中酸化還元電位(ORP)
(糖尿病罹病者群、糖尿病非罹病者群)

糖尿病罹病者群

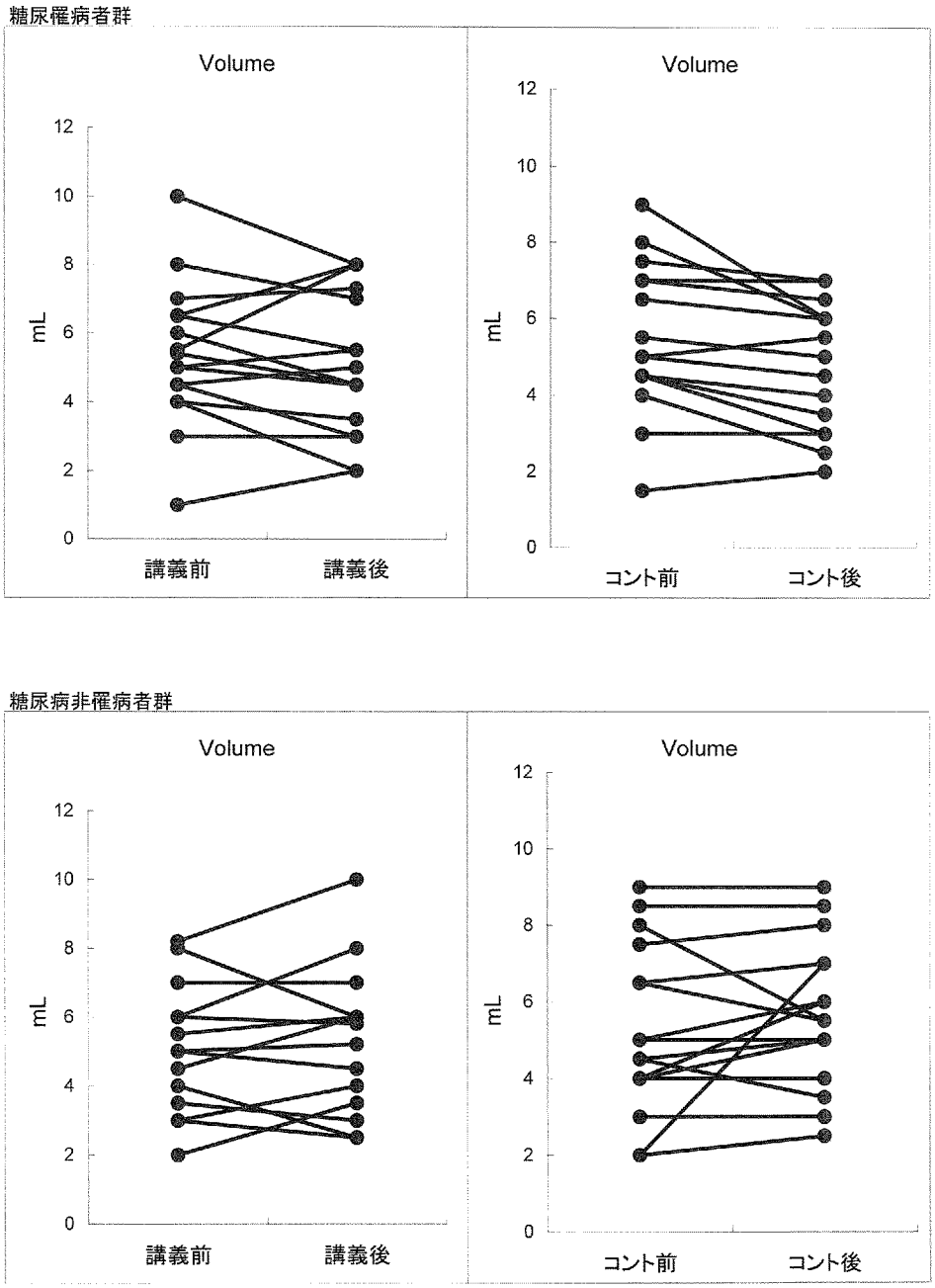


糖尿病非罹病者群



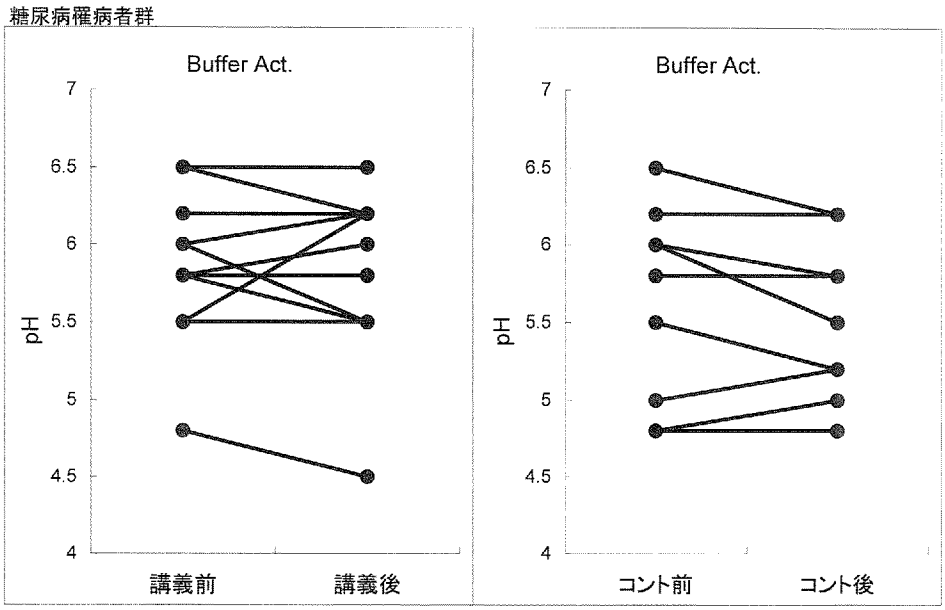
[図93]

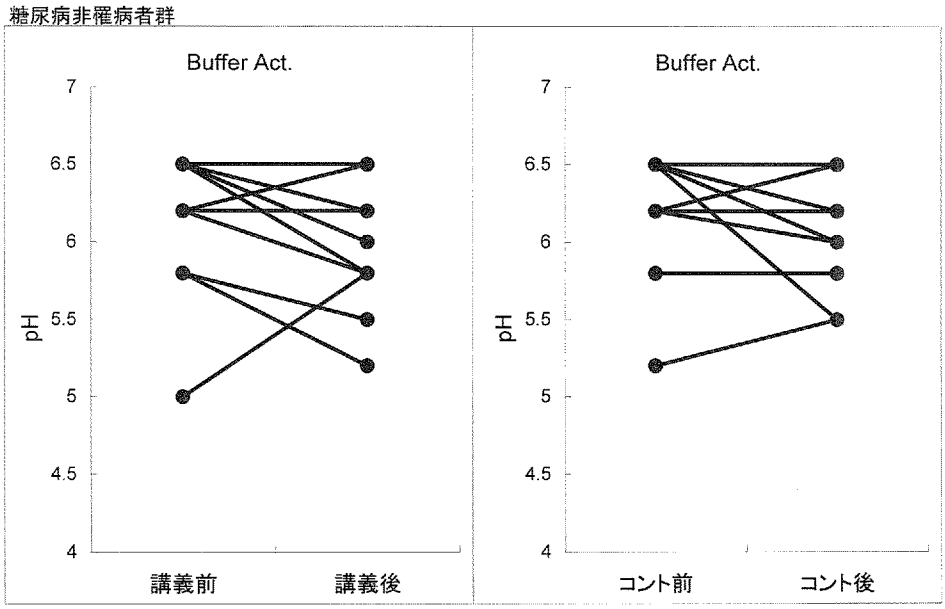
図93 唾液量
(糖尿病罹病者群、糖尿病非罹病者群)



[図94]

図94 唾液緩衝能
（糖尿病罹病者群、糖尿病非罹病者群）

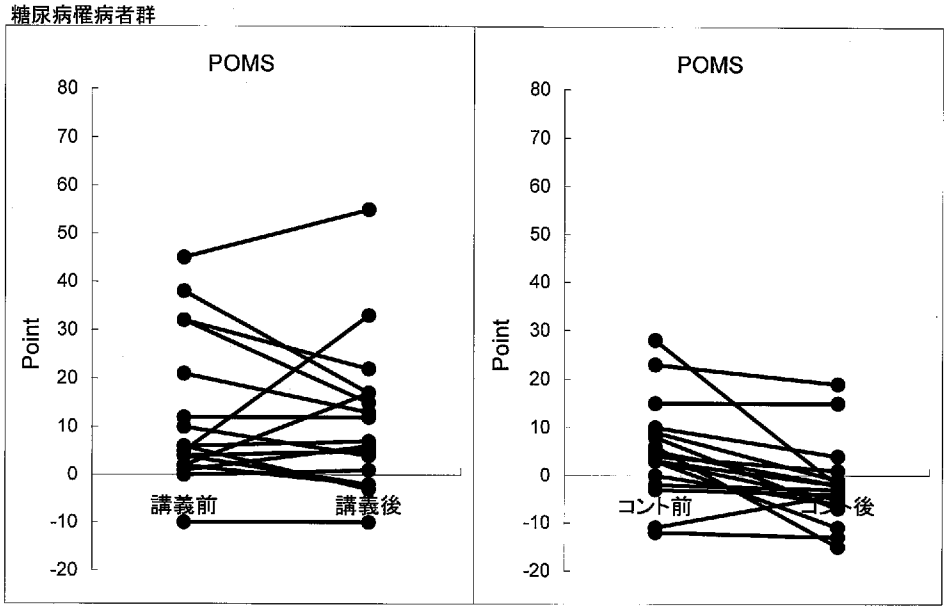




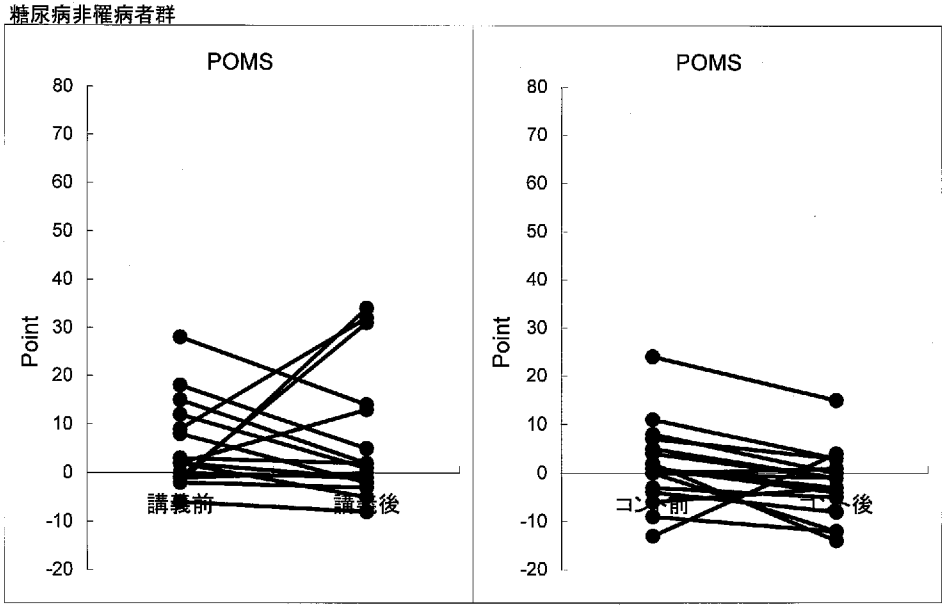
[図95]

図95 総合感情障害度(TMD)
(糖尿病罹病者群、糖尿病非罹病者群)

糖尿病罹病者群



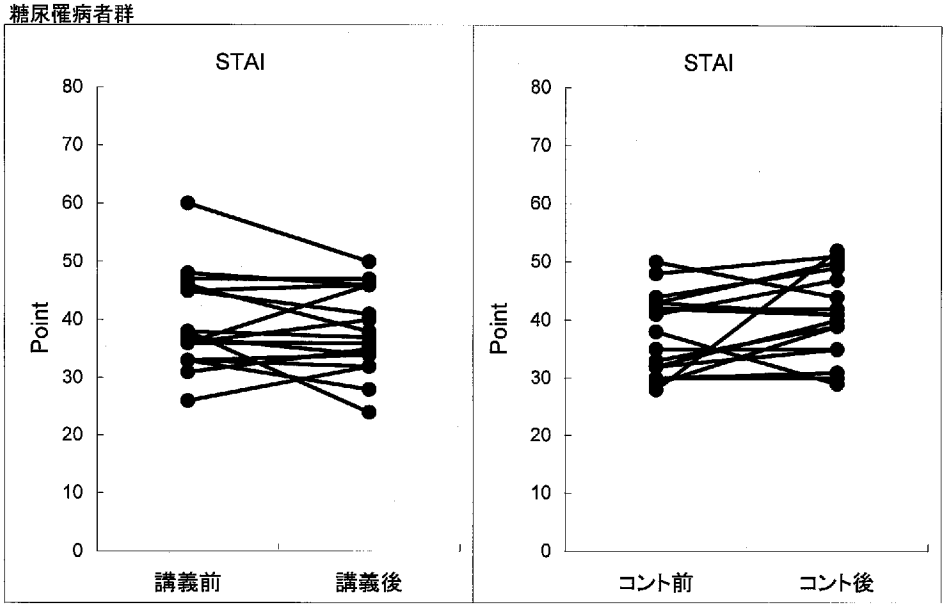
糖尿病非罹病者群



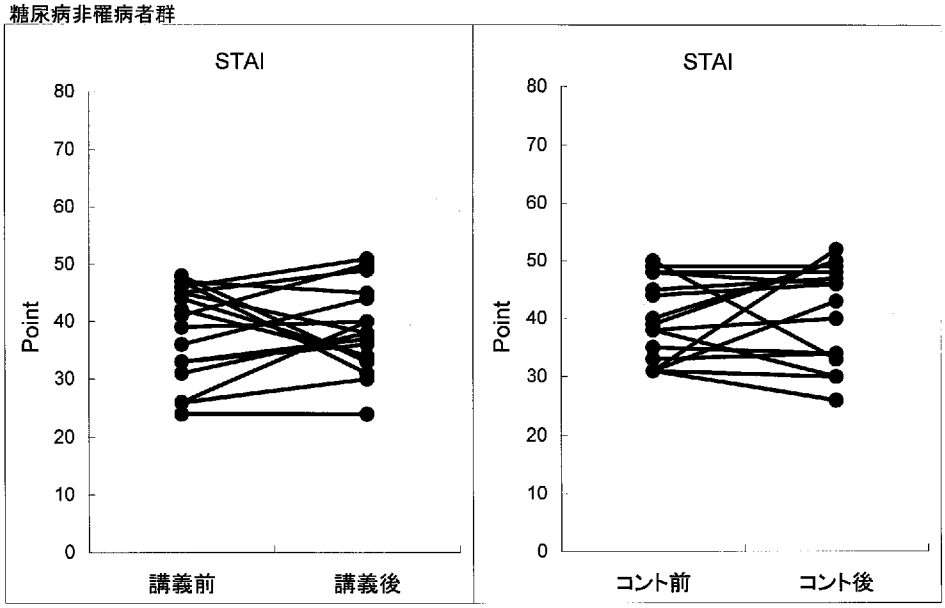
[図96]

図96 不安傾向(STAI)
(糖尿病罹病者群、糖尿病非罹病者群)

糖尿罹病者群



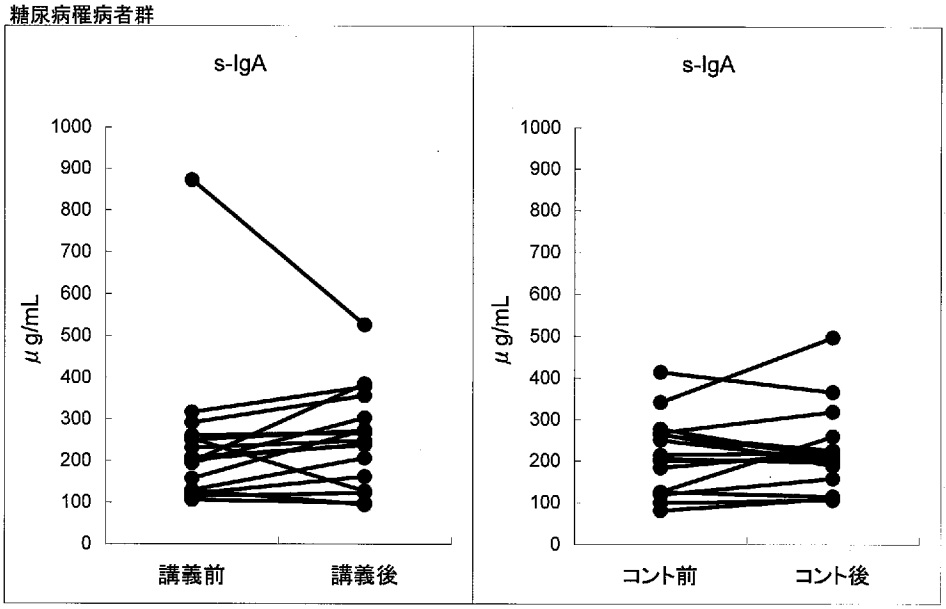
糖尿病非罹病者群



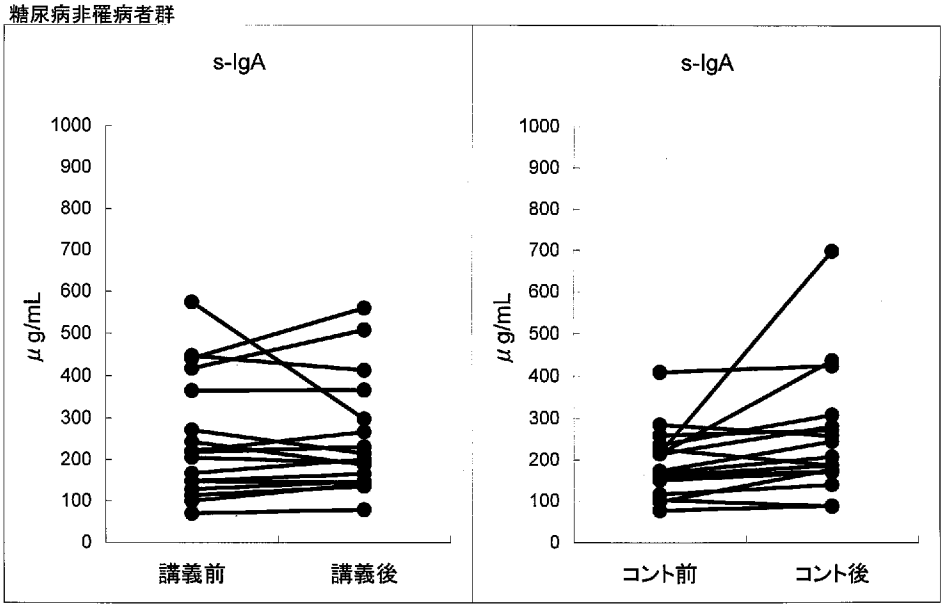
[図97]

図97 唾液中分泌型イムノグロブリン(s-IgA)
(糖尿病罹病者群、糖尿病非罹病者群)

