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(54) **BIOMARKERS OF OOCYTE QUALITY**

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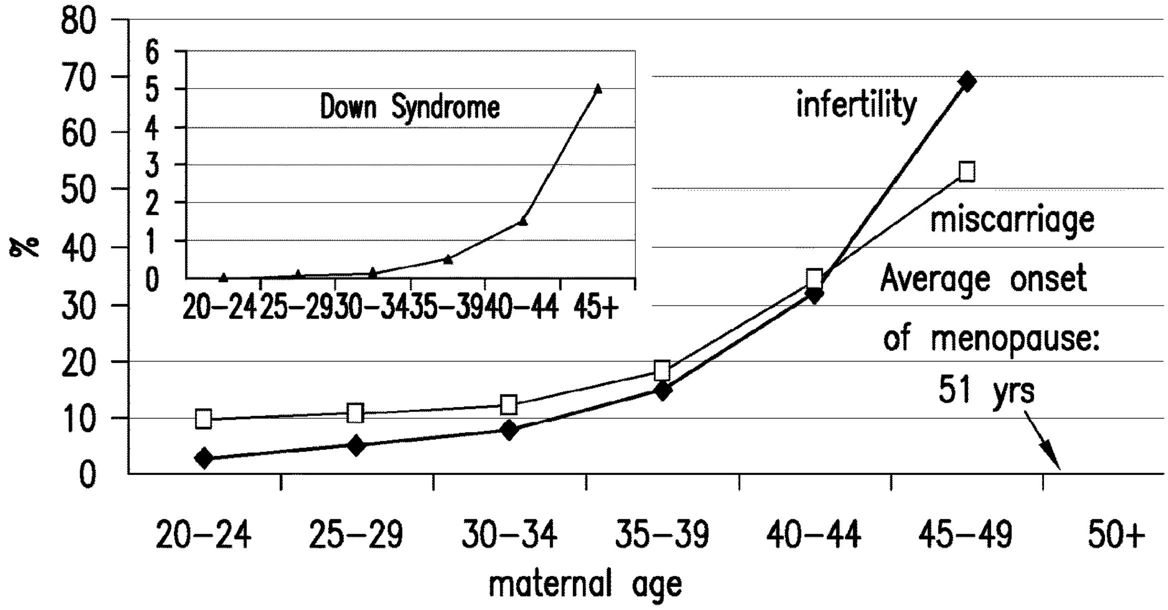
(57) **ABSTRACT**

The present technology relates to biomarkers of oocyte quality and oocyte quality decline, as well as methods in connection with such biomarkers, including method of determining the quality of an oocyte, kits for the same, and libraries, reproductive aging gene expression profiles and profile sets with information relating the same.



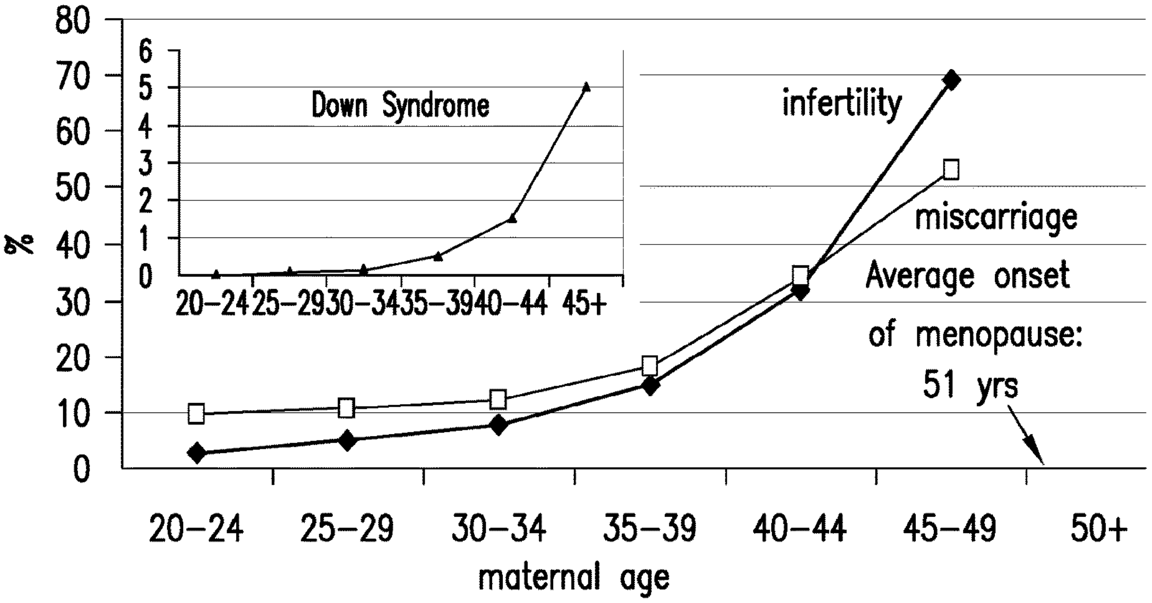

80
70
60
50
40
30
20
10
0
%
6
5
4
3
2
1
0
Down Syndrome
20–24
25–29
30–34
35–39
40–44
45+
infertility
miscarriage
Average onset
of menopause:
51 yrs
20–24
25–29
30–34
35–39
40–44
45–49
50+
maternal age

FIG.1A

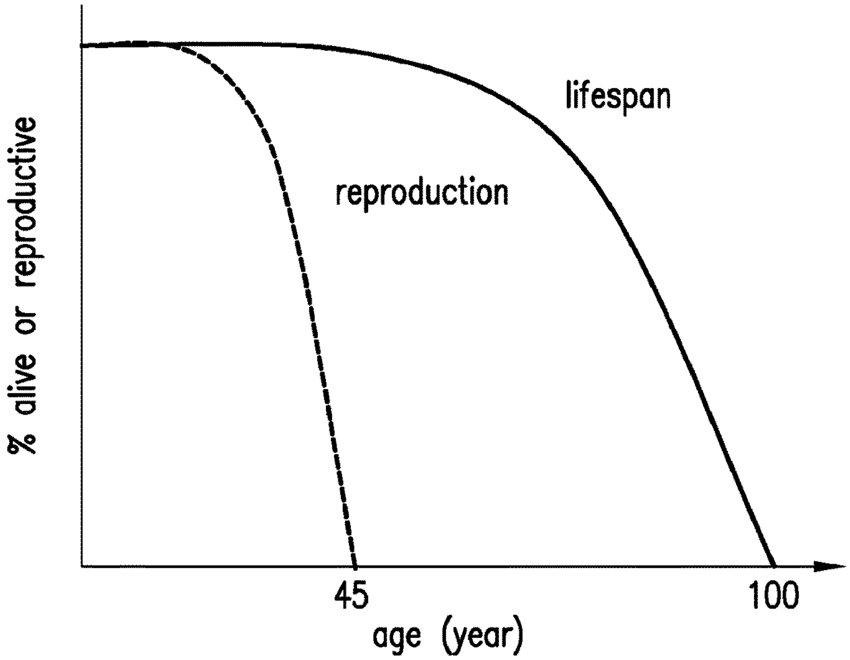

% alive or reproductive
lifespan
reproduction
45
100
age (year)

FIG.1B

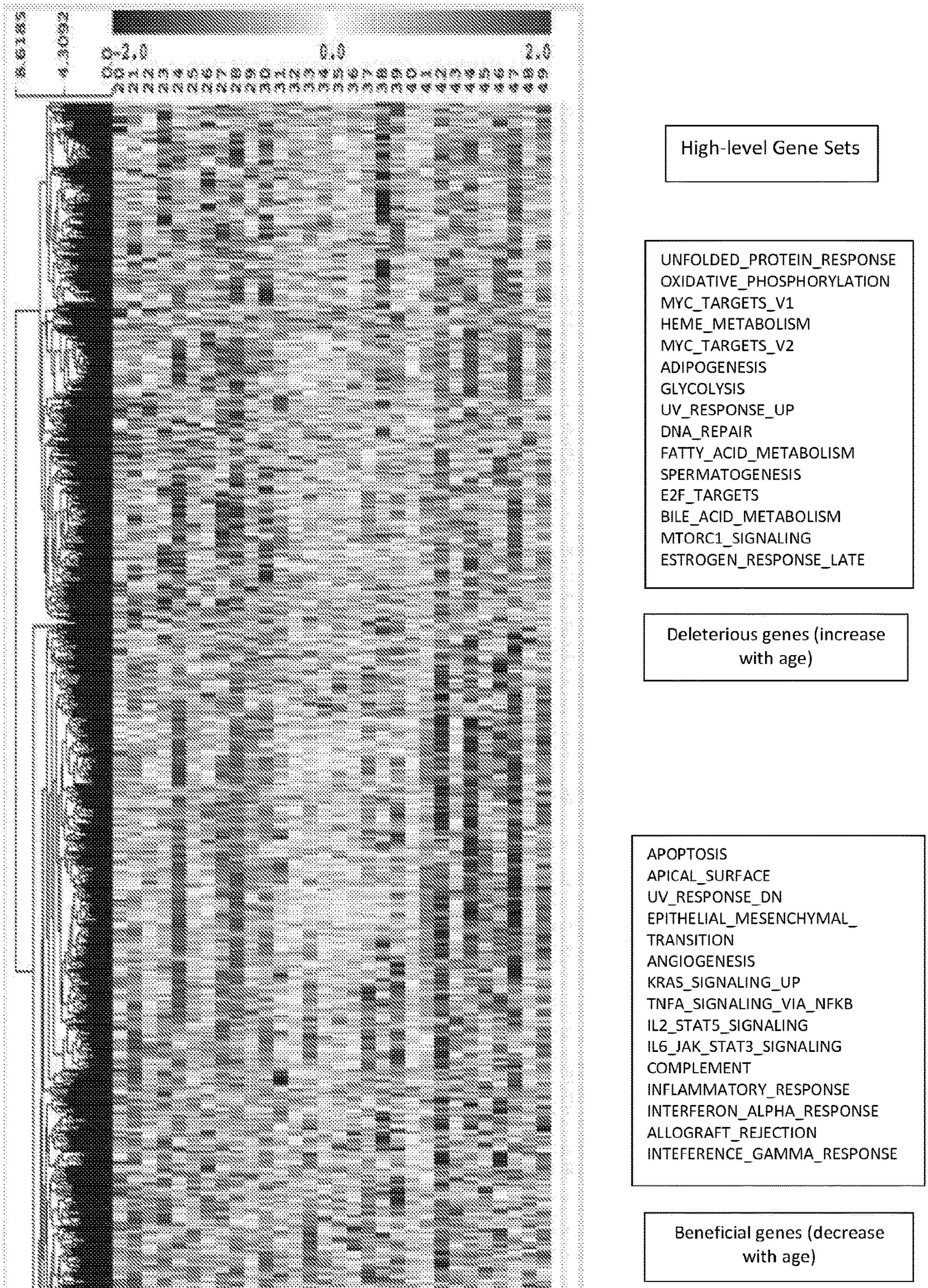

8.6185
4.3092
-2.0
0.0
2.0
High-level Gene Sets
UNFOLDED_PROTEIN_RESPONSE
OXIDATIVE_PHOSPHORYLATION
MYC_TARGETS_V1
HEME_METABOLISM
MYC_TARGETS_V2
ADIPOGENESIS
GLYCOLYSIS
UV_RESPONSE_UP
DNA_REPAIR
FATTY_ACID_METABOLISM
SPERMATOGENESIS
E2F_TARGETS
BILE_ACID_METABOLISM
MTORC1_SIGNALING
ESTROGEN_RESPONSE_LATE
Deleterious genes (increase with age)
APOPTOSIS
APICAL_SURFACE
UV_RESPONSE_DN
EPITHELIAL_MESENCHYMAL_TRANSITION
ANGIOGENESIS
KRAS_SIGNALING_UP
TNFA_SIGNALING_VIA_NFKB
IL2_STAT5_SIGNALING
IL6_JAK_STAT3_SIGNALING
COMPLEMENT
INFLAMMATORY_RESPONSE
INTERFERON_ALPHA_RESPONSE
ALLOGRAFT_REJECTION
INTEFERENCE_GAMMA_RESPONSE
Beneficial genes (decrease with age)

FIGURE 2

BIOMARKERS OF OOCYTE QUALITY

CROSS REFERENCE TO RELATED APPLICATIONS

[0001] This application claims priority to U.S. Provisional Application No. 62/089,604 filed Dec. 9, 2014, and U.S. Provisional Application No. 62/254,356 filed Nov. 12, 2015, the contents of both of which are hereby incorporated by reference.

[0002] This invention was made with government support under Grant No. OD004402 awarded by the National Institutes of Health. The government has certain rights in the invention.

BACKGROUND

[0003] The present technology relates to biomarkers of oocyte quality and oocyte quality decline, as well as methods in connection with such biomarkers.

[0004] The functions of the female reproductive system are known to decline with age. One major factor in decreased fertility is the decline of the quality of the eggs (oocytes) produced by the ovaries as a woman ages. Decline of quality of oocytes and ovarian follicles generally begins sometime in the 30s for most women and eventually leads to menopause, in most cases between ages 45 and 55.

[0005] In certain instances, it can be useful and desirable to determine the quality of an oocyte; for example, when a woman is seeking information about her level of fertility and chances of conception; or when a clinician seeks such information in association with assisted reproductive technologies (ART). Current methods are limited to the determination of oocyte quantity, not quality; furthermore, such methods are generally time consuming, expensive and require destruction of the oocyte itself. For a female subject who may be concerned about declining egg reserve and quality as she ages, a serious disadvantage is associated with any method or kit that requires the destruction of an oocyte in order to measure the subject's chances of conception. Further, since known methods are invasive, currently they can be performed only by medical personnel in a clinic or hospital setting; a woman cannot determine oocyte quality on her own. Thus, the current limitation of the technology to invasive methods has prevented the widespread adoption of diagnostic tests.

[0006] Thus, there is a need for methods and systems that can accurately predict or determine the quality of an oocyte, namely methods that are non-invasive, easy for patients to use, affordable and provide rapid and accurate results.

SUMMARY OF THE DISCLOSED TECHNOLOGY

[0007] In certain embodiments, the present technology is directed to a method of determining the quality of an oocyte in the body of a human without disturbing or destroying the oocyte, the method comprising:

[0008] (a) obtaining a cell sample from a female subject, wherein the cell sample does not include the oocyte;

[0009] (b) measuring a characteristic of a gene or pathway indicative of oocyte quality in the cell sample; and

[0010] (c) predicting or determining the quality of the oocyte based on the characteristic of the gene or pathway.

[0011] In certain embodiments, the present technology is directed to a method of predicting the quality of an oocyte in the body of a mammal without disturbing or destroying the oocyte, the method comprising the steps of:

[0012] (a) obtaining a cell sample from the mammal, wherein the cell sample does not include the oocyte;

[0013] (b) conducting an RT-PCR assay or an ELISA assay on the cell sample using a primer for a gene known to be correlated with aging, and comparing the result with a known value obtained from a library of genes known to be correlated with decreased oocyte quality; and

[0014] (d) predicting the likelihood of oocyte viability based on (b).

[0015] In certain embodiments, the present technology is directed to a kit for predicting a woman's oocyte quality without the need for disturbing or destroying an oocyte, or of measuring a characteristic that correlates with the quality of an oocyte, the kit comprising:

[0016] (a) a collection container for collecting a cell sample obtained from the woman's body, wherein the cell sample does not include an oocyte;

[0017] (b) a testing assay comprising RT-PCR or ELISA, wherein the testing assay measures a characteristic of a gene, pathway or transcriptional profile characteristic of the cell sample, and wherein the characteristic indicates the likely quality of an oocyte; and

[0018] (c) a visual indicator visible to the woman, the visual indicator providing information regarding the predicted quality of the oocyte.

[0019] In certain embodiments, the present technology is directed to a method of producing a library of genes as markers of oocyte quality. Such a method may comprise the steps of correlating a test gene with a quantitative and measured characteristic of oocyte quality, listing the correlation in the library; comparing a measured characteristic of a gene provided by a patient with that listed in the library; and determining the quality of an oocyte of a patient based on the comparison. In certain embodiments, the technology herein contemplates a method of producing a library of genes as markers of oocyte quality, the method comprising the steps of:

[0020] (a) gathering expression data from cells of women in a particular age range;

[0021] (b) calculating an average gene expression for each gene at each age in the range by averaging the expression for that gene in a window of a given period of time;

[0022] (c) comparing the average gene expression of (b) to an "age vector" to indicate which genes change most with age; and

[0023] (d) calculating a FisherZ score, thereby identifying the genes at the tail ends of the distribution as indicators of biological age.

[0024] In certain embodiments, the present technology is directed to a reproductive aging gene expression profile; and a method of developing a reproductive aging gene expression profile and one or more candidate markers of reproductive success.

[0025] In certain embodiments, the present technology is directed to a method of producing a profile set as an indicator of oocyte quality. Such methods discussed herein may be done, for example, with any gene, pathway, or transcriptional profile, or with a library of the same.

BRIEF DESCRIPTION OF THE FIGURES

[0026] FIG. **1***a* is a graph showing the prevalence of Down syndrome and infertility in a typical female human as a function of age. FIG. **1***b* is a graph showing the aging profile of oocytes in a typical female human as a function of age.

[0027] FIG. **2** shows age-dependent gene expression changes in blood from women aged 20 to 50, as a "heat map" which shows on a macro level relative changes.

DETAILED DESCRIPTION

[0028] As used herein, "female subject" and "patient" are used interchangeably to refer to the individual whose oocyte quality is desired to be determined. As discussed herein, a "cell sample" refers to one or more cell from any part of the patient's body, which is desired to be tested in order to perform the diagnostic and scientific methods discussed herein. In various embodiments, a cell sample in accordance with the technology herein may be extracted from any of the following: blood, skin, hair, urine, saliva, sweat, vaginal secretion, any other fluid (including but not limited to intracellular or extracellular fluid, interstitial fluid, lymphatic fluid or transcellular fluid, cerebrospinal fluid, mucus or phlegm).

[0029] Oocyte quantity (the number of viable oocytes produced by a woman, the totality of which is determined long before the onset of puberty) and quality (the likelihood that the oocyte can be successfully fertilized and lead to pregnancy) are two factors of paramount importance in predicting fertility and the likelihood of carrying a pregnancy to term in a female. A woman's oocyte quality is generally predicted to decline after a certain age, until she reaches menopause and her ovaries stop releasing oocytes entirely. That is, with rising maternal age, and as a woman's oocytes age as well, a woman loses the ability to reproduce, and the children she may have are at greater risk for birth defects, chromosomal abnormalities, miscarriage and other problems. These defects start to arise when the woman is in her mid-30s and increase through the 40s, about a decade prior to menopause (the average age of menopause is 51), and are caused by declining oocyte quality.

[0030] Specifically, age-related reproductive decline is characterized by increasing levels of defects in oocyte chromosomal segregation, cell cycle arrest, and oocyte mitochondrial function and morphology, among other factors. Changes in gene expression correlate with these oocyte and egg quality changes, and have been shown in aging human and mouse oocytes. Our work in particular on *C. elegans* oocyte aging, discussed in greater detail below, has highlighted the evolutionary conservation of oocyte quality components. These components, particularly regulators of chromosome segregation fidelity, have been shown to be required for oocyte function and prevention of aneuploidy in worm and mammalian oocytes, and increased fidelity extends reproductive span.

[0031] However, despite the great concern about this problem, the exact age at which any particular woman might have problems is not known, and no diagnostic assay currently exists that can predict long-term age-related fertility status. Thus, a woman who is trying to conceive has limited options for determining the quality of an oocyte any given month or for predicting future success.

[0032] Current methods, such as endocrine tests of the ovarian reserve (oocyte number) predictors follicle stimulating hormone (FSH) and anti-mullerian hormone (AMH), have only immediate, short-term predictability of success with assisted reproductive technologies (ART) such as intrauterine insemination (IUI) in vitro fertilization (IVF), gamete intrafallopian tube transfer (GIFT) and zygote intrafallopian tube transfer (ZIFT). However, such tests cannot generally predict long-term prospective fertility. Similarly, known methods involving transvaginal ultrasound measurements of antral follicle count (AFC) focus on assessing oocyte number. However, oocyte quality, not quantity, is the limiting factor in most age-related fertility decline. In particular, aneuploidies (aberrations in chromosome numbers) and cell cycle arrest/maintenance failures can be a cause of infertility, birth defects, and miscarriage. Morphological assessments are too gross to identify other important measures of quality, such as the levels of particular maternal RNAs that regulate processes in the oocyte. Finally, current measures of oocyte quality require invasive approaches, and the assessment itself can destroy the oocyte in question, further limiting a woman's number of healthy oocytes and potentially requiring a larger pool of donated oocytes for treatment.

[0033] By contrast, bodily fluids such as blood and urine are easy to obtain, and in the case of blood, PBMCs (peripheral blood mononuclear cells) have been shown to provide information about the physiological state of other tissues, including ovarian cells. In fact, a recent study by Gielchinsky et al. in 2008 showed that PBMC expression analysis was able to identify candidate genes up- and down-regulated in women who delivered babies after spontaneous pregnancy at ≥45 years of age. These candidate genes included markers of ovarian function, apoptosis, ubiquitination, energy production, and insulin/IGF-1 signaling the same pathway that we showed extends reproductive span in *C. elegans*. While these factors are good candidates for age-related oocyte quality biomarkers in blood, our work can establish a timecourse for oocyte aging biomarkers in blood throughout the reproductive aging years, allowing us to identify and verify a set of biomarker genes to use for diagnostic purposes.

[0034] A diagnostic of oocyte quality, particularly a non-invasive measure, would be in high demand at several levels: clinics conducting assisted reproductive technology methods such as IVF would like this information before embarking on ART approaches to improve their success rates, egg-freezing companies could use such a diagnostic to predict the success of use of eggs they have frozen, and women could use the data to make informed decisions about their reproductive lives in a manner that is minimally invasive and highly convenient. Thus, in certain embodiments, the technology herein identifies, and permits health care workers or patients to identify biomarkers of oocyte quality in blood or other bodily fluids, as well as the development of a reliable long-term diagnostic of fertility.

[0035] Aging studies have been performed on *Caenorhabditis elegans*, a worm that has been developed as a model of reproductive aging for humans. As demonstrated by data from *C. elegans* and mice, certain genes in an organism are related to the quality of the oocytes of the organism.

[0036] In certain embodiments herein, the quality of an oocyte can be determined by, for example, measuring certain factors and comparing those factors with known values of oocytes of known age. Certain methods herein permit an investigator (including a health care worker or the subject herself) to determine or predict the quality of an oocyte in the body of a human without disturbing (e.g., touching, sampling, moving or altering) or destroying the oocyte itself, and without taking it out of the human's body, e.g., in vivo.

Thus, in certain embodiments, the oocyte itself can be evaluated (or its characteristics determined and predicted) without harming the oocyte, and the oocyte can itself subsequently be fertilized and lead to a successful pregnancy.

[0037] In certain embodiments, the present technology relates to novel methods for assessing or predicting the quality of oocytes without the need for disturbing or destroying the oocytes themselves. These methods are based at least in part on the discovery that genes in *C. elegans*, which display changes as oocytes age, are the same genes as those found in mammals; further, even if no directly associated genes were located, mammalian genes with similar functions to the *C. elegans* genes were located. The *C. elegans* research also revealed data regarding the characteristics of gene expression in mutant *C. elegans* with long reproductive spans. Many of these genes are involved in chromosome segregation, spindle localization, chromosome organization, DNA damage response and repair, and mitochondrial processes such as ATP metabolism. These genes, therefore, are good biomarkers for oocyte quality from oocytes.

[0038] In certain embodiments, the present technology is directed to the exploitation of the non-invasive nature of blood biomarkers, or biomarkers from other bodily fluids. In certain embodiments, the present technology is directed to the development of single-gene markers as biomarkers; in other embodiments, the present technology is directed to profiles or multiple-gene markers, rather than single-gene markers, as biomarkers.

[0039] Table 1 shows pathways that Shown in the Table 1 is a summary of certain genes and pathways that have previously been identified as being of potential interest for human (H), mouse (M) and worm (W), in connection with applications of the present technology.

Gene Ontology	Gene	Genes from oocyte array studies (homologs)		
category	count	Worm (up in sma-2)	Mouse	Human
Cell cycle mitosis^{HMW}	8	cyb-1(Ccnb2), cyb-3(Ccnb3), cdc-25.2(Cdc25a), cki-1*	Ccnb2, Ccna2, Cdc16	CCNA2, CCNG1, CDK7
Chromosome segregation, org'n				
chromosome segregation^{HMW}	7	smc-4(Smc4l1), klp-7, frm-5	Smc4l1, Nin, Kif3b, Bub1	Smc3l1, BUB1B, BUB3
spindle localization^{M}	4	gad-1, mes-1, par-3	Hook1, Nin, Rnf19	
spindle organization^{M}	3	mbk-2, sur-6, goa-1	Tuba2, Tubd1, Pcnt2	
chromosome organization^{MW}	12	spr-5, nurf-1, hpl-1, hil-2	Hdac2, Morf4l2, Rbbp7	
DNA damage response and repair response to DNA damage stim.^{M}	4	mlh-1(MLH1), clk-2, pme-5, uev-2*	Msh-3, Exo1, Shprh	MBD4 (interacts with MLH1), ATR, NBS1
Proteolytic pathway proteolysis^{HM}	19	ubc-1(Ube2a), ubc-2(Ube2d1), ulp-1	Ube2a, Ubc, Usp1	USP1, CTSC, GRP58
Energy pathway, mitochondrial fn. ATP metabolic process^{M}	7	pmr-1(Atp2c1), (Atp6v1a), tat-5(Atp9b)vha-13	Atp2c1, Atp6v1d, Atp5b	
ATP binding^{HMW}	42	pgp-7(Abcb11), mrp-2 (Abcc3), psa-4(SMARCA5), pdk-1, akt-2	Abcb6, Abcf3, Cct2	ABCC4, SMARCA5, SUV3
Cell signalling and communication				
intracellular signaling cascade^{HMW}	11	cdc-42(RHO GTPase), vhp-1, sel-12	Rhoh, Kras2, Mek1	ATF1, CREB1, CLK1
cell-cell signaling^{MW}	5	unc-18, ace1, cab-1	Gja7, Shroom3, Mmp2	
Protein transport protein transport^{HMW}	11	arf-1.1(Arf1), arl-13 (Arl13b), rab-6.2 (Rab6)	Arf1, Arl4, Rab1	ARF4, ARF6 RAB11a
Transcription regulation^{HMW}	19	hlh-1, efl-1, spt-5	Phtf1, Crsp6, Lhx8	PHTF1, NFE2L2, ElF2AK2
Reproductive process				
oogenesis^{M}	5	hrp-1, goa-1, fem-3	Nalp5, Padi5, Nalp9a	
oyiposition^{W}	15	unc-84, cki-1, mtm-3		
Other cell death^{MW}	7	ced-1, ced-8, crn-4	Tnfaip8, Mdm4, BcI2110	
cell differentiation^{W}	24	par-1, eor-2, !in-28		

-continued

Gene Ontology category	Gene count	Genes from oocyte array studies (homologs)		
		Worm (up in sma-2)	Mouse	Human
cell adhesion^{mw}	6	epi-1(Lama2), hmr-1(Cdh11), cdh-3(Cdh23)	Lama2, Cdh2, Pcdhb17	

[0040] In certain embodiments, the genes and pathways further include any of the following:

[0041] Genes in the IIS pathway: RHEB2, 14-3-3 beta/alpha, UDP-D-glucose cytosol, IGF-2, p90Rsk, MEK2 (MAP2K2), c-Myc, IRS-1, PtdIns(3,4,5)P3, PtdIns(4,5)P2, IKK (cat), Erk (MAPK1/3), Hamartin, c-Raf-1, AKT (PKB), PI3K cat class IA, ASK1 (MAP3K5), c-Raf-1, 14-3-3 epsilon, PTEN, 14-3-3 zeta/delta, IGF-1, PI3K reg class IA, p70 S6 kinase1, CREB1, GSK3 alpha/beta, Cyclin D, 3.1.3.67, MEK1 (MAP2K1), Bcl-XL, GRB2, PDK (PDPK1), mTOR, Caspase-9, FOXO3A, Tuberin, 2.7.1.137, Glycogen, I-kB, BAD, 4E-BP1, IGF-1 receptor, H-Ras, IBP, IKK-alpha, GYS1, 2.4.1.11, RPS6, Shc, SOS, NF-kB, Elk-1

[0042] Akt pathway (overlaps with HS): MDM2, HGF receptor (Met), GYS1, 2.7.1.153, Bcl-XL, IKK-alpha, GAB1, Bax, Hamartin, PI3K cat class IA, BAD, IRS-1, PtdIns(3,4,5)P3, PtdIns(4,5)P2, 4E-BP1, mTOR, Caspase-9, FasL(TNFSF6), GSK3 alpha/beta, p21, NF-kB, IGF-1 receptor, RHEB2, PCNA, PI3K reg class IA, PTEN, PP2A catalytic, PDK (PDPK1), Cyclin D3, p53, 3.1.3.67, p27KIP1, AKT(PKB), Tuberin, RPS6, p70 S6 kinase1, c-Myc, HSP90, Cyclin D, IKK (cat), Bim, FOXO3A, I-kB

[0043] PTEN (overlaps with IIS): RHEB2, MEK1 (MAP2K1), PtdIns(4,5)P2, Caspase-3, PDK (PDPK1), 3.1.3.67, ERK1/2, c-Jun, IGF-1, mTOR, PCNA, MEK2 (MAP2K2), FOXO3A, p53, p21, FAK1, p130CAS, c-Cbl, Shc, GSK3 beta, BAD, Paxillin, EGF, PI3K reg class IA, H-Ras, MAGI-2, SOS, PTEN, c-Src, Tcf(Lef), alpha-5/beta-1 integrin, IRS-1, PI3K cat class IA, Beta-catenin, MAGI-3, EGFR, PtdIns(3,4,5)P3, IGF-1 receptor, Tuberin, ILK, GRB2, 2.7.1.137, AKT(PKB), c-Raf-1, MDM2, Caspase-9

[0044] Genes in the TGF-β pathway. p300, MSK1, SOS, NF-kB, TGF-beta receptor type I, SMAD7, p15, Elk-1, TGF-beta 1, SMAD4, Caveolin-1, ErbB2, IKK-beta, TSC-22, TIEG1, FKBP12, SMURF2, APC/hCDH1 complex, FAST-1/2, IKK-alpha, ERK1/2, SMAD3, TAK1(MAP3K7), PAI1, ER81, MEKK4(MAP3K4), NFKBIA, GADD45 beta, H-Ras, Anaphase-promoting complex (APC), c-Raf-1, XIAP, TGF-beta receptor type II, SMURF1, CBP, p21, MEK6(MAP2K6), Sno-N, MEK2(MAP2K2), YY1, MEK3 (MAP2K3), SARA, SP1, Shc, Importin (karyopherin)-beta, SMAD2, TAB1, Ski, p38 MAPK, MEK1(MAP2K1)

[0045] FOXO transcription factors: FOXO1, FOXO3a

[0046] Genes in the Apoptosis pathways: ACVR1, BCL2L1, BIRC1, CAPN2, CAPNS1, CCNG1, CD47, CD81, CD99, CFLAR, CUL1, DAD1, DGKA, DPP4, FST, GZMA, HLA-G, HSPA8, HSPD1, IGF1R, IL15, IL1A, IL2RG, IRS2, ITGB3, MAD2L1, MAP2K1, MAX, NRAS, ODC1, PDGFA, PECAM1, PGRMC1, PRKAR2B, PROS1, PTPN13, RBBP7, RPS3, SERPINB2, SKI, TEGT, TOP1, TPM1, YWHAQ, ZFF148

[0047] Genes in the Ubiquitination pathways: CAPN2, CAST, CD47, CFLAR, CLTC, CUL1, ESPL1, FLNA, HSPA8, IRS2, MAD2L1, MAP2K1, SIRT2, SKI, SNRPN, TOP1, UBQLN4, YWHAB, YWHAQ

[0048] Genes in the Energy Production pathways: ACVR1, BCL2L1, BIRC1, GSS, HLA-G, HSPA8, HSPD1, IGF1R, IRS2, KATNB1, MAP2K1, PGK1, PMS2, PRKD2, SLC25A3, SNRPN, TCF8, TOP1, TPM1

[0049] In certain embodiments, the gene or pathway indicative of oocyte quality is chosen from a gene expressed in connection with one or more of the following categories (reflecting those listed in Table 1): cell cycle (e.g., mitosis); chromosome segregation or organization (e.g., chromosome segregation, spindle localization or chromosome organization); DNA damage response and repair (e.g., response to DNA damage stimulus); proteolytic pathway (e.g., proteolysis); energy pathway or mitochondrial function (e.g., ATP metabolic process or ATP binding); cell signaling and communication (e.g., intracellular signaling cascade or cell-cell signaling); protein transport; transcription regulation; reproductive process (e.g., oogenesis or oviposition); cell death; cell differentiation or cell adhesion.

[0050] Other genes have been found to be of interest—among them, genes of chromatin structure, DNA methylation and genome stability. In particular, genes that have been shown to be associated with both ovarian function and general aging have shown promise in the methods, kits and libraries of the present technology. These include SERPINB2 (serpin peptidase inhibitor, clade B, member 2, also known as PAI-2); IGFIR (insulin-like growth factor 1 receptor); PIK3CB (phosphoinositide-3-kinase, catalytic, beta polypeptide), IRS2 (insulin receptor substrate 2), HSPA8, HSPD1 and HSP60. Two genetic pathways in particular have been found herein to be significant in the regulation of reproductive aging. Specifically, it has previously been determined that TGF-β and insulin/IGF-1 (IIS) signaling pathways regulate reproductive aging cell non-autonomously. That is, these pathways regulate reproductive aging systemically, outside of the oocyte itself rather than by signaling just inside the oocyte. The function of these signaling pathways outside of oocytes (that is, in other areas of the organism's system) can determine the rate of reproductive aging, and analysis of a systemic tissue such as blood or urine for the activity of these pathways can provide useful data, including one or more biological indicators of reproductive aging of the oocytes.

[0051] In certain embodiments, the present technology is directed to transcriptional analysis of peripheral blood mononuclear cells (PMBCs). RNA sequencing is used to achieve greater sensitivity and depth. Biomarkers of reproductive age and reproductive success have been identified. The focus is on the most significant genes associated with reproductive status, regardless of whether the gene function is known or not, thus removing bias in selection. By using a panel of the genes most significantly associated with reproductive success, and then testing the expression of these genes for their predictive power, a diagnostic with a high correlation with outcome has been created. Additionally, analysis of the systemic effects on reproduction can inform subsequent approaches for treatments. Genes that have been shown to be downregulated include members of the insulin/IGF-1 (IIS) pathway (IGFAR, IRS2), and increased SIRT2, a co-regulator of the HS pathway, is associated with late reproductive success. Therefore, previous studies of the *C. elegans* reproductive span correlates exactly with these observations in women, that one of the most important regulators of reproductive span appears to be the IIS pathway. Members of the TGF-β pathway can also be systemic markers of reproductive success. IIS can influence both lifespan and reproductive span, while TGF-β has an effect specifically on reproductive span. Thus, IIS differences in PBMCs are thought also to act as a diagnostic for longevity.

[0052] Thus, in certain embodiments, the technology herein is directed to methods for assessing a woman's likely oocyte quality, chances of conception, comprising developing a quantitative score that offers information regarding chances of conception or otherwise a measure of likelihood of success of an assisted reproductive procedure. In certain embodiments, the score can be calculated as follows: A sample's gene expression values can be obtained, and then how well the genes match a particular age can be determined in one of several ways, including but not limited to the following: (1) by Pearson correlation with a) the set of genes or pathways in the profile, if that is what is available by the gene set qRT-PCR assay, or b) by the Pearson correlation with the entire gene expression profile when the sample's total mRNA-sequence is assessed; or (2) by counting the genes with most extreme FisherZ scores more heavily (weighting) that includes the average expression of all the genes in the set.

[0053] The latter could give a single score that depends most heavily on the set of genes already evaluated. The filmier would likely allow for a better match of the whole transcriptome by age. In certain embodiments, both scores can be used to assess the score of the sample.

[0054] In certain embodiments, a "reproductive age" (as opposed to an actual age) of a given individual can be calculated as follows:

[0055] A pre-calculated age-correlation-score Z_i for each gene i (for a total of ~19,600 genes in the genome) is based on public gene-expression data from blood from females. (These are the "fisherz" scores reported in all the analyses results.)

[0056] Given a new gene-expression sample with normalized expression levels e_i for each gene i, the "reproductive-age" a_{rep} of that sample equals the weighted average of all the genes measured in the sample (N), weighted by the 'age-correlation' scores of those genes, in Equation (I) below:

$$a_{rep} = \frac{\sum_{t=1}^{N} z_i \cdot e_i}{\sum_{t=1}^{N} z_i} \tag{I}$$

[0057] In certain embodiments, the present technology is directed to a kit comprising any one or more of the following: (a) a collection container for collecting a cell sample; and (b) an assay that measures a characteristic of a gene or pathway related to oocyte quality. In use, a medical professional, or the patient herself, may collect the cell sample, subject it to the assay and use the results to predict the patient's oocyte quality. For example, in certain embodiments the kit can predict a woman's likelihood of conceiving, a woman's "reproductive age" (as described later herein) or the likelihood that ovulation will result in a viable oocyte in any given month. Any of these can even be packaged in conjunction with other tools used by women trying to conceive, including but not limited to ovulation predictor kits, tools for measuring body temperature (such as basal body temperature thermometers), tools for measuring or evaluating mucus signs and other physically manifested indicators of fertility and fertile windows.

[0058] In various other embodiments, the kit comprises:

[0059] (a) a collection container for collecting a cell sample obtained from the woman's body;

[0060] (b) a testing assay that measures a characteristic of a gene, pathway or transcriptional profile characteristic of the cell sample, wherein the characteristic indicates the likely quality of an oocyte; and

[0061] (c) a visual indicator visible to the woman, the visual indicator providing information regarding the likely quality of the oocyte.

[0062] The visual indicator can be, for example, a color-coded indicator showing a binary result such as one color for an above average score, and another for a below average score.

[0063] In certain embodiments, the testing assay can be, for example, an RT-PCR assay on blood using the primers for the best genes. In the case of other samples such as urine or other bodily fluids, an assay can include metabolomics to assess metabolites or hormones, such as, for example, an enzyme-linked immunosorbent (ELISA) assay. In other embodiments, a colorimetric test could work in the event that the assay is matter of determining the levels of relatively few (e.g., just one, two or three, or in various embodiments fewer than about 10, fewer than about 25 or fewer than about 50) genes, metabolites or hormones. For example, in certain embodiments, the results of the assay could be displayed as one or more lines that would indicate the score. In certain embodiments, different lines could present different data points or results (for example, different colors or configurations, with the combination providing a score or other type of quantitative or qualitative result).

[0064] In certain embodiments, such a kit could be made commercially available for at-home use, and could include information taken from a library of genes and pathways generated in connection with certain embodiments herein.

[0065] In certain embodiments, the kit will include primers to amplify genes in this set (genes with FisherZ scores above 2 and below −2; see Table 2) from blood. In certain embodiments, any or all of the sample, or any characteristic thereof, can be assigned a score that is equal to the average of the expression level of all the genes in the array weighted by the age-correlation (FisherZ) score of each of the genes. This score conveys the expected oocyte viability for a woman compared to an average for women of the same age.

[0066] In certain embodiments, the present technology is directed to a method for the production of a library of genes, or a reproductive aging gene expression profile, as markers of oocyte quality. Such a method may comprise the steps of correlating a test gene with a quantitative and measured characteristic of oocyte quality, listing the correlation in the library; comparing a measured characteristic of a gene provided by a patient with that listed in the library; and determining the quality of an oocyte of a patient based on the comparison.

[0067] For example, in certain embodiments, a library is produced through any of the following steps: First, list certain genes known or thought to relate to factors such as ovarian function and general aging. Next, obtain samples of oocytes known to be from women of certain ages (for example, age 20, age 25, age 30 and the like) and measure one or more of the characteristics of those oocytes to obtain baseline values. Next, when a patient desires the assay, a cell sample is taken from the patient, the one or more characteristics can be determined by running the assay on the patient's cell sample and comparing the values to those of the library. For example, a patient may be 35 years old but may have oocytes that are typical of a 25 year old or a 40 year old, as determined by a method of the present technology, using the library generated according to this embodiment. This is valuable information that the patient can acquire without the need for invasive testing or destruction of her oocytes, and in certain embodiments, is obtained by implementing a method or kit in accordance with the embodiments herein. In certain embodiments, a yearly clinical assessment of oocyte age could allow a clinician or woman to determine the rate of change of oocyte quality, yet another indicator that could be useful for diagnostics and for advising patients.

[0068] In certain embodiments, a library can be created and used to establish a "profile set" for a user—that is, a set of one or more genes, pathways or transcriptional profiles that indicates various characteristics of a user's oocyte. A candidate gene expression assay can be developed based on the information obtained from bodily fluids such as blood, thus identifying biomarkers that correlate with oocyte quality and pregnancy success.

[0069] In one exemplary method, a library was made by the following steps:

[0070] (1) gathering expression data from samples (whole blood and PBMCs) from women in a particular age range (in certain embodiments, aged 20 to 50, but not so limited). An average gene expression for each gene at each age was calculated by averaging the expression for that gene in a given range of time (e.g., a 2 year window, in overlapping (sliding) windows). This allowed the inclusion of about 30 to about 90 samples in each year. In certain embodiments, an average of about 70 to about 80 GEO female blood samples were used for each 2 year sliding window; for each gene, the Spearmann correlation of the average gene expression to the age vector was determined, and then sorted by the FisherZ score; a score above 2 (top 5%) was used to generate a set of significantly changed age-dependent genes, all candidate biomarkers.

[0071] (2) The gene expression data were compared to an "age vector" to indicate which genes changed most with age. Since most genes do not have an age-related change in expression, the data are normally distributed. The FisherZ score makes it possible to find the genes at the tail ends of the distribution; those genes are most changed with age, and thus are the best indicators of biological age. Such genes are included in the library, and can be used to compare with data acquired from the test subject.

[0072] For the samples of women aged 25 to 50, in certain embodiments only samples from women who have no known fertility defect (i.e., presence at IVF clinic is due to sperm or other pal titer issue) can be used to establish a "young" profile. The expression profiles can then be sorted according to age and further segregated by pregnancy success/failure and other cytological information, and PCA can be performed to identify the genes best correlated with pregnancy success. Using qRT-PCR, the top genes most associated with pregnancy outcome can be tested on a separate sample set prior to IVF (or other ART treatment) to verify predictive power of the gene set. The most predictive genes can be used to develop a diagnostic tool that can be used in clinics after a simple blood draw or urine collection. The clinical procedure RT-PCR can be performed on RNA from blood samples using the mix of primers of the best candidate genes.

[0073] FIG. **2** shows a heat map of the results showing gene trees. Tables 2 and 3 below shows data from FIG. **2** in numerical form. Table 2 shows the results for ages 20-33; Table 3 shows the results for ages 34-40.

TABLE 2

gene	symbol	name	fisherz	20	21	22
56904	SH3GLB2	SH3-domain GRB2-like endophilin B2	3.67	−0.38	−0.45	−1.28
6464	SHC1	SHC (Src homology 2 domain containing) transforming protein 1	3.56	−0.45	−1.44	−0.81
79087	ALG12	ALG12, alpha-1,6-mannosyltransferase	3.45	−0.66	−0.84	−0.31
101928190	LOC101928190	uncharacterized LOC101928190	3.43	−1.81	−1.56	−1.47
3416	IDE	insulin-degrading enzyme	3.17	−0.90	−0.60	−0.59
8001	GLRA3	glycine receptor, alpha 3	3.16	−0.68	−1.27	−1.71
3727	JUND	jun D proto-oncogene	3.13	−0.39	−1.05	−0.07

TABLE 2-continued

10945	KDELR1	KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 1	3.12	−0.05	−1.56	0.01
5025	P2RX4	purinergic receptor P2X, ligand-gated ion channel, 4	3.09	−0.52	−0.03	−0.87
29920	PYCR2	pyrroline-5-carboxylate reductase family, member 2	3.07	−0.44	−0.06	−1.54
101929248	LOC101929248	uncharacterized LOC101929248	3.01	−0.18	−0.66	−0.47
23646	PLD3	phospholipase D family, member 3	2.98	−0.35	−1.18	0.25
10280	SIGMAR1	sigma non-opioid intracellular receptor 1	2.97	−0.26	−0.98	−0.02
140699	MROH8	maestro heat-like repeat family member 8	2.96	−1.96	−1.29	−0.57
4669	NAGLU	N-acetylglucosaminidase, alpha	2.94	1.04	−1.05	−0.47
8341	HIST1H2BN	histone cluster 1, H2bn	2.91	−0.20	−1.26	−1.79
2519	FUCA2	fucosidase, alpha-L-2, plasma	2.90	−2.72	−1.16	−0.08
8985	PLOD3	procollagen-lysine, 2-oxoglutarate 5-dioxygenase 3	2.88	0.48	−0.96	−0.65
1690	COCH	cochlin	2.87	−0.79	−2.11	0.48
51114	ZDHHC9	zinc finger, DHHC-type containing 9	2.86	0.19	−0.88	−0.47
55907	CMAS	cytidine monophosphate N-acetylneuraminic acid synthetase	2.85	−0.20	−0.12	−0.94
144811	LACC1	laccase (multicopper oxidoreductase) domain containing 1	2.84	0.65	−2.69	−0.27
92421	CHMP4C	charged multivesicular body protein 4C	2.84	−1.75	0.40	−0.42
23475	QPRT	quinolinate phosphoribosyltransferase	2.83	0.03	−0.54	−0.22
54913	RPP25	ribonuclease P/MRP 25 kDa subunit	2.77	−1.16	−1.29	0.21
4645	MYO5B	myosin VB	2.76	−1.61	−0.94	0.39
9917	FAM20B	family with sequence similarity 20, member B	2.74	−0.21	−0.82	−0.91
57213	SPRYD7	SPRY domain containing 7	2.73	0.00	−1.85	−0.11
113829	SLC35A4	solute carrier family 35, member A4	2.73	−0.37	−0.56	−1.00
100128164	LOC100128164	four and a half LIM domains 1 pseudogene	2.72	−1.16	−0.96	−0.93
26284	ERAL1	Era-like 1 2S mitochondrial rRNA chaperone 1	2.70	0.75	−0.67	−0.65

TABLE 2-continued

64847	SPATA20	spermatogenesis associated 20	2.70	1.79	−1.47	−0.62
55974	SLC50A1	solute carrier family 50 (sugar efflux transporter), member 1	2.69	−0.45	−0.88	0.39
64405	CDH22	cadherin 22, type 2	2.68	−0.95	−1.41	−2.30
6510	SLC1A5	solute carrier family 1 (neutral amino acid transporter), member 5	2.68	−0.54	−1.66	−0.02
196463	PLBD2	phospholipase B domain containing 2	2.67	−0.48	−1.13	−1.29
741	ZNHIT2	zinc finger, HIT-type containing 2	2.67	−2.15	0.74	−1.37
23568	ARL2BP	ADP-ribosylation factor-like 2 binding protein	2.66	0.53	0.31	−1.77
79144	PPDPF	pancreatic progenitor cell differentiation and proliferation factor	2.66	0.02	−1.75	−1.35
91319	DERL3	derlin 3	2.66	−0.64	−0.55	−0.94
79654	HECTD3	HECT domain containing E3 ubiquitin protein ligase 3	2.64	0.28	−2.10	−0.42
115950	ZNF653	zinc finger protein 653	2.63	−0.11	−0.32	−1.94
1374	CPT1A	carnitine palmitoyltransferase 1A (liver)	2.63	−0.46	−1.45	−0.66
81533	ITFG1	integrin alpha FG-GAP repeat containing 1	2.62	−2.21	−1.14	0.04
201931	TMEM192	transmembrane protein 192	2.60	−1.17	−1.00	−0.12
7979	SHFM1	split hand/foot malformation (ectrodactyly) type 1	2.60	−0.03	0.14	−0.54
159296	NKX2-3	NK2 homeobox 3	2.59	0.18	−0.81	−0.29
51102	MECR	mitochondrial trans-2-enoyl-CoA reductase	2.59	0.73	−0.13	−0.55
8729	GBF1	golgi brefeldin A resistant guanine nucleotide exchange factor 1	2.59	−0.82	−0.51	−1.04
118460	EXOSC6	exosome component 6	2.58	−0.87	0.01	−0.27
79586	CHPF	chondroitin polymerizing factor	2.57	−1.64	−0.31	−1.32
2052	EPHX1	epoxide hydrolase 1, microsomal (xenobiotic)	2.54	0.15	−2.10	0.57
84893	FBXO18	F-box protein, helicase, 18	2.53	−1.99	0.08	0.16
54726	OTUD4	OTU domain containing 4	2.53	−0.35	0.31	−0.91
813	CALU	calumenin	2.53	−0.42	0.21	−0.41
54431	DNAJC10	DnaJ (Hsp40) homolog, subfamily C, member 10	2.52	0.67	−1.18	−0.24
9612	NCOR2	nuclear receptor corepressor 2	2.52	−0.79	−1.22	−1.40

TABLE 2-continued

9829	DNAJC6	DnaJ (Hsp40) homolog, subfamily C, member 6	2.51	−1.56	0.25	−0.84
79036	KXD1	KxDL motif containing 1	2.51	−1.30	−0.97	−0.91
284361	EMC10	ER membrane protein complex subunit 10	2.51	0.21	−0.27	−0.93
131118	DNAJC19	DnaJ (Hsp40) homolog, subfamily C, member 19	2.50	−0.13	−0.23	−0.21
644809	C15orf56	chromosome 15 open reading frame 56	2.50	−2.50	−1.68	0.03
2119	ETV5	ets variant 5	2.50	0.74	−2.06	−0.40
5833	PCYT2	phosphate cytidylyltransferase 2, ethanolamine	2.50	−0.95	−0.34	0.60
922	CD5L	CD5 molecule-like	2.49	0.26	−1.47	1.04
9261	MAPKAPK2	mitogen-activated protein kinase-activated protein kinase 2	2.49	−0.65	−0.96	−0.37
57190	SEPN1	selenoprotein N, 1	2.49	−0.88	−0.59	0.58
79644	SRD5A3	steroid 5 alpha-reductase 3	2.48	1.23	−0.67	−0.27
79058	ASPSCR1	alveolar soft part sarcoma chromosome region, candidate 1	2.48	−0.54	0.00	−0.68
7832	BTG2	BTG family, member 2	2.47	−0.51	−0.67	−0.75
11070	TMEM115	transmembrane protein 115	2.47	0.00	−0.03	−0.31
10847	SRCAP	Snf2-related CREBBP activator protein	2.46	−1.45	−0.63	−1.00
4597	MVD	mevalonate (diphospho) decarboxylase	2.46	−1.41	−1.21	−1.30
100506696	PCAT6	prostate cancer associated transcript 6 (non-protein coding)	2.45	0.45	−0.79	−0.46
100507459	LOC100507459	uncharacterized LOC100507459	2.45	−0.67	−2.06	0.13
100130613	CXorf64	chromosome X open reading frame 64	2.45	−0.70	−0.39	−0.55
5081	PAX7	paired box 7	2.45	−0.18	−0.61	−0.05
100240728	LOC100240728	uncharacterized LOC100240728	2.44	0.45	−0.36	−0.61
26229	B3GAT3	beta-1,3-glucuronyltransferase 3 (glucuronosyltransferase I)	2.44	−0.09	0.75	−0.81
950	SCARB2	scavenger receptor class B, member 2	2.44	0.11	−1.84	−0.51
161882	ZFPM1	zinc finger protein, FOG family member 1	2.44	0.78	−1.19	−0.40
5034	P4HB	prolyl 4-hydroxylase, beta polypeptide	2.43	−0.03	−0.65	0.03
123355	LRRC28	leucine rich repeat containing 28	2.43	−3.02	−0.37	−0.11

TABLE 2-continued

6734	SRPR	signal recognition particle receptor (docking protein)	2.43	−0.95	−0.99	−0.46
9911	TMCC2	transmembrane and coiled-coil domain family 2	2.43	−0.31	−1.12	−0.50
222642	TSPO2	translocator protein 2	2.42	−0.04	−0.31	−0.73
3643	INSR	insulin receptor	2.42	−1.47	−1.69	−0.40
85462	FHDC1	FH2 domain containing 1	2.41	−1.86	−1.61	−0.81
149175	MANEAL	mannosidase, endo-alpha-like	2.40	0.96	−1.03	−1.02
1819	DRG2	developmentally regulated GTP binding protein 2	2.40	−0.30	0.61	−0.59
10370	CITED2	Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain, 2	2.39	−0.55	−1.11	−0.62
25792	CIZ1	CDKN1A interacting zinc finger protein 1	2.39	−0.51	−0.14	−0.05
4072	EPCAM	epithelial cell adhesion molecule	2.39	−0.61	−0.92	0.35
84447	SYVN1	synovial apoptosis inhibitor 1, synoviolin	2.39	−0.16	−1.58	−0.62
527	ATP6V0C	ATPase, H+ transporting, lysosomal 16 kDa, V0 subunit c	2.39	−1.34	−1.27	−1.10
10629	TAF6L	TAF6-like RNA polymerase II, p300/CBP-associated factor (PCAF)-associated factor, 65 kDa	2.38	−0.68	−0.53	−0.44
51150	SDF4	stromal cell derived factor 4	2.38	−0.19	−0.15	0.08
57143	ADCK1	aarF domain containing kinase 1	2.37	−0.37	−0.83	−0.99
682	BSG	basigin	2.37	−0.21	−1.33	0.61
10139	ARFRP1	ADP-ribosylation factor related protein 1	2.37	−1.43	0.38	−0.03
203238	CCDC171	coiled-coil domain containing 171	2.37	0.06	−0.78	−0.07
54805	CNNM2	cyclin M2	2.37	−0.64	0.23	−0.71
1200	TPP1	tripeptidyl peptidase I	2.37	0.19	−2.22	−0.27
2271	FH	fumarate hydratase	2.37	−0.93	−0.36	−0.51
376412	RNF126P1	ring finger protein 126 pseudogene 1	2.37	−0.06	−0.52	−0.30
4924	NUCB1	nucleobindin 1	2.37	−1.22	−1.33	1.30
55132	LARP1B	La ribonucleoprotein domain family, member 1B	2.37	0.00	0.03	−0.14

TABLE 2-continued

9650	MTFR1	mitochondrial fission regulator 1	2.37	0.28	−0.07	−0.47
29803	REPIN1	replication initiator 1	2.36	−0.05	−2.01	−0.66
4507	MTAP	methylthioadenosine phosphorylase	2.36	−0.50	0.16	−1.34
816	CAMK2B	calcium/calmodulin-dependent protein kinase II beta	2.36	−0.96	−1.38	−0.92
120379	PIH1D2	PIH1 domain containing 2	2.36	0.24	−0.66	0.42
91289	LMF2	lipase maturation factor 2	2.36	−0.15	−1.01	−0.77
10905	MAN1A2	mannosidase, alpha, class 1A, member 2	2.35	−0.52	−0.40	−0.47
25930	PTPN23	protein tyrosine phosphatase, non-receptor type 23	2.35	−0.79	−1.96	−0.03
57648	KIAA1522	KIAA1522	2.35	−1.31	−1.46	−0.14
7249	TSC2	tuberous sclerosis 2	2.35	−0.03	−0.57	0.01
55151	TMEM38B	transmembrane protein 38B	2.34	0.29	−0.25	−0.17
160728	SLC5A8	solute carrier family 5 (sodium/monocarboxylate cotransporter), member 8	2.33	−1.06	−1.61	−2.74
148418	SAMD13	sterile alpha motif domain containing 13	2.33	−0.78	0.86	−0.47
646762	LOC646762	uncharacterized LOC646762	2.32	−0.60	−1.03	−0.50
79109	MAPKAP1	mitogen-activated protein kinase associated protein 1	2.32	−0.93	−0.74	0.05
81037	CLPTM1L	CLPTM1-like	2.31	−0.28	−0.13	−0.56
51523	CXXC5	CXXC finger protein 5	2.29	0.91	−1.19	−0.86
55322	C5orf22	chromosome 5 open reading frame 22	2.29	−0.14	−1.05	−1.19
100996671	LOC100996671	uncharacterized LOC100996671	2.29	−1.07	0.25	0.83
55222	LRRC20	leucine rich repeat containing 20	2.29	0.14	0.15	−0.15
55624	POMGNT1	protein O-linked mannose N-acetylglucosaminyltransferase 1 (beta 1,2-)	2.29	0.42	−0.59	0.05
100505983	LOC100505983	uncharacterized LOC100505983	2.28	−0.30	−1.40	−0.22
3069	HDLBP	high density lipoprotein binding protein	2.28	0.02	−0.50	0.20
10959	TMED2	transmembrane emp24 domain trafficking protein 2	2.28	−0.64	0.50	−0.45
6598	SMARCB1	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily b, member 1	2.28	−0.03	−1.04	0.23

TABLE 2-continued

60412	EXOC4	exocyst complex component 4	2.27	−0.97	−0.75	0.09
54982	CLN6	ceroid-lipofuscinosis, neuronal 6, late infantile, variant	2.27	−0.22	−0.05	−1.13
91752	ZNF804A	zinc finger protein 804A	2.27	−0.60	−0.96	−0.74
113178	SCAMP4	secretory carrier membrane protein 4	2.26	−0.63	−0.57	0.58
10	NAT2	N-acetyltransferase 2 (arylamine N-acetyltransferase)	2.26	−2.14	−0.97	−2.02
375	ARF1	ADP-ribosylation factor 1	2.26	−0.93	0.03	−0.04
5589	PRKCSH	protein kinase C substrate 80K-H	2.26	−0.64	−1.59	0.51
9136	RRP9	ribosomal RNA processing 9, small subunit (SSU) processome component, homolog (yeast)	2.26	−0.92	0.08	−1.22
23193	GANAB	glucosidase, alpha; neutral AB	2.26	−0.20	0.04	−0.10
1798	DPAGT1	dolichyl-phosphate (UDP-N-acetylglucosamine) N-acetylglucosaminephosphotransferase 1 (GlcNAc-1-P transferase)	2.25	0.46	−0.97	0.23
85440	DOCK7	dedicator of cytokinesis 7	2.25	0.62	−1.10	0.08
100505794	LOC100505794	uncharacterized LOC100505794	2.24	−1.88	−0.15	−1.64
1173	AP2M1	adaptor-related protein complex 2, mu 1 subunit	2.24	0.00	−0.87	0.19
124540	MSI2	musashi RNA-binding protein 2	2.24	−0.83	−0.24	0.21
8372	HYAL3	hyaluronoglucosaminidase 3	2.24	−0.32	0.20	−0.55
64755	C16orf58	chromosome 16 open reading frame 58	2.24	0.94	−0.41	−0.56
79102	RNF26	ring finger protein 26	2.24	−0.02	−0.85	0.30
10963	STIP1	stress-induced-phosphoprotein 1	2.24	−1.07	−0.30	0.04
375387	NRROS	negative regulator of reactive oxygen species	2.24	0.14	−0.08	−0.66
972	CD74	CD74 molecule, major histocompatibility complex, class II invariant chain	2.23	1.04	−3.36	−0.16
54676	GTPBP2	GTP binding protein 2	2.23	0.44	−1.39	−0.84
192286	HIGD2A	HIG1 hypoxia inducible domain family, member 2A	2.23	1.25	−0.69	−1.21
3295	HSD17B4	hydroxysteroid (17-beta) dehydrogenase 4	2.23	−0.22	−1.28	0.23

TABLE 2-continued

80852	GRIP2	glutamate receptor interacting protein 2	2.23	−1.32	−0.75	−2.48
1298	COL9A2	collagen, type IX, alpha 2	2.22	−1.39	−2.02	−0.09
2004	ELK3	ELK3, ETS-domain protein (SRF accessory protein 2)	2.22	0.12	−0.69	−0.62
10279	PRSS16	protease, serine, 16 (thymus)	2.22	0.08	0.44	−2.85
151790	WDR49	WD repeat domain 49	2.22	−1.01	−1.82	0.21
399664	MEX3D	mex-3 RNA binding family member D	2.21	−1.01	0.55	−2.20
5664	PSEN2	presenilin 2 (Alzheimer disease 4)	2.21	1.22	−1.57	−0.49
51614	ERGIC3	ERGIC and golgi 3	2.21	0.53	−0.17	−0.81
79178	THTPA	thiamine triphosphatase	2.21	0.37	−0.69	−0.20
51726	DNAJB11	DnaJ (Hsp40) homolog, subfamily B, member 11	2.20	−0.15	0.16	−0.46
3425	IDUA	iduronidase, alpha-L-	2.20	0.16	0.01	−0.59
1642	DDB1	damage-specific DNA binding protein 1, 127 kDa	2.20	0.72	−0.92	−1.11
101928770	LOC101928770	uncharacterized LOC101928770	2.19	−1.77	−0.87	0.07
11015	KDELR3	KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 3	2.19	0.74	−1.45	0.13
35	ACADS	acyl-CoA dehydrogenase, C-2 to C-3 short chain	2.19	−0.36	−0.45	−0.31
64798	DEPTOR	DEP domain containing MTOR-interacting protein	2.19	0.99	−0.91	−0.04
23457	ABCB9	ATP-binding cassette, sub-family B (MDR/TAP), member 9	2.19	−0.90	−0.60	−1.70
56132	PCDHB3	protocadherin beta 3	2.19	−1.40	0.21	−2.75
23400	ATP13A2	ATPase type 13A2	2.19	0.69	0.78	−0.24
3980	LIG3	ligase III, DNA, ATP-dependent	2.19	−1.66	0.65	0.25
5690	PSMB2	proteasome (prosome, macropain) subunit, beta type, 2	2.19	−0.48	−1.31	−0.93
7917	BAG6	BCL2-associated athanogene 6	2.19	0.61	−1.07	−0.41
1739	DLG1	discs, large homolog 1 (*Drosophila*)	2.18	−0.19	0.09	−0.49
2837	UTS2R	urotensin 2 receptor	2.18	0.03	−1.24	−0.19
83746	L3MBTL2	l(3)mbt-like 2 (*Drosophila*)	2.18	−0.32	0.57	−1.37

TABLE 2-continued

5962	RDX	radixin	2.18	1.15	−0.45	0.35
9956	HS3ST2	heparan sulfate (glucosamine) 3-O-sulfotransferase 2	2.18	0.52	−0.59	−1.02
162968	ZNF497	zinc finger protein 497	2.18	−0.39	−0.58	−0.52
4192	MDK	midkine (neurite growth-promoting factor 2)	2.18	0.14	−1.17	0.55
54919	HEATR2	HEAT repeat containing 2	2.18	−0.66	−0.12	0.37
10972	TMED10	transmembrane emp24-like trafficking protein 10 (yeast)	2.17	0.29	−0.15	−0.89
23061	TBC1D9B	TBC1 domain family, member 9B (with GRAM domain)	2.17	0.25	−1.61	−0.61
3792	KEL	Kell blood group, metallo-endopeptidase	2.17	−1.53	−0.95	0.95
2063	NR2F6	nuclear receptor subfamily 2, group F, member 6	2.17	0.08	−1.78	−0.45
55177	RMDN3	regulator of microtubule dynamics 3	2.17	−0.02	−0.72	−0.89
11147	HHLA3	HERV-H LTR-associating 3	2.17	−0.01	−0.94	0.21
57486	NLN	neurolysin (metallopeptidase M3 family)	2.17	−0.76	−2.12	0.41
30814	PLA2G2E	phospholipase A2, group IIE	2.16	−1.73	−0.14	−0.20
57414	RHBDD2	rhomboid domain containing 2	2.16	−0.83	0.47	−0.68
84836	ABHD14B	abhydrolase domain containing 14B	2.16	0.25	−0.70	−0.77
8516	ITGA8	integrin, alpha 8	2.16	−1.05	−0.45	0.93
89866	SEC16B	SEC16 homolog B (*S. cerevisiae*)	2.16	0.34	−1.11	−0.52
10491	CRTAP	cartilage associated protein	2.16	−0.42	−1.22	−1.46
11047	ADRM1	adhesion regulating molecule 1	2.16	−0.86	−0.75	−0.35
28971	AAMDC	adipogenesis associated, Mth938 domain containing	2.16	−0.57	−1.44	0.87
8078	USP5	ubiquitin specific peptidase 5 (isopeptidase T)	2.16	−0.20	−1.15	−0.68
37	ACADVL	acyl-CoA dehydrogenase, very long chain	2.16	0.77	−1.27	0.27
145508	CEP128	centrosomal protein 128 kDa	2.15	−1.44	−0.13	−2.43
49861	CLDN20	claudin 20	2.15	−1.53	−0.99	−1.79
5905	RANGAP1	Ran GTPase activating protein 1	2.15	0.36	0.13	−0.26
7542	ZFPL1	zinc finger protein-like 1	2.15	−0.61	−0.83	0.40
9562	MINPP1	multiple inositol-polyphosphate phosphatase 1	2.15	0.75	−0.88	−1.41

