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- (71) 出願人(米国を除く全ての指定国について): 学校
法人慶應義塾(KEIO UNIVERSITY) [JP/JP]; 〒
1088345 東京都港区三田二丁目15番45号
Tokyo (JP).
- (72) 発明者; および
- (75) 発明者/出願人(米国についてのみ): 岡田 洋平
(OKADA, Yohei) [JP/JP]; 〒1608582 東京都新宿区信
濃町35番地 慶應義塾大学医学部内 Tokyo
(JP). 岡野 栄之(OKANO, Hideyuki) [JP/JP]; 〒
1608582 東京都新宿区信濃町35番地 慶應義
塾大学医学部内 Tokyo (JP). 角田 達彦(TSUN-
ODA, Tatsuhiko) [JP/JP]; 〒2300045 神奈川県横浜市
鶴見区末広町1丁目7番22号 独立行政法人
理化学研究所 横浜研究所内 Kanagawa (JP). 宮
冬樹(MIYA, Fuyuki) [JP/JP]; 〒2300045 神奈川県横

浜市鶴見区末広町1丁目7番22号 独立行政
法人理化学研究所 横浜研究所内 Kanagawa (JP).

- (74) 代理人: 一色国際特許業務法人(ISSHIKI & CO.);
〒1050004 東京都港区新橋2丁目12番7号
労金新橋ビル Tokyo (JP).
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— 国際調査報告(条約第21条(3))

(54) Title: METHOD FOR SELECTING IPS CELL CLONE, AND METHOD FOR SELECTING GENE USED IN METHOD FOR SELECTING SAME

(54) 発明の名称: iPS細胞クローンの選択方法、及びその選択方法に用いる遺伝子の選択方法

(57) Abstract: The purpose of the present invention is to provide a method for selecting an iPS cell clone with which tumor formation is less likely even when caused to differentiate, and a method for selecting a gene used in the method for selecting the same. As one embodiment, the expression level is examined with regards to at least one gene in any gene group from among first through tenth gene groups in an iPS cell clone in an undifferentiated state, whereby there is selected an iPS cell clone in which tumor formation is less likely even when caused to differentiate. Also, the expression level of a gene belonging to a candidate gene group including one or more genes is examined in each iPS clone in an undifferentiated state in relation to a plurality of first iPS cell clones that cannot differentiate normally or that are likely to form a tumor when differentiated and a plurality of second iPS cell clones that are less likely to form a tumor, whereby there is selected a gene used in the method for selecting an iPS cell clone with which tumor formation is less likely even when caused to differentiate.

(57) 要約: 本発明は、分化させても腫瘍化が起きにくいiPS細胞クローンの選択方法、及びその選択方法に用いる遺伝子の選択方法を提供することを目的とし、一実施態様として、未分化状態のiPS細胞クローンにおいて、第1~第10遺伝子群のいずれかの遺伝子群において、少なくとも一つの遺伝子について、発現レベルを調べることによって、分化させても腫瘍化が起きにくいiPS細胞クローンを選択する。また、正常に分化できないか、あるいは分化しても腫瘍化を起こしやすい複数の第1のiPS細胞クローンと、腫瘍化を起こしにくい複数の第2のiPS細胞クローンにおいて、未分化状態の各iPS細胞クローンで、1以上の遺伝子を含む候補遺伝子群に属する遺伝子の発現レベルを調べることによって、分化させても腫瘍化が起きにくいiPS細胞クローンの選択方法に用いる遺伝子を選択する。

WO 2012/115270 A1

明 細 書

発明の名称：

i P S細胞クローンの選択方法、及びその選択方法に用いる遺伝子の選択方法

技術分野

[0001] 本発明は、i P S細胞クローンの選択方法、及びその選択方法に用いる遺伝子の選択方法に関する。

背景技術

[0002] i P S細胞 (induced pluripotent stem cells; 人工多能性幹細胞) は、多能性を有し、分化細胞から調製できるため、再生医療において移植に用いるための細胞として期待されている。しかしながら、i P S細胞を分化させて移植しても、in vivoでは、移植されたi P S細胞由来の細胞が腫瘍化する問題が指摘されている (Miura K. et al., Nat Biotechnol. 2009 vol.27: p .743-5.)。

発明の概要

発明が解決しようとする課題

[0003] 本発明は、分化させても腫瘍化が起きにくいi P S細胞クローンの選択方法、及びその選択方法に用いる遺伝子の選択方法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

[0004] 本発明は、以下のような各項からなる。

(1) i P S細胞クローンの選択方法であって、未分化状態のi P S細胞において、以下の第1～第12遺伝子群のいずれかの遺伝子群において、少なくとも一つの遺伝子について、発現レベルを調べる工程、を含む方法。

(2) 第1項に記載の選択方法であって、前記発現レベルを、正常に分化しないか、分化しても腫瘍化を起こしやすいi P S細胞クローンにおける当該遺伝子の発現レベル、及び、腫瘍化を起こしにくいi P S細胞クローンにお

ける当該遺伝子の発現レベルと比較する工程、をさらに含む方法。

(3) 第1項に記載の選択方法であって、前記iPS細胞クローンにおいて、第1～第12遺伝子群のいずれかの遺伝子群に属する全ての遺伝子の発現レベルを調べる工程と、調べた遺伝子群において、発現レベルに異常のある遺伝子の個数を調べる工程と、調べた遺伝子の個数を、正常に分化しないか、分化しても腫瘍化を起こしやすいiPS細胞クローンにおける発現レベルに異常のある遺伝子の個数、及び、腫瘍化を起こしにくいiPS細胞クローンにおける発現レベルに異常のある遺伝子の個数と比較する工程、をさらに含む方法。

(4) 第3項に記載の選択方法であって、腫瘍化を起こしにくい多能性幹細胞の発現レベルと比較することによって、前記発現レベルが異常かどうか判断することを特徴とする、方法。

(5) 第1項に記載の選択方法であって、前記iPS細胞クローンにおいて、第1～第12遺伝子群のいずれかの遺伝子群に属する全ての遺伝子の発現レベルを調べる工程と、調べた遺伝子群について、前記iPS細胞クローンにおける発現レベルと、正常に分化しないか、分化しても腫瘍化を起こしやすいiPS細胞クローンにおける発現レベルとを指標にして、iPS細胞クローンのclustering分析を行う工程と、当該iPS細胞クローンが、腫瘍化を起こしにくいiPS細胞クローンと正常に分化しないか、分化しても腫瘍化を起こしやすいiPS細胞クローンのいずれに分類されるかを調べる工程と、を含む方法。

(6) 第5項に記載の選択方法であって、腫瘍化を起こしにくい多能性幹細胞の発現レベルとの相対値を指標にして、前記iPS細胞クローンのclustering分析を行うことを特徴とする、請求項7に記載の方法。

(7) iPS細胞クローンを選択するために発現レベルを調べる遺伝子の選択方法であって、正常に分化しないか、分化しても腫瘍化を起こしやすい複数の第1のiPS細胞クローンと、腫瘍化を起こしにくい複数の第2のiPS細胞クローンにおいて、未分化状態のiPS細胞で、1以上の遺伝子を含

む候補遺伝子群に属する遺伝子の発現レベルを調べる工程、を含む方法。

(8) 前記候補遺伝子群に属する遺伝子が、多能性幹細胞で分化細胞より発現の高い遺伝子、及びDNA修復に関与する遺伝子であることを特徴とする、第7項に記載の方法。

(9) 前記候補遺伝子群に属する遺伝子が、第1遺伝子群及び第2遺伝子群のいずれかに属する遺伝子であることを特徴とする、第7項に記載の方法。

(10) 第7項に記載の選択方法であって、複数の第1のiPS細胞クローンにおいて得られた第1の発現レベルと、複数の第2のiPS細胞クローンにおいて得られた第2の発現レベルとを比較する工程と、第1の発現レベルと第2の発現レベルとが異なるかどうか調べる工程と、を含む方法。

(11) 第7項に記載の選択方法であって、複数の第1のiPS細胞クローンにおいて得られた発現レベルにおいて、発現レベルに異常のある遺伝子の第1の個数と、複数の第2のiPS細胞クローンにおいて得られた発現レベルのうち、発現レベルに異常のある遺伝子の第2の個数とを比較する工程と、第1の個数と第2の個数とが異なるかどうか調べる工程と、を含む方法。

(12) 第11項に記載の選択方法であって、腫瘍化を起こしにくい多能性幹細胞の発現レベルと比較することによって、前記発現レベルが異常かどうか判断することを特徴とする、方法。

(13) 第7項に記載の選択方法であって、前記iPS細胞クローンについて、前記発現レベルを指標にしてclustering分析を行う工程と、複数の第1のiPS細胞クローンと複数の第2のiPS細胞クローンが、それぞれ別のclusterに分類されるかどうか調べる工程と、を含む方法。

(14) 第13項に記載の選択方法であって、腫瘍化を起こしにくい多能性幹細胞の発現レベルとの相対値を指標にして、前記iPS細胞クローンについてclustering分析を行うことを特徴とする、方法。

[0005] ==関連文献とのクロスリファレンス==

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4 6 6 2 9 8に基づく優先権を主張するものであり、当該基礎出願を引用することにより、本明細書に含めるものとする。

図面の簡単な説明

[0006] [図1]本発明の一実施例において、表1に示した各iPS細胞クローンの発現レベルが、ヒトES細胞(KhES1-S3)の発現レベルの平均に比べて、0.667倍以下あるいは1.5倍以上という異常な発現レベルを示す遺伝子の個数をグラフ化した図である。

[図2]本発明の一実施例において、図中の各クローンにおける、表2に示した遺伝子の発現をclustering解析して得られたtreeを示した図である。

[図3]本発明の一実施例において、図中の各クローンにおける、表3に示した遺伝子の発現をclustering解析して得られたtreeを示した図である。

[図4]本発明の一実施例において、図中の各クローンにおける、表4に示した遺伝子の発現をclustering解析して得られたtreeを示した図である。

[図5]本発明の一実施例において、図中の各クローンにおける、表5に示した遺伝子の発現をclustering解析して得られたtreeを示した図である。

[図6]本発明の一実施例において、図中の各クローンにおける、表6に示した遺伝子の発現をclustering解析して得られたtreeを示した図である。

[図7]本発明の一実施例において、図中の各クローンにおける、表7に示した遺伝子の発現をclustering解析して得られたtreeを示した図である。

[図8]本発明の一実施例において、図中の各クローンにおける、表8に示した遺伝子の発現をclustering解析して得られたtreeを示した図である。

[図9]本発明の一実施例において、図中の各クローンにおける、表9に示した遺伝子の発現をclustering解析して得られたtreeを示した図である。

[図10]本発明の一実施例において、図中の各クローンにおける、表10に示した遺伝子の発現をclustering解析して得られたtreeを示した図である。

[図11]本発明の一実施例において、図中の各クローンにおける、表11に示した遺伝子の発現をclustering解析して得られたtreeを示した図である。

[図12]本発明の一実施例において、図中の各クローンにおける、表12に示

した遺伝子の発現をclustering解析して得られたtreeを示した図である。

[図13]本発明の一実施例において、ヒトiPS細胞を、3次ニューロスフェアに分化誘導し、NOS/SCIDマウスの脳に移植し、in vivoにおける造腫瘍性を解析した結果を示す写真である。

[図14]本発明の一実施例において、ヒトiPS細胞（253G4）を、3次ニューロスフェアに分化誘導し、NOS/SCIDマウスの脳に移植し、in vivoにおける移植iPS細胞の増殖を解析した結果を示す写真である。

[図15]本発明の一実施例において、ヒトiPS細胞を、3次ニューロスフェアに分化誘導し、NOD/SCIDマウスの精巢に注入し、3ヵ月後にテラトーマを摘出し、（A）外見、（B）長軸方向の長さ、（C）iPS細胞作製時に導入した初期化遺伝子の発現を観察した図である。

[図16]本発明の一実施例において、未分化状態のiPS細胞と、各細胞を分化させた3次ニューロスフェアに対し、アレイCGH解析を行なった結果を示す図である。（a）ゲノムDNA上で、異常が検出された場所を矢印で示している。（b）ゲノムDNA上で、異常が生じている遺伝子数がグラフで示されている。

[図17]本発明の一実施例において、全遺伝子を用いて、clustering解析を行なって得られたtreeを表す図である。

[図18]本発明の一実施例において、図中の各クローンにおける、表4に示した遺伝子の発現をclustering解析して得られたtreeを示した図である。

[図19]本発明の一実施例において、図中の各クローンにおける、表12に示した遺伝子の発現をclustering解析して得られたtreeを示した図である。

[図20]本発明の一実施例において、第12遺伝子群のプロープについて、ES細胞における発現の平均値から、シグナル強度に1.5倍以上の差があるプロープの個数を測定した結果を示すグラフである。

[図21]本発明の一実施例において、エピソーマルベクターを用いて作製したヒトiPS細胞を、3次ニューロスフェアに分化誘導し、NOD/SCIDマウスの精巢に注入し、3ヵ月後にテラトーマを摘出し、（A）外見を観察し、（B

）長軸方向の長さを測定した図である。

[図22]本発明の一実施例において、409B2由来の神経幹細胞を移植して得られた精巢の組織切片像及びその拡大図（A，B）である。

[図23]本発明の一実施例において、414C2由来の神経幹細胞を移植して得られた精巢の組織切片像及びその拡大図（A）である。

発明を実施するための形態

[0007] 以下、上記知見に基づき完成した本発明の実施の形態を、実施例を挙げながら詳細に説明する。

実施の形態及び実施例に特に説明がない場合には、J. Sambrook, E. F. Fritsch & T. Maniatis (Ed.), *Molecular cloning, a laboratory manual* (3rd edition), Cold Spring Harbor Press, Cold Spring Harbor, New York (2001); F. M. Ausubel, R. Brent, R. E. Kingston, D. D. Moore, J.G. Seidman, J. A. Smith, K. Struhl (Ed.), *Current Protocols in Molecular Biology*, John Wiley & Sons Ltd.; Juan S. Bonifacino (Bethesda, Maryland); Mary Dasso (Bethesda, Maryland); J. B. Harford, J. L-Schwartz, K. M. Yamada (Ed.), *Current Protocols in Cell Biology*, John Wiley & Sons Ltd.等の標準的なプロトコール集に記載の方法、あるいはそれを修飾したり、改変した方法を用いる。また、市販の試薬キットや測定装置を用いる場合には、特に説明が無い場合、それらに添付のプロトコールを用いる。

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[0008] (1) iPS細胞の作製方法

iPS細胞は、分化した細胞に初期化因子を導入し、脱分化させることに

よって製造できる。(Takahashi K & Yamanaka S. Cell 2006 vol.126: p.663-676; Takahashi K, et al., Cell 2007 vol.131: p.861-872)。

- [0009] 初期化方法は特に限定されないが、核初期化因子を導入することにより、多分化能及び自己増殖能を有するように誘導することが好ましい。例えば国際公開W02005/080598やW02007/069666に記載された初期化方法を用いることができる。
- [0010] 核初期化因子は、特に限定されないが、Oct遺伝子群、Klf遺伝子群、Sox遺伝子群のそれぞれの遺伝子群から選択された遺伝子の遺伝子産物の組み合わせを含むことが好ましく、iPS細胞樹立の効率という点では、遺伝子群の遺伝子産物をさらに含んだ組み合わせを含むことがより好ましい。Oct遺伝子群に属する遺伝子としては、Oct3/4、Oct1A、Oct6などがあり、Klf遺伝子群に属する遺伝子としては、Klf1、Klf2、Klf4、Klf5などがあり、Sox遺伝子群に属する遺伝子としては、Sox1、Sox2、Sox3、Sox7、Sox15、Sox17、Sox18などがある。Myc遺伝子群に属する遺伝子としては、c-Myc、N-Myc、L-Mycなどがある。
- [0011] 核初期化因子としては、上記組み合わせ以外にも、Oct遺伝子群の遺伝子、Sox遺伝子群の遺伝子に加え、Nanog遺伝子、lin-28遺伝子、及び／又はglis1遺伝子を含む組み合わせが挙げられる。また、これらの遺伝子のいずれかの組み合わせに加え、p53を欠損させてもよく、例えば、shp53によってp53遺伝子をノックダウンしてもよい。なお、細胞に導入する場合、上記組み合わせの遺伝子に加え、他にも遺伝子産物を導入してもよく、例えば、不死化誘導因子などが挙げられる。
- [0012] これらの遺伝子は、いずれも、脊椎動物で高度に保存されている遺伝子であり、本明細書では、特に動物名を示さない限り、ホモログを含めた遺伝子を表すものとする。また、polymorphismを含め、変異を有する遺伝子であっても、野生型の遺伝子産物と同等の機能を有する遺伝子もまた、含まれるものとする。
- [0013] さらに、これら遺伝子の組み合わせに加え、サイトカインや化合物を補助

因子として培地に添加しても良い。この場合のサイトカインとして、例えばS CFやbFGFなどが挙げられ、これらは、c-Mycに代替でき、化合物として、例えばバルプロ酸などが挙げられ、これは、c-Myc遺伝子やKlf4遺伝子に代替できる。

[0014] (2) i P S細胞クローンの選択方法

本発明にかかるi P S細胞クローンの選択方法は、未分化状態のi P S細胞において、表1～12に示す第1～第12の遺伝子群など、所定の遺伝子群において、少なくとも一つの遺伝子について、発現レベルを調べる工程を含む。

遺伝子の発現レベルの調べ方は、特に限定されず、例えば、未分化状態のi P S細胞から常法によって全mRNAを抽出し、そのmRNAを用いて、調べたい遺伝子をプローブにしてノザンブロットングを行ったり、逆転写の後PCRを行ったりすることで、その遺伝子の発現レベルを知ることができる。複数の遺伝子について同時に発現を調べる場合は、DNAアレイを用いることが好ましい。すなわち、調べたい遺伝子に対するプローブが固定されたDNAアレイに対し、標識した全mRNAをハイブリダイズさせ、得られたシグナルの強度を解析することによって、その遺伝子の発現レベルを知ることができる。

これまで、未分化状態のi P S細胞の遺伝子発現レベルを調べることによって、そのi P S細胞が分化した時にどのような性状を示すかを予測する方法は知られていなかった。しかし、本発明の一実施形態においては、未分化状態のi P S細胞において特定の遺伝子の発現レベルを調べ、その発現レベルを指標にすることによって、そのi P S細胞が腫瘍化を起こしにくいかどうか、を予測することが可能である。以下、その予測方法について、具体的な方法を説明するが、本発明の方法は、下記のものに限定されない。なお、本明細書で「i P S細胞クローンが腫瘍化を起こしにくい」とだけ言う時、i n vitroで分化した時あるいはi n vivoに移植して分化した場合に、そのクローンが腫瘍化しにくいということを意味するのであって、分化しない場合は

含まないものとする。

[0015] [1] 特定の遺伝子の発現を比較する方法

所定の遺伝子群のうちの少なくとも一つの遺伝子について、予め、正常に分化しないか、分化しても腫瘍化を起こしやすい i P S 細胞クローンにおける当該遺伝子の発現レベルと、腫瘍化を起こしにくい i P S 細胞クローンにおける当該遺伝子の発現レベルとを、それぞれ 1 以上の i P S 細胞クローンを用いて決定し、そして、これらの発現（以下、対象発現と称する）のレベルを、性状を調べたい i P S 細胞クローンにおける当該遺伝子の発現のレベルと比較する。

[0016] ここで、あるクローンが腫瘍を起こしやすいかどうかを判断する方法は特に限定されないが、例えば、i P S 細胞からニューロスフェアを分化させ (Okada et al., Stem Cells. 2008 vol.26: p.3086-98; Miura K. et al., Nat Biotechnol. 2009 vol.27: p.743-5)、NOD/SCIDマウスの線条体や精巢に移植し、1～6ヶ月後にニューロスフェアの分化状態を調べ、腫瘍が形成されたかどうかを調べたり、形成された場合、その大きさや個数を調べたり、移植細胞の異常増殖等を調べたりすればよい (Okada et al., Stem Cells. 2008 vol.26: p.3086-98; Miura K. et al., Nat Biotechnol. 2009 vol.27: p.743-5)。腫瘍を起こしやすいかどうかの基準は、i P S 細胞の使用目的によって、当業者が適切に決定すればよく、例えば、治療目的の移植に用いる場合は、厳しい基準とすればよく、形成された腫瘍を研究する場合は、緩い基準にすれば良い。この時、全ての種類の腫瘍について考慮に入れてもよいが、グリオーマなど特定の腫瘍についてのみ考慮に入れてもよい。

[0017] 対照発現レベルの数値化の方法は特に限定されず、複数のクローンにおける発現レベルのリスト、複数のクローンにおける発現レベルの平均または平均±標準偏差（または誤差）、複数のクローンにおける発現レベルの上限から下限までの範囲、複数のクローンにおける発現レベルから推測または統計的に計算された値または範囲など、性状を調べたいクローンにおいて調べた発現レベルがどちらの発現レベルに適合するかが判定できる限り、いずれの

数値化であってもよい。そして、その数値化のやり方によって、適切な比較方法を選択することができる。例えば、調べた発現レベルと対照発現レベルの間に有意差はあるか、あるいは、調べた発現レベルは対照発現レベルの範囲の中に入っているか等を検定する。そして、調べた発現レベルが、正常に分化しないか、分化しても腫瘍化を起こしやすいクローンの対照発現レベルに適合すると判定された場合、そのクローンは正常に分化しないか、分化しても腫瘍化を起こしやすいクローンである、あるいは腫瘍化を起こしにくいクローンではないと判断し、腫瘍化を起こしにくいクローンにおける対照発現レベルに適合すると判定された場合、そのクローンは腫瘍化を起こしにくい i P S 細胞であると判断する。

[0018] [2] 発現に異常のある遺伝子の個数を比較する方法

あるいは、予め、1以上の正常に分化しないか、分化しても腫瘍化を起こしやすい i P S 細胞クローンと1以上の腫瘍化を起こしにくい i P S 細胞クローンにおいて、所定の遺伝子群の全ての遺伝子の発現レベルを決定し、発現レベルに異常のある遺伝子の個数を算出し、それぞれの i P S 細胞クローンにおいて発現レベルに異常のある遺伝子の個数を決定（以下、対照個数と称する）する。そして、性状を調べたい i P S 細胞クローンにおいて発現レベルに異常のある遺伝子の個数を対照個数と比較する。

[0019] ここで、一つの遺伝子について、複数種類のプローブを用いて調べた結果を用いてclustering解析を行ってもよいが、複数種類のプローブを用いる遺伝子の割合は少ない方が好ましく、全体の20%未満であることが好ましく、10%未満であることがより好ましく、0%であることが最も好ましい。一つの遺伝子について、複数種類のプローブを用いる場合であっても、プローブの種類も少ない方が好ましく、三種類以下のプローブを用いるのが好ましく、二種類以下のプローブを用いるのがより好ましいが、最も好ましいのは一種類のプローブを用いる場合である。また、検出できる遺伝子が特定されていないプローブを用いても良いが、その数は少ない方が好ましく、全体の20%未満であることが好ましく、10%未満であることがより好ましく

、０％であることが最も好ましい。なお、正常に分化しないか、分化しても腫瘍化を起こしやすいか、については、[１]と同様にして判断できる。

[0020] 発現レベルに異常があるかどうかを判断する方法は特に限定されないが、正常な多能性幹細胞クローンと比較して決めることが好ましい。ここで、正常な多能性幹細胞クローンとしては、腫瘍化を起こしにくい多能性幹細胞クローンであればよく、多能性幹細胞は、ＥＳ細胞でもｉＰＳ細胞でもよい。そして、遺伝子群の各遺伝子について、正常な多能性幹細胞クローンにおける発現レベルと比較して、所定の割合以下、及び所定の割合以上の発現レベルを異常とする。例えば、異常とする割合は、１０％以下、２０％以下、５０％以下、６６．７％以下、８０％以下、あるいは、１２０％以上、１２５％以上、１３３．３％以上、１５０％以上、１８０％以上を例示できる。

[0021] ここでも、対照個数の提示の仕方は特に限定されず、複数のクローンにおける個数のリスト、複数のクローンにおける個数の平均または平均±標準偏差（または誤差）、複数のクローンにおける個数の上限から下限までの範囲、複数のクローンにおける個数から推測または統計的に計算された値または範囲など、性状を調べたいクローンにおいて調べた個数がどちらに適合するかが判定できる限り、いずれの表示であってもよい。そして、その表示の仕方によって、適切な比較方法を選択することができる。例えば、調べた個数と対照個数の間に有意差はあるか、あるいは、調べた個数は対照個数の範囲の中に入っているか等を検定する。そして、調べた個数が、正常に分化しないか、分化しても腫瘍化を起こしやすいクローンの対照個数に適合すると判定された場合、そのクローンは正常に分化しないか、分化しても腫瘍化を起こしやすいクローンである、あるいは腫瘍化を起こしにくいクローンではないと判断され、腫瘍化を起こしにくいクローンにおける対照個数に適合すると判定された場合、そのクローンは腫瘍化を起こしにくいクローンであると判断される。

[0022] [３]clustering分析によって分類する方法

あるいは、予め、１以上の正常に分化しないか、分化しても腫瘍化を起こ

しやすい i P S 細胞クローンと 1 以上の腫瘍化を起こしにくい i P S 細胞クローンにおいて、所定の遺伝子群の全ての発現レベルを決定する。ここで、そして、性状を調べたい i P S 細胞クローンにおいても、同じ遺伝子群の全ての発現レベルを決定し、各 i P S 細胞クローンの clustering 解析を行なう。

[0023] ここで、一つの遺伝子について、複数種類のプローブを用いて調べた結果を用いて clustering 解析を行ってもよいが、複数種類のプローブを用いる遺伝子の割合は少ない方が好ましく、全体の 20%未満であることが好ましく、10%未満であることがより好ましく、0%であることが最も好ましい。一つの遺伝子について、複数種類のプローブを用いる場合であっても、プローブの種類も少ない方が好ましく、三種類以下のプローブを用いるのが好ましく、二種類以下のプローブを用いるのがより好ましいが、最も好ましいのは一種類のプローブを用いる場合である。また、検出できる遺伝子が特定されていないプローブを用いても良いが、その数は少ない方が好ましく、全体の 20%未満であることが好ましく、10%未満であることがより好ましく、0%であることが最も好ましい。なお、正常に分化しないか、分化しても腫瘍化を起こしやすいか、及び所定の遺伝子群の中の遺伝子について、発現に異常があるかどうか、については、[1]と同様にして判断できる。

[0024] ここで、clustering 分析を行なう際、調べた発現レベルが異常かどうかを指標にしてもよい。発現レベルに異常があるかどうかを判断する方法は、[2]の記載と同様である。なお、clusteringt は、Cluster 3.0 (東京大学医科学研究所ヒトゲノム解析センター DNA 情報解析分野によるフリーウェア ; M. J. L. de Hoon, S. Imoto, J. Nolan, and S. Miyano: Open Source Clustering Software. Bioinformatics, 20 (9): 1453--1454 (2004). ; <http://bonsai.hgc.jp/~mdehoon/software/cluster/>) や Gene spring GX (Agilent 社) などのソフトを用いて行うことができる。

[0025] clustering 分析の結果、性状を調べたい i P S 細胞が、正常に分化しないか、分化しても腫瘍化を起こしやすいクローンに分類された場合、そのクロ

ーンは正常に分化しないか、分化しても腫瘍化を起こしやすいクローンである、または腫瘍化を起こしにくいクローンではないと判断され、腫瘍化を起こしにくいクローンに分類された場合、そのクローンは腫瘍化を起こしにくい i P S 細胞であると判断される。

[0026] (3) 遺伝子の選択方法

(1) で述べたように、未分化状態の i P S 細胞クローンにおいて、第 1 ～第 1 2 遺伝子群など、所定の遺伝子群のうちの少なくとも一つの遺伝子について、発現レベルを調べることによって、腫瘍化を起こしにくい i P S 細胞クローンを選択できる。

[0027] あるクローンが腫瘍化を起こしにくいかどうかを判断するために、どの遺伝子あるいはどの遺伝子群について発現レベルを調べるかについては、i P S 細胞の起源によっても異なる可能性があるが、当業者が試行錯誤することなく、容易に決定することができる。以下、その決定方法について述べる。

[0028] まず、クローンを選択するための遺伝子として使用できるかどうかを調べる候補遺伝子を選択する。この選択方法は、特に限定されず、ランダムに選んでも良いが、多能性幹細胞で分化細胞より発現の高い遺伝子や D N A 修復に関与する遺伝子から選ぶのが好ましく、さらに第 1 遺伝子群及び第 2 遺伝子群から選ぶのがより好ましい。それによって、極めて高確率で目的のクローンを選択するための遺伝子を選択することが可能になる。それらの遺伝子群からの候補遺伝子の選び方も特に限定されないが、実施例のように、腫瘍化を起こしにくい多能性幹細胞クローンと、正常に分化しないか、分化しても腫瘍化を起こしやすい多能性幹細胞クローンとの間で、発現レベルが顕著に異なるような遺伝子を選択することが好ましい。こうして選択した、1 以上、好ましくは 2 以上の遺伝子を含む遺伝子の群を第 X 遺伝子群とする。

[0029] なお、多能性幹細胞で分化細胞より発現の高い遺伝子は、R T - P C R やマイクロアレイ等を用いて、当業者には容易に調べることが可能である。また、D N A 修復に関与する遺伝子とは、D N A 修復過程のいずれか 1 つの過程に関わっている遺伝子であればよく、論文、特許公報、データベース等で

そのように報告されている遺伝子であってもよい。これらの報告は、例えば、PUBMED、各国（例えば、日本、欧州、米国）特許庁やWIP0のHP、GO（Gene Ontology）などのデータベースからアクセス可能なデータベースに載っている論文や特許公報から検索することができる。すなわち、DNA修復に関与する遺伝子とは、PUBMEDや各国（例えば、日本、欧州、米国）特許庁やWIP0のデータベースやGOのデータベースに含まれている論文、特許公報、遺伝子情報の中に、機能の少なくとも一つがDNA修復に関与していることが報告されている遺伝子であることが最も好ましい。

[0030] 次に、正常に分化しないか、分化しても腫瘍化を起こしやすい1以上の、好ましくは複数の第1のiPS細胞クローンと、腫瘍化を起こしにくい1以上の、好ましくは複数の第2のiPS細胞において、未分化状態の各iPS細胞で、第X遺伝子群に属する遺伝子の発現レベルを調べる。そして、この発現レベルを指標にして、第1のiPS細胞クローンと第2のiPS細胞クローンを比較する。比較の方法は特に限定されないが、以下に、いくつかの具体例を述べる。

[0031] [1]発現レベル自体を比較する方法

例えば、第1のクローンの発現レベルと、第2のクローンの発現レベルが異なるかどうか調べる。

[0032] ここで、発現レベルが異なるという判断は、腫瘍化を起こしにくいかどうか不明のクローンにおいて、同様に第X遺伝子群の遺伝子の発現レベルを調べ、そのクローンが、第1のクローンと第2のクローンのどちらに適合するかが判断できれば、どのような基準で判断してもよい。例えば、第1及び第2のクローンにおける発現レベルを、それぞれ最低レベルと最高レベルの範囲で表し、それらの範囲が重ならない場合に異なると判断しても良く、それぞれ平均値で表し、それらの値に有意差がある場合に異なると判断してもよいが、これらに限定されない。

[0033] このように、第1のクローンと第2のクローンにおける発現レベルを比較し、それらが異なるようであれば、この第X遺伝子群は、腫瘍化を起こしに

くいクローンを選択するための遺伝子群として用いることができる。

[0034] [2] 多能性幹細胞と発現レベルが異なる遺伝子数を比較する方法

あるいは、第X遺伝子群の中で、第1及び第2のiPS細胞クローンにおいて、正常な多能性幹細胞クローンと発現レベルが異なる遺伝子の個数を測定し、それらの個数が異なれば、この第X遺伝子群は、腫瘍化を起こしにくいiPS細胞クローンを選択するための遺伝子群として用いることができる。なお、正常な多能性幹細胞クローンとは、in vitroまたはin vivoに移植した時に、腫瘍化を起こしにくいことが判明している多能性幹細胞クローンのことであって、腫瘍化を起こしにくいのであれば、ES細胞であってもよく、iPS細胞であってもよい。

[0035] ここで、個数が異なるという判断は、腫瘍化を起こしやすいかどうか不明のiPS細胞クローンにおいて、同様に第X遺伝子群の遺伝子の発現レベルを調べ、正常な多能性幹細胞クローンと発現レベルが異なる遺伝子の個数が、第1のiPS細胞クローンと第2のiPS細胞クローンのどちらに適合するかが判断できれば、どのような基準で判断してもよい。ここで、正常な多能性幹細胞クローンと発現レベルが異なると判断するための基準は、[1]に記載の方法と同様の方法で行うことができる。そして、第1のiPS細胞クローンと第2のiPS細胞クローンとの間で、例えば、個数の分布範囲が重ならなかったり、個数の平均値が有意に異なったりするようであれば、この第X遺伝子群は、腫瘍化を起こしにくいiPS細胞クローンを選択するための遺伝子群として用いることができる。

[0036] [3] clustering分析の結果を比較する方法

この方法は、第X遺伝子群に属する遺伝子について、第1及び第2のiPS細胞クローンにおいて、正常な多能性細胞クローンと発現レベルを比較し、その比較結果を用いて、iPS細胞をclustering解析し、第1及び第2のiPS細胞クローンが、それぞれ別のclusterとして分類されれば、腫瘍化を起こしにくいiPS細胞クローンを選択するための遺伝子群として用いることができる。clusteringの方法は、(1)[3]で述べたのと同じ方法を用い

ることができる。

実施例

[0037] (1) 用いた多能性幹細胞クローンの性状の評価

実施例においては、ヒトES細胞クローンとして、KhES1～KhES3の3クローン (Suemori et al. Biochem Biophys Res Commun. 2006 vol.345: p.926-32.)、ヒトiPS細胞クローンとして、201B6、201B7、253G1、253G4の各クローン (Takahashi et al., Cell. 2007 131:861-72; Nakagawa et al. Nat Biotechnol. 2008 vol.26: p.101-6.) を用いた。培養は、通常に使用される方法を用いた (Suemori et al. Biochem Biophys Res Commun. 2006 vol.345: p.926-32.)。

[0038] まず、これらのiPS細胞クローンを、公知の方法 (国際公開W02010/090007号公報) を用いて、in vitroでニューロスフェアに分化させたところ、201B6のみ、ニューロスフェアが形成されなかったが、201B7、253G1、253G4からは、正常にニューロスフェアが形成された。

ニューロスフェアが形成された3系統について、2回継代した後、3次ニューロスフェアを、公知の方法 (国際公開W02010/090007号公報) を用いて神経系細胞に分化誘導したところ、大部分が神経細胞に分化し、グリア細胞はほとんど分化しなかった。なお、対照として、KhES1細胞をin vitroで分化させたものを用いた。

マイクロアレイにより、遺伝子発現profileを検討すると、ヒトiPS細胞から誘導した神経幹細胞も、ヒトES細胞から誘導した神経幹細胞とほぼ同様のProfileを示した (後述の(6)比較例参照)。なお、ヒトiPS細胞分化後の3次ニューロスフェアでは、TRA-1-60、TRA-1-81、NCAMなどの未分化マーカーはほとんど検出されず、これらのヒトiPS細胞クローンには、分化抵抗性の細胞や未分化細胞の残存はほとんど無いことが確認された。

また、ニューロスフェアが形成された3クローンについては、電気生理学的に解析をしたが、ヒトES細胞と同様に活動電位が記録され、これらの3

クローンは機能的なニューロンに分化できることが示された。

[0039] (2) 用いた多能性幹細胞の造腫瘍性の評価

ここでは、これらのヒト i P S 細胞クローンを、3 次ニューロスフェアに分化誘導し、細胞を分離して、NOS/SCIDマウスの脳に移植し、in vivoにおける分化能と造腫瘍性を解析した。

[0040] まず、公知の方法 (Okada et al., Stem Cells, 2008 vol.26: p.3086-98; Miura K. et al., Nat Biotechnol, 2009 vol.27: p.743-5) で、各 i P S 細胞からヒト E B (Embryoid body; 胚様体) を作製し、その後、1 次ニューロスフェアに分化誘導した。なお、i P S 細胞クローンの一つ 2 0 1 B 6 は、正常に分化しなかった。ここで、Venusを発現するレンチウイルス (Okada et al., Stem Cells, 2008 vol.26: p.3086-98) を導入し、Venusを発現する神経幹細胞を製造した。さらに、2 回継代して 3 次ニューロスフェアを作製し、単一の細胞に分離して、 $1 - 5 \times 10^5$ 個の細胞をNOD/SCIDマウスの線条体に注入した (Ogawa et al., J Neurosci Res, 2009 vol.87: p.307-17; Miura K. et al., Nat Biotechnol, 2009 vol.27: p.743-5)。細胞注入 6 ヶ月後、マウスから脳を摘出し、神経細胞、アストロサイト、オリゴデンドロサイト、それぞれのマーカーに対する抗体を用いて、免疫組織化学的に、移植した細胞の分化状態を調べたところ、in vivoでは、3 つの神経系細胞に分化していた。また、分化した神経細胞の種類も、TH陽性カテコラミン作動性ニューロン、ChAT陽性コリン作動性ニューロン、GAD67 陽性GABA作動性ニューロンが検出され、いずれのクローンも正常な分化能を有していた。

[0041] 同時に、マウス脳切片をH E 染色したところ、2 5 3 G 1、2 5 3 G 4 を移植したマウス脳では、低級グリオーマの像が観察され、核異型を有する細胞 (図では鋸で示されている) も観察された (図 1 3)。これに対し、2 0 1 B 7 を移植したマウス脳では、対照のK h E S 1 と同様、正常な脳組織が観察された (図 1 3)。

特に、脳の組織切片上でvenusが発現している面積を調べたところ、2 5 3 G 1 及び 2 5 3 G 4 では腫瘍化の兆候が見られ、特に 2 5 3 G 4 の移植組織

では、移植細胞由来の巨大な腫瘍が観察された（図14）。なお、201B7では、対照のK h E S 1と同様、移植細胞に以上は見られなかった。

[0042] 次に、未分化細胞の残存について、より高感度に解析するために、3次ニューロスフェアを単一の細胞に分離して、 $1-5 \times 10^5$ 個の細胞をNOD/SCIDマウスの精巣に注入し、3ヵ月後に精巣を摘出し、外見（A）、長軸方向の長さ（B）、i P S細胞作製時に導入した初期化遺伝子の発現（C）を観察した（図15）。201B7では、全ての点で、対照のK h E S 1と同様であったが、253G1では、細胞の増殖はほぼ正常だったが、対照のK h E S 1とは異なり、初期化遺伝子（P O U 5 F 1のみ）の発現が認められた。253G4では、細胞の増殖が著しく、初期化遺伝子（特にP O U 5 F 1）の発現も著しく亢進していた。また、組織化学的な解析では、脳の組織切片と同様に、201B7を移植したマウス脳では、対照のK h E S 1と同様、正常組織であったが、253G1及び253G4を移植したマウス脳では低級グリオーマの像が観察され、特に253G4は悪性度が高かった。

[0043] 以上から、201B7は、組織に移植した時、in vivoで腫瘍化を起こしにくいクローンであり、253G1及び253G4は、in vivoで腫瘍化を起こしやすいクローンであると考えられ、以下の実験では、特定の遺伝子群の発現パターンで、201B7がES細胞と同じパターンを取り、253G1及び253G4は、それらと異なるパターンを取ることを示す。

[0044] （3）第1～第10遺伝子群を用いたi P S細胞クローンの分類

ここでは、多能性幹細胞で分化細胞より発現の高い遺伝子群、DNA修復に関与する遺伝子群、及びそれらに共通する遺伝子群から、様々な遺伝子群を抽出し、それらについて、ES細胞及びi P S細胞における未分化状態での発現パターンを調べ、その発現パターンによって、腫瘍化を起こしにくいクローンと、正常に分化しないか、分化しても腫瘍化を起こしやすいクローンが区別できることを示す。

[0045] [1]遺伝子群の抽出

まず、マイクロアレイHuman U-133 Plus 2.0 Array (Affymetrix社)を用い

て、多能性幹細胞で分化細胞より発現の高い遺伝子として、22種類のヒト組織（骨髄、小脳、大脳皮質、胎児脳、心臓、腎臓、肝臓、肺、脾臓、前立腺、唾液腺、骨格筋、小腸、脊髄、脾臓、胃、精巣、胸腺、甲状腺、気管支、子宮）の発現レベルと、K h E S 1～K h E S 3のE S細胞クローンの発現レベルを比較し、

1. F D R (False Discovery Rate) のq値が0.05未満であること
2. E S 3クローン全てがpフラグであること
3. E S 3クローン全てで、ヒト組織の発現レベルの平均より5倍以上高いこと。

の3つの条件を満たすプローブ1340個（表1）（特定された遺伝子種929個；対応遺伝子が特定されていないプローブ102個を含む）を選択し、特定された遺伝子種929個を第1遺伝子群とした。ここで、特定された遺伝子とは、遺伝子名が判明し、単一に数えられた遺伝子のことを言う。

[0046] 第1遺伝子群から、K h E S 1～K h E S 3のE S細胞クローンの発現レベルの平均と201B7の発現レベルが2倍以上であるプローブを除いた1304個のプローブ（表2）（特定された遺伝子種906個；対応遺伝子が特定されていないプローブ96個を含む）からなる遺伝子群を選択し、特定された遺伝子種906個を第2遺伝子群とした。

[0047] 一方、DNA修復に関与する遺伝子群として、G O (Gene Ontology) のデータベースにおいて、DNA repairで登録されているhumanの遺伝子を抽出したところ、DNArepairに関するとされている遺伝子が313個得られた。また、文献中 (Wood et al., Science 2001 vol.291 p.1284; Wood et al., 2005 Mutation research vol.577 p.275; Negrini Nat Rev Mol Cell Biol. 2010 vol.113: p.220-8.) にDNArepairに関するとされている遺伝子163個を得て、重複なく332個抽出して第3遺伝子群を作製し、それらに対応するプローブ676個を選択した（表3）。そして、第2遺伝子群と第3遺伝子群で重複している83個のプローブ（表4）（特定された遺伝子種60個を含む）を選択し、特定された遺伝子種60個を第4遺伝子群とした。

[0048] さらに、第1遺伝子群の遺伝子から、201B6、253G1、253G4すべての発現レベルが、ES3クローンの発現レベルの平均より1.5倍以上であり、201B7の発現レベルとESの平均との差が1.5倍以内である80個のプローブ（表5）（特定された遺伝子種70個；対応遺伝子が特定されていないプローブ3個を含む）を選択し、特定された遺伝子種70個を第5遺伝子群とし；第1遺伝子群の遺伝子から、201B6、253G1、253G4すべての発現レベルがES3クローンの発現レベルの平均より1.5倍以上であり、さらに、ES3クローンと201B7のすべてで、ES3クローンの発現レベルの平均との差が1.5倍以内である72個のプローブ（表6）（特定された遺伝子種63個；対応遺伝子が特定されていないプローブ2個を含む）を選択し、特定された遺伝子種63個を第6遺伝子群とし；第3遺伝子群の遺伝子から、201B6、253G1、253G4のすべての発現レベルが、ES3クローンの発現レベルの平均より1.5倍以上である59個のプローブ（表7）（特定された遺伝子種54個を含む）を選択し、特定された遺伝子種54個を第7遺伝子群とし；第7遺伝子群の遺伝子から、ES3クローンと201B7のすべてで、ES3クローンの発現レベルの平均との差が1.5倍以内である18個のプローブ（表8）（特定された遺伝子種17個を含む）を選択し、特定された遺伝子種17個を第8遺伝子群とし；第4遺伝子群の遺伝子から、201B6、253G1、253G4のいずれかの発現レベルが、ES3クローンの発現レベルの平均より1.5倍以上であり、201B7の発現レベルとESの平均との差が1.5倍以内である13個のプローブ（表9）（特定された遺伝子種13個を含む）を選択し、対応する遺伝子を第9遺伝子群とし；第4遺伝子群の遺伝子から、201B6、253G1、253G4のすべての発現レベルが、ES3クローンの発現レベルの平均より1.5倍以上であり、201B7の発現レベルとESの平均との差が1.5倍以内である5個のプローブ（表10）（特定された遺伝子種5個を含む）を選択し、対応する遺伝子を第10遺伝子群とした。

[0049] <マイクロアレイを用いた解析方法>

マイクロアレイとして、Affymetrix社 U133plus2.0を用いた。

正常ヒト組織（骨髄、小脳、大脳皮質、胎児脳、心臓、腎臓、肝臓、肺、膵臓、前立腺、唾液腺、骨格筋、小腸、脊髄、脾臓、胃、精巣、胸腺、甲状腺、気管支、子宮）のRNAは、Clontech, Ambion, Cell Applications, Stratagene社から購入した。他の細胞などに関しては、Trizol (Invitrogen社) にて全RNAを回収し、RNAeasy mini kit (Qiagen社) を用いてカラム精製を行った。また、キアゲン社のRNAase-free DNaseにより処理し、混入するDNAを分解した。RNAの品質は、Bioanalyzer 2100 (Agilent社)を用いて確認した。

[0050] [2]発現に異常のある遺伝子の個数を比較する方法

ここでは、第1遺伝子群の遺伝子を含むプローブにおいて、各iPS細胞の発現レベルが、ES3クローンの発現レベルの平均に比べて、0.667倍以下あるいは1.5倍以上という異常な発現レベルを示すプローブの個数を調べ、その結果を図1にグラフ化した。

[0051] 腫瘍化を起こしにくいiPS細胞(201B7)と、正常に分化しないか(201B6)、分化しても腫瘍化を起こしやすい(253G1、253G4)iPS細胞とでは、発現に異常のあるプローブの個数に有意な差があった。

[0052] 従って、第1遺伝子群の遺伝子の発現を調べ、腫瘍化を起こしにくい多能性幹細胞に対して発現に異常のある遺伝子の個数を調べることにより、腫瘍化を起こしにくいかどうかを判断できる。

[0053] [3]clustering分析によって分類する方法

ここでは、第2～第10遺伝子群の遺伝子を含むプローブについて、ES3クローンの発現レベルの平均に対する、各iPS細胞の発現レベルの割合を計算し、 $\log_2(\text{ratio})$ で表した(表2～表10)。これらのデータに対し、Cluster 3.0を用いて、clustering解析を行い、得られた結果をJava Treeview(東京大学医科学研究所ヒトゲノム解析センターDNA情報解析分野による

フリーウェア ; M. J. L. de Hoon, S. Imoto, J. Nolan, and S. Miyano: Open Source Clustering Software. *Bioinformatics*, 20 (9): 1453--1454 (2004). ; <http://bonsai.hgc.jp/~mdehoon/software/cluster/>) を用いて、tree を作製した (図 2 ~ 図 10)。

[0054] 図 2 ~ 図 10 の tree に示されているように、調べた iPS 細胞のうち、201B7 だけがヒト ES 細胞と同じグループに分類されており、201B6、253G1、253G4 は、それとは別に一つのグループに分類されている。

[0055] このように、多能性幹細胞で分化細胞より発現の高い遺伝子、及び DNA 修復に関与する遺伝子から選択された遺伝子からなる遺伝子群について、腫瘍化を起こしにくい多能性幹細胞における発現レベルと比較することにより、正常に分化しないか、分化しても腫瘍化を起こしやすい iPS 細胞と、腫瘍化を起こしにくい iPS 細胞に分類ができる。従って、この方法を使えば、腫瘍化を起こしにくいかどうか分からない iPS 細胞についても、どちらのグループに属するかを明らかにでき、その iPS 細胞が腫瘍化を起こしにくいかどうかを判断できる。

[0056] [4] 発現レベル自体を比較する方法

例えば、本実施例では、表 10 に記載の suppressor of Ty 16 homolog (*S. cerevisiae*) の発現レベルは、ES3 クローンと、正常に分化しないか (201B6)、分化しても腫瘍化を起こしやすい (253G1、253G4) とでは、有意に差がある。そして、腫瘍化を起こしにくい iPS 細胞 (201B7) の発現レベルは、ES3 クローンと差がなく、腫瘍化を起こしやすい iPS 細胞とは顕著な差がある。

[0057] このように、発現レベル自体を比較することによっても、iPS 細胞が腫瘍化を起こしにくいかどうかを判断できる。

[0058] (4) 第 11 ~ 第 12 遺伝子群を用いた iPS 細胞クローンの分類

ここでは、第 1 遺伝子群及び第 3 遺伝子群に属する各遺伝子を含むプローブに対し、表 2 及び表 3 に示された発現レベルを表す数値に基づき、ES3

クローンと201B7のグループ及び201B6、253G1、253G4のグループの間でSAMの検定を行い、各遺伝子群で $p < 0.1$ または $p < 0.05$ で有意差のあったプローブを、それぞれ27個（表11）（特定された遺伝子26個を含む）と19個（表12）（特定された遺伝子17個を含む）抽出し、特定された遺伝子種26個と17個を第11遺伝子群及び第12遺伝子群とした。（3）[3]と同様に、clustering解析をしたところ、図11及び図12のtreeに示されているように、調べたiPS細胞のうち、201B7だけがヒトES細胞と同じグループに分類されており、201B6、253G1、253G4は、それとは別に一つのグループに分類されていた。

[0059] このように、統計学的有意性を有する発現レベルの差を用いることによっても、iPS細胞を、正常に分化しないか、分化しても腫瘍化を起こしやすいiPS細胞と、腫瘍化を起こしにくいiPS細胞に分類ができる。

[0060] （5）ゲノムDNAにおける変異

本発明は、未分化状態のiPS細胞における、DNA修復に関与する遺伝子の発現の異常が、分化後のiPS細胞の造腫瘍性に影響があるという発見に基づくものである。以下、そのメカニズムとして、未分化状態におけるDNA修復に関与する遺伝子の異常によって、DNAに多数の傷が生じ、それが原因となって、iPS細胞が正常に分化できないか、あるいはiPS細胞が分化したときに腫瘍化するということを示す。

[0061] まず、未分化状態のiPS細胞（201B6、253G1、253G4、201B7）と、各細胞を分化させた3次ニューロスフェア、iPS細胞作製のもととなる線維芽細胞（HDF）、コントロールとして、ヒト胎児由来神経幹細胞（hNSC）および患者グリオーマ細胞由来細胞（GDC）から、ゲノムDNAを単離し、アレイCGH解析を行なった。

[0062] ゲノムDNAは、各クローンから、そして対照として正常ヒト男性ゲノム（Promega社）から、フェノールクロロホルム法、あるいは、DNeasy Blood & Tissue KitやQIAamp DNA mini Kit（Qiagen社）を用いて抽出し、PicoGreenを用いて定量した。各サンプルとして、500ngから1000ngの二本鎖DNAを

用い、制限酵素（AluIとRsaI）による消化を行い、DNAを断片化した。その後、Genomic DNA Enzymatic Labeling キット（Agilent社）を用いて、DNA断片をCy3またはCy5でラベルし、片方をコントロール、もう片方をサンプルとした。精製後、Sureprint G3 human CGHマイクロアレイ4x180K（Agilent社）を用い、添付プロトコルに従い、ハイブリダイゼーション、Agilent スキャナーを用いたスキャンニング、Feature extractionソフトウェアによるシグナルの数値化を行った。得られたデータは、Agilent Genomic Workbenchを用いて、Aberrationの検出を行った。検出されたAberrationのうち、対照のHDF（ヒト皮膚線維芽細胞）で見られるAberrationは、単なるCNV（copy number variation）の可能性が高いため、解析から除外して、各クローン間のaberrated geneとしての遺伝子数を比較した。

[0063] 図16に示されるように、ES細胞や腫瘍化を起こしにくいiPS細胞（201B7）では、分化しても、ゲノム異常は全体として変化がなく、一方、正常に分化しないか（201B6）、分化しても腫瘍化を起こしやすい（253G1、253G4）では、分化と共に、ゲノム異常が増加しており、その異状のレベルは、患者グリオーマに由来する培養細胞（GDC21、GDC36、GDC40）ほどではないものの、ES細胞や201B7と比べて、はるかに高かった。

[0064] このように、未分化状態のiPS細胞において、DNA修復に関与する遺伝子の発現に異常があると、分化過程で生じるDNA変異が修復できず、そのために正常に分化できないか、あるいは分化させても細胞が腫瘍化するものと考えられる。

[0065] （6）比較例

本比較例では、いずれかのクローン中で発現が検出されたプローブ全てを対象とし、Rというclustering解析用ソフトウェアを用い（<http://www.r-project.org/>）、Ward's hierarchical clustering methodとEuclidian distanceによって、clustering解析を、行なった。その結果を図17に示すが、本発明のように適切な遺伝子群を選択しなければ、腫瘍化を起こしにくいiPS

細胞と、正常に分化しないか、分化しても腫瘍化を起こしやすい i P S 細胞は、clusterによって区別することができなかった。

[0066] (7) エピソーマルベクターを用いて作製したヒト i P S 細胞の解析

エピソーマルベクターを用いて作製したヒト i P S 細胞株 4 0 9 B 2 及び 4 1 4 C 2 (Okita et al., Nat Methods 2011) について、比較する対照の細胞株として、K h E S 1、K h E S 2、K h E S 3、2 0 1 B 7、4 0 9 B 2、4 1 4 C 2、2 0 1 B 6、2 5 3 G 4、2 5 3 G 1 の各クローンを用い、第 4 遺伝子群及び第 1 2 遺伝子群について、マイクロアレイを用いて (3) と同様の方法で、発現の解析及びclustering分析を行った。その結果、図 1 8 及び図 1 9 のtreeに示されるように、どちらの場合も、4 0 9 B 2 及び 4 1 4 C 2 は、E S 細胞及び 2 0 1 B 7 と同じ枝に分類された。

また、第 1 2 遺伝子群の 1 9 プローブについて、3 つの E S 細胞における発現の平均値から、シグナル強度に 1.5 倍以上の差があるプローブの個数を測定したところ、図 2 0 に示すように、その個数が、4 0 9 B 2、4 1 4 C 2、2 0 1 B 7 では 6 個以内、2 0 1 B 6、2 5 3 G 4、2 5 3 G 1 では、1 0 個以上となり、2 つのグループで有意に (t 検定で $p=0.017$) 差が見られた。

次に、4 0 9 B 2 及び 4 1 4 C 2 について、(2) と同様の方法で、造腫瘍性の評価を行なったところ、図 2 1 に示すように、4 0 9 B 2 及び 4 1 4 C 2 は、E S 細胞及び 2 0 1 B 7 と同様に、精巢移植後の腫大は観察されなかった。また、4 0 9 B 2 及び 4 1 4 C 2 を移植した精巢のパラフィン切片を作製し、H E 染色を行なって、移植細胞由来のテラトーマの組織像を観察したところ、図 2 2 及び図 2 3 に示すように、2 5 3 G 4、2 5 3 G 1 より腫瘍化傾向が低く、十分に分化した神経細胞及びグリア細胞が観察された。

このように、本発明の遺伝子群は、i P S 細胞を、正常に分化しないか、分化しても腫瘍化を起こしやすいクローンと、腫瘍化を起こしにくいクローンに分類するのに有用である。

[0067] [表 1 A] 第 1 遺伝子群 (表 1 B) を含むプローブ 1 3 4 0 個において、ヒ

ト E S 細胞クローン (KhES1-S3) の発現レベルの平均に対する、各 E S 細胞クローン及び各 i P S 細胞クローンの発現レベルの割合

	Gene Symbol	Gene Title	KhES1 ES	KhES2 ES	KhES3 ES	201B7 iPS	201B6 iPS	253G4 iPS	253G1 iPS
1	GRIA3	glutamate receptor, ionotropic, AMPA 3	0.53	0.21	-0.74	0.91	1.38	1.03	1.29
2	STC2	stanniocalcin 2	-0.11	0.06	0.04	0.81	1.70	0.38	0.79
3	TFPI2	tissue factor pathway inhibitor 2	-0.09	0.35	-0.27	0.22	0.56	0.08	0.13
4	TFPI2	tissue factor pathway inhibitor 2	-0.24	-0.03	0.27	0.91	0.85	0.83	1.04
5	ZNF85	zinc finger protein 85	0.39	0.53	-0.92	-1.05	-1.46	-0.65	-0.06
6	---	---	0.23	0.71	-0.94	-0.60	-1.21	-1.61	-0.41
7	SLC2A3	solute carrier family 2 (facilitated glucose transporter), member 3	-0.37	-0.43	0.80	-0.62	-0.64	-0.84	-1.26
8	SLC2A3	solute carrier family 2 (facilitated glucose transporter), member 3	-0.53	-0.51	1.04	-0.52	-0.51	-0.59	-0.58
9	TNFRSF8	tumor necrosis factor receptor superfamily, member 8	-0.43	-0.23	0.66	-0.45	-0.58	-0.82	-0.50
10	UTF1	undifferentiated embryonic cell transcription factor 1	-1.24	0.07	1.17	-0.64	-0.43	-0.72	-0.87
11	HMGAI	high mobility group A1-hook 1	-0.81	0.18	0.63	-0.72	-1.22	-0.68	-0.95
12	ZNF678	zinc finger protein 678	0.62	-0.24	-0.39	-0.81	-1.36	-0.42	-1.57
13	FANCB	Fanconi anemia, complementation group B	0.81	-0.21	-0.61	-0.93	-0.83	-0.05	-0.98
14	GNL1	Gingulin-like 1	0.18	-0.36	0.18	-1.38	-1.35	-1.13	-1.15
15	KIF1A	kinesin family member 1A	-0.10	0.24	-0.14	-0.94	-1.08	-1.55	-1.06
16	SYT3	synaptotagmin III	0.00	-0.24	0.24	-1.39	-1.57	-0.90	-1.24
17	DDX11	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 11 (CHL1-like helicase homolog, S. cerevisiae)	-0.27	0.25	0.03	-0.04	-1.07	-1.06	-1.41
18	C14orf106	chromosome 14 open reading frame 106	-0.10	0.04	0.06	0.01	-1.19	-1.01	-1.33
19	ZNF92	zinc finger protein 92	-0.13	0.09	0.04	-0.01	-1.13	-0.98	-0.78
20	ASPM	asp (abnormal spindle) homolog, microcephaly associated (Drosophila)	0.07	0.03	-0.11	-0.58	-1.50	-1.25	-1.87
21	ZNF770	zinc finger protein 770	0.28	0.22	-0.50	-0.52	-1.21	-1.26	-1.05
22	ATP11C	ATPase, class VI, type 11C	0.43	0.14	-0.57	-0.75	-1.02	-0.82	-1.47
23	ZNF92	zinc finger protein 92	0.39	-0.06	-0.32	0.01	-0.69	-1.56	-0.16
24	SNORD116	small nucleolar RNA, C/D box 116 cluster	0.35	0.31	-0.66	0.27	-0.48	-1.72	-0.70
25	GOL11A1	collagen, type XI, alpha 1	0.18	-0.02	-0.16	0.58	-1.42	-1.13	-0.16
26	ANTXR1	antirax toxin receptor 1	0.39	-0.07	-0.32	-0.92	-1.56	-1.64	-0.18
27	GNKSR2	connector enhancer of kinase suppressor of Ras 2	0.59	-0.07	-0.52	0.33	-0.26	-0.05	-0.13
28	DNA2	DNA replication helicase 2 homolog (yeast)	0.48	-0.07	-0.41	0.11	0.05	-0.18	-0.36
29	PLK4	polo-like kinase 4 (Drosophila)	0.49	-0.17	-0.31	0.13	0.09	-0.40	-0.75
30	FLJ35848	hypothetical protein FLJ35848	0.34	-0.15	-0.19	-0.15	-0.54	0.13	-0.27
31	DLGAP5	discs, large (Drosophila) homolog-associated protein 5	0.19	-0.26	0.06	-0.01	-0.24	-0.15	-0.16
32	ELAVL2	ELAV (embryonic lethal, abnormal vision, Drosophila)-like 2 (Hu antigen B)	0.28	-0.31	0.03	-0.06	-0.35	-0.22	-0.29
33	ZNF391	zinc finger protein 391	0.36	-0.42	0.05	0.25	-0.17	-0.30	-0.14
34	NCAPG2	iron-SMC condensin II complex, subunit G2	0.28	-0.34	0.06	0.22	-0.25	-0.29	-0.27
35	SLC16A1	solute carrier family 16, member 1 (monocarboxylic acid transporter 1)	0.34	-0.13	-0.21	0.12	-0.21	-0.19	-0.57
36	MCM4	minichromosome maintenance complex component 4	0.06	-0.03	-0.03	0.12	-0.12	-0.39	-0.59
37	FGD6	FYVE, RhoGEF, and PH domain containing 6	0.14	-0.07	-0.07	0.11	-0.37	0.01	-0.54
38	WDHD1	WD repeat and HMW-box DNA binding protein 1	0.02	-0.17	0.15	0.12	-0.46	-0.20	-0.52
39	CCDC88A	coiled-coil domain containing 88A	0.19	-0.30	0.11	-0.02	-0.60	-0.24	-0.32

40	BIRC5	beculoviral IAP repeat-containing 5	0.14	0.09	-0.23	-0.39	-0.19	-0.44	-0.62
41	—	—	0.11	0.10	-0.20	-0.52	0.18	-0.31	-0.61
42	CCNA2	cyclin A2	0.07	-0.01	-0.06	0.04	0.60	0.22	0.06
43	SRP35	serine-arginine repressor protein (35 kDa)	0.21	-0.10	-0.11	0.21	0.35	0.07	-0.03
44	MAD2L1	MAD2 mitotic arrest deficient-like 1 (yeast)	0.12	0.07	-0.19	0.17	0.37	-0.11	-0.05
45	CCNA2	cyclin A2	0.00	0.03	-0.04	0.14	0.47	-0.07	-0.10
46	PDPN	podocalyxin	0.12	-0.22	0.10	0.33	0.25	0.30	-0.01
47	RAD51AP1	RAD51 associated protein 1	0.20	-0.17	-0.04	0.03	0.24	0.30	-0.01
48	CENPH	centromere protein H	0.09	-0.02	-0.07	0.21	0.41	0.36	-0.03
49	NOAPH	non-SMC condensin I complex subunit H	0.36	-0.40	0.05	0.01	0.26	0.02	0.03
50	FAM72A /// FAM72B /// FAM72C /// FAM72D	family with sequence similarity 72, member A /// family with sequence similarity 72, member B /// family with sequence similarity 72, member C /// family with sequence similarity 72, member D	0.06	-0.25	0.19	-0.12	0.37	0.24	0.04
51	BIRC5	beculoviral IAP repeat-containing 5	0.04	-0.14	0.09	-0.38	0.16	-0.09	-0.14
52	WDHD1	WD repeat and HMG-box DNA binding protein 1	-0.15	0.15	0.01	0.02	0.21	-0.11	-0.47
53	TMEFF1	transmembrane protein with EGF-like and two follistatin-like domains 1	-0.05	-0.02	0.07	-0.17	0.19	-0.07	-0.44
54	PAICS	phosphoribosylaminimidazole carboxylase, phosphoribosylaminimidazole succinocarboxamide synthetase	0.11	-0.12	0.00	0.02	-0.15	0.01	-0.28
55	DBF4	DBF4 homolog (S. cerevisiae)	0.09	-0.05	-0.04	-0.05	-0.16	-0.12	-0.19
56	HMMR	hyaluronan-mediated motility receptor (RHAMM)	0.03	0.05	-0.08	-0.14	-0.09	-0.04	-0.25
57	MGM4	minichromosome maintenance complex component 4	-0.04	-0.02	0.06	0.03	-0.13	-0.14	-0.28
58	FXYD7	FXYD domain containing ion transport regulator 7	-0.12	0.15	-0.03	-0.08	-0.26	-0.12	-0.30
59	—	—	-0.07	0.04	0.02	-0.09	-0.37	-0.15	0.03
60	FEN1	flap structure-specific endonuclease 1	0.02	0.12	-0.14	0.29	0.22	0.26	0.00
61	CDC25C	cell division cycle 25 homolog C (S. pombe)	-0.07	0.24	-0.17	0.01	0.20	0.36	-0.01
62	TPM1	tropomyosin 1 (alpha)	-0.14	0.16	-0.02	-0.12	-0.16	0.11	0.30
63	HMMR	hyaluronan-mediated motility receptor (RHAMM)	-0.12	0.09	0.03	0.24	-0.14	0.08	-0.01
64	CCNF	cyclin F	-0.27	0.11	0.16	0.12	0.20	0.04	0.15
65	CDCA5	cell division cycle associated 5	-0.19	0.10	0.09	0.15	0.07	-0.03	0.04
66	HJURP	Holliday junction recognition protein	-0.08	0.01	0.07	0.18	0.13	0.05	-0.10
67	SPAG5	sperm associated antigen 5	-0.16	0.09	0.07	0.02	0.08	-0.10	0.08
68	RFXWD3	ring finger and WD repeat domain 3	-0.09	-0.02	0.11	0.11	0.14	0.22	-0.08
69	C21orf45	chromosome 21 open reading frame 45	-0.04	0.01	0.04	0.13	-0.03	0.05	0.13
70	CDCA2	cell division cycle associated 2	0.03	-0.03	0.00	0.04	0.06	0.09	0.05
71	MGM4	minichromosome maintenance complex component 4	-0.11	0.06	0.06	0.03	0.06	0.18	0.05
72	TFDP2	transcription factor Dp-2 (E2F dimerization partner 2)	0.12	-0.24	0.12	-0.05	-0.05	-0.05	0.06
73	PRM1	primase, DNA, polypeptide 1 (49kDa)	0.09	-0.16	0.07	0.06	0.09	0.07	0.19
74	SEPHS1	selenophosphate synthetase 1	0.06	-0.18	0.12	0.21	0.13	-0.02	0.11
75	MCM2	minichromosome maintenance complex component 2	-0.04	-0.04	0.08	0.16	0.04	0.02	0.05
76	SEPHS1	selenophosphate synthetase 1	0.01	-0.11	0.10	0.16	-0.06	-0.09	0.02
77	FAM64A	family with sequence similarity 64, member A	-0.10	0.03	0.07	0.05	-0.06	-0.09	-0.05
78	BEND3	BEN domain containing 3	-0.10	-0.06	0.17	-0.05	0.09	0.05	0.19
79	VRR1	vaccinia related kinase 1	0.23	-0.15	-0.07	0.04	0.09	0.19	0.16

80	POLE2	polymerase (DNA directed), epsilon 2 (p99 subunit)	0.16	-0.14	-0.03	0.02	0.15	0.27	0.16
81	DSGCI	defective in sister chromatid cohesion 1 homolog (S. cerevisiae)	0.19	-0.10	-0.09	0.05	0.10	0.25	0.16
82	GINS2	GINS complex subunit 2 (Psi2 homolog)	0.18	-0.14	-0.03	0.05	-0.01	0.27	0.36
83	CCNJ	cyclin J	0.23	-0.07	-0.16	-0.20	0.23	0.24	0.14
84	EXO1	exonuclease 1	0.23	-0.22	-0.01	0.17	-0.05	-0.06	-0.14
85	PDPN	podoplanin	0.30	-0.08	-0.21	0.12	-0.01	-0.16	-0.13
86	GDC2	cell division cycle 2, G1 to S and G2 to M	0.34	-0.20	-0.14	-0.07	-0.06	-0.01	0.03
87	PDPN	podoplanin	0.28	-0.23	-0.05	-0.09	0.10	-0.24	-0.06
88	GDC2	cell division cycle 2, G1 to S and G2 to M	0.34	-0.21	-0.12	-0.12	-0.01	0.01	0.06
89	RCC2	regulator of chromosome condensation 2	0.28	-0.21	-0.06	-0.06	0.08	-0.01	-0.01
90	FLJ20874	hypothetical protein FLJ20874	0.15	-0.11	-0.04	-0.20	-0.05	-0.03	0.14
91	—	—	0.13	-0.05	-0.08	-0.08	-0.05	0.05	0.04
92	CCNB1	cyclin B1	0.11	-0.09	-0.02	-0.12	0.09	0.06	0.02
93	RFC3	replication factor C (activator 1) 3, 38kDa	0.18	-0.01	-0.17	0.06	-0.01	0.05	-0.01
94	FANCD2	Fanconi anemia, complementation group D2	0.12	0.08	-0.20	-0.01	0.07	0.03	-0.01
95	RRM2	ribonucleotide reductase M2	0.16	0.01	-0.17	0.10	0.14	0.16	0.12
96	CCNB1	cyclin B1	0.19	-0.03	-0.16	0.15	0.19	0.05	0.01
97	CENPN	centromere protein N	0.22	-0.04	-0.18	0.00	-0.08	-0.27	0.12
98	RTKN2	growth factor receptor-bound protein 14	0.09	0.05	-0.13	-0.24	-0.08	-0.25	-0.08
99	GRB14	phosphatidylinositol 3-kinase gamma	0.04	-0.21	0.17	0.25	0.00	-0.02	0.27
100	PFAS	phosphoribosylformylglycinamide synthase	0.18	-0.29	0.11	0.24	0.33	0.07	0.23
101	KIF15	kinesin family member 15	0.17	-0.33	0.16	0.05	0.15	0.10	0.19
102	RAD54B	RAD54 homolog B (S. cerevisiae)	0.17	-0.47	0.00	0.37	-0.04	0.28	0.36
103	RAD54L	RAD54-like (S. cerevisiae)	0.17	-0.47	0.30	-0.23	0.11	0.01	-0.08
104	PPA1	phosphoribosyl pyrophosphate amidotransferase	0.35	-0.56	0.20	-0.13	-0.19	-0.01	-0.23
105	SLC16A1	solute carrier family 16, member 1 (monocarboxylic acid transporter 1)	0.38	-0.48	0.10	-0.04	0.23	0.06	-0.12
106	ZNF814	zinc finger protein 814	0.30	-0.49	0.19	-0.02	0.19	0.18	-0.09
107	SLC16A1	solute carrier family 16, member 1 (monocarboxylic acid transporter 1)	0.19	-0.25	0.06	0.07	0.03	-0.06	-0.09
108	ZNF462	zinc finger protein 462	0.23	-0.37	0.14	0.03	-0.04	-0.04	-0.09
109	API3	adaptor-related protein complex 1, sigma 3 subunit	0.18	0.01	-0.19	0.35	0.28	0.52	0.36
110	LHFPL4	lipoma HMGIC fusion partner-like 4	0.24	-0.14	-0.10	0.28	0.36	0.37	0.63
111	GDC2	cell division cycle 2, G1 to S and G2 to M	0.24	-0.16	-0.08	0.04	0.06	0.52	0.51
112	ZNF114	zinc finger protein 114	-0.03	0.14	-0.11	0.03	0.08	0.34	0.31
113	ZWINT	ZW10 interactor	0.20	-0.11	-0.09	0.06	0.27	0.30	0.29
114	G2Lorf45	chromosome 21 open reading frame 45	0.01	0.04	-0.05	0.17	0.25	0.23	0.31
115	G1orf135	chromosome 1 open reading frame 135	0.02	0.07	-0.09	0.17	0.40	0.30	0.65
116	NODAL	nodal homolog (mouse)	-0.02	0.19	-0.16	0.34	0.33	0.64	0.35
117	GBS	cystathionine-beta-synthase	-0.47	0.15	0.33	-0.03	0.33	-0.12	-0.20
118	GBS	cystathionine-beta-synthase	-0.39	0.04	0.35	0.01	-0.31	-0.19	-0.32
119	TPX2	TPX2, microtubule-associated, homolog (Xenopus laevis)	-0.24	-0.07	0.31	-0.11	-0.02	-0.16	-0.43
120	CDT1	chromatin licensing and DNA replication factor 1	-0.29	-0.26	0.55	-0.06	0.04	0.11	-0.17
121	MCM7	minichromosome maintenance complex component 7	-0.34	-0.03	0.37	0.17	-0.01	-0.04	-0.25

	TUBB2A /// TUBB2B	tubulin, beta 2A /// tubulin, beta 2B	-0.59	0.35	0.24	0.29	-0.15	0.01	0.04
122	ESPL1	extra spindle pole bodies homolog 1 (S. cerevisiae)	-0.29	0.10	0.19	-0.28	-0.22	0.09	0.04
123	KCNQ2	potassium voltage-gated channel, KQT-like subfamily, member 2	-0.24	0.24	0.01	0.15	-0.09	0.33	0.35
124	UBE2S	ubiquitin-conjugating enzyme E2S	-0.30	0.15	0.15	0.04	-0.02	0.12	0.14
125	TEAD4	TEA domain family member 4	-0.36	0.16	0.19	0.08	-0.06	0.21	0.14
126	SCLY	selenocysteine lyase	-0.37	0.06	0.30	0.07	0.09	0.23	0.18
127	CENPA	centromere protein A	-0.06	0.06	0.00	-0.23	0.15	0.14	0.20
128	CDCA3	cell division cycle associated 3	-0.06	0.14	-0.08	-0.02	0.00	0.02	0.26
129	HMGA1	high mobility group AT-hook 1	-0.62	0.19	0.43	-0.13	0.09	0.19	-0.02
130	DHFR	dihydrofolate reductase	-0.41	0.09	0.32	-0.15	0.12	-0.01	-0.09
131	PHF17	PHD finger protein 17	-0.36	-0.03	0.39	-0.37	0.28	-0.05	-0.01
132	MSH6	mutS homolog 6 (E. coli)	-0.18	0.02	0.16	0.17	-0.07	-0.09	-0.30
133	CTPS	GTP synthase	-0.01	-0.05	0.06	0.21	0.07	-0.07	-0.15
134	KIF2C	kinesin family member 2C	-0.01	-0.10	0.11	0.11	0.10	-0.02	-0.33
135	FOXO1	forkhead box M1	-0.19	-0.12	0.27	-0.06	0.08	-0.03	-0.13
136	GTSE1	G-2 and S-phase expressed 1	-0.25	0.13	0.12	0.05	0.11	0.13	-0.12
137	AURKA	aurora kinase A	-0.13	0.02	0.11	-0.06	0.25	0.06	-0.07
138	ESPL1	extra spindle pole bodies homolog 1 (S. cerevisiae)	-0.17	-0.02	0.19	-0.08	0.09	0.16	0.03
139	FBXO11	F-box protein 11	-0.24	0.02	0.22	0.32	0.13	-0.10	-0.23
140	NLN	neulysin (metallopeptidase M3 family)	-0.17	-0.01	0.18	-0.04	-0.08	-0.08	-0.21
141	LAPTM4B	lysosomal protein transmembrane 4 beta	-0.08	0.09	-0.01	0.03	0.08	-0.23	-0.28
142	TMPO	thymopoietin	-0.13	0.12	0.01	0.06	0.03	-0.20	-0.09
143	EZH2	enhancer of zeste homolog 2 (Drosophila)	0.06	0.01	-0.07	0.13	0.14	0.04	-0.10
144	CDK7	cell division cycle 7 homolog (S. cerevisiae)	-0.04	0.06	-0.02	0.08	0.24	0.00	-0.20
145	NEF1	neuropilin (NRP) and toll-like 1	-0.12	0.09	0.03	0.22	-0.16	-0.29	0.00
146	KIF23	kinesin family member 23	-0.03	0.00	0.03	0.11	-0.16	-0.08	-0.23
147	KIF18B	kinesin family member 18B	0.03	-0.05	0.02	0.05	-0.27	-0.14	-0.21
148	FANCI	Fanconi anemia, complementation group I	0.00	-0.01	0.01	0.21	-0.28	-0.23	-0.25
149	CDCA2	cell division cycle associated 2	0.03	-0.05	0.02	0.18	-0.08	-0.30	-0.28
150	MCM6	minichromosome maintenance complex component 6	0.25	-0.01	-0.24	0.03	-0.23	-0.10	-0.16
151	MSH2	mutS homolog 2, colon cancer, nonpolyposis type 1 (E. coli)	0.22	-0.10	-0.12	0.04	-0.17	-0.11	-0.43
152	TMEFF1	transmembrane protein with EGF-like and two follistatin-like domains 1	0.02	-0.09	0.07	-0.03	-0.09	-0.12	-0.41
153	NOAPG	iron-SMC condensin I complex, subunit G	0.14	-0.12	-0.01	0.04	-0.15	0.05	-0.30
154	DHFR	dihydrofolate reductase	0.31	-0.17	-0.14	-0.01	-0.15	0.03	-0.45
155	MASTL	microtubule associated serine/threonine kinase-like	0.14	-0.02	-0.13	-0.04	-0.07	-0.11	-0.36
156	FANCI	Fanconi anemia, complementation group I	0.31	-0.24	-0.06	-0.01	-0.09	-0.20	-0.09
157	NOAPG	non-SMC condensin I complex, subunit G	0.26	-0.11	-0.15	0.22	-0.04	-0.06	-0.05
158	CENPJ	centromere protein J	0.40	-0.14	-0.25	-0.10	-0.25	-0.09	-0.02
159	KIF11	kinesin family member 11	0.03	-0.15	0.11	0.02	0.00	-0.02	-0.13
160	KIF2C	kinesin family member 2C	-0.02	-0.13	0.15	-0.08	-0.03	-0.14	-0.14
161	TOP2A	topoisomerase (DNA) II alpha 170kDa	-0.04	0.00	0.04	-0.34	-0.04	-0.03	-0.19
162	ZNF643	zinc finger protein 643	-0.05	0.06	0.00	-0.08	-0.19	0.09	-0.29

164	PSIP1	PC4 and SFRS1 interacting protein 1	0.01	-0.05	0.04	-0.15	-0.13	0.00	-0.23
165	—	—	0.00	-0.03	0.03	-0.23	-0.03	-0.15	-0.19
166	ORC6L	origin recognition complex, subunit 6 like (yeast)	-0.01	-0.04	0.05	-0.14	-0.04	-0.07	-0.18
167	RAD54B	RAD54 homolog B (S. cerevisiae)	0.12	0.00	-0.02	-0.16	-0.09	-0.04	-0.22
168	KPNA2	karyopherin alpha 2 (RAG cohort 1, importin alpha 1)	0.12	-0.10	-0.02	-0.09	0.08	0.05	0.05
169	NOP16	NOP16 nucleolar protein homolog (yeast)	0.13	-0.05	-0.08	-0.05	0.11	0.08	-0.04
170	NUSAP1	nucleolar and spindle associated protein 1	0.19	-0.15	-0.04	-0.03	0.17	0.13	0.00
171	G13orf34	chromosome 13 open reading frame 34	0.19	-0.18	-0.02	-0.03	0.05	0.02	0.02
172	C6orf173	chromosome 6 open reading frame 173	0.15	-0.07	-0.08	-0.07	0.01	0.08	0.16
173	RNASEH2A	ribonuclease H2, subunit A	-0.01	-0.08	0.07	-0.17	0.03	0.05	-0.01
174	CONE1	cyclin E1	0.00	-0.09	0.09	-0.27	0.01	0.18	0.07
175	KIF14	kinesin family member 14	-0.01	-0.15	0.15	-0.33	-0.06	0.08	0.08
176	—	—	0.30	-0.25	-0.05	-0.23	-0.11	0.11	-0.11
177	ZNF788	zinc finger family member 788	0.17	-0.14	-0.03	-0.37	-0.06	-0.11	-0.08
178	CASP3	caspase 3, apoptosis-related cysteine peptidase	0.04	0.20	-0.24	0.22	0.26	0.17	0.04
179	RRM2	ribonucleotide reductase M2	0.26	0.05	-0.30	0.26	0.19	0.12	0.32
180	RAD51	RAD51 homolog (RecA homolog, E. coli) (S. cerevisiae)	0.17	0.03	-0.20	0.10	0.35	0.35	0.32
181	PPAT	phosphoribosyl pyrophosphate amidotransferase	0.21	0.17	-0.38	0.09	0.28	0.40	0.25
182	SUV39H2	suppressor of variegation 3-9 homolog 2 (Drosophila)	0.34	0.03	-0.37	0.01	-0.02	-0.01	0.10
183	UCHL1	ubiquitin carboxyl-terminal esterase L1 (ubiquitin thioesterase)	0.13	0.08	-0.21	0.04	-0.13	-0.01	0.12
184	—	—	0.12	0.26	-0.38	0.23	-0.17	0.21	0.24
185	THAP9	THAP domain containing 9	0.07	0.13	-0.20	0.26	-0.15	0.03	0.02
186	SKP2	S-phase kinase-associated protein 2 (p45)	0.28	-0.15	-0.13	0.21	0.23	0.01	-0.01
187	NUSAP1	nucleolar and spindle associated protein 1	0.31	-0.12	-0.19	0.15	0.01	0.14	-0.27
188	UBE2T	ubiquitin-conjugating enzyme E2T (putative)	0.45	-0.23	-0.22	-0.04	0.18	0.18	0.13
189	NUF2	NUF2, NDC80 kinetochore complex component, homolog (S. cerevisiae)	0.45	-0.23	-0.22	-0.11	0.12	0.17	0.00
190	—	—	0.64	-0.27	-0.36	0.07	0.23	0.05	-0.02
191	RFC4	replication factor C (activator 1) 4, 37kDa	0.25	-0.29	0.04	0.08	0.44	0.24	0.26
192	NDC80	NDC80 homolog, kinetochore complex component (S. cerevisiae)	0.32	-0.29	-0.03	-0.16	0.32	0.22	-0.02
193	NEK2	NIMA (never in mitosis gene a)-related kinase 2	0.16	-0.22	0.06	-0.04	0.35	0.33	0.08
194	AURKA	aurora kinase A	0.17	-0.26	0.09	-0.11	0.31	0.14	0.01
195	TRIM6	tripartite motif-containing 6	0.13	-0.24	0.12	-0.21	0.33	0.13	0.16
196	CKS1B	CDC28 protein kinase regulatory subunit 1B	0.05	-0.15	0.09	0.23	0.33	0.29	0.44
197	CGB2	cyclin B2	0.09	-0.07	-0.03	0.14	0.32	0.34	0.37
198	GMNN	geminin, DNA replication inhibitor	-0.03	0.02	0.00	0.08	0.24	0.16	0.35
199	CENPK	centromere protein K	0.26	-0.18	-0.08	0.24	0.28	0.48	0.22
200	FAM54A	family with sequence similarity 54, member A	0.18	-0.12	-0.06	0.17	0.20	0.36	0.22
201	PTTG1	pituitary tumor-transforming 1	0.01	-0.15	0.15	0.16	0.27	0.28	0.30
202	TEAD2	TEA domain family member 2	0.00	-0.08	0.08	0.25	0.38	0.28	0.29
203	CDC48	cell division cycle associated 8	0.04	-0.06	0.02	0.13	0.54	0.34	0.29
204	NEK2	NIMA (never in mitosis gene a)-related kinase 2	0.18	-0.23	0.05	-0.08	0.24	0.37	-0.02
205	FBXO5	F-box protein 5	0.21	-0.13	-0.08	0.18	0.36	0.31	-0.03

206	BXDC2	brx domain containing 2	0.21	-0.18	-0.03	0.13	0.22	0.45	0.22
207	MTA3	metastasis associated 1 family member 3	0.08	-0.32	0.74	-0.04	0.12	0.19	0.17
208	TIMELESS	timeless homolog (<i>Drosophila</i>)	-0.16	-0.28	0.44	0.28	0.35	0.21	0.15
209	CDCG138	coiled-coil domain containing 138	0.06	-0.24	0.19	0.36	0.33	0.20	-0.03
210	EEF1E1	eukaryotic translation elongation factor 1 epsilon 1	0.26	-0.20	-0.06	0.05	-0.10	0.02	0.21
211	CDCG150	coiled-coil domain containing 150	0.29	-0.24	-0.06	0.18	-0.09	0.03	0.09
212	LYAR	lyl antibody reactive homolog (mouse)	0.25	-0.24	-0.01	0.07	0.05	0.18	0.16
213	SLOC6A15	solute carrier family 6 (neutral amino acid transporter), member 15	0.24	-0.15	-0.09	0.26	0.10	0.16	0.31
214	—	—	0.40	-0.25	-0.16	0.38	0.01	0.19	0.24
215	MRS2	MRS2 magnesium homeostasis factor homolog (S. cerevisiae)	0.39	-0.01	-0.38	0.01	0.00	0.04	0.43
216	FAM64A	family with sequence similarity 54, member A	0.20	-0.07	-0.14	0.02	-0.12	-0.12	0.35
217	BRCA2	breast cancer 2, early onset	0.28	-0.36	0.08	0.15	-0.17	-0.41	-0.03
218	THAP9	THAP domain containing 9	0.45	-0.32	-0.13	0.54	-0.33	-0.33	-0.57
219	—	—	0.49	-0.15	-0.34	0.06	-0.08	-0.61	-0.46
220	MCN10	mitochondrion maintenance complex component 10	0.38	-0.59	0.21	0.50	0.10	-0.09	-0.13
221	C12orf48	chromosome 12 open reading frame 48	0.35	-0.57	0.22	0.29	0.02	0.03	-0.25
222	C12orf48	chromosome 12 open reading frame 48	0.35	-0.50	0.15	0.16	-0.02	0.04	-0.23
223	COL28	chemokine (C-C motif) ligand 26	0.59	-0.68	0.09	0.22	0.06	0.04	-0.04
224	—	—	0.37	-0.46	0.09	0.37	-0.22	0.15	-0.43
225	NSBP1	nucleosomal binding protein 1	-0.04	-0.48	0.51	0.10	-0.34	-0.22	0.29
226	—	—	-0.10	-0.56	0.66	0.40	-0.15	0.14	0.40
227	HESX1	HESX homeobox 1	0.54	-0.42	-0.12	-0.28	0.16	0.03	0.41
228	TNNT1	troponin T type 1 (skeletal, slow)	0.41	-0.21	-0.20	-0.64	0.10	0.25	0.22
229	MAD2L1	MAD2 mitotic arrest deficient-like 1 (yeast)	0.41	-0.04	-0.37	0.08	0.66	0.28	0.33
230	GUCA1A	guanylate cyclase activator 1A (retina)	0.25	-0.13	-0.12	-0.25	0.42	0.40	0.07
231	UBE2C	ubiquitin-conjugating enzyme E2C	0.34	0.19	-0.53	0.10	0.17	0.25	0.29
232	CDC6	cell division cycle 6 homolog (S. cerevisiae)	0.36	0.09	-0.45	0.13	0.05	0.22	-0.01
233	GDC6	cell division cycle 6 homolog (S. cerevisiae)	0.26	0.23	-0.48	0.43	0.10	0.12	-0.01
234	DIAPH2	diaphanous homolog 2 (<i>Drosophila</i>)	0.32	0.15	-0.47	0.34	-0.04	0.29	0.28
235	UCHL1	Ubiquitin carboxyl-terminal esterase L1 (ubiquitin thiolesterase)	0.11	0.20	-0.40	-0.28	-0.21	0.02	-0.17
236	GAL	galanin prepropeptide	0.22	0.22	-0.44	-0.13	-0.27	-0.37	0.01
237	—	—	-0.33	0.19	0.14	-0.03	0.71	0.19	-0.38
238	PLK4	polo-like kinase 4 (<i>Drosophila</i>)	0.13	-0.08	-0.05	0.53	0.50	-0.31	-0.23
239	CHAF1A	chromatin assembly factor 1, subunit A (p150)	-0.37	0.17	0.26	0.30	-0.16	0.17	0.06
240	CHAF1A	chromatin assembly factor 1, subunit A (p150)	-0.40	0.18	0.23	0.12	0.13	0.24	0.06
241	TEAD4	TEA domain family member 4	-0.63	0.41	0.22	0.05	0.03	0.12	0.20
242	MCW5	minichromosome maintenance complex component 5	-0.26	-0.06	0.32	0.20	0.01	-0.35	-0.45
243	GALNT13	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetyltransferase 13 (GALNAc-T13)	-0.29	-0.03	0.32	0.20	0.38	-0.37	-0.04
244	GAL3ST3	galactose-3-O-sulfotransferase 3	-0.69	0.36	0.34	0.28	-0.32	-0.24	-0.20
245	FAM46B	family with sequence similarity 46, member B	-0.52	0.26	0.26	0.25	0.11	0.18	-0.06
246	LOC389857	hypothetical protein	-0.46	0.35	0.11	0.22	0.00	-0.11	-0.11
247	JARD2	jumonji, AT rich interactive domain 2	-0.27	-0.03	0.30	0.19	-0.09	0.10	0.16