糖尿病罹病者群



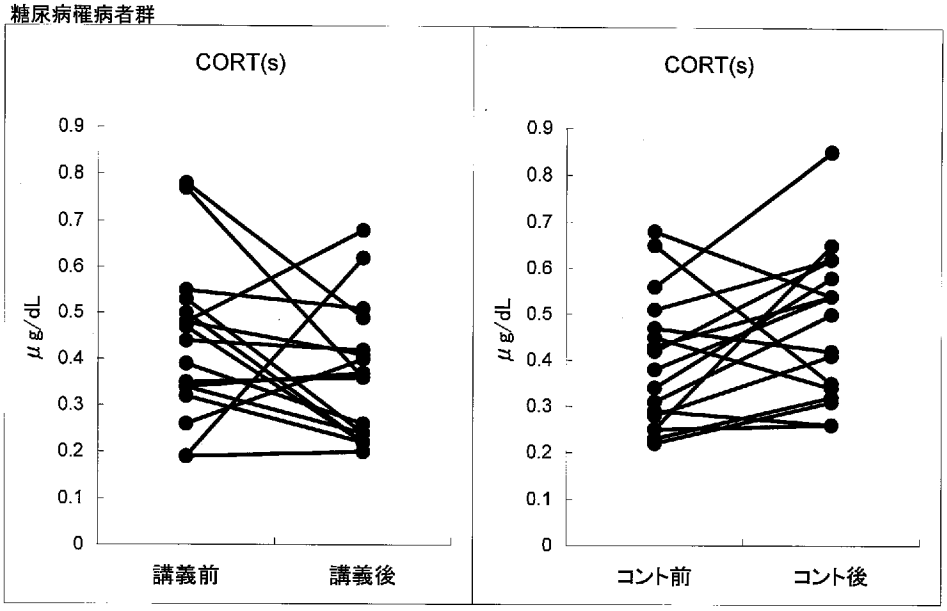
糖尿病非罹病者群



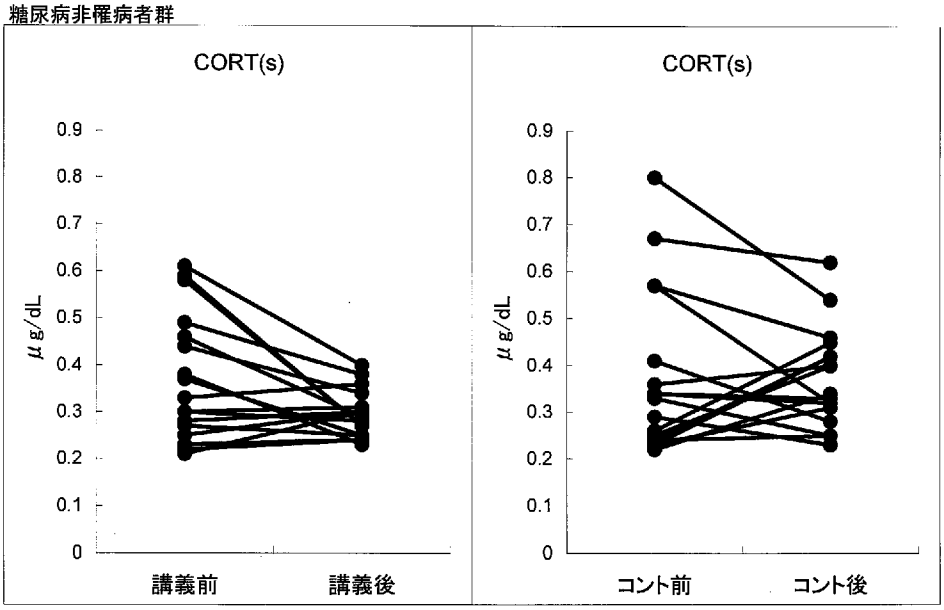
[図98]

図98 唾液中コルチゾール
(糖尿病罹病者群、糖尿病非罹病者群)

糖尿病罹病者群

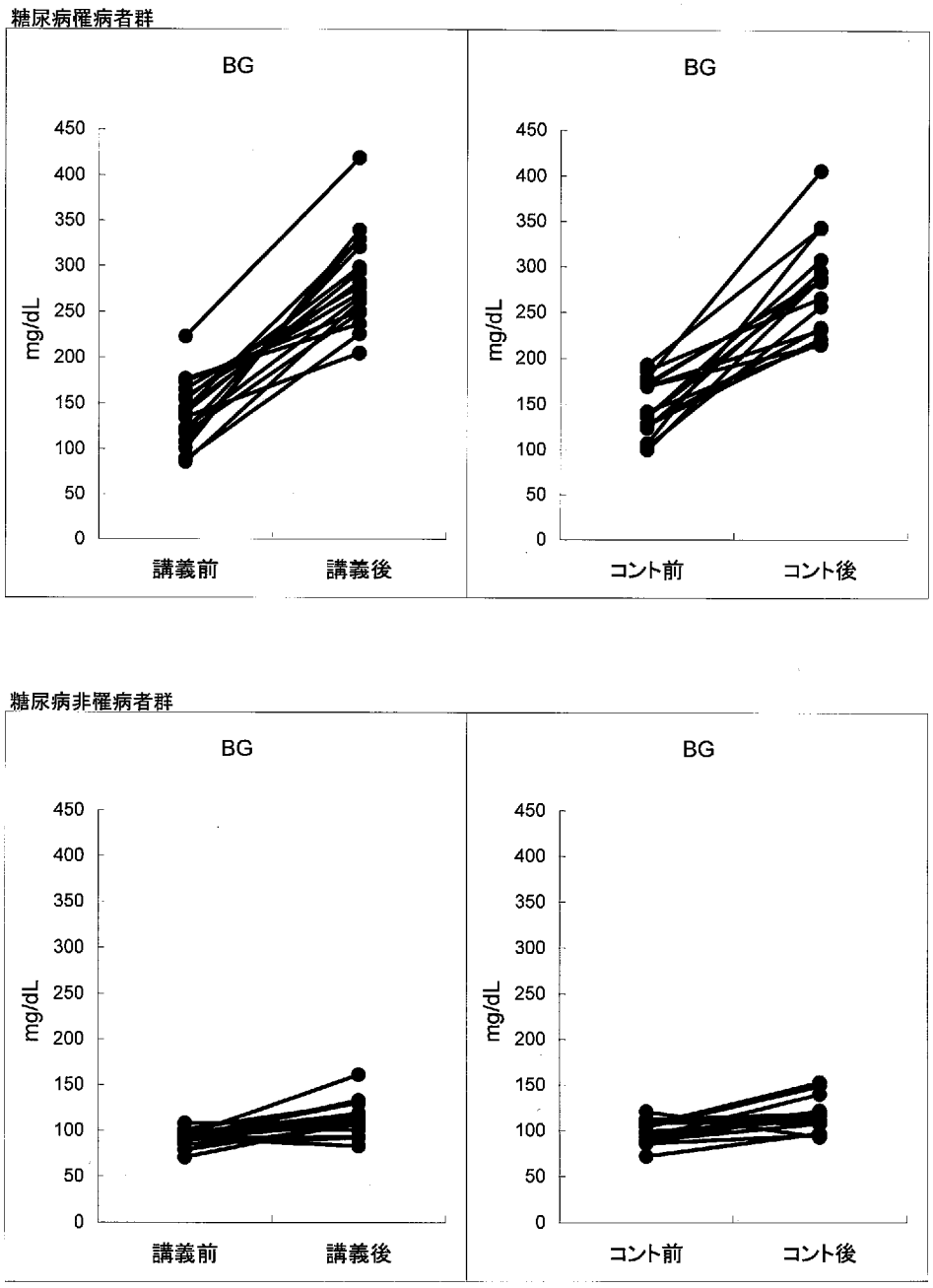


糖尿病非罹病者群



[図99]

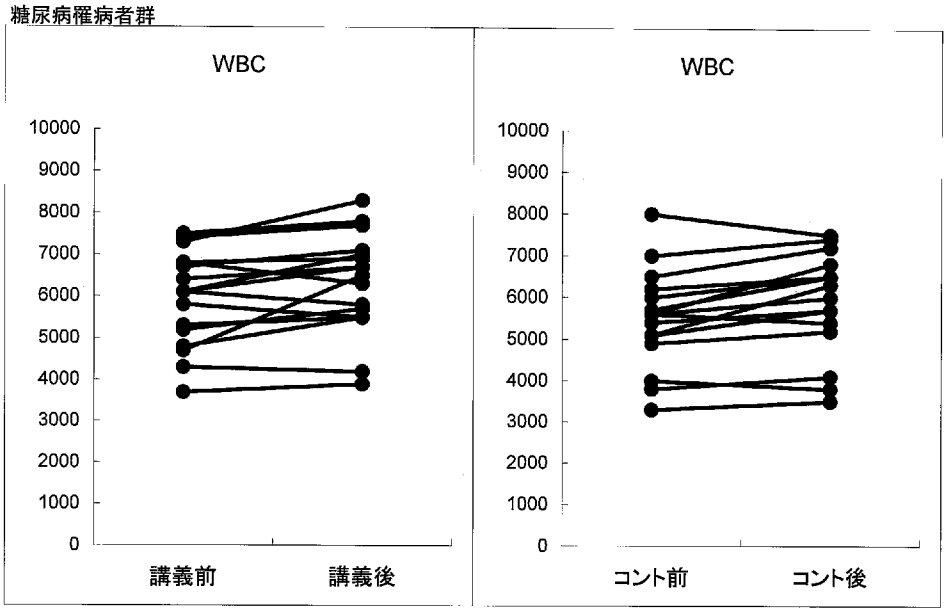
図99 血糖値
（糖尿病罹病者群、糖尿病非罹病者群）



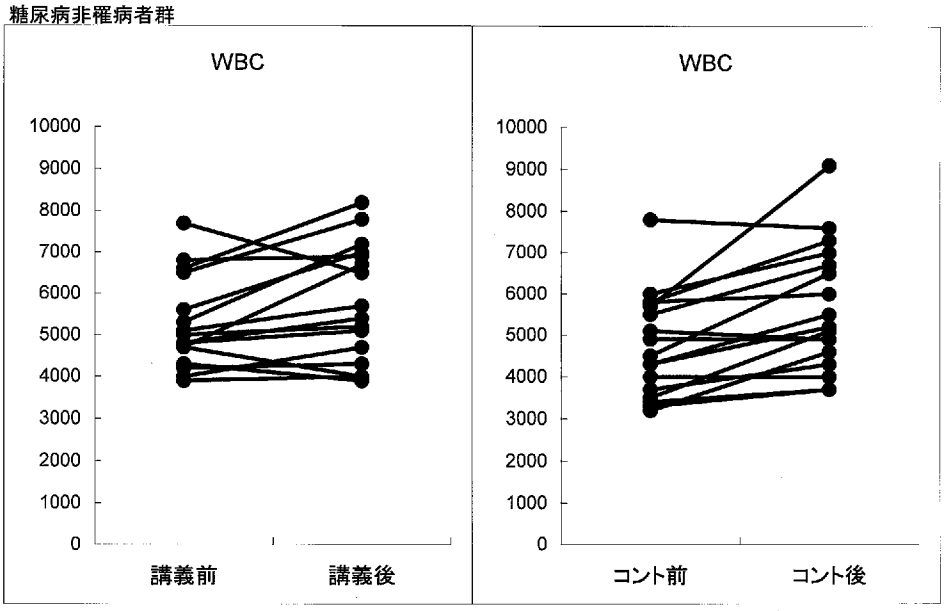
[図100]

図100 白血球数
(糖尿病罹病者群、糖尿病非罹病者群)

糖尿病罹病者群



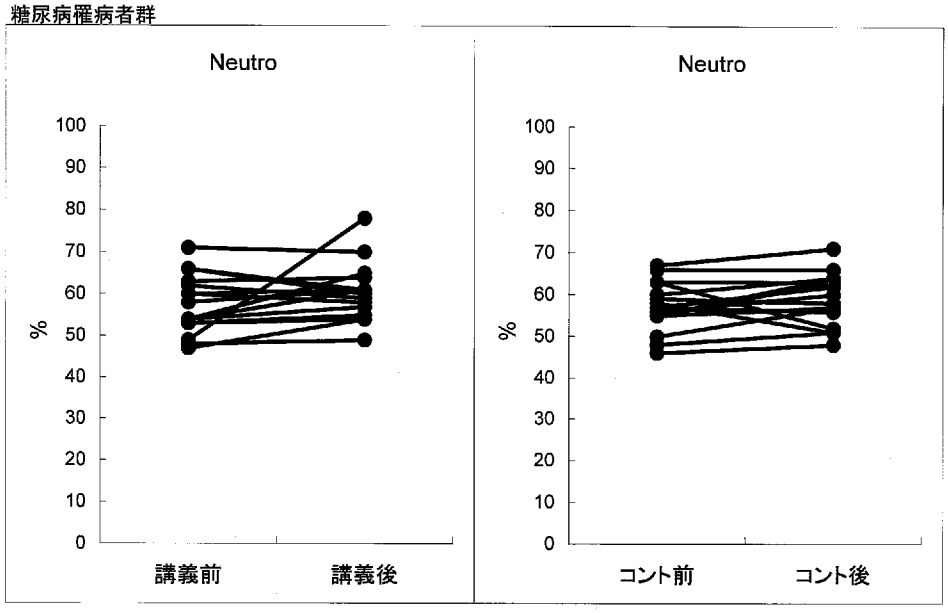
糖尿病非罹病者群



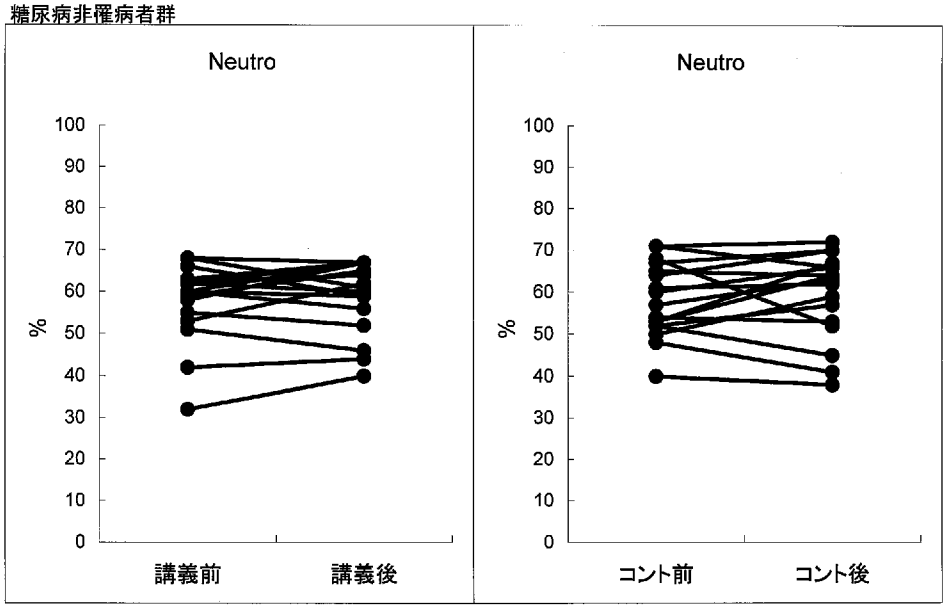
[図101]

図101 好中球比
(糖尿病罹病者群、糖尿病非罹病者群)

糖尿病罹病者群



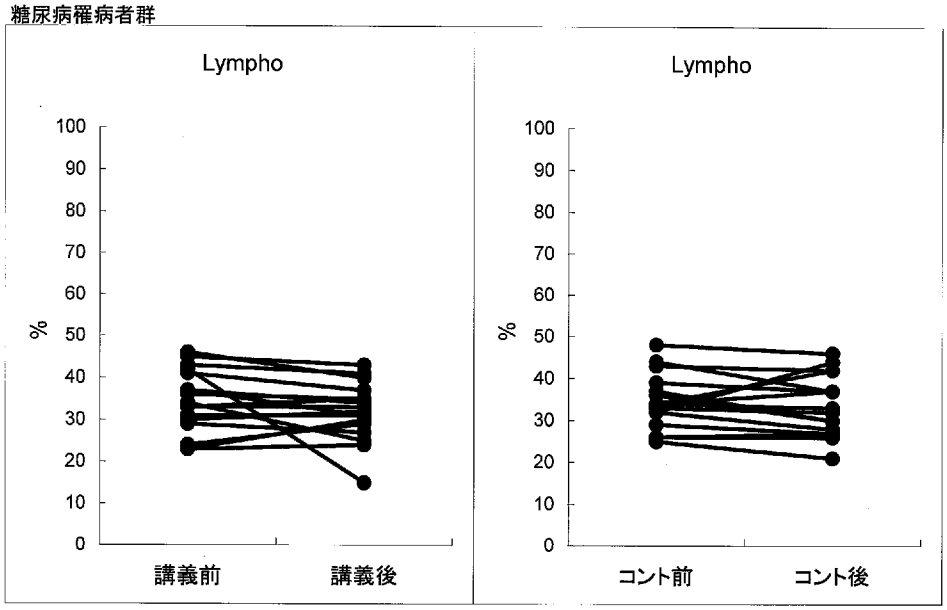
糖尿病非罹病者群



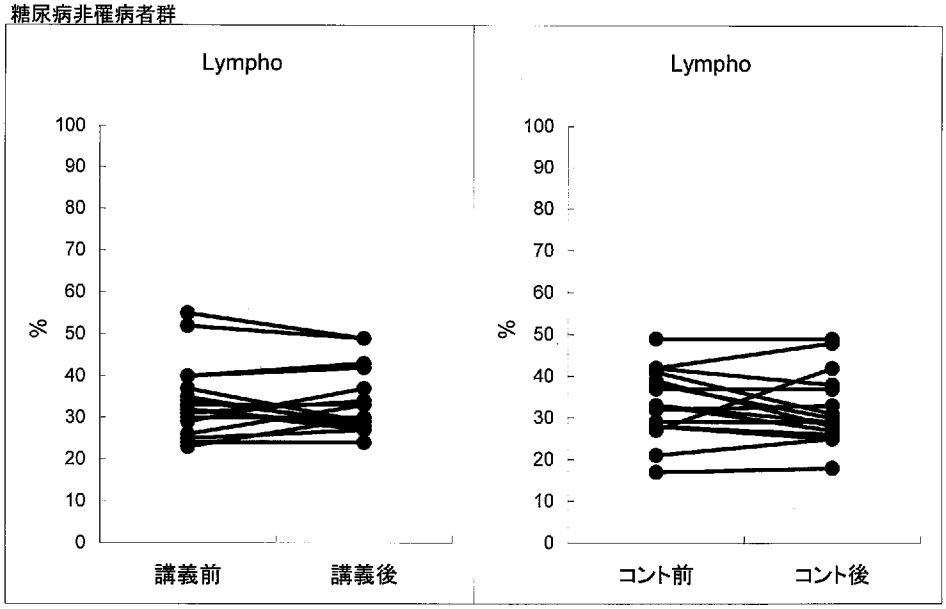
[図102]

図102 リンパ球比
(糖尿病罹病者群、糖尿病非罹病者群)