TABLE 2-continued

79095	C9orf16	chromosome 9 open reading frame 16	2.15	−0.91	−1.40	−0.54
8815	BANF1	barrier to autointegration factor 1	2.15	−0.86	−0.94	0.62
54867	TMEM214	transmembrane protein 214	2.15	−0.36	−1.15	−0.26
6721	SREBF2	sterol regulatory element binding transcription factor 2	2.15	−0.66	−1.09	−0.41
23133	PHF8	PHD finger protein 8	2.15	−2.33	−0.20	−1.80
113675	SDSL	serine dehydratase-like	2.14	−0.45	−1.26	−0.08
129303	TMEM150A	transmembrane protein 150A	2.14	−1.19	−0.27	0.63
57658	CALCOCO1	calcium binding and coiled-coil domain 1	2.14	−0.87	−2.39	−1.31
162	AP1B1	adaptor-related protein complex 1, beta 1 subunit	2.14	0.16	−2.22	−0.01
2873	GPS1	G protein pathway suppressor 1	2.14	−0.39	0.88	0.19
64978	MRPL38	mitochondrial ribosomal protein L38	2.14	−1.05	0.55	0.51
220323	OAF	OAF homolog (*Drosophila*)	2.14	1.31	−1.11	0.05
6006	RHCE	Rh blood group, CcEe antigens	2.14	−0.69	−0.91	−0.21
389812	LCN15	lipocalin 15	2.14	0.12	−1.10	−0.97
2628	GATM	glycine amidinotransferase (L-arginine:glycine amidinotransferase)	2.13	−0.78	−2.26	−0.51
6509	SLC1A4	solute carrier family 1 (glutamate/neutral amino acid transporter), member 4	2.13	−1.52	0.41	0.40
3888	KRT82	keratin 82	2.13	−0.47	−0.10	−0.62
5211	PFKL	phosphofructokinase, liver	2.13	0.14	−1.68	−1.00
55080	TAPBPL	TAP binding protein-like	2.13	−0.22	−1.22	−1.01
2139	EYA2	eyes absent homolog 2 (*Drosophila*)	2.13	−1.64	0.08	0.41
2030	SLC29A1	solute carrier family 29 (equilibrative nucleoside transporter), member 1	2.12	0.75	−0.96	0.08
56005	C19orf10	chromosome 19 open reading frame 10	2.12	−0.77	−0.18	−0.18
6414	SEPP1	selenoprotein P, plasma, 1	2.12	1.63	−1.72	0.86
5184	PEPD	peptidase D	2.12	−0.14	−1.08	−0.28
643783	USP46-AS1	USP46 antisense RNA 1	2.12	0.35	−1.04	−0.30
101928185	LOC101928185	uncharacterized LOC101928185	2.12	−1.31	−1.64	−0.15
22883	CLSTN1	calsyntenin 1	2.12	−0.33	−1.22	−0.04
25800	SLC39A6	solute carrier family 39 (zinc transporter), member 6	2.12	0.89	−1.29	0.19

TABLE 2-continued

54681	P4HTM	prolyl 4-hydroxylase, transmembrane (endoplasmic reticulum)	2.12	1.14	−1.11	−0.26
644150	WIPF3	WAS/WASL interacting protein family, member 3	2.12	−1.29	0.15	−0.20
9048	ARTN	artemin	2.12	0.12	−1.89	−0.02
3054	HCFC1	host cell factor C1 (VP16-accessory protein)	2.11	0.43	−0.62	0.29
115098	CCDC124	coiled-coil domain containing 124	2.11	−1.85	0.10	−0.23
55558	PLXNA3	plexin A3	2.11	0.92	−0.78	−0.16
675	BRCA2	breast cancer 2, early onset	2.11	0.63	−0.16	0.83
9777	TM9SF4	transmembrane 9 superfamily protein member 4	2.11	1.49	−1.09	−0.22
83707	TRPT1	tRNA phosphotransferase 1	2.11	−0.04	−0.15	0.66
55334	SLC39A9	solute carrier family 39, member 9	2.10	−1.47	−2.10	0.10
9793	CKAP5	cytoskeleton associated protein 5	2.10	0.88	−0.71	−0.58
56834	GPR137	G protein-coupled receptor 137	2.10	0.20	−1.10	−0.16
25921	ZDHHC5	zinc finger, DHHC-type containing 5	2.10	0.57	−1.11	0.18
6520	SLC3A2	solute carrier family 3 (amino acid transporter heavy chain), member 2	2.10	−0.83	0.35	−0.52
728591	CCDC169	coiled-coil domain containing 169	2.10	0.35	−1.49	−0.25
7415	VCP	valosin containing protein	2.10	−0.60	−0.61	0.52
130827	TMEM182	transmembrane protein 182	2.09	0.93	−1.07	0.22
9620	CELSR1	cadherin, EGF LAG seven-pass G-type receptor 1	2.09	−0.77	−0.90	−0.16
55335	NIPSNAP3B	nipsnap homolog 3B (*C. elegans*)	2.09	0.69	0.11	−1.05
84988	PPP1R16A	protein phosphatase 1, regulatory subunit 16A	2.08	−0.45	−0.84	0.96
100192378	ZFHX4-AS1	ZFHX4 antisense RNA1	2.08	−2.06	−0.64	−0.08
442524	DPY19L2P3	DPY19L2 pseudogene 3	2.08	−1.30	−0.58	−1.03
51661	FKBP7	FK506 binding protein 7	2.08	−0.88	−0.66	0.68
84922	FIZ1	FLT3-interacting zinc finger 1	2.08	−0.46	0.44	−0.63
84954	MPND	MPN domain containing	2.08	−0.90	−1.51	0.67
245972	ATP6V0D2	ATPase, H+ transporting, lysosomal 38 kDa, V0 subunit d2	2.08	−1.56	−0.90	−1.17

TABLE 2-continued

4316	MMP7	matrix metallopeptidase 7 (matrilysin, uterine)	2.08	0.13	−0.58	−0.85
55157	DARS2	aspartyl-tRNA synthetase 2, mitochondrial	2.08	−0.09	−0.44	−0.11
7466	WFS1	Wolfram syndrome 1 (wolframin)	2.08	−0.39	−1.04	−1.00
79365	BHLHE41	basic helix-loop-helix family, member e41	2.08	−0.44	−0.14	−1.16
10066	SCAMP2	secretory carrier membrane protein 2	2.08	0.95	−0.99	−0.95
203068	TUBB	tubulin, beta class I	2.08	0.35	−0.93	0.23
5780	PTPN9	protein tyrosine phosphatase, non-receptor type 9	2.07	−0.81	−1.50	−2.22
285627	LOC285627	uncharacterized LOC285627	2.07	−0.60	−1.20	−1.77
2058	EPRS	glutamyl-prolyl-tRNA synthetase	2.07	1.25	−0.56	−0.87
1737	DLAT	dihydrolipoamide S-acetyltransferase	2.06	0.55	−0.03	−0.10
22924	MAPRE3	microtubule-associated protein, RP/EB family, member 3	2.06	−1.75	−1.32	1.17
6005	RHAG	Rh-associated glycoprotein	2.06	0.29	−0.86	0.24
5286	PIK3C2A	phosphatidylinositol-4-phosphate 3-kinase, catalytic subunit type 2 alpha	2.06	0.32	−0.71	−1.15
11226	GALNT6	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 6 (GalNAc-T6)	2.06	−0.01	−0.06	−1.72
2762	GMDS	GDP-mannose 4,6-dehydratase	2.06	−0.47	−0.69	0.57
8908	GYG2	glycogenin 2	2.06	−1.16	−0.54	−0.28
10693	CCT6B	chaperonin containing TCP1, subunit 6B (zeta 2)	2.06	−0.80	0.01	−0.01
199953	TMEM201	transmembrane protein 201	2.06	0.96	−0.49	−0.44
2760	GM2A	GM2 ganglioside activator	2.06	−0.83	−2.47	−0.62
8295	TRRAP	transformation/transcription domain-associated protein	2.06	−0.95	0.47	−0.18
1822	ATN1	atrophin 1	2.06	0.34	−1.85	−0.79
55328	RNLS	renalase, FAD-dependent amine oxidase	2.06	−1.82	−1.29	−1.06
2069	EREG	epiregulin	2.05	0.33	−1.08	−1.00
4329	ALDH6A1	aldehyde dehydrogenase 6 family, member A1	2.05	−0.73	−1.24	0.51

TABLE 2-continued

537	ATP6AP1	ATPase, H+ transporting, lysosomal accessory protein 1	2.05	−0.44	−0.63	0.30
64764	CREB3L2	cAMP responsive element binding protein 3-like 2	2.05	0.14	−0.79	−0.67
811	CALR	calreticulin	2.05	−0.14	−0.89	0.33
9779	TBC1D5	TBC1 domain family, member 5	2.05	−1.68	−2.31	−1.07
114815	SORCS1	sortilin-related VPS10 domain containing receptor 1	2.05	0.76	−1.44	0.08
29927	SEC61A1	Sec61 alpha 1 subunit (*S. cerevisiae*)	2.05	0.85	−0.38	−0.14
6007	RHD	Rh blood group, D antigen	2.05	−0.65	−0.49	0.05
5192	PEX10	peroxisomal biogenesis factor 10	2.05	0.46	−0.02	0.03
125875	CLDND2	claudin domain containing 2	2.04	−0.14	−0.57	−1.20
10882	C1QL1	complement component 1, q subcomponent-like 1	2.04	−1.07	−0.41	0.12
192683	SCAMP5	secretory carrier membrane protein 5	2.04	−1.38	−0.77	−0.67
8028	MLLT10	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, *Drosophila*); translocated to, 10	2.04	−0.77	−0.35	−0.59
150368	FAM109B	family with sequence similarity 109, member B	2.04	−2.05	−0.51	−0.22
84206	MEX3B	mex-3 RNA binding family member B	2.04	0.32	−0.13	0.08
101929288	LOC101929288	uncharacterized LOC101929288	2.04	1.28	−1.48	−0.72
826	CAPNS1	calpain, small subunit 1	2.04	0.59	−1.22	−0.28
83440	ADPGK	ADP-dependent glucokinase	2.04	−0.02	−0.60	−0.27
1128	CHRM1	cholinergic receptor, muscarinic 1	2.03	−1.51	−0.76	−0.39
160287	LDHAL6A	lactate dehydrogenase A-like 6A	2.03	−2.65	−1.74	0.06
412	STS	steroid sulfatase (microsomal), isozyme S	2.03	−1.76	−1.65	−0.18
64215	DNAJC1	DnaJ (Hsp40) homolog, subfamily C, member 1	2.03	1.51	−1.51	0.09
7343	UBTF	upstream binding transcription factor, RNA polymerase I	2.03	−0.53	−0.11	−1.28

TABLE 2-continued

25840	METTL7A	methyltransferase like 7A	2.03	−0.61	−2.47	−0.33
55315	SLC29A3	solute carrier family 29 (equilibrative nucleoside transporter), member 3	2.03	−0.28	−1.38	−0.93
100507513	LOC100507513	uncharacterized LOC100507513	2.03	−2.70	−0.19	−0.63
55704	CCDC88A	coiled-coil domain containing 88A	2.03	0.69	−1.77	−0.57
57604	KIAA1456	KIAA1456	2.03	−0.70	−0.30	−0.47
10449	ACAA2	acetyl-CoA acyltransferase 2	2.03	−1.02	0.19	−0.82
1727	CYB5R3	cytochrome b5 reductase 3	2.03	−0.54	−2.22	−0.12
9569	GTF2IRD1	GTF2I repeat domain containing 1	2.03	0.34	−1.07	−0.12
10009	ZBTB33	zinc finger and BTB domain containing 33	2.02	0.14	−0.17	−0.80
5188	PET112	PET112 homolog (yeast)	2.02	0.13	0.24	−0.42
2132	EXT2	exostosin glycosyltransferase 2	2.02	−0.14	−0.75	−0.49
2239	GPC4	glypican 4	2.02	−0.72	−2.04	−0.62
56927	GPR108	G protein-coupled receptor 108	2.02	−1.22	−0.51	0.22
2950	GSTP1	glutathione S-transferase pi 1	2.02	0.65	−1.37	−0.42
342538	NACA2	nascent polypeptide-associated complex alpha subunit 2	2.02	−0.31	−0.61	−0.70
55218	EXD2	exonuclease 3'-5' domain containing 2	2.02	−0.54	−0.04	−0.98
151827	LRRC34	leucine rich repeat containing 34	2.01	0.17	−1.19	0.03
64689	GORASP1	golgi reassembly stacking protein 1, 65 kDa	2.01	0.31	−0.64	−0.05
10324	KLHL41	ketch-like family member 41	2.01	−1.94	−0.23	−0.23
1314	COPA	coatomer protein complex, subunit alpha	2.01	0.86	−0.79	−0.71
54928	IMPAD1	inositol monophosphatase domain containing 1	2.01	−0.51	−0.54	−0.27
8971	H1FX	H1 histone family, member X	2.01	0.81	−0.77	0.07
79832	QSER1	glutamine and serine rich 1	2.01	0.76	−2.38	−0.17
10150	MBNL2	muscleblind-like splicing regulator 2	2.00	0.94	−0.70	−0.95
8744	TNFSF9	tumor necrosis factor (ligand) superfamily, member 9	2.00	−0.11	−0.84	−0.48
23287	AGTPBP1	ATP/GTP binding protein 1	−2.00	−1.57	0.97	1.22
606553	C8orf49	chromosome 8 open reading frame 49	−2.00	2.76	0.90	0.66

TABLE 2-continued

103	ADAR	adenosine deaminase, RNA-specific	−2.01	−0.46	0.24	0.27
55509	BATF3	basic leucine zipper transcription factor, ATF-like 3	−2.01	2.57	−0.14	−0.02
729614	FLJ37453	uncharacterized LOC729614	−2.01	−0.39	1.58	0.81
9241	NOG	noggin	−2.01	0.41	2.02	−0.87
26118	WSB1	WD repeat and SOCS box containing 1	−2.01	1.08	0.29	0.60
64400	AKTIP	AKT interacting protein	−2.01	−0.63	1.59	−0.03
283237	TTC9C	tetratricopeptide repeat domain 9C	−2.01	2.06	1.25	−0.54
51155	HN1	hematological and neurological expressed 1	−2.01	−0.85	0.39	0.68
18	ABAT	4-aminobutyrate aminotransferase	−2.01	−1.10	0.52	0.31
22990	PCNX	pecanex homolog (*Drosophila*)	−2.01	−1.17	0.95	1.00
23347	SMCHD1	structural maintenance of chromosomes flexible hinge domain containing 1	−2.01	−1.02	0.76	−0.33
83988	NCALD	neurocalcin delta	−2.01	1.58	0.85	−0.21
3428	IFI16	interferon, gamma-inducible protein 16	−2.02	−0.62	0.35	−0.23
3700	ITIH4	inter-alpha-trypsin inhibitor heavy chain family, member 4	−2.02	−2.31	1.74	0.75
64859	NABP1	nucleic acid binding protein 1	−2.02	0.63	−0.50	1.06
55192	DNAJC17	DnaJ (Hsp40) homolog, subfamily C, member 17	−2.02	0.76	2.14	−0.39
101928869	LOC101928869	uncharacterized LOC101928869	−2.02	−0.94	0.98	−0.04
10513	APPBP2	amyloid beta precursor protein (cytoplasmic tail) binding protein 2	−2.02	0.18	1.66	0.01
11009	IL24	interleukin 24	−2.02	1.97	0.89	−1.30
169355	IDO2	indoleamine 2,3-dioxygenase 2	−2.02	1.52	0.85	2.06
10109	ARPC2	actin related protein 2/3 complex, subunit 2, 34 kDa	−2.02	0.24	0.98	−1.80
9903	KLHL21	kelch-like family member 21	−2.02	−1.20	1.23	0.43
23150	FRMD4B	FERM domain containing 4B	−2.03	1.12	0.47	0.58
10865	ARID5A	AT rich interactive domain 5A (MRF1-like)	−2.03	0.52	1.51	1.21

TABLE 2-continued

5165	PDK3	pyruvate dehydrogenase kinase, isozyme 3	−2.03	−0.54	0.91	−0.02
57403	RAB22A	RAB22A, member RAS oncogene family	−2.03	−0.08	2.12	−0.13
22900	CARD8	caspase recruitment domain family, member 8	−2.03	0.52	0.73	−0.41
80345	ZSCAN16	zinc finger and SCAN domain containing 16	−2.03	0.80	0.98	0.44
10964	IFI44L	interferon-induced protein 44-like	−2.03	−0.11	1.45	−1.10
27040	LAT	linker for activation of T cells	−2.03	0.98	2.49	−0.63
91010	FMNL3	formin-like 3	−2.03	1.02	1.86	−0.53
29065	ASAP1-IT1	ASAP1 intronic transcript 1 (non-protein coding)	−2.04	−0.30	−0.18	0.47
84078	KBTBD7	kelch repeat and BTB (POZ) domain containing 7	−2.04	−1.19	0.90	0.45
101927910	LOC101927910	keratin-associated protein 5-5-like	−2.04	−0.31	2.24	0.32
51380	CSAD	cysteine sulfinic acid decarboxylase	−2.04	−0.09	−0.06	0.73
10289	EIF1B	eukaryotic translation initiation factor 1B	−2.04	−0.24	0.83	0.31
10296	MAEA	macrophage erythroblast attacher	−2.04	−0.68	0.90	−0.33
114224	PRO2852	uncharacterized protein PRO2852	−2.04	0.11	−0.51	1.25
2153	F5	coagulation factor V (proaccelerin, labile factor)	−2.04	−1.17	0.70	0.31
55825	PECR	peroxisomal trans-2-enoyl-CoA reductase	−2.04	−0.87	0.84	0.04
6503	SLA	Src-like-adaptor	−2.04	−0.29	1.61	−0.56
7913	DEK	DEK oncogene	−2.04	1.72	0.60	0.74
30834	ZNRD1	zinc ribbon domain containing 1	−2.04	−0.10	2.21	−0.49
26999	CYFIP2	cytoplasmic FMR1 interacting protein 2	−2.05	−1.41	2.03	−0.12
286437	LOC286437	uncharacterized LOC286437	−2.05	−1.23	1.77	0.04
4277	MICB	MHC class I polypeptide-related sequence B	−2.05	0.44	0.88	−1.09
5698	PSMB9	proteasome (prosome, macropain) subunit, beta type, 9	−2.05	0.22	0.77	−0.85
4318	MMP9	matrix metallopeptidase 9 (gelatinase B, 92 kDa gelatinase, 92 kDa type IV collagenase)	−2.05	0.13	0.27	0.77

TABLE 2-continued

10616	RBCK1	RanBP-type and C3HC4-type zinc finger containing 1	−2.06	1.31	−0.02	1.30
23012	STK38L	serine/threonine kinase 38 like	−2.06	−0.51	0.07	0.24
100129361	LOC100129361	chromosome X open reading frame 69-like	−2.06	0.66	1.07	0.65
10742	RAI2	retinoic acid induced 2	−2.06	−1.54	0.78	0.22
196264	MPZL3	myelin protein zero-like 3	−2.06	−0.75	1.46	−0.03
27197	GPR82	G protein-coupled receptor 82	−2.06	1.47	−0.05	−0.56
7529	YWHAB	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, beta polypeptide	−2.06	0.12	1.88	−1.43
94235	GNG8	guanine nucleotide binding protein (G protein), gamma 8	−2.06	0.86	1.60	0.38
352961	HCG26	HLA complex group 26 (non-protein coding)	−2.06	0.17	1.72	−1.13
49856	WRAP73	WD repeat containing, antisense to TP73	−2.06	1.00	0.94	−0.34
9448	MAP4K4	mitogen-activated protein kinase kinase kinase kinase 4	−2.06	−0.65	0.97	0.77
9525	VPS4B	vacuolar protein sorting 4 homolog B (*S. cerevisiae*)	−2.06	−0.29	0.95	0.05
100505576	LINC00672	long intergenic non-protein coding RNA 672	−2.06	−0.31	0.81	−1.00
151556	GPR155	G protein-coupled receptor 155	−2.06	−0.84	1.11	−0.76
284613	CYB561D1	cytochrome b561 family, member D1	−2.06	−0.29	1.00	−0.95
286223	C9orf47	chromosome 9 open reading frame 47	−2.06	−0.06	−0.46	−0.10
57061	HYMAI	hydatidiform mole associated and imprinted (non-protein coding)	−2.06	−0.54	−1.51	0.71
9520	NPEPPS	aminopeptidase puromycin sensitive	−2.07	−0.18	0.60	0.67
202299	C5orf27	chromosome 5 open reading frame 27	−2.07	0.22	0.55	1.88
2015	EMR1	egf-like module containing, mucin-like, hormone receptor-like 1	−2.07	0.71	−0.20	1.31
57763	ANKRA2	ankyrin repeat, family A (RFXANK-like), 2	−2.07	1.06	1.86	0.48
54778	RNF111	ring finger protein 111	−2.07	0.08	0.96	−0.42

TABLE 2-continued

762	CA4	carbonic anhydrase IV	−2.07	−1.35	0.56	0.60
192668	CYS1	cystin 1	−2.08	0.29	0.23	1.30
24146	CLDN15	claudin 15	−2.08	0.77	1.30	−1.01
54843	SYTL2	synaptotagmin-like 2	−2.08	1.28	1.88	0.17
55374	TMCO6	transmembrane and coiled-coil domains 6	−2.08	0.23	0.72	0.89
79603	CERS4	ceramide synthase 4	−2.08	−0.79	1.36	0.39
3577	CXCR1	chemokine (C—X—C motif) receptor 1	−2.08	−0.87	0.16	0.02
10385	BTN2A2	butyrophilin, subfamily 2, member A2	−2.08	2.47	0.07	0.09
79792	GSDMD	gasdermin D	−2.08	1.86	−0.51	1.05
84674	CARD6	caspase recruitment domain family, member 6	−2.09	−0.39	0.54	0.60
51131	PHF11	PHD finger protein 11	−2.09	−0.26	1.37	−0.66
5966	REL	v-rel avian reticuloendotheliosis viral oncogene homolog	−2.09	1.12	1.40	1.10
9733	SART3	squamous cell carcinoma antigen recognized by T cells 3	−2.09	2.19	0.91	−1.56
10328	EMC8	ER membrane protein complex subunit 8	−2.09	0.55	1.57	0.44
255231	MCOLN2	mucolipin 2	−2.09	0.84	0.52	−1.56
25801	GCA	grancalcin, EF-hand calcium binding protein	−2.09	0.50	−0.38	−0.16
6352	CCL5	chemokine (C-C motif) ligand 5	−2.09	0.66	2.04	−0.99
54811	ZNF562	zinc finger protein 562	−2.09	0.02	0.03	−0.48
59348	ZNF350	zinc finger protein 350	−2.09	−0.38	1.17	0.72
9967	THRAP3	thyroid hormone receptor associated protein 3	−2.09	0.61	0.79	0.50
2533	FYB	FYN binding protein	−2.10	−0.93	1.62	−0.12
28985	MCTS1	malignant T cell amplified sequence 1	−2.10	1.15	1.28	0.01
55234	SMU1	smu-1 suppressor of mec-8 and unc-52 homolog (*C. elegans*)	−2.10	−0.47	1.24	0.87
1301	COL11A1	collagen, type XI, alpha 1	−2.10	1.40	−0.09	0.56
84803	AGPAT9	1-acylglycerol-3-phosphate O-acyltransferase 9	−2.10	0.07	0.36	0.57
100506779	BZRAP1-AS1	BZRAP1 antisense RNA 1	−2.10	−0.30	1.43	−0.34
197135	PATL2	protein associated with topoisomerase II homolog 2 (yeast)	−2.10	−0.32	1.45	−0.85
3614	IMPDH1	IMP (inosine 5'-monophosphate) dehydrogenase 1	−2.10	−0.75	−0.34	0.30
80781	COL18A1	collagen, type XVIII, alpha 1	−2.10	0.13	0.76	0.35

TABLE 2-continued

5586	PKN2	protein kinase N2	−2.11	0.30	0.71	0.00
79415	C17orf62	chromosome 17 open reading frame 62	−2.11	0.76	−0.67	0.50
8893	EIF2B5	eukaryotic translation initiation factor 2B, subunit 5 epsilon, 82 kDa	−2.11	1.21	1.89	0.97
79736	TEFM	transcription elongation factor, mitochondrial	−2.11	1.33	0.37	0.40
5770	PTPN1	protein tyrosine phosphatase, non-receptor type 1	−2.11	2.04	−0.16	0.32
9360	PPIG	peptidylprolyl isomerase G (cyclophilin G)	−2.11	0.97	1.56	−0.15
29940	DSE	dermatan sulfate epimerase	−2.11	0.87	0.10	0.80
7150	TOP1	topoisomerase (DNA) I	−2.11	2.04	−0.62	0.33
84964	ALKBH6	alkB, alkylation repair homolog 6 (*E. coli*)	−2.11	1.92	−0.46	1.22
10614	HEXIM1	hexamethylene bis-acetamide inducible 1	−2.11	0.25	1.20	0.02
147923	ZNF420	zinc finger protein 420	−2.12	0.88	1.70	0.00
284029	LINC00324	long intergenic non-protein coding RNA 324	−2.12	−1.08	1.66	−0.49
54952	TRNAU1AP	tRNA selenocysteine 1 associated protein 1	−2.12	−0.15	1.42	0.05
57476	GRAMD1B	GRAM domain containing 1B	−2.12	−0.38	0.44	−0.25
8745	ADAM23	ADAM metallopeptidase domain 23	−2.12	2.31	0.05	0.81
22928	SEPHS2	selenophosphate synthetase 2	−2.12	0.67	0.44	0.29
25880	TMEM186	transmembrane protein 186	−2.12	1.09	1.51	−0.68
28638	TRBC2	T cell receptor beta constant 2	−2.12	−0.78	2.11	−1.29
29933	GPR132	G protein-coupled receptor 132	−2.12	0.04	1.76	0.74
30009	TBX21	T-box 21	−2.12	0.92	0.97	−1.29
3554	IL1R1	interleukin 1 receptor, type I	−2.12	0.44	0.16	1.54
8821	INPP4B	inositol polyphosphate-4-phosphatase, type II, 105 kDa	−2.12	1.75	1.83	0.31
10943	MSL3	male-specific lethal 3 homolog (*Drosophila*)	−2.12	−0.77	1.06	0.45
57724	EPG5	ectopic P-granules autophagy protein 5 homolog (*C. elegans*)	−2.12	−0.14	0.63	−0.20
100506282	LOC100506282	uncharacterized LOC100506282	−2.13	1.67	0.76	1.07
147699	PPM1N	protein phosphatase, Mg2+/Mn2+ dependent, 1 N (putative)	−2.13	0.16	0.53	−0.19

TABLE 2-continued

3002	GZMB	granzyme B (granzyme 2, cytotoxic T-lymphocyte-associated serine esterase 1)	−2.13	0.76	0.87	−1.46
389320	C5orf48	chromosome 5 open reading frame 48	−2.13	0.37	1.37	1.13
9914	ATP2C2	ATPase, Ca++ transporting, type 2C, member 2	−2.13	0.23	1.12	0.78
10804	GJB6	gap junction protein, beta 6, 30 kDa	−2.13	−1.12	1.65	0.81
51439	FAM8A1	family with sequence similarity 8, member A1	−2.13	−0.89	1.07	0.42
814	CAMK4	calcium/calmodulin-dependent protein kinase IV	−2.13	−0.47	2.19	−1.77
5272	SERPINB9	serpin peptidase inhibitor, clade B (ovalbumin), member 9	−2.13	−0.34	0.40	−0.98
8428	STK24	serine/threonine kinase 24	−2.13	−1.09	1.59	−0.29
23048	FNBP1	formin binding protein 1	−2.14	1.36	0.52	0.23
344558	SH3RF3	SH3 domain containing ring finger 3	−2.14	−0.73	1.32	−0.41
79078	C1orf50	chromosome 1 open reading frame 50	−2.14	0.08	1.02	−1.09
81606	LBH	limb bud and heart development	−2.14	0.57	2.63	−1.26
64377	CHST8	carbohydrate (N-acetylgalactosamine 4-0) sulfotransferase 8	−2.14	0.58	−0.51	0.79
57501	KIAA1257	KIAA1257	−2.14	−0.10	0.47	0.78
5991	RFX3	regulatory factor X, 3 (influences HLA class II expression)	−2.14	1.47	1.11	2.05
90075	ZNF30	zinc finger protein 30	−2.14	1.82	1.22	0.52
375341	C3orf62	chromosome 3 open reading frame 62	−2.14	−0.26	0.66	0.88
100130548	LOC100130548	uncharacterized LOC100130548	−2.15	−0.64	1.52	0.77
114786	XKR4	XK, Kell blood group complex subunit-related family, member 4	−2.15	0.58	−0.23	0.36
150084	IGSF5	immunoglobulin superfamily, member 5	−2.15	0.75	−0.16	0.36
55012	PPP2R3C	protein phosphatase 2, regulatory subunit B", gamma	−2.15	−0.91	0.93	0.14
147525	LINC00526	long intergenic non-protein coding RNA 526	−2.15	−0.23	1.84	−0.31

TABLE 2-continued

54557	SGTB	small glutamine-rich tetratricopeptide repeat (TPR)-containing, beta	−2.15	−0.86	0.84	0.17
56267	CCBL2	cysteine conjugate-beta lyase 2	−2.15	0.21	1.69	0.59
51176	LEF1	lymphoid enhancer-binding factor 1	−2.15	−1.11	2.08	−1.07
10468	FST	follistatin	−2.15	−0.19	2.02	0.77
23258	DENND5A	DENN/MADD domain containing 5A	−2.15	−0.31	0.08	0.68
90768	MGC45800	uncharacterized LOC90768	−2.15	−0.26	1.01	0.45
134957	STXBP5	syntaxin binding protein 5 (tomosyn)	−2.16	0.06	0.64	0.98
80342	TRAF3IP3	TRAF3 interacting protein 3	−2.16	−0.07	1.61	−0.81
91351	DDX60L	DEAD (Asp-Glu-Ala-Asp) box polypeptide 60-like	−2.16	−0.99	0.41	0.33
29916	SNX11	sorting nexin 11	−2.16	−0.18	−0.11	0.79
8519	IFITM1	interferon induced transmembrane protein 1	−2.16	−0.67	1.50	−1.06
2113	ETS1	v-ets avian erythroblastosis virus E26 oncogene homolog 1	−2.16	−0.80	1.75	−0.93
55770	EXOC2	exocyst complex component 2	−2.16	1.87	1.84	−0.31
91833	WDR20	WD repeat domain 20	−2.16	−0.21	1.84	0.30
117177	RAB3IP	RAB3A interacting protein	−2.16	−0.62	0.78	0.40
546	ATRX	alpha thalassemia/mental retardation syndrome X-linked	−2.16	0.55	0.60	0.60
4253	CTAGE5	CTAGE family, member 5	−2.17	0.57	0.77	−0.38
23214	XPO6	exportin 6	−2.17	−1.37	1.00	0.31
53347	UBASH3A	ubiquitin associated and SH3 domain containing A	−2.17	−1.35	2.45	0.00
56888	KCMF1	potassium channel modulatory factor 1	−2.17	0.00	0.23	−1.20
777	CACNA1E	calcium channel, voltage-dependent, R type, alpha 1E subunit	−2.17	−0.20	0.28	2.32
100216545	KMT2E-AS1	KMT2E antisense RNA1 (head to head)	−2.17	0.71	2.04	0.78
8879	SGPL1	sphingosine-1-phosphate lyase 1	−2.17	1.73	−0.25	0.87
9759	HDAC4	histone deacetylase 4	−2.17	−2.02	1.08	0.56
26578	OSTF1	osteoclast stimulating factor 1	−2.18	−0.80	0.56	0.25

TABLE 2-continued

4050	LTB	lymphotoxin beta (TNF superfamily, member 3)	−2.18	−1.06	1.52	−1.14
4236	MFAP1	microfibrillar-associated protein 1	−2.18	0.60	0.85	−1.82
54491	FAM105A	family with sequence similarity 105, member A	−2.18	−0.93	1.49	−0.02
55847	CISD1	CDGSH iron sulfur domain 1	−2.18	0.64	1.22	1.28
100132707	PAXIP1-AS2	PAXIP1 antisense RNA 2	−2.19	0.24	0.73	−0.19
55884	WSB2	WD repeat and SOCS box containing 2	−2.19	0.99	−0.17	0.61
83607	AMMECR1L	AMMECR1-like	−2.19	1.07	1.60	−0.11
9252	RPS6KA5	ribosomal protein S6 kinase, 90 kDa, polypeptide 5	−2.19	−0.18	0.95	−0.58
55119	PRPF38B	pre-mRNA processing factor 38B	−2.19	1.71	1.08	0.42
57520	HECW2	HECT, C2 and WW domain containing E3 ubiquitin protein ligase 2	−2.19	0.30	0.43	1.06
79818	ZNF552	zinc finger protein 552	−2.19	−1.20	1.23	−0.01
8320	EOMES	eomesodermin	−2.19	0.15	1.44	−0.76
2792	GNGT1	guanine nucleotide binding protein (G protein), gamma transducing activity polypeptide 1	−2.19	1.41	−0.14	0.28
54910	SEMA4C	sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4C	−2.19	1.21	0.99	0.63
55114	ARHGAP17	Rho GTPase activating protein 17	−2.19	0.18	−0.27	−0.27
56253	CRTAM	cytotoxic and regulatory T cell molecule	−2.19	0.83	1.31	0.15
65082	VPS33A	vacuolar protein sorting 33 homolog A (*S. cerevisiae*)	−2.19	−0.65	1.18	−0.57
84719	LINC00260	long intergenic non-protein coding RNA 260	−2.20	1.45	1.51	−0.68
253558	LCLAT1	lysocardiolipin acyltransferase 1	−2.20	0.62	0.95	1.24
6777	STAT5B	signal transducer and activator of transcription 5B	−2.20	−0.54	1.15	0.74
80025	PANK2	pantothenate kinase 2	−2.20	−0.45	0.85	−0.61
84662	GLIS2	GLIS family zinc finger 2	−2.20	0.95	0.42	0.03

TABLE 2-continued

89890	KBTBD6	kelch repeat and BTB (POZ) domain containing 6	−2.20	0.03	1.98	1.00
10390	CEPT1	choline/ethanolamine phosphotransferase 1	−2.20	0.35	1.23	0.57
2841	GPR18	G protein-coupled receptor 18	−2.20	1.15	2.42	−1.03
3904	LAIR2	leukocyte-associated immunoglobulin-like receptor 2	−2.20	0.84	0.21	−0.44
140460	ASB7	ankyrin repeat and SOCS box containing 7	−2.20	0.07	1.03	1.30
9605	VPS9D1	VPS9 domain containing 1	−2.20	−0.23	0.95	0.68
283349	RASSF3	Ras association (RalGDS/AF-6) domain family member 3	−2.21	−0.83	0.96	0.02
51246	SHISA5	shisa family member 5	−2.21	−1.42	0.99	0.13
148268	ZNF570	zinc finger protein 570	−2.21	1.26	2.25	0.36
26589	MRPL46	mitochondrial ribosomal protein L46	−2.21	1.15	1.68	0.71
7049	TGFBR3	transforming growth factor, beta receptor III	−2.21	1.01	2.02	−0.17
2791	GNG11	guanine nucleotide binding protein (G protein), gamma 11	−2.21	−0.39	−0.02	0.39
51455	REV1	REV1, polymerase (DNA directed)	−2.21	1.24	1.77	−0.17
1178	CLC	Charcot-Leyden crystal galectin	−2.22	0.06	0.48	0.09
79153	GDPD3	glycerophosphodiester phosphodiesterase domain containing 3	−2.22	−0.34	0.91	0.18
101928524	LOC101928524	uncharacterized LOC101928524	−2.22	−0.67	0.78	0.40
11064	CNTRL	centriolin	−2.22	0.66	−0.56	1.20
23429	RYBP	RING1 and YY1 binding protein	−2.22	1.35	0.64	0.34
5170	PDPK1	3-phosphoinositide dependent protein kinase-1	−2.22	−0.83	0.31	0.56
10677	AVIL	advillin	−2.23	−0.85	0.84	−0.08
3772	KCNJ15	potassium inwardly-rectifying channel, subfamily J, member 15	−2.23	−1.08	0.27	0.28
128061	C1orf131	chromosome 1 open reading frame 131	−2.23	0.81	1.10	−0.79
50856	CLEC4A	C-type lectin domain family 4, member A	−2.23	−0.08	−0.28	0.35
6198	RPS6KB1	ribosomal protein S6 kinase, 70 kDa, polypeptide 1	−2.23	2.01	1.73	0.04

TABLE 2-continued

101927588	LOC101927588	uncharacterized LOC101927588	−2.24	−0.02	0.56	1.52
2000	ELF4	E74-like factor 4 (ets domain transcription factor)	−2.24	0.13	0.14	0.01
493753	COA5	cytochrome c oxidase assembly factor 5	−2.24	0.79	1.30	0.77
23081	KDM4C	lysine (K)-specific demethylase 4C	−2.24	1.09	0.42	−1.06
4773	NFATC2	nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 2	−2.24	0.57	1.16	−0.30
10178	TENM1	teneurin transmembrane protein 1	−2.25	−0.87	0.62	0.49
4974	OMG	oligodendrocyte myelin glycoprotein	−2.25	−1.43	0.63	1.07
83860	TAF3	TAF3 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 140 kDa	−2.25	0.03	1.69	1.03
91612	CHURC1	churchill domain containing 1	−2.25	−1.11	1.06	0.63
2178	FANCE	Fanconi anemia, complementation group E	−2.26	−0.72	0.82	0.67
55303	GIMAP4	GTPase, IMAP family member 4	−2.26	−0.40	1.33	−0.81
221002	RASGEF1A	RasGEF domain family, member 1A	−2.26	−0.14	0.69	0.68
3930	LBR	lamin B receptor	−2.26	0.12	0.71	0.54
55471	NDUFAF7	NADH dehydrogenase (ubiquinone) complex I, assembly factor 7	−2.26	1.20	1.05	0.71
9354	UBE4A	ubiquitination factor E4A	−2.26	0.81	0.66	0.18
83700	JAM3	junctional adhesion molecule 3	−2.26	−0.33	1.46	1.10
9140	ATG12	autophagy related 12	−2.26	1.06	0.85	0.87
23526	HMHA1	histocompatibility (minor) HA-1	−2.27	0.14	1.43	−0.76
23590	PDSS1	prenyl (decaprenyl) diphosphate synthase, subunit 1	−2.27	0.01	0.69	1.26
9270	ITGB1BP1	integrin beta 1 binding protein 1	−2.27	1.68	0.62	0.35
10627	MYL12A	myosin, light chain 12A, regulatory, non-sarcomeric	−2.27	−0.87	1.16	0.00
26048	ZNF500	zinc finger protein 500	−2.27	3.47	1.42	0.12
917	CD3G	CD3g molecule, gamma (CD3-TCR complex)	−2.27	−0.29	2.30	−1.44
94039	ZNF101	zinc finger protein 101	−2.27	−0.72	1.69	−0.18

TABLE 2-continued

4215	MAP3K3	mitogen-activated protein kinase kinase kinase 3	−2.28	−0.81	1.06	0.08
10663	CXCR6	chemokine (C—X—C motif) receptor 6	−2.28	0.37	1.78	−0.60
10308	ZNF267	zinc finger protein 267	−2.28	0.38	0.74	0.86
8527	DGKD	diacylglycerol kinase, delta 130 kDa	−2.28	0.75	1.41	0.23
926	CD8B	CD8b molecule	−2.28	−0.83	2.69	−0.16
9619	ABCG1	ATP-binding cassette, sub-family G (WHITE), member 1	−2.28	0.94	1.01	0.91
5998	RGS3	regulator of G-protein signaling 3	−2.29	−0.40	0.51	1.00
132625	ZFP42	ZFP42 zinc finger protein	−2.29	0.10	1.45	0.56
88455	ANKRD13A	ankyrin repeat domain 13A	−2.30	−0.39	0.13	0.41
3604	TNFRSF9	tumor necrosis factor receptor superfamily, member 9	−2.30	−0.59	0.42	0.11
100507398	INTS6-AS1	INTS6 antisense RNA 1	−2.30	1.02	1.07	1.97
58517	RBM25	RNA binding motif protein 25	−2.30	2.48	1.59	0.61
51192	CKLF	chemokine-like factor	−2.31	−0.45	0.59	0.36
2177	FANCD2	Fanconi anemia, complementation group D2	−2.31	1.14	1.23	1.11
57097	PARP11	poly (ADP-ribose) polymerase family, member 11	−2.31	−0.19	0.77	0.11
11214	AKAP13	A kinase (PRKA) anchor protein 13	−2.31	0.37	0.68	0.25
4600	MX2	myxovirus (influenza virus) resistance 2 (mouse)	−2.31	−1.58	0.05	0.01
84255	SLC37A3	solute carrier family 37, member 3	−2.31	−0.59	0.93	0.61
11216	AKAP10	A kinase (PRKA) anchor protein 10	−2.32	0.82	1.04	−0.62
162417	NAGS	N-acetylglutamate synthase	−2.32	0.09	1.46	0.28
101928617	LOC101928617	uncharacterized LOC101928617	−2.32	−0.30	0.64	−0.61
10617	STAMBP	STAM binding protein	−2.32	1.84	−0.17	1.19
1326	MAP3K8	mitogen-activated protein kinase kinase kinase 8	−2.32	0.72	0.63	0.15
23315	SLC9A8	solute carrier family 9, subfamily A (NHE8, cation proton antiporter 8), member 8	−2.32	−1.35	0.88	0.60
10791	VAMP5	vesicle-associated membrane protein 5	−2.32	−0.11	1.36	−0.88

TABLE 2-continued

8718	TNFRSF25	tumor necrosis factor receptor superfamily, member 25	−2.32	−0.24	3.91	−0.69
51571	FAM49B	family with sequence similarity 49, member B	−2.33	−0.68	0.75	0.20
283521	LINC00282	long intergenic non-protein coding RNA 282	−2.33	−2.30	1.78	0.05
51122	COMMD2	COMM domain containing 2	−2.33	−0.09	1.53	0.88
5372	PMM1	phosphomanno mutase 1	−2.33	0.16	1.25	0.70
9830	TRIM14	tripartite motif containing 14	−2.33	−0.29	1.44	−0.28
314	AOC2	amine oxidase, copper containing 2 (retina-specific)	−2.33	−0.52	0.23	0.02
51761	ATP8A2	ATPase, aminophospholipid transporter, class I, type 8A, member 2	−2.33	0.45	1.61	−1.13
493861	EID3	EP300 interacting inhibitor of differentiation 3	−2.34	0.84	1.87	0.88
6672	SP100	SP100 nuclear antigen	−2.34	−0.15	0.33	0.13
55578	SUPT20H	suppressor of Ty 20 homolog (*S. cerevisiae*)	−2.34	−0.88	2.05	−0.26
159	ADSS	adenylosuccinate synthase	−2.34	1.28	1.03	0.02
9683	N4BP1	NEDD4 binding protein 1	−2.34	−0.82	0.93	−0.13
26287	ANKRD2	ankyrin repeat domain 2 (stretch responsive muscle)	−2.35	0.96	−1.11	2.34
57147	SCYL3	SCY1-like 3 (*S. cerevisiae*)	−2.35	0.41	1.20	0.45
1808	DPYSL2	dihydropyrimidinase-like 2	−2.35	0.81	−0.69	0.07
23355	VPS8	vacuolar protein sorting 8 homolog (*S. cerevisiae*)	−2.35	−0.37	0.18	1.13
8115	TCL1A	T-cell leukemia/lymphoma 1A	−2.35	0.02	0.58	−1.16
94120	SYTL3	synaptotagmin-like 3	−2.35	0.66	1.11	−0.17
22950	SLC4A1AP	solute carrier family 4 (anion exchanger), member 1, adaptor protein	−2.35	−0.93	1.36	0.15
27342	RABGEF1	RAB guanine nucleotide exchange factor (GEF) 1	−2.35	−0.93	1.58	0.45
64926	RASAL3	RAS protein activator like 3	−2.35	0.01	0.96	0.27
100507331	ZSWIM8-AS1	ZSWIM8 antisense RNA 1	−2.36	0.57	1.26	1.67
4068	SH2D1A	SH2 domain containing 1A	−2.36	1.66	1.54	0.32
60481	ELOVL5	ELOVL fatty acid elongase 5	−2.36	1.02	0.79	−0.43
2634	GBP2	guanylate binding protein 2, interferon-inducible	−2.36	0.00	0.80	−0.31

TABLE 2-continued

55824	PAG1	phosphoprotein associated with glycosphingolipid microdomains 1	−2.36	−1.03	1.59	−0.87
79074	C2orf49	chromosome 2 open reading frame 49	−2.36	1.44	0.56	0.88
220930	ZEB1-AS1	ZEB1 antisense RNA 1	−2.36	1.06	0.36	1.60
64421	DCLRE1C	DNA cross-link repair 1C	−2.36	0.49	0.61	0.27
64121	RRAGC	Ras-related GTP binding C	−2.37	0.32	0.40	−0.50
137835	TMEM71	transmembrane protein 71	−2.37	−0.41	1.11	0.62
57674	RNF213	ring finger protein 213	−2.37	−0.91	0.53	0.09
728392	LOC728392	uncharacterized LOC728392	−2.37	−0.94	0.78	1.08
329	BIRC2	baculoviral IAP repeat containing 2	−2.38	1.72	1.94	0.71
55279	ZNF654	zinc finger protein 654	−2.38	0.07	1.10	0.14
7107	GPR137B	G protein-coupled receptor 137B	−2.38	0.57	0.21	−0.70
9416	DDX23	DEAD (Asp-Glu-Ala-Asp) box polypeptide 23	−2.38	0.21	0.21	0.77
137964	AGPAT6	1-acylglycerol-3-phosphate O-acyltransferase 6	−2.38	1.36	0.99	0.64
3431	SP110	SP110 nuclear body protein	−2.38	−0.53	0.24	−0.78
4140	MARK3	MAP/microtubule affinity-regulating kinase 3	−2.38	1.19	0.52	0.47
59269	HIVEP3	human immunodeficiency virus type I enhancer binding protein 3	−2.38	0.24	0.53	0.70
7846	TUBA1A	tubulin, alpha 1a	−2.38	0.54	0.04	0.66
100652740	C16orf98	chromosome 16 open reading frame 98	−2.38	0.57	1.13	0.08
23398	PPWD1	peptidylprolyl isomerase domain and WD repeat containing 1	−2.38	0.94	1.67	0.73
158747	MOSPD2	motile sperm domain containing 2	−2.39	−0.04	0.20	0.26
285512	FAM13A-AS1	FAM13A antisense RNA 1	−2.39	0.05	0.98	0.11
3937	LCP2	lymphocyte cytosolic protein 2 (SH2 domain containing leukocyte protein of 76 kDa)	−2.39	0.47	1.08	−0.27
730051	ZNF814	zinc finger protein 814	−2.39	0.33	1.83	0.68
9320	TRIP12	thyroid hormone receptor interactor 12	−2.39	1.30	0.94	−0.17
6932	TCF7	transcription factor 7 (T-cell specific, HMG-box)	−2.39	−0.88	2.43	−1.09
79722	ANKRD55	ankyrin repeat domain 55	−2.39	−0.59	1.57	−0.41

TABLE 2-continued

115362	GBP5	guanylate binding protein 5	−2.39	−0.13	0.78	−0.29
29909	GPR171	G protein-coupled receptor 171	−2.39	−0.05	2.07	−0.56
440503	PLIN5	perilipin 5	−2.40	−0.13	−0.04	0.83
80183	KIAA0226L	KIAA0226-like	−2.40	−0.11	−0.47	0.26
80709	AKNA	AT-hook transcription factor	−2.40	−0.40	1.34	−0.21
10562	OLFM4	olfactomedin 4	−2.40	−0.72	1.37	0.89
64780	MICAL1	microtubule associated monooxygenase, calponin and LIM domain containing 1	−2.41	0.90	−0.01	1.48
155038	GIMAP8	GTPase, IMAP family member 8	−2.41	−0.08	1.03	−1.06
1783	DYNC1LI2	dynein, cytoplasmic 1, light intermediate chain 2	−2.41	0.29	0.55	0.93
100287569	LINC00173	long intergenic non-protein coding RNA 173	−2.42	0.79	0.50	0.39
5696	PSMB8	proteasome (prosome, macropain) subunit, beta type, 8	−2.42	1.75	1.55	0.44
11066	SNRNP35	small nuclear ribonucleoprotein 35 kDa (U11/U12)	−2.42	−0.97	0.66	1.09
122553	TRAPPC6B	trafficking protein particle complex 6B	−2.42	1.80	0.59	0.36
50484	RRM2B	ribonucleotide reductase M2 B (TP53 inducible)	−2.43	0.68	0.40	0.71
9847	C2CD5	C2 calcium-dependent domain containing 5	−2.43	−0.31	1.91	0.18
129285	PPP1R21	protein phosphatase 1, regulatory subunit 21	−2.43	0.25	0.06	0.41
9794	MAML1	mastermind-like 1 (*Drosophila*)	−2.43	−0.49	1.65	−0.21
84309	NUDT16L1	nudix (nucleoside diphosphate linked moiety X)-type motif 16-like 1	−2.43	0.68	1.62	1.06
65258	MPPE1	metallophosphoesterase 1	−2.43	0.07	0.99	0.10
5562	PRKAA1	protein kinase, AMP-activated, alpha 1 catalytic subunit	−2.44	0.73	0.77	0.85
123036	TC2N	tandem C2 domains, nuclear	−2.44	−0.21	2.02	−1.10
84166	NLRC5	NLR family, CARD domain containing 5	−2.45	−0.28	1.58	0.03
253143	PRR14L	proline rich 14-like	−2.45	0.27	−0.17	0.16
1236	CCR7	chemokine (C-C motif) receptor 7	−2.45	0.54	2.19	−0.91

TABLE 2-continued

266747	RGL4	ral guanine nucleotide dissociation stimulator-like 4	−2.46	−1.20	1.65	0.35
25988	HINFP	histone H4 transcription factor	−2.46	1.72	0.72	−0.63
6515	SLC2A3	solute carrier family 2 (facilitated glucose transporter), member 3	−2.46	−0.20	0.92	0.47
90592	ZNF700	zinc finger protein 700	−2.46	−0.40	0.59	1.21
6867	TACC1	transforming, acidic coiled-coil containing protein 1	−2.47	0.01	1.16	0.49
23041	MON2	MON2 homolog (*S. cerevisiae*)	−2.47	0.67	1.20	0.77
100289230	LOC100289230	uncharacterized LOC100289230	−2.47	0.61	2.09	0.17
57169	ZNFX1	zinc finger, NFX1-type containing 1	−2.48	−0.54	0.80	0.09
1105	CHD1	chromodomain helicase DNA binding protein 1	−2.48	0.28	1.87	0.72
943	TNFRSF8	tumor necrosis factor receptor superfamily, member 8	−2.48	1.74	−0.67	0.47
3275	PRMT2	protein arginine methyltransferase 2	−2.48	−0.49	1.32	−0.31
8851	CDK5R1	cyclin-dependent kinase 5, regulatory subunit 1 (p35)	−2.49	−0.76	2.06	−0.36
168537	GIMAP7	GTPase, IMAP family member 7	−2.49	0.04	1.78	−1.22
256236	NAPSB	napsin B aspartic peptidase, pseudogene	−2.49	1.72	−0.85	0.59
26235	FBXL4	F-box and leucine-rich repeat protein 4	−2.50	1.20	−0.11	1.21
9363	RAB33A	RAB33A, member RAS oncogene family	−2.50	0.55	2.57	−0.44
729683	LOC729683	uncharacterized LOC729683	−2.50	0.55	1.35	−0.65
388969	C2orf68	chromosome 2 open reading frame 68	−2.51	0.77	1.38	−0.40
4818	NKG7	natural killer cell group 7 sequence	−2.51	0.44	1.69	−0.12
93953	ACRC	acidic repeat containing	−2.51	0.38	1.86	0.00
28982	FLVCR1	feline leukemia virus subgroup C cellular receptor 1	−2.51	1.33	0.57	0.26
84911	ZNF382	zinc finger protein 382	−2.52	1.69	1.32	0.47
66036	MTMR9	myotubularin related protein 9	−2.52	−0.10	1.66	−0.12
9750	FAM65B	family with sequence similarity 65, member B	−2.52	−0.37	1.14	−0.34
9938	ARHGAP25	Rho GTPase activating protein 25	−2.52	0.29	0.14	−0.26

TABLE 2-continued

120425	AMICA1	adhesion molecule, interacts with CXADR antigen 1	−2.52	−0.42	0.68	0.50
6840	SVIL	supervillin	−2.53	−0.64	0.50	0.29
26268	FBXO9	F-box protein 9	−2.53	0.69	1.35	0.19
55206	SBNO1	strawberry notch homolog 1 (*Drosophila*)	−2.53	−0.54	1.57	0.30
355	FAS	Fas cell surface death receptor	−2.54	0.43	0.39	0.75
50615	IL21R	interleukin 21 receptor	−2.54	0.35	1.97	−0.81
221178	SPATA13	spermatogenesis associated 13	−2.54	−2.61	1.22	0.40
11104	KATNA1	katanin p60 (ATPase containing) subunit A1	−2.54	0.20	2.21	0.15
1117	CHI3L2	chitinase 3-like 2	−2.54	0.52	1.23	−0.94
374969	CCDC23	coiled-coil domain containing 23	−2.54	−1.26	1.25	0.52
6285	S100B	S100 calcium binding protein B	−2.55	1.40	1.92	0.66
387357	THEMIS	thymocyte selection associated	−2.55	−0.15	1.81	−0.25
2960	GTF2E1	general transcription factor IIE, polypeptide 1, alpha 56 kDa	−2.56	0.13	0.92	0.46
100129550	LOC100129550	uncharacterized LOC100129550	−2.56	−0.15	0.93	0.40
54520	CCDC93	coiled-coil domain containing 93	−2.56	−1.12	2.30	0.56
10302	SNAPC5	small nuclear RNA activating complex, polypeptide 5, 19 kDa	−2.56	0.07	1.15	0.47
50939	IMPG2	interphotoreceptor matrix proteoglycan 2	−2.56	1.12	1.76	0.25
8802	SUCLG1	succinate-CoA ligase, alpha subunit	−2.56	2.64	1.54	0.65
23332	CLASP1	cytoplasmic linker associated protein 1	−2.57	1.26	2.20	0.71
203328	SUSD3	sushi domain containing 3	−2.57	−0.72	2.46	−0.31
126231	ZNF573	zinc finger protein 573	−2.58	0.65	1.46	−0.25
6993	DYNLT1	dynein, light chain, Tctex-type 1	−2.58	−0.49	1.03	0.82
58500	ZNF250	zinc finger protein 250	−2.59	−0.24	0.92	1.21
10507	SEMA4D	sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4D	−2.59	−1.16	1.46	−0.04
170482	CLEC4C	C-type lectin domain family 4, member C	−2.59	−0.58	0.36	0.78
3004	GZMM	granzyme M (lymphocyte met-ase 1)	−2.59	1.40	2.20	−1.17

TABLE 2-continued

64895	PAPOLG	poly(A) polymerase gamma	−2.59	1.43	0.78	−0.61
7850	IL1R2	interleukin 1 receptor, type II	−2.59	0.45	0.05	0.37
93594	TBC1D31	TBC1 domain family, member 31	−2.59	0.76	0.44	−0.83
23215	PRRC2C	proline-rich coiled-coil 2C	−2.60	−0.05	1.60	0.21
80196	RNF34	ring finger protein 34, E3 ubiquitin protein ligase	−2.60	0.73	1.11	−0.35
284415	VSTM1	V-set and transmembrane domain containing 1	−2.60	−0.29	0.72	0.08
56882	CDC42SE1	CDC42 small effector 1	−2.60	−0.64	1.52	0.06
6508	SLC4A3	solute carrier family 4 (anion exchanger), member 3	−2.60	0.54	0.57	1.27
79663	HSPBAP1	HSPB (heat shock 27 kDa) associated protein 1	−2.61	−0.64	0.48	0.55
474344	GIMAP6	GTPase, IMAP family member 6	−2.61	0.08	1.31	−1.13
100505746	ITGB2-AS1	ITGB2 antisense RNA 1	−2.62	0.00	0.48	0.26
1293	COL6A3	collagen, type VI, alpha 3	−2.62	1.08	0.33	1.42
10294	DNAJA2	DnaJ (Hsp40) homolog, subfamily A, member 2	−2.62	−0.42	0.80	0.61
3091	HIF1A	hypoxia inducible factor 1, alpha subunit (basic helix-loop-helix transcription factor)	−2.62	0.89	0.98	0.92
79573	TTC13	tetratricopeptide repeat domain 13	−2.63	−0.03	1.77	−0.49
9208	LRRFIP1	leucine rich repeat (in FLII) interacting protein 1	−2.63	1.90	0.55	0.36
29116	MYLIP	myosin regulatory light chain interacting protein	−2.63	0.05	1.36	0.05
92370	ACPL2	acid phosphatase-like 2	−2.63	0.23	1.78	0.72
9546	APBA3	amyloid beta (A4) precursor protein-binding, family A, member 3	−2.64	0.44	0.47	−0.42
253018	HCG27	HLA complex group 27 (non-protein coding)	−2.64	−0.10	1.10	−0.40
10096	ACTR3	ARP3 actin-related protein 3 homolog (yeast)	−2.65	1.04	−0.12	−0.18
84138	SLC7A6OS	solute carrier family 7, member 6 opposite strand	−2.65	0.77	0.59	−0.11
8440	NCK2	NCK adaptor protein 2	−2.65	0.72	1.76	−1.44

TABLE 2-continued

7277	TUBA4A	tubulin, alpha 4a	−2.65	−0.26	1.61	−0.14
8269	TMEM187	transmembrane protein 187	−2.66	0.48	0.64	0.72
8807	IL18RAP	interleukin 18 receptor accessory protein	−2.66	−0.44	1.01	−0.16
1235	CCR6	chemokine (C-C motif) receptor 6	−2.67	1.38	2.29	−0.68
7059	THBS3	thrombospondin 3	−2.67	0.99	0.61	1.95
54971	BANP	BTG3 associated nuclear protein	−2.67	−0.13	1.08	−0.42
57677	ZFP14	ZFP14 zinc finger protein	−2.68	1.28	1.43	1.02
6890	TAP1	transporter 1, ATP-binding cassette, sub-family B (MDR/TAP)	−2.68	0.01	1.23	0.39
22944	KIN	KIN, antigenic determinant of recA protein homolog (mouse)	−2.69	0.44	1.04	0.09
26512	INTS6	integrator complex subunit 6	−2.69	0.30	0.91	0.00
92797	HELB	helicase (DNA) B	−2.69	0.69	0.21	1.09
5481	PPID	peptidylprolyl isomerase D	−2.70	0.46	0.93	0.38
22897	CEP164	centrosomal protein 164 kDa	−2.71	−0.13	0.44	0.20
3620	IDO1	indoleamine 2,3-dioxygenase 1	−2.71	0.37	0.85	−0.36
64766	S100PBP	S100P binding protein	−2.71	1.02	0.38	0.93
8809	IL18R1	interleukin 18 receptor 1	−2.71	−0.63	1.28	0.39
116984	ARAP2	ArfGAP with RhoGAP domain, ankyrin repeat and PH domain 2	−2.71	0.12	1.76	−0.12
440823	MIAT	myocardial infarction associated transcript (non-protein coding)	−2.72	1.47	1.42	−0.05
59340	HRH4	histamine receptor H4	−2.72	1.07	0.24	−0.36
197259	MLKL	mixed lineage kinase domain-like	−2.73	0.14	−0.03	−0.41
23670	TMEM2	transmembrane protein 2	−2.73	−0.89	1.36	0.25
643314	KIAA0754	KIAA0754	−2.73	1.42	−0.20	1.32
28526	TRDC	T cell receptor delta constant	−2.73	0.84	1.43	−0.85
55096	EBLN2	endogenous Bornavirus-like nucleoprotein 2	−2.74	0.08	1.21	0.85
2796	GNRH1	gonadotropin-releasing hormone 1 (luteinizing-releasing hormone)	−2.74	1.82	0.79	−0.16
54509	RHOF	ras homolog family member F (in filopodia)	−2.74	2.02	1.91	−0.18
11120	BTN2A1	butyrophilin, subfamily 2, member A1	−2.75	0.47	1.81	−1.10
84869	CBR4	carbonyl reductase 4	−2.75	1.20	0.13	0.50
28991	COMMD5	COMM domain containing 5	−2.76	0.53	0.53	0.04

TABLE 2-continued

154141	MBOAT1	membrane bound O-acyltransferase domain containing 1	−2.79	0.40	0.42	1.28
3659	IRF1	interferon regulatory factor 1	−2.79	0.33	1.23	0.46
154007	SNRNP48	small nuclear ribonucleoprotein 48 kDa (U11/U12)	−2.80	0.64	0.71	0.84
116835	HSPA12B	heat shock 70 kD protein 12B	−2.81	0.73	0.95	0.79
9488	PIGB	phosphatidylinositol glycan anchor biosynthesis, class B	−2.82	−0.03	1.02	0.43
100293516	ZNF587B	zinc finger protein 587B	−2.83	−0.05	0.73	1.59
9217	VAPB	VAMP (vesicle-associated membrane protein)-associated protein B and C	−2.84	0.11	1.97	0.05
10538	BATF	basic leucine zipper transcription factor, ATF-like	−2.84	0.90	0.63	1.05
6935	ZEB1	zinc finger E-box binding homeobox 1	−2.87	0.92	1.75	0.62
10443	N4BP2L2	NEDD4 binding protein 2-like 2	−2.88	0.79	1.38	0.19
3837	KPNB1	karyopherin (importin) beta 1	−2.88	0.72	0.69	−0.05
81698	LINC00597	long intergenic non-protein coding RNA 597	−2.88	0.51	0.98	0.58
2643	GCH1	GTP cyclohydrolase 1	−2.89	1.47	1.66	0.50
57559	STAMBPL1	STAM binding protein-like 1	−2.89	1.12	1.44	−0.87
116842	LEAP2	liver expressed antimicrobial peptide 2	−2.89	1.23	1.24	−0.18
202	AIM1	absent in melanoma 1	−2.90	−0.39	1.31	0.01
9934	P2RY14	purinergic receptor P2Y, G-protein coupled, 14	−2.90	0.39	0.49	0.14
100216546	LINC01004	long intergenic non-protein coding RNA 1004	−2.90	1.20	0.90	0.72
9692	KIAA0391	KIAA0391	−2.90	1.44	1.45	0.30
89845	ABCC10	ATP-binding cassette, sub-family C (CFTR/MRP), member 10	−2.92	1.26	0.32	0.22
26034	IPCEF1	interaction protein for cytohesin exchange factors 1	−2.92	−0.35	1.30	−0.60
10906	TRAFD1	TRAF-type zinc finger domain containing 1	−2.93	0.59	−0.14	0.29
84811	BUD13	BUD13 homolog (*S. cerevisiae*)	−2.94	0.68	2.47	0.33
100527964	LOC100527964	uncharacterized LOC100527964	−2.96	2.19	0.20	0.70