248	SILV	silver homolog (mouse)	-0.23	0.07	0.16	-0.11	0.11	0.47	0.07
249	IGFBP1	insulin-like growth factor binding protein-like 1	-0.29	0.10	0.19	-0.03	-0.03	0.29	-0.10
250	MBD2	methyl-CpG binding domain protein 2	-0.14	0.07	0.08	-0.19	0.25	0.19	0.28
251	GINS1	GINS complex subunit 1 (Psf1 homolog)	0.29	-0.29	0.00	0.25	0.39	0.25	0.11
252	HAS3	hyaluronan synthase 3	0.12	-0.13	0.00	0.24	0.18	0.02	0.25
253	NASP	nuclear autoantigenic sperm protein (histone-binding)	0.06	-0.27	0.21	0.17	0.24	0.25	-0.07
254	MCM5	minichromosome maintenance complex component 5	-0.04	-0.26	0.30	0.15	0.07	0.02	-0.11
255	MTF2	metal response element binding transcription factor 2	-0.11	-0.10	0.20	-0.03	0.28	0.10	-0.06
256	PNAIP1	phorbol-12-myristate-13-acetate-induced protein 1	0.10	-0.14	0.04	0.11	0.24	0.16	-0.05
257	MATR3	Matrin 3	0.00	-0.12	0.12	0.15	0.09	0.13	-0.03
258	CRMP1	collapsin response mediator protein 1	-0.20	-0.07	0.27	0.06	0.16	0.14	-0.03
259	CBX2	chromobox homolog 2 (Pc class homolog, Drosophila)	-0.04	-0.17	0.21	0.01	0.23	0.06	0.07
260	WDR72	WD repeat domain 72	-0.10	-0.23	0.33	0.13	0.29	0.26	0.21
261	CDCA7	cell division cycle associated 7	-0.02	-0.03	0.05	0.12	0.24	0.23	0.17
262	FOXA3	forkhead box A3	-0.12	0.05	0.08	0.21	0.40	0.31	-0.01
263	SPC25	SPC25, NDC80 kinetochore complex component, homolog (S. cerevisiae)	0.25	-0.04	-0.21	0.25	0.02	0.25	0.01
264	BLM	Bloom syndrome, RecQ helicase-like	0.15	-0.15	0.00	0.30	0.03	0.20	0.17
265	C11orf82	chromosome 11 open reading frame 82	0.25	-0.13	-0.12	0.24	0.01	0.09	0.19
266	CHRNA3	cholinergic receptor, nicotinic, alpha 5	0.41	-0.34	-0.07	0.18	-0.17	0.12	-0.03
267	GDAP1	ganglioside-induced differentiation-associated protein 1	0.30	-0.10	-0.20	0.24	-0.22	0.04	0.08
268	MTF2	metal response element binding transcription factor 2	-0.02	-0.01	0.03	0.03	-0.10	-0.02	0.17
269	CHST4	carbohydrate (N-acetylglucosamine 6-O) sulfotransferase 4	-0.02	0.03	-0.01	0.08	-0.11	0.06	0.21
270	DNMT3A	DNA (cytosine-5)-methyltransferase 3 alpha	0.14	-0.16	0.02	0.04	-0.09	-0.03	0.21
271	SEPHS1	selenophosphate synthetase 1	0.06	-0.09	0.03	0.03	-0.13	-0.16	-0.05
272	KLHL7	kelch-like 7 (Drosophila)	0.01	-0.18	0.16	-0.08	-0.24	-0.01	0.07
273	DTL	denticleless homolog (Drosophila)	0.06	-0.03	-0.03	0.22	-0.08	0.06	-0.01
274	DTL	denticleless homolog (Drosophila)	0.06	0.02	-0.07	0.21	-0.11	-0.10	-0.24
275	TNNI3	tropoin 1 type 3 (cardiac)	-0.07	0.23	-0.16	-0.15	0.08	0.24	0.07
276	ZNF738	zinc finger protein 738	0.20	0.09	-0.29	-0.30	-0.10	0.08	-0.08
277	MTF2	metal response element binding transcription factor 2	-0.25	-0.04	0.29	-0.17	-0.13	-0.21	-0.28
278	HOMER1	homer homolog 1 (Drosophila)	-0.12	-0.09	0.22	-0.12	-0.08	-0.05	-0.15
279	TAGC3	transforming, acidic coiled-coil containing protein 3	-0.27	0.08	0.19	-0.12	0.19	-0.09	-0.19
280	—	—	0.00	-0.06	0.06	-0.07	-0.41	-0.01	-0.28
281	MCM3	minichromosome maintenance complex component 3	0.01	-0.03	0.03	-0.02	0.00	0.13	-0.26
282	NASP	nuclear autoantigenic sperm protein (histone-binding)	0.05	-0.08	0.03	0.06	-0.01	-0.01	-0.39
283	MRS2	MRS2 magnesium homeostasis factor homolog (S. cerevisiae)	0.12	-0.10	-0.02	0.08	-0.22	0.09	-0.25
284	REC3	replication factor C (activator 1) 3, 38kDa	0.08	0.04	-0.13	-0.10	0.01	-0.06	-0.34
285	FAM83D	family with sequence similarity 83, member D	0.01	0.00	0.00	-0.13	0.05	0.01	-0.10
286	—	—	-0.01	0.01	0.00	-0.34	-0.09	-0.02	-0.14
287	HOMER1	homer homolog 1 (Drosophila)	-0.04	0.05	-0.01	-0.16	-0.02	-0.16	-0.21
288	PLK4	polo-like kinase 4 (Drosophila)	0.10	-0.05	-0.06	-0.11	-0.02	-0.11	-0.49
289	BUB1	budding uninhibited by benzimidazoles 1 homolog (yeast)	0.13	-0.05	-0.07	-0.01	0.06	-0.08	-0.32

290	JPW	imprinted in Prader-Willi syndrome (non-protein coding)	-0.07	0.11	-0.04	0.06	0.00	-0.02	-0.46
291	CDT1	Chromatin licensing and DNA replication factor 1	-0.07	0.01	0.06	-0.12	-0.11	-0.08	-0.33
292	FERMT1	fermitin family homolog 1 (Drosophila)	0.14	-0.12	-0.02	-0.23	0.13	-0.44	-0.29
293	STRBP	spermatozoal perinuclear RNA binding protein	0.16	-0.46	0.30	-0.33	-0.04	-0.17	-0.31
294	FAM124A	family with sequence similarity 124A	0.13	-0.43	0.29	0.03	-0.04	-0.14	-0.09
295	COMMD7	COMMD domain containing 7	0.04	-0.42	0.37	0.28	-0.37	0.01	-0.50
296	SYT6	synaptotagmin VI	-0.26	-0.31	0.57	-0.03	0.15	0.13	-0.40
297	CLDN7	claudin 7	-0.12	0.29	0.03	0.15	0.27	0.65	0.31
298	RND2	Rho family GTPase 2	-0.12	-0.14	0.26	0.13	0.28	0.32	0.40
299	AIM1L	absent in melanoma 1-like	-0.11	-0.08	0.18	0.29	0.13	0.53	0.57
300	LOC253842	hypothetical protein LOC253842	-0.24	-0.10	0.34	0.09	0.52	0.62	0.50
301	CDC20	cell division cycle 20 homolog (S. cerevisiae)	-0.23	0.11	0.12	0.30	0.36	0.42	0.44
302	AURKB	aurora kinase B	-0.41	0.08	0.32	0.38	0.29	0.44	0.52
303	OIP5	Opa interacting protein 5	-0.06	-0.13	0.19	0.30	0.38	0.46	0.49
304	LOC100128191	hypothetical protein LOC100128191	-0.18	0.16	0.02	0.12	0.41	0.28	0.36
305	—	—	-0.31	0.25	0.06	0.38	0.02	0.51	0.34
306	RASL11B	RAS-like, family 11, member B	0.21	-0.19	-0.02	0.42	0.15	0.57	0.45
307	GULP1	GULP, engulfment adaptor PTB domain containing 1	0.33	-0.33	0.00	0.26	-0.11	0.14	0.53
308	AP3B2	adaptor-related protein complex 3, beta 2 subunit	0.24	0.34	-0.58	0.13	0.72	0.43	0.65
309	HMG3	high-mobility group box 3	0.17	0.47	-0.64	0.18	0.68	0.98	0.70
310	GXCL5	chemokine (G-X-G motif) ligand 5	0.50	-0.15	-0.34	0.16	0.45	1.02	1.32
311	GXCL5	chemokine (C-X-C motif) ligand 5	0.16	0.05	-0.21	0.10	0.04	0.59	1.09
312	PHF21B	PHD finger protein 21B	-0.16	-0.04	0.20	0.27	1.07	0.56	0.85
313	MND1	meiotic nuclear divisions 1 homolog (S. cerevisiae)	0.01	-0.31	0.30	0.37	0.94	0.34	0.34
314	MLF1IP	MLF1 interacting protein	-0.18	0.13	0.05	0.52	0.83	0.59	0.67
315	MLF1IP	MLF1 interacting protein	-0.29	0.38	-0.07	0.81	0.99	0.68	0.75
316	C13orf38	chromosome 13 open reading frame 38	0.42	-0.67	0.25	0.57	0.80	0.31	0.83
317	SLC16A1	solute carrier family 16, member 1 (monocarboxylic acid transporter 1)	0.37	-0.64	0.27	0.38	0.41	0.43	0.39
318	NPM3	nucleophosmin/nucleoplasmin 3	0.28	-0.37	0.08	0.14	0.72	0.85	0.69
319	G16orf75	chromosome 16 open reading frame 75	0.24	-0.46	0.22	0.43	0.80	0.71	0.58
320	SKA1	spindle and kinetochore associated complex subunit 1	-0.27	0.14	0.14	0.72	0.60	0.56	0.30
321	LOC647946	hypothetical protein LOC647946	0.09	-0.28	0.19	0.75	0.65	0.52	0.47
322	NFFR2	neurotrophin receptor 2	-0.03	-0.22	0.26	0.70	0.27	0.98	0.65
323	FAM124A	family with sequence similarity 124A	0.06	-0.23	0.17	0.43	0.36	0.57	0.73
324	GINS4	GINS complex subunit 4 (Sic5 homolog)	-0.08	0.01	0.07	0.01	0.89	0.79	0.98
325	FEN1	flap structure-specific endonuclease 1	0.01	-0.06	0.04	0.28	0.46	0.45	0.65
326	RAB38	RAB38, member RAS oncogene family	0.05	-0.13	0.07	0.24	0.47	0.49	0.74
327	BCL2L12	BCL2-like 12 (proline rich)	-0.25	-0.12	0.37	0.40	0.38	0.59	0.66
328	MLF1IP	MLF1 interacting protein	-0.30	0.34	-0.04	0.67	0.86	0.82	0.57
329	—	—	-0.09	0.18	-0.09	0.47	0.71	0.55	0.86
330	C9orf100	chromosome 9 open reading frame 100	-0.51	0.22	0.29	0.43	0.73	0.14	0.12
331	ZNFR3	zinc finger protein 93	0.53	-0.08	-0.45	-0.18	0.51	0.12	0.28
332	KIAA1661	KIAA1661 protein	0.64	-0.29	-0.35	-0.11	0.73	0.71	0.23
333	USP9X	ubiquitin specific peptidase 9, X-linked	0.09	0.18	-0.26	-0.27	0.47	0.61	0.23

334	HIST1H2AM	histone cluster 1, H2am	0.48	-0.20	-0.28	0.28	0.55	-0.03	0.11
335	LOC284242	hypothetical protein LOC284242	0.53	-0.35	-0.18	0.32	0.56	0.48	0.27
336	MCM6	minichromosome maintenance complex component 6	0.53	-0.40	-0.13	0.44	0.55	0.44	0.06
337	---	---	0.26	0.01	-0.26	0.24	0.88	0.42	0.19
338	BPTF	bromodomain PHD finger transcription factor	0.26	0.06	-0.33	0.59	0.36	0.30	0.55
339	FLJ35934	FLJ35934 protein	-0.07	0.21	-0.14	-0.23	0.07	-1.21	-0.09
340	HOXC6	homeobox C6	-0.30	0.97	-0.67	-0.05	-0.36	-1.09	0.43
341	---	---	-0.60	1.20	-0.60	-0.09	-0.40	-0.64	-0.09
342	---	---	-0.26	0.83	-0.57	0.07	-0.85	-0.58	0.08
343	PODH7	protocadherin 7	-0.55	0.65	-0.10	-0.39	-0.58	-0.21	0.18
344	SLC7A5	solute carrier family 7 (cationic amino acid transporter, y+ system), member 5	-0.41	0.72	-0.31	0.04	-0.30	-0.23	-0.04
345	CUL4A	culin 4A	-0.29	0.74	-0.45	-0.15	-0.41	-0.29	-0.25
346	KIF4A	kinesin family member 4A	-0.27	0.52	-0.26	-0.10	0.04	-0.22	-0.40
347	IL1A	interleukin 1, alpha	-0.05	0.67	-0.62	-0.26	-0.75	0.14	0.38
348	AFP	alpha-fetoprotein	0.34	0.31	-0.65	0.26	-0.63	-0.33	0.79
349	ARHGAP28	Rho GTPase activating protein 28	0.07	0.12	-0.19	0.37	-0.32	-0.46	0.21
350	UPF3B	UPF3 regulator of nonsense transcripts homolog B (yeast)	-0.06	0.44	-0.38	-0.36	0.34	-0.42	0.25
351	HIST1H4J	histone cluster 1, H4j	0.11	0.30	-0.41	-0.15	0.05	-0.32	0.37
352	GPC2	glypican 2	0.14	0.33	-0.47	-0.29	-0.06	-0.11	0.01
353	NLRP12	NLR family, pyrin domain containing 12	0.05	-0.32	0.28	0.05	-0.02	-0.46	-1.32
354	DPYSL3	dihydropyrimidinase-like 3	-0.10	0.02	0.08	-0.12	-0.70	-0.66	-1.22
355	TCF3	transcription factor 3 (E2A immunoglobulin enhancer binding factor E12/E47)	-0.34	0.08	0.25	0.12	-0.54	-0.37	-1.30
356	NP5A2	nuclear receptor subfamily 5, group A, member 2	-0.15	-0.16	0.31	-0.12	-0.68	-1.19	-0.99
357	MYH10	myosin, heavy chain 10, non-muscle	0.00	-0.32	0.32	0.11	-0.80	-0.75	-1.13
358	GLI2	GLI family zinc finger 2	-0.35	-0.31	0.66	-0.10	-0.04	-0.29	-0.59
359	ANKS6	ankyrin repeat and sterile alpha motif domain containing 6	-0.25	-0.16	0.41	-0.41	-0.61	-0.41	-0.57
360	CENPE	centromere protein E, 312kDa	-0.05	0.21	-0.16	-0.46	-0.88	-1.20	-0.33
361	CENPF	centromere protein F, 350/400kDa (mitosis)	0.21	-0.02	-0.20	-0.37	-0.75	-0.91	-0.43
362	CHML	choroideremia-like (Rab escort protein 2)	0.12	0.05	-0.18	-0.22	-0.68	-0.88	-0.32
363	CENPF	centromere protein F, 350/400kDa (mitosis)	0.06	0.08	-0.14	-0.38	-1.05	-0.78	-0.39
364	EDIL3	EGF-like repeats and discoidin I-like domains 3	0.06	0.26	-0.33	-0.23	-0.70	-0.75	-0.80
365	ATAD5	ATPase family, AAA domain containing 5	-0.07	0.32	-0.25	-0.18	-0.57	-0.62	-0.63
366	SKIL	SKI-like oncogene	0.37	-0.10	-0.27	-0.17	-0.75	-0.47	-0.43
367	ASPM	asp (abnormal spindle) homolog, microcephaly associated (Drosophila)	0.12	0.07	-0.19	-0.28	-0.83	-0.62	-0.45
368	KIF18A	kinesin family member 18A	0.34	0.10	-0.44	-0.22	-0.67	-0.57	-0.37
369	N4BP2	NEDD4 binding protein 2	0.16	-0.15	0.00	-0.13	-0.81	-0.63	-0.06
370	TP53	tumor protein p53	-0.22	0.46	-0.24	0.11	-0.49	-0.48	-0.55
371	OSBPL10	oxysterol binding protein-like 10	-0.26	0.30	-0.05	-0.16	-0.65	-0.88	-0.41
372	USP28	ubiquitin specific peptidase 28	0.02	-0.07	0.04	-0.18	-0.47	-0.70	-0.82
373	ZNF398	zinc finger protein 398	0.00	0.09	-0.09	-0.15	-0.40	-0.63	-0.72
374	DEPDC1	DEP domain containing 1	0.11	-0.09	-0.02	0.06	-0.33	-0.55	-0.96

375	CENP1	centromere protein 1	0.12	0.15	-0.27	-0.07	-0.55	-0.63	-0.70
376	G1orf106	chromosome 14 open reading frame 106	0.10	0.12	-0.22	0.04	-0.75	-0.52	-0.76
377	HSPA4	heat shock 70kDa protein 4	0.13	-0.09	-0.10	-0.09	-0.45	-0.44	-0.69
378	HAUS8	HAUS augmin-like complex, subunit 6	0.41	-0.23	-0.19	-0.01	-0.41	-0.45	-0.82
379	ZNZF53	zinc finger protein 253	0.11	0.15	-0.27	-0.26	-0.61	-0.42	-0.66
380	ARHGAP11A	Rho GTPase activating protein 11A	-0.05	0.26	-0.21	-0.50	-0.56	-0.32	-0.67
381	PAP2D	phosphatidic acid phosphatase type 2	0.11	0.10	-0.22	-0.46	-0.42	-0.19	-0.80
382	GULP1	GULP, engulfment adaptor PTB domain containing 1	0.04	-0.12	0.08	-0.21	-0.55	-0.35	-0.34
383	PAICS	phosphoribosylaminimidazole carboxylase, phosphoribosylaminimidazole succinocarboxamide synthase	0.17	-0.11	-0.06	-0.06	-0.46	-0.35	-0.40
384	SMC3	structural maintenance of chromosomes 3	0.22	-0.16	-0.07	-0.36	-0.43	-0.22	-0.21
385	GDYL	chromodomain protein, Y-like	0.33	-0.20	-0.13	-0.16	-0.38	-0.16	-0.45
386	GULP1	GULP, engulfment adaptor PTB domain containing 1	0.27	-0.20	-0.07	-0.18	-0.52	-0.35	-0.46
387	G2E3	G2/M-phase specific E3 ubiquitin ligase	0.31	-0.35	0.04	-0.30	-0.48	-0.27	-0.36
388	MK67	antigen identified by monoclonal antibody KJ-67	0.15	0.00	-0.15	-0.43	-0.54	-0.49	-0.43
389	TRHD3	thyrotropin-releasing hormone degrading enzyme	0.17	-0.10	-0.08	-0.24	-0.24	-0.36	-0.49
390	IGF2BP3	insulin-like growth factor 2 mRNA binding protein 3	0.28	-0.34	0.06	-0.19	-0.24	-0.21	-0.59
391	HAUS6	HAUS augmin-like complex, subunit 6	-0.03	-0.26	0.29	-0.11	-0.32	-0.43	-0.75
392	HSPA4	heat shock 70kDa protein 4	-0.06	-0.07	0.13	-0.11	-0.25	-0.33	-0.53
393	DIAPH3	diaphanous homolog 3 (Drosophila)	-0.04	-0.13	0.17	0.00	-0.30	-0.14	-0.60
394	C4orf21	chromosome 4 open reading frame 21	0.03	-0.05	0.02	-0.24	0.01	-0.28	-0.73
395	MSH6	mutS homolog 6 (E. coli)	-0.10	0.05	0.05	0.18	-0.37	-0.38	-0.68
396	WDHD1	WD repeat and HMG-box DNA binding protein 1	0.21	-0.25	0.04	-0.06	-0.27	-0.31	-0.70
397	KNTC1	kinetochore associated 1	0.19	-0.17	-0.02	-0.04	-0.43	-0.44	-0.47
398	FANCI	Fanconi anemia, complementation group 1	0.19	-0.13	-0.06	0.12	-0.44	-0.50	-0.57
399	ZNZF195	zinc finger protein 195	0.00	0.02	-0.24	-0.33	-0.00	-0.16	-0.29
400	KLHL7	kelch-like 7 (Drosophila)	-0.06	-0.04	0.10	-0.22	-0.28	-0.17	-0.24
401	PSIP1	PC4 and SFRS1 interacting protein 1	0.15	-0.13	-0.02	-0.13	-0.28	-0.19	-0.22
402	C18orf54	chromosome 18 open reading frame 54	0.23	-0.29	0.05	-0.26	-0.32	-0.31	-0.31
403	DKC1	dykeratosis congenita 1, dyskerin	0.00	0.24	-0.24	-0.17	-0.17	-0.04	-0.41
404	FLJ32810	Ruvr-type GTPase-activating protein FLJ32810	0.04	0.05	-0.08	-0.01	-0.20	-0.16	-0.53
405	ZNZF43	zinc finger protein 43	0.22	0.14	-0.36	-0.10	-0.50	-0.28	-0.63
406	CENP1	centromere protein 1	0.18	0.07	-0.24	-0.33	-0.24	-0.23	-0.45
407	DEPDC1	DEP domain containing 1	0.31	-0.15	-0.16	-0.08	-0.44	-0.21	-0.60
408	WDR89	WD repeat domain 89	0.35	-0.13	-0.22	-0.10	-0.31	-0.20	-0.53
409	TTF2	transcription termination factor, RNA polymerase II	0.10	0.05	-0.15	0.07	-0.92	-0.12	-0.64
410	ZNZF254	zinc finger protein 254	0.35	-0.19	-0.16	-0.83	-0.27	-0.88	-0.78
411	OSER1	glutamine and serine rich 1	0.65	-0.27	-0.38	-0.12	-0.83	-0.44	-0.78
412	ZNZF675	zinc finger protein 675	0.30	-0.28	-0.02	-0.26	-0.59	-0.41	-0.63
413	ZNZF721	zinc finger protein 721	0.46	-0.36	-0.10	-0.77	-0.30	-0.52	-0.81
414	ESCO1	establishment of cohesion 1 homolog 1 (S. cerevisiae)	0.31	-0.21	-0.11	-0.43	-0.61	-0.66	-0.65
415	OSER1	glutamine and serine rich 1	0.43	-0.36	-0.07	-0.26	-0.54	-0.37	-0.73
416	NR5A2	nuclear receptor subfamily 5, group A, member 2	0.22	-0.45	0.23	-0.36	-0.18	-0.56	-0.35
417	TOP2A	topoisomerase (DNA) II alpha 170kDa	0.18	-0.20	0.02	-0.15	-0.58	-0.57	-0.78

418	GHML	choroideremia-like (Rab escort protein 2)	0.24	-0.25	0.01	-0.57	-0.50	-0.70	-0.40
419	ASPM	asp (abnormal spindle) homolog, microcephaly associated (Drosophila)	0.19	-0.18	-0.02	-0.31	-0.58	-0.61	-0.42
420	GTSE1	G-2 and S-phase expressed 1	-0.16	-0.01	0.17	-0.35	-0.40	-0.59	-0.57
421	POLQ	polymerase (DNA directed) theta	-0.07	0.09	-0.01	-0.25	-0.42	-0.63	-0.27
422	HMG2	high mobility group A1-hook 2	-0.10	0.06	0.04	-0.16	-0.20	-0.50	-0.20
423	TSR1	TSR1, 20S rRNA accumulation, homolog (S. cerevisiae)	-0.29	0.19	0.11	0.03	-0.42	-0.36	-0.10
424	XPO5	exportin 5	-0.19	0.21	-0.02	-0.07	-0.41	-0.42	-0.17
425	PAWR	PRKC, apoptosis, WT1, regulator	0.04	0.03	-0.07	-0.18	-0.47	-0.32	-0.39
426	KIF14	kinesin family member 14	-0.01	0.10	-0.09	-0.03	-0.50	-0.36	-0.26
427	ZNF708	zinc finger protein 708	-0.01	0.04	-0.04	-0.12	-0.54	-0.05	-0.19
428	ZNF589	zinc finger protein 589	-0.06	0.13	-0.06	-0.29	-0.38	-0.25	-0.28
429	ZIK1	zinc finger protein interacting with K protein 1 homolog (mouse)	0.03	-0.01	-0.02	-0.28	-0.33	-0.23	-0.29
430	STIL	SCL/TAL1 interrupting locus	0.10	0.16	-0.26	-0.21	-0.23	-0.53	-0.38
431	CDK6	cyclin-dependent kinase 6	0.09	0.08	-0.17	-0.28	-0.18	-0.69	-0.53
432	TME448	transmembrane protein 48	0.18	0.00	-0.18	-0.02	-0.40	-0.38	-0.61
433	ZIK1	zinc finger protein interacting with K protein 1 homolog (mouse)	0.17	-0.02	-0.15	-0.09	-0.46	-0.46	-0.46
434	---	---	0.11	0.08	-0.20	-0.40	-0.41	-0.34	-0.49
435	COL11A1	collagen, type XI, alpha 1	0.00	0.08	-0.08	-0.24	-1.36	-0.66	-0.55
436	COL11A1	collagen, type XI, alpha 1	-0.03	0.20	-0.17	0.04	-1.05	-0.49	-0.12
437	PCDH7	protocadherin 7	0.13	-0.19	0.06	-0.07	-0.59	-0.59	-0.44
438	CCDC18	coiled-coil domain containing 18	0.14	-0.22	0.07	-0.43	-1.05	-0.53	-0.27
439	ESF1	ESF1, nucleolar pre-rRNA processing protein, homolog (S. cerevisiae)	0.24	-0.24	0.00	-0.26	-0.75	-0.54	-0.51
440	API5	apoptosis inhibitor 5	0.12	0.01	-0.14	-0.18	-0.88	-0.61	-0.28
441	SGOL2	shogunin-like 2 (S. pombe)	-0.02	-0.21	0.23	-0.18	-0.76	-0.43	-0.19
442	SMC3	structural maintenance of chromosomes 3	0.06	-0.31	0.24	-0.44	-0.54	0.02	-0.32
443	ESCO2	establishment of cohesion 1 homolog 2 (S. cerevisiae)	0.28	-0.32	0.03	-0.36	-0.35	0.01	0.05
444	---	---	0.11	-0.13	0.03	-0.36	-0.55	0.33	-0.37
445	BRCA2	breast cancer 2, early onset	0.33	-0.33	0.00	-0.59	-0.55	-0.10	-0.49
446	ESCO1	establishment of cohesion 1 homolog 1 (S. cerevisiae)	0.46	-0.55	0.09	-0.43	-0.38	0.00	-0.11
447	TMEH132B	transmembrane protein 132B	0.59	-0.20	-0.39	-0.37	0.07	-0.35	-0.52
448	G18orf54	chromosome 18 open reading frame 54	0.56	-0.53	-0.03	-0.32	-0.11	-0.14	-0.49
449	FANCB	Fanconi anemia, complementation group B	0.30	0.26	-0.57	-0.15	-0.41	-0.56	-0.37
450	ZNF107	zinc finger protein 107	0.24	0.14	-0.38	-0.23	-0.97	-0.71	-0.43
451	G3BP2	GTPase activating protein (SH3 domain) binding protein 2	0.44	0.07	-0.50	-0.14	-0.71	-0.87	-0.80
452	IGF2BP3	insulin-like growth factor 2 mRNA binding protein 3	0.38	-0.02	-0.36	-0.15	-0.74	-0.72	-1.02
453	MCM4	minichromosome maintenance complex component 4	0.07	0.00	-0.07	0.36	-0.63	-0.58	-1.23
454	---	---	0.15	0.05	-0.20	0.00	-0.68	-0.76	-0.70
455	CXorf15	chromosome X open reading frame 15	0.56	0.25	-0.81	0.20	-0.58	-0.41	-0.84
456	ZNF589	zinc finger protein 589	-0.12	0.12	0.00	-0.10	-0.48	-0.50	-0.88
457	ZNF589	zinc finger protein 589	-0.06	0.14	-0.07	-0.27	-0.52	-0.42	-0.81
458	---	---	0.04	0.17	-0.21	-0.14	-0.57	-0.53	-1.13

459	PLK1	polo-like kinase 1 (Drosophila)	-0.15	0.02	0.12	-0.01	-0.80	-0.51	-1.07
460	KLRG2	killer cell lectin-like receptor subfamily G, member 2	-0.06	-0.13	0.19	-0.43	-0.63	-0.40	-1.10
461	TEAD2	TEA domain family member 2	-0.35	0.31	0.04	0.19	-0.28	-0.17	-1.16
462	KIF20B	kinesin family member 20B	0.46	-0.41	-0.04	-0.48	-1.09	-0.79	-0.26
463	C12orf35	chromosome 12 open reading frame 35	0.20	-0.22	0.03	-0.39	-1.13	-0.94	-0.86
464	ZNF680	zinc finger protein 680	0.35	-0.22	-0.14	-0.72	-0.93	-0.66	-0.74
465	ACTN3	actinin, alpha 3	-0.59	0.38	0.21	-0.55	-0.22	-0.62	-0.38
466	CENPJ	centromere protein J	-0.46	0.47	-0.01	-0.46	-0.04	-0.34	-1.00
467	SKP2	S-phase kinase-associated protein 2 (p45)	0.42	0.46	-0.86	0.70	-0.23	-0.32	-0.80
468	DOP2	DOP2 decapping enzyme homolog (S. cerevisiae)	0.40	0.25	-0.67	0.13	0.13	0.81	-0.88
469	LOC643401	hypothetical protein LOC643401	0.65	-1.07	0.42	-0.78	0.36	0.11	-0.13
470	---	---	0.55	-0.72	0.17	-1.45	0.21	-0.57	-0.93
471	---	---	0.60	-0.68	0.08	-0.76	0.09	-0.31	-0.81
472	GDA	cytidine deaminase	-0.24	0.27	-0.02	-1.67	0.81	-0.39	0.10
473	TMEM132D	transmembrane protein 132D	-0.07	0.11	-0.04	-0.98	-0.01	0.40	0.34
474	---	---	-0.47	0.51	-0.04	-0.91	0.59	-0.24	-0.59
475	FAM71F1	family with sequence similarity 71, member F1	-0.05	0.33	-0.28	-1.03	0.73	0.10	-0.53
476	---	---	-0.17	0.37	-0.19	-1.45	-0.83	-0.74	-0.13
477	CHM	choroideremia (Rab escort protein 1)	0.60	-0.03	-0.57	0.80	-0.58	-0.24	-0.58
478	ZNF92	zinc finger protein 92	-0.30	-0.13	0.43	0.30	-0.39	-0.75	-0.55
479	PHF3	PHD finger protein 3	-0.27	0.06	0.21	-0.23	-0.91	-0.93	-0.91
480	ZNF644	zinc finger protein 644	0.61	-0.07	-0.55	0.00	-1.05	-0.83	-0.92
481	ANKRD32	ankyrin repeat domain 32	0.10	-0.02	-0.08	0.19	-0.55	-0.52	-1.62
482	TPP2	tripeptidyl peptidase II	0.07	-0.08	0.01	-0.12	-0.57	-0.78	-1.05
483	HSPH1	heat shock 105kDa/110kDa protein 1	0.07	0.10	-0.17	0.04	-0.64	-0.74	-1.09
484	MATR3	matrin 3	0.18	-0.21	0.03	-0.03	-0.62	-0.62	-1.22
485	LOC100129064 /// LOC100131360 /// LOC100131888 /// PPP4R2	hypothetical LOC100129064 /// similar to protein phosphatase 4 regulatory subunit 2 /// similar to PPP4R2 protein /// protein phosphatase 4, regulatory subunit 2	0.11	0.03	-0.15	0.00	-0.47	-0.62	-1.36
486	GNO11	GCR4-NOT transcription complex, subunit 1	-0.13	0.14	-0.01	-0.12	-0.94	-1.12	-1.37
487	PRP44B	PRP4 pre-mRNA processing factor 4 homolog B (yeast)	0.12	0.05	-0.17	-0.10	-0.98	-0.87	-1.11
488	NUPI33	nucleoporin 133kDa	0.17	0.10	-0.27	-0.24	-0.83	-1.33	-1.38
489	LARS	leucyl-tRNA synthetase	0.20	-0.23	0.04	-0.19	-0.84	-1.02	-1.30
490	BCLAF1	BCL2-associated transcription factor 1	0.24	-0.02	-0.22	-0.26	-1.37	-1.13	-1.38
491	BCLAF1	BCL2-associated transcription factor 1	0.11	0.04	-0.16	-0.16	-1.33	-1.33	-1.20
492	DHX9	DEAH (Asp-Glu-Ala-His) box polypeptide 9	0.10	0.09	-0.19	0.27	-0.96	-1.00	-1.45
493	DHX9	DEAH (Asp-Glu-Ala-His) box polypeptide 9	0.31	-0.14	-0.18	-0.02	-1.03	-1.10	-1.35
494	SUPT16H	suppressor of Ty 16 homolog (S. cerevisiae)	0.28	-0.09	-0.19	0.04	-1.21	-1.15	-1.81
495	REAK	RB-associated KRAH zinc finger	0.30	-0.28	-0.02	-0.56	-0.86	-1.07	-1.07
496	ER1	exoribonuclease 1	0.53	-0.55	0.02	-0.68	-0.94	-0.69	-1.23
497	USP25	ubiquitin specific peptidase 25	-0.04	-0.22	0.27	-0.14	-0.60	-0.71	-1.44
498	EPRS	glutamyl-prolyl-tRNA synthetase	0.26	-0.14	-0.12	-0.03	-0.77	-0.89	-1.36
499	RECQL	RecQ protein-like (DNA helicase Q1-like)	-0.11	-0.03	0.14	-0.54	-0.97	-0.94	-1.16
500	GPR176	G protein-coupled receptor 176	0.12	0.01	-0.13	0.38	-0.90	-0.74	-1.05

501	SCD	stearoyl-CoA desaturase (delta-9-desaturase)	0.05	0.33	-0.38	-0.02	-1.00	-0.95	-1.05
502	SCD	stearoyl-CoA desaturase (delta-9-desaturase)	0.16	0.13	-0.29	0.00	-1.06	-1.09	-0.98
503	FAM126A	family with sequence similarity 126, member A	0.27	0.29	-0.56	0.11	-1.11	-0.67	-1.16
504	MIPOL1	mirror-image polyductyl 1	0.03	0.36	-0.38	-0.57	-0.40	-0.34	-0.88
505	GEN1	Gen homolog 1, endonuclease (Drosophila)	0.29	0.10	-0.39	-0.75	-0.40	-0.26	-0.59
506	UBE3A	ubiquitin protein ligase E3A	0.19	0.37	-0.56	-0.42	-1.09	-0.65	-0.70
507	FAR1	fatty acyl CoA reductase 1	-0.12	0.15	-0.03	-0.50	-0.76	-0.56	-1.24
508	ZNF84	zinc finger protein 84	0.07	0.04	-0.11	-0.48	-0.56	-0.57	-0.49
509	DNAJC10	DnaJ (Hsp40) homolog, subfamily C, member 10	0.10	0.05	-0.15	-0.30	-0.69	-0.55	-0.67
510	IGF2BP2	insulin-like growth factor 2 mRNA binding protein 2	0.05	0.23	-0.29	-0.29	-0.50	-0.62	-0.93
511	REB1	RB-associated KRAB zinc finger	0.35	0.05	-0.41	-0.53	-0.72	-0.58	-1.11
512	LRRIG3	leucine-rich repeats and Ig motif containing 3	0.02	0.04	-0.06	-0.46	-1.00	-0.02	-0.91
513	ZNF569	zinc finger protein 569	-0.11	-0.08	0.18	-0.06	-0.41	-0.35	-0.44
514	TRIM37	tripartite motif-containing 37	-0.04	0.04	-0.01	-0.07	-0.29	-0.10	-0.67
515	MTFHD1L	methylentetrahydrofolate dehydrogenase (NADP+-dependent) 1-like	-0.33	0.07	0.26	-0.11	-0.10	-0.04	-0.49
516	PRIM2	primase, DNA, polypeptide 2 (58kDa)	0.18	-0.06	-0.12	-0.23	-0.17	-0.44	-0.50
517	NVL	nuclear VCP-like	0.21	-0.17	-0.04	-0.24	0.00	-0.53	-0.39
518	RPAP3	RNA polymerase II associated protein 3	0.29	-0.15	-0.15	0.03	-0.12	-0.22	-0.41
519	PRIM2	primase, DNA, polypeptide 2 (58kDa)	0.16	-0.01	-0.01	-0.15	-0.26	-0.28	-0.53
520	ATAD2	ATPase family, AAA domain containing 2	0.29	-0.25	-0.03	0.20	-0.36	-0.43	-0.37
521	PRIM2	primase, DNA, polypeptide 2 (58kDa)	0.03	0.07	-0.10	0.07	-0.20	-0.39	-0.58
522	BCAT1	branched chain aminotransferase 1, cytosolic	0.03	0.01	-0.05	0.12	-0.42	-0.55	-0.42
523	ASCC3	activating signal cointegrator 1 complex subunit 3	-0.02	0.16	-0.15	0.03	-0.18	-0.54	-0.31
524	MED20	mediator complex subunit 20	-0.10	0.28	-0.17	-0.18	-0.30	-0.23	-0.58
525	BCAT1	branched chain aminotransferase 1, cytosolic	-0.06	0.30	-0.24	0.11	-0.56	-0.55	-0.42
526	ZNF146	zinc finger protein 146	0.10	-0.06	-0.04	0.17	-0.60	-0.58	-0.71
527	REM26	RNA binding motif protein 26	-0.03	0.10	-0.07	-0.13	-0.37	-0.60	-0.75
528	ESF1	ESF1, nuclear pre-rRNA processing protein, homolog (S. cerevisiae)	-0.18	0.23	-0.04	-0.05	-0.60	-0.60	-0.66
529	ANLN	anillin, actin binding protein	0.04	0.10	-0.14	-0.05	-0.48	-0.49	-0.74
530	HMGCR	3-hydroxy-3-methylglutaryl-Coenzyme A reductase	-0.01	0.00	0.01	-0.21	-0.48	-0.62	-0.70
531	LARP4	La ribonucleoprotein domain family, member 4	-0.02	-0.02	0.03	-0.33	-0.42	-0.43	-0.66
532	SQLE	squalene epoxidase	-0.01	0.03	-0.02	-0.34	-0.53	-0.59	-0.85
533	GZE3	G2/M-phase specific E3 ubiquitin ligase	0.28	-0.04	-0.24	-0.29	-0.47	-0.49	-0.62
534	GART	phosphoribosylglycinamide formyltransferase, phosphoribosylglycinamide synthetase, phosphoribosylaminimidazole synthetase	-0.10	0.17	-0.06	-0.06	-0.33	-0.40	-0.94
535	VCAN	versican	0.13	0.05	-0.18	-0.21	-0.80	-0.81	-0.64
536	VCAN	versican	0.19	0.00	-0.18	-0.34	-0.84	-0.83	-0.87
537	RIF1	RAP1 interacting factor homolog (yeast)	-0.04	0.15	-0.10	-0.03	-0.78	-0.78	-0.86
538	SOC34	suppressor of cytokine signaling 4	0.27	0.17	-0.44	-0.25	-0.77	-0.61	-0.40
539	PHIP	pleckstrin homology domain interacting protein	0.18	0.03	-0.21	-0.41	-0.77	-0.54	-0.16
540	USO1	USO1 homolog, vesicle docking protein (yeast)	0.00	0.04	-0.04	-0.25	-0.65	-0.81	-0.48
541	SR140	U2-associated SR140 protein	0.05	-0.01	-0.04	-0.18	-0.58	-0.49	-0.47
542	VCAN	versican	0.16	-0.03	-0.13	-0.15	-0.54	-0.52	-0.37

543	VCAN	versican		0.10	-0.05	-0.05	-0.17	-0.41	-0.41	-0.37
544	SMARCD1	SWI/SNF-related, matrix-associated actin-dependent regulator of chromatin, subfamily a, containing DEAD/H box 1		0.18	-0.02	-0.15	-0.12	-0.36	-0.36	-0.22
545	G2E3	G2/M-phase specific E3 ubiquitin ligase		0.15	-0.20	0.05	-0.21	-0.50	-0.33	-0.46
546	PRPF40A	PRP40 pre-mRNA processing factor 40 homolog A (S. cerevisiae)		-0.03	-0.09	0.12	-0.23	-0.45	-0.31	-0.30
547	PRPF40A	PRP40 pre-mRNA processing factor 40 homolog A (S. cerevisiae)		0.09	0.03	-0.13	-0.31	-0.61	-0.10	-0.01
548	RNCTT	RNA guanylyltransferase and 5'-phosphatase		-0.11	0.07	0.04	-0.36	-0.33	-0.47	-0.16
549	ARNTL2	aryl hydrocarbon receptor nuclear translocator-like 2		-0.09	0.18	-0.09	-0.43	-0.34	-0.27	-0.12
550	SGOL2	shugoshin-like 2 (S. pombe)		0.04	0.11	-0.15	-0.29	-0.44	-0.31	-0.13
551	ZNF567	zinc finger protein 567		0.03	0.15	-0.19	-0.32	-0.48	-0.31	-0.14
552	PPPDE1	PPPDE peptidase domain containing 1		-0.09	0.33	-0.24	0.09	-0.12	-0.78	-0.99
553	UCMA	upper zone of growth plate and cartilage matrix associated		-0.08	0.43	-0.35	-0.29	-0.50	-0.56	-1.05
554	SPRED1	sprouty-related, EVH1 domain containing 1		-0.02	0.69	-0.68	0.07	-0.68	-0.60	-0.62
555	KPNB1	karyopherin (importin) beta 1		-0.02	-0.23	0.25	-0.94	-0.05	-0.29	-0.61
556	ZNF300	zinc finger protein 300		0.06	-0.11	0.04	-0.59	-0.19	-0.65	-1.05
557	TMTC3	transmembrane and tetratricopeptide repeat containing 3		-0.16	-0.46	0.62	-0.30	-0.88	-0.36	-0.55
558	CGDC88A	coiled-coil domain containing 88A		-0.27	-0.41	0.68	-0.11	-0.58	-0.74	-0.37
559	CGDC18	coiled-coil domain containing 18		0.18	-0.87	0.69	0.09	-0.67	-0.65	-0.54
560	LAMA1	laminin, alpha 1		0.02	-0.44	-0.41	-0.34	-0.39	-0.39	-0.23
561	LOC169834	hypothetical protein LOC169834		0.12	-0.68	0.56	-0.38	-0.33	-0.14	-0.56
562	LMCD1	LM and cysteine-rich domains 1		-0.29	-0.06	0.36	-0.29	-0.61	-0.49	-0.36
563	ZNF684	zinc finger protein 684		0.19	0.05	-0.24	-1.33	-0.93	-0.29	-0.37
564	ZNF638	zinc finger protein 638		-0.08	-0.03	0.11	0.04	-0.49	-0.43	-0.73
565	FGF2	fibroblast growth factor 2 (basic)		-0.20	0.32	-0.12	-0.20	-0.23	-0.32	-0.55
566	KIAA1009	KIAA1009		-0.10	-0.08	0.18	0.13	-0.80	-0.29	-0.04
567	RAI14	retinoic acid induced 14		-0.09	-0.05	0.14	-0.10	-0.61	-0.20	-0.07
568	ASCC3	activating signal cointegrator 1 complex subunit 3		-0.03	-0.06	0.09	-0.28	-0.45	-0.39	-0.34
569	EIF5B	eukaryotic translation initiation factor 5B		-0.13	-0.18	0.31	-0.34	-0.23	-0.01	-0.34
570	—	—		-0.41	0.09	0.32	-0.50	-0.05	-0.19	-0.37
571	TYMS	thymidylate synthetase		0.09	-0.23	0.14	-0.46	-0.26	-0.13	-0.28
572	TYMS	thymidylate synthetase		0.10	-0.07	-0.04	-0.22	-0.34	-0.20	-0.02
573	SIX4	SIX homeobox 4		0.24	-0.08	-0.16	-0.44	-0.18	-0.08	-0.04
574	TPR	translocated promoter region (to activated MET oncogene)		0.44	-0.45	0.01	-0.40	-0.34	-0.33	-0.30
575	KIAA1586	KIAA1586		0.37	-0.23	-0.14	-0.23	-0.48	-0.53	-0.12
576	SYT14	synaptotagmin XIV		0.52	-0.11	-0.41	0.29	-0.48	0.00	0.03
577	RAD18	RAD18 homolog (S. cerevisiae)		0.29	-0.09	-0.20	-0.04	-0.27	-0.38	0.19
578	CWC22	CWC22 spliceosome-associated protein homolog (S. cerevisiae)		0.36	-0.14	-0.22	0.20	-0.33	-0.27	0.04
579	GJA1	gap junction protein, alpha 1, 43kDa		0.01	0.03	-0.04	-0.09	-0.05	-0.09	-0.16
580	MRE11A	MRE11 meiotic recombination 11 homolog A (S. cerevisiae)		0.03	-0.02	-0.01	-0.04	-0.19	-0.06	-0.16

[illegible]

618	SERPINH1	binding protein 2 gamma)	serpin, peptidase inhibitor, clade H (heat shock protein 47), member 1, (collagen binding protein 1)	-0.28	0.23	0.05	-0.11	-0.15	-0.21
619	MFAP2	microfibrillar-associated protein 2	microfibrillar-associated protein 2	-0.42	0.20	0.22	-0.06	0.08	0.37
620	PCNXL2	pecanex-like 2 (Drosophila)	pecanex-like 2 (Drosophila)	-0.12	-0.13	0.26	-0.13	0.13	0.13
621	---	---	---	-0.20	-0.05	0.25	-0.07	-0.03	0.12
622	FAM175A	family with sequence similarity 175, member A	family with sequence similarity 175, member A	0.01	-0.31	0.18	0.12	0.09	-0.46
623	PARS	arginyl-tRNA synthetase	arginyl-tRNA synthetase	0.19	-0.04	-0.15	0.01	0.16	0.07
624	PBK	PDZ binding kinase	PDZ binding kinase	0.34	-0.11	-0.23	-0.17	0.09	0.02
625	GFPT2	glutamine-fructose-6-phosphate transaminase 2	glutamine-fructose-6-phosphate transaminase 2	0.12	-0.13	0.01	0.18	0.01	0.15
626	RPL22L1	ribosomal protein L22-like 1	ribosomal protein L22-like 1	0.11	-0.23	0.12	0.18	0.05	0.27
627	KDEL1C	KDEL (Lys-Asp-Glu-Leu) containing 1	KDEL (Lys-Asp-Glu-Leu) containing 1	0.28	-0.16	-0.12	0.16	0.33	0.07
628	basocnulin 2	basocnulin 2	basocnulin 2	0.12	-0.17	0.05	0.11	0.52	0.02
629	TNPO1	transporin 1	transporin 1	-0.06	0.18	-0.12	0.21	0.04	0.15
630	---	---	---	0.06	0.04	-0.10	0.32	0.23	0.12
631	MGC45800	hypothetical LOC90768	hypothetical LOC90768	0.11	0.10	-0.22	-0.15	0.71	0.01
632	RGS17	regulator of G-protein signaling 17	regulator of G-protein signaling 17	-0.07	-0.20	0.27	0.41	0.39	0.44
633	USP45	ubiquitin specific peptidase 45	ubiquitin specific peptidase 45	0.01	-0.20	0.19	0.27	0.28	0.56
634	PHF19	PHD finger protein 19	PHD finger protein 19	-0.19	-0.16	0.35	0.07	0.20	0.36
635	GDF11	growth differentiation factor 11	growth differentiation factor 11	-0.24	0.47	-0.23	-0.82	-0.30	0.02
636	CABYR	calcium binding tyrosine (Y)-phosphorylation regulated	calcium binding tyrosine (Y)-phosphorylation regulated	-0.35	0.46	-0.11	-0.41	0.28	-0.09
637	AMMEOR1	Alport syndrome, mental retardation, midface hypoplasia and elliptocytosis chromosomal region gene 1	Alport syndrome, mental retardation, midface hypoplasia and elliptocytosis chromosomal region gene 1	0.55	0.04	-0.60	0.23	0.11	-0.03
638	MUDENG	MU-2/APIM2 domain containing, death-inducing	MU-2/APIM2 domain containing, death-inducing	0.35	0.15	-0.51	-0.09	-0.14	-0.21
639	C4orf46	chromosome 4 open reading frame 46	chromosome 4 open reading frame 46	0.27	0.14	-0.41	0.09	0.47	-0.09
640	SMARCA5	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 5	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 5	0.41	-0.31	-0.10	-0.29	0.33	-0.17
641	TWIST2	Twist neighbor	Twist neighbor	0.41	-0.29	-0.13	0.02	0.23	-0.27
642	ATAD2	ATPase family, AAA domain containing 2	ATPase family, AAA domain containing 2	0.52	-0.35	-0.16	-0.23	-0.07	-0.11
643	---	---	---	0.69	-0.49	-0.20	-0.38	-0.25	-0.48
644	TK1	thymidine kinase 1, soluble	thymidine kinase 1, soluble	-0.31	0.48	-0.17	-0.02	0.25	0.57
645	ST6SIA3	ST6 alpha-N-acetyl-neuraminidase alpha-2,8-sialyltransferase 3	ST6 alpha-N-acetyl-neuraminidase alpha-2,8-sialyltransferase 3	-0.42	0.46	-0.04	0.11	0.11	0.57
646	CRYGD	crystallin, gamma D	crystallin, gamma D	-0.24	0.50	-0.26	0.15	0.05	0.22
647	CDKN3	cyclin-dependent kinase inhibitor 3	cyclin-dependent kinase inhibitor 3	-0.17	0.20	-0.03	0.36	0.19	0.28
648	CDKN3	cyclin-dependent kinase inhibitor 3	cyclin-dependent kinase inhibitor 3	-0.18	0.21	-0.03	0.22	-0.03	0.14
649	RG8MTD1	RNA (guanine-9-) methyltransferase domain containing 1	RNA (guanine-9-) methyltransferase domain containing 1	0.09	0.17	-0.26	0.04	-0.01	0.27
650	SNX5	sorting nexin 5	sorting nexin 5	0.11	0.11	-0.22	0.15	0.28	0.32
651	NUFIP1	nuclear fragile X mental retardation protein interacting protein 1	nuclear fragile X mental retardation protein interacting protein 1	-0.19	-0.06	0.25	0.16	0.30	0.29
652	FSD1	fibronectin type III and SPRY domain containing 1	fibronectin type III and SPRY domain containing 1	-0.34	0.09	0.25	0.01	0.11	0.26
653	PIF1	PIF1 5'-to-3' DNA helicase homolog (S. cerevisiae)	PIF1 5'-to-3' DNA helicase homolog (S. cerevisiae)	-0.24	0.04	0.20	-0.08	0.20	0.19
654	DNAH14	dynin, axonemal, heavy chain 14	dynin, axonemal, heavy chain 14	-0.33	0.21	0.13	0.30	0.11	0.22
655	SYNCRIP	synaptoagmin binding, cytoplasmic RNA interacting protein	synaptoagmin binding, cytoplasmic RNA interacting protein	0.39	-0.18	-0.22	-0.01	-0.02	0.01

856	GLMN	glomulin, FKBP associated protein	0.35	-0.14	-0.21	0.09	0.05	0.15	0.31
857	ORC4L	origin recognition complex, subunit 4-like (yeast)	0.27	0.04	-0.31	0.23	0.14	0.03	0.06
858	AMMECR1	Alport syndrome, mental retardation, midface hypoplasia and elliptocytosis chromosomal region gene 1	0.33	0.05	-0.38	0.15	0.28	0.16	0.21
859	BCCIP	BRCA2 and CDKN1A interacting protein	0.29	0.03	-0.32	0.01	0.31	0.07	0.04
860	Glorf112	chromosome 1 open reading frame 112	0.39	-0.22	-0.17	0.20	0.27	0.06	0.02
861	DBC1	deleted in bladder cancer 1	0.13	-0.24	0.11	0.15	0.09	0.01	0.37
862	HAUS1	HAUS augmin-like complex, subunit 1	0.24	-0.30	0.06	-0.05	0.00	0.04	0.25
863	---	---	0.06	-0.18	0.12	-0.03	0.30	0.18	0.27
864	DMKN	dermokine	0.14	-0.19	0.05	0.37	0.21	0.16	0.40
865	EXOSC8	exosome component 8	0.07	-0.06	-0.01	0.09	0.82	0.45	0.10
866	LMNB2	lamin B2	-0.11	-0.11	0.21	0.09	0.56	0.38	0.27
867	NARG1	NMDA receptor regulated 1	-0.01	-0.02	0.03	0.01	0.61	0.20	0.20
868	TRIP13	thyroid hormone receptor interactor 13	0.02	0.05	-0.06	0.36	0.24	0.39	0.15
869	PAK1IP1	PAK1 interacting protein 1	0.11	0.10	-0.22	0.28	0.10	0.32	0.34
870	TIPIN	TIMELESS interacting protein	0.01	0.12	-0.13	0.26	0.34	0.38	0.38
871	MGC11082	hypothetical LOC84777	0.21	0.20	-0.41	0.21	0.19	0.33	0.32
872	UHRF1	ubiquitin-like with PHD and ring finger domains 1	0.16	0.18	-0.34	0.33	0.19	0.30	0.12
873	C16orf88	chromosome 16 open reading frame 88	0.10	-0.08	-0.02	0.25	0.35	0.32	0.11
874	KIF20A	kinesin family member 20A	0.07	0.01	-0.07	0.35	0.34	0.13	0.11
875	CENPQ	centromere protein Q	0.02	0.06	-0.07	0.15	0.20	0.40	0.26
876	GABPB1	GA binding protein transcription factor, beta subunit 1	0.26	-0.13	-0.27	0.21	0.32	0.27	0.27
877	FBXO5	F-box protein 5	0.28	-0.01	-0.27	0.24	0.34	0.28	0.16
878	EXOSC3	exosome component 3	0.17	-0.05	-0.12	0.31	0.45	0.51	0.48
879	MRPS12	mitochondrial ribosomal protein S12	0.34	-0.25	-0.09	0.07	-0.16	0.28	0.68
880	CENPM	centromere protein M	-0.04	0.06	-0.02	0.15	-0.30	0.15	0.69
881	SPC24	SPC24, NDC80 kinetochore complex component, homolog (S. cerevisiae)	0.38	-0.14	-0.24	0.00	-0.22	-0.20	0.41
882	GTSE1	G-2 and S-phase expressed 1	-0.25	-0.16	0.42	-0.08	0.42	-0.01	-0.24
883	AEN	apoptosis enhancing nuclease	-0.14	-0.10	0.24	-0.34	0.01	-0.12	-0.21
884	NUDT1	nucleoside diphosphate linked moiety X)-type motif 1	0.03	-0.14	0.11	-0.45	0.12	0.21	0.25
885	MAP9	microtubule-associated protein 9	0.16	-0.17	0.01	-0.48	0.11	-0.02	0.06
886	FAM155A	family with sequence similarity 155, member A	0.01	-0.44	0.43	-0.05	-0.20	0.33	-0.06
887	KIAA1524	KIAA1524	-0.18	0.31	-0.13	0.18	0.16	0.08	-0.14
888	CHAF1B	chromatin assembly factor 1, subunit B (p60)	0.00	0.17	-0.18	0.32	0.28	0.00	-0.07
889	FGD6	FYVE, RhoGEF and PH domain containing 6	-0.04	0.11	-0.07	0.32	-0.10	0.31	-0.07
890	TAF5L	TAF5-like RNA polymerase II, p300/CBP-associated factor (PCAF)-associated factor, 65kDa	0.02	0.01	-0.04	0.13	0.20	-0.10	0.14
891	TGIF1	TGFB-induced factor homeobox 1	0.01	0.10	-0.11	0.06	0.03	0.08	0.16
892	MELK	maternal embryonic leucine zipper kinase	0.09	0.08	-0.16	0.03	0.08	0.11	0.15
893	DDX21	DEAD (Asp-Glu-Ala-Asp) box polypeptide 21	0.06	0.00	-0.06	-0.03	0.04	0.15	0.10
894	PAOS	phosphoribosylaminimidazole carboxylase, phosphoribosylaminimidazole succinocarboxamide synthetase	-0.08	0.01	0.08	0.00	0.08	-0.02	0.03
895	CENPA	centromere protein A	0.00	0.12	-0.12	-0.15	0.10	0.02	0.11

696	GDCA3	cell division cycle associated 3	-0.09	0.11	-0.02	-0.16	-0.01	-0.05	0.02
697	GEF78	centrosomal protein 78kDa	0.03	0.00	-0.04	0.04	0.15	-0.06	-0.03
698	HDAC2	histone deacetylase 2	-0.02	-0.03	0.06	0.14	0.12	0.09	-0.19
699	ZNF281	zinc finger protein 281	-0.02	-0.03	0.05	-0.04	0.00	-0.11	-0.19
700	RUVBL1	RuvB-like 1 (E. coli)	0.16	-0.12	-0.05	0.01	0.14	0.14	-0.03
701	NUP107	nucleoporin 107kDa	0.06	-0.09	0.03	0.03	0.03	0.01	0.04
702	ZWILCH	Zwisch, kinetochore associated, homolog (Drosophila)	0.12	-0.13	0.01	0.06	-0.02	0.06	0.02
703	VCAN	versican	0.08	-0.06	-0.02	-0.24	-0.10	-0.08	0.00
704	SKA3	spindle and kinetochore associated complex subunit 3	0.02	0.01	-0.03	-0.17	0.04	-0.02	-0.19
705	GULP1	GULP, engulfment adaptor PTB domain containing 1	-0.16	0.01	0.15	-0.06	-0.03	0.17	-0.04
706	TRIM59	tripartite motif-containing 59	-0.25	0.10	0.15	-0.17	-0.09	-0.03	-0.05
707	DIAPH3	diaphanous homolog 3 (Drosophila)	-0.09	0.12	-0.03	0.00	-0.09	-0.06	0.01
708	ZNF215	zinc finger protein 215	-0.06	0.12	-0.06	0.27	-0.22	-0.05	0.04
709	CEMP1	centromere protein 1	0.14	-0.11	-0.03	0.34	-0.02	-0.15	0.09
710	KIAA0020	KIAA0020	0.25	0.05	-0.30	-0.03	-0.22	0.01	0.02
711	CXorf26	chromosome X open reading frame 26	0.23	0.11	-0.35	-0.18	-0.10	-0.13	-0.07
712	CASF5	cancer susceptibility candidate 5	0.16	0.09	-0.25	-0.11	-0.19	-0.17	0.13
713	MTRF1	mitochondrial translational release factor 1	0.22	0.08	-0.31	-0.18	-0.03	0.07	0.01
714	SH2D5	SH2 domain containing 5	-0.02	0.15	-0.13	-0.31	-0.14	-0.09	0.22
715	FZD7	frizzled homolog 7 (Drosophila)	0.18	0.05	-0.24	0.14	-0.11	-0.16	-0.18
716	FZD7	frizzled homolog 7 (Drosophila)	0.15	0.01	-0.16	0.01	0.02	-0.08	-0.12
717	MPP6	membrane protein, palmitoylated 6 (MAGUK p55 subfamily member 6)	0.09	0.10	-0.19	-0.11	0.04	0.06	-0.20
718	CHEK1	CHK1 checkpoint homolog (S. pombe)	0.22	-0.14	-0.07	0.10	0.11	0.09	-0.20
719	CHEK1	CHK1 checkpoint homolog (S. pombe)	0.28	-0.12	-0.17	0.06	0.06	-0.06	-0.28
720	SLC39A10	solute carrier family 39 (zinc transporter), member 10	0.23	-0.30	0.06	0.07	0.12	0.09	-0.11
721	ZWILCH	Zwisch, kinetochore associated, homolog (Drosophila)	0.29	-0.26	-0.03	0.18	0.02	-0.05	-0.11
722	TSR1	TSR1, 20S rRNA accumulation, homolog (S. cerevisiae)	0.28	-0.21	-0.07	-0.02	0.14	-0.05	-0.29
723	WDR75	WD repeat domain 75	0.31	-0.23	-0.08	-0.05	0.07	-0.06	-0.24
724	—	—	0.17	-0.17	0.00	-0.14	-0.17	-0.12	-0.09
725	HAUS6	HAUS augmin-like complex, subunit 6	0.22	-0.20	-0.01	-0.07	-0.20	-0.13	-0.14
726	CEBPZ	CCAAT/enhancer binding protein (C/EBP), zeta	0.15	-0.07	-0.07	-0.05	-0.34	-0.08	-0.19
727	NLN	neurolysin (metallopeptidase M3 family)	0.12	-0.02	-0.11	-0.02	-0.26	-0.19	-0.19
728	GLI2	GLI family zinc finger 2	0.14	-0.09	-0.05	0.15	-0.28	-0.12	-0.06
729	GSE1L	GSE1, chromosome segregation 1-like (yeast)	0.12	-0.18	0.06	0.01	-0.12	-0.11	-0.27
730	WDR89	WD repeat domain 89	0.14	-0.12	-0.02	0.07	-0.19	-0.09	-0.46
731	DEPDC1	DEP domain containing 1	0.15	-0.27	0.12	-0.14	-0.21	-0.17	-0.42
732	KIAA1524	KIAA1524	0.29	-0.18	-0.11	0.07	-0.27	0.13	-0.21
733	ZNF670	zinc finger protein 670	0.11	-0.25	0.14	-0.17	-0.01	0.19	-0.47
734	SMC4	structural maintenance of chromosomes 4	0.11	-0.09	-0.03	0.07	-0.31	-0.24	-0.26
735	KRR1	KRR1, small subunit (SSU) procasome component, homolog (yeast)	-0.03	0.09	-0.07	0.03	-0.18	-0.07	-0.13
736	SYNCRIP	synaptotagmin binding, cytoplasmic RNA interacting protein	0.01	0.07	-0.07	-0.06	-0.20	-0.22	-0.19
737	TARS	threonyl-tRNA synthetase	-0.08	-0.09	0.17	-0.02	-0.08	-0.13	-0.42

738	ZNF397	zinc finger protein 397	0.00	-0.16	0.16	0.19	-0.15	-0.12	-0.11
739	C1orf80	chromosome 17 open reading frame 80	-0.07	-0.19	0.26	0.15	-0.09	-0.27	-0.35
740	SMC1A	structural maintenance of chromosomes 1A	-0.12	-0.12	0.24	-0.10	-0.36	-0.08	-0.20
741	SMARCA5	SMC1/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 5	0.05	-0.06	0.00	-0.10	0.06	-0.22	-0.51
742	DLAT	dihydropyrimidine S-acetyltransferase	0.02	-0.06	0.04	-0.01	-0.16	-0.16	-0.33
743	C1orf183	chromosome 1 open reading frame 183	0.14	-0.15	0.01	-0.20	0.02	-0.02	-0.38
744	SSB	Stogen syndrome antigen B (autoantigen 1a)	0.20	-0.17	-0.03	-0.06	-0.04	-0.04	-0.09
745	IGF2BP3	insulin-like growth factor 2 mRNA binding protein 3	0.17	-0.15	-0.01	-0.08	-0.08	-0.05	-0.28
746	MTAP	methylthadenosine phosphorylase	0.10	-0.08	-0.03	-0.02	-0.08	-0.02	-0.18
747	PIN1	pinin, thiosome associated protein	0.24	-0.13	-0.12	-0.04	-0.17	-0.01	-0.18
748	SKA2	spindle and kinetochore associated complex subunit 2	0.22	-0.15	-0.07	0.01	-0.10	-0.08	-0.13
749	PRPF40A	PRP40 pre-mRNA processing factor 40 homolog A (S. cerevisiae)	0.03	-0.09	0.07	-0.21	-0.29	-0.09	-0.26
750	CENPN	centromere protein N	0.09	-0.12	0.04	-0.18	-0.16	-0.09	-0.11
751	GART	phosphoribosylglycinamide formyltransferase, phosphoribosylglycinamide synthetase, phosphoribosylaminimidazole synthetase	0.04	-0.06	0.02	0.12	0.05	-0.10	-0.15
752	FLJ36848	hypothetical LOC647115	0.07	-0.12	0.05	0.16	-0.21	-0.15	0.01
753	CKS2	CDC28 protein kinase regulatory subunit 2	0.04	-0.03	-0.01	-0.04	-0.04	0.01	-0.07
754	DNAJC2	DnaJ (Hsp40) homolog, subfamily C, member 2	-0.03	0.04	-0.01	-0.11	-0.16	-0.13	0.08
755	C2orf44	chromosome 2 open reading frame 44	-0.10	0.06	0.04	-0.21	-0.08	0.11	-0.13
756	PRC1	protein regulator of cytokinesis 1	0.02	-0.14	0.13	-0.08	0.15	0.10	-0.03
757	ATP5O /// DONSON	ATP synthase, H+ transporting, mitochondrial F1 complex, O subunit /// downstream neighbor of SON	-0.12	-0.07	0.19	-0.15	0.08	0.21	-0.13
758	MKI67	antigen identified by monoclonal antibody Ki-67	0.01	0.15	-0.16	0.25	-0.08	-0.09	-0.23
759	GART	phosphoribosylglycinamide formyltransferase, phosphoribosylglycinamide synthetase, phosphoribosylaminimidazole synthetase	0.04	0.05	-0.09	0.18	-0.07	-0.18	-0.50
760	PNN	pinin, desmosome associated protein	0.23	-0.12	-0.11	-0.13	-0.22	-0.17	-0.32
761	CSE1L	CSE1 chromsome segregation 1-like (yeast)	0.13	0.00	-0.12	-0.03	-0.27	-0.28	-0.37
762	HSPD1	heat shock 60kDa protein 1 (chaperonin)	0.10	0.06	-0.16	-0.04	-0.15	-0.16	-0.23
763	CEP350	centrosomal protein 55kDa	0.09	0.14	-0.23	-0.23	-0.02	-0.26	-0.26
764	DEPDC1	DEP domain containing 1	0.11	0.06	-0.17	0.02	-0.39	-0.32	-0.19
765	ARL5B	ADP-ribosylation factor-like 5B	0.19	0.01	-0.21	0.15	-0.26	-0.36	-0.10
766	KPNA2	karyopherin alpha 2 (RAG cohort 1, importin alpha 1)	0.01	0.09	-0.10	0.00	-0.09	0.04	-0.33
767	ECT2	epithelial cell transforming sequence 2 oncogene	-0.08	0.06	0.01	-0.01	-0.13	-0.04	-0.42
768	HSPA4	heat shock 70kDa protein 4	-0.14	0.06	0.07	-0.09	-0.25	-0.32	-0.21
769	E2F1	E2F transcription factor 1	0.11	-0.15	0.04	-0.05	-0.19	-0.24	-0.11
770	C1orf54	Chromosome 18 open reading frame 54	-0.07	-0.08	0.16	-0.04	-0.23	-0.10	-0.16
771	MATR3 /// SNHG4	matrin 3 /// small nuclear RNA host gene 4 (non-protein coding)	0.33	-0.19	-0.14	0.19	0.22	0.30	-0.42
772	UTP15	UTP15, U3 small nuclear ribonucleoprotein, homolog (S. cerevisiae)	0.26	-0.11	-0.15	0.08	0.15	0.22	-0.26
773	ELOVL6	ELOVL family member 6, elongation of long chain fatty acids (FEN1/Elo2, SUR4/Elo3-like, yeast)	0.33	-0.20	-0.13	-0.15	0.25	-0.01	-0.11

774	ELOVL6	ELOVL family member 6, elongation of long chain fatty acids (FEN1/Elo2, SUR4/Elo3-like, Yeast)	0.20	-0.11	-0.08	-0.18	0.32	-0.01	-0.24
775	RAD18	RAD18 homolog (S. cerevisiae)	0.35	-0.32	-0.04	-0.20	0.03	-0.08	-0.18
776	CHEK1	CHEK1 checkpoint homolog (S. pombe)	0.39	-0.25	-0.15	-0.11	0.02	-0.16	-0.23
777	ZNF616	zinc finger protein 616	0.22	-0.48	0.25	-0.04	0.20	-0.14	-0.20
778	---	---	0.22	-0.20	-0.02	0.00	0.33	-0.02	-0.21
779	ZNF616	zinc finger protein 616	0.28	-0.29	0.01	-0.07	0.12	-0.01	-0.16
780	SMC2	structural maintenance of chromosomes 2	0.38	-0.08	-0.30	0.07	-0.53	-0.36	-0.28
781	ZNF141	zinc finger protein 141	0.18	-0.32	0.14	0.09	-0.62	-0.22	-0.28
782	SMC6	structural maintenance of chromosomes 6	0.13	-0.16	0.04	0.18	-0.53	-0.43	-0.29
783	SMC4	structural maintenance of chromosomes 4	0.27	-0.32	0.05	0.02	-0.32	-0.28	-0.27
784	WDR35	WD repeat domain 35	0.34	-0.17	-0.17	0.08	-0.42	-0.14	-0.20
785	TRIM59	tripartite motif-containing 59	-0.04	-0.28	0.30	0.18	-0.56	-0.28	0.09
786	ZNF334	zinc finger protein 334	0.58	-0.59	0.01	-0.16	-0.32	0.03	-0.13
787	PP1G	peptidyl/prolyl isomerase G (cyclophilin G)	0.24	-0.17	-0.08	-0.07	-0.46	-0.14	0.02
788	MURC	muscle-related coiled-coil protein	0.22	-0.18	-0.04	-0.17	-0.41	0.03	0.15
789	CEP152	centrosomal protein 152kDa	0.29	-0.41	0.12	0.12	-0.40	-0.04	0.07
790	PTTG3P	pituitary tumor-transforming 3 (pseudogene)	0.14	-0.63	0.49	0.06	0.44	0.45	0.17
791	CHEK2	CHEK2 checkpoint homolog (S. pombe)	0.17	-0.30	0.13	0.02	0.28	0.23	-0.08
792	MK167	antigen identified by monoclonal antibody Ki-67	0.07	-0.15	0.08	-0.04	0.38	-0.05	-0.02
793	PHF17	PHF finger protein 17	-0.01	-0.19	0.20	-0.12	0.38	0.00	-0.09
794	NEIL3	nei endonuclease VIII-like 3 (E. coli)	0.39	-0.46	0.07	-0.07	0.56	0.08	0.01
795	C5orf34	chromosome 5 open reading frame 34	0.45	-0.58	0.14	-0.21	0.37	0.24	-0.13
796	GNL2	guanine nucleotide binding protein-like 2 (nucleolar)	0.03	-0.21	0.18	0.09	0.28	0.27	0.02
797	DNTTIP2	deoxynucleotidyltransferase, terminal, interacting protein 2	0.08	0.04	-0.12	0.04	-0.11	0.17	0.01
798	NPM1	nucleophosmin (nucleolar phosphoprotein B23, numatrin)	0.18	-0.05	-0.12	0.03	-0.02	-0.02	0.05
799	SSB	Sjogren syndrome antigen B (autoantigen La)	0.17	-0.11	-0.06	-0.04	-0.02	0.22	-0.11
800	ORC3L	origin recognition complex, subunit 3-like (yeast)	0.09	-0.12	0.03	-0.02	0.06	0.19	0.04
801	ZNF607	zinc finger protein 607	0.09	-0.03	-0.07	0.11	0.06	0.12	0.06
802	PRPF40A	PRP40 pre-mRNA processing factor 40 homolog A (S. cerevisiae)	0.04	-0.12	0.08	0.10	0.03	0.01	0.20
803	BAX	BCL2-associated X protein	0.06	0.03	-0.08	-0.11	0.28	0.19	0.40
804	GDK7	cyclin-dependent kinase 7	0.13	-0.12	-0.01	0.11	0.08	0.28	0.38
805	LOC100292909	hypothetical protein LOC100292909	0.14	-0.19	0.05	0.03	0.32	0.40	0.39
806	G2oorf19	chromosome 20 open reading frame 19	0.07	0.03	-0.10	0.20	0.37	0.34	0.23
807	PGBD1	plagioBac transposable element derived 1	0.10	0.06	-0.16	0.02	0.30	0.41	0.15
808	DCAF13	DDB1 and CUL4 associated factor 13	0.04	-0.06	0.01	0.07	0.39	0.39	0.10
809	PABPC1L	poly(A) binding protein, cytoplasmic 1-like	0.25	-0.20	-0.05	-0.07	0.31	0.34	0.15
810	---	---	0.45	-0.53	0.07	0.08	0.10	-0.03	0.26
811	ROR1	receptor tyrosine kinase-like orphan receptor 1	0.36	-0.43	0.06	0.12	0.20	0.12	0.26
812	TEX9	testis expressed 9	0.21	-0.30	0.09	0.21	-0.01	0.04	0.38
813	MTAP	methylthioadenosine phosphorylase	0.47	-0.17	-0.30	0.28	-0.03	-0.06	0.14
814	NPM1	nucleophosmin (nucleolar phosphoprotein B23, numatrin)	0.29	-0.18	-0.12	0.21	0.09	0.07	0.17

815	NUDCD1	NudC domain containing 1	0.28	-0.14	-0.15	0.25	0.18	0.28	0.17
816	TRMT5	TRMT5 RNA methyltransferase 5 homolog (S. cerevisiae)	0.47	-0.25	-0.22	-0.20	0.08	0.08	0.25
817	KIAA0101	zinc finger protein 613	0.13	0.20	-0.33	0.26	0.04	0.25	0.33
818	ZNF613	receptor tyrosine kinase-like orphan receptor 1	0.05	0.13	-0.18	0.54	0.07	0.50	0.13
819	ROR1	receptor tyrosine kinase-like orphan receptor 1	-0.11	0.15	-0.04	0.30	0.10	0.10	0.04
820	GINS4	GINS complex subunit 4 (Slc5 homolog)	-0.20	0.00	0.20	0.31	0.19	0.23	0.11
821	SMC6	structural maintenance of chromosomes 6	0.11	-0.09	-0.02	0.51	0.41	0.15	0.15
822	GLRX3	glutaredoxin 3	0.06	0.01	-0.07	0.01	0.12	0.32	-0.66
823	NUDCD1	NudC domain containing 1	0.20	-0.21	0.01	0.18	0.50	0.27	-0.47
824	OHML	choroideremia-like (Rab escort protein 2)	-0.21	0.58	-0.37	-0.08	-0.24	-0.54	-0.19
825	ROR1	receptor tyrosine kinase-like orphan receptor 1	-0.31	0.45	-0.13	0.20	0.22	-0.17	-0.28
826	ANLN	anillin, actin binding protein	-0.14	0.32	-0.19	0.17	-0.18	-0.16	-0.28
827	NUDT11	nudix (nucleoside diphosphate linked moiety X)-type motif 11	-0.24	0.46	-0.22	-0.14	0.04	-0.26	-0.22
828	DBN1	desmin 1	-0.60	0.38	0.22	-0.13	-0.33	-0.14	-0.15
829	CABYR	calcium binding tyrosine-(Y)-phosphorylation regulated	-0.38	0.56	-0.19	0.39	-0.16	0.28	-0.31
830	CENPJ	centromere protein J	-0.13	0.05	0.08	0.36	-0.16	-0.10	-0.54
831	---	---	-0.35	0.43	-0.07	0.17	0.36	0.12	-0.53
832	PARD3	par-3 partitioning defective 3 homolog (C. elegans)	-0.18	0.24	-0.06	-0.51	0.27	0.01	-0.09
833	---	---	-0.39	0.32	0.06	-0.20	0.32	0.49	-0.05
834	TRO	trophinin	-0.37	-0.08	0.45	0.73	0.49	0.39	0.15
835	GTSE1	G-2 and S-phase expressed 1	-0.23	-0.23	0.46	0.27	0.47	0.35	-0.21
836	SLC4A5	Solute carrier family 4, sodium bicarbonate cotransporter, member 5	-0.10	-0.17	0.27	0.22	0.71	0.46	0.20
837	CCDC34	coiled-coil domain containing 34	-0.24	-0.43	0.67	0.10	0.40	0.26	0.26
838	NT5DC2	5'-nucleotidase domain containing 2	-0.69	0.13	0.56	0.21	-0.12	-0.06	-0.13
839	SALL1	sal-like 1 (Drosophila)	-0.39	-0.09	0.49	-0.16	-0.01	0.21	-0.04
840	SALL1	sal-like 1 (Drosophila)	-0.39	0.10	0.29	0.04	0.11	0.29	0.01
841	PPP4R4	protein phosphatase 4, regulatory subunit 4	-0.36	0.27	0.08	0.01	-0.08	0.65	0.23
842	CCDC152	coiled-coil domain containing 152	-0.10	-0.42	0.52	0.19	-0.33	0.40	0.18
843	MYOZ3	myozenin 3	-0.12	-0.04	0.17	0.76	0.38	-0.17	0.57
844	BIRC5	baculoviral IAP repeat-containing 5	-0.25	0.37	0.33	0.33	0.66	0.44	0.56
845	CHAC1	ChAC, cation transport regulator homolog 1 (E. coli)	-0.26	0.40	-0.14	0.59	0.51	0.30	0.54
846	SMHG12	small nuclear RNA host gene 12 (non-protein coding)	0.14	-0.16	0.03	0.39	0.43	0.88	0.44
847	GNASAS	GNAS antisense RNA (non-protein coding)	0.16	-0.40	0.24	0.47	0.39	0.58	0.44
848	UGCG2	UDP-glucose glucosyltransferase 2	0.37	-0.62	0.25	0.54	0.53	0.74	0.77
849	SLC6A15	solute carrier family 6 (neutral amino acid transporter), member 15	0.33	-0.43	0.10	0.26	0.43	0.74	0.74
850	LCTL	lactase-like	0.32	0.28	-0.58	0.57	0.07	0.00	0.90
851	AMMEGR1	Alport syndrome, mental retardation, midface hypoplasia and elliptocytosis chromosomal region gene 1	0.40	0.15	-0.56	0.26	0.56	0.35	0.32
852	LOC100289612	arsenic transactivated protein 1	0.33	0.39	-0.72	0.56	0.53	0.90	0.43
853	C4orf43	chromosome 4 open reading frame 43	0.11	-0.13	0.03	0.05	1.00	0.35	-0.79
854	NPPB	neuretic peptide precursor B	-0.64	-0.35	0.99	0.65	1.56	-0.07	0.74
855	CER1	cerberus 1, cysteine knot superfamily, homolog (Xenopus laevis)	-0.65	-0.38	1.02	-0.21	0.64	-0.60	-0.22

856	VWDE	von Willebrand factor D and EGF domains	-0.72	0.15	0.57	0.49	0.70	-0.47	-0.53
857	INI1BE	inhibin, beta E	-0.02	0.44	-0.42	0.97	1.56	0.49	0.91
858	PCSK9	proprotein convertase subtilisin/kexin type 9	-0.34	-0.18	0.52	0.83	1.47	0.84	0.88
859	---	---	0.99	-0.75	-0.24	0.26	0.35	0.21	-0.12
860	MCM10	minichromosome maintenance complex component 10	0.92	-0.60	-0.33	0.63	1.07	1.00	0.12
861	HMG3L1	high-mobility group box 3-like 1	0.37	0.56	-0.93	0.15	1.55	1.00	0.86
862	CDC25A	cell division cycle 25 homolog A (S. pombe)	-0.04	-0.01	0.05	0.18	-0.30	-0.49	-0.81
863	BICD1	bicaudal D homolog 1 (Drosophila)	0.13	0.11	-0.25	-0.37	-0.45	-0.47	-0.47
864	OCLN	occludin	0.15	-0.03	-0.12	0.01	-0.56	-0.49	-0.53
865	DNMT3A	DNA (cytosine-5-)methyltransferase 3 alpha	-0.06	0.18	-0.12	0.00	-0.65	-0.44	-0.46
866	CDC141	coiled-coil domain containing 141	0.64	-0.30	-0.34	-0.02	-0.53	-0.94	-0.47
867	ZNF711	zinc finger protein 711	0.22	0.32	-0.54	-0.37	-0.28	-0.96	-0.82
868	SLC04C1	solute carrier organic anion transporter family, member 4C1	0.24	0.10	-0.34	-0.41	-0.73	-1.01	-0.75
869	---	---	-0.02	0.03	-0.01	-0.38	-1.05	-0.71	-0.97
870	BCL2L11	BCL2-like 11 (apoptosis facilitator)	0.10	0.13	-0.23	-0.11	-0.59	-0.41	-0.80
871	AASS	aminoacetate-semialdehyde synthase	0.11	-0.03	-0.08	-0.27	-0.58	-0.62	-1.09
872	SOX2	SRY (sex determining region Y)-box 2	0.39	0.07	-0.46	0.09	-0.89	-0.82	-1.23
873	SALL3	sal-like 3 (Drosophila)	0.06	-0.16	0.11	-0.65	-1.08	-1.06	-0.42
874	---	---	-0.02	-0.16	0.18	-0.96	-1.10	-1.17	-1.03
875	PCDH5	protocadherin beta 5	0.17	-0.39	0.22	-1.15	-0.62	-1.12	-1.26
876	CALCR	calcitonin receptor	-0.20	-0.21	0.41	-0.77	0.07	-0.65	-1.52
877	LRAT	lecithin retinol acyltransferase (phosphatidylcholine--retinol O-acyltransferase)	0.10	-0.11	0.01	-0.89	0.19	-0.73	-1.08
878	CCND2	cyclin D2	-0.53	0.18	0.36	-0.38	-0.93	-0.72	0.17
879	ETV4	ets variant 4	-0.73	0.58	0.15	-0.17	-0.14	-0.42	-0.41
880	MYBL2	v-myb myeloblastosis viral oncogene homolog (avian)-like 2	-0.55	0.07	0.48	0.13	-0.13	-0.25	-0.37
881	FOXH1	forkhead box H1	-1.14	0.59	0.55	-0.28	-0.40	-0.06	-0.38
882	SOX4	SRY (sex determining region Y)-box 4	-0.77	0.27	0.50	-0.14	-0.66	-0.65	-0.44
883	DBNDD1	dysbindin (dystrobrevin binding protein 1) domain containing 1	-0.52	0.04	0.49	-0.23	-0.75	0.01	-0.29
884	CYP251	cytochrome P450, family 2, subfamily S, polypeptide 1	-0.65	0.29	0.35	0.13	-0.33	-0.08	-0.30
885	FAM111B	family with sequence similarity 111, member B	0.42	-0.69	0.27	-0.37	-0.72	0.10	-0.87
886	SLC16A1	solute carrier family 16, member 1 (monocarboxylic acid transporter 1)	0.46	-0.06	-0.41	0.14	-0.78	-0.83	-1.21
887	BRIP1	BRCA1 interacting protein C-terminal helicase 1	0.50	-0.05	-0.45	-0.14	-0.86	-0.80	-1.28
888	C21orf88	chromosome 21 open reading frame 88	0.49	-0.28	-0.21	0.09	-1.05	-0.66	-0.39
889	SNHG4	small nucleolar RNA host gene 4 (non-protein coding)	0.65	-0.17	-0.48	0.12	-0.34	-0.50	-0.61
890	E2F8	E2F transcription factor 8	0.58	-0.29	-0.30	-0.15	-0.30	-0.34	-0.38
891	SNHG4	small nucleolar RNA host gene 4 (non-protein coding)	0.24	0.09	-0.33	-0.45	-0.36	-0.42	-0.87
892	BUB1	budding uninhibited by benzimidazoles 1 homolog (yeast)	0.32	-0.14	-0.18	-0.05	-0.32	-0.44	-0.99
893	LPAR4	lysophosphatidic acid receptor 4	0.26	-0.05	-0.22	-0.21	-0.71	-0.31	-0.73
894	CDC88A	coiled-coil domain containing 88A	0.18	-0.03	-0.25	-0.25	-0.53	-0.42	-0.87
895	---	---	0.20	0.01	-0.20	0.03	-0.58	-0.02	-0.87
896	CDC25A	cell division cycle 25 homolog A (S. pombe)	0.07	0.03	-0.10	0.12	-0.73	-0.52	-0.61

887	F2RL1	coagulation factor II (thrombin) receptor-like 1	0.16	0.01	-0.17	-0.10	-0.41	-0.57	-0.75
888	ZNF93	zinc finger protein 93	-0.16	0.30	-0.14	0.02	-0.71	-0.31	-0.64
889	B4GALT6	UDP-Gal4betaGlcNAc beta 1,4- galactosyltransferase, polypeptide 6	0.33	-0.35	0.02	-0.33	-0.55	-0.30	-0.36
900	ZNF273	zinc finger protein 273	0.32	0.05	-0.38	-0.07	-0.48	-0.44	-0.30
901	MRS2	MRS2 magnesium homeostasis factor homolog (S. cerevisiae)	0.34	-0.18	-0.16	0.06	-0.48	-0.32	-0.25
902	ZNF649	zinc finger protein 649	0.16	-0.07	-0.09	-0.15	-0.29	-0.38	-0.50
903	ZNF253	zinc finger protein 253	0.30	-0.16	-0.13	-0.17	-0.42	-0.37	-0.41
904	C12orf35	chromosome 12 open reading frame 35	0.17	-0.17	0.00	-0.38	-0.87	-0.71	-0.64
905	ZNF138	zinc finger protein 138	0.27	-0.12	-0.15	-0.42	-0.64	-0.68	-0.73
906	B4GALT6	UDP-Gal4betaGlcNAc beta 1,4- galactosyltransferase, polypeptide 6	0.54	-0.69	0.16	-0.42	-0.69	-0.39	-0.82
907	SIX4	SIX homeobox 4	0.38	-0.72	0.34	-0.59	-0.43	-0.55	-0.71
908	PCDH2	protocadherin beta 2	0.34	-0.47	0.13	-0.36	-0.41	-0.99	-0.52
909	EIF2AK4	eukaryotic translation initiation factor 2 alpha kinase 4	0.31	-0.70	0.39	-0.85	-0.92	-1.11	-0.95
910	RAB39	RAB39, member RAS oncogene family	-0.10	0.26	-0.16	0.36	-0.53	0.03	-0.08
911	TERF1	telomeric repeat binding factor (NIMA-interacting) 1	-0.13	-0.13	0.26	-0.10	-0.05	-0.11	-0.38
912	BUB1B	budding uninhibited by benzimidazoles 1 homolog beta (yeast)	-0.11	-0.12	0.24	-0.20	-0.01	-0.02	-0.19
913	SYT1	synaptotagmin 1	0.04	-0.07	0.03	-0.31	-0.13	-0.06	-0.11
914	POLR3G	polymerase (RNA) III (DNA directed) polypeptide G (32kD)	0.14	-0.24	0.11	-0.18	-0.11	-0.24	-0.24
915	TERF1	telomeric repeat binding factor (NIMA-interacting) 1	-0.26	-0.11	0.38	-0.04	-0.31	-0.06	-0.31
916	RAG3	ras-related G3 botulinum toxin substrate 3 (rho family, small GTP binding protein Rac3)	-0.24	-0.10	0.34	-0.18	-0.24	-0.04	-0.13
917	GDF3	growth differentiation factor 3	-0.09	-0.23	0.31	-0.24	0.05	-0.42	-0.01
918	MMP24	matrix metalloproteinase 24 (membrane-inserted)	-0.38	0.23	0.15	-0.16	-0.57	-0.24	-0.28
919	GAP43	growth associated protein 43	-0.24	0.04	0.20	-0.21	-0.37	-0.45	-0.02
920	ITGB1BP3	integrin beta 1 binding protein 3	-0.20	0.31	-0.11	-0.06	-0.19	-0.11	-0.08
921	CECR2	cat eye syndrome chromosome region, candidate 2	-0.16	0.19	-0.04	-0.22	-0.15	-0.05	0.07
922	AASS	aminoacidipate-semialdehyde synthase	0.23	-0.24	0.01	-0.18	-0.34	-0.03	-0.47
923	TRIM24	tripartite motif-containing 24	-0.03	0.01	0.02	0.05	-0.24	-0.13	-0.20
924	ZNF93	zinc finger protein 93	0.03	0.03	-0.06	0.04	-0.38	-0.25	-0.05
925	TRIM24	tripartite motif-containing 24	0.11	-0.01	-0.10	0.03	-0.27	-0.21	-0.26
926	PHC1	polyhomeotic homolog 1 (Drosophila)	0.21	-0.14	-0.07	0.00	-0.34	-0.24	-0.14
927	MCM10	minichromosome maintenance complex component 10	0.22	0.02	-0.24	0.26	-0.26	-0.29	-0.18
928	IPW	imprinted in Prader-Willi syndrome (non-protein coding)	0.13	0.10	-0.23	-0.25	-0.30	-0.25	-0.41
929	FZD3	frizzled homolog 3 (Drosophila)	0.29	-0.04	-0.26	-0.14	-0.37	-0.40	-0.33
930	SYT1	synaptotagmin 1	-0.19	-0.05	0.24	-0.32	-0.56	-0.47	-0.66
931	PHC1	polyhomeotic homolog 1 (Drosophila)	-0.08	0.08	0.00	-0.15	-0.45	-0.37	-0.56
932	HELLS	helicase, lymphoid-specific	0.14	-0.07	-0.07	-0.33	-0.63	-0.41	-0.50
933	ITK	ITK protein kinase	-0.04	-0.03	0.07	-0.23	-0.56	-0.36	-0.43
934	POLR3G	polymerase (RNA) III (DNA directed) polypeptide G (32kD)	0.08	-0.06	-0.02	0.06	-0.64	-0.50	-0.55
935	KBTBD8	kelch repeat and BTB (POZ) domain containing 8	0.09	0.18	-0.27	-0.21	-0.74	-0.45	-0.35
936	ZNF681	zinc finger protein 681	0.02	0.06	-0.08	0.01	-0.13	-0.79	-0.64
937	DSG2	desmoglein 2	0.00	0.04	-0.04	0.06	-0.45	-0.46	-0.43

938	F2RL1	coagulation factor II (thrombin) receptor-like 1	0.05	0.01	-0.07	0.00	-0.29	-0.42	-0.47
939	—	—	0.28	-0.01	-0.27	-0.23	-0.12	-0.48	-0.22
940	ACOXL	acyl-Coenzyme A oxidase-like	0.21	-0.11	-0.10	-0.03	0.16	-0.28	-0.74
941	—	—	0.35	-0.11	-0.24	-0.31	-0.24	-0.42	-0.81
942	C15orf42	chromosome 15 open reading frame 42	0.15	0.00	-0.15	-0.49	-0.12	-0.18	-0.63
943	PKIB	protein kinase (cAMP-dependent, catalytic) inhibitor beta	0.10	0.17	-0.27	-0.40	0.14	-0.01	-0.46
944	HELLS	helicase, lymphoid-specific	0.07	-0.04	-0.03	-0.73	-0.03	0.16	-0.26
945	LOC100288551	hypothetical protein LOC100288551	-0.02	-0.43	0.45	0.02	0.06	-0.10	-0.83
946	KCNGB3	potassium voltage-gated channel, subfamily G, member 3	0.40	-0.40	0.00	-0.92	-0.25	-0.27	-0.55
947	—	—	-0.03	-0.17	0.20	-0.77	-0.39	-0.50	-0.21
948	ZNF550P	zinc finger protein 550 pseudogene	-0.05	-0.16	0.20	-1.02	-0.06	-0.11	-0.51
949	XRCC3	X-ray repair complementing defective repair in Chinese hamster cells 3	-0.33	0.02	0.31	-0.94	-0.12	-0.83	-0.45
950	ZNF682	zinc finger protein 682	-0.40	0.38	0.01	-0.71	-0.54	-0.37	-0.51
951	CYP2B6	cytochrome P450, family 2, subfamily B, polypeptide 6	-0.05	0.76	-0.70	0.22	-0.07	-0.26	-0.05
952	GYG2	glycogenin 2	0.01	0.56	-0.57	0.43	-0.22	-0.11	-0.41
953	ERCC6L	excision repair cross-complementing rodent repair deficiency, complementation group 6-like	-0.21	0.62	-0.42	-0.10	-0.23	-0.23	-0.36
954	IL17RD	interleukin 17 receptor D	-0.05	0.34	-0.30	0.18	-0.11	-0.24	-0.84
955	RP6-213H19.1	serine/threonine protein kinase MST4	0.42	0.27	-0.68	0.46	-0.27	-0.22	-0.83
956	—	—	-0.16	0.50	-0.34	-0.43	-1.28	0.45	-0.74
957	NFE2L3	nuclear factor (erythroid-derived 2)-like 3	-0.16	-0.65	0.80	0.53	1.02	0.30	0.18
958	—	—	-0.02	-0.51	0.54	-0.55	0.80	0.25	0.21
959	—	—	-0.38	-0.43	0.81	-0.60	1.12	0.47	-0.12
960	—	—	-0.06	-0.22	0.28	-0.57	0.98	1.14	0.10
961	WDR37	WD repeat domain 37	0.25	-0.63	0.43	0.55	0.61	0.73	0.35
962	DAZL	deleted in azoospermia-like	0.79	-0.96	0.18	0.61	0.53	0.37	-0.01
963	—	—	0.59	-0.46	-0.13	0.00	0.34	0.32	0.34
964	SEMG1	semenogelin 1	0.16	0.16	-0.32	0.45	0.56	0.86	1.24
965	KCNE1L	KCNE1-like	0.05	0.74	-0.79	0.48	0.41	0.80	0.92
966	SLC1A6	solite carrier family 1 (high affinity aspartate/glutamate transporter), member 6	0.10	0.06	-0.16	0.58	1.02	1.02	0.70
967	LMNB1	lamin B1	0.06	0.12	-0.18	0.09	0.80	0.77	0.41
968	PKIB	protein kinase (cAMP-dependent, catalytic) inhibitor beta	0.08	0.25	-0.33	-0.02	0.60	0.80	0.45
969	FAM133A	family with sequence similarity 133, member A	0.43	-0.34	-0.09	0.55	0.30	0.74	0.79
970	CNKSR2	connector enhancer of kinase suppressor of Ras 2	0.36	-0.03	-0.34	0.47	0.47	0.73	0.56
971	—	—	0.17	-0.01	-0.16	0.63	0.67	0.45	0.88
972	TRIML2	tripartite motif family-like 2	0.05	-0.13	0.08	-0.82	0.66	-0.20	-0.56
973	LOC285401	hypothetical LOC285401	-0.15	0.10	0.05	-0.56	0.38	0.15	0.01
974	LOC728485	hypothetical protein LOC728485	-0.12	-0.06	0.17	-1.43	0.32	0.16	0.03
975	SALL3	Sal-like 3 (Drosophila)	0.21	-0.48	0.27	-1.08	-0.31	-0.28	0.03
976	GPR64	G protein-coupled receptor 64	0.72	0.00	-0.73	-0.02	-0.32	0.13	0.14
977	—	—	0.35	-0.16	-0.19	-0.23	-0.18	-0.10	-0.02
978	SNRPN	small nuclear ribonucleoprotein polypeptide N	0.72	-0.32	-0.40	-0.31	-0.36	-0.12	-0.20

