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(54) Title: ALTERNATIVELY TRANSCRIBED GENES ASSOCIATED WITH SCHIZOPHRENIA

(57) Abstract: Methods of identifying gene targets associated with schizophrenia or the symptoms thereof, as well as to specific nucleic acid molecules that have been discovered to be associated with schizophrenia are provided. Accordingly, the invention also relates to methods of modulating schizophrenia or the symptoms thereof, methods of diagnosing schizophrenia or the symptoms thereof, methods for predicting the susceptibility to schizophrenia or the symptoms thereof, and methods of identifying compounds that modulate schizophrenia or the symptoms thereof via manipulations of the nucleic acid molecules and their products.



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ALTERNATIVELY TRANSCRIBED GENES ASSOCIATED WITH SCHIZOPHRENIA

FIELD OF INVENTION

[0001] This invention relates generally to schizophrenia and related disorders, and to methods for detecting gene targets associated with these disorders, to methods of predicting susceptibility to schizophrenia, to and methods of diagnosing schizophrenia, to methods of treating schizophrenia, as well as to the gene targets themselves.

BACKGROUND OF THE INVENTION

[0002] The term “schizophrenia” refers to a number of related disorders, and is characterized by a wide range of complex symptoms. Schizophrenia affects more than 1% of the population worldwide, and clinical symptoms include a constellation of positive symptoms (e.g., hallucinations, delusions, racing thoughts), negative symptoms (e.g., apathy, lack of emotion, poor or nonexistent social functioning), and cognitive symptoms (e.g., disorganized thoughts, difficulty concentrating and/or following instructions, difficulty completing tasks, learning and memory deficits). The illness usually develops between adolescence and age thirty. For some patients the disease is consistent and lifelong, whereas others may experience periodic episodes of psychosis.

[0003] Research in recent years has provided information necessary to understand some of the underlying neuropathology and etiology of schizophrenia, and has implicated dozens of genes, neurotransmitters, and neural microcircuits. Unlike other types of dementia, schizophrenia is not associated with visible neuropathological markers such as plaques, tangles, or Lewy bodies. The gliosis that is a marker of neuronal death in many neurodegenerative diseases is not present in schizophrenia. It has been suggested that the etiology and pathophysiology of schizophrenia are related to maturational or developmental brain processes such as the formation of neurites, synaptogenesis, neuronal pruning, or apoptosis.

[0004] Schizophrenia is thought to be the consequence of some combination of inherited genetic factors and external, non-genetic factors that affect the regulation and expression of genes controlling brain function, or that injure the brain directly. It is thought that the disease is likely polygenic with multiple susceptibility loci. Schizophrenia runs in families as indicated by twin and adoption studies which suggest that such familial aggregation is largely accounted for by genetic factors. These same studies, however, also

suggest that familial genetic transmission can only account for some of the cases of schizophrenia. For example, the concordance rate in monozygotic twins is about forty percent, indicating that non-genetic factors must play a role in development of the disease. Further, schizophrenia persists despite the fact that the majority of individuals with the disease do not marry or procreate.

[0005] Research with schizophrenia models has revealed, for example, a possible role for dopamine, glutamate, and serotonin in the development of schizophrenia (see, e.g., Geyer et al., *Psychopharmacology*, 156, 117-154, 2001). Proposal for treatment of schizophrenia with dopamine or dopamine precursors has also been suggested (see, e.g., U.S. Patent No. 7,115,256). In addition, many candidate genes have been identified from human postmortem brains using gene expression microarrays (see, e.g., Mirnics et al., *Trends in Neurosci.*, 24(8), 479-486, 2001; see also U.S. Patent No. 7,220,581). Some of the genes identified have been proposed for use in diagnosis of schizophrenia (see U.S. Patent No. 6,395,482).

[0006] Despite the wealth of information accumulated from years of research, the understanding of schizophrenia remains rudimentary. The neuropathological findings are controversial and not diagnostically useful, relevant genes have been difficult to identify, and treatment has not improved much over time. Current treatments have inadequate efficacy, and often are associated with intolerable side effects which can lead to discontinuation of treatment by patients.

[0007] There is therefore a strong need to identify genes involved in schizophrenia, genes that are useful as biomarkers for diagnosing schizophrenia, as well as for methods that can detect such gene targets so they can be utilized in screening therapeutics, in diagnosing schizophrenia, and in developing treatments for individuals with schizophrenia. There is also a great need for new biomarkers and methods for detecting susceptibility to schizophrenia, as well as for preventing or following up development of the disease. Diagnostic tools could prove extremely useful, as early identification of subjects at risk of developing schizophrenia would enable early intervention and/or prophylactic treatment to be administered. A need therefore exists for new methods and reagents to more accurately and effectively diagnose and treat schizophrenia.

SUMMARY OF THE INVENTION

[0008] As used herein, schizophrenia encompasses any of the many disorders that are characterized by psychosis as a core or fundamental feature. The term schizophrenia refers to schizophrenia, schizophreniform disorder, schizoaffective disorder, schizotypal disorder, schizoid personality disorder, schizotypal personality disorder, delusional disorder, brief psychotic disorder, shared psychotic disorder, psychotic disorder due to a general medical condition, substance-induced psychotic disorder, and psychotic disorder not otherwise specified, as defined in the DSM-IV, DSM-IV-TR, or any other diagnostic criteria. Further, as used in the invention, schizophrenia can refer to the different schizophrenia subtypes, including the paranoid type, the disorganized type, the catatonic type, the undifferentiated type, and the residual type, as well as the symptoms associated with these aspect of the disorders. All possible symptoms of these disorders are also within the scope of the invention, and are encompassed by the term, schizophrenia.

[0009] In one embodiment of the invention, methods are provided for identifying gene targets that are associated with schizophrenia or with the symptoms of schizophrenia. Animal models (using living animals) of schizophrenia are utilized, and initiated, and from tissue obtained from at least one of those animals, transcriptional regulation is assessed over time, relative to the onset of the schizophrenia model. Initiating an animal model refers to the onset of the manipulation that induces the schizophrenia model, whether it is a behavioral, biological, or genetic manipulation, drug administration, or any other manipulation which yields a model of schizophrenia. In some embodiments, it is useful to measure gene expression from animals at time points after, and, optionally, before the initiation of the model and to compare the gene expression from before and after initiation. In some embodiments, it is useful to compare the gene expression, whether from before or after the initiation of the model, or both, to gene expression at one or more time points from control animals, which are not subject to a schizophrenia model. Transcripts are then detected which are dysregulated in tissue from animals that are a model of schizophrenia. Any change in gene expression observed in the schizophrenia model, whether relative to other time points in the same model, relative to another schizophrenia model, or relative to the same time point or time points in control animals can be informative with respect to gene targets for schizophrenia or the symptoms of schizophrenia.

[0010] Systems for carrying out all of the methods described herein are also provided, and optionally comprise a computer system and related software. For example, as relates to

the foregoing method, the system may comprise groups of mice in which an animal model of schizophrenia in living animals has been initiated, and a computer system comprising software, said computer system configured to assess transcriptional regulation in tissue over time in animals that are a model of schizophrenia, wherein the tissue is sampled one or more times after the initiation of the model and optionally one or more times prior to the initiation of the model; compare the transcriptional regulation from prior to initiation of the model with transcriptional regulation from after the initiation of the model, and/or with transcriptional regulation assessed from tissue in living animals not subject to a schizophrenia model; and detect a transcript that is dysregulated in tissue from animals that are a model of schizophrenia. Optionally, the computer system may output a result which is indicative of gene targets associated with schizophrenia or schizophrenia symptoms.

[0011] In some embodiments, transcriptional regulation in the animal model is compared with transcriptional regulation of genes that have previously been identified as associated with schizophrenia or the symptoms thereof. Matching the regulation with these genes with newly identified genes can be informative in identifying new transcripts or known genes which have not been previously identified as associated with schizophrenia or the symptoms of schizophrenia.

[0012] Any model of schizophrenia, whether pharmacological or non-pharmacological, can be used in accordance with the methods of the invention, though in preferred embodiments, the model is the isolation rearing model or the maternal deprivation model

[0013] In some embodiments, the methods for screening for schizophrenia targets relate to gene expression products and the changes observed with respect to those gene expression products.

[0014] In another embodiment of the invention, nucleic acid sequences identified according to the screening methods of the invention are provided. In yet another embodiment, the invention provides nucleic acid sequences that comprises at least SEQ ID NO:1 through SEQ ID NO:16.

[0015] In other embodiments, the invention relates to methods for predicting the susceptibility to schizophrenia or the symptoms of schizophrenia. According to the methods of this invention, an individual provides a biological sample, and from this sample, gene expression or the products of gene expression are measured. The gene or genes measured

include those that have been identified as “pre-symptomatic genes,” described herein, which are associated with circumstances that exist prior to the onset of schizophrenia, and predict the onset of schizophrenia or symptoms associated with schizophrenia. When dysregulation of one or more of these genes is detected, it is informative of the likelihood that schizophrenia or its symptoms will be present in that individual.

[0016] In some embodiments, the pre-symptomatic genes have not been previously identified as being associated with schizophrenia, or as being predictive of the susceptibility to schizophrenia or the symptoms of schizophrenia. In another embodiment, the genes assessed are chosen from among interferon-induced protein, interferon regulatory factor 7, and PKR. In yet another embodiment, the genes assessed are chosen from one or more of SEQ ID NO: 11 through SEQ ID NO: 16.

[0017] In some embodiments, the individual providing the biological sample possesses at least one risk factor for schizophrenia. In other embodiments, the individual is asymptomatic, and in yet other embodiments, the individual presents with one or more symptoms of schizophrenia, but is not clinically diagnosed with schizophrenia.

[0018] In another embodiment, the invention provides methods for diagnosing schizophrenia or the symptoms of schizophrenia. An individual provides a biological sample, and from this sample, gene expression or the products of gene expression is measured. The genes measured include those that have been identified as “symptomatic genes,” described herein, which are associated with schizophrenia or the symptoms of schizophrenia. When dysregulation of one or more of these genes is detected, it is diagnostic of the presence of schizophrenia or its symptoms in that individual.

[0019] In some embodiments, the symptomatic genes have not been previously identified as being associated with schizophrenia, or the symptoms of schizophrenia. In another embodiment, the genes assessed are chosen from among SEQ ID NO:1 through SEQ ID NO: 16.

[0020] In some embodiments, the individual to be diagnosed presents with symptoms or other signs which aid in the diagnosis of schizophrenia. In other embodiments, the diagnosis is aided by other clinical, behavioral, or biological assessment tools.

[0021] In yet another embodiment of the invention, methods for preventing schizophrenia or the symptoms of schizophrenia are provided. The gene targets obtained according to the invention, or which are described herein are upregulated or downregulated,

or the products of the gene targets are increased or decreased. The nature of the dysregulation of the gene associated with the onset of schizophrenia will inform whether to upregulate or downregulate gene expression, or whether to increase or decrease gene expression products. In some embodiments the method for preventing schizophrenia or the symptoms of schizophrenia are performed in conjunction with other methods for preventing schizophrenia or its symptoms. In some embodiments, more than one gene or its expression product is modulated.

[0022] In yet another embodiment of the invention, methods for treating schizophrenia or the symptoms of schizophrenia are provided. The gene targets obtained according to the invention, or which are described herein are upregulated or downregulated, or the products of the gene targets are increased or decreased. The nature of the dysregulation of the gene associated with schizophrenia will inform whether to upregulate or downregulate gene expression, or whether to increase or decrease gene expression products. In some embodiments the method for treating schizophrenia or the symptoms of schizophrenia are performed in conjunction with other treatments for schizophrenia or its symptoms, including any behavioral and drug therapies. In some embodiments, more than one gene or its expression product is modulated.

[0023] In another embodiment, a method is provided of preventing or treating schizophrenia, or the cognitive deficits associated with schizophrenia by administering midkine to an individual in need. As described herein, midkine has positive effects on symptoms of schizophrenia, and its administration can be a beneficial treatment for the disorder, or the symptoms of the disorder.

[0024] Another embodiment of the invention provides a method for screening compounds for their ability to increase or decrease the activity of one or more of the gene targets associated with schizophrenia or the symptoms of schizophrenia. By utilizing animal models of schizophrenia as described herein, and assessing dysregulation of genes associated with schizophrenia, it can be determined which compounds have an influence on this dysregulation. Gene expression can be assessed prior to and after compound administration in a model of schizophrenia, along with assessment of behavioral and biological manifestations. Changes in gene expression or gene expression products can be meaningful with respect to those compounds as potential therapeutics for schizophrenia or the symptoms of schizophrenia.

[0025] In another embodiment of the invention, pharmaceutical compositions are provided. The pharmaceutical compositions may comprise one or more of the nucleic acids obtained from the methods of the invention, or as described by the invention. The pharmaceutical compositions may also comprise agonists and antagonists of one or more of the genes described in the invention, in order to treat schizophrenia or the symptoms of schizophrenia.

[0026] These and other aspects of the invention may be more clearly understood by reference to the following detailed description of the invention and the appended claims.

BRIEF DESCRIPTION OF THE FIGURES

[0027] FIGS. 1A-1B: Influence of isolation rearing and maternal deprivation on sensorimotor gating in male Wistar rats. Isolation reared animals (n=7-8/group) were raised in single perspex cages from weaning on postnatal day (P) 25. Maternally deprived animals (n=7-8/group) were isolated from their mothers for a single 24-hour period on P9. At the end of the 24-hour period the dams were returned to their litters and left undisturbed until weaning on P25. After weaning on P25 pups were housed in groups of 3-4 per cage. For both models, separate cohorts were analyzed at P30, P40, P60 and P80. Panel A: All isolation reared animals are compared to age-matched social controls (raised in cages of 3-4 from weaning, ns=8/group). Isolated animals exhibited impaired sensorimotor gating (as measured by prepulse inhibition), when analyzed at P60 ($F[1,56]=15.38$; $p=0.0002$). This deficit was maintained at P80 ($F[1,52]=17.35$; $p=0.0001$). Closed circles represent isolation-reared rats; open circles represent social controls. Panel B: All maternally deprived animals are compared to age-matched controls not maternally deprived (raised in cages of 3-4 from weaning, ns=8/group). Maternally deprived animals did not exhibiting a significant difference in prepulse inhibition compared to controls. Data were analyzed using the two-way ANOVA statistical test. Closed circles represent maternally deprived rats; open circles represent non-deprived controls. Db =decibels.

[0028] FIGS. 2A-2B: Influence of isolation rearing and maternal deprivation on spatial learning in male Wistar rats. Isolation reared animals (n=7-8/group) were raised in single perspex cages from weaning on postnatal day (P) 25. Maternally deprived animals (n=7-8/group) were isolated from their mothers for a single 24-hour period on P9. At the end of the 24-hour period the dams were returned to their litters and left undisturbed until weaning on P25. After weaning on P25 pups were housed in groups of 3-4 per cage. For

both models, separate cohorts were analyzed at P30, P40, P60 and P80 in a water maze. Panel A: All isolation reared animals are compared to age-matched social controls (raised in cages of 3-4 from weaning, $n=8/\text{group}$). Isolated animals exhibited impaired spatial learning when analyzed at P60 ($F[1,19]=36.80$; $p<0.0001$). Closed circles represent isolation-reared rats; open circles represent social controls. Panel B: All maternally deprived animals are compared to age-matched controls not maternally deprived (raised in cages of 3-4 from weaning, $n=8/\text{group}$). Maternally deprived animals exhibited impaired spatial learning when analyzed at P60 ($F[1,19]=5.29$; $p=0.0222$). Data were analyzed using the two-way ANOVA statistical test. Closed circles represent maternally deprived rats; open circles represent non-deprived controls.

[0029] FIGS. 3A-3C: Expression of unknown genes in the prefrontal cortex demonstrated by the microarray studies to co-dysregulate with known genes in the medial prefrontal cortex of isolation-reared animals. The known genes are of interest as they are already implicated in schizophrenia-related biology. The unknown ESTs were selected on the basis of their common pattern and, in particular, their substantial up-regulation at P60. Values are represented relative to social controls.

[0030] FIGS. 4A-4C: Genes that relate to reelin-Lis1-DISC1 signaling show altered expression in the medial prefrontal cortex of isolation reared animals. Panel A: The inter-relationship between reelin-, Lis1- and DISC1-associated genes. Genes in the shaded circles were dysregulated in the isolation reared animals. Panel B: The altered expression of Lis1 at mRNA level as indicated by the microarray. Panel C: confirmation of change in Lis1 expression by quantitative real time PCR. Open circles represent socially reared controls and closed circles and filled bars represent isolation-reared animals.

[0031] FIGS. 5A-5F: Genes that relate to GABAergic transmission and synaptic structure show altered expression in the medial prefrontal cortex of isolation-reared animals. Panels A, C and E: The altered expression of GABAA receptor alpha4, complexin I and synapsin II, respectively, at mRNA level as indicated by the microarray. Panels B, D and F: Confirmation of change in GABAA receptor alpha4, complexin I and synapsin II, respectively, expression by quantitative real time PCR. Open circles and clear bars represent socially-reared controls and closed circles and filled bars represent isolation reared animals.

[0032] FIG. 6: Interferon-related gene dysregulation in the medial prefrontal cortex of socially isolated, maternally deprived, and social control animals. Panel A: Interferon-

induced protein with tetratricopeptide repeats 2; Panel B: Interferon regulatory factor 7; Panel C: PKR.

[0033] FIG. 7: Expression of unknown genes in the prefrontal cortex demonstrated by the microarray studies to co-dysregulate with known genes in the medial prefrontal cortex of maternal deprived animals. The known genes are of interest as they are associated with interferon signaling and, thus, viral infection. Maternal viral infection is associated with increased risk of schizophrenia in the unborn child. The unknown ESTs were selected on the basis of their common pattern and, in particular, their substantial up-regulation at P30. Values are represented relative to social controls.

[0034] FIGS. 8A-8B: Influence of prior environmental manipulation on basal dopamine, glutamate and GABA levels in the medial prefrontal cortex of mature Wistar rats on postnatal day 80. Panel A: The concentration of neurotransmitter in dialysate samples collected over a 300 min period is illustrated. Values for social animals (SC; unfilled columns) are compared to those reared in isolation (IR; shaded columns) or with prior maternal deprivation (MD; filled columns) and expressed as the mean and SEM. Those values significantly different ($p < 0.05$) from the control group are indicated with an asterisk. Panel B: Shows the track left by the microdialysis probe with the position of the dialysis membrane indicated with arrowheads.

[0035] FIGS. 9A-9C: Consequence of prior environmental manipulation on parvalbumin cell density in the medial prefrontal cortex. Values for social animals (SC; unfilled columns) and those reared in isolation (IR; shaded columns) or with prior maternal deprivation (MD; filled columns) are shown as the mean and SEM and values significantly different from social controls ($p < 0.05$) are indicated with asterisks (* one-tailed t-test; ** two-tailed t-test).

[0036] FIGS. 10A-10B: Consequence of prior environmental manipulation on synapse density in the medial prefrontal cortex in animals on postnatal day 80. Values for social animals (SC; unfilled columns) and those reared in isolation (IR; shaded columns) or with prior maternal deprivation (MD; filled columns) are shown as the mean and SEM and values significantly different from social controls ($p < 0.05$) are indicated with asterisks (* one-tailed t-test; ** two-tailed t-test).

[0037] FIG. 11: Midkine can reverse isolation rearing-induced sensory processing deficits. Isolation reared animals exhibit a significant deficit in prepulse inhibition (PPI) of

startle. Four daily ICV injections of Midkine (2 μ g/day; filled circles) reversed PPI behavior back to normal compared to vehicle-treated animals (open circles) (Two-way ANOVA, $p < 0.05$ for treatment).

DETAILED DESCRIPTION OF THE INVENTION

[0038] This invention relates to nucleic acid molecules and their products which have been discovered to be associated with schizophrenia and related disorders and the symptoms thereof via screening methods of the invention, which are described herein. Accordingly, this invention also relates to methods of diagnosing schizophrenia as well as to methods of predicting the susceptibility of an individual to developing schizophrenia and related disorders. This invention also relates to methods of identifying compounds that modulate schizophrenia or the symptoms thereof via manipulations of the nucleic acid molecules and their products. Accordingly, the invention also relates to methods of modulating symptoms of schizophrenia and to treating schizophrenia and related disorders or the symptoms thereof. The invention also relates to methods of treating schizophrenia or the symptoms thereof with midkine.

[0039] The term “schizophrenia” as used herein encompasses many different mental disorders characterized by psychosis as a core or fundamental feature, including, but not limited to those that are outlined in the Diagnostic and Statistical Manual of Mental Disorders, Fourth Edition (DSM-IV; or the DSM-IV–Text Revision (TR)), or any other diagnostic sources used by mental health care professionals, as well as the individual features and symptoms of the disorders. As used herein, schizophrenia refers to schizophrenia; schizophreniform disorder; schizoaffective disorder (including the bipolar type and the depressive type); schizotypal disorder; schizoid personality disorder; schizotypal personality disorder; delusional disorder (including the erotomaniac type, the grandiose type, the jealous type, the persecutory type, and somatic type, the mixed type, and the unspecified type); brief psychotic disorder (with or without marked stressors, including with postpartum onset); shared psychotic disorder; psychotic disorder due to a general medical condition (including with delusions or hallucinations); substance-induced psychotic disorder (including with delusions or hallucinations, with onset during intoxication, and with onset during withdrawal); and psychotic disorder not otherwise specified, as defined in the DSM-IV, DSM-IV-TR, or any other diagnostic criteria. Further, as used in the invention, schizophrenia encompasses the different schizophrenia subtypes, and various psychotic disorders, including, without limitation, the paranoid type, the disorganized type, the

catatonic type, the undifferentiated type, and the residual type, as well as the symptoms associated with these aspect of the disorders and other psychotic disorders.

[0040] All possible symptoms of schizophrenia and related disorders are within the scope of this invention, and are included with the use of the term, schizophrenia. The characteristic symptoms of psychosis and schizophrenia include a range of behavioral, cognitive and emotional dysfunctions that include alterations in perception, inferential thinking, language and communication, behavioral monitoring, affect, fluency and productivity of thought and speech, hedonic capacity, volition and drive, and attention. No single symptom is pathognomonic of the diseases, but rather the diagnosis includes the recognition of a constellation of signs and symptoms that are associated with impaired occupational and/or social functioning.

[0041] In a clinical evaluation, schizophrenia is commonly marked by two broad categories: positive symptoms and negative symptoms, which are encompassed by the invention. Positive symptoms of schizophrenia and related disorders reflect an excess or distortion of normal functions and include distortions in thought content (delusions), perception of reality (hallucinations, which can be auditory, visual, olfactory, gustatory, and/or tactile), language and thought process (disorganized speech), and self-monitoring of behavior (grossly disorganized and catatonic behavior).

[0042] The negative symptoms of schizophrenia are a class of symptoms of schizophrenia which can be considered to reflect a loss or diminution of normal functions. Negative symptoms of schizophrenia and related disorders include affective flattening (characterized by, for example, an immobile and/or unresponsive facial expression, poor eye contact and reduced body language), alogia ('poverty of speech' or brief, laconic and/or empty replies), avolition (characterized by a reduced or absent ability to initiate and carry out goal-directed activities), anhedonia (loss of interest or pleasure), social withdrawal, apathy and other negative symptoms known to those of skill in the art.

[0043] The positive and negative symptoms of schizophrenia may be assessed using any methodology known in the art including, but not limited to, the Brief Psychiatric Rating Scale (BPRS), the Positive and Negative Symptom Scale (PANSS), the Rorschach Schizophrenia Index (SCZI), and the Scale for the Assessment of Negative Symptoms (SANS), and the Scale for the Assessment of Positive Symptoms (PANS).

[0044] Utilizing animal models of schizophrenia, the inventors have observed particular patterns of gene expression which are diagnostic of the disease, and have observed particular patterns of gene expression in the same animal models which are predictive of developing the disease, using the screening methods of the invention. The inventors have discovered a group of previously unknown nucleic acids that are useful for diagnosing schizophrenia. They have also discovered a group of previously identified genes as newly associated with schizophrenia and the symptoms thereof.

[0045] As used herein, measuring gene expression refers to detecting any nucleic acid sequence, gene, gene fragment, gene transcript, expressed sequence tags (ESTs) and the like, and are all encompassed by the invention in all aspects.

[0046] In one embodiment of the invention, methods for identifying gene targets associated with schizophrenia or the symptoms thereof are provided. Transcriptional regulation is assessed over time in tissue obtained from live animals that are a model of schizophrenia. In some embodiments, only one group of animals is used. When at least two groups of animals are utilized, one of the groups serves as a control group which has not been manipulated or is not an animal model of schizophrenia. Each group contains at least one animal. Gene expression is assessed at different time points relative to the schizophrenia model utilized, and values are compared to those of control animals to determine which transcripts are associated with schizophrenia. For example, with respect to the social isolation model, gene expression may be measured at time points prior to isolation, throughout the isolation period, and after the isolation period, and at the same developmental time points in control animals. In some instances, gene expression is measured prior to the onset of the schizophrenia model, and at times after the model is initiated, so that animals can serve as their own control group, and gene expression after the model onset is compared with gene expression prior to the model onset. In some embodiments, more than two groups of animals are utilized, such that gene expression can be compared among a control group and different models of schizophrenia. The ultimate comparison, whether between a control group and schizophrenia model group, or within a group, prior to and after the onset of the schizophrenia model, is a change in gene expression. The nature of the changes in gene expression assessed are described further herein. Any change in gene expression at any time point can be informative with respect to a gene target's role in schizophrenia or the symptoms thereof.

[0047] In some embodiments, gene expression products, rather than gene expression is measured and applied to the same methods described herein, and can be equally informative with respect to what genes and their products are associated with schizophrenia or the symptoms thereof, and which may serve as useful targets.

[0048] Any animal model of schizophrenia known in the art is contemplated for use with the methods of the invention, including pharmacological and non-pharmacological models, and models utilizing neurodevelopmental manipulations, as well as manipulations performed prior to birth and genetic manipulations. In a preferred embodiment, the animal model is the social isolation rearing model, which is a widely used, recognized, and validated schizophrenia model (e.g., Geyer et al., *Biol. Psychiatry*, 34, 361-372, 1993). Social isolation rearing comprises housing an animal in a cage by itself from the time of weaning, and for the duration of experimental procedures. This model can be applied to any species of animal for experimental purposes, all of which are encompassed by the invention. Social isolation rearing leads to a number of behavioral and neurobiological changes which are consistent with typical schizophrenia-related deficits that are observed in schizophrenic patients. As provided in the Examples herein, the inventors have illustrated the power of this model by demonstrating substantial deficits in pre-pulse inhibition, which is a widely used measure of sensorimotor gating, as well as deficits in spatial memory, and, among other things, a reduction in glutamate and parvalbumin cell density in the prefrontal cortex.

[0049] Any animal is contemplated in the methods of the invention, though preferably the animal is a mammal. The mammal can include, but is not limited to rodents, including mice, rats, hamsters, voles, guinea pigs, squirrels, prairie dogs, marmots, and gophers. Also within the scope of the invention are non-human primates and avian species. In some embodiments of the invention, humans that either have schizophrenia or the symptoms thereof, or that do not have schizophrenia or the symptoms thereof, or are at risk for developing schizophrenia or the symptoms thereof can provide tissue samples for assessment of gene expression or gene expression products.

[0050] Prepulse inhibition reflects a mechanism that allows an individual to filter incoming sensory information such that irrelevant external stimuli are ignored, and important stimuli are attended to (Van den Buuse et al., *Curr. Mol. Med.*, 3, 459-471, 2003). Schizophrenia patients have fundamental deficits in attention and sensory information processing, and these deficits are reflected in prepulse inhibition deficits observed in these patients. These deficits can be reversed in schizophrenia patients by administering, for

example, antipsychotic drugs. Prepulse inhibition is a robust phenomenon observed across many species, including humans and rodents, so that it has become a widely used tool in studies of schizophrenia, and a widely accepted means of validating animal models of schizophrenia (Van den Buuse et al., *Curr. Mol. Med.*, 3, 459-471, 2003).

[0051] In another preferred embodiment, the animal model is the maternal deprivation model, which includes separating the animals from their mothers for a distinct period of time prior to weaning (e.g., Ellenbroek et al., *Schizophr. Res.*, 30(3), 251-260, 1998). For example, rat pups are isolated from their mothers for a single 24-hour period on postnatal day 9, after which they are returned to their mothers until weaning. This model is also well accepted as a neurodevelopmental model for schizophrenia, leading to pharmacological and behavioral indicators of schizophrenia. As observed in the social isolation model, prefrontal hyperglutamatergia was observed in maternally deprived animals. In addition, maternally deprived animals exhibited a non-statistically significant decrement in pre-pulse inhibition. Without being bound by theory, it is believed that compensatory mechanisms in the maternal deprivation model may prevent full emergence of schizophrenic symptoms. In this regard, it is interesting to note that in addition to the hypoglutamatergia, maternally deprived animals also exhibit a concomitant prefrontal hypergabergia which could represent a component of this proposed protection adaptation facilitating normal sensorimotor function. Importantly, treatment of the maternally deprived animals with the anti-psychotic clozapine actually unmasks a PPI deficient and normalises the GABA levels in the prefrontal cortex further supporting the hypothesis that high GABA levels in the maternal deprivation animals may indeed represent some form of compensation mechanism that restores normal mPFC function even in the presence of low glutamate.

[0052] Pharmacological models of schizophrenia are also contemplated by the invention, including those which are based on alterations in the dopamine, GABA, glutamate, and serotonin systems (Van den Buuse et al., *Curr. Mol. Med.*, 3, 459-471, 2003). Also contemplated by the invention are models which involve neonatal brain lesions of the hippocampus, the amygdala, the frontal cortex, and any other brain region with a potential role in schizophrenia or the symptoms thereof, as well as prenatal and neonatal infection models and other prenatal and neonatal models such as early exposure to anesthetics, cannabinoids, epidermal growth factor, and ethanol (Van den Buuse et al., *Curr. Mol. Med.*, 3, 459-471, 2003).

[0053] One example of a pharmacological model encompassed by the invention is the phencyclidine (PCP) model of schizophrenia, which suggests that N-methyl--aspartate (NMDA) receptor hypofunction and its consequences may play an important role in the pathophysiology of schizophrenia (e.g., Jentsch and Roth, *Neuropsychopharmacology*, 20(3), 201-225, 1999). The schizophreniform psychosis caused by PCP resembles schizophrenia in all of the relevant domains of psychopathology, especially with respect to the negative symptoms and cognitive dysfunction. In this model, animals are administered PCP or an analogue via systemic injection, and within thirty minutes, symptoms are apparent. This model is often utilized in rodents and non-human primates, but humans that abuse the drug may also be considered within the scope of the invention. Another pharmacological model used is ketamine administration, which antagonizes NMDA receptors and its administration is thought to resemble the psychotic state, and in particular, the delusions associated with schizophrenia, and to provide a window to the early stages of the disease process (e.g., Lahti et al., *Neuropsychopharmacology*, 13, 9-19, 1995).

[0054] In some embodiments of the invention, transcriptional regulation is assessed from brain tissue. Many brain regions are implicated in schizophrenia and the symptoms thereof, which are all contemplated as useful in the methods of the invention (e.g., Pinkham et al., *Schizophr. Res.*, 2007). These brain regions include, but are not limited to the prefrontal cortex, anterior cingulate gyrus, hippocampus, the cortex, neocortex, amygdala, striatum, caudate nucleus, temporal lobes, corpus callosum, and cerebellum. These regions, among others, can all be used to assess for transcriptional regulation prior to, during, and after the manipulation which initiates the schizophrenia model. In a preferred embodiment, the brain tissue assessed is from the medial prefrontal cortex. It is also contemplated by the invention that transcriptional regulation can be assessed from other tissue including without limitation, blood, plasma, lymph, urine, mucus, sputum, saliva, CSF, or tissue from other organs of the body.

[0055] Depending on the schizophrenia model utilized with the methods of the invention, transcriptional regulation is assessed from tissue at various time points relative to the induction of the model. In embodiments using the social isolation model, for example, transcriptional regulation may be assessed at one or more time intervals prior to (for baseline comparisons) and following isolation (e.g., postnatal day 25) in experimental animals, and at the same or different time intervals for socially-reared control animals. Gene expression is measured in all groups of animals, for ultimate comparison to the gene expression of control

animals. Gene expression that varies in the schizophrenia model as compared to the control animals is indicative of potential relevance of the transcript or its products' role in schizophrenia. Changes in gene expression observed prior to symptom onset in that particular model can be informative with respect to prodromal gene markers, and changes in gene expression concurrent with or following the presence of symptoms in the model used can be informative with respect to diagnostic markers of the disease.

[0056] In some embodiments of the invention, expression of genes that have previously been identified as associated with schizophrenia or the symptoms of schizophrenia are particularly useful, as changes in their regulation relative to control animals can be informative with respect to identifying novel transcripts or other genes that are newly identified as associated with schizophrenia. Changes in known genes previously identified as associated with schizophrenia at particular time points can be used to match with unknown transcripts, or with genes not previously associated with schizophrenia, thereby indicating a role for those transcripts or genes in schizophrenia.

[0057] Therefore, the expression of the new transcripts (or newly associated genes or transcripts) that are identified as regulated following the onset of the schizophrenia model are compared with the expression genes previously identified as being associated with schizophrenia or the symptoms thereof at the same time points. The previously identified genes can be chosen from any gene or transcript that has been previously associated with schizophrenia. For example, they can include, but are not limited to, complexin 1, GABAAR α 4, synapsin 2, parvalbumin, Lis-1, DISC1, DISC2, DIS1 reelin, neuregulin-1, COMT, dysbindin, G72, G30, DTNBP1, DAO, DAOA, brain-derived neurotrophic factor, Akt, DAAO, GRIN2B, RGS4, GRM3, calcineurin, α -7 nicotinic receptor gene, PRODH2, CAPON, TRAR, PPP3CC, midkine, transthyretin, USAG-1, and eNNP2.

[0058] In one embodiment, the average temporal pattern of the genes previously identified as associated with schizophrenia is used as a "seed pattern" and all regulated genes are ranked for their similarity to this pattern based on the time points and amplitude as described herein. This seed pattern may include 2 or more previously identified genes. In some embodiments of the invention, the seed pattern may include 5 or 10 identified genes, and in some embodiments it may include 20, 30, 50, 100, 200, 500, 1000 or more previously identified genes. In one embodiment, the top 100 matches to the seed pattern are chosen as the transcripts with the strongest relevance for schizophrenia. In another embodiment, the top 50 matches to the seed pattern are chosen as the transcripts with the strongest relevance

for schizophrenia. In yet another embodiment, the top 25 matches to the seed pattern are chosen as the transcripts with the strongest relevance for schizophrenia.

[0059] Any detectable change in amplitude of gene expression is included as meaningful for identifying transcripts associated with schizophrenia or the symptoms thereof. The change in amplitude of gene expression may be an upregulation or downregulation. Any degree of change in amplitude may be relevant and within the scope of this invention provided such change is sufficiently correlated with development of or expression of schizophrenic symptoms. Such changes in amplitude may, without limitation be a change of 1%, 10%, 50%, or 100%, and in some embodiments the change in amplitude of gene expression may be 3-fold, 5-fold, 10-fold, 20-fold, 50-fold, 100-fold or greater. In some embodiments, no change in gene expression at one or more of the assessed time points may be meaningful, particularly in the context of gene expression at nearby time points, and is within the scope of this invention. The change in expression can be either an increase or a decrease from baseline expression, or it may be an increase or decrease in gene expression relative to the gene expression at other time points within the temporal pattern, or it can be an increase or decrease relative to control animals at the same time point. The gene transcripts identified according to the methods of the invention are indicative of their role in schizophrenia. Compounds that increase or decrease the activity of the genes, gene fragments, and gene products identified as targets associated with schizophrenia using the methods of the invention described above, may also be drug candidates for modulating schizophrenia or its symptoms, or for preventing or delaying the onset of schizophrenia.

[0060] Changes in gene expression over any period of time relative to the onset of schizophrenia model used are within the scope of this invention and may vary greatly depending on the species that is evaluated and the model that is used. In some embodiments, depending on the model utilized, the gene expression is regulated within 6 months of the onset of the model. In another embodiment, the gene expression is regulated within one week of the onset of the model. In another embodiment, the gene expression is regulated within one month of the onset of the model. In yet another embodiment, the gene expression is regulated within two months of onset of the model, and in some embodiments, the gene expression is regulated within three months of the onset of the schizophrenia model. In another embodiment, the gene expression is regulated 10 minutes, 20 minutes, 30 minutes, one hour, two hours, four hours, six hours, or twelve hours after the onset of the model. In some embodiments the gene expression is regulated within one year of the onset of the

model, within five years of the onset of the model, or within ten or more years of the onset of the model.

[0061] For example, when utilizing the social isolation rearing model of schizophrenia, measurement of gene expression or the products thereof can be performed prior to isolation and at postnatal days 30, 40, 60, and 80. When utilizing the maternal deprivation model of schizophrenia, measurement of gene expression can be performed, for example prior to deprivation and at postnatal days 30, 40, 60, and 80. As another example, when the schizophrenia model is PCP, gene expression may be measured prior to drug administration, and 10, 20, 30, 60, and 120 minutes after drug administration. In humans, in the case of a drug-induced psychosis, for example, gene expression or the products thereof may be measured prior to drug administration and at 10, 20, 30, 60, and 120 minutes after drug administration, as well as up to several days and months following drug administration. As another example, in humans, after an early life stressor which may lead to schizophrenia or the symptoms thereof, gene expression or the products thereof may be measured within hours of the event, prior to the event, and after 1, 2, 3, 4, 5, 6, 12, and 24 months after the event, as well as up to 10, 20, and 30 years after the stressful event.

[0062] In some embodiments of the invention, gene expression products are assessed relative to the schizophrenia model or models utilized, and amplitude and time points comparisons are carried out as described herein for gene expression. According to the invention, gene expression products include any products which have been or may be determined to be associated with, or be capable of modulating schizophrenia or the symptoms thereof, but are not limited to proteins, peptides, or nucleic acid molecules (e.g., mRNA, tRNA, rRNA, or cRNA) that are involved in transcription or translation.

[0063] In one embodiment, the social isolation rearing model is used in rats, and gene expression is measured from the prefrontal cortex in rats that undergo isolation, as well as in control, socially reared animals at postnatal days 30, 40, 60, and 80. In some embodiments, mRNA of at least one or more of complexin 1, GABAAR α , synapsin 2, parvalbumin, and the genes from Figures 11 through 14 are measured at the time points indicated. In other embodiments, mRNA of at least one or more of interferon-induced protein, interferon regulatory factor 7, PKR, Ifi44, Ifit2, Irf7, Isgf3g, G1p2, Mx1, Mx2, and SEQ ID NO: 1 through SEQ ID NO: 16 are measured at the time points indicated.

[0064] According to the methods of the invention, gene expression levels may be detected by methods known to those skilled in the art and may be obtained, for example using any apparatus that can measure gene expression levels which are widely known in the art. The nucleic acid molecule levels measured can be derived directly from the gene or, alternatively, from a corresponding regulatory gene. All forms of gene expression products can be measured, including, for example, spliced variants. Similarly, gene expression can be measured by assessing the level of protein or derivative thereof translated from mRNA. This may, however, also reflect posttranslational modifications and other forms of processing. If the gene expression assessed is at the mRNA level, it can, for example, also be measured by in situ hybridization, Northern blot analysis, dot-blot hybridization analysis, microarray analysis, or by PCR. Such methods are described in detail, for example, in Ausubel et al., *Current Protocols In Molecular Biology* (New York: John Wiley & Sons) (1998); and Sambrook et al., *Molecular Cloning: A Laboratory Manual*, 2nd edition (New York: Cold Spring Harbor University Press (1989).

[0065] In another embodiment of the invention, gene expression levels can be obtained by contacting the sample of interest with a suitable microarray, and determining the extent of hybridization of the nucleic acid in the sample to the probes on the microarray. It is also contemplated by the invention that gene expression assessed by methods such as microarray can be validated by using quantitative real-time PCR analysis at the time points determined to be relevant from the temporal profile of gene expression observed. It will be apparent to those skilled in the art that any methodology that can be utilized for measuring gene expression will be suitable for use in the invention. Microarray analysis and PCR analysis can be carried out according to the Examples described herein, or by any of the available methods known in the art (see, e.g., Avison, *Measuring Gene Expression*, Taylor & Francis Group, NY, NY, 2007).

[0066] If the gene expression product is a protein or polypeptide, transcriptional regulation can be measured using techniques for protein detection and quantification that are known in the art. Antibodies, for example, can be generated which are specific to the protein using routine methods known in the art, which specifically bind to the protein of interest so that they can be detected and measured. Protein measurement can be carried out by any methods known in the art, including histochemistry, immunoblot analysis, in vitro binding studies, radioimmunoassay, and ELISAs.

[0067] In one embodiment, the transcripts which are identified as associated with schizophrenia or the symptoms thereof are expressed sequence tags (ESTs). ESTs are short single-pass sequence reads from mRNA (cDNA). They may be of various lengths. For use in this invention, it is preferred, but not required, that they be of sufficient length to identify a unique expressed sequence. Typically, they are about 300-500 bp in length. However, sequences as short as about 16 bases may be sufficient to identify a specific sequence. ESTs represent a snapshot of genes expressed in a given tissue and/or at a given developmental stage. They are tags (some coding, others not) of expression for a given cDNA library. There are now well over one million of these sequences in the publicly available database and these sequences are believed to represent more than half of all human genes. The ESTs of, and for use with the invention, however, are not meant to be limited by what is available in public databases, and also may be novel ESTs that are generated and identified according to the methods of the invention described herein.