TABLE 2-continued

118426	LOH12CR1	loss of heterozygosity, 12, chromosomal region 1	−2.97	0.48	1.63	0.15
54331	GNG2	guanine nucleotide binding protein (G protein), gamma 2	−2.98	−0.03	0.87	−0.04
94081	SFXN1	sideroflexin 1	−2.99	0.80	1.65	0.60
145474	LOC145474	uncharacterized LOC145474	−2.99	−0.36	0.65	0.87
84969	TOX2	TOX high mobility group box family member 2	−3.00	0.40	2.29	0.74
4907	NT5E	5'-nucleotidase, ecto (CD73)	−3.02	1.48	0.94	−0.61
51735	RAPGEF6	Rap guanine nucleotide exchange factor (GEF) 6	−3.03	0.23	2.17	−0.04
9953	HS3ST3B1	heparan sulfate (glucosamine) 3-O-sulfotransferase 3B1	−3.03	0.28	1.28	0.36
23112	TNRC6B	trinucleotide repeat containing 6B	−3.04	−0.25	1.32	−0.24
91526	ANKRD44	ankyrin repeat domain 44	−3.05	0.02	1.28	0.18
101928017	LOC101928017	uncharacterized LOC101928017	−3.08	1.33	2.56	−0.17
84859	LRCH3	leucine-rich repeats and calponin homology (CH) domain containing 3	−3.08	1.45	0.64	−0.48
159013	CXorf38	chromosome X open reading frame 38	−3.11	−0.05	0.79	−0.09
23208	SYT11	synaptotagmin XI	−3.19	2.10	0.96	0.61
101928649	LOC101928649	uncharacterized LOC101928649	−3.23	2.32	0.72	1.25
85459	KIAA1731	KIAA1731	−3.28	0.85	0.74	0.76
9617	MTRF1	mitochondrial translational release factor 1	−3.31	0.72	1.67	0.54
56898	BDH2	3-hydroxybutyrate dehydrogenase, type 2	−3.50	1.08	1.68	1.59
387882	C12orf75	chromosome 12 open reading frame 75	−3.61	1.40	1.07	1.33
677769	SCARNA17	small Cajal body-specific RNA17	−3.64	1.73	0.35	0.50

gene	23	24	25	26	27	28	29	30	31	32	33
56904	−1.83	−1.21	−1.05	−0.66	−0.43	−1.78	−0.69	−1.58	0.44	1.01	−0.76
6464	−1.13	−1.00	−1.03	−0.56	−1.20	−0.33	−0.28	−1.31	0.34	0.51	−0.13
79087	−2.90	−0.53	−0.29	−0.66	−0.35	−0.03	−0.18	−1.81	−0.22	0.44	−0.73
101928190	−0.25	−1.19	−1.22	−0.40	−0.39	−1.16	−0.67	0.23	0.08	−0.21	−0.22
3416	−0.45	−1.01	−1.58	−0.51	−0.95	−1.91	−0.71	0.15	−0.62	0.07	0.00
8001	−0.80	−0.48	−1.40	−1.24	0.01	−1.10	−1.56	−0.51	0.69	−0.22	−0.24
3727	−1.14	−1.52	−0.73	−1.41	−1.82	−1.51	−0.20	−1.07	1.02	0.47	−0.41
10945	−0.88	−1.24	−1.27	−1.42	−0.93	−1.21	−0.26	−1.24	0.72	0.71	−1.17
5025	−0.79	−1.00	−1.24	−0.59	−0.49	−1.65	−0.52	−1.23	−0.24	1.11	−0.76
29920	−2.73	−0.24	−0.34	0.17	−0.54	−1.47	−0.54	−0.92	−0.26	1.05	0.64
101929248	−0.98	−0.65	−0.85	−0.61	−1.35	−0.22	−0.65	−2.54	−0.18	−0.62	0.23
23646	−1.68	−1.32	−0.48	−0.76	−0.64	−1.76	−0.22	−1.69	0.35	0.61	−0.46

TABLE 2-continued

10280	−1.39	−2.09	−0.07	−0.19	−0.76	−1.03	−0.53	−1.88	0.14	0.20	0.17
140699	−1.14	−1.47	−0.35	0.30	−0.45	−0.69	−0.25	−0.56	−0.93	−0.15	0.62
4669	−1.76	−1.51	−0.69	−0.46	−0.80	−0.95	−0.60	−1.13	0.61	−0.69	−1.08
8341	−0.53	−0.66	−2.02	−0.06	−0.55	−1.55	0.83	0.33	0.10	−1.31	−0.85
2519	−0.83	−0.05	−0.54	−0.22	−0.07	−0.77	−0.76	−0.44	−1.20	0.37	−0.76
8985	−0.90	−1.85	−0.41	−0.45	−1.61	−1.23	−1.48	0.02	1.31	−0.16	−0.18
1690	−0.84	−0.58	−1.09	−0.97	−2.01	−0.69	−0.58	0.82	−0.57	−0.36	−0.26
51114	−0.20	−1.68	−0.68	−2.12	−1.33	−0.96	−0.36	−0.56	−0.61	0.86	0.09
55907	−2.31	−0.59	0.30	−0.38	−1.00	−0.93	−0.24	−0.94	−0.46	−0.09	−0.01
144811	−1.17	−0.87	−0.18	−1.12	−0.19	−0.07	−1.80	0.53	−1.35	−0.94	0.83
92421	−2.35	−0.64	−0.34	−1.10	0.72	−1.28	−1.34	−1.09	−0.85	1.39	−0.10
23475	−0.75	−1.34	−0.29	−0.98	−1.44	−1.67	−1.38	−0.50	0.13	−0.15	−1.58
54913	−1.45	−0.52	−0.96	−0.73	0.41	−1.10	−0.99	−0.08	−1.89	1.72	0.18
4645	−0.57	−1.59	−1.36	−0.92	0.78	−1.14	−0.16	−0.26	0.48	−0.44	−0.56
9917	−1.04	−0.90	−0.17	−2.40	−0.36	−0.74	−0.39	−0.28	−0.24	0.79	0.49
57213	−0.01	−1.02	−0.38	−1.40	−1.66	−0.89	−0.57	−0.24	0.64	−0.12	−0.12
113829	−0.66	−0.97	−0.50	−0.62	−0.35	−1.90	−1.13	−1.82	0.44	0.07	0.00
100128164	−1.50	−1.29	−0.90	−0.90	−0.44	−2.12	−0.20	0.18	1.48	−0.25	0.99
26284	−1.15	−1.48	−0.12	−1.63	−1.48	−1.39	−1.07	−0.54	0.46	−0.15	−0.42
64847	−1.92	−1.96	−0.13	−0.02	−0.58	−0.71	−1.04	−0.62	−0.12	−1.53	−0.35
55974	−1.37	−1.53	−0.83	0.39	−0.73	−1.67	0.03	−1.45	−0.84	0.27	−0.77
64405	0.28	−1.42	0.70	−1.02	−0.86	−0.51	−0.35	−0.10	−0.82	−0.53	0.03
6510	−0.23	−1.46	−1.54	0.84	−1.10	−1.53	−1.06	−1.39	0.33	0.39	−0.85
196463	−0.53	0.13	−0.08	−0.93	−0.44	0.11	−0.72	−0.89	−0.78	−1.26	−0.54
741	−3.02	0.00	0.07	−0.16	0.09	−0.92	−0.36	−0.79	−0.99	−0.83	−0.17
23568	−0.16	−1.18	−0.81	−2.57	−0.51	−1.35	−1.08	−0.44	0.18	0.40	−0.47
79144	−0.47	−1.91	−0.40	−0.61	−1.14	−0.69	−1.72	0.25	0.75	0.04	−0.05
91319	1.17	−0.93	−1.11	−0.59	−1.45	−1.01	−0.61	−1.22	0.69	−0.01	−0.98
79654	−1.14	−1.00	−0.09	−1.03	−1.33	−1.32	−1.46	0.30	0.85	−0.15	0.17
115950	−0.21	−0.26	0.09	−1.18	0.55	−0.81	−2.66	−0.81	−0.28	−0.64	0.54
1374	−1.14	0.77	−1.00	−0.91	−1.78	−0.13	−0.16	0.02	−0.29	−1.12	−0.12
81533	−1.03	0.34	−0.28	−2.54	0.09	−0.12	−0.45	−1.29	−0.70	0.74	−0.35
201931	−0.79	−0.56	−0.56	−1.24	−0.23	−0.93	−0.61	−1.18	−0.14	1.05	1.26
7979	−1.85	−1.60	−0.34	−0.51	−0.74	−2.66	−0.05	−1.07	0.47	0.57	0.10
159296	−2.23	−1.09	−0.47	−1.19	−1.19	−0.70	−1.29	−0.45	−1.48	0.39	0.44
51102	−1.70	−2.25	−0.26	0.01	−0.88	−1.89	−1.05	−1.02	0.73	−0.27	−0.01
8729	−2.12	−0.75	−0.91	0.64	−0.47	−1.75	−0.60	−1.64	0.81	1.01	−0.03
118460	−1.68	−0.53	−0.13	−0.67	−1.68	−0.83	−0.05	−2.45	1.05	0.82	0.02
79586	−0.05	−0.27	0.04	−0.77	−0.24	−1.94	−0.42	0.14	0.47	0.85	−1.27
2052	−0.57	−1.45	−0.72	−1.12	−0.34	−1.22	−1.19	−0.72	−0.45	1.06	−0.72
84893	−1.13	−1.60	−0.80	1.38	−1.32	−0.62	−0.94	−0.82	−0.21	−0.18	−0.09
54726	−1.46	−0.26	−0.32	−0.48	0.01	−0.61	−1.37	−0.16	−2.12	0.27	0.69
813	−0.68	−1.55	−0.84	−0.35	−0.55	−1.41	−0.79	−0.81	0.15	0.89	−0.93
54431	−0.94	−1.36	−0.25	−1.86	−0.57	−0.40	−0.67	0.04	−0.18	−0.12	0.19
9612	−0.81	−0.67	−1.56	−0.53	−2.17	0.00	−0.71	−0.15	1.43	0.81	−0.51
9829	−1.18	0.51	−0.02	−0.51	0.15	−0.61	0.37	0.70	−2.38	−0.42	−0.55
79036	−1.36	−1.06	−0.27	−0.70	−0.22	−1.02	−0.22	−0.39	1.03	0.00	−0.92
284361	−0.39	−1.29	−0.05	−1.87	−0.60	−1.53	−0.98	−1.21	0.35	0.79	−0.74
131118	−1.71	−1.73	−0.31	0.25	0.06	−1.88	−0.71	−0.67	0.06	−0.02	0.91
644809	−0.72	−0.54	−1.48	0.15	−0.39	−0.20	−0.50	−1.93	−0.92	0.89	0.93
2119	−0.52	−1.29	−0.50	−1.03	−0.50	−0.28	−0.92	−2.05	0.97	0.94	−1.10
5833	−0.87	−1.39	−0.89	−0.33	−1.09	−2.70	−0.29	−0.55	1.50	−0.13	−0.64
922	−1.78	−1.65	−0.19	−0.25	−1.34	−0.88	0.64	−2.09	−0.07	−0.15	−0.01
9261	−0.46	−0.25	−1.13	−1.38	−0.95	−0.90	0.00	−2.42	1.26	1.47	−1.44
57190	−1.54	−0.12	−1.04	−1.51	−0.51	0.19	−1.52	0.70	−0.67	1.23	−0.29
79644	−0.81	−1.01	−0.45	−2.99	−0.84	−0.84	−0.75	−0.73	−0.14	0.74	−0.03
79058	−2.55	−1.65	−1.17	1.07	−1.90	−1.07	−0.50	−1.01	0.76	−0.18	−0.25
7832	−0.80	1.75	−0.97	−1.72	0.60	−0.34	−0.58	−1.79	−1.22	0.20	−0.75
11070	−1.85	−0.85	−0.67	−1.96	0.67	−0.29	−1.12	−1.17	−1.09	0.85	−0.04
10847	−0.84	−0.94	−0.74	−0.27	−0.99	−1.16	−0.22	−0.68	2.32	0.59	−0.72
4597	−0.64	0.43	−0.66	0.62	−0.59	−1.03	−1.00	−0.89	−0.32	−0.72	−1.64
100506696	−0.28	−1.50	−0.99	−1.11	−1.28	−1.19	−1.05	−0.97	0.69	0.83	−0.65
100507459	−0.44	−1.72	−1.06	0.52	0.04	−1.09	−0.21	−1.81	0.60	0.41	−0.41
100130613	−0.91	−0.72	−0.29	−1.82	−1.75	−1.36	−0.10	−0.54	0.44	1.21	0.32
5081	−2.10	−1.71	−0.98	0.31	−0.49	−0.67	−0.54	−2.58	0.31	0.21	0.68
100240728	−1.48	−1.29	0.18	−0.53	−1.28	−1.80	−0.35	−1.66	1.60	−1.14	−0.16
26229	−2.19	−1.42	−0.62	−0.44	−1.67	−1.24	−0.10	−1.09	1.04	−0.35	−0.10
950	0.23	−1.23	−0.64	−0.61	0.58	−1.21	−0.71	−1.21	−0.52	1.47	−0.41
161882	−0.48	−1.15	−1.45	−1.12	−0.53	−0.79	−1.05	−1.85	1.20	−0.43	−0.39
5034	−0.90	−1.26	−0.72	−1.37	−1.06	−2.03	−0.52	−1.36	0.68	0.97	−0.45
123355	−1.46	−0.65	−1.18	0.74	−0.82	−0.18	−0.86	−0.79	0.71	0.54	0.02
6734	−1.37	−0.59	−0.55	−1.25	−0.25	−0.54	−0.25	−0.02	−0.30	0.10	0.54
9911	0.14	−0.95	−1.31	−0.60	−1.53	−1.37	−0.86	0.64	−0.61	−0.20	−0.91
222642	−0.25	0.39	−0.95	−1.52	−1.68	−0.71	−0.93	0.44	−1.02	−1.00	−1.54
3643	−0.21	−1.22	−0.76	−1.70	−1.17	0.68	−0.88	−0.92	1.24	−0.15	−0.62
85462	−0.67	0.75	0.12	−0.65	0.05	−1.41	−1.02	0.54	−0.51	−0.90	−0.39
149175	−0.86	−0.89	0.07	0.22	−1.72	−1.95	−0.40	−1.95	0.41	−0.35	−0.10

TABLE 2-continued

1819	−2.41	−0.72	−0.95	0.00	−0.78	−1.19	−0.94	−1.34	−0.10	0.60	−0.48
10370	−1.04	−0.27	0.09	−1.87	−0.74	−0.30	−1.07	0.04	0.42	0.80	−0.26
25792	−1.30	−0.78	−0.73	−1.09	−1.18	−0.71	−0.53	−0.61	0.86	0.57	−0.14
4072	−1.47	−1.29	−0.52	−0.06	−0.55	−1.07	−0.51	−1.51	0.54	−0.64	−0.97
84447	−0.51	−0.82	−0.07	−0.69	−1.53	−0.53	−0.87	−0.63	1.35	−0.03	−0.26
527	−0.71	0.26	−1.08	−1.38	−1.11	−1.26	−0.47	−1.00	0.53	1.03	−0.13
10629	−0.46	−1.55	−1.87	0.86	−1.13	−2.13	−1.10	−0.15	0.89	0.86	−0.60
51150	−0.87	−0.86	−0.98	−2.08	−1.07	−0.97	−0.52	−1.61	0.18	0.65	0.01
57143	0.37	−2.09	0.44	0.53	−2.14	−0.98	−1.30	−0.25	1.34	−0.33	−0.70
682	−1.96	−0.72	−1.18	−0.56	−0.79	−1.33	−0.03	−0.85	−0.05	0.29	−1.11
10139	−1.44	−0.88	−1.19	0.15	−0.10	−1.03	−1.09	−2.20	0.12	0.61	0.24
203238	−1.31	−2.56	0.15	−0.77	−1.35	−0.24	0.80	−1.81	0.39	0.47	−1.01
54805	−0.19	−0.69	−0.53	−1.14	−0.89	−2.27	−0.46	−1.16	0.42	−0.95	−0.04
1200	−1.56	−0.55	−0.04	−0.17	−1.95	−1.26	−0.68	0.97	−0.16	0.11	0.49
2271	−0.72	−0.29	0.39	−0.72	0.11	−2.07	−1.33	−2.12	−0.19	0.26	−0.53
376412	−0.59	−1.49	−0.81	0.10	−1.53	−1.99	−0.59	−1.49	1.02	0.36	0.28
4924	−2.44	−0.35	−0.63	−1.12	−0.38	−1.00	0.02	−0.94	0.15	0.09	−0.41
55132	−0.36	−0.74	−0.76	−1.46	−1.45	−1.07	−1.06	−0.86	0.31	−0.92	−0.11
9650	−2.56	−0.84	−0.51	−0.78	−0.38	−1.17	−0.77	−0.31	−0.27	−0.58	−0.60
29803	−0.23	−1.24	−0.42	−0.37	−1.50	−1.76	−0.78	−1.36	1.43	0.63	0.34
4507	−0.25	−1.03	−0.78	−0.51	−1.08	−0.71	−1.44	−0.62	0.31	1.21	1.00
816	−1.72	−0.50	−2.28	−0.06	−1.48	−1.37	0.91	0.17	0.67	0.44	−0.01
120379	0.09	−0.74	−2.12	−2.85	0.20	−1.88	−0.51	−0.61	0.50	−0.07	0.03
91289	0.02	−1.30	−0.42	0.39	−1.30	−1.02	−0.83	−2.28	0.92	−0.22	−0.63
10905	−1.17	0.50	−1.56	−1.18	−0.65	0.10	−0.93	−0.18	−0.28	0.54	−0.14
25930	−1.18	−0.27	0.57	−2.29	−2.08	−0.50	−0.90	0.10	0.69	0.20	0.71
57648	−0.35	−0.88	−0.42	−0.20	0.17	−1.18	0.01	0.41	0.19	0.45	−0.22
7249	−2.52	−0.50	−0.69	−1.10	−0.75	−0.32	−0.30	−1.75	0.18	0.74	−0.06
55151	−0.96	−0.14	−0.33	−1.17	0.40	−1.88	−0.70	−0.12	−1.22	−0.12	0.04
160728	−0.89	0.44	0.81	−1.06	−1.07	−0.70	−0.41	−0.74	0.19	0.24	−0.70
148418	−1.41	−0.78	−1.09	−0.57	−1.40	−1.27	−1.02	−0.98	1.80	1.04	−1.05
646762	0.05	−1.42	−0.18	−0.11	−1.67	−1.88	−1.42	0.23	1.52	0.15	−0.80
79109	−0.62	−0.40	−0.58	−1.97	−0.53	−0.98	0.65	−2.58	−0.26	0.40	0.20
81037	0.12	−1.47	−0.44	−0.95	−1.21	−1.68	−0.82	−1.86	0.99	0.53	−0.60
51523	0.69	−0.77	−0.96	−1.13	−1.08	−1.31	−1.02	−0.68	−0.33	0.23	−0.98
55322	−1.92	−0.84	−0.43	0.08	−0.06	−1.94	−0.30	−0.46	0.04	0.66	1.47
100996671	−2.37	−0.81	−2.13	−0.74	−1.37	−0.90	0.07	−0.24	0.59	−0.06	−0.83
55222	−0.38	−2.38	−1.07	0.40	−0.33	−1.72	−0.20	−1.69	−0.75	0.47	−1.05
55624	−0.95	−2.00	−0.16	−1.30	−1.25	−1.45	−0.62	−1.24	0.38	0.43	0.58
100505983	−1.36	−0.31	−0.14	0.80	−0.64	−0.81	−0.39	0.10	−1.00	−0.77	−1.21
3069	−0.05	−1.09	−0.89	−0.54	−1.77	−1.65	−0.48	−1.57	1.64	−0.17	−0.39
10959	−1.37	−0.78	−0.66	−1.67	−0.30	−1.87	−0.27	−1.19	0.35	1.51	0.14
6598	−1.33	−1.85	−0.82	−0.83	−1.68	−0.75	−0.49	−0.64	1.09	0.22	−1.02
60412	−0.82	−1.06	−0.22	1.00	0.34	−2.64	−0.77	−0.34	−0.03	0.34	−0.47
54982	−0.14	−0.97	−0.85	−0.43	−0.81	−1.53	0.19	−2.33	0.61	0.38	−0.88
91752	−0.90	−0.06	−0.82	0.39	−1.31	−1.41	−1.05	0.19	−0.79	0.26	−1.36
113178	−2.16	0.01	−0.48	−1.48	−0.91	−0.98	0.52	−1.27	0.00	0.41	−0.64
10	−1.50	−0.51	−0.82	0.00	1.29	0.07	−0.19	−0.94	−0.06	0.31	0.49
375	−1.44	−0.75	−0.71	−0.31	−0.59	−1.57	0.25	−1.27	0.54	1.30	−1.11
5589	−0.95	−1.22	−0.60	−0.45	−1.20	−1.19	0.19	−1.22	1.45	0.22	−0.09
9136	−1.47	0.45	0.16	−0.13	−0.18	−1.11	−0.12	−2.21	−1.46	−0.45	0.16
23193	−1.18	−0.78	−0.57	−1.28	−1.20	−2.09	−0.13	−0.77	0.29	1.21	−0.14
1798	−0.18	−2.01	−0.74	−0.59	−1.17	−1.80	−0.78	−0.66	0.56	0.23	−0.25
85440	−0.45	−1.70	−0.49	−1.37	−0.71	−1.44	−0.34	−0.15	−0.53	−0.03	0.71
100505794	−0.18	0.84	0.07	−0.81	−1.09	0.79	−0.19	−0.74	−0.81	0.69	−0.41
1173	−0.83	−0.58	0.01	−1.24	−0.72	−1.26	−0.17	−1.41	0.52	0.41	0.49
124540	−0.60	−1.31	−0.30	−1.63	−1.61	−1.18	−0.02	−1.23	0.49	0.32	0.17
8372	−0.71	−2.60	−0.63	−0.10	−1.86	−0.78	0.12	1.45	−0.18	−1.76	−0.41
64755	−0.55	−1.42	−0.35	−0.24	−1.81	−1.76	−0.68	−1.66	0.41	0.59	−0.48
79102	−1.43	−0.70	−1.38	0.39	−1.46	−2.44	−0.21	−1.16	1.19	0.28	−0.77
10963	−2.09	−0.40	−0.42	−0.73	−0.21	−1.47	0.49	−1.67	−0.12	1.24	−0.17
375387	−0.87	−0.01	−0.17	−0.11	−1.28	−0.50	−0.60	0.24	−1.54	−0.83	−0.65
972	−0.28	−1.43	−0.11	−0.01	−0.70	−1.47	−0.12	−0.90	0.20	0.38	−0.74
54676	−2.43	−0.14	−0.94	0.04	−1.20	−1.73	−0.38	−1.14	−0.52	−0.67	0.09
192286	−0.95	−1.64	−0.10	−0.35	−0.96	−1.57	−0.62	−0.45	−0.12	−0.06	0.30
3295	−0.96	−1.28	−0.07	−1.22	−0.35	−1.62	−0.12	−0.33	−0.44	0.74	0.28
80852	0.46	−0.23	−1.00	−0.28	−0.56	−1.60	0.29	−0.25	0.99	−0.45	0.32
1298	−1.17	−1.30	0.06	−0.27	−1.24	0.45	0.11	−2.40	1.06	−0.53	−0.79
2004	1.45	−0.81	−0.93	−0.98	−0.84	−1.47	−1.45	−0.39	−2.20	−0.39	0.73
10279	−1.22	−0.19	−0.43	0.00	0.14	−0.38	−1.05	−0.19	−0.73	−1.41	0.10
151790	−0.42	−0.58	0.23	−0.53	−0.55	−0.87	−0.58	−1.29	−0.51	−0.23	−0.55
399664	0.21	−0.20	−1.11	0.19	−0.11	−0.84	−1.00	−2.02	0.71	0.86	−0.53
5664	−0.06	−0.67	−0.95	−1.10	−0.55	−0.82	−1.52	−0.69	−0.48	0.70	−1.26
51614	−0.96	−1.69	−1.06	−0.57	−0.66	−1.27	−0.86	−1.00	1.10	0.44	−0.68
79178	−0.91	−0.99	−0.52	−0.45	−0.70	−1.55	0.06	−2.35	0.14	0.23	−0.52
51726	−0.02	−1.07	−0.56	−1.29	−1.52	−1.64	−0.24	−2.37	0.98	0.57	−0.65
3425	−0.24	−1.67	0.48	−1.44	−1.45	−1.37	−1.23	−1.32	0.23	0.19	0.15

TABLE 2-continued

1642	−0.14	−1.68	−0.30	0.04	−1.21	−1.77	−1.06	−1.05	0.65	−0.11	−0.13
101928770	−2.41	0.42	−0.74	−0.38	−1.28	1.03	−1.00	−0.24	0.14	−0.97	0.15
11015	−0.90	−1.05	−1.01	−0.66	0.40	−1.50	−1.03	−1.40	0.20	1.30	−0.43
35	−0.92	−1.80	−1.34	−0.11	−1.72	−0.57	−0.59	−1.68	1.63	−0.30	0.76
64798	0.17	−1.91	−0.69	−1.41	−1.48	−1.15	−0.95	−0.40	0.49	0.30	−0.05
23457	0.23	0.95	−0.75	−0.57	−2.38	−2.52	−0.49	0.58	0.06	1.04	−0.19
56132	−1.26	−0.74	0.98	−0.40	0.17	0.89	−0.77	−0.68	−0.57	−1.01	−0.72
23400	−0.55	−0.61	−0.38	−1.52	−1.24	−1.72	−1.52	−1.07	−1.03	0.51	−0.12
3980	−0.89	−2.55	−0.81	−0.74	0.02	−2.38	−1.06	0.51	0.52	0.50	−0.07
5690	−0.06	−1.09	−0.42	0.34	−2.37	−1.23	0.14	−0.81	1.55	−1.12	0.64
7917	−0.50	−1.20	−1.11	−0.12	−1.42	−1.52	−1.02	−0.94	0.53	0.32	−0.02
1739	−0.98	−0.97	−0.58	−1.71	−1.05	−1.23	0.06	−1.57	0.23	0.49	1.12
2837	0.46	−1.16	−1.84	0.00	−1.49	−2.39	0.82	0.24	−0.42	−0.46	0.40
83746	−0.75	−2.66	−0.21	1.28	−0.65	−2.26	−0.13	−1.23	0.41	−0.08	−0.23
5962	−1.71	−0.86	−0.84	−1.85	−0.50	−0.59	0.17	−1.83	−1.01	−0.33	−0.52
9956	0.24	−1.50	−0.94	−0.36	−0.32	−0.42	−0.53	−2.99	0.42	−0.16	−0.13
162968	−1.78	−1.45	0.14	−0.66	0.23	0.98	−1.94	−0.57	−1.14	0.93	−0.68
4192	0.08	−0.98	−0.23	−1.37	−0.57	−1.05	−1.01	−2.53	0.54	1.26	−0.99
54919	−0.55	−1.79	−0.04	−1.01	0.14	−1.22	−0.85	−2.07	−0.84	0.81	−0.31
10972	−0.25	−0.98	−0.40	−1.46	−0.19	−1.53	−0.52	−0.83	−0.04	0.35	0.62
23061	0.36	−2.05	−0.57	0.68	−1.81	−2.03	−0.54	−0.50	1.07	0.38	−0.24
3792	−0.63	−1.58	0.55	−0.34	−0.72	−0.74	−1.03	0.51	−1.59	−0.61	−0.82
2063	−1.95	−0.34	−0.82	−0.42	−0.19	−0.82	−0.99	−1.05	1.04	−0.08	−1.50
55177	−0.07	−2.03	−0.04	0.26	−0.51	−1.87	−1.07	−0.42	−0.46	0.51	−0.67
11147	−1.73	−0.67	−0.17	0.33	0.02	−1.46	−0.63	−0.49	−1.48	−0.53	−0.15
57486	0.16	−0.80	−1.04	−0.54	−1.81	0.10	0.08	−0.39	−0.68	−0.02	−0.44
30814	−1.11	−1.25	−1.55	−0.09	0.17	−1.32	1.17	−1.13	1.76	0.08	0.07
57414	−0.87	−0.95	−0.83	−0.40	−0.34	−1.04	−0.51	−1.61	1.09	1.76	−0.93
84836	0.14	−1.42	−0.30	−0.83	−1.04	−1.21	−1.88	−1.02	0.71	0.55	0.04
8516	−1.32	0.38	−1.48	0.19	−0.48	0.22	−1.34	−0.59	−0.80	−0.71	−0.91
89866	−1.19	−2.47	−0.47	−1.09	−1.23	−1.28	−0.86	1.00	0.80	0.49	−0.17
10491	1.30	−0.37	−0.39	−1.44	−1.15	−0.34	−1.17	−0.38	0.86	0.22	0.63
11047	−1.14	−1.04	−0.78	1.01	−1.44	−1.42	−0.65	−1.92	0.73	0.22	−0.91
28971	0.17	−2.19	−0.58	0.06	−1.82	−1.72	−1.03	−1.00	1.01	0.39	−0.43
8078	−0.66	−1.54	−0.64	0.06	−1.61	−0.79	−0.05	0.00	0.26	0.29	0.46
37	−0.90	−1.46	−0.37	−0.18	−1.67	−1.00	−0.69	−2.44	0.71	0.40	−0.81
145508	0.86	−0.27	−0.22	−1.14	−0.22	−0.88	−1.73	0.49	−0.87	0.38	−0.08
49861	−1.45	−1.00	−0.62	−0.48	0.21	−0.66	−0.44	0.45	1.92	0.48	−0.68
5905	−0.19	−1.82	−0.41	−0.21	−1.01	−1.46	−0.07	−2.74	0.95	−0.20	−0.18
7542	−1.75	0.16	−0.45	−0.49	−0.71	−0.43	−0.82	−2.69	−0.62	1.20	−0.85
9562	−1.06	−0.10	0.68	−1.68	0.34	−0.44	−0.28	−0.58	−1.52	−0.25	0.18
79095	−1.81	−1.41	−0.33	0.96	−0.80	−0.84	−0.51	−1.63	0.97	0.93	−0.10
8815	−1.77	−0.92	−0.97	−0.73	−0.13	−1.25	0.19	−0.20	−0.05	0.57	0.37
54867	−1.31	−1.25	−0.40	−2.00	−0.89	−0.75	−0.56	0.61	1.97	−0.05	0.68
6721	−0.84	−1.28	−0.71	−0.20	−1.67	−0.98	0.44	−1.03	1.08	1.63	−1.16
23133	0.31	−0.51	−1.00	−0.42	−1.45	−0.75	−0.02	−0.49	1.72	−0.57	0.70
113675	−0.65	−0.86	−0.59	−0.23	0.05	−1.80	−0.22	−1.55	−0.74	−0.31	−0.39
129303	−0.87	−1.14	−0.18	−1.12	−2.01	−2.22	−1.38	0.92	−0.08	0.79	0.77
57658	−0.60	−0.22	−0.57	−0.06	−1.37	−1.12	−0.15	0.04	2.19	0.40	0.59
162	−0.65	−1.04	−0.46	0.39	−1.24	−0.53	−0.45	−2.53	0.87	0.24	−1.00
2873	−0.64	−1.89	−0.46	0.03	−1.64	−1.37	−0.52	−1.98	−0.63	0.97	−0.55
64978	−2.16	−0.49	−0.44	0.02	−0.43	−1.89	−0.71	−1.57	−0.49	1.44	0.29
220323	−0.21	−1.96	−1.16	−1.10	−1.46	−0.88	−0.76	−0.15	0.57	−0.16	−0.45
6006	0.44	−0.98	−0.96	0.11	−0.35	−0.32	−2.07	1.25	−0.63	−1.58	−0.47
389812	−1.86	−0.92	−0.47	0.18	−1.89	−1.46	0.51	−0.27	0.30	−0.11	0.54
2628	−0.24	−0.77	−0.41	−0.50	0.76	−1.29	−0.12	−0.63	−0.91	0.26	−0.80
6509	0.52	−0.81	−0.96	−0.62	−0.94	−1.58	−1.54	−0.58	0.41	0.35	−1.26
3888	−0.26	−1.61	−1.47	−0.07	−2.05	−0.47	−0.53	−0.82	2.32	0.46	−0.22
5211	0.14	−1.54	−0.58	0.42	−1.76	−1.34	−0.31	−1.71	1.16	0.16	−0.38
55080	−0.64	0.06	−0.50	0.32	−0.05	−0.43	−1.30	−1.03	−0.22	0.34	1.22
2139	−1.52	−1.27	−0.08	0.94	0.72	−1.22	−1.55	−0.82	−0.31	−0.73	−0.04
2030	−1.26	−1.36	−0.97	−0.26	−1.64	−0.75	−0.98	−0.28	−0.02	0.19	−1.69
56005	0.35	−1.40	−0.24	−0.71	−0.49	−1.30	−0.95	−1.94	0.46	0.86	−0.87
6414	−1.04	−1.09	−0.68	−1.59	−0.49	−0.89	−0.68	0.14	−1.32	0.19	−0.45
5184	0.05	−0.97	−0.12	−0.53	−0.49	−0.93	−0.41	−0.92	0.78	0.21	0.29
643783	−0.73	−0.39	−1.05	−0.58	0.11	−0.85	−2.07	−0.01	−0.15	−0.59	−0.69
101928185	−1.37	−0.63	−0.59	−1.98	0.77	−0.44	−1.62	1.00	−0.18	2.19	−0.74
22883	0.08	−1.78	0.15	−0.12	−1.13	−1.16	−1.23	−0.93	1.48	0.62	0.54
25800	−1.18	−1.06	−0.44	−2.67	−0.39	−0.57	−0.39	−1.73	0.50	0.69	−0.05
54681	−0.49	−2.25	−0.14	−0.71	−0.87	−1.45	−1.29	−1.09	0.79	0.73	0.36
644150	−1.36	−0.25	−1.42	−1.20	0.56	−1.50	0.02	−0.58	0.38	1.10	−0.66
9048	−0.51	−1.44	−0.70	−1.11	−1.39	−0.58	−0.96	0.03	1.54	−0.41	−0.20
3054	−0.46	−1.57	−0.46	−0.74	−1.34	−2.37	−1.10	−1.16	1.18	0.15	−0.53
115098	−1.33	−0.65	−0.49	−0.36	0.11	−0.91	−0.95	−1.73	0.73	−0.10	−0.74
55558	−0.98	−1.98	−0.76	−0.43	−1.30	−1.51	−0.78	−0.45	0.20	0.59	0.09
675	−0.67	−0.79	−0.77	−1.18	−1.71	−0.78	−1.13	−1.61	−0.06	−0.15	−1.28
9777	−0.71	−0.94	−0.60	−1.42	−1.36	−0.78	−0.99	−1.21	−0.17	0.44	−0.12

TABLE 2-continued

83707	−0.32	−0.96	0.26	−1.13	−0.12	−1.86	−1.51	−1.91	0.78	0.09	0.07
55334	−1.24	0.02	−0.97	0.16	−0.36	−2.12	0.21	−0.09	0.21	0.56	−0.75
9793	−0.79	−2.20	−0.63	−0.99	−1.59	−1.83	−1.05	−0.61	0.33	0.21	0.14
56834	−1.80	−0.65	−0.91	1.33	−1.08	−1.71	−0.58	−0.68	−0.32	1.03	−1.49
25921	−0.80	−1.37	−0.94	−0.61	−1.61	−1.67	0.08	−2.40	0.82	1.06	−0.75
6520	−1.00	−1.42	−0.24	−0.20	−1.68	−1.78	−0.18	−0.41	0.14	0.70	−0.34
728591	−2.19	−1.03	−0.77	−0.31	−2.56	−0.93	0.44	−0.52	1.26	0.29	0.26
7415	−0.15	−1.24	−0.38	−0.49	−1.55	−1.45	−0.43	−2.29	1.44	0.18	−1.31
130827	−0.27	−1.98	0.13	−1.18	0.68	−2.05	−1.40	−0.24	−0.42	0.11	−0.11
9620	−1.36	−1.62	−0.97	−1.27	0.61	0.57	−0.53	−0.17	−0.14	0.46	−0.19
55335	−1.02	−0.39	−0.77	−0.14	−1.00	−0.52	−1.05	0.17	0.33	−0.47	−0.28
84988	−0.89	−1.50	0.07	−0.98	−0.32	−1.33	0.34	−1.48	−2.09	1.44	−0.70
100192378	−0.77	−0.53	−0.89	0.11	−1.09	−1.44	0.41	1.80	−0.16	0.04	−0.76
442524	−1.65	−0.06	0.00	−1.42	−0.34	−0.81	0.06	1.36	−0.63	−0.05	−0.84
51661	−0.53	−2.05	−0.71	0.13	−2.12	−1.11	−0.33	−0.66	0.39	0.71	−0.07
84922	−1.48	−0.47	0.27	−1.56	−0.92	−1.93	−0.11	−1.40	0.08	1.24	0.55
84954	−0.29	−0.31	−1.39	−0.88	−0.83	−0.64	−0.60	−1.29	0.77	0.85	−0.79
245972	−0.90	−1.01	−0.54	1.67	0.72	−0.73	−1.14	−1.10	2.12	−0.40	−0.49
4316	−0.80	−0.12	−1.04	0.22	−0.85	−1.80	0.25	−0.51	1.17	−0.52	−1.12
55157	−1.26	−0.46	−1.05	−0.51	−1.34	−1.89	−0.78	0.46	−0.81	−1.38	0.79
7466	−0.86	−1.74	0.06	0.43	0.75	−0.51	−0.61	−0.56	0.08	0.30	−1.23
79365	−0.08	0.05	−0.90	−0.83	−0.38	−0.80	−0.68	0.48	−0.30	−0.18	−1.83
10066	−0.61	−1.47	−0.69	1.05	−1.45	−1.85	−0.43	−0.89	0.58	0.69	−0.79
203068	−0.33	−2.04	−0.26	0.25	−1.53	−1.88	−0.53	−1.11	0.26	0.37	−0.66
5780	−1.05	−1.09	−0.58	0.00	−0.65	−1.00	0.38	1.20	1.33	−0.33	0.72
285627	−1.12	−1.14	−1.16	−1.29	−1.59	1.73	1.59	−0.91	1.41	−0.14	−0.38
2058	0.10	−1.92	0.06	−1.23	−1.51	−1.23	−0.94	−1.00	0.01	−0.09	−0.50
1737	−1.31	−0.80	−0.29	−1.99	−0.31	−1.56	0.19	−0.58	−0.82	−0.05	0.58
22924	−0.15	0.38	−0.71	−1.23	−0.23	−1.47	−0.27	−1.47	−0.69	0.59	−1.26
6005	−0.48	−1.01	−1.18	−1.11	−1.20	−0.26	−0.87	0.90	−1.20	−1.47	−1.03
5286	−1.64	−0.64	−1.00	−1.04	−0.21	−0.37	−0.59	−1.00	0.03	1.31	1.20
11226	0.35	−0.68	−1.38	−0.95	−0.33	−0.02	−0.95	−0.32	−0.54	0.45	−0.30
2762	0.14	−1.22	−0.97	−1.65	−1.27	−1.53	−1.62	−0.14	0.97	0.37	−0.72
8908	−0.02	−1.42	−0.38	0.32	−1.32	−0.94	−1.34	−1.44	1.24	1.45	0.28
10693	0.37	−2.13	−0.77	−1.54	−1.52	−0.52	−0.51	−0.44	1.00	0.31	−0.72
199953	0.07	−1.27	−0.22	−0.53	−1.57	−1.59	−1.06	−1.95	0.05	−0.05	−0.50
2760	−1.84	0.43	0.17	−1.04	0.52	−0.49	−0.16	−0.08	−1.11	0.30	−1.44
8295	−1.13	−1.01	−0.82	−0.91	−1.02	−1.77	0.63	−0.62	0.38	0.59	0.06
1822	−0.49	−0.97	−0.03	0.16	−1.02	−1.34	−0.29	−2.32	1.03	1.63	−0.72
55328	1.34	−0.21	−0.33	0.71	−1.28	−2.18	−2.27	−0.14	0.91	−0.29	0.76
2069	−0.53	0.62	−0.30	−1.99	0.27	−0.52	−0.37	0.14	−1.07	−0.64	0.43
4329	−0.52	−1.68	−0.34	−1.07	−1.27	−1.02	−0.75	1.43	−0.14	0.25	0.69
537	−0.83	−0.17	−0.66	−1.80	−0.72	−0.99	0.01	−2.03	0.38	1.24	−1.43
64764	0.24	−1.41	−0.28	0.06	−1.22	−1.72	−0.95	−1.13	1.14	−0.04	−0.24
811	−0.75	−1.02	−0.65	−1.40	−1.73	−0.91	−0.32	−1.64	1.61	0.75	−0.66
9779	−0.28	−0.56	−0.45	0.87	−1.17	−1.16	−0.75	−0.74	1.42	−0.18	0.54
114815	−1.45	−1.03	0.21	−0.07	−1.12	−2.49	−1.23	0.55	0.79	−0.85	0.62
29927	−0.62	−1.01	−0.41	−0.78	−0.95	−1.19	−0.23	−2.17	−0.18	0.62	−0.99
6007	−0.52	0.15	−0.04	−0.41	−0.29	−0.43	1.20	−1.27	−0.94	−1.67	−0.20
5192	−0.69	−1.31	−1.10	−0.21	−0.63	−1.40	−1.44	−1.37	0.00	0.02	−0.26
125875	−1.36	−0.94	1.20	−0.52	−2.27	−1.61	−0.41	−1.06	1.40	0.32	0.31
10882	−0.68	1.53	−2.31	−0.49	−0.46	−1.90	0.23	−0.81	−0.39	−0.73	−0.03
192683	−0.51	−1.23	−0.40	1.20	−1.41	−1.53	−0.61	1.28	1.53	0.28	0.34
8028	−0.34	−0.03	−0.41	−1.91	−0.70	−0.92	−0.78	−1.75	0.00	0.39	0.32
150368	−0.51	−1.64	−0.79	2.53	0.69	−0.58	−1.82	−0.74	−0.54	0.51	−0.42
84206	−1.12	−0.84	−0.63	−1.18	−1.68	−1.75	−0.56	−1.05	0.44	0.65	−0.93
101929288	−0.69	−1.90	−0.51	0.48	−0.39	−0.37	−0.77	−0.73	−0.43	1.18	−0.22
826	−1.17	−0.41	−0.58	−0.49	−0.98	−1.05	−0.41	−0.81	0.56	0.39	−0.04
83440	−1.11	−0.98	−0.85	−0.09	−0.84	−1.59	−0.01	−1.58	1.21	1.63	0.05
1128	−1.54	−1.81	0.21	0.16	−2.12	−0.69	−0.41	0.70	0.97	−0.80	0.89
160287	−0.43	0.03	−1.50	0.34	−0.90	−0.38	0.88	0.17	1.52	−0.43	−0.05
412	−1.81	0.82	−0.89	0.39	0.73	0.64	−0.94	−0.24	−0.63	−0.84	0.20
64215	−0.31	−1.81	−0.25	−1.24	−1.03	−1.72	−0.20	−0.01	0.04	−0.02	0.19
7343	−0.70	−0.63	−0.59	0.26	−1.18	−2.83	0.15	−1.14	1.93	1.57	−0.26
25840	−0.25	0.09	−0.10	−0.81	−0.75	−1.86	−0.40	−0.04	1.14	0.65	0.04
55315	0.75	−0.81	−0.31	−0.96	1.87	−0.86	−0.42	0.21	−0.79	0.44	−0.22
100507513	0.14	−0.76	−0.08	−1.02	−0.93	−0.07	−1.63	1.20	−0.27	0.38	−0.66
55704	−1.65	−0.54	−0.10	−1.07	−2.00	−0.06	−0.13	−1.38	0.49	0.56	−0.85
57604	−2.21	−0.46	0.23	−2.17	−0.35	0.05	−1.66	0.20	1.17	0.48	−0.67
10449	0.15	0.45	−2.21	−1.40	−0.69	−1.52	−0.28	0.20	−0.35	−0.94	−0.91
1727	−0.36	−0.55	−1.16	0.35	−0.69	−2.32	−0.50	−0.95	0.87	0.62	−0.36
9569	−1.84	−2.20	−0.34	−0.82	−0.24	−0.72	−0.16	−1.93	1.36	0.32	0.33
10009	−1.16	−1.08	−0.18	−0.96	−0.80	−0.59	−1.24	0.32	0.35	0.29	0.00
5188	−3.01	−1.09	0.55	0.26	−0.06	−2.33	0.25	−0.43	−0.53	0.25	−0.38
2132	−1.19	0.06	0.42	−2.44	−0.51	0.41	−1.46	1.70	−0.51	0.07	0.93
2239	−0.72	−1.45	−1.88	−0.30	0.56	0.00	−0.65	−0.13	0.61	1.59	−0.09
56927	−2.64	−0.20	−0.50	−0.38	0.59	0.43	−0.48	−0.59	−0.46	0.96	−0.92

TABLE 2-continued

2950	−1.24	−1.53	−0.25	−0.04	−0.52	−1.24	−0.17	−1.67	0.19	0.49	−0.84
342538	−0.33	−1.80	1.04	−0.70	−1.75	−0.48	−0.70	−2.09	1.11	−0.08	1.12
55218	0.35	−1.78	−0.68	−0.02	−1.07	−2.27	−0.41	−0.07	0.83	0.78	0.28
151827	−0.68	−2.19	−0.20	−0.84	−0.06	−1.75	−0.08	−0.62	0.50	0.73	−0.80
64689	−1.44	0.10	−0.65	−1.71	0.34	−0.40	−0.98	−1.40	−0.45	0.37	−0.81
10324	−0.90	−1.52	0.79	1.46	0.27	0.19	−1.04	−0.47	−1.27	−1.22	−0.13
1314	−1.48	−0.79	−1.03	0.16	−0.59	−1.60	0.16	−1.99	−0.28	1.25	0.04
54928	−0.35	−0.05	−0.79	−2.08	−0.33	0.07	−0.26	−1.04	−0.86	0.44	−0.36
8971	−0.49	−1.86	−0.38	−0.69	−1.67	−1.08	−0.99	−1.20	1.07	−0.15	−0.43
79832	−0.86	−0.28	−0.33	−0.67	−0.55	−0.15	−0.41	−0.49	−0.51	0.73	1.29
10150	−1.27	−1.00	−0.38	−1.14	0.64	−1.05	−0.17	−0.74	−0.42	0.85	0.01
8744	0.26	−1.51	−0.14	−1.47	−1.51	−0.99	−0.47	−1.18	0.51	0.11	−0.78
23287	−0.26	2.13	0.44	−0.11	0.13	1.42	1.05	0.79	0.77	−0.25	0.62
606553	0.81	0.08	1.02	0.43	−1.56	−0.86	0.62	0.74	−0.22	0.97	−0.84
103	0.23	0.58	0.50	1.37	0.61	2.05	0.95	0.87	−0.45	0.75	0.64
55509	0.69	−0.21	0.45	0.60	1.32	1.27	0.90	−1.19	−1.38	−0.01	−0.22
729614	−0.62	1.52	0.73	0.20	0.30	1.52	1.04	0.56	0.04	−0.53	0.27
9241	2.11	0.05	0.74	−0.47	−0.65	0.35	0.07	1.78	1.04	0.16	1.41
26118	−0.84	0.72	0.11	−0.10	1.28	1.04	0.96	0.73	0.36	0.70	0.02
64400	−0.16	1.10	0.53	0.44	1.81	1.33	1.01	1.39	−0.44	0.28	1.03
283237	0.23	0.98	0.19	0.50	0.70	0.13	0.91	−0.85	−0.34	0.49	1.61
51155	−0.19	1.52	0.82	0.58	0.64	0.87	1.25	0.22	−0.07	−0.03	−0.24
18	0.33	1.74	0.49	0.10	1.28	1.60	0.61	0.95	−0.86	0.15	0.58
22990	−0.21	1.87	0.84	−0.13	0.50	1.60	1.32	0.89	0.16	0.09	0.51
23347	0.55	1.55	0.38	0.49	0.74	1.69	0.44	1.37	0.40	0.26	0.27
83988	1.14	−1.32	0.36	1.67	0.69	0.42	0.04	0.26	0.61	−0.31	1.21
3428	0.76	0.89	0.80	1.81	1.23	0.86	0.99	1.04	−0.54	−0.22	0.79
3700	0.42	1.03	0.85	0.10	0.96	0.79	0.32	1.18	−0.41	0.25	0.56
64859	−0.95	1.92	0.65	−0.52	1.36	1.76	1.07	0.79	−0.98	−0.24	0.27
55192	−0.81	1.37	−0.26	0.92	1.29	0.70	1.13	0.36	−2.35	1.03	0.10
101928869	1.75	0.91	0.85	1.93	1.19	0.15	−0.60	−0.16	0.06	0.17	0.19
10513	0.67	1.59	0.67	−0.63	1.67	1.45	0.81	0.31	−0.53	0.18	0.91
11009	2.52	−0.08	−0.13	0.06	−0.20	0.75	−0.56	1.34	0.24	−0.01	0.48
169355	1.60	0.56	1.18	−0.24	0.98	0.94	−0.33	−0.81	−1.63	−0.34	0.14
10109	0.01	2.33	0.80	0.71	0.77	0.54	0.29	1.02	0.04	−0.34	1.13
9903	0.47	2.17	1.10	−0.11	0.89	1.64	0.08	0.63	−0.97	0.08	1.22
23150	0.34	1.40	0.90	−1.32	1.36	1.19	0.20	1.31	−0.63	0.07	0.83
10865	−0.41	0.75	0.12	0.34	0.22	1.51	1.44	−1.16	0.65	0.52	−0.43
5165	0.28	1.95	0.00	0.19	1.47	1.77	1.18	0.96	−0.93	0.10	−0.07
57403	0.51	2.05	0.52	−0.33	1.09	1.44	0.70	1.31	−0.64	−0.45	0.29
22900	−0.17	1.69	1.03	0.65	0.18	1.44	0.44	1.64	−0.19	−0.12	1.43
80345	−0.40	1.15	0.61	0.78	0.37	1.82	1.31	0.13	−0.62	−1.06	1.05
10964	1.33	0.19	0.77	0.76	1.61	0.71	0.31	1.37	−0.46	−0.81	0.84
27040	2.03	−1.09	1.40	0.58	0.63	−0.26	−0.09	0.57	0.41	0.15	1.44
91010	2.18	1.05	0.47	0.06	0.82	0.25	0.46	0.00	−2.78	0.17	0.34
29065	0.25	1.51	1.33	0.21	0.72	1.55	1.02	1.40	−0.68	−0.21	−0.34
84078	−0.01	2.40	0.74	−0.25	1.25	1.94	0.29	0.93	−0.39	0.06	0.84
101927910	0.06	0.88	0.83	2.09	0.79	−0.52	0.79	0.42	0.18	−0.05	−0.41
51380	−0.40	1.68	0.42	0.27	1.05	1.50	1.50	0.48	0.11	0.31	−0.12
10289	0.91	2.11	0.60	−3.60	−0.01	1.16	0.60	0.77	−1.07	−0.39	0.69
10296	0.38	0.97	0.18	−0.05	0.73	0.88	1.42	0.80	1.48	0.27	0.65
114224	0.59	1.30	0.74	0.54	0.37	0.83	0.70	0.88	0.59	−0.44	0.93
2153	0.23	1.78	0.32	0.84	1.13	1.30	0.99	1.49	−0.18	−0.35	0.03
55825	−0.20	1.43	0.82	0.75	1.90	0.91	0.93	1.53	−1.12	0.04	0.44
6503	1.07	1.09	0.58	0.45	0.79	1.27	0.61	0.40	0.20	1.09	0.51
7913	0.74	0.38	0.75	−0.88	−0.27	0.55	0.95	0.62	−1.06	−1.38	1.70
30834	1.36	−0.23	0.88	1.26	1.21	−0.55	−0.36	0.45	0.30	−0.01	0.31
26999	0.95	1.08	1.08	1.14	0.68	0.40	0.80	0.79	−0.58	−0.01	1.71
286437	0.27	1.68	0.85	0.55	1.37	1.97	0.57	0.98	−0.83	−0.43	0.89
4277	1.15	1.68	1.25	0.76	−0.04	1.39	−0.16	2.18	−0.58	−1.13	0.64
5698	1.13	0.20	0.73	3.00	1.24	0.60	0.14	0.18	−1.15	0.05	0.24
4318	−0.48	1.42	0.57	−0.07	1.19	2.13	1.22	0.92	−0.52	0.09	−0.85
10616	−0.93	0.33	0.37	−0.37	−0.11	0.63	1.17	1.32	0.23	0.23	0.83
23012	−0.12	1.99	0.83	0.14	0.66	2.08	2.05	1.25	−0.19	0.30	−0.10
100129361	−0.41	1.17	0.12	−0.87	0.69	2.17	0.22	1.48	−0.03	−0.69	1.23
10742	1.27	−0.11	−0.07	0.50	2.51	1.59	−0.28	1.29	0.20	0.53	1.14
196264	0.53	1.90	0.23	0.40	1.52	1.72	0.64	1.46	−1.03	−0.46	0.35
27197	0.52	1.68	0.11	0.86	1.19	0.76	0.01	1.50	−1.24	0.30	0.62
7529	0.90	1.85	0.66	−1.22	1.39	1.01	0.50	1.01	0.01	0.24	0.87
94235	−0.99	1.29	0.27	1.86	1.27	1.57	−0.33	0.76	−1.95	−0.40	−1.23
352961	1.94	0.65	0.87	1.11	0.46	0.69	−0.22	−0.68	0.31	1.29	1.04
49856	−1.11	2.08	1.20	0.31	1.03	0.65	1.78	0.14	−0.41	−0.03	0.28
9448	−0.22	1.73	0.69	−0.29	0.59	1.97	1.05	1.19	0.25	−0.01	0.44
9525	1.17	1.85	1.07	−0.99	0.07	1.39	0.89	1.57	0.61	−0.67	1.62
100505576	0.50	2.03	0.82	1.04	1.15	1.21	0.48	1.14	0.14	−0.51	0.25
151556	0.53	1.62	0.66	0.75	1.94	1.56	0.24	0.92	−0.43	0.40	1.22
284613	0.94	1.30	1.37	1.91	0.38	0.31	0.18	0.03	−0.32	0.27	1.14

TABLE 2-continued

286223	2.67	1.01	0.83	0.81	0.27	0.89	−0.37	0.97	−0.53	−0.27	−0.69
57061	1.37	1.32	1.18	1.46	0.26	0.77	1.33	−1.18	0.40	0.72	−0.91
9520	−0.29	2.38	0.32	−0.37	1.33	1.67	1.14	0.32	−0.53	0.09	−0.23
202299	0.47	0.12	0.22	1.70	0.34	0.42	1.23	−0.34	−2.27	0.04	−0.76
2015	0.23	1.65	0.33	−0.38	0.60	1.18	0.76	1.35	−1.49	−0.84	0.54
57763	0.65	0.70	1.43	−0.90	0.38	0.55	0.90	0.97	0.05	−0.81	1.86
54778	0.18	2.08	0.55	−0.12	1.49	1.21	0.92	1.13	−0.69	0.52	1.05
762	0.10	2.14	−0.06	0.38	1.31	1.77	1.01	0.66	−0.24	0.19	−0.53
192668	−0.16	0.38	0.06	2.18	1.76	0.63	0.93	1.55	−1.64	−0.80	−1.50
24146	0.61	0.75	0.70	−1.11	0.19	0.64	0.85	0.52	−0.09	0.53	1.15
54843	1.23	−0.47	0.27	0.31	1.88	0.79	0.52	0.71	−0.62	0.25	1.08
55374	−1.38	1.73	0.98	0.78	1.09	1.26	0.80	0.41	−1.71	0.14	1.19
79603	0.24	1.41	0.56	−0.14	2.37	1.73	0.22	0.87	−1.87	0.41	−0.18
3577	0.41	1.65	0.38	0.78	1.05	1.94	1.08	0.95	0.22	0.20	−0.45
10385	1.37	−0.04	1.81	0.77	1.33	1.48	0.17	−0.19	−0.89	−0.75	−0.27
79792	0.44	−0.84	1.06	1.48	−0.70	0.09	0.76	−0.06	0.83	0.04	−0.91
84674	−0.10	1.92	0.49	−0.08	0.89	1.17	1.17	1.35	−0.49	0.06	0.21
51131	2.53	0.00	0.42	1.15	1.55	0.04	−0.15	0.76	−0.34	0.45	1.57
5966	−0.25	2.05	0.05	−1.56	0.88	0.99	0.70	0.06	−1.99	0.25	0.28
9733	1.24	0.09	1.24	−0.12	0.44	1.04	1.05	−0.65	0.71	0.62	0.22
10328	1.46	0.72	1.45	−0.45	0.42	1.19	0.22	−0.96	−0.08	−0.14	−0.22
255231	1.36	−0.16	0.87	0.96	1.48	0.44	0.65	−0.22	−0.43	−0.38	0.83
25801	0.75	1.99	0.56	−0.33	0.66	0.95	1.23	1.93	−0.35	−0.04	−0.34
6352	0.77	0.97	0.84	0.75	0.81	0.56	−0.17	1.43	−1.63	−0.89	1.85
54811	2.78	0.89	0.42	−0.23	0.04	0.69	−0.38	−0.41	1.33	0.16	0.03
59348	0.92	1.52	−0.06	−1.02	0.65	1.83	0.48	1.01	−0.88	0.18	0.58
9967	0.34	1.38	0.42	−0.18	0.82	1.13	1.04	0.01	0.19	0.42	−1.21
2533	0.63	1.64	0.60	0.06	1.33	0.87	0.79	1.42	−0.11	0.06	0.98
28985	0.87	0.08	1.86	0.77	0.38	2.11	−0.30	0.53	−0.45	−0.71	1.60
55234	1.08	1.66	0.78	−0.39	−0.24	1.02	0.09	1.09	0.76	0.11	1.58
1301	0.58	0.52	0.09	1.35	1.68	0.40	1.30	0.14	−1.27	−0.59	−1.00
84803	0.77	1.75	0.09	−0.19	1.09	1.49	1.32	1.46	−1.63	−0.04	0.34
100506779	1.03	0.52	1.04	0.95	−0.25	0.59	0.61	1.56	0.60	−0.84	1.97
197135	0.86	0.54	0.70	1.70	1.12	1.12	−0.13	1.75	−1.20	−0.31	1.55
3614	0.96	1.83	0.45	1.02	0.05	1.63	0.31	1.20	0.04	−0.59	0.18
80781	0.34	0.80	−0.26	1.12	1.50	1.39	0.87	−0.60	0.01	1.40	0.88
5586	0.82	2.16	0.30	−1.31	1.42	1.77	0.51	−0.09	0.04	1.01	−0.23
79415	−0.90	0.99	1.16	0.88	0.65	0.73	1.39	0.74	0.29	0.33	0.22
8893	1.33	−1.57	1.62	0.98	−0.49	0.54	−0.32	1.23	0.11	−2.02	0.86
79736	−0.29	1.26	0.56	0.09	1.61	0.35	0.66	−0.24	−1.38	−0.24	−0.37
5770	0.41	1.10	0.12	0.64	0.96	1.02	0.64	0.10	−0.69	0.96	−1.02
9360	0.55	1.10	0.39	−0.08	0.54	1.34	0.98	0.83	1.00	−0.98	0.10
29940	0.95	2.13	−0.14	−1.14	1.24	0.94	1.56	0.98	−1.34	0.34	−0.17
7150	2.22	0.31	0.27	−0.34	−0.25	1.11	0.48	−0.64	0.16	−0.13	−0.72
84964	0.31	−0.89	1.78	1.24	−0.29	−0.06	0.67	1.82	−0.02	−0.78	1.67
10614	1.76	1.99	0.77	−1.31	−0.09	1.62	0.85	0.60	−1.08	−0.71	−0.06
147923	0.45	0.82	0.57	0.48	1.70	1.89	−0.09	1.09	−0.96	0.36	0.87
284029	0.56	1.66	0.65	0.91	1.60	1.44	0.87	1.52	−0.73	−0.02	0.54
54952	−1.00	1.41	1.18	0.24	1.67	1.29	0.71	0.98	−1.15	−1.42	0.67
57476	1.90	−0.34	0.80	1.04	0.08	1.05	1.07	1.17	−0.65	0.31	0.53
8745	−0.18	−0.01	2.00	−0.14	0.00	0.11	0.78	0.86	−0.61	0.67	−0.09
22928	−0.55	2.68	0.68	0.38	0.74	0.84	0.96	0.53	−0.67	−1.04	0.61
25880	1.35	−0.51	0.99	1.52	0.32	1.42	0.81	0.68	1.25	−1.14	0.66
28638	1.68	−0.07	0.91	1.16	0.90	0.34	0.41	1.54	0.06	0.48	1.13
29933	−0.12	2.20	−0.13	−0.29	0.67	0.55	1.14	−0.22	−0.91	0.64	−0.33
30009	1.57	0.87	1.50	1.10	0.29	0.91	0.31	1.27	−0.98	−0.42	1.09
3554	−0.20	1.25	0.05	0.01	1.49	1.69	1.08	1.14	−1.73	0.14	−1.36
8821	1.81	−0.27	0.79	0.11	0.92	0.10	−0.38	1.87	−1.03	0.37	1.31
10943	−0.82	1.44	0.47	0.70	1.31	1.19	0.71	1.43	0.23	0.14	1.36
57724	0.61	1.42	0.76	0.56	0.27	1.57	−0.17	1.99	0.49	−0.19	1.02
100506282	−0.07	0.74	−0.53	0.01	0.89	1.95	−1.25	0.53	−1.01	0.05	−0.26
147699	0.22	1.70	0.96	0.95	0.97	0.78	1.39	0.99	−0.81	0.07	−0.33
3002	1.40	0.57	0.71	0.54	0.99	1.01	0.60	1.91	−1.01	−0.19	1.05
389320	1.57	1.12	2.12	0.00	−1.54	0.65	−0.73	−1.55	1.05	−0.61	0.70
9914	−0.40	1.76	−0.16	0.77	1.89	1.04	1.22	−0.06	−0.19	0.43	−1.13
10804	0.49	1.50	0.51	−0.28	1.35	2.22	0.90	0.30	−0.80	0.74	−0.01
51439	0.69	1.97	0.43	−0.38	1.46	1.59	0.98	1.18	−0.17	0.32	0.55
814	0.95	0.46	1.09	1.10	1.19	1.02	0.51	1.22	−0.06	−0.03	1.23
5272	2.13	1.17	0.13	1.86	0.91	1.06	0.87	0.19	−0.51	−0.21	1.19
8428	1.84	1.70	0.16	1.13	0.66	0.00	0.54	0.98	0.51	−0.54	1.42
23048	2.57	−0.01	0.94	0.21	−0.59	0.81	0.85	−0.35	0.48	−0.79	0.91
344558	0.74	0.36	0.16	0.16	1.04	2.22	0.64	1.22	0.82	0.42	0.44
79078	2.24	0.25	0.60	0.34	1.06	1.02	−0.36	−0.43	0.20	−0.55	0.20
81606	2.52	0.10	0.75	0.87	0.65	−0.09	−0.51	0.85	0.30	0.08	1.25
64377	2.02	1.14	−0.65	0.58	0.67	0.51	1.91	1.05	−0.55	0.16	−0.13
57501	1.58	0.16	0.24	1.80	0.46	0.96	0.62	0.91	−0.83	−0.51	0.22
5991	−0.76	1.31	−0.08	−0.70	1.25	1.43	0.81	−0.71	−0.33	0.77	−0.36