979	FANCB	Farcon anemia, complementation group B	0.67	-0.25	-0.42	0.18	-0.60	0.80	-0.10
980	UGT3A1	UDP glucosyltransferase 3 family, polypeptide A1	0.32	-0.36	0.04	0.36	-0.51	-0.01	-0.21
981	DPPA4	developmental pluripotency associated 4	0.67	-0.73	0.06	-0.39	-0.14	-0.34	-0.41
982	---	---	1.24	-0.85	-0.39	-0.20	-0.23	0.31	0.13
983	G1orf187	chromosome 1 open reading frame 187	-0.19	0.06	0.13	-0.12	0.25	-0.33	-0.08
984	FLJ36116	hypothetical locus LOC388666	-0.26	0.03	0.23	0.17	0.39	-0.18	0.15
985	AP1M2	adaptor-related protein complex 1, mu 2 subunit	-0.33	0.02	0.31	-0.04	0.12	0.19	0.05
986	DPPA2	developmental pluripotency associated 2	-0.37	0.18	0.19	-0.14	0.31	0.01	0.04
987	EPHA1	EPH receptor A1	-0.34	-0.14	0.48	0.20	-0.12	0.19	0.33
988	ARID3B	AT rich interactive domain 3B (BRIGHT-like)	-0.25	-0.24	0.50	-0.19	0.15	0.19	0.07
989	PODXL	podocalyxin-like	-0.05	-0.01	0.06	0.02	-0.24	-0.01	-0.04
990	FSRP2	epithelial splicing regulatory protein 2	-0.11	0.12	-0.01	0.01	-0.39	-0.09	-0.12
991	SALL2	sal-like 2 (Drosophila)	-0.10	-0.13	0.23	0.01	-0.23	-0.15	-0.16
992	GDC25A	cell division cycle 25 homolog A (S. pombe)	0.07	-0.18	0.11	-0.10	0.10	0.23	0.09
993	ACVR2B	activin A receptor, type IIB	0.26	-0.32	0.06	-0.04	0.24	0.05	0.03
994	FAM60A	family with sequence similarity 60, member A	0.06	-0.11	0.05	0.15	-0.01	-0.05	-0.03
995	ADD2	adducin 2 (beta)	0.22	-0.13	-0.10	0.17	0.08	0.05	-0.02
996	IDO1	indoleamine 2,3-dioxygenase 1	0.17	-0.52	0.35	-0.10	-0.04	0.09	0.21
997	ELAVL2	ELAV (embryonic lethal, abnormal vision, Drosophila)-like 2 (Hu antigen B)	0.30	-0.48	0.18	0.11	0.19	0.14	0.21
998	LOC157627	hypothetical LOC157627	0.16	-0.34	0.18	-0.25	0.11	0.02	-0.19
999	---	---	0.40	-0.45	0.04	-0.42	0.12	-0.17	0.10
1000	G1orf38 /// SOHLH2	chromosome 13 open reading frame 38 /// ispermato-genesis and oogenesis specific basic helix-loop-helix 2	0.44	-0.53	0.08	-0.31	0.28	0.07	-0.18
1001	RECQL4	RecQ protein-like 4	-0.28	0.09	0.19	0.22	-0.36	0.18	-0.07
1002	CAMKV	CaM kinase-like vesicle-associated	-0.20	-0.12	0.31	0.29	0.01	0.23	0.14
1003	EPHX3	epoxide hydrolase 3	-0.43	0.08	0.35	0.05	-0.02	0.25	0.34
1004	FAM19A4	family with sequence similarity 19 (chemokine (C-C motif)-like), member A4	-0.27	-0.01	0.28	0.26	0.01	0.43	-0.28
1005	TNFSF11	tumor necrosis factor (ligand) superfamily, member 11	0.33	-0.03	-0.30	0.34	-0.12	0.09	0.27
1006	PIPOX	pipicolinic acid oxidase	0.19	-0.05	-0.14	-0.06	-0.15	0.29	0.08
1007	MIR17HG	MIR17 host gene (non-protein coding)	0.21	-0.12	-0.09	-0.15	-0.10	0.03	0.14
1008	G14orf115	chromosome 14 open reading frame 115	-0.05	0.13	-0.07	0.06	0.10	-0.05	0.19
1009	E2F5	E2F transcription factor 5, p130-binding	-0.02	0.02	0.00	0.19	0.02	0.18	0.14
1010	TET1	tet oncogene 1	0.00	-0.20	0.20	-0.02	0.25	-0.04	-0.05
1011	GUCA1A	guanylate cyclase activator 1A (retina)	0.43	-0.47	0.04	-0.04	0.41	0.55	0.31
1012	---	---	0.32	-0.45	0.13	0.27	0.52	0.46	0.57
1013	FANCD2	Farcon anemia, complementation group D2	0.09	-0.25	0.17	-0.08	0.31	0.30	0.52
1014	FZD5	frizzled homolog 5 (Drosophila)	-0.06	-0.17	0.23	0.16	0.32	0.40	0.27
1015	DEPDC1B	DEP domain containing 1B	-0.01	-0.17	0.18	0.17	0.61	0.58	0.05
1016	PNAIP1	phorbol-12-myristate-13-acetate-induced protein 1	0.30	-0.32	0.03	-0.01	0.61	0.41	0.13
1017	IGSF1	immunoglobulin superfamily, member 1	0.36	-0.11	-0.25	0.22	0.79	0.36	0.09
1018	---	---	0.26	-0.27	0.01	0.27	0.78	0.32	0.56
1019	C15orf12	cathepsin L2	0.02	-0.43	0.41	0.15	0.04	0.38	0.40
1020	---	---	0.14	-0.72	0.58	0.15	0.29	0.22	0.18

1021	HELLS	helicase, lymphoid-specific	0.47	-0.97	0.50	0.01	0.24	0.27	0.12
1022	IGF2BP1	insulin-like growth factor 2 mRNA binding protein 1	0.19	-0.62	0.44	0.06	0.37	0.21	0.07
1023	NFE2L3	nuclear factor (erythroid-derived 2)-like 3	0.38	-0.61	0.22	0.05	0.62	-0.03	-0.04
1024	HELLS	helicase, lymphoid-specific	0.34	-0.91	0.58	-0.33	-0.03	0.04	-0.23
1025	HELLS	helicase, lymphoid-specific	0.27	-0.62	0.35	-0.08	0.24	0.12	-0.32
1026	ST8SIA3	ST8 alpha-N-acetyl-neuraminidase alpha-2,8-sialyltransferase 3	0.00	0.54	-0.55	0.52	0.30	0.25	0.25
1027	PCYT1B	phosphate cytidylyltransferase 1, choline, beta	0.50	0.38	-0.87	0.17	0.22	0.21	0.48
1028	AP1S2	adaptor-related protein complex 1, sigma 2 subunit	0.36	0.31	-0.66	0.10	-0.11	0.07	0.21
1029	ZNF114	zinc finger protein 114	0.02	0.21	-0.23	0.30	0.45	0.44	0.51
1030	SLOC25A21	solite carrier family 25 (mitochondrial oxodicarboxylate carrier), member 21	0.38	0.10	-0.48	0.35	0.70	0.61	0.60
1031	LOC253842	hypothetical protein LOC253842	0.04	0.06	-0.11	0.16	0.56	0.48	0.91
1032	DCAF12L1	DDB1 and CUL4 associated factor 12-like 1	0.48	-0.08	-0.40	0.23	0.16	0.28	0.71
1033	GYG2	glycogenin 2	0.41	0.05	-0.46	0.57	0.46	0.36	0.27
1034	CDC25C	cell division cycle 25 homolog C (S. pombe)	0.11	0.32	-0.44	0.44	0.32	0.26	0.16
1035	RP6-213H19.1	serine/threonine protein kinase MS14	0.29	0.11	-0.40	0.31	0.10	0.17	0.04
1036	LOC100216479	hypothetical LOC100216479	0.04	0.13	-0.17	0.70	0.27	0.18	0.16
1037	HMG83	high-mobility group box 3	0.23	0.40	-0.63	-0.09	0.46	0.33	0.27
1038	---	---	0.18	0.24	-0.42	-0.09	0.09	0.12	0.37
1039	ZNF90	zinc finger protein 90	0.69	-0.14	-0.55	-0.34	-2.01	-1.62	-1.93
1040	NRK	Nrk related kinase	0.25	0.49	-0.74	-0.41	-1.53	-1.05	-1.49
1041	GRPR	gastrin-releasing peptide receptor	0.62	0.48	-1.10	-0.30	-1.27	-0.36	-0.49
1042	SERPINE9	serpin peptidase inhibitor, clade B (ovalbumin), member 9	0.03	0.81	-0.84	-0.43	-1.47	-0.56	-0.85
1043	---	---	0.54	0.67	-1.21	0.34	-1.66	-1.06	-0.84
1044	---	---	0.09	0.91	-1.00	-0.24	-0.88	-0.98	-0.12
1045	PNKD	paroxysmal nonkinetic dyskinesia	-0.12	1.12	-1.00	-0.34	-0.69	-0.91	0.26
1046	RBW17	RNA binding motif protein 17	-0.03	0.88	-0.84	-0.19	-0.32	-0.76	0.25
1047	---	---	-0.45	1.44	-0.99	-0.44	-0.87	-1.26	-0.31
1048	RNF5	ring finger protein 5	0.02	0.98	-1.00	0.15	-0.42	-0.55	0.26
1049	---	---	0.09	1.20	-1.29	-0.22	-0.74	-0.94	0.11
1050	---	---	0.00	1.32	-1.32	-0.22	-0.46	-0.71	0.44
1051	---	---	-0.08	0.85	-0.76	-0.34	-0.35	-0.79	-0.14
1052	SPB1	Sp1-B transcription factor (Sp1-1/PU.1 related)	-0.28	0.73	-0.45	-0.36	-0.14	-0.10	0.39
1053	LOC652147	similar to U5 snRNP-specific protein, 200 kDa	-0.59	1.13	-0.53	-0.09	-0.92	-0.73	-0.16
1054	NLRP7	NLR family, pyrin domain containing 7	-0.75	1.38	-0.62	-0.10	-0.56	-0.52	-0.04
1055	C21orf105	chromosome 21 open reading frame 105	-0.70	0.77	-0.07	-1.01	-0.48	-0.56	-1.32
1056	---	---	-1.00	0.75	0.24	-1.48	-1.68	-1.60	-1.07
1057	CYP26A1	cytochrome P450, family 26, subfamily A, polypeptide 1	-0.87	-0.41	1.27	-0.57	0.74	-1.27	-0.65
1058	---	---	-1.53	0.39	1.14	0.07	1.14	0.22	0.27
1059	ZNF560	zinc finger protein 560	-0.55	-0.53	1.08	-1.99	-0.46	-0.14	-1.54
1060	C18orf54	chromosome 18 open reading frame 54	0.06	-0.26	0.20	-0.98	-0.25	-1.60	-1.18
1061	ZNF829	zinc finger protein 829	-0.04	-0.02	0.06	-1.73	0.10	-0.83	-0.97
1062	ERBB2	v-erb-b2 erythroblastic leukemia viral oncogene homolog 2, neuro/glioblastoma derived oncogene homolog (avian)	-0.33	0.19	0.13	0.34	-2.23	-2.77	-2.12

1083	DAPK1	death-associated protein kinase 1	-0.05	0.36	-0.31	0.24	-1.51	-2.20	-2.21
1084	Sepr9	seprin 9	0.07	0.08	-0.15	-1.36	-1.21	-0.88	-1.77
1085	ATRX	alpha thalassemia/mental retardation syndrome X-linked (RAD54 homolog, <i>S. cerevisiae</i>)	-0.02	0.00	0.03	-1.00	-2.06	-1.55	-1.42
1086	ATRX	alpha thalassemia/mental retardation syndrome X-linked (RAD54 homolog, <i>S. cerevisiae</i>)	0.04	0.07	-0.11	-1.00	-1.75	-1.71	-1.33
1087	SLG6A6	solite carrier family 6 (neurotransmitter transporter, laurine), member 6	-0.40	0.50	-0.10	-0.82	-1.25	-1.08	-2.31
1088	PHF12	PHD finger protein 12	-0.17	0.19	-0.02	-0.77	-1.36	-1.11	-2.70
1089	HEATR1	HEAT repeat containing 1	-0.03	-0.07	0.10	0.23	-1.00	-1.44	-2.89
1090	MYO10	myosin X	-0.22	-0.07	0.29	0.44	-0.91	-1.21	-2.63
1091	MYO10	myosin X	0.15	-0.10	-0.05	0.24	-1.75	-1.52	-1.94
1092	MDM2	Mdm2 p53 binding protein homolog (mouse)	0.49	-0.49	0.00	0.25	-0.50	-1.05	-2.77
1093	TFRC	transferrin receptor (p90, CD71)	0.36	-0.30	-0.05	-0.19	-1.01	-1.37	-1.94
1094	TPR	translocated promoter region (to activated MET oncogene)	-0.41	0.17	0.24	-0.22	-2.07	-1.28	-3.58
1095	NUP188	nucleoporin 188kDa	0.12	0.05	-0.17	0.05	-4.03	-1.49	-3.48
1096	DYNC2H1	dynein, cytoplasmic 2, heavy chain 1	0.19	0.11	-0.30	0.02	-2.11	-1.78	-2.18
1097	MME	membrane metallo-endopeptidase	0.28	-0.33	0.11	-0.50	-1.05	-1.04	-0.59
1098	BDNF	brain-derived neurotrophic factor	-0.51	0.50	0.01	-0.37	-0.29	-1.00	0.25
1099	MMP14	matrix metalloproteinase 14 (membrane-inserted)	-0.64	0.94	-0.30	-0.34	-0.59	-0.58	0.02
1099	UHRF1BP1L	UHRF1 binding protein, 1-like	0.06	-0.02	-0.04	0.43	-0.73	-0.71	-0.12
1081	ODZ3	odc, odd Oz/ten-m homolog 3 (<i>Drosophila</i>)	-0.01	-0.08	0.07	0.20	-1.31	-1.24	-0.36
1082	SLC4A7	solite carrier family 4, sodium bicarbonate cotransporter, member 7	0.05	0.41	-0.45	-0.19	-0.60	-1.10	-1.26
1083	TRPC4	transient receptor potential cation channel, subfamily C, member 4	-0.16	-0.03	0.19	-0.02	-0.45	-0.95	-1.47
1084	SEMA3A	sema domain, immunoglobulin domain (lg), short basic domain, secreted, (semaphorin) 3A	0.21	-0.41	0.20	-0.08	-0.79	-0.18	-0.50
1085	LOC100288985	hypothetical protein LOC100288985	0.00	-0.45	0.45	-0.47	-0.53	-0.77	-0.62
1086	RAB3B	RAB3B, member RAS oncogene family	-0.33	0.20	0.13	-0.29	-0.58	-0.26	-0.51
1087	RAB3B	RAB3B, member RAS oncogene family	-0.29	0.26	0.03	-0.31	-0.65	-0.55	-0.79
1088	RALGPS2	Ral GEF with PH domain and SH3 binding motif 2	-0.03	0.20	-0.17	-0.51	-0.38	-0.24	-0.86
1089	FGF2	fibroblast growth factor 2 (basic)	0.20	0.24	-0.44	-0.31	-0.30	-0.66	-0.55
1090			0.17	-0.13	-0.04	-0.51	-0.32	-0.35	-0.21
1091	KIAA1826	KIAA1826	0.24	-0.04	-0.20	-0.05	-0.47	-0.52	-0.85
1092	RALGPS2	Ral GEF with PH domain and SH3 binding motif 2	0.33	-0.10	-0.23	0.04	-0.65	-0.60	-0.93
1093	FST	folistatin	-0.31	-0.34	0.65	-0.49	0.09	-0.47	-0.30
1094	TRPC4	transient receptor potential cation channel, subfamily C, member 4	0.32	-0.53	0.21	-1.09	-0.29	-1.39	-0.98
1095	LOC401074	hypothetical LOC401074	0.17	0.18	-0.35	0.17	0.35	0.61	1.05
1096	MAP9	microtubule-associated protein 9	-0.17	0.38	-0.22	0.34	0.50	0.70	0.43
1097	SLC7A11	solite carrier family 7, (cationic amino acid transporter, y+ system) member 11	0.08	-0.10	0.02	0.33	0.85	-0.13	0.40
1098	SLC7A11	solite carrier family 7, (cationic amino acid transporter, y+ system) member 11	0.14	-0.08	-0.06	0.04	0.77	-0.01	0.26

1099	BBS7	Bardet-Biedl syndrome 7	0.04	-0.15	0.11	0.20	0.93	0.39	-0.15
1100	GRBP2	cellular retinoic acid binding protein 2	-0.14	0.01	0.13	-0.27	-0.18	0.44	0.28
1101	GPX8	glutathione peroxidase 8 (putative)	0.22	-0.01	-0.21	0.27	-0.02	0.06	0.18
1102	---	---	-0.04	-0.06	0.10	-0.04	0.10	0.13	0.09
1103	RAB3B	RAB3B, member, RAS oncogene family	0.22	-0.46	0.24	-0.30	0.01	0.11	-0.07
1104	---	---	0.61	-0.40	-0.22	-0.10	0.26	0.16	-0.08
1105	SFRP2	secreted frizzled-related protein 2	-0.47	-0.31	0.78	-0.08	0.89	0.49	0.54
1106	SEMA3A	sema domain, immunoglobulin domain (lg), short basic domain, secreted, (semaphorin) 3A	0.66	-1.03	0.37	0.04	0.48	-0.36	-2.19
1107	IRX2	iroquois homeobox 2	-0.36	0.30	0.06	-0.13	-3.03	-0.12	-0.12
1108	LOC339260	Hypothetical protein LOC339260	0.52	0.30	-1.24	0.99	1.46	1.11	1.72
1109	SERPINF4	serpin peptidase inhibitor, clade B (ovalbumin), member 4	1.00	-0.44	-0.56	0.79	0.04	1.37	1.53
1110	VNDE	von Willebrand factor D and EGF domains	0.83	-0.83	0.00	-0.61	-0.78	-0.59	-0.46
1111	SSX4 /// SSX4B	synovial sarcoma, X breakpoint 4 /// synovial sarcoma, X breakpoint 4B	-0.01	-0.21	0.22	-0.59	0.17	-0.69	-0.66
1112	CHST9	carbohydrate (N-acetyl)galactosamine 4-O-sulfotransferase 9	0.18	-0.40	0.22	-0.37	-0.43	-0.63	-0.38
1113	ZNF682	zinc finger protein 682	0.33	-0.40	0.07	-1.09	-1.03	-0.82	-1.09
1114	GNTI2	glucosaminyl (N-acetyl) transferase 2, I-branching enzyme (I blood group)	0.11	-0.10	0.00	-0.38	-0.70	-0.90	-1.41
1115	SLC12A1	solute carrier family 12 (sodium/potassium/chloride transporters), member 1	0.02	-0.02	0.01	-0.55	-0.73	-0.73	-1.41
1116	DSC2	desmocollin 2	0.16	-0.08	-0.08	0.28	-0.96	-0.58	-0.47
1117	NRK	Nrk related kinase	0.12	0.13	-0.25	-0.19	-1.02	-0.98	-0.49
1118	LOC729993	hypothetical protein LOC729993	-0.03	0.33	-0.30	-0.61	-1.36	-0.99	-0.81
1119	---	---	0.32	-0.44	0.12	-1.81	-0.46	-0.70	-0.50
1120	---	---	0.62	-0.62	0.00	-2.19	-0.58	-0.61	-1.87
1121	---	---	0.89	-0.21	-0.68	-0.26	0.69	0.79	0.25
1122	LOC347475	UPF0825 coiled-coil domain-containing protein ENSP00000359845	0.60	0.54	-1.14	0.15	0.68	0.51	0.53
1123	LOC100129662	hypothetical protein LOC100129662	0.54	0.07	-0.61	0.51	0.49	0.49	0.56
1124	ZNF876P	zinc finger protein 876 (pseudogene)	0.45	0.16	-0.60	0.81	0.53	-0.07	0.26
1125	GPC4	glypican 4	0.33	0.29	-0.61	0.33	0.31	0.43	0.20
1126	GYG2	glycogenin 2	0.27	0.33	-0.60	0.56	0.11	0.11	0.13
1127	SH3GL3	SH3 domain GRB2-like 3	0.08	0.07	-0.15	0.44	0.01	0.19	0.57
1128	NODAL	nodal homolog (mouse)	-0.27	0.33	-0.06	0.54	0.44	0.47	0.63
1129	FAM71F1	family with sequence similarity 71, member F1	-0.52	0.79	-0.28	0.50	0.26	0.24	0.25
1130	BIK	BCL2-interacting killer (apoptosis-inducing)	-0.13	0.00	0.13	-0.10	0.16	0.03	0.46
1131	RIT2	Ras-like without CAAX 2	0.13	-0.09	-0.04	-0.02	0.10	0.08	0.42
1132	---	---	0.21	-0.38	0.17	0.25	0.28	0.28	0.44
1133	NAPIL3	nucleosome assembly protein 1-like 3	-0.04	0.35	-0.31	0.43	0.19	0.49	0.24
1134	PCYT1B	phosphatase cytidylyltransferase 1, choline, beta	0.29	0.08	-0.36	0.13	0.12	0.34	0.41
1135	LOC389895	hypothetical LOC389895	0.30	0.00	-0.30	-0.04	0.26	0.69	0.79
1136	---	---	0.92	-0.72	-0.20	0.41	0.25	0.66	0.21
1137	G30r38	chromosome 13 open reading frame 38	0.50	-0.67	0.17	0.52	-0.09	0.05	0.23
1138	FABP7	fatty acid binding protein 7, brain	0.26	-0.24	-0.03	0.46	0.68	0.39	0.50

1139	KLKB1	kallikrein B, plasma (Fletcher factor) 1	0.31	-0.42	0.11	0.27	0.80	0.14	0.49
1140	HLA-DPB2	major histocompatibility complex, class II, DP beta 2 (pseudogene)	0.53	-0.36	-0.17	0.45	0.60	0.55	0.72
1141	GALOB	calcitonin-related polypeptide beta	-0.28	-0.15	0.44	0.37	0.26	0.45	0.96
1142	ZFR2	zinc finger RNA binding protein 2	0.05	-0.36	0.31	0.43	0.55	0.82	0.94
1143	LOC151627	hypothetical LOC151627	0.25	-0.69	0.44	0.01	0.35	0.47	0.04
1144	ZIC2	Zic family member 2 (odd paired homolog, Drosophila)	-0.28	-0.40	0.68	0.38	0.42	0.63	0.16
1145	LOC730125	Hypothetical LOC730125	-0.07	-0.34	0.41	0.27	0.19	0.40	0.26
1146	—	—	-0.15	-0.57	0.72	0.05	0.49	0.37	0.31
1147	ADAMTS19	ADAM metalloproteinase with thrombospondin type 1 motif, 19	-0.36	-0.19	0.55	-0.26	-0.01	-0.26	-0.79
1148	C1orf187	chromosome 1 open reading frame 187	0.01	-0.40	0.39	-0.44	0.28	-0.12	-0.39
1149	—	—	-0.09	-0.41	0.30	-0.32	-0.07	-0.01	-0.50
1150	FGFR4	fibroblast growth factor receptor 4	-0.54	0.07	0.47	-0.30	0.03	0.16	-0.27
1151	SEMA6A	sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6A	-0.44	-0.20	0.65	-0.58	0.11	-0.21	0.00
1152	SALL3	sal-like 3 (Drosophila)	-0.30	-0.14	0.44	-0.66	-0.10	-0.04	-0.27
1153	ADD2	adducin 2 (beta)	-0.51	0.22	0.28	0.17	0.03	-0.32	-0.11
1154	ETV4	ets variant 4	-0.37	0.21	0.16	-0.35	-0.09	-0.23	-0.27
1155	IGFBP1	insulin-like growth factor 2 mRNA binding protein 1	-0.40	0.46	-0.06	-0.15	0.02	-0.51	-0.35
1156	DPPA3	developmental pluripotency associated 3	-0.43	0.28	0.16	-0.29	0.00	-0.67	-0.71
1157	—	—	-0.53	0.24	0.29	-0.53	0.47	0.24	-0.37
1158	DPPA5	developmental pluripotency associated 5	-0.98	0.34	0.64	-0.52	-0.16	-0.27	-0.35
1159	HS6ST2	heparan sulfate 6-O-sulfotransferase 2	0.35	-0.20	-0.15	0.14	0.30	0.15	-0.62
1160	GLDC	glycine dehydrogenase (decarboxylating)	0.13	0.03	-0.16	-0.13	-0.30	-0.38	-0.45
1161	NLGN4X	neuroligin 4, X-linked	0.22	0.20	-0.42	0.02	-0.45	-0.21	-0.35
1162	MEGF10	multitide EGF-like domains 10	0.38	0.16	-0.54	-0.21	-0.40	-0.16	-0.17
1163	KLHDC7A	kelch domain containing 7A	-0.01	0.31	-0.31	-0.38	-0.73	-0.10	0.11
1164	PALM3	Paralemnin-3	-0.04	0.15	-0.11	-0.50	-0.42	-0.18	-0.06
1165	GPR19	G protein-coupled receptor 19	0.40	-0.04	-0.36	-0.17	0.08	-0.13	0.19
1166	ORC1L	origin recognition complex, subunit 1-like (yeast)	0.06	0.09	-0.15	0.32	0.13	-0.10	-0.26
1167	COCH	coagulation factor G homolog, cochlin (Limulus polyphemus)	0.21	-0.26	0.05	0.24	0.04	-0.14	0.05
1168	GABRB3	gamma-aminobutyric acid (GABA) A receptor, beta 3	0.21	-0.20	0.00	-0.04	-0.12	-0.20	-0.17
1169	GABRB3	gamma-aminobutyric acid (GABA) A receptor, beta 3	0.08	-0.21	0.13	0.09	-0.30	-0.29	-0.39
1170	—	—	0.01	-0.03	0.02	-0.17	-0.10	-0.42	-0.12
1171	COCH	coagulation factor G homolog, cochlin (Limulus polyphemus)	0.34	-0.23	-0.11	0.27	0.02	-0.19	0.15
1172	DSC2	desmoglein 2	0.34	-0.24	-0.11	-0.05	-0.06	0.01	0.11
1173	FAM80A /// LOC728115	family with sequence similarity 80, member A /// similar to family with sequence similarity 60, member A	0.18	-0.21	0.03	0.13	-0.05	0.02	-0.09
1174	CNTNAP2	contactin associated protein-like 2	0.30	-0.09	-0.20	0.64	0.11	0.09	0.17
1175	C8orf42	chromosome 8 open reading frame 42	0.09	0.01	-0.09	0.44	-0.08	-0.22	0.01
1176	ZSCAN10	zinc finger and SCAN domain containing 10	-0.29	0.06	0.23	-0.06	-0.30	-0.30	-0.19
1177	NXPH2	neurexophilin 2	-0.19	-0.06	0.25	-0.17	-0.21	-0.06	-0.34
1178	PRDM14	PR domain containing 14	-0.33	0.20	0.13	-0.19	-0.40	-0.07	-0.09

1179	FOXO3	forkhead box D3	-0.36	0.17	0.19	0.10	-0.44	-0.04	-0.34
1180	KIF1A	kinesin family member 1A	-0.29	0.13	0.16	-0.29	-0.40	-0.48	-0.06
1181	ADAMTS19	ADAM metalloproteinase with thrombospondin type 1 motif 19	-0.43	0.02	0.41	-0.10	-0.16	-0.14	0.05
1182	FOXH1	forkhead box H1	-0.46	-0.04	0.51	-0.32	0.00	0.17	0.14
1183	—	—	-0.28	-0.13	0.41	-0.18	0.21	0.14	0.00
1184	PLEKHG4B	pleckstrin homology domain containing, family G (with RhoGef domain) member 4B	-0.44	-0.02	0.46	0.32	-0.10	0.04	0.10
1185	LOC728342	Hypothetical protein LOC728342	-0.09	-0.28	0.38	0.13	-0.28	0.18	0.10
1186	PDZD4	PDZ domain containing 4	-0.43	0.61	-0.18	-0.41	-0.49	-0.22	0.03
1187	C9orf135	chromosome 9 open reading frame 135	-0.33	0.19	-0.63	-0.79	-0.33	-0.24	-0.24
1188	TMSB15A	thymosin beta 15a	-0.13	0.32	-0.19	-0.05	0.68	-0.21	0.01
1189	GNG4	guanine nucleotide binding protein (G protein), gamma 4	-0.26	0.27	-0.01	0.46	0.44	0.27	0.23
1190	C1orf135	chromosome 1 open reading frame 135	0.01	0.19	-0.20	0.12	0.25	0.18	0.29
1191	—	—	0.14	-0.02	-0.11	0.10	0.14	0.24	0.21
1192	CA14	carbonic anhydrase XIV	-0.03	-0.03	0.06	0.27	0.36	0.50	0.70
1193	SOX3	SRY (sex determining region Y)-box 3	-0.28	0.14	0.14	0.02	0.50	0.31	0.40
1194	—	—	-0.20	-0.02	0.22	-0.01	0.24	0.17	0.36
1195	ATCAV	ataxia cerebellar, Cayman type	-0.59	0.41	0.18	0.30	0.15	0.55	0.57
1196	PIM2	pim-2 oncogene	0.23	0.50	-0.73	0.06	0.10	-0.06	0.05
1197	TEX14	testis expressed 14	-0.23	0.42	-0.19	0.30	-0.39	0.17	0.25
1198	ZNF488	zinc finger protein 488	0.07	0.41	-0.48	0.17	-0.33	0.19	0.45
1199	—	—	0.02	0.41	-0.43	-0.02	-0.06	0.52	0.52
1200	ATXN7L1	ataxin 7-like 1	-0.05	0.20	-0.15	0.87	-0.28	0.31	0.10
1201	IGDCC3	immunoglobulin superfamily, DCC subclass, member 3	-0.75	0.70	0.05	0.01	-0.34	-0.04	0.58
1202	SLC1A6	solute carrier family 1 (high affinity aspartate/glutamate transporter), member 6	0.02	0.04	-0.07	0.67	0.83	0.80	0.88
1203	SOX11	SRY (sex determining region Y)-box 11	0.21	-0.65	0.44	0.70	0.63	0.65	0.64
1204	LEFTY1	left-right determination factor 1	-0.15	0.27	-0.12	0.53	0.52	0.87	0.81
1205	ME1	malic enzyme 1, NADP(+)-dependent, cytosolic	-0.49	1.26	-0.77	-0.74	-1.01	-1.11	-0.41
1206	—	—	-0.32	1.25	-0.93	-0.11	-0.58	-1.05	0.16
1207	—	—	0.08	0.61	-0.69	-0.22	-0.53	-0.80	0.05
1208	GPR143	G protein-coupled receptor 143	-0.47	1.05	-0.58	-0.16	-0.29	0.14	0.28
1209	—	—	0.19	1.06	-1.26	-0.10	-0.42	-0.48	0.54
1210	LOC153469	hypothetical protein LOC153469	0.82	0.17	-0.99	0.40	0.01	0.34	0.24
1211	GPC4	glycan 4	0.35	0.55	-0.90	0.44	-0.21	0.12	-0.05
1212	SMFDL3B	schlingomyelin phosphodiesterase, acid-like 3B	0.36	0.20	-0.56	0.11	-0.37	-0.29	0.14
1213	WNK3	WNK lysine deficient protein kinase 3	0.44	0.04	-0.47	0.07	0.17	0.06	-0.02
1214	ZFP42	zinc finger protein 42 homolog (mouse)	-0.85	0.58	0.27	0.46	0.72	0.27	-0.15
1215	ZFP42	zinc finger protein 42 homolog (mouse)	-0.02	0.39	-0.37	0.17	0.46	-0.08	-0.60
1216	NMU	neuromedin U	-0.06	-0.13	0.19	0.10	-0.21	-0.01	0.41
1217	CD24	CD24 molecule	0.03	-0.08	0.04	-0.04	0.04	0.08	0.04
1218	CD24	CD24 molecule	-0.05	-0.08	0.12	0.00	0.10	0.21	0.03
1219	SCNN1A	sodium channel, nonvoltage-gated 1 alpha	-0.04	-0.27	0.32	-0.28	-0.02	-0.12	-0.01
1220	REPMS2	RNA binding protein with multiple splicing 2	-0.30	-0.05	0.36	-0.02	0.05	0.05	0.14

1221	FREM2	FRAS1 related extracellular matrix protein 2	-0.16	-0.09	0.25	-0.13	0.23	0.08	-0.02
1222	LOC100131138	similar to HCG2040918	-0.43	0.22	0.21	-0.15	0.09	-0.17	-0.03
1223	CALB1	calbindin 1, 28kDa	-0.11	0.04	0.07	0.03	0.16	0.10	0.07
1224	POU5F1B	POU class 5 homeobox 1B	-0.15	0.02	0.13	0.11	-0.04	0.09	0.15
1225	OTX2	orthodenticle homeobox 2	0.08	-0.16	0.08	0.17	0.04	0.02	-0.18
1226	SOX2	SRY (sex determining region Y)-box 2	-0.26	-0.09	0.34	0.13	-0.03	-0.01	-0.24
1227	LIN28B	lin-28 homolog B (C. elegans)	0.13	-0.21	0.07	-0.09	-0.20	-0.15	-0.25
1228	GD24	GD24 molecule	-0.14	-0.03	0.16	-0.04	0.02	-0.39	-0.35
1229	C1orf187	chromosome 1 open reading frame 187	-0.42	-0.09	0.51	-0.15	0.50	0.28	0.48
1230	---	---	-0.20	-0.17	0.37	-0.01	0.35	0.12	0.28
1231	ZFP42	zinc finger protein 42 homolog (mouse)	-0.40	0.05	0.35	0.14	0.33	0.24	0.33
1232	RMST	rhabdomyosarcoma 2 associated transcript (non-protein coding)	0.48	-0.57	0.09	0.15	0.13	0.27	0.36
1233	---	---	0.30	-0.29	0.00	-0.14	0.26	0.29	0.24
1234	CXADR	coxsackie virus and adenovirus receptor	0.23	0.15	-0.39	0.01	-0.60	-0.48	-0.72
1235	GABRB3	gamma-aminobutyric acid (GABA) A receptor, beta 3	0.31	-0.15	-0.16	0.03	-0.43	-0.28	-0.55
1236	KCNN2	potassium intermediate/small conductance calcium-activated channel, subfamily N, member 2	0.11	0.01	-0.13	-0.12	-0.45	-0.05	-0.19
1237	IGF2BP1	insulin-like growth factor 2 mRNA binding protein 1	0.17	-0.25	0.08	0.12	-0.28	-0.49	-0.84
1238	CLDN6	claudin 6	-0.25	0.14	0.11	-0.72	-0.04	-0.77	-0.77
1239	TEX15	testis expressed 15	0.13	-0.26	0.13	-0.49	-0.86	-0.72	-0.71
1240	ZIC3	Zic family member 3 (odd-paired homolog, Drosophila)	0.05	0.32	-0.37	-0.12	-0.22	-0.33	-0.19
1241	RPRM	reptino, TP53 dependent, G2 arrest mediator candidate	-0.36	0.49	-0.13	-0.36	-0.07	-0.25	-0.33
1242	GD24	GD24 molecule	0.01	0.05	-0.06	0.01	0.12	-0.03	-0.46
1243	---	---	-0.14	0.19	-0.05	-0.19	0.11	-0.21	-0.20
1244	GDH3	cadherin 3, type 1, P-cadherin (placental)	-0.52	0.24	0.28	-0.18	-0.37	-0.11	-0.36
1245	LINGO1	leucine rich repeat and Ig domain containing 1	-0.33	0.17	0.15	-0.11	-0.60	-0.46	-0.40
1246	SEMA6A	sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6A	-0.62	-0.08	0.70	-0.31	-0.34	-0.58	-0.43
1247	LEGT1	leukocyte cell derived chemotaxin 1	0.47	-0.42	-0.05	-0.03	0.16	0.55	0.46
1248	DOX	doublecortin	0.88	-0.54	-0.34	0.00	0.41	-0.13	0.07
1249	GLB1L3	galactosidase, beta 1-like 3	0.49	-0.28	-0.21	-0.05	0.10	-0.04	0.26
1250	OTX2	orthodenticle homeobox 2	0.45	-0.32	-0.13	0.07	0.07	0.10	-0.12
1251	SOX11	SRY (sex determining region Y)-box 11	0.03	-0.09	0.06	-0.08	0.33	0.16	0.37
1252	ZNF165	zinc finger protein 165	0.19	-0.16	-0.03	0.01	0.39	0.12	0.10
1253	SOX11	SRY (sex determining region Y)-box 11	-0.03	-0.23	0.26	0.15	0.29	0.22	0.19
1254	---	---	-0.12	-0.23	0.35	-0.25	0.25	0.05	0.05
1255	MYCN	v-myc myelocytomatosis viral related oncogene, neuroblastoma derived (avian)	-0.11	0.01	0.10	-0.03	0.23	-0.01	-0.15
1256	NANOG	Nanog homeobox	-0.12	0.13	-0.01	0.07	0.27	0.00	-0.12
1257	POU5F1 /// POU5F1B /// POU5FIP3 /// POU5FIP4	POU class 5 homeobox 1 /// POU class 5 homeobox 1B /// POU class 5 homeobox 1 pseudogene 3 /// POU class 5 homeobox 1 pseudogene 4	-0.10	0.07	0.03	-0.02	-0.03	0.03	0.06
1258	---	---	0.09	0.04	-0.13	-0.01	0.02	-0.03	0.09
1259	CALB1	calbindin 1, 28kDa	-0.14	0.03	0.10	0.25	0.27	0.13	0.15

1250	G6orf168	chromosome 6 open reading frame 168	-0.01	0.27	-0.26	0.07	0.16	0.21	0.34
1261	SLC7A3	solute carrier family 7 (cationic amino acid transporter, y+ system), member 3	-0.40	0.33	0.08	-0.10	0.27	-0.01	-0.20
1262	KIF29A	kinesin family member 26A	0.07	0.10	-0.17	-0.31	0.46	0.25	-0.08
1263	GAP43	growth associated protein 43	-0.23	-0.04	0.27	-0.26	0.18	-0.03	0.06
1264	JPH3	junctophilin 3	-0.33	-0.17	0.36	-0.29	0.22	0.20	0.22
1265	CR1 /// OR1L	complement component (3b/4b) receptor 1 (Knops blood group) /// complement component (3b/4b) receptor 1—like	-0.12	0.01	0.11	-0.30	-0.02	0.31	0.00
1266	GABRA5	gamma-aminobutyric acid (GABA) A receptor, alpha 5	-0.06	-0.31	0.37	0.03	-0.09	-0.26	-0.20
1267	KIF5C	kinesin family member 5C	-0.01	0.13	-0.12	0.09	-0.36	-0.06	-0.24
1268	TUBB2B	tubulin, beta 2B	-0.09	0.08	0.01	0.05	-0.21	-0.28	-0.12
1269	DNMT3B	DNA (cytosine-5)-methyltransferase 3 beta	-0.05	-0.01	0.06	0.00	-0.14	-0.03	-0.15
1270	SOX2	SRF (sex determining region Y)-box 2	0.07	-0.15	0.07	-0.15	-0.30	-0.26	-0.33
1271	DDX25	DEAD (Asp-Glu-Ala-Asp) box polypeptide 25	-0.01	0.03	-0.02	-0.47	-0.04	0.03	-0.09
1272	PTPRZ1	protein tyrosine phosphatase, receptor-type, Z polypeptide 1	0.17	-0.14	-0.03	-0.12	-0.17	-0.13	-0.15
1273	UNC5D	unc-5 homolog D (C. elegans)	0.08	-0.11	0.02	-0.07	-0.06	-0.10	-0.25
1274	---	---	0.19	-0.12	-0.07	-0.40	-0.12	-0.24	-0.24
1275	VASH2	vesohilin 2	-0.13	-0.07	0.19	-0.34	-0.24	-0.25	-0.36
1276	GINTAP2	contactin associated protein-like 2	0.15	-0.26	0.10	-0.37	-0.26	-0.34	-0.19
1277	ORF135	chromosome 9 open reading frame 135	0.17	-0.22	0.06	-0.21	-0.69	-0.34	0.08
1278	LRRTM4	leucine rich repeat transmembrane neuronal 4	0.15	-0.28	0.13	0.09	-0.34	-0.42	0.18
1279	MBD2	methyl-CpG binding domain protein 2	0.42	-0.28	-0.14	-0.10	0.06	-0.01	0.16
1280	MARVELD3	MARVEL domain containing 3	0.12	-0.10	-0.02	-0.03	-0.08	0.03	0.01
1281	---	---	0.29	0.03	-0.31	-0.24	-0.32	0.09	0.29
1282	---	---	0.38	0.34	-0.72	0.57	-0.48	-0.47	-0.89
1283	SEMA6B	sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6B	-0.28	-0.04	0.31	-1.30	-1.00	-1.05	-0.59
1284	ONTNAP2	contactin associated protein-like 2	0.00	-0.54	0.54	-0.96	-0.39	-0.76	-0.16
1285	---	---	0.02	-0.86	0.85	-0.73	-0.52	-0.72	-0.69
1286	---	---	-0.39	-0.46	0.85	-0.29	1.03	0.40	0.18
1287	LEFTY2	left-right determination factor 2	-0.56	0.52	0.04	0.22	0.04	0.28	-0.01
1288	POU5F1P3	POU class 5 homeobox 1 pseudogene 3	-0.45	0.18	0.27	0.16	0.04	0.14	0.16
1289	POU6F1P4	POU class 5 homeobox 1 pseudogene 4	-0.24	0.19	0.06	0.11	-0.08	0.02	0.14
1290	EPCAM	epithelial cell adhesion molecule	0.09	-0.08	-0.01	0.32	0.10	-0.01	0.15
1291	GD24	GD24 molecule	-0.09	0.13	-0.04	0.09	-0.12	-0.23	-0.01
1292	GD24	GD24 molecule	-0.17	-0.11	0.27	-0.02	0.24	0.26	-0.20
1293	LIN28	lin-28 homolog (C. elegans)	-0.13	0.02	0.10	0.10	0.11	0.07	-0.11
1294	GAL	galanin prepropeptide	-0.46	0.40	0.06	-0.17	0.03	-0.23	0.13
1295	L1TD1	L1NE-1 type transposase domain containing 1	0.10	-0.04	-0.06	-0.01	-0.40	-0.29	-0.03
1296	NLGN4X	neuroligin 4, X-linked	0.19	0.16	-0.35	0.09	-0.04	0.16	0.22
1297	DPPA4	developmental pluripotency associated 4	0.04	-0.27	0.23	-0.02	0.22	0.08	-0.61
1298	USP44	ubiquitin specific peptidase 44	0.11	-0.19	0.08	0.00	-0.15	-0.31	-0.50
1299	ESRP1	epithelial splicing regulatory protein 1	0.21	-0.27	0.06	-0.03	0.04	-0.07	-0.21
1300	BEND4	BEIN domain containing 4	-0.02	-0.51	0.53	0.01	0.14	-0.18	-0.38

1301	---	---	-0.25	-0.19	0.44	-0.50	-0.06	-0.27	-0.44
1302	---	---	0.08	-0.02	-0.06	-0.88	-0.02	-0.73	-0.61
1303	---	---	0.18	0.45	-0.63	-0.16	-0.21	-0.17	0.15
1304	---	---	0.31	-0.23	-0.07	-0.15	-0.18	0.18	-0.10
1305	TOX3	TOX high mobility group box family member 3	0.54	-0.38	-0.15	-0.27	-0.17	-0.18	-0.30
1306	---	---	0.27	-0.14	-0.13	-0.13	-0.06	0.02	0.20
1307	CNTNAP2	contactin associated protein-like 2	-0.02	0.19	-0.17	0.80	0.26	0.20	0.19
1308	SCG3	secretogranin III	0.17	-0.28	0.11	-0.09	-0.04	-0.19	0.21
1309	ESRP1	epithelial splicing regulatory protein 1	0.02	-0.18	0.16	0.02	0.02	-0.25	-0.81
1310	CRISPLD1	cysteine-rich secretory protein LOC1 domain containing 1	-0.08	-0.12	0.20	0.10	-0.39	-0.12	-0.17
1311	SALL4	sal-like 4 (Drosophila)	-0.03	-0.13	0.15	0.12	-0.16	-0.19	-0.19
1312	GABRB3	gamma-aminobutyric acid (GABA) A receptor, beta 3	0.00	-0.24	0.24	-0.06	-0.02	-0.01	-0.12
1313	DPPA4	developmental pluripotency associated 4	0.15	-0.16	0.01	0.04	-0.03	0.02	-0.29
1314	LRRN1	leucine rich repeat neuronal 1	-0.20	0.23	-0.04	0.01	0.03	0.10	-0.05
1315	CRABP1	cellular retinoic acid binding protein 1	-0.16	0.70	-0.54	0.01	-1.14	-0.67	-0.41
1316	NFS	neurotensin	-0.59	0.03	0.56	-0.07	-1.18	-0.45	-0.35
1317	ZSCAN10	zinc finger and SCAN domain containing 10	-0.74	0.30	0.44	0.00	-0.56	-0.40	-0.29
1318	CLDN6	claudin 6	-0.48	0.14	0.34	0.03	-1.00	-0.71	-0.68
1319	VASH2	vasohibin 2	-0.27	-0.07	0.34	-0.46	-0.72	-0.62	-0.53
1320	CHST9	carbohydrate (N-acetyl)galactosamine 4-O) sulfotransferase 9	0.07	-0.19	0.13	-0.58	-0.52	-0.49	-0.67
1321	MEGF10	multiple EGF-like-domains 10	0.39	0.29	-0.68	-0.22	-0.63	-0.52	-0.72
1322	LITD1	LITD-1 type transposase domain containing 1	0.11	0.33	-0.44	-0.08	-0.49	-0.45	-0.82
1323	SCGB3A2	secretoglobins, family 3A, member 2	0.47	-0.34	-0.14	-1.01	-0.90	-1.06	-1.12
1324	COX6A1	cytochrome c oxidase subunit VIa polypeptide 1	0.11	1.07	-1.18	-0.37	-0.87	-1.15	0.05
1325	TDGF1 /// TDGF3	teratocarcinoma-derived growth factor 1 /// teratocarcinoma-derived growth factor 3, pseudogene	-0.15	0.05	0.09	-0.01	0.05	-0.06	-0.01
1326	HESRG	hypothetical LOC790952	0.24	-0.27	0.03	-0.02	-0.01	-0.01	-0.09
1327	NLRP2	NLR family, pyrin domain containing 2	-0.71	-0.10	0.81	0.62	-3.20	1.27	0.48
1328	PSPH	phosphoserine phosphatase	-0.03	-0.02	0.04	-2.11	-1.67	-2.19	-2.64
1329	LOC100132181	Hypothetical protein LOC100132181	-0.12	0.49	-0.37	-2.69	-2.36	-2.66	-2.50
1330	---	---	0.42	-0.28	-0.14	-3.42	-0.84	-3.16	-4.09
1331	GNAS	GNAS complex locus	-0.26	-0.12	0.38	-1.95	-1.51	-3.29	-1.17
1332	LOC100132181	Hypothetical protein LOC100132181	0.24	-0.33	0.09	-1.49	-1.51	-3.65	-1.89
1333	G13orf35 /// SOHLH2	chromosome 13 open reading frame 38 /// spermatogenesis and oogenesis specific basic helix-loop-helix 2	0.15	0.02	-0.17	-1.44	-2.25	-2.06	-1.84
1334	NECAB1	N-terminal EF-hand calcium binding protein 1	-0.20	0.57	-0.37	-2.23	-1.95	-1.82	-2.00
1335	HHLA1	HERV-H LTR-associating 1	-0.39	0.36	0.02	-1.77	1.15	-1.66	-1.92
1336	ASHD12B	abhydrolase domain containing 12B	-2.06	1.03	1.03	-1.52	1.37	-1.69	-2.47
1337	REM15	RNA binding motif protein 15	-0.03	0.39	-0.36	-0.48	-2.36	-2.05	-6.57
1338	ZNF208	zinc finger protein 208	0.16	-0.52	0.36	-8.95	-5.39	-6.59	-4.26
1339	ZNF257	zinc finger protein 257	0.19	0.03	0.36	-8.95	-5.39	-6.59	-4.26
1340	RBM46	RNA binding motif protein 46	1.60	-1.20	-0.41	-6.56	-2.66	-1.69	-2.56

[0068] [表 1 B] 第 1 遺伝子群

	Gene Symbol	Gene Title
1	GRIA3	glutamate receptor, ionotropic, AMPA 3
2	STC2	stanniocalcin 2
3	TFPI2	tissue factor pathway inhibitor 2
4	ZNF85	zinc finger protein 85
5	SLC2A3	solute carrier family 2 (facilitated glucose transporter), member 3
6	TNFRSF8	tumor necrosis factor receptor superfamily, member 8
7	UTF1	undifferentiated embryonic cell transcription factor 1
8	HMGAI	high mobility group AT-hook 1
9	ZNF678	zinc finger protein 678
10	FANCB	Fanconi anemia, complementation group B
11	CGNL1	Cingulin-like 1
12	KIF1A	kinesin family member 1A
13	SYT3	synaptotagmin III
14	DDX11	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 11 (CHL1-like helicase homolog, <i>S. cerevisiae</i>)
15	C14orf106	chromosome 14 open reading frame 106
16	ZNF92	zinc finger protein 92
17	ASPM	asp (abnormal spindle) homolog, microcephaly associated (<i>Drosophila</i>)
18	ZNF770	zinc finger protein 770
19	ATP11C	ATPase, class VI, type 11C
20	SNORD116@	small nucleolar RNA, C/D box 116 cluster
21	COL11A1	collagen, type XI, alpha 1
22	ANTXR1	anthrax toxin receptor 1
23	CNKSR2	connector enhancer of kinase suppressor of Ras 2
24	DNA2	DNA replication helicase 2 homolog (yeast)
25	PLK4	polo-like kinase 4 (<i>Drosophila</i>)
26	FLJ35848	hypothetical protein FLJ35848
27	DLGAP5	discs, large (<i>Drosophila</i>) homolog-associated protein 5
28	ELAVL2	ELAV (embryonic lethal, abnormal vision, <i>Drosophila</i>)-like 2 (Hu antigen B)
29	ZNF391	zinc finger protein 391
30	NCAPG2	non-SMC condensin II complex, subunit G2
31	SLC16A1	solute carrier family 16, member 1 (monocarboxylic acid transporter 1)
32	MCM4	minichromosome maintenance complex component 4
33	FGD6	FYVE, RhoGEF and PH domain containing 6
34	WDHD1	WD repeat and HMG-box DNA binding protein 1
35	CCDC88A	coiled-coil domain containing 88A
36	BIRC5	baculoviral IAP repeat-containing 5
37	CCNA2	cyclin A2
38	SRp35	serine-arginine repressor protein (35 kDa)
39	MAD2L1	MAD2 mitotic arrest deficient-like 1 (yeast)
40	PDPN	podoplanin
41	RAD51AP1	RAD51 associated protein 1
42	CENPH	centromere protein H
43	NCAPH	non-SMC condensin I complex, subunit H
44	FAM72A /// FAM72B /// FAM72C /// FAM72D	family with sequence similarity 72, member A /// family with sequence similarity 72, member B /// family with sequence similarity 72, member C /// family with sequence similarity 72, member D
45	TMEFF1	transmembrane protein with EGF-like and two follistatin-like domains 1
46	PAICS	phosphoribosylaminoimidazole carboxylase, phosphoribosylaminoimidazole succinocarboxamide synthetase
47	DBF4	DBF4 homolog (<i>S. cerevisiae</i>)
48	HMMR	hyaluronan-mediated motility receptor (RHAMM)
49	FXVD7	FXVD domain containing ion transport regulator 7
50	FEN1	flap structure-specific endonuclease 1
51	CDC25C	cell division cycle 25 homolog C (<i>S. pombe</i>)
52	TPM1	tropomyosin 1 (alpha)
53	CCNF	cyclin F
54	CDCA5	cell division cycle associated 5

55	HJURP	Holliday junction recognition protein
56	SPAG5	sperm associated antigen 5
57	RFWD3	ring finger and WD repeat domain 3
58	C21orf45	chromosome 21 open reading frame 45
59	CDCA2	cell division cycle associated 2
60	TFDP2	transcription factor Dp-2 (E2F dimerization partner 2)
61	PRIM1	primase, DNA, polypeptide 1 (49kDa)
62	SEPHS1	selenophosphate synthetase 1
63	MCM2	minichromosome maintenance complex component 2
64	FAM64A	family with sequence similarity 64, member A
65	BEND3	BEN domain containing 3
66	VRK1	vaccinia related kinase 1
67	POLE2	polymerase (DNA directed), epsilon 2 (p59 subunit)
68	DSCC1	defective in sister chromatid cohesion 1 homolog (S. cerevisiae)
69	GIN52	GIN5 complex subunit 2 (Psf2 homolog)
70	CCNJ	cyclin J
71	EXO1	exonuclease 1
72	CDC2	cell division cycle 2, G1 to S and G2 to M
73	RCC2	regulator of chromosome condensation 2
74	FLJ20674	hypothetical protein FLJ20674
75	CCNB1	cyclin B1
76	RFC3	replication factor C (activator 1) 3, 38kDa
77	FANCD2	Fanconi anemia, complementation group D2
78	RRM2	ribonucleotide reductase M2
79	CENPN	centromere protein N
80	RTKN2	rhotekin 2
81	GRB14	growth factor receptor-bound protein 14
82	PFAS	phosphoribosylformylglycinamide synthase
83	KIF15	kinesin family member 15
84	RAD54B	RAD54 homolog B (S. cerevisiae)
85	RAD54L	RAD54-like (S. cerevisiae)
86	PPAT	phosphoribosyl pyrophosphate amidotransferase
87	ZNF814	zinc finger protein 814
88	ZNF462	zinc finger protein 462
89	AP1S3	adaptor-related protein complex 1, sigma 3 subunit
90	LHFPL4	lipoma HMGIC fusion partner-like 4
91	ZNF114	zinc finger protein 114
92	ZWINT	ZW10 interactor
93	C1orf135	chromosome 1 open reading frame 135
94	NODAL	nodal homolog (mouse)
95	CBS	cystathionine-beta-synthase
96	TPX2	TPX2, microtubule-associated, homolog (Xenopus laevis)
97	CDT1	chromatin licensing and DNA replication factor 1
98	MCM7	minichromosome maintenance complex component 7
99	TUBB2A /// TUBB2B	tubulin, beta 2A /// tubulin, beta 2B
100	ESPL1	extra spindle pole bodies homolog 1 (S. cerevisiae)
101	KCNQ2	potassium voltage-gated channel, KQT-like subfamily, member 2
102	UBE2S	ubiquitin-conjugating enzyme E2S
103	TEAD4	TEA domain family member 4
104	SCLY	selenocysteine lyase
105	CENPA	centromere protein A
106	CDCA3	cell division cycle associated 3
107	DHFR	dihydrofolate reductase
108	PHF17	PHD finger protein 17
109	MSH6	mutS homolog 6 (E. coli)
110	CTPS	CTP synthase
111	KIF2C	kinesin family member 2C
112	FOXM1	forkhead box M1
113	GTSE1	G-2 and S-phase expressed 1
114	AURKA	aurora kinase A
115	FBXO11	F-box protein 11
116	NLN	neurolysin (metallopeptidase M3 family)
117	LAPTM4B	lysosomal protein transmembrane 4 beta
118	TMPO	thymopoietin

119	EZH2	enhancer of zeste homolog 2 (Drosophila)
120	CDC7	cell division cycle 7 homolog (S. cerevisiae)
121	NETO1	neuropilin (NRP) and tolloid (TLL)-like 1
122	KIF23	kinesin family member 23
123	KIF18B	kinesin family member 18B
124	FANCI	Fanconi anemia, complementation group I
125	MCM6	minichromosome maintenance complex component 6
126	MSH2	mutS homolog 2, colon cancer, nonpolyposis type 1 (E. coli)
127	NCAPG	non-SMC condensin I complex, subunit G
128	MASTL	microtubule associated serine/threonine kinase-like
129	CENPJ	centromere protein J
130	KIF11	kinesin family member 11
131	TOP2A	topoisomerase (DNA) II alpha 170kDa
132	ZNF643	zinc finger protein 643
133	PSIP1	PC4 and SFRS1 interacting protein 1
134	ORC6L	origin recognition complex, subunit 6 like (yeast)
135	KPNA2	karyopherin alpha 2 (RAG cohort 1, importin alpha 1)
136	NOP16	NOP16 nucleolar protein homolog (yeast)
137	NUSAP1	nucleolar and spindle associated protein 1
138	C13orf34	chromosome 13 open reading frame 34
139	C6orf173	chromosome 6 open reading frame 173
140	RNASEH2A	ribonuclease H2, subunit A
141	CCNE1	cyclin E1
142	KIF14	kinesin family member 14
143	ZNF788	zinc finger family member 788
144	CASP3	caspase 3, apoptosis-related cysteine peptidase
145	RAD51	RAD51 homolog (RecA homolog, E. coli) (S. cerevisiae)
146	SUV39H2	suppressor of variegation 3-9 homolog 2 (Drosophila)
147	UCHL1	ubiquitin carboxyl-terminal esterase L1 (ubiquitin thiolesterase)
148	THAP9	THAP domain containing 9
149	SKP2	S-phase kinase-associated protein 2 (p45)
150	UBE2T	ubiquitin-conjugating enzyme E2T (putative)
151	NUF2	NUF2, NDC80 kinetochore complex component, homolog (S. cerevisiae)
152	RFC4	replication factor C (activator 1) 4, 37kDa
153	NDC80	NDC80 homolog, kinetochore complex component (S. cerevisiae)
154	NEK2	NIMA (never in mitosis gene a)-related kinase 2
155	TRIM6	tripartite motif-containing 6
156	CKS1B	CDC28 protein kinase regulatory subunit 1B
157	CCNB2	cyclin B2
158	GMNN	geminin, DNA replication inhibitor
159	CENPK	centromere protein K
160	FAM54A	family with sequence similarity 54, member A
161	PTTG1	pituitary tumor-transforming 1
162	TEAD2	TEA domain family member 2
163	CDCA8	cell division cycle associated 8
164	FBXO5	F-box protein 5
165	BXDC2	brix domain containing 2
166	MTA3	metastasis associated 1 family, member 3
167	TIMELESS	timeless homolog (Drosophila)
168	CCDC138	coiled-coil domain containing 138
169	EEF1E1	eukaryotic translation elongation factor 1 epsilon 1
170	CCDC150	coiled-coil domain containing 150
171	LYAR	Ly1 antibody reactive homolog (mouse)
172	SLC6A15	solute carrier family 6 (neutral amino acid transporter), member 15
173	MRS2	MRS2 magnesium homeostasis factor homolog (S. cerevisiae)
174	BRCA2	breast cancer 2, early onset
175	MCM10	minichromosome maintenance complex component 10
176	C12orf48	chromosome 12 open reading frame 48
177	CCL26	chemokine (C-C motif) ligand 26
178	NSBP1	nucleosomal binding protein 1

179	HESX1	HESX homeobox 1
180	TNNT1	troponin T type 1 (skeletal, slow)
181	GUCA1A	guanylate cyclase activator 1A (retina)
182	UBE2C	ubiquitin-conjugating enzyme E2C
183	CDC8	cell division cycle 8 homolog (S. cerevisiae)
184	DIAPH2	diaphanous homolog 2 (Drosophila)
185	GAL	galanin prepropeptide
186	CHAF1A	chromatin assembly factor 1, subunit A (p150)
187	MCM5	minichromosome maintenance complex component 5
188	GALNT13	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 13 (GalNAc-T13)
189	GAL3ST3	galactose-3-O-sulfotransferase 3
190	FAM46B	family with sequence similarity 46, member B
191	LOC389857	hypothetical protein
192	JARID2	jumonji, AT rich interactive domain 2
193	SILV	silver homolog (mouse)
194	IGFBPL1	insulin-like growth factor binding protein-like 1
195	MBD2	methyl-CpG binding domain protein 2
196	GINS1	GINS complex subunit 1 (Psf1 homolog)
197	HAS3	hyaluronan synthase 3
198	NASP	nuclear autoantigenic sperm protein (histone-binding)
199	MTF2	metal response element binding transcription factor 2
200	PMAIP1	phorbol-12-myristate-13-acetate-induced protein 1
201	MATR3	Matrin 3
202	CRMP1	collapsin response mediator protein 1
203	CBX2	chromobox homolog 2 (Pc class homolog, Drosophila)
204	WDR72	WD repeat domain 72
205	CDCA7	cell division cycle associated 7
206	FOXA3	forkhead box A3
207	SPC25	SPC25, NDC80 kinetochore complex component, homolog (S. cerevisiae)
208	BLM	Bloom syndrome, RecQ helicase-like
209	C11orf82	chromosome 11 open reading frame 82
210	CHRNA5	cholinergic receptor, nicotinic, alpha 5
211	GDAP1	ganglioside-induced differentiation-associated protein 1
212	GHST4	carbohydrate (N-acetylglucosamine 6-O) sulfotransferase 4
213	DNMT3A	DNA (cytosine-5-)-methyltransferase 3 alpha
214	KLHL7	kelch-like 7 (Drosophila)
215	DTL	denticless homolog (Drosophila)
216	TNNI3	troponin I type 3 (cardiac)
217	ZNF738	zinc finger protein 738
218	HOMER1	homer homolog 1 (Drosophila)
219	TACC3	transforming, acidic coiled-coil containing protein 3
220	MCM3	minichromosome maintenance complex component 3
221	FAM83D	family with sequence similarity 83, member D
222	BUB1	budding uninhibited by benzimidazoles 1 homolog (yeast)
223	IPW	imprinted in Prader-Willi syndrome (non-protein coding)
224	FERMT1	fermitin family homolog 1 (Drosophila)
225	STRBP	spermatid perinuclear RNA binding protein
226	FAM124A	family with sequence similarity 124A
227	COMM7	COMM domain containing 7
228	SYT6	synaptotagmin VI
229	CLDN7	claudin 7
230	RND2	Rho family GTPase 2
231	AIM1L	absent in melanoma 1-like
232	LOC253842	hypothetical protein LOC253842
233	CDC20	cell division cycle 20 homolog (S. cerevisiae)
234	AURKB	aurora kinase B
235	OIP5	Opa interacting protein 5
236	LOC100128191	hypothetical protein LOC100128191
237	RASL11B	RAS-like, family 11, member B
238	GULP1	GULP, engulfment adaptor PTB domain containing 1
239	AP3B2	adaptor-related protein complex 3, beta 2 subunit
240	HMGB3	high-mobility group box 3
241	CXCL5	chemokine (C-X-C motif) ligand 5

242	PHF21B	PHD finger protein 21B
243	MND1	meiotic nuclear divisions 1 homolog (S. cerevisiae)
244	MLF1IP	MLF1 interacting protein
245	C13orf38	chromosome 13 open reading frame 38
246	NPM3	nucleophosmin/nucleoplasmin 3
247	C16orf75	chromosome 16 open reading frame 75
248	SKA1	spindle and kinetochore associated complex subunit 1
249	LOC647946	hypothetical protein LOC647946
250	NPFRR2	neuropeptide FF receptor 2
251	GINS4	GINS complex subunit 4 (Sld5 homolog)
252	RAB38	RAB38, member RAS oncogene family
253	BCL2L12	BCL2-like 12 (proline rich)
254	C9orf100	chromosome 9 open reading frame 100
255	ZNF93	zinc finger protein 93
256	KIAA1661	KIAA1661 protein
257	USP9X	ubiquitin specific peptidase 9, X-linked
258	HIST1H2AM	histone cluster 1, H2am
259	LOC284242	hypothetical protein LOC284242
260	BPTF	bromodomain PHD finger transcription factor
261	FLJ35934	FLJ35934 protein
262	HOXC6	homeobox C6
263	PCDH7	protocadherin 7
264	SLC7A5	solute carrier family 7 (cationic amino acid transporter, y ⁺ system), member 5
265	CUL4A	cullin 4A
266	KIF4A	kinesin family member 4A
267	IL1A	interleukin 1, alpha
268	AFP	alpha-fetoprotein
269	ARHGAP28	Rho GTPase activating protein 28
270	UPF3B	UPF3 regulator of nonsense transcripts homolog B (yeast)
271	HIST1H4J	histone cluster 1, H4j
272	GPC2	glypican 2
273	NLRP12	NLR family, pyrin domain containing 12
274	DPYSL3	dihydropyrimidinase-like 3
275	TGF3	transcription factor 3 (E2A immunoglobulin enhancer binding factors E12/E47)
276	NR5A2	nuclear receptor subfamily 5, group A, member 2
277	MYH10	myosin, heavy chain 10, non-muscle
278	GLI2	GLI family zinc finger 2
279	ANKS6	ankyrin repeat and sterile alpha motif domain containing 6
280	CENPE	centromere protein E, 312kDa
281	CENPF	centromere protein F, 350/400kDa (mitotin)
282	CHML	choroideremia-like (Rab escort protein 2)
283	EDIL3	EGF-like repeats and discoidin I-like domains 3
284	ATAD5	ATPase family, AAA domain containing 5
285	SKI1	SKI-like oncogene
286	KIF18A	kinesin family member 18A
287	N4BP2	NEDD4 binding protein 2
288	TP53	tumor protein p53
289	OSBPL10	oxysterol binding protein-like 10
290	USP28	ubiquitin specific peptidase 28
291	ZNF398	zinc finger protein 398
292	DEPDC1	DEP domain containing 1
293	CENPI	centromere protein I
294	HSPA4	heat shock 70kDa protein 4
295	HAUS6	HAUS augmin-like complex, subunit 6
296	ZNF253	zinc finger protein 253
297	ARHGAP11A	Rho GTPase activating protein 11A
298	PAP2D	phosphatidic acid phosphatase type 2
299	SMC3	structural maintenance of chromosomes 3
300	CDYL	chromodomain protein, Y-like
301	G2E3	G2/M-phase specific E3 ubiquitin ligase
302	MKI67	antigen identified by monoclonal antibody Ki-67
303	TRHDE	thyrotropin-releasing hormone degrading enzyme

304	IGF2BP3	insulin-like growth factor 2 mRNA binding protein 3
305	DIAPH3	diaphanous homolog 3 (Drosophila)
306	C4orf21	chromosome 4 open reading frame 21
307	KNTC1	kinetochore associated 1
308	ZNF195	zinc finger protein 195
309	C18orf54	chromosome 18 open reading frame 54
310	DKC1	dyskeratosis congenita 1, dyskerin
311	FLJ32810	Rho-type GTPase-activating protein FLJ32810
312	ZNF43	zinc finger protein 43
313	WDR89	WD repeat domain 89
314	TTF2	transcription termination factor, RNA polymerase II
315	ZNF254	zinc finger protein 254
316	QSER1	glutamine and serine rich 1
317	ZNF675	zinc finger protein 675
318	ZNF721	zinc finger protein 721
319	ESCO1	establishment of cohesion 1 homolog 1 (S. cerevisiae)
320	POLQ	polymerase (DNA directed), theta
321	HMG2	high mobility group AT-hook 2
322	TSR1	TSR1, 20S rRNA accumulation, homolog (S. cerevisiae)
323	XPO5	exportin 5
324	PAWR	PRKC, apoptosis, WT1, regulator
325	ZNF708	zinc finger protein 708
326	ZNF589	zinc finger protein 589
327	ZIK1	zinc finger protein interacting with K protein 1 homolog (mouse)
328	STIL	SCL/TAL1 interrupting locus
329	CDK6	cyclin-dependent kinase 6
330	TMEM48	transmembrane protein 48
331	CCDC18	coiled-coil domain containing 18
332	ESF1	ESF1, nucleolar pre-rRNA processing protein, homolog (S. cerevisiae)
333	API5	apoptosis inhibitor 5
334	SGOL2	shugoshin-like 2 (S. pombe)
335	ESCO2	establishment of cohesion 1 homolog 2 (S. cerevisiae)
336	TMEM132B	transmembrane protein 132B
337	ZNF107	zinc finger protein 107
338	G3BP2	GTPase activating protein (SH3 domain) binding protein 2
339	CXorf15	chromosome X open reading frame 15
340	PLK1	polo-like kinase 1 (Drosophila)
341	KLRG2	killer cell lectin-like receptor subfamily G, member 2
342	KIF20B	kinesin family member 20B
343	C12orf35	chromosome 12 open reading frame 35
344	ZNF680	zinc finger protein 680
345	ACTN3	actinin, alpha 3
346	DGP2	DGP2 decapping enzyme homolog (S. cerevisiae)
347	LOC643401	hypothetical protein LOC643401
348	CDA	cytidine deaminase
349	TMEM132D	transmembrane protein 132D
350	FAM71F1	family with sequence similarity 71, member F1
351	CHM	choroideremia (Rab escort protein 1)
352	PHF3	PHD finger protein 3
353	ZNF644	zinc finger protein 644
354	ANKRD32	ankyrin repeat domain 32
355	TPP2	tripeptidyl peptidase II
356	HSPH1	heat shock 105kDa/110kDa protein 1
357	LOC100129064 /// LOC100131360 /// LOC100131868 /// PPP4R2	hypothetical LOC100129064 /// similar to protein phosphatase 4 regulatory subunit 2 /// similar to PPP4R2 protein /// protein phosphatase 4, regulatory subunit 2
358	CNOT1	CCR4-NOT transcription complex, subunit 1
359	PRPF4B	PRP4 pre-mRNA processing factor 4 homolog B (yeast)
360	NUP133	nucleoporin 133kDa
361	LARS	leucyl-tRNA synthetase
362	BCLAF1	BCL2-associated transcription factor 1
363	DHX9	DEAH (Asp-Glu-Ala-His) box polypeptide 9

364	SUPT16H	suppressor of Ty 16 homolog (S. cerevisiae)
365	RBAK	RB-associated KRAB zinc finger
366	ERI1	exoribonuclease 1
367	USP25	ubiquitin specific peptidase 25
368	EPRS	glutamyl-prolyl-tRNA synthetase
369	RECQL	RecQ protein-like (DNA helicase Q1-like)
370	GPR176	G protein-coupled receptor 176
371	SCD	stearoyl-CoA desaturase (delta-9-desaturase)
372	FAM126A	family with sequence similarity 126, member A
373	MIPOL1	mirror-image polydactyly 1
374	GEN1	Gen homolog 1, endonuclease (Drosophila)
375	UBE3A	ubiquitin protein ligase E3A
376	FAR1	fatty acyl CoA reductase 1
377	ZNF84	zinc finger protein 84
378	DNAJC10	DnaJ (Hsp40) homolog, subfamily C, member 10
379	IGF2BP2	insulin-like growth factor 2 mRNA binding protein 2
380	LRRIG3	leucine-rich repeats and IQ motif containing 3
381	ZNF569	zinc finger protein 569
382	TRIM37	tripartite motif-containing 37
383	MTHFD1L	methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 1-like
384	PRIM2	primase, DNA, polypeptide 2 (58kDa)
385	NVL	nuclear VOP-like
386	RPAP3	RNA polymerase II associated protein 3
387	ATAD2	ATPase family, AAA domain containing 2
388	BCAT1	branched chain aminotransferase 1, cytosolic
389	ASCC3	activating signal cointegrator 1 complex subunit 3
390	MED20	mediator complex subunit 20
391	ZNF146	zinc finger protein 146
392	RBM26	RNA binding motif protein 26
393	ANLN	anillin, actin binding protein
394	HMGCR	3-hydroxy-3-methylglutaryl-Coenzyme A reductase
395	LARP4	La ribonucleoprotein domain family, member 4
396	SQLE	squalene epoxidase
397	GART	phosphoribosylglycinamide formyltransferase, phosphoribosylglycinamide synthetase, phosphoribosylaminoimidazole synthetase
398	VCAN	versican
399	RIF1	RAP1 interacting factor homolog (yeast)
400	SOCS4	suppressor of cytokine signaling 4
401	PHIP	pleckstrin homology domain interacting protein
402	USO1	USO1 homolog, vesicle docking protein (yeast)
403	SR140	U2-associated SR140 protein
404	SMARCD1	SWI/SNF-related, matrix-associated actin-dependent regulator of chromatin, subfamily a, containing DEAD/H box 1
405	PRPF40A	PRP40 pre-mRNA processing factor 40 homolog A (S. cerevisiae)
406	RNGTT	RNA guanylyltransferase and 5'-phosphatase
407	ARNTL2	aryl hydrocarbon receptor nuclear translocator-like 2
408	ZNF567	zinc finger protein 567
409	PPPDE1	PPPDE peptidase domain containing 1
410	UCMA	upper zone of growth plate and cartilage matrix associated
411	SPRED1	sprouty-related, EVH1 domain containing 1
412	KPNB1	karyopherin (importin) beta 1
413	ZNF300	zinc finger protein 300
414	TMTC3	transmembrane and tetratricopeptide repeat containing 3
415	LAMA1	laminin, alpha 1
416	LOC169834	hypothetical protein LOC169834
417	LMCD1	LIM and cysteine-rich domains 1
418	ZNF684	zinc finger protein 684
419	ZNF638	zinc finger protein 638
420	FGF2	fibroblast growth factor 2 (basic)
421	KIAA1009	KIAA1009

422	RAI14	retinoic acid induced 14
423	EIF5B	eukaryotic translation initiation factor 5B
424	TYMS	thymidylate synthetase
425	SIX4	SIX homeobox 4
426	TPR	translocated promoter region (to activated MET oncogene)
427	KIAA1586	KIAA1586
428	SYT14	synaptotagmin XIV
429	RAD18	RAD18 homolog (S. cerevisiae)
430	CWC22	CWC22 spliceosome-associated protein homolog (S. cerevisiae)
431	GJA1	gap junction protein, alpha 1, 43kDa
432	MRE11A	MRE11 meiotic recombination 11 homolog A (S. cerevisiae)
433	RBBP6	retinoblastoma binding protein 6
434	RRAS2	related RAS viral (r-ras) oncogene homolog 2
435	ZMYM1	zinc finger, MYM-type 1
436	ZNF268	zinc finger protein 268
437	ELOVL4	elongation of very long chain fatty acids (FEN1/Elo2, SUR4/Elo3, yeast)-like 4
438	hCQ_2024410 /// RPE	rcRPE /// ribulose-5-phosphate-3-epimerase
439	SHCBP1	SHC SH2-domain binding protein 1
440	IWS1	IWS1 homolog (S. cerevisiae)
441	RAB34	RAB34, member RAS oncogene family
442	CDC5L	CDC5 cell division cycle 5-like (S. pombe)
443	MPHOSPH10	M-phase phosphoprotein 10 (U3 small nucleolar ribonucleoprotein)
444	CTSC	cathepsin C
445	CCDC99	coiled-coil domain containing 99
446	MAGED4 /// MAGED4B	melanoma antigen family D, 4 /// melanoma antigen family D, 4B
447	SMARCA1	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 1
448	HIST1H2AG	histone cluster 1, H2ag
449	PSAT1	phosphoserine aminotransferase 1
450	GABPA	GA binding protein transcription factor, alpha subunit 60kDa
451	C10orf28	chromosome 10 open reading frame 28
452	UBA6	ubiquitin-like modifier activating enzyme 6
453	ALKBH8	alkB, alkylation repair homolog 8 (E. coli)
454	DIS3	DIS3 mitotic control homolog (S. cerevisiae)
455	TFAP2C	transcription factor AP-2 gamma (activating enhancer binding protein 2 gamma)
456	SERPINH1	serpin peptidase inhibitor, clade H (heat shock protein 47), member 1, (collagen binding protein 1)
457	MFAP2	microfibrillar-associated protein 2
458	PCNXL2	pecanex-like 2 (Drosophila)
459	FAM175A	family with sequence similarity 175, member A
460	RARS	arginyl-tRNA synthetase
461	PBK	PDZ binding kinase
462	GFPT2	glutamine-fructose-6-phosphate transaminase 2
463	RPL22L1	ribosomal protein L22-like 1
464	KDELG1	KDEL (Lys-Asp-Glu-Leu) containing 1
465	BNC2	basenuclin 2
466	TNPO1	transportin 1
467	MGC45800	hypothetical LOC90768
468	RGS17	regulator of G-protein signaling 17
469	USP45	ubiquitin specific peptidase 45
470	PHF19	PHD finger protein 19
471	GDF11	growth differentiation factor 11
472	CABYR	calcium binding tyrosine-(Y)-phosphorylation regulated
473	AMMECR1	Alport syndrome, mental retardation, midface hypoplasia and elliptocytosis chromosomal region gene 1
474	MUDENG	MU-2/AP1M2 domain containing, death-inducing
475	C4orf46	chromosome 4 open reading frame 46
		SWI/SNF related, matrix associated, actin dependent

476	SMARCA5	regulator of chromatin, subfamily a, member 5
477	TWISTNB	TWIST neighbor
478	TK1	thymidine kinase 1, soluble
479	ST8SIA3	ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 3
480	CRYGD	crystallin, gamma D
481	CDKN3	cyclin-dependent kinase inhibitor 3
482	RG9MTD1	RNA (guanine-9-) methyltransferase domain containing 1
483	SNX5	sorting nexin 5
484	NUFIP1	nuclear fragile X mental retardation protein interacting protein 1
485	FSD1	fibronectin type III and SPRY domain containing 1
486	PIF1	PIF1 5'-to-3' DNA helicase homolog (S. cerevisiae)
487	DNAH14	dynein, axonemal, heavy chain 14
488	SYNCRIP	synaptotagmin binding, cytoplasmic RNA interacting protein
489	GLMN	glomulin, FKBP associated protein
490	ORC4L	origin recognition complex, subunit 4-like (yeast)
491	BGGIP	BRCA2 and GSKN1A interacting protein
492	C1orf112	chromosome 1 open reading frame 112
493	DBC1	deleted in bladder cancer 1
494	HAUS1	HAUS augmin-like complex, subunit 1
495	DMKN	dermokine
496	EXOSC9	exosome component 9
497	LMNB2	lamin B2
498	NARG1	NMDA receptor regulated 1
499	TRIP13	thyroid hormone receptor interactor 13
500	PAK1IP1	PAK1 interacting protein 1
501	TIPIN	TIMELESS interacting protein
502	MGC11082	hypothetical LOC84777
503	UHRF1	ubiquitin-like with PHD and ring finger domains 1
504	C16orf88	chromosome 16 open reading frame 88
505	KIF20A	kinesin family member 20A
506	CENPQ	centromere protein Q
507	GABPB1	GA binding protein transcription factor, beta subunit 1
508	EXOSC3	exosome component 3
509	MRPS12	mitochondrial ribosomal protein S12
510	CENPM	centromere protein M
511	SPC24	SPC24, NDC80 kinetochore complex component, homolog (S. cerevisiae)
512	AEN	apoptosis enhancing nuclease
513	NUDT1	nudix (nucleoside diphosphate linked moiety X)-type motif 1
514	MAP9	microtubule-associated protein 9
515	FAM155A	family with sequence similarity 155, member A
516	KIAA1524	KIAA1524
517	CHAF1B	chromatin assembly factor 1, subunit B (p60)
518	TAF5L	TAF5-like RNA polymerase II, p300/CBP-associated factor (PCAF)-associated factor, 65kDa
519	TGIF1	TGFB-induced factor homeobox 1
520	MELK	maternal embryonic leucine zipper kinase
521	DDX21	DEAD (Asp-Glu-Ala-Asp) box polypeptide 21
522	CEP78	centrosomal protein 78kDa
523	HDAC2	histone deacetylase 2
524	ZNF281	zinc finger protein 281
525	RUVBL1	RuvB-like 1 (E. coli)
526	NUP107	nucleoporin 107kDa
527	ZWILCH	Zwilch, kinetochore associated, homolog (Drosophila)
528	SKA3	spindle and kinetochore associated complex subunit 3
529	TRIM59	tripartite motif-containing 59
530	ZNF215	zinc finger protein 215
531	CENPO	centromere protein O
532	KIAA0020	KIAA0020
533	CXorf26	chromosome X open reading frame 26
534	CASC5	cancer susceptibility candidate 5

535	MTRF1	mitochondrial translational release factor 1
536	SH2D5	SH2 domain containing 5
537	FZD7	frizzled homolog 7 (Drosophila)
538	MPP6	membrane protein, palmitoylated 6 (MAGUK p55 subfamily member 6)
539	CHEK1	CHK1 checkpoint homolog (S. pombe)
540	SLC39A10	solute carrier family 39 (zinc transporter), member 10
541	WDR75	WD repeat domain 75
542	CEBPZ	CCAAT/enhancer binding protein (C/EBP), zeta
543	CSE1L	CSE1 chromosome segregation 1-like (yeast)
544	ZNF670	zinc finger protein 670
545	SMC4	structural maintenance of chromosomes 4
546	KRR1	KRR1, small subunit (SSU) processome component, homolog (yeast)
547	TARS	threonyl-tRNA synthetase
548	ZNF397	zinc finger protein 397
549	C17orf80	chromosome 17 open reading frame 80
550	SMC1A	structural maintenance of chromosomes 1A
551	DLAT	dihydrolipoamide S-acetyltransferase
552	C1orf163	chromosome 1 open reading frame 163
553	SSB	Sjogren syndrome antigen B (autoantigen La)
554	MTAP	methylthioadenosine phosphorylase
555	PNN	pinin, desmosome associated protein
556	SKA2	spindle and kinetochore associated complex subunit 2
557	FLJ36848	hypothetical LOC647115
558	GKS2	CDC28 protein kinase regulatory subunit 2
559	DNAJC2	DnaJ (Hsp40) homolog, subfamily C, member 2
560	C2orf44	chromosome 2 open reading frame 44
561	PRC1	protein regulator of cytokinesis 1
562	ATP5O /// DONSON	ATP synthase, H+ transporting, mitochondrial F1 complex, O subunit /// downstream neighbor of SON
563	HSPD1	heat shock 60kDa protein 1 (chaperonin)
564	CEP55	centrosomal protein 55kDa
565	ARL5B	ADP-ribosylation factor-like 5B
566	ECT2	epithelial cell transforming sequence 2 oncogene
567	E2F7	E2F transcription factor 7
568	MATR3 /// SNHG4	matrin 3 /// small nucleolar RNA host gene 4 (non-protein coding)
569	UTP15	UTP15, U3 small nucleolar ribonucleoprotein, homolog (S. cerevisiae)
570	ELOVL6	ELOVL family member 6, elongation of long chain fatty acids (FEN1/Elo2, SUR4/Elo3-like, yeast)
571	ZNF616	zinc finger protein 616
572	SMC2	structural maintenance of chromosomes 2
573	ZNF141	zinc finger protein 141
574	SMC6	structural maintenance of chromosomes 6
575	WDR35	WD repeat domain 35
576	ZNF334	zinc finger protein 334
577	PPIG	peptidylprolyl isomerase G (cyclophilin G)
578	MURC	muscle-related coiled-coil protein
579	CEP152	centrosomal protein 152kDa
580	PTTG3P	pituitary tumor-transforming 3 (pseudogene)
581	CHEK2	CHK2 checkpoint homolog (S. pombe)
582	NEIL3	nei endonuclease VIII-like 3 (E. coli)
583	C5orf34	chromosome 5 open reading frame 34
584	GNL2	guanine nucleotide binding protein-like 2 (nucleolar)
585	DNTTIP2	deoxynucleotidyltransferase, terminal, interacting protein 2
586	NPM1	nucleophosmin (nucleolar phosphoprotein B23, numatrin)
587	ORC3L	origin recognition complex, subunit 3-like (yeast)
588	ZNF607	zinc finger protein 607
589	BAX	BCL2-associated X protein
590	CDK7	cyclin-dependent kinase 7
591	LOC100292909	hypothetical protein LOC100292909
592	C20orf19	chromosome 20 open reading frame 19

593	PGBD1	piggyBac transposable element derived 1
594	DCAF13	DDB1 and CUL4 associated factor 13
595	PABPC1L	poly(A) binding protein, cytoplasmic 1-like
596	ROR1	receptor tyrosine kinase-like orphan receptor 1
597	TEX9	testis expressed 9
598	NUDCD1	NudC domain containing 1
599	TRMT5	TRM5 tRNA methyltransferase 5 homolog (S. cerevisiae)
600	KIAA0101	KIAA0101
601	ZNF613	zinc finger protein 613
602	GLRX3	glutaredoxin 3
603	NUDT11	nudix (nucleoside diphosphate linked moiety X)-type motif 11
604	DBN1	drebrin 1
605	PARD3	par-3 partitioning defective 3 homolog (C. elegans)
606	TRO	trophinin
607	SLC4A5	Solute carrier family 4, sodium bicarbonate cotransporter, member 5
608	CCDC34	coiled-coil domain containing 34
609	NT5DC2	5'-nucleotidase domain containing 2
610	SALL1	sal-like 1 (Drosophila)
611	PPP4R4	protein phosphatase 4, regulatory subunit 4
612	CCDC152	coiled-coil domain containing 152
613	MYOZ3	myozenin 3
614	CHAC1	ChaC, cation transport regulator homolog 1 (E. coli)
615	SNHG12	small nucleolar RNA host gene 12 (non-protein coding)
616	GNASAS	GNAS antisense RNA (non-protein coding)
617	UGGT2	UDP-glucose glycoprotein glucosyltransferase 2
618	LCTL	lactase-like
619	LOC100289612	arsenic transactivated protein 1
620	C4orf43	chromosome 4 open reading frame 43
621	NPPB	natriuretic peptide precursor B
622	CER1	cerberus 1, cysteine knot superfamily, homolog (Xenopus laevis)
623	VWDE	von Willebrand factor D and EGF domains
624	INHBE	inhibin, beta E
625	PCSK9	proprotein convertase subtilisin/kexin type 9
626	HMGB3L1	high-mobility group box 3-like 1
627	CDC25A	cell division cycle 25 homolog A (S. pombe)
628	BICD1	bicaudal D homolog 1 (Drosophila)
629	OCLN	occludin
630	CCDC141	coiled-coil domain containing 141
631	ZNF711	zinc finger protein 711
632	SLCO4C1	solute carrier organic anion transporter family, member 4C1
633	BCL2L11	BCL2-like 11 (apoptosis facilitator)
634	AASS	aminoadipate-semialdehyde synthase
635	SOX2	SRY (sex determining region Y)-box 2
636	SALL3	sal-like 3 (Drosophila)
637	PCDH5	protocadherin beta 5
638	CALCR	calcitonin receptor
639	LRAT	lecithin retinol acyltransferase (phosphatidylcholine--retinol O-acyltransferase)
640	CCND2	cyclin D2
641	ETV4	ets variant 4
642	MYBL2	v-myb myeloblastosis viral oncogene homolog (avian)-like 2
643	FOXH1	forkhead box H1
644	SOX4	SRY (sex determining region Y)-box 4
645	DNDD1	dysbindin (dystrobrevin binding protein 1) domain containing 1
646	CYP2S1	cytochrome P450, family 2, subfamily S, polypeptide 1
647	FAM111B	family with sequence similarity 111, member B
648	BRIP1	BRCA1 interacting protein C-terminal helicase 1
649	C21orf88	chromosome 21 open reading frame 88
650	SNHG4	small nucleolar RNA host gene 4 (non-protein coding)
651	E2F8	E2F transcription factor 8

652	LPAR4	lysophosphatidic acid receptor 4
653	F2RL1	coagulation factor II (thrombin) receptor-like 1
654	B4GALT6	UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, polypeptide 6
655	ZNF273	zinc finger protein 273
656	ZNF649	zinc finger protein 649
657	ZNF138	zinc finger protein 138
658	PCDHB2	protocadherin beta 2
659	EIF2AK4	eukaryotic translation initiation factor 2 alpha kinase 4
660	RAB39	RAB39, member RAS oncogene family
661	TERF1	telomeric repeat binding factor (NIMA-interacting) 1
662	BUB1B	budding uninhibited by benzimidazoles 1 homolog beta (yeast)
663	SYT1	synaptotagmin I
664	POLR3G	polymerase (RNA) III (DNA directed) polypeptide G (32kD)
665	RAC3	ras-related G3 botulinum toxin substrate 3 (rho family, small GTP binding protein Rac3)
666	GDF3	growth differentiation factor 3
667	MMP24	matrix metalloproteinase 24 (membrane-inserted)
668	GAP43	growth associated protein 43
669	ITGB1BP3	integrin beta 1 binding protein 3
670	CECR2	cat eye syndrome chromosome region, candidate 2
671	TRIM24	tripartite motif-containing 24
672	PHC1	polyhomeotic homolog 1 (Drosophila)
673	FZD3	frizzled homolog 3 (Drosophila)
674	HELLS	helicase, lymphoid-specific
675	TTK	TTK protein kinase
676	KBTBD8	kelch repeat and BTB (POZ) domain containing 8
677	ZNF681	zinc finger protein 681
678	DSG2	desmoglein 2
679	ACOXL	acyl-Coenzyme A oxidase-like
680	C15orf42	chromosome 15 open reading frame 42
681	PKJB	protein kinase (cAMP-dependent, catalytic) inhibitor beta
682	LOC100288551	hypothetical protein LOC100288551
683	KCNK3	potassium voltage-gated channel, subfamily G, member 3
684	ZNF850P	zinc finger protein 850 pseudogene
685	XRCC3	X-ray repair complementing defective repair in Chinese hamster cells 3
686	ZNF682	zinc finger protein 682
687	CYP2B6	cytochrome P450, family 2, subfamily B, polypeptide 6
688	GYG2	glycogenin 2
689	ERCC6L	excision repair cross-complementing rodent repair deficiency, complementation group 6-like
690	IL17RD	interleukin 17 receptor D
691	RP6-213H19.1	serine/threonine protein kinase MST4
692	NFE2L3	nuclear factor (erythroid-derived 2)-like 3
693	WDR67	WD repeat domain 67
694	DAZL	deleted in azoospermia-like
695	SEMG1	semenogelin I
696	KCNE1L	KCNE1-like
697	SLC1A6	solute carrier family 1 (high affinity aspartate/glutamate transporter), member 6
698	LMNB1	lamin B1
699	FAM133A	family with sequence similarity 133, member A
700	TRIML2	tripartite motif family-like 2
701	LOC285401	hypothetical LOC285401
702	LOC728485	hypothetical protein LOC728485
703	GPR64	G protein-coupled receptor 64
704	SNRPN	small nuclear ribonucleoprotein polypeptide N
705	UGT3A1	UDP glycosyltransferase 3 family, polypeptide A1
706	DPPA4	developmental pluripotency associated 4
707	C1orf187	chromosome 1 open reading frame 187
708	FLJ36116	hypothetical locus LOC388666
709	AP1M2	adaptor-related protein complex 1, mu 2 subunit
710	DPPA2	developmental pluripotency associated 2