[0068] The ESTs detected according to the invention are useful for elucidating the genes and gene products responsible for regulating schizophrenia, the symptoms thereof, and the onset of schizophrenia and therefore for understanding the mechanisms underlying schizophrenia and the symptoms thereof. The ESTs detected according to the methods of this invention demonstrate specific regulation at time points relative to the schizophrenia models utilized. Such involvement may be to contribute, or be required for the onset of and maintenance of schizophrenia or the symptoms thereof. For the purposes of the invention, it is not necessary to know what genes the ESTs are associated with, because changes in amplitude at particular time points relative to the schizophrenia model or models utilized are useful in themselves as markers for diagnosing and predicting the onset of schizophrenia or the symptoms thereof.

[0069] Once these ESTs are identified as being associated with schizophrenia or the symptoms thereof, they are useful for detecting or diagnosing schizophrenia either prior, to or concurrent with the appearance of its symptoms, as well as for modulating the onset of schizophrenia or the symptoms thereof by either enhancing or inhibiting EST expression or the products thereof.

[0070] Similarly, the ESTs for use with the invention are useful for development of new pharmaceutical agents for treatment of or prevention of schizophrenia or the symptoms thereof. Pharmaceutical agents may be useful to modulate relevant ESTs identified as

associated with schizophrenia or the symptoms thereof, to either increase or decrease their expression or the products thereof.

[0071] Systems for carrying out all of the methods described herein are also provided, and optionally comprise a computer system and related software. For example, as relates to the foregoing method, the system may comprise groups of mice in which an animal model of schizophrenia in living animals has been initiated, and a computer system comprising software, said computer system configured to assess transcriptional regulation in tissue over time in animals that are a model of schizophrenia, wherein the tissue is sampled one or more times after the initiation of the model and optionally one or more times prior to the initiation of the model; compare the transcriptional regulation from prior to initiation of the model with transcriptional regulation from after the initiation of the model, and/or with transcriptional regulation assessed from tissue in living animals not subject to a schizophrenia model; and detect a transcript that is dysregulated in tissue from animals that are a model of schizophrenia. Optionally, the computer system may output a result which is indicative of gene targets associated with schizophrenia or schizophrenia symptoms.

[0072] In one embodiment, the invention comprises nucleic acid sequences obtained according to the screening methods of the invention. In another embodiment, the invention comprises a nucleic acid sequence selected from the group consisting of SEQ ID NO:1 through SEQ ID NO:16.

[0073] In yet another embodiment of the invention, a method is provided of predicting the susceptibility to schizophrenia or the symptoms thereof in an individual. A biological sample is provided by an individual to determine the susceptibility to onset of schizophrenia or the symptoms thereof, and from the sample provided gene expression or gene expression products are measured which have been identified to be informative regarding the onset of schizophrenia or the symptoms thereof; these genes are considered “pre-symptomatic genes” and are described herein. If the gene expression or products thereof measured are considered to be dysregulated, then there is an increased likelihood for developing schizophrenia or the symptoms thereof, compared to an individual who does not demonstrate dysregulation of those same genes or products thereof or compared to an earlier time point within the same individual, in which dysregulation of those same genes or products thereof was not demonstrated.

[0074] Dysregulation refers to any change in gene expression or the products thereof relative to the gene expression or products thereof in an individual, at the same general time point or time points, who have been determined to not have ever presented with symptoms of schizophrenia or who have never developed schizophrenia. It can also refer to any change in gene expression or the products thereof relative to a baseline measure in the same individual, at a time, for example, when certain external or internal factors that initiate the onset of schizophrenia were not present or had not yet caused pathologic or prepathologic changes.

[0075] The inventors have identified several genes, the dysregulation of which are predictive of the onset of schizophrenia, or the susceptibility to schizophrenia in a widely accepted and validated animal model of schizophrenia. These genes have been discovered to be associated with schizophrenia or the symptoms thereof. Utilizing the screening methods described herein, the inventors have identified genes that are dysregulated prior to the onset of the symptoms of schizophrenia, including interferon-induced protein, interferon regulatory factor 7, PKR, Ifi44, Ifit2, Irf7, Isgf3g, G1p2, Mx1, Mx2, SEQ ID NO: 11 through SEQ ID NO: 16, and in some embodiments, the genes or fragments listed in Tables 3, 4, 7, and 8.

[0076] As demonstrated in the Examples described herein, when utilizing the social isolation rearing model for schizophrenia in rats, symptoms are present on postnatal day 60, including deficits in prepulse inhibition and the neurobiological measures described herein. In assessing gene expression at various intervals from animals after initiating the schizophrenia model, it was determined that certain genes exhibited dysregulation (relative to control animals) prior to the time of symptoms on postnatal day 60, including genes exhibiting dysregulation (relative to control animals) at postnatal day 30 and postnatal day 40. Accordingly any transcripts or genes identified as dysregulated at any time point prior to the onset of symptoms in a model of schizophrenia can be used as predictive of schizophrenia or the symptoms thereof, or as a drug target and are within the scope of this invention. Also within the scope of the invention is the detection of gene expression or product dysregulation that occurs at a point where just some symptoms of schizophrenia are present, but prior to a set of circumstances that are diagnostic of schizophrenia.

[0077] As described above, the genes or the products thereof for use with the invention include, but are not limited to proteins, peptides, or nucleic acid molecules (e.g., mRNA, tRNA, rRNA, or cRNA) that are involved in transcription or translation. Also as described above, any detectable change in gene expression, or the products thereof, whether upregulated or downregulated, are contemplated as useful in the methods of the invention, as

well as any time points prior to the onset of schizophrenia or the symptoms thereof. Any methods available and known to one of ordinary skill in the art are contemplated for measuring gene expression or the products thereof, as described herein.

[0078] In some preferred embodiments of the invention, the relevant genes for which expression or expression products are identified as being dysregulated include, but are not limited to interferon-induced protein, interferon regulatory factor 7, PKR, Ifi44, Ifit2, Irf7, Isgf3g, G1p2, Mx1, Mx2, and SEQ ID NO: 11 through SEQ ID NO: 16. In yet other embodiments of the invention, the relevant genes whose expression or expression products are identified as being dysregulated include those described in Tables 3, 4, 7, and 8. In another embodiment of the invention, the relevant genes for which expression or expression products are identified as being dysregulated have been previously identified as being associated with schizophrenia or the symptoms thereof. In another embodiment of the invention, one or more genes identified as being dysregulated include, but are not limited to genes that are involved in synaptogenesis, synaptic pruning, synaptic drive, synaptic communication, synapse formation, synaptic activity, synaptic plasticity, neuritogenesis, neurite architecture, neuronal migration, intracellular transport, integrator genes, signal transduction, microtubule assembly, axon elongation, cell motility, and G-protein coupled receptor signaling. All of these genes, collectively, which may be used to predict the onset or susceptibility to schizophrenia or the symptoms thereof, are referred to herein as “pre-symptomatic” genes.

[0079] In one embodiment of the invention, in determining the susceptibility to schizophrenia or the symptoms thereof, one or more of the pre-symptomatic genes are downregulated in an individual prior to the onset of schizophrenia or the symptoms thereof, which is informative of the susceptibility of the individual to schizophrenia or the symptoms thereof. In another embodiment, one or more of the pre-symptomatic genes are upregulated in an individual prior to the onset of schizophrenia or the symptoms thereof, which is informative of the susceptibility of the individual to schizophrenia or the symptoms thereof. In some embodiments, one or more of the pre-symptomatic genes will be upregulated, and one or more of the symptomatic genes will be downregulated, which is informative of the susceptibility of the individual to schizophrenia or the symptoms thereof.

[0080] In some embodiments, one gene or its expression product is predictive of the susceptibility to schizophrenia, and in other embodiments, two or more genes or their

expression products are predictive of the susceptibility to schizophrenia or the symptoms thereof.

[0081] In some embodiments, the individual providing the biological sample is an individual that possess at least one or more risk factors for schizophrenia. Risk factors contemplated by the invention include, but are not limited to family history of schizophrenia, schizophrenia-like psychoses, and other mental disorders; genetic factors; place of birth, including urbanicity; season of birth; obstetric complications; infections; diet; toxic exposures; household crowding; exposure to pets; breast-feeding; family history of Gaucher's disease; maternal infection, such as herpes simplex virus-2; prenatal and/or postnatal stress; enhanced maternal immune activation; handedness; childhood exposure to social adversity, including social defeat or social exclusion; and alterations in neurotransmitter levels, including, but not limited to dopamine, glutamate, GABA, acetylcholine, and serotonin. Any number of these factors either alone or in combination can be indicative of increased risk of developing schizophrenia or the symptoms thereof, which may be an indication for assessing the genes identified by the inventors and identified by the methods described herein, to determine the susceptibility to developing schizophrenia or the symptoms thereof. The presence of one or more risk factors may also be useful in determining the susceptibility of an individual to schizophrenia, when used in combination with detection of pre-symptomatic gene dysregulation. In some embodiments, the individual does not have any known risk factors for schizophrenia.

[0082] In some embodiments of the invention, the individual is completely asymptomatic, presenting with no known symptoms of schizophrenia. In other embodiments, the individual presents with one or more symptoms of schizophrenia, which include, but are not limited to the symptoms described herein, such as any of the positive and negative symptoms characterized by clinicians. Any potential symptom that is indicative of schizophrenia is within the scope of the invention. The individual may present with one or more symptoms that, taken together, do not constitute a clinical diagnosis for schizophrenia or related disorders, as for example, defined in the DSM-IV. For example, the individual may not present with a sufficient number of symptoms, they may not have had the symptoms for a sufficient duration, or they may present with symptoms which resemble schizophrenia or a related disorder, but for some reason do not fit into the defined categories for clinical diagnosis and therefore would not be diagnosed by a clinician as having schizophrenia or a related disorder.

[0083] The biological sample from which gene expression or a product thereof is measured can include any biological tissue provided by an individual. In particular, genes or the expression products thereof can be evaluated from blood, plasma, saliva, CSF, urine, lymph, sputum, or other tissues of the body. In a preferred embodiment, the measurement is made from peripheral blood mononuclear cells.

[0084] In another embodiment, this invention provides methods of diagnosing schizophrenia or the symptoms thereof in an individual. A biological sample is provided by an individual, to determine if the individual has schizophrenia or the symptoms thereof, and from the sample provided, gene expression or the products thereof are measured which have been identified to be informative regarding diagnosis of schizophrenia; these genes are considered “symptomatic genes” and are described herein. If the gene expression or products thereof are considered to be dysregulated, it is diagnostic of schizophrenia. The presence of dysregulation or more than one symptomatic gene is greater evidence of the presence of schizophrenia.

[0085] Dysregulation refers to any change in gene expression or the products thereof relative to the gene expression or products thereof in an individual, at the same general time point or time points, who have been determined not to have schizophrenia, or in some embodiments, who have never developed schizophrenia, or who never develop schizophrenia. It can also refer to any change in gene expression or the products thereof relative to a baseline measure in the same individual, at a time, for example, prior to the onset of schizophrenia, and in some embodiments, prior to the onset of any symptoms of schizophrenia.

[0086] The inventors have identified several genes, the dysregulation of which are indicative of the presence of schizophrenia or the symptoms thereof in a widely accepted and validated animal model of schizophrenia, and which can be considered as biomarkers for schizophrenia and the symptoms thereof. Using the methods of the invention as described herein, the inventors have discovered many genes to be associated with schizophrenia or the symptoms thereof, including but not limited to those listed in Tables 5, 6, 9, and 10, and SEQ ID NO: 1 through SEQ ID NO: 10. In another embodiment of the invention, one or more genes identified as being dysregulated include, but are not limited to genes that are involved in synaptogenesis, synaptic pruning, synaptic drive, synaptic communication, synapse formation, synaptic activity, synaptic plasticity, neuritogenesis, neurite architecture, neuronal migration, intracellular transport, integrator genes, signal transduction, microtubule assembly,

axon elongation, cell motility, and G-protein coupled receptor signaling. Many genes that have been previously associated with schizophrenia are within the scope of the invention, including GABAA receptor $\alpha 4$, complexin 1, and synapsin 2, parvalbumin, and Lis-1. Further, the inventors have identified several novel ESTs, the dysregulation of which can serve as biomarkers for schizophrenia or the symptoms thereof. Utilizing the screening methods described herein, comprising assessing gene transcription or the products thereof over time in animal models of schizophrenia, the inventors have identified genes that are dysregulated concurrent with or after the onset of the symptoms of schizophrenia. As demonstrated in the Examples described herein, when utilizing the social isolation rearing model for schizophrenia, symptoms are present on postnatal day 60, including deficits in prepulse inhibition and the neurobiological measures described herein. In assessing gene expression at various intervals from animals after the onset of the schizophrenia model, it was determined that certain genes exhibited dysregulation (relative to control animals) concurrent with the presence of symptoms on postnatal day 60. In some instances, dysregulation was also observed on postnatal day 80. Within the scope of the invention for use in diagnosis are any transcripts or genes identified as dysregulated at any time point concurrent with, and after the onset of symptoms in a model of schizophrenia.

[0087] As described in other embodiments herein, detecting dysregulation of relevant genes, transcripts, or their expression products, as used herein, refers to any difference in gene expression or gene expression product relative to individuals who have been assessed at the same general time point, concurrent with or after the onset of schizophrenia or the symptoms thereof.

[0088] As described above, the genes or the products thereof for use with the invention include, but are not limited to proteins, peptides, or nucleic acid molecules (e.g., mRNA, tRNA, rRNA, or cRNA) that are involved in transcription or translation. Also as described above, any detectable change in gene expression, or the products thereof, whether upregulated or downregulated, are contemplated as useful in the methods of the invention, as well as any time points concurrent with or following the onset of schizophrenia or the symptoms thereof. Any methods available and known to one of ordinary skill in the art are contemplated for measuring gene expression or the products thereof, as described herein.

[0089] In some embodiments of the invention, the relevant genes whose expression or expression products are identified as being dysregulated concurrent with, or following the onset of schizophrenia or the symptoms thereof include genes or transcripts, or the expression

products thereof, that have not previously identified as associated with schizophrenia or the symptoms thereof. These include, but are not limited to the ESTs identified according to the invention, including SEQ ID NO:1 through SEQ ID NO:10. Also contemplated for use in the invention are the genes identified in Tables 3 through 10, which the inventors have discovered to be associated with schizophrenia or the symptoms thereof using the methods described herein. Also within the scope of the invention for purposes of diagnosis or predicting onset of schizophrenia or the symptoms thereof are genes which have been previously identified as associated with schizophrenia or the symptoms thereof, including any of the genes identified herein as associated with schizophrenia or the symptoms thereof, and any genes identified according to the methods of the invention. In another embodiment of the invention, one or more genes identified as being dysregulated include, but are not limited to genes that are involved in synaptogenesis, synaptic pruning, synaptic drive, synaptic communication, synapse formation, synaptic activity, synaptic plasticity, neuritogenesis, neurite architecture, neuronal migration, intracellular transport, integrator genes, signal transduction, microtubule assembly, axon elongation, cell motility, and G-protein coupled receptor signaling. All of these genes and transcripts, collectively, are referred to as “symptomatic” genes.

[0090] In one embodiment of the invention, one or more of the symptomatic genes is downregulated in an individual concurrent with or following the onset of schizophrenia or the symptoms thereof, and is informative as a diagnostic marker. In another embodiment, one or more of the symptomatic genes is upregulated in an individual concurrent with or following the onset of schizophrenia or the symptoms thereof, and is informative as a diagnostic marker. In some embodiments, one or more of the symptomatic genes is upregulated, and one or more of the symptomatic genes is downregulated, which is informative as a diagnostic marker. In some embodiments, a distinctive pattern of gene expression regulation, comprising more than one time point of regulation is informative for diagnosis or prediction of schizophrenia or the symptoms thereof.

[0091] In another embodiment of the invention, the symptomatic gene, genes, or the expression products thereof that are dysregulated have been previously identified as being associated with schizophrenia or the symptoms thereof.

[0092] In some embodiments, one symptomatic gene or its expression product is a biomarker for schizophrenia or the symptoms thereof, and in other embodiments, two or

more symptomatic genes or their expression products are biomarkers for schizophrenia or the symptoms thereof.

[0093] It is of particular importance to utilize one or biomarkers as described herein for diagnosing schizophrenia or the symptoms thereof because traditional diagnoses on their own are not always accurate. For example, inaccurate diagnosis can be the result of overlap in diagnostic criteria between mood and psychotic disorders, provider bias, miscommunication between patient and provider, changes in diagnostic criteria, differences in diagnostic practice between providers, assessment at a time when symptom acuity is severe, influence of substance abuse, and a lack of sufficient data obtained. In addition, cultural differences can lead to inaccurate diagnoses; for example, multiple studies have shown that significant disparities exist in the diagnosis of schizophrenia between African Americans and Caucasians (e.g., Hampton, Br. J. Psychiatry Suppl., 50, s46-51, 2007). The use of the symptomatic genes may be able to yield a reliable diagnosis of schizophrenia or the symptoms thereof in advance of traditional diagnostic tools which often rely on the presence of a certain number of symptoms for a specified amount of time. Therefore, with earlier diagnosis, earlier treatment and care of patients can be initiated.

[0094] Evaluation of dysregulation of symptomatic genes or their expression products may be performed alone or in combination with one or more of any clinical, behavioral, or biological assessment tools used for diagnosing schizophrenia or the symptoms thereof. Use of the symptomatic genes or their expression products as described herein can be particularly powerful when used in combination with other diagnostic tools. For example, they may be utilized in conjunction with diagnoses made in accordance with the DSM-IV (or DSM-IV-TR); the Comprehensive Assessment of Symptoms and History (CASH), or an adapted version using a cultural formulation to make the instrument more culturally sensitive (CASH-CS); the Positive and Negative Syndrome Scale (PANSS) for typological and dimensional assessment; the Brief Psychiatric Rating Scale (BPRS); the Rorschach Schizophrenia Index (SCZI); the Scale for the Assessment of Negative Symptoms (SANS); the Scale for the Assessment of Positive Symptoms (PANS); the Bonn Scale for the Assessment of Basic Symptoms (BSABS); the Instrument for the Retrospective Assessment of the Onset of Schizophrenia; the Present State Examination; the Structured Interview for Prodromal Syndromes; the Global Assessment of Functioning; neuroimaging; use of other biomarkers or genetic factors; family history of psychotic disorders; and assessment of any risk factor for schizophrenia or the symptoms thereof.

[0095] In another embodiment, the targets obtained according to the methods of the invention, as well as the targets described herein, are used to prevent schizophrenia or the symptoms thereof by either upregulating or downregulating them, or by increasing or decreasing their products. Depending on the nature of the dysregulation of the target in association with predicting susceptibility to schizophrenia or the symptoms thereof, it may be desirable to increase or decrease the function of the gene of interest, or a product of the gene of interest.

[0096] Included among the gene targets to be modified for preventing schizophrenia or the symptoms thereof are the pre-symptomatic genes as described herein. In some embodiments it will be necessary to modify only one such gene or gene product, and in other embodiments it may be desirable to modify more than one pre-symptomatic gene or gene product. In one embodiment, the genes to be modified include interferon-induced protein, interferon regulatory factor 7, or PKR, or a combination thereof. As an example, it may be desirable to increase the expression of these genes or their products, as they have been found to be decreased under circumstances leading to the onset of schizophrenia as compared to circumstances that do not lead to schizophrenia. In another embodiment, it may be useful to modify one or more of the genes from Tables 3, 4, 7 and 8. In other embodiments, it may be useful to modify one or more of the genes from Tables 5, 6, 9, and 10. In yet other embodiments, it may be useful to modify one or more of SEQ ID NO:1 through SEQ ID NO:16.

[0097] In another embodiment, the targets obtained according to the methods of the invention, as well as the targets described herein, are used to treat schizophrenia or the symptoms thereof by either upregulating or downregulating them, or by increasing or decreasing their products. Depending on the nature of the dysregulation of the target in association with schizophrenia or the symptoms thereof, it may be desirable to increase or decrease the function of the gene of interest, or a product of the gene of interest.

[0098] Included among the gene targets to be modified for treating schizophrenia or the symptoms thereof are the symptomatic genes as described herein. In some embodiments it will be necessary to modify only one such gene or gene product, and in other embodiments it may be desirable to modify more than one symptomatic gene or gene product. Included among the gene targets to modulate for treating schizophrenia or the symptoms thereof are nucleic acid sequences selected from the group consisting of SEQ ID NO:1 through SEQ ID NO:16. Any one or more of the genes from Tables 5, 6, 9, and 10 or their products, may also

be modulated for treating schizophrenia or the symptoms thereof. As an example, it may be desirable to decrease the expression of these nucleic acids (e.g., the ESTs) or their products, as they have been found to increase in association with schizophrenia relative to circumstances where no symptoms of schizophrenia are present. In other embodiments, it may be useful to modulate one or more of the genes from Tables 3, 4, 7, and 8.

[0099] In some embodiments, it may be desirable to modulate the expression or expression product of at least one pre-symptomatic gene in combination with modulating the expression or expression product of at least one symptomatic gene, and in some cases this combination for treatment or prevention of schizophrenia or the symptoms thereof may be enhanced by the addition of other treatments.

[00100] In some embodiments, treatment by modulating symptomatic or pre-symptomatic genes or their products might be indicated for individuals for whom other schizophrenia treatments are ineffective or to which they have become resistant, or for individuals who have had improved symptoms but experienced a relapse or no further improvement.

[00101] In some embodiments, the individual receiving treatment or prophylactic treatment is an adult, in some embodiments the individual is an adolescent, and in some embodiments the individual is a child.

[00102] In some embodiments, prevention of schizophrenia or the symptoms thereof by modulating at least one pre-symptomatic gene or expression product, or treatment of schizophrenia or the symptoms thereof by modulating at least one symptomatic gene or expression product may be performed in combination with one or more other preventative or treating agents or regimens. For example, the prevention or treatment methods described herein can be combined with traditional behavioral or drug therapies. These therapies can be those administered to treat schizophrenia, or to target individual symptoms of schizophrenia. These therapies include, but are not limited to cognitive-behavioral therapy; social skills training; psychotherapy; cognitive remediation; family intervention; first and second generation antipsychotics, such as haloperidol, clozapine, risperidone, and olanzapine; neuroleptics such as chlorpromazine and paliperidone; quetiapine; aripiprazole; ziprasidone; trifluoperazine; flupenthixol; loxapine; perphenazine; fluvoxamine; iloperidone; osanetant; MEM 3454; ORG 5222; DU 127090; DTA 201A; psychostimulants; drugs that act as dopamine or acetylcholine antagonists; dopamine reuptake inhibitors; glutamate antagonists;

serotonin antagonists; drugs that enhance cognitive abilities; electric shock therapy; eicosapentaenoic acid; hormone therapy, such as testosterone; and antidepressants.

[00103] According to the invention, gene expression products include, but are not limited to proteins, peptides, or nucleic acid molecules (e.g., mRNA, tRNA, rRNA, or cRNA) that are involved in transcription or translation.

[00104] In one embodiment of the invention, gene expression products can refer to epigenetic changes such as DNA methylation and chromatin remodeling. Chromatin remodeling is initiated by the posttranslational modification of the amino acids that make up histone proteins, or by the addition of methyl groups to the DNA at CpG sites to convert cytosine to 5-methylcytosine. Any epigenetic modulation known to one of skill in the art is contemplated by the invention.

[00105] Any means of enhancing gene expression, or the gene expression product in an individual that is known by one of skill in the art may be used to modulate gene expression or a gene expression product as contemplated for methods of prevention or treatment in the invention. For example, pharmaceutical compositions which are agonists for the gene product of interest may be used to prevent or treat schizophrenia or the symptoms thereof.

[00106] Any means of reducing gene expression, or the gene expression product in an individual that is known by one of skill in the art may be used to reduce gene expression or a gene expression product as contemplated for methods of prevention or treatment in the invention. Non-limiting examples for use in reducing gene expression or gene expression products according to the invention include RNA interference, antisense RNA, antibodies, and pharmaceutical compositions that antagonize the activity of the gene product of interest.

[00107] In certain embodiments, antisense is used to decrease expression of a gene. Antisense is used in reference to RNA sequences that are complementary to a specific RNA sequence (e.g., mRNA). Included within antisense are antisense RNA ("asRNA") molecules involved in gene regulation by bacteria. Antisense RNA may be produced by any method, including synthesis by splicing the gene(s) of interest in a reverse orientation to a viral promoter that permits the synthesis of a coding strand. Once introduced, this transcribed strand combines with natural mRNA to form duplexes. These duplexes then block either the further transcription of the mRNA or its translation. Regions of a nucleic acid sequences that are accessible to antisense molecules can be determined using available computer analysis methods.

[00108] In certain embodiments, an RNA interference (RNAi) molecule is used to decrease expression of a gene. RNA interference (RNAi) is defined as the ability of double-stranded RNA (dsRNA) to suppress the expression of a gene corresponding to its own sequence. RNAi is also called post-transcriptional gene silencing or PTGS. Since the only RNA molecules normally found in the cytoplasm of a cell are molecules of single-stranded mRNA, the cell has enzymes that recognize and cut dsRNA into fragments containing 21-25 base pairs (approximately two turns of a double helix). The antisense strand of the fragment separates enough from the sense strand so that it hybridizes with the complementary sense sequence on a molecule of endogenous cellular mRNA. This hybridization triggers cutting of the mRNA in the double-stranded region, thus destroying its ability to be translated into a polypeptide. Introducing dsRNA corresponding to a particular gene thus knocks out the cell's own expression of that gene in particular tissues and/or at a chosen time.

[00109] Double-stranded RNA can be used to interfere with gene expression in mammals (Wianny & Zemicka-Goetz, 2000, Nature Cell Biology 2: 70-75; incorporated herein by reference in its entirety). dsRNA is used as inhibitory RNA or RNAi of the function of the gene of interest to produce a phenotype that is the same as that of a null mutant of the gene of interest (Wianny & Zernicka-Goetz, 2000, Nature Cell Biology).

[00110] In another embodiment, a method is provided which comprises screening compounds for their ability to increase or decrease the activity of one or more of the targets identified according to the methods of the invention. Accordingly, an assay is provided which comprises measuring gene expression (pre-symptomatic or symptomatic) in an animal model of schizophrenia at relevant time points previously determined, and comparing it to the same time points in control animals, or to earlier time points within the same animals, to establish dysregulation. Once these targets are identified as described by the methods herein as being relevant for schizophrenia or the symptoms thereof, they can be utilized in order to screen for compounds that modulate the gene targets or products thereof.

[00111] In some embodiments, a test compound, which is any compound of interest, is administered to animals displaying dysregulation of the targets that have been identified, and in some embodiments, the compound is also administered to control animals. It is then determined if the compound has any influence on the gene expression or the products thereof. Concurrent with this, symptoms of schizophrenia, and other behavioral and biological measures can be assessed from those animals in order to more fully elucidate the effects that the compound has on gene expression relevant to schizophrenia, and on the behavioral and

biological manifestations of schizophrenia or the symptoms thereof. Compounds that bind to the gene products either competitively or non-competitively, or otherwise affect their activity may be useful as drug candidates for preventing or treating schizophrenia or the symptoms thereof. For example, if utilizing the social isolation rearing model in rats, compounds that can counteract the dysregulation of gene expression or products thereof at postnatal day 60, by, for example, reducing mRNA of GABAAR α 4 complexin 1, synapsin 2, or parvalbumin, or SEQ ID NO: 1 through SEQ ID NO: 10, may be useful for modulating, preventing, or treating schizophrenia or the symptoms thereof.

[00112] In another embodiment of the invention, a method is provided of preventing or treating schizophrenia, or the symptoms thereof, or the cognitive deficits associated with schizophrenia by administering to an individual in need thereof an effective amount of midkine. As described herein, cognitive abnormalities are a core symptom of schizophrenia, which can be manifest in numerous ways, and are not the result of medication. All cognitive deficits are within the scope of the invention, including all variations of abnormalities in learning; abnormalities in any kind of memory, including but not limited to short term memory, long term memory, episodic memory, working memory, declarative (explicit) and procedural (implicit) memory, semantic memory, spatial memory, visuospatial memory, memory consolidation, memory re-consolidation; as well as abnormalities in thought, verbal skills, language processing,; as well reduced mental speed and reduced reaction time; thought disorder; problems with planning and complex sentences; difficulty generating novel strategies to solve a problem; and the failure to show mental flexibility.

[00113] As described herein, prepulse inhibition is used as a readout of sensorimotor processing in the prefrontal cortex, and is closely tied with working memory function, and as demonstrated herein, is greatly reduced in an animal model of schizophrenia. As demonstrated in the Examples herein, administration of midkine into the 3rd cerebral ventricle of the brain reverses the deficit observed in prepulse inhibition of startle in animals that have been reared in isolation.

[00114] Pharmaceutical compositions comprising the genes or gene fragments derived according to the methods of the invention, or comprising one or more of the genes and gene fragments or their products as described herein are contemplated by the invention. Also within the scope of the invention are pharmaceutical compositions comprising agonists and antagonists of one or more of the genes, fragments, or products thereof, which are useful in the prevention or treatment of schizophrenia or the symptoms thereof.

[00115] The pharmaceutical compositions of the invention can be formulated as neutral or salt forms. Pharmaceutically acceptable non-toxic salts include the base addition salts (formed with free carboxyl or other anionic groups) which may be derived from inorganic bases such as, for example, sodium, potassium, ammonium, calcium, or ferric hydroxides, and such organic bases as isopropylamine, trimethylamine, 2-ethylamino-ethanol, histidine, procaine, and the like. Such salts may also be formed as acid addition salts with any free cationic groups and will generally be formed with inorganic acids such as, for example, hydrochloric, sulfuric, or phosphoric acids, or organic acids such as acetic, p-toluenesulfonic, methanesulfonic acid, oxalic, tartaric, mandelic, and the like. Salts of the invention include amine salts formed by the protonation of an amino group with inorganic acids such as hydrochloric acid, hydrobromic acid, hydroiodic acid, sulfuric acid, phosphoric acid, and the like. Salts of the invention also include amine salts formed by the protonation of an amino group with suitable organic acids, such as p-toluenesulfonic acid, acetic acid, and the like. Additional excipients which are contemplated for use in the practice of the present invention are those available to those of ordinary skill in the art, for example, those found in the United States Pharmacopeia Vol. XXII and National Formulary Vol. XVII, U.S. Pharmacopcia Convention, Inc., Rockville, Md. (1989), the relevant contents of which are incorporated herein by reference.

[00116] Pharmaceutically acceptable carriers for use in the invention can be determined in part by the specific composition administered, as well as by the particular method used to administer the composition. Accordingly, there are a wide variety of suitable formulations of pharmaceutical compositions of the present invention (see, e.g., Remington's Pharmaceutical Sciences, 20th ed., 2003).

[00117] The term "pharmaceutically acceptable" can mean approved by a regulatory agency of the Federal or a state government or listed in the U.S. Pharmacopeia or other generally recognized pharmacopeia for use in animals, and for use in humans. The term "carrier" can mean a diluent, excipient, or vehicle with which the therapeutic is administered. Such pharmaceutical carriers can be sterile liquids, such as water and oils, including those of petroleum, animal, vegetable or synthetic origin, such as peanut oil, soybean oil, mineral oil, sesame oil and the like. Saline is a preferred carrier when the pharmaceutical composition is administered intravenously. Aqueous dextrose and glycerol solutions can also be employed as liquid carriers, particularly for injectable solutions. Suitable pharmaceutical excipients include starch, glucose, lactose, sucrose, gelatin, malt, rice, flour, chalk, silica gel, sodium

stearate, glycerol monostearate, talc, sodium chloride, dried skim milk, glycerol, propylene, glycol, water, ethanol and the like. The composition, if desired, can also contain minor amounts of wetting or emulsifying agents, or pH buffering agents. These compositions can take the form of solutions, suspensions, emulsion, tablets, pills, capsules, powders, sustained-release formulations and the like. Oral formulation can include standard carriers such as pharmaceutical grades of mannitol, lactose, starch, magnesium stearate, sodium saccharine, cellulose, magnesium carbonate, etc. Examples of suitable pharmaceutical carriers are described in "Remington's Pharmaceutical Sciences" by E. W. Martin. Such compositions will contain a prophylactically or therapeutically effective amount of a prophylactic or therapeutic agent preferably in purified form, together with a suitable amount of carrier so as to provide the form for proper administration to the patient. The formulation should suit the mode of administration. In a preferred embodiment, the pharmaceutical compositions are sterile and in suitable form for administration to a subject, preferably an animal subject, more preferably a mammalian subject, and most preferably a human subject.

[00118] In another embodiment, the composition can be delivered in a vesicle, in particular a liposome (see Langer, *Science* 249:1527-1533 (1990); Treat et al., in *Liposomes in the Therapy of Infectious Disease and Cancer*, Lopez-Berestein and Fidler (eds.), Liss, New York, pp. 353-365 (1989); Lopez-Berestein, pp. 317-327).

[00119] In yet another embodiment of the invention, the composition can be delivered in a controlled release or sustained release system. In one embodiment, a pump may be used to achieve controlled or sustained release (see Langer, *supra*; Sefton, 1987, *CRC Crit. Rev. Biomed. Eng.* 14:20; Buchwald et al., 1980, *Surgery* 88:507; Saudek et al., 1989, *N. Engl. J. Med.* 321:574). In another embodiment, polymeric materials can be used to achieve controlled or sustained release of the nucleic acids of the invention or fragments thereof (see e.g., *Medical Applications of Controlled Release*, Langer and Wise (eds.), CRC Pres., Boca Raton, Fla. (1974); *Controlled Drug Bioavailability, Drug Product Design and Performance*, Smolen and Ball (eds.), Wiley, N.Y. (1984); Ranger and Peppas, 1983, *J. Macromol. Sci. Rev. Macromol. Chem.* 23:61; see also Levy et al., 1985, *Science* 228:190; During et al., 1989, *Ann. Neurol.* 25:351; Howard et al., 1989, *J. Neurosurg.* 71:105); U.S. Pat. No. 5,679,377; U.S. Pat. No. 5,916,597; U.S. Pat. No. 5,912,015; U.S. Pat. No. 5,989,463; U.S. Pat. No. 5,128,326; International Publication No. WO 99/15154; and International Publication No. WO 99/20253. Examples of polymers used in sustained release formulations include, but are not limited to, poly(2-hydroxy ethyl methacrylate), poly(methyl

methacrylate), poly(acrylic acid), poly(ethylene-co-vinyl acetate), poly(methacrylic acid), polyglycolides (PLG), polyanhydrides, poly(N-vinyl pyrrolidone), poly(vinyl alcohol), polyacrylamide, poly(ethylene glycol), polylactides (PLA), poly(lactide-co-glycolides) (PLGA), and polyorthoesters. In a preferred embodiment, the polymer used in a sustained release formulation is inert, free of leachable impurities, stable on storage, sterile, and biodegradable. In yet another embodiment, a controlled or sustained release system can be placed in proximity of the therapeutic target, i.e., the lungs, thus requiring only a fraction of the systemic dose (see, e.g., Goodson, in *Medical Applications of Controlled Release*, supra, vol. 2, pp. 115-138 (1984)).

[00120] Controlled release systems are discussed in Langer (1990, *Science* 249:1527-1533). Any technique known to one of skill in the art can be used to produce sustained release formulations comprising one or more genes of the invention or fragments thereof. See, e.g., U.S. Pat. No. 4,526,938, International publication No. WO 91/05548, International publication No. WO 96/20698, Ning et al., 1996, "Intratumoral Radioimmunotherapy of a Human Colon Cancer Xenograft Using a Sustained-Release Gel," *Radiotherapy & Oncology* 39:179-189, Song et al., 1995, "Antibody Mediated Lung Targeting of Long-Circulating Emulsions," *PDA Journal of Pharmaceutical Science & Technology* 50:372-397, Cleek et al., 1997, "Biodegradable Polymeric Carriers for a bFGF Antibody for Cardiovascular Application," *Pro. Int'l. Symp. Control. Rel. Bioact. Mater.* 24:853-854, and Lam et al., 1997, "Microencapsulation of Recombinant Humanized Monoclonal Antibody for Local Delivery," *Proc. Int'l. Symp. Control Rel. Bioact. Mater.* 24:759-760, each of which is incorporated herein by reference in their entirety.

[00121] In some embodiments of the invention, in which the composition is one or more nucleic acid molecules obtained according to the methods of the invention as described herein, the nucleic acid or nucleic acids can be administered in vivo by constructing it as part of an appropriate nucleic acid expression vector and administering it so that it becomes intracellular, e.g., by use of a retroviral vector (see U.S. Pat. No. 4,980,286), or by direct injection, or by use of microparticle bombardment (e.g., a gene gun; Biolistic, Dupont), or coating with lipids or cell-surface receptors or transfecting agents, or by administering it in linkage to a homeobox-like peptide which is known to enter the nucleus (see e.g., Joliot et al., 1991, *Proc. Natl. Acad. Sci. USA* 88:1864-1868), etc. Alternatively, a nucleic acid can be introduced intracellularly and incorporated within host cell DNA for expression by homologous recombination.

[00122] Pharmaceutical compositions of the invention are formulated to be compatible with their intended route of administration. Examples of suitable routes of administration include, but are not limited to, parenteral (e.g., intravenous, intramuscular, intradermal, intra-tumoral, intra-synovial, and subcutaneous), oral (e.g., inhalation), intranasal, transdermal (topical), transmucosal, intra-tumoral, intra-synovial, vaginal, and rectal administration. In a specific embodiment, the composition is formulated in accordance with routine procedures as a pharmaceutical composition adapted for intravenous, subcutaneous, intramuscular, oral, intra-tumoral, intra-synovial, intranasal or topical administration to human beings. Typically, compositions for intravenous administration are solutions in sterile isotonic aqueous buffer. Where necessary, the composition may also include a solubilizing agent and a local anesthetic such as lignocaine to ease pain at the site of the injection.

[00123] If the compositions of the invention are to be administered orally, the compositions can be formulated orally in the form of, e.g., gum, tablets, capsules, cachets, gelcaps, solutions, suspensions and the like. Tablets or capsules can be prepared by conventional means with pharmaceutically acceptable excipients such as binding agents (e.g., pregelatinised maize starch, polyvinylpyrrolidone or hydroxypropyl methylcellulose); fillers (e.g., lactose, microcrystalline cellulose or calcium hydrogen phosphate); lubricants (e.g., magnesium stearate, talc or silica); disintegrants (e.g., potato starch or sodium starch glycolate); or wetting agents (e.g., sodium lauryl sulphate). The tablets may be coated by methods well-known in the art. Liquid preparations for oral administration may take the form of, for example, solutions, syrups or suspensions, or they may be presented as a dry product for constitution with water or other suitable vehicle before use. Such liquid preparations may be prepared by conventional means with pharmaceutically acceptable additives such as suspending agents (e.g., sorbitol syrup, cellulose derivatives or hydrogenated edible fats); emulsifying agents (e.g., lecithin or acacia); non-aqueous vehicles (e.g., almond oil, oily esters, ethyl alcohol or fractionated vegetable oils); and preservatives (e.g., methyl or propyl-p-hydroxybenzoates or sorbic acid). The preparations may also contain buffer salts, flavoring, coloring and sweetening agents as appropriate. Preparations for oral administration may be suitably formulated for slow release, controlled release or sustained release of a prophylactic or therapeutic agent(s).

[00124] If the compositions of the invention are to be administered intranasally, the compositions can be formulated in an aerosol form, spray, mist or in the form of drops. In particular, prophylactic or therapeutic agents for use according to the present invention can be

conveniently delivered in the form of an aerosol spray presentation from pressurized packs or a nebuliser, with the use of a suitable propellant, e.g., dichlorodifluoromethane, trichlorofluoromethane, dichlorotetrafluoroethane, carbon dioxide or other suitable gas. In the case of a pressurized aerosol the dosage unit may be determined by providing a valve to deliver a metered amount. Capsules and cartridges of, e.g., gelatin for use in an inhaler or insufflator may be formulated containing a powder mix of the compound and a suitable powder base such as lactose or starch.

[00125] The compositions of the invention may be formulated for parenteral administration by injection, e.g., by bolus injection or continuous infusion. Formulations for injection may be presented in unit dosage form, e.g., in ampoules or in multi-dose containers, with an added preservative. The compositions may take such forms as suspensions, solutions or emulsions in oily or aqueous vehicles, and may contain formulatory agents such as suspending, stabilizing and/or dispersing agents. Alternatively, the active ingredient may be in powder form for constitution with a suitable vehicle, e.g., sterile pyrogen-free water, before use.

[00126] If the compositions of the invention are to be administered topically, the compositions can be formulated in the form of, e.g., an ointment, cream, transdermal patch, lotion, gel, oral gel, spray, aerosol, solution, emulsion, or other form well-known to one of skill in the art. See, e.g., Remington's Pharmaceutical Sciences and Introduction to Pharmaceutical Dosage Forms, 4^{sup}.th ed., Lea & Febiger, Philadelphia, Pa. (1985). For non-sprayable topical dosage forms, viscous to semi-solid or solid forms comprising a carrier or one or more excipients compatible with topical application and having a dynamic viscosity preferably greater than water are typically employed. Suitable formulations include, without limitation, solutions, suspensions, emulsions, creams, ointments, powders, liniments, salves, and the like, which are, if desired, sterilized or mixed with auxiliary agents (e.g., preservatives, stabilizers, wetting agents, buffers, or salts) for influencing various properties, such as, for example, osmotic pressure. Other suitable topical dosage forms include sprayable aerosol preparations wherein the active ingredient, preferably in combination with a solid or liquid inert carrier, is packaged in a mixture with a pressurized volatile (e.g., a gaseous propellant, such as freon), or in a squeeze bottle. Moisturizers or humectants can also be added to pharmaceutical compositions and dosage forms if desired. Examples of such additional ingredients are well-known in the art.