TABLE 2-continued

90075	1.22	0.04	1.13	−0.22	0.09	0.17	−0.46	1.92	−0.28	−0.05	0.73
375341	−0.16	2.46	0.28	−0.15	0.87	1.81	0.37	0.21	−0.73	0.03	0.21
100130548	−0.28	0.79	−0.17	1.39	1.47	−0.18	1.85	1.51	−0.18	−0.70	0.20
114786	0.18	−0.33	0.18	0.15	1.43	1.42	0.86	2.80	−1.10	0.01	−0.43
150084	1.25	0.66	−1.41	0.71	0.30	−0.46	2.19	0.68	0.28	0.00	0.06
55012	0.42	2.15	0.26	−0.14	1.51	1.48	1.12	0.75	−0.90	−0.32	0.57
147525	−0.06	1.45	0.95	2.63	1.24	−1.14	0.73	0.72	−1.12	0.69	0.95
54557	0.59	2.07	0.35	−0.05	1.50	1.79	0.93	0.64	−0.54	−0.02	0.72
56267	0.68	1.12	0.66	0.00	1.40	0.55	0.51	−1.04	−0.31	−1.27	2.06
51176	0.94	0.73	1.19	0.97	1.09	1.34	−0.10	1.68	−0.17	0.40	1.23
10468	0.69	0.48	0.50	0.02	0.92	0.94	1.12	−1.83	−0.50	1.95	−1.06
23258	0.33	2.08	0.61	0.09	0.54	1.76	1.08	0.95	−0.33	0.11	0.44
90768	0.94	0.64	0.78	1.61	1.01	0.49	0.60	1.84	−1.64	−1.32	−0.38
134957	−0.56	2.12	0.46	−0.53	0.73	1.82	0.91	1.02	−0.17	−0.11	0.44
80342	1.33	0.34	0.89	0.53	0.13	0.34	0.28	1.29	0.80	−0.40	1.93
91351	0.10	1.95	0.83	0.14	1.02	1.47	0.92	1.37	−0.12	0.11	0.83
29916	−0.08	1.78	0.79	0.64	0.74	1.63	1.25	−0.33	−0.90	−0.74	−0.48
8519	0.89	1.30	0.22	1.44	1.02	0.77	0.61	1.56	−0.27	0.36	0.81
2113	2.02	0.13	0.53	1.00	0.61	0.39	0.46	1.48	0.16	0.65	1.32
55770	0.60	0.06	0.36	0.01	0.40	1.04	−0.23	0.99	0.29	0.76	1.44
91833	0.45	2.25	0.37	−0.15	1.37	1.26	0.24	0.42	−0.54	0.23	0.99
117177	−0.60	1.24	0.82	0.82	1.56	1.51	0.97	1.34	−1.48	0.31	0.76
546	−0.01	1.70	0.81	−0.48	0.46	1.21	0.85	0.12	0.44	0.92	0.15
4253	−0.14	1.90	0.97	0.59	1.30	1.46	0.76	0.17	−0.48	0.41	1.74
23214	0.36	1.22	0.42	0.52	0.44	1.66	1.25	0.88	0.49	−0.29	0.40
53347	1.13	0.52	0.51	0.39	1.80	0.65	0.03	1.42	0.08	−0.21	1.10
56888	0.83	1.90	0.98	0.93	1.15	0.21	0.71	1.29	0.74	1.09	0.34
777	−0.64	1.29	0.70	0.27	0.87	1.67	0.84	0.60	−0.91	0.25	−0.91
100216545	0.22	1.92	1.46	0.35	−0.38	2.02	0.78	−1.40	−0.32	−1.32	−0.63
8879	0.44	1.20	0.78	−0.59	1.65	1.47	1.07	−0.07	−0.56	0.00	0.19
9759	0.72	2.01	0.65	0.21	0.45	1.28	0.07	1.02	0.52	−0.27	0.34
26578	0.68	1.82	0.77	−0.03	1.27	1.69	0.70	0.87	−0.17	0.31	−0.22
4050	1.24	0.75	1.10	0.97	1.15	1.11	0.84	1.04	0.10	−0.02	0.83
4236	1.39	1.80	0.64	0.59	1.39	0.06	0.29	0.08	0.28	−0.44	0.50
54491	0.58	1.64	0.86	0.89	0.86	0.49	0.77	1.34	0.12	0.11	1.09
55847	0.70	1.63	0.58	−0.42	2.24	0.33	0.51	0.95	−1.47	−1.03	0.25
100132707	−0.29	1.25	1.04	1.40	1.93	1.29	−0.14	1.03	−0.96	−0.49	0.84
55884	0.84	1.93	−0.23	−0.12	1.56	2.12	0.32	0.51	−1.73	−0.19	−0.43
83607	2.29	1.09	1.92	−0.29	−1.00	1.17	0.14	0.69	0.39	−0.23	0.70
9252	0.79	1.76	0.63	−0.51	1.63	2.18	0.01	0.87	−0.60	0.79	1.59
55119	−0.47	0.89	1.10	−1.07	0.09	1.28	0.93	0.92	−0.05	0.27	1.60
57520	−0.19	1.25	0.23	0.17	1.25	2.16	0.89	1.30	−1.12	−0.70	−0.46
79818	0.32	2.65	0.87	−0.10	2.00	1.00	0.88	0.39	−0.87	−0.27	0.61
8320	0.99	0.59	0.27	1.15	1.49	0.52	0.78	1.25	−0.66	−0.29	2.05
2792	0.50	0.39	0.84	0.38	−0.25	0.04	−0.08	1.59	0.58	−0.57	−0.11
54910	2.60	−0.10	−0.02	−1.29	0.13	0.44	0.65	0.36	0.67	0.85	−0.63
55114	2.50	0.98	0.68	1.83	0.11	0.88	−0.55	0.52	0.26	−1.49	−0.30
56253	1.02	0.85	0.39	−0.53	1.13	1.34	−0.02	1.25	−0.01	0.41	1.86
65082	1.06	1.62	0.08	−0.31	1.29	0.88	1.13	0.98	−0.34	−0.93	2.21
84719	−1.18	1.53	0.94	0.46	1.00	1.54	1.14	0.61	−0.14	0.05	0.66
253558	0.01	0.49	1.38	0.35	−0.13	1.26	1.05	1.19	−0.40	0.30	2.03
6777	−0.50	1.64	0.39	0.78	0.54	1.17	1.41	0.11	0.29	0.21	0.33
80025	1.82	1.80	0.20	0.10	1.03	1.26	0.57	1.24	−0.42	−0.59	−0.24
84662	0.61	1.80	−0.94	−0.33	1.78	2.12	1.20	−0.62	0.32	−0.66	0.02
89890	−0.65	2.49	1.13	−0.34	1.21	0.86	0.32	−0.65	−0.49	0.46	1.02
10390	0.67	1.39	0.54	−0.69	1.68	0.96	0.88	1.49	−0.90	0.27	−0.72
2841	2.51	0.55	0.30	−0.18	0.62	0.06	−0.10	0.97	−1.02	−0.39	1.74
3904	0.77	−0.42	0.80	2.51	0.13	0.95	1.18	0.65	0.84	−1.06	1.43
140460	−0.11	2.16	0.77	−0.72	0.50	1.35	1.65	0.95	−0.18	−0.56	0.11
9605	−1.02	1.87	0.88	1.02	0.03	1.54	1.51	−0.21	1.08	−0.21	−0.15
283349	0.63	1.99	0.51	−0.21	1.09	1.87	0.57	1.23	−0.11	−0.47	0.95
51246	0.60	0.57	0.51	2.19	0.73	1.63	0.37	0.08	0.50	0.06	0.81
148268	0.60	1.09	0.73	0.63	1.36	−0.69	0.19	0.55	0.08	0.28	−0.67
26589	−0.10	−0.28	2.06	1.41	1.27	0.48	0.64	−1.12	−0.65	−0.67	0.72
7049	1.32	0.17	1.16	0.92	0.95	1.02	−0.25	1.40	−0.92	−0.32	1.46
2791	0.42	1.64	0.34	1.17	1.26	2.19	1.17	1.24	−1.01	−0.53	0.44
51455	0.25	1.09	1.24	−0.48	0.99	0.97	0.45	1.46	−0.58	0.15	1.21
1178	0.20	1.78	0.51	−0.13	0.64	1.87	0.98	2.19	−0.60	0.32	−0.25
79153	−0.58	1.62	0.72	1.27	0.78	1.50	0.97	1.38	−0.35	−0.30	0.47
101928524	0.08	1.77	1.16	−0.46	0.73	0.94	1.31	1.31	−0.02	−0.31	0.93
11064	0.12	−0.51	1.36	1.59	0.01	−0.03	0.05	0.79	1.94	0.51	0.43
23429	0.90	1.15	0.20	−1.70	0.21	1.99	1.03	0.49	0.29	0.20	0.01
5170	0.68	1.76	0.38	0.14	0.81	2.13	0.73	1.11	0.69	−0.52	0.06
10677	0.35	1.90	0.81	0.36	1.44	1.66	0.83	0.69	0.22	0.20	0.19
3772	0.14	2.03	0.52	0.51	1.10	1.60	0.82	1.35	−0.24	0.07	−0.32
128061	0.76	1.14	1.31	1.07	0.65	2.07	0.85	1.41	−0.41	−0.93	1.16
50856	1.13	1.69	0.48	−0.23	1.62	1.62	1.15	1.23	−1.44	−0.54	0.24

TABLE 2-continued

6198	1.34	0.64	0.55	−3.33	0.42	0.38	1.20	0.40	0.29	−0.61	0.63
101927588	1.05	1.26	0.45	2.73	0.04	−0.27	−0.20	1.03	−1.19	0.20	−0.19
2000	1.08	2.17	0.66	−0.34	0.03	1.33	0.91	1.07	−0.17	−0.57	0.68
493753	0.60	0.88	1.75	−0.83	1.79	0.96	0.54	0.70	−1.86	−0.62	1.51
23081	1.82	1.08	1.58	−0.25	0.68	1.35	−0.19	1.59	0.01	−0.37	1.24
4773	1.31	0.77	0.35	−0.14	1.02	1.27	−0.15	1.62	−0.86	0.63	1.80
10178	0.94	1.45	1.09	0.56	0.80	1.72	1.02	1.43	−0.28	−0.48	0.71
4974	0.11	2.44	0.35	0.13	−0.07	1.00	0.14	0.44	1.03	0.18	0.37
83860	0.98	1.57	0.03	−0.62	0.37	1.25	0.73	1.36	−1.88	−1.19	0.73
91612	0.76	1.04	0.38	0.62	2.28	0.47	−0.43	1.24	0.05	−0.19	1.48
2178	0.55	1.26	2.07	1.92	−0.26	1.78	0.19	1.00	−0.18	−0.95	0.29
55303	1.32	1.02	0.67	0.91	1.67	0.74	0.48	1.27	−0.46	0.03	1.72
221002	0.33	1.15	0.77	0.59	0.99	1.68	0.12	1.29	−0.88	−0.21	1.82
3930	0.30	1.44	0.47	0.22	0.11	1.61	1.22	1.38	−0.60	−1.01	0.90
55471	−1.10	1.68	1.02	−0.60	1.18	1.09	1.62	−0.08	−0.28	0.03	1.16
9354	1.46	0.54	0.75	0.02	0.38	1.12	1.15	−0.05	0.60	−0.09	1.36
83700	0.50	0.45	−0.11	0.81	−0.48	1.17	0.99	1.41	−0.76	0.43	1.16
9140	−0.73	0.84	1.14	0.11	0.89	0.88	1.51	0.57	−0.51	0.79	0.68
23526	1.54	0.94	0.81	0.93	−0.64	1.23	0.37	0.55	0.58	−1.06	1.41
23590	−0.05	1.26	0.78	0.60	−0.05	1.57	1.36	0.50	−0.54	0.09	−0.78
9270	0.84	0.38	1.22	−1.18	−0.41	1.27	0.87	0.46	−0.44	0.06	1.13
10627	0.44	1.93	0.96	−0.62	1.75	1.01	−0.14	0.95	−0.08	−0.14	1.40
26048	0.24	0.49	1.43	1.06	−0.63	0.73	−0.32	−0.65	1.04	−0.25	0.28
917	1.55	−0.41	0.92	1.54	1.57	0.96	0.01	1.21	0.31	0.74	1.00
94039	0.83	0.62	0.80	1.02	1.49	1.14	0.52	1.38	0.03	−0.66	1.61
4215	0.86	1.75	0.38	0.31	0.62	2.04	0.84	0.33	0.39	−0.56	−0.11
10663	2.22	0.22	0.33	0.83	2.29	0.13	−0.30	1.03	−1.04	0.77	1.09
10308	−0.09	1.79	0.22	−0.93	1.12	1.95	1.16	1.19	−0.74	−0.57	0.04
8527	0.20	0.57	0.04	0.51	−1.51	1.22	0.55	−0.40	2.52	−0.15	0.52
926	0.61	0.47	0.71	1.26	0.68	0.83	0.32	1.73	−0.67	0.70	1.62
9619	1.62	0.12	0.71	0.50	1.60	1.43	0.88	−0.69	−1.34	0.63	0.66
5998	0.62	0.40	0.66	1.43	1.44	0.38	0.92	−0.51	0.37	−0.43	0.62
132625	1.09	1.45	0.38	0.01	0.27	0.66	1.12	1.63	−0.10	−0.30	0.31
88455	0.85	2.27	0.47	0.15	0.62	2.02	0.41	1.14	−0.11	−0.13	1.04
3604	0.10	1.56	0.22	0.88	2.06	1.57	1.63	0.00	−0.42	−0.06	−0.08
100507398	−0.25	1.82	0.07	−0.32	0.82	0.17	0.71	0.47	−0.82	−1.01	1.65
58517	0.66	0.22	0.90	−0.78	−0.82	1.14	0.53	−1.04	1.36	0.06	−0.21
51192	−0.18	1.98	0.69	0.41	0.96	1.55	1.30	1.40	0.22	−0.50	0.29
2177	0.65	0.97	1.23	−0.22	−0.14	1.53	0.87	0.09	−0.85	−1.31	−0.41
57097	0.50	0.85	0.54	0.62	0.51	0.58	−0.07	2.33	−1.58	0.72	1.28
11214	0.59	0.75	0.43	0.66	0.71	1.74	1.23	0.55	0.35	0.42	0.28
4600	1.21	1.31	0.41	1.55	0.72	1.01	0.83	1.26	0.04	0.03	0.38
84255	−0.05	1.47	0.53	0.24	1.59	1.69	1.15	1.45	−1.07	0.11	0.34
11216	0.19	1.36	0.45	−0.89	1.30	0.18	0.87	0.61	0.07	0.80	1.27
162417	0.06	1.77	0.33	0.19	1.35	1.42	0.28	−0.08	−1.94	−0.09	0.91
101928617	1.50	1.43	0.45	2.39	0.53	0.62	0.59	1.14	0.11	−1.13	1.12
10617	0.41	−0.15	0.84	0.50	−0.06	0.63	1.59	0.03	0.90	−1.13	1.28
1326	0.53	2.43	0.34	−1.12	1.37	1.18	0.88	1.00	−1.77	0.23	−0.12
23315	0.19	1.76	0.60	0.89	0.67	1.35	0.90	−0.11	0.73	0.17	0.38
10791	0.35	0.03	0.73	2.07	1.02	0.89	0.75	1.02	−0.63	0.56	0.26
8718	0.85	0.36	1.17	0.14	1.06	0.42	−0.22	0.55	−0.19	0.23	1.01
51571	0.99	1.67	0.76	0.02	0.74	1.74	1.09	0.96	0.20	−0.06	0.70
283521	1.12	0.70	0.42	1.45	0.85	0.92	0.74	1.41	−0.07	−0.18	1.04
51122	0.73	1.30	0.91	0.33	0.54	1.71	0.83	0.87	−1.63	−0.91	1.59
5372	0.87	1.51	−0.30	0.03	1.53	1.61	0.65	0.66	0.40	0.84	−0.63
9830	1.60	0.34	1.21	1.44	1.06	−0.50	0.32	1.02	−0.07	1.06	0.50
314	0.87	2.05	0.30	0.23	0.51	2.08	1.28	0.83	0.42	−0.07	−0.06
51761	1.10	0.25	0.58	−0.01	0.67	0.45	0.84	3.18	0.18	−0.06	−0.39
493861	0.96	−0.75	1.10	0.37	0.11	1.50	0.27	0.40	−0.55	0.44	1.12
6672	0.53	1.85	0.28	0.38	1.94	1.21	0.99	0.92	−0.22	0.13	0.07
55578	−0.67	0.83	0.70	0.55	0.67	1.37	1.08	1.45	0.14	0.60	1.26
159	0.98	1.82	0.16	−1.09	0.25	0.00	0.37	1.31	1.43	0.31	0.48
9683	0.83	1.89	0.35	0.69	1.18	1.74	0.67	1.27	−0.16	−0.02	0.27
26287	0.73	0.27	−0.10	0.70	0.88	0.95	0.53	1.32	−0.41	0.70	0.07
57147	−0.84	1.60	0.94	0.45	1.55	1.49	1.10	0.58	−0.29	−0.29	0.92
1808	1.64	0.89	0.96	0.15	0.52	1.13	0.85	1.00	−0.53	−0.26	1.02
23355	−0.35	1.71	0.76	0.83	1.12	1.25	1.07	0.16	−0.04	0.80	0.19
8115	1.01	1.89	−0.31	1.19	1.25	1.15	0.86	1.26	−0.42	−0.68	−0.61
94120	1.37	1.68	0.14	−0.31	1.89	1.29	0.21	0.72	−0.94	0.11	1.11
22950	0.63	1.64	1.21	0.76	1.55	1.81	0.87	0.90	−1.41	−1.03	0.58
27342	0.16	2.11	0.06	−0.21	1.34	1.20	1.26	1.38	−0.14	0.34	0.14
64926	1.48	0.15	0.69	0.94	−1.20	0.52	0.77	1.39	0.60	−0.20	1.57
100507331	0.99	0.83	0.89	−0.67	−0.38	0.68	0.17	−0.24	1.46	−0.53	−0.02
4068	1.15	−0.38	0.44	−0.19	0.42	1.40	0.95	1.39	−0.63	−0.42	1.64
60481	1.66	1.09	0.23	−0.45	1.43	−0.01	0.72	0.06	1.43	−0.25	0.41
2634	1.17	1.10	0.29	1.72	1.38	1.24	0.69	1.45	−0.97	0.08	0.36
55824	1.01	1.35	0.89	0.88	0.78	1.87	0.94	1.37	0.01	−0.14	0.95

TABLE 2-continued

79074	0.01	1.34	0.51	−0.92	0.49	1.07	0.88	0.72	−0.71	−0.15	1.07
220930	−0.60	1.48	−0.06	0.33	0.26	2.02	1.50	0.91	−0.30	−0.09	0.65
64421	0.78	1.57	0.87	0.15	0.12	1.70	0.38	1.38	−0.35	−0.41	0.79
64121	1.60	2.31	0.25	0.49	1.30	1.49	1.24	−0.35	−0.52	−0.20	0.12
137835	0.67	1.50	0.48	−0.21	0.62	1.64	0.32	1.77	−0.46	−0.75	1.12
57674	0.75	0.98	0.66	0.81	1.43	1.18	1.14	1.29	−1.06	0.98	0.24
728392	0.94	0.69	−0.12	0.59	1.80	1.62	0.62	0.60	0.17	−0.26	1.61
329	0.38	0.64	0.85	−1.56	0.82	1.38	0.85	0.41	−0.11	−1.01	1.38
55279	0.32	2.40	0.68	−0.06	1.46	1.26	0.80	1.11	−0.85	−0.02	0.71
7107	0.82	1.49	0.72	0.40	2.26	1.48	0.57	1.00	−1.92	−0.21	0.14
9416	−0.06	0.23	1.52	−0.15	0.69	1.76	1.16	−0.29	0.75	−0.61	0.98
137964	2.56	0.12	0.97	−1.16	−0.65	0.42	1.16	−2.19	0.86	0.70	0.57
3431	0.86	1.19	0.66	1.43	1.56	1.06	0.55	1.33	−0.27	0.16	1.14
4140	0.60	1.73	0.75	0.26	−0.47	1.08	1.16	−0.18	0.35	−0.66	0.53
59269	0.58	0.60	1.36	1.52	0.02	1.56	1.60	1.17	−1.21	−0.51	0.45
7846	1.03	0.56	0.63	0.04	0.74	0.87	0.79	0.77	0.19	−0.39	−0.33
100652740	0.30	0.97	1.47	0.59	0.24	0.29	0.92	1.69	0.07	−0.62	−0.89
23398	0.21	0.44	1.35	−1.17	0.10	0.47	0.70	0.67	0.97	−0.42	2.08
158747	−0.04	2.04	0.63	0.13	1.51	1.61	1.18	1.23	−0.74	0.10	0.42
285512	0.28	1.69	0.75	0.26	0.30	2.21	0.39	1.10	−0.19	−0.46	0.95
3937	0.84	0.90	0.75	−0.13	0.47	0.49	0.50	1.43	−0.03	0.81	1.85
730051	1.09	1.57	0.62	−0.82	−0.93	0.66	0.22	1.04	0.32	−0.14	1.42
9320	1.55	1.08	0.07	−2.00	0.47	0.79	0.86	0.14	0.43	0.46	0.76
6932	1.37	0.50	0.73	0.44	1.17	0.61	0.47	1.06	0.39	0.39	1.63
79722	0.88	1.17	0.74	0.27	1.50	1.30	0.56	1.77	−0.89	0.27	0.12
115362	1.49	−0.02	1.26	1.46	1.19	0.55	−0.05	1.99	−0.51	0.69	1.24
29909	0.88	1.28	0.65	0.90	1.66	0.88	0.47	1.80	−1.36	0.24	1.33
440503	0.33	2.05	0.14	0.45	0.59	0.93	1.69	0.32	1.11	−0.18	−0.34
80183	0.27	1.91	0.48	0.38	1.01	1.58	1.33	1.23	−0.22	−0.40	−0.76
80709	0.67	0.92	0.61	0.58	0.59	1.01	0.60	1.04	0.99	0.16	1.28
10562	−0.39	2.05	0.92	0.49	0.72	1.00	1.20	1.78	−1.10	0.02	−0.06
64780	0.26	0.63	1.04	−0.26	−0.09	2.00	1.38	0.06	1.25	0.02	−0.14
155038	1.56	1.12	0.57	0.95	1.41	1.01	0.72	0.50	−0.21	0.33	1.28
1783	0.38	1.95	0.70	−1.11	1.71	1.64	0.68	−0.45	−0.12	0.68	0.07
100287569	0.32	1.40	0.59	0.71	−0.45	1.00	1.34	0.79	−0.50	−0.35	0.59
5696	1.12	0.03	1.78	0.93	0.89	−0.08	0.22	−2.47	−0.20	0.67	0.03
11066	−0.04	1.16	0.44	1.21	0.14	0.91	1.70	1.01	0.41	0.62	−0.32
122553	−0.63	1.39	0.56	−0.93	0.77	0.80	1.42	0.31	0.49	−0.09	1.37
50484	0.41	2.16	0.69	−0.45	1.31	1.81	1.13	−0.29	−0.26	0.13	0.17
9847	0.82	1.07	1.59	0.11	1.41	0.76	0.81	0.31	−0.69	0.01	1.15
129285	−0.58	1.41	0.55	0.54	0.61	0.82	0.98	0.85	0.04	0.54	2.65
9794	0.86	2.10	0.43	0.18	0.45	1.39	1.23	0.21	0.26	−0.07	1.37
84309	1.08	0.92	1.33	−1.60	0.08	1.20	−0.35	−0.09	0.78	−0.73	0.06
65258	0.91	2.01	0.10	−1.04	1.16	2.05	0.81	0.84	−0.12	−0.49	0.44
5562	−0.31	2.07	0.30	−0.88	0.95	1.03	0.81	1.47	0.02	0.12	1.35
123036	1.32	0.58	0.73	0.34	1.88	0.62	0.25	1.61	−1.02	0.44	1.77
84166	1.45	0.08	1.27	1.65	−0.26	0.73	0.73	1.25	0.76	0.07	0.89
253143	0.30	1.74	1.33	1.03	0.73	1.99	0.97	0.09	−0.11	0.01	−0.40
1236	1.10	−0.17	0.59	1.24	0.65	0.70	0.96	1.18	−0.18	0.29	1.06
266747	0.48	1.77	0.88	0.42	0.75	1.35	0.73	1.32	−0.25	−0.07	0.66
25988	0.89	0.80	1.02	−0.37	0.31	0.61	0.39	0.38	0.39	0.75	0.64
6515	0.65	1.85	0.11	−0.06	0.41	1.51	1.55	1.39	−0.40	−0.12	−0.35
90592	−0.05	1.09	1.02	0.46	0.73	1.68	1.49	−0.92	0.64	−0.39	1.35
6867	0.94	2.45	0.30	−0.47	0.69	1.84	0.32	0.56	−0.40	−1.37	−0.74
23041	−1.09	0.76	0.48	−0.39	0.74	1.89	0.63	1.64	−0.08	0.66	1.60
100289230	0.81	1.13	0.29	−1.19	1.80	1.95	0.86	0.19	−2.01	0.16	0.13
57169	0.55	1.50	0.33	0.83	1.63	1.61	0.13	1.45	−0.63	0.03	0.98
1105	0.97	1.24	0.49	−1.30	0.11	1.55	0.86	0.95	−0.32	0.12	0.77
943	0.19	1.34	0.36	1.00	0.25	1.11	2.05	−0.21	−0.35	0.17	−1.44
3275	0.48	1.06	0.41	0.95	1.11	0.74	0.81	0.07	1.71	0.51	1.21
8851	0.57	2.04	−0.04	0.72	1.27	0.56	0.68	1.06	−0.27	0.48	0.78
168537	1.09	0.82	1.02	0.81	1.09	1.16	0.58	1.38	0.38	−0.37	1.66
256236	0.85	0.80	0.33	1.03	0.91	0.55	1.48	1.29	−1.55	−0.27	0.15
26235	−0.26	1.84	0.70	−0.39	1.09	2.06	0.36	1.17	−1.42	−0.11	0.64
9363	1.27	1.45	−0.19	−0.26	1.01	0.60	0.92	−0.10	−0.16	1.03	−0.53
729683	0.87	1.30	0.21	1.98	0.50	0.61	−0.72	0.38	1.28	0.16	1.17
388969	1.18	1.54	0.74	−1.94	0.39	1.23	0.79	−0.18	1.07	−0.04	1.74
4818	0.57	0.76	1.05	0.49	0.11	0.45	0.90	2.00	−0.75	0.16	1.11
93953	−0.35	1.64	1.34	−0.42	0.96	1.36	0.82	1.36	−0.55	−0.15	0.92
28982	1.27	1.28	1.42	−0.60	0.68	1.61	−0.22	−0.74	−0.24	−0.61	1.83
84911	−0.60	0.73	0.60	0.16	1.09	1.40	−0.04	2.50	−0.92	−0.46	0.44
66036	1.79	1.40	0.57	−0.19	0.54	2.24	0.42	1.37	−0.11	−0.52	1.38
9750	0.82	1.48	0.74	0.49	0.52	0.91	0.47	1.42	0.37	−0.08	1.47
9938	1.05	1.22	0.74	0.82	0.41	1.80	0.81	0.70	0.64	0.06	0.58
120425	0.77	1.52	0.76	0.58	1.25	1.31	1.33	0.85	−0.58	−0.15	0.79
6840	0.86	1.20	0.59	0.19	0.74	1.52	0.40	1.72	−0.21	0.39	0.62
26268	1.31	1.98	1.07	−0.61	1.10	1.08	−0.30	1.30	−0.88	0.14	0.52

TABLE 2-continued

55206	0.70	2.42	0.60	−0.30	0.70	2.19	0.42	0.46	0.47	−0.23	0.26
355	−0.19	1.88	0.04	0.15	2.14	1.10	0.82	1.07	−1.25	−0.22	0.34
50615	1.49	1.00	0.22	0.90	1.16	0.94	0.97	0.88	−1.86	0.04	−0.03
221178	1.14	1.04	0.40	0.98	1.33	0.19	1.08	1.15	0.26	0.44	1.42
11104	−0.35	1.56	1.05	1.98	0.36	1.03	1.12	−0.19	0.52	−1.14	0.36
1117	1.73	0.09	0.77	1.18	2.05	−0.83	1.49	−0.09	0.11	0.27	0.61
374969	0.95	1.62	0.39	0.72	1.64	1.69	0.74	0.50	−0.87	−0.15	0.19
6285	1.66	0.22	−0.29	0.23	0.47	2.40	−0.14	1.60	0.08	−0.53	0.23
387357	0.42	0.58	0.88	0.38	1.49	1.05	0.38	1.75	−0.66	0.32	2.20
2960	0.05	1.75	0.60	0.45	1.98	1.10	0.63	0.93	−0.86	0.37	0.93
100129550	0.98	2.25	0.42	−0.51	0.93	1.92	0.54	0.95	0.15	−0.23	−0.07
54520	1.00	1.95	0.57	0.20	0.83	1.02	0.45	1.01	0.46	−0.36	0.04
10302	1.39	0.92	0.94	2.08	1.20	0.86	−0.13	0.27	−0.68	−0.41	1.09
50939	0.88	1.11	1.52	0.97	−0.52	0.34	−0.48	0.70	0.57	−1.29	−0.37
8802	0.50	1.05	1.24	−2.63	1.10	0.94	0.44	−0.40	−0.45	0.01	−0.50
23332	0.25	1.48	1.22	−0.75	0.32	1.97	0.41	−1.34	−0.45	0.38	0.22
203328	0.84	0.94	0.92	0.73	1.34	1.12	0.86	0.63	−1.00	−0.47	0.74
126231	2.14	0.29	1.06	0.34	0.75	1.21	−0.48	0.66	0.36	0.13	1.63
6993	0.55	1.52	−0.09	0.35	2.13	1.40	0.11	1.40	−0.55	0.33	0.40
58500	1.15	2.33	0.54	−0.27	0.72	0.78	0.11	−0.64	0.90	−0.60	0.86
10507	1.02	1.83	0.47	0.44	0.19	1.52	0.86	0.83	0.35	0.01	0.98
170482	1.64	0.77	0.99	−0.35	2.06	0.48	0.57	2.67	−0.61	−0.90	−0.37
3004	0.69	−0.20	1.10	1.03	1.29	−0.34	0.50	0.91	0.71	1.02	1.57
64895	0.09	1.82	0.86	0.06	1.01	1.49	1.11	0.78	0.00	−0.08	0.87
7850	0.31	1.82	0.25	0.17	0.98	1.74	1.34	0.74	−0.71	−0.03	−0.58
93594	1.85	−0.23	1.06	0.91	0.06	1.25	0.46	1.95	0.16	−0.09	1.96
23215	1.43	0.54	0.85	0.29	−0.17	1.41	0.17	−0.20	1.44	0.15	−0.23
80196	0.42	1.89	0.77	0.07	1.69	1.03	1.17	1.06	−0.58	0.14	0.84
284415	0.88	2.09	1.00	0.02	−0.40	1.54	1.87	1.64	−0.13	−0.06	−1.12
56882	0.75	2.04	0.57	−0.17	0.59	2.13	0.25	0.42	0.57	0.11	−0.13
6508	1.67	0.97	0.51	0.51	1.58	1.36	0.27	−0.80	−0.44	0.23	0.78
79663	0.94	2.44	0.67	−0.06	1.07	1.48	0.26	1.56	−0.03	−0.58	0.72
474344	1.63	0.77	0.91	0.90	1.05	0.46	0.33	0.94	0.17	−0.10	1.94
100505746	1.02	0.80	1.13	0.83	0.59	1.35	1.54	1.32	−0.57	−0.63	1.22
1293	0.70	0.20	0.95	0.85	1.33	1.54	0.96	1.16	−0.57	−0.23	−0.15
10294	0.81	1.92	0.29	−2.02	1.93	0.68	0.58	1.76	−0.19	0.13	1.26
3091	0.47	1.45	0.07	0.04	0.63	1.66	1.04	0.98	−2.00	−0.71	0.26
79573	0.89	1.51	1.47	0.14	0.83	0.66	0.81	0.93	−0.70	−0.33	2.34
9208	0.68	1.13	0.63	−1.15	0.13	1.25	1.10	−0.10	0.95	−0.35	0.52
29116	2.07	0.69	0.37	−0.43	0.03	1.95	0.12	0.83	−0.33	0.11	1.50
92370	0.55	1.14	0.71	0.13	1.12	1.67	1.06	0.80	0.04	−0.29	1.12
9546	0.93	1.19	0.64	1.81	0.58	1.19	0.26	−1.08	0.38	0.71	0.90
253018	0.37	1.54	0.33	0.70	1.54	2.03	0.29	1.51	0.00	−0.62	0.35
10096	0.65	1.15	1.29	−0.25	0.38	0.69	1.65	1.38	−0.20	−0.45	0.82
84138	1.94	0.71	0.61	0.92	1.42	0.62	0.53	−0.60	−0.02	−1.03	0.89
8440	1.15	0.75	0.32	1.35	0.51	1.57	0.37	1.51	0.32	−0.17	1.03
7277	0.59	1.42	0.67	1.32	0.97	0.98	0.59	1.01	−0.39	−0.49	0.50
8269	0.93	1.95	0.42	0.54	1.96	−0.12	0.60	−0.65	−0.21	0.84	0.28
8807	0.55	1.98	0.82	0.56	0.78	1.65	1.12	1.70	−0.51	−0.05	0.59
1235	1.67	1.50	0.33	0.37	1.55	0.12	−0.25	0.85	−0.46	−0.84	0.85
7059	0.89	1.47	−0.02	1.14	−0.06	−0.22	0.71	−0.72	0.00	0.33	−0.07
54971	1.75	2.08	0.38	0.58	0.76	1.60	0.63	0.70	0.64	−0.99	−0.06
57677	0.18	0.05	0.35	−0.01	0.40	2.20	0.17	0.56	0.74	−0.57	0.90
6890	0.26	0.79	0.72	0.98	1.34	1.71	0.64	0.63	−1.03	−0.17	0.66
22944	−0.32	1.94	0.73	0.00	1.44	1.28	1.19	1.12	−0.05	−0.18	1.23
26512	0.49	1.72	0.26	−0.96	1.66	1.82	1.78	0.92	0.02	−0.55	1.06
92797	−0.03	1.19	1.08	−0.37	0.13	1.17	1.27	2.08	0.29	0.15	0.28
5481	−0.13	1.29	0.80	−0.54	1.49	0.89	1.07	−0.15	−0.44	−0.16	1.25
22897	1.63	−0.43	0.51	3.52	0.05	0.28	0.09	0.02	1.28	−0.28	1.15
3620	0.77	1.28	0.63	0.56	1.92	1.06	0.66	1.37	−1.58	0.08	0.03
64766	0.83	0.37	1.77	0.42	−0.57	0.49	1.17	0.48	1.12	−0.57	1.49
8809	0.19	1.61	0.57	0.17	1.19	1.66	1.13	1.69	−0.60	0.21	0.52
116984	1.32	0.97	1.27	1.02	0.99	1.41	1.06	1.03	−1.31	−0.37	1.42
440823	0.90	0.56	0.24	0.70	0.92	−0.15	1.56	1.36	0.18	0.96	0.39
59340	−0.17	1.40	0.32	1.80	0.61	1.00	1.12	1.55	0.73	0.56	0.03
197259	0.04	2.12	0.83	1.57	1.26	0.65	0.65	1.09	−0.49	−0.28	1.28
23670	0.73	1.86	0.32	0.66	1.42	1.25	0.79	1.14	−0.51	0.44	0.65
643314	0.38	0.60	0.37	−0.32	0.79	1.39	1.01	0.50	0.14	0.09	0.93
28526	1.74	0.35	1.07	0.55	0.93	0.70	−0.11	1.52	0.75	−0.26	1.46
55096	1.02	1.94	0.13	−0.08	1.22	1.64	0.56	0.61	−0.58	−0.16	0.11
2796	0.76	0.78	0.24	1.70	0.70	0.46	0.48	−0.44	0.63	0.13	1.22
54509	1.61	0.96	0.22	0.15	0.33	−0.36	1.34	0.29	−1.91	−0.14	−0.07
11120	0.74	1.59	1.22	1.25	0.54	1.62	0.07	0.36	0.70	0.07	0.37
84869	0.27	0.41	1.51	0.07	1.46	1.79	1.91	0.17	0.75	−0.61	0.70
28991	0.57	2.23	0.61	0.06	1.64	1.49	0.50	−0.44	−0.56	−0.06	0.31
154141	−0.32	1.71	0.48	0.68	0.97	1.43	0.93	0.11	0.16	0.55	−0.53
3659	0.85	1.63	0.44	0.41	0.87	2.23	−0.13	1.69	−0.78	−0.51	0.22

TABLE 2-continued

154007	−0.19	1.65	0.32	0.02	0.39	1.85	1.53	1.44	−0.29	−0.70	0.17
116835	0.78	−0.15	−0.17	2.37	0.99	0.77	0.54	1.12	0.12	0.26	−0.34
9488	0.80	1.28	0.77	1.28	−0.25	2.06	0.67	−0.14	0.41	−0.12	0.82
100293516	0.62	0.76	1.92	0.19	0.23	1.07	0.75	0.57	1.62	−0.80	1.85
9217	1.47	1.18	0.82	0.73	1.49	1.54	−0.05	0.49	0.58	−0.07	0.14
10538	−0.09	0.04	1.11	0.93	1.13	1.13	1.29	−0.07	0.25	−0.27	0.46
6935	0.40	0.57	0.10	−0.09	0.26	1.22	1.16	0.67	0.42	0.47	0.38
10443	0.33	0.96	1.05	0.11	0.71	1.52	0.69	0.92	−0.06	0.56	1.76
3837	1.52	1.10	1.48	0.98	0.29	0.83	1.02	0.88	0.28	0.41	0.01
81698	0.50	1.27	−0.17	1.15	1.10	1.20	0.94	−0.19	−0.26	0.57	−0.32
2643	0.99	1.44	−0.26	0.30	0.89	0.61	−0.21	1.51	−2.32	−0.02	1.22
57559	1.17	0.28	0.80	1.87	1.24	0.52	0.84	0.96	−0.53	−0.33	1.18
116842	1.22	1.47	1.24	−0.34	1.56	0.50	0.64	1.46	−0.72	−0.53	1.59
202	1.52	1.00	0.75	0.90	0.73	0.66	0.40	1.37	0.03	−0.21	1.09
9934	0.61	1.54	0.87	0.14	1.44	2.04	0.82	0.82	−1.17	0.24	0.64
100216546	0.98	1.37	0.09	−0.33	1.60	1.27	1.30	1.61	−0.28	−0.58	0.24
9692	1.02	0.38	−0.56	2.06	0.68	0.52	1.27	0.32	0.38	−0.74	0.68
89845	1.66	0.08	1.44	1.47	0.53	0.21	1.07	−0.51	0.40	−0.76	1.25
26034	1.24	1.25	0.80	1.40	1.07	1.25	0.92	1.34	−0.11	−0.16	1.08
10906	0.91	1.62	0.23	1.86	1.01	1.12	1.38	0.13	0.05	0.27	−0.50
84811	0.74	1.40	1.66	0.12	−0.13	1.56	1.04	0.52	0.12	−0.11	0.46
100527964	0.47	0.30	1.34	0.37	−0.34	−0.21	1.15	0.84	1.60	−0.37	1.50
118426	1.01	0.95	0.81	0.19	1.80	1.21	1.04	1.61	−0.72	0.09	0.21
54331	0.27	1.33	0.71	0.62	0.50	1.62	1.42	1.14	0.13	0.26	0.49
94081	0.43	1.31	1.26	−0.58	1.19	0.68	1.33	0.42	−0.71	0.21	0.72
145474	1.04	1.28	0.06	0.15	1.37	2.52	1.11	1.12	−0.57	−0.27	0.00
84969	0.73	0.71	0.64	0.33	1.83	1.20	0.92	0.57	−0.79	−0.46	−0.03
4907	2.13	0.02	0.50	−0.38	0.88	0.65	−0.17	1.47	1.62	0.16	0.74
51735	1.08	1.90	0.65	−0.13	1.37	1.58	0.38	1.25	−0.35	−0.08	0.48
9953	1.18	1.23	1.47	0.26	0.98	1.12	0.86	0.96	−0.19	0.40	1.56
23112	1.51	1.77	0.55	0.67	1.02	1.48	0.19	0.40	1.01	0.23	0.65
91526	0.97	1.90	1.07	0.55	1.12	0.46	1.14	0.65	−0.09	−0.04	1.26
101928017	1.87	0.03	0.21	0.43	1.92	0.24	0.61	0.89	−0.88	−0.07	−0.43
84859	0.28	1.08	1.43	1.70	0.97	0.72	0.52	0.21	0.59	0.52	1.69
159013	0.87	2.04	1.26	0.08	0.73	1.49	1.14	0.74	−0.06	−0.34	1.06
23208	1.08	1.11	1.25	0.52	0.54	0.41	1.02	0.94	−1.17	−0.67	1.05
101928649	−0.40	1.41	1.37	0.14	−0.38	1.40	1.81	−0.35	−0.41	−1.01	0.57
85459	0.54	1.00	0.69	−0.64	0.10	2.21	1.43	0.35	0.59	−0.59	−0.20
9617	−0.11	0.92	1.44	0.33	0.80	1.02	0.78	0.74	−0.78	−0.53	2.48
56898	0.83	0.88	0.66	0.29	0.73	−0.24	1.14	0.11	0.60	−1.18	0.62
387882	1.38	1.03	0.70	0.51	0.55	0.32	0.55	1.23	−0.65	−0.91	1.27
677769	2.09	0.27	0.72	0.83	1.44	0.65	1.55	0.36	0.16	−0.28	−0.25

TABLE 3

gene	symbol	name	fisherz	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49
56904	SH3GLB2	SH3-domain GRB2-like endophilin B2	3.67	0.86	0.03	0.37	0.71	0.24	−0.28	−0.23	−0.13	0.98	1.54	1.43	0.73	1.10	1.44	0.98	0.90
6464	SHC1	SHC (Src homology 2 domain containing) transforming protein 1	3.56	−0.43	−1.06	−1.09	−0.27	0.99	1.19	−0.30	0.90	1.11	0.57	2.34	1.40	0.45	1.58	0.72	0.74
79087	ALG12	ALG12, alpha-1,6-mannosyltransferase	3.45	1.14	−0.24	0.59	0.10	−1.45	0.11	1.19	0.28	−0.15	1.43	1.19	0.41	0.95	1.63	0.72	1.15
101928190	LOC101928190	uncharacterized LOC101928190	3.43	1.24	0.71	0.74	0.31	0.91	−1.41	0.23	0.13	1.68	0.42	0.86	0.70	0.39	1.90	−0.10	1.52
3416	IDE	insulin-degrading enzyme	3.17	0.76	0.80	−1.08	−0.57	−0.36	1.61	0.57	−0.39	1.73	0.21	1.68	−0.09	1.19	1.50	0.54	1.52
8001	GLRA3	glycine receptor, alpha 3	3.16	−0.21	1.30	0.32	0.98	1.09	0.47	0.48	1.52	−0.17	1.03	−0.17	0.38	0.08	0.91	2.51	−0.03
3727	JUND	jun D proto-oncogene	3.13	0.20	−0.25	0.01	1.09	−0.01	1.40	−0.11	0.06	1.11	1.34	1.26	0.72	−0.14	2.08	0.75	0.33
10945	KDELR1	KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 1	3.12	0.44	−0.09	−0.61	0.81	−0.57	0.88	0.08	0.06	1.39	1.53	1.53	0.60	1.11	1.64	−0.08	1.05
5025	P2RX4	purinergic receptor P2X, ligand-gated ion channel, 4	3.09	0.96	−0.42	0.15	0.62	−1.94	0.26	−0.16	0.05	1.94	0.87	1.26	1.11	1.26	1.57	0.26	1.03
29920	PYCR2	pyrroline-5-carboxylate reductase family, member 2	3.07	−0.04	0.00	0.49	−0.15	−2.15	0.68	0.75	0.48	1.18	1.28	1.23	0.34	1.12	0.99	0.24	0.75
101929248	LOC101929248	uncharacterized LOC101929248	3.01	0.19	−0.17	−0.18	0.01	1.61	0.18	0.53	−0.20	2.59	0.99	1.20	0.97	−0.79	1.22	1.06	0.49
23646	PLD3	phospholipase D family, member 3	2.98	0.65	−0.64	0.06	0.24	−1.13	0.96	0.34	0.11	1.35	1.31	1.68	0.05	1.50	1.28	0.51	1.07
10280	SIGMAR1	sigma non-opioid intracellular receptor 1	2.97	0.22	0.01	0.14	−0.50	0.10	0.93	0.34	−0.69	1.01	0.31	2.78	0.98	0.78	1.56	−0.44	1.14

TABLE 3-continued

gene	symbol	name	fisherz	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49
140699	MROH8	maestro heat-like repeat family member 8	2.96	0.32	1.56	−0.41	−0.07	0.94	0.59	−0.16	−0.42	1.76	−0.96	0.53	2.62	0.53	0.98	0.67	0.42
4669	NAGLU	N-acetylglucosaminidase, alpha	2.94	0.38	−0.30	−0.61	0.46	−0.07	0.27	−0.03	−0.46	1.51	0.78	2.04	1.01	1.38	1.43	0.27	1.47
8341	HIST1H2BN	histone cluster 1, H2bn	2.91	0.70	−0.94	0.44	−0.67	0.97	0.77	0.30	−0.01	2.01	1.24	0.65	1.12	0.86	1.20	0.48	0.38
2519	FUCA2	fucosidase, alpha-L-2, plasma	2.90	0.53	−0.11	0.73	−0.27	−1.09	0.71	0.23	0.25	1.18	1.07	1.39	−0.27	2.25	0.60	0.35	1.70
8985	PLOD3	procollagen-lysine, 2-oxoglutarate 5-dioxygenase 3	2.88	−0.01	−0.40	−0.24	1.02	−1.43	0.95	−0.02	−0.03	1.07	0.69	1.71	0.83	0.14	1.52	0.71	1.59
1690	COCH	cochlin	2.87	1.54	0.02	0.18	0.15	−0.68	1.61	0.98	0.17	−0.16	0.42	1.49	0.75	−0.39	0.43	1.26	1.76
51114	ZDHHC9	zinc finger, DHHC-type containing 9	2.86	−0.02	0.17	0.23	0.73	−1.38	0.85	−0.58	0.03	1.59	0.00	1.31	1.14	0.51	1.71	0.63	1.78
55907	CMAS	cytidine monophosphate N-acetylneuraminic acid synthetase	2.85	1.20	−0.01	0.04	0.81	−2.74	0.89	0.74	0.54	0.58	0.73	−0.47	0.55	1.49	1.08	1.05	1.41
144811	LACC1	laccase (multicopper oxidoreductase) domain containing 1	2.84	0.36	−0.91	0.83	0.37	−0.37	−0.14	0.49	0.06	1.38	0.64	0.73	1.51	1.22	0.69	0.76	1.00
92421	CHMP4C	charged multivesicular body protein 4C	2.84	0.78	−0.20	−0.06	0.22	1.10	−0.83	1.09	0.01	0.80	−0.05	1.13	0.48	1.25	1.21	0.87	0.92
23475	QPRT	quinolinate phosphoribosyltransferase	2.83	0.37	0.89	−0.26	1.13	0.03	1.45	0.18	−1.05	2.00	0.68	0.81	0.87	0.86	0.95	0.15	1.62
54913	RPP25	ribonuclease P/MRP 25 kDa subunit	2.77	−0.43	0.75	−0.35	−0.37	−0.10	0.09	0.93	−0.40	0.59	1.07	0.84	0.03	2.18	1.76	0.04	1.03
4645	MYO5B	myosin VB	2.76	−0.18	−0.49	−1.23	0.10	1.08	0.83	1.07	−0.70	2.24	−0.22	0.09	0.28	1.06	1.74	1.21	1.03
9917	FAM20B	family with sequence similarity 20, member B	2.74	0.12	−0.53	0.50	0.28	−2.09	1.80	0.57	−0.51	0.78	1.31	0.41	1.53	1.01	1.80	0.01	0.21
57213	SPRYD7	SPRY domain containing 7	2.73	−1.19	−0.63	−0.47	−0.17	−0.47	1.72	0.94	−0.10	0.64	0.21	0.64	1.98	1.98	0.86	0.23	1.56
113829	SLC35A4	solute carrier family 35, member A4	2.73	0.87	1.35	−0.10	−0.15	−1.18	0.18	0.72	−0.67	1.02	0.55	1.40	0.75	1.65	1.90	−0.25	1.33

TABLE 3-continued

gene	symbol	name	fisherz	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49
100128164	LOC100128164	four and a half LIM domains 1 pseudogene	2.72	0.42	0.07	0.32	0.00	0.66	0.24	0.79	−0.33	1.45	0.81	−0.54	2.29	0.34	−0.05	1.56	−0.04
26284	ERAL1	Era-like 12S mitochondrial rRNA chaperone 1	2.70	−0.05	0.90	0.35	0.49	−0.61	1.23	0.18	−1.13	0.39	1.23	1.88	0.52	1.45	1.48	0.12	1.12
64847	SPATA20	spermatogenesis associated 20	2.70	−0.42	0.01	0.46	0.25	0.15	1.21	0.86	−0.40	1.35	0.50	1.60	0.61	0.38	0.91	0.46	1.37
55974	SLC50A1	solute carrier family 50 (sugar efflux transporter), member 1	2.69	0.40	0.27	0.44	0.44	−1.19	0.22	−0.25	−0.17	1.56	1.31	1.64	0.74	0.76	1.89	−0.13	1.52
64405	CDH22	cadherin 22, type 2	2.68	−0.66	0.02	0.78	0.79	2.12	1.83	−0.24	0.12	0.77	0.44	−0.42	0.71	0.71	1.44	1.18	−0.31
6510	SLC1A5	solute carrier family 1 (neutral amino acid transporter), member 5	2.68	0.25	1.07	0.13	0.83	−0.44	0.26	−0.15	−0.18	1.32	1.39	1.65	0.26	0.81	1.40	−0.12	1.32
196463	PLBD2	phospholipase B domain containing 2	2.67	−1.07	−0.43	0.96	−0.66	0.81	1.69	0.38	−0.60	0.20	0.29	2.42	1.83	−0.31	1.22	0.44	1.67
741	ZNHIT2	zinc finger, HIT-type containing 2	2.67	0.67	0.08	0.56	1.43	0.01	1.55	0.14	0.43	−0.19	0.73	0.61	0.99	0.83	0.88	0.39	0.75
23568	ARL2BP	ADP-ribosylation factor-like 2 binding protein	2.66	−0.14	0.26	−0.22	1.22	−0.32	0.30	−0.88	−0.15	1.16	0.99	1.12	0.79	0.98	1.69	1.16	0.98
79144	PPDPF	pancreatic progenitor cell differentiation and proliferation factor	2.66	0.31	0.19	−0.47	0.46	0.47	0.81	−0.24	0.16	0.77	1.88	1.68	1.18	1.54	1.28	−0.38	−0.60
91319	DERL3	derlin 3	2.66	−0.62	0.03	−0.15	0.15	1.29	0.46	−0.42	−0.44	0.92	0.20	2.64	−0.29	1.45	1.91	0.19	0.85
79654	HECTD3	HECT domain containing E3 ubiquitin protein ligase 3	2.64	0.18	−0.01	0.20	0.36	−1.15	1.05	0.58	0.20	1.06	1.44	1.00	0.38	0.57	2.48	−0.53	0.64
115950	ZNF653	zinc finger protein 653	2.63	0.27	0.87	0.00	0.98	−2.01	0.67	0.83	−0.26	0.33	1.07	0.48	1.16	1.11	0.89	0.15	1.50
1374	CPT1A	carnitine palmitoyltransferase 1A (liver)	2.63	0.10	−0.31	−0.13	1.44	−1.60	1.16	0.66	0.87	0.43	1.77	0.21	−0.73	0.37	2.11	1.09	1.00

TABLE 3-continued

gene	symbol	name	fisherz	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49
81533	ITFG1	integrin alpha FG-GAP repeat containing 1	2.62	0.64	−0.23	0.72	0.46	−0.86	0.92	0.52	0.43	1.00	−0.07	0.63	0.37	1.91	0.63	0.03	1.80
201931	TMEM192	transmembrane protein 192	2.60	0.09	0.73	−0.14	−0.82	−2.06	−0.53	0.31	−0.18	2.23	1.04	1.20	0.53	1.56	1.34	0.23	0.69
7979	SHFM1	split hand/foot malformation (ectrodactyly) type 1	2.60	1.12	−0.09	−0.10	0.73	−1.07	0.61	0.16	−0.93	0.91	0.91	1.92	0.99	1.14	0.74	0.36	0.72
159296	NKX2-3	NK2 homeobox 3	2.59	0.50	1.03	1.28	−0.20	0.57	1.82	−0.28	−0.20	0.96	1.31	−0.11	1.55	0.42	−0.02	0.07	1.47
51102	MECR	mitochondrial trans-2-enoyl-CoA reductase	2.59	0.16	0.07	0.17	0.04	−0.44	0.71	−0.09	−0.58	1.10	0.34	1.23	1.17	0.60	2.12	0.26	1.67
8729	GBF1	golgi brefeldin A resistant guanine nucleotide exchange factor 1	2.59	1.24	−0.79	0.52	−1.28	0.35	0.14	0.64	0.31	1.47	0.10	1.60	0.65	0.89	1.14	0.80	0.37
118460	EXOSC6	exosome component 6	2.58	0.83	−0.62	0.09	−0.58	−0.27	−0.35	0.30	−0.12	1.27	1.31	0.60	1.80	0.06	2.06	0.33	0.56
79586	CHPF	chondroitin polymerizing factor	2.57	0.08	−0.01	−0.27	0.24	−0.60	−1.04	0.71	−0.82	0.39	0.20	2.85	1.40	1.12	0.23	0.71	1.54
2052	EPHX1	epoxide hydrolase 1, microsomal (xenobiotic)	2.54	0.28	−0.62	−0.70	1.11	−0.86	2.09	0.72	0.28	1.09	0.47	1.12	0.36	1.57	0.82	0.19	0.90
84893	FBXO18	F-box protein, helicase, 18	2.53	0.06	−0.86	0.82	−0.01	−0.98	2.23	0.80	−0.29	0.24	0.32	1.65	0.78	0.83	0.44	0.61	1.43
54726	OTUD4	OTU domain containing 4	2.53	−0.54	0.74	−0.10	0.36	−2.67	1.55	0.71	1.09	1.10	0.96	1.20	0.32	−0.03	0.73	0.08	1.29
813	CALU	calumenin	2.53	0.77	−0.57	−0.59	0.26	−1.77	0.48	−0.37	−0.09	2.63	0.58	1.67	0.30	1.18	1.13	0.50	1.34
54431	DNAJC10	DnaJ (Hsp40) homolog, subfamily C, member 10	2.52	−0.14	−0.64	−0.26	−0.41	−1.83	1.24	0.87	−0.15	1.57	−0.13	1.61	0.61	0.78	1.91	−0.13	1.95
9612	NCOR2	nuclear receptor corepressor 2	2.52	0.79	0.41	1.31	−0.10	0.09	0.14	−0.93	0.39	1.90	0.95	1.41	−0.26	−0.32	1.42	0.35	0.75
9829	DNAJC6	DnaJ (Hsp40) homolog, subfamily C, member 6	2.51	−1.46	−1.60	0.51	−1.21	0.40	0.88	0.92	0.09	1.51	0.12	0.63	1.34	0.66	1.03	1.20	1.07

TABLE 3-continued

gene	symbol	name	fisherz	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49
79036	KXD1	KxDL motif containing 1	2.51	1.09	1.96	0.12	0.68	−1.54	−1.19	−0.11	−0.10	1.36	1.66	0.70	0.74	1.82	0.10	0.48	0.54
284361	EMC10	ER membrane protein complex subunit 10	2.51	0.39	−0.02	−0.10	1.36	−1.21	0.58	−0.70	−0.61	1.09	0.91	1.93	0.32	1.33	1.47	0.50	1.25
131118	DNAJC19	DnaJ (Hsp40) homolog, subfamily C, member 19	2.50	−0.86	−0.69	−0.12	−0.13	0.65	0.03	−0.07	−1.13	0.97	−0.11	2.78	1.05	0.56	1.43	0.50	1.46
644809	C15orf56	chromosome 15 open reading frame 56	2.50	1.27	0.33	−0.45	1.00	0.30	−0.28	0.83	1.34	0.41	0.93	1.19	−0.58	0.70	0.54	0.97	0.36
2119	ETV5	ets variant 5	2.50	−0.01	−0.98	0.28	1.06	0.15	0.03	0.09	−0.07	1.55	1.30	1.41	1.18	0.92	−0.35	0.12	1.33
5833	PCYT2	phosphate cytidylyltransferase 2, ethanolamine	2.50	0.56	−0.12	−0.20	0.58	1.23	0.12	0.06	−1.29	1.50	1.58	0.65	0.81	−0.02	1.44	0.61	0.56
922	CD5L	CD5 molecule-like	2.49	−0.83	−0.01	−0.54	0.77	−0.08	0.71	0.85	−0.09	−0.20	0.71	2.07	0.84	1.11	1.13	0.30	1.17
9261	MAPKAPK2	mitogen-activated protein kinase-activated protein kinase 2	2.49	0.73	0.00	−0.02	0.75	−0.75	0.99	−0.36	0.30	0.92	1.06	1.74	0.14	0.06	1.46	0.69	0.45
57190	SEPN1	selenoprotein N, 1	2.49	0.30	−2.37	−0.29	0.02	−1.13	0.88	0.47	0.45	0.55	1.53	0.97	0.91	1.00	1.45	0.83	0.39
79644	SRD5A3	steroid 5 alpha-reductase 3	2.48	0.19	−0.30	−1.11	0.87	0.35	0.34	0.38	−0.24	2.00	−0.02	0.97	0.20	1.39	1.28	−0.14	1.40
79058	ASPSCR1	alveolar soft part sarcoma chromosome region, candidate 1	2.48	1.16	−0.14	−0.09	1.45	0.52	0.80	0.92	−0.07	0.73	0.52	−0.13	1.04	0.44	1.18	0.39	0.97
7832	BTG2	BTG family, member 2	2.47	0.09	−0.36	−0.33	−0.31	−0.16	−0.29	0.98	1.51	1.17	0.00	0.95	0.05	0.18	0.88	2.64	0.53
11070	TMEM115	transmembrane protein 115	2.47	0.04	0.53	0.48	0.98	−2.10	0.09	0.54	1.10	0.79	1.15	0.75	0.01	−0.40	1.70	1.24	0.96
10847	SRCAP	Snf2-related CREBBP activator protein	2.46	0.51	0.46	−1.01	0.38	−1.04	0.23	1.10	−0.37	1.36	1.79	−0.19	0.04	1.17	0.48	1.85	−0.04
4597	MVD	mevalonate (diphospho) decarboxylase	2.46	0.97	0.72	0.94	0.62	1.96	0.27	−0.81	−0.64	1.37	0.62	0.46	0.04	1.90	−0.04	0.65	1.32

TABLE 3-continued

gene	symbol	name	fisherz	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49
100506696	PCAT6	prostate cancer associated transcript 6 (non-protein coding)	2.45	0.60	0.46	−0.56	0.92	−0.60	1.38	−0.08	−1.22	1.34	−0.28	1.60	0.90	0.86	1.72	−0.26	1.49
100507459	LOC100507459	uncharacterized LOC100507459	2.45	−0.40	0.61	0.49	0.11	0.49	0.31	0.51	−1.15	1.83	0.59	0.69	0.69	1.37	0.93	−1.09	1.81
100130613	CXorf64	chromosome X open reading frame 64	2.45	0.41	−0.67	−0.83	0.89	−0.92	0.94	−0.43	0.70	2.62	0.62	1.00	−0.14	0.72	1.62	0.67	−0.06
5081	PAX7	paired box 7	2.45	0.92	1.45	−0.72	−0.11	−0.28	0.03	0.14	−0.03	1.12	1.76	1.27	0.76	−0.18	0.73	0.94	0.62
100240728	LOC100240728	uncharacterized LOC100240728	2.44	−0.30	0.84	−0.05	−0.08	1.21	0.24	0.14	−0.85	1.34	−0.18	0.72	0.70	0.95	2.04	0.91	0.79
26229	B3GAT3	beta-1,3-glucuronyltransferase 3 (glucuronosyltransferase I)	2.44	0.41	0.51	−0.10	0.60	0.07	−0.02	−0.13	−0.99	0.96	0.01	1.74	1.11	0.29	2.12	0.36	1.40
950	SCARB2	scavenger receptor class B, member 2	2.44	0.02	−0.02	−0.25	0.56	−1.75	0.16	−0.31	−0.33	2.17	0.29	0.82	0.32	1.94	1.07	0.30	1.53
161882	ZFPM1	zinc finger protein, FOG family member 1	2.44	−0.12	0.46	0.89	1.03	−1.82	0.50	0.42	0.44	0.06	1.41	1.20	1.53	1.01	1.28	0.50	0.03
5034	P4HB	prolyl 4-hydroxylase, beta polypeptide	2.43	0.81	0.23	−0.36	1.07	−0.87	1.03	−0.19	−0.65	1.45	1.15	1.79	0.03	1.05	1.54	−0.09	0.67
123355	LRRC28	leucine rich repeat containing 28	2.43	0.93	0.57	0.85	−0.04	−1.58	1.12	0.24	−0.15	−0.31	0.69	0.79	0.81	−0.05	1.64	0.68	1.25
6734	SRPR	signal recognition particle receptor (docking protein)	2.43	1.45	−0.69	0.11	−0.77	−1.71	0.60	0.75	0.84	0.69	−0.07	2.54	−0.27	−0.67	2.25	1.01	0.82
9911	TMCC2	transmembrane and coiled-coil domain family 2	2.43	−0.95	−0.25	0.73	2.21	0.29	0.89	0.19	0.45	0.69	1.42	1.32	−0.55	1.64	1.70	−0.42	0.14
222642	TSPO2	translocator protein 2	2.42	−0.73	−0.46	0.66	0.63	−0.26	1.40	0.44	0.78	0.73	1.00	1.86	0.59	1.95	0.76	−0.74	1.21
3643	INSR	insulin receptor	2.42	0.82	0.91	−0.72	0.88	−0.54	0.97	0.74	0.48	1.94	1.22	0.41	−0.68	1.40	0.37	0.39	0.70
85462	FHDCI	FH2 domain containing 1	2.41	−1.49	−0.58	0.18	1.72	0.44	1.64	1.34	0.98	0.71	−0.13	0.84	1.24	0.87	−0.77	0.78	0.63