糖尿病罹病者群

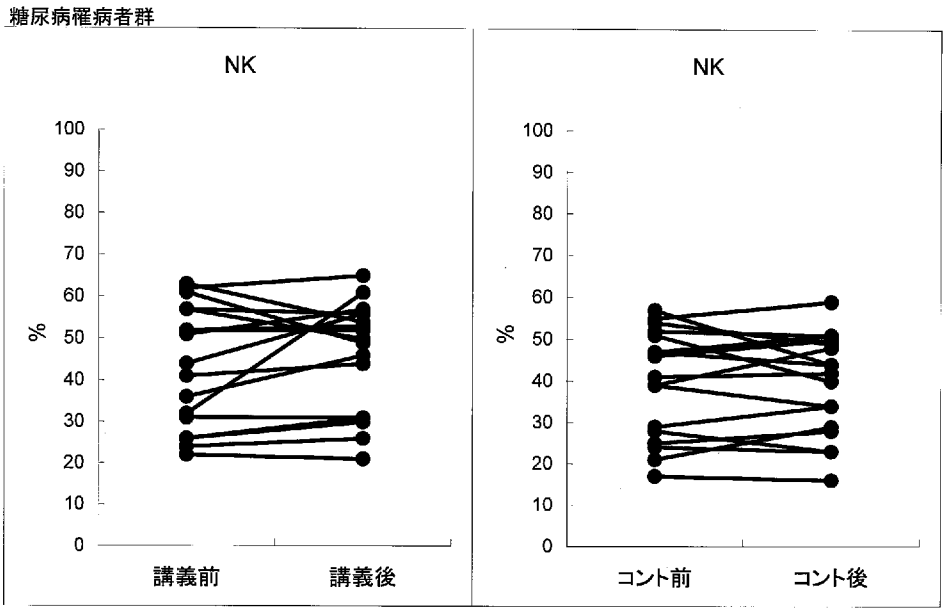


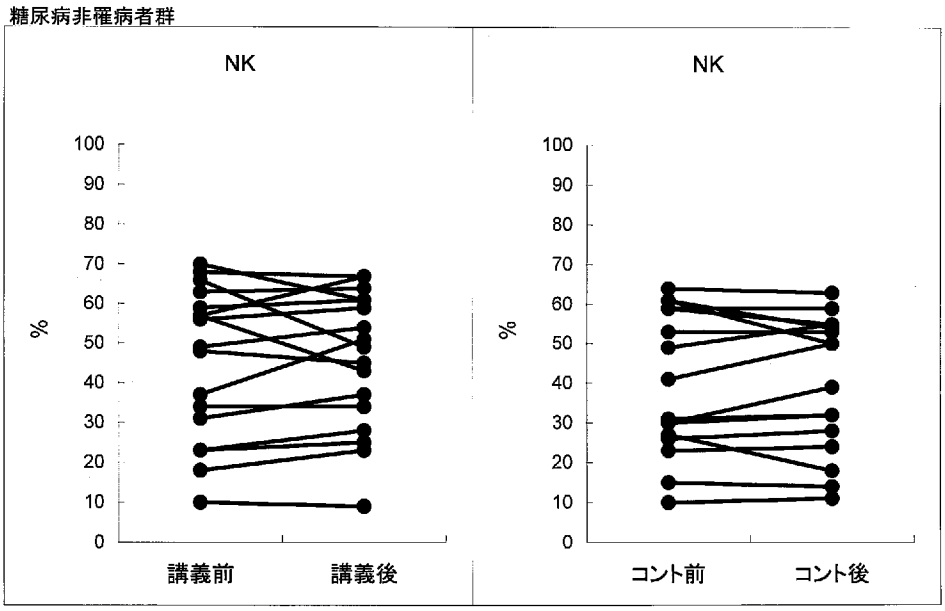
糖尿病非罹病者群



[図103]

図103 NK細胞活性
(糖尿病罹病者群、糖尿病非罹病者群)

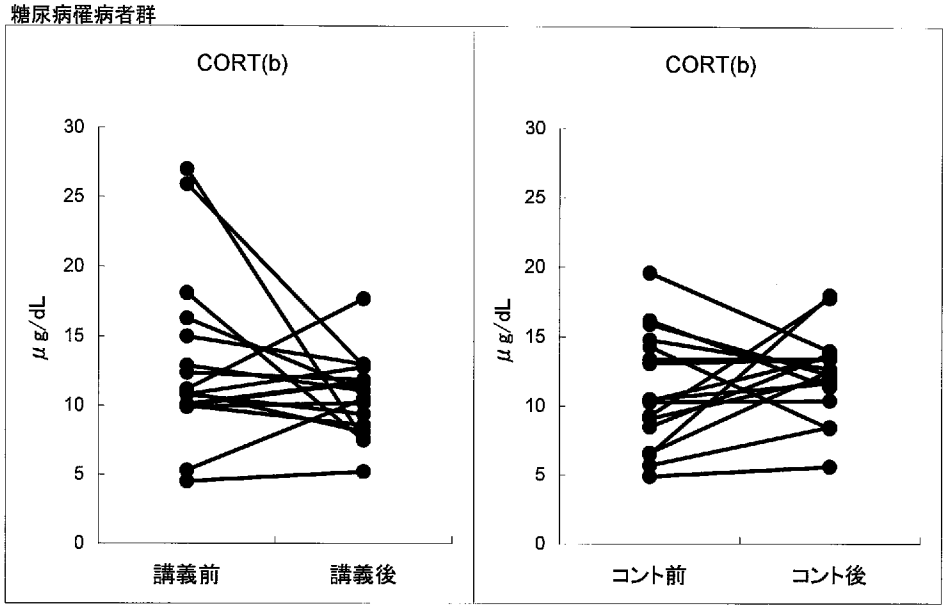




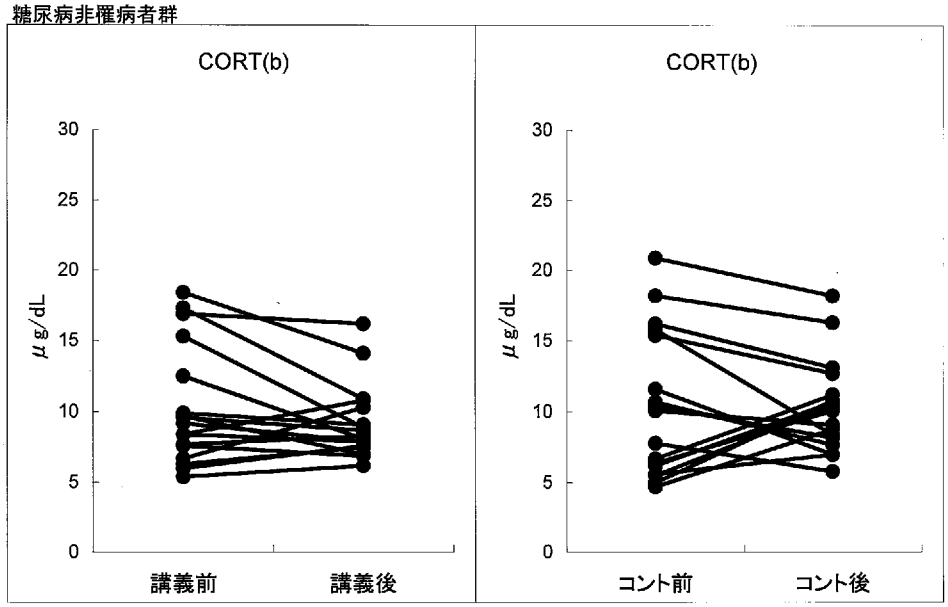
[図104]

図104 血中コルチゾール
（糖尿病罹病者群、糖尿病非罹病者群）

糖尿病罹病者群



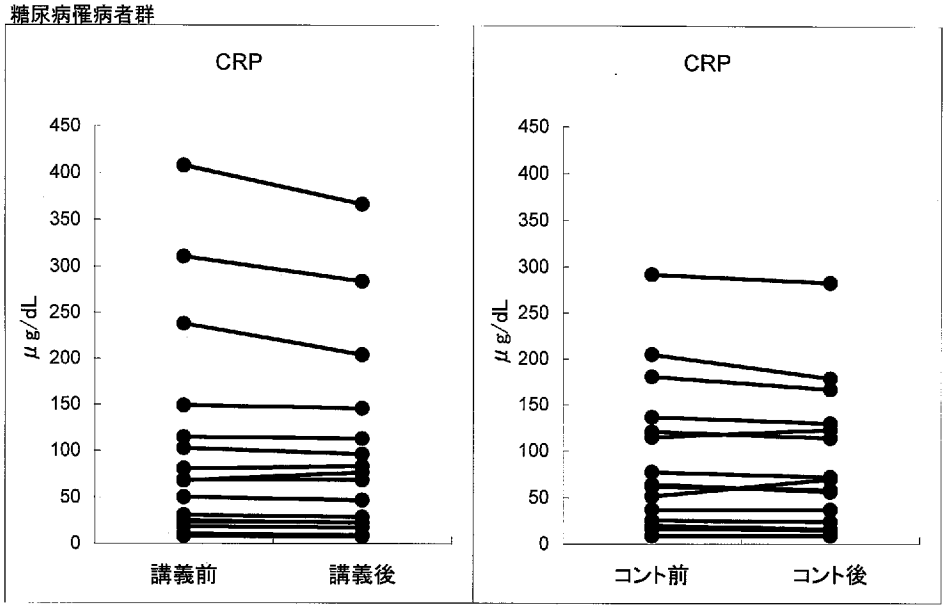
糖尿病非罹病者群



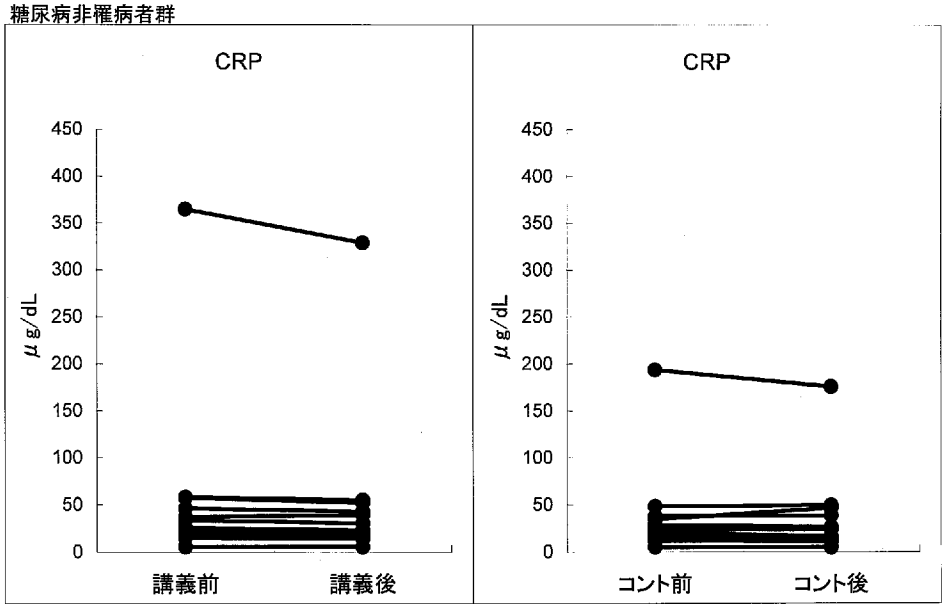
[図105]

図105 C反応性蛋白
（糖尿病罹病者群、糖尿病非罹病者群）

糖尿病罹病者群



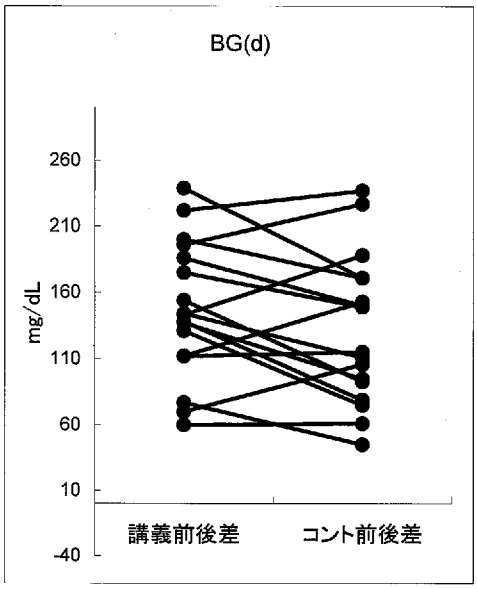
糖尿病非罹病者群



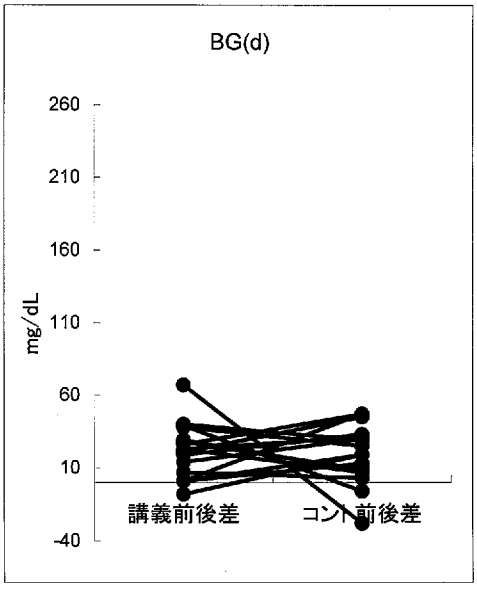
[図106]

図106 血糖値(前後差)
(糖尿病罹病者群、糖尿病非罹病者群)

糖尿病罹病者群



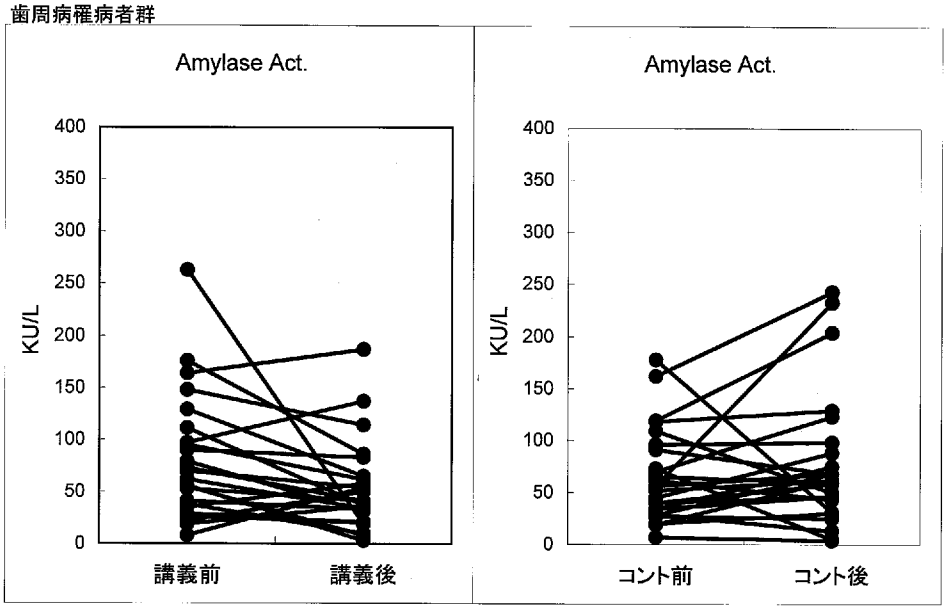
糖尿病非罹病者群



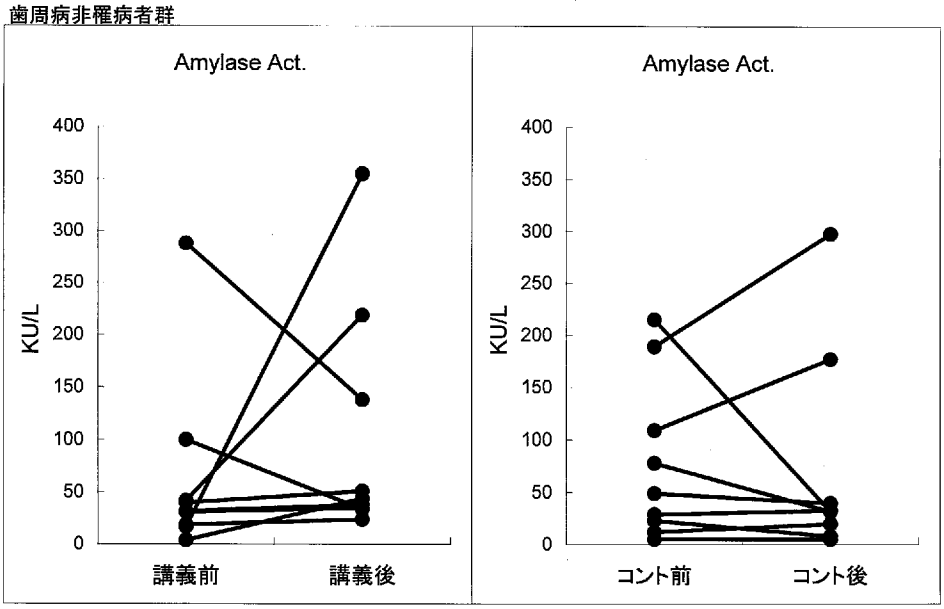
[図107]

図107 唾液アミラーゼ活性
（歯周病罹病者群、歯周病非罹病者群）

歯周病罹病者群



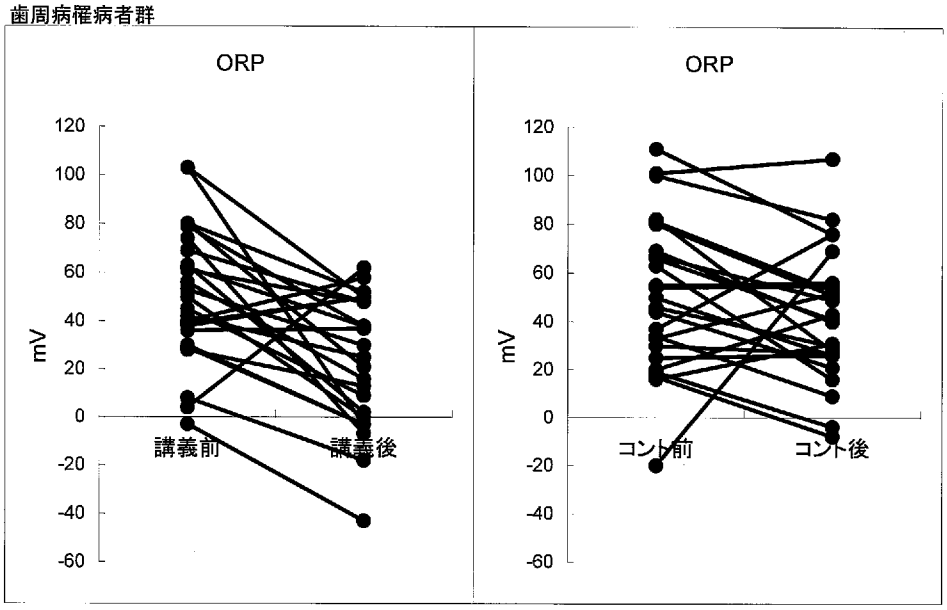
歯周病非罹病者群



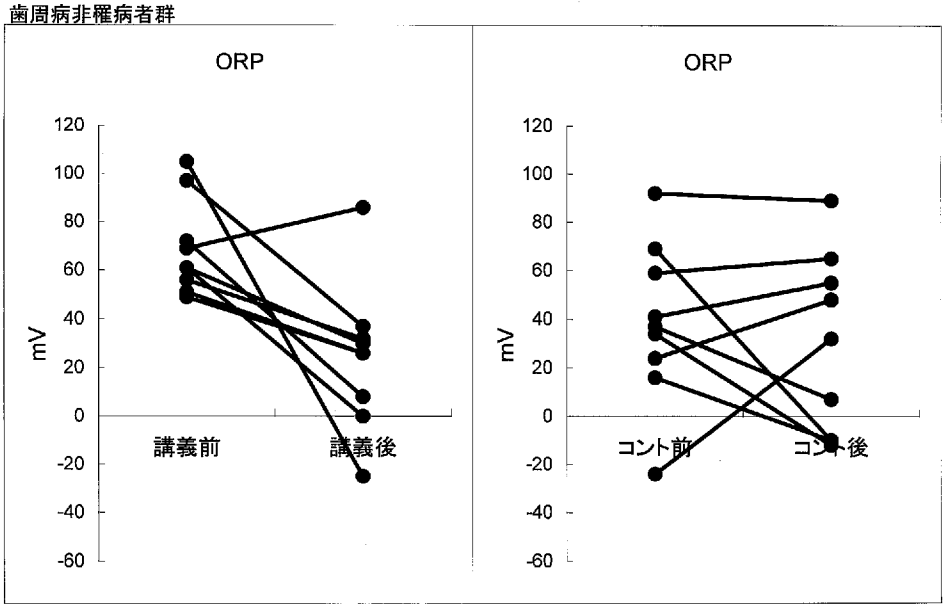
[図108]