[00127] In addition to the formulations described above, the compositions of the invention may also be formulated as a depot preparation. Such long acting formulations may be administered by implantation (for example subcutaneously or intramuscularly) or by intramuscular injection. Thus, for example, the compositions may be formulated with suitable polymeric or hydrophobic materials (for example as an emulsion in an acceptable oil) or ion exchange resins, or as sparingly soluble derivatives, for example, as a sparingly soluble salt.

[00128] Generally, the ingredients of compositions of the invention, such as nucleic acids or proteins are supplied either separately or mixed together in unit dosage form, for example, as a dry lyophilized powder or water free concentrate in a hermetically sealed container such as an ampoule or sachette indicating the quantity of active agent. If the composition is to be administered by infusion, it can be dispensed with an infusion bottle containing sterile pharmaceutical grade water or saline. Where the composition is administered by injection, an ampoule of sterile water for injection or saline can be provided so that the ingredients may be mixed prior to administration.

EXAMPLES

[00129] It is understood that the following examples and embodiments described herein are for illustrative purposes only and that various modifications or changes in light thereof will be suggestive to persons skilled in the art and are to be included within the spirit and purview of this application and the scope of the appended claims. All publications, patents, and patent applications cited herein are hereby incorporated by reference in their entirety for all purposes.

[00130] Unless otherwise specified, in the examples provided below, animals were maintained as follows.

[00131] Animal maintenance

[00132] Postnatal day 80 male Wistar rats (300-350g) were obtained from the Biomedical Facility at University College Dublin and were group housed on a 12:12 light/dark cycle, with ad libitum access to food and water. The animals were introduced into the experimental rooms 5 days prior to commencement of training. On the 2 days prior to training the animals were handled, their weights monitored and spontaneous behavior assessed in an open field apparatus (620 mm long, 620 mm wide, 150 mm high). The floor of the open field was ruled into a series of squares (77x77 mm), the animal was placed in the

centre and the number of lines crossed in a 5-minute period counted. Other behaviors assessed included rearing, grooming, piloerection, defecation and posture. All observations were carried out in the quiet room under low-level red illumination between 08:00 and 12:00 to minimize circadian influence. Naïve littermates were treated precisely as their trained counterparts except they were not exposed to the training environment prior to sacrifice.

EXAMPLE 1

Social Isolation Rearing Leads to Deficits in Sensorimotor Gating

[00133] **Materials and Methods**

[00134] ***Isolation rearing***

[00135] Isolation-reared animals (isolated animals) were housed singly in non-soft bottom cages (22.5 cm x 34.5 cm x 17 cm), from time of weaning (postnatal day 25, P25) until completion of behavioral testing. A standard 12 hour light/dark cycle was observed and food and water was provided ad libitum. Noise and visual stimuli were kept to an absolute minimum as described previously by Geyer et al., 1993. Socially reared animals (social animals) were housed in groups of 4 from time of weaning until surgical implantation of a guide cannula on P80, there after they were housed singly. Soft bottom cages were used (27.5 cm x 40.5 cm x 20.1 cm), a standard 12 hour light/dark cycle observed and food and water provided ad libitum. The cages were floored with sawdust and contained a single open-ended cardboard cylinder for environmental enrichment.

[00136] ***Maternal Deprivation***

[00137] The maternal deprivation protocol employed was as described previously (Ellenbroek et al 1998). Briefly, rat pups were isolated from their mothers for a single 24-hour period on P9. The dams were housed in the same room as the pups but in a separate cage. At the end of the 24-hour period the dams were returned to their litters and left undisturbed until weaning on P25. After weaning on P25 pups were housed in groups of four per cage. Social control animals were reared in groups of four under standard conditions. All animals were housed singly from P80, just prior to behavioral manipulation and/or surgery.

[00138] ***Prepulse inhibition of startle response*** (Ellenbroek et al., 1998)

[00139] The startle apparatus consisted of a sound attenuating chamber (54.6 x 50.8 x 30.5 cm), a startle platform which measured the startle response, and an audio stimulator, controlled by the startle reflex software (MED Associates Inc.). Animals were restrained in

an appropriately sized animal holder, placed on the startle platform. Animals were placed in the apparatus and allowed to acclimatize to a background noise of 70dB[A] for 5 minutes. Subsequently, the animals received five startle trials (120bD[A] burst of white noise lasting 20ms). Next, the rats received five blocks of trials, consisting of two startle trials and four prepulse inhibition trials (of differing prepulse intensity), as well as a no stimulus condition. The prepulse inhibition trials consisted of a prepulse stimulus of 72, 76, 80 or 84dB[A] burst of white noise, followed 100ms later by the startle stimulus of 120dB[A]. The inter-trial interval was between 10 and 20s. The session terminated with five further startle trials. The resulting movement of the rats was measured during 100ms after startle stimulus onset, and then rectified, amplified and analyzed by computer and the maximal response and average response over the 100ms period determined. Baseline startle amplitude was determined as the mean response of all startle trials. The per cent prepulse inhibition was determined according to the following formula: $100 - ([\text{startle amplitude at prepulse trial} / \text{startle amplitude at startle trial}] \times 100\%)$. The effect on baseline startle amplitude was analyzed by a one-way analysis of variance (ANOVA). The effect of rearing on PPI was determined by 2-way ANOVA (factors: rearing and prepulse intensity), with post-hoc Bonferroni tests.

[00140] Separate cohorts of animals were analyzed at P30, P40, P60 and P80 (P = postnatal day). All isolation reared animals were compared to age-matched social controls and all maternally deprived animals were compared to age-matched non-deprived controls (raised in cages of 3-4 from weaning, n=8/group). Isolated animals exhibited impaired sensorimotor gating as measured by prepulse inhibition, when analyzed at P60, and this deficit was maintained at P80 (FIG. 1A).

EXAMPLE 2

Social Isolation Rearing and Maternal Deprivation Lead to Deficits in Spatial Memory

[00141] Materials and Methods

[00142] Isolation reared animals, maternally deprived animals, socially reared controls, and non-deprived controls were maintained as described in Example 1.

[00143] *Water maze training*

[00144] The spatial learning task has been described in detail previously (Murphy et al., 1996). The water maze apparatus consisted of a large circular pool (1 m diameter, 80 cm

high, temperature $26 \pm 1^\circ\text{C}$) with a platform (11 cm diameter) submerged 1.5 cm below the water surface. Both the pool and the platform were constructed of black polyvinyl plastic and offered no intra-maze cues to guide escape behavior. The experimental room contained several extra-maze visual cues. During training the platform was hidden in the same quadrant 30 cm from the edge of the maze. Each trial started with the rat facing the wall of the maze at one of three locations. The time taken by the rat to find the hidden platform within a 60 sec period was recorded. On the first trial, rats failing to find the platform within the 60 sec period were placed on it for 10 sec. Times to the platform were measured over 5 trials in the training session with an inter-trial interval of 300 sec. To control for stress and other non-learning associated factors during water maze training each trained animal was paired with a corresponding passive control animal that was allowed to swim in the maze for a time matching its trained counterpart for each trial but in the absence of a platform.

[00145] Separate cohorts were analyzed at P30, P40, P60 and P80. All isolation reared animals were compared to age-matched social controls and all maternally deprived animals were compared to age-matched non-deprived controls (raised in cages of 3-4 from weaning, $n=8/\text{group}$). Socially isolated animals and maternally deprived exhibited impaired spatial learning when analyzed at P60 in the Water Maze task (FIG. 2).

EXAMPLE 3

mRNA Expression Profiles in Prefrontal Cortex (PFC) in Socially Isolated Animals and Maternally Deprived Animals

[00146] Materials and Methods

[00147] Isolation reared animals, maternally deprived animals, socially reared controls, and non-deprived controls were maintained as described in Example 1.

[00148] *Sample collection*

[00149] In order to determine schizophrenia-associated developmental alterations of mRNA expression in the rat medial prefrontal cortex, this brain region was dissected from postnatal day 30, 40, 60 and 80 in isolation reared animals, socially housed control counterparts, maternally deprived animals, and non-deprived counterparts. Animals were killed by cervical dislocation, the medial prefrontal cortex rapidly dissected and snap frozen. All experimental procedures were approved by the Animal Research Ethics Committee of the Biomedical Facility at University College, Dublin, and were carried out by individuals who held the appropriate license issued by the Minister for Health and Children.

[00150] *Microarray and Real-time Sample preparation*

[00151] Total RNA was extracted from each medial prefrontal cortex by homogenisation in TRIzol reagent (Invitrogen, Carlsbad, CA, USA) and following the TRIzol protocol. The resulting RNA samples were purified using an RNeasy mini kit (Qiagen, UK). RNA concentration was determined spectrophotometrically, and RNA integrity was confirmed by agarose gel electrophoresis. Double-stranded cDNA was synthesised from 10µg total RNA (Superscript System, Invitrogen, Carlsbad, CA, USA). Briefly, the RNA was mixed with 100pmol oligonucleotide GGCCATGGAATTGTAATACGACTCACTATAGGGAGGCGG (dT)₂₄ in 20µl water, annealed at 70°C for 10 min, and quick-chilled. Buffer, dithiothreitol, and dNTP mix were then added and incubated at 37°C for 2 min. Second-strand synthesis was performed by adding reaction buffer, dNTPs (200M), DNA ligase (10U), DNA polymerase (40U), ribonuclease H (2U), and water (to a final volume of 150µl), and the reaction was incubated for 2h at 16°C. This was followed by addition of 10U T4 DNA polymerase and incubation at 16°C for 5 min. The cDNA was purified by phenol/chloroform extraction, precipitated, and transcribed in vitro using T7 RNA polymerase. Biotinylated cRNA was generated using the BioArray HighYield RNA Transcription Kit (Enzo Diagnostics, Inc., Farmingdale, NY). The cRNA was purified by RNeasy minispin columns and fragmented by incubation in 40mM Tris (pH 8.1), 100mM potassium acetate, and 30mM magnesium acetate buffer at 94°C for 35 min.

[00152] *Microarray analysis*

[00153] Fragmented cRNA for each sample was hybridised to the Affymetrix rat genome RG230.02 chip using the protocol outlined in the GeneChip Expression Analysis Technical Manual (Affymetrix Inc., Santa Clara, CA, USA). Hybridized chips were washed and stained using Affymetrix Fluidics Station 400 and EukGE-WS1 Standard Format as recommended by the manufacturer. The staining was performed using streptavidin-phycoerythrin conjugate (SAPE; Molecular Probes, Eugene, OR, USA), followed by biotinylated antibody against streptavidin (Vector Laboratories, Burlingame, CA, USA), and then SAPE. The chips were scanned using a Hewlett-Packard GeneArray Scanner and analyzed using Affymetrix MAS5.0 software. Hybridization intensities were normalized using a method featuring a pool of 11 biotin-labeled cRNA control transcripts, derived by in vitro transcription of 11 cloned *Bacillus subtilis* genes, which were spiked into each hybridization experiment. This normalization method has been described in detail previously

(Hill et al., 2001). The 5'/3' ratio for glyceraldehydes-3-phosphate dehydrogenase (GAPDH) and for beta-actin ranged from 0.8 to 1.1.

[00154] DNA microarrays were used to study the mRNA expression profiles of rat prefrontal cortex over time following social isolation rearing. The prefrontal cortex is the area of the brain attributed to processing deficits associated with schizophrenia. Identification of time for emergence of sensory processing and cognition deficits in the animal models of isolation rearing allowed analysis of transcriptional change in the presymptomatic (postnatal days 30 and 40) and symptomatic periods. Over the developmental timeframe investigated, in excess of 2000 genes were observed to change significantly in animals maintained in isolation from time of weaning. A transient increase in 600-700 transcripts was observed at postnatal 60, the so-called 'P60 spike' (FIG. 3 represents a fraction of these transcripts).

[00155] The P60 spike was associated with a substantial number of unknown ESTs that exhibited the same significant elevations in transcription at this postnatal age as was observed with genes known to be associated with schizophrenia (FIG. 3). Analysis of the known genes in this core group revealed several transcripts of interest with respect to a potential role in schizophrenia signaling cascades, such as GABAA receptor alpha4 and complexin I, as well as parvalbumin (FIG. 3). These transcripts shared a characteristic temporal pattern of regulation following social isolation rearing, with decreases in expression at P40, and sharp increases in expression at P60 (FIG. 3).

[00156] This distinctive pattern of transcript modulation was used to develop a 'seed pattern' with which the entire transcriptional data set could be interrogated. This has generated a unique database of ESTs likely to have a significant role in schizophrenia. Collectively, these genes can be considered a core transcriptional program for schizophrenia. The potential of the unknown genes as targets for regulating schizophrenia and its symptoms is underpinned by the validation of the co-regulating known genes at message, protein and functional levels. Information about the unknown gene transcripts is provided in Table 1.

TABLE 1.

Code	Affy ID	Gene Name
UK1	1390262_a_at	DnaJ (Hsp40) homolog, subfamily C, member 9 (predicted)
UK2	1384043_at	Transcribed locus
UK3	1376245_x_at	DnaJ (Hsp40) homolog, subfamily C, member 9 (predicted)

UK4	1375443_at	Similar to gene trap ROSA b-geo 22
UK5	1381054_at	Similar to KIAA0980 protein (predicted)
UK6	1382299_at	Transcribed locus
UK7	1380870_at	Similar to RIKEN cDNA 1700040L02 (predicted)
UK8	1375648_at	Similar to hypothetical protein (predicted)
UK9	1391249_at	Similar to DD1 (predicted)
UK10	1377448_at	Similar to RIKEN cDNA 1110001E17 (predicted)

[00157] The P30 spike was associated with a substantial number of unknown ESTs that exhibited the same significant elevations in transcription at this postnatal age as was observed with genes known to be associated with an anti-viral response (FIG. 7). Analysis of the known genes in this core group revealed several transcripts of interest with respect to interferon signaling, including interferon regulatory factor 7, PKR, Ifi44, Ifit2, Irf7, Isgf3g, G1p2, Mx1, Mx2, and SEQ ID NO: 11 through SEQ ID NO: 16 (FIG. 7). These transcripts shared a characteristic temporal pattern of regulation following maternal deprivation, with increases in expression at P30, and sharp decreases in expression at P40 (FIG. 7).

[00158] Collectively, these genes can be considered a core transcriptional program for schizophrenia. The potential of the unknown genes as targets for regulating schizophrenia and its symptoms is underpinned by the validation of the co-regulating known genes at message, protein and functional levels. Information about the unknown gene transcripts is provided in Table 2.

TABLE 2

Code	Affy ID	Gene Name
UK11	1391754_at	(2',5'-oligoadenylate synthetase 1, 40/46kDa, 2'-5' oligoadenylate synthetase 1F, 2'-5' oligoadenylate synthetase 1I)
UK12	1370913_at	(Best5 protein, hypothetical gene supported by NM_138881)
UK13	1372604_at	(hypothetical protein LOC503164, similar to RIKEN cDNA 2210421G13)
UK14	1379285_at	similar to 5830458K16Rik protein (predicted)
UK15	1397304_at	Transcribed locus
UK16	1378082_at	Transcribed locus
Ifi44	1381014_at	interferon-induced protein 44 (predicted)
Ifit2	1379568_at	interferon-induced protein with tetratricopeptide repeats 2 (predicted)
Irf7	1383564_at	interferon regulatory factor 7 (predicted)
Isgf3g	1374627_at	interferon dependent positive acting transcription factor 3 gamma (predicted)

G1p2	1382314_at	interferon, alpha-inducible protein (clone IFI-15K) (predicted)
Mx1	1371015_at	myxovirus (influenza virus) resistance 1
Mx2	1369202_at	myxovirus (influenza virus) resistance 2

[00159] Genes and gene fragments identified as changing significantly in animals that were reared in social isolation, relative to social control animals on postnatal day 30 (P30) are provided in Table 3.

TABLE 3

Fragment Name	Gene Name	Gene Symbol
1394490_at	(ATP-binding cassette, sub-family A (ABC1), member 1, hypothetical gene supported by NM_178095)	(Abca1, LOC497803)
1392108_at	(ATP-binding cassette, sub-family C (CFTR/MRP), member 3, aldehyde oxidase 3, chemokine (C-C motif) ligand 9 (predicted), enoyl-Coenzyme A, hydratase/3-hydroxyacyl Coenzyme A dehydrogenase, guanosine monophosphate reductase 2, tumor necrosis factor receptor)	(Abcc3, Aox3, Ccl9_predicted, Ehadh, Gmpr2, Tnfrsf1b)
1387210_at	(discs, large homolog 4 (Drosophila), hypothetical gene supported by NM_019621)	(Dlgh4, LOC497670)
1369471_at	(LOC499775, rapostlin)	(Frbp1, LOC499775)
1370454_at	(HS1 binding protein, homer homolog 1 (Drosophila))	(Homer1, Hs1bp1)
1370997_at	(HS1 binding protein, homer homolog 1 (Drosophila))	(Homer1, Hs1bp1)
1382331_at	(similar to RIKEN cDNA 0610038L10 gene, similar to riboflavin kinase)	(LOC317214, LOC499328)
1389734_x_at	(MHC class I RT1.O type 149 processed pseudogene, RT1 class I, T24, gene 4, RT1 class Ib, locus H2-TL-like (S2), RT1 class Ib, locus S3, similar to class I histocompatibility antigen alpha chain - cotton-top tamarin)	(LOC360231, LOC499402, RT1-149, RT1-S2, RT1-S3)
1370428_x_at	(RT1 class I, A3, RT1 class I, CE10, RT1 class I, CE3, RT1 class I, CE7, RT1 class Ia, locus A2, RT1 class Ib, locus Aw2)	(RT1-A2, RT1-A3, RT1-Aw2, RT1-CE10, RT1-CE3, RT1-CE7)
1390706_at	(short form of beta II spectrin, spectrin beta 2)	(Spnb1, Spnb2)
1380577_at	ATP-binding cassette, sub-family G (WHITE), member 2	Abcg2
1398836_s_at	actin, beta	Actb
1374419_at	adenylate cyclase 9 (predicted)	Adcy9_predicted
1369326_at	A kinase (PRKA) anchor protein 6	Akap6
1369063_at	acidic (leucine-rich) nuclear phosphoprotein 32 family, member A	Anp32a

1387068_at	activity regulated cytoskeletal-associated protein	Arc
1391658_at	archain	Arcn1
1380525_at	arylsulfatase E (chondrodysplasia punctata 1) (predicted)	Arse_predicted
1387234_at	alpha-2-glycoprotein 1, zinc	Azgp1
1391293_at	butyrobetaine (gamma), 2-oxoglutarate dioxygenase 1 (gamma-butyrobetaine hydroxylase)	Bbox1
1369733_at	catenin beta	Catnb
1388026_at	CD3 antigen, zeta polypeptide	Cd3z
1371278_at	cell division cycle 34 homolog (S. cerevisiae) (predicted)	Cdc34_predicted
1397673_at	CUG triplet repeat,RNA-binding protein 2	Cugbp2
1375231_a_at	CXXC finger 5	Cxxc5
1371142_at	cytochrome P450, subfamily 2G, polypeptide 1	Cyp2g1
1385871_at	DEAH (Asp-Glu-Ala-His) box polypeptide 36 (predicted)	Dhx36_predicted
1391602_at	developmentally regulated GTP binding protein 1 (predicted)	Drg1_predicted
1368146_at	dual specificity phosphatase 1	Dusp1
1368321_at	early growth response 1	Egr1
1387306_a_at	early growth response 2	Egr2
1387442_at	early growth response 4	Egr4
1375043_at	FBJ murine osteosarcoma viral oncogene homolog	Fos
1390686_at	gamma-aminobutyric acid (GABA) A receptor, subunit gamma 3	Gabrg3
1368074_at	galactose-4-epimerase, UDP	Gale
1379926_at	guanine nucleotide binding protein, alpha 12	Gna12
1388085_at	glutathione peroxidase 6	Gpx6
1376412_at	glutamate receptor, ionotropic, 4	Gria4
1379546_at	hematological and neurological expressed sequence 1	Hn1
1383564_at	interferon regulatory factor 7 (predicted)	Irf7_predicted

1376845_at	putative ISG12(b) protein	isg12(b)
1382535_at	potassium channel tetramerisation domain containing 12 (predicted)	Kctd12_predicted
1384608_at	RN protein	LOC171116
1391426_a_at	similar to PEST-containing nuclear protein	LOC288165
1393436_at	similar to potential ligand-binding protein	LOC309100
1399073_at	similar to HSPC263	LOC314660
1385832_s_at	similar to RIKEN cDNA 1200013B08	LOC317578
1389270_x_at	similar to ATPase inhibitor	LOC497829
1374328_at	similar to hypothetical protein	LOC499213
1385656_at	similar to hypothetical protein MGC13034	LOC499516
1376792_at	similar to CDNA sequence BC014699	LOC500221
1375073_at	similar to sterile alpha motif domain containing 11	LOC500601
1391595_at	similar to ribosomal protein L21	LOC503211
1380177_at	methionine adenosyltransferase II, alpha	Mat2a
1379333_at	similar to ALEX3 protein; arm protein lost in epithelial cancers, X chromosome, 3	MGC93796
1369623_at	morphine related protein-1 (RefSeq = NM_022613)	Morp1
1375180_at	MARVEL (membrane-associating) domain containing 1 (predicted)	Mrvldc1_predicted
1370783_a_at	membrane-spanning 4-domains, subfamily A, member 2	Ms4a2
1385125_at	transcription factor myocardin	Myocd
1386935_at	nuclear receptor subfamily 4, group A, member 1	Nr4a1
1368958_at	protein kinase C and casein kinase substrate in neurons 1	Pacsin1
1377122_at	phosphodiesterase 1A, calmodulin-dependent	Pde1a
1383294_at	prodynorphin	Pdyn
1371250_at	platelet factor 4	Pf4
1383037_at	polymerase (DNA-directed), delta interacting protein 2 (predicted)	Poldip2_predicted

1375328_at	protease, serine, 21	Prss21
1380604_at	pumilio 2 (Drosophila) (predicted)	Pum2_predicted
1386900_at	ribosome associated membrane protein 4	RAMP4
1369614_at	RAP2B, member of RAS oncogene family	Rap2b
1378287_at	radixin	Rdx
1375542_at	radixin	Rdx
1391042_at	similar to Metal-response element-binding transcription factor 2 (Metal-response element DNA-binding protein M96) (predicted)	RGD1304727_predicted
1397194_at	similar to CG5554-PA (predicted)	RGD1305146_predicted
1385426_at	similar to hypothetical protein FLJ20647 (predicted)	RGD1305326_predicted
1398609_at	similar to Rnf37-pending protein (predicted)	RGD1305440_predicted
1384553_at	similar to hypothetical protein FLJ13089 (predicted)	RGD1305685_predicted
1374258_at	similar to hypothetical protein MGC13138 (predicted)	RGD1306928_predicted
1375648_at	similar to hypothetical protein (predicted)	RGD1307966_predicted
1389269_at	similar to RIKEN cDNA 4933433P14 gene (predicted)	RGD1308470_predicted
1373814_at	similar to mKIAA1002 protein (predicted)	RGD1310066_predicted
1391387_s_at	similar to RIKEN cDNA 0610039G24 gene (predicted)	RGD1310828_predicted
1376152_at	similar to flavoprotein oxidoreductase MICAL2 (predicted)	RGD1311773_predicted
1398854_at	ribosomal protein L24	Rpl24
1375788_at	ribosomal protein L7	Rpl7
1390919_at	splicing factor, arginine/serine-rich 8 (suppressor-of-white-apricot homolog, Drosophila) (predicted)	Sfrs8_predicted
1389949_at	sialyltransferase 7c	Siat7c
1369020_at	solute carrier family 5 (sodium iodide symporter), member 5	Slc5a5
1389067_at	solute carrier organic anion transporter family, member 4a1	Slco4a1
1381394_at	PDZ protein Mrt1	Snx27

1388396_at	serine/threonine kinase 25 (STE20 homolog, yeast)	Stk25
1397148_at	stomatin (Epb7.2)-like 3 (predicted)	Stoml3_predicted
1387662_at	synaptotagmin 4	Syt4
1387484_at	transforming growth factor, beta receptor 3	Tgfb3
1368650_at	TGFB inducible early growth response	Tieg
1371029_at	tuberous sclerosis 2	Tsc2
1367598_at	transthyretin	Ttr
1369413_at	Unc4.1 homeobox (C. elegans)	Uncx4.1
1386909_a_at	voltage-dependent anion channel 1	Vdac1
1396688_at	voltage-dependent anion channel 2	Vdac2

[00160] Genes and gene fragments identified as changing significantly in animals that were reared in social isolation, relative to social control animals on postnatal day 40 (P40) are provided in Table 4.

TABLE 4

Fragment Name	Gene Name	Gene Symbol
1370464_at	(ATP-binding cassette, sub-family B (MDR/TAP), member 1, ATP-binding cassette, sub-family B (MDR/TAP), member 1A, ATP-binding cassette, sub-family B (MDR/TAP), member 4)	(Abcb1, Abcb1a, Abcb4)
1392108_at	(ATP-binding cassette, sub-family C (CFTR/MRP), member 3, aldehyde oxidase 3, chemokine (C-C motif) ligand 9 (predicted), enoyl-Coenzyme A, hydratase/3-hydroxyacyl Coenzyme A dehydrogenase, guanosine monophosphate reductase 2, tumor necrosis factor receptor (acid phosphatase 1, soluble, son of sevenless homolog 2 (Drosophila)))	(Abcc3, Aox3, Ccl9_predicted, Ehadh, Gmpr2, Tnfrsf1b)
1387840_at	(acid phosphatase 1, soluble, son of sevenless homolog 2 (Drosophila))	(Acp1, Sos2)
1383079_at	(apoptotic peptidase activating factor 1, ceroid-lipofuscinosis, neuronal 2, chemokine (C-C) receptor 5, galactose mutarotase (aldose 1-epimerase), glycine C-acetyltransferase (2-amino-3-ketobutyrate-coenzyme A ligase) (predicted), proteasome (prosome, ma	(Apaf1, Ccr5, Cln2, Galm, Gcat_predicted, LOC501658, Psmid9)
1391673_at	(Rho GTPase activating protein 20, hypothetical gene supported by NM_213629)	(Arhgap20, LOC497830)
1370913_at	(Best5 protein, hypothetical gene supported by NM_138881)	(Best5, LOC497812)
1370892_at	(complement component 4, gene 2, complement component 4a)	(C4-2, C4a)
1395412_at	(GPI-anchored membrane protein 1 (predicted), similar to GPI-anchored membrane protein 1)	(Gpiap1_predicted, LOC362174)
1371245_a_at	(beta-glo, hemoglobin beta chain complex)	(Hbb, MGC72973)
1369868_at	(hypothetical gene supported by NM_053946, implantation-associated protein)	(Iag2, LOC497846)
1387770_at	(interferon, alpha-inducible protein 27-like, putative ISG12(a) protein)	(Ifi271, isg12(a))
1387995_a_at	(interferon induced transmembrane protein 2 (1-8D), interferon induced transmembrane protein 3)	(Ifitm2, Ifitm3)
1370801_at	(integrin, beta 5, similar to integrin beta-5)	(Itgb5, LOC498091)

1381030_at	(similar to step II splicing factor SLU7; DNA segment, Chr 11, ERATO Doi 730, expressed; DNA segment, Chr 3, Brigham & Womens Genetics 0878 expressed, step II splicing factor SLU7 (S. cerevisiae))	(LOC303057, Slu7)
1398588_at	(similar to step II splicing factor SLU7; DNA segment, Chr 11, ERATO Doi 730, expressed; DNA segment, Chr 3, Brigham & Womens Genetics 0878 expressed, step II splicing factor SLU7 (S. cerevisiae))	(LOC303057, Slu7)
1397824_at	similar to WAC	(LOC307029, LOC361260)
1372604_at	(hypothetical protein LOC503164, similar to RIKEN cDNA 2210421G13)	(LOC315106, LOC503164)
1382331_at	(similar to RIKEN cDNA 0610038L10 gene, similar to riboflavin kinase)	(LOC317214, LOC499328)
1388212_a_at	(MHC class I RT1.O type 149 processed pseudogene, RT1 class I, T24, gene 4, RT1 class Ib, locus H2-TL-like (S2), RT1 class Ib, locus S3, similar to class I histocompatibility antigen alpha chain - cotton-top tamarin)	(LOC360231, LOC499402, RT1-149, RT1-S2, RT1-S3)
1389734_x_at	(MHC class I RT1.O type 149 processed pseudogene, RT1 class I, T24, gene 4, RT1 class Ib, locus H2-TL-like (S2), RT1 class Ib, locus S3, similar to class I histocompatibility antigen alpha chain - cotton-top tamarin)	(LOC360231, LOC499402, RT1-149, RT1-S2, RT1-S3)
1388164_at	(MHC class I RT1.O type 149 processed pseudogene, RT1 class I, T24, gene 4, RT1 class Ib, locus H2-TL-like (S2), RT1 class Ib, locus S3, similar to class I histocompatibility antigen alpha chain - cotton-top tamarin)	(LOC360231, LOC499402, RT1-149, RT1-S2, RT1-S3)
1371123_x_at	(MHC class I RT1.O type 149 processed pseudogene, RT1 class I, T24, gene 4, RT1 class Ib, locus H2-TL-like (S2), RT1 class Ib, locus S3, similar to class I histocompatibility antigen alpha chain - cotton-top tamarin)	(LOC360231, LOC499402, RT1-149, RT1-S2, RT1-S3)
1388213_a_at	(MHC class I RT1.O type 149 processed pseudogene, RT1 class I, T24, gene 4, RT1 class Ib, locus H2-TL-like (S2), RT1 class Ib, locus S3, similar to class I histocompatibility antigen alpha chain - cotton-top tamarin)	(LOC360231, LOC499402, RT1-149, RT1-S2, RT1-S3)
1370500_a_at	(hypothetical gene supported by NM_012720, myelin-associated oligodendrocytic basic protein)	(LOC360443, Mobp)
1377174_at	(SET binding factor 1 (predicted), similar to mKIAA3020 protein)	(LOC362985, Sbf1_predicted)
1397522_at	(SET binding factor 1 (predicted), similar to mKIAA3020 protein)	(LOC362985, Sbf1_predicted)
1370642_s_at	(hypothetical gene supported by NM_031525, platelet derived growth factor receptor, beta polypeptide)	(LOC497724, Pdgfrb)
1368150_at	(hypothetical gene supported by NM_031736, solute carrier family 27 (fatty acid transporter), member 2)	(LOC497779, Slc27a2)

1387837_at	adenomatosis polyposis coli	Apc
1395894_at	apoptosis inhibitor 5 (predicted)	Api5_predicted
1380533_at	amyloid beta (A4) precursor protein	App
1387068_at	activity regulated cytoskeletal-associated protein	Arc
1398817_at	ADP-ribosylation factor 1	Arf1
1368925_a_at	Rho guanine nucleotide exchange factor 7	Arhgef7
1371108_a_at	ATPase, Na ⁺ /K ⁺ transporting, alpha 1 polypeptide	Atp1a1
1369798_at	ATPase, Na ⁺ /K ⁺ transporting, beta 2 polypeptide	Atp1b2
1377386_at	ATPase, Ca ⁺⁺ -sequestering	Atp2c1
1389470_at	B-factor, properdin	Bf
1386994_at	B-cell translocation gene 2, anti-proliferative	Btg2
1398251_a_at	calcium/calmodulin-dependent protein kinase II beta subunit	Camk2b
1369993_at	calcium/calmodulin-dependent protein kinase II gamma	Camk2g
1371687_at	calnexin	Canx
1369733_at	catenin beta	Catnb
1392937_at	cyclin I (predicted)	Ccni_predicted
1368976_at	CD38 antigen	Cd38
1369025_at	CD5 antigen	Cd5
1387695_at	Cdc42-binding protein kinase beta	Cdc42bpb
1375719_s_at	cadherin 13	Cdh13
1369538_at	cyclin-dependent kinase 5, regulatory subunit 1 (p35)	Cdk5r
1368449_at	centaurin, alpha 1	Centa1
1380063_at	cholesterol 25-hydroxylase (predicted)	Ch25h_predicted
1369239_at	chloride channel 5	Clcn5
1369609_at	claudin 11	Cldn11

1370693_a_at	cyclic nucleotide phosphodiesterase 1	Cnp1
1370864_at	collagen, type 1, alpha 1	Col1a1
1388116_at	collagen, type 1, alpha 1	Col1a1
1370155_at	procollagen, type I, alpha 2	Col1a2
1369811_at	complexin 1	Cplx1
1369495_at	corticotropin releasing hormone receptor 2	Crhr2
1383761_at	Chorionic somatomammotropin hormone 1 variant; Placental lactogen-1	Csh1v
1387879_a_at	CUG triplet repeat,RNA-binding protein 2	Cugbp2
1369136_at	Cytochrome P450, subfamily IIA (phenobarbital-inducible)/ (Cytochrome P450 IIA3)	Cyp2a3a
1368608_at	cytochrome P450, family 2, subfamily f, polypeptide 2	Cyp2f2
1371142_at	cytochrome P450, subfamily 2G, polypeptide 1	Cyp2g1
1370387_at	cytochrome P450, family 3, subfamily a, polypeptide 13	Cyp3a13
1390738_at	DAMP-1 protein	Damp1
1391463_at	DEAD (Asp-Glu-Ala-Asp) box polypeptide 58 (predicted)	Ddx58_predicted
1391406_at	degenerative spermatocyte homolog (Drosophila)	Degs
1391602_at	developmentally regulated GTP binding protein 1 (predicted)	Drg1_predicted
1395586_at	eukaryotic translation elongation factor 1 alpha 1	Eef1a1
1387306_a_at	early growth response 2	Egr2
1387442_at	early growth response 4	Egr4
1397520_at	eukaryotic translation initiation factor 4 gamma, 2	Elf4g2
1382710_at	ectodermal-neural cortex 1	Enc1
1386907_at	enolase 3, beta	Eno3
1397826_at	erythrocyte protein band 4.9 (predicted)	Epb4.9_predicted
1387715_at	extracellular peptidase inhibitor	Expi
1382173_at	fibrillarin (predicted)	Fbl_predicted

1393252_at	fibulin 1 (predicted)	Fbln1_predicted
1387351_at	fibrillin 1	Fbn1
1383354_a_at	F-box only protein 33 (predicted)	Fbxo33_predicted
1392820_at	fibroblast growth factor 1	Fgf1
1370747_at	fibroblast growth factor 9	Fgf9
1390049_at	four and a half LIM domains 1	Fhl1
1375043_at	FBJ murine osteosarcoma viral oncogene homolog	Fos
1382314_at	interferon, alpha-inducible protein (clone IFI-15K) (predicted)	G1p2_predicted
1369905_at	gamma-aminobutyric acid (GABA-A) receptor, subunit alpha 4	Gabra4
1395269_s_at	gamma-aminobutyric acid A receptor, delta	Gabrd
1388792_at	growth arrest and DNA-damage-inducible 45 gamma (predicted)	Gadd45g_predicted
1368332_at	guanylate nucleotide binding protein 2	Gbp2
1380230_at	GTP cyclohydrolase 1	Gch
1369640_at	gap junction membrane channel protein alpha 1	Gja1
1367633_at	glutamine synthetase 1	Glul
1369278_at	guanine nucleotide binding protein, alpha 12	Gna12
1368952_at	G protein-coupled receptor 51	Gpr51
1388085_at	glutathione peroxidase 6	Gpx6
1391731_at	high mobility group box transcription factor 1	Hbp1
1382902_at	potential ubiquitin ligase	Herc6
AFFX_Rat_Hexokinase_3_at	hexokinase 1	Hk1
AFFX_Rat_Hexokinase_5_at	hexokinase 1	Hk1
AFFX_Rat_Hexokinase_M_at	hexokinase 1	Hk1
1388080_a_at	histamine receptor H3	Hrh3
1382697_at	heterogeneous nuclear ribonucleoprotein methyltransferase-like 3 (S. cerevisiae)	Hrmt113

1387994_at	hydroxysteroid (17-beta) dehydrogenase 9	Hsd17b9
1375335_at	heat shock 90kDa protein 1, beta	Hspcb
1369456_at	5-hydroxytryptamine (serotonin) receptor 2B	Htr2b
1371442_at	hypoxia up-regulated 1	Hyou1
1368416_at	integrin binding sialoprotein	Ibsp
1391489_at	interferon inducible protein 1 (predicted)	Ifi1_predicted
1381014_at	interferon-induced protein 44 (predicted)	Ifi44_predicted
1384180_at	interferon-induced protein with tetratricopeptide repeats 2 (predicted)	Ifit2_predicted
1379568_at	interferon-induced protein with tetratricopeptide repeats 2 (predicted)	Ifit2_predicted
1371148_s_at	internexin, alpha	Inexa
1383564_at	interferon regulatory factor 7 (predicted)	Irf7_predicted
1376845_at	putative ISG12(b) protein	isg12(b)
1383448_at	interferon dependent positive acting transcription factor 3 gamma (predicted)	Isgf3g_predicted
1374627_at	interferon dependent positive acting transcription factor 3 gamma (predicted)	Isgf3g_predicted
1374404_at	v-jun sarcoma virus 17 oncogene homolog (avian)	Jun
1396701_at	kalirin, RhoGEF kinase	Kalm
1382787_at	kinesin family member 5A	Kif5a
1388125_a_at	kinesin 2	Kns2
1383145_at	lysosomal-associated membrane protein 3 (predicted)	Lamp3_predicted
1387946_at	lectin, galactoside-binding, soluble, 3 binding protein	Lgals3bp
1370853_at	CaM-kinase II inhibitor alpha	LOC287005
1385546_at	similar to IQ motif and WD repeats 1	LOC289181
1371382_at	similar to Filamin A (Alpha-filamin) (Filamin 1) (Endothelial actin-binding protein) (Actin-binding protein 280) (ABP-280) (Nonmuscle filamin)	LOC293860
1397512_at	similar to Vps41 protein	LOC306991
1393436_at	similar to potential ligand-binding protein	LOC309100

1379748_at	similar to minor histocompatibility antigen precursor	LOC310968
1389034_at	similar to ubiquitin specific protease UBP43	LOC312688
1396803_at	similar to THO complex 2	LOC313308
1399073_at	similar to HSPC263	LOC314660
1377498_at	similar to adenosine monophosphate deaminase 2 (isoform L)	LOC362015
1391564_at	similar to zinc finger protein 426	LOC363022
1394299_at	similar to brain expressed X-linked protein 2	LOC363498
1373975_at	similar to thioether S-methyltransferase	LOC368066
1381556_at	similar to BC013672 protein	LOC498673
1384547_at	similar to antimicrobial peptide RY2G5	LOC499925
1376693_at	similar to OEF2	LOC500011
1397815_at	similar to ADP-ribosylation factor-like 10C	LOC500282
1387373_at	myomegalin	LOC64183
1368666_a_at	calcium-independent alpha-latrotoxin receptor homolog 3	Lphn3
1384361_at	mal, T-cell differentiation protein 2	Mal2
1387737_at	methionine adenosyltransferase II, alpha	Mat2a
1387341_a_at	myelin basic protein	Mbp
1381403_at	malic enzyme 2, NAD(+)-dependent, mitochondrial (predicted)	Me2_predicted
1372389_at	similar to immediate early response 2	MGC72578
1379891_at	scotin	MGC94600
1370129_at	meningioma expressed antigen 5 (hyaluronidase)	Mgea5
1388204_at	matrix metalloproteinase 13	Mmp13
1372800_at	myeloid ecotropic viral integration site-related gene 2 (predicted)	Mrg2_predicted
1371015_at	myxovirus (influenza virus) resistance 1	Mx1
1369202_at	myxovirus (influenza virus) resistance 2	Mx2

1387283_at	myxovirus (influenza virus) resistance 2	Mx2
1393881_at	NMDA receptor-regulated gene 1 (predicted)	Narg1_predicted
1392581_at	neurocalcin delta	Ncald
1375119_at	neural precursor cell expressed, developmentally down-regulated gene 4A	Nedd4a
1368820_at	nuclear transcription factor-Y gamma	Nfyc
1395408_at	nitric oxide synthase trafficking	Nostrin
1386935_at	nuclear receptor subfamily 4, group A, member 1	Nr4a1
1369689_at	N-ethylmaleimide sensitive fusion protein	Nsf
1396684_at	NTE-related protein	Ntcl
1387639_at	neural visinin-like Ca2+-binding protein type 2	Nvjp2
1369835_at	olfactory marker protein	Omp
1390923_a_at	oxysterol binding protein-like 1A	Osbp11a
1369209_at	p34 protein	P34
1368958_at	protein kinase C and casein kinase substrate in neurons 1	Pacsin1
1396267_at	p21 (CDKN1A)-activated kinase 2	Pak2
1385116_at	protocadherin beta 21 (predicted)	Pcdhb21_predicted
1377122_at	phosphodiesterase 1A, calmodulin-dependent	Pde1a
1369044_a_at	phosphodiesterase 4B	Pde4b
1370833_at	peroxin 2	Pex2
1367970_at	profilin 2	Pfn2
1387238_at	paired-like homeobox 2a	Phox2a
1376137_at	pleckstrin homology domain containing, family B (evectins) member 2 (predicted)	Plekhb2_predicted
1368213_at	P450 (cytochrome) oxidoreductase	Por
1395236_at	protein phosphatase 1, regulatory (inhibitor) subunit 3C (predicted)	Ppp1r3c_predicted
1381024_at	protein phosphatase 2 (formerly 2A), regulatory subunit A (PR 65), alpha	Ppp2r1a

	isoform	
1369297_at	protein phosphatase 2 (formerly 2A), regulatory subunit B (PR 52), gamma isoform	Ppp2r2c
1395409_at	protein phosphatase 2A, regulatory subunit B' (PR 53) (predicted)	Ppp2r4_predicted
1369152_at	protein phosphatase 3, regulatory subunit B, alpha isoform, type 1	Ppp3r1
1394416_at	prickle-like 2 (Drosophila) (predicted)	Prickle2_predicted
1388182_at	DNA primase, p49 subunit	Prim1
1368240_a_at	protein kinase C, beta 1	Prkcb1
1387242_at	Protein kinase, interferon-inducible double stranded RNA dependent	Prkr
1375476_at	muscle glycogen phosphorylase	Pygm
1376029_at	RAB2, member RAS oncogene family-like	Rab2l
1393288_at	RAB5B, member RAS oncogene family (predicted)	Rab5b_predicted
1371103_at	RAB6B, member RAS oncogene family	Rab6b
1398838_at	RAB7, member RAS oncogene family	Rab7
1389811_at	RasGEF domain family, member 1C (predicted)	Rasgef1c_predicted
1369129_at	RAS guanyl releasing protein 1	Rasgrp1
1387622_at	radical fringe gene homolog (Drosophila)	Rfng
1395739_at	similar to RIKEN cDNA C920006C10 (predicted)	RGD1305976_predicted
1379285_at	similar to 5830458K16Rik protein (predicted)	RGD1306974_predicted
1391908_at	similar to retinoid x receptor interacting protein (predicted)	RGD1307009_predicted
1389044_at	similar to golgi-specific brefeldin A-resistance guanine nucleotide exchange factor 1 (predicted)	RGD1307160_predicted
1376144_at	similar to B aggressive lymphoma (predicted)	RGD1307534_predicted
1377683_at	similar to hypothetical protein FLJ13045 (predicted)	RGD1307615_predicted
1385105_at	similar to DKFZP434B168 protein (predicted)	RGD1308014_predicted
1375829_at	similar to RIKEN cDNA 1810055E12 (predicted)	RGD1308326_predicted

1395533_at	similar to KIAA0564 protein (predicted)	RGD1308772_predicted
1377950_at	similar to interferon-inducible GTPase (predicted)	RGD1309362_predicted
1396137_at	similar to RIKEN cDNA C230075L19 gene (predicted)	RGD1310284_predicted
1372034_at	similar to hypothetical protein MGC29390 (predicted)	RGD1310490_predicted
1384334_at	similar to RIKEN cDNA C330023F11 (predicted)	RGD1311440_predicted
1374142_at	similar to RIKEN cDNA E130201N16 (predicted)	RGD1311589_predicted
1394427_at	similar to 4921517L17Rik protein (predicted)	RGD1311678_predicted
1398444_at	similar to RIKEN cDNA 5133400G04 (predicted)	RGD1311742_predicted
1391249_at	similar to DD1 (predicted)	RGD1312005_predicted
1368144_at	regulator of G-protein signaling 2	Rgs2
1369332_a_at	regulating synaptic membrane exocytosis 1	RIMS1
1395699_at	RIO kinase 3 (yeast) (predicted)	RioK3_predicted
1398824_at	coated vesicle membrane protein	Rnp24
1375788_at	ribosomal protein L7	Rpl7
1390777_at	sterol-C5-desaturase (fungal ERG3, delta-5-desaturase) homolog (S. cerevisiae)	Sc5d
1387926_at	sterol-C5-desaturase (fungal ERG3, delta-5-desaturase) homolog (S. cerevisiae)	Sc5d
1386889_at	stearoyl-Coenzyme A desaturase 2	Scd2
1369265_at	SUMO/sentrin specific protease 2	Senp2
1371310_s_at	serine (or cysteine) proteinase inhibitor, clade H, member 1	Serpinh1
1371063_at	SH3 domain protein 2A	Sh3gl2
1368986_at	solute carrier family 17 (sodium-dependent inorganic phosphate cotransporter), member 7	Slc17a7
1388064_a_at	solute carrier family 1 (glial high affinity glutamate transporter), member 3	Slc1a3
1367810_at	choline transporter	Slc6a8
1387094_at	solute carrier organic anion transporter family, member 1a4	Slco1a4

1367563_at	secreted acidic cysteine rich glycoprotein	Sparc
1386541_at	spermatogenesis associated 9 (predicted)	Spat9_predicted
1368835_at	signal transducer and activator of transcription 1	Stat1
1387354_at	signal transducer and activator of transcription 1	Stat1
1372757_at	signal transducer and activator of transcription 1	Stat1
1368844_at	stress 70 protein chaperone, microsome-associated, 60kD human homolog	Stch
1397148_at	stomatin (Epb7.2)-like 3 (predicted)	Stom13_predicted
1387359_at	syntaxin 1A (brain)	Stx1a
1384716_at	synaptotagmin 1	Syt1
1387662_at	synaptotagmin 4	Syt4
1370323_at	thimet oligopeptidase 1	Thop1
1371194_at	tumor necrosis factor alpha induced protein 6	Tnfaip6
1378572_at	toll interacting protein (predicted)	Tollip_predicted
1395794_at	tropomyosin 1, alpha	Tpm1
1385252_at	tripartite motif protein 34 (predicted)	Trim34_predicted
1367598_at	transthyretin	Ttr
1373037_at	ubiquitin-conjugating enzyme E2L 6 (predicted)	Ube2l6_predicted
1384053_at	ubiquitin conjugation factor E4 A	Ube4a
1368858_at	UDP-glucuronosyltransferase 8	Ugt8
1388088_a_at	upstream transcription factor 2	Usf2
1386909_a_at	voltage-dependent anion channel 1	Vdac1
1396462_at	vacuolar protein sorting 4a (yeast)	Vps4a
1396170_at	WW domain binding protein 4 (formin binding protein 21)	Wbp4
1376256_at	WD repeat and FYVE domain containing 1 (predicted)	Wdly1_predicted
1382192_at	extra cellular link domain-containing 1 (predicted)	Xlkd1_predicted

1380071_at	zinc finger CCCH type domain containing 1 (predicted)	Zc3hdc1_predicted
1394975_at	zinc finger, matrin-like (predicted)	Zfml_predicted
1393080_at	zinc finger RNA binding protein (predicted)	Zfr_predicted
1377837_at	zinc finger protein 183 (RING finger, C3HC4 type)	Znf183

[00161] Genes and gene fragments identified as changing significantly in animals that were reared in social isolation, relative to social control animals on postnatal day 60 (P60) are provided in Table 5.