TABLE 3-continued

gene	symbol	name	fisherz	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49
149175	MANEAL	mannosidase, endo-alpha-like	2.40	−0.21	1.02	−0.57	0.94	−0.11	0.62	0.36	−0.87	1.31	−0.24	1.27	0.71	1.31	1.65	0.25	1.16
1819	DRG2	developmentally regulated GTP binding protein 2	2.40	0.10	−0.07	0.40	1.15	−1.28	1.82	0.23	−1.07	1.27	0.83	0.77	1.38	0.79	1.44	0.17	0.66
10370	CITED2	Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain, 2	2.39	0.05	−1.13	−0.29	−0.11	−1.87	1.52	1.11	0.32	1.35	1.00	2.19	−0.28	0.37	1.78	−0.04	0.50
25792	CIZ1	CDKN1A interacting zinc finger protein 1	2.39	0.29	0.30	−0.16	1.23	−3.21	1.91	0.78	0.20	0.41	1.30	0.87	0.30	0.40	1.17	−0.14	0.71
4072	EPCAM	epithelial cell adhesion molecule	2.39	−0.86	−0.35	0.43	1.47	1.86	1.30	−0.31	−0.08	1.58	0.17	−0.06	1.18	1.61	1.63	−0.46	0.14
84447	SYVN1	synovial apoptosis inhibitor 1, synoviolin	2.39	0.55	−0.02	−1.26	0.17	−0.81	0.81	0.33	0.20	0.83	0.15	3.04	−0.74	−0.15	1.60	1.15	1.11
527	ATP6V0C	ATPase, H+ transporting, lysosomal 16 kDa, V0 subunit c	2.39	0.82	0.46	0.25	1.67	−1.27	0.53	−0.19	0.22	0.99	2.28	1.05	0.52	1.37	0.07	−0.15	0.44
10629	TAF6L	TAF6-like RNA polymerase II, p300/CBP-associated factor (PCAF)-associated factor, 65 kDa	2.38	0.86	0.07	0.15	0.72	−0.79	0.18	−0.37	−0.96	0.72	1.25	1.36	0.81	0.49	1.62	0.83	1.07
51150	SDF4	stromal cell derived factor 4	2.38	0.64	−0.15	−0.38	1.14	−1.29	0.94	−0.01	−0.16	0.84	1.00	2.12	−0.61	0.65	1.83	0.48	1.32
57143	ADCK1	aarF domain containing kinase 1	2.37	−0.13	−0.14	−0.63	1.06	−1.36	0.60	0.80	0.12	1.28	0.45	1.08	0.00	0.96	1.52	0.37	1.31
682	BSG	basigin	2.37	1.54	−0.94	0.51	1.17	−1.40	1.79	0.29	0.58	0.24	1.35	1.35	0.01	0.28	0.94	0.86	0.64
10139	ARFRP1	ADP-ribosylation factor related protein 1	2.37	0.91	−0.06	−0.20	0.67	0.22	0.55	−1.51	−0.77	1.82	1.50	1.33	1.42	0.31	0.73	0.40	0.56

TABLE 3-continued

gene	symbol	name	fisherz	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49
203238	CCDC171	coiled-coil domain containing 171	2.37	0.55	−0.41	−0.27	0.81	0.36	0.98	0.27	0.00	2.16	−0.98	0.49	1.18	0.10	1.11	0.59	1.07
54805	CNNM2	cyclin M2	2.37	−0.82	0.70	0.73	0.69	−1.02	1.36	0.29	−0.21	1.05	−0.04	1.84	0.68	0.60	2.24	−0.39	1.30
1200	TPP1	tripeptidyl peptidase I	2.37	0.44	−1.00	0.97	−0.89	−0.66	1.35	0.23	0.58	0.63	1.99	0.41	0.33	0.30	1.89	0.03	0.51
2271	FH	fumarate hydratase	2.37	1.67	1.85	−0.14	0.05	−1.23	0.68	−0.07	−0.06	1.25	1.51	0.16	0.33	1.52	0.89	0.46	0.12
376412	RNF126P1	ring finger protein 126 pseudogene 1	2.37	0.37	−0.03	0.02	0.11	−0.29	0.56	0.07	−0.79	2.48	0.85	−0.14	1.86	0.35	1.91	0.17	0.12
4924	NUCB1	nucleobindin 1	2.37	1.68	−0.36	0.75	0.29	−1.49	0.63	−0.05	1.13	−0.32	1.41	1.06	0.50	0.08	1.40	0.89	0.68
55132	LARP1B	La ribonucleoprotein domain family, member 1B	2.37	0.33	−0.97	−0.07	−0.41	−0.06	1.04	0.62	−0.36	2.03	−0.55	2.66	0.91	0.20	1.79	0.48	0.96
9650	MTFR1	mitochondrial fission regulator 1	2.37	0.55	−1.00	0.41	−0.59	0.91	0.94	0.64	−0.88	1.53	0.05	2.22	0.00	1.53	0.97	0.24	1.52
29803	REPIN1	replication initiator 1	2.36	0.71	0.46	−1.02	0.72	0.31	1.07	0.30	−0.59	0.61	0.78	0.74	0.33	0.58	2.47	0.04	0.49
4507	MTAP	methylthioadenosine phosphorylase	2.36	−0.31	−0.03	0.15	0.50	−2.09	−0.40	−0.55	−0.25	1.46	0.89	0.40	0.50	1.74	2.40	0.24	0.89
816	CAMK2B	calcium/calmodulin-dependent protein kinase II beta	2.36	0.87	0.30	−0.16	1.51	0.03	0.88	−0.66	0.50	1.32	0.83	1.59	−0.29	−0.16	0.82	1.01	0.12
120379	PIH1D2	PIH1 domain containing 2	2.36	−0.30	0.35	−0.39	−0.51	1.52	0.81	0.62	−0.08	1.13	0.31	0.51	0.91	1.86	0.68	−0.05	0.60
91289	LMF2	lipase maturation factor 2	2.36	0.26	0.57	−0.74	1.31	−0.30	−0.03	0.09	−0.47	1.31	1.83	2.32	0.17	0.26	1.18	0.08	0.76
10905	MAN1A2	mannosidase, alpha, class 1A, member 2	2.35	−0.51	0.22	0.09	0.26	−2.42	0.90	1.97	−0.62	1.19	−0.05	1.84	0.33	−0.35	1.88	0.67	0.92
25930	PTPN23	protein tyrosine phosphatase, non-receptor type 23	2.35	0.19	−0.75	0.81	−0.12	1.67	0.28	0.92	0.50	0.02	0.77	0.84	1.54	−0.81	1.10	0.40	0.38
57648	KIAA1522	KIAA1522	2.35	−0.40	0.20	−0.30	1.23	−3.21	1.11	0.50	−0.47	2.10	1.08	0.71	0.23	1.36	0.17	0.16	0.50
7249	TSC2	tuberous sclerosis 2	2.35	1.12	0.34	−0.58	0.67	−1.88	1.60	1.13	0.49	0.06	0.98	0.12	1.11	−0.24	1.74	0.08	0.95
55151	TMEM38B	transmembrane protein 38B	2.34	−0.35	−1.27	−0.84	−1.50	0.61	−0.02	−0.12	0.00	2.10	0.27	2.35	1.09	0.85	1.35	0.51	1.28

TABLE 3-continued

gene	symbol	name	fisherz	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49
160728	SLC5A8	solute carrier family 5 (sodium/mono carboxylate cotransporter), member 8	2.33	0.23	1.90	0.52	0.37	0.89	0.94	1.04	−0.98	0.68	0.87	0.89	−0.03	1.18	0.88	−0.30	0.24
148418	SAMD13	sterile alpha motif domain containing 13	2.33	−0.47	−1.02	0.15	0.56	0.26	−0.01	0.66	0.27	0.01	0.99	0.48	1.10	0.63	2.51	−0.04	1.03
646762	LOC646762	uncharacterized LOC646762	2.32	−0.74	0.22	0.58	1.62	−1.26	1.30	0.75	−0.35	0.56	0.69	0.75	0.65	0.29	1.65	−0.33	1.30
79109	MAPKAP1	mitogen-activated protein kinase associated protein 1	2.32	1.94	1.42	−0.40	0.88	0.18	−0.23	−0.30	−0.65	0.49	0.44	1.00	−0.21	0.50	1.70	−0.01	1.53
81037	CLPTM1L	CLPTM1-like	2.31	−0.21	0.34	−0.22	0.69	−0.33	0.40	−0.03	−0.82	1.54	0.31	2.15	0.68	1.36	1.40	−0.36	1.46
51523	CXXC5	CXXC finger protein 5	2.29	−0.06	0.22	−0.21	0.55	−1.23	1.07	0.16	−0.55	1.11	0.59	1.55	0.71	1.32	1.90	−0.56	1.92
55322	C5orf22	chromosome 5 open reading frame 22	2.29	0.39	0.87	−0.82	−1.06	0.01	−0.25	0.45	0.07	0.44	1.40	1.68	−1.07	0.53	2.29	0.47	0.65
100996671	LOC100996671	uncharacterized LOC100996671	2.29	0.80	−0.60	0.34	0.08	1.80	0.16	1.43	0.04	0.39	0.99	1.48	0.91	−0.57	0.38	0.90	0.25
55222	LRRC20	leucine rich repeat containing 20	2.29	0.23	−0.12	0.22	0.24	1.55	1.03	0.51	−1.06	0.66	0.18	0.59	2.49	0.37	0.82	−0.19	1.05
55624	POMGNT1	protein O-linked mannose N-acetylglucosaminyltransferase 1 (beta 1,2-)	2.29	−0.06	0.70	−0.71	0.71	−0.89	0.73	0.36	−0.90	1.34	0.54	2.05	0.93	0.16	1.95	−0.11	0.91
100505983	LOC100505983	uncharacterized LOC100505983	2.28	−1.93	−0.81	0.07	1.41	1.83	1.16	0.13	−0.75	1.06	−0.02	0.56	0.93	0.48	1.69	1.73	0.10
3069	HDLBP	high density lipoprotein binding protein	2.28	−0.16	0.12	−0.65	0.76	−1.02	0.55	0.09	−0.32	1.25	0.11	2.33	0.43	0.56	1.76	0.03	1.39
10959	TMED2	transmembrane emp24 domain trafficking protein 2	2.28	0.83	0.00	−0.50	0.52	−1.89	0.52	0.09	−0.10	1.62	1.12	1.53	−0.30	0.48	1.62	0.76	0.43

TABLE 3-continued

gene	symbol	name	fisherz	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49
6598	SMARCB1	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily b, member 1	2.28	1.36	0.07	−0.79	0.70	0.16	1.80	0.11	−0.46	1.24	1.23	1.83	1.00	−0.41	0.86	−0.20	0.45
60412	EXOC4	exocyst complex component 4	2.27	1.43	−0.21	0.74	0.01	−2.40	0.19	−0.05	0.04	1.19	0.19	0.03	0.92	0.66	1.98	0.47	1.10
54982	CLN6	ceroid-lipofuscinosis, neuronal 6, late infantile, variant	2.27	−0.12	1.03	−0.50	0.73	−0.65	0.76	0.09	−1.20	1.12	0.57	1.61	0.39	1.37	1.49	−0.31	1.79
91752	ZNF804A	zinc finger protein 804A	2.27	1.42	−0.14	0.19	0.13	−0.40	2.06	0.44	0.71	2.19	0.00	−0.85	0.36	0.48	−0.20	0.59	2.17
113178	SCAMP4	secretory carrier membrane protein 4	2.26	1.06	−0.85	0.25	−0.20	−2.04	1.61	0.32	0.51	0.52	1.13	0.55	1.03	0.38	1.46	1.48	0.38
10	NAT2	N-acetyltransferase 2 (arylamine N-acetyltransferase)	2.26	0.44	−0.98	1.14	−0.91	1.22	−0.17	0.67	0.24	1.69	0.65	−0.79	1.15	0.49	1.03	1.20	−0.08
375	ARF1	ADP-ribosylation factor 1	2.26	1.14	0.27	0.39	0.74	−2.81	0.22	−0.31	0.50	1.12	1.33	0.52	−0.06	0.47	1.27	1.07	0.74
5589	PRKCSH	protein kinase C substrate 80K-H	2.26	0.76	−0.28	−0.42	0.65	−2.02	0.91	0.53	0.31	0.81	1.04	1.69	0.50	−0.72	1.94	0.34	0.73
9136	RRP9	ribosomal RNA processing 9, small subunit (SSU) processome component, homolog (yeast)	2.26	0.58	1.04	0.45	−0.65	−1.29	0.83	0.24	−0.27	0.33	1.05	0.96	0.76	1.39	1.46	−0.50	2.04
23193	GANAB	glucosidase, alpha; neutral AB	2.26	0.68	−0.80	−0.03	−0.26	−1.54	0.58	0.22	−0.34	1.11	1.13	2.19	0.18	1.02	2.08	0.17	0.50

TABLE 3-continued

gene	symbol	name	fisherz	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49
1798	DPAGT1	dolichyl-phosphate (UDP-N-acetylglucosamine) N-acetylglucosaminephosphotransferase 1 (GlcNAc-1-P transferase)	2.25	0.11	0.64	−1.27	0.51	−0.74	0.31	−0.10	−0.74	1.69	0.40	1.59	0.99	1.79	1.26	−0.13	1.36
85440	DOCK7	dedicator of cytokinesis 7	2.25	0.22	−0.02	−0.61	1.02	−2.22	1.47	0.95	−0.35	1.14	−0.12	1.20	0.71	−0.01	2.02	0.22	1.28
100505794	LOC100505794	uncharacterized LOC100505794	2.24	−0.85	−1.84	−0.01	0.14	1.13	−1.40	0.80	−0.18	1.52	0.28	1.05	1.35	0.82	1.63	0.98	0.10
1173	AP2M1	adaptor-related protein complex 2, mu 1 subunit	2.24	0.69	0.34	0.20	0.65	−3.44	1.20	0.32	0.34	0.23	1.42	0.43	0.23	0.47	1.69	−0.21	0.91
124540	MSI2	musashi RNA-binding protein 2	2.24	0.42	0.40	0.33	1.53	−1.37	1.31	0.75	−1.35	0.55	0.43	0.72	0.45	−0.09	2.03	−0.18	1.83
8372	HYAL3	hyaluronoglucosaminidase 3	2.24	−0.17	0.81	−0.39	0.57	0.63	0.87	−0.29	0.03	1.00	2.11	1.17	0.30	−0.05	1.43	0.16	−0.04
64755	C16orf58	chromosome 16 open reading frame 58	2.24	0.26	−0.77	−0.46	0.24	−0.44	1.02	0.33	−0.45	1.37	0.83	1.34	0.29	0.65	2.50	0.19	1.08
79102	RNF26	ring finger protein 26	2.24	0.59	0.25	−0.41	1.17	−0.35	1.28	0.15	−0.79	0.77	1.30	0.89	0.00	0.46	1.97	0.33	0.63
10963	STIP1	stress-induced-phosphoprotein 1	2.24	1.54	0.24	0.38	0.39	−2.44	0.54	0.24	0.18	1.18	1.18	1.06	−0.52	0.50	1.12	0.88	0.39
375387	NRROS	negative regulator of reactive oxygen species	2.24	0.14	−0.62	0.52	−1.49	−2.04	1.82	1.02	0.80	0.78	2.50	0.31	0.28	0.63	1.24	0.04	0.99
972	CD74	CD74 molecule, major histocompatibility complex, class II invariant chain	2.23	1.35	0.06	−0.03	0.45	−1.10	0.36	0.22	−0.06	0.94	1.05	0.53	1.14	0.80	1.59	0.02	0.34
54676	GTPBP2	GTP binding protein 2	2.23	1.23	0.20	1.63	0.41	1.10	1.61	0.46	0.82	0.86	0.85	0.48	−0.30	0.08	1.32	0.31	−0.23
192286	HIGD2A	HIG1 hypoxia inducible domain family, member 2A	2.23	0.13	−0.59	0.61	−0.93	−1.19	1.07	−0.25	−0.86	1.32	1.09	1.57	1.38	1.15	1.75	−0.10	1.02
3295	HSD17B4	hydroxysteroid (17-beta) dehydrogenase 4	2.23	0.58	.25	−0.54	0.87	−2.80	1.49	0.77	−0.06	1.32	1.16	−0.03	0.15	1.18	0.17	0.00	1.16

TABLE 3-continued

gene	symbol	name	fisherz	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49
80852	GRIP2	glutamate receptor interacting protein 2	2.23	−1.75	0.47	0.38	0.71	0.57	0.30	0.05	0.54	1.02	−0.38	2.14	−0.44	1.91	0.67	0.34	0.32
1298	COL9A2	collagen, type IX, alpha 2	2.22	0.82	0.86	0.11	0.64	1.33	0.56	0.37	0.00	2.13	0.83	0.67	−0.08	0.10	0.21	0.35	0.61
2004	ELK3	ELK3, ETS-domain protein (SRF accessory protein 2)	2.22	−0.85	0.96	−0.24	0.61	0.13	0.42	0.09	−0.66	1.55	0.98	1.45	0.65	1.35	1.54	0.13	0.37
10279	PRSS16	protease, serine, 16 (thymus)	2.22	0.07	0.07	−0.15	0.31	0.82	−0.14	0.21	−0.26	1.11	−1.71	2.05	1.03	1.08	1.35	1.07	0.80
151790	WDR49	WD repeat domain 49	2.22	0.39	0.65	−0.20	0.87	−1.62	0.76	0.78	0.00	2.14	1.03	−0.14	1.45	2.44	0.44	−0.90	0.42
399664	MEX3D	mex-3 RNA binding family member D	2.21	−0.89	0.64	−0.40	0.08	−0.89	0.24	0.58	−0.83	2.15	0.82	0.42	0.57	1.84	1.06	0.51	0.60
5664	PSEN2	presenilin 2 (Alzheimer disease 4)	2.21	0.07	−0.24	0.53	−0.14	0.28	0.06	0.64	−0.30	2.65	−0.12	0.78	−0.07	1.74	0.55	−0.24	2.05
51614	ERGIC3	ERGIC and golgi 3	2.21	0.14	−0.32	−0.36	0.90	−0.92	0.50	0.13	−0.86	1.60	0.13	2.12	0.34	0.84	2.19	0.03	1.23
79178	THTPA	thiamine triphosphatase	2.21	0.18	1.08	0.08	0.68	−1.53	0.69	−0.05	−0.69	0.93	0.76	1.46	−0.25	2.19	1.12	−0.18	1.61
51726	DNAJB11	DnaJ (Hsp40) homolog, subfamily B, member 11	2.20	0.26	0.41	−0.49	1.02	−0.53	0.36	0.10	−0.70	1.88	0.46	1.61	0.24	1.27	1.21	−0.02	1.16
3425	IDUA	iduronidase, alpha-L-	2.20	−0.08	−0.06	−0.61	0.23	−0.33	1.39	0.21	−0.83	1.37	0.55	2.21	0.42	0.93	1.79	−0.31	1.22
1642	DDB1	damage-specific DNA binding protein 1, 127 kDa	2.20	−0.46	0.93	−0.32	0.82	0.26	0.71	−0.23	−1.49	1.42	0.80	1.27	1.21	0.97	1.91	−0.64	0.89
101928770	LOC101928770	uncharacterized LOC101928770	2.19	0.42	−0.39	1.97	−0.05	−0.75	1.30	−0.42	0.22	0.39	0.06	−0.18	0.88	1.13	1.91	0.96	0.40
11015	KDELR3	KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 3	2.19	0.54	−0.29	−1.29	0.96	0.95	−0.77	0.24	−0.94	1.34	−0.28	1.49	−0.18	1.11	1.12	1.25	1.41
35	ACADS	acyl-CoA dehydrogenase, C-2 to C-3 short chain	2.19	1.08	−0.33	0.02	1.25	0.88	0.45	0.33	−1.07	−0.63	0.70	2.04	0.58	−0.21	0.90	0.85	0.93

TABLE 3-continued

gene	symbol	name	fisherz	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49
64798	DEPTOR	DEP domain containing MTOR-interacting protein	2.19	−0.97	−0.54	−0.53	1.14	−0.50	0.90	0.64	−0.81	0.91	0.34	1.30	1.17	0.54	2.26	−0.13	1.32
23457	ABCB9	ATP-binding cassette, sub-family B (MDR/TAP), member 9	2.19	−0.12	1.07	−0.70	−0.22	0.74	0.32	0.07	0.08	0.78	0.09	2.03	1.05	0.73	0.22	0.46	0.65
56132	PCDHB3	protocadherin beta 3	2.19	0.22	−0.59	1.11	−0.10	0.17	0.49	1.08	0.93	2.27	0.23	−0.14	1.28	−0.57	0.24	1.04	0.39
23400	ATP13A2	ATPase type 13A2	2.19	−0.18	−0.61	0.41	−0.57	0.06	0.84	0.17	−1.01	0.01	1.55	1.71	1.58	0.81	1.67	0.46	1.14
3980	LIG3	ligase III, DNA, ATP-dependent	2.19	−0.46	0.56	0.18	0.36	−0.54	0.48	0.86	−0.21	1.56	0.80	0.39	0.02	1.11	1.28	0.03	1.27
5690	PSMB2	proteasome (prosome, macropain) subunit, beta type, 2	2.19	0.25	0.78	−0.61	0.57	−0.70	1.14	0.01	−0.55	0.18	0.83	1.46	0.33	−0.16	2.18	0.18	1.27
7917	BAG6	BCL2-associated athanogene 6	2.19	0.11	0.58	−0.49	1.38	−1.40	1.08	0.01	−0.80	0.97	1.34	1.73	0.60	1.00	1.81	−0.75	0.71
1739	DLG1	discs, large homolog 1 (*Drosophila*)	2.18	0.29	−0.28	0.06	−0.75	−0.96	1.19	0.48	−0.38	1.57	−0.07	1.94	0.87	−0.62	2.35	0.56	0.51
2837	UTS2R	urotensin 2 receptor	2.18	1.12	−0.79	−1.10	0.22	0.05	0.23	−0.10	0.19	0.95	0.95	0.99	1.56	−0.42	1.90	0.81	0.66
83746	L3MBTL2	l(3)mbt-like 2 (*Drosophila*)	2.18	0.03	0.30	−0.18	0.89	−0.51	0.42	0.04	−0.22	1.29	1.21	1.06	−0.15	1.10	1.67	0.02	0.65
5962	RDX	radixin	2.18	0.90	−0.78	−0.53	−0.63	0.90	0.24	0.52	−0.06	2.04	0.60	1.77	0.50	0.72	1.01	1.07	0.56
9956	HS3ST2	heparan sulfate (glucosamine) 3-O-sulfotransferase 2	2.18	0.67	0.26	−0.67	0.27	0.74	0.52	−0.45	−0.25	3.02	0.28	−0.01	1.34	0.80	0.38	0.50	0.39
162968	ZNF497	zinc finger protein 497	2.18	0.06	0.30	−0.31	1.56	2.47	−1.23	0.27	−0.36	0.45	0.25	0.24	1.17	1.14	−0.12	0.59	0.97
4192	MDK	midkine (neurite growth-promoting factor 2)	2.18	−0.74	−0.74	0.03	0.81	0.61	0.59	−0.39	−0.31	0.92	0.47	2.08	0.74	1.48	0.74	−0.09	1.14
54919	HEATR2	HEAT repeat containing 2	2.18	0.58	0.20	−1.69	0.26	0.87	1.46	0.50	−0.57	1.29	0.54	0.96	−0.12	1.96	1.12	−0.28	1.02

TABLE 3-continued

gene	symbol	name	fisherz	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49
10972	TMED10	transmembrane emp24-like trafficking protein 10 (yeast)	2.17	0.24	0.15	−0.92	0.23	−2.06	−0.13	0.02	−0.74	1.77	0.23	2.46	0.42	1.56	1.44	0.21	1.12
23061	TBC1D9B	TBC1 domain family, member 9B (with GRAM domain)	2.17	−0.48	0.44	−0.23	1.47	−0.17	0.78	−0.15	−0.54	1.50	0.81	0.61	0.50	−0.02	1.88	−0.13	0.96
3792	KEL	Kell blood group, metallo-endopeptidase	2.17	−0.27	−1.35	1.11	0.27	0.74	1.85	0.31	−0.05	0.68	0.56	1.10	0.83	1.13	0.58	−0.81	1.84
2063	NR2F6	nuclear receptor subfamily 2, group F, member 6	2.17	−0.44	0.57	0.74	0.43	2.13	0.83	0.19	−0.08	0.90	0.72	0.27	0.73	2.32	−0.26	−0.53	0.72
55177	RMDN3	regulator of microtubule dynamics 3	2.17	−0.50	−0.29	−0.19	0.44	0.38	0.90	−0.31	−0.97	1.51	−0.17	1.73	0.72	1.80	1.84	−0.38	1.52
11147	HHLA3	HERV-H LTR-associating 3	2.17	0.24	−0.04	0.74	0.13	−2.30	0.11	0.71	−0.24	1.31	0.62	1.61	1.44	1.52	0.99	−0.64	1.50
57486	NLN	neurolysin (metallopeptidase M3 family)	2.17	1.46	1.23	−0.04	0.19	−1.92	0.21	0.51	0.33	1.15	1.70	−0.82	0.09	1.67	0.27	0.48	1.34
30814	PLA2G2E	phospholipase A2, group IIE	2.16	0.03	−0.89	0.15	0.91	0.07	0.49	−0.23	−1.35	0.01	0.00	2.32	1.05	0.30	1.56	0.28	0.57
57414	RHBDD2	rhomboid domain containing 2	2.16	−0.01	−0.77	−0.70	0.76	−0.84	−0.49	−0.74	0.32	2.32	−0.19	1.24	0.89	0.83	0.18	1.65	1.21
84836	ABHD14B	abhydrolase domain containing 14B	2.16	−0.24	0.04	−0.02	0.50	−1.38	1.10	−0.20	−0.91	1.01	0.94	1.68	1.17	1.06	2.18	−0.34	0.87
8516	ITGA8	integrin, alpha 8	2.16	−0.45	−0.84	−0.31	−0.09	−0.90	−0.03	1.49	0.25	1.21	0.02	2.41	1.07	0.22	0.17	1.02	2.16
89866	SEC16B	SEC16 homolog B (*S. cerevisiae*)	2.16	−0.12	0.36	1.15	0.30	0.07	0.92	1.22	−0.67	1.20	−0.94	0.19	1.74	0.58	1.43	−0.32	0.67
10491	CRTAP	cartilage associated protein	2.16	−0.69	0.36	0.47	0.31	−2.19	0.24	−0.11	−0.70	0.36	1.16	1.65	0.39	1.08	1.97	−0.10	1.15
11047	ADRM1	adhesion regulating molecule 1	2.16	−0.45	1.09	0.59	1.78	0.53	1.42	−0.82	−0.35	1.12	1.04	0.91	0.66	1.05	0.97	−0.49	0.27

TABLE 3-continued

gene	symbol	name	fisherz	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49
28971	AAMDC	adipogenesis associated, Mth938 domain containing	2.16	0.19	0.18	0.52	2.32	0.38	0.56	−0.35	−0.63	0.91	−0.04	0.74	0.41	0.55	0.75	0.52	1.27
8078	USP5	ubiquitin specific peptidase 5 (isopeptidase T)	2.16	0.09	0.52	−0.61	1.26	−1.97	1.65	−0.60	−0.79	0.83	1.03	1.70	1.40	−0.20	1.71	−0.58	0.82
37	ACADVL	acyl-CoA dehydrogenase, very long chain	2.16	0.58	−0.03	−0.12	1.26	−0.92	1.19	0.62	−0.34	1.34	0.92	0.66	0.12	0.99	1.25	−0.18	1.30
145508	CEP128	centrosomal protein 128 kDa	2.15	−0.23	0.18	−0.41	−0.20	0.67	0.60	0.28	−0.19	1.59	−0.82	1.68	1.14	1.20	1.82	−0.36	0.73
49861	CLDN20	claudin 20	2.15	0.38	0.63	−0.14	1.58	−1.01	0.53	0.41	−0.64	1.75	0.12	1.45	0.94	−1.19	0.64	0.71	0.43
5905	RANGAP1	Ran GTPase activating protein 1	2.15	0.08	0.44	0.11	0.78	−0.96	0.63	−0.14	−1.29	0.65	1.09	1.62	0.41	0.84	1.96	0.02	0.88
7542	ZFPL1	zinc finger protein-like 1	2.15	1.34	0.05	1.09	0.51	−1.65	1.04	−0.56	0.27	0.76	1.26	1.06	0.37	0.64	0.81	0.68	0.85
9562	MINPP1	multiple inositol-polyphosphate phosphatase 1	2.15	−0.37	−0.97	−0.14	−0.65	−1.76	0.37	1.29	0.08	0.78	0.44	1.99	0.48	1.37	1.34	0.26	1.74
79095	C9orf16	chromosome 9 open reading frame 16	2.15	0.05	0.44	0.56	0.89	0.96	−0.21	−0.58	−0.46	−0.13	1.85	1.41	1.20	−0.57	1.83	0.41	−0.24
8815	BANF1	barrier to autointegration factor 1	2.15	1.25	0.40	0.35	0.39	−3.22	0.98	0.62	0.38	0.81	0.91	0.85	0.22	0.02	1.60	−0.32	0.80
54867	TMEM214	transmembrane protein 214	2.15	1.05	0.54	−0.11	−0.14	−1.99	0.06	0.49	0.55	0.73	0.90	1.61	0.99	−1.05	1.10	0.44	0.55
6721	SREBF2	sterol regulatory element binding transcription factor 2	2.15	1.52	−1.11	0.63	−0.36	−0.39	1.66	−0.57	−0.09	0.41	2.01	1.07	0.36	−0.13	0.81	0.28	0.77
23133	PHF8	PHD finger protein 8	2.15	−0.14	0.85	−1.47	0.16	0.98	0.12	0.56	1.06	1.95	0.14	1.21	0.50	−0.54	0.82	0.11	0.49
113675	SDSL	serine dehydratase-like	2.14	0.18	0.46	0.40	0.65	−0.53	1.95	0.34	−1.22	1.71	0.59	0.29	1.64	1.52	−0.21	−0.65	1.96
129303	TMEM150A	transmembrane protein 150A	2.14	0.67	−0.67	0.33	0.71	−0.48	−0.19	−0.01	0.70	−0.43	1.43	0.59	1.14	0.72	1.91	0.34	0.60

TABLE 3-continued

gene	symbol	name	fisherz	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49
57658	CALCOCO1	calcium binding and coiled-coil domain 1	2.14	−0.17	−0.13	−0.05	1.18	−1.65	0.80	1.39	0.87	0.49	1.24	0.11	0.05	−0.45	1.13	0.89	−0.26
162	AP1B1	adaptor-related protein complex 1, beta 1 subunit	2.14	0.94	1.04	−0.67	1.27	−0.68	1.09	−0.54	−0.32	0.67	1.06	0.49	0.79	0.53	1.48	0.46	0.87
2873	GPS1	G protein pathway suppressor 1	2.14	0.97	0.03	−0.43	0.31	−1.03	0.65	0.32	−0.93	0.91	1.18	1.35	0.91	0.61	1.78	0.24	1.14
64978	MRPL38	mitochondrial ribosomal protein L38	2.14	0.70	−0.93	−0.17	0.07	−1.17	0.11	0.22	−0.02	0.45	1.55	1.48	0.58	0.56	2.00	0.13	0.90
220323	OAF	OAF homolog (*Drosophila*)	2.14	−0.95	−0.74	0.44	0.73	−0.83	1.76	0.61	−0.26	0.80	1.35	1.56	−0.15	0.53	1.59	−0.16	1.20
6006	RHCE	Rh blood group, CcEe antigens	2.14	−1.22	−1.53	1.05	0.71	0.38	1.81	−0.52	0.25	0.25	0.61	0.83	1.04	1.81	1.10	0.07	0.74
389812	LCN15	lipocalin 15	2.14	−0.38	0.83	0.01	0.45	1.73	0.80	−0.48	−0.46	1.02	0.52	2.10	−1.40	1.21	0.82	−0.27	0.91
2628	GATM	glycine amidinotransferase (L-arginine:glycine amidinotransferase)	2.13	1.24	0.66	−0.73	−0.16	0.93	0.13	0.50	−0.81	1.86	−0.24	0.43	0.20	0.65	2.88	−0.31	0.94
6509	SLC1A4	solute carrier family 1 (glutamate/neutral amino acid transporter), member 4	2.13	−0.32	−0.44	−1.07	0.07	0.08	0.64	0.35	−0.34	1.69	−0.05	1.52	0.04	2.06	0.78	0.89	1.80
3888	KRT82	keratin 82	2.13	−0.02	0.75	−0.44	1.04	0.07	0.05	−0.43	−1.20	1.84	−0.10	1.27	1.39	−0.20	1.34	0.54	0.02
5211	PFKL	phosphofructokinase, liver	2.13	0.63	1.37	−0.29	1.47	−0.49	0.49	−0.55	−0.40	0.72	1.58	0.63	0.70	0.30	1.64	−0.31	0.77
55080	TAPBPL	TAP binding protein-like	2.13	0.69	0.59	0.34	0.26	−3.02	−0.36	−0.02	0.35	−0.03	0.62	1.57	−1.06	1.71	1.57	0.45	1.03
2139	EYA2	eyes absent homolog 2 (*Drosophila*)	2.13	−0.64	−0.46	−0.24	−0.28	0.42	0.05	0.27	−0.62	1.63	−0.03	1.74	0.11	2.34	1.54	0.63	0.55
2030	SLC29A1	solute carrier family 29 (equilibrative nucleoside transporter), member 1	2.12	0.37	0.86	−0.34	1.33	−0.19	1.48	0.26	−0.95	0.67	1.88	0.44	0.37	1.31	1.52	−0.80	0.96
56005	C19orf10	chromosome 19 open reading frame 10	2.12	0.10	0.03	−0.14	0.99	−1.11	0.16	−0.30	−0.75	1.32	0.38	2.37	0.01	0.96	1.24	−0.03	2.13

TABLE 3-continued

gene	symbol	name	fisherz	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49
6414	SEPP1	selenoprotein P, plasma, 1	2.12	−0.17	−1.23	−0.28	0.31	0.01	1.70	0.16	−0.48	0.45	0.27	1.23	1.28	1.49	0.67	−0.01	1.71
5184	PEPD	peptidase D	2.12	0.58	1.17	−0.10	1.00	−3.74	0.88	−0.36	−0.47	0.26	0.95	0.76	0.83	1.24	0.61	−0.30	1.24
643783	USP46-AS1	USP46 antisense RNA 1	2.12	0.11	−0.67	0.36	−0.25	0.81	−0.06	1.37	−1.02	2.72	0.30	0.24	0.11	2.25	−0.47	0.80	1.42
101928185	LOC101928185	uncharacterized LOC101928185	2.12	0.62	1.07	−0.29	0.04	0.22	0.57	−0.44	0.27	1.62	−0.09	0.39	0.27	1.04	1.36	−0.27	0.32
22883	CLSTN1	calsyntenin 1	2.12	−0.88	0.33	−1.64	0.78	−0.52	0.11	0.20	−0.78	0.83	0.11	1.34	1.41	0.80	2.32	−0.15	0.83
25800	SLC39A6	solute carrier family 39 (zinc transporter), member 6	2.12	1.32	−0.10	−0.45	−0.17	−1.15	0.57	0.92	0.61	1.45	0.29	1.08	0.34	−0.45	1.40	0.76	1.11
54681	P4HTM	prolyl 4-hydroxylase, transmembrane (endoplasmic reticulum)	2.12	−0.37	−0.25	−0.91	0.75	−0.35	0.64	−0.03	−0.56	1.97	0.06	1.79	0.92	0.52	1.43	0.09	0.95
644150	WIPF3	WAS/WASL interacting protein family, member 3	2.12	0.18	−1.20	−0.10	0.67	1.88	−0.20	−0.63	−0.96	1.19	−0.90	1.97	1.37	0.78	1.04	0.38	0.75
9048	ARTN	artemin	2.12	1.14	0.34	−0.47	0.42	−0.31	1.27	0.26	−0.87	2.97	0.99	0.80	0.44	0.17	0.56	−0.49	0.30
3054	HCFC1	host cell factor C1 (VP16-accessory protein)	2.11	−0.38	0.24	0.51	0.88	0.82	0.36	−0.16	−0.94	1.52	0.39	1.81	0.82	0.29	1.87	−0.23	0.53
115098	CCDC124	coiled-coil domain containing 124	2.11	−0.46	0.69	1.79	1.66	−1.30	1.67	0.58	−0.42	0.22	1.05	0.24	0.41	−0.38	1.85	0.01	0.78
55558	PLXNA3	plexin A3	2.11	0.55	−0.45	−0.92	0.83	−0.91	0.78	0.31	−0.98	1.18	0.35	1.76	1.14	0.35	2.29	0.12	0.93
675	BRCA2	breast cancer 2, early onset	2.11	0.23	0.24	0.06	−0.24	−0.02	3.09	0.09	−0.64	0.94	0.65	0.36	1.01	0.61	1.52	0.45	0.48
9777	TM9SF4	transmembrane 9 superfamily protein member 4	2.11	0.69	0.39	−0.54	−0.38	−1.21	0.51	−0.17	0.05	1.45	1.76	0.99	−0.82	1.31	1.67	0.50	1.49
83707	TRPT1	tRNA phosphotransferase 1	2.11	0.84	0.89	−0.54	0.43	−2.69	0.74	0.16	−0.10	1.04	0.33	1.49	0.78	1.06	0.48	0.29	0.96
55334	SLC39A9	solute carrier family 39, member 9	2.10	1.31	1.47	−0.86	0.12	0.94	−0.80	0.19	0.14	1.20	0.80	−0.06	1.19	1.37	−0.87	1.39	0.28
9793	CKAP5	cytoskeleton associated protein 5	2.10	0.83	0.75	0.01	0.54	0.26	1.41	0.58	−0.83	1.16	0.98	0.68	0.72	0.41	2.14	−0.53	0.27

TABLE 3-continued

gene	symbol	name	fisherz	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49
56834	GPR137	G protein-coupled receptor 137	2.10	0.97	−1.57	1.00	−0.34	0.81	0.36	−0.05	0.56	1.20	1.44	0.83	−0.19	1.06	−0.02	1.44	0.42
25921	ZDHHC5	zinc finger, DHHC-type containing 5	2.10	1.06	1.03	−0.01	0.57	−0.90	0.11	0.66	0.16	0.73	1.29	1.18	−0.32	1.05	0.46	0.36	1.11
6520	SLC3A2	solute carrier family 3 (amino acid transporter heavy chain), member 2	2.10	0.59	0.18	−0.52	0.66	−1.50	1.41	0.09	−0.74	1.85	0.84	1.55	−0.55	0.56	1.54	−0.14	1.60
728591	CCDC169	coiled-coil domain containing 169	2.10	−0.73	0.49	0.38	0.41	1.32	1.49	−0.12	0.40	0.33	0.33	0.74	0.72	−0.82	1.65	0.69	0.17
7415	VCP	valosin containing protein	2.10	0.38	0.37	−0.38	1.27	−0.80	1.30	0.34	−0.40	1.57	0.03	1.03	0.73	0.36	1.30	−0.08	1.33
130827	TMEM182	transmembrane protein 182	2.09	−0.70	0.39	−0.81	0.17	−0.95	0.49	0.94	−0.69	0.85	−0.21	1.07	1.40	0.88	2.10	0.50	1.22
9620	CELSR1	cadherin, EGF LAG seven-pass G-type receptor 1	2.09	0.64	−1.29	0.72	−1.74	1.90	0.13	0.81	−0.25	1.91	0.05	−0.65	1.54	1.44	0.76	−0.01	0.47
55335	NIPSNAP3B	nipsnap homolog 3B (*C. elegans*)	2.09	0.24	−0.35	0.20	0.75	−3.17	0.61	0.07	0.04	1.59	0.27	0.23	0.88	0.22	2.57	0.02	1.21
84988	PPP1R16A	protein phosphatase 1, regulatory subunit 16A	2.08	0.17	0.65	−0.18	0.53	−1.39	0.79	0.62	−0.42	1.14	1.45	0.97	0.35	1.71	0.57	0.14	0.69
100192378	ZFHX4-AS1	ZFHX4 antisense RNA 1	2.08	−0.02	−0.09	0.21	−0.51	3.12	−0.66	0.35	0.57	0.93	0.54	−0.86	1.05	0.27	−0.40	0.80	0.75
442524	DPY19L2P3	DPY19L2 pseudogene 3	2.08	−0.04	0.55	−0.86	−0.37	0.85	1.79	0.02	−0.39	1.24	1.42	−0.45	−0.65	0.75	1.42	−0.31	2.31
51661	FKBP7	FK506 binding protein 7	2.08	0.48	−0.50	0.03	0.37	−0.06	0.46	0.66	−1.13	0.65	0.33	1.51	0.87	−0.21	2.34	−0.48	1.88
84922	FIZ1	FLT3-interacting zinc finger 1	2.08	0.63	−0.74	0.21	−0.69	−1.35	0.98	−0.19	−0.25	0.91	0.94	1.99	1.15	−0.01	1.58	1.00	0.23
84954	MPND	MPN domain containing	2.08	0.62	1.05	−0.42	1.93	−1.93	0.97	−0.04	−0.08	0.28	0.53	1.07	−0.52	1.06	1.48	−0.35	1.49
245972	ATP6V0D2	ATPase, H+ transporting, lysosomal 38 kDa, V0 subunit d2	2.08	0.45	0.17	−0.66	0.73	0.96	−0.51	−1.18	−0.41	1.48	−0.24	1.44	−0.04	1.00	0.54	0.87	0.85

TABLE 3-continued

gene	symbol	name	fisherz	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49
4316	MMP7	matrix metallopeptidase 7 (matrilysin, uterine)	2.08	0.46	0.54	−1.74	0.50	−0.74	0.00	−0.69	0.28	2.65	0.49	0.76	1.87	0.90	1.03	−0.57	0.71
55157	DARS2	aspartyl-tRNA synthetase 2, mitochondrial	2.08	0.58	1.19	0.48	−1.34	2.38	2.03	0.58	−0.35	0.16	0.51	0.50	0.78	0.68	0.81	0.00	−0.10
7466	WFS1	Wolfram syndrome 1 (wolframin)	2.08	0.26	−0.65	0.19	−0.24	−0.07	−1.03	−0.58	−0.50	2.42	−0.37	2.50	0.94	1.76	0.61	0.18	0.91
79365	BHLHE41	basic helix-loop-helix family, member e41	2.08	0.26	−0.23	−0.71	0.08	0.73	−1.29	0.71	−0.12	2.56	−1.17	1.10	0.06	1.88	0.41	0.94	1.97
10066	SCAMP2	secretory carrier membrane protein 2	2.08	0.03	0.23	0.02	0.20	−1.15	−0.05	−0.17	−0.69	1.39	0.88	1.43	−0.21	1.61	1.91	0.43	0.98
203068	TUBB	tubulin, beta class I	2.08	0.67	0.41	−0.39	0.71	−0.84	1.86	−0.22	−0.95	1.14	1.02	0.59	0.57	0.72	2.13	−0.52	0.91
5780	PTPN9	protein tyrosine phosphatase, non-receptor type 9	2.07	1.31	0.61	−1.20	0.51	−1.65	0.38	0.53	0.14	0.48	1.64	−0.13	0.64	−0.46	0.92	0.83	1.05
285627	LOC285627	uncharacterized LOC285627	2.07	0.41	0.40	0.33	−0.58	1.13	−0.65	0.35	0.49	1.01	0.69	1.52	0.44	0.72	−0.07	0.39	−0.01
2058	EPRS	glutamyl-prolyl-tRNA synthetase	2.07	0.11	1.90	−0.12	0.72	−0.88	0.55	0.12	−1.04	1.09	−0.01	1.42	0.45	1.01	1.70	0.16	1.26
1737	DLAT	dihydrolipoamide S-acetyltransferase	2.06	0.30	0.31	−1.50	−0.45	−1.31	1.03	0.49	−0.54	1.36	0.57	1.87	0.02	1.13	1.88	−0.02	1.39
22924	MAPRE3	microtubule-associated protein, RP/EB family, member 3	2.06	1.73	−0.26	−0.87	0.07	0.88	0.45	−0.25	0.11	1.38	1.16	−0.52	0.97	0.99	0.18	1.74	0.64
6005	RHAG	Rh-associated glycoprotein	2.06	−0.62	−0.69	0.67	0.86	0.57	3.03	0.53	0.47	0.50	1.47	0.28	0.66	0.59	1.08	−0.15	0.00
5286	PIK3C2A	phosphatidylinositol-4-phosphate 3-kinase, catalytic subunit type 2 alpha	2.06	0.79	−0.57	0.10	−1.19	−1.43	0.09	0.38	0.29	1.07	0.06	2.18	0.35	−0.03	2.31	1.09	−0.01

TABLE 3-continued

gene	symbol	name	fisherz	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49
11226	GALNT6	UDP-N-acetyl-alpha-D-galactosamine: polypeptide N-acetylgalactosaminyltransferase 6 (GalNAc-T6)	2.06	0.02	0.84	−0.35	0.53	−1.82	0.65	−0.03	−1.12	1.89	0.71	0.39	0.59	3.15	0.17	0.41	0.42
2762	GMDS	GDP-mannose 4,6-dehydratase	2.06	0.22	0.98	−0.90	0.90	0.10	1.55	0.55	−0.41	0.02	0.53	0.41	−0.39	0.63	1.39	0.18	2.47
8908	GYG2	glycogenin 2	2.06	−0.24	−0.32	−0.68	1.05	−1.41	0.20	0.81	−0.82	0.61	0.23	1.55	1.12	0.69	2.25	0.15	0.33
10693	CCT6B	chaperonin containing TCP1, subunit 6B (zeta 2)	2.06	0.21	0.55	0.00	0.92	−0.10	1.02	−0.68	−1.48	1.36	−0.08	0.87	0.36	0.52	2.67	0.11	1.01
199953	TMEM201	transmembrane protein 201	2.06	0.09	0.13	0.12	0.77	−0.08	1.18	0.08	−0.88	0.76	1.19	1.04	1.03	1.33	1.95	−1.28	1.17
2760	GM2A	GM2 ganglioside activator	2.06	2.00	0.33	0.39	−0.75	0.96	0.03	−0.31	1.15	0.97	1.25	−0.21	−0.02	0.89	−0.31	1.09	1.20
8295	TRRAP	transformation/transcription domain-associated protein	2.06	0.95	0.39	−1.52	−0.66	−1.04	0.80	0.51	−0.24	0.95	0.18	1.77	1.14	0.54	2.43	−0.75	0.82
1822	ATN1	atrophin 1	2.06	0.48	−0.10	−0.77	1.14	−0.25	0.58	−0.28	0.19	1.99	0.05	0.06	0.65	1.87	0.66	0.22	0.19
55328	RNLS	renalase, FAD-dependent amine oxidase	2.06	−0.14	0.34	1.00	0.33	−0.12	0.29	0.14	−0.25	0.92	0.14	1.12	0.14	1.28	0.84	−0.08	1.21
2069	EREG	epiregulin	2.05	−0.72	−0.16	−0.15	−0.18	−2.29	2.31	1.04	0.24	1.36	0.69	−0.88	1.00	0.78	1.25	1.02	0.40
4329	ALDH6A1	aldehyde dehydrogenase 6 family, member A1	2.05	−0.31	0.26	−1.79	1.04	−0.62	1.18	1.06	−0.76	0.97	0.40	1.85	−0.13	0.26	1.84	−0.13	0.76
537	ATP6AP1	ATPase, H+ transporting, lysosomal accessory protein 1	2.05	0.66	−0.23	−0.66	1.00	−0.94	0.77	0.13	0.12	1.97	1.12	0.18	−0.33	1.86	0.64	0.06	1.40
64764	CREB3L2	cAMP responsive element binding protein 3-like 2	2.05	−0.55	0.39	−0.70	0.62	−1.03	0.46	−0.15	−0.75	1.59	0.40	1.99	0.36	1.11	2.16	−0.35	1.33
811	CALR	calreticulin	2.05	−0.06	0.62	−0.98	1.94	−0.71	2.17	0.49	−0.11	0.57	0.99	1.10	0.03	0.56	0.67	0.12	0.04
9779	TBC1D5	TBC1 domain family, member 5	2.05	0.62	1.10	0.35	0.80	−1.77	0.91	0.05	0.19	1.03	0.86	0.13	1.84	0.24	0.47	0.56	0.13

TABLE 3-continued

gene	symbol	name	fisherz	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49
114815	SORCS1	sortilin-related VPS10 domain containing receptor 1	2.05	−1.22	−0.43	−0.11	0.82	0.65	−0.25	−0.06	0.04	0.99	0.57	0.76	1.29	−0.08	1.90	0.36	1.41
29927	SEC6IA1	Sec61 alpha 1 subunit (*S. cerevisiae*)	2.05	0.72	0.17	−0.26	0.80	−1.90	0.82	−0.28	−0.38	1.10	0.65	2.00	−0.15	1.09	1.95	0.27	0.98
6007	RHD	Rh blood group, D antigen	2.05	0.25	−0.06	0.38	−0.30	−2.21	3.60	−0.25	0.13	0.60	0.99	−0.08	0.48	0.37	0.65	0.37	0.58
5192	PEX10	peroxisomal biogenesis factor 10	2.05	0.52	0.47	−0.95	0.35	−0.98	0.89	0.02	−0.94	1.06	1.04	1.71	0.04	1.83	2.25	−0.46	1.06
125875	CLDND2	claudin domain containing 2	2.04	−0.13	0.77	−0.29	0.93	−0.02	0.38	0.44	−1.04	1.04	0.88	2.06	0.43	−0.30	1.44	−0.09	0.34
10882	C1QL1	complement component 1, q subcomponent-like 1	2.04	0.92	0.57	0.80	−0.87	−0.34	−1.38	0.32	−0.02	1.27	1.32	0.79	1.36	0.30	0.22	1.82	0.33
192683	SCAMP5	secretory carrier membrane protein 5	2.04	−0.03	−0.60	−0.44	1.06	0.02	−1.29	0.08	−0.28	1.01	−0.25	1.66	−0.27	0.06	1.83	−0.39	1.72
8028	MLLT10	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, *Drosophila*); translocated to, 10	2.04	0.60	0.73	0.59	1.30	−2.16	2.07	0.31	−0.49	0.97	1.24	0.85	−0.16	0.70	1.64	−0.36	0.04
150368	FAM109B	family with sequence similarity 109, member B	2.04	−0.82	0.11	0.24	1.27	1.03	−0.45	−0.18	0.17	0.44	1.40	0.28	0.88	1.54	0.22	−0.17	0.13
84206	MEX3B	mex-3 RNA binding family member B	2.04	−0.09	0.73	0.38	0.97	−0.59	1.57	−0.11	−0.57	1.38	0.68	0.54	0.48	−0.44	2.61	−0.37	1.23
101929288	LOC101929288	uncharacterized LOC101929288	2.04	−0.50	−0.12	−0.51	−0.28	2.96	−0.22	−0.54	−0.33	2.22	0.77	0.83	−0.08	−0.07	0.05	0.09	1.00
826	CAPNS1	calpain, small subunit 1	2.04	0.93	0.42	0.36	0.76	−3.26	0.77	0.52	−0.19	0.63	1.61	0.43	0.34	0.84	1.83	−0.77	0.68
83440	ADPGK	ADP-dependent glucokinase	2.04	0.83	0.18	−0.39	0.42	−2.56	1.02	−0.08	0.21	1.32	1.35	0.92	−0.34	0.12	1.56	0.15	0.35
1128	CHRM1	cholinergic receptor, muscarinic 1	2.03	0.85	0.38	−0.13	−0.37	2.25	−0.48	0.10	−0.18	0.73	0.05	1.25	0.26	−0.43	0.61	1.71	0.51

TABLE 3-continued

gene	symbol	name	fisherz	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49
160287	LDHAL6A	lactate dehydrogenase A-like 6A	2.03	−0.04	−1.64	0.41	−0.28	0.07	0.91	0.85	0.11	0.18	0.66	0.28	0.68	0.11	2.53	−0.18	0.41
412	STS	steroid sulfatase (microsomal), isozyme S	2.03	1.18	0.39	0.83	−1.11	−1.51	0.72	0.07	0.57	1.03	0.93	−0.82	1.08	1.31	−0.81	1.12	1.14
64215	DNAJC1	DnaJ (Hsp40) homolog, subfamily C, member 1	2.03	−0.78	−0.10	0.34	0.20	−1.07	0.99	0.80	−0.64	0.86	−0.78	2.20	0.77	0.66	1.91	0.24	0.70
7343	UBTF	upstream binding transcription factor, RNA polymerase I	2.03	0.61	0.51	−0.33	0.98	−1.66	0.77	0.02	−0.03	0.29	0.99	0.42	0.51	0.18	1.34	0.59	0.16
25840	METTL7A	methyltransferase like 7A	2.03	−0.80	−0.40	0.64	0.14	−1.69	1.19	1.40	0.47	0.39	1.15	−0.10	−0.54	1.51	1.92	−0.12	0.55
55315	SLC29A3	solute carrier family 29 (equilibrative nucleoside transporter), member 3	2.03	−0.65	−1.04	0.67	−0.05	−2.89	0.22	0.73	0.18	1.30	0.53	−0.16	0.98	1.67	0.74	0.33	1.12
100507513	LOC100507513	uncharacterized LOC100507513	2.03	−1.15	0.05	0.97	−0.41	1.70	1.86	−0.44	1.18	0.40	0.37	0.99	0.10	−0.43	1.39	0.32	0.33
55704	CCDC88A	coiled-coil domain containing 88A	2.03	1.88	0.22	0.49	0.02	−1.39	1.97	0.78	0.13	0.51	1.04	0.49	0.85	−0.34	0.43	0.52	0.76
57604	KIAA1456	KIAA1456	2.03	−0.16	−0.62	0.49	0.26	2.66	0.32	0.10	0.14	1.47	0.03	1.45	0.27	−0.63	0.66	−0.09	0.52
10449	ACAA2	acetyl-CoA acyltransferase 2	2.03	1.55	0.62	1.05	−0.83	−0.87	1.95	0.82	0.20	0.95	0.10	−0.05	−0.18	0.42	0.62	1.18	1.64
1727	CYB5R3	cytochrome b5 reductase 3	2.03	0.58	0.39	0.45	1.79	−0.87	0.66	−0.72	0.46	1.17	1.60	0.04	−0.02	1.71	0.91	−0.16	−0.05
9569	GTF2IRD1	GTF2I repeat domain containing 1	2.03	0.08	0.45	−0.51	0.73	−0.35	−0.45	0.62	0.33	2.30	−0.20	1.25	0.37	−0.25	1.63	0.86	0.20
10009	ZBTB33	zinc finger and BTB domain containing 33	2.02	0.68	0.25	−0.42	0.91	−2.59	0.73	0.21	−0.67	1.84	0.66	1.07	0.79	0.11	2.29	−0.96	0.99
5188	PET112	PET112 homolog (yeast)	2.02	0.76	−0.91	−0.05	0.70	−0.48	0.86	−0.21	−1.05	0.26	0.91	0.62	0.23	1.35	1.55	0.61	1.43
2132	EXT2	exostosin glycosyltransferase 2	2.02	−1.04	−0.77	0.03	0.95	−2.00	0.62	0.74	−0.48	0.94	−0.04	0.48	0.27	0.65	1.17	0.66	1.71
2239	GPC4	glypican 4	2.02	0.42	0.29	−0.66	−0.15	−0.28	0.39	0.79	−0.19	1.41	−0.42	0.93	1.42	2.37	−1.21	0.29	0.45
56927	GPR108	G protein-coupled receptor 108	2.02	1.42	−0.90	0.43	−1.02	−1.68	−0.23	−0.22	0.77	2.08	0.82	0.82	0.14	0.79	0.49	0.45	1.53

TABLE 3-continued

gene	symbol	name	fisherz	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49
2950	GSTP1	glutathione S-transferase pi 1	2.02	0.83	0.88	0.20	0.98	−1.26	0.89	−0.03	−0.99	1.37	1.32	1.22	−0.36	1.90	0.92	−0.83	0.91
342538	NACA2	nascent polypeptide-associated complex alpha subunit 2	2.02	−0.55	0.84	−0.30	1.23	−1.03	0.64	0.13	−0.73	1.23	0.43	1.25	1.38	−0.27	1.43	0.73	−0.15
55218	EXD2	exonuclease 3'-5' domain containing 2	2.02	−1.15	0.39	−0.59	0.53	−0.23	−0.13	−0.15	−1.17	1.10	0.06	1.99	0.33	1.73	1.83	0.10	0.96
151827	LRRC34	leucine rich repeat containing 34	2.01	0.27	−0.27	−0.19	1.39	−0.77	1.21	0.52	−1.65	1.81	0.37	0.06	0.74	1.01	1.65	−0.42	1.26
64689	GORASP1	golgi reassembly stacking protein 1, 65 kDa	2.01	0.93	−0.18	0.50	0.08	−2.07	0.91	0.29	0.13	2.07	0.49	−0.23	0.57	2.58	0.79	0.00	0.58
10324	KLHL41	kelch-like family member 41	2.01	0.59	−0.19	−0.04	−0.29	−1.73	0.06	0.91	0.17	0.97	−0.64	0.64	0.86	0.92	2.07	1.62	0.33
1314	COPA	coatomer protein complex, subunit alpha	2.01	0.99	0.14	0.28	−0.31	−1.53	0.17	−0.25	0.03	1.81	0.95	0.85	−0.14	1.37	2.06	0.17	0.19
54928	IMPAD1	inositol monophosphatase domain containing 1	2.01	0.18	−0.91	0.38	−0.21	−0.95	−0.60	0.54	−0.73	1.67	−0.06	2.31	−0.34	1.27	1.44	0.61	2.35
8971	H1FX	H1 histone family, member X	2.01	−0.07	0.18	0.12	1.22	−1.08	1.32	0.14	−0.62	1.00	0.80	1.63	−0.05	0.09	2.19	−0.36	1.27
79832	QSER1	glutamine and serine rich 1	2.01	−0.02	−0.81	0.24	−2.49	−1.52	0.70	1.10	0.11	1.21	0.61	0.89	0.57	0.98	1.65	0.73	0.10
10150	MBNL2	muscleblind-like splicing regulator 2	2.00	0.03	−0.91	0.81	−0.96	−2.54	0.40	0.41	0.14	1.33	0.56	1.87	0.64	0.77	1.81	0.32	0.70
8744	TNFSF9	tumor necrosis factor (ligand) superfamily, member 9	2.00	1.07	1.23	−0.89	0.62	−0.81	2.05	−0.42	−0.12	0.96	1.22	0.80	1.53	−0.82	1.58	0.02	0.57
23287	AGTPBP1	ATP/GTP binding protein 1	−2.00	0.35	−0.29	−0.37	−0.35	−0.87	0.12	0.37	1.18	−1.12	−0.39	−1.56	−1.62	−1.70	−0.40	0.63	−1.34
606553	C8orf49	chromosome 8 open reading frame 49	−2.00	0.29	0.31	−1.93	0.80	0.43	−1.17	0.19	−0.21	0.00	−0.54	−2.01	−0.21	−0.94	−0.65	0.62	−0.49

TABLE 3-continued

gene	symbol	name	fisherz	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49
103	ADAR	adenosine deaminase, RNA-specific	−2.01	0.26	0.29	0.17	−1.46	−0.07	−1.40	0.49	1.34	−2.23	−0.75	−2.19	−0.03	−0.75	−0.40	−0.28	−1.14
55509	BATF3	basic leucine zipper transcription factor, ATF-like 3	−2.01	0.59	0.32	0.49	0.04	1.55	−1.39	−0.53	0.07	−0.14	−0.66	−1.83	−0.27	0.13	−2.02	−0.56	−0.41
729614	FLJ37453	uncharacterized LOC729614	−2.01	0.28	−0.34	0.59	0.07	−1.57	0.43	0.27	0.77	−1.70	−0.66	−1.90	0.16	−2.60	−0.54	0.29	−0.58
9241	NOG	noggin	−2.01	−0.80	0.41	−1.06	0.88	−1.73	0.06	0.16	−0.73	−0.95	−0.22	−0.28	−0.44	−1.29	0.18	−1.27	−1.07
26118	WSB1	WD repeat and SOCS box containing 1	−2.01	1.16	−0.20	0.02	−0.15	−0.19	−0.31	0.00	1.41	−0.86	0.27	−2.11	−1.09	−1.61	−2.21	0.74	−1.83
64400	AKTIP	AKT interacting protein	−2.01	0.09	−0.33	−0.94	−0.99	−0.87	−1.59	0.31	0.97	−1.54	−1.03	−0.14	−0.57	−1.48	−1.36	0.78	−0.56
283237	TTC9C	tetratricopeptide repeat domain 9C	−2.01	0.08	0.60	−0.31	−0.96	1.03	−1.94	−1.20	−0.43	−1.28	−0.77	1.16	−2.11	0.05	−0.53	−0.09	−0.63
51155	HN1	hematological and neurological expressed 1	−2.01	0.74	1.29	0.20	0.79	0.88	0.23	−0.33	0.52	−2.59	−0.80	−2.20	−0.80	−0.61	−1.84	−0.24	−0.84
18	ABAT	4-aminobutyrate aminotransferase	−2.01	0.33	0.20	0.86	−0.07	0.23	−1.00	0.09	1.20	−0.87	−0.67	−1.89	−1.07	−0.72	−2.52	0.26	−1.09
22990	PCNX	pecanex homolog (*Drosophila*)	−2.01	0.31	−0.50	−0.92	−0.70	−0.04	−0.10	0.09	1.21	−1.80	−0.41	−1.79	−0.56	−1.40	−0.91	0.81	−1.51
23347	SMCHD1	structural maintenance of chromosomes flexible hinge domain containing 1	−2.01	0.42	0.17	−0.12	−0.57	−1.02	−0.30	0.96	1.36	−1.86	0.02	−1.45	−1.07	−1.65	−1.25	0.48	−1.67
83988	NCALD	neurocalcin delta	−2.01	0.18	1.54	−1.04	−1.32	0.80	−0.67	−0.18	−1.06	−1.26	−1.77	−0.36	−0.25	0.63	0.14	−2.05	−0.35
3428	IFI16	interferon, gamma-inducible protein 16	−2.02	0.40	0.91	−0.30	−0.71	−0.35	−2.27	0.36	1.03	−1.98	−0.26	−1.64	−0.84	−0.24	−0.74	0.07	−1.35
3700	ITIH4	inter-alpha-trypsin inhibitor heavy chain family, member 4	−2.02	0.45	−0.47	1.50	−1.37	−0.94	−0.27	0.57	0.90	−0.48	−1.42	−1.48	0.17	−1.47	−0.58	−0.73	−0.61

TABLE 3-continued

gene	symbol	name	fisherz	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49
64859	NABP1	nucleic acid binding protein 1	−2.02	0.54	−0.50	−0.09	−0.71	0.95	−0.52	0.24	1.35	−1.50	−0.53	−0.83	−1.35	−1.05	−1.81	0.25	−0.76
55192	DNAJC17	DnaJ (Hsp40) homolog, subfamily C, member 17	−2.02	0.39	−0.28	0.68	−0.36	−1.27	−1.02	0.30	0.26	−0.04	0.26	−1.02	−1.41	−0.09	−1.61	0.07	−0.88
101928869	LOC101928869	uncharacterized LOC101928869	−2.02	0.74	1.59	−0.82	−0.04	−0.18	−0.34	−0.03	−0.20	−1.62	0.28	−0.38	−1.14	−2.14	−1.96	0.32	−0.51
10513	APPBP2	amyloid beta precursor protein (cytoplasmic tail) binding protein 2	−2.02	−0.07	−0.32	−0.95	−0.91	−2.38	−1.45	1.01	0.73	−1.27	−0.41	−0.50	−1.08	−0.79	−0.63	0.36	−0.28
11009	IL24	interleukin 24	−2.02	−0.42	1.84	−1.37	−0.17	−0.02	−1.06	−0.11	−0.40	−0.24	−0.31	−0.49	1.07	−1.28	−0.76	−0.82	−1.43
169355	IDO2	indoleamine 2,3-dioxygenase 2	−2.02	−1.28	0.08	0.42	−0.74	0.89	−1.74	−0.24	−0.11	−1.68	−0.53	−1.14	0.17	−0.75	−0.36	0.76	−0.22
10109	ARPC2	actin related protein 2/3 complex, subunit 2, 34 kDa	−2.02	0.60	0.53	−0.23	−0.15	−0.55	−0.35	−0.38	1.11	−2.14	0.28	−1.34	0.37	−1.69	−0.56	−1.07	−1.15
9903	KLHL21	kelch-like family member 21	−2.02	0.11	0.37	−0.40	0.16	−1.06	−1.62	0.12	0.82	−2.22	0.19	−0.73	−1.04	−0.25	−1.14	−0.14	−0.84
23150	FRMD4B	FERM domain containing 4B	−2.03	0.52	−1.03	−0.23	−0.48	−1.24	−0.60	0.19	1.33	−1.92	0.26	−1.59	−0.43	−1.37	−1.04	0.84	−1.00
10865	ARID5A	AT rich interactive domain 5A (MRF1-like)	−2.03	1.11	−0.22	−0.06	−0.30	0.80	−1.15	−0.75	0.53	−2.27	0.05	−1.26	−0.97	−2.05	−0.69	0.88	−0.42
5165	PDK3	pyruvate dehydrogenase kinase, isozyme 3	−2.03	0.23	−0.04	0.48	−1.00	0.12	−0.47	−0.12	1.13	−1.66	−0.37	−2.01	−0.97	−0.88	−1.78	0.70	−0.63
57403	RAB22A	RAB22A, member RAS oncogene family	−2.03	0.07	−0.46	−0.43	−1.54	−1.06	−1.47	0.28	0.75	−1.03	−0.80	−0.40	−1.70	−0.82	−0.52	1.01	−0.26
22900	CARD8	caspase recruitment domain family, member 8	−2.03	0.12	−0.63	0.28	−1.94	−1.12	−0.87	0.59	0.84	−2.04	−0.17	−0.92	−0.63	−1.41	−0.57	0.67	−1.07