図108 唾液中酸化還元電位
（歯周病罹病者群、歯周病非罹病者群）

歯周病罹病者群



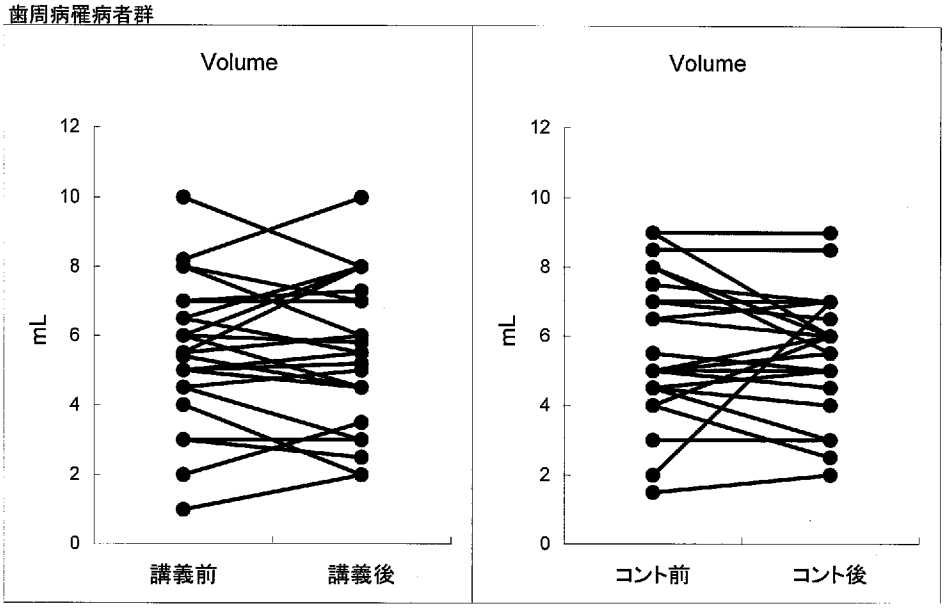
歯周病非罹病者群



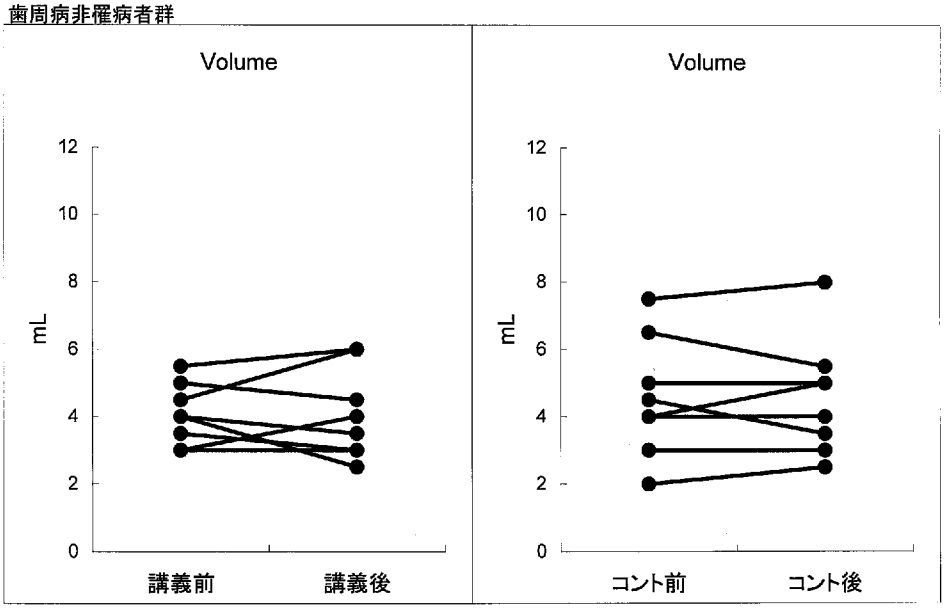
[図109]

図109 唾液量
（歯周病罹病者群、歯周病非罹病者群）

歯周病罹病者群



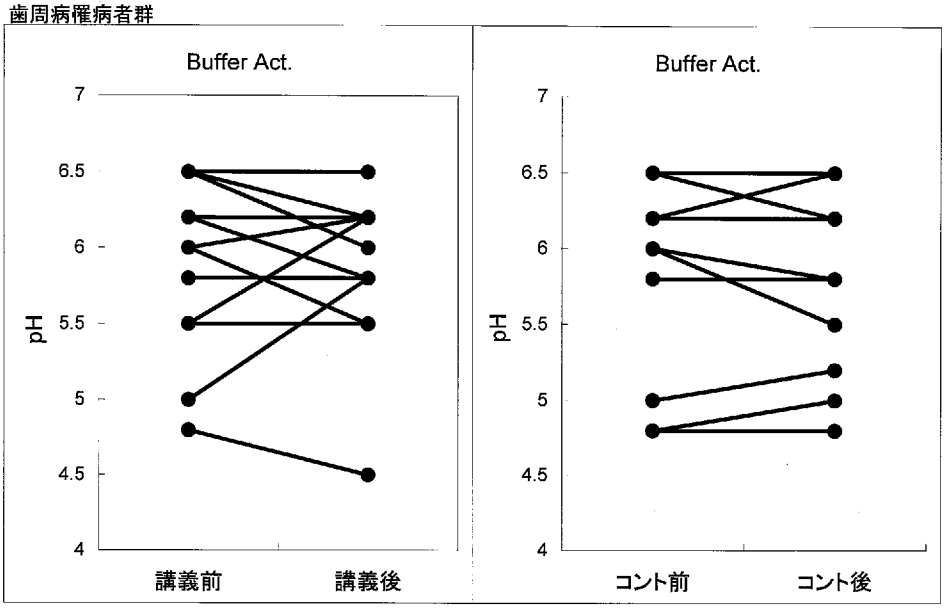
歯周病非罹病者群



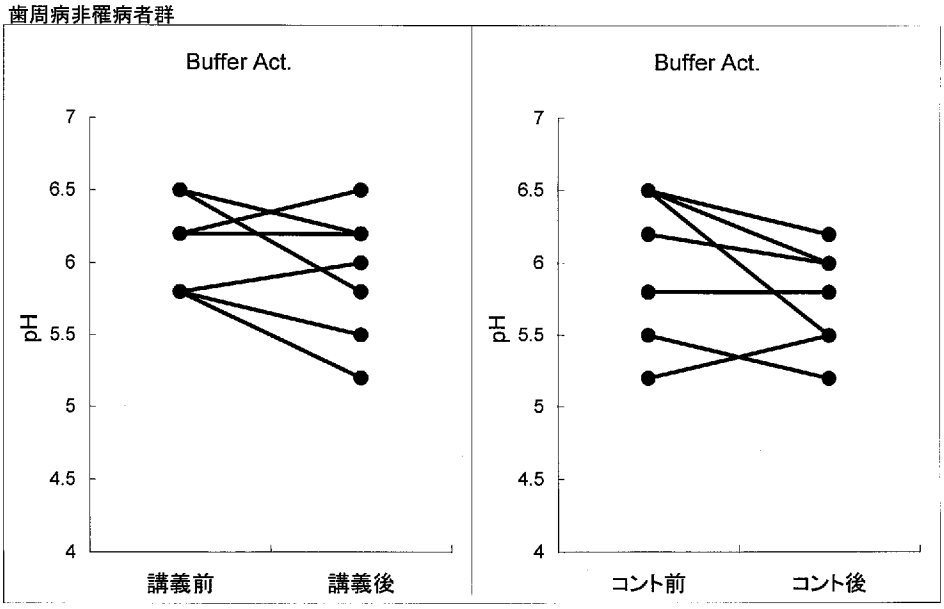
[図110]

図110 唾液緩衝能
(歯周病罹病者群、歯周病非罹病者群)

歯周病罹病者群



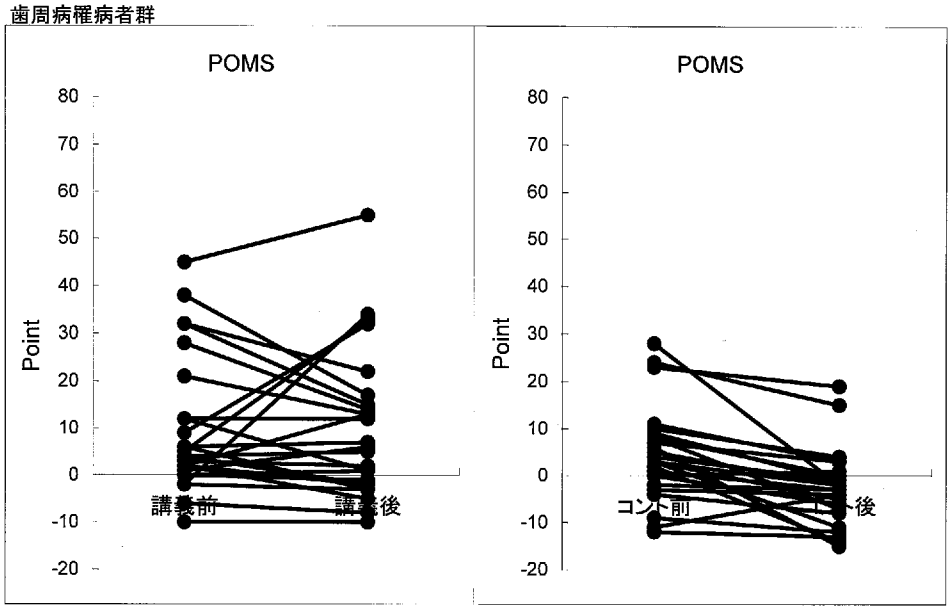
歯周病非罹病者群



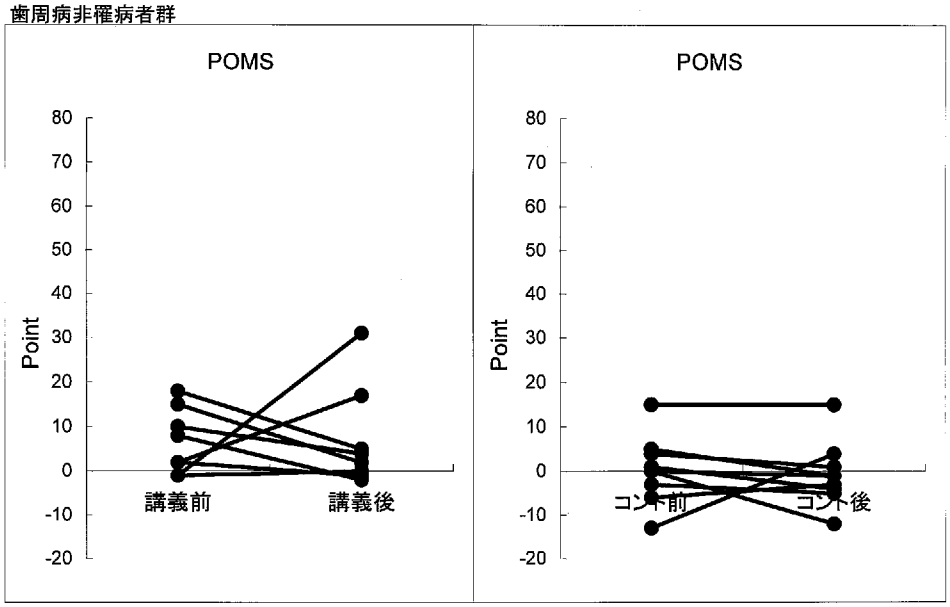
[図111]

図111 総合感情障害度(TMD)
(歯周病罹病者群、歯周病非罹病者群)

歯周病罹病者群



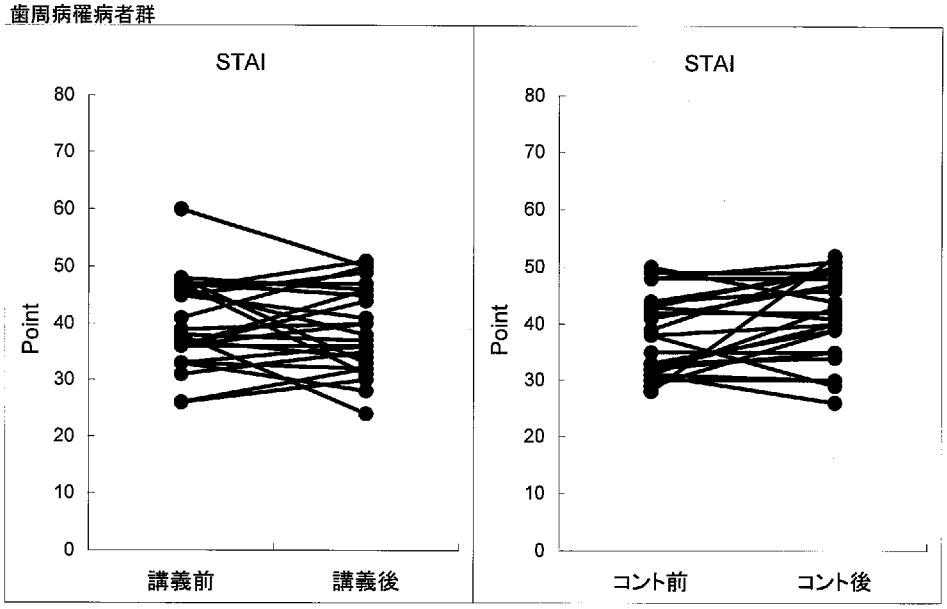
歯周病非罹病者群



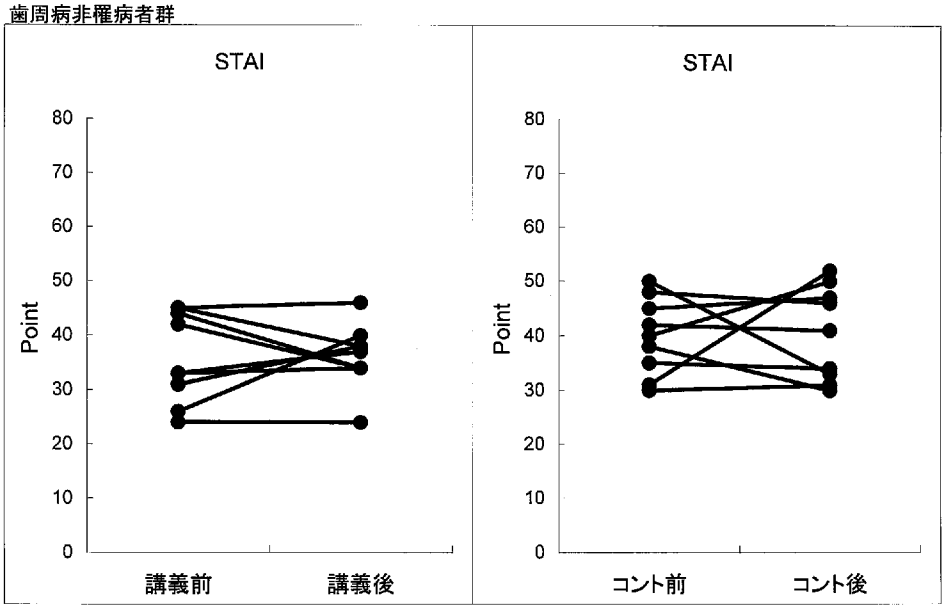
[図112]

図112 不安傾向(STAI)
(歯周病罹病者群、歯周病非罹病者群)

歯周病罹病者群



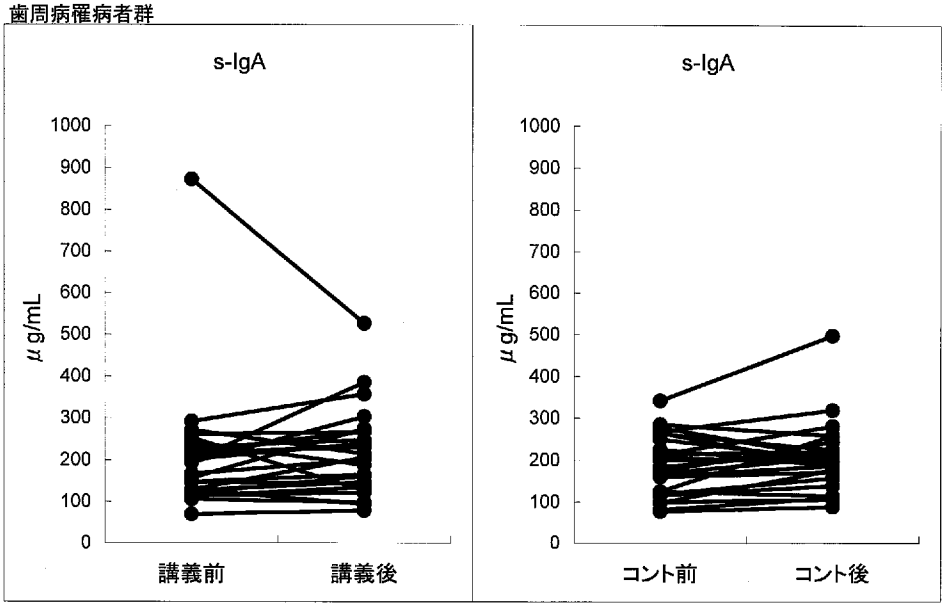
歯周病非罹病者群



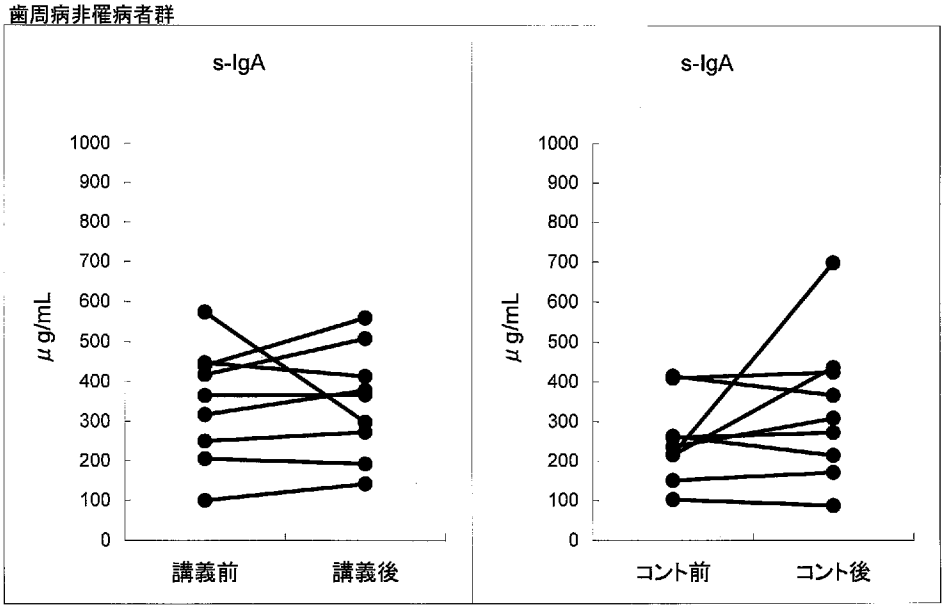
[図113]