TABLE 5

Fragment Name	Gene Name	Gene Symbol
1370116_at	septin 3	3-Sep
1387436_at	septin 7	7-Sep
1386906_a_at	septin 9	9-Sep
1392108_at	(ATP-binding cassette, sub-family C (CFTR/MRP), member 3, aldehyde oxidase 3, chemokine (C-C motif) ligand 9 (predicted), enoyl-Coenzyme A, hydratase/3-hydroxyacyl Coenzyme A dehydrogenase, guanosine monophosphate reductase 2, tumor necrosis factor receptor	(Abcc3, Aox3, Ccl9_predicted, Ehadh, Gmpr2, Tnfrsf1b)
1383140_at	(5 nucleotidase, 6-pyruvoyl-tetrahydropterin synthase, Ras homolog enriched in brain like 1, angiotensin II receptor-associated protein, apoptotic peptidase activating factor 1, ceroid-lipofuscinosis, neuronal 2, cyclin-dependent kinase-like 1 (CDC2-relat	(Agtrap, Apaf1, Cdkl1_predicted, Cln2, Gcat_predicted, Hspa1b, Keg1, LOC293989, MGC95001, Nt5, Pgsg, Pts, Rhebl1, Spock2_predicted, Tsarg1, Ttc4_predicted, sag)
1370686_at	(SEC6-like 1 (S. cerevisiae), aryl-hydrocarbon receptor repressor)	(Ahrr, Sec6l1)
1383079_at	(apoptotic peptidase activating factor 1, ceroid-lipofuscinosis, neuronal 2, chemokine (C-C) receptor 5, galactose mutarotase (aldose 1-epimerase), glycine C-acetyltransferase (2-amino-3-ketobutyrate-coenzyme A ligase) (predicted), proteasome (prosome, ma	(Apaf1, Ccr5, Cln2, Galm, Gcat_predicted, LOC501658, Psmd9)
1383096_at	(LOC500962, amyloid beta (A4) precursor-like protein 2)	(Aplp2, LOC500962)
1396944_at	(LOC500760, bromodomain adjacent to zinc finger domain, 2A (predicted))	(Baz2a_predicted, LOC500760)
1369211_at	(calcium channel, voltage-dependent, alpha 1I subunit, hypothetical gene supported by NM_020084)	(Cacna1i, LOC497824)
1382113_at	(chemokine (C-C motif) ligand 9 (predicted), similar to expressed sequence A1449175)	(Ccl9_predicted, MGC72612)

1372977_at	(atlastin-like, cyclin-dependent kinase-like 1 (CDC2-related kinase) (predicted), similar to mitogen-activated protein kinase kinase kinase 5 isoform 2)	(Cdkl1_predicted, LOC362750, LOC503027)
1389625_at	(coiled-coil-helix-coiled-coil-helix domain containing 4 (predicted), similar to Coiled-coil-helix-coiled-coil-helix domain containing 4)	(Chchd4_predicted, LOC309309)
1377671_at	(colony stimulating factor 2 receptor, beta 1, low-affinity (granulocyte-macrophage), hypothetical gene supported by NM_133555)	(Csf2rb1, LOC497822)
1368738_at	(cytochrome P450, family 11, subfamily B, polypeptide 2, cytochrome P450, subfamily 11B, polypeptide 1, similar to Cytochrome P450 11B1, mitochondrial precursor (CYPXIB1) (P450C11) (Steroid 11-beta-hydroxylase) (P450(11 beta)-DS))	(Cyp11b1, Cyp11b2, LOC500892)
1372247_at	(dolichyl-di-phosphooligosaccharide-protein glycotransferase, dolichyl-di-phosphooligosaccharide-protein glycotransferase (predicted))	(Ddost, Ddost_predicted)
1388057_a_at	(PSD-95 binding protein, discs, large (Drosophila) homolog-associated protein 1)	(Dlgap1, LOC245710)
1375388_at	(elongation factor RNA polymerase II-like 3 (predicted), glucose regulated protein, 58 kDa)	(Eli3_predicted, Grp58)
1369621_s_at	(FK506 binding protein 2, FK506-binding protein 1a)	(Fkbp1a, Fkbp2)
AFFX_Rat_GAPDH_5_at	(glyceraldehyde-3-phosphate dehydrogenase, similar to glyceraldehyde-3-phosphate dehydrogenase)	(Gapd, LOC498123, LOC500506)
1395412_at	(GPI-anchored membrane protein 1 (predicted), similar to GPI-anchored membrane protein 1)	(Gpiap1_predicted, LOC362174)
1395173_at	(GPI-anchored membrane protein 1 (predicted), similar to GPI-anchored membrane protein 1)	(Gpiap1_predicted, LOC362174)
1370454_at	(HS1 binding protein, homer homolog 1 (Drosophila))	(Homer1, Hs1bp1)
1370997_at	(HS1 binding protein, homer homolog 1 (Drosophila))	(Homer1, Hs1bp1)
1369868_at	(hypothetical gene supported by NM_053946, implantation-associated protein)	(lag2, LOC497846)
1369323_at	(leptin receptor, leptin receptor overlapping transcript)	(Lepr, Leprot)
1398875_at	(estrous-specific protein, 250 kDa, similar to RIKEN cDNA 1500004O14)	(LOC246270, LOC366277)
1398303_s_at	(tropomyosin 3, gamma, tropomyosin isoform 6)	(LOC286890, Tpm3)

1387617_at	(tropomyosin 3, gamma, tropomyosin isoform 6)	(LOC286890, Tpm3)
1367452_at	(SMT3 suppressor of mif two 3 homolog 2 (yeast), similar to SMT3 suppressor of mif two 3 homolog 2)	(LOC287993, Sumo2)
1394943_at	(similar to RIKEN cDNA 1810020E01 (predicted), similar to tyrosine kinase-associated leucine zipper protein LAZip1)	(LOC293112, RGD1305677_predicted)
1383116_at	(similar to RIKEN cDNA 4833435D08, similar to glycosyltransferase 28 domain containing 1)	(LOC300284, LOC367759)
1393152_at	similar to Mut protein	(LOC301276, LOC363201)
1391020_at	(similar to CG1841-PA, isoform A, similar to seven transmembrane helix receptor)	(LOC303660, LOC498020)
1387458_at	(ring finger protein 4, similar to CG14998-PC, isoform C)	(LOC305453, Rnf4)
1397824_at	similar to WAC	(LOC307029, LOC361260)
1398965_at	(eomesodermin, similar to golgi autoantigen golgin subtype a4; tGolgin-1)	(LOC316052, LOC501069)
1382331_at	(similar to RIKEN cDNA 0610038L10 gene, similar to riboflavin kinase)	(LOC317214, LOC499328)
1370500_a_at	(hypothetical gene supported by NM_012720, myelin-associated oligodendrocytic basic protein)	(LOC360443, Mobp)
1377174_at	(SET binding factor 1 (predicted), similar to mKIAA3020 protein)	(LOC362985, Sbf1_predicted)
1372968_at	(SET binding factor 1 (predicted), similar to mKIAA3020 protein)	(LOC362985, Sbf1_predicted)
1397522_at	(SET binding factor 1 (predicted), similar to mKIAA3020 protein)	(LOC362985, Sbf1_predicted)
1390576_at	similar to RIKEN cDNA 4921537P18	(LOC364620, LOC498649)
1395363_at	(methionine-tRNA synthetase (predicted), similar to glyceraldehyde-3-phosphate dehydrogenase)	(LOC366910, Mars_predicted)
1382522_at	(hypothetical gene supported by NM_019149, matrin 3)	(LOC497720, Matr3)
1367823_at	(similar to testis specific protein, Ddc8, tissue inhibitor of metalloproteinase 2)	(LOC498028, Timp2)
1395426_at	similar to ubiquitin-conjugating enzyme E2 variant 1	(LOC498326, LOC499945)
1377986_at	(short coiled-coil protein (predicted), similar to short coiled-coil protein)	(LOC498931, Scoc_predicted)
1384257_at	(non-POU domain containing, octamer-binding, similar to Non-POU-domain-containing, octamer binding protein, similar to Nono protein)	(LOC499170, LOC501589, Nono)

1384965_at	(LOC499369, serine/threonine kinase 2)	(LOC499369, SIk)
1387971_a_at	(mitogen activated protein kinase 8 interacting protein, similar to RIKEN cDNA 1700029115)	(LOC499836, Mapk8ip)
1390906_at	(similar to hypothetical protein 3010020C06, tropomodulin 1)	(LOC500455, Tmod1)
1370081_a_at	(LOC501102, vascular endothelial growth factor A)	(LOC501102, Vegfa)
1374129_at	(similar to RNA binding protein with multiple splicing 2, similar to product is unknown~seizure-related gene)	(LOC501454, LOC503214)
1383276_at	(LanC (bacterial lantibiotic synthetase component C)-like 2 (predicted), similar to LanC-like protein 2 (Testis-specific adriamycin sensitivity protein))	(LOC503420, Lancl2_predicted)
1374606_at	(MYST histone acetyltransferase 1 (predicted), protease, serine, 8 (prostasin))	(Myst1_predicted, Prss8)
1397468_at	(ROD1 regulator of differentiation 1 (S. pombe), similar to RIKEN cDNA 2610207116 (predicted))	(RGD1305387_predicted, Rod1)
1371839_at	(similar to hypothetical protein ET (predicted), similar to splicing factor, arginine/serine-rich 2)	(RGD1307394_predicted, Sfrs2)
1370428_x_at	(RT1 class I, A3, RT1 class I, CE10, RT1 class I, CE3, RT1 class I, CE7, RT1 class Ia, locus A2, RT1 class Ib, locus Aw2)	(RT1-A2, RT1-A3, RT1-Aw2, RT1-CE10, RT1-CE3, RT1-CE7)
1388071_x_at	(RT1 class I, A3, RT1 class I, CE10, RT1 class I, CE7, RT1 class Ib, locus Aw2)	(RT1-A3, RT1-Aw2, RT1-CE10, RT1-CE7)
1388203_x_at	(RT1 class I, A3, RT1 class I, CE1, RT1 class I, CE3, RT1 class I, CE5)	(RT1-A3, RT1-CE1, RT1-CE3, RT1-CE5)
1369085_s_at	(SNRPN upstream reading frame, small nuclear ribonucleoprotein N)	(Snrpn, Snurf)
1374780_at	(zinc finger protein 22 (KOX 15), zinc finger protein 422 (predicted))	(Zfp422_predicted, Znf22)
1395346_at	angio-associated migratory protein (predicted)	Aamp_predicted
1368484_at	ATP-binding cassette, sub-family B (MDR/TAP), member 9	Abcb9
1375468_at	ATP-binding cassette, sub-family C (CFTR/MRP), member 5	Abcc5
1368465_at	amiloride-sensitive cation channel 1, neuronal (degenerin)	Accn1
1371140_a_at	amiloride-sensitive cation channel 1, neuronal (degenerin)	Accn1

1398294_at	actinin, alpha 1	Actn1
1379687_at	ARP2 actin-related protein 2 homolog (yeast) (predicted)	Actr2_predicted
1388161_at	a disintegrin and metalloprotease domain 10	Adam10
1368973_at	adenosine deaminase, RNA-specific	Adar
1368729_a_at	adenylate cyclase activating polypeptide 1 receptor 1	Adcyap1r1
1370121_at	adducin 1 (alpha)	Add1
1397519_at	adiponectin receptor 2 (predicted)	Adipor2_predicted
1369629_at	adenosine kinase	Adk
1369402_at	activity-dependent neuroprotective protein	Adnp
1370584_a_at	adenosine A1 receptor	Adora1
1388757_at	adrenergic receptor kinase, beta 1	Adrbk1
1387861_at	amino-terminal enhancer of split	Aes
1392763_at	1-acylglycerol-3-phosphate O-acyltransferase 1	Agpat1
1371748_at	1-acylglycerol-3-phosphate O-acyltransferase 1	Agpat1
1383759_at	ATP/GTP binding protein 1 (predicted)	Agtpbp1_predicted
1391891_at	ATP/GTP binding protein 1 (predicted)	Agtpbp1_predicted
1388922_at	aryl-hydrocarbon receptor-interacting protein	Aip
1369069_at	A kinase (PRKA) anchor protein 1	Akap1
1387493_at	A kinase (PRKA) anchor protein 5	Akap5
1392079_at	A kinase (PRKA) anchor protein 7	Akap7
1368862_at	v-akt murine thymoma viral oncogene homolog 1	Akt1
1368832_at	murine thymoma viral (v-akt) oncogene homolog 2	Akt2
1380381_at	asparagine-linked glycosylation 2 homolog (yeast, alpha-1,3-mannosyltransferase) (predicted)	Alg2_predicted
1371132_a_at	ankyrin 3, epithelial isoform g	Ank3
1396195_at	ankyrin repeat domain 13 (predicted)	Ankrd13_predicted

1368908_at	annexin A4	Anxa4
1377769_at	adaptor protein complex AP-1, sigma 1 (predicted)	Ap1s1_predicted
1370662_a_at	adaptor-related protein complex 2, beta 1 subunit	Ap2b1
1386877_at	adaptor-related protein complex 2, sigma 1 subunit	Ap2s1
1387289_at	amyloid beta (A4) precursor protein-binding, family A, member 2	Apba2
1397670_at	autophagy 12-like (<i>S. cerevisiae</i>) (predicted)	Apg12l_predicted
1382735_at	autophagy 12-like (<i>S. cerevisiae</i>) (predicted)	Apg12l_predicted
1368258_at	apelin, AGTRL1 ligand	ApIn
1380533_at	amyloid beta (A4) precursor protein	App
1387068_at	activity regulated cytoskeletal-associated protein	Arc
1391658_at	archain	Arcn1
1398817_at	ADP-ribosylation factor 1	Arf1
1387447_at	ADP-ribosylation factor 3	Arf3
1384938_at	Rho GTPase activating protein 1 (predicted)	Arhgap1_predicted
1383813_at	ADP-ribosylation factor-like 2 binding protein	Arl2bp
1369729_at	ADP-ribosylation factor-like 5	Arl5
1384131_at	ADP-ribosylation factor-like 6 interacting protein 2 (predicted)	Arl6ip2_predicted
1369319_at	ADP-ribosylation factor-like 6 interacting protein 5	Arl6ip5
1370611_at	aryl hydrocarbon receptor nuclear translocator 2	Arnt2
1375137_at	actin related protein 2/3 complex, subunit 2 (predicted)	Arpc2_predicted
1394318_at	cAMP-regulated phosphoprotein 19	Arpp19
1369077_at	N-acylsphingosine amidohydrolase 1	Asah1
1383535_at	ankyrin repeat and SOCS box-containing protein 8 (predicted)	Asb8_predicted
1370964_at	arginosuccinate synthetase	Ass
1371108_a_at	ATPase, Na ⁺ /K ⁺ transporting, alpha 1 polypeptide	Atp1a1

1368701_at	ATPase, Na ⁺ /K ⁺ transporting, alpha 3 polypeptide	Atp1a3
1369798_at	ATPase, Na ⁺ /K ⁺ transporting, beta 2 polypeptide	Atp1b2
1387285_at	ATPase, Ca ⁺⁺ transporting, plasma membrane 2	Atp2b2
1396279_at	ATPase, H ⁺ transporting, lysosomal accessory protein 2	Atp6ap2
1387664_at	ATPase, H ⁺ transporting, V1 subunit B, isoform 2	Atp6v1b2
1369256_at	beta-site APP cleaving enzyme	Bace
1374117_at	brain-specific angiogenesis inhibitor 1-associated protein 2	Baiap2
1369520_a_at	branched chain aminotransferase 1, cytosolic	Bcat1
1368999_a_at	brain-enriched guanylate kinase-associated	Begain
1388733_at	bifunctional apoptosis regulator (predicted)	Bfar_predicted
1369032_at	bladder cancer associated protein homolog (human)	Blcap
1393641_at	B-cell linker	Blnk
1398004_at	BMP/retinoic acid-inducible neural-specific protein 2	Brinp2
1386774_at	BMP/retinoic acid-inducible neural-specific protein 2	Brinp2
1387629_at	B-box and SPRY domain containing	Bspry
1369886_a_at	calcium binding protein 1	Cabp1
1370757_at	calcium channel, voltage-dependent, gamma subunit 3	Cacng3
1370775_a_at	calcitonin/calcitonin-related polypeptide, alpha	Calca
1367889_at	calcium/calmodulin-dependent protein kinase I	Camk1
1377518_at	calcium/calmodulin-dependent protein kinase I gamma	Camk1g
1371263_a_at	calcium/calmodulin-dependent protein kinase II, delta	Camk2d
1369993_at	calcium/calmodulin-dependent protein kinase II gamma	Camk2g
1371687_at	calhexin	Canx
1368808_at	CAP, adenylate cyclase-associated protein 1 (yeast)	Cap1
1368894_at	CAP, adenylate cyclase-associated protein, 2 (yeast)	Cap2

1387292_s_at	calpain 8	Capn8
1391572_at	cysteinyl-tRNA synthetase (predicted)	Cars_predicted
1397571_at	metastatic lymph node 51	Casc3
1387401_at	calsequestrin 2	Casq2
1369733_at	catenin beta	Catnb
1382842_at	cyclin H	Ccnh
1395508_at	chaperonin containing TCP1, subunit 5 (epsilon)	Cct5
1394997_at	congenital dyserythropoietic anemia, type I (predicted)	Cdan1_predicted
1371278_at	cell division cycle 34 homolog (S. cerevisiae) (predicted)	Cdc34_predicted
1387695_at	Cdc42-binding protein kinase beta	Cdc42bpb
1375719_s_at	cadherin 13	Cdh13
1395122_s_at	cyclin-dependent kinase (CDC2-like) 10 (predicted)	Cdk10_predicted
1394320_at	cyclin dependent kinase 2	Cdk2
1369538_at	cyclin-dependent kinase 5, regulatory subunit 1 (p35)	Cdk5r
1393441_at	similar to cyclin-dependent kinase inhibitor 2D	Cdkn2d
1387636_a_at	P11 protein	Cdtw1
1379130_at	CDW92 antigen	Cdw92
1387726_at	caudal type homeo box 2	Cdx2
1368449_at	centaurin, alpha 1	Centa1
1370184_at	cofilin 1	Cfl1
1397200_at	chromodomain helicase DNA binding protein 4	Chd4
1387388_at	calcium binding protein p22	Chp
1369112_at	cholinergic receptor, muscarinic 3	Chrm3
1369019_at	cholinergic receptor, nicotinic, alpha polypeptide 5	Chrna5
1367740_at	creatine kinase, brain	Ckb

1384015_at	cytoplasmic linker associated protein 1 (predicted)	Clasp1_predicted
1369791_at	putative chloride channel (similar to Mm Clcn4-2)	Clcn4-2
1369609_at	claudin 11	Clcn11
1377765_at	chloride intracellular channel 4	Clic4
1384336_at	Cln3p	Cln3
1370991_at	camello-like 3	Cml3
1388176_at	camello-like 5	Cml5
1370693_a_at	cyclic nucleotide phosphodiesterase 1	Cnp1
1394008_x_at	ciliary neurotrophic factor receptor	Cntfr
1376868_at	Cobl-like 1 (predicted)	Cobl1_predicted
1395352_at	COP9 constitutive photomorphogenic homolog subunit 3	Cops3
1395565_at	COP9 signalosome subunit 4	Cops4
1399010_at	COP9 (constitutive photomorphogenic) homolog, subunit 7a (Arabidopsis thaliana) (predicted)	Cops7a_predicted
1389897_at	COP9 (constitutive photomorphogenic) homolog, subunit 7a (Arabidopsis thaliana) (predicted)	Cops7a_predicted
1394565_at	coatamer protein complex, subunit zeta 1 (predicted)	Copz1_predicted
1369811_at	complexin 1	Cplx1
1377549_at	copine V (predicted)	Cpne5_predicted
1373429_at	cAMP responsive element binding protein-like 1	Crebl1
1378925_at	cAMP responsive element modulator	Crem
1382037_at	cysteine-rich motor neuron 1 (predicted)	Crim1_predicted
1387183_at	carnitine O-octanoyltransferase	Crot
1376051_at	crystallin, lamda 1	Cryl1
1384201_at	citrate synthase	Cs
1369967_at	citrate synthase	Cs

1395914_at	casein kinase 1, delta	Csnk1d
1370527_a_at	casein kinase 1, delta	Csnk1d
1386693_at	casein kinase 1, epsilon	Csnk1e
1394731_at	casein kinase 1, gamma 3	Csnk1g3
1368685_at	chondroitin sulfate proteoglycan 4	Cspg4
1368704_a_at	chondroitin sulfate proteoglycan 5	Cspg5
1379238_at	CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) small phosphatase-like (predicted)	Ctdspl_predicted
1397808_at	cathepsin C	Ctsc
1367651_at	cathepsin D	Ctsd
1370922_at	cortixin	Ctxn
1387879_a_at	CUG triplet repeat, RNA-binding protein 2	Cugbp2
1387880_at	CUG triplet repeat, RNA-binding protein 2	Cugbp2
1379365_at	chemokine (C-X-C motif) ligand 11	Cxcl11
1379911_at	death associated protein kinase 1 (predicted)	Dapk1_predicted
1387874_at	D site albumin promoter binding protein	Dbp
1389553_at	dendritic cell inhibitory receptor 3	Dcir3
1371834_at	dynactin 2	Dctn2
1399162_a_at	damage-specific DNA binding protein 1	Ddb1
1397405_at	DEAD (Asp-Glu-Ala-Asp) box polypeptide 17 (predicted)	Ddx17_predicted
1385214_at	DEAD (Asp-Glu-Ala-Asp) box polypeptide 3, X-linked	Ddx3x
1381384_at	degenerative spermatocyte homolog (Drosophila)	Degs
1385871_at	DEAH (Asp-Glu-Ala-His) box polypeptide 36 (predicted)	Dhx36_predicted
1380807_at	discs, large homolog 1 (Drosophila)	Dlgh1
1368944_at	discs, large homolog 1 (Drosophila)	Dlgh1
1388280_a_at	discs, large homolog 3 (Drosophila)	Dlgh3

1382024_at	DnaJ (Hsp40) homolog, subfamily B, member 6 (predicted)	Dnajb6_predicted
1369714_at	DnaJ (Hsp40) homolog, subfamily C, member 14	Dnajc14
1369390_a_at	dipeptidylpeptidase 6	Dpp6
1391602_at	developmentally regulated GTP binding protein 1 (predicted)	Drg1_predicted
1368146_at	dual specificity phosphatase 1	Dusp1
1377064_at	dual specificity phosphatase 6	Dusp6
1391510_at	estrogen receptor-binding fragment-associated gene 9 (predicted)	Ebag9_predicted
1395586_at	eukaryotic translation elongation factor 1 alpha 1	Eef1a1
1385625_at	EGF-containing fibulin-like extracellular matrix protein 2	Efemp2
1387306_a_at	early growth response 2	Egr2
1387442_at	early growth response 4	Egr4
1372317_at	EH-domain containing 1 (predicted)	Ehd1_predicted
1387588_at	EH-domain containing 3	Ehd3
1368866_at	GERp95	Eif2c2
1397693_at	eukaryotic translation initiation factor 2, subunit 3, structural gene X-linked	Eif2s3x
1387630_at	ELOVL family member 5, elongation of long chain fatty acids (yeast)	Elovl5
1390174_at	echinoderm microtubule associated protein like 1 (predicted)	Eml1_predicted
1369702_at	endosulfine alpha	Ensa
1369212_s_at	erythrocyte protein band 4.1-like 1	Epb4.1l1
1388061_a_at	Eph receptor A7	Epha7
1369453_at	Epsin 1	Epn1
1387849_at	epsin 2	Epn2
1370007_at	protein disulfide isomerase related protein (calcium-binding protein, intestinal-related)	Erp70
1370625_at	Fas apoptotic inhibitory molecule 2	Faim2
1392339_at	phenylalanine-tRNA synthetase-like, beta subunit	Farslb

1392875_at	F-box and leucine-rich repeat protein 4 (predicted)	Fbxl4_predicted
1376500_at	F-box only protein 23 (predicted)	Fbxo23_predicted
1381903_at	F-box only protein 33 (predicted)	Fbxo33_predicted
1370707_at	FEV (ETS oncogene family)	Fev
1387498_a_at	Fibroblast growth factor receptor 1	Fgfr1
1384829_at	fibroblast growth factor receptor 3	Fgfr3
1390049_at	four and a half LIM domains 1	Fhl1
1390995_at	FK506 binding protein-like	Fkbp1
1369087_at	FMS-like tyrosine kinase 1	Flt1
1375043_at	FBJ murine osteosarcoma viral oncogene homolog	Fos
1395802_at	fucosyltransferase 11	Fut11
1373435_at	fragile X mental retardation gene 2, autosomal homolog (predicted)	Fxr2h_predicted
1368696_at	FXYD domain-containing ion transport regulator 7	Fxyd7
1369103_at	fyn proto-oncogene	Fyn
1381189_at	fizzy/cell division cycle 20 related 1 (Drosophila) (predicted)	Fzr1_predicted
1378239_at	glucosidase, alpha; acid (Pompe disease, glycogen storage disease type II)	Gaa
1388030_a_at	gamma-aminobutyric acid (GABA) B receptor 1	Gabbr1
1369371_a_at	gamma-aminobutyric acid (GABA) B receptor 1	Gabbr1
1369905_at	gamma-aminobutyric acid (GABA-A) receptor, subunit alpha 4	Gabra4
1395269_s_at	gamma-aminobutyric acid A receptor, delta	Gabrd
1370760_a_at	glutamate decarboxylase 1	Gad1
1372016_at	growth arrest and DNA-damage-inducible 45 beta (predicted)	Gadd45b_predicted
1368332_at	guanylate nucleotide binding protein 2	Gbp2
1375135_at	GCN1 general control of amino-acid synthesis 1-like 1 (yeast) (predicted)	Gcn1l1_predicted
1398822_at	GDP dissociation inhibitor 2	Gdi2

1375359_at	glial cell line derived neurotrophic factor family receptor alpha 2	Gfra2
1373803_a_at	growth hormone receptor	Ghr
1370730_a_at	growth hormone releasing hormone receptor	Ghrhr
1368775_at	gonadotropin inducible ovarian transcription factor 1	Giot1
1369640_at	gap junction membrane channel protein alpha 1	Gja1
1370146_at	glycine receptor, beta subunit	Glrbb
1367705_at	glutaredoxin 1 (thioltransferase)	Glrx1
1367633_at	glutamine synthetase 1	Glul
1387505_at	guanine nucleotide binding protein, alpha inhibiting 1	Gnai1
1367844_at	guanine nucleotide binding protein, alpha inhibiting 2	Gnai2
1368030_at	guanine nucleotide binding protein, alpha inhibiting 3	Gnai3
1381988_at	guanine nucleotide binding protein, alpha q polypeptide	Gnaq
1387095_at	guanine nucleotide binding protein, alpha z subunit	Gnaz
1368957_at	guanine nucleotide binding protein, gamma 7	Gng7
1369571_at	golgi phosphoprotein 3	Golph3
1369410_at	golgi SNAP receptor complex member 1	Gosr1
1368272_at	glutamate oxaloacetate transaminase 1	Got1
1382739_at	G protein-coupled receptor 19	Gpr19
1368952_at	G protein-coupled receptor 51	Gpr51
1388066_a_at	G protein-coupled receptor kinase 6	Gprk6
1370590_at	G-protein signalling modulator 1 (AGS3-like, C. elegans)	Gpsm1
1386871_at	glutathione peroxidase 4	Gpx4
1389900_at	glutamate receptor, ionotropic, N-methyl D-aspartate 1	Grin1
1371051_at	glutamate receptor, ionotropic, N-methyl D-aspartate-like 1A	Grin1a
1369781_at	glutamate receptor, metabotropic 7	Grm7

1383627_a_at	general transcription factor IIF, polypeptide 1, 74kDa	Gtf2f1
1387390_at	granzyme K	Gzmk
1367759_at	H1 histone family, member 0	H1f0
1398849_at	H3 histone, family 3B	H3f3b
AFFX_Rat_Hexokinase_3_at	hexokinase 1	Hk1
AFFX_Rat_Hexokinase_5_at	hexokinase 1	Hk1
AFFX_Rat_Hexokinase_M_at	hexokinase 1	Hk1
1386983_at	hydroxymethylbilane synthase	Hmbs
1388309_at	high mobility group AT-hook 1	Hmga1
1387848_at	3-hydroxy-3-methylglutaryl-Coenzyme A reductase	Hmgcr
1375612_at	heterogeneous nuclear ribonucleoprotein A1	Hnrpa1
1369562_at	neural visinin-like Ca2+-binding protein type 3	Hpcal1
1371510_at	HCF-1 beta-propeller interacting protein	Hpip
1393790_at	HRAS-like suppressor (predicted)	Hrasls_predicted
1388080_a_at	histamine receptor H3	Hrh3
1391423_at	heat shock factor 2	Hsf2
1387430_at	heat shock factor 2	Hsf2
1385620_at	heat shock protein 105 (predicted)	Hsp105_predicted
1369124_at	5-hydroxytryptamine (serotonin) receptor 2A	Htr2a
1371442_at	hypoxia up-regulated 1	Hyou1
1393710_at	intercellular adhesion molecule 5, telencephalin (predicted)	Icam5_predicted
1387769_a_at	Inhibitor of DNA binding 3, dominant negative helix-loop-helix protein	Id3
1385923_at	inhibitor of DNA binding 4	Idb4
1375183_at	inhibitor of DNA binding 4	Idb4
1375696_at	interferon (alpha and beta) receptor 1 (predicted)	Ifnar1_predicted

1394668_at	immunoglobulin superfamily, member 4B (predicted)	Igsf4b_predicted
1390033_at	immunoglobulin superfamily, member 4B (predicted)	Igsf4b_predicted
1395339_at	imprinted and ancient	Impact
1375754_at	imprinted and ancient	Impact
1370232_at	isovaleryl coenzyme A dehydrogenase	Ivd
1368251_at	Janus kinase 3	Jak3
1369847_at	potassium voltage-gated channel, shaker-related subfamily, beta member 1	Kcnab1
1370558_a_at	potassium voltage gated channel, Shaw-related subfamily, member 2	Kcnc2
1370773_a_at	Kv channel-interacting protein 2	Kcnp2
1370595_a_at	potassium channel interacting protein 4	Kcnp4
1368793_at	potassium inwardly-rectifying channel, subfamily J, member 2	Kcnj2
1369487_a_at	potassium inwardly-rectifying channel, subfamily J, member 4	Kcnj4
1369418_at	potassium inwardly-rectifying channel, subfamily J, member 9	Kcnj9
1375190_at	potassium channel tetramerisation domain containing 13	Kctd13
1387260_at	Kruppel-like factor 4 (gut)	Klf4
1385961_at	Kruppel-like factor 5	Klf5
1397386_at	lymphoid nuclear protein related to AF4-like (predicted)	Laf4l_predicted
1387844_at	LIM and SH3 protein 1	Lasp1
1388747_at	leucine carboxyl methyltransferase 1	Lcmt1
1381369_at	leucine-rich repeat LGI family, member 3 (predicted)	Lgi3_predicted
1370108_a_at	lin-7 homolog a (C. elegans)	Lin7a
1369610_at	lin-7 homolog C (C. elegans)	Lin7c
1390379_at	LIM domain only 4 (predicted)	Lmo4_predicted
1379803_at	LIM domain only 4 (predicted)	Lmo4_predicted
1369408_at	BMP/retinoic acid-inducible neural-specific protein	LOC140610

1384608_at	RN protein	LOC171116
1369922_at	RDCR-0918-3 protein	LOC246120
1397843_at	WD-containing protein Rab11BP/Rabphilin-11	LOC246152
1397846_at	cytosolic leucine-rich protein	LOC246768
1370853_at	CaM-kinase II inhibitor alpha	LOC287005
1398316_at	similar to LEYDIG CELL TUMOR 10 KD PROTEIN	LOC288913
1392723_at	similar to ankyrin repeat domain protein 17 isoform b	LOC289521
1394536_at	similar to Ubiquitin carboxyl-terminal hydrolase 4 (Ubiquitin thiolesterase 4) (Ubiquitin-specific processing protease 4) (Deubiquitinating enzyme 4) (Ubiquitous nuclear protein)	LOC290864
1371365_at	similar to Ubiquitin-conjugating enzyme E2S	LOC292588
1373149_at	similar to yippee-like 3	LOC293491
1399155_at	similar to RIKEN cDNA 5830434P21	LOC296637
1388315_at	similar to neuronal protein 15.6	LOC299310
1378149_at	similar to RIKEN cDNA 2310075A12	LOC300472
1392122_x_at	similar to Btk-PH-domain binding protein	LOC301119
1395379_at	similar to U2af1-rs2	LOC302670
1383335_at	hypothetical protein LOC303515	LOC303515
1374579_at	similar to RIKEN cDNA E230015L20 gene	LOC306238
1397512_at	similar to Vps41 protein	LOC306991
1396106_at	similar to dystrobrevin alpha isoform 1	LOC307548
1391786_at	similar to Murine homolog of human ffp-3	LOC308650
1379123_at	similar to Seizure related 6 homolog (mouse)-like 2	LOC308988
1390175_at	similar to Delta-interacting protein A (Hepatitis delta antigen interacting protein A)	LOC309161
1375311_at	similar to Delta-interacting protein A (Hepatitis delta antigen interacting protein A)	LOC309161

1384525_at	similar to spleen specific 238 kDa protein with PH domain	LOC313438
1380314_at	similar to hypothetical protein FLJ38984	LOC313595
1373018_at	similar to hypothetical protein FLJ14800	LOC315327
1384550_at	similar to RIKEN cDNA 1810030O07	LOC317344
1373603_at	similar to RIKEN cDNA 0610007P22	LOC360494
1382805_at	similar to myosin XVIIa	LOC360570
1383555_at	similar to RIKEN cDNA 4930579G22	LOC360799
1393604_at	similar to RIKEN cDNA A930018B01	LOC360810
1381611_at	similar to transcription factor ELYS	LOC360886
1379740_at	similar to chromosome 18 open reading frame 54	LOC361346
1371712_at	similar to autoantigen	LOC361399
1377498_at	similar to adenosine monophosphate deaminase 2 (isoform L)	LOC362015
1377580_at	similar to mKIAA0738 protein	LOC362353
1390040_at	brain and reproductive organ-expressed protein	LOC362704
1388984_at	similar to RNA polymerase III subunit RPC2	LOC362858
1382533_at	similar to HIV-1 Rev binding protein	LOC363266
1394991_at	similar to interleukin-1 receptor associated kinase 1 splice form 3	LOC363520
1386580_at	similar to Wdr8 protein	LOC366515
1382029_at	similar to CDNA sequence BC017647	LOC497960
1378587_at	similar to RIKEN cDNA 5530600A18	LOC497981
1378966_at	LOC498061	LOC498061
1388705_at	similar to selenoprotein SelM	LOC498398
1373569_at	similar to cDNA sequence BC018601	LOC498404
1375718_at	Bm403207	LOC498525
1390756_at	similar to expressed sequence AW121567	LOC498667