711	EPHA1	EPH receptor A1
712	ARID3B	AT rich interactive domain 3B (BRIGHT-like)
713	PODXL	podocalyxin-like
714	ESRP2	epithelial splicing regulatory protein 2
715	SALL2	sal-like 2 (Drosophila)
716	ACVR2B	activin A receptor, type IIB
717	FAM60A	family with sequence similarity 60, member A
718	ADD2	adducin 2 (beta)
719	IDO1	indoleamine 2,3-dioxygenase 1
720	LOC157627	hypothetical LOC157627
721	C13orf38 /// SOHLH2	chromosome 13 open reading frame 38 /// spermatogenesis and oogenesis specific basic helix-loop-helix 2
722	RECQL4	RecQ protein-like 4
723	CAMKV	CaM kinase-like vesicle-associated
724	EPHX3	epoxide hydrolase 3
725	FAM19A4	family with sequence similarity 19 (chemokine (C-C motif)-like), member A4
726	TNFSF11	tumor necrosis factor (ligand) superfamily, member 11
727	PIPOX	pipecolic acid oxidase
728	MIR17HG	MIR17 host gene (non-protein coding)
729	C14orf115	chromosome 14 open reading frame 115
730	E2F5	E2F transcription factor 5, p130-binding
731	TET1	tet oncogene 1
732	FZD5	frizzled homolog 5 (Drosophila)
733	DEPDC1B	DEP domain containing 1B
734	IGSF1	immunoglobulin superfamily, member 1
735	CTSL2	cathepsin L2
736	IGF2BP1	insulin-like growth factor 2 mRNA binding protein 1
737	PCYT1B	phosphate cytidyltransferase 1, choline, beta
738	AP1S2	adaptor-related protein complex 1, sigma 2 subunit
739	SLC25A21	solute carrier family 25 (mitochondrial oxodicarboxylate carrier), member 21
740	DCAF12L1	DDB1 and CUL4 associated factor 12-like 1
741	LOC100216479	hypothetical LOC100216479
742	ZNF90	zinc finger protein 90
743	NRK	Nik related kinase
744	GRPR	gastrin-releasing peptide receptor
745	SERPINB9	serpin peptidase inhibitor, clade B (ovalbumin), member 9
746	PNKD	paroxysmal nonkinesigenic dyskinesia
747	RBM17	RNA binding motif protein 17
748	RNF5	ring finger protein 5
749	SP1B	Spi-B transcription factor (Spi-1/PU.1 related)
750	LOC652147	similar to U5 snRNP-specific protein, 200 kDa
751	NLRP7	NLR family, pyrin domain containing 7
752	C21orf105	chromosome 21 open reading frame 105
753	CYP26A1	cytochrome P450, family 26, subfamily A, polypeptide 1
754	ZNF560	zinc finger protein 560
755	ZNF829	zinc finger protein 829
756	ERBB2	v-erb-b2 erythroblastic leukemia viral oncogene homolog 2, neuro/glioblastoma derived oncogene homolog (avian)
757	DAPK1	death-associated protein kinase 1
758	Sep9	septin 9
759	ATRX	alpha thalassemia/mental retardation syndrome X-linked (RAD54 homolog, S. cerevisiae)
760	SLC6A6	solute carrier family 6 (neurotransmitter transporter, taurine), member 6
761	PHF12	PHD finger protein 12
762	HEATR1	HEAT repeat containing 1
763	MYO10	myosin X
764	JMJD1C	jumonji domain containing 1C
765	MDM2	Mdm2 p53 binding protein homolog (mouse)
766	TFRC	transferrin receptor (p90, CD71)
767	NUP188	nucleoporin 188kDa
768	DYNC2H1	dynein, cytoplasmic 2, heavy chain 1

769	MME	membrane metallo-endopeptidase
770	BDNF	brain-derived neurotrophic factor
771	MMP14	matrix metallopeptidase 14 (membrane-inserted)
772	UHRF1BP1L	UHRF1 binding protein 1-like
773	ODZ3	odz, odd Oz/ten-m homolog 3 (Drosophila)
774	SLC4A7	solute carrier family 4, sodium bicarbonate cotransporter, member 7
775	TRPC4	transient receptor potential cation channel, subfamily C, member 4
776	SEMA3A	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3A
777	LOC100288985	hypothetical protein LOC100288985
778	RAB3B	RAB3B, member RAS oncogene family
779	RALGPS2	Ral GEF with PH domain and SH3 binding motif 2
780	KIAA1826	KIAA1826
781	FST	folistatin
782	LOC401074	hypothetical LOC401074
783	SLC7A11	solute carrier family 7, (cationic amino acid transporter, y+ system) member 11
784	BBS7	Bardet-Biedl syndrome 7
785	CRABP2	cellular retinoic acid binding protein 2
786	GPX8	glutathione peroxidase 8 (putative)
787	SFRP2	secreted frizzled-related protein 2
788	IRX2	iroquois homeobox 2
789	LOC339260	Hypothetical protein LOC339260
790	SERPINF4	serpin peptidase inhibitor, clade B (ovalbumin), member 4
791	SSX4 /// SSX4B	synovial sarcoma, X breakpoint 4 /// synovial sarcoma, X breakpoint 4B
792	GHST9	carbohydrate (N-acetylgalactosamine 4-O) sulfotransferase 9
793	GCNT2	glucosaminyl (N-acetyl) transferase 2, I-branching enzyme (I blood group)
794	SLC12A1	solute carrier family 12 (sodium/potassium/chloride transporters), member 1
795	DSC2	desmocollin 2
796	LOC729993	hypothetical protein LOC729993
797	LOC347475	UPF0625 coiled-coil domain-containing protein ENSP00000359845
798	LOC100129662	hypothetical protein LOC100129662
799	ZNF876P	zinc finger protein 876 (pseudogene)
800	GPC4	glypican 4
801	SH3GL3	SH3-domain GRB2-like 3
802	BIK	BCL2-interacting killer (apoptosis-inducing)
803	RIT2	Ras-like without CAAX 2
804	NAP1L3	nucleosome assembly protein 1-like 3
805	LOC389895	hypothetical LOC389895
806	FABP7	fatty acid binding protein 7, brain
807	KLKB1	kallikrein B, plasma (Fletcher factor) 1
808	HLA-DPB2	major histocompatibility complex, class II, DP beta 2 (pseudogene)
809	CALCB	calcitonin-related polypeptide beta
810	ZFR2	zinc finger RNA binding protein 2
811	ZIC2	Zic family member 2 (odd-paired homolog, Drosophila)
812	LOC730125	Hypothetical LOC730125
813	ADAMTS19	ADAM metallopeptidase with thrombospondin type 1 motif, 19
814	FGFR4	fibroblast growth factor receptor 4
815	SEMA6A	sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6A
816	DPPA3	developmental pluripotency associated 3
817	DPPA5	developmental pluripotency associated 5
818	HS6ST2	heparan sulfate 6-O-sulfotransferase 2
819	GLDC	glycine dehydrogenase (decarboxylating)
820	NLGN4X	neuroligin 4, X-linked
821	MEGF10	multiple EGF-like-domains 10
822	KLHDC7A	kelch domain containing 7A

823	PALM3	Paralemmin-3
824	GPR19	G protein-coupled receptor 19
825	ORC1L	origin recognition complex, subunit 1-like (yeast)
826	COCH	coagulation factor C homolog, cochlin (Limulus polyphemus)
827	GABRB3	gamma-aminobutyric acid (GABA) A receptor, beta 3
828	FAM60A /// LOC728115	family with sequence similarity 60, member A /// similar to family with sequence similarity 60, member A
829	CNTNAP2	contactin associated protein-like 2
830	C8orf42	chromosome 8 open reading frame 42
831	ZSCAN10	zinc finger and SCAN domain containing 10
832	NXPH2	neurexophilin 2
833	PRDM14	PR domain containing 14
834	FOXD3	forkhead box D3
835	PLEKHG4B	pleckstrin homology domain containing, family G (with RhoGef domain) member 4B
836	LOC728342	Hypothetical protein LOC728342
837	PDZD4	PDZ domain containing 4
838	C9orf135	chromosome 9 open reading frame 135
839	TMSB15A	thymosin beta 15a
840	GNG4	guanine nucleotide binding protein (G protein), gamma 4
841	CA14	carbonic anhydrase XIV
842	SOX3	SRY (sex determining region Y)-box 3
843	ATCAY	ataxia, cerebellar, Cayman type
844	PIM2	pim-2 oncogene
845	TEX14	testis expressed 14
846	ZNF488	zinc finger protein 488
847	ATXN7L1	ataxin 7-like 1
848	IGDCC3	immunoglobulin superfamily, DCC subclass, member 3
849	SOX11	SRY (sex determining region Y)-box 11
850	LEFTY1	left-right determination factor 1
851	ME1	malic enzyme 1, NADP(+)-dependent, cytosolic
852	GPR143	G protein-coupled receptor 143
853	LOC153469	hypothetical protein LOC153469
854	SMPDL3B	sphingomyelin phosphodiesterase, acid-like 3B
855	WNK3	WNK lysine deficient protein kinase 3
856	ZFP42	zinc finger protein 42 homolog (mouse)
857	NMU	neuromedin U
858	CD24	CD24 molecule
859	SCNN1A	sodium channel, nonvoltage-gated 1 alpha
860	RBPMS2	RNA binding protein with multiple splicing 2
861	FREM2	FRAS1 related extracellular matrix protein 2
862	LOC100131138	similar to hCG2040918
863	CALB1	calbindin 1, 28kDa
864	POU5F1B	POU class 5 homeobox 1B
865	OTX2	orthodenticle homeobox 2
866	LIN28B	lin-28 homolog B (C. elegans)
867	RMST	rhabdomyosarcoma 2 associated transcript (non-protein coding)
868	CXADR	coxsackie virus and adenovirus receptor
869	KCNN2	potassium intermediate/small conductance calcium-activated channel, subfamily N, member 2
870	CLDN6	claudin 6
871	TEX15	testis expressed 15
872	ZIC3	Zic family member 3 (odd-paired homolog, Drosophila)
873	RPRM	reprimin, TP53 dependent G2 arrest mediator candidate
874	CDH3	cadherin 3, type 1, P-cadherin (placental)
875	LINGO1	leucine rich repeat and Ig domain containing 1
876	LECT1	leukocyte cell derived chemotaxin 1
877	DCX	doublecortin
878	GLB1L3	galactosidase, beta 1-like 3
879	ZNF165	zinc finger protein 165
880	MYCN	v-myc myelocytomatosis viral related oncogene, neuroblastoma derived (avian)
881	NANOG	Nanog homeobox
		POU class 5 homeobox 1 /// POU class 5 homeobox

882	POU5F1 /// POU5F1B /// POU5F1P3 /// POU5F1P4	1B /// POU class 5 homeobox 1 pseudogene 3 /// POU class 5 homeobox 1 pseudogene 4
883	C6orf168	chromosome 6 open reading frame 168
884	SLC7A3	solute carrier family 7 (cationic amino acid transporter, y+ system), member 3
885	KIF26A	kinesin family member 26A
886	JPH3	junctophilin 3
887	CR1 /// CR1L	complement component (3b/4b) receptor 1 (Knops blood group) /// complement component (3b/4b) receptor 1-like
888	GABRA5	gamma-aminobutyric acid (GABA) A receptor, alpha 5
889	KIF5C	kinesin family member 5C
890	TUBB2B	tubulin, beta 2B
891	DNMT3B	DNA (cytosine-5-)-methyltransferase 3 beta
892	DDX25	DEAD (Asp-Glu-Ala-Asp) box polypeptide 25
893	PTPRZ1	protein tyrosine phosphatase, receptor-type, Z polypeptide 1
894	UNC5D	unc-5 homolog D (C. elegans)
895	VASH2	vasohibin 2
896	LRRTM4	leucine rich repeat transmembrane neuronal 4
897	MARVELD3	MARVEL domain containing 3
898	SEMA6B	sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6B
899	LEFTY2	left-right determination factor 2
900	POU5F1P3	POU class 5 homeobox 1 pseudogene 3
901	POU5F1P4	POU class 5 homeobox 1 pseudogene 4
902	EPCAM	epithelial cell adhesion molecule
903	LIN28	lin-28 homolog (C. elegans)
904	L1TD1	LINE-1 type transposase domain containing 1
905	USP44	ubiquitin specific peptidase 44
906	ESRP1	epithelial splicing regulatory protein 1
907	BEND4	BEN domain containing 4
908	TOX3	TOX high mobility group box family member 3
909	SCG3	secretogranin III
910	CRISPLD1	cysteine-rich secretory protein LCCL domain containing 1
911	SALL4	sal-like 4 (Drosophila)
912	LRRN1	leucine rich repeat neuronal 1
913	CRABP1	cellular retinoic acid binding protein 1
914	NTS	neurotensin
915	SCGB3A2	secretoglobin, family 3A, member 2
916	COX8A1	cytochrome c oxidase subunit VIa polypeptide 1
917	TDGF1 /// TDGF3	teratocarcinoma-derived growth factor 1 /// teratocarcinoma-derived growth factor 3, pseudogene
918	HESRG	hypothetical LOC790952
919	NLRP2	NLR family, pyrin domain containing 2
920	PSPH	phosphoserine phosphatase
921	LOC100132181	Hypothetical protein LOC100132181
922	GNAS	GNAS complex locus
923	NECAB1	N-terminal EF-hand calcium binding protein 1
924	HHLA1	HERV-H LTR-associating 1
925	ABHD12B	abhydrolase domain containing 12B
926	RBM15	RNA binding motif protein 15
927	ZNF208	zinc finger protein 208
928	ZNF257	zinc finger protein 257
929	RBM46	RNA binding motif protein 46

[0069] [表2 A] 第2 遺伝子群 (表2 B) を含むプローブ1 3 0 4 個において、ヒトES細胞クローン (KhES1-S3) の発現レベルの平均に対する、各ES細胞クローン及び各iPS細胞クローンの発現レベルの割合

Gene Symbol	Gene Title	KHES2 ES	KHES1 ES	201B7 iPS	KHES3 ES	201B6 iPS	253G4 iPS	253G1 iPS
1 GRIA3	glutamate receptor, ionotropic, AMPA 3	0.21	0.53	0.91	-0.74	1.38	1.03	1.29
2 STC2	stanniocalcin 2	0.06	-0.11	0.81	0.04	1.70	0.38	0.79
3 TFPI2	tissue factor pathway inhibitor 2	0.35	-0.09	0.22	-0.27	0.56	0.08	0.13
4 TFPI2	tissue factor pathway inhibitor 2	-0.03	-0.24	0.91	0.27	0.85	0.83	1.04
5 NPPB	inatriuretic peptide precursor B	-0.35	-0.64	0.65	0.99	1.56	-0.07	0.74
6 INHBE	inhibin, beta E	0.44	-0.02	0.97	-0.42	1.56	0.49	0.91
7 PCSK9	proprotein convertase subtilisin/kexin type 9	-0.18	-0.34	0.83	0.52	1.47	0.84	0.88
8 SLC2A3	solute carrier family 2 (facilitated glucose transporter), member 3	-0.43	-0.37	-0.62	0.80	-0.64	-0.84	-1.28
9 SLC2A3	solute carrier family 2 (facilitated glucose transporter), member 3	-0.51	-0.53	-0.52	1.04	-0.51	-0.59	-0.58
10 TNFRSF8	tumor necrosis factor receptor superfamily, member 8	-0.23	-0.43	-0.45	0.66	-0.58	-0.92	-0.50
11 UTF1	undifferentiated embryonic cell transcription factor 1	0.07	-1.24	-0.64	1.17	-0.43	-0.72	-0.87
12 HMGA1	high mobility group AT-hook 1	0.18	-0.81	-0.72	0.83	-1.22	-0.68	-0.95
13 KIF1A	kinesin family member 1A	0.24	-0.10	-0.94	-0.14	-1.08	-1.55	-1.06
14 —	—	0.71	0.23	-0.60	-0.94	-1.21	-1.61	-0.41
15 ZNF678	zinc finger protein 678	-0.24	0.62	-0.81	-0.39	-1.36	-0.42	-1.57
16 FANCB	Fanconi anemia, complementation group B	-0.21	0.81	-0.93	-0.61	-0.83	-0.05	-0.98
17 DDX11	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 11 (CHLI-like helicase homolog, S. cerevisiae)	0.25	-0.27	-0.04	0.03	-1.07	-1.06	-1.41
18 C14orf106	chromosome 14 open reading frame 106	0.04	-0.10	0.01	0.06	-1.19	-1.01	-1.33
19 ZNF92	zinc finger protein 92	0.09	-0.13	-0.01	0.04	-1.13	-0.98	-0.78
20 ASPM	aspm (abnormal spindle) homolog, microcephaly associated (Drosophila)	0.03	0.07	-0.58	-0.11	-1.50	-1.25	-1.87
21 ZNF770	zinc finger protein 770	0.22	0.28	-0.52	-0.50	-1.21	-1.26	-1.05
22 ATP11C	ATPase, class VI, type 11C	0.14	0.43	-0.75	-0.57	-1.02	-0.82	-1.47
23 ATRX	alpha thalassemia/mental retardation syndrome X-linked (RAD54 homolog, S. cerevisiae)	0.07	0.04	-1.00	-0.11	-1.75	-1.71	-1.33
24 ANTXR1	anthrax toxin receptor 1	-0.07	0.39	-0.92	-0.32	-1.56	-1.64	-0.18
25 ZNF92	zinc finger protein 92	-0.06	0.39	0.01	-0.32	-0.69	-1.56	-0.18
26 SNORD116	small nucleolar RNA, C/D box 116 cluster	0.31	0.35	0.27	-0.66	-0.48	-1.72	-0.70
27 COL11A1	collagen, type XI, alpha 1	-0.02	0.18	0.58	-0.16	-1.42	-1.13	-0.16
28 LOC643401	hypothetical protein LOC643401	-1.07	0.65	-0.78	0.42	0.36	0.11	-0.13
29 CNKSR2	connector enhancer of kinase suppressor of Ras 2	-0.07	0.59	0.33	-0.52	-0.26	-0.05	-0.13
30 DNA2	DNA replication helicase 2 homolog (yeast)	-0.07	0.48	0.11	-0.41	0.05	-0.18	-0.36
31 PIK4	polo-like kinase 4 (Drosophila)	-0.17	0.49	0.13	-0.31	0.09	-0.40	-0.75
32 FLJ35848	hypothetical protein FLJ35848	-0.15	0.34	-0.15	-0.19	-0.54	0.13	-0.27
33 DLGAP5	discs large (Drosophila) homolog associated protein 5	-0.26	0.19	-0.01	0.06	-0.24	-0.15	-0.16
34 ELAVL2	ELAV (embryonic lethal, abnormal vision, Drosophila)-like 2 (Hu antigen B)	-0.31	0.28	-0.06	0.03	-0.35	-0.22	-0.29
35 ZNF391	zinc finger protein 391	-0.42	0.36	0.25	0.05	-0.17	-0.30	-0.14
36 NCAPG2	non-SMC condensin II complex, subunit G2	-0.34	0.28	0.22	0.06	-0.25	-0.29	-0.27
37 SLC16A1	solute carrier family 16, member 1 (monocarboxylic acid transporter 1)	-0.13	0.34	0.12	-0.21	-0.21	-0.19	-0.57
38 MCM4	minichromosome maintenance complex component 4	-0.03	0.06	0.12	-0.03	-0.12	-0.39	-0.59

39	F-GD6	F-YVE, RhoGEF and PH domain containing 8	-0.07	0.14	0.11	-0.07	-0.37	0.01	-0.54
40	WDHD1	WD repeat and HMG-box DNA binding protein 1	-0.17	0.02	0.12	0.15	-0.46	-0.20	-0.52
41	CCDC88A	coiled-coil domain containing 88A	-0.30	0.19	-0.02	0.11	-0.60	-0.24	-0.32
42	BIRC5	baculoviral IAP repeat-containing 5	0.09	0.14	-0.39	-0.23	-0.19	-0.44	-0.82
43	—	—	0.10	0.11	-0.52	-0.20	0.18	-0.31	-0.61
44	CCNA2	cyclin A2	-0.01	0.07	0.04	-0.06	0.60	0.22	0.06
45	SRP35	serine-arginine repressor protein (35 kDa)	-0.10	0.21	0.21	-0.11	0.35	0.07	-0.03
46	MAD2L1	MAD2 mitotic arrest deficient-like 1 (yeast)	0.03	0.00	0.12	0.17	0.37	-0.11	-0.05
47	CCNA2	cyclin A2	0.03	0.00	0.14	-0.04	0.47	-0.07	-0.10
48	PDPN	podoplanin	-0.22	0.12	0.33	0.10	0.25	0.30	-0.01
49	RAD51AP1	RAD51 associated protein 1	-0.17	0.20	0.03	-0.04	0.24	0.30	-0.01
50	CENPH	centromere protein H	-0.02	0.09	0.21	-0.07	0.41	0.36	-0.03
51	NCAPH	non-SMC condensin I complex, subunit H	-0.40	0.36	0.01	0.05	0.26	0.02	0.03
52	FAM72A /// FAM72B /// FAM72C /// FAM72D	family with sequence similarity 72, member A /// family with sequence similarity 72, member B /// family with sequence similarity 72, member C /// family with sequence similarity 72, member D	-0.25	0.06	-0.12	0.19	0.37	0.24	0.04
53	BIRC5	baculoviral IAP repeat-containing 5	-0.14	0.04	-0.38	0.09	0.16	-0.09	-0.14
54	WDHD1	WD repeat and HMG-box DNA binding protein 1	0.15	-0.15	0.02	0.01	0.21	-0.11	-0.47
55	TMEFF1	transmembrane protein with EGF-like and two follistatin-like domains 1	-0.02	-0.05	-0.17	0.07	0.19	-0.07	-0.44
56	PAOS	phosphoribosylaminimidazole carboxylase, phosphoribosylaminimidazole succinocarboxamide synthetase	-0.12	0.11	0.02	0.00	-0.15	0.01	-0.28
57	DBF4	DBF4 homolog (S. cerevisiae)	-0.05	0.09	-0.05	-0.04	-0.16	-0.12	-0.19
58	HMMR	hyaluronan-mediated motility receptor (RHAMM)	0.05	0.03	-0.14	-0.08	-0.09	-0.04	-0.25
59	MCM4	mitochondrion maintenance complex component 4	-0.02	-0.04	0.03	0.06	-0.13	-0.14	-0.26
60	FXYD7	FXYD domain containing ion transport regulator 7	0.15	-0.12	-0.08	-0.03	-0.26	-0.12	-0.30
61	—	—	0.04	-0.07	-0.09	0.02	-0.37	-0.15	0.03
62	FEN1	flap structure-specific endonuclease 1	0.12	0.02	0.29	-0.14	0.22	0.26	0.00
63	CDC25C	cell division cycle 25 homolog C (S. pombe)	0.24	-0.07	0.01	-0.17	0.20	0.36	-0.01
64	TPM1	tropomyosin 1 (alpha)	0.16	-0.14	-0.12	-0.02	-0.16	0.11	0.30
65	HMMR	hyaluronan-mediated motility receptor (RHAMM)	0.09	-0.12	0.24	0.03	-0.14	0.08	-0.01
66	CCNF	cyclin F	0.11	-0.27	0.12	0.16	0.20	0.04	0.15
67	CDC45	cell division cycle associated 5	0.10	-0.19	0.15	0.09	0.07	-0.03	0.04
68	HJURP	Holliday junction recognition protein	0.01	-0.08	0.18	0.07	0.13	0.05	-0.10
69	SPAG5	sperm associated antigen 5	0.09	-0.16	0.02	0.07	0.08	-0.10	0.08
70	RFWD3	ring finger and WD repeat domain 3	-0.02	-0.09	0.11	0.11	0.14	0.22	-0.06
71	C21orf45	chromosome 21 open reading frame 45	0.01	-0.04	0.13	0.04	-0.03	0.05	0.13
72	CDC42	cell division cycle associated 2	-0.03	0.03	0.04	0.00	0.06	0.09	0.05
73	MCM4	mitochondrion maintenance complex component 4	0.06	-0.11	0.03	0.06	0.06	0.18	0.05
74	TDFP2	transcription factor Dp-2 (E2F dimerization partner 2)	-0.24	0.12	-0.05	0.12	-0.05	-0.05	0.06
75	PRIM1	primase, DNA, polypeptide 1 (43kDa)	-0.16	0.09	0.06	0.07	0.09	0.07	0.19
76	SEPHS1	selenophosphate synthetase 1	-0.18	0.06	0.21	0.12	0.13	-0.02	0.11
77	MCM2	mitochondrion maintenance complex component 2	-0.04	-0.04	0.16	0.06	0.04	0.02	0.05
78	SEPHS1	selenophosphate synthetase 1	-0.11	0.01	0.16	0.10	-0.05	-0.09	0.02

79	FAM64A	family with sequence similarity 64, member A	0.03	-0.10	0.05	0.07	-0.06	0.04	-0.05
80	BEND3	BEN domain containing 3	-0.06	-0.10	-0.05	0.17	-0.09	0.05	0.19
81	VRK1	vaccinia related kinase 1	-0.15	0.23	0.04	-0.07	0.09	0.19	0.16
82	POLE2	polymerase (DNA directed) epsilon 2 (p59 subunit)	-0.14	0.16	0.02	-0.03	0.15	0.27	0.16
83	DSGCI	defective in sister chromatid cohesion 1 homolog (S. cerevisiae)	-0.10	0.19	0.05	-0.09	0.10	0.25	0.16
84	GNS2	GIN5 complex subunit 2 (Psf2 homolog)	-0.14	0.18	0.05	-0.03	-0.01	0.27	0.36
85	CCNJ	cyclin J	-0.07	0.23	-0.20	-0.16	0.23	0.24	0.14
86	EXO1	endonuclease 1	-0.22	0.23	0.17	-0.01	-0.05	-0.06	-0.14
87	PDPN	podoplanin	-0.08	0.30	0.12	-0.21	-0.01	-0.16	-0.13
88	CDC2	cell division cycle 2, G1 to S and G2 to M	-0.20	0.34	-0.07	-0.14	-0.06	-0.01	0.03
89	PDPN	podoplanin	-0.23	0.28	-0.09	-0.05	0.10	-0.24	-0.06
90	CDC2	cell division cycle 2, G1 to S and G2 to M	-0.21	0.34	-0.12	-0.12	-0.01	0.01	0.06
91	RCC2	regulator of chromosome condensation 2	-0.21	0.28	-0.06	-0.06	0.08	-0.01	-0.01
92	FLJ20874	hypothetical protein FLJ20874	-0.11	0.15	-0.20	-0.04	-0.05	-0.03	0.14
93	—	—	-0.05	0.13	-0.08	-0.08	-0.05	0.05	0.04
94	CCNB1	cyclin B1	-0.09	0.11	-0.12	-0.02	0.09	0.08	0.02
95	RFC3	replication factor C (activator 1) 3, 38kDa	-0.01	0.18	0.06	-0.17	0.07	0.05	-0.01
96	FANCD2	Fanconi anemia, complementation group D2	0.08	0.12	-0.01	-0.20	0.07	0.03	-0.01
97	RRM2	ribonucleotide reductase M2	0.01	0.16	0.10	-0.17	0.14	0.16	0.12
98	CCNB1	cyclin B1	-0.03	0.19	0.15	-0.16	0.19	0.05	0.01
99	CENPN	centromere protein N	-0.04	0.22	0.00	-0.18	-0.08	-0.27	0.12
100	RTKN2	rhokin 2	0.05	0.09	-0.24	-0.13	-0.08	-0.25	-0.06
101	GRB14	growth factor receptor-bound protein 14	-0.21	0.04	0.25	0.17	0.00	-0.02	0.27
102	PFAS	phosphoribosylformylglycinamide synthase	-0.29	0.18	0.24	0.11	0.11	0.07	0.33
103	KIF15	kinesin family member 15	-0.33	0.17	0.05	0.16	0.15	0.10	0.19
104	RAD54B	RAD54 homolog B (S. cerevisiae)	-0.17	0.17	0.37	0.00	-0.04	0.28	0.36
105	RAD54L	RAD54-like (S. cerevisiae)	-0.47	0.17	-0.23	0.30	0.11	0.01	-0.06
106	PPAT	phosphoribosyl pyrophosphate amidotransferase	-0.56	0.35	-0.13	0.20	-0.19	-0.01	-0.23
107	SLC16A1	solute carrier family 16, member 1 (monocarboxylic acid transporter 1)	-0.48	0.38	-0.04	0.10	0.23	0.06	-0.12
108	ZNF814	zinc finger protein 814	-0.49	0.30	-0.02	0.19	0.19	0.18	-0.09
109	SLC16A1	solute carrier family 16, member 1 (monocarboxylic acid transporter 1)	-0.25	0.19	0.07	0.06	0.03	-0.06	-0.09
110	ZNF462	zinc finger protein 462	-0.37	0.23	0.03	0.14	-0.04	-0.04	-0.09
111	AP1S3	adaptor-related protein complex 1, sigma 3 subunit	0.01	0.18	0.35	-0.19	0.28	0.52	0.36
112	LHFPL4	lipoma HMGIC fusion partner-like 4	-0.14	0.24	0.28	-0.10	0.36	0.37	0.83
113	CDC2	cell division cycle 2, G1 to S and G2 to M	-0.16	0.24	0.04	-0.08	0.06	0.52	0.51
114	ZNF114	zinc finger protein 114	0.14	-0.03	0.03	-0.11	0.08	0.34	0.34
115	ZWINT	ZW10 interactor	-0.11	0.20	0.06	-0.09	0.27	0.30	0.29
116	G2Iorf45	chromosome 21 open reading frame 45	0.04	0.01	0.17	-0.05	0.25	0.23	0.31
117	G1orf135	chromosome 1 open reading frame 135	0.07	0.02	0.17	-0.09	0.40	0.30	0.85
118	NODAL	nodal homolog (mouse)	0.19	-0.02	0.34	-0.16	0.33	0.64	0.35
119	CBS	cystathionine-beta-synthase	0.15	-0.47	-0.03	0.33	-0.20	-0.12	-0.20
120	CBS	cystathionine-beta-synthase	0.04	-0.39	0.01	0.35	-0.31	-0.19	-0.32

121	TPX2	TPX2, microtubule-associated, homolog (Xenopus laevis)	-0.07	-0.24	-0.11	0.31	-0.02	-0.16	-0.43
122	CDT1	chromatin licensing and DNA replication factor 1	-0.26	-0.29	-0.06	0.55	0.04	0.11	-0.17
123	MCM7	minichromosome maintenance complex component 7	-0.03	-0.34	0.17	0.37	-0.01	-0.04	-0.25
124	TUBB2A TUBB2B	tubulin, beta 2A /// tubulin, beta 2B	0.35	-0.59	0.29	0.24	-0.15	0.01	0.04
125	ESPL1	extra spindle pole bodies homolog 1 (S. cerevisiae)	0.10	-0.29	-0.26	0.19	-0.22	0.09	0.04
126	KONQ2	potassium voltage-gated channel, KQT-like subfamily, member 2	0.24	-0.24	0.15	0.01	-0.09	0.33	0.35
127	UBE2S	ubiquitin-conjugating enzyme E2S	0.15	-0.30	0.04	0.15	-0.02	0.12	0.14
128	TEAD4	TEA domain family member 4	0.16	-0.36	0.08	0.19	-0.06	0.21	0.14
129	SCLY	selenocysteine lyase	0.06	-0.37	0.07	0.30	0.09	0.23	0.18
130	CENPA	centromere protein A	0.06	-0.06	-0.23	0.00	0.15	0.14	0.20
131	GDCA3	cell division cycle associated 3	0.14	-0.06	-0.02	-0.08	0.00	0.02	0.28
132	HMGAI	high mobility group AT-hook 1	0.19	-0.62	-0.13	0.43	0.09	0.19	-0.02
133	DHFR	dihydrofolate reductase	0.09	-0.41	-0.15	0.32	0.12	-0.01	-0.09
134	PHF17	PHD finger protein 17	-0.03	-0.36	-0.37	0.39	0.28	-0.05	-0.01
135	MSH6	mutS homolog 6 (E. coli)	0.02	-0.18	0.17	0.16	-0.07	-0.09	-0.30
136	GTPS	GTP synthase	-0.05	-0.01	0.21	0.06	0.07	-0.07	-0.15
137	KIF2C	kinesin family member 2C	-0.10	-0.01	0.11	0.11	0.10	-0.02	-0.33
138	FOXMI	forkhead box M1	-0.12	-0.15	-0.06	0.27	0.08	-0.03	-0.13
139	GTSE1	G-2 and S-phase expressed 1	0.13	-0.25	0.05	0.12	0.11	0.13	-0.12
140	AURKA	aurora kinase A	0.02	-0.13	-0.06	0.11	0.25	0.06	-0.07
141	ESPL1	extra spindle pole bodies homolog 1 (S. cerevisiae)	-0.02	-0.17	-0.08	0.19	0.09	0.16	0.03
142	FBXO11	F-box protein 11	0.02	-0.24	0.32	0.22	0.13	-0.10	-0.23
143	NLN	neurolysin (metallopeptidase M3 family)	-0.01	-0.17	-0.04	0.18	-0.08	-0.06	-0.21
144	LAPTM4B	lysosomal protein transmembrane 4 beta	0.09	-0.08	0.03	-0.01	0.08	-0.23	-0.26
145	TMPO	thymopoietin	0.12	-0.13	0.06	0.01	0.03	-0.20	-0.09
146	EZH2	enhancer of zeste homolog 2 (Drosophila)	0.01	0.06	0.13	-0.07	0.14	0.04	-0.10
147	CDC7	cell division cycle 7 homolog (S. cerevisiae)	0.06	-0.04	0.06	-0.02	0.24	0.00	-0.20
148	NETO1	neuropilin (NRP) and tolloid (TLL)-like 1	0.09	-0.12	0.22	0.03	-0.16	-0.29	0.00
149	KIF23	kinesin family member 23	0.00	-0.03	0.11	0.03	-0.16	-0.08	-0.23
150	KIF18B	kinesin family member 18B	-0.05	0.03	0.05	0.02	-0.27	-0.14	-0.21
151	FANCI	Fanconi anemia, complementation group I	-0.01	0.00	0.21	0.01	-0.28	-0.23	-0.25
152	GDCA2	cell division cycle associated 2	-0.05	0.03	0.18	0.02	-0.08	-0.30	-0.28
153	MCM6	minichromosome maintenance complex component 6	-0.01	0.25	0.03	-0.24	-0.23	-0.10	-0.16
154	MSH2	mutS homolog 2, colon cancer, nonpolyposis type 1 (E. coli)	-0.10	0.22	0.04	-0.12	-0.17	-0.11	-0.43
155	TMEFF1	transmembrane protein with EGF-like and two follistatin-like domains 1	-0.09	0.02	-0.03	0.07	-0.09	-0.12	-0.41
156	NCAPG	non-SMC condensin I complex, subunit G	-0.12	0.14	0.04	-0.01	-0.15	0.05	-0.30
157	DHFR	dihydrofolate reductase	-0.17	0.31	-0.01	-0.14	-0.15	0.03	-0.45
158	MASTL	microtubule associated serine/threonine kinase-like	-0.02	0.14	-0.04	-0.13	-0.07	-0.11	-0.36
159	FANCI	Fanconi anemia, complementation group I	-0.24	0.31	-0.01	-0.06	-0.09	-0.20	-0.09
160	NCAPG	non-SMC condensin I complex, subunit G	-0.11	0.28	0.22	-0.15	-0.06	-0.06	-0.05
161	CENPJ	centromere protein J	-0.14	0.40	-0.10	-0.25	-0.25	-0.09	-0.02
162	KIF11	kinesin family member 11	-0.15	0.03	0.02	0.11	0.00	-0.02	-0.13

163	KIF2C	kinesin family member 2C	-0.13	-0.02	-0.08	0.15	-0.03	-0.14	-0.14
164	TOP2A	topoisomerase (DNA) II alpha 170kDa	0.00	-0.04	-0.34	0.04	-0.04	-0.03	-0.19
165	ZNF643	zinc finger protein 643	0.06	-0.05	-0.08	0.00	-0.19	0.09	-0.29
166	PSIP1	PC4 and SFRS1 interacting protein 1	-0.05	0.01	-0.15	0.04	-0.13	0.00	-0.23
167	—	—	-0.03	0.00	-0.23	0.03	-0.03	-0.15	-0.19
168	ORC6L	origin recognition complex, subunit 6 like (yeast)	-0.04	-0.01	-0.14	0.05	-0.04	-0.07	-0.18
169	RAD54B	RAD54 homolog B (S. cerevisiae)	0.00	0.12	-0.16	-0.12	-0.09	-0.04	-0.22
170	KPNA2	karyopherin alpha 2 (RAG cohort 1, importin alpha 1)	-0.10	0.12	-0.09	-0.02	0.08	0.05	0.05
171	NOP16	NOP16 nucleolar protein homolog (yeast)	-0.05	0.13	-0.05	-0.08	0.11	0.09	-0.04
172	NUSAP1	nucleolar and spindle associated protein 1	-0.15	0.19	-0.03	-0.04	0.17	0.13	0.00
173	C13orf34	chromosome 13 open reading frame 34	-0.18	0.19	-0.03	-0.02	0.05	0.02	0.02
174	C6orf173	chromosome 6 open reading frame 173	-0.07	0.15	-0.07	-0.08	0.01	0.06	0.16
175	RNAHEH2A	ribonuclease H2, subunit A	-0.06	-0.01	-0.17	0.07	0.03	0.05	-0.01
176	CCNE1	cyclin E1	-0.09	0.00	-0.27	0.09	0.01	0.18	0.07
177	KIF14	kinesin family member 14	-0.15	-0.01	-0.33	0.15	-0.06	0.08	0.08
178	—	—	-0.25	0.30	-0.23	-0.05	-0.11	0.11	-0.11
179	ZNF788	zinc finger family member 788	-0.14	0.17	-0.37	-0.03	-0.06	-0.11	-0.08
180	CASP3	caspase 3, apoptosis-related cysteine peptidase	0.20	0.04	0.22	-0.24	0.26	0.17	0.04
181	RRM2	ribonucleotide reductase M2	0.05	0.26	0.26	-0.30	0.19	0.12	0.32
182	RAD51	RAD51 homolog (RecA homolog, E. coli) (S. cerevisiae)	0.03	0.17	0.10	-0.20	0.35	0.35	0.32
183	PPAT	phosphoribosyl pyrophosphate amidotransferase	0.17	0.21	0.09	-0.38	0.28	0.40	0.25
184	SUV39H2	suppressor of variegation 3-9 homolog 2 (Drosophila)	0.03	0.34	0.01	-0.37	-0.02	-0.01	0.10
185	UGHL1	ubiquitin carboxyl-terminal esterase L1 (ubiquitin thioesterase)	0.08	0.13	0.04	-0.21	-0.13	-0.01	0.12
186	—	—	0.26	0.12	0.23	-0.38	-0.17	0.21	0.24
187	THAP9	THAP domain containing 9	0.13	0.07	0.26	-0.20	-0.15	0.03	0.02
188	SKP2	S-phase kinase-associated protein 2 (p45)	-0.15	0.28	0.21	-0.13	0.23	0.01	-0.01
189	NUSAP1	nucleolar and spindle associated protein 1	-0.12	0.31	0.15	-0.19	0.01	0.14	-0.27
190	UBE2T	ubiquitin-conjugating enzyme E2T (putative)	-0.23	0.45	-0.04	-0.22	0.18	0.18	0.13
191	NUF2	NUF2, NDC80 kinetochore complex component, homolog (S. cerevisiae)	-0.23	0.45	-0.11	-0.22	0.12	0.17	0.00
192	—	—	-0.27	0.64	0.07	-0.36	0.23	0.05	-0.02
193	RFC4	replication factor C (activator 1) 4, 37kDa	-0.29	0.25	0.08	0.04	0.44	0.24	0.26
194	NDC80	NDC80 homolog, kinetochore complex component (S. cerevisiae)	-0.29	0.32	-0.16	-0.03	0.32	0.22	-0.02
195	NEK2	NIMA (never in mitosis gene a)-related kinase 2	-0.22	0.16	-0.04	0.06	0.35	0.33	0.08
196	AURKA	aurora kinase A	-0.26	0.17	-0.11	0.09	0.31	0.14	0.01
197	TRIM6	tripartite motif-containing 6	-0.24	0.13	-0.21	0.12	0.33	0.13	0.18
198	CKS1B	CDK28 protein kinase regulatory subunit 1B	-0.15	0.05	0.23	0.09	0.33	0.29	0.44
199	CCNB2	cyclin B2	-0.07	0.09	0.14	-0.03	0.32	0.34	0.37
200	GMNN	geminin, DNA replication inhibitor	0.02	-0.03	0.08	0.00	0.24	0.16	0.35
201	GENPK	centromere protein K	-0.18	0.26	0.24	-0.08	0.28	0.48	0.22
202	FAM54A	family with sequence similarity 54, member A	-0.12	0.18	0.17	-0.06	0.20	0.36	0.22
203	PTTG1	pituitary tumor-transforming 1	-0.15	0.01	0.16	0.15	0.27	0.28	0.30
204	TEAD2	TEA domain family member 2	-0.08	0.00	0.25	0.08	0.38	0.28	0.29

205	CDC43	cell division cycle associated 8	-0.06	0.04	0.13	0.02	0.54	0.34	0.02	0.25
206	NFK2	NIMA (never in mitosis gene a)-related kinase 2	-0.23	0.18	-0.08	0.05	0.24	0.37	-0.02	-0.02
207	FBX05	F-box protein 5	-0.13	0.21	0.18	-0.08	0.36	0.31	-0.03	-0.03
208	BXDC2	bix domain containing 2	-0.18	0.21	0.13	-0.03	0.22	0.45	0.22	0.45
209	MTA3	metastasis associated 1 family, member 3	-0.32	0.08	-0.04	0.24	0.12	0.19	0.17	0.17
210	TIMELESS	timeless homolog (Drosophila)	-0.28	-0.16	0.28	0.44	0.35	0.21	0.44	0.15
211	CCDC38	coiled-coil domain containing 38	-0.24	0.06	0.36	0.19	0.33	0.20	-0.03	-0.03
212	EEF1E1	eukaryotic translation elongation factor 1 epsilon 1	-0.24	0.26	0.05	-0.06	0.21	0.02	0.21	0.02
213	CCDC50	coiled-coil domain containing 50	-0.24	0.29	0.18	-0.06	-0.09	0.03	0.09	0.09
214	LYAR	Lyl antibody reactive homolog (mouse)	-0.24	0.25	0.07	-0.01	0.05	0.18	0.16	0.16
215	SLOC415	solute carrier family 6 (neutral amino acid transporter), member 15	-0.15	0.24	0.26	-0.09	0.10	0.16	0.31	0.31
216	---	---	-0.25	0.40	0.38	-0.16	0.01	0.19	0.24	0.24
217	MRS2	MRS2 magnesium homeostasis factor homolog (S. cerevisiae)	-0.01	0.39	0.01	-0.38	0.00	0.04	0.43	0.43
218	FAM54A	family with sequence similarity 54, member A	-0.07	0.20	0.02	-0.14	-0.17	-0.12	0.35	0.35
219	BRGA2	breast cancer 2, early onset	-0.36	0.28	0.15	0.08	-0.17	-0.41	-0.03	-0.03
220	THAP9	THAP domain containing 9	-0.32	0.45	0.54	-0.13	-0.33	-0.33	-0.57	-0.57
221	---	---	-0.15	0.49	0.06	-0.34	-0.08	-0.61	-0.46	-0.46
222	MCM10	minichromosome maintenance complex component 10	-0.59	0.38	0.50	0.21	0.10	-0.09	-0.13	-0.13
223	C12orf48	chromosome 12 open reading frame 48	-0.57	0.35	0.29	0.22	0.02	0.03	-0.25	-0.25
224	C12orf48	chromosome 12 open reading frame 48	-0.50	0.35	0.16	0.15	-0.02	0.04	-0.23	-0.23
225	GCL26	chemokine (C-C motif) ligand 26	-0.68	0.59	0.22	0.09	0.06	0.04	-0.04	-0.04
226	---	---	-0.46	0.37	0.37	0.09	-0.22	0.15	-0.43	-0.43
227	NSBPI	nucleosomal binding protein 1	-0.48	-0.04	0.10	-0.04	0.29	-0.22	0.51	0.29
228	---	---	-0.56	-0.10	0.40	0.68	-0.15	0.14	0.40	0.40
229	HESX1	HESX homeobox 1	-0.42	0.54	-0.28	-0.12	0.16	0.03	0.41	0.41
230	TNNT1	tropinin T type 1 (skeletal, slow)	-0.21	0.41	-0.64	-0.20	0.10	0.25	0.22	0.22
231	MAD2L1	MAD2 mitotic arrest deficient-like 1 (yeast)	-0.04	0.41	0.06	-0.37	0.66	0.28	0.33	0.33
232	GUCAT1A	guanylate cyclase activator 1A (retina)	-0.13	0.25	-0.25	-0.12	0.42	0.40	0.07	0.07
233	UBE2C	ubiquitin-conjugating enzyme E2C	0.19	0.34	0.10	-0.53	0.17	0.25	0.29	0.29
234	CDC6	cell division cycle 6 homolog (S. cerevisiae)	0.09	0.36	0.13	-0.45	0.05	0.13	-0.01	-0.01
235	GDC6	cell division cycle 6 homolog (S. cerevisiae)	0.23	0.26	0.43	-0.48	0.10	0.12	-0.01	-0.01
236	DIAPH2	diaphanous homolog 2 (Drosophila)	0.15	0.32	0.34	-0.47	-0.04	0.29	0.28	0.28
237	UOHL1	Ubiquitin carboxyl-terminal esterase L1 (ubiquitin thiolesterase)	0.29	0.11	-0.28	-0.40	-0.21	0.02	-0.17	-0.17
238	GAL	galanin prepropeptide	0.22	0.22	-0.13	-0.44	-0.27	-0.37	0.01	0.01
239	---	---	0.19	-0.33	-0.03	0.14	0.19	0.19	-0.38	-0.38
240	PLK4	polo-like kinase 4 (Drosophila)	-0.08	0.13	0.53	-0.05	0.50	-0.31	-0.23	-0.23
241	CHAF1A	chromatin assembly factor 1, subunit A (p150)	0.17	-0.37	0.20	0.20	-0.16	0.17	0.06	0.06
242	CHAF1A	chromatin assembly factor 1, subunit A (p150)	0.18	-0.40	0.12	0.23	0.13	0.24	0.06	0.06
243	TEAD4	TEA domain family member 4	0.41	-0.63	0.05	0.22	0.03	0.12	0.20	0.20
244	MCM5	minichromosome maintenance complex component 5	-0.06	-0.26	0.20	0.32	0.01	-0.35	-0.45	-0.45
245	GALNT13	UDP-N-acetyl-alpha-D-galactosaminepolypeptide N-acetylgalactosaminyltransferase 13 (GalNAc-T13)	-0.03	-0.29	0.20	0.32	0.38	-0.37	-0.04	-0.04
246	GAL3ST3	galactose 3-O-sulfotransferase 3	0.36	-0.69	0.28	0.34	-0.32	-0.24	-0.20	-0.20

		Family with sequence similarity 46, member B	0.26	-0.52	0.25	0.28	0.11	0.18	-0.08
247	FAM46B								
248	LOC389857	hypothetical protein	0.35	-0.46	0.22	0.11	0.00	-0.11	-0.11
249	JARD2	jumonji, AT rich interactive domain 2	-0.03	-0.27	0.19	0.30	-0.09	0.10	0.19
250	SILV	silver homolog (mouse)	0.07	-0.23	-0.11	0.16	0.11	0.47	0.07
251	IGFBPL1	insulin-like growth factor binding protein-like 1	0.10	-0.29	-0.03	0.19	-0.03	0.29	-0.10
252	MBD2	methy-CpG binding domain protein 2	0.07	-0.14	-0.19	0.08	0.25	0.19	0.28
253	GINS1	GINS complex subunit 1 (Psf1 homolog)	-0.29	0.29	0.25	0.00	0.39	0.25	0.11
254	HAS3	hyaluronan synthase 3	-0.13	0.12	0.25	0.00	0.22	0.00	0.25
255	NASP	nuclear autoantigenic sperm protein (histone-binding)	-0.27	0.06	0.17	0.21	0.24	0.25	-0.07
256	MCM5	minichromosome maintenance complex component 5	-0.26	-0.04	0.15	0.30	0.07	0.02	-0.11
257	MTF2	metal response element binding transcription factor 2	-0.10	-0.11	-0.03	0.20	0.28	0.10	-0.06
258	PMAPI1	phorbol-12-myristate-13-acetate-induced protein 1	-0.14	0.10	0.11	0.04	0.24	0.16	-0.05
259	MATR3	Matrin 3	-0.12	0.00	0.15	0.12	0.09	0.13	-0.03
260	CRMP1	collapsin response mediator protein 1	-0.07	-0.20	0.06	0.27	0.16	0.14	-0.03
261	CBX2	chromobox homolog 2 (Pc class homolog, Drosophila)	-0.17	-0.04	0.01	0.21	0.23	0.06	0.07
262	WDR72	WD repeat domain 72	-0.23	-0.10	0.13	0.33	0.29	0.26	0.21
263	ODCA7	cell division cycle associated 7	-0.03	-0.02	0.12	0.05	0.24	0.23	0.17
264	FOXA3	forkhead box A3	0.05	-0.12	0.21	0.08	0.40	0.31	-0.01
265	SPC25	SPC25, NDC80 kinetochore complex component, homolog (S. cerevisiae)	-0.04	0.25	0.25	-0.21	0.02	0.25	0.01
266	BLM	Blom syndrome, RecQ helicase-like	-0.15	0.15	0.30	0.00	0.03	0.20	0.17
267	C11orf82	chromosome 11 open reading frame 82	-0.13	0.25	0.24	-0.12	0.01	0.09	0.19
268	CHRNA5	cholinergic receptor, nicotinic, alpha 5	-0.34	0.41	0.18	-0.07	-0.17	0.12	-0.03
269	GDAP1	ganglioside-induced differentiation-associated protein 1	-0.10	0.30	0.03	-0.20	-0.22	0.04	0.08
270	MTF2	metal response element binding transcription factor 2	-0.01	-0.02	0.04	0.03	-0.10	-0.02	0.17
271	CHST4	carbohydrate (N-acetylglucosamine 6-O) sulfotransferase 4	0.03	-0.02	0.08	-0.01	-0.11	0.06	0.21
272	DNMT3A	DNA (cytosine-5)-methyltransferase 3 alpha	-0.16	0.14	0.04	0.02	-0.09	-0.03	0.21
273	SEPHS1	selenophosphate synthetase 1	-0.09	0.06	0.03	0.03	-0.13	-0.16	-0.05
274	KLHL7	kelch-like 7 (Drosophila)	-0.18	0.01	-0.08	0.16	-0.24	-0.01	0.07
275	D1L	denticleless homolog (Drosophila)	-0.03	0.06	0.22	-0.03	-0.08	0.06	-0.01
276	D1L	denticleless homolog (Drosophila)	0.02	0.06	0.21	-0.07	-0.11	-0.10	-0.24
277	TNNI3	troponin I type 3 (cardiac)	0.23	-0.07	-0.15	-0.16	0.08	0.24	0.07
278	ZNF738	zinc finger protein 738	0.09	0.20	-0.30	-0.29	-0.10	0.08	-0.08
279	MTF2	metal response element binding transcription factor 2	-0.04	-0.25	-0.17	0.29	-0.13	-0.21	-0.28
280	HOMER1	hommer homolog 1 (Drosophila)	-0.09	-0.12	0.22	0.22	-0.08	-0.05	-0.19
281	TACG3	transforming, acidic coiled-coil containing protein 3	0.08	-0.27	-0.12	0.19	-0.19	-0.09	-0.19
282	---	---	-0.06	0.00	-0.07	0.06	-0.41	-0.01	-0.28
283	MCM3	minichromosome maintenance complex component 3	-0.03	0.01	-0.02	0.03	0.00	0.13	-0.26
284	NASP	nuclear autoantigenic sperm protein (histone-binding)	-0.08	0.05	0.06	0.03	-0.01	-0.01	-0.39
285	MRS2	MRS2 magnesium homeostasis factor homolog (S. cerevisiae)	-0.10	0.12	0.08	-0.02	-0.22	0.09	-0.25
286	RFC3	replication factor C (activator 1) 3, 38kDa	0.04	0.08	-0.10	-0.13	0.01	-0.06	-0.34
287	FAM63D	family with sequence similarity 83, member D	0.00	0.01	-0.13	0.00	0.05	0.01	-0.10
288	---	---	0.01	-0.01	-0.34	0.00	-0.09	-0.02	-0.14

289	HOMER1	homer homolog 1 (Drosophila)	0.05	-0.04	-0.16	-0.01	-0.02	-0.16	-0.21
290	PLK4	ipolo-like kinase 4 (Drosophila)	-0.05	0.10	-0.11	-0.06	0.13	-0.21	-0.49
291	BUB1	budding uninhibited by benzimidazoles 1 homolog (yeast)	-0.05	0.13	-0.01	-0.07	0.06	-0.06	-0.32
292	IPW	imprinted in Prader-Willi syndrome (non-protein coding)	0.11	-0.07	0.06	-0.04	0.00	-0.02	-0.46
293	CDT1	Chromatin licensing and DNA replication factor 1	0.01	-0.07	-0.12	0.06	-0.11	-0.08	-0.33
294	FERMT1	fermitin family homolog 1 (Drosophila)	-0.12	0.14	-0.23	-0.02	0.13	-0.44	-0.29
295	STRBP	spermatid perinuclear RNA binding protein	-0.48	0.16	-0.33	0.30	-0.13	-0.17	-0.31
296	FAM124A	family with sequence similarity 124A	-0.43	0.13	0.03	0.29	-0.04	-0.14	-0.08
297	COMMD7	COMM domain containing 7	-0.42	0.04	0.28	0.37	-0.37	0.01	-0.50
298	SYT8	synaptotagmin VI	-0.31	-0.26	-0.03	0.57	0.15	0.13	-0.40
299	CLDN7	claudin 7	0.29	-0.32	0.15	0.03	0.27	0.65	0.31
300	RND2	Rho family GTPase 2	-0.14	-0.12	0.13	0.26	0.28	0.32	0.40
301	AIM1L	absent in melanoma 1-like	-0.06	-0.11	0.29	0.18	0.13	0.53	0.57
302	LOC253842	hypothetical protein LOC253842	-0.10	-0.24	0.09	0.34	0.52	0.62	0.50
303	CDC20	cell division cycle 20 homolog (S. cerevisiae)	0.11	-0.23	0.30	0.12	0.36	0.42	0.44
304	AURKB	aurora kinase B	0.08	-0.41	0.38	0.32	0.29	0.44	0.52
305	OIP5	Opa interacting protein 5	-0.13	-0.08	0.30	0.19	0.38	0.46	0.49
306	LOC100128191	hypothetical protein LOC100128191	0.16	-0.18	0.12	0.02	0.41	0.28	0.36
307	---	---	0.25	-0.31	0.38	0.06	0.02	0.51	0.34
308	RASL11B	RAS-like, family 11, member B	-0.19	0.21	0.42	-0.02	0.15	0.57	0.45
309	GULP1	GULP, engulfment adaptor PTB domain containing 1	-0.33	0.33	0.26	0.00	-0.11	0.14	0.53
310	AP3B2	adaptor-related protein complex 3, beta 2 subunit	0.34	0.24	0.13	-0.58	0.72	0.43	0.65
311	HMG3	high-mobility group box 3	0.47	0.17	0.18	-0.64	0.68	0.96	0.70
312	CXCL5	chemokine (C-X-C motif) ligand 5	-0.15	0.50	0.16	-0.34	0.45	1.02	1.32
313	CXCL5	chemokine (C-X-C motif) ligand 5	0.05	0.16	0.10	-0.21	0.04	0.59	1.06
314	PHF21B	PHD finger protein 21B	-0.04	-0.18	0.27	0.20	1.07	0.58	0.85
315	MND1	meiotic nuclear divisions 1 homolog (S. cerevisiae)	-0.31	0.01	0.37	0.30	0.94	0.44	0.34
316	MLF1IP	MLF1 interacting protein	0.13	-0.18	0.52	0.05	0.83	0.59	0.67
317	MLF1IP	MLF1 interacting protein	0.36	-0.29	0.61	-0.07	0.99	0.68	0.75
318	ZNF93	zinc finger protein 93	-0.08	0.53	-0.18	-0.45	0.51	0.12	0.28
319	KIAA1661	KIAA1661 protein	-0.29	0.64	-0.11	-0.35	0.73	0.71	0.23
320	USP9X	ubiquitin specific peptidase 9, X-linked	0.18	0.09	-0.27	-0.26	0.47	0.81	0.23
321	HIST1H2AM	histone cluster 1, H2am	-0.20	0.48	0.28	-0.28	0.55	-0.03	0.11
322	LOC284242	hypothetical protein LOC284242	-0.35	0.53	0.32	-0.18	0.56	0.48	0.27
323	MDM6	minichromosome maintenance complex component 6	-0.40	0.53	0.44	-0.13	0.55	0.44	0.06
324	---	---	0.01	0.26	0.24	-0.26	0.88	0.42	0.19
325	BPTF	bromodomain PHD finger transcription factor	0.06	0.26	0.59	-0.33	0.36	0.30	0.55
326	C13orf38	chromosome 13 open reading frame 38	-0.67	0.42	0.57	0.25	0.80	0.31	0.83
327	SLC16A1	solute carrier family 16, member 1 (monocarboxylic acid transporter 1)	-0.64	0.37	0.38	0.27	0.41	0.43	0.39
328	NPM3	nucleophosmin/nucleoplasm 3	-0.37	0.28	0.14	0.08	0.72	0.85	0.69
329	C16orf75	chromosome 16 open reading frame 75	-0.46	0.24	0.43	0.22	0.80	0.71	0.58
330	SKA1	spindle and kinetochore associated complex subunit 1	0.14	-0.27	0.72	0.14	0.60	0.56	0.30
331	LOC647946	hypothetical protein LOC647946	-0.28	0.09	0.75	0.19	0.65	0.52	0.47
332	NPF42	neuropeptide FF receptor 2	-0.22	-0.03	0.70	0.26	0.27	0.98	0.65

[illegible]

374	OSBPL10	oxysterol binding protein-like 10	0.30	-0.26	-0.16	-0.05	-0.85	-0.89	-0.41
375	USP28	ubiquitin specific peptidase 28	-0.07	0.02	-0.18	0.04	-0.47	-0.70	-0.82
376	ZNF398	zinc finger protein 398	0.09	0.00	-0.15	-0.09	-0.40	-0.63	-0.72
377	DEPDC1	DEP domain containing 1	-0.09	0.11	0.06	-0.02	-0.33	-0.55	-0.96
378	CENPI	centromere protein 1	0.15	0.12	-0.07	-0.27	-0.55	-0.63	-0.70
379	G14orf106	chromosome 14 open reading frame 106	0.12	0.10	0.04	-0.22	-0.75	-0.62	-0.76
380	HSPA4	heat shock 70kDa protein 4	-0.03	0.13	-0.09	-0.10	-0.45	-0.44	-0.89
381	HAUS6	HAUS augmin-like complex subunit 6	-0.23	0.41	-0.01	-0.19	-0.45	-0.62	-0.82
382	ZNF253	zinc finger protein 253	0.15	0.11	-0.26	-0.27	-0.61	-0.42	-0.66
383	ARRGAP11A	Rho GTPase activating protein 11A	0.26	-0.05	-0.50	-0.21	-0.56	-0.32	-0.87
384	PAP2D	phosphatidic acid phosphatase type 2	0.10	0.11	-0.46	-0.22	-0.42	-0.19	-0.80
385	GULP1	GULP, engulfment adaptor PTB domain containing 1	-0.12	0.04	-0.21	0.08	-0.55	-0.35	-0.34
386	PAICS	phosphoribosylaminimidazole succinocarboxamide synthetase	-0.11	0.17	-0.06	-0.06	-0.46	-0.35	-0.40
387	SMC3	structural maintenance of chromosomes 3	-0.16	0.22	-0.36	-0.07	-0.43	-0.22	-0.21
388	CDYL	chromodomain protein, Y-like	-0.20	0.33	-0.16	-0.13	-0.38	-0.16	-0.45
389	GULP1	GULP, engulfment adaptor PTB domain containing 1	-0.20	0.27	-0.18	-0.07	-0.52	-0.35	-0.46
390	G2E3	G2/M-phase specific E3 ubiquitin ligase	-0.35	0.31	-0.30	0.04	-0.48	-0.27	-0.36
391	MKI67	antigen identified by monoclonal antibody Ki-67	0.00	0.15	-0.43	-0.15	-0.54	-0.49	-0.43
392	TRHDE	thyrotropin-releasing hormone degrading enzyme	-0.10	0.17	-0.42	-0.08	-0.24	-0.38	-0.49
393	IGF2BP3	insulin-like growth factor 2 mRNA binding protein 3	-0.34	0.28	-0.19	0.06	-0.24	-0.21	-0.59
394	HAUS6	HAUS augmin-like complex subunit 6	-0.26	-0.03	-0.11	0.29	-0.32	-0.43	-0.75
395	HSPA4	heat shock 70kDa protein 4	-0.07	-0.06	-0.11	0.13	-0.25	-0.33	-0.53
396	DIAPH3	diaphanous homolog 3 (Drosophila)	-0.13	-0.04	0.00	0.17	-0.30	-0.14	-0.66
397	G4orf21	chromosome 4 open reading frame 21	-0.05	0.03	-0.24	0.02	0.01	-0.26	-0.73
398	MSH6	mutS homolog 6 (E. coli)	0.05	-0.10	0.18	0.05	-0.37	-0.38	-0.68
399	WDHD1	WD repeat and HMG-box DNA binding protein 1	-0.25	0.21	-0.06	0.04	-0.27	-0.31	-0.70
400	KNTG1	kinetochore associated 1	-0.17	0.19	-0.04	-0.02	-0.43	-0.44	-0.47
401	FANCI	Fanconi anemia, complementation group 1	-0.13	0.19	0.12	-0.06	-0.44	-0.50	-0.57
402	ZNF195	zinc finger protein 195	0.02	0.00	-0.24	-0.02	-0.33	-0.16	-0.29
403	KLHL7	kelch-like 7 (Drosophila)	-0.04	-0.06	-0.22	0.10	-0.28	-0.17	-0.24
404	PSIP1	PC4 and SFRS1 interacting protein 1	-0.13	0.15	-0.13	-0.02	-0.28	-0.19	-0.22
405	G18orf54	chromosome 18 open reading frame 54	-0.29	0.23	-0.26	0.05	-0.32	-0.31	-0.31
406	DKC1	diskeratosis congenita 1, dyskerin	0.24	0.00	-0.02	-0.24	-0.17	-0.04	-0.41
407	FLJ32810	Rho-type GTPase-activating protein FLJ32810	0.05	0.04	-0.01	-0.08	-0.20	-0.16	-0.53
408	ZNF43	zinc finger protein 43	0.14	0.22	-0.10	-0.36	-0.50	-0.28	-0.63
409	GNP1	centromere protein 1	0.07	0.18	-0.24	-0.33	-0.23	-0.45	-0.45
410	DEPDC1	DEP domain containing 1	-0.15	0.31	-0.08	-0.16	-0.21	-0.66	-0.66
411	WDR89	WD repeat domain 89	-0.13	0.35	-0.10	-0.22	-0.31	-0.20	-0.53
412	TTF2	transcription termination factor, RNA polymerase II	0.05	0.10	0.07	-0.15	-0.92	-0.12	-0.64
413	ZNF254	zinc finger protein 254	-0.19	0.35	0.07	-0.16	-0.83	-0.27	-0.88
414	QSER1	glutamine and serine rich 1	-0.27	0.65	-0.12	-0.38	-0.83	-0.44	-0.78
415	ZNF675	zinc finger protein 675	-0.28	0.30	-0.26	-0.02	-0.59	-0.41	-0.63
416	ZNF721	zinc finger protein 721	-0.36	0.46	-0.30	-0.10	-0.77	-0.52	-0.81

417	ESCO1	establishment of cohesion 1 homolog 1 (S. cerevisiae)	-0.21	0.31	-0.43	-0.11	-0.61	-0.66	-0.65
418	QSER1	glutamine and serine rich 1	-0.36	0.43	-0.26	-0.07	-0.54	-0.57	-0.73
419	NR5A2	nuclear receptor subfamily 5, group A, member 2	-0.45	0.22	-0.36	0.23	-0.18	-0.56	-0.35
420	TOP2A	topoisomerase (DNA) II alpha 170kDa	-0.20	0.18	-0.15	0.02	-0.58	-0.57	-0.76
421	CHML	choroideremia-like (Rab escort protein 2)	-0.25	0.24	-0.57	0.01	-0.50	-0.70	-0.40
422	ASPM	asp (abnormal spindle) homolog, microcephaly associated (Drosophila)	-0.18	0.19	-0.31	-0.02	-0.58	-0.61	-0.42
423	GTSE1	G-2 and S-phase expressed 1	-0.01	-0.16	-0.35	0.17	-0.40	-0.59	-0.57
424	POLQ	polymerase (DNA directed) theta	0.09	-0.07	-0.25	-0.01	-0.42	-0.63	-0.27
425	HMG2	high mobility group AT-hook 2	0.06	-0.10	-0.16	0.04	-0.42	-0.50	-0.20
426	TSR1	TSR1, 20S rRNA accumulation, homolog (S. cerevisiae)	0.19	-0.29	0.03	0.11	-0.42	-0.36	-0.10
427	XPO5	exportin 5	0.21	-0.19	-0.07	-0.02	-0.41	-0.42	-0.17
428	PAWR	PRKC, apoptosis, WT1, regulator	0.03	0.04	-0.18	-0.07	-0.47	-0.32	-0.39
429	KIF14	kinesin family member 14	0.10	-0.01	-0.03	-0.03	-0.50	-0.36	-0.26
430	ZNF708	zinc finger protein 708	0.04	-0.01	-0.12	-0.04	-0.54	-0.05	-0.19
431	ZNF589	zinc finger protein 589	0.13	-0.06	-0.29	-0.06	-0.38	-0.25	-0.28
432	ZIK1	zinc finger protein interacting with K protein 1 homolog (mouse)	-0.01	0.03	-0.28	-0.02	-0.33	-0.23	-0.29
433	STIL	SCL/TAL 1 interrupting locus	0.16	0.10	-0.21	-0.26	-0.23	-0.53	-0.36
434	CDK6	cyclin-dependent kinase 6	0.08	0.09	-0.28	-0.17	-0.18	-0.69	-0.53
435	TNEM48	transmembrane protein 48	0.00	0.18	-0.02	-0.18	-0.40	-0.38	-0.61
436	ZIK1	zinc finger protein interacting with K protein 1 homolog (mouse)	-0.02	0.17	-0.09	-0.15	-0.40	-0.46	-0.46
437	—	—	0.08	0.11	-0.40	-0.20	-0.41	-0.34	-0.49
438	COL11A1	collagen, type XI, alpha 1	0.08	0.00	-0.24	-0.08	-1.36	-0.66	-0.55
439	COL11A1	collagen, type XI, alpha 1	0.20	-0.03	0.04	-0.17	-1.05	-0.49	-0.12
440	PCDH7	protocadherin 7	-0.19	0.13	-0.07	0.06	-0.92	-0.59	-0.44
441	CCDC18	coiled-coil domain containing 18	-0.22	0.14	-0.43	0.07	-1.05	-0.53	-0.27
442	ESF1	ESF1, nuclear pre-rRNA processing protein, homolog (S. cerevisiae)	-0.24	0.24	-0.26	0.00	-0.75	-0.64	-0.51
443	AP5	apoptosis inhibitor 5	0.01	0.12	-0.18	-0.14	-0.88	-0.61	-0.28
444	SGOL2	shugoshin-like 2 (S. pombe)	-0.21	-0.02	-0.18	0.23	-0.76	-0.43	-0.19
445	SMC3	structural maintenance of chromosomes 3	-0.31	0.06	-0.44	0.24	-0.54	0.02	-0.32
446	ESCO2	establishment of cohesion 1 homolog 2 (S. cerevisiae)	-0.32	0.28	-0.36	0.03	-0.55	0.01	0.05
447	—	—	-0.13	0.11	-0.36	0.03	-0.55	0.33	-0.37
448	BRCA2	breast cancer 2, early onset	-0.33	0.33	-0.59	0.00	-0.55	-0.10	-0.49
449	ESCO1	establishment of cohesion 1 homolog 1 (S. cerevisiae)	-0.55	0.46	-0.43	0.09	-0.38	0.00	-0.11
450	TNEM132B	transmembrane protein 132B	-0.20	0.59	-0.37	-0.39	0.07	-0.35	-0.52
451	C18orf54	chromosome 18 open reading frame 54	-0.53	0.58	-0.32	-0.03	-0.11	-0.14	-0.49
452	FANCB	Fanconi anemia, complementation group B	0.26	0.30	-0.15	-0.57	-0.41	-0.56	-0.37
453	ZNF107	zinc finger protein 107	0.14	0.24	-0.23	-0.38	-0.57	-0.71	-0.43
454	G3BP2	GTPase activating protein, (SH3 domain) binding protein 2	0.07	0.44	-0.14	-0.50	-0.71	-0.87	-0.80
455	IGF2BP3	insulin-like growth factor 2 mRNA binding protein 3	-0.02	0.38	-0.15	-0.36	-0.74	-0.72	-1.02
456	MCM4	minichromosome maintenance complex component 4	0.00	0.07	0.36	-0.07	-0.63	-0.58	-1.23
457	—	—	0.05	0.15	0.00	-0.20	-0.68	-0.76	-1.22

458	CXorf15	chromosome X open reading frame 15	0.25	0.56	0.20	-0.81	-0.58	-0.41	-0.84
459	ZNF589	zinc finger protein 589	0.12	-0.12	-0.10	0.00	-0.48	-0.50	-0.88
460	ZNF589	zinc finger protein 589	0.14	-0.06	-0.27	-0.07	-0.52	-0.42	-0.81
461	---	---	0.17	0.04	-0.14	-0.21	-0.57	-0.53	-1.13
462	PLK1	polo-like kinase 1 (Drosophila)	0.02	-0.15	-0.01	0.12	-0.60	-0.51	-1.01
463	KLRG2	killer cell lectin-like receptor subfamily G, member 2	-0.13	-0.06	-0.43	0.19	-0.63	-0.40	-1.10
464	TEAD2	TEA domain family member 2	0.31	-0.35	0.19	0.04	-0.28	-0.17	-1.16
465	KIF20B	kinesin family member 20B	-0.41	0.46	-0.46	-0.04	-1.09	-0.79	-0.26
466	C12orf35	chromosome 12 open reading frame 35	-0.22	0.20	-0.39	0.03	-1.13	-0.94	-0.86
467	ZNF680	zinc finger protein 680	-0.22	0.35	-0.72	-0.14	-0.93	-0.86	-0.74
468	ACTN3	actinin, alpha 3	0.38	-0.59	-0.55	0.21	-0.22	-0.62	-0.38
469	CENPJ	centromere protein J	0.47	-0.46	-0.46	-0.01	-0.04	-0.34	-1.00
470	SKP2	S-phase kinase-associated protein 2 (p45)	0.46	0.40	0.70	-0.88	-0.23	-0.32	-0.80
471	DCP2	DCP2 decapping enzyme homolog (S. cerevisiae)	0.25	0.42	0.13	-0.67	0.13	-0.61	-0.88
472	GER1	cerberus 1, cysteine knot superfamily, homolog (Xenopus laevis)	-0.38	-0.65	-0.21	1.02	0.64	-0.60	-0.22
473	VWDE	von Willebrand factor D and EGF domains	0.15	-0.72	0.49	0.57	0.70	-0.47	-0.53
474	---	---	0.51	-0.47	-0.91	-0.04	0.59	-0.24	-0.59
475	CHM	choroideremia (Rab escort protein 1)	-0.03	0.60	0.80	-0.57	0.73	-0.24	-0.58
476	C18orf54	chromosome 18 open reading frame 54	-0.26	0.06	-0.98	0.20	-0.25	-1.80	-1.18
477	ZNF92	zinc finger protein 92	-0.13	-0.30	0.30	0.43	-0.59	-0.75	-0.55
478	PHF3	PHD finger protein 3	0.06	-0.27	-0.23	0.21	-1.12	-0.93	-0.91
479	ZNF644	zinc finger protein 644	-0.07	0.61	0.00	-0.55	-1.05	-0.83	-0.92
480	ANKRD32	ankyrin repeat domain 32	-0.02	0.10	0.19	-0.08	-0.55	-0.52	-1.82
481	TPP2	tripeptidyl peptidase II	-0.08	0.07	-0.12	0.01	-0.57	-0.78	-1.05
482	HSPH1	heat shock 105kDa/110kDa protein 1	0.10	0.07	0.04	-0.17	-0.64	-0.74	-1.09
483	MATR3	matrin 3	-0.21	0.18	-0.03	0.03	-0.62	-0.62	-1.22
484	LOC100129064 /// LOC100131360 /// LOC100131868 /// PPP4R2	hypothetical LOC100129064 /// similar to protein phosphatase 4 regulatory subunit 2 /// similar to PPP4R2 protein /// protein phosphatase 4, regulatory subunit 2	0.03	0.11	0.00	-0.15	-0.47	-0.62	-1.36
485	CNOT1	CCR4-NOT transcription complex, subunit 1	0.14	-0.13	-0.12	-0.01	-0.84	-1.12	-1.37
486	PRPF4B	PRP4 pre-mRNA processing factor 4 homolog B (yeast)	0.05	0.12	-0.10	-0.17	-0.98	-0.87	-1.11
487	NUP133	nucleoporin 133kDa	0.10	0.17	-0.24	-0.27	-0.83	-1.33	-1.38
488	LARS	leucyl-tRNA synthetase	-0.23	0.20	-0.19	0.04	-0.84	-1.02	-1.30
489	BCLAF1	BCL2-associated transcription factor 1	-0.02	0.24	-0.26	-0.22	-1.37	-1.13	-1.38
490	BCLAF1	BCL2-associated transcription factor 1	0.04	0.11	-0.16	-0.16	-1.33	-1.33	-1.20
491	DHX9	DEAH (Asp-Glu-Ala-His) box polypeptide 9	0.09	0.10	0.27	-0.19	-0.96	-1.00	-1.45
492	DHX9	DEAH (Asp-Glu-Ala-His) box polypeptide 9	-0.14	0.31	-0.02	-0.18	-1.03	-1.10	-1.35
493	SUPT16H	suppressor of Ty 16 homolog (S. cerevisiae)	-0.09	0.28	0.04	-0.19	-1.21	-1.15	-1.61
494	RBK1	RB-associated KRAB zinc finger	-0.28	0.30	-0.56	-0.02	-1.23	-0.66	-1.07
495	ERH1	exoribonuclease 1	-0.55	0.53	-0.88	0.02	-0.94	-0.69	-1.23
496	USP25	ubiquitin specific peptidase 25	-0.22	-0.04	-0.14	0.27	-0.60	-0.71	-1.44
497	EPRS	glutamyl-prolyl-tRNA synthetase	-0.14	0.26	-0.03	-0.12	-0.77	-0.89	-1.36
498	RECQL	RecQ protein-like (DNA helicase Q1-like)	-0.03	-0.11	-0.54	0.14	-0.97	-0.94	-1.16

	GPR176	G protein-coupled receptor 176	0.01	0.12	0.38	-0.13	-0.90	-0.74	-1.05
499	SCD	stearoyl-CoA desaturase (delta-9-desaturase)	0.33	0.05	-0.02	-0.38	-1.00	-0.95	-1.05
500	SCD	stearoyl-CoA desaturase (delta-9-desaturase)	0.13	0.16	0.00	-0.29	-1.06	-1.09	-0.98
501	FAM126A	family with sequence similarity 126, member A	0.29	0.27	0.11	-0.56	-1.11	-0.87	-1.16
502	MIPOL1	mirror-image polydactyl 1	0.36	0.03	-0.57	-0.38	-0.40	-0.34	-0.68
503	GEN1	Gen homolog 1, endonuclease (Drosophila)	0.10	0.29	-0.39	-0.39	-0.40	-0.26	-0.59
504	UBP3A	ubiquitin protein ligase E3A	0.37	0.19	-0.42	-0.56	-1.09	-0.85	-0.70
505	FAR1	fatty acyl CoA reductase 1	0.15	-0.12	-0.50	-0.03	-0.76	-0.56	-1.24
506	ZNF84	zinc finger protein 84	0.04	0.07	-0.48	-0.11	-0.56	-0.57	-0.49
507	DNAJC10	DNAJ (Hsp40) homolog, subfamily C, member 10	0.05	0.10	-0.30	-0.15	-0.89	-0.55	-0.87
508	IGF2BP2	insulin-like growth factor 2 mRNA binding protein 2	0.23	0.05	-0.29	-0.29	-0.50	-0.62	-0.93
509	RBK3	RB-associated KRAB zinc finger	0.05	0.35	-0.53	-0.41	-0.72	-0.58	-1.11
510	LRRIQ3	leucine-rich repeats and IQ motif containing 3	0.04	0.02	-0.46	-0.06	-1.00	-0.02	-0.91
511	ZNF569	zinc finger protein 569	-0.08	-0.11	-0.06	0.18	-0.41	-0.35	-0.44
512	TRIM37	tripartite motif-containing 37	0.04	-0.04	-0.07	-0.01	-0.29	-0.10	-0.87
513	MTF1	methyltetrahydrofolate dehydrogenase (NADP+ dependent) 1-like	0.07	-0.33	-0.11	0.28	-0.10	-0.04	-0.49
514	PRIM2	primase, DNA, polypeptide 2 (58kDa)	-0.06	0.18	-0.23	-0.12	-0.17	-0.44	-0.50
515	NVL	nuclear VCP-like	-0.17	0.21	-0.24	-0.04	0.00	-0.53	-0.39
516	RPAP3	RNA polymerase II associated protein 3	-0.15	0.29	0.03	-0.15	-0.12	-0.22	-0.41
517	PRIM2	primase, DNA, polypeptide 2 (58kDa)	-0.01	0.16	0.05	-0.15	-0.26	-0.28	-0.53
518	ATAD2	ATPase family, AAA domain containing 2	-0.25	0.29	0.20	-0.03	-0.36	-0.43	-0.37
519	PRIM2	primase, DNA, polypeptide 2 (58kDa)	0.07	0.03	0.07	-0.10	-0.20	-0.39	-0.58
520	BCAT1	branched chain aminotransferase 1, cytosolic	0.01	0.03	0.12	-0.05	-0.42	-0.55	-0.42
521	ASCC3	activating signal co-receptor 1 complex subunit 3	0.16	-0.02	0.03	-0.15	-0.18	-0.54	-0.31
522	MED20	mediator complex subunit 20	0.28	-0.10	-0.18	-0.17	-0.30	-0.23	-0.58
523	BCAT1	branched chain aminotransferase 1, cytosolic	0.30	-0.06	0.11	-0.24	-0.56	-0.55	-0.42
524	ZNF146	zinc finger protein 146	-0.06	0.10	0.17	-0.04	-0.80	-0.58	-0.71
525	RNA	RNA binding motif protein 26	0.10	-0.03	-0.13	-0.07	-0.37	-0.60	-0.75
526	ESF1	ESF1, nuclear pre-rRNA processing protein, homolog (S. cerevisiae)	0.23	-0.18	-0.05	-0.04	-0.60	-0.80	-0.69
527	ANLN	anillin, actin binding protein	0.10	0.04	-0.05	-0.14	-0.48	-0.49	-0.74
528	HMGR	3-hydroxy-3-methylglutaryl-Coenzyme A reductase	0.00	-0.01	-0.21	0.01	-0.48	-0.62	-0.70
529	LARP4	La ribonucleoprotein domain family, member 4	-0.02	-0.02	-0.33	0.03	-0.42	-0.43	-0.66
530	SCLE	squalene epoxidase	0.03	-0.01	-0.34	-0.02	-0.53	-0.59	-0.85
531	G2E3	G2/M-phase specific E3 ubiquitin ligase	-0.04	0.28	-0.29	-0.24	-0.47	-0.49	-0.62
532	GART	phosphoribosylglycinamide formyltransferase, phosphoribosylglycinamide synthetase, phosphoribosylaminoimidazole synthetase	0.17	-0.10	-0.06	-0.06	-0.33	-0.40	-0.94
533	VCAN	versican	0.05	0.13	-0.21	-0.18	-0.80	-0.81	-0.64
534	VCAN	versican	0.00	0.19	-0.34	-0.18	-0.84	-0.83	-0.87
535	REF1	RAP1 interacting factor homolog (yeast)	0.15	-0.04	-0.03	-0.10	-0.78	-0.76	-0.66
536	SOC34	suppressor of cytokine signaling 4	0.17	0.27	-0.25	-0.44	-0.77	-0.61	-0.40
537	PHIP	pleckstrin homology domain interacting protein	0.03	0.18	-0.41	-0.21	-0.77	-0.54	-0.16
538	USO1	USO1 homolog, vesicle docking protein (yeast)	0.04	0.00	-0.25	-0.04	-0.65	-0.61	-0.48
539	SR140	U2-associated SR140 protein	-0.01	0.05	-0.18	-0.04	-0.58	-0.49	-0.47

541	VCAN	versican	-0.03	0.16	-0.15	-0.13	-0.54	-0.52	-0.37
542	VCAN	SWI/ SNF-related, matrix-associated actin-dependent regulator of chromatin, subfamily a, containing DEAD/H box 1	-0.05	0.10	-0.17	-0.05	-0.41	-0.41	-0.37
543	SMARCA1		-0.02	0.18	-0.12	-0.15	-0.36	-0.36	-0.22
544	G2E3	G2/M-phase specific E3 ubiquitin ligase	-0.20	0.15	-0.21	0.05	-0.50	-0.33	-0.46
545	PRPF40A	PRP40 pre-mRNA processing factor 40 homolog A (S. cerevisiae)	-0.09	-0.03	-0.23	0.12	-0.45	-0.31	-0.30
546	PRPF40A	PRP40 pre-mRNA processing factor 40 homolog A (S. cerevisiae)	0.03	0.09	-0.31	-0.13	-0.61	-0.10	-0.01
547	RNGTT	RNA guanylyltransferase and 5'-phosphatase	0.07	-0.11	-0.36	0.04	-0.33	-0.47	-0.16
548	ARNTL2	aryl hydrocarbon receptor nuclear translocator-like 2	0.18	-0.09	-0.43	-0.09	-0.34	-0.27	-0.12
549	SGOL2	slugosin-like 2 (S. pombe)	0.11	0.04	-0.29	-0.15	-0.44	-0.31	-0.13
550	ZNF367	zinc finger protein 367	0.15	0.03	-0.32	-0.19	-0.48	-0.31	-0.14
551	PPPDE1	PPPDE peptidase domain containing 1	0.33	-0.09	0.09	-0.24	-0.12	-0.78	-0.99
552	UCMA	upper zone of growth plate and cartilage matrix associated	0.43	-0.08	-0.29	-0.35	-0.50	-0.56	-1.05
553	SPRED1	sprouty-related, EVH1 domain containing 1	0.69	-0.02	0.07	-0.68	-0.68	-0.60	-0.62
554	KPNB1	karyopherin (importin) beta 1	-0.23	-0.02	-0.94	0.25	-0.05	-0.29	-0.81
555	ZNF300	zinc finger protein 300	-0.11	0.06	-0.59	0.04	-0.19	-0.65	-1.05
556	TMT03	transmembrane and tetratricopeptide repeat containing 3	-0.46	-0.16	-0.30	0.62	-0.68	-0.36	-0.55
557	CCDC88A	coiled-coil domain containing 88A	-0.41	-0.27	-0.11	0.68	-0.58	-0.74	-0.37
558	CCDC18	coiled-coil domain containing 18	-0.87	0.18	0.09	0.69	-0.67	-0.65	-0.54
559	LAMA1	laminin, alpha 1	-0.44	0.02	-0.41	0.42	-0.34	-0.39	-0.23
560	LOC169834	hypothetical protein LOC169834	-0.68	0.12	-0.38	0.56	-0.33	-0.14	-0.56
561	LMCD1	LM and cysteine-rich domains 1	-0.06	-0.29	-0.29	0.36	-0.61	-0.49	0.36
562	ZNF638	zinc finger protein 638	-0.03	-0.08	0.04	0.11	-0.49	-0.43	-0.73
563	FGF2	fibroblast growth factor 2 (basic)	0.32	-0.20	-0.20	-0.12	-0.23	-0.32	-0.55
564	KIAA1009	KIAA1009	-0.08	-0.10	0.13	0.18	-0.60	-0.29	-0.04
565	RAI14	retinoic acid induced 14	-0.05	-0.09	-0.10	0.14	-0.61	-0.20	-0.07
566	ASCC3	activating signal cointegrator 1 complex subunit 3	-0.06	-0.03	-0.28	0.09	-0.45	-0.39	-0.34
567	EIF5B	eukaryotic translation initiation factor 5B	-0.18	-0.13	-0.34	0.31	-0.23	-0.01	-0.34
568	---	---	0.09	-0.41	-0.50	0.32	-0.05	-0.19	-0.37
569	TYMS	thymidylate synthetase	-0.23	0.09	-0.46	0.14	-0.26	-0.13	-0.28
570	TYMS	thymidylate synthetase	-0.07	0.10	-0.22	-0.04	-0.24	-0.20	-0.02
571	SIX4	SIX homeobox 4	-0.08	0.24	-0.44	-0.16	-0.18	-0.08	-0.04
572	TPR	translocated promoter region (to activated MET oncogene)	-0.45	0.44	-0.40	0.01	-0.34	-0.33	-0.30
573	KIAA1586	KIAA1586	-0.23	0.37	-0.23	-0.14	-0.48	-0.53	-0.12
574	SYT14	synaptotagmin XIV	-0.11	0.52	0.29	-0.41	-0.48	0.00	0.03
575	RAD18	RAD18 homolog (S. cerevisiae)	-0.09	0.29	-0.04	-0.20	-0.27	-0.38	0.19
576	CWC22	CWC22 spliceosome-associated protein homolog (S. cerevisiae)	-0.14	0.36	0.20	-0.22	-0.33	-0.27	0.04
577	GJA1	gap junction protein, alpha 1, 43kDa	0.03	0.01	-0.09	-0.04	-0.05	-0.09	-0.16
578	MRE11A	MRE11 meiotic recombination 11 homolog A (S. cerevisiae)	-0.02	0.03	-0.04	-0.01	-0.19	-0.06	-0.16

579	RBAP6	retinoblastoma binding protein 6	-0.06	0.06	-0.30	-0.01	-0.20	-0.10	-0.10
580	RRAS2	related RAS viral (v-ras) oncogene homolog 2	0.14	-0.11	-0.03	-0.03	-0.22	-0.12	-0.29
581	RPAP3	RNA polymerase II associated protein 3	0.13	-0.03	-0.10	-0.10	-0.37	-0.09	-0.31
582	USO1	USO1 homolog, vesicle docking protein (yeast)	-0.15	0.05	0.05	0.09	-0.36	-0.17	-0.13
583	ZMYM1	zinc finger, MYM-type 1	-0.13	0.13	0.24	0.01	-0.08	-0.08	0.07
584	—	—	-0.08	0.01	0.06	0.06	-0.16	0.05	0.11
585	ZNF268	zinc finger protein 268	-0.17	0.13	0.07	0.04	-0.26	-0.05	-0.05
586	GPR176	G protein-coupled receptor 176	-0.13	0.14	0.11	-0.01	-0.19	-0.07	0.02
587	ELOVL4	elongation of very long chain fatty acids (FEN1/Elo2, SUR4/Elo3, yeast)-like 4	-0.26	0.17	0.09	0.08	-0.05	-0.08	-0.20
588	BCAT1	branched chain aminotransferase 1, cytosolic	-0.21	0.15	-0.07	0.06	-0.23	-0.21	-0.08
589	BCAT1	branched chain aminotransferase 1, cytosolic	-0.16	0.17	-0.02	-0.01	-0.16	-0.29	-0.11
590	PCG_2024410 /// RPE	pcrPE /// ribulose-5-phosphate-3-epimerase	-0.04	0.26	-0.04	-0.22	-0.12	-0.01	-0.05
591	SHCBP1	SHC SH2-domain binding protein 1	-0.11	0.05	0.05	0.06	0.00	-0.30	-0.30
592	IWS1	IWS1 homolog (S. cerevisiae)	-0.19	-0.03	0.20	0.20	-0.06	-0.18	-0.25
593	RAB34	RAB34, member RAS oncogene family	0.11	-0.11	0.06	0.00	-0.18	-0.19	0.13
594	RAB34	RAB34, member RAS oncogene family	0.03	-0.08	0.12	0.05	-0.11	-0.06	0.27
595	MTFHD1L	methylenetetrahydrofolate dehydrogenase (NADP+-dependent) 1-like	-0.08	-0.10	0.14	0.18	0.15	-0.08	-0.05
596	CDC5L	CDC5 cell division cycle 5-like (S. pombe)	0.08	0.12	0.20	-0.19	0.08	0.03	-0.26
597	MPHOSPH10	M-phase phosphoprotein 10 (U3 small nucleolar ribonucleoprotein)	0.12	-0.08	0.11	-0.04	-0.05	0.20	-0.04
598	CTSC	cathepsin C	0.20	-0.12	0.12	-0.08	-0.10	0.00	-0.11
599	CDC39	coiled-coil domain containing 99	-0.03	0.02	0.15	0.01	0.04	0.04	-0.08
600	REBP6	retinoblastoma binding protein 6	0.26	-0.25	-0.10	0.00	-0.16	-0.11	-0.08
601	MAGED4 /// MAGED4B	melanoma antigen family D, 4 /// melanoma antigen family D, 4B	0.29	-0.34	-0.08	0.05	-0.21	-0.06	0.08
602	MAGED4 /// MAGED4B	melanoma antigen family D, 4 /// melanoma antigen family D, 4B	0.26	-0.51	-0.18	0.24	-0.14	0.08	-0.07
603	SMARCA1	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 1	0.10	0.35	0.36	-0.45	0.12	0.06	-0.16
604	HIST1H2AG	histone cluster 1, H2ag	0.24	-0.03	0.44	-0.21	0.51	-0.15	-0.19
605	PSAT1	phosphoserine aminotransferase 1	0.17	-0.15	0.25	-0.01	0.24	-0.20	-0.18
606	PSAT1	phosphoserine aminotransferase 1	0.07	-0.12	0.04	0.05	0.29	-0.11	-0.26
607	GABPA	GA binding protein transcription factor, alpha subunit 80kDa	0.11	0.29	0.17	-0.40	-0.52	-0.15	-0.59
608	G10orf28	chromosome 10 open reading frame 28	0.09	0.31	0.21	-0.41	-0.44	-0.53	-0.82
609	RRAS2	related RAS viral (v-ras) oncogene homolog 2	0.15	0.09	-0.06	-0.25	-0.38	-0.33	-0.34
610	UBA6	ubiquitin-like modifier activating enzyme 6	0.24	0.06	0.12	-0.30	-0.37	-0.40	-0.40
611	FAM126A	family with sequence similarity 126, member A	-0.11	0.33	0.17	-0.22	-0.30	-0.08	-0.15
612	ALKBH8	alkB, alkylator repair homolog 8 (E. coli)	-0.11	0.23	0.33	-0.12	-0.18	-0.16	-0.39
613	DIS3	DIS3 mitotic control homolog (S. cerevisiae)	0.07	0.24	0.07	-0.31	-0.24	-0.11	-0.35
614	FAM126A	family with sequence similarity 126, member A	-0.06	0.27	0.21	-0.21	-0.54	-0.28	-0.50
615	TFAP2C	transcription factor AP-2 gamma (activating enhancer	0.06	-0.34	-0.04	0.28	0.08	-0.02	-0.08