図113 唾液中分泌型イムノグロブリンA
（歯周病罹病者群、歯周病非罹病者群）

歯周病罹病者群



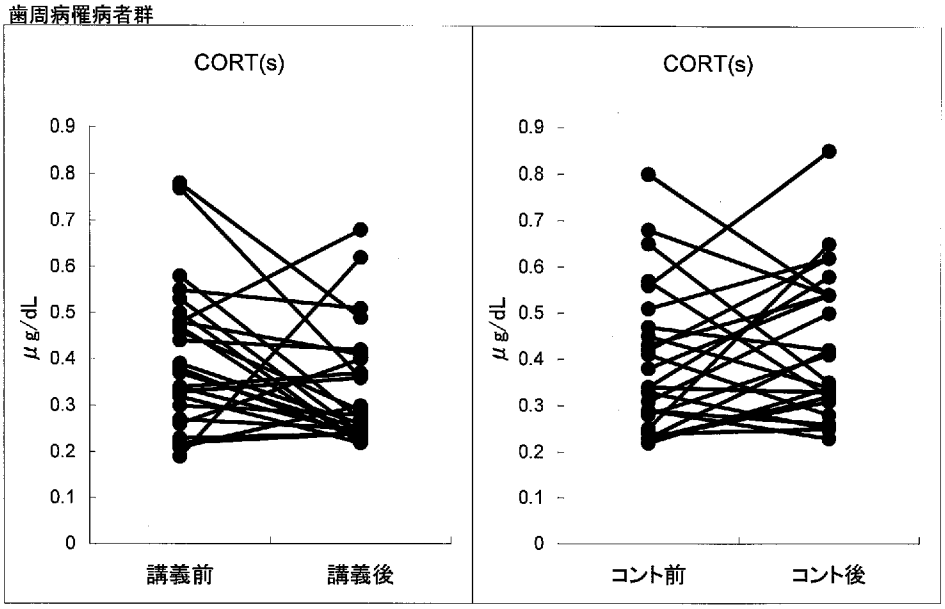
歯周病非罹病者群



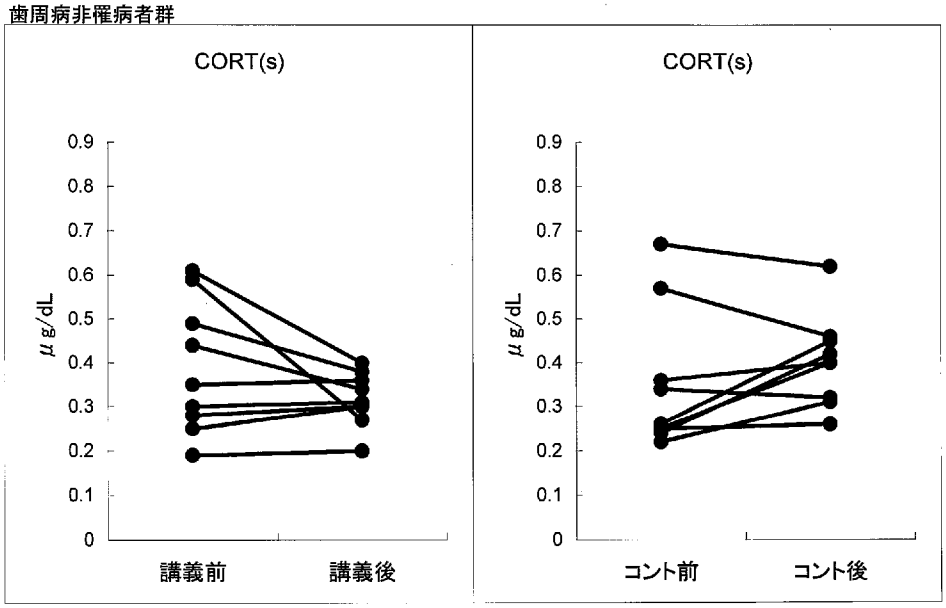
[図114]

図114 唾液中コルチゾール
（歯周病罹病者群、歯周病非罹病者群）

歯周病罹病者群



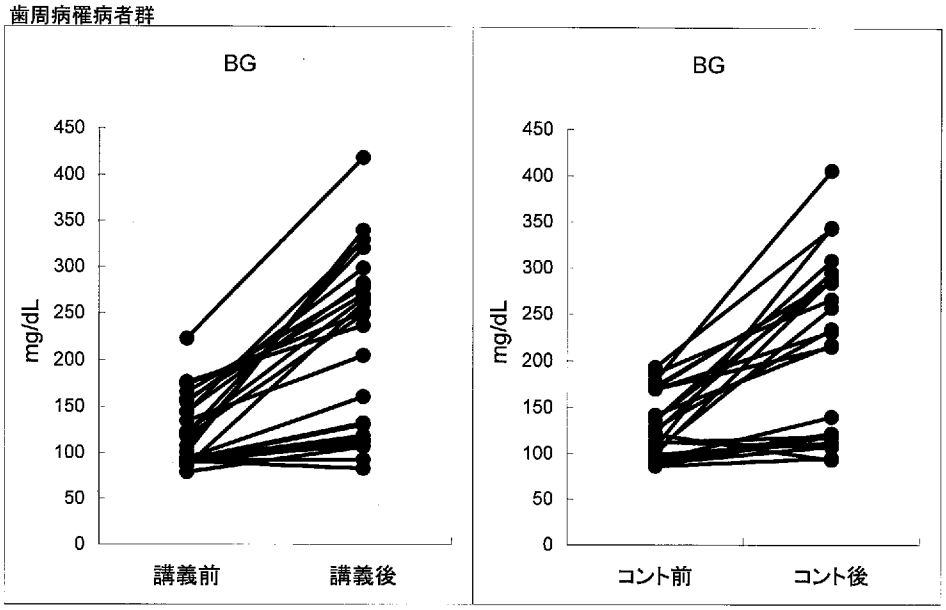
歯周病非罹病者群



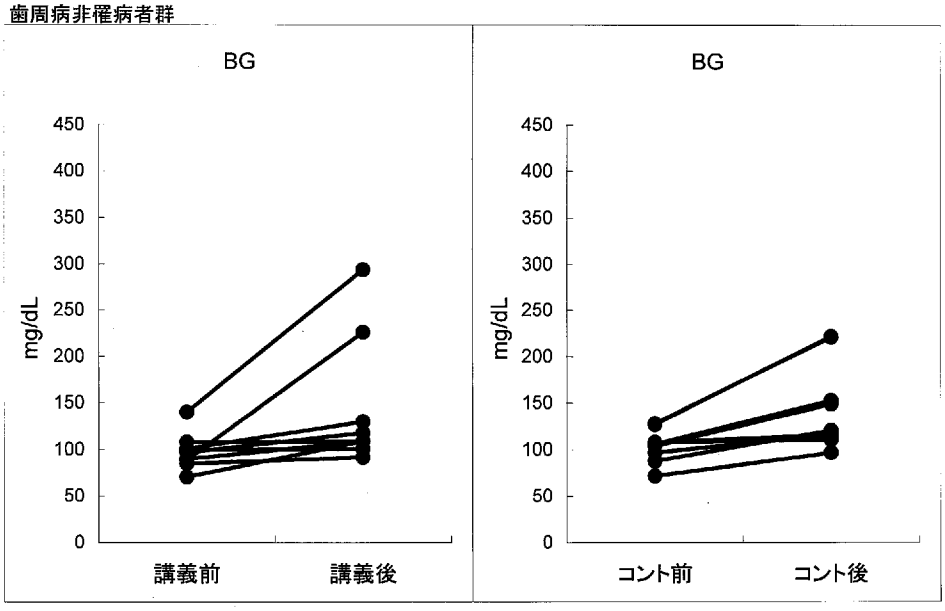
[図115]

図115 血糖値
（歯周病罹病者群、歯周病非罹病者群）

歯周病罹病者群



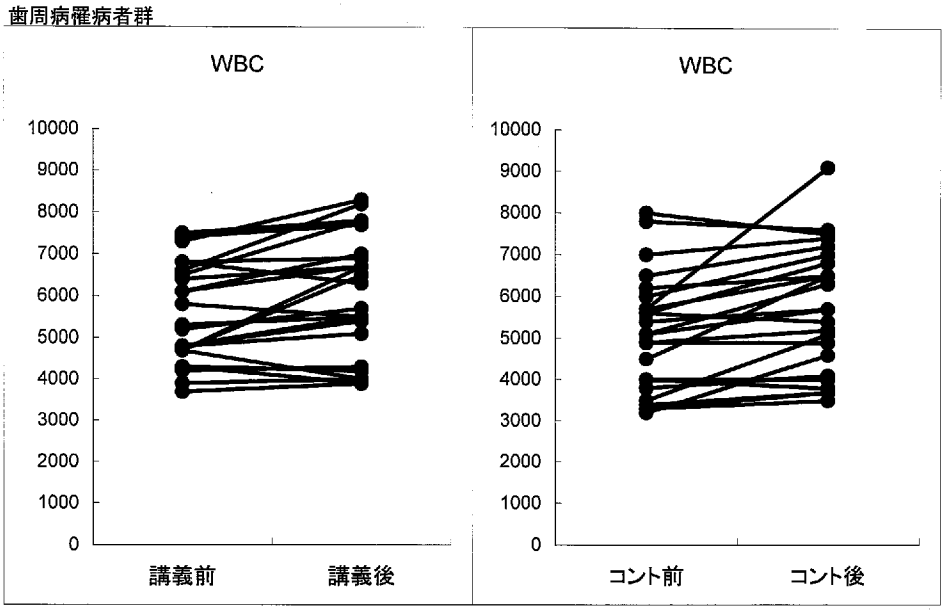
歯周病非罹病者群



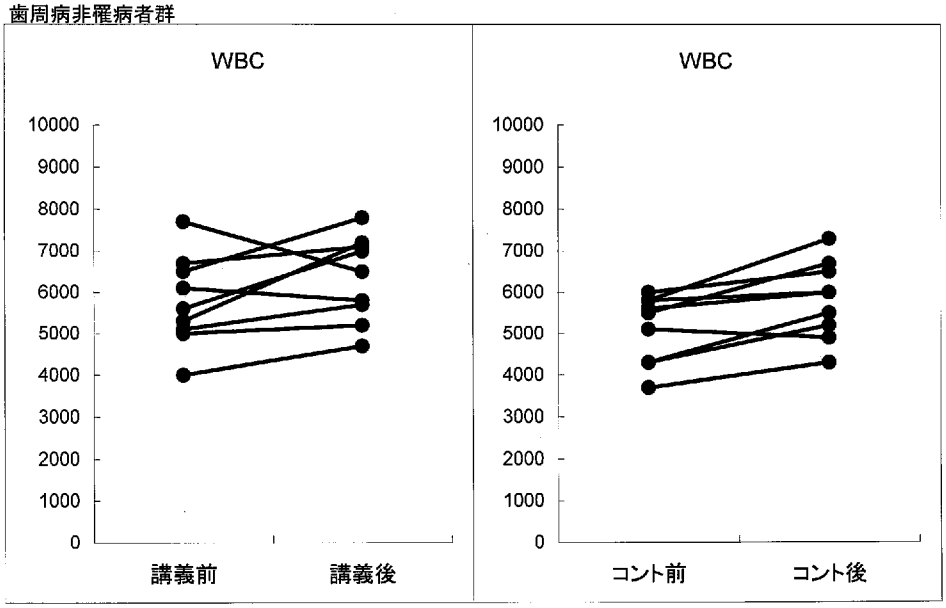
[図116]

図116 白血球数
(歯周病罹病者群、歯周病非罹病者群)

歯周病罹病者群



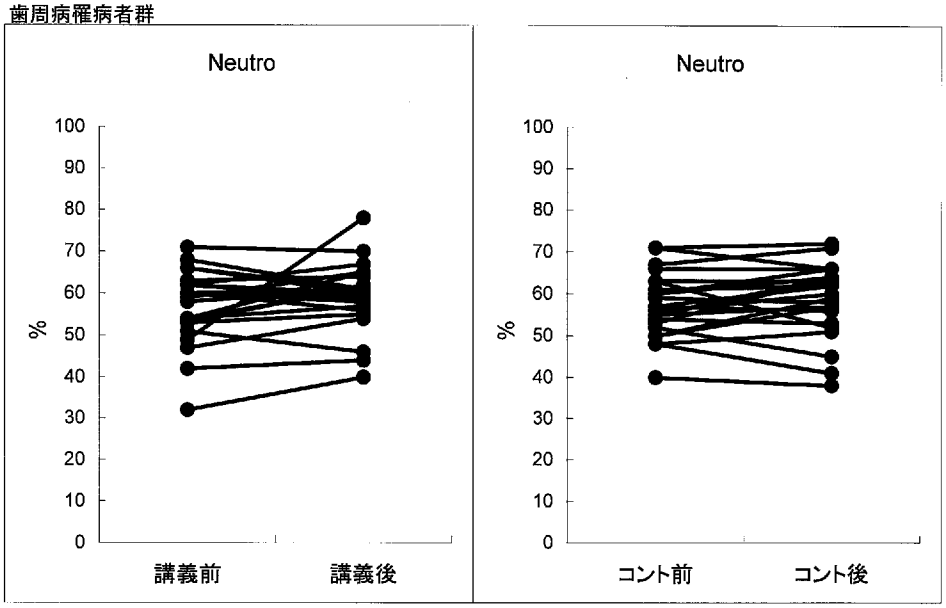
歯周病非罹病者群



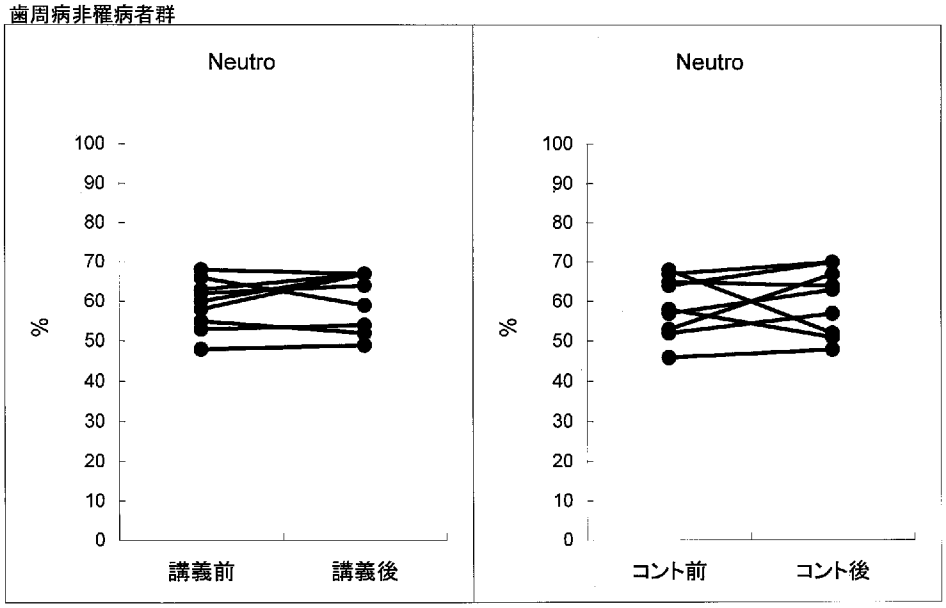
[図117]

図117 好中球比
(歯周病罹病者群、歯周病非罹病者群)

歯周病罹病者群



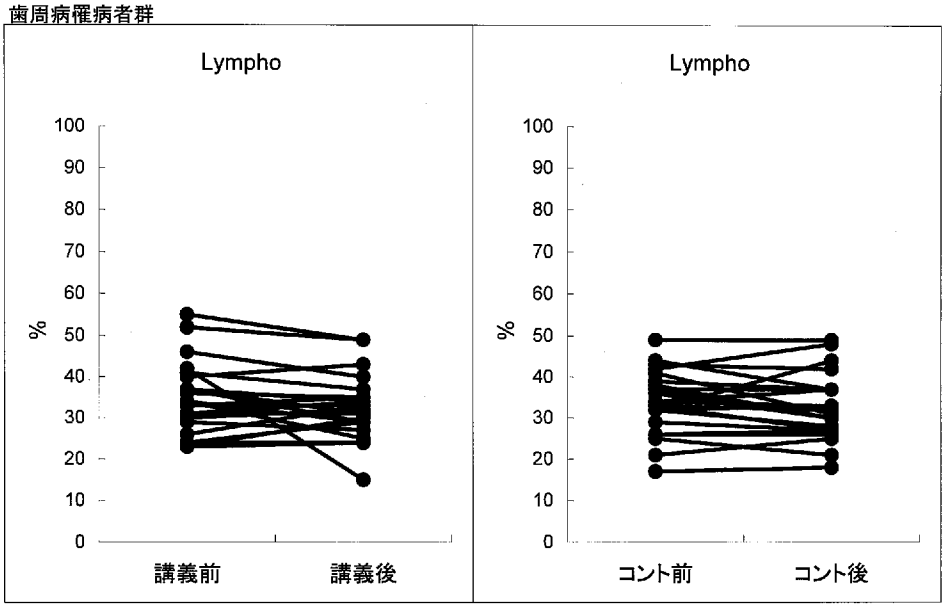
歯周病非罹病者群



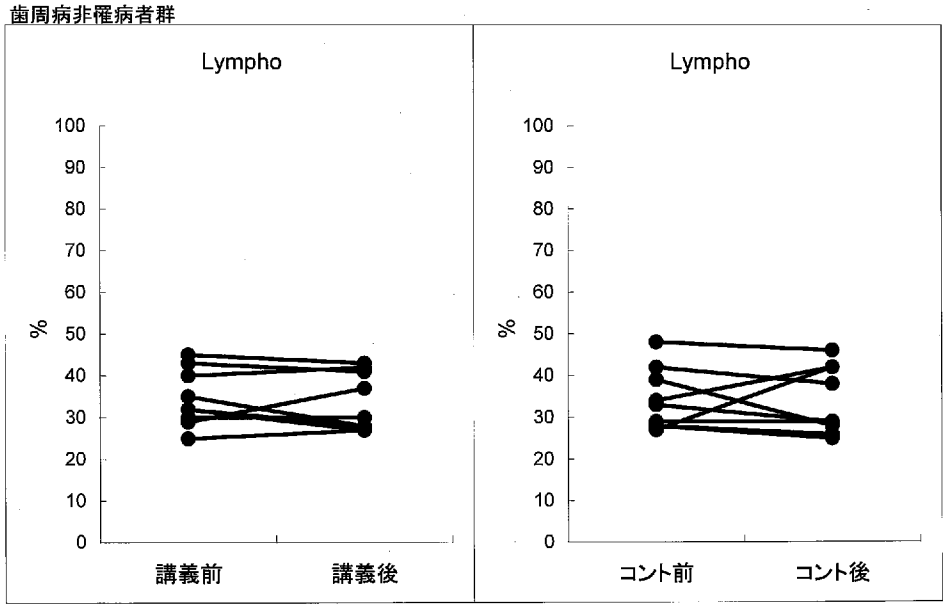
[図118]