1380055_at	similar to 2010004A03Rik protein	LOC498951
1398453_at	similar to cDNA sequence BC025816	LOC498957
1382563_at	similar to hypothetical protein FLJ38944	LOC499112
1378731_at	similar to CDNA sequence BC006909	LOC499267
1372760_at	LOC499304	LOC499304
1388452_at	LOC499428	LOC499428
1393346_at	similar to RIKEN cDNA 5830436D01	LOC499518
1382138_at	similar to hypothetical protein FLJ20433	LOC499745
1393458_s_at	similar to PHD finger protein 14 isoform 1	LOC500030
1392452_at	similar to PHD finger protein 14 isoform 1	LOC500030
1396099_at	similar to Hypothetical protein MGC30714	LOC500065
1395610_at	similar to Hypothetical protein MGC30714	LOC500065
1397815_at	similar to ADP-ribosylation factor-like 10C	LOC500282
1394639_at	similar to CDC42 small effector 2	LOC501691
1392257_at	hypothetical protein LOC501706	LOC501706
1396206_at	similar to Docking protein 5 (Downstream of tyrosine kinase 5) (Protein dok-5)	LOC502694
1394923_at	similar to neuronal interacting factor X 1 (NIX1)	LOC502898
1367984_at	CTD-binding SR-like rA1	LOC56081
1387373_at	myomegalin	LOC64183
1368666_a_at	calcium-independent alpha-latrotoxin receptor homolog 3	Lphn3
1395472_at	leucine rich repeat containing 17	Lrrc17
1375149_at	leucine rich repeat containing 4B (predicted)	Lrrc4b_predicted
1395706_at	leucine rich repeat neuronal 6A (predicted)	Lrrn6a_predicted
1369066_at	MAP-kinase activating death domain	Madd
1392566_at	v-maf musculoaponeurotic fibrosarcoma (avian) oncogene homolog (c-maf)	Maf

1367669_a_at	microtubule-associated proteins 1A/1B light chain 3	Map1lc3b
1369078_at	mitogen activated protein kinase 1	Mapk1
1380024_at	mitogen-activated protein kinase 9	Mapk9
1368646_at	mitogen-activated protein kinase 9	Mapk9
1370792_at	microtubule-associated protein, RP/EB family, member 1	Mapre1
1383114_at	serine/threonine kinase	Mark2
1375140_at	muscleblind-like 2 (predicted)	Mbnl2_predicted
1387341_a_at	myelin basic protein	Mbp
1369793_a_at	melanoma cell adhesion molecule	Mcam
1369820_at	mcf.2 transforming sequence-like	Mcf2l
1394616_at	mesoderm development candidate 2 (predicted)	Mesdc2_predicted
1367796_at	Alpha-1,3-mannosyl-glycoprotein 2-beta-N-acetylglucosaminyltransferase	Mgat1
1382946_a_at	similar to Ras-related protein Rab-1B	MGC105830
1392855_x_at	similar to Ras-related protein Rab-1B	MGC105830
1398982_at	similar to Ras-related protein Rab-1B	MGC105830
1385270_s_at	similar to Ras-related protein Rab-1B	MGC105830
1393669_at	similar to Ras-related protein Rab-1B	MGC105830
1372260_at	leucine zipper domain protein	MGC116147
1372389_at	similar to immediate early response 2	MGC72578
1375630_at	similar to NHP2-like protein 1 (High mobility group-like nuclear protein 2 homolog 1) ([U4/U6.U5] tri-snRNP 15.5 kDa protein) (OTK27)	MGC72932
1392979_at	similar to calcyclin binding protein	MGC93921
1380072_at	similar to 231004H10Rik protein	MGC93975
1371919_at	similar to RP2 protein, testosterone-regulated - ricefield mouse (Mus caroli)	MGC94056
1395526_at	similar to RIKEN cDNA 1700006D24	MGC94361
1395655_at	phosphatidylinositol 4-kinase type-II beta	MGC94512

1379891_at	scotin	MGC94600
1379325_at	similar to Mkrn1 protein	MGC94941
1370129_at	meningioma expressed antigen 5 (hyaluronidase)	Mgea5
1383025_at	meningioma expressed antigen 5 (hyaluronidase)	Mgea5
1367609_at	macrophage migration inhibitory factor	Mif
1375656_at	muscle, intestine and stomach expression 1	Mist1
1369623_at	morphine related protein-1 (RefSeq = NM_022613)	Morp1
1383650_at	MAS-related G protein-coupled receptor, member B4	Mrgprb4
1383649_a_at	MAS-related G protein-coupled receptor, member B4	Mrgprb4
1386114_at	MAS-related G protein-coupled receptor, member B4	Mrgprb4
1371604_at	mitochondrial ribosomal protein L34	Mrpl34
1397604_at	membrane-spanning 4-domains, subfamily A, member 3 (predicted)	Ms4a3_predicted
1368411_a_at	microtubule-associated protein 2	Mtap2
1384314_at	mitochondrial translational initiation factor 2	Mtif2
1394182_at	myotubularin related protein 4 (predicted)	Mtmr4_predicted
1387785_at	myotrophin	Mtpn
1387786_at	myotrophin	Mtpn
1368232_at	mevalonate kinase	Mvk
1384095_at	myosin VIIA and Rab interacting protein	Myrip
1384255_at	N-ethylmaleimide-sensitive factor attachment protein, gamma (predicted)	Napg_predicted
1386951_at	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex 5	Ndufa5
1395157_at	neural precursor cell expressed, developmentally down-regulated gene 4A	Nedd4a
1369081_at	neuraminidase 1	Neu1
1396092_at	NFKB inhibitor interacting Ras-like protein 1 (predicted)	Nkiras1_predicted
1368895_at	neuroligin 2	Nlgn2

1391256_at	N-myristoyltransferase 2	Nmt2
1368929_at	nuclear protein localization 4	Npl4
1384331_at	neoplastic progression 3 (predicted)	Npn3_predicted
1386935_at	nuclear receptor subfamily 4, group A, member 1	Nr4a1
1372032_at	neuroblastoma RAS viral (v-ras) oncogene homolog	Nras
1390469_at	nurim (nuclear envelope membrane protein)	Nrm
1370570_at	neuropilin 1	Nrp1
1369689_at	N-ethylmaleimide sensitive fusion protein	Nsf
1369690_at	N-ethylmaleimide sensitive fusion protein	Nsf
1383957_at	nudix (nucleotide diphosphate linked moiety X)-type motif 3 (predicted)	Nudt3_predicted
1387639_at	neural visinin-like Ca2+-binding protein type 2	Nvjp2
1384144_at	nucleoredoxin (predicted)	Nxn_predicted
1368962_at	neurexophilin 3	Nxph3
1367729_at	ornithine aminotransferase	Oat
1369417_a_at	opioid-binding protein/cell adhesion molecule-like	Opcml
1387461_at	opioid receptor, mu 1	Oprm1
1373442_at	amplified in osteosarcoma	Os-9
1390923_a_at	oxysterol binding protein-like 1A	Osbpl1a
1369209_at	p34 protein	P34
1368958_at	protein kinase C and casein kinase substrate in neurons 1	Pacsin1
1392890_at	platelet-activating factor acetylhydrolase, isoform Ib, alpha subunit 45kDa	Pafah1b1
1387377_a_at	p21 (CDKN1A)-activated kinase 1	Pak1
1396267_at	p21 (CDKN1A)-activated kinase 2	Pak2
1383274_at	poly(rC) binding protein 3 (predicted)	Pcbp3_predicted
1395441_at	poly(rC) binding protein 4 (predicted)	Pcbp4_predicted

1393454_at	protocadherin 17 (predicted)	Pcdh17_predicted
1368956_at	protocadherin 8	Pcdh8
1398271_at	piccolo (presynaptic cytomatrix protein)	Pclo
1369044_a_at	phosphodiesterase 4B	Pde4b
1386961_at	phosphofructokinase, muscle	Pfkm
1367605_at	profilin 1	Pfn1
1367970_at	profilin 2	Pfn2
1369473_at	phosphoglucomutase 1	Pgm1
1379427_at	progesterone receptor membrane component 2 (predicted)	Pgrmc2_predicted
1367927_at	prohibitin	Phb
1369357_at	phosphorylase kinase alpha 1	Phka1
1397572_at	phosphatidylinositol glycan, class M	Pigm
1397753_at	phosphatidylinositol glycan, class Q	Pigq
1379515_at	phosphatidylinositol glycan, class T (predicted)	Pigt_predicted
1370531_a_at	phospholipase D1	Pld1
1373272_at	pleckstrin homology domain containing, family A member 5	Plekha5
1376137_at	pleckstrin homology domain containing, family B (evectins) member 2 (predicted)	Plekha2_predicted
1384325_at	palate, lung, and nasal epithelium carcinoma associated	Plunc
1370504_a_at	peripheral myelin protein 22	Pmp22
1388717_at	protein O-fucosyltransferase 2 (predicted)	Pofut2_predicted
1383037_at	polymerase (DNA-directed), delta interacting protein 2 (predicted)	Poldip2_predicted
1368213_at	P450 (cytochrome) oxidoreductase	Por
1368859_at	protein phosphatase 1A, magnesium dependent, alpha isoform	Ppm1a
1381024_at	protein phosphatase 2 (formerly 2A), regulatory subunit A (PR 65), alpha isoform	Ppp2r1a

1375245_at	protein phosphatase 2 (formerly 2A), regulatory subunit A (PR 65), alpha isoform	Ppp2r1a
1395409_at	protein phosphatase 2A, regulatory subunit B' (PR 53) (predicted)	Ppp2r4_predicted
1395826_at	protein phosphatase 2, regulatory subunit B (B56), epsilon isoform (predicted)	Ppp2r5e_predicted
1369152_at	protein phosphatase 3, regulatory subunit B, alpha isoform, type 1	Ppp3r1
1398242_at	protein phosphatase 5, catalytic subunit	Ppp5c
1369236_at	PR domain containing 4	Prdm4
1367969_at	peroxiredoxin 6	Prdx6
1368240_a_at	protein kinase C, beta 1	Prkcb1
1383722_at	proline synthetase co-transcribed (predicted)	Prosc_predicted
1387085_at	phosphoribosyl pyrophosphate synthetase 1	Prps1
1368551_at	phosphoribosyl pyrophosphate synthetase 2	Prps2
1368507_at	proteasome (prosome, macropain) subunit, alpha type 3	Pasma3
1398812_at	proteasome (prosome, macropain) subunit, beta type 1	Psemb1
1383426_at	proline-serine-threonine phosphatase-interacting protein 1 (predicted)	Pstpip1_predicted
1372663_at	phosphatidylserine synthase 2 (predicted)	Ptdss2_predicted
1367851_at	prostaglandin D2 synthase	Ptgds
1368527_at	prostaglandin-endoperoxide synthase 2	Ptgs2
1369688_s_at	protein tyrosine kinase 2 beta	Plk2b
1370243_a_at	prothymosin alpha	Ptma
1386892_at	parathymosin	Ptms
1370574_a_at	protein tyrosine phosphatase, non-receptor type substrate 1	Ptpns1
1370599_a_at	protein tyrosine phosphatase, receptor type, D	Ptprd
1370488_a_at	protein tyrosine phosphatase, receptor type, D	Ptprd
1368035_a_at	protein tyrosine phosphatase, receptor type, F	Ptprf

1370214_at	parvalbumin	Pvalb
1395279_at	PX domain containing serine/threonine kinase	Pxk
1383072_at	muscle glycogen phosphorylase	Pygm
1398825_at	RAB11B, member RAS oncogene family	Rab11b
1371055_at	RAB12, member RAS oncogene family	Rab12
1370758_at	RAB15, member RAS oncogene family	Rab15
1370780_at	RAB31, member RAS oncogene family	Rab31
1369816_at	RAB3A, member RAS oncogene family	Rab3a
1387641_at	RAB5A, member RAS oncogene family	Rab5a
1393288_at	RAB5B, member RAS oncogene family (predicted)	Rab5b_predicted
1399153_at	RAB5B, member RAS oncogene family (predicted)	Rab5b_predicted
1371836_at	RAB5C, member RAS oncogene family (predicted)	Rab5c_predicted
1371103_at	RAB6B, member RAS oncogene family	Rab6b
1398838_at	RAB7, member RAS oncogene family	Rab7
1398780_at	Rab acceptor 1 (prenylated)	Rabac1
1372513_at	ras-related C3 botulinum toxin substrate 1	Rac1
1395465_at	RAE1 RNA export 1 homolog (S. pombe) (predicted)	Rae1_predicted
1387389_at	receptor (calcitonin) activity modifying protein 3	Ramp3
1386900_at	ribosome associated membrane protein 4	RAMP4
1379552_s_at	Rap2 interacting protein	Rap2ip
1370373_at	RASD family, member 2	Rasd2
1369130_at	RAS guanyl releasing protein 1	Rasgrp1
1369129_at	RAS guanyl releasing protein 1	Rasgrp1
1399063_at	retinoblastoma-associated factor 600	Rbatf600
1375921_at	reticulocalbin (predicted)	Rcn_predicted

1378287_at	radixin	Rdx
1375542_at	radixin	Rdx
1374448_at	reversion-inducing-cysteine-rich protein with kazal motifs (predicted)	Reck_predicted
1369093_at	reelin	ReIn
1387622_at	radical fringe gene homolog (Drosophila)	Rfng
1373747_at	similar to cornichon-like protein (predicted)	RGD1304930_predicted
1378137_at	similar to ribosome-binding protein p34 - rat (predicted)	RGD1305092_predicted
1381448_at	similar to CG6796-PA (predicted)	RGD1305145_predicted
1393610_at	similar to hypothetical protein BC008163 (predicted)	RGD1305162_predicted
1388959_at	similar to KIAA0153 protein (predicted)	RGD1305319_predicted
1379793_at	similar to RIKEN cDNA 3110031B13 (predicted)	RGD1305356_predicted
1379706_at	similar to dJ1033H22.1 (KIAA0554 protein) (predicted)	RGD1305386_predicted
1388306_at	similar to RIKEN cDNA 1810042K04 (predicted)	RGD1305593_predicted
1374438_at	similar to mKIAA1046 protein (predicted)	RGD1305606_predicted
1390730_at	similar to 1810009O10Rik protein (predicted)	RGD1305651_predicted
1390037_at	similar to chromosome 20 open reading frame 58 (predicted)	RGD1305809_predicted
1395078_at	similar to semaphorin sem2 (predicted)	RGD1306079_predicted
1373300_at	similar to hypothetical protein DKFZp761D0211 (predicted)	RGD1306151_predicted
1392617_at	similar to hypothetical protein DKFZp761D0211 (predicted)	RGD1306151_predicted
1375700_at	similar to hypothetical protein FLJ14360 (predicted)	RGD1306288_predicted
1393846_at	similar to downregulated in renal cell carcinoma (predicted)	RGD1306327_predicted
1395791_at	similar to mKIAA1402 protein (predicted)	RGD1306404_predicted
1379795_at	similar to RIKEN cDNA 2410002O22 gene (predicted)	RGD1306583_predicted
1392938_s_at	similar to C11orf17 protein (predicted)	RGD1306959_predicted
1373534_at	similar to SR rich protein (predicted)	RGD1307395_predicted

1396086_at	similar to RIKEN cDNA 1810014L12 (predicted)	RGD1307423_predicted
1373095_at	similar to mKIAA0317 protein (predicted)	RGD1307597_predicted
1373753_at	similar to RIKEN cDNA 2510010F15 (predicted)	RGD1307608_predicted
1384388_at	similar to gp25L2 protein (predicted)	RGD1307627_predicted
1395550_at	similar to MEGF6 (4P83) (predicted)	RGD1307670_predicted
1375627_at	similar to hypothetical protein FLJ10342 (predicted)	RGD1307791_predicted
1379206_at	similar to RIKEN cDNA 1110001E17 (predicted)	RGD1307901_predicted
1377448_at	similar to RIKEN cDNA 1110001E17 (predicted)	RGD1307901_predicted
1375648_at	similar to hypothetical protein (predicted)	RGD1307966_predicted
1384615_at	similar to cisplatin resistance-associated overexpressed protein (predicted)	RGD1307981_predicted
1372563_at	similar to D330021B20 protein (predicted)	RGD1308143_predicted
1383837_at	similar to DNA segment, Chr 17, Wayne State University 94, expressed (predicted)	RGD1308185_predicted
1375206_at	hypothetical LOC287466 (predicted)	RGD1308212_predicted
1393086_at	similar to RIKEN cDNA 5730469D23 (predicted)	RGD1308324_predicted
1395334_at	similar to pancreatitis-induced protein 49 (predicted)	RGD1308600_predicted
1375540_at	similar to hypothetical protein D11Ert497e (predicted)	RGD1308696_predicted
1395533_at	similar to KIAA0564 protein (predicted)	RGD1308772_predicted
1373071_at	similar to RIKEN cDNA 1810054G18 (predicted)	RGD1308901_predicted
1376254_at	similar to KIAA1440 protein (predicted)	RGD1308908_predicted
1392621_at	similar to FKSG26 protein (predicted)	RGD1309054_predicted
1393673_at	similar to HCDI protein (predicted)	RGD1309307_predicted
1390315_a_at	similar to KIAA0913 protein (predicted)	RGD1309414_predicted
1373814_at	similar to mKIAA1002 protein (predicted)	RGD1310066_predicted
1376727_at	similar to RIKEN cDNA 2310034L04 (predicted)	RGD1310157_predicted
1389302_at	similar to RIKEN cDNA D030070L09 (predicted)	RGD1310199_predicted

1396137_at	similar to RIKEN cDNA C230075L19 gene (predicted)	RGD1310284_predicted
1372438_at	similar to Nit protein 2 (predicted)	RGD1310494_predicted
1371747_at	similar to RIKEN cDNA 2700038C09 (predicted)	RGD1310660_predicted
1396708_at	similar to hypothetical protein MGC33486 (predicted)	RGD1310680_predicted
1375674_at	similar to chromosome 16 open reading frame 5 (predicted)	RGD1310686_predicted
1379763_at	similar to chromosome 1 open reading frame 16 (predicted)	RGD1310761_predicted
1398664_at	similar to RIKEN cDNA 9130427A09 (predicted)	RGD1311016_predicted
1382187_at	similar to RIKEN cDNA 2610029K21 (predicted)	RGD1311086_predicted
1394760_at	similar to KIAA1409 protein (predicted)	RGD1311117_predicted
1376303_a_at	membralin (predicted)	RGD1311136_predicted
1373971_at	similar to PCPD protein (predicted)	RGD1311177_predicted
1393826_at	similar to apolipoprotein F-like (predicted)	RGD1311384_predicted
1376152_at	similar to flavoprotein oxidoreductase MICAL2 (predicted)	RGD1311773_predicted
1383097_at	similar to RIKEN cDNA 2010012O05 (predicted)	RGD1311783_predicted
1385302_at	similar to RIKEN cDNA 2610020H15 (predicted)	RGD1311813_predicted
1391249_at	similar to DD1 (predicted)	RGD1312005_predicted
1373486_at	similar to scotin (predicted)	RGD1312041_predicted
1368065_at	regulator of G-protein signaling 19 interacting protein 1	Rgs19ip1
1368144_at	regulator of G-protein signaling 2	Rgs2
1370130_at	ras homolog gene family, member A	Rhoa
1370627_at	ras homolog gene family, member V	Rhov
1385790_at	ring finger protein 153 (predicted)	Rnf153_predicted
1398824_at	coated vesicle membrane protein	Rnp24
1369054_at	rabphilin 3A homolog (mouse)	Rph3a
1398854_at	ribosomal protein L24	Rpl24

1376110_at	ribonuclease P 25 subunit (human) (predicted)	Rpp25_predicted
1398617_at	ribosomal protein S27a	Rps27a
1387888_at	ribosomal protein S9	Rps9
1382537_at	Ras-related GTP binding C (predicted)	Rragc_predicted
1369293_at	reticulon 4 receptor	Rtn4r
1393404_at	reticulon 4 receptor-like 1	Rtn4rl1
1391739_at	RUN domain containing 1 (predicted)	Rundc1_predicted
1369805_at	synaptonemal complex protein SC65	Sc65
1367959_a_at	sodium channel, voltage-gated, type I, beta polypeptide	Scn1b
1387010_s_at	sodium channel, voltage-gated, type I, beta polypeptide	Scn1b
1389582_at	stromal cell-derived factor 2-like 1 (predicted)	Sdf2l1_predicted
1387252_at	SEC14-like 2 (S. cerevisiae)	Sec14l2
1382868_at	sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6A (predicted)	Sema6a_predicted
1369265_at	SUMO/sentrin specific protease 2	Senp2
1367593_at	selenoprotein W, muscle 1	Sepw1
1368444_at	small glutamine-rich tetratricopeptide repeat (TPR)-containing, alpha	Sgta
1371063_at	SH3 domain protein 2A	Sh3gl2
1368931_at	SH3 domain protein 2 C1	Sh3gl3
1373267_at	Sh3 domain YSC-like 1 (predicted)	Sh3yl1_predicted
1380435_at	soc-2 (suppressor of clear) homolog (C. elegans) (predicted)	Shoc2_predicted
1390600_at	alpha-2,6-sialyltransferase ST6GalNAc IV	siat7D
1372572_at	sialyltransferase 7F	Siat7F
1392269_at	transcriptional regulator, SIN3A (yeast) (predicted)	Sin3a_predicted
1388059_a_at	solute carrier family 11 (proton-coupled divalent metal ion transporters), member 2	Slc11a2

1388064_a_at	solute carrier family 1 (glial high affinity glutamate transporter), member 3	Slc1a3
1371130_at	solute carrier family 1 (glial high affinity glutamate transporter), member 3	Slc1a3
1369234_at	solute carrier family 20, member 2	Slc20a2
1388221_at	solute carrier family 24 (sodium/potassium/calcium exchanger), member 3	Slc24a3
1397647_at	solute carrier family 25 (mitochondrial carrier; ornithine transporter) member 15 (predicted)	Slc25a15_predicted
1387707_at	solute carrier family 2 (facilitated glucose transporter), member 3	Slc2a3
1390825_at	solute carrier family 35, member B3 (predicted)	Slc35b3_predicted
1381922_at	solute carrier family 5 (sodium/glucose cotransporter), member 11	Slc5a11
1377455_at	solute carrier family 6 (neurotransmitter transporter, GABA), member 11	Slc6a11
1369237_at	solute carrier family 6 (neurotransmitter transporter, L-proline), member 7	Slc6a7
1369772_at	solute carrier family 6 (neurotransmitter transporter, glycine), member 9	Slc6a9
1387280_a_at	tumor-associated protein 1	Slc7a5
1379701_at	solute carrier family 8 (sodium/calcium exchanger), member 3	Slc8a3
1368296_at	solute carrier organic anion transporter family, member 2b1	Slco2b1
1392178_at	SLIT and NTRK-like family, member 1 (predicted)	Slitrk1_predicted
1385011_at	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 4	Smarca4
1384246_at	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 5 (predicted)	Smarca5_predicted
1369924_at	synuclein, beta	Sncb
1386282_x_at	SNF related kinase	Snrk
1379275_at	sorting nexin 10 (predicted)	Snx10_predicted
1396278_at	sorting nexin 11 (predicted)	Snx11_predicted
1369635_at	sorbitol dehydrogenase	Sord
1398274_at	spermatogenesis associated 2	Spata2
1373636_at	sparc/osteonectin, cwcv and kazal-like domains proteoglycan 1 (predicted)	Spock1_predicted

1379466_at	shadow of prion protein	Sprn
1371104_at	sterol regulatory element binding factor 1	Srebf1
1367834_at	spermidine synthase	Srm
1382166_at	signal recognition particle receptor, B subunit (predicted)	Srprb_predicted
1398877_at	stress-induced-phosphoprotein 1 (Hsp70/Hsp90-organizing protein)	Stip1
1388396_at	serine/threonine kinase 25 (STE20 homolog, yeast)	Stk25
1367799_at	statin-like	Stnl
1387359_at	syntaxin 1A (brain)	Stx1a
1386853_s_at	syntaxin 5a	Stx5a
1370519_at	syntaxin binding protein 1	Stxbp1
1370840_at	syntaxin binding protein 1	Stxbp1
1370518_a_at	syntaxin binding protein 1	Stxbp1
1368771_at	sulfatase 1	Sulf1
1369627_at	synaptic vesicle glycoprotein 2b	Sv2b
1369022_at	SV2 related protein	Svop
1382850_at	synapsin II	Syn2
1369482_a_at	synapsin II	Syn2
1384716_at	synaptotagmin 1	Syt1
1369135_at	synaptotagmin XI	Syt11
1387517_at	synaptotagmin 13	Syt13
1387662_at	synaptotagmin 4	Syt4
1368417_at	synaptotagmin 5	Syt5
1394802_at	synaptotagmin 7	Syt7
1381181_at	tachykinin receptor 1	Tacr1
1377147_at	TBC1 domain family, member 7 (predicted)	Tbc1d7_predicted

1380200_at	transcription factor 8 (represses interleukin 2 expression)	Tcf8
1388011_a_at	transforming growth factor, beta 2	Tgfb2
1377596_a_at	thyroid hormone receptor associated protein 6 (predicted)	Thrap6_predicted
1387983_at	thyroid hormone receptor beta	Thrb
1370150_a_at	thyroid hormone responsive protein	Thrsp
1387852_at	thyroid hormone responsive protein	Thrsp
1369651_at	thymus cell antigen 1, theta	Thy1
1368650_at	TGFB inducible early growth response	Tieg
1387495_at	transducin-like enhancer of split 4, E(spl) homolog (Drosophila)	Tle4
1392651_at	transmembrane 4 superfamily member 3	Tm4sf3
1387850_at	transmembrane protein with EGF-like and two follistatin-like domains 1	Tmeff1
1393418_at	tropomodulin 2	Tmod2
1393423_at	tankyrase, TRF1-interacting ankyrin-related ADP-ribose polymerase 2 (predicted)	Tnks2_predicted
1375664_at	trinucleotide repeat containing 6 (predicted)	Tnrc6_predicted
1378572_at	toll interacting protein (predicted)	Tollip_predicted
1384328_at	target of myb1 homolog (chicken) (predicted)	Tom1_predicted
1375420_at	tumor protein p53 inducible protein 11 (predicted)	Tp53i11_predicted
1367976_at	tripeptidyl peptidase II	Tpp2
1371060_at	tripartite motif protein 23	Trim23
1398823_at	translin-associated factor X	Tsnax
1371594_at	tetratricopeptide repeat domain 11 (predicted)	Ttc11_predicted
1371618_s_at	tubulin, beta 3	Tubb3
1395719_at	Tu translation elongation factor, mitochondrial (predicted)	Tufm_predicted
1385754_s_at	p105 coactivator	U83883
1385548_at	ubiquitin-conjugating enzyme E2D 1, UBC4/5 homolog (yeast) (predicted)	Ube2d1_predicted

1369617_at	ubiquitin-conjugating enzyme E2N (homologous to yeast UBC13)	Ube2n
1385615_at	ubiquitin conjugation factor E4 A	Ube4a
1371188_a_at	upstream binding transcription factor, RNA polymerase I	Ubf
1369977_at	ubiquitin carboxy-terminal hydrolase L1	Uchl1
1382257_at	uridine monophosphate synthetase (predicted)	Umps_predicted
1369394_at	unc-5 homolog A (C. elegans)	Unc5a
1387624_at	upstream transcription factor 1	Usf1
1388088_a_at	upstream transcription factor 2	Usf2
1387703_a_at	ubiquitin specific protease 2	Usp2
1376127_at	UDP-glucuronate decarboxylase 1	Uxs1
1369597_at	vesicle-associated membrane protein, associated protein B and C	Vapb
1386909_a_at	voltage-dependent anion channel 1	Vdac1
1370549_at	vacuolar protein sorting 45 (yeast)	Vps45
1369667_at	vacuolar protein sorting 52 (yeast)	Vps52
1368853_at	visinin-like 1	Vsnl1
1397675_at	eukaryotic translation initiation factor 4H	Wbscr1
1381070_at	WD repeat domain 36 (predicted)	Wdr36_predicted
1369344_at	WD repeat domain 7	Wdr7
1386807_at	wingless-related MMTV integration site 2	Wnt2
1383451_at	WD SOCS-box protein 2	Wsb2
1385343_at	X-box binding protein 1	Xbp1
1375903_a_at	YY1 associated factor 2 (predicted)	Yaf2_predicted
1376444_at	YY1 transcription factor	Yy1
1388731_at	zinc binding alcohol dehydrogenase, domain containing 2 (predicted)	Zadh2_predicted
1384783_at	zinc finger protein 161	Zfp161

1380106_at	zinc finger protein 162	Zfp162
1380416_at	zinc finger protein 191	Zfp191
1380529_at	zinc finger protein 207 (predicted)	Zfp207_predicted
1387512_at	zinc finger protein 238	Zfp238
1369501_at	zinc finger protein 260	Zfp260
1385658_at	zinc finger protein 313	Znf313
1388919_at	zinc finger protein 541 (predicted)	Znf541_predicted
1388130_at	zyxin	Zyx
1390019_at	H3 histone, family 3B	H3f3b
1380025_at	Rattus norvegicus catechol-O-methyltransferase (Comt), mRNA.	Comt
1396820_at	histone deacetylase 1 (predicted)	Hdac1_predicted
1389787_at	serum response factor (predicted)	Srf_predicted

[00162] Genes and gene fragments identified as changing significantly in animals that were reared in social isolation, relative to social control animals on postnatal day 80 (P80) are provided in Table 6.

TABLE 6

Fragment Name	Gene Name	Gene Symbol
1369997_at	(dishevelled, dsh homolog 1 (Drosophila), limitrin)	(1200013a08rik, Dvl1)
1392108_at	(ATP-binding cassette, sub-family C (CFTR/MRP), member 3, aldehyde oxidase 3, chemokine (C-C motif) ligand 9 (predicted), enoyl-Coenzyme A, hydratase/3-hydroxyacyl Coenzyme A dehydrogenase, guanosine monophosphate reductase 2, tumor necrosis factor receptor)	(Abcc3, Aox3, Ccl9_predicted, Ehadh, Gmpr2, Tnfrsf1b)
1372087_at	(a disintegrin and metalloproteinase domain 17 (tumor necrosis factor, alpha, converting enzyme), hypertrophic agonist responsive protein)	(Adam17, harpb64)
1385577_at	(5 nucleotidase, 6-pyruvoyl-tetrahydropterin synthase, Ras homolog enriched in brain like 1, alcohol dehydrogenase 6 (class V) (predicted), angiotensin II receptor-associated protein, apoptotic peptidase activating factor 1, ceroid-lipofuscinosis, neurona)	(Adh6_predicted, Agtrap, Apaf1, Cdkl1_predicted, Cln2, Galm, Gcat_predicted, Hspa1b, Keg1, LOC293989, LOC499300, MGC95001, Nt5, Pgsg, Pts, Rhebl1, Rps6kb2_predicted, Tsarg1, Ttc4_predicted, sag)
1383377_at	(ATP synthase, H ⁺ transporting, mitochondrial F0 complex, subunit F6, GA repeat binding protein, alpha (predicted))	(Atp5j, Gabpa_predicted)
1370913_at	(Best5 protein, hypothetical gene supported by NM_138881)	(Best5, LOC497812)
1370892_at	(complement component 4, gene 2, complement component 4a)	(C4-2, C4a)
1370891_at	(CD48 antigen, similar to cytokine receptor related protein 4)	(Cd48, Cytora4)
1372977_at	(atlastin-like, cyclin-dependent kinase-like 1 (CDC2-related kinase) (predicted), similar to mitogen-activated protein kinase kinase kinase 5 isoform 2)	(Cdkl1_predicted, LOC362750, LOC503027)
1387305_s_at	(cytochrome P450, family 11, subfamily B, polypeptide 2, cytochrome P450, subfamily 11B, polypeptide 1)	(Cyp11b1, Cyp11b2)
1391661_at	(glycerol kinase, hypothetical gene supported by NM_024381)	(Gyk, LOC497845)

1371102_x_at	(beta-glo, hemoglobin beta chain complex)	(Hbb, MGC72973)
1368255_at	(hypothetical gene supported by NM_017354, neurotrimin)	(Hnt, LOC360435)
1388850_at	(heat shock 90kDa protein 1, alpha-like 3 (predicted), heat shock protein 1, alpha)	(Hspca, Hspcal3_predicted)
1387995_a_at	(interferon induced transmembrane protein 2 (1-8D), interferon induced transmembrane protein 3)	(Ifitm2, Ifitm3)
1376758_at	(LOC498665, inhibitor of growth family, member 1 (predicted))	(Ing1_predicted, LOC498665)
1369035_a_at	(hypothetical gene supported by NM_013192, potassium inwardly-rectifying channel, subfamily J, member 6)	(Kcnj6, LOC497678)
1397130_at	(mitogen activated protein kinase 10, similar to binding protein)	(LOC293702, Mapk10)
1381030_at	(similar to step II splicing factor SLU7; DNA segment, Chr 11, ERATO Doi 730, expressed; DNA segment, Chr 3, Brigham & Womens Genetics 0878 expressed, step II splicing factor SLU7 (S. cerevisiae))	(LOC303057, Slu7)
1372604_at	(hypothetical protein LOC503164, similar to RIKEN cDNA 2210421G13)	(LOC315106, LOC503164)
1388164_at	(MHC class I RT1.O type 149 processed pseudogene, RT1 class I, T24, gene 4, RT1 class Ib, locus H2-TL-like (S2), RT1 class Ib, locus S3, similar to class I histocompatibility antigen alpha chain - cotton-top tamarin)	(LOC360231, LOC499402, RT1-149, RT1-S2, RT1-S3)
1395691_at	(similar to phosphoserine-tRNA kinase, zinc finger protein, subfamily 1A, 5 (predicted))	(LOC361661, Zfpn1a5_predicted)
1368993_at	(hypothetical gene supported by NM_020088, odd Oz/ten-m homolog 2 (Drosophila))	(LOC497664, Odz2)
1387071_a_at	(hypothetical gene supported by NM_017212, microtubule-associated protein tau)	(LOC497674, Mapt)
1398861_at	(hypothetical gene supported by NM_021579, nuclear RNA export factor 1)	(LOC497739, Nxf1)
1371230_x_at	(serine protease inhibitor, Kazal type 1, similar to ATPase inhibitor)	(LOC497807, Spink1)
1368261_at	(hypothetical gene supported by NM_053817, neurexin 3)	(LOC497817, Nrnx3)
1392316_at	(LOC498458, protein tyrosine phosphatase, receptor type, G)	(LOC498458, Ptpg)
1373992_at	(similar to MGC108823 protein, similar to interferon-inducible GTPase)	(LOC498872, MGC108823)
1369896_s_at	(LOC499013, RNA binding motif protein 16)	(LOC499013, Rbm16)

1373782_a_at	(LOC499769, similar to LOC495800 protein)	(LOC499769, LOC499770)
1373666_at	(Rap guanine nucleotide exchange factor (GEF) 5, similar to Rap guanine nucleotide exchange factor 5 (Guanine nucleotide exchange factor for Rap1) (M-Ras-regulated Rap GEF) (MR-GEF))	(LOC500748, Rapgef5)
1371017_at	(T-cell receptor gamma chain, similar to TCR V gamma 3)	(LOC502132, Tcrg)
1369138_a_at	(parkin, similar to mature parasite-infected erythrocyte surface antigen like precursor (2N179))	(LOC502231, Park2)
1371152_a_at	(2',5'-oligoadenylate synthetase 1, 40/46kDa, 2'-5' oligoadenylate synthetase 1L, 2'-5' oligoadenylate synthetase 1K)	(Oas1, Oas1i, Oas1k)
1378934_at	(zinc responsive protein ZD10B, zinc responsive protein Zd10A)	(ZD10B, Zd10A)
1368330_at	apoptosis antagonizing transcription factor	Aatf
1388153_at	acyl-CoA synthetase long-chain family member 1	Acs11
1388179_at	activin receptor IIB	Acvr2b
1383418_at	a disintegrin and metalloprotease domain 11 (predicted)	Adam11_predicted
1374419_at	adenylate cyclase 9 (predicted)	Adcy9_predicted
1382981_at	Abelson helper integration site 1	Ahi1
1368558_s_at	allograft inflammatory factor 1	Aif1
1367555_at	albumin	Alb
1368776_at	arachidonate 5-lipoxygenase	Alox5
1367775_at	alpha-methylacyl-CoA racemase	Amacr
1381042_at	anaphase promoting complex subunit 10 (predicted)	Anapc10_predicted
1374163_at	anaphase promoting complex subunit 4 (predicted)	Anapc4_predicted
1395313_s_at	annexin A3	Anxa3
1376413_at	amyloid beta (A4) precursor protein-binding, family A, member 1	Apba1
1398258_at	apolipoprotein D	Apod
1395053_at	androgen-induced proliferation inhibitor (predicted)	Aprin_predicted
1392864_at	Rho GTPase activating protein 5 (predicted)	Arhgap5_predicted

1370002_at	Rho guanine nucleotide exchange factor (GEF) 1	Arhgef1
1368916_at	argininosuccinate lyase	Asl
1368701_at	ATPase, Na ⁺ /K ⁺ transporting, alpha 3 polypeptide	Atp1a3
1386426_at	ATPase, Ca ⁺⁺ transporting, plasma membrane 1	Atp2b1
1387126_at	ATPase, Ca ⁺⁺ -sequestering	Atp2c1
1367724_a_at	ATPase, H ⁺ transporting, V0 subunit E isoform 1	Atp6v0e1
1373087_at	axotrophin (predicted)	Axot_predicted
1379419_at	DNA sequence AY228474	AY228474
1392421_at	bromodomain adjacent to zinc finger domain, 2B (predicted)	Baz2b_predicted
1371391_at	bone morphogenetic protein 6	Bmp6
1386994_at	B-cell translocation gene 2, anti-proliferative	Btg2
1397151_at	calcium channel, voltage-dependent, alpha 2/delta 3 subunit	Cacna2d3
1367889_at	calcium/calmodulin-dependent protein kinase I	Camk1
1370438_at	C-terminal PDZ domain ligand of neuronal nitric oxide synthase	Capon
1370810_at	cyclin D2	Ccnd2
1374540_at	cell division cycle associated 7 (predicted)	Cdca7_predicted
1392140_at	cadherin 11	Cdh11
1368887_at	cadherin 22	Cdh22
1368545_at	CASP8 and FADD-like apoptosis regulator	Cflar
1380063_at	cholesterol 25-hydroxylase (predicted)	Ch25h_predicted
1370991_at	camello-like 3	Cml3
1381294_at	cyclin M1 (predicted)	Cnm1_predicted
1394008_x_at	ciliary neurotrophic factor receptor	Cntrf
1370376_a_at	cold shock domain protein A	Csda
1367631_at	connective tissue growth factor	Ctgf

1397217_at	CUG triplet repeat, RNA-binding protein 2	Cugbp2
1369068_at	cullin 5	Cul5
1387913_at	cytochrome P450, family 2, subfamily d, polypeptide 22	Cyp2d22
1379855_at	deleted in colorectal carcinoma	Dcc
1386535_at	DEAD (Asp-Glu-Ala-Asp) box polypeptide 3, X-linked	Ddx3x
1380807_at	discs, large homolog 1 (Drosophila)	Dlgh1
1375139_at	discs, large homolog 2 (Drosophila)	Dlgh2
1370073_at	protein kinase inhibitor p58	Dnajc3
1398803_at	dynein, cytoplasmic, heavy chain 1	Dnch1
1383895_at	dynein, cytoplasmic, light chain 2B (predicted)	Dncl2b_predicted
1388134_at	eukaryotic translation elongation factor 1 delta (guanine nucleotide exchange protein)	Eef1d
1368867_at	GERp95	Elf2c2
1370542_a_at	E74-like factor 1	Elf1
1369453_at	Epsin 1	Epn1
1387964_a_at	ERO1-like (S. cerevisiae)	Ero1l
1372823_at	family with sequence similarity 36, member A (predicted)	Fam36a_predicted
1383354_a_at	F-box only protein 33 (predicted)	Fbxo33_predicted
1384829_at	fibroblast growth factor receptor 3	Fgfr3
1383904_at	fibronin-like protein 1	Fgl1
1379263_at	fukutin related protein (predicted)	Fkrp_predicted
1375043_at	FBJ murine osteosarcoma viral oncogene homolog	Fos
1390936_at	FXYD domain-containing ion transport regulator 3	Fxyd3
1382314_at	interferon, alpha-inducible protein (clone IFI-15K) (predicted)	G1p2_predicted
1388792_at	growth arrest and DNA-damage-inducible 45 gamma (predicted)	Gadd45g_predicted
1378900_at	GCN5 general control of amino acid synthesis-like 2 (yeast) (predicted)	Gcn5l2_predicted

1369640_at	gap junction membrane channel protein alpha 1	Gja1
1387906_a_at	GNAS complex locus	Gnas
1375705_at	guanine nucleotide binding protein, beta 1	Gnb1
1387670_at	glycerol-3-phosphate dehydrogenase 2	Gpd2
1394578_at	glutamate receptor, ionotropic, 2	Gria2
1393995_at	glutamate receptor, ionotropic, 2	Gria2
1389574_at	general transcription factor IIIC, polypeptide 2, beta 110kDa	Gtf3c2
1376285_at	GULP, engulfment adaptor PTB domain containing 1 (predicted)	Gulp1_predicted
1367759_at	H1 histone family, member 0	H1f0
1378614_at	Huntington disease gene homolog	Hdh
1374599_at	hect (homologous to the E6-AP (UBE3A) carboxyl terminus) domain and RCC1 (CHC1)-like domain (RLD) 1 (predicted)	Herc1_predicted
1394746_at	hect (homologous to the E6-AP (UBE3A) carboxyl terminus) domain and RCC1 (CHC1)-like domain (RLD) 1 (predicted)	Herc1_predicted
1388309_at	high mobility group AT-hook 1	Hmga1
1371336_at	hematological and neurological expressed sequence 1	Hn1
1371510_at	HCF-1 beta-propeller interacting protein	Hpip
1371255_at	Harvey rat sarcoma viral (v-Ha-ras) oncogene homolog	Hras
1368416_at	integrin binding sialoprotein	Ibsp
1375532_at	Inhibitor of DNA binding 2, dominant negative helix-loop-helix protein	Id2
1385923_at	inhibitor of DNA binding 4	Icb4
1381014_at	interferon-induced protein 44 (predicted)	Iff44_predicted
1384180_at	interferon-induced protein with tetratricopeptide repeats 2 (predicted)	Ifft2_predicted
1387625_at	insulin-like growth factor binding protein 6	Igfbp6
1390715_at	insulin-like growth factor binding protein-like 1 (predicted)	Igfbpl1_predicted
1370331_at	interleukin 11 receptor, alpha chain 1	Il11ra1