616	SERPINH1	binding protein 2 gamma)	0.23	-0.28	-0.05	0.05	-0.11	-0.15	-0.21
617	MFAP2	serpin, peptidase inhibitor, clade H (heat shock protein 47), member 1, (collagen binding protein 1)	0.20	-0.42	0.32	0.22	-0.06	0.08	0.37
618	PCNXL2	microfibrillar-associated protein 2	-0.13	-0.12	0.05	0.26	-0.13	0.13	0.13
619	—	pecanex-like 2 (<i>Drosophila</i>)	-0.05	-0.20	-0.07	0.25	0.11	-0.03	0.12
620	FAM175A	family with sequence similarity 175, member A	-0.31	-0.31	0.18	0.30	0.12	0.09	-0.46
621	PARS	arginyl-tRNA synthetase	-0.04	0.19	0.01	-0.15	0.20	0.16	0.07
622	PBK	PDZ binding kinase	-0.11	0.34	-0.17	-0.23	0.09	0.03	0.02
623	GFPT2	glutamine-fructose-6-phosphate transaminase 2	-0.13	0.12	0.18	0.01	0.01	0.30	0.15
624	RPL22L1	ribosomal protein L22-like 1	-0.23	0.11	0.18	0.12	0.05	0.27	0.20
625	KDELC1	KDEL (Lys-Asp-Glu-Leu) containing 1	-0.16	0.28	0.16	-0.12	0.45	0.33	0.07
626	basocucin 2	—	-0.17	0.12	0.11	0.05	0.52	0.33	0.02
627	TNPO1	transporin 1	0.18	-0.06	0.21	-0.12	0.04	0.15	0.41
628	—	—	0.04	0.06	0.32	-0.10	0.23	0.12	0.31
629	MGC45800	hypothetical LOC90768	0.10	0.11	-0.15	-0.22	0.71	0.01	0.29
630	RGS17	regulator of G-protein signaling 17	-0.20	-0.07	0.41	0.27	0.39	0.44	0.80
631	USP45	ubiquitin specific peptidase 45	-0.20	0.01	0.27	0.19	0.28	0.56	0.47
632	PHF19	PHD finger protein 19	-0.16	-0.19	0.35	0.20	0.36	0.47	0.47
633	GDF11	growth differentiation factor 11	0.47	-0.24	-0.62	-0.23	-0.22	-0.30	0.02
634	CABYR	calcium binding tyrosine (Y)-phosphorylation regulated	0.46	-0.35	-0.41	-0.11	0.28	-0.09	0.13
635	AMMEOR1	Alport syndrome, mental retardation, midface hypoplasia and elliptocytosis chromosomal region gene 1	0.04	0.55	0.23	-0.80	0.11	-0.03	-0.32
636	MUDENG	MU-2/APIM2 domain containing, death-inducing	0.15	0.35	-0.09	-0.51	-0.14	-0.14	-0.21
637	C4orf46	chromosome 4 open reading frame 46	0.14	0.27	0.09	-0.41	0.47	-0.09	-0.35
638	SMARCA5	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 5	-0.31	0.41	-0.29	-0.10	0.33	-0.17	-0.66
639	TWISTB	TWIST neighbor	-0.29	0.41	0.02	-0.13	0.23	-0.27	-0.65
640	ATAD2	ATPase family, AAA domain containing 2	-0.35	0.52	-0.23	-0.16	-0.07	-0.11	-0.50
641	—	—	-0.49	0.69	-0.38	-0.20	-0.08	-0.25	-0.48
642	TK1	thymidine kinase 1, soluble	0.48	-0.31	-0.02	-0.17	0.25	0.21	0.57
643	ST8SIA3	ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 3	0.46	-0.42	0.11	-0.04	0.11	0.57	0.61
644	CRYGD	crystallin, gamma D	0.50	-0.24	0.15	-0.26	0.05	0.22	0.73
645	CDK3	cyclin-dependent kinase inhibitor 3	0.20	-0.17	0.36	-0.03	0.19	0.28	0.48
646	CDKN3	cyclin-dependent kinase inhibitor 3	0.21	-0.18	0.22	-0.03	-0.03	0.14	0.52
647	RG8MTD1	RNA (guanine-9-) methyltransferase domain containing 1	0.17	0.09	0.04	-0.26	-0.01	0.27	0.34
648	SNX5	sorting nexin 5	0.11	0.11	0.15	-0.22	-0.03	0.28	0.32
649	NUFIP1	nuclear fragile X mental retardation protein interacting protein 1	-0.06	-0.19	0.16	0.25	0.30	0.29	0.41
650	FSD1	fibronectin type III and SPRY domain containing 1	0.09	-0.34	0.01	0.25	0.11	0.26	0.34
651	PIF1	PIF1 5'-to-3' DNA helicase homolog (S. cerevisiae)	0.04	-0.24	-0.08	0.20	0.20	0.19	0.30
652	DNAH14	dynlin, axonemal, heavy chain 14	0.21	-0.33	0.30	0.13	0.11	0.22	0.20
653	SYNCRIP	synapto-agmin binding, cytoplasmic RNA interacting protein	-0.18	0.39	-0.01	-0.22	-0.02	0.01	0.02

854	GLMN	glomulin, FKBP associated protein	-0.14	0.35	0.09	-0.21	0.05	0.15	0.31
855	ORC4L	origin recognition complex, subunit 4-like (yeast)	0.04	0.27	0.23	-0.31	0.14	0.03	0.06
856	AMMECR1	Alport syndrome, mental retardation, midface hypoplasia and elliptocytosis chromosomal region gene 1	0.05	0.33	0.15	-0.38	0.28	0.16	0.21
857	BCCIP	BRCA2 and CDKN1A interacting protein	0.03	0.29	0.01	-0.32	0.31	0.07	0.04
858	Glorf112	chromosome 1 open reading frame 112	-0.22	0.39	0.20	-0.17	0.27	0.06	0.02
859	DBC1	deleted in bladder cancer 1	-0.24	0.13	0.15	0.11	0.09	0.01	0.37
860	HAUS1	HAUS augmin-like complex, subunit 1	-0.30	0.24	-0.05	0.06	0.00	0.04	0.25
861	—	—	-0.18	0.06	-0.03	0.12	0.30	0.18	0.27
862	DMKN	dermokine	-0.19	0.14	0.37	0.05	0.21	0.16	0.40
863	EXOSC8	exosome component 8	-0.06	0.07	0.09	-0.01	0.82	0.45	0.10
864	LMNB2	lamin B2	-0.11	-0.11	0.09	0.21	0.56	0.38	0.27
865	NARG1	NMDA receptor regulated 1	-0.02	-0.01	0.01	0.03	0.61	0.20	0.20
866	TRIP13	thyroid hormone receptor interactor 13	0.05	0.02	0.36	-0.06	0.24	0.39	0.15
867	PAK1IP1	PAK1 interacting protein 1	0.10	0.11	0.26	-0.22	0.10	0.32	0.34
868	TIPIN	TIMELESS interacting protein	0.12	0.01	0.26	-0.13	0.34	0.38	0.38
869	MGC11082	hypothetical LOC84777	0.20	0.21	0.21	-0.41	0.19	0.33	0.32
870	UHRF1	ubiquitin-like with PHD and ring finger domains 1	0.18	0.16	0.33	-0.34	0.19	0.30	0.12
871	G1orf88	chromosome 16 open reading frame 88	-0.08	0.10	0.25	-0.02	0.35	0.32	0.11
872	KIF20A	kinesin family member 20A	0.01	0.07	0.35	-0.07	0.34	0.13	0.11
873	CENPQ	centromere protein Q	0.06	0.02	0.15	-0.07	0.20	0.40	0.26
874	GABPB1	GA binding protein transcription factor, beta subunit 1	-0.13	0.26	0.21	-0.13	0.32	0.27	0.27
875	FBXO5	F-box protein 5	-0.01	0.28	0.24	-0.27	0.34	0.28	0.16
876	EXOSC3	exosome component 3	-0.05	0.17	0.31	-0.12	0.45	0.51	0.48
877	MRPS12	mitochondrial ribosomal protein S12	-0.25	0.34	0.07	-0.09	-0.16	0.28	0.68
878	CENPM	centromere protein M	0.06	-0.04	0.15	-0.02	-0.30	0.15	0.69
879	SPC24	SPC24, NDC80 kinetochore complex component, homolog (S. cerevisiae)	-0.14	0.38	0.00	-0.24	-0.22	-0.20	0.41
880	GTSE1	G-2 and S-phase expressed 1	-0.16	-0.25	-0.08	0.42	0.42	-0.01	-0.24
881	AEN	apoptosis enhancing nuclease	-0.10	-0.14	-0.34	0.24	0.01	-0.12	-0.21
882	NUDT1	nucleoside diphosphate linked moiety X-type motif 1	-0.14	0.03	-0.45	0.11	0.12	0.21	0.25
883	MAP9	microtubule-associated protein 9	-0.17	0.16	-0.48	0.01	0.11	-0.02	0.06
884	FAM155A	family with sequence similarity 155, member A	-0.44	0.01	-0.05	0.43	-0.20	0.33	-0.06
885	KIAA1524	KIAA1524	0.31	-0.18	0.18	-0.13	0.16	0.08	-0.14
886	CHAF1B	chromatin assembly factor 1, subunit B (p60)	0.17	0.00	0.32	-0.18	0.28	0.00	-0.07
887	FGD6	FYVE, RhoGEF and PH domain containing 6	0.11	-0.04	0.32	-0.07	-0.10	0.31	-0.07
888	TAF5L	TAF5-like RNA polymerase II, p300/CBP-associated factor (PCAF)-associated factor, 65kDa	0.01	0.02	0.13	-0.04	0.20	-0.10	0.14
889	TGIF1	TGFB-induced factor homeobox 1	0.10	0.01	0.06	-0.11	0.03	0.08	0.16
890	MELK	maternal embryonic leucine zipper kinase	0.08	0.09	0.03	-0.16	0.08	0.11	0.15
891	DDX21	DEAD (Asp-Glu-Ala-Asp) box polypeptide 21	0.00	0.06	-0.03	-0.06	0.04	0.15	0.10
892	PAOS	phosphoribosylaminimidazole carboxylase, phosphoribosylaminimidazole succinocarboxamide synthetase	0.01	-0.08	0.00	0.08	0.08	-0.02	0.03
893	CENPA	centromere protein A	0.12	0.00	-0.15	-0.12	0.10	0.02	0.11

894	CDCA3	cell division cycle associated 3	0.11	-0.09	-0.16	-0.02	-0.01	-0.05	0.02
895	CEP78	centrosomal protein 78kDa	0.00	0.03	0.04	-0.04	0.15	-0.06	-0.09
896	HDAC2	histone deacetylase 2	-0.03	-0.02	0.14	0.06	0.12	0.09	-0.19
897	ZNF281	zinc finger protein 281	-0.03	-0.02	-0.04	0.05	0.00	-0.11	-0.19
898	RUVBL1	RuvB-like 1 (E. coli)	-0.12	0.16	0.01	-0.05	0.14	0.14	-0.03
899	NUPI07	nucleoporin 107kDa	-0.09	0.06	0.08	0.03	0.03	0.01	0.04
900	ZWILCH	Zwilch, kinetochore associated, homolog (Drosophila)	-0.13	0.12	0.06	0.01	-0.02	0.06	0.02
901	VGAN	version	-0.06	0.08	-0.24	-0.02	-0.10	-0.08	0.00
902	SKA3	spindle and kinetochore associated complex subunit 3	0.01	0.02	-0.17	-0.03	0.04	-0.02	-0.19
903	GULP1	GULP, engulfment adaptor PIB domain containing 1	0.01	-0.16	-0.06	0.15	-0.03	0.17	-0.04
904	TRIM59	tripartite motif-containing 59	0.10	-0.25	-0.17	0.15	-0.09	-0.03	-0.05
905	DIAPH3	diaphanous homolog 3 (Drosophila)	0.12	-0.09	0.00	-0.03	-0.09	-0.06	0.01
906	ZNF215	zinc finger protein 215	0.12	-0.06	0.27	-0.06	-0.22	-0.05	0.04
907	CENPO	centromere protein O	-0.11	0.14	0.34	-0.03	-0.02	-0.15	0.09
908	KIAA0020		0.05	0.25	-0.03	-0.30	-0.22	0.01	0.02
909	CXorf26	chromosome X open reading frame 26	0.11	0.23	-0.18	-0.35	-0.10	-0.13	-0.07
910	CASC5	cancer susceptibility candidate 5	0.09	0.16	-0.11	-0.25	-0.19	-0.17	0.13
911	MTRE1	mitochondrial translational release factor 1	0.08	0.22	-0.18	-0.31	-0.03	0.07	0.01
912	SH2D5	SH2 domain containing 5	0.15	-0.02	-0.31	-0.13	-0.14	-0.09	0.22
913	FZD7	frazzled homolog 7 (Drosophila)	0.05	0.18	0.14	-0.24	-0.11	-0.16	-0.18
914	FZD7	frazzled homolog 7 (Drosophila)	0.01	0.15	0.01	-0.16	0.02	-0.09	-0.12
915	MPP6	membrane protein, palmitoylated 6 (MAGUK p55 subfamily member 6)	0.10	0.09	-0.11	-0.19	0.04	0.06	-0.20
916	CHEK1	CHEK1 checkpoint homolog (S. pombe)	-0.14	0.22	0.10	-0.07	0.11	0.09	-0.20
917	CHEK1	CHEK1 checkpoint homolog (S. pombe)	-0.12	0.28	0.06	-0.17	0.06	-0.06	-0.28
918	SLC39A10	solute carrier family 39 (zinc transporter), member 10	-0.30	0.23	0.07	0.06	0.12	0.09	-0.11
919	ZWILCH	Zwilch, kinetochore associated, homolog (Drosophila)	-0.26	0.29	0.18	-0.03	0.02	-0.05	-0.11
920	TSR1	TSR1, 20S rRNA accumulation, homolog (S. cerevisiae)	-0.21	0.28	-0.02	-0.07	0.14	-0.05	-0.29
921	WDR75	WD repeat domain 75	-0.23	0.31	-0.05	-0.08	0.07	-0.06	-0.24
922	—	—	-0.17	0.17	-0.14	0.00	-0.17	-0.12	-0.09
923	HAUS6	HAUS augmin-like complex, subunit 6	-0.20	0.22	-0.07	-0.01	-0.20	-0.13	-0.14
924	CEBPZ	CCAAT/enhancer binding protein (C/EBP), zeta	-0.07	0.15	-0.05	-0.07	-0.34	-0.08	-0.19
925	NLN	neurolysin (metallopeptidase M3 family)	-0.02	0.12	-0.02	-0.11	-0.26	-0.19	-0.19
926	GLI2	GLI family zinc finger 2	-0.09	0.14	0.15	-0.05	-0.28	-0.12	-0.06
927	CSE1L	CSE1 chromosome segregation 1-like (yeast)	-0.18	0.12	0.01	0.06	-0.12	-0.11	-0.27
928	WDR89	WD repeat domain 89	-0.12	0.14	0.07	-0.02	-0.19	-0.09	-0.46
929	DEPDC1	DEP domain containing 1	-0.27	0.15	-0.14	0.12	-0.21	-0.17	-0.42
930	KIAA1524	KIAA1524	-0.18	0.29	0.07	-0.11	-0.27	0.13	-0.21
931	ZNF670	zinc finger protein 670	-0.25	0.11	-0.17	0.14	-0.01	0.19	-0.47
932	SMC4	structural maintenance of chromosomes 4	-0.09	0.11	0.07	-0.03	-0.31	-0.24	-0.26
933	KRR1	KRR1 small subunit (SSU) processome component, homolog (yeast)	0.09	-0.03	0.03	-0.07	-0.18	-0.07	-0.13
934	SYNCRIP	synaptotagmin binding, cytoplasmic RNA interacting protein	0.07	0.01	-0.06	-0.07	-0.20	-0.22	-0.19
935	TARS	threonyl-tRNA synthetase	-0.09	-0.08	-0.02	0.17	-0.08	-0.13	-0.42

736	ZNF397	zinc finger protein 397	-0.16	0.00	0.19	0.16	-0.15	-0.12	-0.11
737	C1orf80	chromosome 17 open reading frame 80	-0.19	-0.07	0.15	0.26	-0.09	-0.27	-0.35
738	SMC1A	structural maintenance of chromosomes 1A	-0.12	-0.12	-0.10	0.24	-0.36	-0.08	-0.20
739	SMARCA5	SMC1/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 5	-0.06	0.05	-0.10	0.00	0.06	-0.22	-0.51
740	DLAT	dlivoylopoamide S-acetyltransferase	-0.06	0.02	-0.01	0.04	-0.16	-0.16	-0.33
741	C1orf183	chromosome 1 open reading frame 183	-0.15	0.14	-0.20	0.01	0.02	-0.02	-0.38
742	SSB	Stogen syndrome antigen B (autoantigen Ia)	-0.17	0.20	-0.06	-0.03	-0.27	-0.04	-0.09
743	IGF2BP3	insulin-like growth factor 2 mRNA binding protein 3	-0.15	0.17	-0.08	-0.01	-0.08	-0.05	-0.28
744	MTAP	methylthioadenosine phosphorylase	-0.08	0.10	-0.02	-0.03	-0.08	-0.02	-0.18
745	PNN	pinin, desmosome associated protein	-0.13	0.24	-0.04	-0.12	-0.17	-0.01	-0.20
746	SKA2	spindle and kinetochore associated complex subunit 2	-0.15	0.22	0.01	-0.07	-0.10	-0.06	-0.13
747	PRPF40A	PRP40 pre-mRNA processing factor 40 homolog A (S. cerevisiae)	-0.09	0.03	-0.21	0.07	-0.29	-0.09	-0.26
748	CENPN	centromere protein N	-0.12	0.09	-0.18	0.04	-0.16	-0.09	-0.11
749	GART	phosphoribosylglycinamide formyltransferase, phosphoribosylglycinamide synthetase, phosphoribosylaminimidazole synthetase	-0.06	0.04	0.12	0.02	0.05	-0.10	-0.15
750	FLJ36848	hypothetical LOC647115	-0.12	0.07	0.16	0.05	-0.21	-0.15	0.01
751	CKS2	CDC28 protein kinase regulatory subunit 2	-0.03	0.04	-0.05	-0.01	-0.04	0.01	-0.07
752	DNAJC2	DnaJ (Hsp40) homolog, subfamily C, member 2	0.04	-0.03	-0.11	-0.01	-0.16	-0.13	0.08
753	C2orf44	chromosome 2 open reading frame 44	0.06	-0.10	-0.21	0.04	-0.08	0.11	-0.13
754	PRC1	protein regulator of cytokinesis 1	-0.14	0.02	-0.08	0.13	0.15	0.10	-0.03
755	ATP5O /// DONSON	ATP synthase, H+ transporting, mitochondrial F1 complex, O subunit /// downstream neighbor of SON	-0.07	-0.12	-0.15	0.19	0.08	0.21	-0.13
756	MKI67	antigen identified by monoclonal antibody Ki-67	0.15	0.01	0.25	-0.16	-0.08	-0.09	-0.23
757	GART	phosphoribosylglycinamide formyltransferase, phosphoribosylglycinamide synthetase, phosphoribosylaminimidazole synthetase	0.05	0.04	0.18	-0.09	-0.07	-0.18	-0.50
758	PNN	pinin, desmosome associated protein	-0.12	0.23	-0.13	-0.11	-0.22	-0.17	-0.32
759	CSE1L	CSE1 chromsome segregation 1-like (yeast)	0.00	0.13	-0.03	-0.12	-0.27	-0.28	-0.37
760	HSPD1	heat shock 60kDa protein 1 (chaperonin)	0.06	0.10	-0.04	-0.16	-0.15	-0.16	-0.23
761	CEP35	centrosomal protein 55kDa	0.14	0.09	-0.23	-0.23	-0.21	-0.02	-0.26
762	DEPDC1	DEP domain containing 1	0.06	0.11	0.02	-0.17	-0.39	-0.32	-0.19
763	ARL5B	ADP-ribosylation factor-like 5B	0.01	0.19	0.15	-0.21	-0.36	-0.10	-0.19
764	KPNA2	karyopherin alpha 2 (RAG cohort 1, importin alpha 1)	0.09	0.01	0.00	-0.10	-0.09	0.04	-0.33
765	ECT2	epithelial cell transforming sequence 2 oncogene	0.06	-0.08	-0.01	0.01	-0.13	-0.04	-0.42
766	HSPA4	heat shock 70kDa protein 4	0.06	-0.14	-0.09	0.07	-0.25	-0.32	-0.21
767	E2F7	E2F transcription factor 7	-0.15	0.11	-0.05	0.04	-0.19	-0.24	-0.11
768	C1orf54	chromosome 18 open reading frame 54	-0.08	-0.07	-0.04	0.16	-0.23	-0.10	-0.16
769	MATR3 /// SNHG4	matrin 3 /// small nuclear RNA host gene 4 (non-protein coding)	-0.19	0.33	0.19	-0.14	0.22	0.30	-0.42
770	UTP15	UTP15, U3 small nuclear ribonucleoprotein, homolog (S. cerevisiae)	-0.11	0.26	0.08	-0.15	0.16	0.22	-0.26
771	ELOVL6	ELOVL family member 6, elongation of long chain fatty acids (FEN1/Elo2, SUR4/Elo3-like, yeast)	-0.20	0.33	-0.15	-0.13	0.25	-0.01	-0.11

772	ELOVL6	ELOVL family member 6, elongation of long chain fatty acids (FEN1/Elo2, SUR4/Elo3-like, Yeast)	-0.11	0.20	-0.18	-0.08	0.32	-0.01	-0.24
773	RAD18	RAD18 homolog (S. cerevisiae)	-0.32	0.35	-0.20	-0.04	0.03	-0.08	-0.18
774	CHEK1	CHK1 checkpoint homolog (S. pombe)	-0.25	0.39	-0.11	-0.15	-0.02	-0.16	-0.23
775	ZNF616	zinc finger protein 616	-0.43	0.22	-0.04	0.25	0.20	-0.14	-0.20
776	---	---	-0.20	0.22	0.00	-0.02	0.33	-0.02	-0.21
777	ZNF616	zinc finger protein 616	-0.29	0.28	-0.07	0.01	0.12	-0.01	-0.16
778	SMC2	structural maintenance of chromosomes 2	-0.08	0.38	0.07	-0.30	-0.53	-0.36	-0.28
779	ZNF141	zinc finger protein 141	-0.32	0.18	0.09	0.14	-0.62	-0.22	-0.28
780	SMC6	structural maintenance of chromosomes 6	-0.16	0.13	0.18	0.04	-0.53	-0.43	-0.29
781	SMC4	structural maintenance of chromosomes 4	-0.32	0.27	0.02	0.05	-0.32	-0.28	-0.29
782	WDR35	WD repeat domain 35	-0.17	0.34	0.08	-0.17	-0.42	-0.14	-0.20
783	TRIM59	tripartite motif-containing 59	-0.26	-0.04	0.18	0.30	-0.56	-0.28	0.09
784	ZNF334	zinc finger protein 334	-0.59	0.58	-0.16	0.01	-0.32	0.03	-0.13
785	PP1G	peptidyl/prolyl isomerase G (cyclophilin G)	-0.17	0.24	-0.07	-0.08	-0.46	-0.14	0.02
786	MURC	muscle-related coiled-coil protein	-0.18	0.22	-0.17	-0.04	-0.41	0.03	0.15
787	CEP152	centrosomal protein 152kDa	-0.41	0.29	0.12	0.12	-0.40	-0.04	0.07
788	PTTG3P	pituitary tumor-transforming 3 (pseudogene)	-0.63	0.14	0.06	0.49	0.44	0.45	0.17
789	CHEK2	CHK2 checkpoint homolog (S. pombe)	-0.30	0.17	0.02	0.13	0.28	0.23	-0.08
790	MK167	antigen identified by monoclonal antibody Ki-67	-0.15	0.07	-0.04	0.08	0.38	-0.05	-0.02
791	PHF17	PHF finger protein 17	-0.19	-0.01	-0.12	0.20	0.38	0.00	-0.09
792	NEIL3	nei endonuclease VIII-like 3 (E. coli)	-0.46	0.39	-0.07	0.56	0.07	0.08	0.01
793	C5orf34	chromosome 5 open reading frame 34	-0.58	0.45	-0.21	0.14	0.37	0.24	-0.13
794	GNL2	guanine nucleotide binding protein-like 2 (nucleolar)	-0.21	0.03	0.08	0.18	0.28	0.27	0.02
795	DNTTIP2	deoxynucleotidyltransferase, terminal, interacting protein 2	0.04	0.08	0.04	-0.12	-0.11	0.17	0.01
796	NPM1	nucleophosmin (nucleolar phosphoprotein B23, numatrin)	-0.05	0.18	0.03	-0.12	-0.02	-0.02	0.05
797	SSB	Sjogren syndrome antigen B (autoantigen La)	-0.11	0.17	-0.04	-0.08	-0.02	0.22	-0.11
798	ORC3L	origin recognition complex, subunit 3-like (yeast)	-0.12	0.09	-0.02	0.03	0.06	0.19	0.04
799	ZNF607	zinc finger protein 607	-0.03	0.09	0.11	-0.07	0.06	0.12	0.06
800	PRPF40A	PRP40 pre-mRNA processing factor 40 homolog A (S. cerevisiae)	-0.12	0.04	0.10	0.08	0.03	0.01	0.20
801	BAX	BCL2-associated X protein	0.03	0.06	-0.11	-0.08	0.28	0.19	0.40
802	GDK7	cyclin-dependent kinase 7	-0.12	0.13	0.11	-0.01	0.08	0.28	0.38
803	LOC100292909	hypothetical protein LOC100292909	-0.19	0.14	0.03	0.05	0.32	0.40	0.39
804	G2oorf19	chromosome 20 open reading frame 19	0.03	0.07	0.20	-0.10	0.37	0.34	0.23
805	PGBD1	piGyBac transposable element derived 1	0.06	0.10	0.02	-0.16	0.30	0.41	0.15
806	DCAF13	DDB1 and CUL4 associated factor 13	-0.06	0.04	0.07	0.25	0.39	0.39	0.01
807	PABPC1L	poly(A) binding protein, cytoplasmic, 1-like	-0.20	0.25	-0.07	-0.05	0.31	0.34	0.15
808	---	---	-0.53	0.45	0.08	0.07	0.10	-0.03	0.26
809	ROR1	receptor tyrosine kinase-like orphan receptor 1	-0.43	0.36	0.12	0.06	0.20	0.12	0.26
810	TEX9	testis expressed 9	-0.30	0.21	0.21	0.09	-0.01	0.04	0.38
811	MTAP	methylthioadenosine phosphorylase	-0.17	0.47	0.28	-0.30	-0.03	-0.06	0.14
812	NPM1	nucleophosmin (nucleolar phosphoprotein B23, numatrin)	-0.13	0.29	0.21	-0.12	0.09	0.07	0.17

813	NUCD01	NudC domain containing 1	-0.14	0.28	0.25	-0.15	0.18	0.28	0.17
814	TRMT5	TRMT5 RNA methyltransferase 5 homolog (S. cerevisiae)	-0.25	0.47	-0.20	-0.22	0.08	0.08	0.25
815	KIAA0101	KIAA0101	0.20	0.13	0.26	-0.33	0.04	0.25	0.33
816	ZNF613	zinc finger protein 613	0.13	0.05	0.54	-0.18	0.07	0.50	0.13
817	ROR1	receptor tyrosine kinase-like orphan receptor 1	0.15	-0.11	0.30	-0.04	0.10	0.10	0.04
818	GINS4	GINS complex subunit 4 (Slc5 homolog)	0.00	-0.20	0.31	0.20	0.19	0.23	0.11
819	SMC6	structural maintenance of chromosomes 6	-0.09	0.11	0.51	-0.02	0.41	0.15	0.15
820	GLRX3	glucuradixin 3	0.01	0.06	0.01	-0.07	0.12	0.32	-0.07
821	NUCD01	NudC domain containing 1	-0.21	0.20	0.18	0.01	0.50	0.27	-0.47
822	CHML	choroideremia-like (Rab escort protein 2)	0.58	-0.21	-0.06	-0.37	-0.24	-0.54	-0.19
823	ROR1	receptor tyrosine kinase-like orphan receptor 1	0.45	-0.31	0.20	-0.13	-0.22	-0.17	-0.28
824	ANLN	anillin, actin binding protein	0.32	-0.14	0.17	-0.19	-0.18	-0.16	-0.28
825	NUDT11	nudix (nucleoside diphosphate linked moiety X)-type motif 11	0.46	-0.24	-0.14	-0.22	0.04	-0.26	-0.22
826	DBN1	drebrin 1	0.38	-0.60	-0.13	0.22	-0.33	-0.14	-0.15
827	CABYR	calcium binding tyrosine-(Y)-phosphorylation regulated	0.56	-0.38	0.39	-0.19	-0.16	0.28	-0.31
828	CENPJ	centromere protein J	0.05	-0.13	0.36	0.08	-0.16	-0.10	-0.54
829	—	—	0.43	-0.35	0.17	-0.07	0.36	0.12	-0.53
830	PAR3	par-3 partitioning defective 3 homolog (C. elegans)	0.24	-0.18	-0.51	-0.06	0.27	0.01	-0.09
831	—	—	0.32	-0.29	0.20	0.06	-0.32	0.49	-0.05
832	TRO	trophinin	-0.08	-0.37	0.73	0.45	0.49	0.39	0.15
833	GTSE1	G-2 and S-phase expressed 1	-0.23	-0.23	0.27	0.46	0.47	0.35	-0.21
834	SLC4A5	Solute carrier family 4, sodium bicarbonate cotransporter, member 5	-0.17	-0.10	0.22	0.27	0.71	0.46	0.20
835	CCDC34	coiled-coil domain containing 34	-0.43	-0.24	0.10	0.67	0.40	0.26	0.26
836	NTSDC2	5'-nucleotidase domain containing 2	0.13	-0.69	0.21	0.56	-0.12	-0.06	-0.13
837	SALL1	sal-like 1 (Drosophila)	-0.09	-0.39	-0.16	0.49	-0.01	0.21	-0.04
838	SALL1	sal-like 1 (Drosophila)	0.10	-0.39	0.29	0.11	0.29	0.01	0.01
839	PPP4R4	protein phosphatase 4, regulatory subunit 4	0.27	-0.36	0.01	0.08	-0.08	0.65	0.23
840	CCDC152	coiled-coil domain containing 152	-0.42	-0.10	0.19	0.52	-0.33	0.40	0.18
841	MYO23	myozenin 3	-0.04	-0.12	0.76	0.17	0.38	-0.17	0.57
842	BIRC5	baculoviral IAP repeat-containing 5	0.37	0.44	0.33	-0.12	0.66	0.34	0.56
843	CHAC1	ChAc, cation transport regulator homolog 1 (E. coli)	0.40	-0.26	0.59	-0.14	0.51	0.30	0.54
844	SNHG12	small nucleolar RNA host gene 12 (non-protein coding)	-0.16	0.14	0.39	0.03	0.43	0.68	0.44
845	GNAS	GNAS antisense RNA (non-protein coding)	-0.40	0.16	0.47	0.24	0.39	0.59	0.44
846	UGT2	UDP-glucose glycoprotein glucosyltransferase 2	-0.62	0.37	0.54	0.25	0.53	0.74	0.77
847	SLC6A15	solute carrier family 6 (neutral amino acid transporter), member 15	-0.43	0.33	0.26	0.10	0.43	0.74	0.74
848	LCTL	lactase-like	0.26	0.32	0.57	-0.53	0.07	0.00	0.90
849	AMMEOR1	Alport syndrome, mental retardation, midface hypoplasia and elliptocytosis chromosomal region gene 1	0.15	0.40	0.26	-0.55	0.56	0.35	0.32
850	LOC100289612	arsenic transactivated protein 1	0.39	0.33	0.56	-0.72	0.53	0.90	0.43
851	C1orf43	chromosome 4 open reading frame 43	-0.13	0.11	0.05	0.03	1.00	0.35	-0.79
852	DYN2H1	dynein, cytoplasmic 2, heavy chain 1	0.11	0.19	0.02	-0.30	-2.11	-1.78	-2.18
853	MME	membrane metallo-endopeptidase	-0.38	0.28	0.50	0.11	-1.05	-1.04	-0.59
854	BDNF	brain-derived neurotrophic factor	0.50	-0.51	-0.37	0.01	-0.29	-1.00	0.25

855	MMP14	matrix metalloproteinase 14 (membrane-inserted)	0.94	-0.64	-0.34	-0.30	-0.59	-0.58	0.02
856	UHRF1BP1L	UHRF1 binding protein 1-like	-0.02	0.06	0.43	-0.04	-0.73	-0.71	-0.12
857	ODZ3	odd Oz/ter-m homolog 3 (Drosophila)	-0.06	-0.01	0.20	0.07	-1.31	-1.24	-0.36
858	SLC4A7	solute carrier family 4, sodium bicarbonate cotransporter, member 7	0.41	0.05	-0.19	-0.45	-0.60	-1.10	-1.26
859	TRPC4	transient receptor potential cation channel, subfamily C, member 4	-0.03	-0.18	-0.02	0.19	-0.45	-0.95	-1.47
860	SEMA3A	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3A	-0.41	0.21	-0.08	0.20	-0.79	-0.18	-0.50
861	LOC100288985	hypothetical protein LOC100288985	-0.45	0.00	-0.47	0.45	-0.93	-0.77	-0.82
862	RAB3B	RAB3B, member RAS oncogene family	0.20	-0.33	-0.29	0.13	-0.58	-0.26	-0.51
863	RAB3B	RAB3B, member RAS oncogene family	0.26	-0.29	-0.31	0.03	-0.65	-0.55	-0.79
864	RALGAP-S2	Ral GEF with PH domain and SH3 binding motif 2	0.20	-0.03	-0.51	-0.17	-0.38	-0.24	-0.98
865	FGF2	fibroblast growth factor-2 (basic)	0.24	0.20	-0.31	-0.44	-0.30	-0.66	-0.55
866	—	—	-0.13	0.17	-0.51	-0.04	-0.32	-0.35	-0.21
867	KIAA1826	KIAA1826	-0.04	0.24	-0.05	-0.20	-0.47	-0.52	-0.85
868	RALGPS2	Ral GEF with PH domain and SH3 binding motif 2	-0.10	0.33	0.04	-0.23	-0.65	-0.80	-0.93
869	FST	folistatin	-0.34	-0.31	-0.49	0.85	0.09	-0.47	-0.30
870	LOC401074	hypothetical LOC401074	0.18	0.17	0.17	-0.35	0.35	0.61	1.05
871	MAP9	microtubule-associated protein 9	0.38	-0.17	0.34	-0.22	0.50	0.70	0.43
872	SLC7A11	solute carrier family 7, (cationic amino acid transporter, y+ system) member 11	-0.10	0.08	0.33	0.02	0.85	-0.13	0.40
873	SLC7A11	solute carrier family 7, (cationic amino acid transporter, y+ system) member 11	-0.08	0.14	0.04	-0.06	0.77	-0.01	0.26
874	BBS7	Bardet-Biedl syndrome 7	-0.15	0.04	0.20	0.11	0.93	0.39	-0.15
875	CRABP2	cellular retinoic acid binding protein 2	0.01	-0.14	-0.27	0.13	-0.18	0.44	0.28
876	GPX8	glutathione peroxidase 8 (putative)	-0.01	0.22	0.27	-0.21	-0.02	0.06	0.18
877	—	—	-0.06	-0.04	-0.04	0.10	0.10	0.13	0.09
878	RAB3B	RAB3B, member RAS oncogene family	-0.46	0.22	-0.30	0.24	0.01	0.11	-0.07
879	—	—	-0.40	0.61	-0.10	-0.22	0.26	0.16	-0.08
880	SFRP2	secreted frizzled-related protein 2	-0.31	-0.47	-0.06	0.78	0.89	0.49	0.54
881	SEMA3A	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3A	-1.03	0.66	0.04	0.37	0.48	-0.38	-2.19
882	IRX2	irradiation induced homeobox 2	0.30	-0.36	-0.13	0.06	-3.03	-0.12	-0.12
883	TPR	translocated promoter region (to activated MET oncogene)	0.17	-0.41	-0.22	0.24	-2.07	-1.28	-3.58
884	NUPT188	nucleoporin 188kDa	0.05	0.12	0.05	-0.17	-4.03	-1.49	-3.48
885	FRBB2	v-erb-b2 erythroblastic leukemia viral oncogene homolog 2, neuro/glioblastoma derived oncogene homolog (avian)	0.19	-0.33	0.34	0.13	-2.23	-2.77	-2.12
886	DAPK1	death-associated protein kinase 1	0.36	-0.05	0.24	-0.31	-1.51	-2.20	-2.21
887	HEATR1	HEAT repeat containing 1	-0.07	-0.03	0.23	0.10	-1.00	-1.44	-2.89
888	MYO10	myosin X	-0.07	-0.22	0.44	0.29	-0.91	-1.21	-2.63
889	JMJD1C	jumonji domain containing 1C	-0.10	0.15	0.24	-0.05	-1.75	-1.52	-1.94
890	SLC6A6	solute carrier family 6 (neurotransmitter transporter, taurine), member 6	0.50	-0.40	-0.82	-0.10	-1.25	-1.09	-2.31

891	PHF12	pHD finger protein 12	0.19	-0.17	-0.77	-0.02	-1.36	-1.11	-2.70
892	MDM2	Mein2 p53 binding protein homolog (mouse)	-0.49	0.49	0.25	0.00	-0.50	-1.05	-2.77
893	TFRC	transferrin receptor (p90, CD71)	-0.30	0.36	-0.19	-0.05	-1.01	-1.37	-1.94
894	HMG3L1	high-mobility group box 3-like 1	0.56	0.37	0.15	-0.93	1.65	1.60	0.86
895	CDC25A	cell division cycle 25 homolog A (S. pombe)	-0.01	-0.04	0.18	0.05	-0.30	-0.49	-0.81
896	BICD1	bicaudal D homolog 1 (Drosophila)	0.11	0.13	-0.37	-0.25	-0.57	-0.45	-0.47
897	OCLN	occludin	-0.03	0.15	0.01	-0.12	-0.56	-0.48	-0.53
898	DNMT3A	DNA (cytosine-5)-methyltransferase 3 alpha	0.18	-0.06	0.00	-0.12	-0.65	-0.44	-0.46
899	CDC41	coiled-coil domain containing 141	-0.30	0.64	-0.02	-0.34	-0.53	-0.94	-0.47
900	ZNF711	zinc finger protein 711	0.32	0.22	-0.37	-0.54	-0.28	-0.96	-0.82
901	SLOC4G1	solute carrier organic anion transporter family, member 4C1	0.10	0.24	-0.41	-0.34	-0.73	-1.01	-0.75
902	---	---	---	---	---	---	---	---	---
903	BCL2L11	BCL2-like 11 (apoptosis facilitator)	0.03	-0.02	-0.38	-0.01	-1.05	-0.71	-0.97
904	AASS	aminoacylate-semialdehyde synthase	-0.03	0.11	-0.11	-0.23	-0.59	-0.41	-0.80
905	SOX2	SRY (sex determining region Y)-box 2	0.07	0.39	0.09	-0.46	-0.89	-0.82	-1.23
906	SALL3	sal-like 3 (Drosophila)	-0.16	0.06	-0.65	0.11	-1.08	-1.06	-0.42
907	---	---	-0.16	-0.02	-0.96	0.18	-1.10	-1.17	-1.03
908	GONT2	glucosaminyl (N-acetyl) transferase 2, I-branching enzyme (I blood group)	-0.10	0.11	-0.38	0.00	-0.70	-0.90	-1.41
909	SLOC12A1	solute carrier family 12 (sodium/potassium/chloride transporters), member 1	-0.02	0.02	-0.55	0.01	-0.73	-0.73	-1.41
910	DSC2	desmocollin 2	-0.08	0.16	0.28	-0.08	-0.96	-0.58	-0.47
911	NRK	Nrk-related kinase	0.13	0.12	-0.19	-0.25	-1.02	-0.98	-0.49
912	LOC729993	hypothetical protein LOC729993	0.33	-0.03	-0.61	-0.30	-1.36	-0.99	-0.81
913	ZNF90	zinc finger protein 90	-0.14	0.69	-0.34	-0.55	-2.01	-1.62	-1.93
914	NRK	zinc finger protein 90	0.49	0.25	-0.41	-0.74	-1.53	-1.05	-1.49
915	GRPR	gastrin-releasing peptide receptor	0.48	0.62	-0.30	-1.10	-1.27	-0.36	-0.49
916	SERPINE9	serpin peptidase inhibitor, clade B (ovalbumin), member 9	0.81	0.03	-0.43	-0.84	-1.47	-0.56	-0.85
917	---	---	0.67	0.54	0.34	-1.21	-1.66	-1.08	-0.84
918	---	---	0.91	0.09	-0.24	-1.00	-0.88	-0.98	-0.12
919	PNKD	paroxysmal nonkinetic dyskinesia	1.12	-0.34	-0.34	-1.00	-0.69	-0.91	0.26
920	RBM17	RNA binding motif protein 17	0.88	-0.03	-0.19	-0.84	-0.32	-0.76	0.25
921	---	---	1.44	-0.45	-0.44	-0.99	-0.87	-1.26	-0.31
922	RMF5	ring finger protein 5	0.98	0.02	0.15	-1.00	-0.42	-0.55	0.26
923	---	---	1.20	0.09	-0.22	-1.29	-0.74	-0.94	0.11
924	---	---	1.32	0.00	-0.22	-1.32	-0.46	-0.71	0.44
925	---	---	0.85	-0.08	-0.34	-0.76	-0.35	-0.79	-0.14
926	SPIB	Sp1-B transcription factor (Sp1-1/PU.1 related)	0.73	-0.28	-0.36	-0.45	-0.14	-0.10	0.39
927	LOC652147	similar to U5 snRNP-specific protein, 200 kDa	1.13	-0.59	-0.09	-0.53	-0.92	-0.73	-0.16
928	NLRP7	NLR family, pyrin domain containing 7	1.38	-0.75	-0.10	-0.62	-0.75	-0.52	-0.04
929	---	---	-0.75	0.99	0.26	-0.24	0.35	0.21	-0.12
930	MDM10	minichromosome maintenance complex component 10	-0.60	0.92	0.63	-0.33	1.07	1.00	0.12
931	CALCR	calcitonin receptor	-0.21	-0.20	-0.77	0.41	0.07	-0.65	-1.52
932	LRAT	lecithin retinol acyltransferase (phosphatidylcholine--retinol O-acyltransferase)	-0.11	0.10	-0.89	0.01	0.19	-0.73	-1.08

933	CCND2	cyclin D2		0.18	-0.53	-0.38	0.36	-0.93	-0.72	0.17
934	ETV4	ets variant 4		0.58	-0.73	-0.17	0.15	-0.14	-0.42	-0.41
935	MYBL2	v-myb myeloblastosis viral oncogene homolog (avian)-like 2		0.07	-0.55	0.13	0.48	-0.13	-0.25	-0.37
936	FOXH1	forkhead box H1		0.59	-1.14	-0.28	0.55	-0.40	-0.06	-0.36
937	SOX4	SRY (sex determining region Y)-box 4		0.27	-0.77	-0.14	0.50	-0.66	-0.65	-0.44
938	DBNDD1	dysbindin (dystrobrevin binding protein 1) domain containing 1		0.04	-0.52	-0.23	0.49	-0.75	0.01	-0.29
939	CYP2S1	cytochrome P450, family 2, subfamily S, polypeptide 1		0.29	-0.65	0.13	0.35	-0.33	-0.08	-0.30
940	SLC16A1	solute carrier family 16, member 1 (monocarboxylic acid transporter 1)		-0.06	0.46	0.14	-0.41	-0.78	-0.83	-1.21
941	BRIP1	BRCA1 interacting protein C-terminal helixase 1		-0.05	0.50	-0.14	-0.45	-0.86	-0.80	-1.28
942	C21orf88	chromosome 21 open reading frame 88		-0.28	0.49	0.09	-0.21	-1.05	-0.66	-0.39
943	SNHG4	small nucleolar RNA host gene 4 (non-protein coding)		-0.17	0.65	0.12	-0.48	-0.34	-0.50	-0.61
944	E2F8	E2F transcription factor 8		-0.29	0.58	-0.15	-0.30	-0.30	-0.34	-0.36
945	SNHG4	small nucleolar RNA host gene 4 (non-protein coding)		0.09	0.24	-0.45	-0.33	-0.35	-0.42	-0.87
946	BUB1	budding uninhibited by benzimidazoles 1 homolog (yeast)		-0.14	0.32	-0.06	-0.18	-0.32	-0.44	-0.99
947	LPAR4	lysophosphatidic acid receptor 4		-0.05	0.26	-0.21	-0.22	-0.71	-0.31	-0.73
948	CDC88A	coiled-coil domain containing 88A		-0.03	0.18	-0.25	-0.15	-0.53	-0.42	-0.87
949	—	—		0.01	0.20	0.03	-0.20	-0.58	-0.02	-0.67
950	CDC25A	cell division cycle 25 homolog A (S. pombe)		0.03	0.07	0.12	-0.10	-0.73	-0.52	-0.81
951	F2RL1	coagulation factor II (thrombin) receptor-like 1		0.01	0.16	-0.10	-0.17	-0.41	-0.57	-0.75
952	ZNF93	zinc finger protein 93		0.30	-0.16	0.02	-0.14	-0.71	-0.31	-0.84
953	B4GALT6	UDP-Gal4betaGlcNAc beta 1,4- galactosyltransferase, polypeptide 6		-0.35	0.33	-0.33	0.02	-0.55	-0.30	-0.36
954	ZNF273	zinc finger protein 273		0.05	0.32	-0.07	-0.38	-0.48	-0.44	-0.30
955	MRS2	MRS2 magnesium homeostasis factor homolog (S. cerevisiae)		-0.18	0.34	0.06	-0.16	-0.48	-0.32	-0.25
956	ZNF649	zinc finger protein 649		-0.07	0.16	-0.15	-0.09	-0.29	-0.38	-0.50
957	ZNF253	zinc finger protein 253		-0.16	0.30	-0.17	-0.13	-0.42	-0.37	-0.41
958	C12orf35	chromosome 12 open reading frame 35		-0.17	0.17	-0.38	0.00	-0.87	-0.71	-0.64
959	ZNF138	zinc finger protein 138		-0.12	0.27	-0.42	-0.15	-0.64	-0.68	-0.73
960	B4GALT6	UDP-Gal4betaGlcNAc beta 1,4- galactosyltransferase, polypeptide 6		-0.69	0.54	-0.42	0.16	-0.69	-0.39	-0.82
961	SIX4	SIX homeobox 4		-0.72	0.38	-0.59	0.34	-0.43	-0.55	-0.71
962	PCDH2	protocadherin beta 2		-0.47	0.34	-0.36	0.13	-0.41	-0.96	-0.52
963	EF2AK4	eukaryotic translation initiation factor 2 alpha kinase 4		-0.70	0.31	-0.85	0.39	-0.92	-1.11	-0.95
964	FAM111B	family with sequence similarity 111, member B		-0.69	0.42	-0.37	0.27	-0.72	0.10	-0.87
965	—	—		-0.68	0.60	-0.76	0.06	0.09	-0.31	-0.61
966	LOC100288551	hypothetical protein LOC100288551		-0.43	-0.02	0.02	0.45	0.06	-0.10	-0.83
967	RAB39	RAB39, member RAS oncogene family		0.26	-0.10	0.36	-0.16	-0.53	0.03	-0.08
968	TERF1	telomeric repeat binding factor (NIMA-interacting) 1		-0.13	-0.13	-0.10	0.28	-0.05	-0.11	-0.38
969	BUB1B	budding uninhibited by benzimidazoles 1 homolog beta (yeast)		-0.12	-0.11	-0.20	0.24	-0.01	-0.02	-0.19
970	SYT1	synaptotagmin 1		-0.07	0.04	-0.31	0.03	-0.13	-0.06	-0.11
971	POLR3G	polymerase (RNA) III (DNA directed) polypeptide G (32KD)		-0.24	0.14	-0.18	0.11	-0.11	-0.24	-0.24

972	TERF1	telomeric repeat binding factor (NIMA-interacting) 1	-0.11	-0.26	-0.04	0.38	-0.31	-0.06	-0.31
973	RAC3	ras-related G3 botulinum toxin substrate 3 (rho family, small GTP binding protein Rac3)	-0.10	-0.24	-0.18	0.34	-0.24	-0.04	-0.13
974	GDF3	growth differentiation factor 3	-0.23	-0.09	-0.24	0.31	0.05	-0.42	-0.01
975	MMP24	matrix metalloproteinase 24 (membrane-inserted)	0.23	-0.38	-0.16	0.15	-0.57	-0.24	-0.26
976	GAP43	growth associated protein 43	0.04	-0.24	-0.21	0.20	-0.45	-0.37	-0.02
977	ITGB1BP3	integrin beta 1 binding protein 3	0.31	-0.20	-0.06	-0.11	-0.19	-0.11	-0.08
978	CECR2	cat eye syndrome chromosome region, candidate 2	0.19	-0.16	-0.22	-0.04	-0.15	-0.05	0.07
979	AASS	aminoadipate-semialdehyde synthase	-0.24	0.23	-0.18	0.01	-0.34	-0.03	-0.47
980	TRIM24	tripartite motif-containing 24	0.01	-0.03	0.05	0.02	-0.24	-0.13	-0.20
981	ZNF93	zinc finger protein 93	0.03	0.03	0.04	-0.06	-0.38	-0.25	-0.05
982	TRIM24	tripartite motif-containing 24	-0.01	0.11	0.03	-0.10	-0.27	-0.21	-0.26
983	PHC1	polyhomeotic homolog 1 (Drosophila)	-0.14	0.21	0.00	-0.07	-0.34	-0.24	-0.14
984	MCM10	mitochondrion maintenance complex component 10	0.02	0.22	0.26	-0.24	-0.26	-0.29	-0.18
985	IPW	imprinted in Prader-Willi syndrome (non-protein coding)	0.10	0.13	-0.25	-0.23	-0.30	-0.25	-0.41
986	FZD3	frizzled homolog 3 (Drosophila)	-0.04	0.29	-0.14	-0.26	-0.37	-0.40	-0.33
987	SYT1	synaptotagmin 1	-0.05	-0.19	-0.32	0.24	-0.56	-0.47	-0.66
988	PHC1	polyhomeotic homolog 1 (Drosophila)	0.08	-0.08	-0.15	0.00	-0.45	-0.37	-0.56
989	HELLS	helicase, lymphoid-specific	-0.07	0.14	-0.33	-0.07	-0.63	-0.41	-0.50
990	ITK	ITK protein kinase	-0.03	-0.04	-0.23	0.07	-0.56	-0.36	-0.43
991	POLR3G	polymerase (RNA) III (DNA directed) polypeptide G (32kD)	-0.06	0.08	0.06	-0.02	-0.64	-0.50	-0.55
992	KBTBD8	kelch repeat and BTB (POZ) domain containing 8	0.18	0.02	-0.21	-0.27	-0.74	-0.45	-0.35
993	ZNF681	zinc finger protein 681	0.06	0.09	0.01	-0.08	-0.13	-0.79	-0.64
994	DSG2	desmoglein 2	0.04	0.00	0.06	-0.04	-0.45	-0.46	-0.43
995	F2RL1	coagulation factor II (thrombin) receptor-like 1	0.01	0.05	0.00	-0.07	-0.29	-0.42	-0.47
996	—	—	-0.01	0.28	-0.23	-0.27	-0.12	-0.48	-0.22
997	ACOXL	acyl-Coenzyme A oxidase-like	-0.11	0.21	-0.03	-0.10	0.16	-0.28	-0.74
998	—	—	-0.11	0.35	-0.31	-0.24	-0.24	-0.42	-0.81
999	C15orf42	chromosome 15 open reading frame 42	0.00	0.15	-0.49	-0.15	-0.12	-0.18	-0.83
1000	PKIB	protein kinase (cAMP-dependent, catalytic) inhibitor beta	0.17	0.10	-0.40	-0.27	0.14	-0.01	-0.46
1001	HELLS	helicase, lymphoid-specific	-0.04	0.07	-0.73	-0.03	-0.03	0.16	-0.26
1002	KCNQ3	potassium voltage-gated channel, subfamily G, member 3	-0.40	0.40	-0.92	0.00	-0.25	-0.27	-0.55
1003	—	—	-0.17	-0.03	-0.77	0.20	-0.39	-0.50	-0.21
1004	XRCC3	X-ray repair complementing defective repair in Chinese hamster cells 3	0.02	-0.33	-0.94	0.31	-0.12	-0.63	-0.45
1005	ZNF682	zinc finger protein 682	0.38	-0.40	-0.71	0.01	-0.54	-0.37	-0.51
1006	CYP2B6	cytochrome P450, family 2, subfamily B, polypeptide 6	0.76	-0.05	0.22	-0.70	-0.07	-0.26	-0.05
1007	GYG2	glycogenin 2	0.56	0.01	0.43	-0.57	-0.22	-0.11	-0.41
1008	ERCC6L	excision repair cross-complementing rodent repair deficiency, complementation group 6-like	0.62	-0.21	-0.10	-0.42	-0.23	-0.23	-0.36
1009	IL17RD	interleukin 17 receptor D	0.34	-0.05	0.18	-0.30	-0.11	-0.24	-0.84
1010	RP6-213H19.1	serine/threonine protein kinase MS14	0.27	0.42	0.46	-0.68	-0.27	-0.22	-0.63
1011	—	—	0.50	-0.16	-0.43	-0.34	-1.28	0.45	-0.74
1012	WDR67	WD repeat domain 67	-0.68	0.25	0.55	0.43	0.61	0.73	0.35
1013	DAZL	deleted in azoospermia-like	-0.96	0.79	0.61	0.18	0.53	0.37	-0.01

1014	---		-0.46	0.59	0.00	-0.13	0.34	0.32	0.34
1015	SEMGI	semenogelin I	0.16	0.16	0.45	-0.32	0.56	0.86	1.24
1016	KONEIL	KONEI-like	0.74	0.05	0.48	-0.79	0.41	0.80	0.92
1017	SLCIA6	solute carrier family 1 (high affinity aspartate/glutamate transporter), member 6	0.06	0.10	0.58	-0.16	1.02	1.02	0.70
1018	LMBN1	lamin B1	0.12	0.06	0.09	-0.18	0.80	0.77	0.41
1019	PKIB	protein kinase (cAMP-dependent, catalytic) inhibitor beta	0.25	0.08	-0.02	-0.33	0.60	0.80	0.45
1020	FAM133A	family with sequence similarity 133, member A	-0.34	0.43	0.55	-0.09	0.30	0.74	0.79
1021	CNKSR2	connector enhancer of kinase suppressor of Ras 2	-0.03	0.36	0.47	-0.34	0.47	0.73	0.56
1022	---	---	-0.01	0.17	0.63	-0.16	0.67	0.45	0.68
1023	GPR64	G protein-coupled receptor 64	0.00	0.72	-0.02	-0.73	-0.32	0.13	0.14
1024	---	---	-0.16	0.35	-0.23	-0.19	-0.02	-0.10	-0.20
1025	SNRPN	small nuclear ribonucleoprotein polypeptide N	-0.32	0.72	-0.31	-0.40	-0.36	-0.12	-0.20
1026	FANGB	Fancconi anemia, complementation group B	-0.25	0.67	0.18	-0.42	-0.60	0.60	-0.10
1027	UGT3A1	UDP glucosyltransferase 3 family, polypeptide A1	-0.36	0.32	0.36	0.04	-0.51	-0.01	-0.21
1028	DHPA4	developmental pluripotency associated 4	-0.73	0.67	-0.39	0.06	-0.14	-0.34	-0.41
1029	---	---	-0.85	1.24	-0.20	-0.39	0.31	0.13	0.20
1030	TRIML2	tripartite motif family-like 2	-0.13	0.05	-0.82	0.08	0.66	-0.20	-0.56
1031	LOC285401	hypothetical LOC285401	0.10	-0.15	-0.56	0.05	0.38	0.15	0.01
1032	C1orf187	chromosome 1 open reading frame 187	0.06	-0.19	-0.12	0.13	0.25	-0.33	-0.08
1033	FLJ38116	hypothetical locus LOC388668	0.03	-0.26	0.17	0.23	0.39	-0.18	0.15
1034	AP1M2	adaptor-related protein complex 1, mu, 2 subunit	0.02	-0.33	-0.04	0.31	0.12	0.19	0.05
1035	DPPIA2	developmental pluripotency associated 2	0.18	-0.37	-0.14	0.19	0.31	0.01	0.04
1036	EPHA1	EPH receptor A1	-0.14	-0.34	0.20	0.48	-0.12	0.19	0.33
1037	ARID3B	AT rich interactive domain 3B (BRG1T-like)	-0.24	-0.25	-0.19	0.50	0.15	0.19	0.07
1038	PODXL	podocalyxin-like	-0.01	-0.05	0.02	0.06	-0.24	-0.01	-0.04
1039	ESRP2	epithelial splicing regulatory protein 2	0.12	-0.11	0.01	-0.01	-0.39	-0.09	-0.12
1040	SALL2	tsal-like 2 (Drosophila)	-0.13	-0.10	0.01	0.23	-0.15	-0.16	-0.16
1041	GDC25A	cell division cycle 25 homolog A (S. pombe)	-0.18	0.07	-0.10	0.11	0.10	0.23	0.09
1042	ACVR2B	activin A receptor, type IIb	-0.32	0.26	-0.04	0.06	0.24	0.05	0.03
1043	FAM60A	family with sequence similarity 60, member A	-0.11	0.06	0.15	0.05	-0.01	-0.05	-0.03
1044	ADD2	jadducin 2 (beta)	-0.13	0.22	0.17	-0.10	0.08	0.05	-0.02
1045	IDO1	indoleamine 2,3-dioxygenase 1	-0.52	0.17	-0.10	0.35	-0.04	0.08	0.21
1046	ELAVL2	ELAV (embryonic lethal, abnormal vision, Drosophila)-like 2 (Hu antigen B)	-0.48	0.30	0.11	0.18	0.19	0.14	0.21
1047	LOG157627	hypothetical LOC157627	-0.34	0.16	-0.25	0.18	0.11	0.02	-0.19
1048	---	---	-0.45	0.40	-0.42	0.04	0.12	-0.17	0.10
1049	C13orf38 /// SOHLH2	chromosome 13 open reading frame 38 /// spermatogenesis and oogenesis specific basic helix-loop-helix 2	-0.53	0.44	-0.31	0.08	0.28	0.07	-0.18
1050	RECQL4	RecQ protein-like 4	0.09	-0.28	0.22	0.19	-0.36	0.18	-0.07
1051	CAMKV	CaM kinase-like vesicle-associated	-0.12	-0.20	0.29	0.31	0.01	0.23	0.14
1052	EPHX3	epoxide hydrolase 3	0.08	-0.43	0.05	0.35	-0.02	0.25	0.34
1053	FAM19A4	family with sequence similarity 19 (hemokine C-C motif)-like, member A4	-0.01	-0.27	0.26	0.28	0.01	0.43	-0.28

1054	TNFSF11	tumor necrosis factor (ligand) superfamily, member 11	-0.03	0.33	0.34	-0.30	-0.12	0.09	0.27
1055	PIPOX	peroxisomal acid oxidase	-0.05	0.19	-0.06	-0.14	-0.15	0.29	0.08
1056	MIR17HG	MIR17 host gene (non-protein coding)	-0.12	0.21	-0.15	-0.09	-0.10	0.03	0.14
1057	CL4orf115	chromosome 14 open reading frame 115	0.13	-0.05	0.06	-0.07	0.10	-0.05	0.19
1058	E2F5	E2F transcription factor 5, p130-binding	0.02	-0.02	0.19	0.00	0.15	0.18	0.14
1059	TET1	tet oncogene 1	-0.20	0.00	-0.02	0.20	0.25	-0.04	-0.05
1060	GUCA1A	guanylate cyclase activator 1A (retina)	-0.47	0.43	-0.04	0.04	0.41	0.55	0.31
1061	---	---	-0.45	0.32	0.27	0.13	0.52	0.46	0.57
1062	FANCD2	Fanconi anemia, complementation group D2	-0.25	0.09	-0.08	0.17	0.31	0.30	0.52
1063	FZD5	fizzled homolog 5 (Drosophila)	-0.17	-0.08	0.16	0.23	0.32	0.40	0.27
1064	DEPDC1B	DEP domain containing 1B	-0.17	-0.01	0.17	0.18	0.61	0.56	0.05
1065	PMAIP1	phorbol-12-myristate-13-acetate-induced protein 1	-0.32	0.30	-0.01	0.03	0.61	0.41	0.13
1066	IGSF1	immunoglobulin superfamily, member 1	-0.11	0.36	0.22	-0.25	0.79	0.36	0.09
1067	---	---	-0.27	0.26	0.27	0.01	0.78	0.32	0.56
1068	CTSL2	cathepsin L2	-0.43	0.02	0.15	0.41	0.04	0.38	0.40
1069	---	---	-0.72	0.14	0.15	0.58	0.29	0.22	0.18
1070	HELLS	helicase, lymphoid-specific	-0.97	0.47	0.01	0.50	0.24	0.27	0.12
1071	IGF2BP1	insulin-like growth factor 2 mRNA binding protein 1	-0.62	0.19	0.06	0.44	0.37	0.21	0.07
1072	NFE2L3	nuclear factor (erythroid-derived 2)-like 3	-0.61	0.38	0.05	0.22	0.62	-0.03	-0.04
1073	HELLS	helicase, lymphoid-specific	-0.91	0.34	-0.33	0.58	-0.03	0.04	-0.23
1074	HELLS	helicase, lymphoid-specific	-0.62	0.27	-0.08	0.35	0.24	0.12	-0.32
1075	ST8SIA3	ST8 alpha-N-acetyl-neuraminidase alpha-2,3-sialyltransferase 3	0.54	0.00	0.52	-0.55	0.30	0.25	0.25
1076	PCYT1B	phosphate cytidylyltransferase 1, choline, beta	0.38	0.50	0.17	-0.87	0.22	0.21	0.48
1077	AP1S2	adaptor-related protein complex 1, sigma 2 subunit	0.31	0.36	0.10	-0.66	-0.11	0.07	0.21
1078	ZNFX14	zinc finger protein 114	0.21	0.02	0.30	-0.23	0.45	0.44	0.51
1079	SLC25A21	solute carrier family 25 (mitochondrial oxodicarboxylate carrier), member 21	0.10	0.38	0.35	-0.48	0.70	0.61	0.60
1080	LOC253842	hypothetical protein LOC253842	0.06	0.04	0.16	-0.11	0.56	0.48	0.91
1081	DCAF12L1	DDB1 and CUL4 associated factor 12-like 1	-0.08	0.48	0.23	-0.40	0.16	0.28	0.71
1082	GYG2	glycogenin 2	0.05	0.41	0.57	-0.46	0.46	0.36	0.27
1083	CDC25C	cell division cycle 25 homolog C (S. pombe)	0.32	0.11	0.44	-0.44	0.32	0.26	0.16
1084	RP6-213H19.1	serine/threonine protein kinase MST4	0.11	0.29	0.31	-0.40	0.10	0.17	0.04
1085	LOC100216479	hypothetical LOC100216479	0.13	0.04	0.70	-0.17	0.27	0.18	0.16
1086	HMGCB3	high-mobility group box 3	0.40	0.23	-0.08	-0.63	0.46	0.33	0.27
1087	---	---	-0.65	0.18	-0.09	-0.42	0.09	0.12	0.37
1088	NFE2L3	nuclear factor (erythroid-derived 2)-like 3	-0.51	-0.02	-0.55	0.54	0.80	0.25	0.21
1089	---	---	-0.43	-0.38	-0.60	0.81	1.12	0.47	-0.12
1090	---	---	-0.22	-0.06	-0.57	0.28	0.88	1.14	0.10
1091	CYP26A1	cytochrome P450, family 26, subfamily A, polypeptide 1	-0.41	-0.87	-0.57	1.27	0.74	-1.27	-0.65
1093	---	---	0.39	-1.53	0.07	1.14	1.14	0.22	0.27
1094	LOC339260	Hypothetical protein LOC339260	0.72	0.52	0.99	-1.24	1.46	1.11	1.72
1095	SERPINF4	serpin peptidase inhibitor, clade B (ovalbumin), member 4	-0.44	1.00	0.79	-0.56	0.04	1.37	1.53
1096	---	---	-0.21	0.89	-0.26	-0.88	0.69	0.79	0.25

1097	LOC347475	UPF0625 coiled-coil domain-containing protein ENSP00000359845	0.54	0.60	0.15	-1.14	0.68	0.51	0.53
1098	LOC100129662	hypothetical protein LOC100129662	0.07	0.54	0.51	-0.81	0.49	0.49	0.56
1099	ZNF878P	zinc finger protein 876 (pseudogene)	0.16	0.45	0.81	-0.80	0.53	-0.07	0.26
1100	GPC4	glypican 4	0.29	0.33	0.33	-0.81	0.31	0.43	0.20
1101	GYG2	glycogenin 2	0.33	0.27	0.56	-0.60	0.27	0.11	0.13
1102	SH3GL3	SH3-domain GRB2-like 3	0.07	0.08	0.44	-0.15	0.01	0.19	0.57
1103	NODAL	nodal homolog (mouse)	0.33	-0.27	0.34	-0.27	0.44	0.47	0.63
1104	FAM71F1	family with sequence similarity 71, member F1	0.79	-0.52	0.50	-0.28	0.26	0.24	0.25
1105	BIK	BCL2-interacting killer (apoptosis-inducing)	0.00	-0.13	-0.10	0.13	0.15	0.03	0.46
1106	RT2	Ras-like without CAAX 2	-0.09	0.13	-0.02	-0.04	0.10	0.08	0.42
1107	—	—	-0.38	0.21	0.20	0.17	0.25	0.28	0.44
1108	NAP1L3	nucleosome assembly protein 1-like 3	0.35	-0.04	0.43	-0.31	0.19	0.49	0.24
1109	PCYT1B	phosphate cytidylyltransferase 1, choline, beta	0.08	0.29	0.13	-0.36	0.12	0.34	0.41
1110	LOC389895	hypothetical LOC389895	0.00	0.30	-0.04	-0.30	0.26	0.69	0.79
1111	—	—	-0.72	0.92	0.41	-0.20	0.25	0.66	0.21
1112	G13orf38	chromosome 13 open reading frame 38	-0.67	0.50	0.52	0.17	-0.09	0.05	0.23
1113	FABP7	fatty acid binding protein 7, brain	-0.24	0.28	0.46	-0.03	0.68	0.39	0.50
1114	KLKB1	kallikrein B, plasma (Fletcher factor) 1	-0.42	0.31	0.27	0.11	0.80	0.14	0.49
1115	HLA-DPB2	major histocompatibility complex, class II, DP beta 2 (pseudogene)	-0.36	0.53	0.45	-0.17	0.60	0.55	0.72
1116	ALOB	calcitonin-related polypeptide beta	-0.15	-0.28	0.37	0.44	0.26	0.45	0.96
1117	ZFR2	zinc finger RNA binding protein 2	-0.36	0.05	0.43	0.31	0.55	0.82	0.94
1118	LOC157827	hypothetical LOC157827	-0.69	0.25	0.01	0.44	0.35	0.47	0.04
1119	ZIG2	Zig family member 2 (odd-paired homolog, Drosophila)	-0.40	-0.28	0.38	0.69	0.42	0.63	0.16
1120	LOC730125	Hypothetical LOC730125	-0.34	-0.07	0.27	0.41	0.19	0.40	0.26
1121	—	—	-0.57	-0.15	0.05	0.72	0.49	0.37	0.31
1122	ADAMTS19	ADAM metalloproteinase with thrombospondin type 1 motif, 19	-0.19	-0.36	-0.26	0.55	-0.01	-0.26	-0.79
1123	C1orf187	chromosome 1 open reading frame 187	-0.40	0.01	-0.44	0.39	0.28	-0.12	-0.39
1124	—	—	-0.41	-0.09	-0.32	0.50	-0.07	-0.01	-0.50
1125	FGFR4	fibroblast growth factor receptor 4	0.07	-0.54	-0.30	0.47	0.03	0.16	-0.27
1126	SEMA6A	sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6A	-0.20	-0.44	-0.58	0.65	0.11	-0.21	0.00
1127	SALL3	sall-like 3 (Drosophila)	-0.14	-0.30	-0.66	0.44	-0.10	-0.04	-0.27
1128	ADD2	adducin 2 (beta)	0.22	-0.51	0.17	0.28	0.03	-0.32	-0.11
1129	ETV4	ets variant 4	0.21	-0.37	-0.35	0.16	-0.09	-0.23	-0.27
1130	IGFBP1	insulin-like growth factor 2 mRNA binding protein 1	0.46	-0.40	-0.16	-0.06	0.02	-0.51	-0.35
1131	DPPA3	developmental pluripotency associated 3	0.28	-0.43	-0.29	0.16	0.00	-0.67	-0.71
1132	—	—	0.24	-0.53	-0.53	0.29	0.47	0.24	-0.37
1133	DPPA5	developmental pluripotency associated 5	0.34	-0.98	-0.52	0.64	-0.16	-0.27	-0.35
1134	HS6ST2	heparan sulfate 6-O-sulfotransferase 2	-0.20	0.35	0.14	-0.15	0.30	0.15	-0.62
1135	GLDC	glycine dehydrogenase (decarboxylating)	0.03	0.13	-0.13	-0.16	-0.30	-0.38	-0.45
1136	NLGNA4	neuroligin 4, X-linked	0.20	0.22	0.02	-0.42	-0.45	-0.21	-0.35
1137	MEGF10	multiple EGF-like-domains 10	0.16	0.38	-0.21	-0.54	-0.40	-0.16	-0.17
1138	KLHDC7A	kelch domain containing 7A	0.31	-0.01	-0.38	-0.31	-0.73	-0.10	0.11

1139	PALM3	Paralemmin-3	0.15	-0.04	-0.50	-0.11	-0.42	-0.18	-0.06
1140	GPR19	G protein-coupled receptor 19	-0.04	0.40	-0.17	-0.36	0.08	-0.13	0.19
1141	ORC1L	origin recognition complex, subunit 1-like (yeast)	0.09	0.06	0.32	-0.15	0.13	-0.10	-0.26
1142	COCH	coagulation factor C homolog, cochlin (Limulus polyphemus)	-0.26	0.21	0.24	0.05	0.04	-0.14	0.05
1143	GABRB3	gamma-aminobutyric acid (GABA) A receptor, beta 3	-0.20	0.21	-0.04	0.00	-0.12	-0.20	-0.17
1144	GABRB3	gamma-aminobutyric acid (GABA) A receptor, beta 3	-0.21	0.08	0.08	0.13	-0.30	-0.28	-0.39
1145	—	—	-0.03	0.01	-0.17	0.02	-0.10	-0.42	-0.12
1146	COCH	coagulation factor C homolog, cochlin (Limulus polyphemus)	-0.23	0.34	0.27	-0.11	0.02	-0.19	0.15
1147	DSG2	desmoglein 2	-0.24	0.34	-0.05	-0.11	-0.06	0.01	0.11
1148	FAM60A /// LOC728115	family with sequence similarity 80, member A /// similar to family with sequence similarity 80, member A	-0.21	0.18	0.13	0.03	-0.05	0.02	-0.09
1149	CNTNAP2	contactin associated protein-like 2	-0.09	0.30	0.64	-0.20	0.11	0.09	0.17
1150	C9orf42	chromosome 9 open reading frame 42	0.01	0.09	0.44	-0.09	-0.08	-0.22	0.01
1151	ZSCAN10	zinc finger and SCAN domain containing 10	0.06	-0.29	-0.06	0.23	-0.30	-0.30	-0.19
1152	NXPH2	neurexophilin 2	-0.06	-0.19	-0.17	0.25	-0.21	-0.06	-0.34
1153	PRDM14	PR domain containing 14	0.20	-0.33	-0.19	0.13	-0.40	-0.07	-0.09
1154	FOXO3	forkhead box D3	0.17	-0.36	0.10	0.19	-0.44	-0.04	-0.34
1155	KIF1A	kinesin family member 1A	0.13	-0.29	-0.29	0.15	-0.40	-0.48	-0.06
1156	ADAMTS19	ADAM metalloproteinase with thrombospondin type 1 motif, 19	0.02	-0.43	-0.10	0.41	-0.16	-0.14	0.05
1157	FOXH1	forkhead box H1	-0.04	-0.46	-0.32	0.51	0.00	0.17	0.14
1158	—	—	-0.13	-0.28	-0.18	0.41	0.21	0.14	0.00
1159	PLEKHG4B	pleckstrin homology domain containing, family G (with RhoGef domain) member 4B	-0.02	-0.44	0.32	0.46	-0.10	0.04	0.10
1160	LOC728342	Hypothetical protein LOC728342	-0.28	-0.09	0.13	0.38	-0.28	0.18	0.10
1161	PDZD4	PDZ domain containing 4	0.61	-0.43	-0.41	-0.18	-0.49	-0.22	0.03
1162	C9orf135	chromosome 9 open reading frame 135	0.19	-0.33	-0.63	0.14	-0.79	-0.33	-0.24
1163	TMSB15A	thymosin beta 15a	0.32	-0.13	-0.05	-0.19	0.68	-0.21	0.01
1164	GNG4	guanine nucleotide binding protein (G protein), gamma 4	0.27	-0.26	0.46	-0.01	0.44	0.27	0.23
1165	C1orf135	chromosome 1 open reading frame 135	0.19	0.01	0.12	-0.20	0.25	0.18	0.29
1166	—	—	-0.02	0.14	0.10	-0.11	0.14	0.24	0.21
1167	CA14	carbonic anhydrase XIV	-0.03	-0.03	0.27	0.06	0.36	0.50	0.70
1168	SOX3	SRY (sex determining region Y)-box 3	0.14	-0.28	0.02	0.14	0.50	0.31	0.40
1169	—	—	-0.02	-0.20	-0.01	0.22	0.24	0.17	0.36
1170	ATGAY	ataxia, cerebellar, Cayman type	0.41	-0.59	0.30	0.18	0.15	0.55	0.57
1171	PIM2	pim-2 oncogene	0.50	0.23	0.06	-0.73	0.10	-0.06	0.05
1172	TEX14	testis expressed 14	0.42	-0.23	0.30	-0.19	-0.39	0.17	0.25
1173	ZNF468	zinc finger protein 468	0.41	0.07	0.17	-0.48	-0.33	0.19	0.45
1174	—	—	0.41	0.02	-0.02	-0.43	-0.06	0.52	0.52
1175	ATXN7L1	ataxin 7-like 1	0.20	-0.05	0.87	-0.15	-0.28	0.31	0.10
1176	IGDCC3	immunoglobulin superfamily, DCC subclass, member 3	0.70	-0.75	0.01	0.05	-0.34	-0.04	0.58
1177	MEI	malic enzyme 1, NADP(+)-dependent, cytosolic	1.26	-0.49	-0.74	-0.77	-1.01	-1.11	-0.41
1178	—	—	1.25	-0.32	-0.11	-0.93	-0.58	-1.05	0.16
1179	—	—	0.61	0.08	-0.22	-0.69	-0.53	-0.80	0.05

1180	GPR143	G protein-coupled receptor 143	1.06	-0.47	-0.16	-0.58	-0.29	0.14	0.28
1181	—	—	1.06	0.19	-0.10	-1.26	-0.42	-0.48	0.54
1182	VWDE	von Willebrand factor D and EGF domains	-0.83	0.83	-0.61	0.00	-0.78	-0.59	-0.46
1183	SSX4 /// SSX4B	synovial sarcoma, X breakpoint 4 /// synovial sarcoma, X breakpoint 4B	-0.21	-0.01	-0.59	0.22	0.17	-0.69	-0.66
1184	CHST9	carbohydrate (N-acetyl)galactosamine 4-O sulfotransferase 9	-0.40	0.18	-0.37	0.22	-0.43	-0.63	-0.38
1185	GNTNAP2	contactin associated protein-like 2	-0.54	0.00	-0.96	0.54	-0.39	-0.76	-0.16
1186	—	—	-0.86	0.02	-0.73	0.85	-0.52	-0.72	-0.69
1187	LOC153469	hypothetical protein LOC153469	0.17	0.82	0.40	-0.99	0.01	0.34	0.24
1188	GPC4	glypican 4	0.55	0.35	0.44	-0.80	-0.21	0.12	-0.05
1189	SMPDL3B	sphingomyelin phosphodiesterase, acid-like 3B	0.20	0.36	0.11	-0.56	-0.37	-0.29	0.14
1190	WNK3	WNK lysine deficient protein kinase 3	0.04	0.44	0.07	-0.47	0.17	0.06	-0.02
1191	ZFP42	zinc finger protein 42 homolog (mouse)	0.58	-0.85	0.46	0.27	0.72	0.27	-0.15
1192	ZFP42	zinc finger protein 42 homolog (mouse)	0.39	-0.02	0.17	-0.37	0.46	-0.08	-0.60
1193	NMU	neuromedin U	-0.13	-0.06	0.10	0.19	-0.21	-0.01	0.41
1194	CD24	CD24 molecule	-0.08	0.03	-0.04	0.04	0.04	0.08	0.04
1195	CD24	CD24 molecule	-0.08	-0.05	0.00	0.12	0.10	0.21	0.03
1196	SCNN1A	sodium channel, nonvoltage-gated 1 alpha	-0.27	-0.04	-0.28	0.32	-0.02	-0.12	-0.01
1197	RPMS2	RNA binding protein with multiple splicing 2	-0.05	-0.30	-0.02	0.38	0.05	0.05	0.14
1198	FREM2	FRAS1 related extracellular matrix protein 2	-0.09	-0.16	-0.13	0.25	0.23	0.08	-0.02
1199	LOC100131138	similar to hCG2040918	0.22	-0.43	-0.15	0.21	0.09	-0.17	-0.05
1200	GALB1	galbindin 1, 28kDa	0.04	-0.11	0.03	0.07	0.16	0.10	0.07
1201	POU5F1B	POU class 5 homeobox 1B	0.02	-0.15	0.11	0.13	-0.04	0.09	0.15
1202	OTX2	orthodenticle homeobox 2	-0.16	0.08	0.17	0.08	0.04	0.02	-0.18
1203	SOX2	SRY (sex determining region Y)-box 2	-0.09	-0.26	0.13	0.34	-0.03	-0.01	-0.24
1204	LRN28B	lin-28 homolog B (C. elegans)	-0.21	0.13	-0.09	0.07	-0.20	-0.15	-0.25
1205	CD24	CD24 molecule	-0.03	-0.14	-0.04	0.16	0.11	0.02	-0.39
1206	C1orf187	chromosome 1 open reading frame 187	-0.09	-0.42	-0.15	0.51	0.50	0.28	0.48
1207	—	—	-0.17	-0.20	-0.01	0.37	0.35	0.12	0.28
1208	ZFP42	zinc finger protein 42 homolog (mouse)	0.05	-0.40	0.14	0.35	0.33	0.24	0.33
1209	RMST	rhabdomyosarcoma 2 associated transcript (non-protein coding)	-0.57	0.48	0.15	0.09	0.13	0.27	0.36
1210	—	—	-0.29	0.30	-0.14	0.00	0.26	0.29	0.24
1211	CXADR	coxsaackie virus and adanavirus receptor	0.15	0.23	0.01	-0.39	-0.60	-0.48	-0.72
1212	GABRB3	gamma-aminobutyric acid (GABA) A receptor, beta 3	-0.15	0.31	0.03	-0.15	-0.43	-0.28	-0.55
1213	KCNN2	potassium intermediate/small conductance calcium-activated channel, subfamily N, member 2	0.01	0.11	-0.12	-0.13	-0.45	-0.05	-0.19
1214	IGF2BP1	insulin-like growth factor 2 mRNA binding protein 1	-0.25	0.17	0.12	0.08	-0.28	-0.49	-0.84
1215	CLDN6	claudin 6	0.14	-0.25	-0.04	0.11	-1.17	-0.72	-0.77
1216	TEX15	testis expressed 15	-0.26	0.13	-0.49	0.13	-0.86	-0.72	-0.71
1217	ZIC3	Zic family member 3 (odd-paired homolog, Drosophila)	0.32	0.05	-0.37	-0.37	-0.22	-0.33	-0.19
1218	PRPM4	reprimo, TP53 dependent G2 arrest mediator candidate	0.49	-0.36	-0.36	-0.13	-0.07	-0.25	-0.33
1219	CD24	CD24 molecule	0.05	0.01	0.01	-0.06	0.12	-0.03	-0.46
1220	—	—	0.19	-0.14	-0.19	-0.05	0.11	-0.21	-0.20
1221	CDH3	cadherin 3, type 1, P-cadherin (placental)	0.24	-0.52	-0.16	0.28	-0.37	-0.11	-0.36

1222	LINGO1	leucine rich repeat and Ig domain containing 1	0.17	-0.33	-0.11	0.15	-0.60	-0.46	-0.40
1223	SEMA6A	sem domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6A	-0.08	-0.62	-0.31	0.70	-0.34	-0.58	-0.43
1224	LECT1	leukocyte cell derived chemotaxin 1	-0.42	0.47	-0.03	-0.05	0.16	0.55	0.46
1225	DCX	doublecortin	-0.54	0.88	0.00	-0.34	0.41	-0.13	0.07
1226	GLIL3	galactosidase, beta 1-like 3	-0.28	0.49	-0.05	0.21	0.10	-0.04	0.26
1227	OTX2	orthodenticle homeobox 2	-0.32	0.45	0.07	-0.13	0.07	0.10	-0.12
1228	SOX11	SRY (sex determining region, Y)-box 11	-0.09	0.03	-0.08	0.06	0.33	0.16	0.37
1229	ZNF165	zinc finger protein 165	-0.16	0.19	0.01	-0.03	0.39	0.12	0.10
1230	SOX11	SRY (sex determining region, Y)-box 11	-0.23	-0.03	0.15	0.28	0.25	0.22	0.19
1231	—	—	-0.23	-0.12	-0.25	0.35	0.25	0.05	0.05
1232	MYCN	v-myc myelocytomatosis viral related oncogene, neuroblastoma derived (avian)	0.01	-0.11	-0.03	0.10	0.23	-0.01	-0.15
1233	NANOG	Nanog homeobox	0.13	-0.12	0.07	-0.01	0.27	0.00	-0.12
1234	POU5F1 /// POU5F1B /// POU5F1P3 /// POU5F1P4	POU class 5 homeobox 1 /// POU class 5 homeobox 1B /// POU class 5 homeobox 1 pseudogene 3 /// POU class 5 homeobox 1 pseudogene 4	0.07	-0.10	-0.02	0.03	-0.03	0.03	0.06
1235	—	—	0.04	0.09	-0.01	-0.13	0.02	-0.03	0.09
1236	GALB1	calbindin 1, 28kDa	0.03	-0.14	0.25	0.10	0.27	0.13	0.15
1237	C8orf168	chromosome 8 open reading frame 168	0.27	-0.01	0.07	-0.26	0.16	0.21	0.34
1238	SLC7A3	solute carrier family 7 (cationic amino acid transporter, y+ system), member 3	0.33	-0.40	-0.10	0.08	0.27	-0.01	-0.20
1239	KIF26A	kinesin family member 26A	0.10	0.07	-0.31	-0.17	0.46	0.25	-0.08
1240	GAP43	growth associated protein 43	-0.04	-0.23	-0.26	0.27	0.18	-0.03	0.06
1241	JPH3	junctophilin 3	-0.17	-0.33	-0.29	0.50	0.22	0.20	0.22
1242	CR1 /// CR1L	complement component (3b/4b) receptor 1 (Knops blood group) /// complement component (3b/4b) receptor 1-like	0.01	-0.12	-0.30	0.11	-0.02	0.31	0.00
1243	GABRA5	gamma-aminobutyric acid (GABA) A receptor, alpha 5	-0.31	-0.06	0.08	0.37	-0.09	-0.26	-0.20
1244	KIF5C	kinesin family member 5C	0.13	-0.01	0.09	-0.12	-0.36	-0.06	-0.24
1245	TUBB2B	tubulin, beta 2B	0.08	-0.09	0.05	0.01	-0.21	-0.28	-0.12
1246	DNMT3B	DNA (cytosine-5-) methyltransferase 3 beta	-0.01	-0.05	0.00	0.08	-0.14	-0.03	-0.15
1247	SOX2	SRY (sex determining region, Y)-box 2	-0.15	0.07	-0.15	0.07	-0.30	-0.26	-0.33
1248	DDX25	DEAD (Asp-Glu-Ala-Asp) box polypeptide 25	0.03	-0.01	-0.47	-0.02	-0.04	0.03	-0.09
1249	PTPRZ1	protein tyrosine phosphatase, receptor-type, Z polypeptide 1	-0.14	0.17	-0.12	-0.03	-0.17	-0.13	-0.15
1250	UNC5D	unc-5 homolog D (C. elegans)	-0.11	0.08	-0.07	0.02	-0.06	-0.10	-0.25
1251	—	—	-0.12	0.19	-0.40	-0.07	-0.12	-0.24	-0.24
1252	VASH2	vasohibin 2	-0.07	-0.13	-0.34	0.19	-0.24	-0.25	-0.36
1253	GNTAP2	contactin associated protein-like 2	-0.26	0.15	-0.37	0.10	-0.57	-0.34	-0.19
1254	C9orf135	chromosome 9 open reading frame 135	-0.22	0.17	-0.21	0.05	-0.69	-0.34	0.08
1255	LRRTM4	leucine rich repeat transmembrane neuronal 4	-0.28	0.15	0.09	0.13	-0.34	-0.42	0.18
1256	MBD2	methyl-CpG binding domain protein 2	-0.28	0.42	-0.10	-0.14	0.06	-0.01	0.16
1257	MARVELD3	methyl-CpG binding domain protein 3	-0.10	0.12	-0.03	-0.02	-0.08	0.03	0.01
1258	—	—	0.03	0.29	-0.24	-0.31	-0.32	0.08	0.29

[illegible]

1301	COX6A1	cytochrome c oxidase subunit VIa polypeptide 1	1.07	0.11	-0.37	-1.18	-0.87	-1.15	0.05
1302	TDGF1 /// TDGF3	teratocarcinoma-derived growth factor 1 ///	0.05	-0.15	-0.01	0.09	0.05	-0.06	-0.01
1303	HESRG	teratocarcinoma-derived growth factor 3, pseudogene hypothetical LOC790952	-0.27	0.24	-0.02	0.03	-0.01	-0.01	-0.09
1304	NLRP2	NLR family, pyrin domain containing 2	-0.10	-0.71	0.62	0.81	-3.20	1.27	0.48

[0070] [表 2 B] 第 2 遺伝子群

	Gene Symbol	Gene Title
1	GRIA3	glutamate receptor, ionotropic, AMPA 3
2	STC2	stanniocalcin 2
3	TFPI2	tissue factor pathway inhibitor 2
4	NPPB	natriuretic peptide precursor B
5	INHBE	inhibin, beta E
6	PCSK9	proprotein convertase subtilisin/kexin type 9
7	SLC2A3	solute carrier family 2 (facilitated glucose transporter), member 3
8	TNFRSF8	tumor necrosis factor receptor superfamily, member 8
9	UTF1	undifferentiated embryonic cell transcription factor 1
10	HMGAI	high mobility group A1-hook 1
11	KIF1A	kinesin family member 1A
12	ZNF678	zinc finger protein 678
13	FANCB	Fanconi anemia, complementation group B
14	DDX11	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 11 (CHL1-like helicase homolog, <i>S. cerevisiae</i>)
15	C14orf106	chromosome 14 open reading frame 106
16	ZNF92	zinc finger protein 92
17	ASPM	asp (abnormal spindle) homolog, microcephaly associated (<i>Drosophila</i>)
18	ZNF770	zinc finger protein 770
19	ATP11C	ATPase, class VI, type 11C
20	ATRXL	alpha thalassemia/mental retardation syndrome X-linked (RAD54 homolog, <i>S. cerevisiae</i>)
21	ANTXR1	anthrax toxin receptor 1
22	SNORD116@	small nucleolar RNA, C/D box 116 cluster
23	COL1A1	collagen, type XI, alpha 1
24	LOC643401	hypothetical protein LOC643401
25	CNKSR2	connector enhancer of kinase suppressor of Ras 2
26	DNA2	DNA replication helicase 2 homolog (yeast)
27	PLK4	polo-like kinase 4 (<i>Drosophila</i>)
28	FLJ35848	hypothetical protein FLJ35848
29	DLGAP5	discs, large (<i>Drosophila</i>) homolog-associated protein 5
30	ELAVL2	ELAV (embryonic lethal, abnormal vision, <i>Drosophila</i>)-like 2 (Hu antigen B)
31	ZNF391	zinc finger protein 391
32	NCAPG2	non-SMC condensin II complex, subunit G2
33	SLC16A1	solute carrier family 16, member 1 (monocarboxylic acid transporter 1)
34	MCM4	minichromosome maintenance complex component 4
35	FGD6	FYVE, RhoGEF and PH domain containing 6
36	WDHD1	WD repeat and HMG-box DNA binding protein 1
37	CCDC88A	coiled-coil domain containing 88A
38	BIRC5	baculoviral IAP repeat-containing 5
39	CCNA2	cyclin A2
40	SRp35	serine-arginine repressor protein (35 kDa)
41	MAD2L1	MAD2 mitotic arrest deficient-like 1 (yeast)
42	PDPN	podoplanin
43	RAD51AP1	RAD51 associated protein 1
44	CENPH	centromere protein H
45	NCAPH	non-SMC condensin I complex, subunit H
46	FAM72A /// FAM72B /// FAM72C /// FAM72D	family with sequence similarity 72, member A /// family with sequence similarity 72, member B /// family with sequence similarity 72, member C /// family with sequence similarity 72, member D
47	TMEFF1	transmembrane protein with EGF-like and two follistatin-like domains 1
48	PAICS	phosphoribosylaminoimidazole carboxylase, phosphoribosylaminoimidazole succinocarboxamide synthetase
49	DBF4	DBF4 homolog (<i>S. cerevisiae</i>)
50	HMMR	hyaluronan-mediated motility receptor (RHAMM)
51	FXSD7	FXSD domain containing ion transport regulator 7
52	FEN1	flap structure-specific endonuclease 1
53	CDG25C	cell division cycle 25 homolog C (<i>S. pombe</i>)