図118 リンパ球比
（歯周病罹病者群、歯周病非罹病者群）

歯周病罹病者群



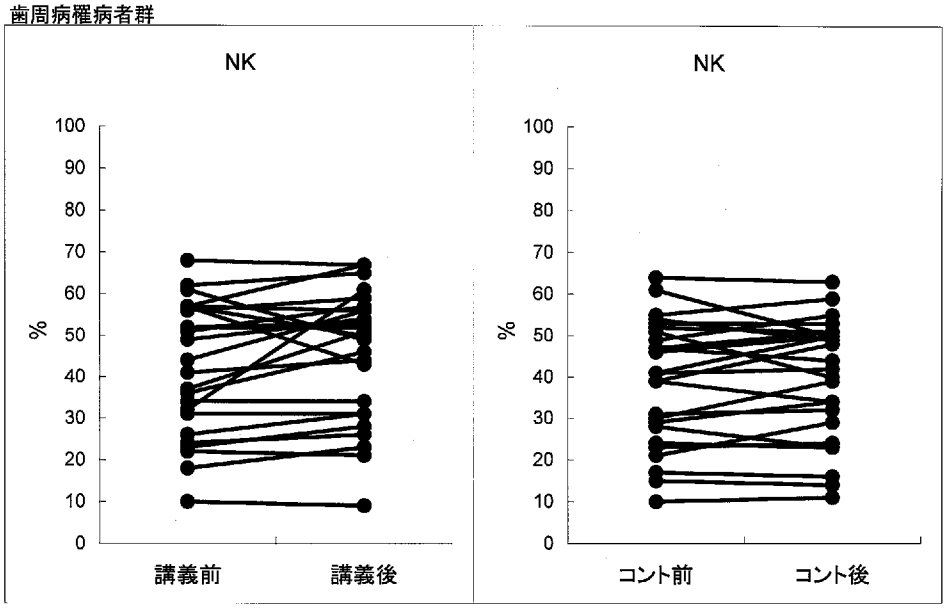
歯周病非罹病者群



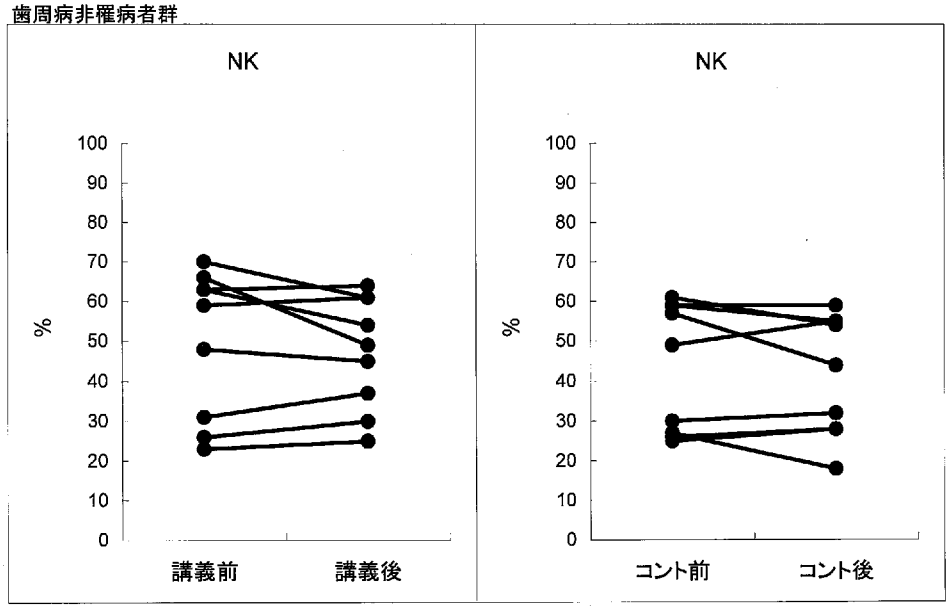
[図119]

図119
（歯周病罹病者群、歯周病非罹病者群）

歯周病罹病者群



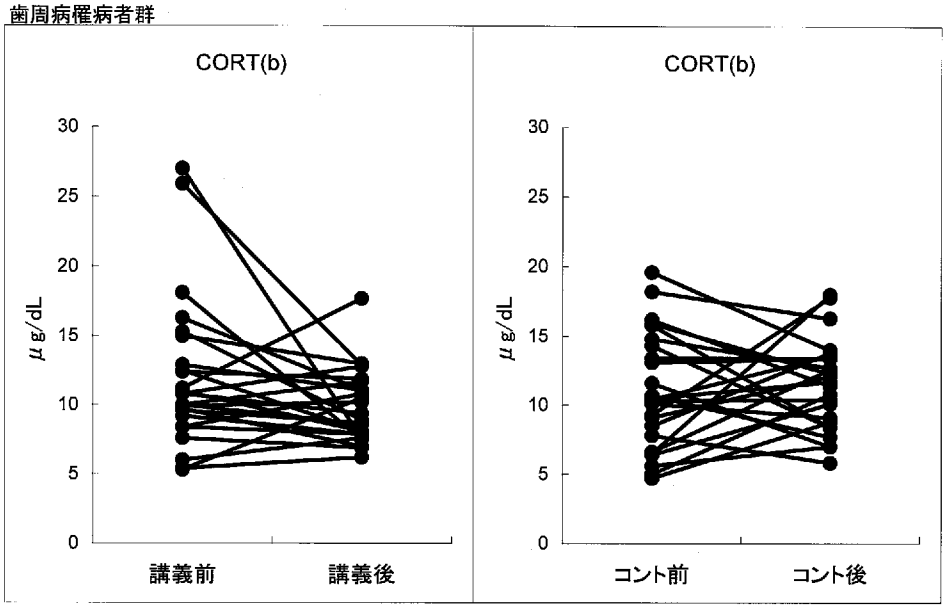
歯周病非罹病者群



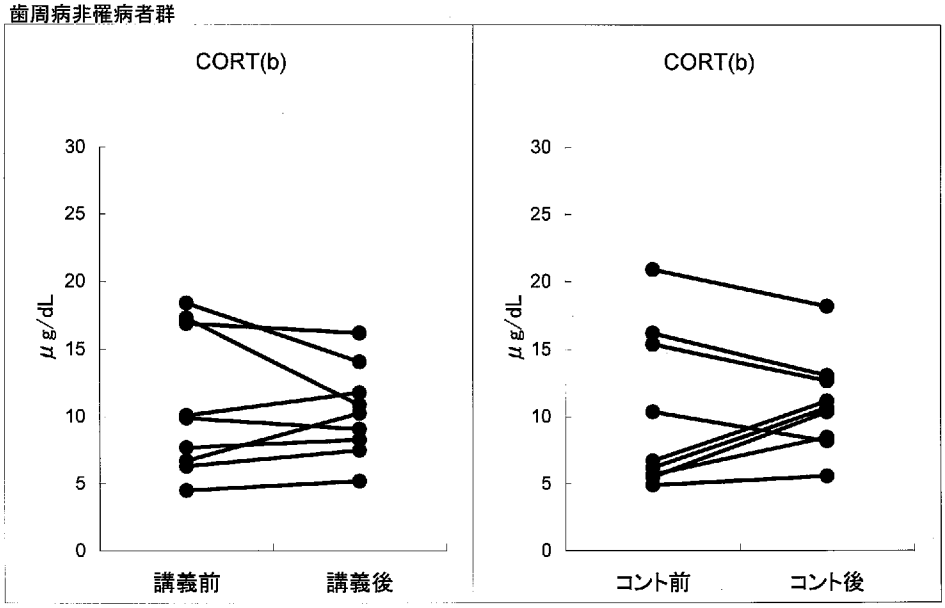
[図120]

図120 血中コルチゾール
（歯周病罹病者群、歯周病非罹病者群）

歯周病罹病者群



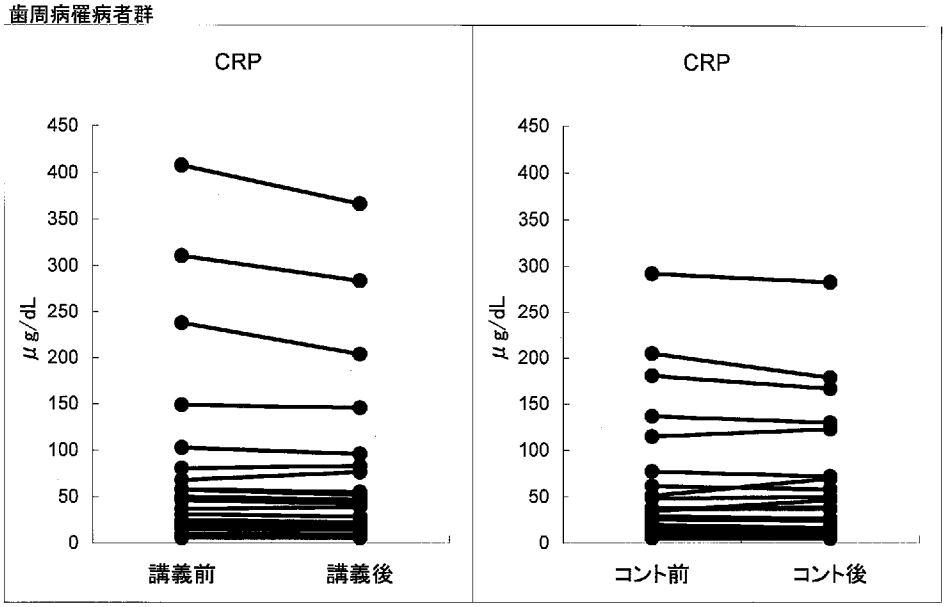
歯周病非罹病者群



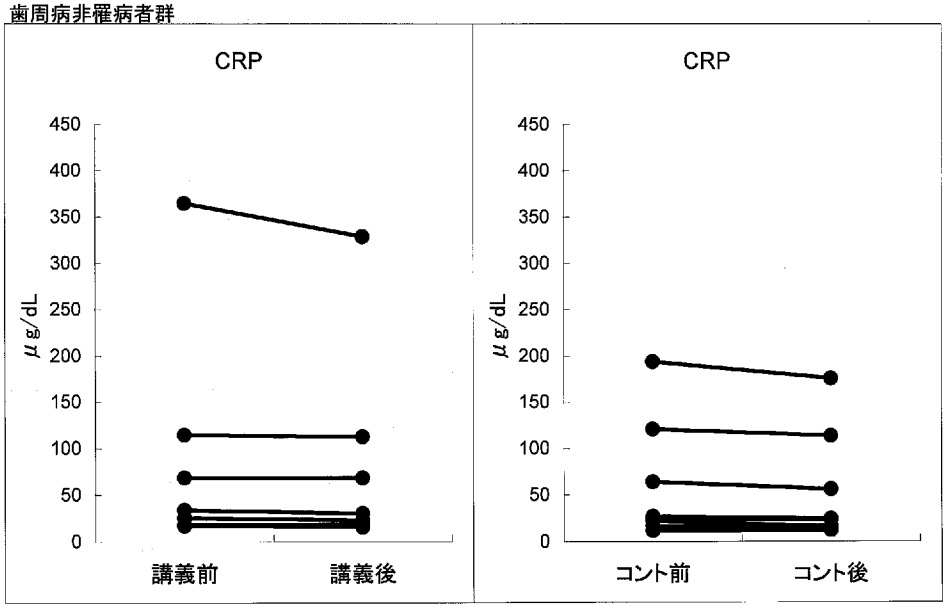
[図121]

図121 CRP
(歯周病罹病者群、歯周病非罹病者群)

歯周病罹病者群



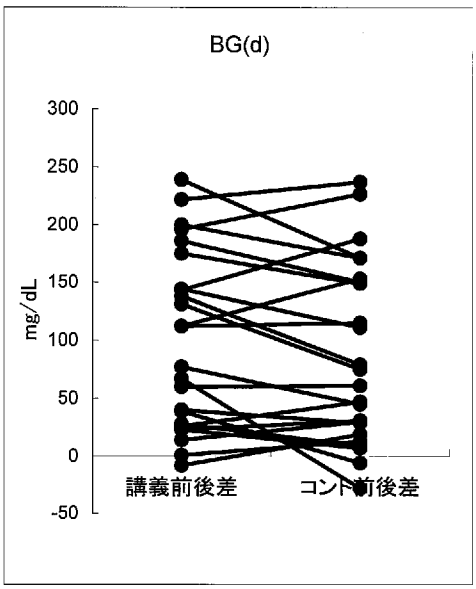
歯周病非罹病者群



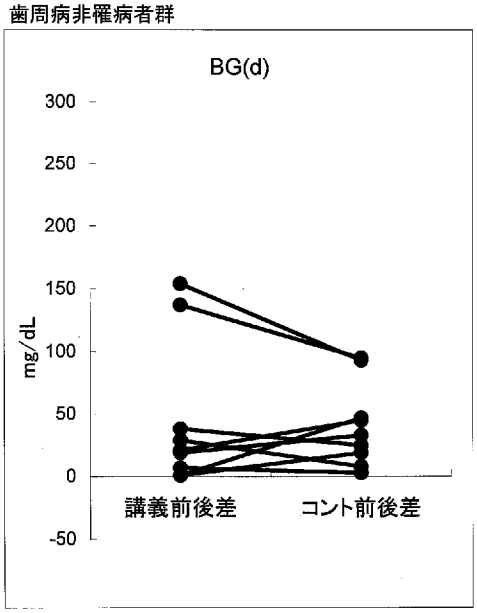
[図122]

図122 血糖値(前後差)
(歯周病罹病者群、歯周病非罹病者群)

歯周病罹病者群



歯周病非罹病者群



[図123]

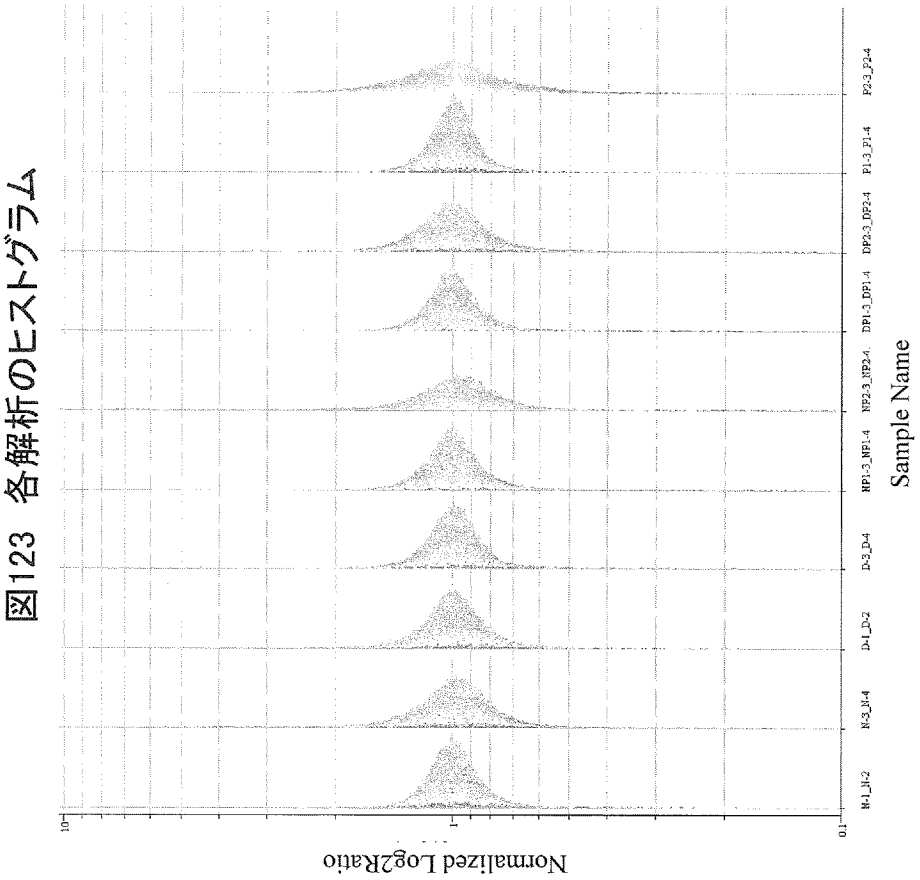


図123 各解析のヒストグラム

[図124]

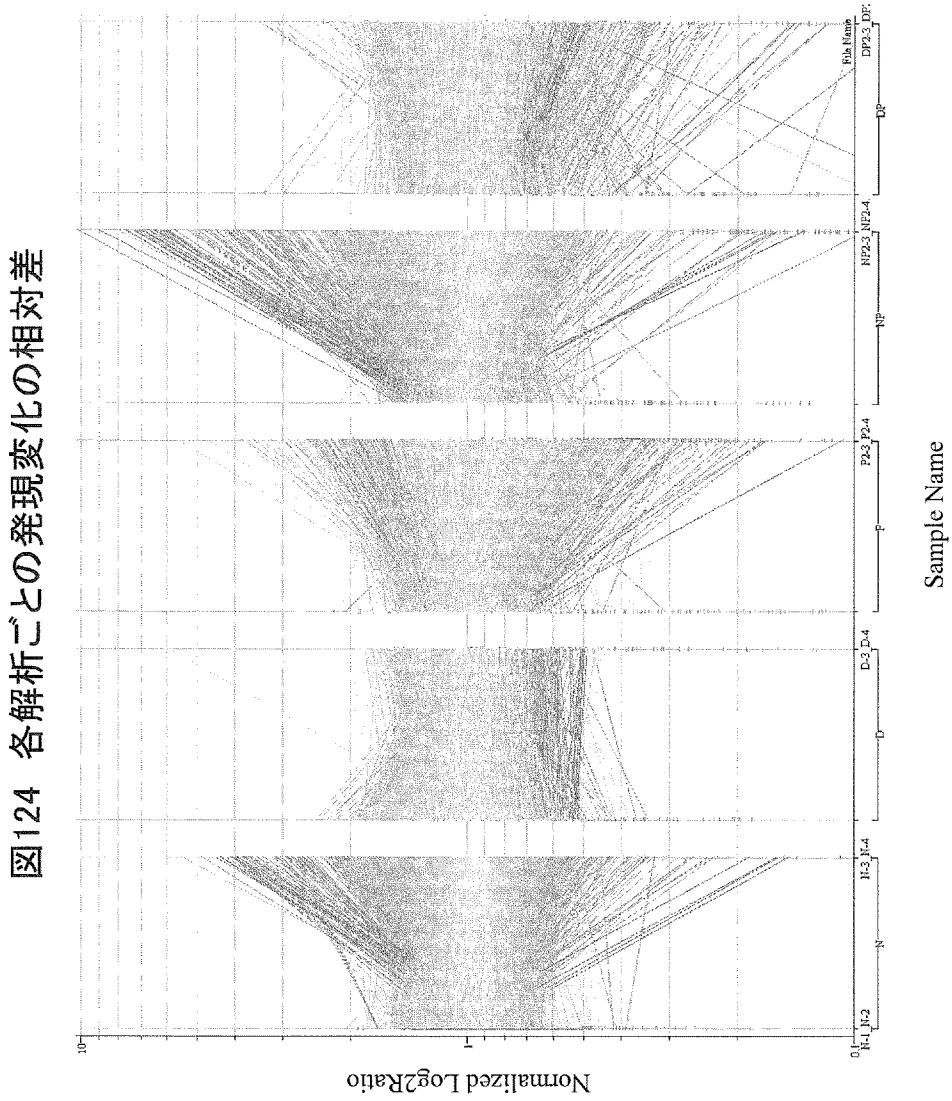
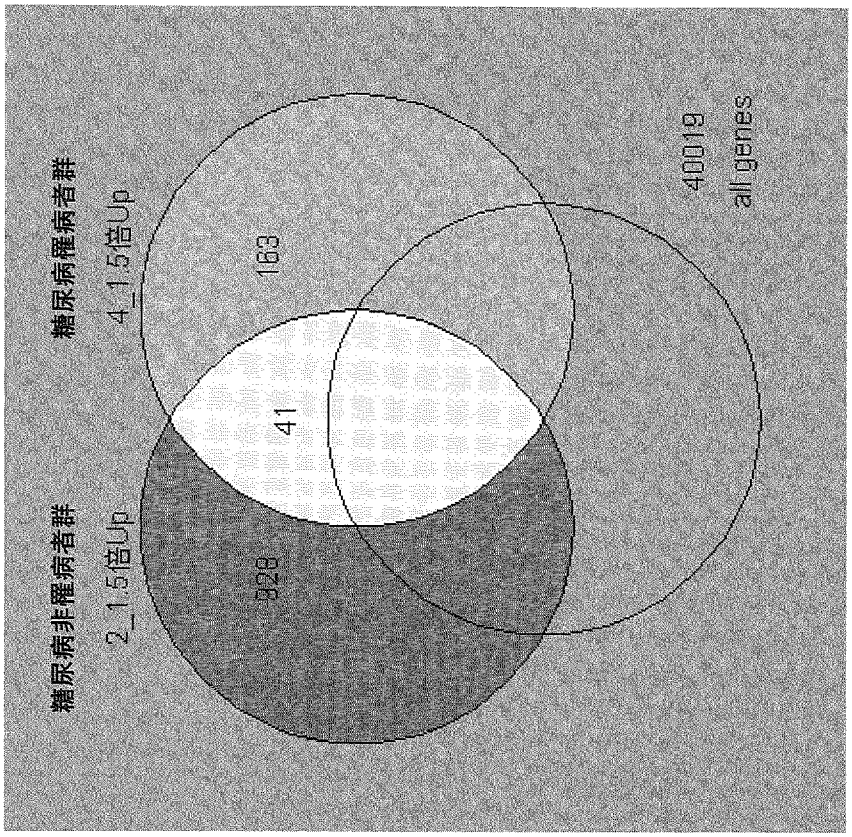