TABLE 3-continued

gene	symbol	name	fisherz	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49
80345	ZSCAN16	zinc finger and SCAN domain containing 16	−2.03	0.25	0.38	−0.29	−0.21	−2.60	−0.38	0.41	−0.12	−1.55	−0.83	−0.44	−1.71	−1.62	0.69	0.30	0.35
10964	IFI44L	interferon-induced protein 44-like	−2.03	0.51	0.65	1.14	−0.66	0.15	−2.49	−1.00	−0.09	−1.41	−0.56	−0.82	−0.56	0.68	−0.79	−1.42	−0.16
27040	LAT	linker for activation of T cells	−2.03	−1.26	0.22	0.00	−0.32	−1.34	−1.39	0.27	−0.40	−1.06	−0.92	−0.17	0.50	−1.30	0.11	−0.74	−0.80
91010	FMNL3	formin-like 3	−2.03	−0.46	0.53	−1.06	−0.53	0.41	−1.24	0.65	−0.86	0.52	−1.00	−0.68	1.01	−0.58	−0.89	−0.51	−0.66
29065	ASAP1-IT1	ASAP1 intronic transcript 1 (non-protein coding)	−2.04	−0.05	−0.37	0.50	−0.60	0.41	−0.52	0.23	1.63	−1.15	−0.81	−1.37	−0.47	−0.63	−2.39	0.67	−1.85
84078	KBTBD7	kelch repeat and BTB (POZ) domain containing 7	−2.04	0.25	0.37	−0.64	−0.88	−0.25	−1.55	0.01	1.20	−1.58	−0.27	−0.77	−0.63	−0.74	−1.72	0.06	−0.83
101927910	LOC101927910	keratin-associated protein 5-5-like	−2.04	−0.79	0.91	0.09	−2.83	−0.49	−0.84	0.04	0.19	0.00	−0.97	0.65	−1.69	−0.02	−0.74	0.07	−0.89
51380	CSAD	cysteine sulfinic acid decarboxylase	−2.04	0.77	−0.68	0.23	−0.27	−0.09	−0.14	0.06	1.55	−1.54	−0.38	−1.37	−1.24	−1.69	−1.78	0.90	−1.71
10289	EIF1B	eukaryotic translation initiation factor 1B	−2.04	−0.15	−0.05	0.65	0.70	0.21	0.46	0.08	0.41	−0.51	−0.02	−0.29	−1.10	−1.16	−0.63	−0.81	−0.43
10296	MAEA	macrophage erythroblast attacher	−2.04	0.53	0.45	−0.22	0.57	−2.49	−0.23	0.10	1.41	−1.69	0.09	−0.72	−1.92	−1.38	−0.70	−0.29	−1.12
114224	PRO2852	uncharacterized protein PRO2852	−2.04	−0.57	−0.16	0.15	1.01	−2.13	0.84	−0.01	1.21	−0.48	−1.25	−1.88	−1.10	−0.21	−1.29	0.11	−2.10
2153	F5	coagulation factor V (proaccelerin, labile factor)	−2.04	−0.02	−0.21	0.56	−1.29	0.22	−0.50	−0.01	1.46	−1.68	−0.34	−1.54	−0.84	−0.80	−1.89	0.71	−1.23
55825	PECR	peroxisomal trans-2-enoyl-CoA reductase	−2.04	0.44	−0.03	0.40	−1.39	1.16	−1.50	0.14	0.50	−1.38	−0.96	−1.34	−0.69	−0.12	−1.71	−0.01	−0.95
6503	SLA	Src-like-adaptor	−2.04	−1.37	−0.53	−0.03	−0.44	−0.09	−0.92	0.16	1.22	−2.09	0.47	−1.85	0.18	−0.46	−1.63	0.31	−1.76

TABLE 3-continued

gene	symbol	name	fisherz	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49
7913	DEK	DEK oncogene	−2.04	0.66	0.32	−0.64	0.15	−1.37	1.58	0.40	0.13	−1.63	0.91	−0.68	−0.60	−1.29	−0.28	−1.34	−1.48
30834	ZNRD1	zinc ribbon domain containing 1	−2.04	0.24	2.03	−1.06	1.04	−1.30	−0.83	−0.48	0.06	−1.36	−0.55	0.30	−2.11	−0.36	−0.68	−1.02	−0.18
26999	CYFIP2	cytoplasmic FMR1 interacting protein 2	−2.05	−0.51	0.45	−0.46	−1.11	0.10	−0.79	−0.07	−0.13	−2.15	−0.90	−0.81	−0.06	−1.87	0.74	−0.38	−0.59
286437	LOC286437	uncharacterized LOC286437	−2.05	−0.30	−0.30	0.06	−1.27	−0.01	−1.52	0.19	0.46	−1.54	−1.44	−0.75	−0.03	−0.47	−1.27	0.36	−0.61
4277	MICB	MHC class I polypeptide-related sequence B	−2.05	−0.08	0.21	−0.19	−1.44	0.62	−1.13	0.56	0.54	−1.42	−0.74	−0.78	−1.71	−0.92	−0.51	−0.43	0.06
5698	PSMB9	proteasome (prosome, macropain) subunit, beta type, 9	−2.05	−0.12	1.18	0.14	−0.74	−0.24	−2.61	−0.38	−0.29	−1.17	−0.56	−0.36	−0.77	0.95	−0.86	−0.57	−0.11
4318	MMP9	matrix metallopeptidase 9 (gelatinase B, 92 kDa gelatinase, 92 kDa type IV collagenase)	−2.05	0.33	−1.02	−0.43	−0.23	1.00	0.27	−0.31	1.28	−1.31	−0.21	−1.42	−0.85	−0.67	−2.52	0.23	−0.94
10616	RBCK1	RanBP-type and C3HC4-type zinc finger containing 1	−2.06	1.08	0.35	0.94	0.00	−0.64	−0.41	0.26	1.27	−2.22	0.34	−1.99	−1.68	−1.40	−1.02	−0.42	−0.76
23012	STK38L	serine/threonine kinase 38 like	−2.06	0.24	−0.56	0.06	−1.49	0.02	−1.09	0.19	0.86	−1.70	−0.05	−1.23	−1.13	−1.30	−0.69	0.13	−0.95
100129361	LOC100129361	chromosome X open reading frame 69-like	−2.06	−0.72	−1.53	1.08	−0.01	0.92	0.17	−0.23	−0.04	−1.34	0.07	−2.27	−0.84	−1.20	−1.04	−0.25	−0.24
10742	RAI2	retinoic acid induced 2	−2.06	−0.16	0.32	−1.10	−0.44	1.06	−0.25	−0.59	0.49	−1.56	−1.22	−1.14	−0.12	−1.02	−1.37	−0.42	−0.51
196264	MPZL3	myelin protein zero-like 3	−2.06	0.06	−0.05	−0.10	−0.69	−0.50	−1.07	0.00	1.02	−1.32	−0.48	−1.80	−0.41	−0.64	−1.82	0.63	−0.78
27197	GPR82	G protein-coupled receptor 82	−2.06	−0.33	0.39	0.98	−1.16	−0.23	−1.77	0.46	0.82	−1.73	0.57	−1.82	−0.67	−0.18	−1.45	−0.35	−0.68

TABLE 3-continued

gene	symbol	name	fisherz	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49
7529	YWHAB	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, beta polypeptide	−2.06	−0.33	0.35	−0.87	−0.63	−0.57	−0.75	−0.06	0.72	−0.99	0.33	−1.52	−0.06	0.35	−1.67	−0.38	−1.73
94235	GNG8	guanine nucleotide binding protein (G protein), gamma 8	−2.06	0.07	0.57	1.14	−0.82	−0.23	−0.73	0.29	0.22	−0.97	−0.62	−0.56	−0.99	−0.15	−1.35	0.41	−1.24
352961	HCG26	HLA complex group 26 (non-protein coding)	−2.06	−0.34	0.92	−0.34	−1.67	0.70	−1.42	−0.25	−0.11	−1.35	−2.01	−0.19	−0.28	0.23	−0.23	−0.65	−1.23
49856	WRAP73	WD repeat containing, antisense to TP73	−2.06	0.36	0.65	−0.16	−0.78	−0.95	−1.29	0.12	1.13	−1.50	0.37	−0.93	−0.90	−1.08	−2.01	0.19	−0.77
9448	MAP4K4	mitogen-activated protein kinase kinase kinase kinase 4	−2.06	−0.11	−0.96	−0.07	−0.59	−0.35	0.04	0.68	1.15	−2.04	−0.12	−1.91	−0.40	−1.10	−1.66	0.12	−1.12
9525	VPS4B	vacuolar protein sorting 4 homolog B (*S. cerevisiae*)	−2.06	−0.15	−0.27	−1.47	−1.02	−0.95	−1.20	0.70	0.48	−1.00	−0.15	−0.43	−0.62	−1.54	−0.17	−1.44	−0.08
100505576	LINC00672	long intergenic non-protein coding RNA 672	−2.06	−0.65	−1.38	0.24	−0.20	1.06	−0.59	0.47	1.10	−1.72	−0.75	−0.39	−0.39	−2.04	−1.16	−0.01	−1.34
151556	GPR155	G protein-coupled receptor 155	−2.06	0.09	0.08	−0.13	−1.59	−0.55	−1.77	0.02	0.50	−1.78	−0.89	−0.59	−0.56	−0.09	−1.22	0.53	−0.98
284613	CYB561D1	cytochrome b561 family, member D1	−2.06	−0.63	0.38	−0.70	0.91	0.39	−0.85	−0.12	0.97	−2.62	−0.18	−0.51	−0.35	−0.17	−2.08	−0.40	−1.31
286223	C9orf47	chromosome 9 open reading frame 47	−2.06	−0.58	1.33	0.81	−0.48	0.97	−0.62	0.21	0.71	−0.77	−0.45	−1.48	−1.30	0.34	−2.48	−0.60	−0.58

TABLE 3-continued

gene	symbol	name	fisherz	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49
57061	HYMAI	hydatidiform mole associated and imprinted (non-protein coding)	−2.06	0.13	1.06	−0.57	1.15	0.29	0.43	−0.06	0.34	−1.58	−1.46	−0.71	−0.12	−0.65	−1.03	−0.97	−1.63
9520	NPEPPS	aminopeptidase puromycin sensitive	−2.07	0.62	0.08	0.22	−0.82	−1.10	−0.44	0.24	1.34	−0.81	0.12	−2.17	−1.52	−0.54	−1.61	0.38	−0.92
202299	C5orf27	chromosome 5 open reading frame 27	−2.07	−0.25	0.66	1.19	0.02	1.74	−0.68	−0.85	−0.39	−0.23	−1.28	−0.44	−0.75	0.44	−1.28	−1.92	0.19
2015	EMR1	egf-like module containing, mucin-like, hormone receptor-like 1	−2.07	0.55	0.65	0.29	−0.20	−0.94	0.30	−0.01	1.19	−2.03	0.02	−2.16	−0.53	−1.57	−1.09	0.30	−0.51
57763	ANKRA2	ankyrin repeat, family A (RFXANK-like), 2	−2.07	−0.20	−1.67	−0.42	−1.70	−1.43	−0.82	0.78	−0.05	−0.21	−0.99	0.70	−1.42	−0.84	0.16	−0.67	−0.40
54778	RNF111	ring finger protein 111	−2.07	0.23	−0.89	−1.05	−1.92	−0.72	−0.97	0.80	1.12	−0.70	0.23	−0.85	−1.81	−0.24	−1.06	−0.22	−0.91
762	CA4	carbonic anhydrase IV	−2.07	0.62	−0.41	0.08	0.07	0.13	−0.68	−0.21	1.50	−0.79	−0.07	−1.15	−1.51	−0.94	−2.12	0.33	−1.40
192668	CYS1	cystin 1	−2.08	−0.24	0.82	0.06	0.07	0.31	−0.07	0.20	−0.21	−1.54	−0.90	−1.06	0.13	−0.71	−2.03	0.03	−0.05
24146	CLDN15	claudin 15	−2.08	−1.46	0.60	0.44	0.57	−0.18	1.72	0.41	0.85	−1.60	−0.24	−1.45	−0.07	−0.51	−2.01	−1.50	−1.37
54843	SYTL2	synaptotagmin-like 2	−2.08	−2.09	−0.12	−0.38	−1.38	−1.01	−1.25	0.18	−0.75	−0.04	−1.66	−0.28	−0.58	1.24	0.13	−0.37	−0.93
55374	TMCO6	transmembrane and coiled-coil domains 6	−2.08	−0.03	0.41	−0.36	−0.83	0.19	−1.37	0.42	0.91	−1.48	−0.88	−0.97	−0.16	0.36	−1.93	−0.18	−1.23
79603	CERS4	ceramide synthase 4	−2.08	−0.47	1.17	0.72	−0.73	−0.21	−0.90	0.12	−0.61	−1.48	−0.26	−0.66	−0.63	−0.38	−1.90	−0.01	−0.32
3577	CXCR1	chemokine (C—X—C motif) receptor 1	−2.08	0.24	0.01	−0.45	−0.04	0.43	−0.27	0.43	1.29	−1.93	−0.32	−1.75	−1.66	−0.23	−1.89	−0.08	−1.31
10385	BTN2A2	butyrophilin, subfamily 2, member A2	−2.08	−0.42	0.63	−0.30	−1.49	0.56	−1.86	−0.62	−0.12	−0.69	−1.36	−1.25	0.44	0.16	−0.50	−0.48	−0.10
79792	GSDMD	gasdermin D	−2.08	0.07	0.24	0.78	1.85	0.17	1.00	−0.35	−0.52	−2.17	0.45	−0.87	−1.13	−0.69	−1.75	−0.79	−0.88
84674	CARD6	caspase recruitment domain family, member 6	−2.09	−0.13	−0.05	0.28	−0.39	0.05	−0.19	0.34	1.37	−1.70	0.42	−2.50	−1.07	−0.34	−2.10	−0.21	−1.12

TABLE 3-continued

gene	symbol	name	fisherz	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49
51131	PHF11	PHD finger protein 11	−2.09	−0.45	0.25	−2.32	−0.38	0.81	−0.74	−0.55	−0.13	−0.73	−0.79	−0.86	−0.73	0.52	0.05	−1.42	−0.95
5966	REL	v-rel avian reticuloendotheliosis viral oncogene homolog	−2.09	0.51	−0.20	0.66	−1.03	−0.68	0.41	−0.67	0.93	−0.94	0.69	−1.60	−0.40	−0.69	0.27	−0.70	−1.64
9733	SART3	squamous cell carcinoma antigen recognized by T cells 3	−2.09	−0.26	0.49	0.20	−1.84	−2.27	−1.93	0.44	−0.36	−0.14	0.08	−0.14	−0.95	0.00	−0.16	−0.46	−0.12
10328	EMC8	ER membrane protein complex subunit 8	−2.09	0.24	0.80	0.87	−0.84	−0.29	0.70	−1.49	−0.78	−0.56	−0.38	−0.75	−2.76	0.90	−1.61	−0.76	0.54
255231	MCOLN2	mucolipin 2	−2.09	0.64	1.81	−0.22	−1.14	1.95	−1.46	−0.26	−0.20	−0.85	−1.39	−0.57	0.18	−0.52	−1.59	−0.56	−1.02
25801	GCA	grancalcin, EF-hand calcium binding protein	−2.09	−0.11	0.32	−0.21	−0.06	0.10	−0.23	0.59	1.47	−1.92	0.28	−1.92	−1.40	−0.67	−1.50	−0.35	−1.36
6352	CCL5	chemokine (C-C motif) ligand 5	−2.09	−1.08	0.65	0.03	−1.13	−0.16	−1.00	0.05	−0.07	−1.25	−0.09	−1.39	−0.26	0.33	0.52	−0.51	−1.62
54811	ZNF562	zinc finger protein 562	−2.09	−1.12	0.98	−0.04	1.20	2.25	−1.15	−0.23	−0.50	−0.68	−0.11	−1.60	−1.46	−0.18	−1.10	−0.54	−0.62
59348	ZNF350	zinc finger protein 350	−2.09	0.46	−0.12	−0.32	0.55	−0.83	−0.28	−0.22	1.63	−1.49	−0.35	−0.93	−0.55	−2.61	−1.32	0.26	−0.61
9967	THRAP3	thyroid hormone receptor associated protein 3	−2.09	0.95	0.42	0.34	−0.31	−0.87	−0.25	0.01	0.70	−0.70	0.62	−2.98	−1.66	−0.15	−1.91	0.73	−1.22
2533	FYB	FYN binding protein	−2.10	−0.23	−0.56	0.49	−0.40	−0.87	−0.40	0.06	1.06	−2.02	0.17	−1.55	−0.84	−0.88	−1.34	0.27	−1.79
28985	MCTS1	malignant T cell amplified sequence 1	−2.10	−0.66	−0.50	−1.27	−1.57	−0.57	−0.96	−0.69	0.21	−0.17	−0.96	0.87	−1.37	0.61	−0.33	−1.51	−0.31
55234	SMU1	smu-1 suppressor of mec-8 and unc-52 homolog (*C. elegans*)	−2.10	0.13	−0.04	−0.20	−1.39	−2.16	−1.95	0.25	0.29	−0.42	−0.78	−0.59	−0.55	−1.61	−0.87	0.97	−0.28
1301	COL11A1	collagen, type XI, alpha 1	−2.10	0.31	0.13	1.14	−0.13	1.76	−1.45	−0.27	−0.05	−1.79	−1.32	−0.94	0.75	−0.96	−1.31	−0.01	−0.94
84803	AGPAT9	1-acylglycerol-3-phosphate O-acyltransferase 9	−2.10	0.07	−0.17	0.02	−0.92	−0.99	−1.14	−0.01	1.86	−0.86	0.07	−1.55	−0.99	−0.15	−1.58	0.12	−1.23

TABLE 3-continued

gene	symbol	name	fisherz	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49
100506779	BZRAP1-AS1	BZRAP1 antisense RNA 1	−2.10	−0.43	0.34	0.18	0.11	−0.93	0.03	−0.08	−0.09	−1.76	−0.13	−0.93	−0.30	−2.04	0.68	−1.88	−1.36
197135	PATL2	protein associated with topoisomerase II homolog 2 (yeast)	−2.10	−0.08	0.66	0.09	−0.71	−1.13	−0.76	0.19	0.09	−0.76	−1.29	−1.80	0.64	−0.31	−0.37	−0.89	−1.55
3614	IMPDH1	IMP (inosine 5'-monophosphate) dehydrogenase 1	−2.10	0.10	1.24	0.26	0.41	−0.03	−0.14	0.07	1.18	−2.13	0.07	−1.98	−0.72	−0.93	−1.80	−0.74	−1.13
80781	COL18A1	collagen, type XVIII, alpha 1	−2.10	−1.15	−0.88	−0.81	−0.36	1.09	0.29	0.23	0.48	−2.93	−0.38	−1.04	−0.37	−0.56	−1.58	0.24	−0.97
5586	PKN2	protein kinase N2	−2.11	−0.01	−1.33	−1.12	−0.31	−0.29	0.73	1.12	0.96	−0.76	−0.58	−0.99	−1.76	−0.22	−1.49	−0.10	−1.25
79415	C17orf62	chromosome 17 open reading frame 62	−2.11	0.36	0.69	−0.55	−0.20	1.48	−1.49	0.25	0.88	−1.73	−0.49	−1.76	−0.33	−0.83	−2.30	0.17	−1.22
8893	EIF2B5	eukaryotic translation initiation factor 2B, subunit 5 epsilon, 82 kDa	−2.11	−0.42	0.14	0.02	−0.65	−0.39	0.08	0.31	0.39	−1.42	−0.96	−0.56	0.04	−1.19	−0.43	−1.52	0.22
79736	TEFM	transcription elongation factor, mitochondrial	−2.11	0.10	−0.38	0.03	−1.14	3.19	−1.06	0.01	−0.12	−0.70	−0.69	0.46	−1.94	0.18	−1.26	−0.34	−0.43
5770	PTPN1	protein tyrosine phosphatase, non-receptor type 1	−2.11	−0.21	−0.09	0.43	−1.06	2.10	−1.28	−1.53	0.49	0.56	−1.06	−0.82	−1.28	−0.47	−2.00	0.18	−0.38
9360	PPIG	peptidylprolyl isomerase G (cyclophilin G)	−2.11	0.14	−1.09	−0.02	−0.68	−2.03	−0.70	0.86	0.70	−0.97	−0.23	−0.08	−0.90	−2.21	−1.17	1.25	−1.04
29940	DSE	dermatan sulfate epimerase	−2.11	0.22	0.11	0.18	−0.62	−0.15	−1.11	−0.67	1.04	−1.20	0.40	−2.00	−0.83	−0.01	−1.81	−0.31	−0.37
7150	TOP1	topoisomerase (DNA) I	−2.11	0.15	0.58	1.17	1.30	−0.27	1.04	−0.87	0.47	−0.47	−1.72	−0.75	−0.91	0.28	−1.96	−0.92	−1.33
84964	ALKBH6	alkB, alkylation repair homolog 6 (E. coli)	−2.11	0.05	0.45	0.79	−1.20	−1.09	−0.79	0.00	−0.12	−1.18	−1.16	−0.27	−0.20	−1.63	−0.65	−0.37	−0.76

TABLE 3-continued

gene	symbol	name	fisherz	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49
10614	HEXIM1	hexamethylene bis-acetamide inducible 1	−2.11	−0.43	−0.78	1.49	0.54	−0.15	−0.65	0.38	0.47	−0.81	0.27	−1.58	−1.76	−0.81	−1.05	−0.18	−0.73
147923	ZNF420	zinc finger protein 420	−2.12	−1.30	−0.74	−0.71	−1.74	−0.94	−1.51	0.60	−0.09	−1.63	−0.55	0.36	−0.63	−0.38	0.39	−1.12	0.25
284029	LINC00324	long intergenic non-protein coding RNA 324	−2.12	−0.70	−0.55	0.21	−1.11	−0.39	−1.60	0.16	0.48	−1.30	−0.09	−0.50	−0.76	−1.67	−1.15	0.35	−0.48
54952	TRNAU1AP	tRNA selenocysteine 1 associated protein 1	−2.12	0.49	0.10	0.73	−1.46	1.17	−0.06	−0.13	0.17	−1.51	−0.47	−1.76	−0.16	−1.05	−1.15	−0.21	−0.62
57476	GRAMD1B	GRAM domain containing 1B	−2.12	−0.35	1.18	0.80	0.02	−0.31	0.34	−0.79	0.02	−0.67	0.11	−1.52	0.28	−1.39	−3.16	−0.48	−0.86
8745	ADAM23	ADAM metallopeptidase domain 23	−2.12	0.14	−0.79	0.23	−1.00	2.21	−1.70	0.15	−0.53	−1.38	−0.67	0.52	−0.98	−0.15	−0.31	−1.72	−0.57
22928	SEPHS2	selenophosphate synthetase 2	−2.12	0.48	−0.36	−0.41	−1.01	1.46	−1.28	0.09	1.20	−1.64	0.24	−1.43	−0.05	−1.22	−1.37	−0.81	−0.45
25880	TMEM186	transmembrane protein 186	−2.12	−0.84	0.69	−0.26	−1.50	−0.80	−2.08	−0.40	−1.10	0.01	0.03	−0.25	−1.55	−0.01	−0.60	−0.71	0.09
28638	TRBC2	T cell receptor beta constant 2	−2.12	−0.74	0.65	0.15	−0.81	−0.39	−0.41	0.46	−0.02	−2.19	−0.98	−0.89	−0.47	−0.37	−0.06	−1.20	−1.32
29933	GPR132	G protein-coupled receptor 132	−2.12	1.64	−0.07	−0.04	−2.06	−0.25	−0.38	−0.49	0.42	−0.91	0.62	−0.86	−0.39	−1.87	−1.08	1.13	−1.16
30009	TBX21	T-box 21	−2.12	−1.00	1.25	0.12	−0.97	−1.71	−0.78	0.60	−0.43	−1.69	0.15	−0.49	−1.41	−0.50	−0.50	0.12	−0.86
3554	IL1R1	interleukin 1 receptor, type I	−2.12	0.17	−0.48	−0.46	−0.65	0.83	−0.21	−0.33	1.37	−0.71	−0.41	−1.50	−0.30	−0.57	−2.20	0.41	−0.67
8821	INPP4B	inositol polyphosphate-4-phosphatase, type II, 105 kDa	−2.12	−1.19	−0.83	0.02	−0.97	−1.09	−1.49	0.05	−0.07	−1.31	−1.14	−0.75	0.07	−0.20	0.56	−0.75	−0.39
10943	MSL3	male-specific lethal 3 homolog (*Drosophila*)	−2.12	0.46	0.07	0.11	−1.31	−1.19	−1.00	−0.44	1.30	−1.21	−0.83	−0.87	−0.80	−1.68	−1.18	0.84	−1.16
57724	EPG5	ectopic P-granules autophagy protein 5 homolog (*C. elegans*)	−2.12	−0.33	−0.06	0.11	−0.68	−1.69	−0.69	0.63	1.42	−1.81	−0.82	−1.44	−0.38	−1.68	−0.92	0.62	−0.92

TABLE 3-continued

gene	symbol	name	fisherz	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49
100506282	LOC100506282	uncharacterized LOC100506282	−2.13	0.16	0.83	1.50	−0.29	0.27	−0.26	−0.12	0.68	−0.35	−0.98	−0.98	−1.08	−0.06	−2.92	−0.12	−0.82
147699	PPM1N	protein phosphatase, Mg2+/Mn2+ dependent, 1N (putative)	−2.13	−1.19	−0.54	0.79	−0.62	1.75	−1.43	−0.70	0.66	−0.47	−0.55	−0.25	0.21	−1.24	−2.57	−0.15	−1.07
3002	GZMB	granzyme B (granzyme 2, cytotoxic T-lymphocyte-associated serine esterase 1)	−2.13	−1.41	0.38	0.70	−1.15	0.41	−0.41	0.43	−0.49	−2.73	−0.62	−0.77	0.01	−0.74	−0.32	−0.57	−0.47
389320	C5orf48	chromosome 5 open reading frame 48	−2.13	0.36	0.46	−0.93	−0.31	−0.38	0.35	0.10	−0.39	−0.84	−0.47	−1.76	0.86	−0.73	−1.12	0.34	−1.18
9914	ATP2C2	ATPase, Ca++ transporting, type 2C, member 2	−2.13	−0.05	−0.48	−0.11	−0.06	−0.08	−0.22	−0.27	0.80	0.22	−0.95	−2.55	−0.89	−0.10	−2.35	0.50	−0.73
10804	GJB6	gap junction protein, beta 6, 30 kDa	−2.13	0.05	−0.09	−0.70	−1.01	0.54	−0.19	−0.43	0.58	−1.29	−0.76	−1.39	−0.73	−1.88	−1.23	0.69	−0.43
51439	FAM8A1	family with sequence similarity 8, member A1	−2.13	−0.42	−1.15	−0.36	−0.48	−0.61	−0.63	0.86	1.25	−1.58	−0.76	−1.01	−1.56	−0.15	−1.57	−0.26	−0.82
814	CAMK4	calcium/calmodulin-dependent protein kinase IV	−2.13	0.28	0.24	0.04	−1.73	−0.04	−0.95	−0.33	0.13	−1.58	−1.12	−0.34	0.13	−1.29	−0.65	−0.19	−1.21
5272	SERPINB9	serpin peptidase inhibitor, clade B (ovalbumin), member 9	−2.13	0.11	1.70	0.00	−1.10	−0.25	−2.20	−0.80	−0.23	−1.26	−0.35	−0.72	−0.86	−0.60	−0.26	−0.12	−0.92
8428	STK24	serine/threonine kinase 24	−2.13	−0.94	0.54	0.28	−1.13	0.33	−1.44	−0.51	0.40	−1.37	−1.13	−1.10	−1.13	0.08	−0.07	−1.59	0.17
23048	FNBP1	formin binding protein 1	−2.14	−0.45	1.48	0.04	0.03	−1.09	−0.69	−0.25	−0.71	−1.04	0.16	−2.43	0.32	−1.89	0.24	−0.36	−0.47
344558	SH3RF3	SH3 domain containing ring finger 3	−2.14	0.78	−0.14	−0.92	0.38	−1.43	−0.23	0.37	0.84	−0.85	−1.23	−0.98	−0.77	−0.98	−2.71	0.02	−0.55

TABLE 3-continued

gene	symbol	name	fisherz	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49
79078	C1orf50	chromosome 1 open reading frame 50	−2.14	−0.55	1.96	1.42	0.84	1.26	−0.45	−0.84	−0.66	−1.15	−1.62	−0.53	−1.13	−0.96	−0.37	−1.31	−0.53
81606	LBH	limb bud and heart development	−2.14	−1.45	0.75	−0.43	−0.77	−0.26	−0.68	0.22	−0.84	−0.89	−1.14	−0.64	−0.51	0.12	−0.38	−1.14	−0.68
64377	CHST8	carbohydrate (N-acetylgalactosamine 4-0) sulfotransferase 8	−2.14	−0.27	0.39	−0.34	−0.28	−0.62	0.40	−1.62	0.74	0.06	0.41	−0.88	−1.46	0.18	−2.43	−1.63	−0.24
57501	KIAA1257	KIAA1257	−2.14	−0.35	−0.74	0.39	−0.26	−1.75	−0.53	0.75	1.97	0.31	−0.22	−1.43	−0.32	−0.91	−2.19	0.08	−1.54
5991	RFX3	regulatory factor X, 3 (influences HLA class II expression)	−2.14	0.67	−0.98	0.29	−0.25	−0.83	−0.59	−0.03	0.64	−0.01	−1.33	−1.75	−0.60	−1.37	−1.44	0.78	−0.46
90075	ZNF30	zinc finger protein 30	−2.14	−0.45	0.73	−0.98	−0.52	−3.01	−0.88	0.01	−0.66	−0.83	−0.40	1.16	−0.24	−1.24	0.28	−0.67	−0.14
375341	C3orf62	chromosome 3 open reading frame 62	−2.14	0.54	0.27	0.16	0.05	−0.22	−0.54	0.14	1.34	−1.74	0.35	−1.40	−0.79	−0.99	−2.42	0.03	−1.27
100130548	LOC100130548	uncharacterized LOC100130548	−2.15	−0.60	0.80	0.14	0.03	0.85	−0.60	−1.07	0.34	−1.10	−0.90	−1.79	−0.35	−1.83	−0.97	0.72	−1.00
114786	XKR4	XK, Kell blood group complex subunit-related family, member 4	−2.15	−0.80	−0.51	−0.43	−0.34	2.61	−0.79	−0.89	0.13	−0.43	−0.67	−0.14	−0.52	−0.96	−1.69	−0.07	−0.36
150084	IGSF5	immunoglobulin superfamily, member 5	−2.15	0.53	0.83	−0.22	0.26	2.32	−0.73	−0.69	−0.08	−1.24	−0.37	−1.74	−0.43	−1.38	−1.92	0.06	−0.44
55012	PPP2R3C	protein phosphatase 2, regulatory subunit B", gamma	−2.15	0.50	−0.18	0.28	−0.01	−1.68	−0.07	0.12	1.40	−1.31	0.07	−0.91	−1.72	−0.95	−1.60	−0.18	−0.83
147525	LINC00526	long intergenic non-protein coding RNA 526	−2.15	0.01	−0.55	0.90	−0.70	−1.00	−0.83	−0.17	−1.52	−0.38	−0.91	0.19	−0.71	−0.84	−0.58	−0.82	−0.39

TABLE 3-continued

gene	symbol	name	fisherz	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49
54557	SGTB	small glutamine-rich tetratricopeptide repeat (TPR)-containing, beta	−2.15	0.23	−0.78	0.10	−1.25	−0.02	−1.12	−0.10	1.46	−0.88	−0.39	−0.96	−0.64	−1.86	−1.56	0.65	−1.02
56267	CCBL2	cysteine conjugate-beta lyase 2	−2.15	0.68	0.94	−1.30	−0.02	−0.14	−0.75	−0.28	−1.12	−0.42	−1.14	−0.82	−0.48	−0.27	1.02	−2.34	−0.40
51176	LEF1	lymphoid enhancer-binding factor 1	−2.15	−0.06	−0.04	0.50	−1.53	−0.45	−1.54	−0.32	−0.05	−1.34	−0.85	−0.51	−0.22	−1.20	−0.16	−0.27	−1.17
10468	FST	follistatin	−2.15	−0.20	0.87	0.11	−0.41	0.93	−0.11	−1.12	−0.03	−1.05	−1.27	0.56	−0.16	−0.64	−2.11	−0.52	−0.69
23258	DENND5A	DENN/MADD domain containing 5A	−2.15	0.12	0.07	−0.02	0.32	−0.76	0.02	−0.59	0.55	−1.68	0.62	−2.38	−0.05	−0.91	−1.51	0.21	−2.12
90768	MGC45800	uncharacterized LOC90768	−2.15	−1.02	1.59	0.00	−0.58	1.12	0.26	0.23	−0.48	−1.60	−0.91	−1.54	0.08	−0.85	−0.77	−0.32	−0.98
134957	STXBP5	syntaxin binding protein 5 (tomosyn)	−2.16	0.01	−0.56	−0.01	−0.54	−0.10	−0.13	0.71	1.17	−1.58	−0.11	−2.33	−0.72	−1.75	−0.99	0.26	−1.15
80342	TRAF3IP3	TRAF3 interacting protein 3	−2.16	−0.22	1.35	−0.63	−0.25	−0.55	−0.84	0.10	0.11	−1.93	−0.35	−1.02	0.37	−1.99	0.27	−0.76	−1.84
91351	DDX60L	DEAD (Asp-Glu-Ala-Asp) box polypeptide 60-like	−2.16	0.33	−0.81	−0.18	−0.74	0.01	−0.59	0.60	1.32	−1.63	−0.05	−2.06	−0.68	−0.68	−1.66	−0.08	−1.48
29916	SNX11	sorting nexin 11	−2.16	0.44	0.38	0.62	−0.46	1.95	−0.44	−0.31	0.77	−1.33	0.26	−1.32	−1.11	−0.88	−2.44	−0.26	−0.66
8519	IFITM1	interferon induced transmembrane protein 1	−2.16	0.04	0.54	0.00	−0.76	−0.30	−1.74	0.29	0.34	−2.52	−0.89	−0.22	−0.60	−1.53	0.06	−0.06	−1.10
2113	ETS1	v-ets avian erythroblastosis virus E26 oncogene homolog 1	−2.16	−0.22	1.20	−0.30	−1.60	−0.14	−1.05	0.30	−0.03	−1.65	−0.90	−1.05	−0.60	−1.34	0.39	−0.66	−1.13
55770	EXOC2	exocyst complex component 2	−2.16	0.23	−0.28	−2.07	−2.56	0.21	−1.23	0.15	−0.30	−0.49	−0.58	−1.55	0.49	−0.51	0.16	−0.60	−0.17
91833	WDR20	WD repeat domain 20	−2.16	0.26	−0.47	−0.62	−1.23	−1.50	−0.67	0.59	1.04	−1.43	−0.63	−0.27	−1.31	−1.88	−0.88	0.38	−0.19
117177	RAB3IP	RAB3A interacting protein	−2.16	−0.84	−0.71	0.52	−1.59	1.31	−0.65	−0.08	0.89	−0.71	−0.88	−1.16	−0.75	−1.01	−1.50	0.26	−0.90

TABLE 3-continued

gene	symbol	name	fisherz	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49
546	ATRX	alpha thalassemia/mental retardation syndrome X-linked	−2.16	0.61	0.17	0.22	−0.93	−1.67	−0.52	1.13	1.20	−0.88	−0.27	−2.36	−1.28	−0.88	−1.67	0.53	−1.32
4253	CTAGE5	CTAGE family, member 5	−2.17	−0.29	−0.89	−0.52	−1.90	−0.69	−1.65	0.19	0.88	−1.89	−0.62	0.12	−0.65	0.22	−0.93	0.02	−1.04
23214	XPO6	exportin 6	−2.17	0.22	0.51	−0.08	−0.12	0.65	−0.96	−0.26	1.31	−2.20	−0.32	−1.58	−0.25	−1.06	−1.95	0.27	−1.48
53347	UBASH3A	ubiquitin associated and SH3 domain containing A	−2.17	−0.77	0.40	0.23	−1.17	0.06	−1.49	0.38	0.10	−2.00	−1.10	−1.07	−0.09	−0.73	−0.10	−0.42	−0.77
56888	KCMF1	potassium channel modulatory factor 1	−2.17	−1.33	−0.12	−0.16	−1.40	0.87	−1.07	−0.32	0.72	−1.51	−0.61	−0.42	−0.43	0.28	−1.98	−0.08	−1.65
777	CACNA1E	calcium channel, voltage-dependent, R type, alpha 1E subunit	−2.17	0.75	−0.59	0.85	−0.79	1.01	−0.83	−0.03	0.84	−1.28	−0.47	−1.27	−0.72	−1.42	−1.81	0.15	−0.79
100216545	KMT2E-AS1	KMT2E antisense RNA 1 (head to head)	−2.17	−0.69	−0.17	0.88	−0.54	0.46	−0.48	−0.56	−0.03	−0.90	−0.53	−1.13	−0.29	0.82	−0.67	−1.17	−1.23
8879	SGPL1	sphingosine-1-phosphate lyase 1	−2.17	0.23	−0.11	−1.18	−1.11	0.24	−1.42	0.65	0.59	−0.06	−0.38	−1.86	−1.11	−0.18	−2.25	0.61	−0.61
9759	HDAC4	histone deacetylase 4	−2.17	−0.04	0.01	−0.28	0.23	−0.08	0.09	0.27	1.34	−1.51	−0.13	−1.25	−1.48	−0.76	−2.24	0.33	−1.13
26578	OSTF1	osteoclast stimulating factor 1	−2.18	0.31	−0.12	0.48	−0.67	0.07	−1.40	−0.27	1.20	−0.79	−0.03	−2.32	−1.19	0.08	−2.20	0.24	−1.08
4050	LTB	lymphotoxin beta (TNF superfamily, member 3)	−2.18	−0.37	0.26	0.38	−0.82	0.62	−1.48	−0.55	0.43	−2.57	−0.56	−0.84	0.10	−1.01	−0.82	0.03	−1.25
4236	MFAP1	microfibrillar-associated protein 1	−2.18	0.04	2.06	−1.26	−0.18	−1.23	−2.07	0.31	0.18	−0.97	0.20	−0.26	−0.47	0.19	−1.47	−0.87	−0.39
54491	FAM105A	family with sequence similarity 105, member A	−2.18	−0.90	−0.58	−0.19	−0.18	−0.19	−0.82	−0.18	1.20	−2.00	−0.23	−1.14	−0.81	−0.98	−1.99	0.94	−1.25
55847	CISD1	CDGSH iron sulfur domain 1	−2.18	−0.27	−0.72	−0.14	−1.02	0.61	−1.21	0.24	0.40	−0.68	−0.97	−0.65	−0.96	0.74	−2.26	−0.27	−0.24
100132707	PAXIP1-AS2	PAXIP1 antisense RNA 2	−2.19	0.30	0.46	−0.02	−0.76	0.74	−1.35	0.02	0.17	−1.37	−0.59	−1.98	0.34	−0.03	−1.43	−0.28	−1.92

TABLE 3-continued

gene	symbol	name	fisherz	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49
55884	WSB2	WD repeat and SOCS box containing 2	−2.19	0.26	0.47	−0.19	0.05	−0.61	−0.29	−0.28	0.99	−0.99	0.25	−1.75	−1.46	0.14	−2.04	0.02	−0.57
83607	AMMECR1L	AMMECR1-like	−2.19	−1.27	−0.33	−0.57	−0.59	−0.06	−1.35	0.21	−0.43	−0.91	−1.12	−0.48	−1.57	−1.31	−0.27	−0.09	0.72
9252	RPS6KA5	ribosomal protein S6 kinase, 90 kDa, polypeptide 5	−2.19	−0.65	−0.33	−0.72	−1.32	−0.44	−1.20	0.91	0.26	−1.21	−0.52	−0.80	0.20	−0.28	−1.31	−0.59	−1.33
55119	PRPF38B	pre-mRNA processing factor 38B	−2.19	0.01	−0.47	−2.06	−1.09	0.27	−0.06	0.39	0.22	−0.87	−0.57	0.05	−1.42	−2.27	0.10	0.15	−1.08
57520	HECW2	HECT, C2 and WW domain containing E3 ubiquitin protein ligase 2	−2.19	0.49	0.23	0.37	−0.74	0.28	−0.53	0.15	0.91	−1.68	−0.49	−1.38	−0.61	−0.37	−2.56	0.35	−0.97
79818	ZNF552	zinc finger protein 552	−2.19	0.12	−0.32	−0.44	−0.47	0.26	−0.51	0.22	0.99	−0.88	−0.62	−1.53	−1.27	−0.62	−1.71	0.09	−0.82
8320	EOMES	eomesodermin	−2.19	−1.37	0.09	0.09	−1.77	0.29	−1.43	0.48	−0.02	−1.81	−0.84	−0.37	0.13	−0.95	−0.36	0.13	−1.27
2792	GNGT1	guanine nucleotide binding protein (G protein), gamma transducing activity polypeptide 1	−2.19	−1.06	1.52	−0.42	0.02	2.78	−0.16	−0.25	−1.65	0.61	−0.71	−0.92	0.08	−1.85	−1.34	−0.51	−1.02
54910	SEMA4C	sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4C	−2.19	0.12	1.29	−0.78	0.05	−0.12	−1.15	1.12	−0.47	−1.37	−0.55	0.69	−1.74	0.02	−1.01	−1.07	−1.56
55114	ARHGAP17	Rho GTPase activating protein 17	−2.19	1.40	1.57	0.35	−0.95	−1.23	−0.04	−0.11	−1.05	−0.74	0.80	−0.73	−0.56	−1.20	−0.93	−0.46	−1.20
56253	CRTAM	cytotoxic and regulatory T cell molecule	−2.19	−1.83	−1.11	−0.04	−1.84	−1.29	−0.99	0.87	0.45	−0.64	−0.53	0.08	0.29	−0.75	−1.28	−0.12	−1.25

TABLE 3-continued

gene	symbol	name	fisherz	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49
65082	VPS33A	vacuolar protein sorting 33 homolog A (*S. cerevisiae*)	−2.19	−0.53	0.02	−0.62	−0.83	1.05	−1.49	0.36	0.74	−1.11	−0.28	−0.95	0.35	−0.90	−0.98	−1.28	−1.16
84719	LINC00260	long intergenic non-protein coding RNA 260	−2.20	−0.34	−0.71	−0.06	−0.86	−0.17	−0.67	−0.08	0.75	−2.13	−0.68	−1.17	−0.22	0.45	−1.53	0.12	−1.57
253558	LCLAT1	lysocardiolipin acyltransferase 1	−2.20	−0.69	−1.32	−1.73	−1.11	−1.35	−0.66	1.02	−0.05	−1.53	−0.55	−0.37	0.62	−0.35	−1.38	−0.65	−0.24
6777	STAT5B	signal transducer and activator of transcription 5B	−2.20	0.44	0.37	0.15	0.02	−0.23	−0.53	−0.12	0.89	−2.10	0.25	−2.31	−0.90	−1.35	−1.31	0.73	−1.74
80025	PANK2	pantothenate kinase 2	−2.20	−0.25	1.01	0.64	−0.20	0.07	−0.74	−0.02	0.85	−1.77	0.02	−2.35	−0.53	0.04	−1.74	−0.74	−0.84
84662	GLIS2	GLIS family zinc finger 2	−2.20	0.50	0.17	0.54	0.43	0.14	−1.59	−0.74	0.25	−0.94	−0.71	−1.16	0.07	−0.24	−2.45	−0.66	−0.34
89890	KBTBD6	kelch repeat and BTB (POZ) domain containing 6	−2.20	0.15	−0.79	−1.41	−1.72	−0.04	0.42	0.18	0.43	−1.23	−0.10	−0.07	−0.81	−0.85	−1.57	−0.42	−0.54
10390	CEPT1	choline/ethanolamine phosphotransferase 1	−2.20	0.37	−0.08	−0.71	−0.80	−0.63	−1.10	0.83	0.88	−0.61	0.05	−1.78	−1.48	0.33	−2.30	−0.44	−0.26
2841	GPR18	G protein-coupled receptor 18	−2.20	−0.65	0.95	−0.34	−1.00	0.35	−0.03	−0.24	−1.02	−1.34	−0.62	−0.20	−0.38	−0.87	−0.60	−0.68	−0.92
3904	LAIR2	leukocyte-associated immunoglobulin-like receptor 2	−2.20	−1.10	1.23	0.37	−1.27	−0.05	−0.10	0.25	−0.57	−1.85	−0.92	−0.17	−1.43	−1.08	−0.08	−0.63	−0.98
140460	ASB7	ankyrin repeat and SOCS box containing 7	−2.20	−0.05	−0.77	0.23	−0.82	−0.71	−0.46	0.20	1.10	−1.47	−1.03	−0.58	−0.39	−2.59	−0.74	0.08	−0.34
9605	VPS9D1	VPS9 domain containing 1	−2.20	0.25	−0.40	0.11	−0.29	0.40	−0.60	−0.59	1.34	−1.24	0.07	−2.10	−0.90	−0.63	−1.97	−0.03	−1.15
283349	RASSF3	Ras association (RalGDS/AF-6) domain family member 3	−2.21	0.55	−0.19	−0.38	−0.92	−0.34	−0.79	0.51	1.04	−1.69	0.23	−1.49	−0.90	−0.82	−1.37	0.11	−1.75
51246	SHISA5	shisa family member 5	−2.21	−0.38	−0.02	−0.61	0.34	0.24	−1.03	0.03	0.78	−2.49	0.37	−1.40	−1.50	−0.04	−1.70	−0.38	0.05
148268	ZNF570	zinc finger protein 570	−2.21	0.02	−1.49	−0.35	−0.99	−1.73	−1.60	−0.07	−0.57	0.77	−0.95	1.75	−0.12	−0.87	−0.64	−1.25	0.08

TABLE 3-continued

gene	symbol	name	fisherz	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49
26589	MRPL46	mitochondrial ribosomal protein L46	−2.21	−0.39	0.36	0.93	−1.74	0.63	−1.78	−0.28	−0.38	−1.26	−0.14	−0.30	−1.52	−0.79	−0.24	−0.62	0.24
7049	TGFBR3	transforming growth factor, beta receptor III	−2.21	−0.97	−0.32	0.21	−1.90	−1.61	−1.36	0.04	−0.01	−1.15	−0.85	−0.57	−0.04	0.33	−0.21	−0.29	−1.06
2791	GNG11	guanine nucleotide binding protein (G protein), gamma 11	−2.21	−0.32	−1.05	0.18	−1.21	0.83	−1.14	0.12	1.08	−1.49	−0.33	−1.29	−0.73	−0.55	−1.54	−0.67	−0.20
51455	REV1	REV1, polymerase (DNA directed)	−2.21	−0.30	−1.28	−1.13	−1.21	−1.82	0.29	0.51	0.49	−0.63	−0.75	−1.54	0.65	−1.07	−0.93	0.16	−1.02
1178	CLC	Charcot-Leyden crystal galectin	−2.22	−0.06	−0.39	−0.16	−0.98	−1.21	−0.20	0.76	1.10	−1.44	0.64	−1.52	−1.51	−0.40	−1.14	−0.19	−1.44
79153	GDPD3	glycerophosphodiester phosphodiesterase domain containing 3	−2.22	0.49	−0.68	−0.16	−0.96	0.09	−0.61	0.39	1.34	−2.08	−0.64	−1.63	−0.33	−1.50	−1.42	0.37	−0.93
101928524	LOC101928524	uncharacterized LOC101928524	−2.22	0.14	−0.26	−0.07	−0.96	−0.25	0.18	0.69	1.46	−1.91	−0.79	−1.20	−0.18	−0.88	−1.38	−0.31	−2.25
11064	CNTRL	centriolin	−2.22	0.51	0.62	−0.38	−0.04	−1.09	0.45	0.85	0.69	−0.39	−0.56	−2.19	−1.16	−1.33	−0.95	−0.48	−2.11
23429	RYBP	RING1 and YY1 binding protein	−2.22	−1.24	0.30	1.60	−0.59	−0.34	−1.62	0.38	0.67	−0.86	−0.27	−0.37	−1.80	−1.65	−0.85	0.28	−0.75
5170	PDPK1	3-phosphoinositide dependent protein kinase-1	−2.22	0.00	−0.60	0.45	−0.25	0.04	−1.85	0.36	1.42	−1.14	−0.82	−1.01	−0.75	−1.27	−2.15	0.19	−0.62
10677	AVIL	advillin	−2.23	0.30	−0.08	−0.01	−0.59	−1.56	−1.14	0.60	1.13	−0.90	−0.31	−1.31	−1.48	−0.50	−1.58	0.66	−1.78
3772	KCNJ15	potassium inwardly-rectifying channel, subfamily J, member 15	−2.23	0.23	0.26	−0.02	−0.26	0.26	−0.83	0.31	1.35	−1.79	−0.07	−1.86	−1.14	−0.39	−1.96	0.17	−1.31
128061	C1orf131	chromosome 1 open reading frame 131	−2.23	−0.47	−0.90	−0.33	−1.37	−1.22	−1.10	0.05	0.13	−1.44	−0.10	0.09	−1.60	−1.12	−0.13	−0.55	−0.13
50856	CLEC4A	C-type lectin domain family 4, member A	−2.23	0.15	0.14	0.43	−0.80	−0.14	−0.73	−0.26	1.51	−1.39	0.13	−1.57	−0.86	−0.45	−1.89	−0.14	−1.09

TABLE 3-continued

gene	symbol	name	fisherz	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49
6198	RPS6KB1	ribosomal protein S6 kinase, 70 kDa, polypeptide 1	−2.23	−0.21	−0.73	−0.35	−0.80	−0.72	0.28	0.63	−0.06	−0.70	−0.59	−0.05	−0.17	−1.42	−0.33	0.07	−0.55
101927588	LOC101927588	uncharacterized LOC101927588	−2.24	0.09	0.17	−0.36	−0.41	−1.22	0.16	0.27	0.13	−2.50	−0.30	−1.65	−0.53	−0.11	0.85	−1.05	−0.52
2000	ELF4	E74-like factor 4 (ets domain transcription factor)	−2.24	0.39	0.72	−0.14	−0.44	−0.50	0.34	0.29	1.34	−1.71	0.34	−2.31	−0.96	−1.05	−1.26	−0.58	−1.61
493753	COA5	cytochrome c oxidase assembly factor 5	−2.24	−0.80	−0.63	−1.24	−1.03	−0.96	−0.07	0.34	0.31	−0.40	−0.77	0.51	−1.30	−0.67	−0.03	−1.50	−0.01
23081	KDM4C	lysine (K)-specific demethylase 4C	−2.24	−0.52	−0.13	−1.00	−0.29	0.76	−1.48	−0.18	−0.42	−0.09	−1.54	−0.30	0.17	0.03	−0.59	−1.80	−1.60
4773	NFATC2	nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 2	−2.24	−1.02	0.77	−0.22	−1.07	−0.29	−1.21	0.64	−0.31	−2.29	−1.08	−1.41	−0.48	−0.99	0.59	−0.23	−0.44
10178	TENM1	teneurin transmembrane protein 1	−2.25	−0.12	−0.96	0.43	−0.60	−1.74	−0.17	−0.15	0.71	−1.79	−0.36	−0.90	−0.05	−1.71	−1.43	0.64	−1.03
4974	OMG	oligodendrocyte myelin glycoprotein	−2.25	0.29	−0.19	0.31	−0.02	−0.46	0.21	−0.48	2.07	−0.83	0.00	−1.24	−1.35	−1.53	−1.45	0.10	−1.83
83860	TAF3	TAF3 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 140 kDa	−2.25	0.12	0.93	0.61	−1.02	−0.93	−0.32	0.41	0.59	−1.52	−1.30	−0.48	−0.02	−1.12	−1.50	−0.25	−0.28
91612	CHURC1	churchill domain containing 1	−2.25	−0.24	0.27	−0.30	−1.06	−0.04	−0.28	−0.52	1.40	−2.64	−0.26	−1.08	−0.26	−0.72	−0.86	−0.69	−1.00
2178	FANCE	Fanconi anemia, complementation group E	−2.26	−0.56	0.71	−0.52	−1.03	−0.35	0.26	−0.13	−0.49	−1.83	−0.98	0.03	0.31	−1.52	−1.42	−0.93	0.00
55303	GIMAP4	GTPase, IMAP family member 4	−2.26	−0.37	0.14	−0.44	−0.87	−1.15	−1.59	0.33	0.66	−1.98	−0.02	−1.10	−0.42	−0.09	−1.03	−0.12	−1.45

TABLE 3-continued

gene	symbol	name	fisherz	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49
221002	RASGEF1A	RasGEF domain family, member 1A	−2.26	−0.30	−0.94	−0.21	−0.36	−0.68	0.34	−0.10	0.88	−2.51	−0.46	−1.53	−0.07	−0.60	−1.68	0.48	−1.14
3930	LBR	lamin B receptor	−2.26	0.09	0.14	−0.49	−0.30	−0.94	0.64	1.15	0.88	−2.36	0.28	−1.48	−0.55	−1.62	−0.79	−0.69	−1.40
55471	NDUFAF7	NADH dehydrogenase (ubiquinone) complex I, assembly factor 7	−2.26	0.97	−0.55	−0.62	−1.46	−0.11	−0.98	0.29	0.52	−1.80	−0.54	−0.64	−1.01	−1.67	−0.87	0.30	−0.50
9354	UBE4A	ubiquitination factor E4A	−2.26	−0.27	−0.43	−2.87	−0.96	0.06	−0.87	1.19	0.75	−1.29	−0.70	0.18	−2.14	−0.21	−0.90	0.03	−0.44
83700	JAM3	junctional adhesion molecule 3	−2.26	0.00	−0.65	0.67	−0.42	0.58	−0.84	−0.28	0.75	−1.51	0.07	−1.05	−0.33	−3.25	−0.20	−0.58	−0.77
9140	ATG12	autophagy related 12	−2.26	−0.12	−1.78	1.02	−1.95	−1.03	−1.15	0.04	0.41	−0.50	−0.97	0.50	−1.80	−1.54	−0.29	0.65	−0.46
23526	HMHA1	histocompatibility (minor) HA-1	−2.27	−0.29	0.34	0.54	−0.41	−0.11	−0.57	0.13	0.31	−2.31	−0.19	−1.01	0.47	−2.56	−0.43	−0.27	−1.12
23590	PDSS1	prenyl (decaprenyl) diphosphate synthase, subunit 1	−2.27	1.23	0.14	−1.07	−0.31	1.31	0.51	−0.76	0.14	−0.39	−1.10	−1.56	−1.76	−1.89	−1.66	0.54	−0.07
9270	ITGB1BP1	integrin beta 1 binding protein 1	−2.27	−0.53	0.25	−0.72	0.76	1.53	0.81	−0.86	−1.50	−1.05	0.26	−0.42	−0.21	−0.32	−1.49	−2.35	−1.03
10627	MYL12A	myosin, light chain 12A, regulatory, non-sarcomeric	−2.27	0.89	0.00	0.29	−0.64	0.67	−1.59	0.02	0.56	−1.76	−0.04	−1.38	−1.28	−0.41	−1.13	−1.24	−0.71
26048	ZNF500	zinc finger protein 500	−2.27	−1.18	0.18	0.15	−0.86	−0.82	−1.17	−0.58	−1.27	−1.06	−0.65	0.24	−0.03	0.13	−0.37	−0.83	−0.30
917	CD3G	CD3g molecule, gamma (CD3-TCR complex)	−2.27	−1.58	0.01	−0.12	−0.61	−0.23	−0.59	−0.63	−0.25	−1.30	−0.55	−0.61	−0.94	−0.64	−0.88	0.01	−1.05
94039	ZNF101	zinc finger protein 101	−2.27	0.06	−0.61	−0.07	−1.58	−0.20	−0.55	−0.21	0.60	−1.98	−1.00	−0.46	−0.66	−2.00	−0.56	0.33	−0.69
4215	MAP3K3	mitogen-activated protein kinase kinase kinase 3	−2.28	0.26	−0.02	−0.10	−0.33	0.94	−0.99	0.16	1.29	−1.86	−0.07	−2.04	−0.76	−0.96	−1.93	0.09	−0.84
10663	CXCR6	chemokine (C—X—C motif) receptor 6	−2.28	−1.52	0.47	−0.52	−0.61	0.00	−0.11	−0.52	−0.32	−1.86	−1.03	−0.32	−0.78	−0.29	−1.10	−0.34	−0.28

TABLE 3-continued

gene	symbol	name	fisherz	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49
10308	ZNF267	zinc finger protein 267	−2.28	0.84	−0.65	0.10	−1.27	0.56	−0.76	0.39	1.09	−1.16	−0.14	−0.73	−1.57	−1.56	−1.40	0.17	−1.00
8527	DGKD	diacylglycerol kinase, delta 130 kDa	−2.28	0.47	0.01	0.03	0.72	−1.78	0.40	−0.07	0.08	−1.31	0.56	−0.50	−0.08	−2.37	−0.25	−1.31	−1.08
926	CD8B	CD8b molecule	−2.28	−0.59	−0.11	−0.36	−1.18	−0.55	−0.81	0.55	−0.10	−1.69	−0.98	−1.18	−0.39	−0.43	−1.18	−0.37	−0.57
9619	ABCG1	ATP-binding cassette, sub-family G (WHITE), member 1	−2.28	−0.04	−0.78	−0.92	−0.95	−1.71	−1.39	0.19	0.25	−1.65	−0.97	−0.44	0.85	−0.19	−1.13	0.71	−0.82
5998	RGS3	regulator of G-protein signaling 3	−2.29	0.44	0.97	1.13	0.12	−0.09	−0.71	−0.41	0.61	−2.74	−1.13	−1.33	−1.18	−1.52	−1.56	0.59	−0.17
132625	ZFP42	ZFP42 zinc finger protein	−2.29	0.20	−1.36	0.61	−0.55	0.75	−1.95	0.44	0.70	−1.62	−0.62	−0.68	−1.55	−0.90	−1.92	0.44	−0.61
88455	ANKRD13A	ankyrin repeat domain 13A	−2.30	−0.11	−0.08	−0.02	−0.84	−2.13	−0.37	0.72	0.85	−1.99	−0.03	−1.34	−0.09	−0.81	−1.18	−0.69	−0.76
3604	TNFRSF9	tumor necrosis factor receptor superfamily, member 9	−2.30	0.91	0.58	−0.73	−1.34	1.26	−1.09	−0.57	0.06	−1.35	−0.53	−1.48	−0.11	0.01	−1.98	−0.13	−0.90
100507398	INTS6-AS1	INTS6 antisense RNA1	−2.30	−0.45	−0.55	0.49	−0.85	0.37	−0.46	0.34	0.77	−1.77	−0.71	−1.14	−0.32	−2.18	0.16	0.06	−1.13
58517	RBM25	RNA binding motif protein 25	−2.30	−0.20	0.40	−0.90	0.10	−1.85	0.94	0.79	−0.21	0.21	−0.47	−0.65	−0.35	−1.86	−0.87	−0.62	−1.17
51192	CKLF	chemokine-like factor	−2.31	−0.14	−0.30	−0.10	−0.27	−0.11	−0.68	0.28	1.55	−1.90	−0.08	−1.66	−1.17	−1.09	−1.56	−0.01	−1.36
2177	FANCD2	Fanconi anemia, complementation group D2	−2.31	0.35	−0.30	−0.42	−0.66	1.24	1.48	0.09	−0.26	−1.98	−0.30	−1.33	0.22	−2.11	−0.83	−0.27	−0.81
57097	PARP11	poly (ADP-ribose) polymerase family, member 11	−2.31	−0.33	0.54	−0.09	−0.32	0.82	0.52	0.03	−0.01	−1.43	−0.35	−3.05	−1.39	−0.09	−0.76	−0.41	−0.66
11214	AKAP13	A kinase (PRKA) anchor protein 13	−2.31	0.03	−0.10	0.38	−1.00	−1.64	−1.56	0.34	1.77	−1.50	0.10	−1.01	−1.23	−1.10	−1.81	0.71	−1.36
4600	MX2	myxovirus (influenza virus) resistance 2 (mouse)	−2.31	0.55	0.95	0.27	−0.80	0.35	−1.01	0.08	0.25	−1.65	−0.19	−2.24	−0.30	−0.11	−2.28	−0.48	−0.62

TABLE 3-continued

gene	symbol	name	fisherz	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49
84255	SLC37A3	solute carrier family 37, member 3	−2.31	0.14	−0.49	0.05	−1.38	0.56	−1.07	0.15	1.24	−1.24	−0.65	−1.50	−0.74	−0.80	−1.81	0.14	−0.97
11216	AKAP10	A kinase (PRKA) anchor protein 10	−2.32	0.60	0.72	−0.32	0.00	−1.12	0.04	−0.06	0.95	−2.21	−0.23	−2.27	−0.62	−0.37	−0.24	−0.09	−2.24
162417	NAGS	N-acetylglutamate synthase	−2.32	0.51	0.99	−0.07	−0.45	0.84	−1.89	−0.91	0.31	−1.88	−0.31	−0.40	−0.18	−0.15	−2.05	0.12	−0.51
101928617	LOC101928617	uncharacterized LOC101928617	−2.32	−0.16	−0.52	0.77	−0.33	−0.13	−1.42	−0.77	0.14	−0.75	−1.36	0.18	0.28	−1.93	−0.63	−0.22	−1.64
10617	STAMBP	STAM binding protein	−2.32	−0.46	1.22	−0.28	0.00	−1.32	0.00	0.79	0.29	−1.28	0.10	−0.42	−1.20	−2.04	−1.04	−1.88	−0.16
1326	MAP3K8	mitogen-activated protein kinase kinase kinase 8	−2.32	0.35	−0.48	−0.27	−0.16	0.20	0.31	0.65	0.85	−1.70	−0.27	−1.87	−1.05	−0.40	−1.26	−0.31	−1.05
23315	SLC9A8	solute carrier family 9, subfamily A (NHE8, cation proton antiporter 8), member 8	−2.32	0.18	0.29	0.24	0.29	−1.41	−0.05	0.21	1.18	−1.91	0.16	−1.48	−1.08	−1.48	−1.43	0.32	−1.70
10791	VAMP5	vesicle-associated membrane protein 5	−2.32	0.11	0.52	0.99	0.51	0.67	−0.26	−0.75	−0.17	−1.95	−0.11	−1.46	−1.66	−0.85	−1.80	0.15	−1.38
8718	TNFRSF25	tumor necrosis factor receptor superfamily, member 25	−2.32	−0.41	−0.63	−0.05	−0.19	−0.08	−0.68	−0.95	−0.16	−1.46	−0.49	−0.53	0.53	−1.09	−0.42	−0.44	−1.31
51571	FAM49B	family with sequence similarity 49, member B	−2.33	−0.21	−0.09	−0.32	−0.36	0.28	−0.19	−0.30	1.04	−2.19	0.09	−1.88	−0.54	−1.55	−1.73	0.20	−1.32
283521	LINC00282	long intergenic non-protein coding RNA 282	−2.33	0.15	−0.37	−0.21	−0.31	0.14	−0.78	−0.12	0.31	−2.02	−0.58	−0.39	0.07	−1.90	−0.61	0.01	−1.31
51122	COMMD2	COMM domain containing 2	−2.33	0.10	−0.79	−0.17	−1.84	−0.88	−0.11	0.65	−0.23	−1.70	−0.71	−0.94	−0.83	−0.72	−0.30	−0.81	0.68
5372	PMM1	phosphomannomutase 1	−2.33	0.90	−0.91	−0.37	−2.17	−1.48	−0.74	−0.21	0.48	−0.93	−1.09	−0.48	−0.66	−0.38	−1.91	0.83	−0.14
9830	TRIM14	tripartite motif containing 14	−2.33	−1.08	0.02	−0.05	0.03	0.09	−0.20	−0.73	0.40	−1.10	−0.73	−3.08	−1.12	0.74	−1.12	−0.29	−0.62