54	TPM1	tropomyosin 1 (alpha)
55	CCNF	cyclin F
56	CDCA5	cell division cycle associated 5
57	HJURP	Holliday junction recognition protein
58	SPAG5	sperm associated antigen 5
59	RFWF3	ring finger and WD repeat domain 3
60	C21orf45	chromosome 21 open reading frame 45
61	CDCA2	cell division cycle associated 2
62	TFDP2	transcription factor Dp-2 (E2F dimerization partner 2)
63	PRIM1	primase, DNA, polypeptide 1 (49kDa)
64	SEPHS1	selenophosphate synthetase 1
65	MCM2	minichromosome maintenance complex component 2
66	FAM64A	family with sequence similarity 64, member A
67	BEND3	BEN domain containing 3
68	VRK1	vaccinia related kinase 1
69	POLE2	polymerase (DNA directed), epsilon 2 (p59 subunit)
70	DSCC1	defective in sister chromatid cohesion 1 homolog (S. cerevisiae)
71	GIN52	GIN5 complex subunit 2 (Psf2 homolog)
72	CCNJ	cyclin J
73	EXO1	exonuclease 1
74	CDG2	cell division cycle 2, G1 to S and G2 to M
75	RCO2	regulator of chromosome condensation 2
76	FLJ20674	hypothetical protein FLJ20674
77	CCNB1	cyclin B1
78	RFC3	replication factor C (activator 1) 3, 38kDa
79	FANCD2	Fanconi anemia, complementation group D2
80	RRM2	ribonucleotide reductase M2
81	CENPN	centromere protein N
82	RTKN2	rotectin 2
83	GRB14	growth factor receptor-bound protein 14
84	PFAS	phosphoribosylformylglycinamide synthase
85	KIF15	kinesin family member 15
86	RAD54B	RAD54 homolog B (S. cerevisiae)
87	RAD54L	RAD54-like (S. cerevisiae)
88	PPAT	phosphoribosyl pyrophosphate amidotransferase
89	ZNF814	zinc finger protein 814
90	ZNF462	zinc finger protein 462
91	APIS3	adaptor-related protein complex 1, sigma 3 subunit
92	LHFPL4	lipoma HMGIC fusion partner-like 4
93	ZNF114	zinc finger protein 114
94	ZWINT	ZW10 interactor
95	C1orf135	chromosome 1 open reading frame 135
96	NODAL	nodal homolog (mouse)
97	CBS	cystathionine-beta-synthase
98	TPX2	TPX2, microtubule-associated, homolog (Xenopus laevis)
99	CDT1	chromatin licensing and DNA replication factor 1
100	MCM7	minichromosome maintenance complex component 7
101	TUBB2A /// TUBB2B	tubulin, beta 2A /// tubulin, beta 2B
102	ESPL1	extra spindle pole bodies homolog 1 (S. cerevisiae)
103	KCNQ2	potassium voltage-gated channel, KQT-like subfamily, member 2
104	UBE2S	ubiquitin-conjugating enzyme E2S
105	TEAD4	TEA domain family member 4
106	SCLY	selenocysteine lyase
107	CENPA	centromere protein A
108	CDCA3	cell division cycle associated 3
109	DHFR	dihydrofolate reductase
110	PHF17	PHD finger protein 17
111	MSH6	mutS homolog 6 (E. coli)
112	CTPS	CTP synthase
113	KIF2C	kinesin family member 2C
114	FOXM1	forkhead box M1
115	GTSE1	G-2 and S-phase expressed 1
116	AURKA	aurora kinase A
117	FBXO11	F-box protein 11

118	NLN	neurolysin (metallopeptidase M3 family)
119	LAPTM4B	lysosomal protein transmembrane 4 beta
120	TMPO	thymopoietin
121	EZH2	enhancer of zeste homolog 2 (Drosophila)
122	CDG7	cell division cycle 7 homolog (S. cerevisiae)
123	NETO1	neuropilin (NRP) and tolloid (TLL)-like 1
124	KIF23	kinesin family member 23
125	KIF18B	kinesin family member 18B
126	FANCI	Fanconi anemia, complementation group I
127	MCM6	minichromosome maintenance complex component 6
128	MSH2	mutS homolog 2, colon cancer, nonpolyposis type 1 (E. coli)
129	NGAPG	non-SMC condensin I complex, subunit G
130	MASTL	microtubule associated serine/threonine kinase-like
131	CENPJ	centromere protein J
132	KIF11	kinesin family member 11
133	TOP2A	topoisomerase (DNA) II alpha 170kDa
134	ZNF643	zinc finger protein 643
135	PSIP1	PC4 and SFRS1 interacting protein 1
136	ORC6L	origin recognition complex, subunit 6 like (yeast)
137	KPNA2	karyopherin alpha 2 (RAG cohort 1, importin alpha 1)
138	NOP16	NOP16 nucleolar protein homolog (yeast)
139	NUSAP1	nucleolar and spindle associated protein 1
140	CT3orf34	chromosome 13 open reading frame 34
141	C6orf173	chromosome 6 open reading frame 173
142	RNASEH2A	ribonuclease H2, subunit A
143	CCNE1	cyclin E1
144	KIF14	kinesin family member 14
145	ZNF788	zinc finger family member 788
146	CASP3	caspase 3, apoptosis-related cysteine peptidase
147	RAD51	RAD51 homolog (RecA homolog, E. coli) (S. cerevisiae)
148	SUV39H2	suppressor of variegation 3-9 homolog 2 (Drosophila)
149	UCHL1	ubiquitin carboxyl-terminal esterase L1 (ubiquitin thiolesterase)
150	THAP9	THAP domain containing 9
151	SKP2	S-phase kinase-associated protein 2 (p45)
152	UBE2T	ubiquitin-conjugating enzyme E2T (putative)
153	NUF2	NUF2, NDC80 kinetochore complex component, homolog (S. cerevisiae)
154	RFC4	replication factor C (activator 1) 4, 37kDa
155	NDC80	NDC80 homolog, kinetochore complex component (S. cerevisiae)
156	NEK2	NIMA (never in mitosis gene a)-related kinase 2
157	TRIM6	tripartite motif-containing 6
158	CKS1B	CDC28 protein kinase regulatory subunit 1B
159	CCNB2	cyclin B2
160	GMNN	geminin, DNA replication inhibitor
161	CENPK	centromere protein K
162	FAM54A	family with sequence similarity 54, member A
163	PTTG1	pituitary tumor-transforming 1
164	TEAD2	TEA domain family member 2
165	CDCA8	cell division cycle associated 8
166	FBXO5	F-box protein 5
167	BXDC2	brix domain containing 2
168	MTA3	metastasis associated 1 family, member 3
169	TIMELESS	timeless homolog (Drosophila)
170	CCDC138	coiled-coil domain containing 138
171	EEF1E1	eukaryotic translation elongation factor 1 epsilon 1
172	CCDC150	coiled-coil domain containing 150
173	LYAR	Ly1 antibody reactive homolog (mouse)
174	SLC6A15	solute carrier family 6 (neutral amino acid transporter), member 15
175	MRS2	MRS2 magnesium homeostasis factor homolog (S. cerevisiae)
176	BRCA2	breast cancer 2, early onset
177	MCM10	minichromosome maintenance complex component 10

178	IC12orf48	chromosome 12 open reading frame 48
179	CCL26	chemokine (C-C motif) ligand 26
180	NSBP1	nucleosomal binding protein 1
181	HESX1	HESX homeobox 1
182	TNNT1	troponin T type 1 (skeletal, slow)
183	GUCA1A	guanylate cyclase activator 1A (retina)
184	UBE2C	ubiquitin-conjugating enzyme E2C
185	CDC6	cell division cycle 6 homolog (S. cerevisiae)
186	DIAPH2	diaphanous homolog 2 (Drosophila)
187	GAL	galanin prepropeptide
188	CHAF1A	chromatin assembly factor 1, subunit A (p150)
189	MCM5	minichromosome maintenance complex component 5
190	GALNT13	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 13 (GalNAc-T13)
191	GAL3ST3	galactose-3-O-sulfotransferase 3
192	FAM46B	family with sequence similarity 46, member B
193	LOC389857	hypothetical protein
194	JARID2	jumonji, AT rich interactive domain 2
195	SILV	silver homolog (mouse)
196	IGFBPL1	insulin-like growth factor binding protein-like 1
197	MBD2	methyl-CpG binding domain protein 2
198	GINS1	GINS complex subunit 1 (Psf1 homolog)
199	HAS3	hyaluronan synthase 3
200	NASP	nuclear autoantigenic sperm protein (histone-binding)
201	MTF2	metal response element binding transcription factor 2
202	PMAIP1	phorbol-12-myristate-13-acetate-induced protein 1
203	MATR3	Matrin 3
204	CRMP1	collapsin response mediator protein 1
205	CBX2	chromobox homolog 2 (Pc class homolog, Drosophila)
206	WDR72	WD repeat domain 72
207	CDCA7	cell division cycle associated 7
208	FOXA3	forkhead box A3
209	SPC25	SPC25, NDC80 kinetochore complex component, homolog (S. cerevisiae)
210	BLM	Bloom syndrome, RecQ helicase-like
211	C11orf82	chromosome 11 open reading frame 82
212	CHRNA5	cholinergic receptor, nicotinic, alpha 5
213	GDAP1	ganglioside-induced differentiation-associated protein 1
214	CHST4	carbohydrate (N-acetylglucosamine 6-O) sulfotransferase 4
215	DNMT3A	DNA (cytosine-5)-methyltransferase 3 alpha
216	KLHL7	kelch-like 7 (Drosophila)
217	DTL	denticless homolog (Drosophila)
218	TNNI3	troponin I type 3 (cardiac)
219	ZNF738	zinc finger protein 738
220	HOMER1	homer homolog 1 (Drosophila)
221	TACC3	transforming, acidic coiled-coil containing protein 3
222	MCM3	minichromosome maintenance complex component 3
223	FAM83D	family with sequence similarity 83, member D
224	BUB1	budding uninhibited by benzimidazoles 1 homolog (yeast)
225	IPW	imprinted in Prader-Willi syndrome (non-protein coding)
226	FERMT1	fermitin family homolog 1 (Drosophila)
227	STRBP	spermatid perinuclear RNA binding protein
228	FAM124A	family with sequence similarity 124A
229	COMM7	COMM domain containing 7
230	SYT6	synaptotagmin VI
231	CLDN7	claudin 7
232	RND2	Rho family GTPase 2
233	AIM1L	absent in melanoma 1-like
234	LOC253842	hypothetical protein LOC253842
235	CDC20	cell division cycle 20 homolog (S. cerevisiae)
236	AURKB	aurora kinase B
237	OIP5	Opa interacting protein 5
238	LOC100128191	hypothetical protein LOC100128191
239	RASL11B	RAS-like, family 11, member B
240	GULP1	GULP, engulfment adaptor PTB domain containing 1

241	AP3B2	adaptor-related protein complex 3, beta 2 subunit
242	HMGB3	high-mobility group box 3
243	CXCL5	chemokine (C-X-C motif) ligand 5
244	PHF21B	PHD finger protein 21B
245	MND1	meiotic nuclear divisions 1 homolog (S. cerevisiae)
246	MLF1IP	MLF1 interacting protein
247	ZNF93	zinc finger protein 93
248	KIAA1661	KIAA1661 protein
249	USP9X	ubiquitin specific peptidase 9, X-linked
250	HIST1H2AM	histone cluster 1, H2am
251	LOC284242	hypothetical protein LOC284242
252	BPTF	bromodomain PHD finger transcription factor
253	C13orf38	chromosome 13 open reading frame 38
254	NPM3	nucleophosmin/nucleoplasmin 3
255	C16orf75	chromosome 16 open reading frame 75
256	SKA1	spindle and kinetochore associated complex subunit 1
257	LOC647946	hypothetical protein LOC647946
258	NPFFR2	neuropeptide FF receptor 2
259	GIN54	GIN5 complex subunit 4 (Sld5 homolog)
260	RAB38	RAB38, member RAS oncogene family
261	BCL2L12	BCL2-like 12 (proline rich)
262	C9orf100	chromosome 9 open reading frame 100
263	TMEM132D	transmembrane protein 132D
264	FLJ35934	FLJ35934 protein
265	HOXC6	homeobox C6
266	PCDH7	protocadherin 7
267	SLC7A5	solute carrier family 7 (cationic amino acid transporter, y+ system), member 5
268	CUL4A	cullin 4A
269	KIF4A	kinesin family member 4A
270	IL1A	interleukin 1, alpha
271	AFP	alpha-fetoprotein
272	ARHGAP28	Rho GTPase activating protein 28
273	UPF3B	UPF3 regulator of nonsense transcripts homolog B (yeast)
274	HIST1H4J	histone cluster 1, H4j
275	GPC2	glypican 2
276	NLRP12	NLR family, pyrin domain containing 12
277	DPYSL3	dihydropyrimidinase-like 3
278	TCF3	transcription factor 3 (E2A immunoglobulin enhancer binding factors E12/E47)
279	NR5A2	nuclear receptor subfamily 5, group A, member 2
280	MYH10	myosin, heavy chain 10, non-muscle
281	GLI2	GLI family zinc finger 2
282	ANKS6	ankyrin repeat and sterile alpha motif domain containing 6
283	CENPE	centromere protein E, 312kDa
284	CENPF	centromere protein F, 350/400ka (mitotin)
285	CHML	choroideremia-like (Rab escort protein 2)
286	EDIL3	EGF-like repeats and discoidin I-like domains 3
287	ATAD5	ATPase family, AAA domain containing 5
288	SKIL	SKI-like oncogene
289	KIF18A	kinesin family member 18A
290	N4BP2	NEDD4 binding protein 2
291	TP53	tumor protein p53
292	OSBPL10	oxysterol binding protein-like 10
293	USP28	ubiquitin specific peptidase 28
294	ZNF398	zinc finger protein 398
295	DEPDC1	DEP domain containing 1
296	CENPI	centromere protein I
297	HSPA4	heat shock 70kDa protein 4
298	HAUS6	HAUS augmin-like complex, subunit 6
299	ZNF253	zinc finger protein 253
300	ARHGAP11A	Rho GTPase activating protein 11A
301	PAP2D	phosphatidic acid phosphatase type 2
302	SMC3	structural maintenance of chromosomes 3

303	CDYL	chromodomain protein, Y-like
304	G2E3	G2/M-phase specific E3 ubiquitin ligase
305	MKI67	antigen identified by monoclonal antibody Ki-67
306	TRHDE	thyrotropin-releasing hormone degrading enzyme
307	IGF2BP3	insulin-like growth factor 2 mRNA binding protein 3
308	DIAPH3	diaphanous homolog 3 (Drosophila)
309	C4orf21	chromosome 4 open reading frame 21
310	KNTC1	kinetochore associated 1
311	ZNF195	zinc finger protein 195
312	C18orf54	chromosome 18 open reading frame 54
313	DKC1	dyskeratosis congenita 1, dyskerin
314	FLJ32810	Rho-type GTPase-activating protein FLJ32810
315	ZNF43	zinc finger protein 43
316	WDR89	WD repeat domain 89
317	ITTF2	transcription termination factor, RNA polymerase II
318	ZNF254	zinc finger protein 254
319	QSER1	glutamine and serine rich 1
320	ZNF675	zinc finger protein 675
321	ZNF721	zinc finger protein 721
322	ESCO1	establishment of cohesion 1 homolog 1 (S. cerevisiae)
323	POLQ	polymerase (DNA directed), theta
324	HIMGA2	high mobility group AT-hook 2
325	TSR1	TSR1, 20S rRNA accumulation, homolog (S. cerevisiae)
326	XPO5	exportin 5
327	PAWR	PRKC, apoptosis, WT1, regulator
328	ZNF708	zinc finger protein 708
329	ZNF589	zinc finger protein 589
330	ZIK1	zinc finger protein interacting with K protein 1 homolog (mouse)
331	STIL	SCL/TAL1 interrupting locus
332	CDK6	cyclin-dependent kinase 6
333	TMEM48	transmembrane protein 48
334	CCDC18	coiled-coil domain containing 18
335	ESF1	ESF1, nucleolar pre-rRNA processing protein, homolog (S. cerevisiae)
336	API5	apoptosis inhibitor 5
337	SGOL2	shugoshin-like 2 (S. pombe)
338	ESCO2	establishment of cohesion 1 homolog 2 (S. cerevisiae)
339	TMEM132B	transmembrane protein 132B
340	ZNF107	zinc finger protein 107
341	G3BP2	GTPase activating protein (SH3 domain) binding protein 2
342	CXorf15	chromosome X open reading frame 15
343	PLK1	polo-like kinase 1 (Drosophila)
344	KLRG2	killer cell lectin-like receptor subfamily G, member 2
345	KIF20B	kinesin family member 20B
346	C12orf35	chromosome 12 open reading frame 35
347	ZNF680	zinc finger protein 680
348	ACTN3	actinin, alpha 3
349	DGP2	DGP2 decapping enzyme homolog (S. cerevisiae)
350	CER1	cerberus 1, cysteine knot superfamily, homolog (Xenopus laevis)
351	VWDE	von Willebrand factor D and EGF domains
352	CHM	choroideremia (Rab escort protein 1)
353	PHF3	PHD finger protein 3
354	ZNF644	zinc finger protein 644
355	ANKRD32	ankyrin repeat domain 32
356	TPP2	tripeptidyl peptidase II
357	HSPH1	heat shock 105kDa/110kDa protein 1
358	LOC100129064 /// LOC100131360 /// LOC100131868 /// PPP4R2	hypothetical LOC100129064 /// similar to protein phosphatase 4 regulatory subunit 2 /// similar to PPP4R2 protein /// protein phosphatase 4, regulatory subunit 2
359	CNOT1	CCR4-NOT transcription complex, subunit 1
360	PRPF4B	PRP4 pre-mRNA processing factor 4 homolog B (yeast)
361	NUP133	nucleoporin 133kDa

362	LARS	leucyl-tRNA synthetase
363	BCLAF1	BCL2-associated transcription factor 1
364	DHX9	DEAH (Asp-Glu-Ala-His) box polypeptide 9
365	SUPT16H	suppressor of Ty 16 homolog (S. cerevisiae)
366	RBAK	RB-associated KRAB zinc finger
367	ERI1	exoribonuclease 1
368	USP25	ubiquitin specific peptidase 25
369	EPRS	glutamyl-prolyl-tRNA synthetase
370	RECQL	RecQ protein-like (DNA helicase Q1-like)
371	GPR176	G protein-coupled receptor 176
372	SCD	stearoyl-CoA desaturase (delta-9-desaturase)
373	FAM126A	family with sequence similarity 126, member A
374	MIPOL1	mirror-image polydactyly 1
375	GEN1	Gen homolog 1, endonuclease (Drosophila)
376	UBE3A	ubiquitin protein ligase E3A
377	FAR1	fatty acyl CoA reductase 1
378	ZNF84	zinc finger protein 84
379	DNAJC10	DnaJ (Hsp40) homolog, subfamily C, member 10
380	IGF2BP2	insulin-like growth factor 2 mRNA binding protein 2
381	LRRIG3	leucine-rich repeats and IQ motif containing 3
382	ZNF569	zinc finger protein 569
383	TRIM37	tripartite motif-containing 37
384	MTHFD1L	methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 1-like
385	PRIM2	primase, DNA, polypeptide 2 (58kDa)
386	NVL	nuclear VCP-like
387	RPAP3	RNA polymerase II associated protein 3
388	ATAD2	ATPase family, AAA domain containing 2
389	BCAT1	branched chain aminotransferase 1, cytosolic
390	ASCC3	activating signal cointegrator 1 complex subunit 3
391	MED20	mediator complex subunit 20
392	ZNF146	zinc finger protein 146
393	RBM26	RNA binding motif protein 26
394	ANLN	anillin, actin binding protein
395	HMGCR	3-hydroxy-3-methylglutaryl-Coenzyme A reductase
396	LARP4	La ribonucleoprotein domain family, member 4
397	SQLE	squalene epoxidase
398	GART	phosphoribosylglycinamide formyltransferase, phosphoribosylglycinamide synthetase, phosphoribosylaminoimidazole synthetase
399	VCAN	versican
400	RIF1	RAP1 interacting factor homolog (yeast)
401	SOCS4	suppressor of cytokine signaling 4
402	PHIP	pleckstrin homology domain interacting protein
403	USO1	USO1 homolog, vesicle docking protein (yeast)
404	SR140	U2-associated SR140 protein
405	SMARCA4	SWI/SNF-related, matrix-associated actin-dependent regulator of chromatin, subfamily a, containing DEAD/H box 1
406	PRPF40A	PRP40 pre-mRNA processing factor 40 homolog A (S. cerevisiae)
407	RNGTT	RNA guanylyltransferase and 5'-phosphatase
408	ARNTL2	aryl hydrocarbon receptor nuclear translocator-like 2
409	ZNF567	zinc finger protein 567
410	PPPDE1	PPPDE peptidase domain containing 1
411	UCMA	upper zone of growth plate and cartilage matrix associated
412	SPRED1	sprouty-related, EVH1 domain containing 1
413	KPNB1	karyopherin (importin) beta 1
414	ZNF300	zinc finger protein 300
415	TMTC3	transmembrane and tetratricopeptide repeat containing 3
416	LAMA1	laminin, alpha 1
417	LOC169834	hypothetical protein LOC169834
418	LMCD1	LIM and cysteine-rich domains 1
419	ZNF638	zinc finger protein 638

420	FGF2	fibroblast growth factor 2 (basic)
421	KIAA1009	KIAA1009
422	RAI14	retinoic acid induced 14
423	EIF5B	eukaryotic translation initiation factor 5B
424	TYMS	thymidylate synthetase
425	SIX4	SIX homeobox 4
426	TPR	translocated promoter region (to activated MET oncogene)
427	KIAA1586	KIAA1586
428	SYT14	synaptotagmin XIV
429	RAD18	RAD18 homolog (S. cerevisiae)
430	CWC22	CWC22 spliceosome-associated protein homolog (S. cerevisiae)
431	GJA1	gap junction protein, alpha 1, 43kDa
432	MRE11A	MRE11 meiotic recombination 11 homolog A (S. cerevisiae)
433	RBBP6	retinoblastoma binding protein 6
434	RRAS2	related RAS viral (r-ras) oncogene homolog 2
435	ZMYM1	zinc finger, MYM-type 1
436	ZNF268	zinc finger protein 268
437	ELOVL4	elongation of very long chain fatty acids (FEN1/Elo2, SUR4/Elo3, yeast)-like 4
438	hCG 2024410 /// RPE	rcRPE /// ribulose-5-phosphate-3-epimerase
439	SHCBP1	SHC SH2-domain binding protein 1
440	IWS1	IWS1 homolog (S. cerevisiae)
441	RAB34	RAB34, member RAS oncogene family
442	CDC5L	CDC5 cell division cycle 5-like (S. pombe)
443	MPHOSPH10	M-phase phosphoprotein 10 (U3 small nucleolar ribonucleoprotein)
444	CTSC	cathepsin C
445	CCDC99	coiled-coil domain containing 99
446	MAGED4 /// MAGED4B	melanoma antigen family D, 4 /// melanoma antigen family D, 4B
447	SMARCA1	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 1
448	HIST1H2AG	histone cluster 1, H2ag
449	PSAT1	phosphoserine aminotransferase 1
450	GABPA	GA binding protein transcription factor, alpha subunit 60kDa
451	C10orf28	chromosome 10 open reading frame 28
452	UBA6	ubiquitin-like modifier activating enzyme 6
453	ALKBH8	alkB, alkylation repair homolog 8 (E. coli)
454	DIS3	DIS3 mitotic control homolog (S. cerevisiae)
455	TFAP2C	transcription factor AP-2 gamma (activating enhancer binding protein 2 gamma)
456	SERPINH1	serpin peptidase inhibitor, clade H (heat shock protein 47), member 1, (collagen binding protein 1)
457	MFAP2	microfibrillar-associated protein 2
458	PCNXL2	pecanex-like 2 (Drosophila)
459	FAM175A	family with sequence similarity 175, member A
460	RARS	arginyl-tRNA synthetase
461	PBK	PDZ binding kinase
462	GFPT2	glutamine-fructose-6-phosphate transaminase 2
463	RPL22L1	ribosomal protein L22-like 1
464	KDELCL1	KDEL (Lys-Asp-Glu-Leu) containing 1
465	BNC2	basenuclin 2
466	TNPO1	transportin 1
467	MGC45800	hypothetical LOC90768
468	RGS17	regulator of G-protein signaling 17
469	USP45	ubiquitin specific peptidase 45
470	PHF19	PHD finger protein 19
471	GDF11	growth differentiation factor 11
472	CABYR	calcium binding tyrosine-(Y)-phosphorylation regulated
473	AMMECR1	Alport syndrome, mental retardation, midface hypoplasia and elliptocytosis chromosomal region gene 1
474	MUDENG	MU-2/AP1M2 domain containing, death-inducing

475	C4orf46	chromosome 4 open reading frame 46
476	SMARCA5	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 5
477	TWISTNB	TWIST neighbor
478	TK1	thymidine kinase 1, soluble
479	ST8SIA3	ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 3
480	CRYGD	crystallin, gamma D
481	CDKN3	cyclin-dependent kinase inhibitor 3
482	RG9MTD1	RNA (guanine-9-) methyltransferase domain containing 1
483	SNX5	sorting nexin 5
484	NUFIP1	nuclear fragile X mental retardation protein interacting protein 1
485	FSD1	fibronectin type III and SPRY domain containing 1
486	PIF1	PIF1 5'-to-3' DNA helicase homolog (S. cerevisiae)
487	DNAH14	dynein, axonemal, heavy chain 14
488	SYNCRIP	synaptotagmin binding, cytoplasmic RNA interacting protein
489	GLMN	glomulin, FKBP associated protein
490	ORC4L	origin recognition complex, subunit 4-like (yeast)
491	BCCIP	BRCA2 and CDKN1A interacting protein
492	C1orf112	chromosome 1 open reading frame 112
493	DBC1	deleted in bladder cancer 1
494	HAUS1	HAUS augmin-like complex, subunit 1
495	DMKN	dermokine
496	EXOSC9	exosome component 9
497	LMNB2	lamin B2
498	NARG1	NMDA receptor regulated 1
499	TRIP13	thyroid hormone receptor interactor 13
500	PAK1IP1	PAK1 interacting protein 1
501	TIPIN	TIMELESS interacting protein
502	MGC11082	hypothetical LOC84777
503	UHRF1	ubiquitin-like with PHD and ring finger domains 1
504	C16orf88	chromosome 16 open reading frame 88
505	KIF20A	kinesin family member 20A
506	CENPQ	centromere protein Q
507	GABPB1	GA binding protein transcription factor, beta subunit 1
508	EXOSC3	exosome component 3
509	MRPS12	mitochondrial ribosomal protein S12
510	CENPM	centromere protein M
511	SPC24	SPC24, NDC80 kinetochore complex component, homolog (S. cerevisiae)
512	AEN	apoptosis enhancing nuclease
513	NUDT1	nudix (nucleoside diphosphate linked moiety X)-type motif 1
514	MAP9	microtubule-associated protein 9
515	FAM155A	family with sequence similarity 155, member A
516	KIAA1524	KIAA1524
517	CHAF1B	chromatin assembly factor 1, subunit B (p60)
518	TAF5L	TAF5-like RNA polymerase II, p300/CBP-associated factor (PCAF)-associated factor, 65kDa
519	TGIF1	TGFB-induced factor homeobox 1
520	MELK	maternal embryonic leucine zipper kinase
521	DDX21	DEAD (Asp-Glu-Ala-Asp) box polypeptide 21
522	CEP78	centrosomal protein 78kDa
523	HDAC2	histone deacetylase 2
524	ZNF281	zinc finger protein 281
525	RUVBL1	RuvB-like 1 (E. coli)
526	NUP107	nucleoporin 107kDa
527	ZWILCH	Zwilch, kinetochore associated, homolog (Drosophila)
528	SKA3	spindle and kinetochore associated complex subunit 3
529	TRIM59	tripartite motif-containing 59
530	ZNF215	zinc finger protein 215
531	CENPO	centromere protein O
532	KIAA0020	KIAA0020

533	ICXorf26	chromosome X open reading frame 26
534	CASC5	cancer susceptibility candidate 5
535	MTRF1	mitochondrial translational release factor 1
536	SH2D5	SH2 domain containing 5
537	FZD7	frizzled homolog 7 (Drosophila)
538	MPP6	membrane protein, palmitoylated 6 (MAGUK p55 subfamily member 6)
539	CHK1	CHK1 checkpoint homolog (S. pombe)
540	SLC39A10	solute carrier family 39 (zinc transporter), member 10
541	WDR75	WD repeat domain 75
542	CEBPZ	CCAAT/enhancer binding protein (C/EBP), zeta
543	CSE1L	CSE1 chromosome segregation 1-like (yeast)
544	ZNF670	zinc finger protein 670
545	SMC4	structural maintenance of chromosomes 4
546	KRR1	KRR1, small subunit (SSU) processome component, homolog (yeast)
547	TARS	threonyl-tRNA synthetase
548	ZNF397	zinc finger protein 397
549	IC17orf80	chromosome 17 open reading frame 80
550	SMC1A	structural maintenance of chromosomes 1A
551	DLAT	dihydrolipoamide S-acetyltransferase
552	IC1orf163	chromosome 1 open reading frame 163
553	SSB	Sjogren syndrome antigen B (autoantigen La)
554	MTAP	methylthioadenosine phosphorylase
555	PNN	pinin, desmosome associated protein
556	SKA2	spindle and kinetochore associated complex subunit 2
557	FLJ36848	hypothetical LOC647115
558	CKS2	CDC28 protein kinase regulatory subunit 2
559	DNAJC2	DnaJ (Hsp40) homolog, subfamily C, member 2
560	IC2orf44	chromosome 2 open reading frame 44
561	PRC1	protein regulator of cytokinesis 1
562	ATP5O /// DONSON	ATP synthase, H ⁺ transporting, mitochondrial F1 complex, O subunit /// downstream neighbor of SON
563	HSPD1	heat shock 60kDa protein 1 (chaperonin)
564	CEP55	centrosomal protein 55kDa
565	ARL5B	ADP-ribosylation factor-like 5B
566	ECT2	epithelial cell transforming sequence 2 oncogene
567	E2F7	E2F transcription factor 7
568	MATR3 /// SNHG4	matrin 3 /// small nucleolar RNA host gene 4 (non-protein coding)
569	UTP15	UTP15, U3 small nucleolar ribonucleoprotein, homolog (S. cerevisiae)
570	ELOVL6	ELOVL family member 6, elongation of long chain fatty acids (FEN1/Elo2, SUR4/Elo3-like, yeast)
571	ZNF616	zinc finger protein 616
572	SMG2	structural maintenance of chromosomes 2
573	ZNF141	zinc finger protein 141
574	SMC6	structural maintenance of chromosomes 6
575	WDR35	WD repeat domain 35
576	ZNF334	zinc finger protein 334
577	PIPG	peptidylprolyl isomerase G (cyclophilin G)
578	MURC	muscle-related coiled-coil protein
579	CEP152	centrosomal protein 152kDa
580	PTTG3P	pituitary tumor-transforming 3 (pseudogene)
581	CHK2	CHK2 checkpoint homolog (S. pombe)
582	NEIL3	nei endonuclease VIII-like 3 (E. coli)
583	IC5orf34	chromosome 5 open reading frame 34
584	GNL2	guanine nucleotide binding protein-like 2 (nucleolar)
585	DNTTIP2	deoxynucleotidyltransferase, terminal, interacting protein 2
586	NPM1	nucleophosmin (nucleolar phosphoprotein B23, numatrin)
587	ORC3L	origin recognition complex, subunit 3-like (yeast)
588	ZNF607	zinc finger protein 607
589	BAX	BCL2-associated X protein
590	CDK7	cyclin-dependent kinase 7

591	LOC100292909	hypothetical protein LOC100292909
592	C20orf19	chromosome 20 open reading frame 19
593	PGBD1	piggyBac transposable element derived 1
594	DCAF13	DDB1 and CUL4 associated factor 13
595	PABPC1L	poly(A) binding protein, cytoplasmic 1-like
596	ROR1	receptor tyrosine kinase-like orphan receptor 1
597	TEX9	testis expressed 9
598	NUDCD1	NudC domain containing 1
599	TRMT5	TRM5 tRNA methyltransferase 5 homolog (S. cerevisiae)
600	KIAA0101	KIAA0101
601	ZNF613	zinc finger protein 613
602	GLRX3	glutaredoxin 3
603	NUDT11	nudix (nucleoside diphosphate linked moiety X)-type motif 11
604	DBN1	drebrin 1
605	PARD3	par-3 partitioning defective 3 homolog (C. elegans)
606	TRO	trophinin
607	SLC4A5	Solute carrier family 4, sodium bicarbonate cotransporter, member 5
608	CCDC34	coiled-coil domain containing 34
609	NT5DC2	5'-nucleotidase domain containing 2
610	SALL1	sall-like 1 (Drosophila)
611	PPP4R4	protein phosphatase 4, regulatory subunit 4
612	CCDC152	coiled-coil domain containing 152
613	MYOZ3	myozenin 3
614	CHAOT	ChaO, cation transport regulator homolog 1 (E. coli)
615	SNHG12	small nucleolar RNA host gene 12 (non-protein coding)
616	GNASAS	GNAS antisense RNA (non-protein coding)
617	UGGT2	UDP-glucose glycoprotein glucosyltransferase 2
618	LCTL	lactase-like
619	LOC100289612	arsenic transactivated protein 1
620	C4orf43	chromosome 4 open reading frame 43
621	DYNC2H1	dynein, cytoplasmic 2, heavy chain 1
622	MME	membrane metallo-endopeptidase
623	BDNF	brain-derived neurotrophic factor
624	MMP14	matrix metalloproteinase 14 (membrane-inserted)
625	UHRF1BP1L	UHRF1 binding protein 1-like
626	ODZ3	odz, odd Oz/ten-m homolog 3 (Drosophila)
627	SLC4A7	solute carrier family 4, sodium bicarbonate cotransporter, member 7
628	TRPC4	transient receptor potential cation channel, subfamily C, member 4
629	SEMA3A	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3A
630	LOC100288985	hypothetical protein LOC100288985
631	RAB38	RAB38, member RAS oncogene family
632	RALGPS2	Ral GEF with PH domain and SH3 binding motif 2
633	KIAA1826	KIAA1826
634	FST	follicle-stimulating
635	LOC401074	hypothetical LOC401074
636	SLC7A11	solute carrier family 7, (cationic amino acid transporter, y ⁺ system) member 11
637	BBS7	Bardet-Biedl syndrome 7
638	CRABP2	cellular retinoic acid binding protein 2
639	GPX8	glutathione peroxidase 8 (putative)
640	SFRP2	secreted frizzled-related protein 2
641	IRX2	iroquois homeobox 2
642	NUP188	nucleoporin 188kDa
643	ERBB2	v-erb-b2 erythroblastic leukemia viral oncogene homolog 2, neuro/glioblastoma derived oncogene homolog (avian)
644	DAPK1	death-associated protein kinase 1
645	HEATR1	HEAT repeat containing 1
646	MYO10	myosin X
647	JMJD1C	jumonji domain containing 1C
		solute carrier family 6 (neurotransmitter transporter,

648	SLC6A6	taurine), member 6
649	PHF12	PHD finger protein 12
650	MDM2	Mdm2 p53 binding protein homolog (mouse)
651	TFRC	transferrin receptor (p90, CD71)
652	HMGB3L1	high-mobility group box 3-like 1
653	CDC25A	cell division cycle 25 homolog A (S. pombe)
654	BICD1	bicaudal D homolog 1 (Drosophila)
655	OCLN	occludin
656	CCDC141	coiled-coil domain containing 141
657	ZNF711	zinc finger protein 711
658	SLCO4C1	solute carrier organic anion transporter family, member 4C1
659	BCL2L11	BCL2-like 11 (apoptosis facilitator)
660	AASS	aminoadipate-semialdehyde synthase
661	SOX2	SRY (sex determining region Y)-box 2
662	SALL3	sal-like 3 (Drosophila)
663	GCNT2	glucosaminyl (N-acetyl) transferase 2, 1-branching enzyme (1 blood group)
664	SLC12A1	solute carrier family 12 (sodium/potassium/chloride transporters), member 1
665	DSC2	desmocollin 2
666	NRK	Nik related kinase
667	LOC729993	hypothetical protein LOC729993
668	ZNF90	zinc finger protein 90
669	GRPR	gastrin-releasing peptide receptor
670	SERPINF9	serpin peptidase inhibitor, clade B (ovalbumin), member 9
671	PNKD	paroxysmal nonkinesigenic dyskinesia
672	RBM17	RNA binding motif protein 17
673	RNF5	ring finger protein 5
674	SP1B	Spi-B transcription factor (Spi-1/PU.1 related)
675	LOC652147	similar to U5 snRNP-specific protein, 200 kDa
676	NLRP7	NLR family, pyrin domain containing 7
677	CALCR	calcitonin receptor
678	LRAT	lecithin retinol acyltransferase (phosphatidylcholine--retinol O-acyltransferase)
679	CCND2	cyclin D2
680	ETV4	ets variant 4
681	MYBL2	v-myb myeloblastosis viral oncogene homolog (avian)-like 2
682	FOXH1	forkhead box H1
683	SOX4	SRY (sex determining region Y)-box 4
684	DBNDD1	dysbindin (dystrobrevin binding protein 1) domain containing 1
685	CYP2S1	cytochrome P450, family 2, subfamily S, polypeptide 1
686	BRIP1	BRCA1 interacting protein C-terminal helicase 1
687	C21orf88	chromosome 21 open reading frame 88
688	SNHG4	small nucleolar RNA host gene 4 (non-protein coding)
689	E2F8	E2F transcription factor 8
690	LPAR4	lysophosphatidic acid receptor 4
691	F2RL1	coagulation factor II (thrombin) receptor-like 1
692	B4GALT6	UDP-GalbetaGlcNAc beta 1,4- galactosyltransferase, polypeptide 6
693	ZNF273	zinc finger protein 273
694	ZNF649	zinc finger protein 649
695	ZNF138	zinc finger protein 138
696	PCDH2	protocadherin beta 2
697	EIF2AK4	eukaryotic translation initiation factor 2 alpha kinase 4
698	FAM111B	family with sequence similarity 111, member B
699	LOC100288551	hypothetical protein LOC100288551
700	RAB39	RAB39, member RAS oncogene family
701	TERF1	telomeric repeat binding factor (NIMA-interacting) 1
702	BUB1B	budding uninhibited by benzimidazoles 1 homolog beta (yeast)
703	SYT1	synaptotagmin I
704	POLR3G	polymerase (RNA) III (DNA directed) polypeptide G (32kD)
		ras-related C3 botulinum toxin substrate 3 (rho family,

705	RAC3	small GTP binding protein Rac3)
706	GDF3	growth differentiation factor 3
707	MMP24	matrix metalloproteinase 24 (membrane-inserted)
708	GAP43	growth associated protein 43
709	ITGB1BP3	integrin beta 1 binding protein 3
710	CECR2	cat eye syndrome chromosome region, candidate 2
711	TRIM24	tripartite motif-containing 24
712	PHC1	polyhomeotic homolog 1 (Drosophila)
713	FZD3	frizzled homolog 3 (Drosophila)
714	HELLS	helicase, lymphoid-specific
715	TTK	TTK protein kinase
716	KBTD8	kelch repeat and BTB (POZ) domain containing 8
717	ZNF681	zinc finger protein 681
718	DSG2	desmoglein 2
719	ACOXL	acyl-Coenzyme A oxidase-like
720	C15orf42	chromosome 15 open reading frame 42
721	PKIB	protein kinase (cAMP-dependent, catalytic) inhibitor beta
722	KCNGB3	potassium voltage-gated channel, subfamily G, member 3
723	XRCC3	X-ray repair complementing defective repair in Chinese hamster cells 3
724	ZNF682	zinc finger protein 682
725	CYP2B6	cytochrome P450, family 2, subfamily B, polypeptide 6
726	GYG2	glycogenin 2
727	ERCC6L	excision repair cross-complementing rodent repair deficiency, complementation group 6-like
728	IL17RD	interleukin 17 receptor D
729	RP6-213H19.1	serine/threonine protein kinase MST4
730	WDR67	WD repeat domain 67
731	DAZL	deleted in azoospermia-like
732	SEMG1	semenogelin I
733	KCNE1L	KCNE1-like
734	SLC1A6	solute carrier family 1 (high affinity aspartate/glutamate transporter), member 6
735	LMNB1	lamin B1
736	FAM133A	family with sequence similarity 133, member A
737	GPR64	G protein-coupled receptor 64
738	SNRPN	small nuclear ribonucleoprotein polypeptide N
739	UGT3A1	UDP glycosyltransferase 3 family, polypeptide A1
740	DPPA4	developmental pluripotency associated 4
741	TRIML2	tripartite motif family-like 2
742	LOC285401	hypothetical LOC285401
743	C1orf187	chromosome 1 open reading frame 187
744	FLJ36116	hypothetical locus LOC388666
745	AP1M2	adaptor-related protein complex 1, mu 2 subunit
746	DPPA2	developmental pluripotency associated 2
747	EPHA1	EPH receptor A1
748	ARID3B	AT rich interactive domain 3B (BRIGHT-like)
749	PODXL	podocalyxin-like
750	ESRP2	epithelial splicing regulatory protein 2
751	SALL2	sal-like 2 (Drosophila)
752	ACVR2B	activin A receptor, type IIb
753	FAM60A	family with sequence similarity 60, member A
754	ADD2	adducin 2 (beta)
755	IDO1	indoleamine 2,3-dioxygenase 1
756	LOC157627	hypothetical LOC157627
757	C13orf38 /// SOHLH2	chromosome 13 open reading frame 38 /// spermatogenesis and oogenesis specific basic helix-loop-helix 2
758	RECQL4	RecQ protein-like 4
759	CAMKV	CaM kinase-like vesicle-associated
760	EPHX3	epoxide hydrolase 3
761	FAM19A4	family with sequence similarity 19 (chemokine (C-C motif)-like), member A4
762	TNFSF11	tumor necrosis factor (ligand) superfamily, member 11
763	PIPOX	pipecolic acid oxidase

764	MIR17HG	MIR17 host gene (non-protein coding)
765	C14orf115	chromosome 14 open reading frame 115
766	E2F5	E2F transcription factor 5, p130-binding
767	TET1	tet oncogene 1
768	FZD5	frizzled homolog 5 (Drosophila)
769	DEPDC1B	DEP domain containing 1B
770	IGSF1	immunoglobulin superfamily, member 1
771	CTSL2	cathepsin L2
772	IGF2BP1	insulin-like growth factor 2 mRNA binding protein 1
773	NFE2L3	nuclear factor (erythroid-derived 2)-like 3
774	PCYT1B	phosphate cytidyltransferase 1, choline, beta
775	AP1S2	adaptor-related protein complex 1, sigma 2 subunit
776	SLOC25A21	solute carrier family 25 (mitochondrial oxodicarboxylate carrier), member 21
777	DCAF12L1	DOB1 and CUL4 associated factor 12-like 1
778	LOC100216479	hypothetical LOC100216479
779	CYP26A1	cytochrome P450, family 26, subfamily A, polypeptide 1
780	LOC339260	Hypothetical protein LOC339260
781	SERPINF4	serpin peptidase inhibitor, clade B (ovalbumin), member 4
782	LOC347475	UPF0625 coiled-coil domain-containing protein ENSP00000359845
783	LOC100129662	hypothetical protein LOC100129662
784	ZNF876P	zinc finger protein 876 (pseudogene)
785	GPC4	glypican 4
786	SH3GL3	SH3-domain GRB2-like 3
787	FAM71F1	family with sequence similarity 71, member F1
788	BIK	BCL2-interacting killer (apoptosis-inducing)
789	RIT2	Ras-like without CAAX 2
790	NAP1L3	nucleosome assembly protein 1-like 3
791	LOC389895	hypothetical LOC389895
792	FABP7	fatty acid binding protein 7, brain
793	KLKB1	kallikrein B, plasma (Fletcher factor) 1
794	HLA-DPB2	major histocompatibility complex, class II, DP beta 2 (pseudogene)
795	CALCB	calcitonin-related polypeptide beta
796	ZFR2	zinc finger RNA binding protein 2
797	ZIC2	Zic family member 2 (odd-paired homolog, Drosophila)
798	LOC730125	Hypothetical LOC730125
799	ADAMTS19	ADAM metalloproteinase with thrombospondin type 1 motif, 19
800	FGFR4	fibroblast growth factor receptor 4
801	SEMA6A	sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6A
802	DPPA3	developmental pluripotency associated 3
803	DPPA5	developmental pluripotency associated 5
804	HS6ST2	heparan sulfate 6-O-sulfotransferase 2
805	GLDC	glycine dehydrogenase (decarboxylating)
806	NLGN4X	neuroligin 4, X-linked
807	MEGF10	multiple EGF-like-domains 10
808	KLHDC7A	kelch domain containing 7A
809	PALM3	Paralemmin-3
810	GPR19	G protein-coupled receptor 19
811	ORC1L	origin recognition complex, subunit 1-like (yeast)
812	COCH	coagulation factor C homolog, cochlin (Limulus polyphemus)
813	GABRB3	gamma-aminobutyric acid (GABA) A receptor, beta 3
814	FAM60A /// LOC728115	family with sequence similarity 60, member A /// similar to family with sequence similarity 60, member A
815	CNTNAP2	contactin associated protein-like 2
816	C8orf42	chromosome 8 open reading frame 42
817	ZSCAN10	zinc finger and SCAN domain containing 10
818	NXPH2	neurexophilin 2
819	PRDM14	PR domain containing 14
820	FOXO3	forkhead box D3
821	PLEKHG4B	pleckstrin homology domain containing, family G (with RhoGef domain) member 4B

822	LOC728342	Hypothetical protein LOC728342
823	PDZD4	PDZ domain containing 4
824	C9orf135	chromosome 9 open reading frame 135
825	TMSB15A	thymosin beta 15a
826	GNG4	guanine nucleotide binding protein (G protein), gamma 4
827	CA14	carbonic anhydrase XIV
828	SOX3	SRY (sex determining region Y)-box 3
829	ATCAY	ataxia, cerebellar, Cayman type
830	PIM2	pim-2 oncogene
831	TEX14	testis expressed 14
832	ZNF488	zinc finger protein 488
833	ATXN7L1	ataxin 7-like 1
834	IGDCC3	immunoglobulin superfamily, DCC subclass, member 3
835	ME1	malic enzyme 1, NADP(+)-dependent, cytosolic
836	GPR143	G protein-coupled receptor 143
837	SSX4 /// SSX4B	synovial sarcoma, X breakpoint 4 /// synovial sarcoma, X breakpoint 4B
838	CHST9	carbohydrate (N-acetyl)galactosamine 4-O sulfotransferase 9
839	LOC153469	hypothetical protein LOC153469
840	SMPDL3B	sphingomyelin phosphodiesterase, acid-like 3B
841	WNK3	WNK lysine deficient protein kinase 3
842	ZFP42	zinc finger protein 42 homolog (mouse)
843	NMU	neuromedin U
844	CD24	CD24 molecule
845	SCNN1A	sodium channel, nonvoltage-gated 1 alpha
846	RBPM52	RNA binding protein with multiple splicing 2
847	FREM2	FRAS1 related extracellular matrix protein 2
848	LOC100131138	similar to hCG2040918
849	CALB1	calbindin 1, 28kDa
850	POU5F1B	POU class 5 homeobox 1B
851	OTX2	orthodenticle homeobox 2
852	LIN28B	lin-28 homolog B (C. elegans)
853	RMST	rhabdomyosarcoma 2 associated transcript (non-protein coding)
854	CXADR	coxsackie virus and adenovirus receptor
855	KCNN2	potassium intermediate/small conductance calcium-activated channel, subfamily N, member 2
856	CLDN6	claudin 6
857	TEX15	testis expressed 15
858	ZIC3	Zic family member 3 (odd-paired homolog, Drosophila)
859	RPRM	reprimin, TP53 dependent G2 arrest mediator candidate
860	CDH3	cadherin 3, type 1, P-cadherin (placental)
861	LINGO1	leucine rich repeat and Ig domain containing 1
862	LECT1	leukocyte cell derived chemotaxin 1
863	DCX	doublecortin
864	GLB1L3	galactosidase, beta 1-like 3
865	SOX11	SRY (sex determining region Y)-box 11
866	ZNF165	zinc finger protein 165
867	MYCN	v-myc myelocytomatosis viral related oncogene, neuroblastoma derived (avian)
868	NANOG	Nanog homeobox
869	POU5F1 /// POU5F1B /// POU5F1P3 /// POU5F1P4	POU class 5 homeobox 1 /// POU class 5 homeobox 1B /// POU class 5 homeobox 1 pseudogene 3 /// POU class 5 homeobox 1 pseudogene 4
870	C6orf168	chromosome 6 open reading frame 168
871	SLC7A3	solute carrier family 7 (cationic amino acid transporter, y+ system), member 3
872	KIF26A	kinesin family member 26A
873	JPH3	junctophilin 3
874	CR1 /// CR1L	complement component (3b/4b) receptor 1 (Knops blood group) /// complement component (3b/4b) receptor 1-like
875	GABRA5	gamma-aminobutyric acid (GABA) A receptor, alpha 5
876	KIF5C	kinesin family member 5C
877	TUBB2B	tubulin, beta 2B

878	DNMT3B	DNA (cytosine-5)-methyltransferase 3 beta
879	DDX25	DEAD (Asp-Glu-Ala-Asp) box polypeptide 25
880	PTPRZ1	protein tyrosine phosphatase, receptor-type, Z polypeptide 1
881	UNC5D	unc-5 homolog D (C. elegans)
882	VASH2	vasohibin 2
883	LRRTM4	leucine rich repeat transmembrane neuronal 4
884	MARVELD3	MARVEL domain containing 3
885	RBM15	RNA binding motif protein 15
886	LEFTY1	left-right determination factor 1
887	LEFTY2	left-right determination factor 2
888	POU5F1P3	POU class 5 homeobox 1 pseudogene 3
889	POU5F1P4	POU class 5 homeobox 1 pseudogene 4
890	EPCAM	epithelial cell adhesion molecule
891	LIN28	lin-28 homolog (C. elegans)
892	L1TD1	LINE-1 type transposase domain containing 1
893	USP44	ubiquitin specific peptidase 44
894	ESRP1	epithelial splicing regulatory protein 1
895	BEND4	BEN domain containing 4
896	TOX3	TOX high mobility group box family member 3
897	SCG3	secretogranin III
898	CRISPLD1	cysteine-rich secretory protein LCCL domain containing 1
899	SALL4	sal-like 4 (Drosophila)
900	LRRN1	leucine rich repeat neuronal 1
901	CRABP1	cellular retinoic acid binding protein 1
902	NTS	neurotensin
903	COX6A1	cytochrome c oxidase subunit VIa polypeptide 1
904	TDGF1 /// TDGF3	teratocarcinoma-derived growth factor 1 /// teratocarcinoma-derived growth factor 3, pseudogene
905	HESRG	hypothetical LOC790952
906	NLRP2	NLR family, pyrin domain containing 2

[0071] [表 3 A] 第 3 遺伝子群 (表 3 B) を含むプローブ 6 7 6 個において、ヒト E S 細胞クローン (KhES1-S3) の発現レベルの平均に対する、各 E S 細胞クローン及び各 i P S 細胞クローンの発現レベルの割合

Gene Symbol	Gene Title	Khes1 ES	Khes3 ES	Khes2 ES	201B7 IPS	201B6 IPS	253G4 IPS	253G1 IPS
1 RECQL5	RecQ protein-like 5	0.97	0.17	-1.14	-5.28	-1.11	-0.38	-4.48
2 FANCM	Fanconi anemia, complementation group M	1.08	1.05	-2.11	0.71	-3.35	-3.36	-0.93
3 RTEL1	regulator of telomere elongation helicase 1	0.71	1.39	-2.10	1.09	-3.86	-4.51	-2.80
4 ATM	ataxia telangiectasia mutated	-2.06	1.07	0.98	-1.37	-2.30	0.72	-2.08
5 ATXN3	Ataxin 3	-0.16	0.04	0.12	0.47	-3.25	0.06	-3.85
6 FANCG	Fanconi anemia, complementation group C	0.16	-0.01	-0.14	-3.21	-0.39	-1.88	0.81
7 SPO11	SPO11 meiotic protein covalently bound to DSB homolog (S. cerevisiae)	-0.96	-0.20	1.16	-2.00	0.35	-1.94	0.91
8 EYA2	eyes absent homolog 2 (Drosophila)	-1.16	1.68	-0.51	0.49	-1.11	-1.71	-0.93
9 POLE	polymerase (DNA directed), epsilon	-1.03	-0.89	1.92	1.67	-1.48	-0.18	-0.64
10 NCOA6	nuclear receptor coactivator 6	0.00	-1.78	1.77	0.51	-0.73	-0.52	0.67
11 PRKDC	Protein kinase, DNA-activated, catalytic polypeptide	-1.37	-0.61	1.98	2.39	0.71	-0.92	1.18
12 RNF168	ring finger protein 168	1.36	-0.08	-1.28	-1.07	1.71	1.09	-0.61
13 WRNIP1	Werner helicase interacting protein 1	0.66	0.09	-0.76	-1.24	0.88	0.95	-1.36
14 ERCC8	excision repair cross-complementing rodent repair deficiency, complementation group 8	0.40	0.17	-0.57	0.01	0.20	-0.25	0.85
15 FDXO18	F-box protein, helicase, 18	0.33	0.39	-0.72	0.45	0.24	-0.25	0.93
16 DMC1	DMC1 dosage suppressor of mck1 homolog, meiosis-specific homologous recombination (yeast)	0.53	0.51	-1.03	0.58	0.66	0.33	0.36
17 KIF22	kinesin family member 22	-0.31	0.19	0.12	0.22	0.20	0.27	0.07
18 FANCA	Fanconi anemia, complementation group A	-0.32	0.25	0.06	0.33	0.32	0.21	0.07
19 POLD1	polymerase (DNA directed), delta 1, catalytic subunit 125kDa	-0.26	0.24	0.02	0.09	0.13	0.08	0.02
20 MUTHYH	mutY homolog (E. coli)	-0.24	0.16	0.09	-0.10	0.16	0.23	0.04
21 BRCA1	breast cancer 1, early onset	-0.52	0.12	0.41	0.01	0.34	0.27	0.22
22 UNG	uracil-DNA glycosylase	-0.28	0.14	0.13	0.36	0.31	0.29	0.06
23 TRIP13	thyroid hormone receptor interactor 13	0.02	-0.06	0.05	0.36	0.24	0.39	0.15
24 HMG2	high mobility group box 2	-0.20	0.16	0.04	0.20	0.60	0.16	-0.09
25 KIF22	kinesin family member 22	-0.36	0.10	0.26	0.45	0.32	-0.10	-0.06
26 H2AFX	H2A histone family, member X	-0.40	0.23	0.17	-0.21	0.03	0.02	0.00
27 CHEK1	CHK1 checkpoint homolog (S. pombe)	0.22	-0.07	-0.14	0.10	0.11	0.09	-0.20
28 CHEK1	CHK1 checkpoint homolog (S. pombe)	0.28	-0.17	-0.12	0.06	0.06	-0.06	-0.28
29 HMOB1	high mobility group box 1	0.21	-0.10	-0.11	0.04	0.03	0.03	0.01
30 PAXP1	PAX interacting (with transcription-activation domain) protein 1	0.10	0.03	-0.12	0.23	0.03	0.06	-0.10
31 POLR2D	polymerase (RNA) II (DNA directed) polypeptide D	0.08	0.08	-0.16	-0.15	0.00	0.08	-0.03
32 RPA3	replication protein A3, 14kDa	0.15	0.02	-0.17	-0.18	-0.02	0.12	0.16
33 BRCA2	breast cancer 2, early onset	0.28	0.08	-0.36	0.15	-0.17	-0.41	-0.03
34 FANCI	Fanconi anemia, complementation group I	0.31	-0.06	-0.24	-0.01	-0.09	-0.20	-0.09
35 GTF2H4	general transcription factor IIH, polypeptide 4, 52kDa	-0.05	-0.15	0.20	0.09	0.07	-0.12	-0.09
36 LIG3	ligase III, DNA, ATP-dependent	-0.08	-0.06	0.13	0.05	-0.09	-0.18	-0.18
37 CHAF1B	chromatin assembly factor 1, subunit B (p60)	0.00	-0.18	0.17	0.32	0.28	0.00	-0.07
38 CHAF1A	chromatin assembly factor 1, subunit A (p150)	0.00	-0.17	0.17	0.23	0.06	0.07	0.11
39 SIRT1	sirtuin (silent mating type information regulation 2 homolog) 1 (S. cerevisiae)	-0.15	-0.07	0.22	0.18	0.13	0.20	-0.13

40	SSRP1	structure specific recognition protein 1	-0.05	0.11	-0.05	0.07	-0.07	-0.06	-0.02
41	AXIN2	axin 2	-0.16	-0.05	-0.16	0.08	-0.16	-0.10	0.00
42	TDP1	tyrosyl-DNA phosphodiesterase 1	-0.27	0.11	-0.27	-0.20	-0.21	-0.21	-0.25
43	LIG1	ligase I, DNA ATP-dependent	-0.29	0.16	-0.29	0.06	-0.46	-0.26	-0.21
44	MSH6	mutS homolog 6 (E. coli)	-0.18	0.16	-0.18	0.02	-0.07	-0.09	-0.30
45	TOP2A	topoisomerase (DNA) II alpha 170kDa	-0.04	0.04	-0.04	0.00	-0.34	-0.03	-0.19
46	RAD54B	RAD54 homolog B (S. cerevisiae)	0.12	-0.12	0.12	-0.16	-0.09	-0.04	-0.22
47	FANCI	Fanconi anemia, complementation group I	0.00	0.01	0.00	0.21	-0.28	-0.23	-0.25
48	MSH2	mutS homolog 2, colon cancer, nonpolyposis type 1 (E. coli)	0.22	-0.12	0.22	0.04	-0.17	-0.11	-0.43
49	HMGB1	high-mobility group box 1	0.18	-0.15	0.18	-0.10	-0.38	-0.11	-0.31
50	POLQ	polymerase (DNA directed), theta	-0.07	-0.01	-0.07	0.09	-0.42	-0.63	-0.27
51	REC2	replication factor C (activator 1) 2, 40kDa	0.31	-0.08	0.31	-0.08	0.54	0.47	0.22
52	RFC4	replication factor C (activator 1) 4, 37kDa	0.25	0.04	0.25	0.08	0.44	0.24	0.26
53	PTTG1	pituitary tumor-transforming 1	0.01	0.15	0.01	0.16	0.27	0.28	0.30
54	RAD51	RAD51 homolog (RecA homolog E. coli) (S. cerevisiae)	0.17	-0.20	0.17	0.10	0.35	0.35	0.32
55	BARD1	BRCA1 associated RING domain 1	0.14	0.28	0.14	-0.41	0.26	0.42	-0.01
56	RFC5	replication factor C (activator 1) 5, 36.5kDa	0.36	-0.10	0.36	0.11	-0.02	-0.02	0.29
57	UBE2T	ubiquitin-conjugating enzyme E2T (putative)	0.45	-0.22	0.45	-0.04	0.18	0.18	0.13
58	RAD54B	RAD54 homolog B (S. cerevisiae)	0.17	0.00	0.17	0.37	-0.04	0.28	0.36
59	POLA1	polymerase (DNA directed), alpha 1, catalytic subunit	0.47	-0.66	0.47	0.25	0.10	0.12	0.00
60	TDG	thymine-DNA glycosylase	0.24	-0.39	0.24	0.22	0.09	0.07	0.12
61	UHRF1	ubiquitin-like with PHD and ring finger domains 1	0.16	-0.34	0.16	0.33	0.19	0.30	0.12
62	RPAIN	RPA structure-specific endonuclease 1	0.17	-0.32	0.17	0.55	0.26	0.07	0.33
63	FEN1	flap structure-specific endonuclease 1	0.04	0.04	0.04	0.28	0.46	0.45	0.65
64	FANCB	Fanconi anemia, complementation group B	0.51	-0.28	0.51	-0.23	0.06	0.27	0.34
65	CHAF1A	Chromatin assembly factor 1, subunit A (p150)	-0.69	0.50	-0.69	0.21	-0.11	-0.07	0.61
66	EYA3	eyes absent homolog 3 (Drosophila)	0.32	0.34	0.32	0.11	0.32	0.35	-0.73
67	GLSPN	classin homolog (Xenopus laevis)	0.76	-1.07	0.76	0.42	0.20	0.29	-0.31
68	EME2	essential meiotic endonuclease 1 homolog 2 (S. pombe)	0.39	-0.72	0.39	0.06	-0.11	0.15	0.21
69	PARG	poly (ADP-ribose) glycohydrolase	0.12	-0.46	0.12	0.33	-0.11	0.03	-0.47
70	RPAIN	RPA interacting protein	-0.08	0.05	-0.08	0.17	0.80	0.30	0.11
71	DMC1	DMC1 dosage suppressor of mek1 homolog, meiosis-specific homologous recombination (yeast)	0.27	-0.32	0.27	0.13	0.65	-0.03	0.01
72	REC2	replication factor C (activator 1) 2, 40kDa	-0.08	-0.09	-0.08	0.08	0.22	0.32	0.32
73	RPA2	replication protein A2, 32kDa	-0.02	-0.02	-0.02	-0.12	0.30	0.24	0.15
74	PRPF19	PRP19/PSO4 pre-mRNA processing factor 19 homolog (S. cerevisiae)	-0.03	0.02	-0.03	0.02	0.28	0.23	0.27
75	RUVBL2	RuvB-like 2 (E. coli)	0.13	0.12	0.13	0.07	0.31	0.22	0.30
76	MDC1	mediator of DNA-damage checkpoint 1	-0.01	0.07	-0.01	0.13	0.31	0.21	0.25
77	UBE2N	ubiquitin-conjugating enzyme E2N (UBC13 homolog, yeast)	0.14	0.01	0.14	0.21	0.31	0.30	0.23
78	POLQ2	polymerase (DNA directed), gamma 2, accessory subunit	0.19	0.10	0.19	-0.29	0.31	0.33	0.11
79	NUDT1	nucleoside diphosphate linked moiety X)-type motif 1	0.03	0.11	0.03	-0.14	0.12	0.21	0.25
80	POLE	polymerase (DNA directed), epsilon	-0.20	0.24	-0.20	-0.04	0.13	0.30	0.02

[illegible]

120	NPM1	nucleophosmin (nucleolar phosphoprotein B23, numatrin)	0.29	-0.12	-0.18	0.21	0.09	0.07	0.17
121	STRA13	stimulated by retinoic acid 13 homolog (mouse)	-0.02	0.04	-0.03	0.17	-0.04	0.14	0.48
122	POLR2K	polymerase (RNA) II (DNA directed) polypeptide K, 70kDa	0.26	-0.11	-0.16	0.17	0.08	0.19	0.19
123	WDR33	WD repeat domain 33	0.21	-0.06	-0.15	0.22	0.05	0.23	0.21
124	CDK7	cyclin-dependent kinase 7	0.13	-0.01	-0.12	0.11	0.08	0.28	0.38
125	FANCF	Fanconi anemia, complementation group F	0.30	-0.16	-0.13	0.28	0.33	0.46	0.42
126	FANCF	Fanconi anemia, complementation group F	0.15	-0.05	-0.10	0.40	0.25	0.31	0.43
127	BCCIP	BRCA2 and CDKN1A interacting protein	0.16	0.09	-0.25	0.15	0.27	0.53	0.33
128	NTHL1	nth endonuclease III-like 1 (E. coli)	0.03	0.16	-0.19	0.30	0.45	0.27	0.19
129	EME1	essential meiotic endonuclease 1 homolog 1 (S. pombe)	0.13	-0.13	0.00	0.53	0.26	0.22	0.20
130	SMC6	structural maintenance of chromosomes 6	0.11	-0.02	-0.09	0.51	0.41	0.15	0.15
131	XRCC6	X-ray repair complementing defective repair in Chinese hamster cells 6	-0.46	0.46	0.00	-0.01	0.77	0.59	0.25
132	CSNK1E	casein kinase 1, epsilon	-0.23	0.27	-0.04	-0.25	0.35	0.59	0.11
133	CLK2	CLK-like kinase 2	-0.30	0.13	0.17	-0.25	0.04	0.00	-0.12
134	HINFP	histone H4 transcription factor	-0.11	0.09	0.01	-0.17	-0.01	-0.17	-0.08
135	ATXN3	ataxin 3	0.10	0.09	-0.19	-0.16	-0.02	0.13	-0.26
136	MRE11A	MRE11 meiotic recombination 11 homolog A (S. cerevisiae)	0.03	-0.01	-0.02	-0.04	-0.19	-0.06	-0.16
137	DUT	deoxyuridine triphosphatase	0.09	-0.01	-0.08	-0.03	-0.01	0.02	-0.09
138	VOP	valosin-containing protein	-0.09	0.04	0.05	-0.13	-0.03	-0.21	-0.13
139	RPA1	replication protein A1, 70kDa	0.23	0.04	-0.27	0.21	0.12	0.08	-0.05
140	XRCC5	X-ray repair complementing defective repair in Chinese hamster cells 5 (double-strand-break rejoining)	0.16	0.05	-0.22	0.25	0.00	0.07	-0.20
141	DCLRE1A	DNA cross-link repair 1A (PSO2 homolog, S. cerevisiae)	0.12	-0.02	-0.10	0.17	0.30	-0.04	-0.17
142	XRCC6	X-ray repair complementing defective repair in Chinese hamster cells 6	0.05	0.04	-0.09	-0.07	0.01	-0.03	-0.18
143	CRY1	cryptochrome 1 (photolyase-like)	0.03	-0.02	-0.01	-0.06	-0.03	-0.04	-0.07
144	SUMO1	SMT3 suppressor of mit two 3 homolog 1 (S. cerevisiae)	0.08	0.00	-0.08	-0.02	0.03	0.04	0.03
145	SUMO1	SMT3 suppressor of mit two 3 homolog 1 (S. cerevisiae)	0.21	-0.02	-0.19	-0.03	0.02	0.02	-0.06
146	APEX1	APEX nuclease (multifunctional DNA repair enzyme) 1	0.10	-0.07	-0.03	0.13	0.02	0.02	0.20
147	NPM1	nucleophosmin (nucleolar phosphoprotein B23, numatrin)	0.18	-0.12	-0.05	0.03	-0.02	-0.02	0.05
148	RAO21	RAO21 homolog (S. pombe)	0.01	-0.01	0.00	0.16	0.05	0.08	-0.42
149	RPA1	replication protein A1, 70kDa	0.17	-0.03	-0.15	0.21	0.08	-0.06	-0.56
150	XRCC2	X-ray repair complementing defective repair in Chinese hamster cells 2	0.23	0.18	-0.41	0.15	0.19	-0.12	-0.51
151	DCLRE1B	DNA cross-link repair 1B (PSO2 homolog, S. cerevisiae)	-0.09	0.15	-0.06	0.38	0.23	-0.01	-0.38
152	DCLRE1B	DNA cross-link repair 1B (PSO2 homolog, S. cerevisiae)	-0.24	0.31	-0.07	0.25	0.12	0.00	-0.16
153	NBN	nibrin	-0.01	0.07	-0.06	-0.28	-0.38	-0.26	-0.12
154	POLR2B	polymerase (RNA) II (DNA directed) polypeptide B, 140kDa	0.10	-0.01	-0.09	-0.09	-0.12	-0.26	-0.33
155	NBN	nibrin	0.26	0.01	-0.28	-0.04	-0.23	-0.31	-0.29
156	POLR2B	polymerase (RNA) II (DNA directed) polypeptide B, 140kDa	0.24	-0.10	-0.14	-0.07	-0.26	-0.25	-0.39
157	ASF1A	ASF1 anti-silencing function 1 homolog A (S. cerevisiae)	0.14	-0.09	-0.05	0.05	-0.22	-0.30	-0.35

158	CHD1L	chromodomain helicase DNA binding protein 1-like	0.10	-0.15	0.05	0.03	-0.27	-0.48	-0.56
159	EPC2	enhancer of polycomb homolog 2 (Drosophila)	0.01	-0.11	0.10	0.02	-0.18	-0.25	-0.33
160	RFC1	replication factor C (activator 1) 1, 145kDa	-0.01	0.10	-0.09	0.05	-0.35	-0.41	-0.49
161	CHD1L	chromodomain helicase DNA binding protein 1-like	-0.04	0.14	-0.10	-0.19	-0.36	-0.32	-0.31
162	CHD1L	chromodomain helicase DNA binding protein 1-like	0.09	-0.01	-0.09	-0.33	-0.29	-0.23	-0.28
163	TYMS	thymidylate synthetase	0.10	0.14	-0.23	-0.46	-0.26	-0.13	-0.28
164	TYMS	thymidylate synthetase	0.10	-0.04	-0.07	-0.22	-0.34	-0.20	-0.02
165	REV1	REV1 homolog (S. cerevisiae)	0.29	-0.08	-0.21	-0.22	-0.20	-0.27	-0.02
166	PMS1	PMS1 postmeiotic segregation increased 1 (S. cerevisiae)	0.38	-0.06	-0.32	-0.24	-0.34	-0.19	-0.23
167	SFPQ	Splicing factor proline/glutamine-rich (polypyrimidine tract binding protein associated)	0.37	-0.14	-0.23	-0.22	-0.13	-0.21	-0.15
168	NONO	iron-POU domain containing, octamer-binding	-0.13	-0.18	0.31	0.06	-0.10	-0.22	-0.27
169	UBE2D3	ubiquitin-conjugating enzyme E2D 3 (UBC4/5 homolog, yeast)	0.00	-0.25	0.26	0.02	0.19	-0.18	-0.15
170	ZW10	ZW10, kinetochore associated, homolog (Drosophila)	0.24	-0.46	0.22	-0.09	-0.14	-0.26	-0.20
171	NBN	nibrin	-0.11	-0.18	0.29	0.00	-0.37	-0.38	-0.11
172	USP1	ubiquitin specific peptidase 1	0.23	-0.21	-0.02	0.06	-0.19	-0.15	-0.28
173	SMC3	structural maintenance of chromosomes 3	0.11	-0.21	0.10	0.10	-0.40	-0.29	-0.23
174	JMY	junction mediating and regulatory protein, c53 cofactor	0.12	-0.10	-0.03	0.01	-0.40	-0.33	-0.16
175	HMGB1	high-mobility group box 1	0.03	-0.19	0.16	0.12	-0.23	-0.20	0.10
176	ASF1A	ASF1 anti-silencing function 1 homolog A (S. cerevisiae)	0.21	-0.20	-0.02	0.37	-0.24	0.02	-0.13
177	WRN	Werner syndrome, RecQ helicase-like	0.40	-0.33	-0.07	0.15	-0.07	-0.04	0.26
178	SHPRH	SNF2 histone linker PHD RING helicase	0.40	-0.22	-0.18	0.02	-0.19	-0.07	-0.03
179	RAD18	RAD18 homolog (S. cerevisiae)	0.29	-0.20	-0.09	-0.04	-0.27	-0.38	0.19
180	PMS2L2	postmeiotic segregation increased 2-like 2 pseudogene	0.08	-0.13	0.04	-0.09	0.09	0.49	-0.80
181	ERCC3	exonin repair cross-complementing rodent repair deficiency, complementation group 3 (keroderm pigmentosum group B complementing)	0.12	0.00	-0.12	-0.31	-0.19	-0.26	-0.52
182	PRKDC	protein kinase, DNA-activated, catalytic polypeptide	0.08	0.01	-0.09	-0.12	-0.14	-0.18	-0.80
183	SMC1A	structural maintenance of chromosomes 1A	-0.12	0.24	-0.12	-0.10	-0.36	-0.08	-0.20
184	USP1	ubiquitin specific peptidase 1	0.04	0.16	-0.20	0.07	-0.34	-0.16	-0.01
185	XRCC5	X-ray repair complementing defective repair in Chinese hamster cells 5 (double-strand-break rejoining)	0.08	0.07	-0.15	0.07	0.06	0.02	-0.23
186	PRMT6	protein arginine methyltransferase 6	0.13	-0.11	-0.03	0.25	-0.04	-0.06	-0.27
187	HMGB1	high-mobility group box 1	0.00	0.00	0.00	0.06	-0.18	-0.14	-0.34
188	SUPT16H	suppressor of Ty 16 homolog (S. cerevisiae)	0.16	-0.07	-0.10	0.08	-0.20	-0.16	-0.29
189	USP28	ubiquitin specific peptidase 28	0.04	-0.13	0.09	0.05	-0.08	-0.31	-0.30
190	POLR2F	polymerase (RNA) II (DNA directed) polypeptide F	0.11	-0.15	0.04	-0.25	-0.65	-0.42	-0.26
191	SMC3	structural maintenance of chromosomes 3	0.22	-0.07	-0.16	-0.36	-0.22	-0.22	-0.21
192	ZSWIM7	zinc finger, SWIM-type containing 7	0.12	-0.09	-0.03	-0.38	-0.39	-0.36	-0.07
193	SMC6	structural maintenance of chromosomes 6	0.13	0.04	-0.16	-0.53	-0.36	-0.43	-0.29
194	ESCO1	establishment of cohesion 1 homolog 1 (S. cerevisiae)	0.15	-0.03	-0.12	-0.05	-0.45	-0.41	-0.15
195	ASF1A	ASF1 anti-silencing function 1 homolog A (S. cerevisiae)	0.22	-0.26	0.04	-0.07	-0.15	-0.16	0.02
196	UBE2N	ubiquitin-conjugating enzyme E2N (UBC13 homolog, yeast)	0.27	-0.29	0.02	0.10	0.02	0.05	0.13

197	BCCIP	BRC2 and CDKN1A interacting protein	0.29	-0.32	0.03	0.01	0.31	0.07	0.04
198	POLD3	polymerase (DNA-directed), delta 3, accessory subunit	0.33	-0.19	-0.14	0.16	0.15	0.08	-0.03
199	GTF2H2	general transcription factor IIH, polypeptide 2, 44kDa	0.35	-0.24	-0.11	0.07	-0.04	-0.05	-0.04
200	SHFM1	split hand/foot malformation (ectrodactyly) type 1	0.55	-0.19	-0.36	0.00	-0.05	0.04	0.07
201	RAD18	RAD18 homolog (S. cerevisiae)	0.35	-0.04	-0.32	-0.20	0.03	-0.08	-0.18
202	CHEK1	CHK1 checkpoint homolog (S. pombe)	0.39	-0.15	-0.25	-0.11	-0.02	-0.16	-0.23
203	BCCIP	BRC2 and CDKN1A interacting protein	0.28	-0.23	-0.04	-0.42	0.08	0.11	-0.02
204	SMC3	structural maintenance of chromosomes 3	0.06	0.24	-0.31	-0.44	0.24	0.32	-0.32
205	ESCO2	establishment of cohesion 1 homolog 2 (S. cerevisiae)	0.28	0.03	-0.32	-0.38	-0.35	0.01	0.05
206	USP10	ubiquitin specific peptidase 10	0.13	0.27	-0.40	0.00	-0.17	-0.16	-0.37
207	TDP1	tyrosyl-DNA phosphodiesterase 1	0.15	0.24	-0.39	-0.32	-0.01	-0.15	-0.31
208	USP28	ubiquitin specific peptidase 28	0.23	0.07	-0.29	-0.12	0.04	-0.20	-0.40
209	EYA3	eyes absent homolog 3 (Drosophila)	0.38	0.16	-0.54	0.21	-0.11	0.17	0.15
210	MSH6	MutS homolog 6 (E. coli)	0.26	0.18	-0.44	0.18	-0.40	0.54	0.18
211	UBE2B	ubiquitin-conjugating enzyme E2B (RAD6 homolog)	0.74	-0.03	-0.71	0.10	-0.27	-0.23	0.27
212	SFPQ	Splicing factor proline/ glutamine-rich (polypyrimidine tract binding protein associated)	0.51	-0.26	-0.25	0.03	-0.50	-0.32	0.13
213	RBM14	RNA binding motif protein 14	0.52	-0.38	-0.13	0.15	0.36	-0.49	-0.13
214	BUB1	budding uninhibited by benzimidazoles 1 homolog (yeast)	0.10	-0.37	0.27	0.67	-1.02	0.09	-0.52
215	ATXN3	ataxin 3	-0.24	0.38	-0.14	0.34	-0.75	0.05	-0.24
216	RBM14	RNA binding motif protein 14	-0.39	-0.01	0.40	0.00	-0.88	-0.84	-0.88
217	CEPHE	centromere protein E, 312kDa	-0.05	-0.16	0.21	-0.46	-0.68	-1.20	-0.33
218	SSRP1	structure specific recognition protein 1	-0.31	0.18	0.13	0.30	-0.46	-0.35	-0.51
219	RAD21	RAD21 homolog (S. pombe)	0.03	-0.14	0.11	0.06	-0.80	-0.60	-1.07
220	PRKDC	protein kinase, DNA-activated, catalytic polypeptide	0.22	-0.23	0.01	0.01	-0.49	-0.50	-0.81
221	USP10	ubiquitin specific peptidase 10	-0.07	0.07	0.00	0.04	-0.67	-0.78	-0.98
222	NONO	iron-POU domain containing, octamer-binding	-0.30	-0.30	0.60	0.03	-0.38	-0.50	-0.79
223	NONO	iron-POU domain containing, octamer-binding	-0.19	-0.35	0.54	0.04	-0.48	-0.53	-0.75
224	TP53	tumor protein p53	-0.22	-0.24	0.46	0.11	-0.24	-0.48	-0.55
225	BRC41	breast cancer 1, early onset	-0.01	-0.36	0.37	-0.22	-0.19	-0.72	-0.39
226	GADD45G	growth arrest and DNA-damage-inducible, gamma	-0.09	-0.39	0.48	-0.31	-0.54	0.20	0.01
227	SMC1A	structural maintenance of chromosomes 1A	-0.12	-0.28	0.40	-0.29	-0.69	-0.15	-0.02
228	FANCB	Fanconi anemia, complementation group B	0.30	-0.57	0.26	-0.15	-0.41	-0.56	-0.37
229	AXIN2	axin 2	0.27	-0.36	-0.09	-0.30	-0.74	-0.63	-0.81
230	TOP2A	topoisomerase (DNA) II alpha 170kDa	0.18	0.02	-0.20	-0.15	-0.58	-0.57	-0.78
231	USP28	ubiquitin specific peptidase 28	0.02	0.04	-0.07	-0.18	-0.47	-0.70	-0.82
232	ESCO1	establishment of cohesion 1 homolog 1 (S. cerevisiae)	0.31	-0.11	-0.21	-0.43	-0.61	-0.66	-0.85
233	SFPQ	soliding factor proline/ glutamine-rich (polypyrimidine tract binding protein associated)	0.24	-0.20	-0.05	0.20	-0.41	-0.23	-0.58
234	KNTC1	kinetochore associated 1	0.19	-0.02	-0.17	-0.04	-0.43	-0.44	-0.47
235	FANCI	Fanconi anemia, complementation group I	0.19	-0.06	-0.13	0.12	-0.44	-0.50	-0.57
236	LIG3	ligase III, DNA, ATP-dependent	0.02	0.04	-0.06	0.19	-0.13	-0.36	-0.55
237	MSH6	mutS homolog 6 (E. coli)	-0.10	0.05	0.06	0.18	-0.37	-0.38	-0.68
238	BRC42	breast cancer 2, early onset	0.33	0.00	-0.33	-0.59	-0.55	-0.10	-0.49
239	ESCO1	establishment of cohesion 1 homolog 1 (S. cerevisiae)	0.46	0.09	-0.55	-0.43	-0.38	0.00	-0.11

240	EPC2	Enhancer of polycomb homolog 2 (Drosophila)	0.17	0.44	-0.62	0.07	-0.94	-0.54	0.09
241	H2AFX	H2A histone family, member X	-0.54	0.41	0.13	-0.54	-0.81	-0.20	-0.52
242	TDG	thymine-DNA glycosylase	0.24	-0.12	-0.12	-0.52	-0.46	-0.24	-0.65
243	MRE11A	MRE11 meiotic recombination 11 homolog A (S. cerevisiae)	0.36	-0.09	-0.27	-0.47	-0.49	-0.28	-0.52
244	FANCM	Fanconi anemia, complementation group M	0.46	-0.15	-0.32	-0.42	-0.51	-0.48	-0.36
245	GEN1	Gen homolog 1, endonuclease (Drosophila)	0.29	-0.39	0.10	-0.75	-0.40	-0.26	-0.59
246	MUM1	melanoma associated antigen (mutated), 1	0.58	-0.30	-0.29	-1.03	-1.12	-0.74	-0.36
247	CHD1L	Chromodomain helicase DNA binding protein 1-like	0.82	-0.69	-0.13	-0.81	-0.71	0.00	0.18
248	POLQ	polymerase (DNA directed), theta	0.82	-0.44	-0.38	-0.04	0.04	-0.48	0.65
249	FANCA	Fanconi anemia, complementation group A	0.63	-0.04	-0.60	-0.49	0.20	-0.43	0.15
250	CHRNA4	cholinergic receptor, nicotinic, alpha 4	-0.42	-0.47	0.89	0.21	-0.89	-0.38	0.75
251	FZR1	fizzy/cell division cycle 20 related 1 (Drosophila)	-0.85	0.12	0.73	-0.21	-0.85	-0.76	0.21
252	FZR1	fizzy/cell division cycle 20 related 1 (Drosophila)	-0.67	0.18	0.48	0.12	-0.78	-0.26	0.31
253	ATRIP	ATR interacting protein	-1.07	0.84	0.23	0.47	0.18	0.09	-0.03
254	TNP1	transition protein 1 (during histone to protamine replacement)	-1.07	1.03	0.04	0.50	0.20	1.08	0.43
255	PER1	period homolog 1 (Drosophila)	-0.63	0.78	-0.15	0.16	0.46	0.92	1.18
256	SETMAR	SET domain and mariner transposase fusion gene	0.12	-0.06	-0.06	0.03	1.17	0.92	0.86
257	XRCC1	X-ray repair complementing defective repair in Chinese hamster cells 1	-0.11	0.30	-0.20	0.55	0.59	0.81	0.26
258	UBE2V2	ubiquitin-conjugating enzyme E2 variant 2	-0.18	0.26	-0.08	0.30	0.34	0.34	0.33
259	FANCA	Fanconi anemia, complementation group A	-0.06	0.06	0.00	0.79	0.62	0.93	0.83
260	PMS2L2	postmeiotic segregation increased 2-like 2 pseudogene	-0.05	0.27	-0.23	0.81	0.80	0.70	0.88
261	SMC1A	structural maintenance of chromosomes 1A	0.15	-0.55	0.40	0.21	0.63	0.73	-0.08
262	EME1	essential meiotic endonuclease 1 homolog 1 (S. pombe)	-0.35	-0.14	0.48	0.80	0.74	0.64	0.39
263	RAD51C	RAD51 homolog C (S. cerevisiae)	-0.35	-0.09	0.44	0.87	0.43	0.71	0.90
264	RAD51C	RAD51 homolog C (S. cerevisiae)	-0.18	-0.26	0.44	0.49	0.51	0.69	0.89
265	ATXN3	Ataxin 3	0.01	-0.46	0.45	1.00	0.87	0.66	0.92
266	UVRAG	UV radiation resistance associated gene	-0.30	-0.07	0.37	0.33	0.91	0.45	0.65
267	UBE2B	ubiquitin-conjugating enzyme E2B (RAD6 homolog)	0.32	-0.15	-0.17	0.42	0.39	0.38	0.26
268	UBE2B	ubiquitin-conjugating enzyme E2B (RAD6 homolog)	0.24	-0.24	0.01	0.27	0.50	0.48	0.13
269	NCOA6	nuclear receptor coactivator 6	0.08	-0.13	0.04	0.59	0.76	0.50	0.21
270	ERCC1	excision repair cross-complementing rodent repair deficiency, complementation group 1 (includes overlapping antisense sequence)	0.04	0.07	-0.11	0.01	0.59	1.73	0.84
271	BRE	brain and reproductive organ-expressed (TNFRSF1A modulator)	0.23	0.05	-0.29	0.09	0.63	0.43	0.37
272	MC1R	melanocortin 1 receptor (alpha melanocyte stimulating hormone receptor)	0.07	0.15	-0.22	-0.33	0.18	0.57	0.97
273	BRE	brain and reproductive organ-expressed (TNFRSF1A modulator)	0.30	0.17	-0.47	0.23	0.59	0.48	1.00
274	CUL4B	cullin 4B	-0.10	-0.17	0.27	-0.31	0.48	-0.53	-0.19
275	PARP4	poly (ADP-ribose) polymerase family, member 4	-0.42	-0.12	0.54	0.53	0.14	0.02	0.27
276	ERCC1	excision repair cross-complementing rodent repair deficiency, complementation group 1 (includes overlapping	-0.33	-0.11	0.45	0.15	0.09	0.17	0.43

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314	ERCC4	excision repair cross-complementing rodent repair deficiency, complementation group 4	0.05	0.32	-0.37	-0.55	0.24	0.21	-0.06
315	DBP2	damage-specific DNA binding protein 2, 48kDa	-0.18	0.62	-0.44	-0.26	0.66	-0.08	-0.10
316	ATXN3	ataxin 3	0.09	0.49	-0.58	-0.43	0.74	0.01	-0.45
317	ATM	ataxia telangiectasia mutated	0.04	0.12	-0.16	-0.63	-0.05	0.16	0.32
318	RAD23B	RAD23 homolog B (S. cerevisiae)	0.19	0.08	-0.27	-1.00	-0.14	0.33	0.29
319	POLR2F	Polymerase (RNA) II (DNA directed) polypeptide F	0.42	-0.27	-0.15	-0.57	0.49	0.66	0.55
320	RAD51L1	RAD51-like 1 (S. cerevisiae)	0.67	-0.33	-0.34	-0.46	0.29	0.18	-0.27
321	DCLRE1C	DNA cross-link repair 1C (PSO2 homolog, S. cerevisiae)	0.59	-0.15	-0.45	-0.30	0.39	0.15	0.17
322	POL1	polymerase (DNA directed) iota	0.71	-0.17	-0.53	-0.08	0.63	0.42	0.16
323	ALKBH1	alkB, alkylation repair homolog 1 (E. coli)	0.23	0.10	-0.32	-0.40	0.47	0.42	0.08
324	UBE2D3	ubiquitin-conjugating enzyme E2D 3 (UBC4/5 homolog, yeast)	0.55	0.04	-0.59	-0.35	0.56	-0.35	0.08
325	NEIL1	neri endonuclease VIII-like 1 (E. coli)	0.93	-0.06	-0.87	-0.32	1.00	0.02	0.54
326	UBE2B	ubiquitin-conjugating enzyme E2B (RAD6 homolog)	0.81	0.24	-1.05	-0.28	0.35	0.16	0.50
327	HUS1	HUS1 checkpoint homolog (S. pombe)	-0.12	-0.42	0.55	1.08	0.26	0.38	-0.24
328	BAP1	BRCA1 associated protein 1 (ubiquitin carboxy terminal hydrolase)	-0.82	0.20	0.62	0.48	0.42	0.13	0.15
329	PMS2L11	postmeiotic segregation increased 2-like 11 pseudogene	-0.55	-0.34	0.89	0.55	-0.13	0.20	0.35
330	MUM1	melanoma associated antigen (mutated) 1	-0.63	-0.12	0.74	0.20	-0.10	0.19	-0.11
331	PMS1	PMS1 postmeiotic segregation increased 1 (S. cerevisiae)	-0.52	0.18	0.34	-0.20	0.74	0.65	0.15
332	UBE2A	ubiquitin-conjugating enzyme E2A (RAD6 homolog)	-0.41	-0.29	0.69	-0.15	0.70	0.16	0.22
333	FANCC	Fanconi anemia, complementation group C	-0.92	-0.28	1.20	0.23	0.75	0.55	-0.05
334	RAD51L3	RAD51-like 3 (S. cerevisiae)	-0.89	0.58	0.32	0.61	0.61	0.56	0.01
335	FANCD2	Fanconi anemia, complementation group D2	-0.78	0.18	0.60	-0.57	-0.16	-0.37	0.26
336	POLR2A	polymerase (RNA) II (DNA directed) polypeptide A, 220kDa	-0.71	0.69	0.01	-0.58	-0.14	0.25	-0.37
337	ATM	ataxia telangiectasia mutated	0.10	-0.04	-0.06	0.60	0.01	0.08	0.85
338	CDKN2D	cyclin-dependent kinase inhibitor 2D (p19, inhibits CDK4)	-0.02	0.02	0.01	0.02	-0.25	0.28	0.81
339	IRG3	ligase III, DNA, ATP-dependent	0.43	-0.25	-0.18	0.78	0.06	0.58	0.19
340	HELQ	helicase, POLQ-like	0.50	-0.09	-0.41	0.32	0.66	0.67	0.58
341	ERCC8	excision repair cross-complementing rodent repair deficiency, complementation group 8	0.33	-0.18	-0.16	0.43	0.70	0.54	0.25
342	HELQ	helicase, POLQ-like	0.40	-0.23	-0.17	0.10	0.27	0.36	0.48
343	XRCC4	X-ray repair complementing defective repair in Chinese hamster cells 4	0.47	-0.06	-0.41	0.31	0.26	0.27	0.50
344	TMEM161A	transmembrane protein 161A	0.19	0.21	-0.40	0.21	0.48	0.59	0.53
345	POLR2C	polymerase (RNA) II (DNA directed) polypeptide C, 33kDa	0.13	0.08	-0.19	0.45	0.51	0.50	0.66
346	XRCC6BP1	XRCC6 binding protein 1	0.15	-0.02	-0.13	0.36	0.59	0.49	0.55
347	TTC5	tetratricopeptide repeat domain 5	-0.01	-0.19	0.19	0.23	0.33	0.43	0.71
348	NEIL2	neri like 2 (E. coli)	0.10	-0.06	-0.04	0.24	0.24	0.47	0.67
349	INTS3	integrator complex subunit 3	0.26	-0.16	-0.10	0.27	-0.21	-0.40	-0.33
350	EME2	essential meiotic endonuclease 1 homolog 2 (S. pombe)	0.34	-0.35	0.01	-0.01	-0.36	-0.33	-0.18
351	BRCC3	BRCA1/BRCA2-containing complex subunit 3	0.03	-0.19	0.16	-0.10	-0.21	-0.43	-0.09