1371148_s_at	internexin, alpha	Inexa
1383564_at	interferon regulatory factor 7 (predicted)	Irf7_predicted
1383448_at	interferon dependent positive acting transcription factor 3 gamma (predicted)	Isgf3g_predicted
1374627_at	interferon dependent positive acting transcription factor 3 gamma (predicted)	Isgf3g_predicted
1387788_at	Jun-B oncogene	Junb
1396701_at	kalirin, RhoGEF kinase	Kalrn
1381010_at	potassium voltage gated channel, Shal-related family, member 2	Kcnd2
1370970_at	potassium inwardly-rectifying channel, subfamily J, member 14	Kcnj14
1397599_at	potassium voltage-gated channel, subfamily Q, member 3	Kcnq3
1392717_at	kinesin family member 1B	Kif1b
1380172_at	kinesin family member 5C (predicted)	Kif5c_predicted
1367880_at	laminin, beta 2	Lamb2
1387946_at	lectin, galactoside-binding, soluble, 3 binding protein	Lgals3bp
1389329_at	lectin, galactose binding, soluble 8	Lgals8
1381798_at	LIM domain only protein 7	LMO7
1389560_at	Vps24p protein	LOC282834
1370853_at	CaM-kinase II inhibitor alpha	LOC287005
1375526_at	similar to novel protein of unknown function (DUF423) family member	LOC287442
1391416_at	similar to ankyrin repeat domain protein 17 isoform b	LOC289521
1392723_at	similar to ankyrin repeat domain protein 17 isoform b	LOC289521
1375046_at	hypothetical protein LOC289786	LOC289786
1376562_at	similar to Traf2 and NCK interacting kinase, splice variant 4	LOC294917
1385713_at	similar to NAKAP95	LOC299569
1390375_at	similar to NAKAP95	LOC299569
1382111_at	similar to RIKEN cDNA 2010001H14	LOC302554

1378730_at	similar to BCL6 co-repressor-like 1	LOC302810
1378347_at	similar to hypothetical protein FLJ34512	LOC302996
1383920_at	similar to aminomethyltransferase	LOC306586
1371389_at	hypothetical LOC306766	LOC306766
1396232_at	similar to hypothetical protein FLJ25333	LOC309925
1375539_at	similar to T-Brain-1	LOC311078
1389034_at	similar to ubiquitin specific protease UBP43	LOC312688
1396803_at	similar to THO complex 2	LOC313308
1372496_at	similar to hypothetical protein MGC19604	LOC313786
1396567_at	similar to Set alpha isoform	LOC317165
1383673_at	similar to Nap1l2	LOC317247
1384550_at	similar to RIKEN cDNA 1810030O07	LOC317344
1374494_at	similar to testis-specific chromodomain Y-like protein	LOC361237
1381966_at	similar to transcription factor 1	LOC361475
1389099_at	similar to hypothetical protein MGC51082	LOC361519
1372075_at	similar to dJ862K6.2.2 (splicing factor, arginine/serine-rich 6 (SRP55-2)(isoform 2))	LOC362264
1374421_at	similar to Williams-Beuren syndrome deletion transcript 9 homolog	LOC368002
1372324_at	similar to thyroid hormone receptor interactor 3	LOC497975
1378966_at	LOC498061	LOC498061
1396530_at	Ab2-093	LOC498084
1373575_at	similar to NADH dehydrogenase (ubiquinone) Fe-S protein 2	LOC498279
1398390_at	similar to Small inducible cytokine B13 precursor (CXCL13) (B lymphocyte chemoattractant) (CXC chemokine BLC)	LOC498335
1380728_at	similar to collapsin response mediator protein-2A	LOC498539
1381556_at	similar to BC013672 protein	LOC498673

1375821_at	similar to ankyrin repeat domain 26	LOC498767
1381230_at	similar to RIKEN cDNA 2610039E05	LOC498963
1391748_at	similar to Myb protein P42POP	LOC499090
1386793_at	similar to zinc finger protein 61	LOC499094
1373410_at	similar to MADS box transcription enhancer factor 2, polypeptide C (myocyte enhancer factor 2C)	LOC499497
1392070_at	similar to Lix1 homolog (mouse) like	LOC499677
1376693_at	similar to OEF2	LOC500011
1393201_at	similar to lymphoid-restricted membrane protein	LOC500361
1393866_at	similar to WSL-1-like protein	LOC500592
1397700_x_at	LOC500721	LOC500721
1378099_at	LOC500721	LOC500721
1398716_at	LOC500721	LOC500721
1381758_at	similar to MDM2 Binding protein	LOC500870
1380184_at	similar to TAFA5	LOC500915
1374028_at	similar to CDNA sequence BC024479	LOC500974
1398659_at	similar to PSST739 protein	LOC501231
1399041_at	similar to OPA3 protein	LOC502305
1371405_at	similar to hypothetical protein MGC52110	LOC503252
1367984_at	CTD-binding SR-like rA1	LOC56081
1389510_at	Ly1 antibody reactive clone (predicted)	Lyar_predicted
1398834_at	mitogen activated protein kinase kinase 2	Map2k2
1386959_a_at	mitogen activated protein kinase kinase 5	Map2k5
1375673_at	mitogen activated protein kinase kinase kinase 1	Map3k1
1368710_at	serine/threonine kinase	Mark2
1387834_at	megakaryocyte-associated tyrosine kinase	Matk

1379456_at	mitochondrial carrier triple repeat 1 (predicted)	Mcart1_predicted
1376986_at	methytransferase-like 3 (predicted)	Mettl3_predicted
1368071_at	Mg87 protein	Mg87
1372389_at	similar to immediate early response 2	MGC72578
1372967_at	RAC/CDC42 exchange factor	MGC72605
1373023_at	similar to RIKEN cDNA 2010200123	MGC94262
1377935_at	similar to Protein C3orf4 homolog	MGC94479
1379891_at	scotin	MGC94600
1395223_at	similar to hypothetical protein MGC35097	MGC94736
1372599_at	microsomal glutathione S-transferase 2 (predicted)	Mgst2_predicted
1385422_at	myeloid/lymphoid or mixed-lineage leukemia 5 (trithorax homolog, Drosophila) (predicted)	MLI5_predicted
1375703_at	myeloid/lymphoid or mixed-lineage leukemia 5 (trithorax homolog, Drosophila) (predicted)	MLI5_predicted
1369825_at	matrix metalloproteinase 2	Mmp2
1388853_at	mitochondrial ribosomal protein L54 (predicted)	Mrpl54_predicted
1371015_at	myxovirus (influenza virus) resistance 1	Mx1
1387283_at	myxovirus (influenza virus) resistance 2	Mx2
1376648_at	v-myc myelocytomatosis viral related oncogene, neuroblastoma derived (avian)	Mycn
1370174_at	myeloid differentiation primary response gene 116	Myd116
1368450_at	myosin Va	Myo5a
1387866_at	myosin IXb	Myo9b
1373304_at	alpha-N-acetylglucosaminidase	Naglu
1396264_at	nuclear cap binding protein subunit 2 (predicted)	Ncbp2_predicted
1387577_at	neurogenic differentiation 2	Neurod2
1388167_at	nuclear factor I/B	Nfib

1371202_a_at	nuclear factor I/B	Nfib
1395083_at	neuro-oncological ventral antigen 1	Nova1
1387099_at	natriuretic peptide receptor 2	Npr2
1397004_at	nuclear receptor subfamily 3, group C, member 1	Nr3c1
1372032_at	neuroblastoma RAS viral (v-ras) oncogene homolog	Nras
1369404_a_at	neurexin 1	Nrxn1
1388340_at	Ns5atp9 protein	Ns5atp9
1385280_at	nucleotide binding protein 1 (predicted)	Nubp1_predicted
1368466_a_at	outer dense fiber of sperm tails 2	Odf2
1379481_at	poly(A) binding protein, nuclear 1	Pabpn1
1392480_at	poly(A) binding protein, nuclear 1	Pabpn1
1368958_at	protein kinase C and casein kinase substrate in neurons 1	Pacsin1
1376247_at	phosphoenolpyruvate carboxykinase 2 (mitochondrial) (predicted)	Pck2_predicted
1388020_a_at	phosphodiesterase 1C	Pde1c
1398472_at	progressive external ophthalmoplegia 1 (predicted)	Peo1_predicted
1372923_at	peroxisomal biogenesis factor 11b (predicted)	Pex11b_predicted
1370833_at	peroxin 2	Pex2
1368264_at	peroxisomal biogenesis factor 6	Pex6
1370447_at	phospholipase B	Phlpp
1369177_at	phosphatidylinositol 4-kinase type 2 alpha	Pi4k2a
1384558_at	placenta-specific 9 (predicted)	Plac9_predicted
1381133_at	phospholipase C, beta 1	Plcb1
1398899_at	polymerase (RNA) II (DNA directed) polypeptide C (predicted)	Polr2c_predicted
1379832_at	polymerase (RNA) II (DNA directed) polypeptide D (predicted)	Polr2d_predicted
1386971_at	protein phosphatase 1, regulatory subunit 10	Ppp1r10

1376938_at	protein phosphatase 2 (formerly 2A), regulatory subunit B (PR 52), alpha isoform	Ppp2r2a
1384815_at	protein phosphatase 3, catalytic subunit, alpha isoform	Ppp3ca
1368507_at	proteasome (prosome, macropain) subunit, alpha type 3	Psma3
1376069_at	proteasome (prosome, macropain) 26S subunit, non-ATPase, 11 (predicted)	Psmc11_predicted
1374803_at	proteasome (prosome, macropain) 26S subunit, non-ATPase, 11 (predicted)	Psmc11_predicted
1388430_at	prostate tumor over expressed gene 1 (predicted)	Ptov1_predicted
1370181_at	RAB4A, member RAS oncogene family	Rab4a
1367981_at	rabaptin 5	Rabep1
1390941_at	retinoblastoma binding protein 6 (predicted)	Rbbp6_predicted
1370356_at	RNA binding motif protein 10	Rbm10
1396401_at	RNA binding motif protein 17 (predicted)	Rbm17_predicted
1395271_at	RNA binding motif protein 27 (predicted)	Rbm27_predicted
1383164_at	replication factor C (activator 1) 3 (predicted)	Rfc3_predicted
1377532_at	similar to Hepatocellular carcinoma-associated antigen 58 homolog (predicted)	RGD1305020_predicted
1372795_at	similar to hypothetical protein FLJ20511 (predicted)	RGD1305127_predicted
1381448_at	similar to CG6796-PA (predicted)	RGD1305145_predicted
1385862_at	similar to RIKEN cDNA 4930438O05 (predicted)	RGD1305615_predicted
1397513_at	hypothetical LOC294883 (predicted)	RGD1305844_predicted
1395448_at	similar to hypothetical protein FLJ13511 (predicted)	RGD1305857_predicted
1393326_s_at	similar to Pseudoautosomal GTP-binding protein-like protein (predicted)	RGD1305954_predicted
1395637_at	similar to aspartyl beta-hydroxylase; calsequestrin-binding protein; 3110001L23Rik (predicted)	RGD1306020_predicted
1380228_at	similar to hypothetical protein MGC47816 (predicted)	RGD1306880_predicted
1379285_at	similar to 5830458K16Rik protein (predicted)	RGD1306974_predicted
1389203_at	hypothetical LOC287306 (predicted)	RGD1307036_predicted

1397848_at	similar to RIKEN cDNA 6330406115 (predicted)	RGD1307396_predicted
1373920_at	similar to 106 kDa O-GlcNAc transferase-interacting protein (predicted)	RGD1307844_predicted
1383265_at	similar to RIKEN cDNA 4930451A13 (predicted)	RGD1307925_predicted
1377996_at	hypothetical LOC304497 (predicted)	RGD1308037_predicted
1389769_at	similar to KIAA1440 protein (predicted)	RGD1308908_predicted
1391346_at	similar to FKSG26 protein (predicted)	RGD1309054_predicted
1377950_at	similar to interferon-inducible GTPase (predicted)	RGD1309362_predicted
1376221_at	similar to DNA segment, Chr 7, ERATO Doi 462, expressed (predicted)	RGD1309393_predicted
1373814_at	similar to mKIAA1002 protein (predicted)	RGD1310066_predicted
1372433_at	similar to CG11030-PA (predicted)	RGD1310211_predicted
1381513_at	similar to RIKEN cDNA 1300017J02 (predicted)	RGD1310507_predicted
1374139_at	similar to cerebellar degeneration-related 2 (predicted)	RGD1310578_predicted
1393460_at	similar to GARP protein precursor (Garpin) (Glycoprotein A repetitions predominant) (predicted)	RGD1310771_predicted
1388790_at	similar to hypothetical protein D5Etd33e (predicted)	RGD1310857_predicted
1376612_at	similar to RIKEN cDNA 1810033A06 (predicted)	RGD1311144_predicted
1372784_at	similar to Muf1-pending protein (predicted)	RGD1311221_predicted
1392797_at	similar to CGI-41 protein (predicted)	RGD1311265_predicted
1377995_at	similar to hypothetical protein DKFZp761D0211 (predicted)	RGD1311484_predicted
1376136_at	MIRO2 protein	Rhot2
1381967_at	RNA-binding region (RNP1, RRM) containing 2 (predicted)	Rnpc2_predicted
1379737_a_at	RNA-binding region (RNP1, RRM) containing 2 (predicted)	Rnpc2_predicted
1384654_at	roundabout homolog 1 (Drosophila)	Robo1
1377029_at	RAR-related orphan receptor alpha (predicted)	Rora_predicted
1375788_at	ribosomal protein L7	Rpl7
1389051_at	retinoid X receptor beta	Rxrb

1373188_at	sodium channel, voltage-gated, type IV, beta	Scn4b
1372180_at	syndecan 3	Sdc3
1371706_at	serologically defined colon cancer antigen 3 (predicted)	Sdccag3_predicted
1368109_at	sialyltransferase 9 (CMP-NeuAc:lactosylceramide alpha-2,3-sialyltransferase)	Siat9
1389747_at	solute carrier family 26, member 8 (predicted)	Slc26a8_predicted
1368483_a_at	slit homolog 1 (Drosophila)	Slit1
1374391_at	sarcolipin (predicted)	Sln_predicted
1382020_at	sperm associated antigen 9 (predicted)	Spag9_predicted
1395014_at	spastic paraplegia 7 homolog (human)	Spg7
1375374_at	sequestosome 1	Sqstm1
1389030_a_at	Rous sarcoma oncogene	Src
1375459_at	serine/arginine-rich protein specific kinase 2 (predicted)	Srpk2_predicted
1378431_at	serine/arginine-rich protein specific kinase 2 (predicted)	Srpk2_predicted
1398940_at	serine/arginine repetitive matrix 2 (predicted)	Srm2_predicted
1373670_at	signal transducer and activator of transcription 2 (predicted)	Stat2_predicted
1369047_at	sulfotransferase family 1D, member 1	Sult1d1
1376690_at	SRB7 (suppressor of RNA polymerase B) homolog (S. cerevisiae) (predicted)	Surb7_predicted
1371791_at	surfeit 1	Surf1
1379635_at	SYAP1 protein	Syap1
1378886_x_at	Nuclear envelope spectrin repeat protein 1	Syne1
1396512_at	synaptogyrin 1	Syng1
1389778_a_at	transcription elongation factor B (SIII), polypeptide 3	Tceb3
1397286_at	transcription factor 4	Tcf4
1377340_at	tissue factor pathway inhibitor 2	Tfpi2
1370323_at	thimet oligopeptidase 1	Thop1

1370691_a_at	thyroid hormone receptor alpha	Thra
1397692_at	cytotoxic granule-associated RNA binding protein 1 (predicted)	Tia1_predicted
1381557_at	TGFB inducible early growth response 3 (predicted)	Tieg3_predicted
1390125_at	transmembrane 9 superfamily member 1 (predicted)	Tm9sf1_predicted
1380060_at	DNA topoisomerase I, mitochondrial	Top1mt
1388650_at	topoisomerase (DNA) 2 alpha	Top2a
1368840_at	TORID	Torid
1378617_at	transcriptional regulating factor 1 (predicted)	Tref1_predicted
1392188_at	thioredoxin domain containing 9	Txndc9
1373037_at	ubiquitin-conjugating enzyme E2L 6 (predicted)	Ube2l6_predicted
1382741_at	ubiquitin protein ligase E3A (predicted)	Ube3a_predicted
1383510_at	ubiquitin protein ligase E3A (predicted)	Ube3a_predicted
1381542_at	UBX domain containing 2 (predicted)	Ubx2_predicted
1367938_at	UDP-glucose dehydrogenase	Ugdh
1371415_at	ubiquinol-cytochrome c reductase hinge protein (predicted)	Uqcrh_predicted
1367574_at	vimentin	Vim
1368889_at	vesicle transport through interaction with t-SNAREs homolog 1A (yeast)	Vti1a
1369263_at	wingless-type MMTV integration site 5A	Wnt5a
1385343_at	X-box binding protein 1	Xbp1
1380071_at	zinc finger CCH type domain containing 1 (predicted)	Zc3hdc1_predicted
1384452_at	zinc finger, CCHC domain containing 7 (predicted)	Zcchc7_predicted
1394975_at	zinc finger, matrin-like (predicted)	Zfml_predicted
1383053_x_at	zinc finger protein 91	Zfp91
1383052_a_at	zinc finger protein 91	Zfp91
1376917_at	zinc finger protein 292	Znf292

1380025_at	Rattus norvegicus catechol-O-methyltransferase (Comt), mRNA.	Comt
1380240_at	Bone morphogenetic protein 1	Bmp1

[00163] Genes and gene fragments identified as changing significantly in animals that were maternally deprived, relative to non-deprived control animals on postnatal day 30 (P30) are provided in Table 7.

TABLE 7

Fragment Name	Gene Name	Gene Symbol
1370913_at	(Best5 protein, hypothetical gene supported by NM_138881)	(Best5, LOC497812)
1370892_at	(complement component 4, gene 2, complement component 4a)	(C4-2, C4a)
1387210_at	(discs, large homolog 4 (Drosophila), hypothetical gene supported by NM_019621)	(Dlgh4, LOC497670)
1387995_a_at	(interferon induced transmembrane protein 2 (1-8D), interferon induced transmembrane protein 3)	(Ifitm2, Ifitm3)
1372604_at	(hypothetical protein LOC503164, similar to RIKEN cDNA 2210421G13)	(LOC315106, LOC503164)
1382331_at	(similar to RIKEN cDNA 0610038L10 gene, similar to riboflavin kinase)	(LOC317214, LOC499328)
1388212_a_at	(MHC class I RT1.O type 149 processed pseudogene, RT1 class I, T24, gene 4, RT1 class Ib, locus H2-TL-like (S2), RT1 class Ib, locus S3, similar to class I histocompatibility antigen alpha chain - cotton-top tamarin)	(LOC360231, LOC499402, RT1-149, RT1-S2, RT1-S3)
1393663_at	(hypothetical gene supported by NM_139339, tramdorin 1)	(LOC497667, Slc36a2)
1373992_at	(similar to MGC108823 protein, similar to interferon-inducible GTPase)	(LOC498872, MGC108823)
1391754_at	(2',5'-oligoadenylate synthetase 1, 40/46kDa, 2'-5' oligoadenylate synthetase 1F, 2'-5' oligoadenylate synthetase 1I)	(Oas1, Oas1f, Oas1i)
1370428_x_at	(RT1 class I, A3, RT1 class I, CE10, RT1 class I, CE3, RT1 class I, CE7, RT1 class Ia, locus A2, RT1 class Ib, locus Aw2)	(RT1-A2, RT1-A3, RT1-Aw2, RT1-CE10, RT1-CE3, RT1-CE7)
1390706_at	(short form of beta II spectrin, spectrin beta 2)	(Spm1, Spnb2)
1374780_at	(zinc finger protein 22 (KOX 15), zinc finger protein 422 (predicted))	(Zfp422_predicted, Znf22)
1380577_at	(ATP-binding cassette, sub-family G (WHITE), member 2)	Abcg2
1398836_s_at	actin, beta	Actb
1369063_at	acidic (leucine-rich) nuclear phosphoprotein 32 family, member A	Anp32a
1385017_at	aquarius (predicted)	Aqr_predicted
1383691_at	activating transcription factor 2	Atf2
1389470_at	B-factor, propeptidin	Bf
1388187_at	calcium/calmodulin-dependent protein kinase II alpha subunit	Camk2a
1371278_at	cell division cycle 34 homolog (S. cerevisiae) (predicted)	Cdc34_predicted
1369239_at	chloride channel 5	Clcn5
1387420_at	chloride intracellular channel 4	Clc4
1369136_at	Cytochrome P450, subfamily IIA (phenobarbital-inducible) (Cytochrome P450)	Cyp2a3a

	IIA3)	
1371142_at	cytochrome P450, subfamily 2G, polypeptide 1	Cyp2g1
1391463_at	DEAD (Asp-Glu-Ala-Asp) box polypeptide 58 (predicted)	Ddx58_predicted
1391602_at	developmentally regulated GTP binding protein 1 (predicted)	Drg1_predicted
1395274_at	dystonin (predicted)	Dst_predicted
1382314_at	interferon, alpha-inducible protein (clone IFI-15K) (predicted)	G1p2_predicted
1368332_at	guanylate nucleotide binding protein 2	Gbp2
1369640_at	gap junction membrane channel protein alpha 1	Gja1
1387906_a_at	GNAS complex locus	Gnas
1388085_at	glutathione peroxidase 6	Gpx6
1381014_at	interferon-induced protein 44 (predicted)	Ifi44_predicted
1384180_at	interferon-induced protein with tetratricopeptide repeats 2 (predicted)	Ifit2_predicted
1379568_at	interferon-induced protein with tetratricopeptide repeats 2 (predicted)	Ifit2_predicted
1383564_at	interferon regulatory factor 7 (predicted)	Irf7_predicted
1383448_at	interferon dependent positive acting transcription factor 3 gamma (predicted)	Isgf3g_predicted
1374627_at	interferon dependent positive acting transcription factor 3 gamma (predicted)	Isgf3g_predicted
1369846_at	involutrin	Ivl
1382535_at	potassium channel tetramerisation domain containing 12 (predicted)	Kctd12_predicted
1394068_x_at	Kruppel-like factor	Klf2
1390615_at	karyopherin alpha 1 (importin alpha 5)	Kpna1
1387946_at	lectin, galactoside-binding, soluble, 3 binding protein	Lgals3bp
1387027_a_at	lectin, galactose binding, soluble 9	Lgals9
1369149_at	LIM motif-containing protein kinase 1	Limk1
1391426_a_at	similar to PEST-containing nuclear protein	LOC288165
1393436_at	similar to potential ligand-binding protein	LOC309100
1375539_at	similar to T-Brain-1	LOC311078
1389034_at	similar to ubiquitin specific protease UBP43	LOC312688
1399073_at	similar to HSPC263	LOC314660
1393711_at	similar to epididymal protein	LOC361599
1381556_at	similar to BC013672 protein	LOC498673
1385397_at	Ab1-219	LOC499991
1376693_at	similar to OEF2	LOC500011
1376908_at	similar to This ORF is capable of encoding 404aa which is homologous to two human interferon-inducible proteins, 54 kDa and 56 kDa proteins; ORF	MGC94037
1380037_at	hypothetical LOC292764	MGC94040
1383606_at	membrane targeting (tandem) C2 domain containing 1	Mtac2d1
1371015_at	myxovirus (influenza virus) resistance 1	Mx1
1369202_at	myxovirus (influenza virus) resistance 2	Mx2
1387283_at	myxovirus (influenza virus) resistance 2	Mx2

1390633_at	cystatin related protein 2	P22k15
1368958_at	protein kinase C and casein kinase substrate in neurons 1	Pacsin1
1381386_at	processing of precursor 5, ribonuclease P/MRP family (S. cerevisiae) (predicted)	Pop5_predicted
1370995_at	POU domain, class 2, transcription factor 1	Pou2f1
1387242_at	Protein kinase, interferon-inducible double stranded RNA dependent	Prkr
1378287_at	radixin	Rdx
1375542_at	radixin	Rdx
1376719_at	similar to hypothetical protein D4Ert89e (predicted)	RGD1305703_predicted
1376789_at	similar to Myosin light chain kinase 2, skeletal/cardiac muscle (MLCK2) (predicted)	RGD1305801_predicted
1379285_at	similar to 5830458K16Rik protein (predicted)	RGD1306974_predicted
1377950_at	similar to interferon-inducible GTPase (predicted)	RGD1309362_predicted
1397691_at	similar to KIAA2026 protein (predicted)	RGD1311595_predicted
1387189_at	solute carrier family 22, member 3	Slc22a3
1381394_at	PDZ protein Mrt1	Snx27
1368835_at	signal transducer and activator of transcription 1	Stat1
1387354_at	signal transducer and activator of transcription 1	Stat1
1397148_at	stomatin (Epb7.2)-like 3 (predicted)	Stoml3_predicted
1379567_at	thyroid hormone receptor associated protein 1 (predicted)	Thrap1_predicted
1384419_at	thymocyte selection-associated HMG box gene (predicted)	Tox_predicted
1367598_at	transthyretin	Ttr
1368591_at	upstream transcription factor 2	Usf2
1386909_a_at	voltage-dependent anion channel 1	Vdac1
1389993_at	WD repeat domain 33 (predicted)	Wdr33_predicted
1381034_at	wingless related MMTV integration site 10a (predicted)	Wnt10a_predicted
1380071_at	zinc finger CCCH type domain containing 1 (predicted)	Zc3hdc1_predicted
1385658_at	zinc finger protein 313	Znf313

[00164] Genes and gene fragments identified as changing in animals that were maternally deprived, relative to non-deprived control animals on postnatal day 40 (P40) are provided in Table 8.

TABLE 8

Fragment Name	Gene Name	Gene Symbol
1370116_at	septin 3	3-Sep
1370913_at	(Best5 protein, hypothetical gene supported by NM_138881)	(Best5, LOC497812)
1368000_at	(complement component 3, hypothetical gene supported by NM_016994)	(C3, LOC497841)
1370892_at	(complement component 4, gene 2, complement component 4a)	(C4-2, C4a)
1381314_at	(cadherin 4, similar to R-cadherin)	(Cdh4, LOC311710)
1370363_at	(carboxylesterase 3, carboxylesterase-like)	(Ces3, LOC291863)
1369984_at	(COX17 homolog, cytochrome c oxidase assembly protein (yeast), popeye domain containing 2)	(Cox17, Popdc2)
1395412_at	(GPI-anchored membrane protein 1 (predicted), similar to GPI-anchored membrane protein 1)	(Gpiap1_predicted, LOC362174)
1395173_at	(GPI-anchored membrane protein 1 (predicted), similar to GPI-anchored membrane protein 1)	(Gpiap1_predicted, LOC362174)
1368319_a_at	(HS1 binding protein, homer homolog 1 (Drosophila))	(Homer1, Hs1bp1)
1387995_a_at	(interferon induced transmembrane protein 2 (1-8D), interferon induced transmembrane protein 3)	(Ifitm2, Ifitm3)
1387458_at	(ring finger protein 4, similar to CG14998-PC, isoform C)	(LOC305453, Rnf4)
1372604_at	(hypothetical protein LOC503164, similar to RIKEN cDNA 2210421G13)	(LOC315106, LOC503164)
1388212_a_at	(MHC class I RT1.O type 149 processed pseudogene, RT1 class I, T24, gene 4, RT1 class Ib, locus H2-TL-like (S2), RT1 class Ib, locus S3, similar to class I histocompatibility antigen alpha chain - cotton-top tamarin)	(LOC360231, LOC499402, RT1-149, RT1-S2, RT1-S3)
1389734_x_at	(MHC class I RT1.O type 149 processed pseudogene, RT1 class I, T24, gene 4, RT1 class Ib, locus H2-TL-like (S2), RT1 class Ib, locus S3, similar to class I histocompatibility antigen alpha chain - cotton-top tamarin)	(LOC360231, LOC499402, RT1-149, RT1-S2, RT1-S3)

1388164_at	(MHC class I RT1.O type 149 processed pseudogene, RT1 class I, T24, gene 4, RT1 class Ib, locus H2-TL-like (S2), RT1 class Ib, locus S3, similar to class I histocompatibility antigen alpha chain - cotton-top tamarin)	(LOC360231, LOC499402, RT1-149, RT1-S2, RT1-S3)
1377174_at	(SET binding factor 1 (predicted), similar to mKIAA3020 protein)	(LOC362985, Sbf1_predicted)
1392655_at	(similar to Nuclear autoantigen Sp-100 (Speckled 100 kDa) (Nuclear dot-associated Sp100 protein), similar to SP140 nuclear body protein isoform 1)	(LOC363269, LOC501175)
1369973_at	(hypothetical gene supported by NM_017154, xanthine dehydrogenase)	(LOC497811, Xdh)
1380446_at	(LOC498801, myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 10 (predicted))	(LOC498801, Mllt10_predicted)
1373992_at	(similar to MGC108823 protein, similar to interferon-inducible GTPase)	(LOC498872, MGC108823)
1393540_at	(myosin heavy chain, polypeptide 6, myosin, heavy polypeptide 7, cardiac muscle, beta)	(Myh6, Myh7)
1391754_at	(2',5'-oligoadenylate synthetase 1, 40/46kDa, 2'-5' oligoadenylate synthetase 1F, 2'-5' oligoadenylate synthetase 1I)	(Oas1, Oas1f, Oas1i)
1371152_a_at	(2',5'-oligoadenylate synthetase 1, 40/46kDa, 2'-5' oligoadenylate synthetase 1I, 2'-5' oligoadenylate synthetase 1K)	(Oas1, Oas1i, Oas1k)
1370428_x_at	(RT1 class I, A3, RT1 class I, CE10, RT1 class I, CE3, RT1 class I, CE7, RT1 class Ia, locus A2, RT1 class Ib, locus Aw2)	(RT1-A2, RT1-A3, RT1-Aw2, RT1-CE10, RT1-CE3, RT1-CE7)
1388071_x_at	(RT1 class I, A3, RT1 class I, CE10, RT1 class I, CE7, RT1 class Ib, locus Aw2)	(RT1-A3, RT1-Aw2, RT1-CE10, RT1-CE7)
1370429_at	(RT1 class I, A3, RT1 class I, CE10, RT1 class I, CE7, RT1 class Ib, locus Aw2)	(RT1-A3, RT1-Aw2, RT1-CE10, RT1-CE7)
1387555_at	amiloride-sensitive cation channel 2, neuronal	Accn2
1380533_at	amyloid beta (A4) precursor protein	App
1391658_at	archain	Arctn1
1381151_at	AT rich interactive domain 4B (Rbp1 like)	Arid4b
1377191_at	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit e	Atp5i
1396279_at	ATPase, H+ transporting, lysosomal accessory protein 2	Atp6ap2

1389470_at	B-factor, properdin	Bf
1386774_at	BMP/retinoic acid-inducible neural-specific protein 2	Brinp2
1379157_at	calcium channel, voltage-dependent, L type, alpha 1C subunit	Cacna1c
1371687_at	calnexin	Canx
1387178_a_at	cystathionine beta synthase	Cbs
1368887_at	cadherin 22	Cdh22
1387420_at	chloride intracellular channel 4	Clic4
1370864_at	collagen, type 1, alpha 1	Col1a1
1387854_at	procollagen, type I, alpha 2	Col1a2
1370155_at	procollagen, type I, alpha 2	Col1a2
1370959_at	collagen, type III, alpha 1	Col3a1
1387243_at	cytochrome P450, family 1, subfamily a, polypeptide 2	Cyp1a2
1369136_at	Cytochrome P450, subfamily IIA (phenobarbital-inducible) (Cytochrome P450 IIA3)	Cyp2a3a
1368608_at	cytochrome P450, family 2, subfamily f, polypeptide 2	Cyp2f2
1371142_at	cytochrome P450, subfamily 2G, polypeptide 1	Cyp2g1
1370387_at	cytochrome P450, family 3, subfamily a, polypeptide 13	Cyp3a13
1390738_at	DAMP-1 protein	Damp1
1399162_a_at	damage-specific DNA binding protein 1	Ddb1
1391463_at	DEAD (Asp-Glu-Ala-Asp) box polypeptide 58 (predicted)	Ddx58_predicted
1394715_at	Dicer1, Dcr-1 homolog (Drosophila) (predicted)	Dicer1_predicted
1380807_at	discs, large homolog 1 (Drosophila)	Dlgh1
1393756_at	dentin matrix protein 1	Dmp1
1388022_a_at	dynamitin 1-like	Dnm1l
1395586_at	eukaryotic translation elongation factor 1 alpha 1	Eef1a1
1383447_at	ets variant gene 5 (ets-related molecule) (predicted)	Etv5_predicted

1387715_at	extracellular peptidase inhibitor	Expi
1390049_at	four and a half LIM domains 1	Fhl1
1377635_at	flavin containing monooxygenase 2	Fmo2
1369258_at	fucosyltransferase 9	Fut9
1393145_at	follicular lymphoma variant translocation 1 (predicted)	Fvt1_predicted
1382314_at	interferon, alpha-inducible protein (clone IFI-15K) (predicted)	G1p2_predicted
1368332_at	guanylate nucleotide binding protein 2	Gbp2
1395370_at	germ cell-less protein	Gcl
1370146_at	glycine receptor, beta subunit	Glr1b
1388066_a_at	G protein-coupled receptor kinase 6	Gprk6
1388085_at	glutathione peroxidase 6	Gpx6
1370952_at	glutathione S-transferase, mu 2	Gstm2
1382902_at	potential ubiquitin ligase	Herc6
AFFX_Rat_Hexokinase_M_at	hexokinase 1	Hk1
1387994_at	hydroxysteroid (17-beta) dehydrogenase 9	Hsd17b9
1374551_at	interferon-induced protein 35 (predicted)	Ifi35_predicted
1381014_at	interferon-induced protein 44 (predicted)	Ifi44_predicted
1384180_at	interferon-induced protein with tetratricopeptide repeats 2 (predicted)	Ifit2_predicted
1379568_at	interferon-induced protein with tetratricopeptide repeats 2 (predicted)	Ifit2_predicted
1383564_at	interferon regulatory factor 7 (predicted)	Irf7_predicted
1376845_at	putative ISG12(b) protein	isg12(b)
1383448_at	interferon dependent positive acting transcription factor 3 gamma (predicted)	Isfg3g_predicted
1374627_at	interferon dependent positive acting transcription factor 3 gamma (predicted)	Isfg3g_predicted
1370773_a_at	Kv channel-interacting protein 2	Kcni2
1387657_at	kinesin family member 3C	Kif3c

1368723_at	linker for activation of T cells	Lat
1387946_at	lectin, galactoside-binding, soluble, 3 binding protein	Lgals3bp
1385601_at	similar to FSHD region gene 1	LOC304454
1397512_at	similar to Vps41 protein	LOC306991
1393436_at	similar to potential ligand-binding protein	LOC309100
1379748_at	similar to minor histocompatibility antigen precursor	LOC310968
1389034_at	similar to ubiquitin specific protease UBP43	LOC312688
1394459_at	similar to Protein CXorf17 homolog	LOC317423
1390024_at	similar to osteoclast inhibitory lectin	LOC362447
1373975_at	similar to thioether S-methyltransferase	LOC368066
1390506_at	similar to peroxisome proliferator-activated receptor binding protein	LOC497991
1397230_at	similar to hypothetical protein C130098D09	LOC498201
1385213_at	similar to epithelial stromal interaction 1 isoform a	LOC498547
1383708_at	similar to integrin, beta-like 1	LOC498564
1381556_at	similar to BC013672 protein	LOC498673
1371679_at	similar to Synaptopodin-2 (Myopodin)	LOC499702
1384547_at	similar to antimicrobial peptide RY2G5	LOC499925
1385397_at	Ab1-219	LOC499991
1376693_at	similar to OEF2	LOC500011
1396099_at	similar to Hypothetical protein MGC30714	LOC500065
1382273_at	similar to Apoptosis facilitator Bcl-2-like protein 14	LOC500348
1375073_at	similar to sterile alpha motif domain containing 11	LOC500601
1398688_at	similar to Spink5 protein	LOC502158
1375193_at	low density lipoprotein receptor-related protein 11 (predicted)	Lrp11_predicted
1370792_at	microtubule-associated protein, RP/EB family, member 1	Mapre1

1379363_at	maltase-glucoamylase (predicted)	Mgam_predicted
1376908_at	similar to This ORF is capable of encoding 404aa which is homologous to two human interferon-inducible proteins, 54 kDa and 56 kDa proteins; ORF	MGC94037
1388204_at	matrix metalloproteinase 13	Mmp13
1372683_at	molybdenum cofactor sulfurase (predicted)	Mocos_predicted
1394182_at	myotubularin related protein 4 (predicted)	Mtmr4_predicted
1371015_at	myxovirus (influenza virus) resistance 1	Mx1
1369202_at	myxovirus (influenza virus) resistance 2	Mx2
1387283_at	myxovirus (influenza virus) resistance 2	Mx2
1384255_at	N-ethylmaleimide-sensitive factor attachment protein, gamma (predicted)	Napg_predicted
1383899_at	neural precursor cell expressed, developmentally down-regulated gene 4A	Nedd4a
1395157_at	neural precursor cell expressed, developmentally down-regulated gene 4A	Nedd4a
1395408_at	nitric oxide synthase trafficking	Nostrin
1377497_at	2'-5' oligoadenylate synthetase-like 1 (predicted)	Oas1_predicted
1369835_at	olfactory marker protein	Omp
1394973_at	phosphodiesterase 1C	Pde1c
1372923_at	peroxisomal biogenesis factor 11b (predicted)	Pex11b_predicted
1390423_at	pam, highwire, rpm 1 (predicted)	Phr1_predicted
1369039_at	phosphatidylinositol 4-kinase, catalytic, beta polypeptide	Pik4cb
1371447_at	placenta-specific 8 (predicted)	Plac8_predicted
1387242_at	Protein kinase, interferon-inducible double stranded RNA dependent	Prkr
1376029_at	RAB2, member RAS oncogene family-like	Rab2l
1387641_at	RAB5A, member RAS oncogene family	Rab5a
1371103_at	RAB6B, member RAS oncogene family	Rab6b
1391347_at	RAB8B, member RAS oncogene family	Rab8b
1386900_at	ribosome associated membrane protein 4	RAMP4

1396207_at	radixin	Rdx
1390037_at	similar to chromosome 20 open reading frame 58 (predicted)	RGD1305809_predicted
1397861_at	similar to contains transmembrane (TM) region (predicted)	RGD1306235_predicted
1379795_at	similar to RIKEN cDNA 2410002O22 gene (predicted)	RGD1306583_predicted
1390113_a_at	similar to KIAA0731 protein (predicted)	RGD1306683_predicted
1379285_at	similar to 5830458K16Rik protein (predicted)	RGD1306974_predicted
1389849_at	similar to RIKEN cDNA 0610027O18 (predicted)	RGD1307118_predicted
1376144_at	similar to B aggressive lymphoma (predicted)	RGD1307534_predicted
1374337_at	similar to chromosome 17 open reading frame 27 (predicted)	RGD1308168_predicted
1380444_at	similar to RIKEN cDNA 1110017I16 (predicted)	RGD1308977_predicted
1377950_at	similar to interferon-inducible GTPase (predicted)	RGD1309362_predicted
1373262_at	similar to 2310014H01Rik protein (predicted)	RGD1309543_predicted
1385109_at	similar to RIKEN cDNA 4930553M18 (predicted)	RGD1309627_predicted
1373814_at	similar to mKIAA1002 protein (predicted)	RGD1310066_predicted
1372034_at	similar to hypothetical protein MGC29390 (predicted)	RGD1310490_predicted
1372438_at	similar to Nit protein 2 (predicted)	RGD1310494_predicted
1394940_at	similar to hypothetical protein FLJ20037 (predicted)	RGD1311381_predicted
1394695_at	similar to hypothetical protein FLJ20037 (predicted)	RGD1311381_predicted
1379459_at	similar to intracellular membrane-associated calcium-independent phospholipase A2 gamma (predicted)	RGD1311444_predicted
1398824_at	coated vesicle membrane protein	Rnp24
1367661_at	S100 calcium binding protein A6 (calyculin)	S100a6
1390777_at	sterol-C5-desaturase (fungal ERG3, delta-5-desaturase) homolog (S. cerevisiae)	Sc5d
1384173_at	src family associated phosphoprotein 1	Scap1
1368539_at	sodium channel, voltage-gated, type 9, alpha polypeptide	Scn9a

1371063_at	SH3 domain protein 2A	Sh3gl2
1388064_a_at	solute carrier family 1 (glial high affinity glutamate transporter), member 3	Slc1a3
1390825_at	solute carrier family 35, member B3 (predicted)	Slc35b3_predicted
1383970_at	solute carrier family 35, member C2 (predicted)	Slc35c2_predicted
1381922_at	solute carrier family 5 (sodium/glucose cotransporter), member 11	Slc5a11
1374391_at	sarcophilin (predicted)	Sln_predicted
1392965_a_at	SPARC related modular calcium binding 2 (predicted)	Smoc2_predicted
1372930_at	SP110 nuclear body protein (predicted)	Sp110_predicted
1368835_at	signal transducer and activator of transcription 1	Stat1
1372757_at	signal transducer and activator of transcription 1	Stat1
1387876_at	signal transducer and activator of transcription 5B	Stat5b
1397148_at	stomatin (Epb7.2)-like 3 (predicted)	Stoml3_predicted
1369919_at	thyrotroph embryonic factor	Tef
1375951_at	thrombomodulin	Thbd
1374529_at	thrombospondin 2 (predicted)	Thbs2_predicted
1370323_at	thimet oligopeptidase 1	Thop1
1371785_at	tumor necrosis factor receptor superfamily, member 12a	Tnfrsf12a
1393423_at	tankyrase, TRF1-interacting ankyrin-related ADP-ribose polymerase 2 (predicted)	Tnks2_predicted
1371060_at	tripartite motif protein 23	Trim23
1385252_at	tripartite motif protein 34 (predicted)	Trim34_predicted
1387565_at	transient receptor potential cation channel, subfamily V, member 6	Trpv6
1391228_at	testis specific gene A2 (predicted)	Tsga2_predicted
1373037_at	ubiquitin-conjugating enzyme E2L 6 (predicted)	Ube2l6_predicted
1385615_at	ubiquitin conjugation factor E4 A	Ube4a
1369850_at	UDP glycosyltransferase 2 family, polypeptide A1	Ugt2a1

1369394_at	unc-5 homolog A (C. elegans)	Unc5a
1369597_at	vesicle-associated membrane protein, associated protein B and C	Vapb
1380071_at	zinc finger CCHH type domain containing 1 (predicted)	Zc3hdc1_predicted
1394975_at	zinc finger, matrin-like (predicted)	Zfml_predicted

[00165] Genes and gene fragments identified as changing in animals that were maternally deprived, relative to non-deprived control animals on postnatal day 60 (P60) are provided in Table 9.