TABLE 3-continued

gene	symbol	name	fisherz	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49
314	AOC2	amine oxidase, copper containing 2 (retina-specific)	−2.33	−0.51	−0.06	−1.03	−0.02	−0.33	−2.07	1.07	1.57	−1.23	−0.80	−1.22	−0.38	−0.59	−1.39	−0.19	−1.00
51761	ATP8A2	ATPase, aminophospholipid transporter, class I, type 8A, member 2	−2.33	−0.45	0.23	−1.08	−0.93	−0.14	−0.03	−0.38	−1.36	−0.65	−0.54	1.55	−0.02	−0.98	−0.61	−1.49	−0.85
493861	EID3	EP300 interacting inhibitor of differentiation 3	−2.34	−0.28	−0.02	0.74	−1.01	−1.02	−0.25	−0.37	−0.05	−1.53	−2.15	0.38	−0.49	−2.59	−0.08	0.16	0.02
6672	SP100	SP100 nuclear antigen	−2.34	0.20	0.18	0.29	−0.41	0.50	−0.77	−0.06	1.15	−1.70	−0.90	−1.74	−1.19	−0.95	−2.04	0.43	−1.38
55578	SUPT20H	suppressor of Ty 20 homolog (*S. cerevisiae*)	−2.34	0.36	0.25	−1.31	−0.42	−0.89	−0.07	0.42	0.77	−1.89	−0.01	−1.18	−0.27	−0.89	−1.29	−0.89	−1.58
159	ADSS	adenylosuccinate synthase	−2.34	−0.25	0.57	−1.73	−0.38	−2.06	−0.30	1.09	0.51	−0.30	−0.27	−1.80	−1.71	−0.41	−0.20	−0.33	−0.77
9683	N4BP1	NEDD4 binding protein 1	−2.34	−0.14	−0.22	−0.13	−1.00	0.16	−1.58	−0.06	1.46	−1.10	−0.25	−1.54	−0.89	−0.87	−1.95	0.43	−1.02
26287	ANKRD2	ankyrin repeat domain 2 (stretch responsive muscle)	−2.35	0.50	1.19	−0.57	−0.28	0.14	−2.07	−0.55	−0.55	0.17	−0.35	−1.33	−0.93	−2.17	−1.12	0.32	−0.24
57147	SCYL3	SCY1-like 3 (*S. cerevisiae*)	−2.35	0.42	−0.45	−1.01	−1.47	0.05	−1.41	0.71	0.69	−2.01	−1.00	−1.14	−0.81	−1.05	−0.23	0.39	−0.94
1808	DPYSL2	dihydropyrimidinase-like 2	−2.35	1.25	0.58	0.09	−0.22	−0.47	−1.14	−0.65	0.75	−0.78	0.37	−2.35	−0.52	0.18	−1.30	−2.15	−1.19
23355	VPS8	vacuolar protein sorting 8 homolog (*S. cerevisiae*)	−2.35	0.05	−0.51	0.89	−0.48	−0.24	−0.28	−0.07	1.12	−1.94	−0.06	−2.23	0.37	−0.82	−1.73	−0.97	−1.56
8115	TCL1A	T-cell leukemia/lymphoma 1A	−2.35	0.74	1.27	0.86	−0.57	0.60	−0.25	0.24	−0.46	−2.10	−0.35	−1.33	−0.75	−0.66	−1.09	−1.39	−0.80
94120	SYTL3	synaptotagmin-like 3	−2.35	−0.12	0.30	−0.73	−0.86	0.19	−1.81	−0.17	0.71	−1.58	−0.70	−1.19	−0.14	−0.54	−2.10	0.21	−0.36
22950	SLC4A1AP	solute carrier family 4 (anion exchanger), member 1, adaptor protein	−2.35	0.00	0.35	0.02	−0.66	−0.53	−0.79	0.36	0.13	−1.50	−0.47	−1.02	−1.13	−0.41	−1.89	−0.61	0.07

TABLE 3-continued

gene	symbol	name	fisherz	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49
27342	RABGEF1	RAB guanine nucleotide exchange factor (GEF) 1	−2.35	0.57	−0.34	−0.05	−1.20	−0.21	−0.90	−0.53	0.85	−1.17	−0.26	−1.49	−1.08	−1.28	−1.85	0.56	−0.35
64926	RASAL3	RAS protein activator like 3	−2.35	−0.38	1.18	−0.59	0.67	−0.44	−0.48	−0.27	−0.27	−2.56	−0.64	−0.64	0.56	−2.27	−0.17	−0.48	−1.15
100507331	ZSWIM8-AS1	ZSWIM8 antisense RNA 1	−2.36	0.19	0.03	−0.24	1.34	−0.27	0.43	−0.89	0.40	−2.05	−1.05	−0.39	−0.93	−2.45	−0.39	0.96	−1.35
4068	SH2D1A	SH2 domain containing 1A	−2.36	−0.89	−0.83	0.04	−1.01	−0.22	0.40	0.02	−0.21	−2.34	−0.74	−0.80	0.12	−1.55	0.21	−0.10	−1.40
60481	ELOVL5	ELOVL fatty acid elongase 5	−2.36	0.40	0.75	−0.39	−0.39	−0.20	−0.29	0.00	1.18	−1.30	−0.65	−1.44	−1.94	−1.89	0.69	−0.40	−1.84
2634	GBP2	guanylate binding protein 2, interferon-inducible	−2.36	−0.33	−0.07	−0.24	−0.85	0.18	−1.26	0.37	0.70	−2.05	−0.70	−1.66	−0.31	−0.49	−1.33	0.63	−1.57
55824	PAG1	phosphoprotein associated with glycosphingolipid microdomains 1	−2.36	−0.30	−0.42	−0.20	−1.00	0.72	−1.17	−0.25	0.35	−1.53	−0.45	−1.67	−0.32	−0.81	−1.38	−0.13	−1.04
79074	C2orf49	chromosome 2 open reading frame 49	−2.36	0.81	0.03	0.36	−0.95	−1.85	0.70	0.02	−0.21	−1.12	−1.22	0.15	−3.02	−1.03	0.18	−0.03	−0.02
220930	ZEB1-AS1	ZEB1 antisense RNA 1	−2.36	0.53	−1.05	−1.07	−0.97	−0.59	−0.10	0.55	0.82	−1.48	−0.65	−1.51	−0.43	−2.00	−0.83	0.09	−0.45
64421	DCLRE1C	DNA cross-link repair 1C	−2.36	0.02	−1.42	0.49	−1.38	−0.41	1.35	−0.05	0.33	−2.20	−1.18	0.35	0.33	−1.79	−0.72	−1.04	−1.03
64121	RRAGC	Ras-related GTP binding C	−2.37	−0.29	0.24	1.00	−0.12	−1.83	−1.21	−1.34	0.81	−0.98	−0.65	−0.70	−1.84	−0.51	−0.63	−0.09	0.21
137835	TMEM71	transmembrane protein 71	−2.37	−0.30	−0.26	−0.04	0.07	−0.14	0.09	0.36	1.00	−1.85	0.42	−2.21	−1.08	−1.10	−0.98	−0.35	−1.63
57674	RNF213	ring finger protein 213	−2.37	0.30	0.22	0.34	−0.63	−0.06	−1.12	−0.34	0.91	−1.72	−0.17	−2.68	−0.41	−0.08	−1.31	0.01	−1.34
728392	LOC728392	uncharacterized LOC728392	−2.37	0.26	−0.69	−0.19	−0.47	−1.67	−1.25	0.51	0.90	−1.31	−0.73	−1.15	−0.31	−0.39	−1.57	0.52	−1.60
329	BIRC2	baculoviral IAP repeat containing 2	−2.38	−0.70	−2.00	0.48	−1.04	−0.08	−0.52	0.06	0.31	−0.83	−1.06	−0.26	−1.27	−1.30	−0.16	0.34	−0.37
55279	ZNF654	zinc finger protein 654	−2.38	0.07	−1.37	−0.19	−1.93	−0.33	−0.99	0.23	1.02	−0.61	−0.75	−0.51	−0.88	−1.07	−1.48	0.68	−1.01
7107	GPR137B	G protein-coupled receptor 137B	−2.38	0.31	−0.09	0.76	−1.59	0.04	−1.07	−0.16	0.53	0.03	−0.78	−1.82	−0.40	0.21	−1.56	−0.30	−0.94

TABLE 3-continued

gene	symbol	name	fisherz	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49
9416	DDX23	DEAD (Asp-Glu-Ala-Asp) box polypeptide 23	−2.38	0.38	0.91	−0.29	0.12	−0.24	−0.34	1.24	0.90	−2.37	−0.67	−1.75	−1.61	−0.95	−0.70	−1.50	−0.29
137964	AGPAT6	1-acylglycerol-3-phosphate O-acyltransferase 6	−2.38	−0.25	0.41	0.24	0.48	0.30	−1.74	−1.21	−0.72	−0.46	−0.21	−0.05	0.01	−1.19	−0.90	−0.49	−0.57
3431	SP110	SP110 nuclear body protein	−2.38	0.04	0.94	0.17	−0.81	0.06	−1.66	0.16	0.61	−2.33	−0.79	−1.41	−0.68	−0.59	−1.17	0.04	−1.18
4140	MARK3	MAP/microtubule affinity-regulating kinase 3	−2.38	−0.45	−0.24	0.14	0.33	−2.26	1.20	0.34	1.36	−1.48	−0.08	−1.08	−1.61	−0.20	−1.79	−0.41	−1.11
59269	HIVEP3	human immunodeficiency virus type I enhancer binding protein 3	−2.38	0.03	−0.99	−0.81	−1.56	0.96	−0.87	0.22	0.42	−2.34	−0.13	−1.08	−0.23	−0.51	−1.23	0.23	−0.72
7846	TUBA1A	tubulin, alpha 1a	−2.38	0.29	−0.02	0.07	1.15	0.38	0.81	−0.15	0.60	−1.60	0.50	−3.59	−0.28	−0.39	−1.42	−1.04	−1.45
100652740	C16orf98	chromosome 16 open reading frame 98	−2.38	0.39	−1.72	0.89	−1.07	0.95	0.20	1.02	0.50	−1.37	−0.22	−1.35	0.04	−2.28	−1.01	−0.74	−1.02
23398	PPWD1	peptidylprolyl isomerase domain and WD repeat containing 1	−2.38	0.12	−0.31	−0.95	−0.18	−2.18	−0.09	0.31	0.17	−1.09	−1.11	0.12	−0.20	−2.03	0.44	−0.38	−1.37
158747	MOSPD2	motile sperm domain containing 2	−2.39	0.20	−0.33	−0.87	−0.72	−0.10	−0.85	0.40	1.42	−1.32	−0.33	−1.63	−1.05	−0.12	−2.05	0.13	−1.29
285512	FAM13A-AS1	FAM13A antisense RNA1	−2.39	−0.02	−0.56	0.34	−0.14	−1.10	0.10	0.28	1.52	−1.51	−0.57	−1.58	−1.01	−1.46	−1.35	0.30	−1.66
3937	LCP2	lymphocyte cytosolic protein 2 (SH2 domain containing leukocyte protein of 76 kDa)	−2.39	−0.40	−0.18	−0.43	−0.89	−1.73	−0.40	0.43	1.05	−1.78	0.46	−1.89	−0.05	−1.12	0.40	−0.53	−2.09

TABLE 3-continued

gene	symbol	name	fisherz	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49
730051	ZNF814	zinc finger protein 814	−2.39	0.06	0.80	1.10	−1.31	−1.84	0.31	0.38	−0.96	−0.51	−0.83	−0.49	−1.42	−1.81	0.15	−0.75	−0.79
9320	TRIP12	thyroid hormone receptor interactor 12	−2.39	0.32	0.77	−0.44	0.26	−1.55	−0.22	0.30	0.50	−0.17	−0.29	−1.37	−2.81	0.55	−0.58	−0.84	−1.13
6932	TCF7	transcription factor 7 (T-cell specific, HMG-box)	−2.39	−0.20	0.72	−0.19	−0.92	−0.43	−1.09	−0.03	−0.53	−1.59	−1.02	0.11	0.18	−1.29	−0.63	−0.51	−1.80
79722	ANKRD55	ankyrin repeat domain 55	−2.39	−0.17	−0.26	0.25	−0.99	0.95	−0.94	−0.09	0.87	−1.27	−0.47	−1.36	−0.59	−1.49	−1.80	0.39	−1.29
115362	GBP5	guanylate binding protein 5	−2.39	−0.84	−0.21	0.15	−0.30	−1.02	−1.53	0.78	−0.34	−2.54	−0.70	−0.59	−0.85	−0.17	0.08	−0.48	−1.08
29909	GPR171	G protein-coupled receptor 171	−2.39	−0.45	−0.41	−0.68	−1.22	−0.44	−1.16	0.03	0.30	−1.52	−0.96	−1.01	−0.31	−0.55	−0.79	−0.09	−0.92
440503	PLIN5	perilipin 5	−2.40	0.00	−0.42	−0.55	0.25	−0.90	−0.19	0.33	1.56	−1.19	−0.22	−0.90	−0.78	0.32	−2.39	−0.32	−2.34
80183	KIAA0226L	KIAA0226-like	−2.40	1.05	0.47	0.24	−0.83	0.89	−0.52	0.15	0.73	−2.17	−0.34	−1.21	−0.48	−0.74	−2.22	−0.53	−0.99
80709	AKNA	AT-hook transcription factor	−2.40	0.01	0.62	−0.58	0.09	−2.39	−0.62	0.31	0.80	−2.55	−0.14	−1.07	−0.94	−0.94	−0.22	0.00	−1.57
10562	OLFM4	olfactomedin 4	−2.40	−0.05	−0.92	−0.43	−0.75	0.44	0.17	−0.56	1.51	−1.13	−0.46	−1.88	−0.91	−0.68	−0.89	−0.47	−1.15
64780	MICAL1	microtubule associated monooxygenase, calponin and LIM domain containing 1	−2.41	0.42	−1.67	−0.46	−0.90	1.05	0.18	0.23	0.51	−1.46	0.12	−1.72	−0.22	−1.71	−1.15	−0.35	−1.39
155038	GIMAP8	GTPase, IMAP family member 8	−2.41	−0.10	0.79	−0.31	−0.94	−0.77	−1.95	0.23	0.80	−1.81	−0.05	−1.44	−0.35	−0.69	−1.34	0.14	−1.36
1783	DYNC1LI2	dynein, cytoplasmic 1, light intermediate chain 2	−2.41	0.19	−0.77	−0.07	−0.57	0.21	−0.31	0.22	0.85	−0.48	−0.89	−2.29	−1.25	−0.18	−1.93	0.60	−1.22
100287569	LINC00173	long intergenic non-protein coding RNA 173	−2.42	0.45	0.86	0.65	−0.35	−0.49	0.06	0.02	0.75	−2.53	−0.06	−2.53	−0.08	−1.06	−1.68	0.15	−1.27
5696	PSMB8	proteasome (prosome, macropain) subunit, beta type, 8	−2.42	0.36	0.79	0.06	−0.81	0.01	−1.36	−1.04	−0.42	−1.07	−0.25	−0.81	−1.51	0.41	0.08	−1.32	0.22

TABLE 3-continued

gene	symbol	name	fisherz	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49
11066	SNRNP35	small nuclear ribonucleoprotein 35 kDa (U11/U12)	−2.42	0.50	0.48	0.36	0.13	−0.68	−0.85	0.13	0.95	−2.53	−0.69	−0.99	−1.24	−1.33	−1.92	0.26	−0.60
122553	TRAPPC6B	trafficking protein particle complex 6B	−2.42	0.43	−0.02	−0.27	−0.16	−2.71	0.00	0.32	0.98	−1.18	0.01	−0.87	−1.43	−1.56	−0.59	−0.44	−0.71
50484	RRM2B	ribonucleotide reductase M2B (TP53 inducible)	−2.43	0.65	−0.60	−0.74	−1.12	−1.43	−1.00	0.67	0.90	−1.30	0.32	−1.62	−0.86	−0.36	−1.86	0.18	−0.46
9847	C2CD5	C2 calcium-dependent domain containing 5	−2.43	−0.11	−0.34	−0.35	−1.83	−2.61	−0.61	1.06	−0.25	−0.77	−0.92	−0.46	−0.99	0.45	−0.49	−0.83	−0.10
129285	PPP1R21	protein phosphatase 1, regulatory subunit 21	−2.43	0.74	0.78	−0.73	−1.01	−0.36	−1.61	0.01	0.43	−1.50	−0.58	−1.33	−0.80	−0.92	−0.14	−0.04	−2.08
9794	MAML1	mastermind-like 1 (*Drosophila*)	−2.43	−0.38	0.25	−1.74	−0.52	0.35	−1.25	0.17	0.85	−1.59	−0.01	−1.42	−0.69	−1.64	−0.49	−0.21	−1.03
84309	NUDT16L1	nudix (nucleoside diphosphate linked moiety X)-type motif 16-like 1	−2.43	−0.63	0.85	0.02	1.49	0.08	0.02	−0.09	0.08	−1.18	−0.84	−0.74	−1.04	−2.16	−1.98	0.01	0.06
65258	MPPE1	metallophosphoesterase 1	−2.43	0.16	0.09	−0.45	−0.21	−0.75	0.15	0.66	0.67	−2.29	−0.16	−1.27	−1.19	−0.31	−1.91	−0.08	−0.93
5562	PRKAA1	protein kinase, AMP-activated, alpha 1 catalytic subunit	−2.44	−0.34	−0.85	0.48	−0.29	−0.88	−0.50	−0.09	1.12	−1.01	−0.88	−1.07	−1.58	−2.04	−0.86	0.59	−1.07
123036	TC2N	tandem C2 domains, nuclear	−2.44	0.01	−0.08	−0.30	−1.17	−1.17	−1.30	0.09	0.14	−0.60	−1.59	−0.52	−0.41	−0.32	−0.38	−0.26	−1.35
84166	NLRC5	NLR family, CARD domain containing 5	−2.45	−0.28	−0.25	−0.33	−0.79	0.79	−0.88	−0.40	0.14	−2.19	−1.22	−1.14	0.27	−1.78	−0.60	0.19	−1.49
253143	PRR14L	proline rich 14-like	−2.45	−0.36	−0.38	−0.61	−0.68	−0.07	−0.86	0.70	1.64	−0.89	0.03	−2.02	−0.93	−0.57	−2.32	0.25	−0.87
1236	CCR7	chemokine (C-C motif) receptor 7	−2.45	0.05	0.49	−0.12	−1.52	0.66	−1.45	−0.86	−0.73	−0.87	−1.44	0.22	−0.11	−1.92	0.11	−0.20	−1.57

TABLE 3-continued

gene	symbol	name	fisherz	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49
266747	RGL4	ral guanine nucleotide dissociation stimulator-like 4	−2.46	−0.19	0.00	−0.25	−0.28	−0.18	−0.28	−0.09	0.92	−2.31	−0.37	−1.04	−1.25	−1.62	−1.49	0.51	−0.93
25988	HINFP	histone H4 transcription factor	−2.46	−0.11	2.05	−0.48	−0.34	−1.43	−2.67	0.53	−0.80	−0.42	−0.62	−0.04	−2.16	0.17	−0.14	−0.49	−0.67
6515	SLC2A3	solute carrier family 2 (facilitated glucose transporter), member 3	−2.46	0.39	0.08	0.20	−0.25	0.29	−0.33	−0.24	1.00	−1.44	0.08	−2.10	−1.18	−1.10	−1.80	0.39	−1.73
90592	ZNF700	zinc finger protein 700	−2.46	0.71	−1.32	−0.79	−0.72	0.55	0.31	0.50	0.89	−1.42	−1.32	−0.56	−1.19	−1.39	−1.18	−0.12	−1.47
6867	TACC1	transforming, acidic coiled-coil containing protein 1	−2.47	1.05	−0.07	0.50	−0.74	−0.18	−0.34	0.25	1.10	−1.44	0.24	−1.55	−0.49	−1.01	−1.79	−0.35	−0.95
23041	MON2	MON2 homolog (*S. cerevisiae*)	−2.47	0.02	−1.18	−0.17	−2.09	0.71	−0.91	0.18	0.34	−0.58	−1.37	−0.78	−0.13	−0.60	−1.10	−0.26	−1.54
100289230	LOC100289230	uncharacterized LOC100289230	−2.47	−0.65	0.54	−0.02	−0.74	−0.15	−0.65	0.44	−0.37	−0.81	−1.55	−0.52	0.23	−0.16	−1.57	−0.03	−0.99
57169	ZNFX1	zinc finger, NFX1-type containing 1	−2.48	0.01	−0.28	0.54	−0.37	−0.23	−1.52	−0.22	1.44	−1.50	−0.82	−1.07	−1.29	−1.01	−1.68	0.38	−1.13
1105	CHD1	chromodomain helicase DNA binding protein 1	−2.48	0.32	−1.07	0.09	−1.16	−1.37	0.21	0.35	0.63	−0.87	0.00	−0.31	−1.67	−2.36	−0.12	0.20	−1.18
943	TNFRSF8	tumor necrosis factor receptor superfamily, member 8	−2.48	1.03	1.09	0.96	−1.09	0.72	−1.48	−0.68	−0.11	−1.16	−0.49	−0.72	−0.28	−0.76	−1.78	−0.22	−1.05
3275	PRMT2	protein arginine methyltransferase 2	−2.48	0.64	−0.31	0.34	−0.11	−1.52	−2.05	−0.60	1.07	−1.13	−0.52	−1.13	−0.80	−1.50	−0.76	0.33	−1.53
8851	CDK5R1	cyclin-dependent kinase 5, regulatory subunit 1 (p35)	−2.49	0.52	0.25	−0.10	−1.27	0.09	−0.75	0.10	0.45	−1.69	−0.87	−0.37	−0.74	−1.32	−2.10	0.18	−1.17
168537	GIMAP7	GTPase, IMAP family member 7	−2.49	−0.53	−0.08	−0.09	−1.13	−1.10	−1.52	0.37	0.42	−1.80	−0.20	−0.77	−0.64	−1.19	−0.60	−0.16	−1.21

TABLE 3-continued

gene	symbol	name	fisherz	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49
256236	NAPSB	napsin B aspartic peptidase, pseudogene	−2.49	0.84	0.02	0.41	−1.01	1.15	−0.08	−0.58	−0.57	−1.84	0.10	−1.95	0.05	−0.45	−0.98	−1.51	−0.67
26235	FBXL4	F-box and leucine-rich repeat protein 4	−2.50	−0.08	−0.17	0.44	−0.25	−0.66	−0.27	0.77	0.54	−1.25	−1.17	−1.40	−1.58	−0.75	−1.63	0.03	−0.55
9363	RAB33A	RAB33A, member RAS oncogene family	−2.50	−0.30	0.49	0.73	−0.84	1.47	−1.22	−1.17	−0.10	−0.94	−1.70	−0.30	−1.62	−0.65	−0.77	−0.17	−0.65
729683	LOC729683	uncharacterized LOC729683	−2.50	0.17	0.43	0.05	−1.51	−1.17	−1.00	0.20	0.39	−2.26	−1.09	−1.07	−1.69	−0.11	−0.15	0.29	−0.48
388969	C2orf68	chromosome 2 open reading frame 68	−2.51	−0.79	0.31	0.01	−0.04	−0.67	−0.04	0.22	0.21	−2.41	0.05	−0.82	−0.96	−0.78	−0.39	−0.91	−1.23
4818	NKG7	natural killer cell group 7 sequence	−2.51	−0.88	−0.05	0.13	−0.26	−0.75	0.53	0.48	−0.50	−2.79	0.79	−1.43	−0.75	−1.10	−0.10	−0.96	−1.22
93953	ACRC	acidic repeat containing	−2.51	0.21	−0.99	0.29	−1.27	−0.44	−0.68	0.34	0.61	−1.30	−0.72	−0.35	−1.00	−2.04	−1.08	0.47	−1.21
28982	FLVCR1	feline leukemia virus subgroup C cellular receptor 1	−2.51	0.14	0.27	−2.04	−1.05	0.19	−0.75	1.20	0.49	−1.00	−0.62	−0.80	−0.40	−0.43	−0.71	−1.68	−0.66
84911	ZNF382	zinc finger protein 382	−2.52	−0.59	0.61	−0.52	−0.32	−1.23	−0.59	−0.19	−0.09	−0.52	0.34	−1.03	−0.06	−0.71	0.23	−2.34	−1.33
66036	MTMR9	myotubularin related protein 9	−2.52	−0.62	−1.12	0.10	−1.26	−0.33	−1.11	−0.15	−0.23	−0.73	−1.47	−0.41	−0.08	−1.49	−1.18	−0.11	−0.14
9750	FAM65B	family with sequence similarity 65, member B	−2.52	−0.02	0.69	−0.35	−0.24	−0.58	−0.72	0.43	0.77	−2.15	−0.04	−2.13	−0.75	−1.28	−1.12	0.23	−1.78
9938	ARHGAP25	Rho GTPase activating protein 25	−2.52	−0.43	−0.14	−0.46	−0.08	0.04	−0.70	0.37	1.18	−2.93	−0.02	−1.38	−0.37	−1.88	−1.30	0.26	−1.17
120425	AMICA1	adhesion molecule, interacts with CXADR antigen 1	−2.52	0.03	−0.08	0.09	−0.83	0.04	−1.15	−0.35	1.21	−2.05	−0.06	−2.25	0.07	−0.63	−1.63	−0.35	−1.23
6840	SVIL	supervillin	−2.53	−0.28	−0.45	0.12	0.18	0.30	−0.33	−0.12	1.48	−1.28	−0.22	−2.26	−0.72	−0.77	−2.56	0.14	−1.39
26268	FBXO9	F-box protein 9	−2.53	−1.93	−1.19	0.51	−0.65	0.06	−0.29	−0.20	0.81	−1.06	−0.47	−0.45	−1.31	0.04	−1.88	0.01	−0.93
55206	SBNO1	strawberry notch homolog 1 (*Drosophila*)	−2.53	−0.52	−1.01	−0.74	−0.15	−0.54	−0.19	0.59	0.92	−1.47	−0.44	−0.58	−0.84	−1.87	−1.48	0.18	−0.88

TABLE 3-continued

gene	symbol	name	fisherz	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49
355	FAS	Fas cell surface death receptor	−2.54	0.71	0.41	0.30	−0.75	−0.30	−0.75	0.02	0.98	−1.06	−0.27	−1.99	−1.22	−0.61	−1.13	0.19	−1.96
50615	IL21R	interleukin 21 receptor	−2.54	−0.27	0.71	0.03	−1.20	1.61	−1.16	−0.50	−0.32	−1.31	−0.43	−0.83	0.10	−0.72	−1.50	−0.50	−0.95
221178	SPATA13	spermatogenesis associated 13	−2.54	−0.05	0.34	−0.29	−0.17	−0.98	−1.13	−0.24	0.81	−1.02	−0.12	−1.30	−0.70	−1.05	−0.99	−0.18	−1.39
11104	KATNA1	katanin p60 (ATPase containing) subunit A1	−2.54	0.66	−0.03	−1.98	−1.00	−1.29	0.07	−0.20	0.39	−0.45	−0.69	−0.95	−1.39	−0.74	−0.44	−0.90	0.07
1117	CHI3L2	chitinase 3-like 2	−2.54	0.43	1.36	−0.47	−0.37	−0.35	−0.97	0.81	−0.79	−0.82	−1.19	−0.97	−0.89	−1.52	−1.55	−0.62	−0.26
374969	CCDC23	coiled-coil domain containing 23	−2.54	0.15	−0.06	0.88	0.47	−1.69	−0.62	−0.62	0.37	−1.67	0.07	−1.58	−0.60	−0.27	−1.79	−0.36	−0.59
6285	S100B	S100 calcium binding protein B	−2.55	−0.38	−1.44	−0.44	−0.37	−0.57	−0.75	−1.27	−0.47	−0.98	−0.60	−1.02	−0.51	0.51	0.26	−1.69	−0.19
387357	THEMIS	thymocyte selection associated	−2.55	−0.69	−0.77	−0.13	−1.81	−0.37	−1.07	0.36	0.17	−1.84	−0.85	−0.59	0.09	−0.85	−0.32	−0.57	−0.95
2960	GTF2E1	general transcription factor IIE, polypeptide 1, alpha 56 kDa	−2.56	−0.21	0.05	−1.50	−2.33	−0.14	−1.93	−0.30	0.30	−0.34	−0.32	0.37	−1.63	0.30	−1.06	−0.21	−0.49
100129550	LOC100129550	uncharacterized LOC100129550	−2.56	−0.35	−0.66	−0.15	−0.56	−0.87	−0.55	0.51	1.52	−1.52	−0.52	−1.34	−0.69	−0.99	−1.72	0.73	−1.33
54520	CCDC93	coiled-coil domain containing 93	−2.56	0.13	−0.47	−0.50	−0.61	−0.60	−1.14	−0.17	0.93	0.13	−1.33	−0.77	−0.86	−1.40	−2.10	0.55	−0.69
10302	SNAPC5	small nuclear RNA activating complex, polypeptide 5, 19 kDa	−2.56	−0.81	0.12	0.51	−2.51	0.24	−1.32	−0.11	−0.67	−1.51	−0.84	−0.30	−1.00	0.64	−1.00	−0.62	−0.01
50939	IMPG2	interphotoreceptor matrix proteoglycan 2	−2.56	0.15	0.32	−1.16	0.55	1.26	0.53	0.01	−0.91	−2.42	−1.58	−1.16	−0.05	−0.93	−0.40	0.13	−0.90
8802	SUCLG1	succinate-CoA ligase, alpha subunit	−2.56	−0.31	0.44	−0.77	−0.26	−0.40	0.15	−0.86	0.56	−0.18	−0.38	−0.80	−0.66	−0.41	−1.01	−1.39	0.16
23332	CLASP1	cytoplasmic linker associated protein 1	−2.57	0.16	−1.50	−0.09	−0.73	−0.60	0.25	0.40	0.05	−1.67	0.15	−0.75	−1.95	−0.31	−0.74	−0.40	−0.16
203328	SUSD3	sushi domain containing 3	−2.57	0.78	−0.01	0.01	−1.37	0.50	−1.02	−0.79	0.35	−1.87	0.00	−0.97	−0.06	−0.86	−1.48	−0.06	−1.23

TABLE 3-continued

gene	symbol	name	fisherz	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49
126231	ZNF573	zinc finger protein 573	−2.58	−0.54	0.54	−1.59	0.39	−2.26	−1.23	0.00	−0.56	−0.68	−1.32	−1.10	−0.61	0.39	−0.15	−0.50	−0.74
6993	DYNLT1	dynein, light chain, Tctex-type 1	−2.58	−0.22	0.12	0.22	−0.51	0.41	−1.39	−0.72	1.05	−1.49	−0.91	−1.51	−1.17	−0.20	−1.94	0.11	−0.78
58500	ZNF250	zinc finger protein 250	−2.59	0.73	0.63	−0.05	−0.54	−0.79	−1.35	0.42	0.53	−1.82	−0.65	−0.18	−1.35	−0.15	−2.17	0.21	−1.24
10507	SEMA4D	sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4D	−2.59	0.09	0.59	0.54	−0.38	−1.18	−1.00	0.33	0.36	−2.64	−0.26	−0.57	−0.68	−1.26	−1.14	−0.30	−1.26
170482	CLEC4C	C-type lectin domain family 4, member C	−2.59	0.33	1.01	0.08	−0.98	0.02	−0.07	−0.63	−0.22	−1.15	−0.35	−1.45	−0.35	−0.72	−0.99	−1.52	−0.54
3004	GZMM	granzyme M (lymphocyte met-ase 1)	−2.59	−0.20	−0.15	0.23	−0.95	−0.97	−0.91	−0.77	−0.18	−1.88	−0.71	−1.09	−0.30	−1.04	−0.53	−0.22	−1.04
64895	PAPOLG	poly(A) polymerase gamma	−2.59	−0.46	−0.57	−0.15	−1.67	−0.42	−1.03	0.44	0.98	−1.73	−0.15	−0.71	−0.87	−1.84	−0.75	0.61	−1.30
7850	IL1R2	interleukin 1 receptor, type II	−2.59	0.24	−0.03	0.07	−0.67	1.29	−0.64	0.00	1.32	−1.10	−0.32	−1.90	−1.20	−0.47	−2.35	0.09	−1.24
93594	TBC1D31	TBC1 domain family, member 31	−2.59	−0.35	0.31	−1.26	−0.52	−0.18	−1.15	1.02	−0.26	−1.63	−0.65	−0.63	−0.60	−0.77	−1.58	−0.53	−0.92
23215	PRRC2C	proline-rich coiled-coil 2C	−2.60	0.23	0.47	0.90	−0.02	−0.02	−1.17	−0.27	0.75	−0.74	−0.41	−1.26	−0.24	−1.50	−1.71	0.38	−2.86
80196	RNF34	ring finger protein 34, E3 ubiquitin protein ligase	−2.60	−0.06	0.49	−0.53	−1.40	−1.60	−1.67	0.19	0.54	−1.47	−0.38	−0.43	−1.78	−0.28	−1.10	−0.15	−0.36
284415	VSTM1	V-set and transmembrane domain containing 1	−2.60	−0.60	0.30	0.84	−0.02	−0.90	0.30	−0.09	0.39	−1.80	−0.45	−1.49	−1.23	−0.58	−1.27	−0.30	−0.93
56882	CDC42SE1	CDC42 small effector 1	−2.60	−0.19	0.12	−0.34	−0.02	−0.23	−0.45	0.56	1.08	−1.26	0.00	−1.70	−1.27	−0.51	−2.48	−0.24	−1.13
6508	SLC4A3	solute carrier family 4 (anion exchanger), member 3	−2.60	−0.21	−0.74	0.20	−0.25	−1.12	−0.36	−0.53	0.56	−2.53	−0.17	−0.62	−0.30	−1.95	−1.06	1.04	−1.00

TABLE 3-continued

gene	symbol	name	fisherz	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49
79663	HSPBAP1	HSPB (heat shock 27 kDa) associated protein 1	−2.61	−0.19	0.15	−0.38	−0.27	−1.40	−0.24	0.30	1.15	−1.04	−0.50	−1.65	−0.67	−0.77	−1.79	−0.15	−1.43
474344	GIMAP6	GTPase, IMAP family member 6	−2.61	−0.31	0.86	−0.14	−0.72	−1.37	−2.10	0.05	0.03	−1.97	−0.13	−1.39	−0.03	−0.36	−0.19	−0.44	−1.05
100505746	ITGB2-AS1	ITGB2 antisense RNA 1	−2.62	0.34	−0.47	0.12	−1.28	−0.13	−0.74	−0.08	0.88	−1.59	−0.13	−1.86	0.40	−1.70	−1.08	−0.35	−1.67
1293	COL6A3	collagen, type VI, alpha 3	−2.62	−0.52	−1.29	−0.64	−1.17	1.62	−0.54	−0.45	0.44	−1.67	−0.99	−1.27	0.38	−1.26	−1.50	−0.17	−0.57
10294	DNAJA2	DnaJ (Hsp40) homolog, subfamily A, member 2	−2.62	0.13	0.40	−0.18	−0.59	−1.32	−0.43	0.01	0.45	−0.06	−0.97	−0.98	−1.82	−0.63	−0.48	−0.63	−1.05
3091	HIF1A	hypoxia inducible factor 1, alpha subunit (basic helix-loop-helix transcription factor)	−2.62	0.83	−0.75	−0.17	−0.70	0.99	0.89	−0.76	0.21	−1.25	0.00	−2.32	−0.13	−0.97	−1.08	−0.59	−0.88
79573	TTC13	tetratricopeptide repeat domain 13	−2.63	−0.32	−0.92	−0.75	−1.41	−0.10	−0.94	0.62	0.43	−0.44	−1.60	−0.96	−0.73	−1.13	−0.97	−0.08	−0.50
9208	LRRFIP1	leucine rich repeat (in FLII) interacting protein 1	−2.63	0.81	0.12	−0.23	0.56	−0.76	−0.82	0.46	0.85	−1.06	0.13	−1.92	−1.27	−1.78	−0.81	0.08	−1.97
29116	MYLIP	myosin regulatory light chain interacting protein	−2.63	−0.28	−0.62	0.05	−0.27	−2.58	1.19	0.46	0.32	−0.74	−0.61	−0.90	−0.53	−0.89	−1.47	−0.42	−1.07
92370	ACPL2	acid phosphatase-like 2	−2.63	−1.54	−0.45	−0.71	−1.62	−0.80	−0.74	0.67	0.91	−1.12	−0.78	−0.24	−0.84	−1.53	−1.46	0.25	−0.82
9546	APBA3	amyloid beta (A4) precursor protein-binding, family A, member 3	−2.64	0.21	1.01	−0.23	0.00	0.07	−0.75	−0.16	0.97	−0.85	−1.10	−2.63	−1.00	−0.08	−2.03	−0.36	−1.09
253018	HCG27	HLA complex group 27 (non-protein coding)	−2.64	−0.05	0.09	0.27	−0.64	−0.72	−0.47	−0.28	1.22	−1.80	−0.80	−1.19	−0.64	−0.53	−2.19	0.31	−1.22

TABLE 3-continued

gene	symbol	name	fisherz	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49
10096	ACTR3	ARP3 actin-related protein 3 homolog (yeast)	−2.65	0.49	−0.28	0.34	−0.79	−0.13	0.15	0.42	1.60	−1.46	−0.39	−1.67	−0.94	−2.34	−1.00	−0.52	−1.31
84138	SLC7A6OS	solute carrier family 7, member 6 opposite strand	−2.65	−0.42	1.70	−0.20	0.84	−1.16	−0.64	0.40	0.22	−2.19	−0.53	−0.75	−1.75	0.11	−1.27	−1.19	−0.40
8440	NCK2	NCK adaptor protein 2	−2.65	−1.07	0.79	0.13	−0.60	−0.88	−1.96	−0.14	−0.16	−0.66	−0.67	−0.59	−0.68	−0.08	−0.17	−1.75	−1.26
7277	TUBA4A	tubulin, alpha 4a	−2.65	0.48	0.19	0.19	−1.39	0.66	−1.25	−0.13	0.96	−1.88	−0.51	−0.40	−0.36	−1.78	−2.08	−0.03	−1.07
8269	TMEM187	transmembrane protein 187	−2.66	−0.27	0.56	−1.62	0.26	−2.71	−2.09	0.21	−0.25	−0.22	−0.46	0.48	−0.52	−0.13	−1.15	−0.51	0.06
8807	IL18RAP	interleukin 18 receptor accessory protein	−2.66	−0.04	−0.09	0.08	−0.75	0.15	−1.18	0.04	0.86	−1.98	−0.68	−1.33	−0.87	−1.01	−1.47	−0.05	−1.30
1235	CCR6	chemokine (C-C motif) receptor 6	−2.67	−0.28	1.66	−0.57	−1.09	−0.52	−1.19	−0.47	−0.71	−0.95	−0.92	−1.19	−0.36	−0.29	−0.45	−0.48	−0.84
7059	THBS3	thrombospondin 3	−2.67	−0.20	−0.07	−0.91	1.44	0.21	0.44	−0.70	0.17	−0.78	0.31	−2.87	−0.05	−0.46	−0.82	−0.56	−2.14
54971	BANP	BTG3 associated nuclear protein	−2.67	−0.34	0.29	−0.19	−0.04	0.35	−1.94	0.12	0.56	−0.90	−0.97	−1.54	−0.70	−0.60	−2.09	0.10	−0.72
57677	ZFP14	ZFP14 zinc finger protein	−2.68	0.38	−1.14	−0.27	−0.82	1.21	−1.02	0.25	1.22	−1.04	−1.24	−0.91	−1.59	−1.39	−1.38	0.08	−1.02
6890	TAP1	transporter 1, ATP-binding cassette, sub-family B (MDR/TAP)	−2.68	0.05	0.37	0.20	−1.12	1.35	−2.35	−0.28	0.60	−1.63	−1.24	−1.25	−0.70	−0.27	−1.54	−0.02	−0.33
22944	KIN	KIN, antigenic determinant of recA protein homolog (mouse)	−2.69	0.36	−1.20	−0.67	−0.59	−0.67	−0.86	0.25	1.10	−1.47	−0.52	−0.53	−1.37	−2.18	−0.74	−0.02	−0.84
26512	INTS6	integrator complex subunit 6	−2.69	−0.14	0.22	−0.75	−0.86	−0.50	−0.82	0.25	0.70	−1.38	−0.56	−0.29	−0.82	−1.28	−1.37	−0.09	−1.73
92797	HELB	helicase (DNA) B	−2.69	0.17	−0.33	0.01	−1.34	−0.36	−0.87	0.98	1.14	−1.92	0.04	−1.62	−1.14	−1.06	−1.18	−0.46	−1.27
5481	PPID	peptidylprolyl isomerase D	−2.70	0.38	1.67	−0.63	0.41	−0.37	−0.66	−0.08	0.36	−0.38	−0.04	−1.15	−3.10	−0.34	−0.76	−1.56	−0.92
22897	CEP164	centrosomal protein 164 kDa	−2.71	−0.53	1.08	−0.97	−0.12	−0.91	−0.53	−0.46	−0.49	−0.66	−0.50	−1.20	−0.15	−0.12	−0.78	−0.17	−1.82

TABLE 3-continued

gene	symbol	name	fisherz	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49
3620	IDO1	indoleamine 2,3-dioxygenase 1	−2.71	−0.70	0.25	0.59	−0.02	0.84	−1.89	−0.16	0.34	−0.54	−0.76	−1.61	−0.41	0.02	−2.38	−0.88	−0.33
64766	S100PBP	S100P binding protein	−2.71	−0.27	0.58	−1.38	−0.78	0.05	−0.24	1.04	0.31	−1.50	−0.70	−1.26	−1.77	−1.72	0.08	−0.33	−1.45
8809	IL18R1	interleukin 18 receptor 1	−2.71	0.21	0.39	−0.32	−1.30	−0.28	−1.05	0.20	1.05	−1.61	−0.70	−1.51	−0.97	−1.04	−1.44	0.04	−1.06
116984	ARAP2	ArfGAP with RhoGAP domain, ankyrin repeat and PH domain 2	−2.71	−0.28	−0.80	−0.35	−1.14	−0.26	−1.85	−0.25	0.54	−1.26	−0.93	−0.94	−0.72	−0.79	−0.48	−0.15	−0.90
440823	MIAT	myocardial infarction associated transcript (non-protein coding)	−2.72	−0.95	−0.55	−0.22	−1.34	1.31	−1.31	−0.75	0.29	−1.84	−1.26	−0.78	−0.53	−0.71	−0.46	0.38	−1.74
59340	HRH4	histamine receptor H4	−2.72	0.21	−0.90	−0.79	−0.83	−0.38	−2.29	0.82	0.85	−0.82	−0.18	−0.27	−0.82	−1.15	−0.41	−1.10	−1.82
197259	MLKL	mixed lineage kinase domain-like	−2.73	0.03	0.50	−0.43	−0.21	0.32	−0.72	0.01	1.28	−1.69	−0.61	−2.04	−0.74	−0.70	−1.19	−0.54	−1.66
23670	TMEM2	transmembrane protein 2	−2.73	0.16	0.22	−0.71	−0.67	−1.12	−0.96	0.44	0.99	−1.40	−0.20	−1.98	−0.94	−1.09	−1.23	0.23	−1.20
643314	KIAA0754	KIAA0754	−2.73	0.87	0.06	0.11	−0.32	0.34	−0.53	0.57	0.62	−2.15	−1.32	−1.91	−0.16	−1.25	−1.16	−0.01	−2.19
28526	TRDC	T cell receptor delta constant	−2.73	−1.25	0.37	0.10	−0.33	0.10	−1.60	0.78	−0.68	−2.09	−0.85	−0.73	−0.60	−1.17	−0.48	−0.75	−0.92
55096	EBLN2	endogenous Bornavirus-like nucleoprotein 2	−2.74	−0.05	−0.03	0.57	0.28	−0.35	0.33	−0.78	0.63	−2.07	−1.96	−1.31	−0.66	−0.55	−1.70	0.36	−1.25
2796	GNRH1	gonadotropin-releasing hormone 1 (luteinizing-releasing hormone)	−2.74	−0.88	0.11	−0.38	−0.66	−2.90	0.38	−0.08	−0.04	−2.13	0.07	0.42	−0.22	−0.28	−0.14	−0.85	−1.54
54509	RHOF	ras homolog family member F (in filopodia)	−2.74	0.31	0.83	1.43	−0.80	0.32	−1.43	−1.08	−0.54	−0.76	0.25	−0.90	−1.00	−0.42	−0.88	−0.38	−1.12
11120	BTN2A1	butyrophilin, subfamily 2, member A1	−2.75	0.52	−0.22	−1.12	0.07	−1.63	−0.62	−0.13	0.65	−0.96	−0.54	−1.58	−1.21	−1.08	−0.76	0.42	−1.52
84869	CBR4	carbonyl reductase 4	−2.75	0.31	−0.35	−0.28	−1.53	−0.83	−1.22	0.27	0.12	−0.85	−0.74	−1.13	−1.13	0.70	−1.53	−1.57	−0.51

TABLE 3-continued

gene	symbol	name	fisherz	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49
28991	COMMD5	COMM domain containing 5	−2.76	0.41	0.45	−0.17	−0.58	−0.24	−1.90	−0.12	1.08	−0.75	−0.13	−0.51	−2.03	−0.07	−2.53	−0.10	−0.26
154141	MBOAT1	membrane bound O-acyltransferase domain containing 1	−2.79	0.06	0.08	0.22	0.00	−2.65	−0.96	0.23	0.95	−0.25	0.11	−2.56	−0.86	−0.20	−1.10	−0.21	−1.12
3659	IRF1	interferon regulatory factor 1	−2.79	−0.54	−0.36	−0.28	−0.18	−0.21	−1.33	−0.05	1.12	−2.24	−0.61	−1.14	−1.09	−0.73	−0.41	0.38	−1.25
154007	SNRNP48	small nuclear ribonucleoprotein 48 kDa (U11/U12)	−2.80	0.44	−0.26	−0.32	−0.20	−0.06	−0.13	0.34	0.70	−2.02	−0.47	−1.60	−0.35	−1.79	−1.87	0.29	−1.08
116835	HSPA12B	heat shock 70 kD protein 12B	−2.81	0.14	−0.16	0.30	−1.12	0.68	−1.54	0.24	0.80	−1.18	−0.33	−2.58	−1.03	−0.89	−1.03	0.09	−1.15
9488	PIGB	phosphatidylinositol glycan anchor biosynthesis, class B	−2.82	0.68	0.08	−0.07	−1.72	−0.07	−0.55	0.53	0.32	−1.55	0.30	−2.07	−1.93	−0.62	−1.05	−0.04	−1.24
100293516	ZNF587B	zinc finger protein 587B	−2.83	−0.09	0.21	−1.06	−1.76	−1.15	−0.55	0.34	−0.74	−1.19	−0.96	−0.71	−0.49	−1.11	0.00	−0.92	−0.87
9217	VAPB	VAMP (vesicle-associated membrane protein)-associated protein B and C	−2.84	−1.12	−1.05	−0.01	−1.39	0.45	−1.31	0.22	0.31	−1.69	−0.91	−0.14	−0.47	0.21	−1.60	−0.55	−1.38
10538	BATF	basic leucine zipper transcription factor, ATF-like	−2.84	0.51	0.53	0.52	−0.20	1.16	−0.96	−1.16	0.40	−2.02	−0.61	−1.84	−0.45	−1.32	−1.77	0.27	−1.54
6935	ZEB1	zinc finger E-box binding homeobox 1	−2.87	0.56	−0.27	−0.22	−1.18	−0.24	−0.24	−0.04	0.41	−2.43	−0.58	−0.53	−0.58	−3.17	−0.48	0.80	−0.66
10443	N4BP2L2	NEDD4 binding protein 2-like 2	−2.88	−0.84	−1.29	−0.96	−0.53	−0.16	−0.41	0.56	0.54	−2.02	−0.84	−1.19	0.30	−1.54	−0.75	0.00	−1.76
3837	KPNB1	karyopherin (importin) beta 1	−2.88	−1.28	0.25	−0.60	−0.67	−3.06	−0.44	0.00	0.76	−0.97	0.33	−1.43	−0.63	0.10	−1.19	−0.47	−0.87
81698	LINC00597	long intergenic non-protein coding RNA 597	−2.88	−0.07	0.72	−0.14	0.15	0.90	−0.22	−0.31	0.27	−1.29	−2.39	−2.45	0.03	0.43	−1.90	−0.50	−1.09

TABLE 3-continued

gene	symbol	name	fisherz	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49
2643	GCH1	GTP cyclohydrolase 1	−2.89	0.40	−0.06	0.56	−1.53	−1.49	−0.47	−0.24	−0.10	−0.92	−0.26	−0.91	0.08	−0.70	−1.58	−0.30	−0.27
57559	STAMBPL1	STAM binding protein-like 1	−2.89	0.00	0.60	−0.53	−1.08	0.72	−0.73	0.38	−0.75	−1.66	−1.63	−1.12	−1.00	−1.40	−0.22	−0.50	−0.78
116842	LEAP2	liver expressed antimicrobial peptide 2	−2.89	−0.25	−1.30	−0.48	−0.83	−0.27	−0.92	−0.42	0.50	−0.31	−1.47	−0.82	−0.86	−1.33	−1.20	0.53	−0.94
202	AIM1	absent in melanoma 1	−2.90	0.49	0.63	−1.01	−0.59	0.69	−0.56	−0.53	0.42	−1.52	0.10	−2.24	−0.36	−0.70	−1.94	−0.25	−1.80
9934	P2RY14	purinergic receptor P2Y, G-protein coupled, 14	−2.90	0.11	0.00	0.08	−0.93	−0.16	−0.92	0.22	0.90	−2.26	0.01	−1.89	−0.72	−0.65	−1.42	−0.25	−1.14
100216546	LINC01004	long intergenic non-protein coding RNA 1004	−2.90	0.05	−1.36	−0.34	−0.56	−0.82	−0.80	0.04	0.65	−0.82	−2.30	−0.93	−0.17	−0.24	−1.64	−0.02	−0.84
9692	KIAA0391	KIAA0391	−2.90	0.17	0.26	−1.79	0.38	−1.90	−1.18	−0.97	−0.22	−0.70	0.15	0.14	−2.01	−0.92	0.28	−0.30	−0.59
89845	ABCC10	ATP-binding cassette, sub-family C (CFTR/MRP), member 10	−2.92	−0.33	0.85	−1.06	0.54	−0.16	−2.42	0.41	0.04	−0.12	−1.78	−0.04	−0.80	−0.84	−1.59	−0.56	−0.79
26034	IPCEF1	interaction protein for cytohesin exchange factors 1	−2.92	−0.27	0.37	−0.66	−0.98	0.48	−1.28	0.09	0.38	−1.26	−0.81	−1.65	−0.45	−1.23	−1.57	−0.25	−1.32
10906	TRAFD1	TRAF-type zinc finger domain containing 1	−2.93	0.40	0.36	0.88	−0.61	−0.68	−1.48	0.02	0.72	−1.60	−0.28	−2.06	−1.44	−0.57	−1.66	−0.44	−0.41
84811	BUD13	BUD13 homolog (*S. cerevisiae*)	−2.94	−0.56	−0.52	−0.18	−1.59	−1.10	−0.68	−0.44	−0.21	−0.77	−1.39	−1.63	−1.12	−0.57	−0.80	0.75	−0.03
100527964	LOC100527964	uncharacterized LOC100527964	−2.96	−0.38	−0.49	−1.17	0.05	1.04	−0.40	0.00	−0.34	−1.39	−1.20	−0.92	0.41	−1.88	−0.90	−0.84	−1.32
118426	LOH12CR1	loss of heterozygosity, 12, chromosomal region 1	−2.97	0.02	−0.17	−0.21	−1.60	−0.77	−1.09	−0.21	0.73	−1.44	−1.03	−1.56	−0.64	−0.62	−1.07	0.54	−1.33
54331	GNG2	guanine nucleotide binding protein (G protein), gamma 2	−2.98	0.37	0.07	−0.18	−0.48	0.46	−0.38	0.16	0.78	−2.96	−0.45	−1.09	−1.12	−1.74	−0.94	−0.35	−1.45

TABLE 3-continued

gene	symbol	name	fisherz	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49
94081	SFXN1	sideroflexin 1	−2.99	0.15	−0.22	−0.48	−2.28	1.02	−0.14	−0.39	0.15	−2.23	−0.54	−0.65	−0.66	−1.46	−1.12	0.10	−0.57
145474	LOC145474	uncharacterized LOC145474	−2.99	0.22	−0.36	0.36	−0.03	−0.28	−0.80	0.23	0.89	−1.38	−1.25	−1.71	−0.39	−1.06	−1.50	−0.67	−1.24
84969	TOX2	TOX high mobility group box family member 2	−3.00	0.02	−0.66	−0.27	−1.53	1.55	−0.78	−0.37	−0.02	−1.42	−1.61	0.04	−1.08	−1.09	−1.23	−0.27	−0.35
4907	NT5E	5'-nucleotidase, ecto (CD73)	−3.02	0.12	1.19	−0.48	0.06	−1.19	−0.32	−0.13	−0.29	−0.78	−1.18	−0.57	−1.72	−0.69	−1.63	−0.32	−1.49
51735	RAPGEF6	Rap guanine nucleotide exchange factor (GEF) 6	−3.03	−0.09	−0.81	−0.46	−1.21	−0.10	−0.94	0.31	0.41	−1.39	−0.94	−0.52	−1.20	−1.41	−1.43	−0.01	−0.69
9953	HS3ST3B1	heparan sulfate (glucosamine) 3-O-sulfotransferase 3B1	−3.03	−0.12	−1.70	−1.64	−0.53	−0.67	−0.82	0.27	0.65	−1.31	−0.71	−0.50	−0.78	−1.37	−1.29	−0.06	−1.19
23112	TNRC6B	trinucleotide repeat containing 6B	−3.04	−0.93	0.39	−0.92	0.28	−0.77	−0.81	0.84	0.47	−1.45	−1.08	−1.48	−0.92	−0.27	−1.72	−0.35	−1.58
91526	ANKRD44	ankyrin repeat domain 44	−3.05	0.24	0.25	−0.51	−1.20	−0.61	−1.21	−0.03	0.86	−1.42	−0.82	−0.96	−0.97	−2.04	−0.91	0.44	−1.56

TABLE 3-continued

gene	symbol	name	fisherz	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49
101928017	LOC101928017	uncharacterized LOC101928017	−3.08	−0.04	−0.52	−0.33	−0.42	1.09	−0.81	−0.38	−0.52	−1.45	−0.60	−1.46	−0.57	−0.22	−1.75	−0.35	−0.22
84859	LRCH3	leucine-rich repeats and calponin homology (CH) domain containing 3	−3.08	−0.37	−0.52	−0.57	−1.38	−0.85	−2.06	0.23	0.48	−0.68	−0.84	−0.74	−1.35	−0.29	−0.76	0.04	−1.66
159013	CXorf38	chromosome X open reading frame 38	−3.11	0.44	0.69	−0.68	−0.49	−1.10	−0.70	−0.08	0.46	−1.66	0.47	−1.78	−1.91	−0.81	−0.82	−0.56	−1.14
23208	SYT11	synaptotagmin XI	−3.19	0.00	0.62	−0.55	−0.27	−1.12	−0.69	−0.33	−0.57	−1.61	−0.26	−2.00	−0.48	−1.64	−0.96	0.46	−0.34
101928649	LOC101928649	uncharacterized LOC101928649	−3.23	−0.33	−0.10	1.08	−0.60	−0.31	−0.38	0.03	−0.07	−1.16	−0.43	−1.38	−1.48	−1.13	−0.90	−0.62	−0.67
85459	KIAA1731	KIAA1731	−3.28	0.57	0.67	0.61	−0.61	0.37	−0.22	0.15	0.36	−2.16	−1.14	−1.03	−0.96	−1.76	−1.59	0.22	−1.32
9617	MTRF1	mitochondrial translational release factor 1	−3.31	0.69	0.22	−0.22	−0.97	−1.58	−0.41	−0.30	−0.06	−1.36	−1.09	−0.40	−0.87	−1.44	−0.19	−1.02	−1.03
56898	BDH2	3-hydroxybutyrate dehydrogenase, type 2	−3.50	0.36	0.59	−0.70	−0.03	−0.59	0.11	−0.28	−1.73	−2.44	−0.08	−0.40	0.31	−2.06	−0.63	−1.07	−0.16
387882	C12orf75	chromosome 12 open reading frame 75	−3.61	−0.75	0.39	0.39	−0.76	−0.21	−0.74	0.20	−0.52	−1.77	−1.07	−0.65	−1.69	0.18	0.42	−1.73	−1.48
677769	SCARNA17	small Cajal body-specific RNA17	−3.64	−1.27	−0.31	0.25	0.69	0.61	−0.80	−0.90	−0.17	−1.40	−1.81	−0.17	−0.69	−0.97	−1.39	−0.39	−1.39

[0074] High level gene sets for deleterious genes (increase with age) and beneficial genes (decrease with age) were identified, as shown in FIG. **2**, and as summarized here:

[0075] For high level gene sets, the following sets of genes were found to be deleterious (that is, they increase with age): UNFOLDED_PROTEIN-RESPONSE, OXIDATIVE_PHOSPHORYLATION, MYC_TARGETS_V1, ADIPOGENESIS, GLYCOLYSIS, UV_RESPONSE_UP, DNA_REPAIR, FATTY_ACID_METABOLISM, SPERMATOGENESIS, E2F_TARGETS, BILE_ACID_METABOLISM, MTORC1_SIGNALING, ESTROGEN_RESPONSE_LATE.

[0076] The following genes were found to be beneficial (that is, they decrease with age): APOPTOSIS, APICAL_SURFACE, UV_RESPONSE_DN, EPITHELIAL_MESENCHYMAL_TRANSITION, ANGIOGENESIS, KRAS_SIGNALING_UP, TNFA_SIGNALING_VIA_NFKB, IL2_STATS_SIGNALING COMPLEMENT, INFLAMMATORY_RESPONSE, INTERFERON_ALPHA_RESPONSE, ALLOGRAFT_REJECTION AND INTERFERENCE_GAMMA_RESPONSE.

[0077] Table 4 summarizes the data from the high level genesets:

TABLE 4

High Level Genesets

gs.id	gs.desc	gs.ngenes	fisherz
UNFOLDED__PROTEIN__RESPONSE	Genes up-regulated during unfolded protein response, a cellular stress response related to the endoplasmic reticulum.	109	6.005
OXIDATIVE__PHOSPHORYLATION	Genes encoding proteins involved in oxidative phosphorylation.	188	5.683
MYC__TARGETS__V1	A subgroup of genes regulated by MYC - version 1 (v1).	179	5.562
HEME__METABOLISM	Genes involved in metabolism of heme (a cofactor consisting of iron and porphyrin) and erythroblast differentiation.	197	4.56
MYC__TARGETS__V2	A subgroup of genes regulated by MYC - version 2 (v2).	55	3.473
ADIPOGENESIS	Genes up-regulated during adipocyte differentiation (adipogenesis).	196	3.441
GLYCOLYSIS	Genes encoding proteins involved in glycolysis and gluconeogenesis.	198	3.428
UV__RESPONSE__UP	Genes up-regulated in response to ultraviolet (UV) radiation.	157	3.197
DNA__REPAIR	Genes involved in DNA repair.	146	2.991
FATTY__ACID__METABOLISM	Genes encoding proteins involved in metabolism of fatty acids.	151	2.425
SPERMATOGENESIS	Genes up-regulated during production of male gametes (sperm), as in spermatogenesis.	132	2.34
E2F__TARGETS	Genes encoding cell cycle related targets of E2F transcription factors.	192	2.266
BILE__ACID__METABOLISM	Genes involve in metabolism of bile acids and salts.	111	2.149
MTORC1__SIGNALING	Genes up-regulated through activation of mTORC1 complex.	191	2.144
ESTROGEN__RESPONSE__LATE	Genes defining late response to estrogen.	195	2.135
APOPTOSIS	Genes mediating programmed cell death (apoptosis) by activation of caspases.	155	−2.002
APICAL__SURFACE	Genes encoding proteins over-represented on the apical surface of epithelial cells, e.g., important for cell polarity (apical area).	43	−2.272
UV__RESPONSE__DN	Genes down-regulated in response to ultraviolet (UV) radiation.	142	−2.494
EPITHELIAL__MESENCHYMAL__TRANSITION	Genes defining epithelial-mesenchymal transition, as in wound healing, fibrosis and metastasis.	197	−2.866
ANGIOGENESIS	Genes up-regulated during formation of blood vessels (angiogenesis).	36	−3.103
KRAS__SIGNALING__UP	Genes up-regulated by KRAS activation.	198	−3.697
TNFA__SIGNALING__VIA__NFKB	Genes regulated by NF-kB in response to TNF [GeneID = 7124].	199	−3.726
IL2__STAT5__SIGNALING	Genes up-regulated by STAT5 in response to IL2 stimulation.	196	−4.764

TABLE 4-continued

High Level Genesets

gs.id	gs.desc	gs.ngenes	fisherz
IL6_JAK_STAT3_SIGNALING	Genes up-regulated by IL6 [GeneID = 3569] via STAT3 [GeneID = 6774], e.g., during acute phase response.	84	−5.798
COMPLEMENT	Genes encoding components of the complement system, which is part of the innate immune system.	199	−6.829
INFLAMMATORY_RESPONSE	Genes defining inflammatory response.	200	−6.963
INTERFERON_ALPHA_RESPONSE	Genes up-regulated in response to alpha interferon proteins.	94	−7.819
ALLOGRAFT_REJECTION	Genes up-regulated during transplant rejection.	196	−8.52
INTERFERON_GAMMA_RESPONSE	Genes up-regulated in response to IFNG [GeneID = 3458].	194	−10.885

[0078] Table 5 shows GO Biological Processes.