352	NBN	inlbrin	0.55	-0.26	-0.29	0.32	0.02	-0.23	-0.11	-0.23	-0.11
353	MLH3	mutl homolog 3 (E. coli)	0.21	-0.17	-0.04	-0.19	-0.02	-0.01	-0.01	-0.01	0.06
354	RAD50	RAD50 homolog (S. cerevisiae)	0.26	-0.23	-0.03	0.01	-0.05	-0.02	-0.02	-0.02	0.05
355	SMC5	structural maintenance of chromosomes 5	0.24	-0.04	-0.21	-0.13	-0.20	-0.27	-0.07	-0.07	-0.07
356	POL1	polymerase (DNA directed) iota	0.41	-0.20	-0.22	0.03	-0.03	-0.12	-0.12	-0.12	-0.14
357	CUL4A	cullin 4A	0.16	0.07	-0.23	0.30	0.36	0.09	-0.46	0.09	-0.46
358	FAM175A	family with sequence similarity 175, member A	0.01	0.30	-0.31	0.18	0.12	0.09	-0.46	0.09	-0.46
359	XRCC4	X-ray repair complementing defective repair in Chinese hamster cells 4	0.41	0.12	-0.53	0.32	0.05	-0.22	0.27	-0.22	0.27
360	HUS1	HUS1 checkpoint homolog (S. pombe)	0.29	0.31	-0.60	0.30	0.02	-0.15	-0.16	-0.15	-0.16
361	GTF2H3	general transcription factor IIH, polypeptide 3, 34kDa	0.42	0.08	-0.50	0.01	-0.01	-0.06	-0.09	-0.06	-0.09
362	FAM175A	family with sequence similarity 175, member A	0.15	0.17	-0.33	0.01	0.01	0.03	-0.15	0.03	-0.15
363	MGMT	O-6-methylguanine-DNA methyltransferase	0.19	0.02	-0.22	0.16	-0.79	-0.04	0.06	-0.04	0.06
364	CUL4A	Cullin 4A	-0.22	0.31	-0.09	0.03	-0.37	0.09	0.20	-0.37	0.09
365	RAD9A	RAD9 homolog A (S. pombe)	-0.29	0.50	-0.21	-0.32	0.11	-0.15	0.19	-0.32	0.11
366	C19orf40	chromosome 19 open reading frame 40	0.09	0.35	-0.44	-0.02	0.04	-0.24	0.04	-0.44	0.04
367	APEX2	APEX nuclease (apurinic/apyrimidinic endonuclease) 2	-0.43	0.02	0.41	-0.38	-0.09	-0.04	0.23	-0.38	-0.09
368	MMS19	MMS19 nucleotide excision repair homolog (S. cerevisiae)	-0.26	0.25	0.00	0.05	-0.12	-0.01	-0.04	0.05	-0.12
369	VOP	valosin-containing protein	-0.19	0.22	-0.03	-0.05	-0.18	-0.21	-0.34	-0.03	-0.18
370	SUPT6H	suppressor of Ty 6 homolog (S. cerevisiae)	-0.24	0.08	0.16	-0.27	-0.04	-0.20	-0.20	-0.27	-0.04
371	TCEA1	transcription elongation factor A (SII), 1	-0.18	0.13	0.05	-0.22	0.14	-0.02	-0.36	0.05	-0.22
372	HUS1	HUS1 checkpoint homolog (S. pombe)	-0.40	-0.10	0.51	0.08	-0.01	-0.21	0.04	-0.40	0.04
373	MEN1	multiple endocrine neoplasia 1	-0.40	0.19	0.21	0.02	0.06	0.02	-0.09	-0.40	0.21
374	MUS81	MUS81 endonuclease homolog (S. cerevisiae)	-0.33	0.11	0.22	0.06	0.16	-0.08	-0.02	-0.33	0.11
375	POLR2E	polymerase (RNA) II (DNA directed) polypeptide E, 25kDa	-0.50	0.25	0.26	0.01	-0.05	-0.17	0.02	-0.50	0.25
376	POLR2E	polymerase (RNA) II (DNA directed) polypeptide E, 25kDa	-0.44	0.18	0.26	-0.13	-0.21	-0.26	-0.18	-0.44	0.18
377	RAD23A	RAD23 homolog A (S. cerevisiae)	-0.40	0.21	0.19	-0.05	0.15	0.23	0.12	-0.40	0.21
378	DOB1	damage-specific DNA binding protein 1, 127kDa	-0.46	0.35	0.11	0.03	0.20	0.20	0.03	-0.46	0.35
379	CSNK1D	casein kinase 1, delta	-0.44	0.20	0.24	0.03	0.20	0.12	0.22	-0.44	0.20
380	RTEL1	regulator of telomere elongation helicase 1	-0.53	0.35	0.18	0.05	0.07	0.23	-0.15	-0.53	0.35
381	RECQL5	RecQ protein-like 5	-0.65	0.32	0.33	0.11	-0.12	-0.01	0.12	-0.65	0.32
382	ATXN3	ataxin 3	-0.04	0.19	-0.15	-0.22	0.20	0.43	0.20	-0.04	0.19
383	MBD4	methyl-CpG binding domain protein 4	-0.11	0.12	-0.01	-0.12	0.38	0.38	0.04	-0.11	0.12
384	OBFC2B	oligonucleotide/oligosaccharide-binding fold containing 2B	-0.28	0.40	-0.13	-0.11	0.28	0.27	0.13	-0.28	0.40
385	PNKP	polynucleotide kinase 3'-phosphatase	-0.27	0.36	-0.09	-0.11	0.40	0.34	0.15	-0.27	0.36
386	CUL4A	Cullin 4A	-0.12	0.42	-0.30	-0.22	0.20	0.24	0.26	-0.12	0.42
387	ABL1	c-abl oncogene 1, receptor-tyrosine kinase	-0.28	0.18	0.10	0.14	0.10	0.01	-0.05	-0.28	0.18
388	SLC30A9	solute carrier family 30 (zinc transporter), member 9	-0.16	0.29	-0.13	0.17	0.09	0.10	-0.07	-0.16	0.29
389	SOD1	superoxide dismutase 1, soluble	-0.01	-0.01	0.02	0.03	0.15	0.23	0.31	-0.01	-0.01
390	RAD23B	RAD23 homolog B (S. cerevisiae)	-0.06	-0.08	0.14	-0.06	0.22	0.11	0.18	-0.06	-0.08
391	CEBPB	CCAAT/enhancer binding protein (C/EBP), gamma	-0.05	-0.10	0.15	0.01	0.09	0.08	0.19	-0.05	-0.10
392	NSMCE2	non-SMC element 2, MMS21 homolog (S. cerevisiae)	-0.23	0.07	0.16	0.01	0.20	0.13	0.29	-0.23	0.07
393	RAD17	RAD17 homolog (S. pombe)	-0.02	0.03	-0.02	0.10	0.28	0.20	0.01	-0.02	0.03

433	MUM1	melanoma associated antigen (mutated) 1	-0.21	0.07	0.14	0.01	-0.30	-0.13	0.09
434	WDR33	WD repeat domain 33	0.04	-0.04	0.01	-0.19	-0.26	-0.06	0.27
435	PMS2L1	postmeiotic segregation increased 2-like 1 pseudogene	0.34	-0.13	-0.21	0.31	0.01	0.12	0.08
436	TOPBP1	topoisomerase (DNA II) binding protein 1	0.16	-0.15	0.00	0.26	0.01	0.10	0.01
437	SRBD1	S1 RNA binding domain 1	0.17	-0.19	0.02	0.14	0.07	0.00	0.00
438	ALKBH1	alkB, alkylation repair homolog 1 (E. coli)	0.06	-0.02	0.04	0.25	0.03	-0.04	0.11
439	ALKBH2	alkB, alkylation repair homolog 2 (E. coli)	0.20	-0.08	-0.12	0.13	-0.01	-0.07	0.10
440	DDX1	DEAD (Asp-Glu-Ala-Asp) box polypeptide 1	0.04	-0.10	0.06	0.16	0.06	0.12	0.02
441	PMS2L1	postmeiotic segregation increased 2-like 1 pseudogene	0.01	-0.13	0.13	0.14	0.06	0.16	0.02
442	RAD1	RAD1 homolog (S. pombe)	0.10	-0.05	-0.05	0.13	0.23	0.12	0.02
443	RAD17	RAD17 homolog (S. pombe)	0.19	-0.13	-0.06	-0.03	-0.13	-0.01	-0.13
444	PMS2L1	postmeiotic segregation increased 2-like 1 pseudogene	0.12	-0.18	0.06	-0.04	-0.12	-0.17	-0.04
445	UIMC1	ubiquitin interaction motif containing 1	0.00	-0.21	0.20	-0.12	-0.02	-0.14	-0.05
446	SMG1	SMG1 homolog, phosphatidylinositol 3-kinase-related kinase (C. elegans)	0.25	-0.18	-0.07	-0.08	0.16	-0.02	-0.02
447	MLH1	mutL homolog 1, colon cancer, nonpolyposis type 2 (E. coli)	-0.09	0.13	-0.04	0.16	0.24	0.22	0.11
448	MBD4	methyl-CpG binding domain protein 4	0.02	0.04	-0.07	0.12	0.27	0.15	0.28
449	APTD1	apoptosis-inducing, TAF9-like domain 1	-0.03	0.21	-0.17	0.18	0.21	0.19	0.44
450	POLG	polymerase (DNA directed) gamma	-0.16	0.28	-0.10	0.26	0.15	0.13	0.33
451	RAD1	RAD1 homolog (S. pombe)	0.05	-0.14	0.09	0.14	0.10	0.19	0.30
452	PMS2L1	postmeiotic segregation increased 2-like 1 pseudogene	0.06	-0.07	0.01	0.25	0.15	0.18	0.41
453	OGG1	8-oxoguanine DNA glycosylase	-0.17	0.09	0.08	0.05	0.10	0.27	0.04
454	MBD4	methyl-CpG binding domain protein 4	-0.06	0.09	-0.03	0.14	0.13	0.23	0.23
455	REX1	ring-box 1	0.04	0.04	-0.08	0.11	0.20	0.25	0.14
456	KIN	KIN, antigenic determinant of recA protein homolog (mouse)	0.01	0.14	-0.15	0.01	0.24	0.33	0.37
457	APTAX	apataxin	0.09	0.05	-0.14	0.08	0.09	0.23	0.35
458	SUMO1	SMT3 suppressor of mit two 3 homolog 1 (S. cerevisiae)	0.09	-0.09	0.00	0.22	0.37	0.39	0.12
459	CTRF1	chromosome 7 open reading frame 11	-0.05	0.00	0.05	0.19	0.37	0.26	0.25
460	BAZ1B	bromodomain adjacent to zinc finger domain, 1B	0.13	0.01	-0.14	0.02	0.52	0.42	0.36
461	RAD1	RAD1 homolog (S. pombe)	0.19	0.10	-0.29	0.16	0.31	0.40	0.23
462	FANCE	Fanconi anemia, complementation group E	0.07	0.15	-0.22	0.20	0.32	0.41	0.30
463	MBD4	methyl-CpG binding domain protein 4	0.02	0.08	-0.10	0.29	0.35	0.48	0.17
464	CEBPB	CCAAT/enhancer binding protein (C/EBP), gamma	0.23	0.05	-0.28	0.19	0.41	0.17	0.21
465	RAD1	RAD1 homolog (S. pombe)	0.17	-0.09	-0.08	0.15	0.40	0.27	0.31
466	KAT5	K(lysine) acetyltransferase 5	0.16	-0.17	0.01	-0.17	0.00	0.13	-0.11
467	SMUG1	single-strand-selective monofunctional uracil-DNA glycosylase 1	0.21	-0.21	0.00	-0.07	0.18	0.30	0.16
468	XRCC4	X-ray repair complementing defective repair in Chinese hamster cells 4	0.43	-0.06	-0.37	0.14	-0.03	0.13	0.40
469	RAD1	RAD1 homolog (S. pombe)	0.29	-0.20	-0.09	-0.02	-0.06	0.07	0.28
470	NHEJ1	nonhomologous end-joining factor 1	0.25	-0.14	-0.11	-0.04	0.00	-0.02	0.29
471	SFPQ	isolating factor proline/glutamine-rich (polypyrimidine tract binding protein associated)	0.19	-0.04	-0.15	0.05	0.16	0.16	0.43
472	CINP	cyclin-dependent kinase 2 interacting protein	0.16	-0.01	-0.15	-0.12	0.09	0.17	0.26

473	HERC2	fect domain and RLD 2	0.27	-0.10	-0.17	-0.07	0.23	0.04	0.11
474	MORF4L1	mortality factor 4 like 1	0.28	-0.05	-0.22	0.12	0.24	0.18	0.20
475	MORF4L2	mortality factor 4 like 2	0.18	-0.40	0.22	0.17	0.30	0.36	0.12
476	RPAIN	RPA interacting protein	0.03	-0.30	0.27	0.12	0.52	0.21	0.07
477	RAD51L3	RAD51-like 3 (S. cerevisiae)	-0.13	-0.12	0.24	0.14	0.23	0.14	0.31
478	PER1	period homolog 1 (Drosophila)	-0.22	-0.11	0.33	0.16	0.29	0.29	0.22
479	EYA3	eyes absent homolog 3 (Drosophila)	-0.15	-0.01	0.16	-0.08	0.14	0.00	0.23
480	SETMAR	SET domain and mariner transposase fusion gene	0.18	-0.34	0.16	0.40	-0.01	0.23	0.16
481	PMS2L1	postmeiotic segregation increased 2-like 1 pseudogene	-0.08	-0.25	0.33	0.26	-0.10	0.19	0.04
482	IGHMBP2	immunoglobulin mu binding protein 2	0.02	-0.29	0.27	0.30	-0.08	0.10	0.26
483	MORF4L2	Mortality factor 4 like 2	0.53	-0.31	-0.22	-0.02	0.14	0.38	0.20
484	PMS2L2	postmeiotic segregation increased 2-like 2 pseudogene	-0.28	0.00	0.28	0.57	-0.16	0.25	0.22
485	POLR2C	polymerase (RNA) II (DNA directed) polypeptide C. 33kDa	-0.26	0.02	0.23	0.40	0.30	0.36	0.51
486	ESCO2	establishment of cohesion 1 homolog 2 (S. cerevisiae)	-0.30	0.08	0.22	0.54	0.08	0.10	0.56
487	BTG2	BTG family, member 2	-0.17	0.10	0.07	-0.09	-0.56	-0.93	0.08
488	MUTYH	mutY homolog (E. coli)	0.24	-0.31	0.07	-0.35	0.04	-1.03	0.10
489	CIB1	calcium and integrin binding 1 (calmyrin)	-0.03	-0.22	0.25	-0.44	-0.19	-0.32	-0.02
490	TP53BP1	tumor protein p53 binding protein 1	0.04	-0.44	0.40	-0.05	-0.19	-0.18	0.20
491	UBE2B	ubiquitin-conjugating enzyme E2B (RAD6 homolog)	-0.03	-0.30	0.33	-0.19	-0.25	-0.32	0.13
492	GADD45A	growth arrest and DNA-damage-inducible, alpha	-0.06	-0.25	0.30	-0.21	-0.17	-0.34	0.07
493	GETN2	centrin, EF-hand protein, 2	-0.33	-0.31	0.64	-0.31	-0.04	-0.10	0.15
494	GSKN1D	casein kinase 1, delta	-0.31	-0.07	0.38	-0.07	-0.35	-0.42	-0.36
495	SUPT6H	suppressor of Ty 6 homolog (S. cerevisiae)	-0.45	0.18	0.27	-0.31	-0.56	-0.45	-0.42
496	SETX	senataxin	-0.01	0.00	0.01	-0.31	-0.27	-0.04	-0.21
497	RECQL	RecQ protein-like (DNA helicase Q1-like)	0.11	-0.20	0.08	-0.39	-0.49	-0.38	-0.42
498	RECQL	RecQ protein-like (DNA helicase Q1-like)	-0.01	0.01	0.00	-0.45	-0.57	-0.39	-0.41
499	JMY	junction mediating and regulatory protein, p53 cofactor	0.24	-0.12	-0.13	-0.28	-0.54	-0.13	-0.20
500	BRCC3	BRCA1/BRCA2-containing complex, subunit 3	0.24	-0.64	0.41	-0.24	-0.36	-0.33	-0.43
501	BRCC3	BRCA1/BRCA2-containing complex, subunit 3	-0.08	-0.28	0.36	-0.38	-0.51	-0.45	-0.59
502	BRCC3	BRCA1/BRCA2-containing complex, subunit 3	-0.12	-0.34	0.46	-0.08	-0.33	-0.27	-0.38
503	SLK	STE20-like kinase (yeast)	0.10	-0.35	0.25	0.08	-0.47	-0.28	-0.53
504	NBN	Nibrin	-0.02	-0.22	0.25	-0.30	-0.29	-0.21	-0.87
505	CDC14B	CDC14 cell division cycle 14 homolog B (S. cerevisiae)	0.05	-0.44	0.40	-0.77	-0.41	-0.48	-0.66
506	RAD50	RAD50 homolog (S. cerevisiae)	0.33	-0.41	0.07	-0.58	-0.31	0.07	-0.06
507	KIN	KIN antigenic determinant of recA protein homolog (mouse)	0.40	-0.19	-0.21	-1.03	-0.21	-0.13	-0.24
508	IGHMBP2	immunoglobulin mu binding protein 2	0.16	0.17	-0.33	-0.53	-0.19	0.07	-0.48
509	ASTE1	asteroid homolog 1 (Drosophila)	0.10	0.01	-0.11	-0.68	0.07	-0.17	-0.22
510	FANCM	Fanconi anemia, complementation group M	0.18	-0.15	-0.03	-0.48	-0.71	-0.08	-0.47
511	LIG4	ligase IV, DNA, ATP-dependent	0.22	-0.15	-0.07	-0.50	-0.77	-0.66	-0.73
512	RPS27L	ribosomal protein S27-like	0.10	0.37	-0.47	-0.54	-0.90	-0.72	-0.82
513	RECQL	RecQ protein-like (DNA helicase Q1-like)	-0.31	0.36	-0.05	-0.20	-0.59	-0.41	-0.95
514	NSMCE1	non-SMC element 1 homolog (S. cerevisiae)	0.08	0.23	-0.30	-0.65	-0.03	-0.79	-0.56
515	LIG4	ligase IV, DNA, ATP-dependent	0.69	-0.58	-0.11	0.01	-0.50	-0.32	-0.39
516	POLH	Polymerase (DNA directed), eta	0.73	0.22	-0.95	0.06	-0.09	0.40	-0.28

	WD repeat domain 33	0.82	0.64	-1.47	0.38	0.52	0.93	0.33
555	WDR33							
556	ATR	ataxia telangiectasia and Rad3 related	0.63	-0.83	0.47	0.29	0.40	0.38
557	RPS27A	ribosomal protein S27a	0.64	-1.01	0.45	0.29	0.25	0.44
558	PCNA	proliferating cell nuclear antigen	0.28	0.94	0.42	0.37	1.28	-0.11
559	APLF	Aparataxin and PNKP like factor	-0.27	0.53	0.95	0.75	1.81	-0.64
560	CUL4B	cullin 4B	-0.29	-0.19	-0.23	0.05	-0.93	-0.95
561	CUL4B	cullin 4B	-0.22	-0.51	-0.25	-0.34	-1.03	-1.03
562	CUL4B	cullin 4B	-0.25	-0.30	-0.22	-0.08	-0.94	-1.66
563	ERCC4	excision repair cross-complementing rodent repair deficiency, complementation group 4	-0.16	0.01	-0.48	0.29	-0.88	-2.40
564	RPA1	replication protein A1, 70kDa	-0.44	-0.01	0.05	0.18	-0.76	-2.52
565	FZR1	fizzy/cell division cycle 20 related 1 (Drosophila)	-0.07	-0.09	0.31	0.24	0.40	-1.18
566	POLR2A	polymersase (RNA) II (DNA directed) polypeptide A, 220kDa	-0.90	0.23	0.85	0.80	0.34	-2.17
567	RPAIN	RPA interacting protein	0.02	-0.06	0.73	1.27	1.64	0.10
568	SMC3	Structural maintenance of chromosomes 3	0.90	0.30	-0.92	-0.32	0.33	-0.08
569	FANCB	Fanconi anemia, complementation group B	0.81	-0.61	-0.93	-0.83	-0.05	-0.98
570	BUB1	budding uninhibited by benzimidazoles 1 homolog (yeast)	0.32	-0.18	-0.05	-0.32	-0.44	-0.99
571	BRIP1	BRCA1 interacting protein C-terminal helicase 1	0.50	-0.45	-0.14	-0.86	-0.60	-1.28
572	RAD54L	RAD54-like (S. cerevisiae)	0.17	-0.47	-0.23	0.11	0.01	-0.01
573	RAD51AP1	RAD51 associated protein 1	0.20	-0.04	0.03	0.24	0.30	-0.08
574	POLE2	polymersase (DNA directed), epsilon 2 (p59 subunit)	0.16	-0.03	0.02	0.15	0.27	0.16
575	BLM	Bloom syndrome, RecQ helicase-like	0.15	0.00	0.30	0.03	0.20	0.17
576	RFC3	replication factor C (activator 1) 3, 38kDa	0.08	-0.13	0.04	0.01	-0.06	-0.34
577	EXO1	exonuclease 1	0.23	-0.01	-0.22	0.17	-0.05	-0.14
578	RFC3	replication factor C (activator 1) 3, 38kDa	0.18	-0.17	0.08	0.07	0.05	-0.01
579	FANCD2	Fanconi anemia, complementation group D2	0.12	-0.20	0.08	0.01	0.03	-0.01
580	BUB1	budding uninhibited by benzimidazoles 1 homolog (yeast)	0.13	-0.07	-0.05	0.06	-0.08	-0.32
581	DTL	centioleless homolog (Drosophila)	0.06	-0.03	0.22	-0.08	0.06	-0.01
582	DTL	centioleless homolog (Drosophila)	0.06	-0.07	0.02	0.21	-0.11	-0.24
583	MDC1	mediator of DNA-damage checkpoint 1	-0.52	0.19	0.32	-0.26	0.00	-0.08
584	CHAF1A	chromatin assembly factor 1, subunit A (p150)	-0.37	0.20	0.17	0.30	0.17	0.06
585	CHAF1A	chromatin assembly factor 1, subunit A (p150)	-0.40	0.23	0.18	0.12	0.24	0.06
586	FEN1	flap structure-specific endonuclease 1	0.02	-0.14	0.12	0.29	0.26	0.00
587	PARP1	poly (ADP-ribose) polymerase 1	-0.23	0.12	0.11	-0.04	0.05	-0.21
588	GDCA5	cell division cycle associated 5	-0.19	0.09	0.10	0.15	0.07	-0.03
589	RFWD3	ring finger and WD repeat domain 3	-0.09	0.11	-0.02	0.14	0.22	-0.08
590	MAD2L2	MAD2 mitotic arrest deficient-like 2 (yeast)	-0.27	0.23	0.03	0.01	0.16	0.18
591	MRE11A	MRE11 meiotic recombination 11 homolog A (S. cerevisiae)	0.51	-0.41	-0.10	0.24	0.36	-0.04
592	DNA2	DNA replication helicase 2 homolog (yeast)	0.48	-0.41	-0.07	0.11	0.05	-0.36
593	AURKB	aurora kinase B	-0.41	0.32	0.08	0.38	0.29	0.52
594	TP73	tumor protein p73	-0.68	0.25	0.43	0.07	0.57	0.39
595	TTK	TTK protein kinase	-0.04	0.07	-0.03	-0.23	-0.56	-0.43
596	PRKCG	protein kinase C, gamma	-0.53	0.18	0.36	-0.36	-1.04	-0.80

597	CUL4A	culin 4A	-0.29	-0.45	0.74	-0.15	-0.41	-0.29	-0.25
598	AURKB	aurora kinase B	-0.76	0.85	-0.09	0.36	0.31	-0.40	0.44
599	FANCB	Fanconi anemia, complementation group B	0.67	-0.42	-0.25	0.18	-0.60	0.60	-0.10
600	RECQL4	RecQ protein-like 4	-0.28	0.19	0.09	0.22	-0.07	0.18	-0.07
601	RDM1	RAD52 motif 1	-0.08	0.13	-0.05	-0.21	0.91	0.52	0.62
602	FANCD2	Fanconi anemia, complementation group D2	0.09	0.17	-0.25	-0.08	0.31	0.30	0.52
603	BUB1	budding uninhibited by benzimidazoles 1 homolog (yeast)	1.35	0.79	-2.14	0.43	-1.20	-0.78	0.73
604	POLK	polymerase (DNA directed) kappa	-0.25	2.05	-1.80	0.84	-1.84	-0.90	1.35
605	HMBG2	high-mobility group box 2	-1.04	1.34	-0.30	0.74	-2.05	-0.40	1.21
606	REV1	REV1 homolog (S. cerevisiae)	0.88	0.17	-1.06	-0.58	-1.49	-0.78	1.36
607	UBE2B	ubiquitin conjugating enzyme E2B (RAD6 homolog)	0.50	-0.67	0.17	-0.23	0.89	0.74	1.34
608	TYMS	thymidylate synthetase	1.40	-1.16	-0.25	-1.08	1.49	0.65	1.78
609	WRNIP1	Werner helicase interacting protein 1	1.34	-1.90	0.56	0.31	1.23	-0.62	-0.75
610	POLR2B	Polymerase (RNA) II (DNA directed) polypeptide B, 140kDa	0.44	0.07	-0.52	-2.29	-0.41	0.29	0.15
611	BAZ1B	bromodomain adjacent to zinc finger domain, 1B	1.31	0.36	-1.66	-3.13	-0.36	-1.03	0.21
612	BUB1	budding uninhibited by benzimidazoles 1 homolog (yeast)	2.27	-2.14	-0.14	-1.83	-0.69	0.45	0.31
613	OGG1	8-oxoguanine DNA glycosylase	2.05	-1.00	-1.05	-1.03	-1.24	1.25	0.96
614	FGF10	fibroblast growth factor 10	2.08	-1.04	-1.03	-1.12	-0.38	1.28	0.94
615	WDR33	WD repeat domain 33	2.54	-1.19	-1.35	1.56	-1.16	-0.37	0.75
616	ATM	ataxia telangiectasia mutated	0.45	1.37	-1.82	-1.97	1.12	0.12	1.09
617	CRY2	cryptochrome 2 (photolyase-like)	-0.68	2.25	-1.57	-1.80	0.91	-0.93	-0.76
618	USP3	ubiquitin specific peptidase 3	-0.02	0.10	-0.08	-3.09	0.76	0.53	0.64
619	RAD9B	RAD9 homolog B (S. pombe)	-0.32	0.89	-0.57	-0.14	-1.37	2.02	1.07
620	EYA4	eyes absent homolog 4 (Drosophila)	1.14	0.98	-2.13	0.77	-1.26	1.47	1.30
621	CEP164	centrosomal protein 164kDa	0.56	-0.74	0.18	-1.08	0.25	0.10	-0.81
622	POLH	polymerase (DNA directed), eta	1.18	-0.16	-1.02	-0.19	-0.13	-0.75	-0.13
623	POLH	polymerase (DNA directed), eta	0.48	0.55	-1.03	0.03	0.68	-0.52	-0.13
624	GTF2H5	general transcription factor IIH, polypeptide 5	0.53	0.22	-0.74	-0.92	-0.38	1.00	0.34
625	POLK	polymerase (DNA directed) kappa	0.34	-0.27	-0.07	-0.34	-0.66	0.38	0.00
626	PARP3	poly (ADP-ribose) polymerase family, member 3	0.74	-1.08	0.34	-0.09	0.70	0.87	-0.04
627	REV3L	REV3-like, catalytic subunit of DNA polymerase zeta (yeast)	-0.02	-0.03	0.05	-0.02	-0.30	-0.63	-0.05
628	USP3	ubiquitin specific peptidase 3	0.00	-0.16	0.16	0.39	0.56	-0.02	0.09
629	OBFC2A	oligonucleotide/oligosaccharide-binding fold containing 2A	-0.01	-0.10	0.12	-0.33	0.11	0.57	0.24
630	OBFC2A	oligonucleotide/oligosaccharide-binding fold containing 2A	-0.03	0.24	-0.21	-0.31	0.24	0.74	0.67
631	POLH	polymerase (DNA directed), eta	-0.37	1.29	-0.92	-0.40	0.06	0.30	0.66
632	BTG2	BTG family, member 2	-0.56	1.37	-0.81	0.61	1.16	0.44	0.11
633	FBXO6	F-box protein 6	-0.55	0.78	-0.24	0.40	0.74	0.55	-0.40
634	POLH	polymerase (DNA directed), eta	-0.09	0.93	-0.84	0.05	1.37	0.45	0.27
635	TREX1	three prime repair exonuclease 1	-0.37	0.82	-0.44	0.19	0.61	0.43	0.57
636	EYA1	eyes absent homolog 1 (Drosophila)	-0.42	0.65	-0.23	0.81	0.82	-0.71	0.85
637	CDC14B	CDC14 cell division cycle 14 homolog B (S. cerevisiae)	0.20	0.57	-0.77	1.21	-0.78	0.74	0.13
638	POLN	polymerase (DNA directed) nu	0.07	0.57	-0.64	1.06	-0.70	-0.40	-0.26

	three prime repair exonuclease 1	0.73	0.98	-1.71	-0.21	1.07	-0.42	1.30
639	TREX1							
640	FLJ35220	hypothetical protein FLJ35220	-0.82	1.28	-0.46	-0.10	0.36	1.80
641	REV3L	REV3-like, catalytic subunit of DNA polymerase zeta (yeast)	-0.65	1.37	-0.72	1.29	0.59	1.21
642	ATR	ataxia telangiectasia and RadD related	0.14	0.48	-0.61	-0.54	3.46	0.43
643	DCLRE1C	DNA cross-link repair 1C (PSO2 homolog, <i>S. cerevisiae</i>)	0.02	-0.79	0.77	-1.85	2.67	1.81
644	EYA3	eyes absent homolog 3 (<i>Drosophila</i>)	1.79	-1.18	-0.61	1.94	0.79	2.46
645	ZSWIM7	zinc finger, SWIM-type containing 7	-0.83	0.55	0.28	2.05	2.25	2.16
646	FANCM	Fanconi anemia, complementation group M	1.21	-2.19	0.98	1.36	0.01	1.71
647	RPA4	replication protein A4, 34kDa	-0.99	1.85	-0.86	2.02	2.06	1.45
648	ESCO2	Establishment of cohesion 1 homolog 2 (<i>S. cerevisiae</i>)	0.91	-1.67	0.76	1.92	-3.78	0.96
649	DCLRE1C	DNA cross-link repair 1C (PSO2 homolog, <i>S. cerevisiae</i>)	0.49	-0.47	-0.03	-0.54	0.39	1.08
650	SMC5	structural maintenance of chromosomes 5	-0.45	-0.24	0.69	0.11	-3.03	0.73
651	TP53BP1	tumor protein p53 binding protein 1	0.68	0.36	-1.04	-1.69	-0.65	-2.85
652	SUP16H	suppressor of Ty 6 homolog (<i>S. cerevisiae</i>)	-0.96	0.49	0.07	-0.49	-3.16	-3.01
653	MSH6	mutS homolog 6 (<i>E. coli</i>)	-0.51	0.70	-0.19	-2.46	-3.02	-1.53
654	APLF	aplatxin and PNKP like factor	-1.03	0.30	0.73	0.13	-0.25	-4.62
655	CCNO	cyclin O	-1.20	0.88	0.32	0.25	-0.45	-2.99
656	HERC2	hect domain and RLD 2	-0.89	0.22	0.67	0.13	-2.43	-2.99
657	IDP1	Tyrosyl-DNA phosphodiesterase 1	0.05	-0.43	0.38	0.58	-0.97	-3.13
658	USE2D3	ubiquitin-conjugating enzyme E2D 3 (UBC4/5 homolog, yeast)	0.94	0.37	-1.31	0.80	-3.81	-3.42
659	RAD51L1	RAD51-like 1 (<i>S. cerevisiae</i>)	0.16	-0.46	0.31	-1.80	-1.80	-3.01
660	GT2H5	general transcription factor IIH, polypeptide 5	-0.30	0.08	0.22	-2.83	0.15	-3.84
661	HELQ	helicase, POLQ-like	-0.37	-0.03	0.40	-3.39	0.47	-0.56
662	PMS1	PMS1 postmeiotic segregation: increased 1 (<i>S. cerevisiae</i>)	1.52	1.38	-2.90	1.27	2.00	0.98
663	GHD1L	Chromodomain helicase DNA binding protein 1-like	1.66	1.01	-2.67	1.39	1.28	-2.24
664	OBFC2A	oligonucleotide/oligosaccharide-binding fold containing 2A	-0.52	-0.09	0.61	-0.40	-5.54	-1.31
665	GT2H5	general transcription factor IIH, polypeptide 5	-0.94	1.22	-0.28	-0.02	0.76	-1.81
666	RAD51	RAD51 homolog (RecA homolog <i>E. coli</i>) (<i>S. cerevisiae</i>)	0.43	0.81	-1.24	0.05	0.58	-1.59
667	XRCG3	X-ray repair complementing defective repair in Chinese hamster cells 3	-0.33	0.31	0.02	-0.94	-0.83	-0.45
668	TEX15	testis expressed 15	0.38	-0.36	-0.02	0.03	-0.42	-0.83
669	FANCA	Fanconi anemia, complementation group A	0.53	-0.78	0.26	-1.94	-0.92	-1.40
670	TEX15	testis expressed 15	0.13	0.13	-0.26	-0.49	-0.72	-0.71
671	ESCO2	establishment of cohesion 1 homolog 2 (<i>S. cerevisiae</i>)	-0.34	0.58	-0.24	0.00	0.80	-1.21
672	RAD9B	RAD9 homolog B (<i>S. pombe</i>)	-2.05	-1.02	3.07	1.33	2.10	2.50
673	ODC14B	ODC14 cell division cycle 14 homolog B (<i>S. cerevisiae</i>)	-1.36	-0.46	1.82	1.49	1.35	1.52
674	FEED1	endonuclease/exonuclease/phosphatase family domain containing 1	-1.71	0.56	1.16	0.84	1.41	-0.66
675	POLH	polymerase (DNA directed) eta	-0.83	0.46	0.37	2.61	-0.12	2.64
676	EYA4	eyes absent homolog 4 (<i>Drosophila</i>)	-0.43	-0.42	0.85	-0.18	0.11	1.02

[0072] [表3B] 第3遺伝子群

	Gene Symbol	Gene Title
1	RECQL5	RecQ protein-like 5
2	FANCM	Fanconi anemia, complementation group M
3	RTEL1	regulator of telomere elongation helicase 1
4	ATM	ataxia telangiectasia mutated
5	ATXN3	Ataxin 3
6	FANCC	Fanconi anemia, complementation group C
7	SPO11	SPO11 meiotic protein covalently bound to DSB homolog (S. cerevisiae)
8	EYA2	eyes absent homolog 2 (Drosophila)
9	POLE	polymerase (DNA directed), epsilon
10	NCOA6	nuclear receptor coactivator 6
11	PRKDC	Protein kinase, DNA-activated, catalytic polypeptide
12	RNF168	ring finger protein 168
13	WRNIP1	Werner helicase interacting protein 1
14	ERCC8	excision repair cross-complementing rodent repair deficiency, complementation group 8
15	FBXO18	F-box protein, helicase, 18
16	DMC1	DMC1 dosage suppressor of mek1 homolog, meiosis-specific homologous recombination (yeast)
17	KIF22	kinesin family member 22
18	FANCA	Fanconi anemia, complementation group A
19	POLD1	polymerase (DNA directed), delta 1, catalytic subunit 125kDa
20	MUTYH	mutY homolog (E. coli)
21	BRCA1	breast cancer 1, early onset
22	UNG	uracil-DNA glycosylase
23	TRIP13	thyroid hormone receptor interactor 13
24	HMGB2	high-mobility group box 2
25	H2AFX	H2A histone family, member X
26	CHEK1	CHK1 checkpoint homolog (S. pombe)
27	HMGB1	high-mobility group box 1
28	PAXIP1	PAX interacting (with transcription-activation domain) protein 1
29	POLR2D	polymerase (RNA) II (DNA directed) polypeptide D
30	RPA3	replication protein A3, 14kDa
31	BRCA2	breast cancer 2, early onset
32	FANCI	Fanconi anemia, complementation group i
33	GTF2H4	general transcription factor IIH, polypeptide 4, 52kDa
34	LIG3	ligase III, DNA, ATP-dependent
35	CHAF1B	chromatin assembly factor 1, subunit B (p60)
36	CHAF1A	chromatin assembly factor 1, subunit A (p150)
37	SIRT1	sirtuin (silent mating type information regulation 2 homolog) 1 (S. cerevisiae)
38	SSRP1	structure specific recognition protein 1
39	AXIN2	axin 2
40	TDP1	tyrosyl-DNA phosphodiesterase 1
41	LIG1	ligase I, DNA, ATP-dependent
42	MSH6	mutS homolog 6 (E. coli)
43	TOP2A	topoisomerase (DNA) II alpha 170kDa
44	RAD54B	RAD54 homolog B (S. cerevisiae)
45	MSH2	mutS homolog 2, colon cancer, nonpolyposis type 1 (E. coli)
46	POLQ	polymerase (DNA directed), theta
47	RFC2	replication factor C (activator 1) 2, 40kDa
48	RFC4	replication factor C (activator 1) 4, 37kDa
49	PTTG1	pituitary tumor-transforming 1
50	RAD51	RAD51 homolog (RecA homolog, E. coli) (S. cerevisiae)
51	BRAD1	BRCA1 associated RING domain 1
52	RFC5	replication factor C (activator 1) 5, 36.5kDa
53	UBE2T	ubiquitin-conjugating enzyme E2T (putative)
54	POLA1	polymerase (DNA directed), alpha 1, catalytic subunit
55	TDG	thymine-DNA glycosylase
56	UHRF1	ubiquitin-like with PHD and ring finger domains 1
57	RPAIN	RPA interacting protein
58	FEN1	flap structure-specific endonuclease 1

59	FANCB	Fanconi anemia, complementation group B
60	EYA3	eyes absent homolog 3 (Drosophila)
61	CLSPN	claspin homolog (Xenopus laevis)
62	EME2	essential meiotic endonuclease 1 homolog 2 (S. pombe)
63	PARQ	poly (ADP-ribose) glycohydrolase
64	RPA2	replication protein A2, 32kDa
65	PRPF19	PRP19/PSO4 pre-mRNA processing factor 19 homolog (S. cerevisiae)
66	RUVBL2	RuvB-like 2 (E. coli)
67	MDC1	mediator of DNA-damage checkpoint 1
68	UBE2N	ubiquitin-conjugating enzyme E2N (UBC13 homolog, yeast)
69	POLG2	polymerase (DNA directed), gamma 2, accessory subunit
70	NUDT1	nudix (nucleoside diphosphate linked moiety X)-type motif 1
71	CHK2	CHK2 checkpoint homolog (S. pombe)
72	FANCL	Fanconi anemia, complementation group L
73	PARP2	poly (ADP-ribose) polymerase 2
74	NEIL3	nei endonuclease VIII-like 3 (E. coli)
75	SETMAR	SET domain and mariner transposase fusion gene
76	SMC1A	structural maintenance of chromosomes 1A
77	PCNA	proliferating cell nuclear antigen
78	POLB	polymerase (DNA directed), beta
79	CNK1E	casein kinase 1, epsilon
80	POLR2I	polymerase (RNA) II (DNA directed) polypeptide I, 14.5kDa
81	POLR2H	polymerase (RNA) II (DNA directed) polypeptide H
82	SLC30A9	solute carrier family 30 (zinc transporter), member 9
83	RECQL4	RecQ protein-like 4
84	FANCG	Fanconi anemia, complementation group G
85	TP53	tumor protein p53
86	RBBP8	retinoblastoma binding protein 8
87	DUT	deoxyuridine triphosphatase
88	SFPQ	splicing factor proline/glutamine-rich (polypyrimidine tract binding protein associated)
89	PALB2	partner and localizer of BRCA2
90	POLR2G	polymerase (RNA) II (DNA directed) polypeptide G
91	WDR33	WD repeat domain 33
92	MNAT1	menage a trois homolog 1, cyclin H assembly factor (Xenopus laevis)
93	XRCC5	X-ray repair complementing defective repair in Chinese hamster cells 5 (double-strand-break rejoining)
94	POLR2K	polymerase (RNA) II (DNA directed) polypeptide K, 7.0kDa
95	RNF8	ring finger protein 8
96	REV1	REV1 homolog (S. cerevisiae)
97	NPM1	nucleophosmin (nucleolar phosphoprotein B23, numatrin)
98	STRA13	stimulated by retinoic acid 13 homolog (mouse)
99	CDK7	cyclin-dependent kinase 7
100	FANCF	Fanconi anemia, complementation group F
101	BCCIP	BRCA2 and CDKN1A interacting protein
102	NTHL1	nth endonuclease III-like 1 (E. coli)
103	EME1	essential meiotic endonuclease 1 homolog 1 (S. pombe)
104	SMC6	structural maintenance of chromosomes 6
105	XRCC6	X-ray repair complementing defective repair in Chinese hamster cells 6
106	CLK2	CDC-like kinase 2
107	HINFP	histone H4 transcription factor
108	MRE11A	MRE11 meiotic recombination 11 homolog A (S. cerevisiae)
109	VCP	valosin-containing protein
110	RPA1	replication protein A1, 70kDa
111	DCLRE1A	DNA cross-link repair 1A (PSO2 homolog, S. cerevisiae)
112	CRY1	cryptochrome 1 (photolyase-like)
113	SUMO1	SMT3 suppressor of mif two 3 homolog 1 (S. cerevisiae)
114	APEX1	APEX nuclease (multifunctional DNA repair enzyme) 1
115	RAD21	RAD21 homolog (S. pombe)
		X-ray repair complementing defective repair in Chinese

116	XRCC2	hamster cells 2
117	DCLRE1B	DNA cross-link repair 1B (PSO2 homolog, <i>S. cerevisiae</i>)
118	NBN	nibrin
119	POLR2B	polymerase (RNA) II (DNA directed) polypeptide B, 140kDa
120	ASF1A	ASF1 anti-silencing function 1 homolog A (<i>S. cerevisiae</i>)
121	CHD1L	chromodomain helicase DNA binding protein 1-like
122	EPC2	enhancer of polycomb homolog 2 (<i>Drosophila</i>)
123	RFC1	replication factor C (activator 1) 1, 145kDa
124	TYMS	thymidylate synthetase
125	PMS1	PMS1 postmeiotic segregation increased 1 (<i>S. cerevisiae</i>)
126	NONO	non-POU domain containing, octamer-binding
127	UBE2D3	ubiquitin-conjugating enzyme E2D 3 (UBC4/5 homolog, yeast)
128	ZW10	ZW10, kinetochore associated, homolog (<i>Drosophila</i>)
129	USP1	ubiquitin specific peptidase 1
130	SMC3	structural maintenance of chromosomes 3
131	JMY	junction mediating and regulatory protein, p53 cofactor
132	WRN	Werner syndrome, RecQ helicase-like
133	SHPRH	SNF2 histone linker PHD RING helicase
134	RAD18	RAD18 homolog (<i>S. cerevisiae</i>)
135	PMS2L2	postmeiotic segregation increased 2-like 2 pseudogene
136	ERCC3	excision repair cross-complementing rodent repair deficiency, complementation group 3 (xeroderma pigmentosum group B complementing)
137	PRMT6	protein arginine methyltransferase 6
138	SUPT16H	suppressor of Ty 16 homolog (<i>S. cerevisiae</i>)
139	USP28	ubiquitin specific peptidase 28
140	POLR2F	polymerase (RNA) II (DNA directed) polypeptide F
141	ZSWIM7	zinc finger, SWIM-type containing 7
142	ESCO1	establishment of cohesion 1 homolog 1 (<i>S. cerevisiae</i>)
143	POLD3	polymerase (DNA-directed), delta 3, accessory subunit
144	GTF2H2	general transcription factor IIH, polypeptide 2, 44kDa
145	SHFM1	split hand/foot malformation (ectrodactyly) type 1
146	ESCO2	establishment of cohesion 1 homolog 2 (<i>S. cerevisiae</i>)
147	USP10	ubiquitin specific peptidase 10
148	UBE2B	ubiquitin-conjugating enzyme E2B (RAD6 homolog)
149	RBM14	RNA binding motif protein 14
150	BUB1	budding uninhibited by benzimidazoles 1 homolog (yeast)
151	CENPE	centromere protein E, 312kDa
152	GADD45G	growth arrest and DNA-damage-inducible, gamma
153	KNTC1	kinetochore associated 1
154	GEN1	Gen homolog 1, endonuclease (<i>Drosophila</i>)
155	MUM1	melanoma associated antigen (mutated) 1
156	CHRNA4	cholinergic receptor, nicotinic, alpha 4
157	FZR1	fizzy/cell division cycle 20 related 1 (<i>Drosophila</i>)
158	ATRIP	ATR interacting protein
159	TNP1	transition protein 1 (during histone to protamine replacement)
160	PER1	period homolog 1 (<i>Drosophila</i>)
161	XRCC1	X-ray repair complementing defective repair in Chinese hamster cells 1
162	UBE2V2	ubiquitin-conjugating enzyme E2 variant 2
163	RAD51C	RAD51 homolog C (<i>S. cerevisiae</i>)
164	UVRAG	UV radiation resistance associated gene
165	ERCC1	excision repair cross-complementing rodent repair deficiency, complementation group 1 (includes overlapping antisense sequence)
166	BRE	brain and reproductive organ-expressed (TNFRSF1A modulator)
167	MC1R	melanocortin 1 receptor (alpha melanocyte stimulating hormone receptor)
168	CUL4B	cullin 4B
169	PARP4	poly (ADP-ribose) polymerase family, member 4
170	ERCC5	excision repair cross-complementing rodent repair deficiency, complementation group 5
171	XPA	xeroderma pigmentosum, complementation group A

172	CEP164	centrosomal protein 164kDa
173	FTO	fat mass and obesity associated
174	GTF2H1	general transcription factor IIH, polypeptide 1, 62kDa
175	TERF2IP	telomeric repeat binding factor 2, interacting protein
176	ERCC6	excision repair cross-complementing rodent repair deficiency, complementation group 6
177	GTF2H5	general transcription factor IIH, polypeptide 5
178	EEPD1	endonuclease/exonuclease/phosphatase family domain containing 1
179	ALKBH3	alkB, alkylation repair homolog 3 (E. coli)
180	POLD4	polymerase (DNA-directed), delta 4
181	MPG	N-methylpurine-DNA glycosylase
182	POLR2L	polymerase (RNA) II (DNA directed) polypeptide L, 7.6kDa
183	RPS27L	ribosomal protein S27-like
184	XPC	xeroderma pigmentosum, complementation group C
185	NRIH2	nuclear receptor subfamily 1, group H, member 2
186	TCEA1	transcription elongation factor A (SII), 1
187	RAD23A	RAD23 homolog A (S. cerevisiae)
188	ATR	ataxia telangiectasia and Rad3 related
189	SMUG1	single-strand-selective monofunctional uracil-DNA glycosylase 1
190	CDC14B	CDC14 cell division cycle 14 homolog B (S. cerevisiae)
191	OGG1	8-oxoguanine DNA glycosylase
192	POLK	polymerase (DNA directed) kappa
193	HELQ	helicase, POLQ-like
194	ERCC4	excision repair cross-complementing rodent repair deficiency, complementation group 4
195	DDB2	damage-specific DNA binding protein 2, 48kDa
196	RAD23B	RAD23 homolog B (S. cerevisiae)
197	RAD51L1	RAD51-like 1 (S. cerevisiae)
198	DCLRE1C	DNA cross-link repair 1C (PSO2 homolog, S. cerevisiae)
199	POLI	polymerase (DNA directed) iota
200	ALKBH1	alkB, alkylation repair homolog 1 (E. coli)
201	NEIL1	nei endonuclease VII-like 1 (E. coli)
202	HUS1	HUS1 checkpoint homolog (S. pombe)
203	BAP1	BRCA1 associated protein-1 (ubiquitin carboxy-terminal hydrolase)
204	PMS2L11	postmeiotic segregation increased 2-like 11 pseudogene
205	UBE2A	ubiquitin-conjugating enzyme E2A (RAD6 homolog)
206	RAD51L3	RAD51-like 3 (S. cerevisiae)
207	FANCD2	Fanconi anemia, complementation group D2
208	POLR2A	polymerase (RNA) II (DNA directed) polypeptide A, 220kDa
209	CDKN2D	cyclin-dependent kinase inhibitor 2D (p19, inhibits CDK4)
210	XRCC4	X-ray repair complementing defective repair in Chinese hamster cells 4
211	TMEM161A	transmembrane protein 161A
212	POLR2C	polymerase (RNA) II (DNA directed) polypeptide C, 33kDa
213	XRCC6BP1	XRCC6 binding protein 1
214	TTC5	tetratricopeptide repeat domain 5
215	NEIL2	nei like 2 (E. coli)
216	INTS3	integrator complex subunit 3
217	BRCC3	BRCA1/BRCA2-containing complex, subunit 3
218	MLH3	mutL homolog 3 (E. coli)
219	RAD50	RAD50 homolog (S. cerevisiae)
220	SMC5	structural maintenance of chromosomes 5
221	CUL4A	cullin 4A
222	FAM175A	family with sequence similarity 175, member A
223	GTF2H3	general transcription factor IIH, polypeptide 3, 34kDa
224	MGMT	O-6-methylguanine-DNA methyltransferase
225	RAD9A	RAD9 homolog A (S. pombe)
226	C19orf40	chromosome 19 open reading frame 40
227	APEX2	APEX nuclease (apurinic/apyrimidinic endonuclease) 2
228	MMS19	MMS19 nucleotide excision repair homolog (S. cerevisiae)
229	SUPT6H	suppressor of Ty 6 homolog (S. cerevisiae)
230	MEN1	multiple endocrine neoplasia 1
231	MUS81	MUS81 endonuclease homolog (S. cerevisiae)

232	POLR2E	polymerase (RNA) II (DNA directed) polypeptide E, 25kDa
233	DDB1	damage-specific DNA binding protein 1, 127kDa
234	CSNK1D	casein kinase 1, delta
235	MBD4	methyl-CpG binding domain protein 4
236	OBFC2B	oligonucleotide/oligosaccharide-binding fold containing 2B
237	PNKP	polynucleotide kinase 3'-phosphatase
238	ABL1	c-abl oncogene 1, receptor tyrosine kinase
239	SOD1	superoxide dismutase 1, soluble
240	CEBPG	CCAAT/enhancer binding protein (C/EBP), gamma
241	NSMCE2	non-SMC element 2, MMS21 homolog (S. cerevisiae)
242	RAD17	RAD17 homolog (S. pombe)
243	RPS3	ribosomal protein S3
244	KAT5	K(lysine) acetyltransferase 5
245	SETX	senataxin
246	UBB	ubiquitin B
247	POLR2J	polymerase (RNA) II (DNA directed) polypeptide J, 13.3kDa
248	UBC	ubiquitin C
249	PGM3	phosphoglucomutase 3
250	MSH3	mutS homolog 3 (E. coli)
251	APLF	apratxin and PNKP like factor
252	C1orf124	chromosome 1 open reading frame 124
253	POLG	polymerase (DNA directed), gamma
254	RPS27A	ribosomal protein S27a
255	CCNH	cyclin H
256	UPF1	UPF1 regulator of nonsense transcripts homolog (yeast)
257	MORF4L1	mortality factor 4 like 1
258	POLD2	polymerase (DNA directed), delta 2, regulatory subunit 50kDa
259	APTX	apratxin
260	PMS2L5	postmeiotic segregation increased 2-like 5
261	UBA52	ubiquitin A-52 residue ribosomal protein fusion product 1
262	TOPBP1	topoisomerase (DNA) II binding protein 1
263	SRBD1	S1 RNA binding domain 1
264	ALKBH2	alkB, alkylation repair homolog 2 (E. coli)
265	DDX1	DEAD (Asp-Glu-Ala-Asp) box polypeptide 1
266	PMS2L1	postmeiotic segregation increased 2-like 1 pseudogene
267	RAD1	RAD1 homolog (S. pombe)
268	UIMC1	ubiquitin interaction motif containing 1
269	SMG1	SMG1 homolog, phosphatidylinositol 3-kinase-related kinase (C. elegans)
270	MLH1	mutL homolog 1, colon cancer, nonpolyposis type 2 (E. coli)
271	APITD1	apoptosis-inducing, TAF9-like domain 1
272	RBX1	ring-box 1
273	KIN	KIN, antigenic determinant of recA protein homolog (mouse)
274	C7orf11	chromosome 7 open reading frame 11
275	BAZ1B	bromodomain adjacent to zinc finger domain, 1B
276	FANCF	Fanconi anemia, complementation group E
277	NHEJ1	nonhomologous end-joining factor 1
278	CINP	cyclin-dependent kinase 2 interacting protein
279	HERC2	hect domain and RLD 2
280	MORF4L2	mortality factor 4 like 2
281	IGHMBP2	immunoglobulin mu binding protein 2
282	BTG2	BTG family, member 2
283	CIB1	calcium and integrin binding 1 (calmyrin)
284	TP53BP1	tumor protein p53 binding protein 1
285	GADD45A	growth arrest and DNA-damage-inducible, alpha
286	CETN2	centrin, EF-hand protein, 2
287	RECQL	RecQ protein-like (DNA helicase Q1-like)
288	SLK	STE20-like kinase (yeast)
289	ASTE1	asteroid homolog 1 (Drosophila)
290	LIG4	ligase IV, DNA, ATP-dependent
291	NSMCE1	non-SMC element 1 homolog (S. cerevisiae)
292	POLH	Polymerase (DNA directed), eta

293	RAD52	RAD52 homolog (S. cerevisiae)
294	ATRX	alpha thalassemia/mental retardation syndrome X-linked (RAD54 homolog, S. cerevisiae)
295	ERCC2	excision repair cross-complementing rodent repair deficiency, complementation group 2
296	XAB2	XPA binding protein 2
297	RRM2B	ribonucleotide reductase M2 B (TP53 inducible)
298	FLJ35220	hypothetical protein FLJ35220
299	BRIP1	BRCA1 interacting protein C-terminal helicase 1
300	RAD54L	RAD54-like (S. cerevisiae)
301	RAD51AP1	RAD51 associated protein 1
302	POLE2	polymerase (DNA directed), epsilon 2 (p59 subunit)
303	BLM	Bloom syndrome, RecQ helicase-like
304	RFC3	replication factor C (activator 1) 3, 38kDa
305	EXO1	exonuclease 1
306	DTL	denticleless homolog (Drosophila)
307	PARP1	poly (ADP-ribose) polymerase 1
308	CDC45	cell division cycle associated 5
309	RFPD3	ring finger and WD repeat domain 3
310	MAD2L2	MAD2 mitotic arrest deficient-like 2 (yeast)
311	DNA2	DNA replication helicase 2 homolog (yeast)
312	AURKB	aurora kinase B
313	TP73	tumor protein p73
314	TTK	TTK protein kinase
315	PRKCG	protein kinase C, gamma
316	RDM1	RAD52 motif 1
317	FGF10	fibroblast growth factor 10
318	CRY2	cryptochrome 2 (photolyase-like)
319	USP3	ubiquitin specific peptidase 3
320	RAD9B	RAD9 homolog B (S. pombe)
321	EYA4	eyes absent homolog 4 (Drosophila)
322	PARP3	poly (ADP-ribose) polymerase family, member 3
323	REV3L	REV3-like, catalytic subunit of DNA polymerase zeta (yeast)
324	OBFC2A	oligonucleotide/oligosaccharide-binding fold containing 2A
325	FBXO6	F-box protein 6
326	TREX1	three prime repair exonuclease 1
327	EYA1	eyes absent homolog 1 (Drosophila)
328	POLN	polymerase (DNA directed) nu
329	RPA4	replication protein A4, 34kDa
330	CCNO	cyclin O
331	XRCG3	X-ray repair complementing defective repair in Chinese hamster cells 3
332	TEX15	testis expressed 15

[0073] [表 4 A] 第 4 遺伝子群 (表 4 B) を含むプローブ 83 個において、ヒト E S 細胞クローン (KhES1-S3) の発現レベルの平均に対する、各 E S 細胞クローン及び各 i P S 細胞クローンの発現レベルの割合

Gene Symbol	Gene Title	Khes1 ES	Khes2 ES	Khes3 ES	201B7_iPS	201B6_iPS	253G4_iPS	253G1_iPS
1 FANCB	Fanconi anemia, complementation group B	0.81	-0.21	-0.61	-0.93	-0.83	-0.05	-0.98
2 TTK	TTK protein kinase	-0.04	-0.03	0.07	-0.23	-0.56	-0.36	-0.43
3 BUB1	budding uninhibited by benzimidazoles 1 homolog (yeast)	0.32	-0.14	-0.18	-0.05	-0.32	-0.44	-0.99
4 BRIP1	BRCA1 interacting protein C-terminal helicase 1	0.50	-0.05	-0.45	-0.14	-0.86	-0.60	-1.28
5 CHAF1A	chromatin assembly factor 1, subunit A (p150)	-0.37	0.17	0.20	0.30	-0.16	0.17	0.06
6 CHAF1A	chromatin assembly factor 1, subunit A (p150)	-0.40	0.18	0.23	0.12	0.13	0.24	0.06
7 AURKB	aurora kinase B	-0.41	0.08	0.32	0.38	0.29	0.44	0.52
8 RAD54L	RAD54-like (S. cerevisiae)	0.17	-0.47	0.30	-0.23	0.11	0.01	-0.06
9 RAD51AP1	RAD51 associated protein 1	0.20	-0.17	-0.04	0.03	0.24	0.30	-0.01
10 POLE2	polymerease (DNA directed), epsilon 2 (p59 subunit)	0.16	-0.14	-0.03	0.02	0.15	0.27	0.16
11 BLM	Bloom syndrome, RecQ helicase-like	0.15	-0.15	0.00	0.30	0.03	0.20	0.17
12 RFC3	replication factor C (activator 1) 3, 38kDa	0.08	0.04	-0.13	-0.10	0.01	-0.06	-0.34
13 EXO1	exonuclease 1	0.23	-0.22	-0.01	0.17	-0.05	-0.08	-0.14
14 RFC3	replication factor C (activator 1) 3, 38kDa	0.18	-0.01	-0.17	0.06	0.07	0.05	-0.01
15 FANCD2	Fanconi anemia, complementation group D2	0.12	0.08	-0.20	-0.01	0.07	0.03	-0.01
16 BUB1	budding uninhibited by benzimidazoles 1 homolog (yeast)	0.13	-0.05	-0.07	-0.01	0.06	-0.08	-0.32
17 DTL	denticleless homolog (Drosophila)	0.06	-0.03	-0.03	0.22	-0.08	0.06	-0.01
18 DTL	denticleless homolog (Drosophila)	0.06	0.02	-0.07	0.21	-0.11	-0.10	-0.24
19 FANCB	Fanconi anemia, complementation group B	0.30	0.26	-0.57	-0.15	-0.41	-0.56	-0.37
20 DNA2	DNA replication helicase 2 homolog (yeast)	0.48	-0.07	-0.41	0.11	0.05	-0.18	-0.36
21 CUL4A	culin 4A	-0.29	0.74	-0.45	-0.15	-0.41	-0.29	-0.25
22 FEN1	flap structure-specific endonuclease 1	0.01	-0.06	0.04	0.28	0.46	0.45	0.65
23 CHAF1B	chromatin assembly factor 1, subunit B (p60)	0.00	0.17	-0.18	0.32	0.28	0.00	-0.07
24 TRIP13	thyroid hormone receptor interactor 13	0.02	0.05	-0.06	0.36	0.24	0.39	0.15
25 UHRF1	ubiquitin-like with PHD and ring finger domains 1	0.16	0.18	-0.34	0.33	0.19	0.30	0.12
26 MSH6	mutS homolog 6 (E. coli)	-0.18	0.02	0.16	0.17	-0.07	-0.09	-0.30
27 TOP2A	topoisomerase (DNA) II alpha 170kDa	-0.04	0.00	0.04	-0.34	-0.04	-0.03	-0.19
28 RAD54B	RAD54 homolog B (S. cerevisiae)	0.12	0.00	-0.12	-0.16	-0.09	-0.04	-0.22
29 MSH2	mutS homolog 2, colon cancer, nonpolyposis type 1 (E. coli)	0.22	-0.10	-0.12	0.04	-0.17	-0.11	-0.43
30 FANCI	Fanconi anemia, complementation group 1	0.00	-0.01	0.01	0.21	-0.28	-0.23	-0.25
31 CHEK1	CHK1 checkpoint homolog (S. pombe)	0.22	-0.14	-0.07	0.10	0.11	0.09	-0.20
32 CHEK1	CHK1 checkpoint homolog (S. pombe)	0.28	-0.12	-0.17	0.06	0.06	-0.06	-0.28
33 BRCA2	breast cancer 2, early onset	0.28	-0.36	0.08	0.15	-0.17	-0.41	-0.03
34 FANCI	Fanconi anemia, complementation group 1	0.31	-0.24	-0.06	-0.01	-0.09	-0.20	-0.09
35 PTTG1	pituitary tumor-transforming 1	0.01	-0.15	0.15	0.16	0.27	0.28	0.30
36 RFC4	replication factor C (activator 1) 4, 37kDa	0.25	-0.29	0.04	0.08	0.44	0.24	0.26
37 RAD51	RAD51 homolog (RecA homolog E. coli) (S. cerevisiae)	0.17	0.03	-0.20	0.10	0.35	0.35	0.32
38 UBE2T	ubiquitin-conjugating enzyme E2T (putative)	0.45	-0.23	-0.22	-0.04	0.18	0.18	0.13
39 FEN1	flap structure-specific endonuclease 1	0.02	0.12	-0.14	0.29	0.22	0.26	0.00
40 RFW3	ring finger and WD repeat domain 3	-0.09	-0.02	0.11	0.11	0.14	0.22	-0.08
41 CDC45	cell division cycle associated 5	-0.19	0.10	0.09	0.15	0.07	-0.03	0.04
42 RAD54B	RAD54 homolog B (S. cerevisiae)	0.17	-0.17	0.00	0.37	-0.04	0.28	0.36
43 GENPE	centromere protein E, 312kDa	-0.05	0.21	-0.16	-0.46	-0.68	-1.20	-0.33

44	TOP2A	topoisomerase (DNA) II alpha, 170kDa	0.18	-0.20	0.02	-0.15	-0.58	-0.57	-0.78
45	USP28	ubiquitin specific peptidase 28	0.02	-0.07	0.04	-0.18	-0.47	-0.70	-0.82
46	ESCO1	establishment of cohesion 1 homolog 1 (S. cerevisiae)	0.31	-0.21	0.04	-0.43	-0.61	-0.66	-0.65
47	MSH6	mutS homolog 6 (E. coli)	-0.10	0.05	0.05	0.18	-0.37	-0.38	-0.68
48	KNTC1	kinetochore associated 1	0.19	-0.17	-0.02	-0.04	-0.44	-0.44	-0.47
49	FANCI	Fanconi anemia, complementation group I	0.19	-0.13	-0.06	0.12	-0.44	-0.50	-0.57
50	POLQ	polymerase (DNA directed) theta	-0.07	0.09	-0.01	-0.25	-0.42	-0.63	-0.27
51	TP53	tumor protein p53	-0.22	0.46	-0.24	0.11	-0.49	-0.48	-0.55
52	BRCA2	breast cancer 2, early onset	0.33	-0.33	0.00	-0.59	-0.55	-0.10	-0.49
53	ESCO1	establishment of cohesion 1 homolog 1 (S. cerevisiae)	0.46	-0.55	0.09	-0.43	-0.38	0.00	-0.11
54	TYMS	thymidylate synthetase	0.09	-0.23	0.14	-0.46	-0.26	-0.13	-0.28
55	TYMS	thymidylate synthetase	0.10	-0.07	-0.04	-0.22	-0.34	-0.20	-0.02
56	MRE11A	MRE11 meiotic recombination 11 homolog A (S. cerevisiae)	0.03	-0.02	-0.01	-0.04	-0.19	-0.06	-0.16
57	RAD18	RAD18 homolog (S. cerevisiae)	0.29	-0.09	-0.20	-0.04	-0.27	-0.38	0.19
58	CDK7	cyclin-dependent kinase 7	0.13	-0.12	-0.01	0.11	0.08	0.28	0.33
59	NPM1	nucleophosmin (nucleolar phosphoprotein B23, numatrin)	0.18	-0.05	-0.12	0.03	-0.02	-0.02	0.05
60	NPM1	nucleophosmin (nucleolar phosphoprotein B23, numatrin)	0.29	-0.18	-0.12	0.21	0.09	0.07	0.17
61	SMC6	structural maintenance of chromosomes 6	0.11	-0.09	-0.02	0.51	0.41	0.15	0.15
62	SMC1A	structural maintenance of chromosomes 1A	-0.12	-0.12	0.24	-0.10	-0.36	-0.08	-0.20
63	SMC6	structural maintenance of chromosomes 6	0.13	-0.16	0.04	0.18	-0.53	-0.43	-0.29
64	SMC3	structural maintenance of chromosomes 3	0.22	-0.16	0.07	-0.36	-0.43	-0.22	-0.21
65	SMC3	structural maintenance of chromosomes 3	0.06	-0.31	0.24	-0.44	-0.54	0.02	-0.32
66	ESCO2	establishment of cohesion 1 homolog 2 (S. cerevisiae)	0.28	-0.32	0.03	-0.38	-0.35	0.01	0.05
67	NUDT1	nudix (nucleoside diphosphate linked moiety X)-type motif 1	0.03	-0.14	0.11	-0.45	0.12	0.21	0.25
68	CHEK2	CHEK2 checkpoint homolog (S. pombe)	0.17	-0.30	0.13	0.02	0.28	0.23	-0.08
69	NEIL3	nei endonuclease VIII-like 3 (E. coli)	0.39	-0.46	0.07	-0.07	0.56	0.08	0.01
70	BOC1P	BRCA2 and CDKN1A interacting protein	0.29	0.03	-0.32	0.01	0.31	0.07	0.04
71	RAD18	RAD18 homolog (S. cerevisiae)	0.35	-0.32	-0.04	-0.20	-0.08	-0.08	-0.18
72	CHEK1	CHEK1 checkpoint homolog (S. pombe)	0.39	-0.25	-0.15	-0.11	-0.02	-0.16	-0.23
73	GEN1	Gen1 homolog 1, endonuclease (Drosophila)	0.29	0.10	-0.38	-0.75	-0.40	-0.28	-0.59
74	FANM175A	family with sequence similarity 175, member A	0.01	-0.31	0.30	0.18	0.12	0.09	-0.46
75	FANCB	Fanconi anemia, complementation group B	0.67	-0.25	-0.42	0.18	-0.60	0.60	-0.10
76	RECQL4	RecQ protein-like 4	-0.28	0.09	0.19	0.22	-0.36	0.16	-0.07
77	FANCD2	Fanconi anemia, complementation group D2	0.09	-0.25	0.17	-0.08	0.31	0.30	0.52
78	XRCC3	X-ray repair complementing defective repair in Chinese hamster cells 3	-0.33	0.02	0.31	-0.94	-0.12	-0.83	-0.45
79	ATRX	alpha-thalassemia/mental retardation syndrome X-linked (RAD54 homolog, S. cerevisiae)	-0.02	0.00	0.03	-1.00	-2.06	-1.55	-1.42
80	ATRX	alpha-thalassemia/mental retardation syndrome X-linked (RAD54 homolog, S. cerevisiae)	0.04	0.07	-0.11	-1.00	-1.75	-1.71	-1.33
81	RECQL	RecQ protein-like (DNA helicase Q1-like)	-0.11	-0.03	0.14	-0.54	-0.97	-0.94	-1.16
82	SUPT16H	suppressor of Ty 16 homolog (S. cerevisiae)	0.28	-0.09	-0.19	0.04	-1.21	-1.15	-1.61
83	TEX15	testis expressed 15	0.13	-0.26	0.13	-0.49	-0.86	-0.72	-0.71

[0074] [表 4 B] 第 4 遺伝子群

	Gene Symbol	Gene Title
1	FANCB	Fanconi anemia, complementation group B
2	ITK	ITK protein kinase
3	BUB1	budding uninhibited by benzimidazoles 1 homolog (yeast)
4	BRIP1	BRCA1 interacting protein C-terminal helicase 1
5	CHAF1A	chromatin assembly factor 1, subunit A (p150)
6	AURKB	aurora kinase B
7	RAD54L	RAD54-like (S. cerevisiae)
8	RAD51AP1	RAD51 associated protein 1
9	POLE2	polymerase (DNA directed), epsilon 2 (p59 subunit)
10	BLM	Bloom syndrome, RecQ helicase-like
11	RFC3	replication factor C (activator 1) 3, 38kDa
12	EXO1	exonuclease 1
13	FANCD2	Fanconi anemia, complementation group D2
14	DTL	denticleless homolog (Drosophila)
15	DNA2	DNA replication helicase 2 homolog (yeast)
16	CUL4A	cullin 4A
17	FEN1	flap structure-specific endonuclease 1
18	CHAF1B	chromatin assembly factor 1, subunit B (p60)
19	TRIP13	thyroid hormone receptor interactor 13
20	UHRF1	ubiquitin-like with PHD and ring finger domains 1
21	MSH6	mutS homolog 6 (E. coli)
22	TOP2A	topoisomerase (DNA) II alpha 170kDa
23	RAD54B	RAD54 homolog B (S. cerevisiae)
24	MSH2	mutS homolog 2, colon cancer, nonpolyposis type 1 (E. coli)
25	FANCI	Fanconi anemia, complementation group I
26	CHK1	CHK1 checkpoint homolog (S. pombe)
27	BRCA2	breast cancer 2, early onset
28	PTTG1	pituitary tumor-transforming 1
29	RFC4	replication factor C (activator 1) 4, 37kDa
30	RAD51	RAD51 homolog (RecA homolog, E. coli) (S. cerevisiae)
31	UBE2T	ubiquitin-conjugating enzyme E2T (putative)
32	RFWD3	ring finger and WD repeat domain 3
33	CDCA5	cell division cycle associated 5
34	CENPE	centromere protein E, 312kDa
35	USP28	ubiquitin specific peptidase 28
36	ESCO1	establishment of cohesion 1 homolog 1 (S. cerevisiae)
37	KNTC1	kinetochore associated 1
38	POLQ	polymerase (DNA directed), theta
39	TP53	tumor protein p53
40	TYMS	thymidylate synthetase
41	MRE11A	MRE11 meiotic recombination 11 homolog A (S. cerevisiae)
42	RAD18	RAD18 homolog (S. cerevisiae)
43	CDK7	cyclin-dependent kinase 7
44	NPM1	nucleophosmin (nucleolar phosphoprotein B23, numatrin)
45	SMC6	structural maintenance of chromosomes 6
46	SMC1A	structural maintenance of chromosomes 1A
47	SMC3	structural maintenance of chromosomes 3
48	ESCO2	establishment of cohesion 1 homolog 2 (S. cerevisiae)
49	NUDT1	nudix (nucleoside diphosphate linked moiety X)-type motif 1
50	CHK2	CHK2 checkpoint homolog (S. pombe)
51	NEIL3	nei endonuclease VIII-like 3 (E. coli)
52	BCCIP	BRCA2 and CDKN1A interacting protein
53	GEN1	Gen homolog 1, endonuclease (Drosophila)
54	FAM175A	family with sequence similarity 175, member A
55	RECQL4	RecQ protein-like 4
56	XRCC3	X-ray repair complementing defective repair in Chinese hamster cells 3
57	ATRX	alpha thalassemia/mental retardation syndrome X-linked (RAD54 homolog, S. cerevisiae)
58	RECQL	RecQ protein-like (DNA helicase Q1-like)
59	SUPT16H	suppressor of Ty 16 homolog (S. cerevisiae)
60	TEX15	testis expressed 15

[0075] [表 5 A] 第 5 遺伝子群を含むプローブ 80 個において、ヒト ES 細胞クローン (KhES1-S3) の発現レベルの平均に対する、各 ES 細胞クローン及び各 iPS 細胞クローンの発現レベルの割合

	Gene Symbol	Gene Title	Khes1 ES	Khes2 ES	201B7 IPS	Khes3 ES	201B6 IPS	253G4 IPS	253G1 IPS
1	SLC1A6	solute carrier family 1 (high affinity aspartate/glutamate transporter), member 6	0.10	0.06	0.58	-0.16	1.02	1.02	0.70
2	NPM3	nucleophosmin/nucleoplasm 3	0.28	-0.37	0.14	0.08	0.72	0.85	0.89
3	GINS4	GINS complex subunit 4 (Slc6 homolog)	-0.08	0.01	0.01	0.07	0.89	0.79	0.98
4	MLF1IP	MLF1 interacting protein	-0.18	0.13	0.52	0.05	0.83	0.59	0.87
5	HMG3	high-mobility group box 3	0.17	0.47	0.18	-0.64	0.88	0.98	0.70
6	SLC25A21	solute carrier family 25 (mitochondrial oxodicarboxylate carrier), member 21	0.38	0.10	0.35	-0.48	0.70	0.61	0.80
7	HMG3L1	high-mobility group box 3-like 1	0.37	0.56	0.15	-0.93	1.55	1.60	0.86
8	DYNC2H1	dynein, cytoplasmic 2, heavy chain 1	0.19	0.11	0.02	-0.30	-2.11	-1.78	-2.18
9	MME	membrane metallo-endopeptidase	0.28	-0.38	-0.50	0.11	-1.05	-1.04	-0.59
10	ERBB2	v-erb-b2 erythroblastic leukemia viral oncogene homolog 2, neuro/glioblastoma derived oncogene homolog (avian)	-0.33	0.19	0.34	0.13	-2.23	-2.77	-2.12
11	DAPK1	death-associated protein kinase 1	-0.05	0.38	0.24	-0.31	-1.51	-2.20	-2.21
12	HEATR1	HEAT repeat containing 1	-0.03	-0.07	0.23	0.10	-1.00	-1.44	-2.89
13	MYO10	myosin X	-0.22	-0.01	0.44	0.29	-0.91	-1.21	-2.83
14	JMJD1C	jumonji domain containing 1C	0.15	-0.10	0.24	-0.05	-1.75	-1.52	-1.94
15	ZNF644	zinc finger protein 644	0.61	-0.07	0.00	-0.55	-1.05	-0.83	-0.92
16	REAK	RB-associated KRAB zinc finger	0.30	-0.28	-0.56	-0.02	-0.66	-1.07	-1.07
17	HSPH1	heat shock 105kDa/110kDa protein 1	0.07	0.10	0.04	-0.17	-0.64	-0.16	-1.09
18	PRPF4B	PRP4 pre-mRNA processing factor 4 homolog B (yeast)	0.12	0.05	-0.10	-0.17	-0.88	-0.87	-1.11
19	MATR3	matrin 3	0.18	-0.21	-0.03	0.03	-0.82	-0.62	-1.22
20	LARS	leucyl-tRNA synthetase	0.20	-0.23	0.04	0.04	-0.84	-1.02	-1.30
21	CNOT1	GCR4-NOT transcription complex, subunit 1	-0.13	0.14	-0.12	-0.01	-0.94	-1.12	-1.37
22	NUPI33	nucleoporin 133kDa	0.17	0.10	-0.24	-0.27	-0.83	-1.33	-1.38
23	BCLAF1	BCL2-associated transcription factor 1	0.24	-0.02	-0.26	-0.22	-1.37	-1.13	-1.38
24	BCLAF1	BCL2-associated transcription factor 1	0.11	0.04	-0.16	-0.16	-1.33	-1.33	-1.20
25	DHX9	DEAH (Asp-Glu-Ala-His) box polypeptide 9	0.10	0.09	0.27	-0.19	-0.96	-1.00	-1.45
26	DHX9	DEAH (Asp-Glu-Ala-His) box polypeptide 9	0.31	-0.14	-0.02	-0.18	-1.03	-1.10	-1.35
27	SUPT16H	suppressor of Ty 16 homolog (S. cerevisiae)	0.28	-0.09	0.04	-0.19	-1.21	-1.15	-1.81
28	VCAN	versican	0.13	0.05	-0.21	-0.18	-0.80	-0.81	-0.64
29	VCAN	versican	0.19	0.00	-0.34	-0.18	-0.84	-0.83	-0.87
30	RIF1	RAP1 interacting factor homolog (yeast)	-0.04	0.15	-0.03	-0.10	-0.78	-0.76	-0.66
31	ESF1	ESF1, nucleolar pre-rRNA processing protein, homolog (S. cerevisiae)	-0.18	0.23	-0.05	-0.04	-0.60	-0.60	-0.89
32	PHF3	PHD finger protein 3	-0.27	0.06	-0.23	0.21	-1.12	-0.93	-0.91
33	SPRED1	sprouty-related, EVH1 domain containing 1	-0.02	0.69	0.07	-0.68	-0.68	-0.60	-0.62
34	SLC4A7	solute carrier family 4, sodium bicarbonate cotransporter, member 7	0.05	0.41	-0.19	-0.45	-0.60	-1.10	-1.26
35	USP25	ubiquitin specific peptidase 25	-0.04	-0.22	-0.14	0.27	-0.60	-0.71	-1.44
36	EPRS	glutaryl-prolyl-tRNA synthetase	0.26	-0.14	-0.03	-0.12	-0.77	-0.89	-1.36
37	RECQL	RecQ protein-like (DNA helicase Q1-like)	-0.11	-0.03	-0.54	0.14	-0.57	-0.94	-1.16
38	GPR176	G protein-coupled receptor 176	0.12	0.01	0.38	-0.13	-0.90	-0.74	-1.05
39	SCD	stearoyl-CoA desaturase (delta-9-desaturase)	0.05	0.33	-0.02	-0.38	-1.00	-0.95	-1.05

78	CLDN6	claudin 6	-0.25	0.14	-0.04	0.11	-1.17	-0.72	-0.77
79	TEX15	testis expressed 15	0.13	-0.26	-0.49	0.13	-0.86	-0.72	-0.71
80	CLDN6	claudin 6	-0.48	0.14	0.03	0.34	-1.00	-0.71	-0.68

[0076] [表 5 B] 第 5 遺伝子群

	Gene Symbol	Gene Title
1	SLC1A6	solute carrier family 1 (high affinity aspartate/glutamate transporter), member 6
2	NPM3	nucleophosmin/nucleoplasmin 3
3	GINS4	GINS complex subunit 4 (Sld5 homolog)
4	MLF1IP	MLF1 interacting protein
5	HMGB3	high-mobility group box 3
6	SLC25A21	solute carrier family 25 (mitochondrial oxodicarboxylate carrier), member 21
7	HMGB3L1	high-mobility group box 3-like 1
8	DYNC2H1	dynein, cytoplasmic 2, heavy chain 1
9	MME	membrane metallo-endopeptidase
10	ERBB2	v-erb-b2 erythroblastic leukemia viral oncogene homolog 2, neuro/glioblastoma derived oncogene homolog (avian)
11	DAPK1	death-associated protein kinase 1
12	HEATR1	HEAT repeat containing 1
13	MYO10	myosin X
14	UMJD1C	umonji domain containing 1C
15	ZNF644	zinc finger protein 644
16	RBAK	RB-associated KRAB zinc finger
17	HSPH1	heat shock 105kDa/110kDa protein 1
18	PRPF4B	PRP4 pre-mRNA processing factor 4 homolog B (yeast)
19	MATR3	matrin 3
20	LARS	leucyl-tRNA synthetase
21	CNOT1	CCR4-NOT transcription complex, subunit 1
22	NUP133	nucleoporin 133kDa
23	BCLAF1	BCL2-associated transcription factor 1
24	DHX9	DEAH (Asp-Glu-Ala-His) box polypeptide 9
25	SUPT16H	suppressor of Ty 16 homolog (S. cerevisiae)
26	VCAN	versican
27	RIF1	RAP1 interacting factor homolog (yeast)
28	ESF1	ESF1, nucleolar pre-mRNA processing protein, homolog (S. cerevisiae)
29	PHF3	PHD finger protein 3
30	SPRED1	sprouty-related, EVH1 domain containing 1
31	SLC4A7	solute carrier family 4, sodium bicarbonate cotransporter, member 7
32	USP25	ubiquitin specific peptidase 25
33	EPRS	glutamyl-prolyl-tRNA synthetase
34	RECQL	RecQ protein-like (DNA helicase Q1-like)
35	GPR176	G protein-coupled receptor 176
36	SCD	stearoyl-CoA desaturase (delta-9-desaturase)
37	FAM126A	family with sequence similarity 126, member A
38	UBE3A	ubiquitin protein ligase E3A
39	TFR3	transferrin receptor (p90, CD71)
40	LOC100288985	hypothetical protein LOC100288985
41	RALGPS2	Ral GEF with PH domain and SH3 binding motif 2
42	NR5A2	nuclear receptor subfamily 5, group A, member 2
43	MYH10	myosin, heavy chain 10, non-muscle
44	DDX11	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 11 (CHL1-like helicase homolog, S. cerevisiae)
45	C14orf106	chromosome 14 open reading frame 106
46	ZNF92	zinc finger protein 92
47	EDIL3	EGF-like repeats and discoidin I-like domains 3
48	ATAD5	ATPase family, AAA domain containing 5
49	G3BP2	GTPase activating protein (SH3 domain) binding protein 2
50	IGF2BP3	insulin-like growth factor 2 mRNA binding protein 3
51	DPYSL3	dihydropyrimidinase-like 3
52	ESCO1	establishment of cohesion 1 homolog 1 (S. cerevisiae)
53	ASPM	asp (abnormal spindle) homolog, microcephaly associated (Drosophila)
54	ZNF770	zinc finger protein 770
55	SLC16A1	solute carrier family 16, member 1 (monocarboxylic acid transporter 1)

56	BRIP1	BRCA1 interacting protein C-terminal helicase 1
57	C12orf35	chromosome 12 open reading frame 35
58	ZNF138	zinc finger protein 138
59	TPR	translocated promoter region (to activated ME1 oncogene)
60	NUP188	nucleoporin 188kDa
61	RBM15	RNA binding motif protein 15
62	CYP26A1	cytochrome P450, family 26, subfamily A, polypeptide 1
63	SLC04C1	solute carrier organic anion transporter family, member 4C1
64	SOX2	SRY (sex determining region Y)-box 2
65	GCNT2	glucosaminyl (N-acetyl) transferase 2, I-branching enzyme (I blood group)
66	SLC12A1	solute carrier family 12 (sodium/potassium/chloride transporters), member 1
67	ZNF90	zinc finger protein 90
68	NRK	Nrk related kinase
69	CLDN6	claudin 6
70	TEX15	testis expressed 15

[0077] [表 6 A] 第 6 遺伝子群 (表 6 B) を含むプローブ 72 個において、ヒト E S 細胞クローン (KhES1-S3) の発現レベルの平均に対する、各 E S 細胞クローン及び各 i P S 細胞クローンの発現レベルの割合

Gene Symbol	Gene Title	Khes1 ES	Khes3 ES	Khes2 ES	201B7 IPS	201B6 IPS	253G4 IPS	253G1 IPS
1 SLC1A6	solute carrier family 1 (high affinity aspartate/glutamate transporter), member 6	0.10	-0.16	0.06	0.58	1.02	1.02	0.70
2 NPM3	nucleophosmin/nucleoplasm 3	0.28	0.08	-0.37	0.14	0.72	0.85	0.89
3 GINS4	GINS complex subunit 4 (Slc6 homolog)	-0.08	0.07	0.01	0.01	0.89	0.79	0.98
4 MLF1IP	MLF1 interacting protein	-0.18	0.05	0.13	0.52	0.83	0.59	0.87
5 SLC25A21	solute carrier family 25 (mitochondrial oxodicarboxylate carrier), member 21	0.38	-0.48	0.10	0.35	0.70	0.61	0.60
6 DYNC2H1	dynein, cytoplasmic 2, heavy chain 1	0.19	-0.30	0.11	0.02	-2.11	-1.78	-2.18
7 MME	membrane metallo-endopeptidase	0.28	0.11	-0.38	-0.50	-1.05	-1.04	-0.59
8 HEATR1	HEAT repeat containing 1	-0.03	0.10	-0.07	0.23	-1.00	-1.44	-2.89
9 MYO10	myosin X	-0.22	0.29	-0.07	0.44	-0.91	-1.21	-2.83
10 ERBB2	v-erb-b2 erythroblastic leukemia viral oncogene homolog 2, neuro/glioblastoma derived oncogene homolog (avian)	-0.33	0.13	0.19	0.34	-2.23	-2.77	-2.12
11 DAPK1	death-associated protein kinase 1	-0.05	-0.31	0.36	0.24	-1.51	-2.20	-2.21
12 SLC4A7	solute carrier family 4, sodium bicarbonate cotransporter, member 7	0.05	-0.45	0.41	-0.19	-0.80	-1.10	-1.26
13 USP25	ubiquitin specific peptidase 25	-0.04	0.27	-0.22	-0.14	-0.60	-0.71	-1.44
14 EPRS	glutaryl-prolyl-RNA synthetase	0.26	-0.12	-0.14	-0.03	-0.77	-0.89	-1.36
15 RECQL	RecQ protein-like (DNA helicase Q1-like)	-0.11	0.14	-0.03	0.54	-0.97	-0.94	-1.16
16 GPR176	G protein-coupled receptor 176	0.12	-0.13	0.01	0.38	-0.90	-0.74	-1.05
17 SCD	stearoyl-CoA desaturase (delta-9-desaturase)	0.05	-0.38	0.33	-0.02	-1.00	-0.95	-1.05
18 SC3	stearoyl-CoA desaturase (delta-9-desaturase)	0.16	-0.29	0.13	0.00	-1.06	-1.09	-0.88
19 FAM126A	family with sequence similarity 126, member A	0.27	-0.56	0.29	0.11	-1.11	-0.67	-1.16
20 UBE3A	ubiquitin protein ligase E3A	0.19	-0.56	0.37	-0.42	-1.09	-0.65	-0.70
21 RBAK	RB-associated KRAB zinc finger	0.35	-0.41	0.05	-0.53	-0.72	-0.58	-1.11
22 RBAK	RB-associated KRAB zinc finger	0.30	-0.02	-0.28	-0.56	-1.23	-0.66	-1.07
23 HSPH1	heat shock 105kDa/110kDa protein 1	0.07	-0.17	0.10	0.04	-0.84	-0.74	-1.09
24 PRPF4B	PRP4 pre-mRNA processing factor 4 homolog B (yeast)	0.12	-0.17	0.05	-0.10	-0.88	-0.87	-1.11
25 MATR3	matrin 3	0.18	0.03	-0.21	-0.03	-0.62	-0.62	-1.22
26 LARS	leucyl-tRNA synthetase	0.20	0.04	-0.23	-0.19	-0.84	-1.02	-1.30
27 GNOT1	GCR4-NOT transcription complex subunit 1	-0.13	-0.01	0.14	-0.12	-0.94	-1.12	-1.37
28 NUP133	nucleoporin 133kDa	0.17	-0.27	0.10	-0.24	-0.83	-1.33	-1.38
29 BCLAF1	BCL2-associated transcription factor 1	0.24	-0.22	-0.02	-0.26	-1.37	-1.33	-1.38
30 BCLAF1	BCL2-associated transcription factor 1	0.11	-0.16	0.04	-0.16	-1.33	-1.33	-1.20
31 DHX9	DEAH (Asp-Glu-Ala-His) box polypeptide 9	0.10	-0.19	0.09	0.27	-0.96	-1.00	-1.45
32 DHX9	DEAH (Asp-Glu-Ala-His) box polypeptide 9	0.31	-0.18	-0.14	-0.02	-1.03	-1.10	-1.35
33 SUPT16H	suppressor of Ty 16 homolog (S. cerevisiae)	0.28	-0.19	-0.09	0.04	-1.21	-1.15	-1.61
34 VCAN	versican	0.13	-0.18	0.05	-0.21	-0.80	-0.81	-0.84
35 VCAN	versican	0.19	-0.18	0.00	-0.34	-0.84	-0.93	-0.87
36 RIF1	RAP1 interacting factor homolog (yeast)	-0.04	-0.10	0.15	-0.03	-0.78	-0.76	-0.66
37 ESF1	ESF1, nucleolar pre-rRNA processing protein, homolog (S. cerevisiae)	-0.18	-0.04	0.23	-0.05	-0.60	-0.60	-0.69
38 PHF3	PHD finger protein 3	-0.27	0.21	0.06	-0.23	-1.12	-0.93	-0.91
39 TFR3	transferrin receptor (p90, CD71)	0.36	-0.05	-0.30	-0.19	-1.01	-1.37	-1.94