図124 各解析ごとの発現変化の相対差

[図125]

図125 糖尿病非罹病者群と糖尿病罹病者群で笑いにより1.5倍以上の発現変化を認めた遺伝子



[図126]

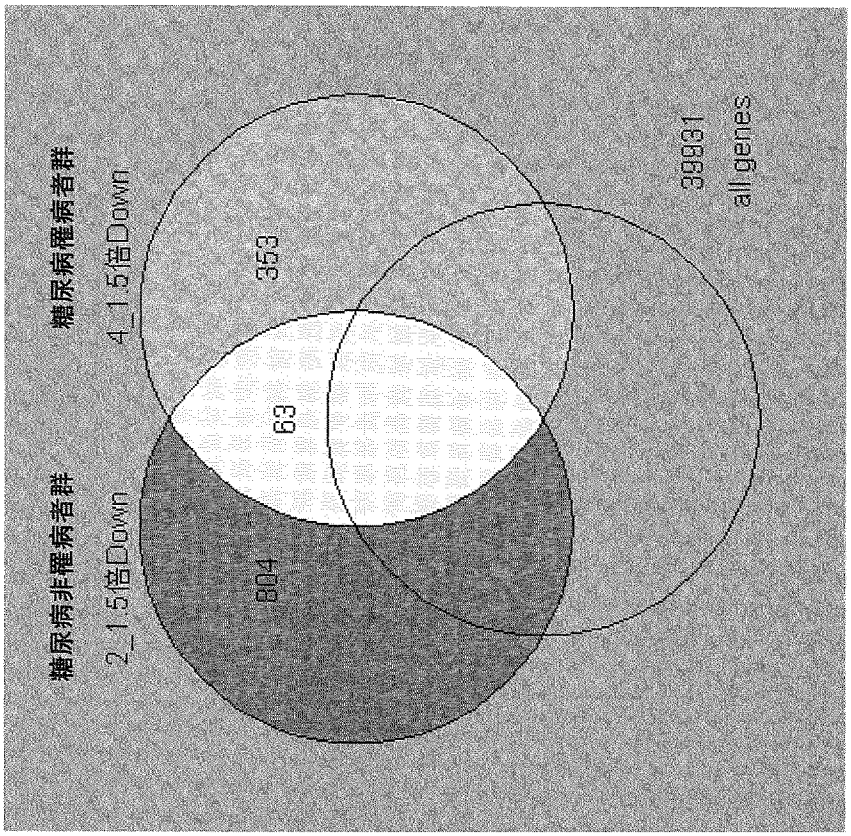
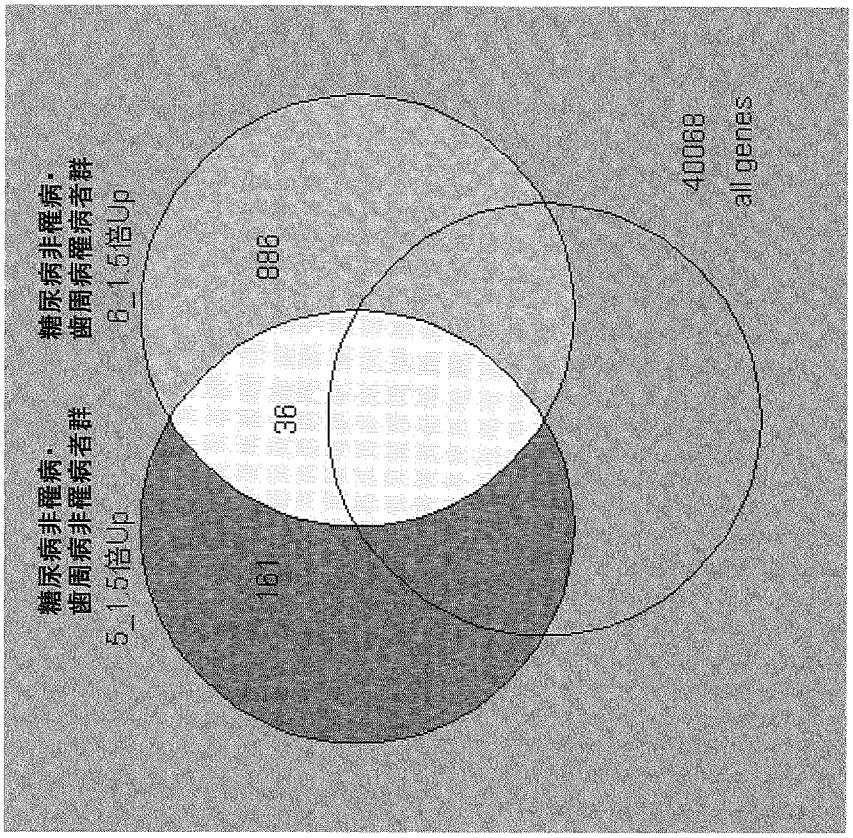


図126 糖尿病非罹病者群と糖尿病罹病者群で笑いにより1/1.5倍以下の発現変化を認めた遺伝子

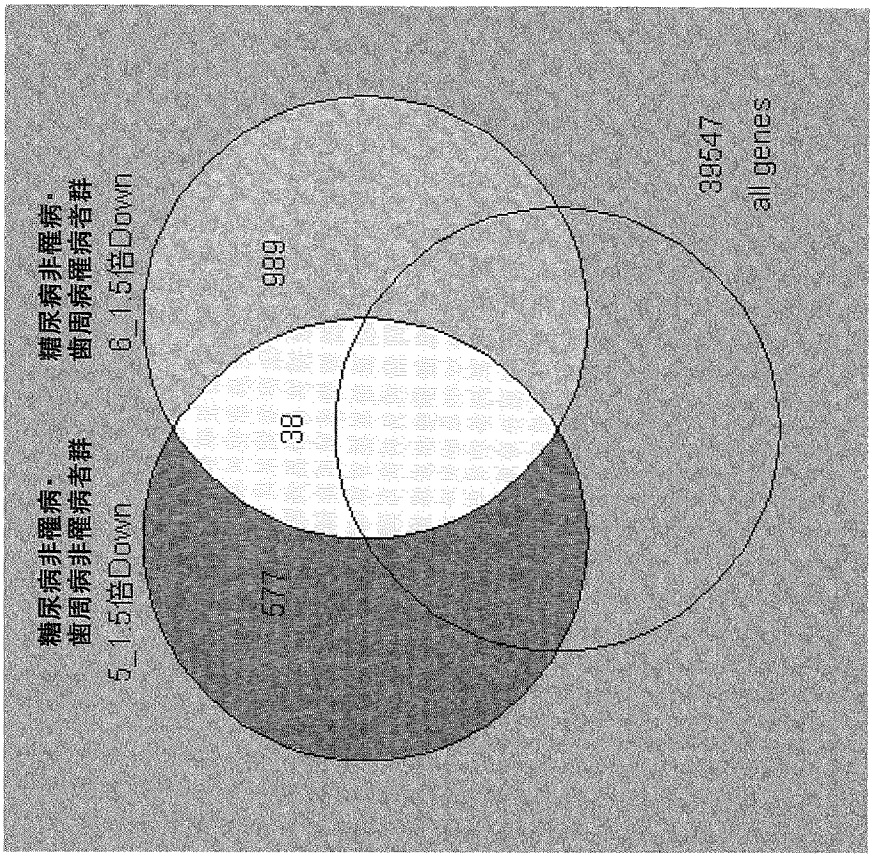
[図127]

図127 糖尿病非罹病・歯周病非罹病者群と糖尿病非罹病・歯周病罹病者群で笑いにより1.5倍以上の発現変化を認めた遺伝子



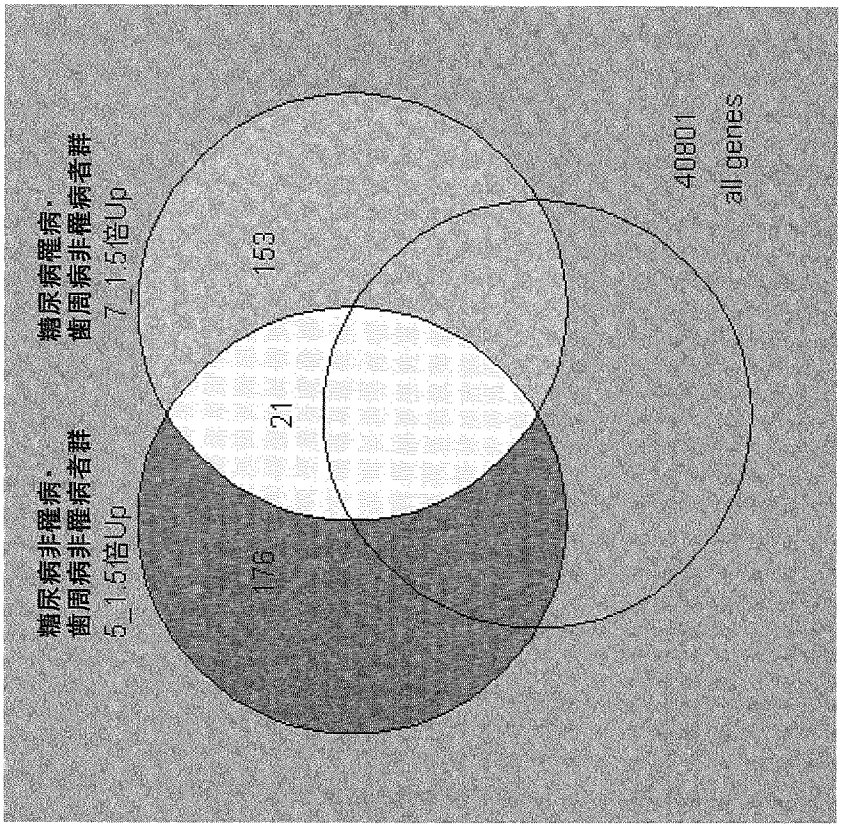
[図128]

図128 糖尿病非罹病・歯周病非罹病者群と糖尿病非罹病・歯周病罹病者群で笑いにより1/1.5倍以下の発現変化を認めた遺伝子



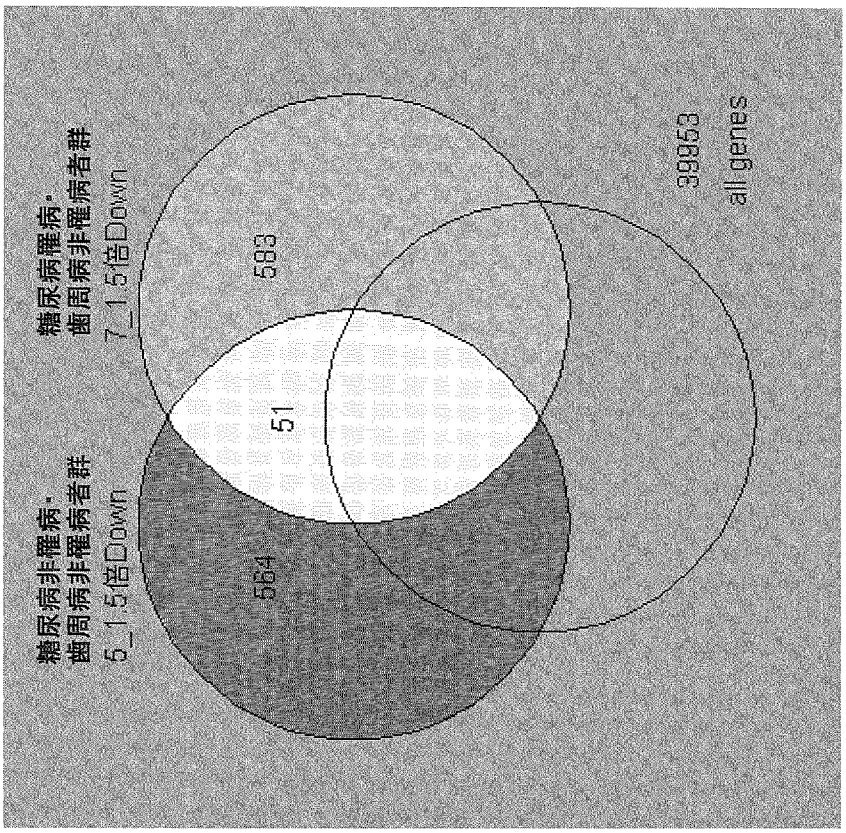
[図129]

図129 糖尿病非罹患・歯周病非罹病者群と糖尿病罹病・歯周病非罹病者群で笑いにより1.5倍以上の発現変化を認めた遺伝子



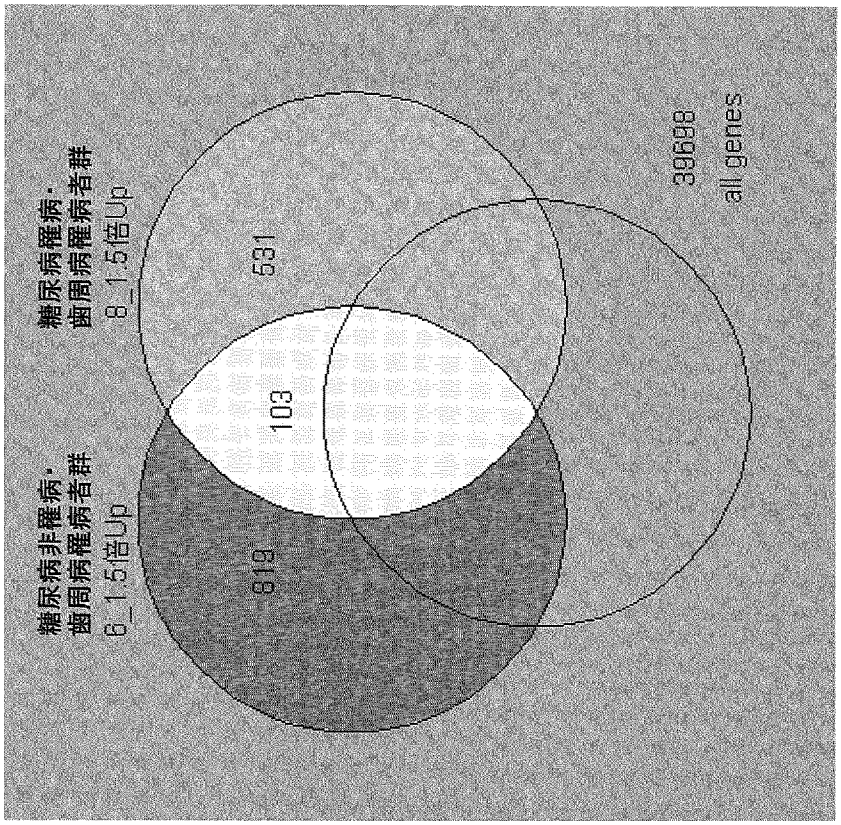
[図130]

図130 糖尿病非罹病・歯周病非罹病者群と糖尿病罹病・歯周病非罹病者群で笑いにより1/1.5倍以下の発現変化を認めた遺伝子



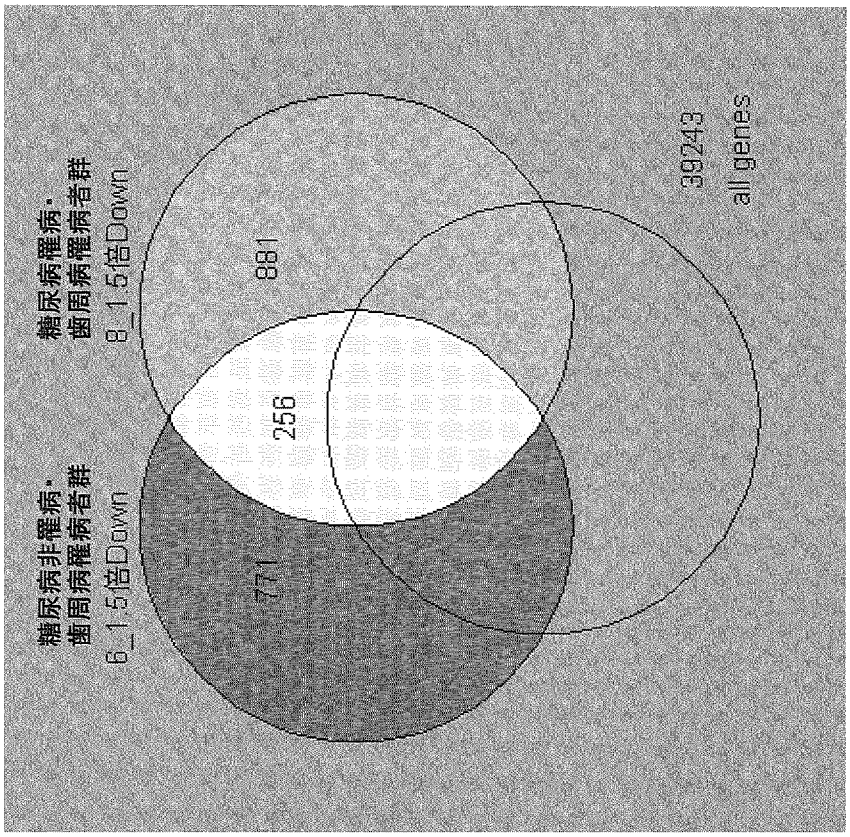
[図131]

図131 糖尿病非罹病・歯周病罹病者群と糖尿病罹病・歯周病罹病者群で笑いにより1.5倍以上の発現変化を認めた遺伝子



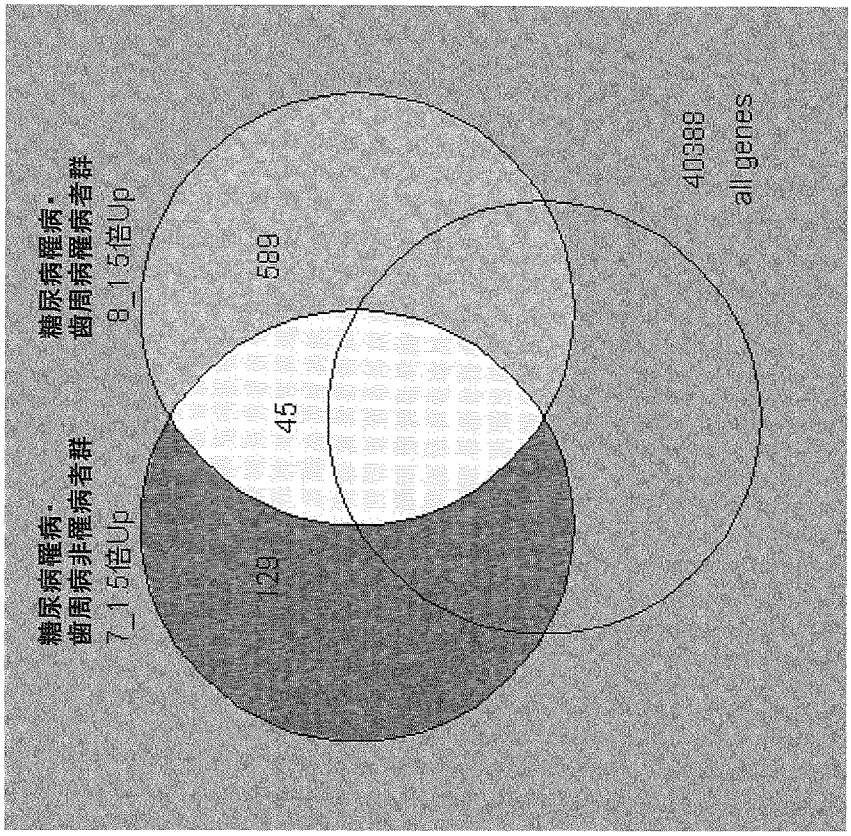
[図132]

図132 糖尿病非罹病・歯周病罹病者群と糖尿病罹病・歯周病罹病者群で笑いにより1/1.5倍以下の発現変化を認めた遺伝子



[図133]