TABLE 9

Fragment Name	Gene Name	Gene Symbol
1383096_at	(LOC500962, amyloid beta (A4) precursor-like protein 2)	(Aplp2, LOC500962)
1372977_at	(atlastin-like, cyclin-dependent kinase-like 1 (CDC2-related kinase) (predicted), similar to mitogen-activated protein kinase kinase 5 isoform 2)	(Cdkl1_predicted, LOC362750, LOC503027)
1387320_a_at	(densin-180, hypothetical gene supported by NM_057142)	(LOC117284, LOC497765)
1384965_at	(LOC499369, serine/threonine kinase 2)	(LOC499369, Slk)
1369063_at	acidic (leucine-rich) nuclear phosphoprotein 32 family, member A	Anp32a
1369752_a_at	calcium/calmodulin-dependent protein kinase IV	Camk4
1379130_at	CDW92 antigen	Cdw92
1368366_at	Camello-like 2	Cml2
1370991_at	camello-like 3	Cml3
1388176_at	camello-like 5	Cml5
1389931_at	corticotropin releasing hormone receptor 2	Crhr2
1394731_at	casein kinase 1, gamma 3	Csnk1g3
1368685_at	chondroitin sulfate proteoglycan 4	Cspg4
1381384_at	degenerative spermatocyte homolog (Drosophila)	Degs
1395572_at	DnaJ (Hsp40) homolog, subfamily A, member 4 (predicted)	Dnaia4_predicted
1387306_a_at	early growth response 2	Egr2
1369371_a_at	gamma-aminobutyric acid (GABA) B receptor 1	Gabbr1
1387935_at	interleukin 3 receptor, alpha chain	Il3ra
1375190_at	potassium channel tetramerisation domain containing 13	Kctd13
1376028_at	similar to RIKEN cDNA 4121402D02	LOC303514
1399118_at	similar to RIKEN cDNA 4121402D02	LOC303514
1394459_at	similar to Protein Cxorf17 homolog	LOC317423
1397334_at	similar to SEC14-like 1	LOC360668
1385455_at	similar to sarcoma antigen NY-SAR-27	LOC499691
1395472_at	leucine rich repeat containing 17	Lrrc17
1393669_at	similar to Ras-related protein Rab-1B	MGC105830
1387365_at	nuclear receptor subfamily 1, group H, member 3	Nr1h3
1391295_at	phosphodiesterase 10A	Pde10a
1372923_at	peroxisomal biogenesis factor 11b (predicted)	Pex11b_predicted

1393673_at		similar to HCDI protein (predicted)	RGD1309307_predicted
1397165_at		SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 2	Smarca2
1387852_at		thyroid hormone responsive protein	Thrsp
1395719_at		Tu translation elongation factor, mitochondrial (predicted)	Tufm_predicted

[00166] Genes and gene fragments identified as changing significantly in animals that were maternally deprived, relative to non-deprived control animals on postnatal day 80 (P80) are provided in Table 10.

TABLE 10

Fragment Name	Gene Name	Gene Symbol
1395545_at	(angiotensin II receptor-associated protein, cytochrome P450-like, heat shock 70kD protein 1B, proteoglycan peptide core protein, similar to CGI-100-like protein)	(Agtrap, Hspa1b, LOC293989, MGC95001, Pgsg)
1370892_at	(complement component 4, gene 2, complement component 4a)	(C4-2, C4a)
1387210_at	(discs, large homolog 4 (Drosophila), hypothetical gene supported by NM_019621)	(Dlgh4, LOC497670)
1368550_at	(HNF-3/forkhead homolog-1, hypothetical gene supported by NM_022858)	(Foxq1, LOC497713)
1374062_x_at	(G protein-coupled receptor kinase 5, microtubule-associated protein, RP/EB family, member 3)	(Gprk5, Mapre3)
1396919_at	(hereditary sensory neuropathy, type II, protein kinase, lysine deficient 1)	(Hsn2, Prkwnk1)
1397130_at	(mitogen activated protein kinase 10, similar to binding protein)	(LOC293702, Mapk10)
1379200_at	(similar to RIKEN cDNA C330027C09 (predicted), similar to Ubiquitin ligase protein DZIP3 (DAZ-interacting protein 3 homolog))	(LOC303963, RGD1310335_predicted)
1389734_x_at	(MHC class I RT1.O type 149 processed pseudogene, RT1 class I, T24, gene 4, RT1 class Ib, locus H2-TL-like (S2), RT1 class Ib, locus S3, similar to class I histocompatibility antigen alpha chain - cotton-top tamarin)	(LOC360231, LOC499402, RT1-149, RT1-S2, RT1-S3)
1372751_at	(LOC500936, hypothetical LOC366994)	(LOC366994, LOC500936)
1392177_at	(LOC498458, protein tyrosine phosphatase, receptor type, G)	(LOC498458, Ptprg)
1372640_at	(LOC499410, protease inhibitor 16 (predicted))	(LOC499410, Pi16_predicted)
1395480_at	(RAD51 homolog (S. cerevisiae) (predicted), similar to AF15q14 protein isoform 2, similar to DNA repair protein RAD51 homolog 1)	(LOC499869, LOC499870, Rad51_predicted)
1383356_at	(LOC500443, similar to dynein, axonemal, intermediate chain 1)	(LOC500442, LOC500443)
1398945_at	(similar to RCK, trehalase (brush-border membrane glycoprotein))	(LOC500988, Treh)
1371017_at	(T-cell receptor gamma chain, similar to TCR V gamma 3)	(LOC502132, Tcrg)
1369138_a_at	(parkin, similar to mature parasite-infected erythrocyte surface antigen like precursor (2N179))	(LOC502231, Park2)
1370428_x_at	(RT1 class I, A3, RT1 class I, CE10, RT1 class I, CE3, RT1 class I, CE7, RT1 class Ia, locus A2, RT1 class Ib, locus Aw2)	(RT1-A2, RT1-A3, RT1-Aw2, RT1-CE10, RT1-CE3, RT1-CE7)
1368330_at	apoptosis antagonizing transcription factor	Aatf
1370955_at	a disintegrin and metalloprotease domain 10	Adam10

1382206_a_at	A kinase (PRKA) anchor protein 2 (predicted)	Akap2_predicted
1388765_at	murine thymoma viral (v-akt) oncogene homolog 2	Akt2
1375263_at	activated leukocyte cell adhesion molecule	Alcam
1368776_at	arachidonate 5-lipoxygenase	Alox5
1396195_at	ankyrin repeat domain 13 (predicted)	Ankrd13_predicted
1369063_at	acidic (leucine-rich) nuclear phosphoprotein 32 family, member A	Anp32a
1398695_at	amyloid beta (A4) precursor protein	App
1387068_at	activity regulated cytoskeletal-associated protein	Arc
1393798_at	alpha thalassemia/mental retardation syndrome X-linked homolog (human)	Atrx
1398004_at	BMP/retnoic acid-inducible neural-specific protein 2	Brinp2
1379157_at	calcium channel, voltage-dependent, L type, alpha 1C subunit	Cacna1c
1397151_at	calcium channel, voltage-dependent, alpha 2/delta 3 subunit	Cacna2d3
1388187_at	calcium/calmodulin-dependent protein kinase II alpha subunit	Camk2a
1387401_at	calsequestrin 2	Casq2
1383075_at	cyclin D1	Ccnd1
1374540_at	cell division cycle associated 7 (predicted)	Cdca7_predicted
1392140_at	cadherin 11	Cdh11
1377402_at	cyclin-dependent kinase (CDC2-like) 10 (predicted)	Cdk10_predicted
1369019_at	cholinergic receptor, nicotinic, alpha polypeptide 5	Chrna5
1394008_x_at	ciliary neurotrophic factor receptor	Cntrf
1384227_at	coronin, actin binding protein 1C (predicted)	Coro1c_predicted
1390399_at	cAMP responsive element binding protein-like 2 (predicted)	Crebl2_predicted
1369912_at	v-crk sarcoma virus CT10 oncogene homolog (avian)	Crk
1384339_s_at	casein kinase II, alpha 1 polypeptide	Csnk2a1
1397217_at	CUG triplet repeat,RNA-binding protein 2	Cugbp2
1369068_at	cullin 5	Cul5
1379855_at	deleted in colorectal carcinoma	Dcc
1376524_at	hypothetical protein	Dd25
1391406_at	degenerative spermatocyte homolog (Drosophila)	Degs
1396063_at	DEK oncogene (DNA binding)	Dek
1380807_at	discs, large homolog 1 (Drosophila)	Dlgh1
1397020_at	discs, large homolog 2 (Drosophila)	Dlgh2
1375139_at	discs, large homolog 2 (Drosophila)	Dlgh2
1368146_at	dual specificity phosphatase 1	Dusp1
1395586_at	eukaryotic translation elongation factor 1 alpha 1	Eef1a1
1369540_at	EF hand calcium binding protein 1	Efcabp1
1370542_a_at	E74-like factor 1	Elf1
1382710_at	ectodermal-neural cortex 1	Enc1

1390054_at	ectodermal-neural cortex 1	Enc1
1369453_at	Epsin 1	Epn1
1372823_at	family with sequence similarity 36, member A (predicted)	Fam36a_predicted
1392339_at	phenylalanine-tRNA synthetase-like, beta subunit	Farslb
1383516_at	fibrinogen-like 2	Fgl2
1390936_at	FXD domain-containing ion transport regulator 3	Fxyd3
1369371_a_at	gamma-aminobutyric acid (GABA) B receptor 1	Gabbr1
1392320_s_at	FKBP-associated protein	Glmn
1384819_at	glucagon-like peptide 2 receptor	Glp2r
1398530_at	guanine nucleotide binding protein (G protein), gamma 11	Gng11
1394578_at	glutamate receptor, ionotropic, 2	Gria2
1393995_at	glutamate receptor, ionotropic, 2	Gria2
1392248_at	glutamate receptor, ionotropic, delta 1	Grid1
1370267_at	glycogen synthase kinase 3 beta	Gsk3b
1378614_at	Huntington disease gene homolog	Hdh
1395981_at	helicase, ATP binding 1 (predicted)	Helic1_predicted
AFFX_Rat_Hexokinase_M_at	hexokinase 1	Hk1
1379546_at	hematological and neurological expressed sequence 1	Hn1
1392329_at	homeodomain leucine zipper-encoding gene	Homez
1385931_at	hook homolog 3	Hook3
1376046_at	hook homolog 3	Hook3
1367648_at	insulin-like growth factor binding protein 2	Igfbp2
1392246_at	immunoglobulin superfamily, member 4A (predicted)	Igsf4a_predicted
1392467_at	inositol (myo)-1(or 4)-monophosphatase 2	Impa2
1396701_at	kalirin, RhoGEF kinase	Kalrn
1369133_a_at	potassium voltage gated channel, Shaw-related subfamily, member 3	Kcnc3
1397599_at	potassium voltage-gated channel, subfamily Q, member 3	Kcnq3
1386041_a_at	Kruppel-like factor	Klf2
1387260_at	Kruppel-like factor 4 (gut)	Klf4
1367880_at	laminin, beta 2	Lamb2
1367628_at	lectin, galactose binding, soluble 1	Lgals1
1369149_at	LIM motif-containing protein kinase 1	Limk1
1370853_at	CaM-kinase II inhibitor alpha	LOC287005
1392723_at	similar to ankyrin repeat domain protein 17 isoform b	LOC289521
1385922_at	similar to RIKEN cDNA 5830434P21	LOC296637
1382881_at	similar to EXCretory canal abnormal EXC-7, ELAV type RNA binding protein (48.7 kD) (exc-7)	LOC298705
1385713_at	similar to NAKAP95	LOC299569
1390375_at	similar to NAKAP95	LOC299569

1384799_at	similar to KIAA2022 protein	LOC302396
1376243_at	similar to serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 12	LOC304692
1377961_at	similar to AT motif-binding factor	LOC307829
1375539_at	similar to T-Brain-1	LOC311078
1396803_at	similar to THO complex 2	LOC313308
1382551_at	similar to Intersectin 2 (SH3 domain-containing protein 1B) (SH3P18) (SH3P18-like WASP associated protein)	LOC313934
1383673_at	similar to Nap1l2	LOC317247
1385427_at	similar to RNA-binding protein Musashi2-S	LOC360596
1389099_at	similar to hypothetical protein MGC51082	LOC361519
1399056_at	similar to CG10585-PA	LOC365592
1386070_at	similar to IRA1 protein	LOC365755
1374421_at	similar to Williams-Beuren syndrome deletion transcript 9 homolog	LOC368002
1380728_at	similar to collapsin response mediator protein-2A	LOC498539
1375821_at	similar to ankryrin repeat domain 26	LOC498767
1395081_at	similar to nuclear receptor coactivator 7	LOC498995
1384809_at	LOC499283	LOC499283
1389986_at	LOC499304	LOC499304
1374028_at	similar to CDNA sequence BC024479	LOC500974
1385686_at	similar to SPRR1b	LOC502543
1371405_at	similar to hypothetical protein MGC52110	LOC503252
1367984_at	CTD-binding SR-like rA1	LOC56081
1368861_a_at	myelin-associated glycoprotein	Mag
1384361_at	mal, T-cell differentiation protein 2	Mal2
1379456_at	mitochondrial carrier triple repeat 1 (predicted)	Mcart1_predicted
1386478_at	mitochondrial carrier triple repeat 1 (predicted)	Mcart1_predicted
1385101_a_at	Unknown (protein for MGC:73017)	MGC73017
1395223_at	similar to hypothetical protein MGC35097	MGC94736
1376853_at	similar to RIKEN cDNA 2310042P20	MGC94954
1368279_at	myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog); translocated to, 3	Mlit3
1377534_at	mannose receptor, C type 1 (predicted)	Mrc1_predicted
1386114_at	MAS-related G protein-coupled receptor, member B4	Mrgprb4
1388853_at	mitochondrial ribosomal protein L54 (predicted)	Mrpl54_predicted
1387786_at	myotrophin	Mtpn
1376648_at	v-myc myelocytomatosis viral related oncogene, neuroblastoma derived (avian)	Mycn
1379472_at	NAD synthetase 1	Nadsyn1

1393881_at	NMDA receptor-regulated gene 1 (predicted)	Narg1_predicted
1388167_at	nuclear factor I/B	Nfib
1394778_at	nuclear factor I/B	Nfib
1391256_at	N-myristoyltransferase 2	Nmt2
1395083_at	neuro-oncological ventral antigen 1	Nova1
1374959_at	NAD(P)H dehydrogenase, quinone 2	Nqo2
1397004_at	nuclear receptor subfamily 3, group C, member 1	Nr3c1
1371069_at	ion transporter protein	Nritp
1391182_at	OTU domain, ubiquitin aldehyde binding 2 (predicted)	Otub2_predicted
1388353_at	proliferation-associated 2G4, 38kDa	Pa2g4
1392480_at	poly(A) binding protein, nuclear 1	Pabpn1
1368958_at	protein kinase C and casein kinase substrate in neurons 1	Pacsin1
1376247_at	phosphoenolpyruvate carboxykinase 2 (mitochondrial) (predicted)	Pck2_predicted
1389396_at	6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase 4	Pfkfb4
1371776_at	phosphatidylinositol 3-kinase, regulatory subunit, polypeptide 1	Pik3r1
1384558_at	placenta-specific 9 (predicted)	Plac9_predicted
1379690_at	polymerase (DNA-directed), delta interacting protein 3 (predicted)	Poldip3_predicted
1384815_at	protein phosphatase 3, catalytic subunit, alpha isoform	Ppp3ca
1379175_at	protein phosphatase 3, catalytic subunit, alpha isoform	Ppp3ca
1398242_at	protein phosphatase 5, catalytic subunit	Ppp5c
1368240_a_at	protein kinase C, beta 1	Prkcb1
1374033_at	proteasome (prosome, macropain) subunit, beta type 10 (predicted)	Psmb10_predicted
1374803_at	proteasome (prosome, macropain) 26S subunit, non-ATPase, 11 (predicted)	Psmc11_predicted
1379859_at	proteasome (prosome, macropain) 26S subunit, non-ATPase, 11 (predicted)	Psmc11_predicted
1383426_at	proline-serine-threonine phosphatase-interacting protein 1 (predicted)	Pstpip1_predicted
1388430_at	prostate tumor over expressed gene 1 (predicted)	Ptov1_predicted
1384485_at	protein tyrosine phosphatase, receptor type, U	Ptpu
1388363_at	hnRNP-associated with lethal yellow (predicted)	Raly_predicted
1369130_at	RAS guanyl releasing protein 1	Rasgrp1
1369129_at	RAS guanyl releasing protein 1	Rasgrp1
1376146_at	similar to RIKEN cDNA 2310033P09 (predicted)	RGD1304587_predicted
1374804_at	similar to Autoantigen NGP-1 (predicted)	RGD1305006_predicted
1386088_at	similar to RIKEN cDNA 1200007B05 gene (predicted)	RGD1305072_predicted
1374764_at	similar to 2610033H07Rik protein (predicted)	RGD1305605_predicted
1385862_at	similar to RIKEN cDNA 4930438O05 (predicted)	RGD1305615_predicted
1390037_at	similar to chromosome 20 open reading frame 58 (predicted)	RGD1305809_predicted
1393326_s_at	similar to Pseudoautosomal GTP-binding protein-like protein (predicted)	RGD1305954_predicted

1376263_at	similar to 1810034B16Rik protein (predicted)	RGD1306222_predicted
1393846_at	similar to downregulated in renal cell carcinoma (predicted)	RGD1306327_predicted
1374516_at	similar to RIKEN cDNA 5830457O10 (predicted)	RGD1306894_predicted
1397848_at	similar to RIKEN cDNA 6330406115 (predicted)	RGD1307396_predicted
1388665_at	similar to RIKEN cDNA 1110020A23 (predicted)	RGD1308134_predicted
1379699_at	similar to FLJ20689 (predicted)	RGD1308907_predicted
1382466_at	similar to RIKEN cDNA 6530403A03 (predicted)	RGD1309020_predicted
1395516_at	similar to hypothetical protein FLJ10154 (predicted)	RGD1310061_predicted
1373814_at	similar to KIAA1002 protein (predicted)	RGD1310066_predicted
1377648_at	similar to KIAA1838 protein (predicted)	RGD1310304_predicted
1381513_at	similar to RIKEN cDNA 1300017J02 (predicted)	RGD1310507_predicted
1393361_at	similar to chromosome 16 open reading frame 33; minus -99 protein (predicted)	RGD1310922_predicted
1376612_at	similar to RIKEN cDNA 1810033A06 (predicted)	RGD1311144_predicted
1373486_at	similar to scotin (predicted)	RGD1312041_predicted
1372639_at	ring finger protein 30 (predicted)	Rnf30_predicted
1379737_a_at	RNA-binding region (RNP1, RRM) containing 2 (predicted)	Rnpc2_predicted
1384654_at	roundabout homolog 1 (Drosophila)	Robo1
1388413_at	ribosome binding protein 1 homolog 180kDa (dog) (predicted)	Rrbp1_predicted
1389051_at	retinoid X receptor beta	Rxrb
1395327_at	CD36 antigen (collagen type I receptor, thrombospondin receptor)-like 2	Scarb2
1378595_at	NonO/p54nrb homolog	Sfpq
1368109_at	sialyltransferase 9 (CMP-NeuAc:lactosylceramide alpha-2,3-sialyltransferase)	Siat9
1395102_at	potassium channel subunit (Slack)	Slack
1389747_at	solute carrier family 26, member 8 (predicted)	Slc26a8_predicted
1387707_at	solute carrier family 2 (facilitated glucose transporter), member 3	Slc2a3
1368046_at	solute carrier family 31 (copper transporters), member 1	Slc31a1
1368440_at	solute carrier family 3, member 1	Slc3a1
1374391_at	sarcophilin (predicted)	Sln_predicted
1398568_at	synaptosomal-associated protein, 91kDa homolog (mouse)	Snap91
1394436_at	sperm associated antigen 9 (predicted)	Spag9_predicted
1377743_at	sprouty protein with EVH-1 domain 1, related sequence (predicted)	Spred1_predicted
1378431_at	serine/arginine-rich protein specific kinase 2 (predicted)	SrpK2_predicted
1398940_at	serine/arginine repetitive matrix 2 (predicted)	Srrm2_predicted
1378886_x_at	Nuclear envelope spectrin repeat protein 1	Syne1
1387517_at	synaptotagmin 13	Syt13
1397286_at	transcription factor 4	Tcf4
1396660_at	transcription factor 4	Tcf4

1392382_at	transforming growth factor, beta 2	Tgfb2
1381557_at	TGFB inducible early growth response 3 (predicted)	Tieg3_predicted
1374446_at	TCDD-inducible poly(ADP-ribose) polymerase (predicted)	Tiparp_predicted
1394160_at	transmembrane protein 2 (predicted)	Tmem2_predicted
1381822_x_at	TP53 regulating kinase (predicted)	Tp53rk_predicted
1371635_at	transmembrane domain protein regulated in adipocytes	Tpra40
1371618_s_at	tubulin, beta 3	Tubb3
1383510_at	ubiquitin protein ligase E3A (predicted)	Ube3a_predicted
1396477_at	unr protein	Unr
1376256_at	WD repeat and FYVE domain containing 1 (predicted)	Wdly1_predicted
1369263_at	wingless-type MMTV integration site 5A	Wnt5a
1385343_at	X-box binding protein 1	Xbp1
1387129_at	X-ray repair complementing defective repair in Chinese hamster cells 1	Xrcc1
1384452_at	zinc finger, CCHC domain containing 7 (predicted)	Zcchc7_predicted
1393795_at	zinc finger homeobox 1b (predicted)	Zfx1b_predicted
1380529_at	zinc finger protein 207 (predicted)	Zfp207_predicted
1379974_at	zinc finger protein 533 (predicted)	Zfp533_predicted
1377105_at	zinc finger protein 91	Zfp91
1397356_at	zinc finger protein 408 (predicted)	Znf408_predicted
1380030_at	zinc finger protein 593 (predicted)	Znf593_predicted

EXAMPLE 4

Lis-1 mRNA Expression Profiles in PFC in Socially Isolated Animals and PCR Confirmation

[00167] This example provides the temporal mRNA expression of Lis-1, a gene that plays a role in signaling cascades involved in schizophrenia in isolation reared animals, as compared to socially reared animals. Isolation reared animals and socially reared controls were maintained as described in Example 1. The microarray was carried out as described in Example 3. Confirmation of the microarray data, using quantitative real-time PCR is described below.

[00168] *Quantitative real-time PCR*

[00169] Real-time PCR was carried out using TaqMan technology on an ABI Prism 7900HT Sequence Detection System (PE Applied Biosystems, UK). cDNAs, from 1µg of DNase treated RNA from each animal (n=6 per group) were produced using SuperScript II RNase H Reverse Transcriptase Kit (Invitrogen) and 50-250ng random primers (Invitrogen). cDNA (0.8µl) from each sample was amplified using TaqMan® Gene Expression Assay primers and probe (Applied Biosystems, UK), Assay ID Rn_00578324_m1. Relative quantitation was determined by constructing a standard curve for each primer and probe set, using pooled DNA from all the samples. A ribosomal RNA control primer and probe set (Applied Biosystems) was used for normalization purposes.

[00170] *Preparation of RNA probes*

[00171] Riboprobes were purchased for Lis-1 (Applied Biosystems, UK). cDNA (0.8µl) from each sample was amplified using TaqMan® Gene Expression Assay primers and probe (Applied Biosystems, UK) designed to the Lis-1 gene (GenBank database accession number NM_031763). Relative quantitation was determined by constructing a standard curve for each primer and probe set, using pooled DNA from all the samples. A ribosomal RNA control primer and probe set (Applied Biosystems) was used for normalization purposes.

[00172] FIG. 4A illustrates an Ingenuity® map demonstrating how Lis-1 is functionally connected to the schizophrenia susceptibility genes DISC1 and RELN. Many other genes in this cluster show dysregulation at the transcriptional level in the isolation rearing model. Lis-1 showed a P60 spike in mRNA expression in isolation reared animals, compared to socially reared animals (FIG. 4B), as with the genes analyzed in Example 3. The temporal pattern of

mRNA expression of Lis-1 was confirmed at the time points of interest following rearing, showing an increase at P60 (FIG. 4C).

EXAMPLE 5

mRNA Expression Profiles of Schizophrenia Signaling Genes in PFC in Socially Isolated Animals and PCR Confirmation

[00173] This example provides the temporal mRNA expression of genes that implicate signal cascades that play a central role in schizophrenia, including GABAergic receptors (GABAA receptor $\alpha 4$ and complexin I) and synaptic structure (synapsin II) in isolation reared animals, as compared to socially reared animals. Isolation reared animals and socially reared controls were maintained as described in Example 1. The microarray was carried out as described in Example 3. Confirmation of the microarray data, using quantitative real-time PCR was carried out as described in Example 4.

[00174] *Preparation of RNA probes*

[00175] Riboprobes were purchased for GABAA receptor $\alpha 4$, complexin I, and synapsin II. cDNA (0.8 μ l) from each sample was amplified using these TaqMan® Gene Expression Assay primers and probe (Applied Biosystems, UK) designed to the GABAA receptor $\alpha 4$, complexin I, and synapsin II genes (GenBank database accession numbers NM_080587, NM_022864 and NM_019159). Relative quantitation was determined by constructing a standard curve for each primer and probe set, using pooled DNA from all the samples. A ribosomal RNA control primer and probe set (Applied Biosystems) was used for normalization purposes.

[00176] The genes GABAA receptor $\alpha 4$, complexin I, and synapsin II showed a P60 spike in mRNA expression in isolation reared animals, compared to socially reared animals (FIGS. 5A, 5C, and 5E), as with the genes analyzed in Examples 3 and 4. The temporal pattern of mRNA expression of these three genes were confirmed at P60 following rearing, validating the P60 spike (FIGS. 5B, 5D, and 5E).

EXAMPLE 6

mRNA Expression Profiles of Interferon-Regulated Genes in PFC in Socially Isolated and Maternally Deprived Animals

[00177] This example provides the temporal mRNA expression of interferon-regulated genes (Interferon-induced protein with tetratricopeptide repeats 2, Interferon regulatory factor 7, and PKR) in isolation reared animals, as compared to maternally-deprived animals, and socially reared animals. Isolation reared animals, maternally deprived animals, and socially reared controls were maintained as described in Example 1. The microarray was carried out as in Example 3. The maternal deprivation model is described below.

[00178] Interferon-regulated genes exhibited a substantial increase in normal social control animals at P40 (FIG. 6). This was absent from both the isolation reared and maternally deprived animals (FIG. 6). The P40 time point is prior to the time when symptoms of the isolation rearing model are present.

EXAMPLE 7

Influence of Prior Environmental Manipulation on Basal Neurotransmitter Levels in The Medial PFC

[00179] This example provides basal levels of dopamine, glutamate and GABA in the medial prefrontal cortex of groups of mature Wistar rats that had either been isolation reared, maternally deprived, or were social controls. Isolation rearing was carried out as described in Example 1, and maternal deprivation was carried out as described in Example 6.

[00180] Materials and Methods

[00181] *Brain microdialysis*

[00182] Male Wistar rats were anaesthetized on P80 using a Univentor 400 anaesthesia unit (Univentor, Malta) under isoflurane inhalation (4% in air delivered at 6.7 ml/min, with an airflow of 500ml/min) until the pedal withdrawal reflex was lost. Once anaesthetised the rat was placed in a Kopf stereotaxic frame (David Kopf Instruments, USA) and stabilised with blunt ear bars. Anaesthesia was maintained by continuous administration of isoflurane (2%, delivered at 3.4 ml/min, air flow 500ml/min). The frontal skull bone was exposed by a sagittal incision of the scalp at the midline. A burr hole of 0.8mm diameter was drilled through the left side of the

skull and the dura was carefully incised. A microdialysis probe of concentric design (CMA/12, Carnegie Medicin AB, Solna, Sweden) outer diameter 0.5mm and a 4mm length of dialysing membrane was carefully implanted in the medial prefrontal cortex (mPFC). The stereotaxic coordinates for the probe in the mPFC (mm from Bregma) were anteroposterior +2.7, mediolateral ± 1.4 , dorsoventral -6.5 (mm from bone) at a 12° angle. The incisor bar was set at -3.3mm (Paxinos and Watson 1998).

[00183] During surgery the body temperature was continuously maintained at 37°C by means of a thermostatically regulated heating pad (CMA 150, Carnegie Medicin AB, Sweden). The flow rate (2µl/ min) of the perfusion medium (sterile Ringer solution, Baxter, UK; formula per 1000ml: sodium chloride 8.6g; potassium chloride 300mg; calcium chloride 300mg; pH~6) was maintained constant by a microperfusion pump (CMA 100; Carnegie Medicin AB, Sweden) during implantation on P80 and also for the duration of the microdialysis experiment on P82. The probe was fixed to the skull with stainless steel screws and metacrylic cement (Svedia, Enköping, Sweden).

[00184] On the day of the microdialysis experiment on P82 dialysate samples were collected in 20min (40µl) aliquots for separation using high performance liquid chromatography followed by fluorimetric (glutamate) or electrochemical (GABA) detection (Kehr et al., 1989, Morari et al, 1994). A new microdialysis probe was used for each rat. At the end of each experiment animals were killed using a CO₂ overdose and the placement of the probes was verified by microscopic examination using a Leitz Cyrostat (Leitz, Germany) or by cresyl violet staining of 30 µM slices cut with a microtome. Animals with incorrect probe position were not included in this study. Data are reported as a percent change from basal values, which were calculated as the mean of the dialysate levels from 3 stable basal samples. All data are expressed as the Mean $\pm$ SEM. ANOVA with repeated measures and Dunnet's post hoc test were used to test for significant differences between groups ($P < 0.05$).

[00185] The neurotransmitter glutamate was determined by precolumn derivatization of a 10 µL dialysate sample with o-phthaldialdehyde/mercaptoethanol reagent and separation by reversed-phase HPLC on a Biophase ODS 5 µM particle column (Knauer, Berlin, Germany). The mobile phase contained 0.1 M sodium acetate, 6.25% methanol, 1.5% tetrahydrofurane, pH 6.95 and was perfused at a flow rate of 1 ml/min. A linear gradient system was used to clean the

column after elution of glutamate. This involved switching to 100% methanol for 2 mins before switching back to the original acetate buffer. The excitation wavelength in the fluorescence detector (CMA/280, Solna, Sweden) was set at 370 nm and the emission cut off filter was set at 450 nm. The limit of detection was 0.5 pmol/sample for glutamate (Morari et al 1994).

[00186] The GABA assay was based on precolumn derivatization of a 10 µl sample with o-phthaldialdehyde/t-butylthiol reagent and separation by reverse-phase HPLC on a Nucleosil 3 C18 column perfused under isocratic conditions at the flow rate of 0.8 mL/min. The mobile phase was 0.15 M sodium acetate, 1 mM EDTA, 50% acetonitrile, pH 5.4. The BAS LC4B electrochemical detector (Bioanalytical Systems, West Lafayette, IN, USA) was set at +0.75V. The limit of detection was 20fmol/sample (Kehr et al 1989).

[00187] Isolation reared animals exhibited a reduction in mPFC glutamate relative to social controls, as did maternally deprived animals. Maternally deprived animals exhibited an increase in mPFC GABA relative to social controls and isolation reared animals (FIG. 8). There were no differences across groups with respect to dopamine in the mPFC (FIG. 8).

EXAMPLE 8

Influence of prior environmental manipulation on parvalbumin cell density in the medial PFC

[00188] This example provides parvalbumin cell density in the medial PFC of groups of mature Wistar rats that had either been isolation reared, maternally deprived, or were social controls. Isolation rearing was carried out as described in Example 1, and maternal deprivation was carried out as described in Example 6.

[00189] Materials and Methods

[00190] *Parvalbumin immunohistochemistry*

[00191] Male Wistar rats were anaesthetized on P80 and perfused with 4% paraformaldehyde (pH 7.4) and brains were removed and stored in the same fixative overnight. Following sacrifice, the whole rat brain was immediately dissected, coated in Optimum Cutting Temperature (OCT) compound to provide an even freezing rate, and lowered into a Cryoprep freezing apparatus (Algen Inc.) containing dry-ice cooled n-hexane. The brains were then stored at -80°C for later analysis. Sections (12µm thick) of the prefrontal cortex were taken at level 3.2mm rostral to bregma using a MICROM Series 550 cryostat at -12°C on the day of the

experiment and were not stored frozen. Sections were thaw mounted onto poly-L-lysine coated slides and immersion fixed for 30 minutes in 70% ethanol followed, by two 10-minute washes in 0.1M PBS (pH 7.3). The sections were then incubated with 80-100 μ l of the mouse monoclonal anti-parvalbumin antibody (Swant, CH; Cat No: 235) diluted 1 in 250 with PBS containing 1% BSA and 1% NGS for 20 hours in a humidified chamber at room temperature. Following two 10 minute washes in 0.1M PBS (pH 7.3), the sections were incubated with the secondary antibody, anti mouse IgG FITC (Calbiochem, UK; Cat No. 401244) diluted 1 in 250 in PBS containing 1% BSA and 1% NGS, for 3 h. The section were counterstained by dipping the sections for 2-3 secs in a solution of Hoechst 33258 nuclear stain (Molecular Probes, US; Cat No. H3569) at a dilution of 1 in 2,000 in PBS followed by a 10 minute wash in 0.1M PBS. The sections were mounted in Vectashield and protected with a coverslip. Sections used to quantify immunopositive cells were not counterstained.

[00192] A montage of four separate images representative of the layers of the prelimbic cortex was created (FIG. 9) using a Leica DMLB fluorescence microscope 20x objective. A counting frame (0.898mm x 0.349mm) with the width of each layer was overlaid on the montage to facilitate counting the layer-specific cell number. Seven separate montages, derived from serial sections obtained from each animal were used to estimate immunopositive cell number and then normalized to cells/mm²/unit area by dividing by the area of each layer.

[00193] Socially reared control animals exhibited an increase in parvalbumin cell density in the medial PFC on P80, relative to P60 in Layer I cells. In Layer II cells, socially reared control animals exhibited an increase in parvalbumin cell density in the medial PFC on P80, relative to P60. In both isolation reared animals and maternally deprived animals, no such change in cell density was observed indicating a substantial dysregulation in the development of GABAergic interneurons (FIG. 9).

EXAMPLE 9

Influence of prior environmental manipulation on synapse density in the medial PFC

[00194] This example provides synapse density in the medial PFC of groups of mature Wistar rats that had either been isolation reared, maternally deprived, or were social controls. Isolation rearing was carried out as described in Example 1, and maternal deprivation was carried out as described in Example 6.

[00195] Materials and Methods

[00196] *Ultrastructural analysis*

[00197] Tissue Processing

[00198] Following transcardial perfusion with a 4% (w/v) paraformaldehyde/2% (w/v) glutaraldehyde solution at pH 7.4, brains were removed from the rats and kept overnight in the same fixative. Following post-fixation, the brains were removed from the storage and the cerebellum was detached. The remaining block was fixed to the stage of a vibroslicer (Campden Instruments), with the rostral face uppermost. Sections of 100µm were collected at a point 3.2mm rostral to bregma and placed into phosphate buffer (0.1 M) in preparation for processing into epoxy resin. Inter-animal consistency was maintained by reference to bregma as described in a rat brain atlas (Paxinos & Watson, 2005). Subsequent to 30 min post-fixation in 0.1% (w/v) osmium tetroxide (Sigma Chemical Co. Ltd, U.K.), slices were dehydrated and flat embedded with epoxy resin (Agar 100; Agar Scientific, U.K.) by routine methods. Polymerization of the resin permitted the prefrontal cortex to be excised from brain slices and re-embedded in resin filled capsules. Using an ultramicrotome, the re-embedded cortex was identified and semithin sections were taken. These sections were stained with 1% Toluidine Blue (Sigma Chemical Co. Ltd, U.K.) to confirm stereotaxic co-ordinates as 3.2mm rostral to bregma. Subsequently, serial ultrathin sections of silver/gold interference colour (80nm thick; Peachey, 1958) were cut from the block face and collected in pairs on electron-lucent coated slot grids (2x1 mm; Agar Scientific, U.K.) Ultrathin sections were counter-stained using uranyl acetate (5% w/v distilled water) and lead citrate (0.3% w/v in 0.1 M sodium hydroxide). Sections were examined in a Tecnai G2 Spirit BioTWIN electron microscope at an accelerating voltage of 120 kV. Images were recorded using a Megaview III CCD, analysed using the analySIS® programme (Soft Imaging Systems) and stored on CD for further analysis.

[00199] Stereology

[00200] Quantification of ultrastructural features employed an unbiased stereological counting technique, termed the double disector. This method of quantification does not require any assumptions about the size or shape of the object under investigation (Sterio, 1984). The sections containing the objects to be quantified were placed in pairs on slot grids and examined under the electron microscope. Corresponding areas from each section were photographed. A

counting frame, drawn in the computer application programme Adobe Photoshop 7®, was placed on the area under investigation on the images obtained from adjacent serial sections. This 'Gundersen frame' (Gundersen, 1977) was designed to have two adjoining dotted lines and two adjoining solid lines. At the magnification used for synaptic density quantification (20,500x), the 'Gundersen frame' included an area of 13.3138µm². One of the pairs of section was randomly, but consistently, selected as the 'look-up' and the other as the 'reference' section. The number of objects counted in the 'reference' image but absent in the 'look-up' image was defined as the Q value. In addition, specific counting rules to eliminate bias were followed. These include counting only objects found within and touching the top and right dotted edges of the Gundersen frame. Also, specific definitions for the identification of a synapse were followed. A synapse was only counted if it contained 3 or more vesicles in the pre-synaptic element and a post-synaptic density. For each animal, several disector pairs were analysed until a progressive mean test of Q values consistently showed the accumulative mean value to deviate by less than 10%, as has been recommended previously (Williams, 1977). Each of the layers from I to VI of the cortex were examined comprehensively using these methods. The region of the cortex that was examined was defined using stereotaxic co-ordinates by reference to a rat brain atlas (Paxinos & Watson, 1998) and the individual layers were defined according to known criteria for each layer. As an example, layer I is a relatively cell sparse layer, and it can easily be distinguished from the more densely packed layer II. Layer V contains predominantly pyramidal shaped soma that runs perpendicular to the pial surface in contrast to the cells of layer VI, which run parallel to the pial surface.

[00201] The density of synapses was then estimated using the following equation:

[00202]
$$N_v = Q/h \cdot a(\text{fra})$$

[00203] Where N_v = density of objects (synapses) per unit volume; Q = (No. objects in 'reference' section) – (No. objects in 'look-up' section); h = thickness of the section; $a(\text{fra})$ = area of Gundersen counting frame. All tissue collected for ultrastructural, and immunohistochemical, studies were evaluated by an observer who was 'blind' to the experimental conditions and the samples were 'unblinded' only when all experiments were complete.

[00204] Isolation reared animals exhibited a significant reduction in synaptic density (both synapses and perforated synapses) in the medial PFC, relative to both socially reared controls and maternally deprived animals, in Layer III. Maternally deprived animals exhibited a reduction in perforated synapse density in Layer VI relative to socially reared controls and isolation reared animals (FIG. 10).

EXAMPLE 10

The deficit in prepulse inhibition is reversed by ICV midkine administration

[00205] Prepulse inhibition of startle, as described in Example 1, is used as a readout of sensorimotor processing in the prefrontal cortex, and is closely tied with working memory. Midkine administration into the 3rd cerebral ventricle of the brain reversed the deficit observed in prepulse inhibition of startle in animals that were reared in isolation. Isolation rearing and prepulse inhibition of startle were performed as described in Example 1. The experimental design of this study dictated surgical implantation of a guide cannula, following which animals were housed in soft bottom cages floored with sawdust, and a daily intracerebroventricular (i.c.v.) of compounds. However in order to maximize the effect of isolation rearing, surgery was carried out on P80 and i.c.v. injections were carried out as quickly and efficiently as possible.

[00206] Animals received an i.c.v. injection of 5 μ l of either midkine 0.4 μ g/ μ l or sterile H₂O for 3 days prior to and on the day of behavioral testing.

[00207] Isolation reared animals exhibited a significant deficit in prepulse inhibition (PPI) of startle. Four daily ICV injections of midkine (2 μ g/day) reversed PPI behavior back to normal compared to vehicle-treated animals (Two-way ANOVA, , $p < 0.05$ for treatment) (FIG. 11).