40	JMJD1C	jumonji domain containing 1C	0.15	-0.05	-0.10	0.24	-1.75	-1.52	-1.94
41	LOC100288385	hypothetical protein LOC100288385	0.00	0.45	-0.45	-0.47	-0.93	-0.77	-0.82
42	RALGPS2	Ral GEF with PH domain and SH3 binding motif 2	0.33	-0.23	-0.10	0.04	-0.65	-0.60	-0.93
43	NR5A2	nuclear receptor subfamily 5, group A, member 2	-0.15	0.31	-0.16	-0.12	-0.68	-1.19	-0.99
44	MYH10	myosin, heavy chain 10, non-muscle	0.00	0.32	-0.32	0.11	-0.80	-0.75	-1.13
45	DDX11	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 11	-0.27	0.03	0.25	-0.04	-1.07	-1.06	-1.41
46	C14orf106	(CHL1-like helicase homolog, S. cerevisiae)	-0.10	0.06	0.04	0.01	-1.19	-1.01	-1.33
47	ZNF92	zinc finger protein 92	-0.13	0.04	0.09	-0.01	-1.13	-0.98	-0.78
48	EDIL3	EGF-like repeats and discoidin I-like domains 3	0.06	-0.33	0.26	-0.23	-0.70	-0.75	-0.80
49	ATAD5	ATPase family, AAA domain containing 5	-0.07	-0.25	0.32	-0.18	-0.97	-0.62	-0.63
50	G3BP2	GTPase activating protein (SH3 domain) binding protein 2	0.44	-0.50	0.07	-0.14	-0.71	-0.87	-0.80
51	IGF2BP3	insulin-like growth factor 2 mRNA binding protein 3	0.38	-0.36	-0.02	-0.15	-0.74	-0.72	-1.02
52	DPYSL3	dihydropyrimidinase-like 3	-0.10	0.08	0.02	-0.12	-0.70	-0.60	-1.22
53	—	—	0.15	-0.20	0.05	0.00	-0.68	-0.76	-1.22
54	ESCO1	establishment of cohesion 1 homolog 1 (S. cerevisiae)	0.31	-0.11	-0.21	-0.43	-0.61	-0.66	-0.65
55	ASPM	asp (abnormal spindle) homolog, microcephaly associated (Drosophila)	0.07	-0.11	0.03	-0.58	-1.50	-1.25	-1.87
56	ZNF770	zinc finger protein 770	0.28	-0.50	0.22	-0.52	-1.21	-1.28	-1.05
57	SLC16A1	solute carrier family 16, member 1 (monocarboxylic acid transporter 1)	0.46	-0.41	-0.06	0.14	-0.78	-0.83	-1.21
58	BRIP1	BRCA1 interacting protein C-terminal helicase 1	0.50	-0.45	-0.05	-0.14	-0.86	-0.60	-1.28
59	C12orf35	chromosome 12 open reading frame 35	0.20	0.03	-0.22	-0.39	-1.13	-0.94	-0.86
60	C12orf35	chromosome 12 open reading frame 35	0.17	0.00	-0.17	-0.38	-0.87	-0.71	-0.64
61	ZNF138	zinc finger protein 138	0.27	-0.15	-0.12	-0.42	-0.64	-0.68	-0.73
62	TPR	translocated promoter region (to activated MET oncogene)	-0.41	0.24	0.17	-0.22	-2.07	-1.28	-3.58
63	NUP188	nucleoporin 188kDa	0.12	-0.17	0.05	0.05	-4.03	-1.49	-3.48
64	RBM15	RNA binding motif protein 15	-0.03	-0.36	0.39	-0.48	-2.36	-2.05	-6.57
65	—	—	-0.02	-0.01	0.03	-0.38	-1.05	-0.71	-0.97
66	SLC04C1	solute carrier organic anion transporter family, member 4C1	0.24	-0.34	0.10	-0.41	-0.73	-1.01	-0.76
67	SOX2	SRY (sex determining region Y)-box 2	0.39	-0.46	0.07	0.09	-0.89	-0.82	-1.23
68	GCNT2	glucosaminyl (N-acetyl) transferase 2, I-branching enzyme (I blood group)	0.11	0.00	-0.10	-0.38	-0.70	-0.90	-1.41
69	SLC12A1	solute carrier family 12 (sodium/potassium/chloride transporters), member 1	0.02	0.01	-0.02	-0.55	-0.73	-0.73	-1.41
70	CLDN6	claudin 6	-0.25	0.11	0.14	-0.04	-1.17	-0.72	-0.77
71	TEX15	testis expressed 15	0.13	0.13	-0.26	-0.49	-0.86	-0.72	-0.71
72	CLDN6	claudin 6	-0.48	0.34	0.14	0.03	-1.00	-0.71	-0.68

[0078] [表 6 B] 第 6 遺伝子群

	Gene Symbol	Gene Title
1	SLC1A6	solute carrier family 1 (high affinity aspartate/glutamate transporter), member 6
2	NPM3	nucleophosmin/nucleoplasmin 3
3	GINS4	GINS complex subunit 4 (Sld5 homolog)
4	MLF1IP	MLF1 interacting protein
5	SLC25A21	solute carrier family 25 (mitochondrial oxodicarboxylate carrier), member 21
6	DYNC2H1	dynein, cytoplasmic 2, heavy chain 1
7	MME	membrane metallo-endopeptidase
8	HEATR1	HEAT repeat containing 1
9	MYO10	myosin X
10	ERBB2	v-erb-b2 erythroblastic leukemia viral oncogene homolog 2, neuro/glioblastoma derived oncogene homolog (avian)
11	DAPK1	death-associated protein kinase 1
12	SLC4A7	solute carrier family 4, sodium bicarbonate cotransporter, member 7
13	USP25	ubiquitin specific peptidase 25
14	EPRS	glutamyl-prolyl-tRNA synthetase
15	RECQL	RecQ protein-like (DNA helicase Q1-like)
16	GPR176	G protein-coupled receptor 176
17	SCD	stearoyl-CoA desaturase (delta-9-desaturase)
18	FAM126A	family with sequence similarity 126, member A
19	UBE3A	ubiquitin protein ligase E3A
20	RBAK	RB-associated KRAB zinc finger
21	HSPH1	heat shock 105kDa/110kDa protein 1
22	PRPF4B	PRP4 pre-mRNA processing factor 4 homolog B (yeast)
23	MATR3	matrin 3
24	LARS	leucyl-tRNA synthetase
25	CNOT1	CCR4-NOT transcription complex, subunit 1
26	NUP133	nucleoporin 133kDa
27	BCLAF1	BCL2-associated transcription factor 1
28	DHX9	DEAH (Asp-Glu-Ala-His) box polypeptide 9
29	SUPT16H	suppressor of Ty 16 homolog (S. cerevisiae)
30	VCAN	versican
31	RIF1	RAP1 interacting factor homolog (yeast)
32	ESF1	ESF1, nucleolar pre-rRNA processing protein, homolog (S. cerevisiae)
33	PHF3	PHD finger protein 3
34	TFRC	transferrin receptor (p90, CD71)
35	JMJD1C	jumonji domain containing 1C
36	LOC100288985	hypothetical protein LOC100288985
37	RALGPS2	Ral GEF with PH domain and SH3 binding motif 2
38	NR5A2	nuclear receptor subfamily 5, group A, member 2
39	MYH10	myosin, heavy chain 10, non-muscle
40	DDX11	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 11 (CHL1-like helicase homolog, S. cerevisiae)
41	C14orf106	chromosome 14 open reading frame 106
42	ZNF92	zinc finger protein 92
43	EDIL3	EGF-like repeats and disoidin I-like domains 3
44	ATAD5	ATPase family, AAA domain containing 5
45	G3BP2	GTPase activating protein (SH3 domain) binding protein 2
46	IGF2BP3	insulin-like growth factor 2 mRNA binding protein 3
47	DPYSL3	dihydropyrimidinase-like 3
48	ESCO1	establishment of cohesion 1 homolog 1 (S. cerevisiae)
49	ASPM	asp (abnormal spindle) homolog, microcephaly associated (Drosophila)
50	ZNF770	zinc finger protein 770
51	SLC16A1	solute carrier family 16, member 1 (monocarboxylic acid transporter 1)
52	BRIP1	BRCA1 interacting protein C-terminal helicase 1
53	C12orf35	chromosome 12 open reading frame 35
54	ZNF138	zinc finger protein 138
		translocated promoter region (to activated MET)

56	NUP188	nucleoporin 188kDa
57	RBM15	RNA binding motif protein 15
58	SLC04C1	solute carrier organic anion transporter family, member 4C1
59	SOX2	SRY (sex determining region Y)-box 2
60	GGNT2	glucosaminyl (N-acetyl) transferase 2, I-branching enzyme (I blood group)
61	SLC12A1	solute carrier family 12 (sodium/potassium/chloride transporters), member 1
62	CLDN6	claudin 6
63	TEX15	testis expressed 15

[0079] [表 7 A] 第 7 遺伝子群 (表 7 B) を含むプローブ 59 個において、ヒト E S 細胞クローン (KhES1-S3) の発現レベルの平均に対する、各 E S 細胞クローン及び各 i P S 細胞クローンの発現レベルの割合

	Gene Symbol	Gene Title	KhES2_ES	KhES1_ES	KhES3_ES	201B7_IPS	201B6_IPS	253G1_IPS	253G4_IPS
1	FANCM	Fanconi anemia, complementation group M	-2.11	1.08	1.05	0.71	-3.35	-0.93	-3.38
2	RTEL1	regulator of telomere elongation helicase 1	-2.10	0.71	1.39	1.09	-3.86	-2.50	-4.51
3	RAD9B	RAD9 homolog B (S. pombe)	-0.57	-0.32	0.89	-0.14	-1.37	1.97	2.02
4	EYA4	eyes absent homolog 4 (Drosophila)	-2.13	1.14	0.88	0.77	-1.28	1.30	1.47
5	CRY2	cryptochrome 2 (photolyase-like)	-1.57	-0.68	2.25	-1.80	0.91	-0.70	-0.93
6	REV3L	REV3-like, catalytic subunit of DNA polymerase zeta (yeast)	-0.72	-0.65	1.37	-1.21	1.29	1.21	0.59
7	EYA3	eyes absent homolog 3 (Drosophila)	-0.61	1.79	-1.18	1.94	1.99	2.46	0.79
8	RNF169	ring finger protein 169	-1.28	1.36	-0.09	-1.07	1.71	-0.81	1.09
9	WRNIP1	Werner helicase interacting protein 1	-0.78	0.66	0.09	-1.24	0.68	-1.36	0.55
10	UBE2B	ubiquitin-conjugating enzyme E2B (RAD5 homolog)	0.17	0.50	-0.67	-0.23	0.89	1.34	0.74
11	ERCC1	excision repair cross-complementing rodent repair deficiency, complementation group 1 (includes overlapping antisense sequence)	-0.11	0.04	0.07	0.01	0.59	0.64	0.73
12	RAD52	RAD52 homolog (S. cerevisiae)	-0.45	0.66	-0.21	0.60	1.02	0.81	0.60
13	SETMAR	SET domain and mariner transposase fusion gene	-0.06	0.12	-0.06	0.03	1.17	0.66	0.92
14	FANCA	Fanconi anemia, complementation group A	0.00	-0.06	0.06	0.78	0.52	0.63	0.53
15	PMS2L2	postmeiotic segregation increased 2-like 2 pseudogene	-0.23	-0.05	0.27	0.81	0.80	0.88	0.70
16	ATXN3	Ataxin 3	0.45	0.01	-0.46	1.00	0.87	0.92	0.66
17	XRCC4	X-ray repair complementing defective repair in Chinese hamster cells 4	-1.12	-0.19	1.30	1.13	0.57	1.24	0.69
18	EYA1	eyes absent homolog 1 (Drosophila)	-0.23	-0.42	0.69	0.81	0.82	0.55	-0.71
19	EEPD1	endonuclease/exonuclease/phosphatase family domain containing 1	1.16	-1.71	0.56	0.84	0.59	-0.66	1.41
20	APLF	Aprataxin and PNKP like factor	0.53	-0.27	-0.26	0.95	0.75	-0.64	1.81
21	TYMS	thymidylate synthetase	-0.25	1.40	-1.16	-1.08	1.49	1.78	0.65
22	WRNIP1	Werner helicase interacting protein 1	0.56	1.34	-1.90	0.31	1.23	-0.75	-0.62
23	CCD14B	CCD14 cell division cycle 14 homolog B (S. cerevisiae)	1.82	-1.36	-0.46	1.49	1.57	1.52	1.35
24	ZSWIM7	zinc finger, SWIM-type containing 7	0.28	-0.83	0.55	2.05	2.07	2.16	2.25
25	RPA4	replications protein A4, 34kDa	-0.96	-0.99	1.85	2.02	2.06	1.45	-1.68
26	PRKDC	Protein kinase, DNA-activated, catalytic polypeptide	1.98	-1.37	-0.61	2.38	0.71	1.18	-0.82
27	PMS1	PMS1 postmeiotic segregation increased 1 (S. cerevisiae)	-2.90	1.52	1.38	1.27	2.00	0.80	1.16
28	CHD1L	chromodomain helicase DNA binding protein 1-like	-2.67	1.66	1.01	1.38	0.85	-2.24	1.28
29	ATM	ataxia telangiectasia mutated	0.98	-2.06	1.07	-1.37	-2.30	-2.08	0.72
30	TP53BP1	tumor protein p53 binding protein 1	-1.04	0.88	0.38	-1.69	-4.04	-2.55	-0.65
31	MSH8	mutS homolog 6 (E. coli)	-0.19	-0.61	0.70	-2.48	-3.02	-1.53	-2.37
32	EYA2	eyes absent homolog 2 (Drosophila)	-0.51	-1.16	1.68	0.48	-1.11	-0.93	-1.71
33	ATRX	alpha thalassemia/mental retardation syndrome X-linked (RAD54 homolog S. cerevisiae)	0.00	-0.02	0.09	-1.00	-2.06	-1.42	-1.55
34	ATRX	alpha thalassemia/mental retardation syndrome X-linked (RAD54 homolog S. cerevisiae)	0.07	0.04	-0.11	-1.00	-1.75	-1.33	-1.71
35	LIQ4	ligase IV, DNA, ATP-dependent	-0.07	0.22	-0.15	-0.66	-0.77	-0.73	-0.66
36	RPS27L	ribosomal protein S27-like	-0.47	0.10	0.37	-0.84	-0.90	-0.92	-0.72
37	RECQL	RecQ protein-like (DNA helicase Q1-like)	-0.33	-0.11	0.14	-0.54	-0.97	-1.16	-0.84

38	TP53BP1	tumor protein p53 binding protein 1	0.28	0.05	-0.33	0.36	-1.49	-1.36	-1.34
39	SETX	senataxin	0.13	0.05	-0.18	-0.03	-1.24	-1.28	-1.23
40	RECQL5	RecQ protein-like 5	-0.51	0.18	0.34	0.56	-1.16	-0.86	-0.75
41	RBM14	RNA binding motif protein 14	0.40	-0.38	-0.01	0.09	-0.88	-0.98	-0.84
42	USP10	ubiquitin specific peptidase 10	0.00	-0.07	0.07	0.04	-0.97	-0.96	-0.78
43	UPF1	UPF1 regulator of nonsense transcripts homolog (yeast)	0.17	-0.54	0.37	-0.08	-0.81	-0.77	-0.88
44	AXIN2	axin 2	0.10	0.16	-0.26	-0.03	-0.59	-1.76	-1.00
45	SUPT16H	suppressor of Ty 16 homolog (S. cerevisiae)	-0.09	0.28	-0.19	0.04	-1.21	-1.61	-1.15
46	AXIN2	axin 2	0.09	0.27	-0.38	-0.30	-0.74	-0.81	-0.63
47	ESQO1	establishment of cohesion 1 homolog 1 (S. cerevisiae)	-0.21	0.31	-0.11	-0.43	-0.51	-0.65	-0.66
48	BRP1	BRQ1 interacting protein C-terminal helix 1	-0.05	0.50	-0.45	-0.14	-0.86	-1.28	-0.60
49	SUPT16H	suppressor of Ty 6 homolog (S. cerevisiae)	0.47	-0.96	0.49	-0.43	-3.16	-3.01	-2.69
50	HERC2	hect domain and RLD 2	0.57	-0.99	0.22	0.13	-0.66	-2.43	-2.45
51	TDP1	(Tyrosyl)-DNA phosphodiesterase 1	0.38	0.05	-0.43	0.58	-0.97	-3.13	-2.53
52	POLK	polymerase (DNA directed) kappa	-1.80	-0.25	2.05	0.94	-1.84	1.35	-0.50
53	BUB1	budding uninhibited by benzimidazoles 1 homolog (yeast)	-2.14	1.35	0.78	0.43	-1.20	0.73	-0.78
54	OGG1	8-oxoguanine DNA glycosylase	-1.05	2.05	-1.00	-1.03	-1.24	0.96	1.25
55	REV1	REV1 homolog (S. cerevisiae)	-1.08	0.88	0.17	-0.50	-1.49	1.36	-0.78
56	OSF02A	oligonucleotide/oligosaccharide-binding fold containing 2A	0.61	-0.52	-0.09	-0.40	-0.53	-1.31	-5.54
57	GTF2H5	general transcription factor IIH polypeptide 5	-0.28	-0.94	1.22	-0.02	0.76	-1.61	-3.15
58	TEX15	testis expressed 15	-0.26	0.13	0.13	-0.48	-0.86	-0.71	-0.72
59	FANCA	Fanconi anemia, complementation group A	0.28	0.53	-0.78	-1.94	-0.93	-1.40	-0.92

[0080] [表 7 B] 第 7 遺伝子群

	Gene Symbol	Gene Title
1	FANCM	Fanconi anemia, complementation group M
2	RTEL1	regulator of telomere elongation helicase 1
3	RAD9B	RAD9 homolog B (S. pombe)
4	EYA4	eyes absent homolog 4 (Drosophila)
5	CRY2	cryptochrome 2 (photolyase-like)
6	REV3L	REV3-like, catalytic subunit of DNA polymerase zeta (yeast)
7	EYA3	eyes absent homolog 3 (Drosophila)
8	RNF168	ring finger protein 168
9	WRNIP1	Werner helicase interacting protein 1
10	UBE2B	ubiquitin-conjugating enzyme E2B (RAD6 homolog)
11	ERCC1	excision repair cross-complementing rodent repair deficiency, complementation group 1 (includes overlapping antisense sequence)
12	RAD52	RAD52 homolog (S. cerevisiae)
13	SETMAR	SET domain and mariner transposase fusion gene
14	FANCA	Fanconi anemia, complementation group A
15	PMS2L2	postmeiotic segregation increased 2-like 2 pseudogene
16	ATXN3	Ataxin 3
17	XRCC4	X-ray repair complementing defective repair in Chinese hamster cells 4
18	EYA1	eyes absent homolog 1 (Drosophila)
19	EEPD1	endonuclease/exonuclease/phosphatase family domain containing 1
20	APLF	Aprataxin and PNKP like factor
21	TYMS	thymidylate synthetase
22	CDC14B	CDC14 cell division cycle 14 homolog B (S. cerevisiae)
23	ZSWIM7	zinc finger, SWIM-type containing 7
24	RPA4	replication protein A4, 34kDa
25	PRKDC	Protein kinase, DNA-activated, catalytic polypeptide
26	PMS1	PMS1 postmeiotic segregation increased 1 (S. cerevisiae)
27	CHD1L	Chromodomain helicase DNA binding protein 1-like
28	ATM	ataxia telangiectasia mutated
29	TP53BP1	tumor protein p53 binding protein 1
30	MSH6	mutS homolog 6 (E. coli)
31	EYA2	eyes absent homolog 2 (Drosophila)
32	ATRX	alpha thalassemia/mental retardation syndrome X-linked (RAD54 homolog, S. cerevisiae)
33	LIG4	ligase IV, DNA, ATP-dependent
34	RPS27L	ribosomal protein S27-like
35	RECQL	RecQ protein-like (DNA helicase Q1-like)
36	SETX	senataxin
37	RECQL5	RecQ protein-like 5
38	RBM14	RNA binding motif protein 14
39	USP10	ubiquitin specific peptidase 10
40	UPF1	UPF1 regulator of nonsense transcripts homolog (yeast)
41	AXIN2	axin 2
42	SUPT16H	suppressor of Ty 16 homolog (S. cerevisiae)
43	ESCO1	establishment of cohesion 1 homolog 1 (S. cerevisiae)
44	BRIP1	BRCA1 interacting protein C-terminal helicase 1
45	SUPT6H	suppressor of Ty 6 homolog (S. cerevisiae)
46	HERC2	hect domain and RLD 2
47	TDP1	Tyrosyl-DNA phosphodiesterase 1
48	POLK	polymerase (DNA directed) kappa
49	BUB1	budding uninhibited by benzimidazoles 1 homolog (yeast)
50	OGG1	8-oxoguanine DNA glycosylase
51	REV1	REV1 homolog (S. cerevisiae)
52	OBFC2A	oligonucleotide/oligosaccharide-binding fold containing 2A
53	GTF2H5	general transcription factor IIH, polypeptide 5
54	TEX15	testis expressed 15

[0081] [表 8 A] 第 8 遺伝子群 (表 8 B) を含むプローブ 18 個において、ヒト ES 細胞クローン (KhES1-S3) の発現レベルの平均に対する、各 ES 細胞クローン及び各 iPS 細胞クローンの発現レベルの割合

	Gene Symbol	Gene Title	Khes1 ES	Khes2 ES	201B7 iPS	Khes3 ES	201B6 iPS	253G1 iPS	253G4 iPS
1	SETMAR	SET domain and mariner transposase fusion gene	0.12	-0.06	0.03	-0.06	1.17	0.86	0.92
2	ERCC1	excision repair cross-complementing rodent repair deficiency, complementation group 1 (includes overlapping antisense sequence)	0.04	-0.11	0.01	0.07	0.59	0.64	0.73
3	LIG4	ligase IV, DNA, ATP-dependent	0.22	-0.07	-0.50	-0.15	-0.77	-0.73	-0.66
4	RPS27L	ribosomal protein S27-like	0.10	-0.47	-0.54	0.37	-0.90	-0.82	-0.72
5	RECQL	RecQ protein-like (DNA helicase Q1-like)	-0.11	-0.03	-0.54	0.14	-0.97	-1.16	-0.94
6	TP53BP1	tumor protein p53 binding protein 1	0.05	0.28	0.39	-0.33	-1.49	-1.36	-1.34
7	SETX	senataxin	0.06	0.13	-0.09	-0.18	-1.24	-1.28	-1.23
8	RECQL5	RecQ protein-like 5	0.18	-0.51	0.56	0.34	-1.16	-0.86	-0.75
9	BRIP1	BRCA1 interacting protein C-terminal helicase 1	0.50	-0.05	-0.14	-0.45	-0.86	-1.28	-0.60
10	REB14	RNA binding motif protein 14	-0.39	0.40	0.00	-0.01	-0.88	-0.88	-0.84
11	USP10	ubiquitin specific peptidase 10	-0.07	0.00	0.04	0.07	-0.67	-0.98	-0.78
12	UPF1	UPF1 regulator of nonsense transcripts homolog (yeast)	-0.54	0.17	-0.08	0.37	-0.81	-0.77	-0.88
13	AXIN2	axin 2	0.16	0.10	-0.03	-0.26	-0.59	-1.76	-1.00
14	SUPT16H	suppressor of Ty 16 homolog (S. cerevisiae)	0.28	-0.09	0.04	-0.19	-1.21	-1.61	-1.15
15	AXIN2	axin 2	0.27	0.09	-0.30	-0.36	-0.74	-0.61	-0.63
16	ESCO1	establishment of cohesion 1 homolog 1 (S. cerevisiae)	0.31	-0.21	-0.43	-0.11	-0.61	-0.85	-0.66
17	TDP1	Tyrosyl-DNA phosphodiesterase 1	0.05	0.38	0.58	-0.43	-0.97	-3.13	-2.53
18	TEX15	testis expressed 15	0.13	-0.26	-0.49	0.13	-0.86	-0.71	-0.72

[0082] [表 8 B] 第 8 遺伝子群

	Gene Symbol	Gene Title
1	SETMAR	SET domain and mariner transposase fusion gene
2	ERCC1	excision repair cross-complementing rodent repair deficiency, complementation group 1 (includes overlapping antisense sequence)
3	LIG4	ligase IV, DNA, ATP-dependent
4	RPS27L	ribosomal protein S27-like
5	RECQL	RecQ protein-like (DNA helicase Q1-like)
6	TP53BP1	tumor protein p53 binding protein 1
7	SETX	senataxin
8	RECQL5	RecQ protein-like 5
9	BRIP1	BRCA1 interacting protein C-terminal helicase 1
10	RBM14	RNA binding motif protein 14
11	USP10	ubiquitin specific peptidase 10
12	UPF1	UPF1 regulator of nonsense transcripts homolog (yeast)
13	AXIN2	axin 2
14	SUPT16H	suppressor of Ty 16 homolog (S. cerevisiae)
15	ESCO1	establishment of cohesion 1 homolog 1 (S. cerevisiae)
16	TDP1	Tyrosyl-DNA phosphodiesterase 1
17	TEX15	testis expressed 15

[0083] [表 9 A] 第 9 遺伝子群 (表 9 B) を含むプローブ 13 個において、ヒト E S 細胞クローン (KhES1-S3) の発現レベルの平均に対する、各 E S 細胞クローン及び各 i P S 細胞クローンの発現レベルの割合

	Gene Symbol	Gene Title	Khes1 ES	Khes2 ES	Khes3 ES	201B7 .IPS	201B6 .IPS	253G1 .IPS	253G4 .IPS
1	FANCB	Fanconi anemia, complementation group B	0.67	-0.25	-0.42	0.18	-0.60	-0.10	0.60
2	TEX15	testis expressed 15	0.13	-0.26	0.13	-0.49	-0.88	-0.71	-0.72
3	RECQL	RecQ protein-like (DNA helicase Q1-like)	-0.11	-0.03	0.14	-0.54	-0.97	-1.16	-0.94
4	FEN1	flap structure-specific endonuclease 1	0.01	-0.06	0.04	0.28	0.46	0.65	0.45
5	CENPE	centromere protein E, 312kDa	-0.05	0.21	-0.16	-0.46	-0.68	-0.33	-1.20
6	TOP2A	topoisomerase (DNA) II alpha 170kDa	0.18	-0.20	0.02	-0.15	-0.58	-0.78	-0.57
7	USP28	ubiquitin specific peptidase 28	0.02	-0.07	0.04	-0.18	-0.47	-0.82	-0.70
8	FSCO1	establishment of cohesion 1 homolog 1 (S. cerevisiae)	0.31	-0.21	-0.11	-0.43	-0.61	-0.65	-0.66
9	MSH6	mutS homolog 6 (E. coli)	-0.10	0.05	0.05	0.18	-0.37	-0.68	-0.38
10	POLQ	polymerase (DNA directed) theta	-0.07	0.09	-0.01	-0.25	-0.42	-0.27	-0.63
11	SUPT16H	suppressor of Ty 16 homolog (S. cerevisiae)	0.28	-0.09	-0.19	0.04	-1.21	-1.61	-1.15
12	BUB1	budding uninhibited by benzimidazoles 1 homolog (yeast)	0.32	-0.14	-0.18	-0.05	-0.32	-0.99	-0.44
13	BRIP1	BRCA1 interacting protein C-terminal helicase 1	0.50	-0.05	-0.45	-0.14	-0.86	-1.28	-0.60

[0084] [表 9 B] 第 9 遺伝子群

	Gene Symbol	Gene Title
1	FANCB	Fanconi anemia, complementation group B
2	TEX15	testis expressed 15
3	RECQL	RecQ protein-like (DNA helicase Q1-like)
4	FEN1	flap structure-specific endonuclease 1
5	CENPE	centromere protein E, 312kDa
6	TOP2A	topoisomerase (DNA) II alpha 170kDa
7	USP28	ubiquitin specific peptidase 28
8	ESCO1	establishment of cohesion 1 homolog 1 (S. cerevisiae)
9	MSH6	mutS homolog 6 (E. coli)
10	POLQ	polymerase (DNA directed), theta
11	SUPT16H	suppressor of Ty 16 homolog (S. cerevisiae)
12	BUB1	budding uninhibited by benzimidazoles 1 homolog (yeast)
13	BRIP1	BRCA1 interacting protein C-terminal helicase 1

[0085] [表10A] 第10遺伝子群 (表10B) を含むプローブ5個において、ヒトES細胞クローン (KhES1-S3) の発現レベルの平均に対する、各ES細胞クローン及び各iPS細胞クローンの発現レベルの割合

	Gene Symbol	Gene Title	Khes1 ES	Khes2 ES	Khes3 ES	201B7 iPS	201B6 iPS	253G4 iPS	253G1 iPS
1	TEX15	testis expressed 15	0.13	-0.26	0.13	-0.49	-0.86	-0.72	-0.71
2	BRIP1	BRCA1 interacting protein C-terminal helicase 1	0.50	-0.05	-0.45	-0.14	-0.88	-0.60	-1.28
3	RECQL	RecQ protein-like (DNA helicase Q1-like)	-0.11	-0.03	0.14	-0.54	-0.97	-0.94	-1.16
4	SUPT16H	suppressor of Ty 16 homolog (S. cerevisiae)	0.28	-0.09	-0.19	0.04	-1.21	-1.15	-1.61
5	ESCO1	establishment of cohesion 1 homolog 1 (S. cerevisiae)	0.31	-0.21	-0.11	-0.43	-0.61	-0.66	-0.65

[0086] [表 1 O B] 第 1 O 遺伝子群

	Gene Symbol	Gene Title
1	TEX15	testis expressed 15
2	BRIP1	BRCA1 interacting protein C-terminal helicase 1
3	RECQL	RecQ protein-like (DNA helicase Q1-like)
4	SUPT16H	suppressor of Ty 16 homolog (S. cerevisiae)
5	ESCO1	establishment of cohesion 1 homolog 1 (S. cerevisiae)

[0087] [表 1 1 A] 第 1 1 遺伝子群 (表 1 1 B) を含むプローブ 2 7 個において、ヒト E S 細胞クローン (KhES1-S3) の発現レベルの平均に対する、各 E S 細胞クローン及び各 i P S 細胞クローンの発現レベルの割合

	Gene Symbol	Gene Title	Khes2 ES	Khes3 ES	Khes1 ES	201B7 IPS	201B6 IPS	253G1 IPS	253G4 IPS
1	ERCC1	exon repair cross-complementing rodent repair deficiency, complementation group 1 (includes overlapping antisense sequence)	-0.11	0.07	0.04	0.01	0.59	0.64	0.73
2	SETMAR	SET domain and mariner transposase fusion gene	-0.06	-0.06	0.12	0.03	1.17	0.86	0.92
3	SETX	senataxin	0.13	-0.18	0.05	-0.09	-1.24	-1.28	-1.23
4	TP53BP1	tumor protein p53 binding protein 1	0.28	-0.33	0.05	0.39	-1.49	-1.36	-1.34
5	RECQL	RecQ protein-like (DNA helicase Q1-like)	-0.03	0.14	-0.11	-0.54	-0.97	-1.16	-0.94
6	RFC1	replication factor C (activator 1) 1, 145kDa	-0.09	0.10	-0.01	0.05	-0.35	-0.49	-0.41
7	SMC5	structural maintenance of chromosomes 5	-0.28	0.11	0.17	-0.09	-0.71	-0.58	-0.81
8	RRM2B	ribonucleotide reductase M2 B (TP53 inducible)	-0.24	0.07	0.16	-0.24	-0.54	-0.75	-0.85
9	UPF1	UPF1 regulator of nonsense transcripts homolog (yeast)	0.17	0.37	-0.54	-0.08	-0.81	-0.77	-0.86
10	RECQL5	RecQ protein-like 5	-0.51	0.34	0.18	0.56	-1.16	-0.88	-0.75
11	ATR	alpha thalassemia/mental retardation syndrome X-linked (RAD54 homolog, S. cerevisiae)	0.00	0.03	-0.02	-1.00	-2.06	-1.42	-1.55
12	ATR	alpha thalassemia/mental retardation syndrome X-linked (RAD54 homolog, S. cerevisiae)	0.07	-0.11	0.04	-1.00	-1.75	-1.33	-1.71
13	FANCI	Fanconi anemia, complementation group I	-0.13	-0.06	0.19	0.12	-0.44	-0.57	-0.50
14	MSH6	mutS homolog 6 (E. coli)	0.05	0.05	-0.10	0.18	-0.37	-0.68	-0.38
15	TOP2A	topoisomerase (DNA) II alpha 170kDa	-0.20	0.02	0.18	-0.15	-0.58	-0.78	-0.57
16	USP28	ubiquitin specific peptidase 28	-0.07	0.04	0.02	-0.18	-0.47	-0.82	-0.70
17	PRM14	RNA binding motif protein 14	0.40	-0.01	-0.39	0.00	-0.88	-0.88	-0.84
18	USP10	ubiquitin specific peptidase 10	0.00	0.07	-0.07	0.04	-0.67	-0.88	-0.78
19	PRKDC	protein kinase, DNA-activated, catalytic polypeptide	0.01	-0.23	0.22	0.01	-0.49	-0.81	-0.50
20	RAD21	RAD21 homolog (S. pombe)	0.11	-0.14	0.03	0.06	-0.48	-1.07	-0.80
21	SUPT16H	suppressor of Ty 16 homolog (S. cerevisiae)	-0.09	-0.19	0.28	0.04	-1.21	-1.61	-1.15
22	AXIN2	axin 2	0.10	-0.26	0.16	-0.03	-0.59	-1.76	-1.00
23	SUPT6H	suppressor of Ty 6 homolog (S. cerevisiae)	0.47	0.49	-0.96	-0.49	-3.16	-3.01	-2.89
24	TDP1	Tyrosyl-DNA phosphodiesterase 1	0.38	-0.43	0.05	0.58	-0.57	-3.13	-2.55
25	HERC2	hect domain and RLD 2	0.67	0.22	-0.89	0.13	-0.66	-2.43	-2.45
26	TEX15	testis expressed 15	-0.02	-0.36	0.38	0.03	-0.42	-0.83	-1.07
27	RTEL1	regulator of telomere elongation helicase 1	-2.10	1.39	0.71	1.09	-3.86	-2.80	-4.51

[0088] [表 1 1 B] 第 1 1 遺伝子群

	Gene Symbol	Gene Title
1	ERCC1	excision repair cross-complementing rodent repair deficiency, complementation group 1 (includes overlapping antisense sequence)
2	SETMAR	SET domain and mariner transposase fusion gene
3	SETX	senataxin
4	TP53BP1	tumor protein p53 binding protein 1
5	RECQL	RecQ protein-like (DNA helicase Q1-like)
6	RFC1	replication factor C (activator 1) 1, 145kDa
7	SMC5	structural maintenance of chromosomes 5
8	RRM2B	ribonucleotide reductase M2 B (TP53 inducible)
9	UPF1	UPF1 regulator of nonsense transcripts homolog (yeast)
10	RECQL5	RecQ protein-like 5
11	ATRX	alpha thalassemia/mental retardation syndrome X-linked (RAD54 homolog, S. cerevisiae)
12	FANCI	Fanconi anemia, complementation group I
13	MSH6	mutS homolog 6 (E. coli)
14	TOP2A	topoisomerase (DNA) II alpha 170kDa
15	USP28	ubiquitin specific peptidase 28
16	RBM14	RNA binding motif protein 14
17	USP10	ubiquitin specific peptidase 10
18	PRKDC	protein kinase, DNA-activated, catalytic polypeptide
19	RAD21	RAD21 homolog (S. pombe)
20	SUPT16H	suppressor of Ty 16 homolog (S. cerevisiae)
21	AXIN2	axin 2
22	SUPT6H	suppressor of Ty 6 homolog (S. cerevisiae)
23	TDP1	Tyrosyl-DNA phosphodiesterase 1
24	HERC2	hect domain and RLD 2
25	TEX15	testis expressed 15
26	RTEL1	regulator of telomere elongation helicase 1

[0089] [表 1 2 A] 第 1 2 遺伝子群 (表 1 2 B) を含むプローブ 1 9 個において、ヒト E S 細胞クローン (KhES1-S3) の発現レベルの平均に対する、各 E S 細胞クローン及び各 i P S 細胞クローンの発現レベルの割合

	Gene Symbol	Gene Title	Khes1 ES	Khes2 ES	Khes3 ES	201B7 .IPS	201B6 .IPS	253G4 .IPS	253G1 .IPS
1	CENPE	centromere protein E 312kDa	-0.05	0.21	-0.16	-0.46	-0.68	-1.20	-0.33
2	TP53	tumor protein p53	-0.22	0.46	-0.24	0.11	-0.49	-0.48	-0.55
3	TOP2A	topoisomerase (DNA) II alpha 170kDa	0.18	-0.20	0.02	-0.15	-0.58	-0.57	-0.78
4	USP28	ubiquitin specific peptidase 28	0.02	-0.07	0.04	-0.18	-0.47	-0.70	-0.82
5	ESCO1	establishment of cohesion I homolog 1 (S. cerevisiae)	0.31	-0.21	-0.11	-0.43	-0.61	-0.86	-0.85
6	MSH6	mutS homolog 6 (E. coli)	-0.10	0.05	0.05	0.18	-0.37	-0.38	-0.68
7	KNTC1	kinetochore associated 1	0.19	-0.17	-0.02	-0.04	-0.43	-0.44	-0.47
8	FANCI	Fanconi anemia, complementation group I	0.19	-0.13	-0.06	0.12	-0.44	-0.50	-0.57
9	FANCI	Fanconi anemia, complementation group I	0.00	-0.01	0.01	0.21	-0.28	-0.23	-0.25
10	POLQ	polymerase (DNA directed) theta	-0.07	0.09	-0.01	-0.25	-0.42	-0.63	-0.27
11	SMC6	structural maintenance of chromosomes 6	0.13	-0.16	0.04	0.18	-0.53	-0.43	-0.29
12	TTK	TTK protein kinase	-0.04	-0.03	0.07	-0.23	-0.56	-0.36	-0.43
13	BUB1	budding uninhibited by benzimidazoles 1 homolog (yeast)	0.32	-0.14	-0.18	-0.05	-0.32	-0.44	-0.99
14	BRIP1	BRCA1 interacting protein C-terminal helicase 1	0.50	-0.05	-0.45	-0.14	-0.86	-0.80	-1.28
15	RECQL	RecQ protein-like (DNA helicase Q1-like)	-0.11	-0.03	0.14	-0.54	-0.97	-0.94	-1.16
16	ATR	alpha thalassemia/mental retardation syndrome X-linked (RAD54 homolog, S. cerevisiae)	-0.02	0.00	0.03	-1.00	-2.06	-1.55	-1.42
17	ATR	alpha thalassemia/mental retardation syndrome X-linked (RAD54 homolog, S. cerevisiae)	0.04	0.07	-0.11	-1.00	-1.75	-1.71	-1.33
18	SUPT16H	suppressor of Ty 16 homolog (S. cerevisiae)	0.28	-0.09	-0.19	0.04	-1.21	-1.15	-1.61
19	TEX15	testis expressed 15	0.13	-0.26	0.13	-0.49	-0.86	-0.72	-0.71

[0090] [表 1 2 B] 第 1 2 遺伝子群

	Gene Symbol	Gene Title
1	CENPE	centromere protein E, 312kDa
2	TP53	tumor protein p53
3	TOP2A	topoisomerase (DNA) II alpha 170kDa
4	USP28	ubiquitin specific peptidase 28
5	ESCO1	establishment of cohesion 1 homolog 1 (S. cerevisiae)
6	MSH6	mutS homolog 6 (E. coli)
7	KNTC1	kinetochore associated 1
8	FANCI	Fanconi anemia, complementation group I
9	POLQ	polymerase (DNA directed), theta
10	SMC6	structural maintenance of chromosomes 6
11	ITK	ITK protein kinase
12	BUB1	budding uninhibited by benzimidazoles 1 homolog (yeast)
13	BRIP1	BRCA1 interacting protein C-terminal helicase 1
14	RECQL	RecQ protein-like (DNA helicase Q1-like)
15	ATRX	alpha thalassemia/mental retardation syndrome X-linked (RAD54 homolog, S. cerevisiae)
16	SUPT16H	suppressor of Ty 16 homolog (S. cerevisiae)
17	TEX15	testis expressed 15

産業上の利用可能性

[0091] 本発明によって、分化させても腫瘍化が起きにくい i P S 細胞クローンの選択方法、及びその選択方法に用いる遺伝子の選択方法が提供できるようになった。

請求の範囲

- [請求項1] i P S細胞クローンの選択方法であって、
 未分化状態のi P S細胞クローンにおいて、第1～第12遺伝子群のいずれかの遺伝子群において、少なくとも一つの遺伝子について、発現レベルを調べる工程、
 を含む方法。
- [請求項2] 請求項1に記載の選択方法であって、
 前記発現レベルを、正常に分化できないか、あるいは分化しても腫瘍化を起こしやすいi P S細胞クローンにおける当該遺伝子の発現レベル、及び、腫瘍化を起こしにくいi P S細胞クローンにおける当該遺伝子の発現レベルと比較する工程、
 をさらに含む方法。
- [請求項3] 請求項1に記載の選択方法であって、
 前記i P S細胞クローンにおいて、第1～第12遺伝子群のいずれかの遺伝子群に属する全ての遺伝子の発現レベルを調べる工程と、
 調べた遺伝子群において、発現レベルに異常のある遺伝子の個数を調べる工程と、
 調べた遺伝子の個数を、正常に分化できないか、あるいは分化しても腫瘍化を起こしやすいi P S細胞クローンにおける発現レベルに異常のある遺伝子の個数、及び、腫瘍化を起こしにくいi P S細胞クローンにおける発現レベルに異常のある遺伝子の個数と比較する工程、
 、
 をさらに含む方法。
- [請求項4] 請求項3に記載の選択方法であって、
 腫瘍化を起こしにくい多能性幹細胞クローンの発現レベルと比較することによって、前記発現レベルが異常かどうか判断することを特徴とする、方法。
- [請求項5] 請求項1に記載の選択方法であって、

前記 i P S 細胞クローンにおいて、第 1 ～第 1 2 遺伝子群のいずれかの遺伝子群に属する全ての遺伝子の発現レベルを調べる工程と、

調べた遺伝子群について、前記 i P S 細胞クローンにおける発現レベルと、正常に分化できないか、あるいは分化しても腫瘍化を起こしやすい i P S 細胞クローンにおける発現レベルと、腫瘍化を起こしやすい i P S 細胞クローンにおける発現レベルとを指標にして、i P S 細胞クローンのclustering分析を行う工程と、

当該 i P S 細胞クローンが、正常に分化できないか、あるいは分化しても腫瘍化を起こしやすい i P S 細胞クローンと、腫瘍化を起こしにくい i P S 細胞クローンのいずれに分類されるかを調べる工程と、

を含む方法。

[請求項6] 請求項 5 に記載の選択方法であって、

腫瘍化を起こしにくい多能性幹細胞クローンの発現レベルとの相対値を指標にして、前記 i P S 細胞クローンのclustering解析を行うことを特徴とする、請求項 7 に記載の方法。

[請求項7] i P S 細胞クローンを選択するために発現レベルを調べる遺伝子の選択方法であって、

正常に分化できないか、あるいは分化しても腫瘍化を起こしやすい複数の第 1 の i P S 細胞クローンと、腫瘍化を起こしにくい複数の第 2 の i P S 細胞クローンにおいて、未分化状態の各 i P S 細胞クローンで、1 以上の遺伝子を含む候補遺伝子群に属する遺伝子の発現レベルを調べる工程、

を含む方法。

[請求項8] 前記候補遺伝子群に属する遺伝子が、多能性幹細胞で分化細胞より発現の高い遺伝子、及びDNA修復に関与する遺伝子であることを特徴とする、請求項 7 に記載の方法。

[請求項9] 前記候補遺伝子群に属する遺伝子が、第 1 遺伝子群及び第 2 遺伝子

群のいずれかに属する遺伝子であることを特徴とする、請求項 7 に記載の方法。

[請求項10] 請求項 7 に記載の選択方法であって、

複数の第 1 の i P S 細胞クローンにおいて得られた第 1 の発現レベルと、複数の第 2 の i P S 細胞クローンにおいて得られた第 2 の発現レベルとを比較する工程と、

第 1 の発現レベルと第 2 の発現レベルとが異なるかどうか調べる工程と、

を含む方法。

[請求項11] 請求項 7 に記載の選択方法であって、

複数の第 1 の i P S 細胞クローンにおいて得られた発現レベルにおいて、発現レベルに異常のある遺伝子の第 1 の個数と、複数の第 2 の i P S 細胞クローンにおいて得られた発現レベルのうち、発現レベルに異常のある遺伝子の第 2 の個数とを比較する工程と、

第 1 の個数と第 2 の個数とが異なるかどうか調べる工程と、

を含む方法。

[請求項12] 請求項 1 1 に記載の選択方法であって、

腫瘍化を起こしにくい多能性幹細胞クローンの発現レベルと比較することによって、前記発現レベルが異常かどうか判断することを特徴とする、方法。

[請求項13] 請求項 7 に記載の選択方法であって、

前記 i P S 細胞クローンについて、前記発現レベルを指標にして clustering 分析を行う工程と、

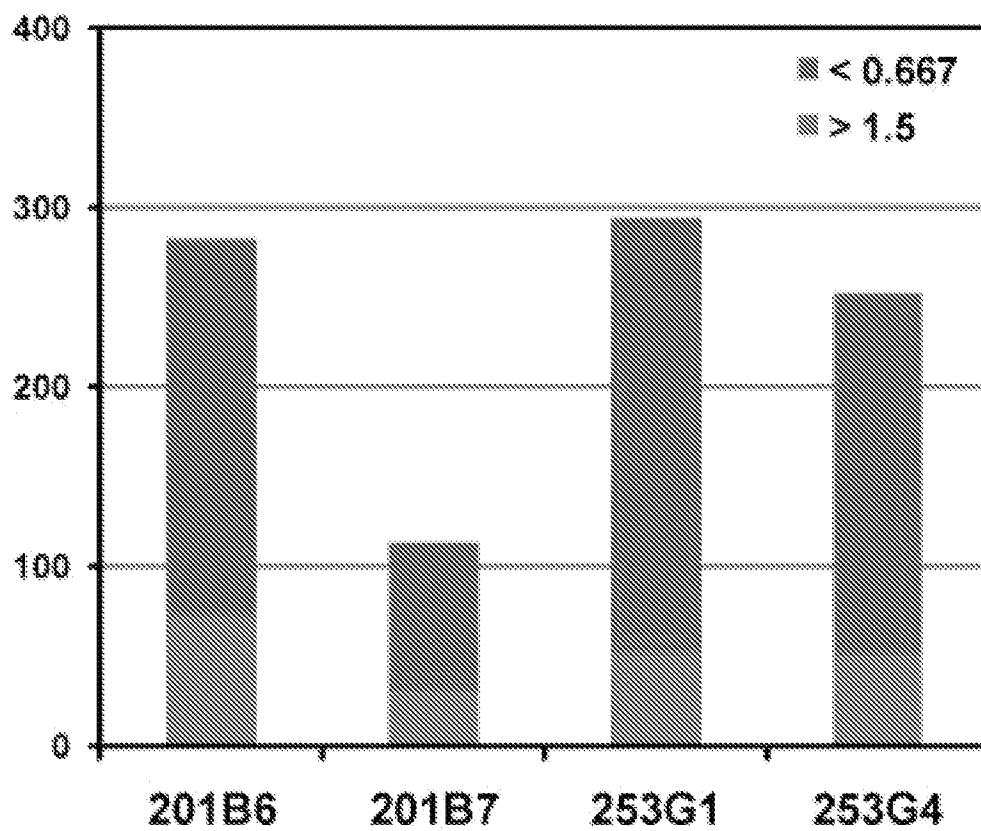
複数の第 1 の i P S 細胞クローンと複数の第 2 の i P S 細胞クローンが、それぞれ別の cluster に分類されるかどうか調べる工程と、
を含む方法。

[請求項14] 請求項 1 3 に記載の選択方法であって、

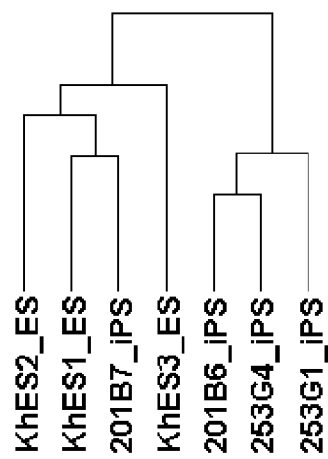
腫瘍化を起こしにくい多能性幹細胞クローンの発現レベルとの相

対値を指標にして、前記 i P S 細胞クローンについて clustering 分析を行うことを特徴とする、方法。

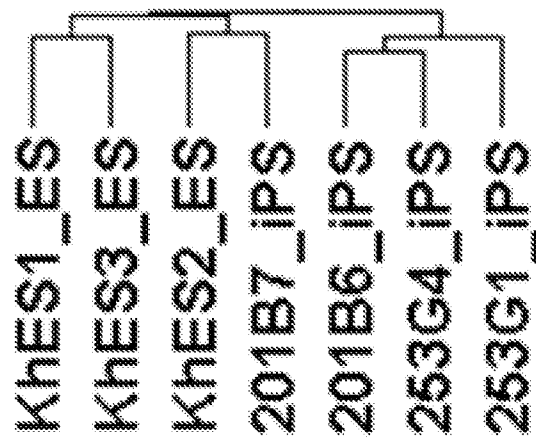
[図1]



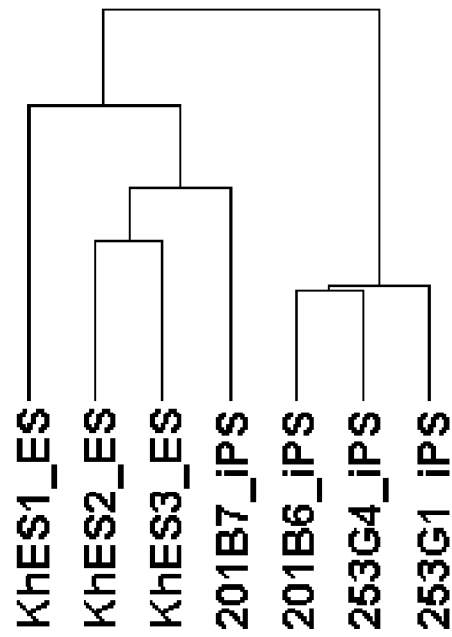
[図2]



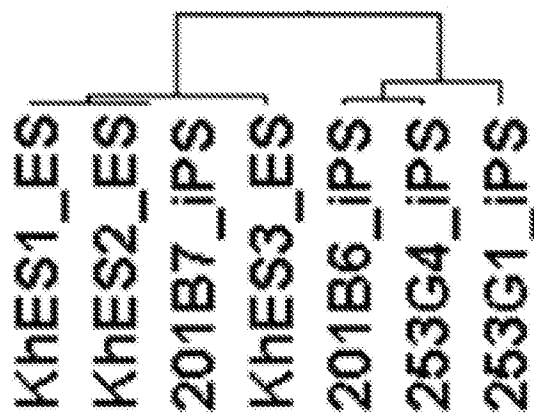
[図3]



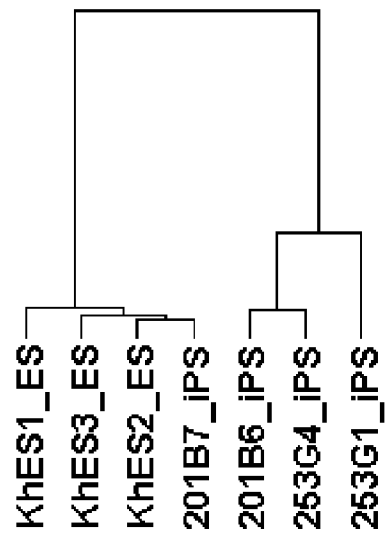
[図4]



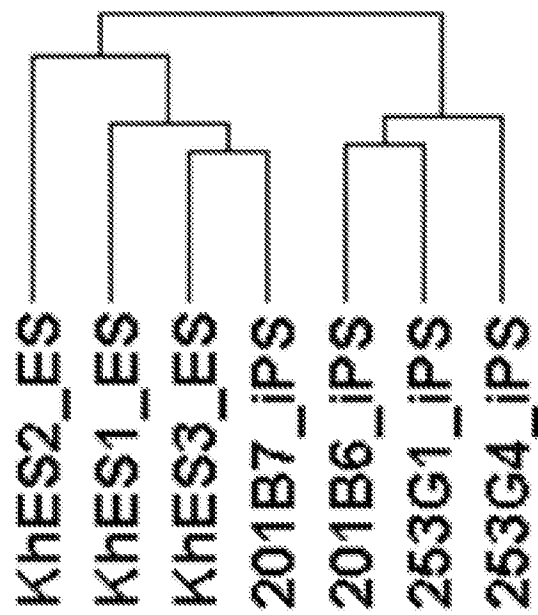
[図5]



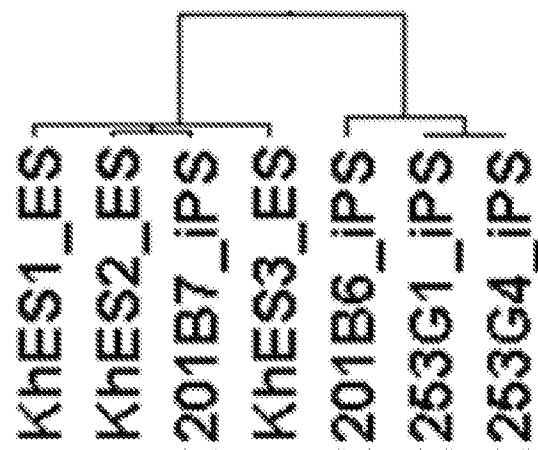
[図6]



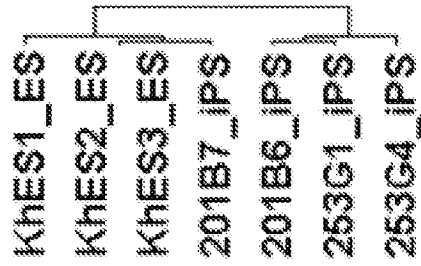
[図7]



[図8]



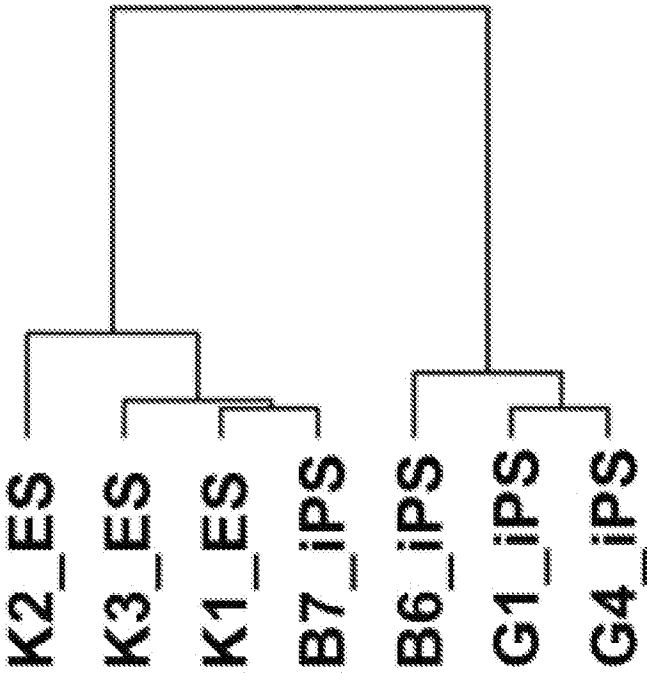
[図9]



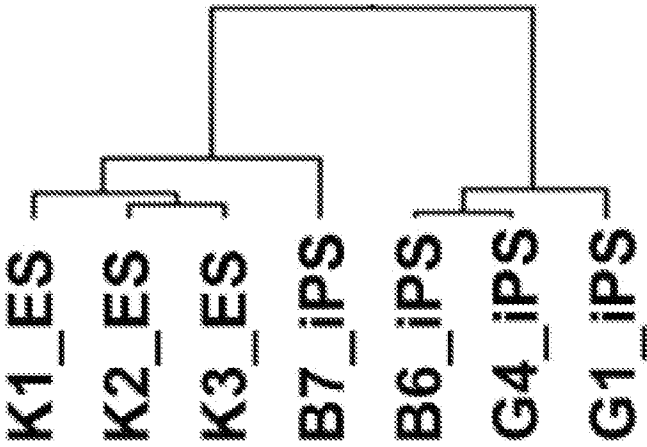
[図10]



[図11]



[図12]

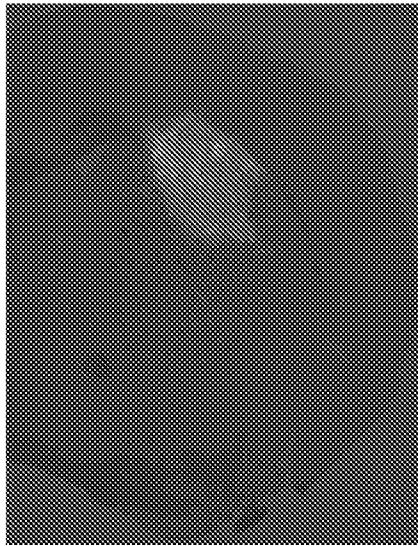


[図13]

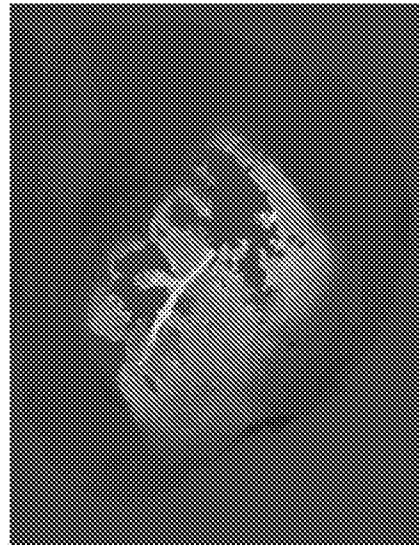
	KhES1	201B7	253G1	253G4	
HE					

[図14]

KhES1

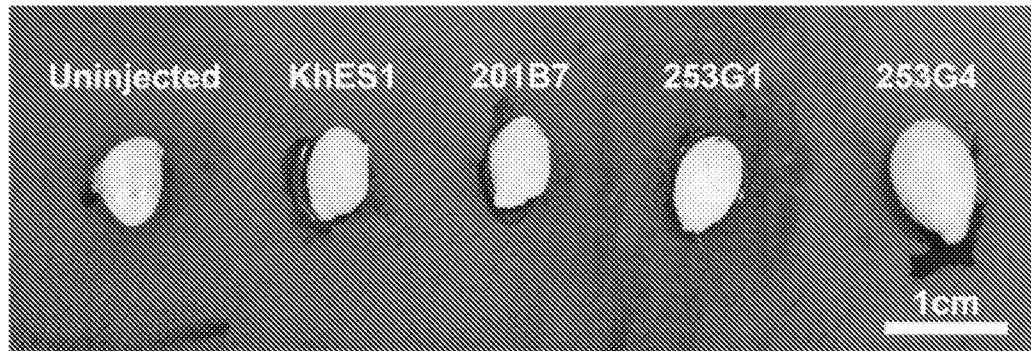


253G4

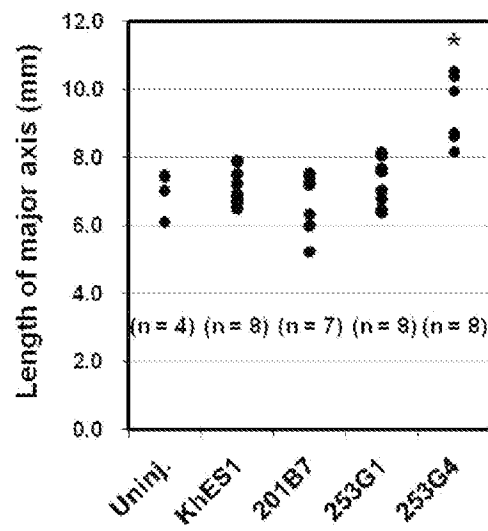


[図15]

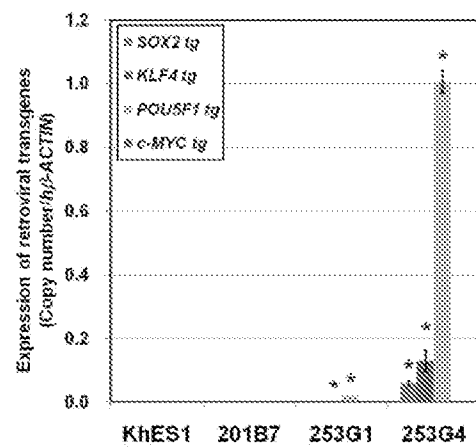
A.



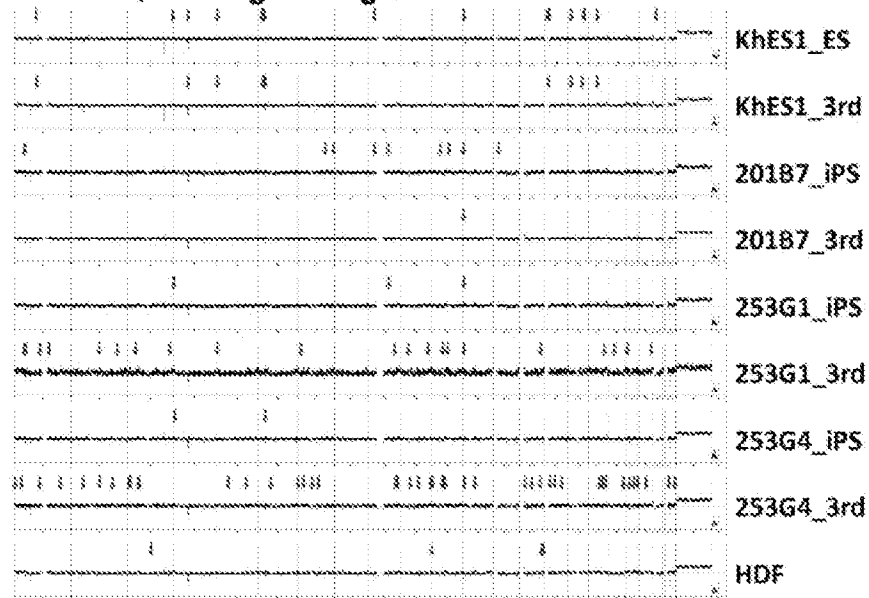
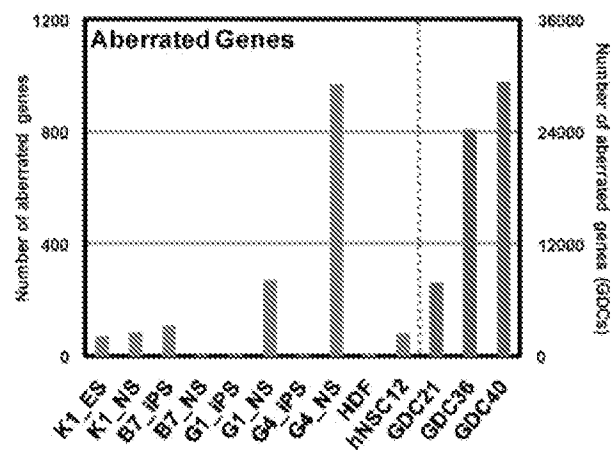
B.



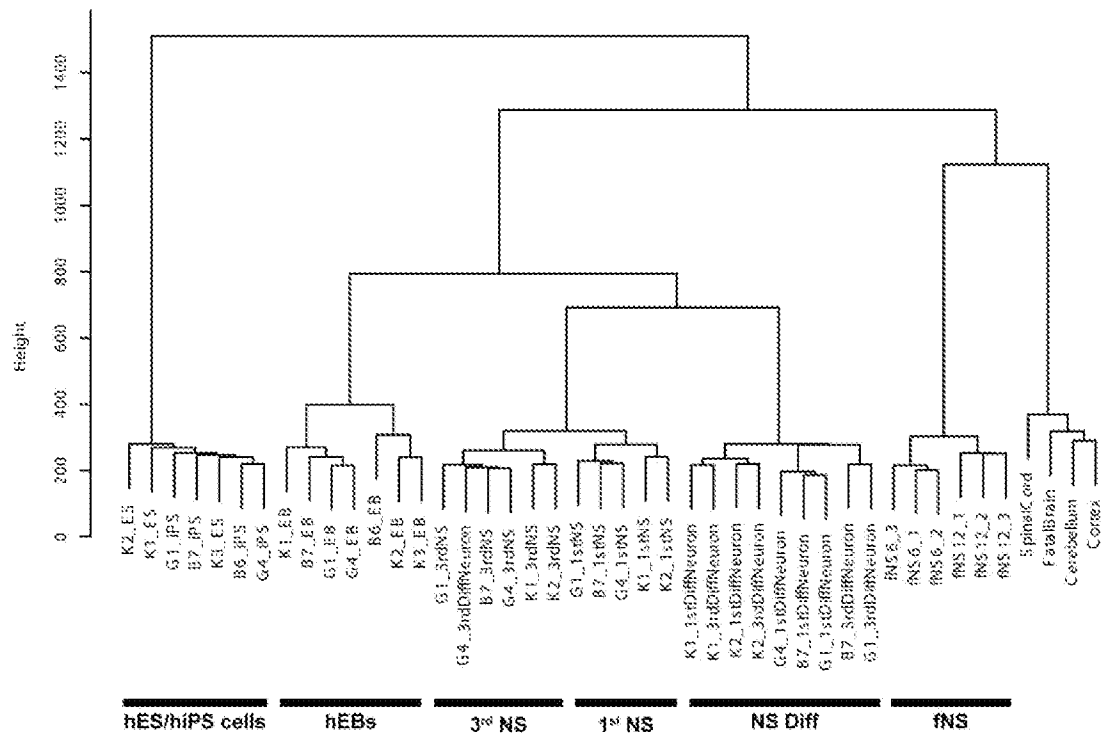
C.



[図16]

a. aCGH, moving average**b**

[図17]



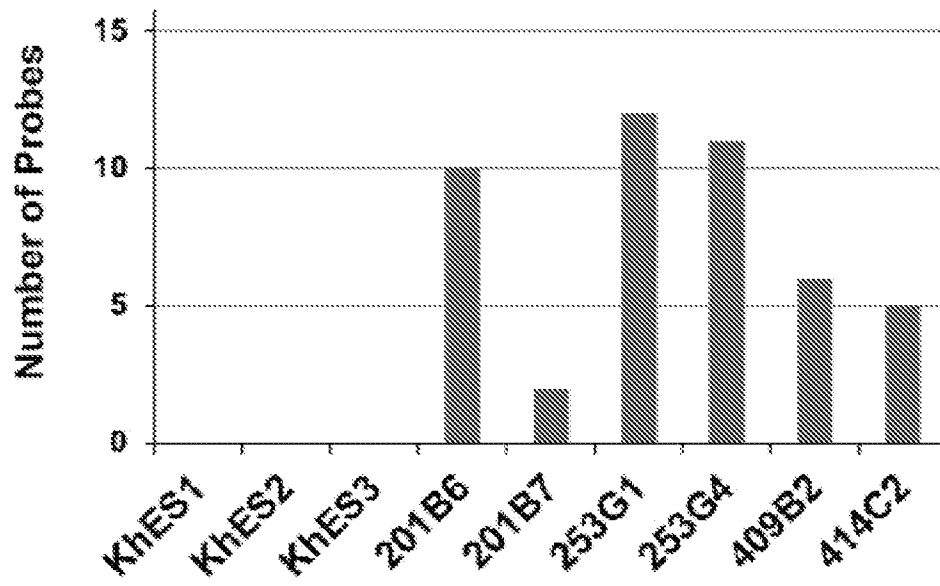
[図18]

KhES1_ES
KhES2_ES
KhES3_ES
201B7_IPS
409B2_IPS
414C2_IPS
201B6_IPS
253G4_IPS
253G1_IPS

[図19]

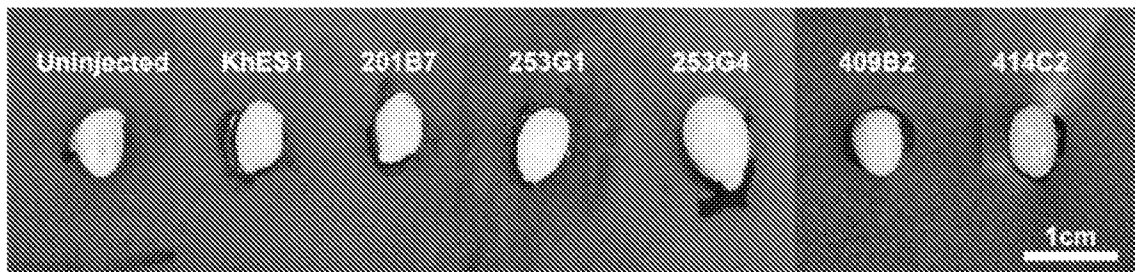
KhES1_ES
KhES2_ES
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201B7_IPS
409B2_IPS
414C2_IPS
201B6_IPS
253G4_IPS
253G1_IPS

[図20]

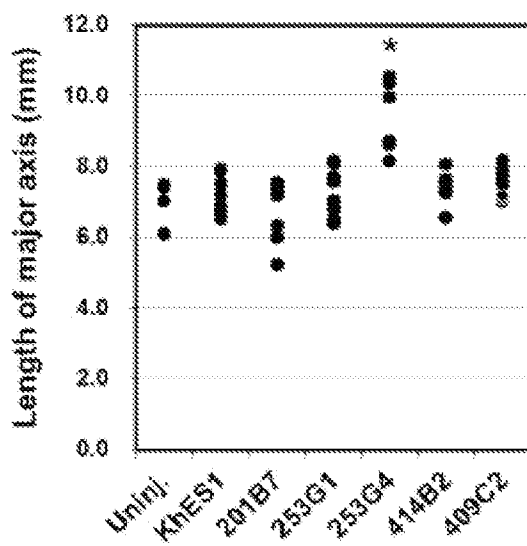


[図21]

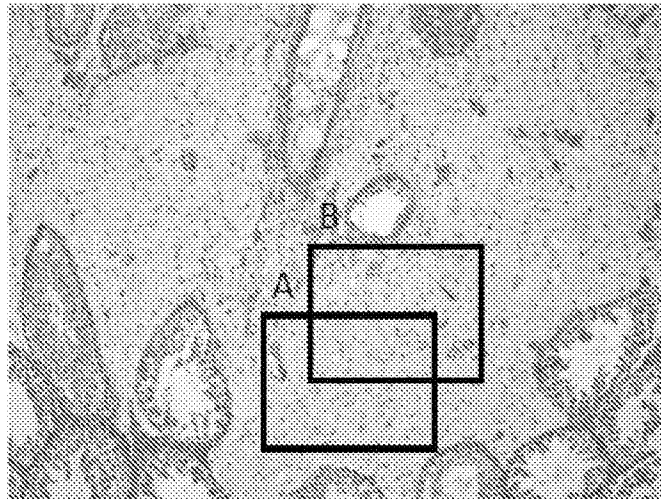
A.



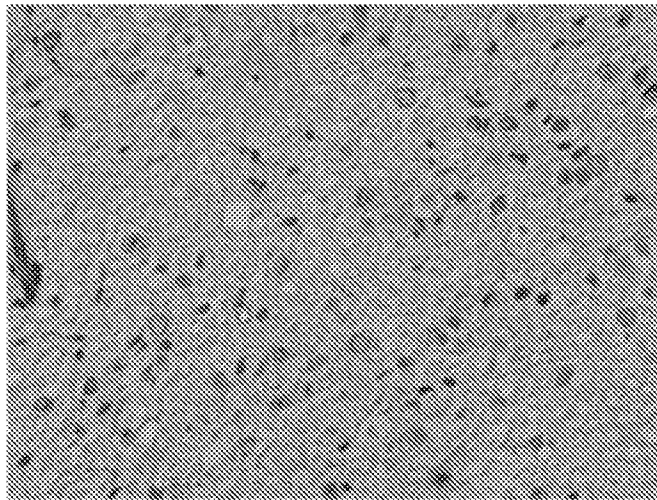
B.



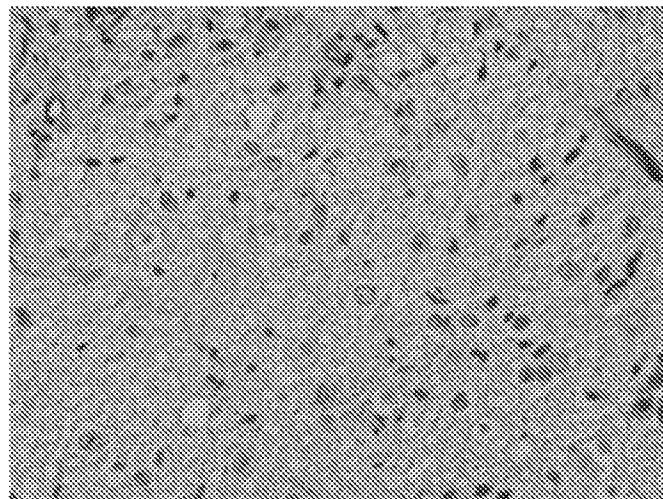
[図22]



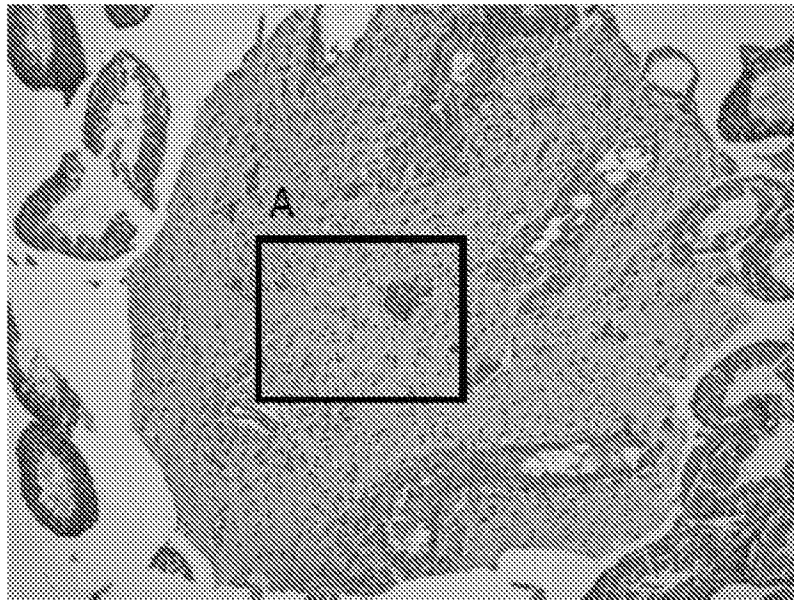
A.



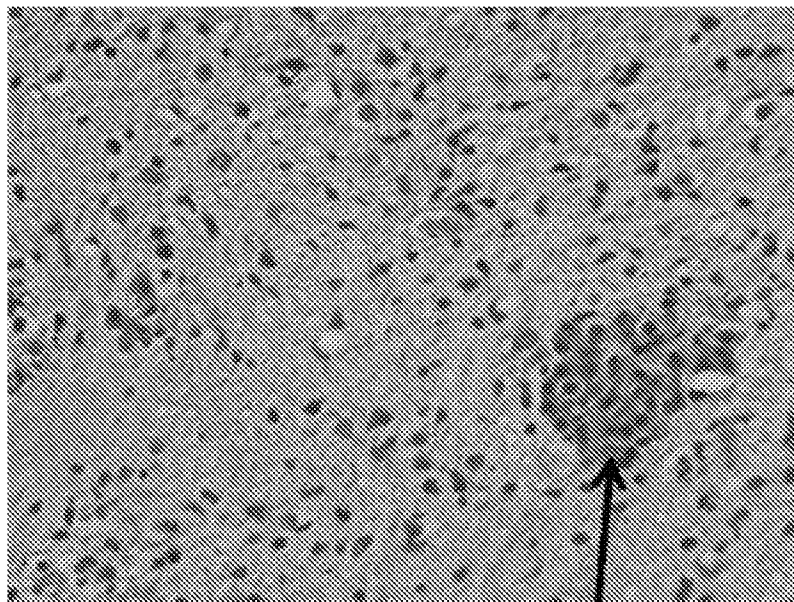
B.



[図23]



A.



精巣由来の細胞
(Leydig cell)

INTERNATIONAL SEARCH REPORT

International application No.

PCT/JP2012/054800

A. CLASSIFICATION OF SUBJECT MATTER

C12Q1/68(2006.01) i, C12N5/10(2006.01) n, C12Q1/02(2006.01) n

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)

C12Q1/68, C12N5/10, C12Q1/02

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	1996-2012
Kokai Jitsuyo Shinan Koho	1971-2012	Toroku Jitsuyo Shinan Koho	1994-2012

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

JSTPlus/JMEDPlus/JST7580 (JDreamII), PubMed, GeneCards

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	WO 2010/038904 A1 (Tottori University), 08 April 2010 (08.04.2010), example 7; fig. 16 (Family: none)	1-6 (Partial)
Y	JP 2010-523117 A (Whitehead Institute for Biomedical Research), 15 July 2010 (15.07.2010), paragraphs [0198] to [0234] & US 2011/0076678 A1 & EP 2145000 A1 & WO 2008/124133 A1 & CA 2683056 A & MX 2009010847 A & ZA 200907185 A & CN 101932705 A & AU 2008236629 A	1-6 (Partial)

☒ 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
08 May, 2012 (08.05.12)

Date of mailing of the international search report
22 May, 2012 (22.05.12)

Name and mailing address of the ISA/
Japanese Patent Office

Authorized officer

Facsimile No.

Telephone No.

INTERNATIONAL SEARCH REPORT

International application No.

PCT/JP2012/054800

C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	JP 2010-528622 A (The General Hospital Corp.), 26 August 2010 (26.08.2010), paragraphs [0070] to [0073] & US 2010/0184051 A1 & EP 2164951 A2 & WO 2008/151058 A2 & CA 2688539 A & CN 101802172 A	1-6(Partial)
Y	WO 2010/134388 A1 (Makoto MIHARA), 25 November 2010 (25.11.2010), paragraphs [0070] to [0072] (Family: none)	1-6(Partial)
Y	RIPKA S. et al., Glutamate receptor GRIA3-- target of CUX1 and mediator of tumor progression in pancreatic cancer., Neoplasia, 2010.08, Vol.12, No.8, p.659-667	1-6(Partial)

INTERNATIONAL SEARCH REPORT

International application No.

PCT/JP2012/054800

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:
See extra sheet.

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.:
In the inventions in claims 1-6, the inventions relating to a method for selecting an iPS cell clone, said method comprising a step for examining the expression level of GRIA3 gene in iPS cell clones in an undifferentiated state.

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest and, where applicable, the 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.

Continuation of Box No.III of continuation of first sheet(2)

Claim 1 and claims 2-6 depending on claim 1 relate to "a method for selecting an iPS cell clone" "said method comprising a step for examining the expression level" "in iPS cell clones in an undifferentiated state" for each of genes that are alternatively selected from among 2492 kinds of genes in total set forth as "one gene group in the 1st to 12th gene groups".

Document 1 discloses a method comprising, in undifferentiated iPS cell clones, examining the expression amounts of endogenous undifferentiated markers Nanog, Oct3/4, Sox2 and Rex1 in subclones with the loss of transferred chromosome, and selecting a cell in a more completely undifferentiated state in which all of these undifferentiated markers are expressed at the same level as in the control iPS cell (See, in particular, Example 7 and Fig. 16).

Document 2 discloses a method for selecting a secondary iPS cell clone, said method comprising a step of, in primary iPS cell clones in an undifferentiated state, examining the expression levels of Nanog-GEP gene and heavy chain and light chain genes (See, in particular, paragraphs [0198]-[0234] and Tables 1 and 2).

Document 3 discloses a method of selecting induced pluripotent stem cells, said method comprising a step for, after re-programming a cell to a pluripotent phenotype, culturing the cell, isolating a clone of cells from the culture which expresses the X-chromosome-linked reporter, and indicating that the clone comprises induced pluripotent stem cells, testing the clone cells with respect to the expression of a stem cell marker that is selected from the group consisting of SSEA1, CD9, Nanog, Fbx15, Ecat1, Esq1, Eras, Gdf3, Fgf4, Cripto, Dax1, Zpf296, Slc2a3, Rex1, Utf1, and Oct4 (See, in particular, paragraphs [0070]-[0073]).

Consequently, "a method for selecting an iPS cell clone, said method comprising a step for examining the expression level in iPS cell clones in an undifferentiated state" does not have a special technical feature within the meaning of PCT Rule 13.2.

Considering the gene names described in Sequence Tables, it does not appear that there is a novel chemical structure common to the 2492 kinds of genes set forth in claim 1 the expression levels of which in iPS are to be examined.

Although these genes have a common technical feature of being a gene expressed in iPS, genes expressed in iPS are as described in Documents 1 to 3. Meanwhile, the mere fact that genes are derived from the same source is not sufficient to meet the criteria for unity of invention (See PCT INTERNATIONAL SEARCH AND PRELIMINARY EXAMINATION GUIDELINES, PCT/GL/ISPE/1, enforced on 2004/03/25, Chapter 10 Unity of Invention, 10.58 Example 32 (<http://www.wipo.int/pct/en/texts/pdf/ispe.pdf>)). Thus, the aforesaid matter cannot be considered as "a special technical feature" in the meaning of PCT Rule 13.2.

Further, there is no other common matter which is considered to be a special technical feature under PCT Rule 13.2.

As a result of judging special technical features with respect to claims dependent on claim 1 at the time of the order for payment of additional fees, two thousand four hundred and ninety three (2,493) inventions (invention groups) are involved in claims.

Respective special technical features of these inventions (invention groups) are as follows.

(Invention group 1) In the inventions in claims 1-6, the inventions relating to the first gene in the 1st gene group.

(Continued to next extra sheet)

"A method for selecting an iPS cell clone, said method comprising a step for examining the expression level of GRIA3 gene in iPS cell clones in an undifferentiated state."

(Invention group 2) In the inventions in claims 1-6, the inventions relating to the second gene in the 1st gene group.

"A method for selecting an iPS cell clone, said method comprising a step for examining the expression level of STC2 gene in iPS cell clones in an undifferentiated state."

(Invention group 2492) In the inventions in claims 1-6, the inventions relating to the seventeenth gene in the 12th gene group "a method for selecting an iPS cell clone, said method comprising a step for examining the expression level of TEX15 gene in iPS cell clones in an undifferentiated state.".

(Invention 2493) the inventions of claims 7-14

"A method for selecting a gene the expression level of which is to be examined to select an iPS cell clone, said method comprising a step for, in a plurality of first iPS cell clones that cannot be normally differentiated or, even in the case of being differentiated, are liable to undergo tumorigenic transformation, and a plurality of second iPS cell clones that scarcely undergo tumorigenic transformation, examining the expression level of a gene belonging to a candidate gene group including one or more genes in the individual iPS cell clones in an undifferentiated state"

document 1: WO 2010/038904 A1 (Tottori University), 08 April 2010 (08.04.2010), example 7; fig. 16 (Family: none)

document 2: JP 2010-523117 A (Whitehead Institute for Biomedical Research), 15 July 2010 (15.07.2010), paragraphs [0198] to [0234] & US 2011/0076678 A1 & EP 2145000 A1 & WO 2008/124133 A1 & CA 2683056 A & MX 2009010847 A & ZA 200907185 A & CN 101932705 A & AU 2008236629 A

document 3: JP 2010-528622 A (The General Hospital Corp.), 26 August 2010 (26.08.2010), paragraphs [0070] to [0073] & US 2010/0184051 A1 & EP 2164951 A2 & WO 2008/151058 A2 & CA 2688539 A & CN 101802172 A

A. 発明の属する分野の分類 (国際特許分類 (I P C))

Int.Cl. C12Q1/68(2006.01)i, C12N5/10(2006.01)n, C12Q1/02(2006.01)n

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 (I P C))

Int.Cl. C12Q1/68, C12N5/10, C12Q1/02

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	1 9 2 2 - 1 9 9 6 年
日本国公開実用新案公報	1 9 7 1 - 2 0 1 2 年
日本国実用新案登録公報	1 9 9 6 - 2 0 1 2 年
日本国登録実用新案公報	1 9 9 4 - 2 0 1 2 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)

JSTPlus/JMEDPlus/JST7580(JDreamII), PubMed, GeneCards

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	WO 2010/038904 A1 (国立大学法人鳥取大学) 2010. 04. 08 実施例 7、図 16 (ファミリーなし)	1-6 の一部

☒ 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

0 8 . 0 5 . 2 0 1 2

国際調査報告の発送日

2 2 . 0 5 . 2 0 1 2

国際調査機関の名称及びあて先

日本国特許庁 (I S A / J P)

郵便番号 1 0 0 - 8 9 1 5

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)

上 條 肇

4 B

9 4 5 3

電話番号 0 3 - 3 5 8 1 - 1 1 0 1 内線 3 4 4 8

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	JP 2010-523117 A(ホワイトヘッド・インスティテュート・フォー・ バイオメディカル・リサーチ) 2010.07.15 【0198】～【0234】段落 & US 2011/0076678 A1 & EP 2145000 A1 & WO 2008/124133 A1 & CA 2683056 A & MX 2009010847 A & ZA 200907185 A & CN 101932705 A & AU 2008236629 A	1-6 の一部
Y	JP 2010-528622 A(ザ ジェネラル ホスピタル コーポレイショ ン) 2010.08.26 【0070】～【0073】段落 & US 2010/0184051 A1 & EP 2164951 A2 & WO 2008/151058 A2 & CA 2688539 A & CN 101802172 A	1-6 の一部
Y	WO 2010/134388 A1(三原 誠) 2010.11.25 【0070】～【0072】段落 (ファミリーなし)	1-6 の一部
Y	RIPKA S. et al., Glutamate receptor GRIA3--target of CUX1 and mediator of tumor progression in pancreatic cancer., Neoplasia, 2010.08, Vol.12, No.8, p.659-667	1-6 の一部

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（P C T 17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P C T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ろの国際調査機関は認めた。
特別ページ参照

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ため、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ため、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。

請求項1～6に係る発明のうち、未分化状態のi P S細胞クローンにおいて、G R I A 3遺伝子について、発現レベルを調べる工程、を含むi P S細胞クローンの選択方法に係る発明

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。

第 III 欄の続き

請求項 1 及び請求項 1 を引用する請求項 2－6 は、「第 1 ～第 1 2 遺伝子群のいずれかの遺伝子群」として挙げられた、合計 2 4 9 2 個の遺伝子から択一的に選択される遺伝子のそれぞれについて、「未分化状態の i P S 細胞クローンにおいて、」「発現レベルを調べる工程、を含む」「i P S 細胞クローンの選択方法」である。

文献 1 には、未分化状態の i P S 細胞クローンにおいて、移入染色体を脱落させたサブクローンの中で、内在性未分化マーカーである N a n o g , O c t 3 / 4 , S o x 2 , R e x 1 の発現量を調べ、これら全ての未分化マーカーがコントロール i P S 細胞と同じレベルで発現しているより完全な未分化状態である細胞を選択する方法が記載されている（特に、実施例 7、図 16 参照）。

また、文献 2 には、未分化状態の一次 i P S 細胞クローンにおいて、Nanog-GFP 遺伝子、重鎖および軽鎖遺伝子の発現レベルを調べる工程、を含む二次 i P S 細胞クローンの選択方法が記載されている（特に、【0198】～【0234】段落表 1、表 2 参照）。

また、文献 3 には、細胞が多能性表現型に再プログラムされ、その後に細胞を培養し、X 染色体連鎖レポーターを発現する培養物から細胞のクローンが単離され、クローンが誘導多能性幹細胞を含むとされた後で、SSEA1、CD9、Nanog、Fbx15、Ecat1、Esg1、Eras、Gdf3、Fgf4、Cripto、Dax1、Zpf296、Slc2a3、Rex1、Utf1、および Oct4 からなる群より選択されうる幹細胞マーカーの発現に関してクローンの細胞を試験する段階を含む誘導多能性幹細胞を選択する方法が記載されている（特に、【0070】～【0073】段落参照）。

したがって、「未分化状態の i P S 細胞クローンにおいて、発現レベルを調べる工程、を含む i P S 細胞クローンの選択方法」であることを P C T 規則 1 3 . 2 における特別な技術的特徴とすることはできない。

そして、請求項 1 に記載された 2 4 9 2 種の i P S において発現レベルを調べる遺伝子は、配列テーブルに記載された遺伝子名からみて互いに共通する新規な化学構造を有しているとはいえない。

これら遺伝子は、i P S において発現する遺伝子である点で共通するものの、i P S において発現する遺伝子は、文献 1 ～ 3 に記載されているとおりであり、また、遺伝子が単に同一の供給源に由来するという関係だけでは発明の単一性を満たすのに十分ではない（「P C T 国際調査及び予備審査のためのガイドライン PCT/GL/ISPE/1」2004 年 3 月 25 日施行, 第 10 章単一性 10.58 事例 32

(<http://www.wipo.int/pct/en/texts/pdf/ispe.pdf> 参照)) から、この点を P C T 規則 13.2 における特別な技術的事項であるとするとはできない。

また、他に、P C T 規則 1 3 . 2 において特別な技術的特徴と考えられる共通の事項は存在しない。

そこで、請求項 1 の従属請求項について手数料の追加納付命令時点での特別な技術的特徴を判断すると、請求の範囲には 2 4 9 3 の発明（群）が含まれる。これらの各発明（群）の特別な技術的特徴は以下のとおりである。

（発明 1）請求項 1 ～ 6 に係る発明のうち、第 1 遺伝子群の第 1 番目の遺伝子に係る発明「未分化状態の i P S 細胞クローンにおいて、G R I A 3 遺伝子について、発現レベルを調べる工程、を含む i P S 細胞クローンの選択方法。」

（発明 2）請求項 1 ～ 6 に係る発明のうち、第 1 遺伝子群の第 2 番目の遺伝子に係る発明「未分化状態の i P S 細胞クローンにおいて、S T C 2 遺伝子について、発現レベルを調べる工程、を含む i P S 細胞クローンの選択方法。」

.....

(発明 2 4 9 2) 請求項 1 ～ 6 に係る発明のうち、第 1 2 遺伝子群の第 1 7 番目の遺伝子に係る発明「未分化状態の i P S 細胞クローンにおいて、T E X 1 5 遺伝子について、発現レベルを調べる工程、を含む i P S 細胞クローンの選択方法。」

(発明 2 4 9 3) 請求項 7 ～ 1 4 に係る発明

「正常に分化できないか、あるいは分化しても腫瘍化を起こしやすい複数の第 1 の i P S 細胞クローンと、腫瘍化を起こしにくい複数の第 2 の i P S 細胞クローンにおいて、未分化状態の各 i P S 細胞クローンで、1 以上の遺伝子を含む候補遺伝子群に属する遺伝子の発現レベルを調べる工程、を含む i P S 細胞クローンを選択するために発現レベルを調べる遺伝子の選択方法」

文献 1 : W O 2010/038904 A1 (国立大学法人鳥取大学) 2010. 04. 08

実施例 7、図 16

(ファミリーなし)

文献 2 : J P 2010-523117 A (ホワイトヘッド・インスティテュート・フォー・バイオメディカル・リサーチ) 2010. 07. 15

【0198】～【0234】段落

& U S 2011/0076678 A1 & E P 2145000 A1 & W O 2008/124133 A1 & C A 2683056 A

& M X 2009010847 A & Z A 200907185 A & C N 101932705 A & A U 2008236629 A

文献 3 : J P 2010-528622 A (ザ ジェネラル ホスピタル コーポレイション) 2010. 08. 26

【0070】～【0073】段落

& U S 2010/0184051 A1 & E P 2164951 A2 & W O 2008/151058 A2 & C A 2688539 A

& C N 101802172 A