図133 糖尿病罹病・歯周病非罹病者群と糖尿病罹病・歯周病罹病者群で笑いにより1.5倍以上の発現変化を認めた遺伝子



[図134]

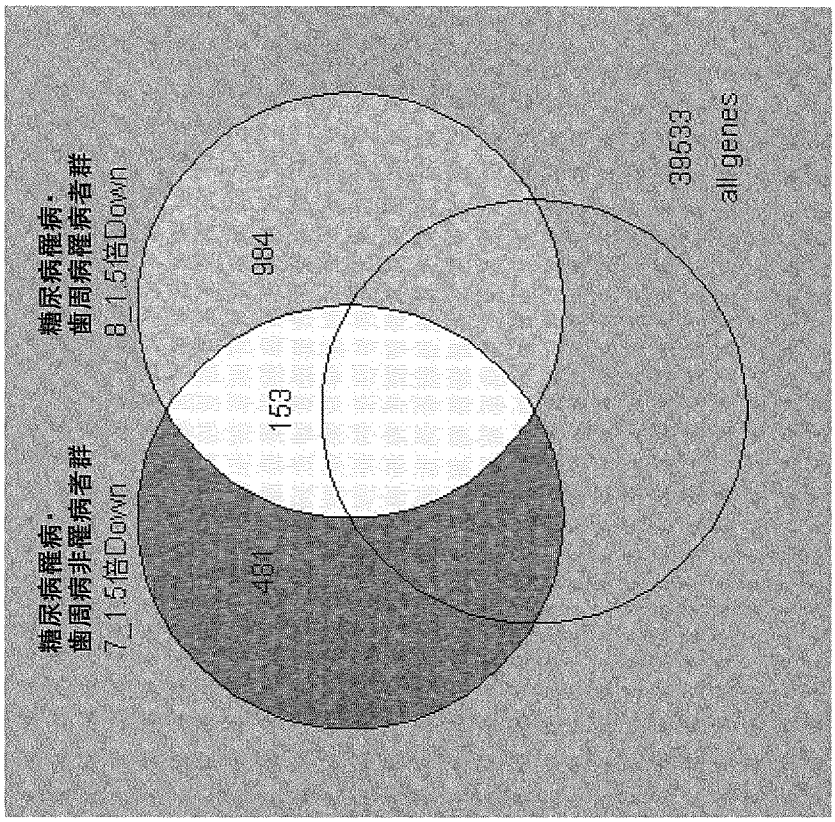


図134 糖尿病罹病・歯周病非罹病者群と糖尿病罹病・歯周病罹病者群で笑いにより1/1.5倍以下の発現変化を認めた遺伝子

[図135]

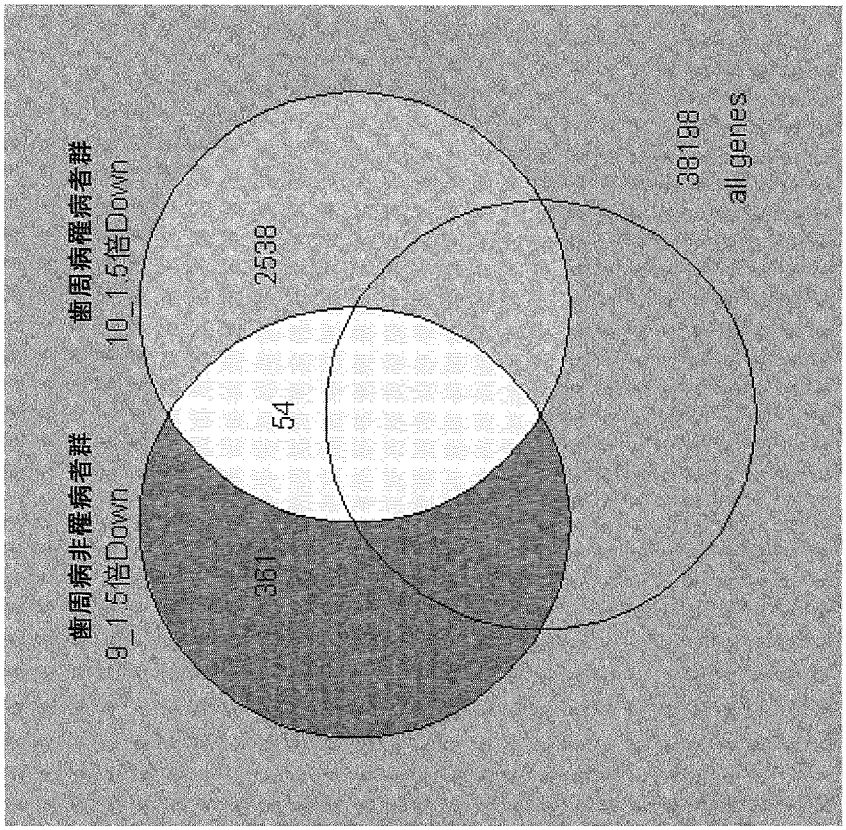


図135 歯周病非罹病者群と歯周病罹病者群で笑いにより1.5倍以上の発現変化を認めた遺伝子

[図136]

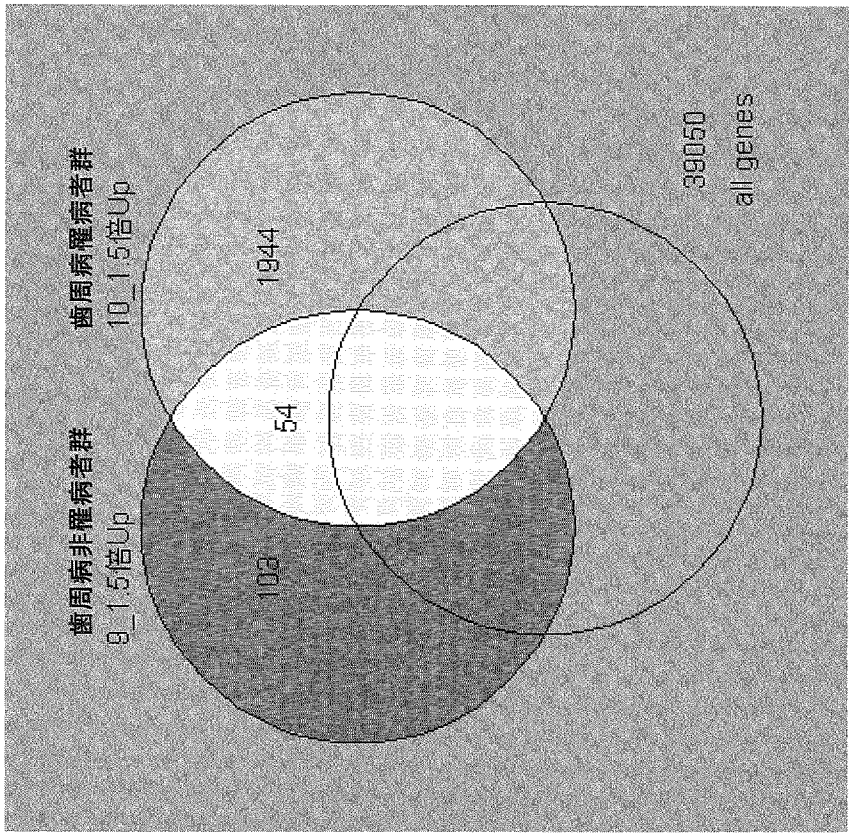


図136 歯周病非罹病者群と歯周病罹病者群で笑いにより1/1.5倍以下の発現変化を認めた遺伝子

INTERNATIONAL SEARCH REPORT

International application No.
PCT/JP2009/003040

A. CLASSIFICATION OF SUBJECT MATTER
C12N15/09(2006.01)i, *C07K16/18*(2006.01)i, *C12Q1/68*(2006.01)i, *G01N33/53*(2006.01)i

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)
C12N15/09, C07K16/18, C12Q1/68, G01N33/53

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched
Jitsuyo Shinan Koho 1922-1996 Jitsuyo Shinan Toroku Koho 1996-2009
Kokai Jitsuyo Shinan Koho 1971-2009 Toroku Jitsuyo Shinan Koho 1994-2009

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)
CAPLUS/BIOSIS/MEDLINE/WPIDS(STN), JSTPlus/JMEDPlus/JST7580(JDreamII)

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	HAYASHI Takashi et al., Laughter up-regulates the genes related to NK cell activity in diabetes, Biomedical Research, 2007, Vol.28, No.6, pp.281-285	1-25
Y	Kazuo MURAKAMI et al., "Kokoro to Karada no Kankei o Idenshi de Toku", Tenri Medical Bulletin, 2004, Vol.7, No.1, pages 1 to 22	1-25
Y	WOLBER K. Paul et al., The Agilent In Situ-Synthesized Microarray Platform, Methods in Enzymology, 2006, Vol.410, pp.28-57	1-25
Y	LU Z. Nick et al., Selective Regulation of Bone Cell Apoptosis by Translational Isoforms of the Glucocorticoid Receptor, Mol. Cel. Biol., 2007, Vol.27, No.20, pp.7143-7160	1-25

☒ Further documents are listed in the continuation of Box C. ☐ See patent family annex.

* Special categories of cited documents:
"A" document defining the general state of the art which is not considered to be of particular relevance
"E" earlier application or patent but published on or after the international filing date
"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)
"O" document referring to an oral disclosure, use, exhibition or other means
"P" document published prior to the international filing date but later than the priority date claimed
"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art
"&" document member of the same patent family

Date of the actual completion of the international search	Date of mailing of the international search report
28 July, 2009 (28.07.09)	11 August, 2009 (11.08.09)
Name and mailing address of the ISA/ Japanese Patent Office	Authorized officer
Facsimile No.	Telephone No.

Form PCT/ISA/210 (second sheet) (April 2007)

INTERNATIONAL SEARCH REPORT

International application No.
PCT/JP2009/003040

C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	PANKSEPP Jaak et al., Neuroevolutionary sources of laughter and social joy: Modeling primal human laughter in laboratory rats, Behavioural Brain Research, 2007, Vol.182, pp.231-244	1-25
Y	BURGDORF Jeffrey et al., Tickling induces reward in adolescent rats, Physiology & Behavior, 2001, Vol.72, pp.167-173	1-25
Y	FRIDLUND J. Alan et al., Relations between tickling and humourous laughter preliminary support for the Darwin-Hecker hypothesis, Biological Psychology, 1990, Vol.30, pp.141-150	1-25
P,X	HAYASHI Takashi et al., The effects of laughter on post-prandial glucose levels and gene expression in type 2 diabetic patients, Life Sciences, 2009, Vol.85, pp.185-187	1-25
A	HAYASHI Takashi et al., Laughter modulates prorenin receptor gene expression in patients with type 2 diabetes, Journal of Psychosomatic Research, 2007, Vol.62, pp.703-706	1-25
A	HAYASHI Keiko et al., Laughter lowered the increase in postprandial blood glucose, Diabetes Care, 2003, Vol.26, No.5, pp.1651-1652	1-25
A	Kazuo MURAKAMI, "Kagaku Gijutsu no Saizensen o Tenbo suru Idenshi Kogaku no Saisentan wa Ima -Anata no Nemureru Idenshi o Okosu-", Gijutsu to Keizai, 2004, No.450, pages 12 to 21	1-25

INTERNATIONAL SEARCH REPORT

International application No.
PCT/JP2009/003040

Box No. II Observations where certain claims were found unsearchable (Continuation of item 2 of first sheet)

This international search report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:

2. ☐ Claims Nos.:
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:

3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box No. III Observations where unity of invention is lacking (Continuation of item 3 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

1225 Types of genes (rat: 805 types of genes, human: 420 types of genes) recited in claims 1-25 share such a common property that the expression levels of the genes are altered by "laughter". However, genes of which the expression levels are altered by "laughter" are known, as disclosed in, for example, a document (Biomedical Research, 2007, Vol.28, No.6, pp281-285). Therefore, the inventions of claims 1-25 do not define a contribution which each of the inventions, considered as a whole, makes over the prior art, and cannot be regarded as being so linked as to form a single general inventive concept.

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.
2. ☒ As all searchable claims could be searched without effort justifying additional fees, this Authority did not invite payment of additional fees.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:

4. ☐ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

Remark on Protest

the

☐ The additional search fees were accompanied by the applicant's protest and, where applicable, payment of a protest fee.

☐ The additional search fees were accompanied by the applicant's protest but the applicable protest fee was not paid within the time limit specified in the invitation.

☐ No protest accompanied the payment of additional search fees.

国際調査報告

国際出願番号　ＰＣＴ／ＪＰ２００９／００３０４０

Ａ．　発明の属する分野の分類（国際特許分類（ＩＰＣ））

Int.Cl.　C12N15/09(2006.01)i, C07K16/18(2006.01)i, C12Q1/68(2006.01)i, G01N33/53(2006.01)i

Ｂ．　調査を行った分野

調査を行った最小限資料（国際特許分類（ＩＰＣ））

Int.Cl.　C12N15/09, C07K16/18, C12Q1/68, G01N33/53

最小限資料以外の資料で調査を行った分野に含まれるもの

日本国実用新案公報	１９２２－１９９６年
日本国公開実用新案公報	１９７１－２００９年
日本国実用新案登録公報	１９９６－２００９年
日本国登録実用新案公報	１９９４－２００９年

国際調査で使用した電子データベース（データベースの名称、調査に使用した用語）

CAPLUS/BIOSIS/MEDLINE/WPIDS(STN), JSTPlus/JMEDPlus/JST7580(JDreamII)

Ｃ．　関連すると認められる文献

引用文献のカテゴリー＊	引用文献名　及び一部の箇所が関連するときは、その関連する箇所の表示	関連する請求項の番号
Y	HAYASHI Takashi et al., Laughter up-regulates the genes related to NK cell activity in diabetes, Biomedical Research, 2007, Vol.28, No.6, pp.281-285	1-25
Y	村上和雄, 心と体の関係を遺伝子で解く, 天理医学紀要, 2004, 第７巻, 第１号, pp.1-22	1-25

☑　Ｃ欄の続きにも文献が列挙されている。　　☐　パテントファミリーに関する別紙を参照。

＊　引用文献のカテゴリー
「Ａ」特に関連のある文献ではなく、一般的技術水準を示すもの
「Ｅ」国際出願日前の出願または特許であるが、国際出願日以後に公表されたもの
「Ｌ」優先権主張に疑義を提起する文献又は他の文献の発行日若しくは他の特別な理由を確立するために引用する文献（理由を付す）
「Ｏ」口頭による開示、使用、展示等に言及する文献
「Ｐ」国際出願日前で、かつ優先権の主張の基礎となる出願の日の後に公表された文献
「Ｔ」国際出願日又は優先日後に公表された文献であって出願と矛盾するものではなく、発明の原理又は理論の理解のために引用するもの
「Ｘ」特に関連のある文献であって、当該文献のみで発明の新規性又は進歩性がないと考えられるもの
「Ｙ」特に関連のある文献であって、当該文献と他の１以上の文献との、当業者にとって自明である組合せによって進歩性がないと考えられるもの
「＆」同一パテントファミリー文献

国際調査を完了した日	国際調査報告の発送日
２８．０７．２００９	１１．０８．２００９

国際調査機関の名称及びあて先
日本国特許庁（ＩＳＡ／ＪＰ）
郵便番号１００－８９１５
東京都千代田区霞が関三丁目４番３号

特許庁審査官（権限のある職員）　４Ｎ　９５４９
引地　進
電話番号　０３－３５８１－１１０１　内線　３４８８

Ｃ（続き）．　関連すると認められる文献

引用文献のカテゴリー＊	引用文献名　及び一部の箇所が関連するときは、その関連する箇所の表示	関連する請求項の番号
Y	WOLBER K. Paul et al., The Agilent In Situ-Synthesized Microarray Platform, Methods in Enzymology, 2006, Vol.410, pp.28-57	1-25
Y	LU Z. Nick et al., Selective Regulation of Bone Cell Apoptosis by Translational Isoforms of the Glucocorticoid Receptor, Mol. Cel. Biol., 2007, Vol.27, No.20, pp.7143-7160	1-25
Y	PANKSEPP Jaak et al., Neuroevolutionary sources of laughter and social joy: Modeling primal human laughter in laboratory rats, Behavioural Brain Research, 2007, Vol.182, pp.231-244	1-25
Y	BURGDORF Jeffrey et al., Tickling induces reward in adolescent rats, Physiology & Behavior, 2001, Vol.72, pp.167-173	1-25
Y	FRIDLUND J. Alan et al., Relations between tickling and humourous laughter preliminary support for the Darwin-Hecker hypothesis, Biological Psychology, 1990, Vol.30, pp.141-150	1-25
PX	HAYASHI Takashi et al., The effects of laughter on post-prandial glucose levels and gene expression in type 2 diabetic patients, Life Sciences, 2009, Vol.85, pp.185-187	1-25
A	HAYASHI Takashi et al., Laughter modulates prorenin receptor gene expression in patients with type 2 diabetes, Journal of Psychosomatic Research, 2007, Vol.62, pp.703-706	1-25
A	HAYASHI Keiko et al., Laughter lowered the increase in postprandial blood glucose, Diabetes Care, 2003, Vol.26, No.5, pp.1651-1652	1-25
A	村上和雄, 科学技術の最前線を展望する　遺伝子工学の最先端は今－あなたの眠れる遺伝子を起こす－, 技術と経済, 2004, 第450号, pp.12-21	1-25

国際調査報告

国際出願番号　ＰＣＴ／ＪＰ２００９／００３０４０

第Ⅱ欄　請求の範囲の一部の調査ができないときの意見（第１ページの２の続き）

法第8条第3項（ＰＣＴ17条(2)(a)）の規定により、この国際調査報告は次の理由により請求の範囲の一部について作成しなかった。

１．☐ 請求項＿＿＿＿＿＿＿＿は、この国際調査機関が調査をすることを要しない対象に係るものである。
つまり、

２．☐ 請求項＿＿＿＿＿＿＿＿は、有意義な国際調査をすることができる程度まで所定の要件を満たしていない国際出願の部分に係るものである。つまり、

３．☐ 請求項＿＿＿＿＿＿＿＿は、従属請求の範囲であってＰＣＴ規則6.4(a)の第２文及び第3文の規定に従って記載されていない。

第Ⅲ欄　発明の単一性が欠如しているときの意見（第１ページの３の続き）

次に述べるようにこの国際出願に二以上の発明があるとこの国際調査機関は認めた。

請求項１－２５に記載された１２２５種類の遺伝子（ラット：８０５種、ヒト４２０種）は、「笑い」によって発現量を変化させる点で共通の性質を有しているが、例えば文献(Biomedical Research, 2007, Vol.28, No.6, pp281-285) に記載されているように、「笑い」によって発現量を変化させる遺伝子は公知であるから、請求項１－２５に係る発明は、全体として先行技術に対して貢献があるとは認められず、単一の一般的発明概念を形成するように連関しているものとは認められない。

１．☐ 出願人が必要な追加調査手数料をすべて期間内に納付したので、この国際調査報告は、すべての調査可能な請求項について作成した。

２．☑ 追加調査手数料を要求するまでもなく、すべての調査可能な請求項について調査することができたので、追加調査手数料の納付を求めなかった。

３．☐ 出願人が必要な追加調査手数料を一部のみしか期間内に納付しなかったので、この国際調査報告は、手数料の納付のあった次の請求項のみについて作成した。

４．☐ 出願人が必要な追加調査手数料を期間内に納付しなかったので、この国際調査報告は、請求の範囲の最初に記載されている発明に係る次の請求項について作成した。

追加調査手数料の異議の申立てに関する注意

☐ 追加調査手数料及び、該当する場合には、異議申立手数料の納付と共に、出願人から異議申立てがあった。

☐ 追加調査手数料の納付と共に出願人から異議申立てがあったが、異議申立手数料が納付命令書に示した期間内に支払われなかった。

☐ 追加調査手数料の納付はあったが、異議申立てはなかった。