Claims:

1. A method of identifying gene targets associated with schizophrenia or schizophrenia symptoms, comprising:
 - (a) initiating an animal model of schizophrenia in living animals;
 - (b) assessing transcriptional regulation in tissue over time in animals that are a model of schizophrenia, wherein the tissue is sampled one or more times after the initiation of the model and optionally one or more times prior to the initiation of the model;
 - (c) comparing the transcriptional regulation from prior to initiation of the model with transcriptional regulation from after the initiation of the model, and/or with transcriptional regulation assessed from tissue in living animals not subject to a schizophrenia model; and
 - (d) detecting a transcript that is dysregulated in tissue from animals that are a model of schizophrenia.
2. The method of claim 1, wherein the model of schizophrenia is isolation rearing.
3. The method of claim 1, wherein the model of schizophrenia is maternal deprivation.
4. The method of claim 2, wherein the transcript is dysregulated at a time point selected from the group consisting of postnatal day 30, postnatal day 40, postnatal day 60, and postnatal day 80.
5. The method of claim 1, further comprising comparing the dysregulated transcript with at least one gene previously associated with schizophrenia.
6. The method of claim 1, wherein the dysregulated transcript is selected from the group consisting of SEQ ID NO:1 through SEQ ID NO:16.
7. The method of claim 1, wherein the dysregulated transcript is selected from the group consisting of interferon-induced protein, interferon regulatory factor 7, and PKR.

8. An isolated nucleic acid molecule comprising at least one transcript identified from the method of claim 1.
9. A method of predicting susceptibility to schizophrenia in an individual comprising detecting dysregulation of one or more pre-symptomatic genes or the products thereof from a biological sample provided by the individual, wherein the dysregulation is correlated with an increased likelihood of developing schizophrenia or the symptoms thereof.
10. The method of claim 9, wherein the dysregulation comprises upregulation.
11. The method of claim 9, wherein the individual is asymptomatic for schizophrenia.
12. The method of claim 9, wherein the individual exhibits symptoms of schizophrenia.
13. The method of claim 9, wherein the individual has not been diagnosed with schizophrenia.
14. The method of claim 9, wherein the individual presents one or more risk factors associated with schizophrenia.
15. The method of claim 9, wherein the biological sample is blood.
16. A method of diagnosing schizophrenia in an individual comprising detecting dysregulation of one or more symptomatic genes or the products thereof from a biological sample provided by the individual.
17. The method of claim 16, wherein the dysregulation is correlated with additional factors diagnostic of schizophrenia.
18. The method of claim 16, wherein the one or more genes is selected from the group consisting of SEQ ID NO:1 through SEQ ID NO:16.
19. The method of claim 16, wherein the one or more genes is selected from Tables 3, 4, 7, or 8.
20. A method of preventing the onset of schizophrenia or its symptoms in an individual in need thereof, comprising modulating the expression of a pre-symptomatic gene or products thereof.

21. The method of claim 20, further comprising administering at least one additional method of prevention.
22. A method of treating schizophrenia or its symptoms in an individual in need thereof, comprising modulating a symptomatic gene or expression thereof.
23. The method of claim 22, further comprising administering at least one additional treatment.
24. The method of claim 22, wherein the gene is selected from the group consisting of SEQ ID NO:1 through SEQ ID NO:16.
25. The method of claim 20, further comprising one or more additional schizophrenia treatments.
26. A method of treating schizophrenia or its symptoms comprising administering midkine to an individual in need thereof.
27. A method of treating cognitive deficits comprising administering midkine to an individual in need thereof.

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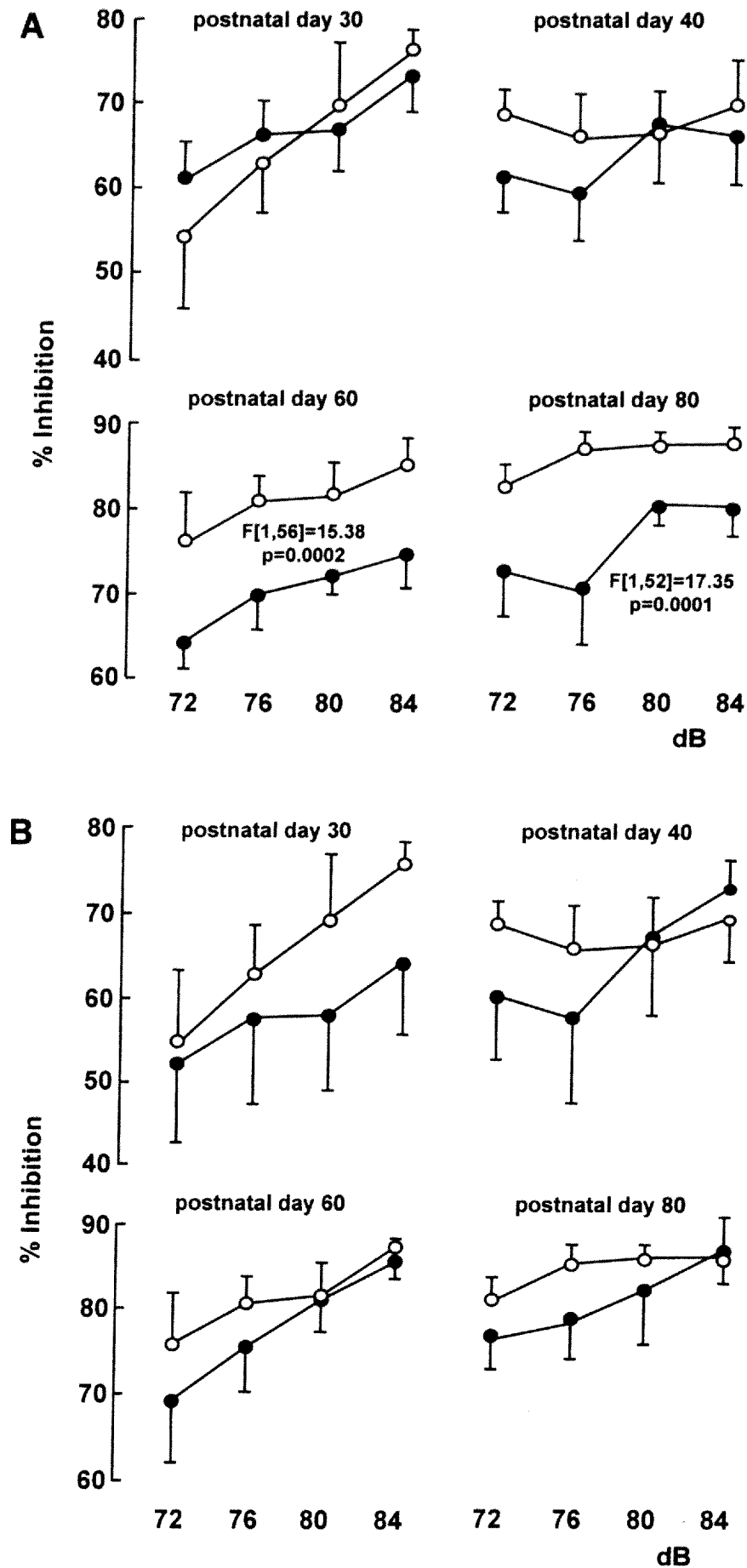


Fig. 1

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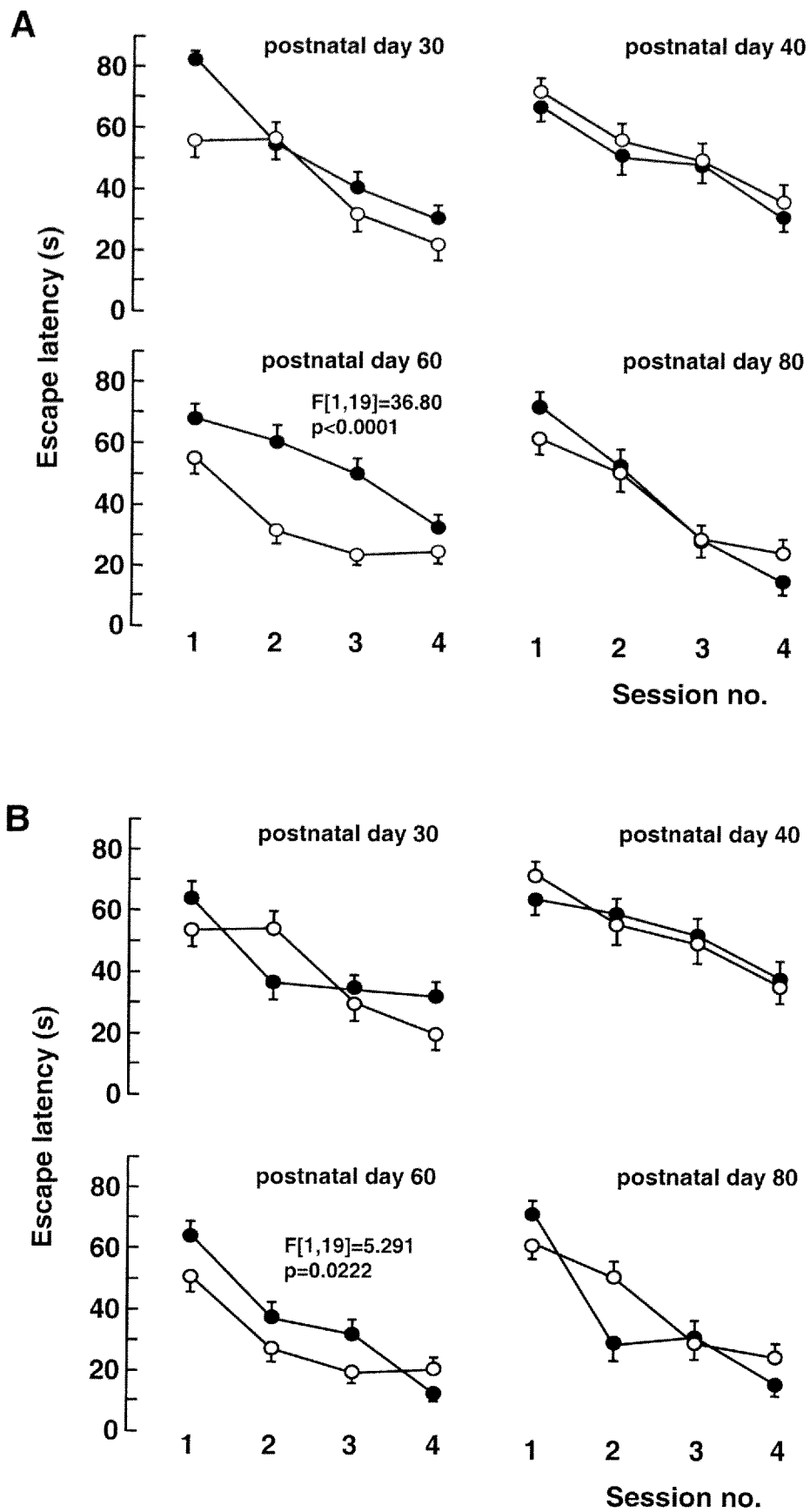


Fig. 2

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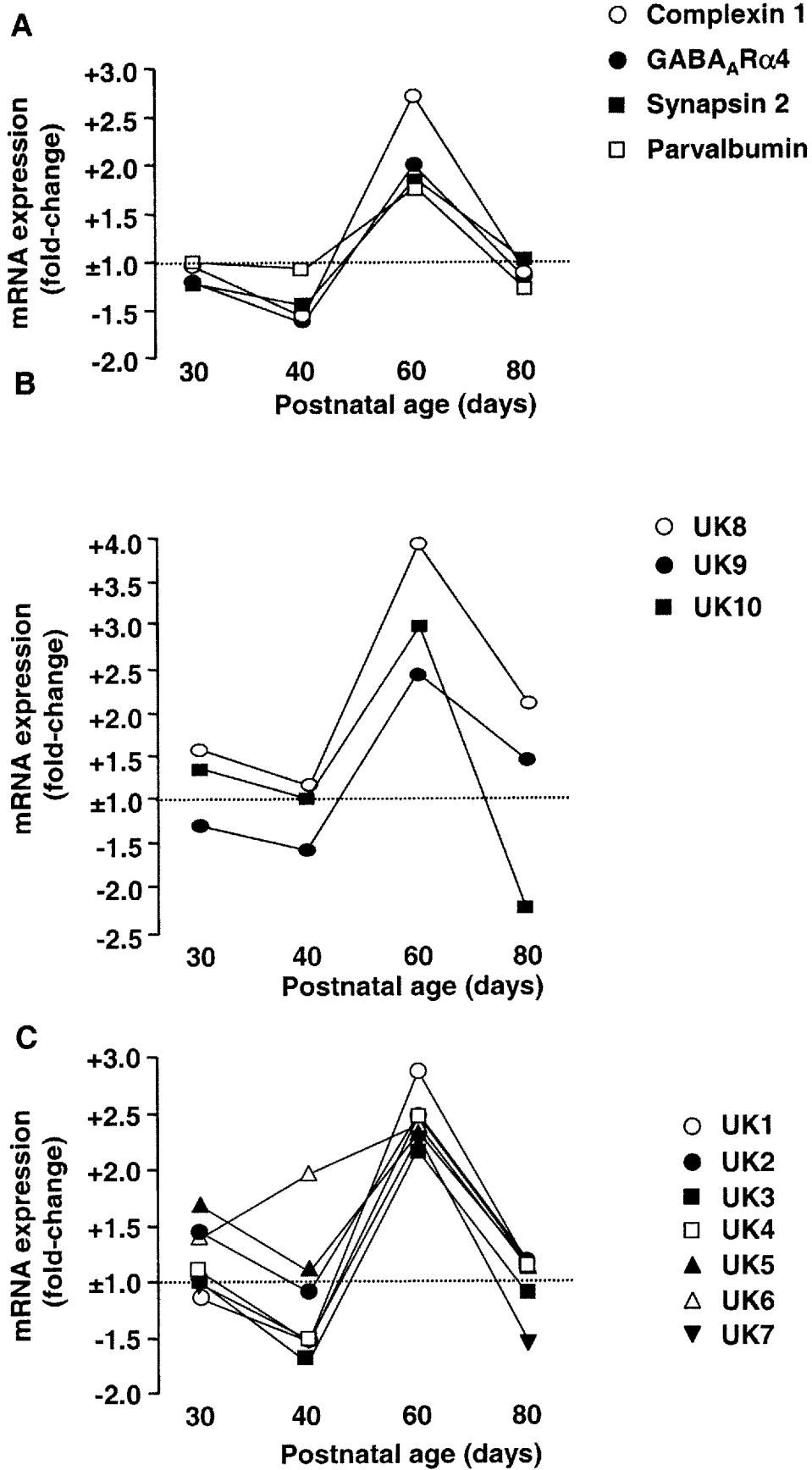


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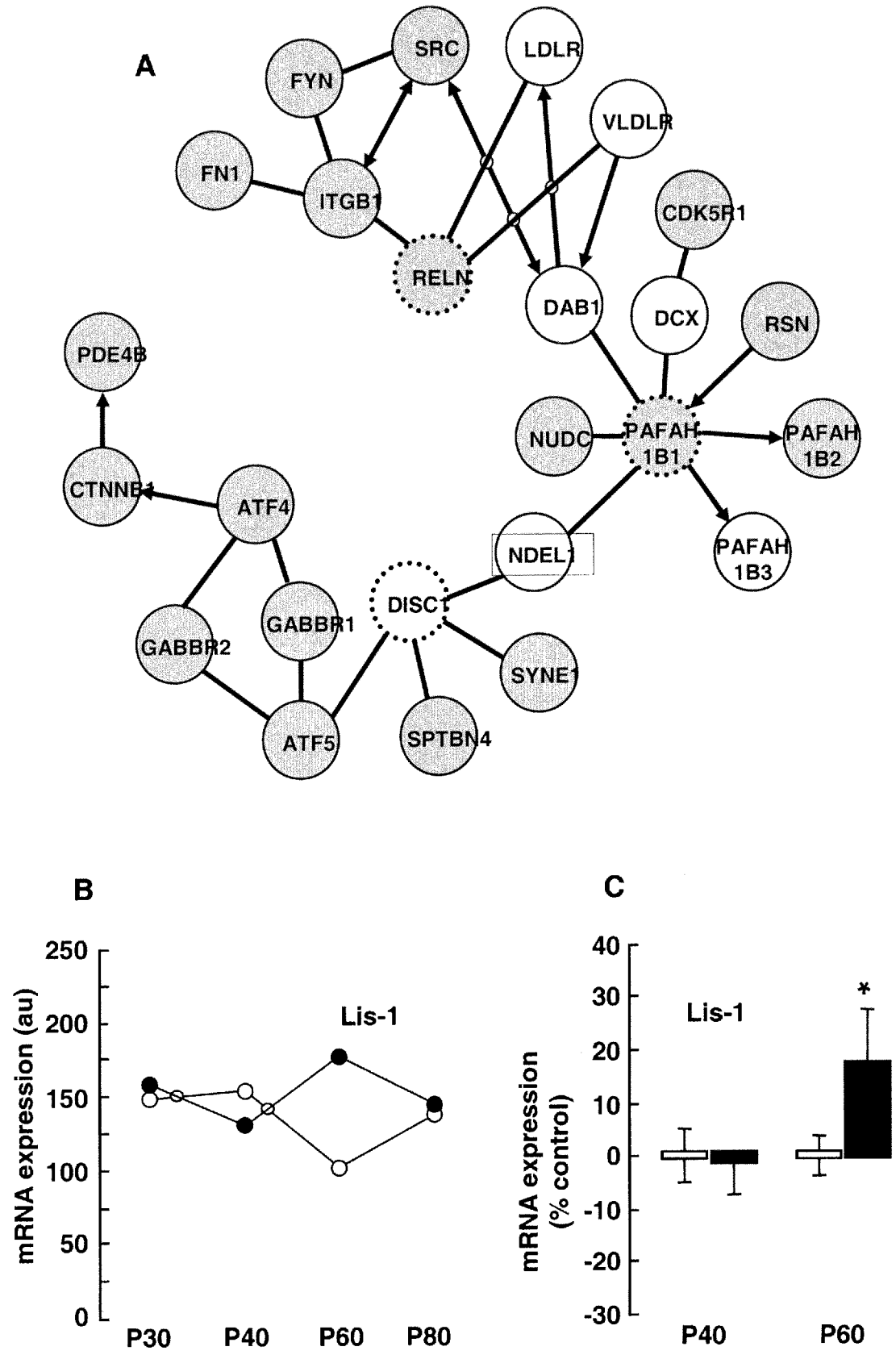


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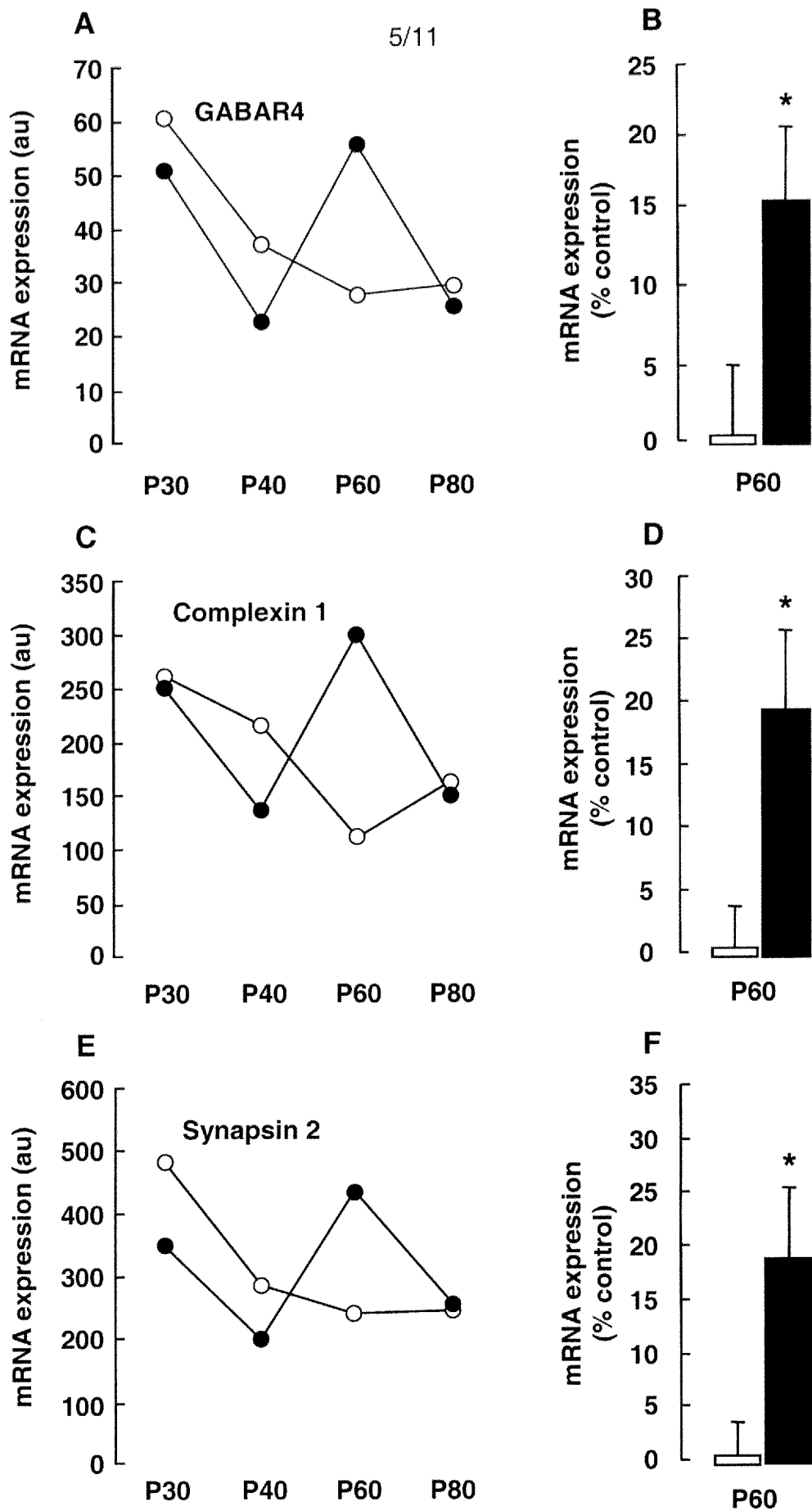


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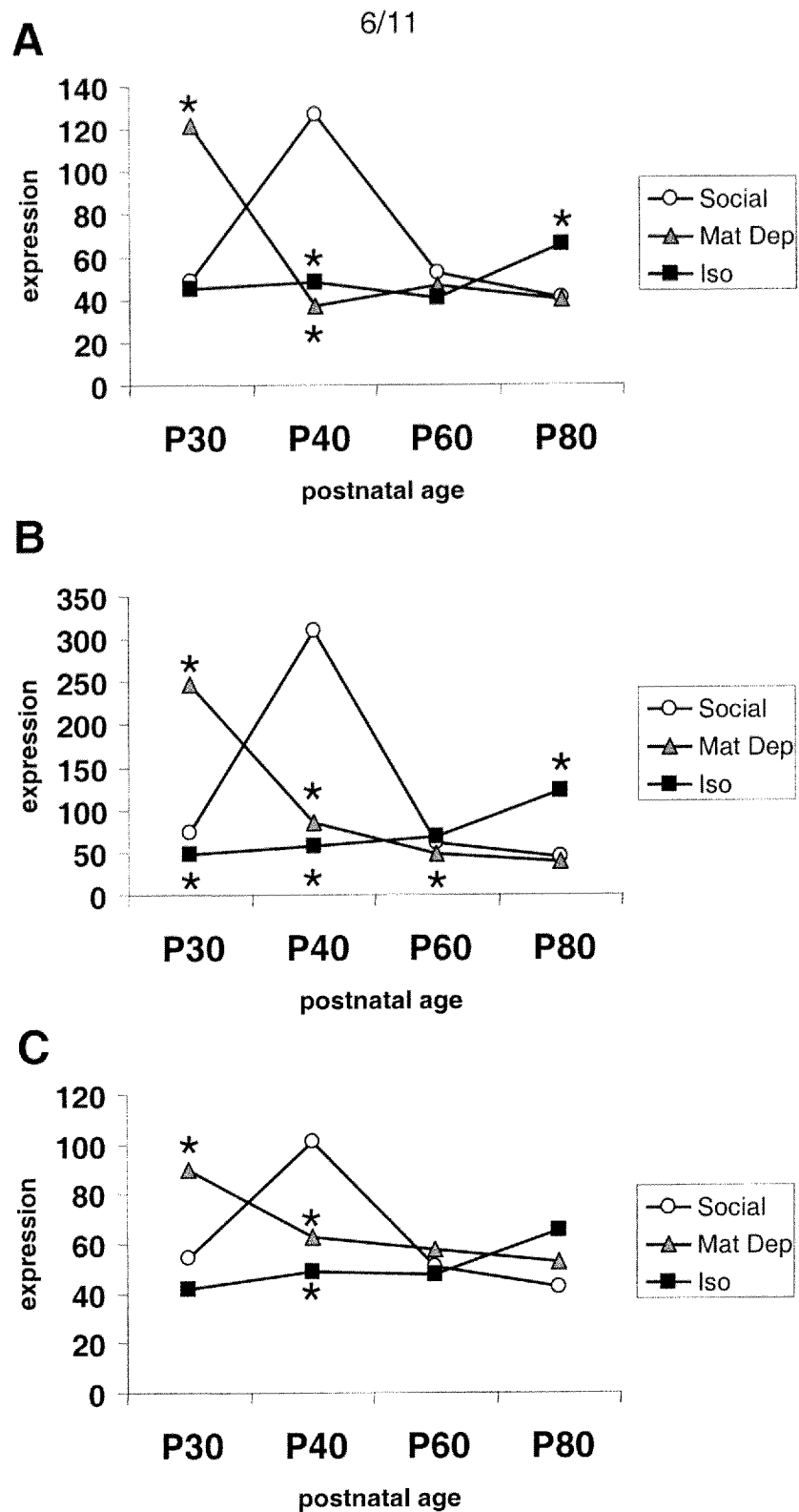


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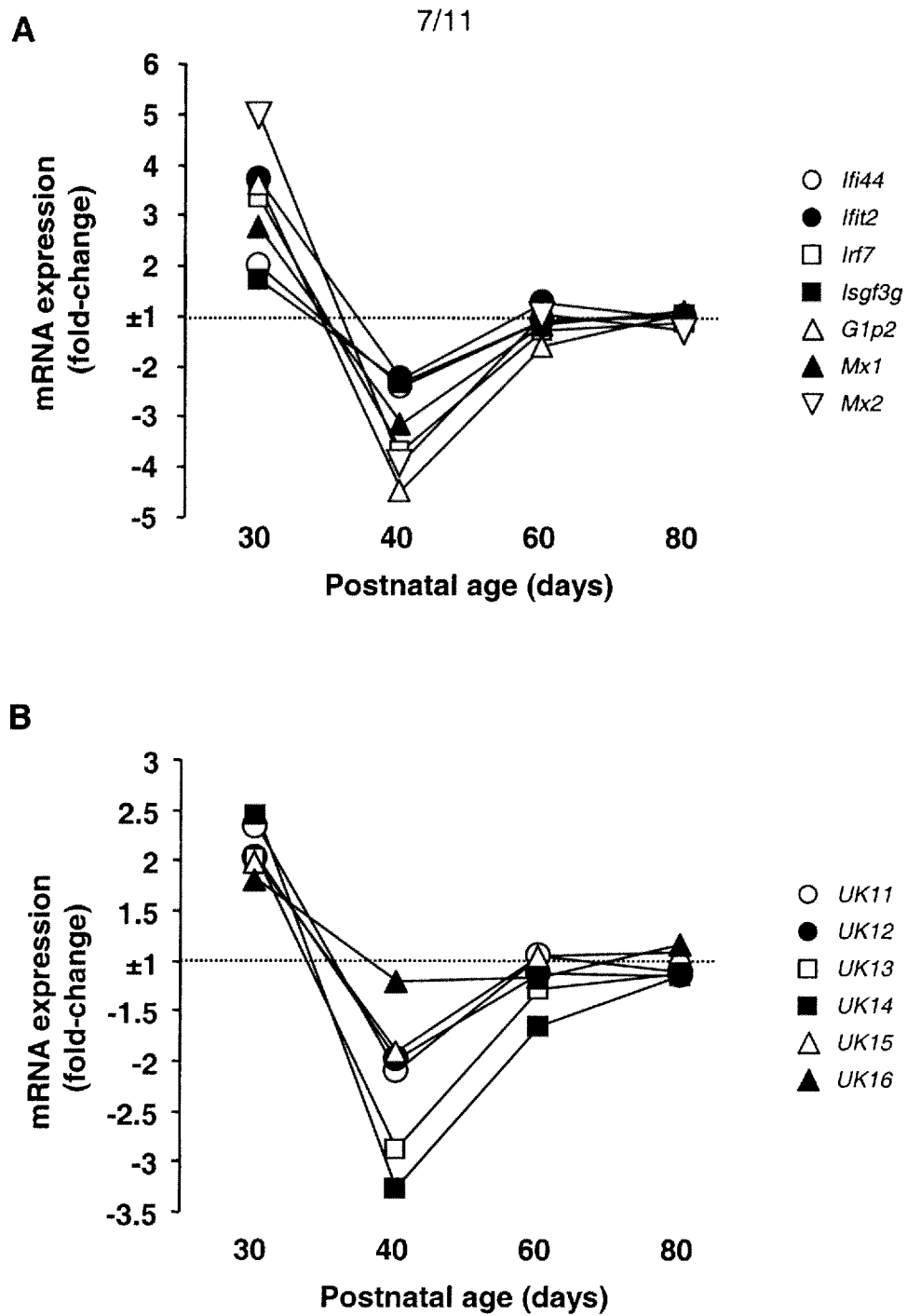


Fig. 7

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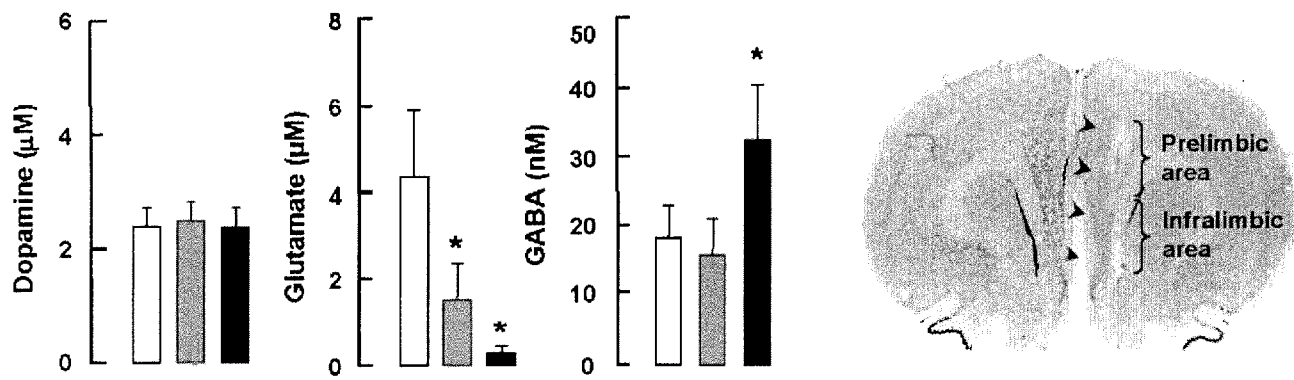


Fig. 8

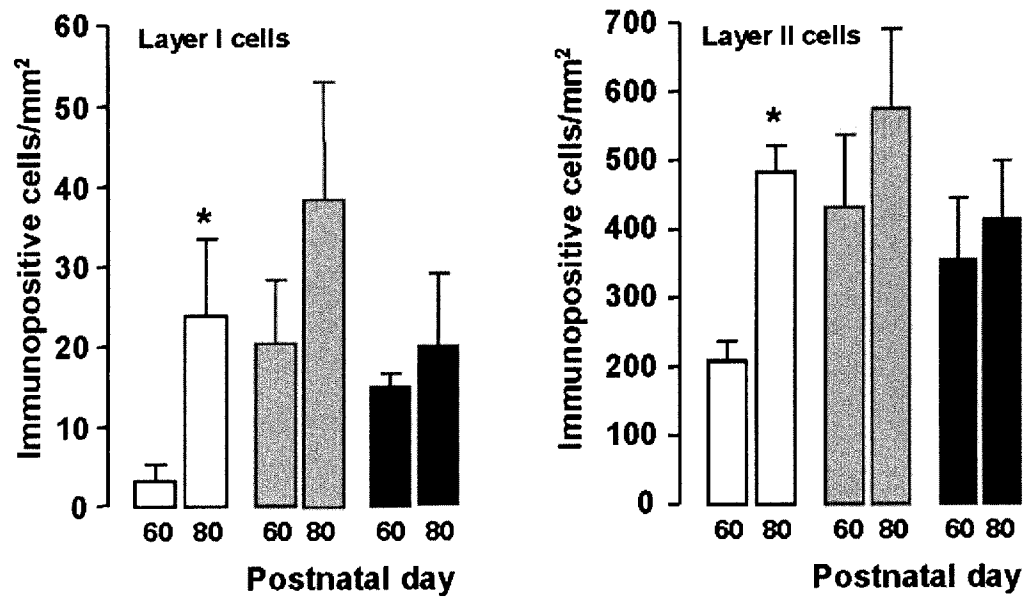
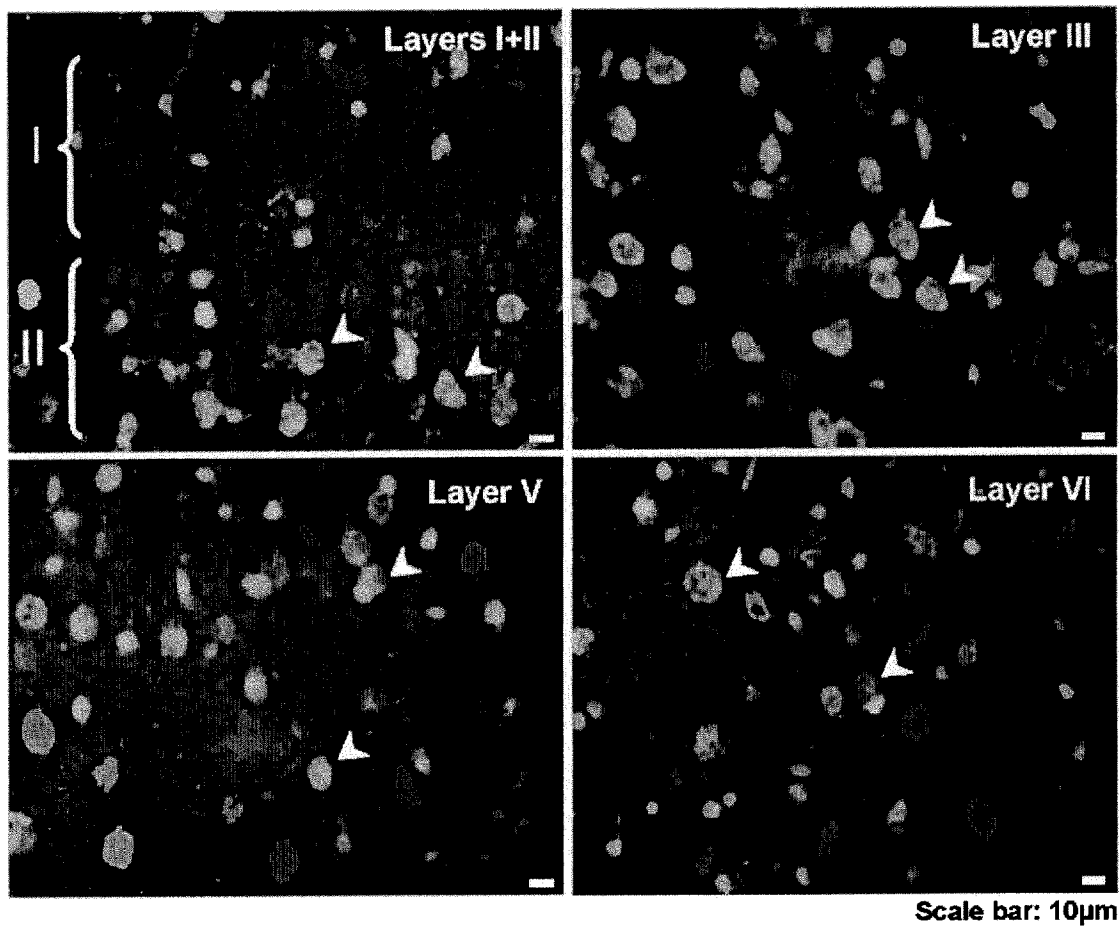


Fig. 9

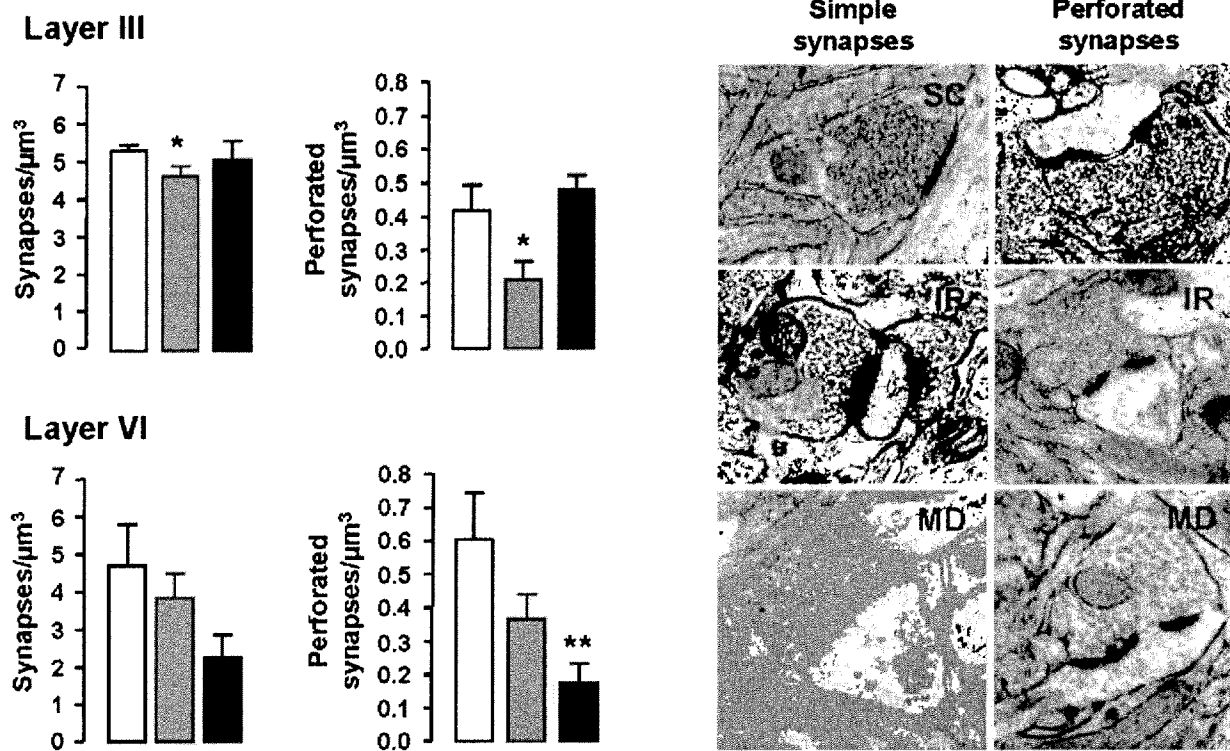


Fig. 10

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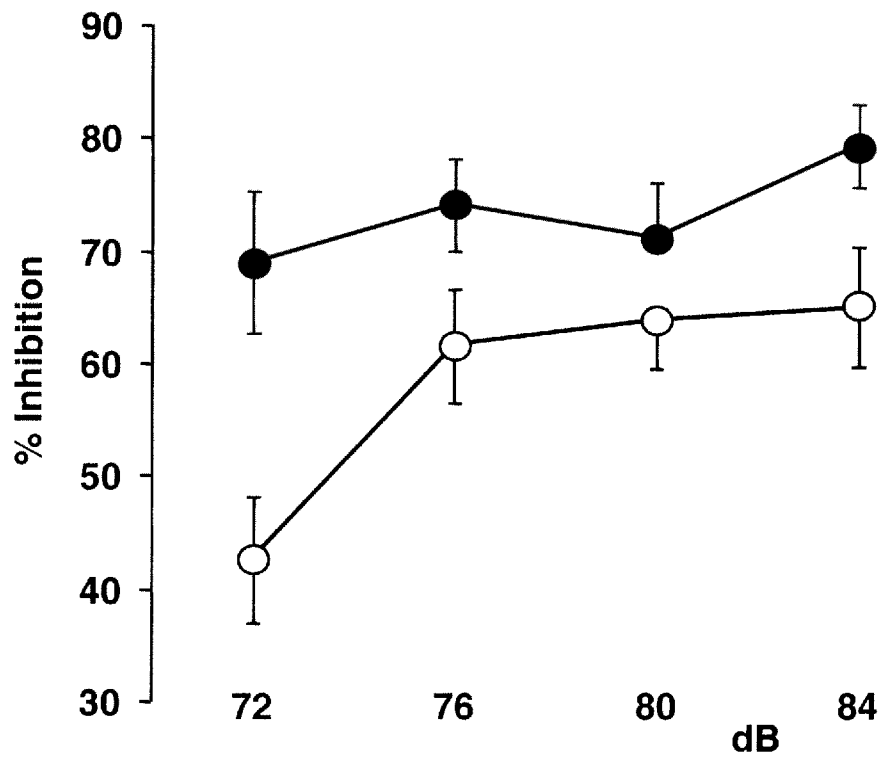


Fig. 11