TABLE 5

GO Biological Processes

gs.id	gs.desc	gs.ngenes	fisherz
GO: 0070085	glycosylation	166	5.578
GO: 0006487	protein N-linked glycosylation	90	5.533
GO: 0006486	protein glycosylation	164	5.486
GO: 0043413	macromolecule glycosylation	164	5.486
GO: 0018279	protein N-linked glycosylation via asparagine	84	4.97
GO: 0018196	peptidyl-asparagine modification	84	4.97
GO: 0043687	post-translational protein modification	126	4.513
GO: 0009101	glycoprotein biosynthetic process	193	4.488
GO: 0030433	ER-associated protein catabolic process	29	4.424
GO: 0016051	carbohydrate biosynthetic process	148	4.249
GO: 0008652	cellular amino acid biosynthetic process	87	4.198
GO: 0045333	cellular respiration	120	4.099
GO: 0033014	tetrapyrrole biosynthetic process	24	4.026
GO: 0006779	porphyrin biosynthetic process	24	4.026
GO: 0006094	gluconeogenesis	39	4.011
GO: 0006783	heme biosynthetic process	19	3.979
GO: 0009311	oligosaccharide metabolic process	61	3.866
GO: 0006457	protein folding	195	3.86
GO: 0051289	protein homotetramerization	40	3.789
GO: 0019319	hexose biosynthetic process	47	3.712
GO: 0009086	methionine biosynthetic process	11	3.628
GO: 0009060	aerobic respiration	33	3.628
GO: 0000097	sulfur amino acid biosynthetic process	14	3.626
GO: 0043039	tRNA aminoacylation	49	3.592
GO: 0043038	amino acid activation	49	3.592
GO: 0006418	tRNA aminoacylation for protein translation	49	3.592
GO: 0009067	aspartate family amino acid biosynthetic process	17	3.582
GO: 0006084	acetyl-CoA metabolic process	35	3.544
GO: 0046148	pigment biosynthetic process	43	3.475
GO: 0009312	oligosaccharide biosynthetic process	42	3.465
GO: 0022900	electron transport chain	122	3.425
GO: 0046395	carboxylic acid catabolic process	148	3.408
GO: 0016054	organic acid catabolic process	148	3.408
GO: 0046364	monosaccharide biosynthetic process	59	3.363
GO: 0048194	Golgi vesicle budding	11	3.306
GO: 0009309	amine biosynthetic process	122	3.303
GO: 0070972	protein localization in endoplasmic reticulum	18	3.29
GO: 0042254	ribosome biogenesis	117	3.267
GO: 0022613	ribonucleoprotein complex biogenesis	190	3.229
GO: 0061136	regulation of proteasomal protein catabolic process	50	3.181
GO: 0006399	tRNA metabolic process	124	3.157
GO: 0006839	mitochondrial transport	77	3.144
GO: 0006555	methionine metabolic process	13	3.107

TABLE 5-continued

GO Biological Processes

gs.id	gs.desc	gs.ngenes	fisherz
GO: 0046165	alcohol biosynthetic process	80	3.079
GO: 0048200	Golgi transport vesicle coating	10	3.059
GO: 0048205	COPI coating of Golgi vesicle	10	3.059
GO: 0048146	positive regulation of fibroblast proliferation	32	3.048
GO: 0006488	dolichol-linked oligosaccharide biosynthetic process	31	3.029
GO: 0009066	aspartate family amino acid metabolic process	34	3.028
GO: 0006829	zinc ion transport	20	3.018
GO: 0051262	protein tetramerization	63	3.008
GO: 0022904	respiratory electron transport chain	87	3.007
GO: 0006664	glycolipid metabolic process	35	2.997
GO: 0006099	tricarboxylic acid cycle	22	2.993
GO: 0048199	vesicle targeting, to, from or within Golgi	21	2.972
GO: 0060425	lung morphogenesis	27	2.963
GO: 0009566	fertilization	79	2.939
GO: 0016042	lipid catabolic process	188	2.931
GO: 0007040	lysosome organization	27	2.926
GO: 0046356	acetyl-CoA catabolic process	23	2.917
GO: 0034637	cellular carbohydrate biosynthetic process	93	2.914
GO: 0042559	pteridine-containing compound biosynthetic process	19	2.897
GO: 0045454	cell redox homeostasis	51	2.89
GO: 0006900	membrane budding	26	2.887
GO: 0009064	glutamine family amino acid metabolic process	53	2.884
GO: 0042558	pteridine-containing compound metabolic process	31	2.87
GO: 0007005	mitochondrion organization	151	2.799
GO: 0019438	aromatic compound biosynthetic process	29	2.797
GO: 0050885	neuromuscular process controlling balance	35	2.744
GO: 0034976	response to endoplasmic reticulum stress	38	2.736
GO: 0046685	response to arsenic-containing substance	13	2.714
GO: 0006901	vesicle coating	25	2.685
GO: 0044243	multicellular organismal catabolic process	25	2.68
GO: 0009310	amine catabolic process	101	2.665
GO: 0006364	rRNA processing	87	2.656
GO: 0034470	ncRNA processing	188	2.656
GO: 0046034	ATP metabolic process	125	2.655
GO: 0006081	cellular aldehyde metabolic process	34	2.619
GO: 0042440	pigment metabolic process	51	2.579
GO: 0032320	positive regulation of Ras GTPase activity	79	−2.624
GO: 0032675	regulation of interleukin-6 production	48	−2.634
GO: 0030041	actin filament polymerization	12	−2.643
GO: 0032651	regulation of interleukin-1 beta production	26	−2.65
GO: 0042098	T cell proliferation	20	−2.652
GO: 0042742	defense response to bacterium	101	−2.653
GO: 0060491	regulation of cell projection assembly	36	−2.665
GO: 0016064	immunoglobulin mediated immune response	59	−2.671
GO: 0007062	sister chromatid cohesion	19	−2.678
GO: 0001837	epithelial to mesenchymal transition	37	−2.68
GO: 0032735	positive regulation of interleukin-12 production	19	−2.682
GO: 0032814	regulation of natural killer cell activation	14	−2.684
GO: 0046634	regulation of alpha-beta T cell activation	45	−2.69
GO: 0045580	regulation of T cell differentiation	68	−2.695
GO: 0045622	regulation of T-helper cell differentiation	19	−2.701
GO: 0045637	regulation of myeloid cell differentiation	97	−2.706
GO: 0040017	positive regulation of locomotion	172	−2.712
GO: 0032733	positive regulation of interleukin-10 production	15	−2.721
GO: 0051480	cytosolic calcium ion homeostasis	132	−2.725
GO: 0070665	positive regulation of leukocyte proliferation	84	−2.726
GO: 0032946	positive regulation of mononuclear cell proliferation	83	−2.731
GO: 0040001	establishment of mitotic spindle localization	11	−2.737
GO: 0043903	regulation of symbiosis, encompassing mutualism through parasitism	17	−2.751
GO: 0045648	positive regulation of erythrocyte differentiation	15	−2.755
GO: 0045070	positive regulation of viral genome replication	10	−2.756

TABLE 5-continued

GO Biological Processes			
gs.id	gs.desc	gs.ngenes	fisherz
GO: 0050718	positive regulation of interleukin-1 beta secretion	13	−2.766
GO: 0050716	positive regulation of interleukin-1 secretion	13	−2.766
GO: 0002275	myeloid cell activation involved in immune response	19	−2.766
GO: 0002714	positive regulation of B cell mediated immunity	10	−2.78
GO: 0002891	positive regulation of immunoglobulin mediated immune response	10	−2.78
GO: 0050671	positive regulation of lymphocyte proliferation	82	−2.793
GO: 0019724	B cell mediated immunity	60	−2.796
GO: 0045954	positive regulation of natural killer cell mediated cytotoxicity	13	−2.819
GO: 0002717	positive regulation of natural killer cell mediated immunity	13	−2.819
GO: 0044126	regulation of growth of symbiont in host	14	−2.829
GO: 0044146	negative regulation of growth of symbiont involved in interaction with host	14	−2.829
GO: 0044130	negative regulation of growth of symbiont in host	14	−2.829
GO: 0044144	modulation of growth of symbiont involved in interaction with host	14	−2.829
GO: 0044060	regulation of endocrine process	14	−2.834
GO: 0032319	regulation of Rho GTPase activity	65	−2.852
GO: 0046636	negative regulation of alpha-beta T cell activation	13	−2.852
GO: 0043901	negative regulation of multi-organism process	21	−2.856
GO: 0002218	activation of innate immune response	113	−2.865
GO: 0051653	spindle localization	13	−2.871
GO: 0051293	establishment of spindle localization	13	−2.871
GO: 0016197	endosome transport	108	−2.881
GO: 0009612	response to mechanical stimulus	107	−2.911
GO: 0032677	regulation of interleukin-8 production	31	−2.925
GO: 0070661	leukocyte proliferation	39	−2.935
GO: 0060389	pathway-restricted SMAD protein phosphorylation	10	−2.941
GO: 0050706	regulation of interleukin-1 beta secretion	15	−2.942
GO: 0002274	myeloid leukocyte activation	48	−2.942
GO: 0050704	regulation of interleukin-1 secretion	15	−2.942
GO: 0045582	positive regulation of T cell differentiation	44	−2.966
GO: 0043547	positive regulation of GTPase activity	132	−2.978
GO: 0045646	regulation of erythrocyte differentiation	23	−2.985
GO: 0050715	positive regulation of cytokine secretion	34	−2.999
GO: 0002286	T cell activation involved in immune response	15	−3.021
GO: 0060323	head morphogenesis	19	−3.03
GO: 0002822	regulation of adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains	63	−3.033
GO: 0002819	regulation of adaptive immune response	66	−3.039
GO: 0045785	positive regulation of cell adhesion	90	−3.039
GO: 0045619	regulation of lymphocyte differentiation	81	−3.053
GO: 0051607	defense response to virus	39	−3.064
GO: 0030335	positive regulation of cell migration	163	−3.068
GO: 0032760	positive regulation of tumor necrosis factor production	28	−3.07
GO: 2000147	positive regulation of cell motility	164	−3.087
GO: 0032943	mononuclear cell proliferation	38	−3.098
GO: 0032647	regulation of interferon-alpha production	11	−3.108
GO: 0001912	positive regulation of leukocyte mediated cytotoxicity	22	−3.119
GO: 0002366	leukocyte activation involved in immune response	53	−3.122
GO: 0002263	cell activation involved in immune response	53	−3.122
GO: 0050707	regulation of cytokine secretion	48	−3.123
GO: 0032479	regulation of type I interferon production	48	−3.129
GO: 0032680	regulation of tumor necrosis factor production	54	−3.135
GO: 0071214	cellular response to abiotic stimulus	95	−3.137
GO: 0070663	regulation of leukocyte proliferation	122	−3.169

TABLE 5-continued

GO Biological Processes

gs.id	gs.desc	gs.ngenes	fisherz
GO: 0042102	positive regulation of T cell proliferation	56	−3.18
GO: 0045621	positive regulation of lymphocyte differentiation	51	−3.181
GO: 0032480	negative regulation of type I interferon production	30	−3.217
GO: 0007259	JAK-STAT cascade	36	−3.221
GO: 0045069	regulation of viral genome replication	20	−3.223
GO: 0042119	neutrophil activation	11	−3.23
GO: 0006569	tryptophan catabolic process	11	−3.232
GO: 0046218	indolalkylamine catabolic process	11	−3.232
GO: 0042436	indole-containing compound catabolic process	11	−3.232
GO: 0007204	elevation of cytosolic calcium ion concentration	117	−3.245
GO: 0032312	regulation of ARF GTP ase activity	24	−3.246
GO: 0006959	humoral immune response	78	−3.258
GO: 0051272	positive regulation of cellular component movement	173	−3.283
GO: 0071346	cellular response to interferon-gamma	73	−3.295
GO: 0032653	regulation of interleukin-10 production	22	−3.307
GO: 0033363	secretory granule organization	10	−3.319
GO: 0035023	regulation of Rho protein signal transduction	132	−3.344
GO: 0050853	B cell receptor signaling pathway	19	−3.349
GO: 0019835	cytolysis	20	−3.366
GO: 0045022	early endosome to late endosome transport	12	−3.38
GO: 0002443	leukocyte mediated immunity	94	−3.383
GO: 0042129	regulation of T cell proliferation	81	−3.406
GO: 0032944	regulation of mononuclear cell proliferation	119	−3.406
GO: 0050856	regulation of T cell receptor signaling pathway	15	−3.407
GO: 0008625	induction of apoptosis via death domain receptors	14	−3.411
GO: 0050727	regulation of inflammatory response	123	−3.42
GO: 0002460	adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains	83	−3.433
GO: 0050670	regulation of lymphocyte proliferation	118	−3.458
GO: 0033209	tumor necrosis factor-mediated signaling pathway	23	−3.486
GO: 0032103	positive regulation of response to external stimulus	111	−3.501
GO: 0045089	positive regulation of innate immune response	138	−3.502
GO: 0006568	tryptophan metabolic process	12	−3.522
GO: 0042108	positive regulation of cytokine biosynthetic process	55	−3.527
GO: 0046651	lymphocyte proliferation	36	−3.536
GO: 0032318	regulation of Ras GTPase activity	119	−3.562
GO: 0070670	response to interleukin-4	12	−3.598
GO: 0002250	adaptive immune response	87	−3.66
GO: 0002697	regulation of immune effector process	161	−3.675
GO: 0060333	interferon-gamma-mediated signaling pathway	62	−3.711
GO: 0002715	regulation of natural killer cell mediated immunity	16	−3.715
GO: 0042269	regulation of natural killer cell mediated cytotoxicity	16	−3.715
GO: 0002699	positive regulation of immune effector process	74	−3.722
GO: 0045071	negative regulation of viral genome replication	11	−3.738
GO: 0048525	negative regulation of viral reproduction	11	−3.738
GO: 0002708	positive regulation of lymphocyte mediated immunity	35	−3.741
GO: 0002705	positive regulation of leukocyte mediated immunity	35	−3.741
GO: 0043122	regulation of I-kappaB kinase/NF-kappaB cascade	144	−3.748
GO: 0031343	positive regulation of cell killing	26	−3.794
GO: 0001910	regulation of leukocyte mediated cytotoxicity	27	−3.795
GO: 0034341	response to interferon-gamma	90	−3.815
GO: 0032655	regulation of interleukin-12 production	32	−3.816

TABLE 5-continued

GO Biological Processes			
gs.id	gs.desc	gs.ngenes	fisherz
GO: 0030811	regulation of nucleotide catabolic process	199	−3.851
GO: 0033121	regulation of purine nucleotide catabolic process	199	−3.851
GO: 0002703	regulation of leukocyte mediated immunity	70	−3.862
GO: 0050854	regulation of antigen receptor-mediated signaling pathway	17	−3.905
GO: 0050900	leukocyte migration	169	−4.01
GO: 0002675	positive regulation of acute inflammatory response	20	−4.028
GO: 0043123	positive regulation of I-kappaB kinase/NF-kappaB cascade	132	−4.059
GO: 0002706	regulation of lymphocyte mediated immunity	57	−4.059
GO: 0001818	negative regulation of cytokine production	100	−4.164
GO: 0002407	dendritic cell chemotaxis	13	−4.165
GO: 0043087	regulation of GTPase activity	176	−4.208
GO: 0042035	regulation of cytokine biosynthetic process	84	−4.23
GO: 0031341	regulation of cell killing	32	−4.238
GO: 0033124	regulation of GTP catabolic process	178	−4.291
GO: 0071260	cellular response to mechanical stimulus	46	−4.33
GO: 0001816	cytokine production	60	−4.396
GO: 0071356	cellular response to tumor necrosis factor	41	−4.406
GO: 0034612	response to tumor necrosis factor	61	−4.513
GO: 0072676	lymphocyte migration	11	−4.521
GO: 0002252	immune effector process	161	−4.563
GO: 0046632	alpha-beta T cell differentiation	20	−4.616
GO: 0030595	leukocyte chemotaxis	56	−4.649
GO: 0060326	cell chemotaxis	71	−4.667
GO: 0031349	positive regulation of defense response	186	−4.725
GO: 0030217	T cell differentiation	71	−4.741
GO: 0006968	cellular defense response	53	−4.787
GO: 0050729	positive regulation of inflammatory response	57	−4.817
GO: 0045088	regulation of innate immune response	185	−4.824
GO: 0031295	T cell costimulation	65	−5.003
GO: 0031294	lymphocyte costimulation	65	−5.003
GO: 0030098	lymphocyte differentiation	106	−5.066
GO: 0046631	alpha-beta T cell activation	26	−5.072
GO: 0001819	positive regulation of cytokine production	137	−5.304
GO: 0071357	cellular response to type I interferon	59	−5.319
GO: 0060337	type I interferon-mediated signaling pathway	59	−5.319
GO: 0009615	response to virus	162	−5.352
GO: 0002521	leukocyte differentiation	141	−5.391
GO: 0034340	response to type I interferon	60	−5.511
GO: 0050852	T cell receptor signaling pathway	74	−6.248
GO: 0051251	positive regulation of lymphocyte activation	180	−6.311
GO: 0019221	cytokine-mediated signaling pathway	188	−6.417
GO: 0042110	T cell activation	130	−6.458
GO: 0002696	positive regulation of leukocyte activation	194	−6.505
GO: 0050867	positive regulation of cell activation	200	−6.557
GO: 0050870	positive regulation of T cell activation	146	−6.662
GO: 0050851	antigen receptor-mediated signaling pathway	92	−6.764
GO: 0050863	regulation of T cell activation	193	−6.787
GO: 0002757	immune response-activating signal transduction	175	−6.928
GO: 0002764	immune response-regulating signaling pathway	178	−6.938
GO: 0002768	immune response-regulating cell surface receptor signaling pathway	100	−7.307
GO: 0002429	immune response-activating cell surface receptor signaling pathway	98	−7.32

[0079] Table 6 shows MeSH Anatomical Contexts.

TABLE 6

MeSH Anatomical Contexts

gs.id	gs.desc	gs.ngenes	fisherz
A11.284.430.214.190.875.811	ribosomes	134	3.695
A11.118.290	erythrocytes	111	3.469
A11.284.430.214.190.875.190.550	lysosomes	114	3.012
A11.284.430.214.190.875.336	golgi_apparatus	183	3.011
A11.118.290.270	erythrocyte_membrane	34	2.932
A11.284.430.106.279.345.175	cell_nucleolus	151	2.897
A11.443	erythroid_cells	157	2.822
A06.407.071	adrenal_glands	26	2.787
A11.284.187.520.300.505.757	chromosomes_human_y	22	2.778
A11.284.187.865	sex_chromosomes	191	2.769
A11.284.430.214.190.875.117.570	micronuclei_chromosome-defective	13	2.675
A11.284.835.626.461	mitochondria_liver	29	2.641
A10.272.491	endothelium	139	−2.555
A11.284.180.700	pseudopodia	40	−2.672
A15.145.229.637.555.567.650	lymphocytes_tumor-infiltrating	11	−2.723
A02.835.583	joints	56	−2.735
A11.284.187.520.300.370.375	chromosomes_human_pair_13	78	−2.794
A11.284.187.520.300.370	chromosomes_human_13-15	191	−2.882
A15.382.520.604.750	thymus_gland	28	−3.166
A11.284.187.520.300.325.330	chromosomes_human_pair_6	161	−3.337
A15.378.316.340	granulocytes	22	−3.725
A15.145.229.637.415.345	eosinophils	42	−4.039
A15.382.680.397	macrophages	135	−4.173
A11.118.637.555.567.569.200.400.905	th2_cells	42	−4.25
A11.284.149.165.570	membrane_microdomains	61	−4.286
A15.382.490.555.567.569.200.700	t-lymphocytes_regulatory	30	−4.303
A15.145.229.188	blood_platelets	100	−4.352
A11.329.372	macrophages	171	−4.359
A15.382.520	lymphatic_system	96	−4.44
A15.382.032	antibody-producing_cells	131	−4.67
A15.382.520.604	lymphoid_tissue	86	−4.791
A11.118.637.555.567.569.200.400.900	th1_cells	35	−5.106
A15.145.229.637.555.567.569.220.200	t-lymphocytes_cytotoxic	38	−5.175
A11.627.624	monocytes	142	−5.806
A15.382.066.270	dendritic_cells	115	−5.827
A11.118.637.555.567.537	killer_cells_natural	95	−5.966
A15.378.316.580	monocytes	117	−6.038
A15.382.490.555.567.569.200.400	t-lymphocytes_helper-inducer	68	−6.297
A11.066	antigen-presenting_cells	127	−6.61
A15.382.490.315.583	neutrophils	86	−6.829
A11.627.340	granulocytes	158	−7.124
A11.118.637.555.567.569.500	t-lymphocyte_subsets	57	−7.292
A15.382.490.555.567.569.440	jurkat_cells	180	−7.396
A15.145.229.637.555.567.550	lymphocyte_subsets	81	−7.646
A15.145.229.637.415	granulocytes	140	−7.65
A11.118.637.555.567.569.220	cd8-positive_t-lymphocytes	90	−7.728
A11.118.637.555.567.569.200	cd4-positive_t-lymphocytes	150	−8.198

[0080] Table 7 shows chemical genetic perturbations.

TABLE 7

Chemical Genetic Perturbations

gs.id	gs.desc	gs.ngenes	fisherz
WELCSH_BRCA1_TARGETS_DN	Down-regulated by induction of exogenous BRCA1 in EcR-293 cells	135	6.537
TARTE_PLASMA_CELL_VS_B_LYMPHOCYTE_UP	Genes up-regulated in plasma cells compared with B lymphocytes.	77	6.053
YAO_TEMPORAL_RESPONSE_TO_PROGESTERONE_CLUSTER_17	Genes co-regulated in uterus during a time course response to progesterone [PubChem = 5994]: SOM cluster 17.	175	6.038
SCHLOSSER_SERUM_RESPONSE_AUGMENTED_BY_MYC	Cluster 2: genes up-regulated in B493-6 cells (B lymphocytes) by serum alone or in combination with MYC [GeneID = 4609] but not by MYC alone.	103	5.872
GRUETZMANN_PANCREATIC_CANCER_DN	Genes down-regulated in pancreatic ductal adenocarcinoma (PDAC) identified in a meta analysis across four independent studies.	192	5.84
TIEN_INTESTINE_PROBIOTICS_24HR_DN	Genes down-regulated in Caco-2 cells (intestinal epithelium) after coculture with the probiotic bacteria *L. casei* for 24 h.	197	5.404
SCHLOSSER_MYC_TARGETS_AND_SERUM_RESPONSE_UP	Cluster 5: genes up-regulated in B493-6 cells (B lymphocytes) by MYC [GeneID = 4609] alone or in combination with serum but not by serum alone.	45	5.36
ELVIDGE_HYPOXIA_DN	Genes down-regulated in MCF7 cells (breast cancer) under hypoxia conditions.	143	4.834
YAO_TEMPORAL_RESPONSE_TO_PROGESTERONE_CLUSTER_14	Genes co-regulated in uterus during a time course response to progesterone [PubChem = 5994]: SOM cluster 14.	137	4.817
YAO_TEMPORAL_RESPONSE_TO_PROGESTERONE_CLUSTER_11	Genes co-regulated in uterus during a time course response to progesterone [PubChem = 5994]: SOM cluster 11.	100	4.763
JIANG_AGING_HYPOTHALAMUS_DN	Down-regulated in the hypothalamus of aged (22 months) BALB/c mice, compared to young (2 months) controls	39	4.74
LIN_APC_TARGETS	Genes up-regulated by forced expression of APC [GeneID = 324] in the APC-deficient SW480 cell line (colon cancer).	76	4.631
PENG_LEUCINE_DEPRIVATION_DN	Genes down-regulated in BJAB cells (B-lymphoma) after leucine [PubChem = 857] deprivation.	176	4.446
CHIANG_LIVER_CANCER_SUBCLASS_UNANNOTATED_DN	Marker genes down-regulated in the 'unannotated' subclass of hepatocellular carcinoma (HCC) samples.	186	4.441
PURBEY_TARGETS_OF_CTBP1_AND_SATB1_DN	Genes down-regulated in HEK-293 cells (fibroblast) upon knockdown of both CTBP1 and SATB1 [GeneID = 1487, 6304] by RNAi.	168	4.261
SHAFFER_IRF4_TARGETS_IN_MYELOMA_VS_MATURE_B_LYMPHOCYTE	IRF4 [GeneID = 3662] target genes up-regulated in primary myeloma vs. mature B lymphocytes.	94	4.132
MENSSEN_MYC_TARGETS	Genes up-regulated by adenoviral expression of c-MYC [GeneID = 4609] in HUVEC cells (umbilical vein endothelium).	49	4.121
HOFMANN_MYELODYSPLASTIC_SYNDROM_RISK_UP	Genes up-regulated in bone marrow hematopoietic stem cells (HSC, CD34+ [GeneID = 947]) from patients with high risk of myelodysplastic syndrome (MDS) compared to the low risk patients.	21	4.077

TABLE 7-continued

Chemical Genetic Perturbations			
gs.id	gs.desc	gs.ngenes	fisherz
BARRIER_COLON_CANCER_RECURRENCE_DN	Down-regulated genes from the 70-gene prognosis predictor for stage 2 colon cancer, based on non-neoplastic mucosa gene expression profiles.	19	4.048
CHAUHAN_RESPONSE_TO_METHOXYESTRADIOL_DN	Genes down-regulated by 2-methoxyestradiol (2ME2) [PubChem = 1573] in the MM.1S cell line (multiple myeloma) sensitive to dexamethasone [PubChem = 5743].	93	3.989
MORI_PLASMA_CELL_UP	Up-regulated genes in the B lymphocyte developmental signature, based on expression profiling of lymphomas from the Emu-myc transgenic mice: plasma cell.	50	3.979
JOHNSTONE_PARVB_TARGETS_2_UP	Genes up-regulated upon overexpression of PARVB [GeneID = 29780] in MDA-MB-231 cells (breast cancer) cultured in 3D collagen I and 3D Matrigel only.	132	3.97
PRAMOONJAGO_SOX4_TARGETS_DN	Genes down-regulated in ACC3 cells (adenoid cystic carcinoma) after knockdown of SOX4 [GeneID = 6659] by RNAi.	48	3.959
SCHUHMACHER_MYC_TARGETS_UP	Genes up-regulated in P493-6 cells (Burkitt's lymphoma) induced to express MYC [GeneID = 4609].	74	3.947
SCHLOSSER_MYC_TARGETS_AND_SERUM_RESPONSE_DN	Cluster 6: genes down-regulated in B493-6 cells (B lymphocytes) by MYC [GeneID = 4609] in combination with serum but not affected by serum alone; they are also up-regulated by MYC alone.	44	3.925
CREIGHTON_AKT1_SIGNALING_VIA_MTOR_UP	Genes in the AKT1 [GeneID = 207] pathway which are independent of MTOR [GeneID = 2475], insensitive to RAD001 (everolimus) [PubChem = 6442177].	34	3.89
NIKOLSKY_BREAST_CANCER_16P13_AMPLICON	Genes within amplicon 16p13 identified in a study of 191 breast tumor samples.	110	3.832
PELLICCIOTTA_HDAC_IN_ANTIGEN_PRESENTATION_UP	Antigen processing and presentation genes up-regulated in JY cells (B lymphocytes) treated with TSA [PubChem = 5562].	63	3.823
VALK_AML_CLUSTER_7	Top 40 genes from cluster 7 of acute myeloid leukemia (AML) expression profile; 61% of the samples are FAB M1 or M2 subtype.	27	3.775
DACOSTA_UV_RESPONSE_VIA_ERCC3_TTD_UP	Genes exclusively up-regulated in fibroblasts expressing the TTD mutant form of ERCC3 [GeneID = 2071], after UVC irradiation.	61	3.769
SANSOM_APC_TARGETS_REQUIRE_MYC	Genes up-regulated after Cre-lox knockout of APC [GeneID = 324] in the small intestine that require functional MYC [GeneID = 4609].	197	3.65
BURTON_ADIPOGENESIS_5	Up-regulated at 48-96 h during differentiation of 3T3-L1 cells (fibroblast) into adipocytes.	120	3.641
DAZARD_UV_RESPONSE_CLUSTER_G5	Cluster G5: genes up-regulated in NHEK cells (normal keratinocyte) at 3 h and 24 h time points after UV-B irradiation.	11	3.638
JIANG_AGING_CEREBRAL_CORTEX_DN	Down-regulated in the cerebral cortex of aged (22 months) BALB/c mice, compared to young (2 months) controls	52	3.618
LI_AMPLIFIED_IN_LUNG_CANCER	Genes with increased copy number that correlates with increased expression across six different lung adenocarcinoma cell lines.	151	3.578

TABLE 7-continued

Chemical Genetic Perturbations			
gs.id	gs.desc	gs.ngenes	fisherz
LUI_THYROID_CANCER_PAX8_PPARG_DN	Top down-regulated genes distinguishing between follicular thyroid carcinoma (FTC) samples by the presence or absence of the PAX8-PPARG [GeneID = 7849; 5468] fusion protein.	36	3.554
VALK_AML_WITH_FLT3_ITD	Genes that best predicted acute myeloid leukemia (AML) with internal tandem duplications (IDT) in FLT3 [GeneID = 2322].	35	3.538
WOO_LIVER_CANCER_RECURRENCE_DN	Genes negatively correlated with recurrence free survival in patients with hepatitis B-related (HBV) hepatocellular carcinoma (HCC).	77	3.529
MORI_LARGE_PRE_BII_LYMPHOCYTE_UP	Up-regulated genes in the B lymphocyte developmental signature, based on expression profiling of lymphomas from the Emu-myc transgenic mice: the Large Pre-BII stage.	80	3.485
JAIN_NFKB_SIGNALING	Genes abnormally regulated in response to CD40L and IL4 [GeneID = 959; 3565] stimulation of B lymphocytes from patients with a hypomorphic mutation of IKBKG [GeneID = 8517].	73	3.481
GUTIERREZ_MULTIPLE_MYELOMA_DN	Genes exclusively down-regulated in plasma cells from MM (multiple myeloma) patients but with a similar expression pattern in the normal cells and in the cells from WM (Waldenstroem's macroblobulinemia) patients.	32	3.481
FALVELLA_SMOKERS_WITH_LUNG_CANCER	Genes that distinguish normal from cancer (lung adenocarcinoma) samples and smokers from non-smoking subjects.	76	3.474
ZHONG_SECRETOME_OF_LUNG_CANCER_AND_FIBROBLAST	Proteins secreted in co-culture of LKR-13 tumor cells (non-small cell lung cancer, NSCLC) and MLg stroma cells (fibroblasts).	125	3.466
JIANG_VHL_TARGETS	Genes up-regulated in 786-0 cells (renal carcinoma, RCC) upon expression of VHL [GeneID = 7428] off a retroviral vector under normoxia (normal oxygen) condition.	126	3.408
MCCLUNG_DELTA_FOSB_TARGETS_8WK	Genes up-regulated in the nucleus accumbens (a major reward center in brain) 8 weeks after induction of deltaFosB, a FOSB [GeneID = 2354] splice variant.	46	3.327
JIANG_TIP30_TARGETS_DN	Down-regulated genes in HepG2 cells (liver cancer) overexpressing an oncogenic variant of tumor suppressor TIP30 [GeneID = 10553] compared to its wild type form.	22	3.262
LI_DCP2_BOUND_MRNA	Genes encoding mRNA transcripts specifically bound by DCP2 [GeneID = 167227].	84	3.245
MODY_HIPPOCAMPUS_POSTNATAL	Genes up-regulated in hyppocampus at late postnatal stages (clusters 11 and 15).	61	3.24
ZHAN_LATE_DIFFERENTIATION_GENES_UP	B lymphocyte late differentiation genes (LDG): top genes up-regulated in plasma cells from tonsils (TPC) compared to those from bone marrow (BPC).	32	3.22

TABLE 7-continued

Chemical Genetic Perturbations			
gs.id	gs.desc	gs.ngenes	fisherz
WAKABAYASHI_ADIPOGENESIS_PPARG_RXRA_BOUND_WITH_H4K20ME1_MARK	Genes with promoters bound by both PPARG and RXRA [GeneID = 5468, 6256] at 8 (but not 0) day time point of adipocyte differentiation of 3T3-L1 cells (preadipocyte) and that were newly modified by H4K20me1.	138	3.213
SCHLOSSER_MYC_AND_SERUM_RESPONSE_SYNERGY	Cluster 3: genes strongly up-regulated in B493-6 cells (B lymphocytes) by a combination of MYC [GeneID = 4609] and serum but not by each of them alone.	30	3.178
ACOSTA_PROLIFERATION_INDEPENDENT_MYC_TARGETS_UP	Genes up-regulated in K562 cells (lymphoblast) by MYC [GeneID = 4609] in the presence of CKN1B [GeneID = 1027].	82	3.167
SHIPP_DLBCL_VS_FOLLICULAR_LYMPHOMA_UP	Top 50 up-regulated markers distinguishing diffuse large B-cell lymphoma (DLBCL) from follicular lymphoma (FL) samples.	40	3.166
DAZARD_UV_RESPONSE_CLUSTER_G4	Cluster G4: genes increasingly up-regulated in NHEK cells (normal keratinocyte) after 12 h time point after UV-B irradiation.	20	3.164
NIKOLSKY_BREAST_CANCER_7P15_AMPLICON	Genes within amplicon 7p15 identified in a copy number alterations study of 191 breast tumor samples.	10	3.162
MCCLUNG_COCAINE_REWARD_5D	Genes up-regulated in the nucleus accumbens (a major reward center in the brain) after 5 days of cocaine [PubChem = 5760] treatment.	78	3.156
MOOTHA_FFA_OXYDATION	Genes involved in free fatty acid oxidation; based on literature and sequence annotation resources and coverted to Affymetrix HG-U133A probe sets.	21	3.09
AMIT_SERUM_RESPONSE_40_MCF10A	Genes whose expression peaked at 40 min after stimulation of MCF10A cells with serum.	32	3.088
WELCH_GATA1_TARGETS	Genes up-regulated after GATA1 [GeneID = 2623] activation in G1E-ER4 cells (erythroid precursors engineered to express GATA1 upon addition of estradiol [PubChemID = 5757]).	20	3.072
SCHLOSSER_MYC_TARGETS_REPRESSED_BY_SERUM	Cluster 7: genes up-regulated in B493-6 cells (B lymphocytes) by MYC [GeneID = 4609] and down-regulated by the combination of MYC and serum.	156	3.069
WALLACE_PROSTATE_CANCER_UP	Genes up-regulated in prostate tumor vs normal tissue samples.	19	3.065
MOOTHA_VOXPHOS	Genes involved in oxidative phosphorylation; based on literature and sequence annotation resources and converted to Affymetrix HG-U133A probe sets.	81	3.053
ZHANG_RESPONSE_TO_CANTHARIDIN_DN	Genes down-regulated in HL-60 cells (promyeloid leukemia) by cantharidin [PubChem = 6708701].	62	3.052
POMEROY_MEDULLOBLASTOMA_PROGNOSIS_DN	Top marker genes in medulloblastoma associated with poor response to treatment (poor outcome).	35	3.052
KIM_GASTRIC_CANCER_CHEMOSENSITIVITY	Genes up-regulated in gastric cancer patients refractory to chemotherapy treatment with 5-fluorouracil and cisplatin [PubChem = 3385; 2767] compared to the sensitive state.	101	3.033

TABLE 7-continued

Chemical Genetic Perturbations			
gs.id	gs.desc	gs.ngenes	fisherz
OXFORD_RALA_OR_RALB_TARGETS_UP	Genes up-regulated after knockdown of RALA or RALB [GeneiD = 5898; 5899], which were also differentially expressed in bladder cancer compared to normal bladder urothelium tissue.	46	3.013
SESTO_RESPONSE_TO_UV_C6	Cluster 6: genes changed in primary keratinocytes by UVB irradiation.	33	3.006
NAKAMURA_CANCER_MICROENVIRONMENT_DN	Genes down-regulated in pancreatic cancer cells grown in orthotopic xenograft tumors compared to those grown in vitro.	45	3.005
BILANGES_RAPAMYCIN_SENSITIVE_VIA_TSC1_AND_TSC2	Genes translationally repressed by rapamycin (sirolimus) [PubChemID = 6610346] in MEF cells (embryonic fibroblast) lacking either TSC1 or TSC2 [GeneID = 7248, 7249] but not in the wild type cells.	63	3
KAYO_CALORIE_RESTRICTION_MUSCLE_DN	Downregulated in the vastus lateralis muscle of middle aged rhesus monkeys subjected to caloric restriction since young adulthood vs age matched controls	80	2.996
SHAFFER_IRF4_TARGETS_IN_PLASMA_CELL_VS_MATURE_B_LYMPHOCYTE	IRF4 [GeneID = 3662] target genes up-regulated in plasma cells compared to mature B lymphocytes.	62	2.992
LUI_TARGETS_OF_PAX8_PPARG_FUSION	Genes down-regulated in follicular thyroid carcinoma (FTC) samples that bear PAX8-PPARG [GeneID = 7849; 5468] fusion protein.	26	2.949
YAO_TEMPORAL_RESPONSE_TO_PROGESTERONE_CLUSTER_12	Genes co-regulated in uterus during a time course response to progesterone [PubChem = 5994]: SOM cluster 12.	76	2.949
RHODES_CANCER_META_SIGNATURE	Genes commonly up-regulated in cancer relative to normal tissue, according to the meta-analysis of the OncoMine gene expression database.	58	2.948
QI_PLASMACYTOMA_DN	Down-regulated genes that best discriminate plasmablastic plasmacytoma from plasmacytic plasmacytoma tumors.	98	2.922
HOFFMANN_LARGE_TO_SMALL_PRE_BII_LYMPHOCYTE_UP	Genes up-regulated during differentiation from large pre-BII to small pre-BII lymphocyte.	157	2.899
FAELT_B_CLL_WITH_VH3_21_UP	Genes up-regulated in samples from B-CLL (B-cell chronic lymphocytic leukemia) with the immunoglobulin heavy chain VH3-21 gene.	42	2.895
ROSS_AML_OF_FAB_M7_TYPE	Top 100 probe sets for pediatric acute myeloid leukemia (AML) subtype FAB M7 (also known as acute megakaryoblastic leukemia, AMKL).	67	2.875
KEEN_RESPONSE_TO_ROSIGLITAZONE_UP	Genes up-regulated in aorta biopsies from mice treated with rosiglitazone [PubChem = 77999].	35	2.873
QI_HYPOXIA_TARGETS_OF_HIF1A_AND_FOXA2	Genes up-regulated by hypoxia in TRAMP-C cells (prostatic cancer) expressing HIF1A and FOXA2 [GeneID = 3091, 3170] off plasmid vectors.	36	2.872
GAZDA_DIAMOND_BLACKFAN_ANEMIA_PROGENITOR_DN	Genes down-regulated in common hematopoietic progenitor cells isolated from bone marrow of patients with Diamond-Blackfan anemia (DBA) and mutated RPS19 [GeneID = 6223].	62	2.851

TABLE 7-continued

Chemical Genetic Perturbations			
gs.id	gs.desc	gs.ngenes	fisherz
ELVIDGE_HYPOXIA_BY_DMOG_DN	Genes down-regulated in MCF7 cells (breast cancer) treated with hypoxia mimetic DMOG [PubChem = 3080614].	58	2.837
GRAHAM_CML_QUIESCENT_VS_NORMAL_QUIESCENT_UP	Genes up-regulated in quiescent (G0) CD34+ [GeneID = 8842] cells isolated from peripheral blood of CML (chronic myeloid leukemia) patients compared to the quiescent cells from normal donors.	85	2.824
GALE_APL_WITH_FLT3_MUTATED_DN	Genes down-regulated in acute promyelocytic leukemia (APL) patients with mutated FLT3 [GeneID = 2322].	17	2.813
TONKS_TARGETS_OF_RUNX1_RUNX1T1_FUSION_SUSTAINED_IN_MONOCYTE_UP	Genes up-regulated by RUNX1-RUNX1T1 [GeneID = 861; 862] fusion protein in normal hematopoietic progenitors; their expression was sustained in subsequently developing monocytes.	20	2.78
KANG_FLUOROURACIL_RESISTANCE_UP	Genes up-regulated in gastric cancer cell lines resistant to 5-fluorouracil [PubChem = 3385].	22	2.755
CHAUHAN_RESPONSE_TO_METHOXYESTRADIOL_UP	Genes up-regulated by 2-methoxyestradiol (2ME2) [PubChem = 1573] in the MM.1S cell line (multiple myeloma) sensitive to dexamethasone [PubChem = 5743].	46	2.755
HEDENFALK_BREAST_CANCER_BRCA1_VS_BRCA2	Genes differentially expressed in hereditary breast cancer tumors with mutated BRCA1 [GeneID = 672] compared to those with mutated BRCA2 [GeneID = 675].	154	2.731
MALONEY_RESPONSE_TO_17AAG_DN	Down-regulated genes in A2780 cells (ovarian cancer) treated with 17AAG [PubChem = 6440175], a chemical with anticancer properties.	69	2.725
IRITANI_MAD1_TARGETS_DN	Genes down-regulated by overexpression of MAD1 [GeneID = 4084] in primary thymocytes from RAG2 [GeneID = 5897] knockout mice.	40	2.719
DELPUECH_FOXO3_TARGETS_DN	Genes down-regulated in DL23 cells (colon cancer) upon expression of an activated form of FOXO3 [GeneID = 2309].	39	2.711
LUI_THYROID_CANCER_CLUSTER_3	Cluster 3: genes with similar expression profiles across follicular thyroid carcinoma (FTC) samples; genes in this cluster correlated well with the presence of PAX8-PPARG [GeneID = 7849; 5468] fusion protein.	18	2.693
DAVIES_MULTIPLE_MYELOMA_VS_MGUS_UP	Genes up-regulated in multiple myeloma (MM) compared to monoclonal gammopathy of uncertain significance (MGUS).	13	2.692
ELLWOOD_MYC_TARGETS_DN	Genes down-regulated in transgenic mice expressing human MYC [GeneID = 4609] in prostate.	40	2.691
TONKS_TARGETS_OF_RUNX1_RUNX1T1_FUSION_MONOCYTE_UP	Genes up-regulated in monocytes by RUNX1-RUNX1T1 [GeneID = 861; 862] fusion.	193	2.685

TABLE 7-continued

Chemical Genetic Perturbations			
gs.id	gs.desc	gs.ngenes	fisherz
WANG_TARGETS_OF_MLL_CBP_FUSION_DN	Top 50 genes down-regulated in granulocyte/macrophage progenitors (GMP) upon expression of MLL-CBP fusion [GeneID = 4297; 1387].	43	2.666
RODWELL_AGING_KIDNEY_NO_BLOOD_DN	Genes whose expression decreases with age in normal kidney, excluding those with higher expression in blood.	146	2.664
MUELLER_COMMON_TARGETS_OF_AML_FUSIONS_UP	Up-regulated target genes shared by acute myeloid leukemia (AML) translocation products PML RARA [GeneID = 5371; 5914], AML1 ETO [GeneID = 861; 862], and PLZF RARA [GeneID = 5914; 7704].	14	2.661
SUZUKI_AMPLIFIED_IN_ORAL_CANCER	High-level amplifications detected in oral squamous cell carcinoma (OSCC) lines by array-CGH analysis.	16	2.655
MARCHINI_TRABECTEDIN_RESISTANCE_DN	Genes down-regulated in chondrosarcoma and ovarian carcinoma cell lines which developed resistance to trabectedin [PubChem = 3199].	48	2.628
NUTT_GBM_VS_AO_GLIOMA_UP	Top 50 marker genes for glioblastoma multiform (GBM), a class of high grade glioma.	45	2.621
ALCALAY_AML_BY_NPM1_LOCALIZATION_UP	Genes up-regulated in acute myeloid leukemia (AML) with respect to cellular localization of NPM1 [GeneID = 4869]: cytoplasmic vs. nucleolar.	133	2.619
AMIT_EGF_RESPONSE_480_HELA	Genes whose expression peaked at 480 min after stimulation of HeLa cells with EGF [GeneID = 1950].	162	2.602
MOOTHA_TCA	Tricarboxylic acid related genes; based on literature and sequence annotation resources and converted to Affymetrix HG-U133A probe sets.	13	2.579
PUJANA_BREAST_CANCER_LIT_INT_NETWORK	Genes constituting the LIT-Int network of proteins interacting with breast cancer reference proteins BRCA1, BRCA2, ATM, and CHEK2 [GeneID = 672; 675; 472; 11200]; the interactions were manually curated from the literature.	99	2.576
ZHONG_SECRETOME_OF_LUNG_CANCER AND_ENDOTHELIUM	Proteins secreted in co-culture of LKR-13 tumor cells (non-small cell lung cancer, NSCLC) and MEC stroma cells (endothelium).	64	2.555
LI_WILMS_TUMOR_VS_FETAL_KIDNEY_1_DN	Genes down-regulated in Wilm's tumor samples compared to fetal kidney.	157	2.553
MUNSHI_MULTIPLE_MYELOMA_UP	Genes up-regulated in multiple myeloma (MM) compared to normal plasma cells from the patient's identical twin.	79	2.551
CHEN_HOXA5_TARGETS_9HR_DN	Genes down-regulated 9 h after induction of HoxA5 [GeneID = 3205] expression in a breast cancer cell line.	40	2.541
AZARE_STAT3_TARGETS	Genes up-regulated in RPWE-1 cells by activated STAT3 [GeneID = 6774].	23	2.537

TABLE 7-continued

Chemical Genetic Perturbations			
gs.id	gs.desc	gs.ngenes	fisherz
DANG_MYC_TARGETS_UP	Genes up-regulated by MYC [GeneID = 4609] and whose promoters are bound by MYC, according to MYC Target Gene Database.	125	2.534
MAYBURD_RESPONSE_TO_L663536_UP	Genes up-regulated in H720 cells (lung cancer) after treatment with L663536 (MK886) [PubChem = 105049], an inhibitor of leukotriene biosynthesis.	29	2.527
YAO_TEMPORAL_RESPONSE_TO_PROGESTERONE_CLUSTER_10	Genes co-regulated in uterus during a time course response to progesterone [PubChem = 5994]: SOM cluster 10.	63	2.519
SHAFFER_IRF4_TARGETS_IN_ACTIVATED_DENDRITIC_CELL	IRF4 [GeneID = 3662] target genes up-regulated in plasmacytoid dendritic cells compared to monocytes.	63	2.509
HUMMERICH_SKIN_CANCER_PROGRESSION_DN	Selected genes down-regulated during progression through benign to malignant skin tumors formed by treatment with DMBA and TPA [PubChem = 6001; 4792] chemicals in the two stage skin carcinogenesis model.	97	2.501
ZHAN_MULTIPLE_MYELOMA_CD1_DN	Top 50 down-regulated genes in cluster CD-1 of multiple myeloma samples with the characteristic expression spike of CCND1 [GeneID = 595].	44	2.501
LIU_LIVER_CANCER	Low abundance transcripts specific to hepatocellular carcinoma (HCC).	37	2.485
ROVERSI_GLIOMA_COPY_NUMBER_UP	Genes in the most frequently gained loci in a panel of glioma cell lines.	94	2.479
MOOTHA_GLUCONEOGENESIS	Genes involved in gluconeogenesis; based on literature and sequence annotation resources and converted to Affymetrix HG-U133A probe sets.	30	2.474
HONMA_DOCETAXEL_RESISTANCE	Genes up-regulated in MCF7-ADR cell line (breast cancer) resistant to docetaxel [PubChem = 148124].	30	2.467
LIU_PROSTATE_CANCER_UP	Genes up-regulated in prostate cancer samples.	91	2.463
COLLER_MYC_TARGETS_UP	Genes up-regulated in 293T (transformed fetal renal cell) upon expression of MYC [GeneID = 4609].	23	2.455
BOYAULT_LIVER_CANCER_SUBCLASS_G123_UP	Up-regulated genes in hepatocellular carcinoma (HCC) subclass G123, defined by unsupervised clustering.	42	2.453
DANG_REGULATED_BY_MYC_UP	Genes up-regulated by MYC [GeneID = 4609], according to the MYC Target Gene Database.	66	2.45
AMIT_SERUM_RESPONSE_480_MCF10A	Genes whose expression peaked at 480 min after stimulation of MCF10A cells with serum.	34	2.442
NADLER_HYPERGLYCEMIA_AT_OBESITY	Genes correlated with the development of hyperglycemia in obese mice.	56	2.395
XU_RESPONSE_TO_TRETINOIN_AND_NSC682994_DN	Genes down-regulated synergistically in NB4 cells (acute promyelocytic leukemia, APL) by tretinoin and NSC682994 [PubChem = 444795; 388304].	14	2.363

TABLE 7-continued

Chemical Genetic Perturbations			
gs.id	gs.desc	gs.ngenes	fisherz
TONKS_TARGETS_OF_RUNX1_RUNX1T1_FUSION_ERYTHROCYTE_UP	Genes up-regulated in erythroid lineage cells by RUNX1-RUNX1T1 [GeneID = 861; 862] fusion.	153	−2.338
BOYAULT_LIVER_CANCER_SUBCLASS_G2	Genes in hepatocellular carcinoma (HCC) subclass G2, defined by unsupervised clustering.	27	−2.358
TSAI_DNAJB4_TARGETS_UP	Genes up-regulated in CL1-5 cells (lung cancer) overexpressing DNAJB4 [GeneID = 11080] off a plasmid vector.	13	−2.389
WILCOX_RESPONSE_TO_PROGESTERONE_UP	Genes up-regulated in primary cultures of ovarian surface epithlium cells exposed to progesterone [PubChem = 5994] for 5 days.	149	−2.394
LEE_AGING_CEREBELLUM_UP	Upregulated in the cerebellum of aged adult mice (30-month) vs young adult (5-month)	82	−2.409
LIEN_BREAST_CARCINOMA_METAPLASTIC_VS_DUCTAL_UP	Genes up-regulated between two breast carcinoma subtypes: metaplastic (MCB) and ductal (DCB).	82	−2.421
STEARMAN_TUMOR_FIELD_EFFECT_UP	Up-regulated genes in the ‘Field Effect’ signature of normal lung tissue adjacent to the tumor.	35	−2.421
MENSE_HYPOXIA_UP	Hypoxia response genes up-regulated in both astrocytes and HeLa cell line.	97	−2.424
PENG_GLUTAMINE_DEPRIVATION_UP	Genes up-regulated in BJAB cells (B-lymphoma) after glutamine [PubChem = 738] deprivation.	36	−2.426
WU_CELL_MIGRATION	Genes associated with migration rate of 40 human bladder cancer cells.	177	−2.433
KYNG_DNA_DAMAGE_BY_UV	UV only responding genes in primary fibroblasts from young donors.	60	−2.441
KOBAYASHI_RESPONSE_TO_ROMIDEPSIN	Genes up-regulated in MM-LH cells (malignant melanoma) after treatment with the HDAC inhibitor romidepsin (FK228) [PubChem = 5352062].	19	−2.446
MCMURRAY_TP53_HRAS_COOPERATION_RESPONSE_DN	Down-regulated ‘cooperation response genes’: responded synergystically to the combination of mutant TP53 and HRAS [GeneID = 7157; 3265] in YAMC cells (colon).	64	−2.447
OSAWA_TNF_TARGETS	Genes up-regulated in Hc cells (normal hepatocyte) by TNF [GeneID = 7124].	10	−2.454
TAKEDA_TARGETS_OF_NUP98_HOXA9_FUSION_3D_DN	Genes down-regulated in CD34+ [GeneID = 947] hematopoetic cells by expression of NUP98-HOXA9 fusion [GeneID = 4928; 3205] off a retroviral vector at 3 days after transduction.	29	−2.467
BROWNE_HCMV_INFECTION_12HR_UP	Genes up-regulated in primary fibroblast cell culture after infection with HCMV (AD169 strain) at 12 h time point that were not up-regulated at the previous time point, 10 h.	107	−2.477
KENNY_CTNNB1_TARGETS_UP	Genes up-regulated in HC11 cells (mammary epithelium) by expression of constantly active CTNNB1 [GeneID = 1499].	50	−2.489
HUMMEL_BURKITTS_LYMPHOMA_DN	Down-regulated genes constituting the molecular signature of Burkitt’s lymphoma.	15	−2.493

TABLE 7-continued

Chemical Genetic Perturbations			
gs.id	gs.desc	gs.ngenes	fisherz
GARGALOVIC_RESPONSE_TO_OXIDIZED_PHOSPHOLIPIDS_YELLOW_UP	Genes from the yellow module which are up-regulated in HAEC cells (primary aortic endothelium) after exposure to the oxidized 1-palmitoyl-2-arachidonyl-sn-3-glycerophosphorylcholine (oxPAPC).	31	−2.509
YE_METASTATIC_LIVER_CANCER	Genes up-regulated in hepatocellular carcinoma (HCC) with intra-hepatic metastasis compared to the non-metastatic tumors.	25	−2.517
NAKAMURA_ADIPOGENESIS_EARLY_DN	Genes down-regulated in mesenchymal stem cells during early phase of adipogenesis, defined as days 1 to 5 of culturing with adipogenic hormones.	38	−2.518
DORSAM_HOXA9_TARGETS_DN	HOXA9 [GeneID = 3205] targets down-regulated in hematopoietic stem cells.	29	−2.536
PLASARI_TGFB1_TARGETS_1HR_UP	Genes up-regulated in MEF cells (embryonic fibroblast) upon stimulation with TGFB1 [GeneID = 7040] for 1 h.	33	−2.546
CHIARETTI_T_ALL_RELAPSE_PROGNOSIS	Genes whose expression predicted relapse in less than 2 years after chemotherapy for adult patients with T-ALL (T cell lymphoblastic leukemia).	19	−2.546
LINDSTEDT_DENDRITIC_CELL_MATURATION_D	Genes down-regulated during the course of maturation of monocyte-derived dendritic cells (DC) in response to inflammatory stimuli (cluster D).	66	−2.549
VERHAAK_AML_WITH_NPM1_MUTATED_UP	Genes up-regulated in acute myeloid leukemia (AML) patients with mutated NPM1 [GeneID = 4869].	173	−2.552
BROWNE_HCMV_INFECTION_20HR_DN	Genes down-regulated in primary fibroblast cell culture after infection with HCMV (AD169 strain) at 20 h time point that were not down-regulated at the previous time point, 18 h.	100	−2.568
PEREZ_TP53_AND_TP63_TARGETS	Genes up-regulated in HMEC cells (primary mammary epithelium) upon expression of both of TP53 [GeneID = 7157] and the transcriptionally active isoform of TP63 [GeneID = 8626] off adenoviral vectors.	196	−2.578
HOFMANN_CELL_LYMPHOMA_DN	Genes down-regulated in lymph nodes from patients with mantle cell lymphoma (MCL) compared to the non-malignant hyperplastic lymph nodes.	39	−2.578
CASORELLI_ACUTE_PROMYELOCYTIC_LEUKEMIA_UP	Genes up-regulated in APL (acute promyeolocytic leukemia) blasts expressing PML-RARA fusion [GeneID = 5371; 5914] compared to normal promyeloblasts.	167	−2.582
XU_CREBBP_TARGETS_DN	Genes down-regulated in pro-B lymphocytes after knockout of CREBBP [GeneID = 1387].	44	−2.586

TABLE 7-continued

Chemical Genetic Perturbations			
gs.id	gs.desc	gs.ngenes	fisherz
DAIRKEE_TERT_TARGETS_DN	Genes down-regulated in non-spontaneously immortalizing (NSI) primary breast cancer tumor cultures upon expression of TERT [GeneID = 7015] off a retroviral vector.	117	−2.589
DAVIES_MULTIPLE_MYELOMA_VS_MGUS_DN	Genes down-regulated in multiple myeloma (MM) compared to monoclonal gammopathy of uncertain significance (MGUS).	26	−2.591
RASHI_RESPONSE_TO_IONIZING_RADIATION_6	Cluster 6: late responding genes activated in ATM [GeneID = 472] deficient but not in the wild type tissues.	83	−2.593
GALE_APL_WITH_FLT3_MUTATED_UP	Genes up-regulated in acute promyelocytic leukemia (APL) patients with mutated FLT3 [GeneID = 2322].	55	−2.593
WAMUNYOKOLI_OVARIAN_CANCER_GRADES_1_2_DN	Genes down-regulated in mucinous ovarian carcinoma tumors of grades 1 and 2 compared to the normal ovarian survace epithelium tissue.	64	−2.597
KLEIN_PRIMARY_EFFUSION_LYMPHOMA_DN	Genes down-regulated in AIDS-related primary effusion lymphoma (PEL) samples compared to other tumor subtypes and normal B lymphocytes.	56	−2.616
HOFMANN_MYELODYSPLASTIC_SYNDROM_RISK_DN	Genes down-regulated in bone marrow hematopoietic stem cells (HSC, CD34+ [GeneID = 947]) from patients with high risk of myelodysplastic syndrome (MDS) compared to the low risk patients.	22	−2.617
TONKS_TARGETS_OF_RUNX1_RUNX1T1_FUSION_HSC_UP	Genes up-regulated in normal hematopoietic progenitors by RUNX1-RUNX1T1 [GeneID = 861; 862] fusion.	182	−2.617
NEWMAN_ERCC6_TARGETS_UP	Genes up-regulated in Cockayne syndrome fibroblasts rescued by expression of ERCC6 [GeneID = 2074] off a plasmid vector.	24	−2.631
KEEN_RESPONSE_TO_ROSIGLITAZONE_DN	Genes down-regulated in aorta biopsies from mice treated with rosiglitazone [PubChem = 77999].	101	−2.643
MCDOWELL_ACUTE_LUNG_INJURY_UP	Genes up-regulated in the mouse model of acute lung injury induced by inhaling nickel sulfate [PubChem = 24586].	44	−2.647
PARK_TRETINOIN_RESPONSE_AND_RARA_PLZF_FUSION	Genes up-regulated by tretinoin (ATRA) [PubChem = 444795] in U937 cells (acute promyelocytic leukemia, APL) made resistant to the drug by expression of the PLZF-RARA fusion [GeneID = 7704, 5914].	22	−2.65
WILLIAMS_ESR2_TARGETS_DN	Genes uniquely down-regulated in T47D cells (breast cancer) by induction of ESR2 [GeneID = 2100] expression in the Tet-Off system.	10	−2.655
LIEN_BREAST_CARCINOMA_METAPLASTIC	Genes up-regulated in metaplastic carcinoma of the breast (MCB) subclass 2 compared to the MCB subclass 1.	33	−2.665
NIKOLSKY_BREAST_CANCER_6P24_P22_AMPLICON	Genes within amplicon 6p24-p22 identified in a copy number alterations study of 191 breast tumor samples.	20	−2.666

TABLE 7-continued

Chemical Genetic Perturbations			
gs.id	gs.desc	gs.ngenes	fisherz
SHETH_LIVER_CANCER_VS_TXNIP_LOSS_PAM2	Cluster PAM2: genes up-regulated in hepatocellular carcinoma (HCC) vs normal liver tissue from mice deficient for TXNIP [GeneID = 10628].	149	−2.671
LINDSTEDT_DENDRITIC_CELL_MATURATION_A	Maturation of monocyte-derived dendritic cells (DC) in response to inflammatory stimuli: genes up-regulated only at 8 hr after the stimulation (cluster A).	63	−2.675
GOLDRATH_IMMUNE_MEMORY	‘Memory genes’ expressed uniquely in CD8+ [GeneID = 925] memory T lymphocytes (compared with effector or naive cells)	64	−2.688
CHIANG_LIVER_CANCER_SUBCLASS_POLYSOMY7_DN	Marker genes down-regulated in the ‘chromosome 7 polysomy’ subclass of hepatocellular carcinoma (HCC); characterized by polysomy of chromosome 7 and by a lack of gains of chromosome 8q.	23	−2.706
GILDEA_METASTASIS	Top genes down-regulated in metastatic (T24T) vs non-metastatic (T24) bladder cancer cell lines.	30	−2.724
FARMER_BREAST_CANCER_CLUSTER_5	Cluster 5: selected 17q21_23 amplicon genes clustered together across breast cancer samples.	19	−2.74
BOYLAN_MULTIPLE_MYELOMA_C_CLUSTER_DN	Genes from cluster 2: down-regulated in group C of tumors arising from overexpression of BCL2L1 and MYC [GeneID = 598; 4609] in plasma cells.	31	−2.74
GRABARCZYK_BCL11B_TARGETS_UP	Genes up-regulated in Jurkat cells (transformed T lymphocytes) after knockdown of BCL11B [GeneID = 64919] by RNAi.	77	−2.756
HALMOS_CEBPA_TARGETS_UP	Genes up-regulated in H358 cells (lung cancer) by inducible expression of CEBPA [GeneID = 1050] off plasmid vector.	48	−2.76
BROWNE_HCMV_INFECTION_6HR_DN	Genes down-regulated in primary fibroblast cell culture point after infection with HCMV (AD169 strain) at 6 h time point that were not down-regulated at the previous time point, 4 h.	157	−2.762
GUTIERREZ_CHRONIC_LYMPHOCYTIC_LEUKEMIA_DN	Genes exclusively down-regulated in B lymphocytes from CLL (chronic lymphocytic leukemia) patients but with a similar expression pattern in the normal cells and in the cells from WM (Waldenstroem’s macroblobulinemia) patients.	56	−2.787
GENTILE_UV_RESPONSE_CLUSTER_D2	Cluster d2: genes down-regulated consistently in WS1 cells (fibroblast) between 6 h and 24 h after irradiation with high dose UV-C.	41	−2.788
CHIARETTI_ACUTE_LYMPHOBLASTIC_LEUKEMIA_ZAP70	Differentially expressed genes between high vs low ZAP70 [GeneID = 7535] acute lymphoblastic leukemia (ALL) cases with no known molecular aberrations.	66	−2.788
RAMALHO_STEMNESS_DN	Genes depleted in embryonic, neural and hematopoietic stem cells.	70	−2.796

TABLE 7-continued

Chemical Genetic Perturbations			
gs.id	gs.desc	gs.ngenes	fisherz
HOOI_ST7_TARGETS_DN	Genes down-regulated in PC-3 cells (prostate cancer) stably expressing ST7 [GeneID = 7982] off a plasmid vector.	117	−2.798
GARGALOVIC_RESPONSE_TO_OXIDIZED_PHOSPHOLIPIDS_BLUE_UP	Genes from the blue module which are up-regulated in HAEC cells (primary aortic endothelium) after exposure to the oxidized 1-palmitoyl-2-arachidonyl-sn-3-glycerophosphorylcholine (oxPAPC).	132	−2.806
GROSS_HYPOXIA_VIA_ELK3_ONLY_UP	Genes specifically up-regulated in SEND cells (skin endothelium) at hypoxia after knockdown of ELK3 [GeneID = 2004] by RNAi.	32	−2.815
BOYAULT_LIVER_CANCER_SUBCLASS_G5_DN	Down-regulated genes in hepatocellular carcinoma (HCC) subclass G5, defined by unsupervised clustering.	27	−2.816
PARK_TRETINOIN_RESPONSE_AND_PML_RARA_FUSION	Genes up-regulated by tretinoin (ATRA) [PubChem = 444795] in U937 cells (acute promyelocytic leukemia, APL) made sensitive to the drug by expression of the PML-RARA fusion [GeneID = 5371; 5914].	30	−2.832
TIAN_TNF_SIGNALING_VIA_NFKB	Genes modulated in HeLa cells (cervical carcinoma) by TNF [GeneID = 7124] via NFKB pathway.	28	−2.834
GROSS_HYPOXIA_VIA_ELK3_DN	Genes down-regulated in SEND cells (skin endothelium) at hypoxia with ELK3 [GeneID = 2004] knockdown by RNAi.	153	−2.87
OKUMURA_INFLAMMATORY_RESPONSE_LPS	Genes up-regulated in mast cells (MC) after stimulation with a bacterial lipopolysaccharide (LPS).	177	−2.885
HAHTOLA_MYCOSIS_FUNGOIDES_CD4_DN	Genes down-regulated in T helper cells (defines as CD4+) isolated from patients with mucosis fungoides compared to those from normal control donors.	114	−2.885
SCHAEFFER_PROSTATE_DEVELOPMENT_6HR_UP	Genes up-regulated in the urogenital sinus (UGS) of day E16 females exposed to the androgen dihydrotestosterone [PubChem = 10635] for 6 h.	168	−2.891
ZHAN_MULTIPLE_MYELOMA_PR_DN	Top 50 down-regulated genes in cluster PR of multiple myeloma samples characterized by increased expression of proliferation and cell cycle genes.	44	−2.897
LU_TUMOR_VASCULATURE_UP	Genes up-regulated in endothelial cells derived from invasive ovarian cancer tissue.	29	−2.899
LEE_DOUBLE_POLAR_THYMOCYTE	Genes enriched in the double polar (DP) thymocyte compared to all other T lymphocyte differentiation stages.	26	−2.906
MAHADEVAN_RESPONSE_TO_MP470_UP	Top genes up-regulated in the GIST (gastrointestinal stromal tumor) cell line resistant to imatinib [PubChem = 5291] after treatment with MP470, a protein kinase inhibitor.	19	−2.906

TABLE 7-continued

Chemical Genetic Perturbations			
gs.id	gs.desc	gs.ngenes	fisherz
MORI_IMMATURE_B_LYMPHOCYTE_UP	Up-regulated genes in the B lymphocyte developmental signature based on expression profiling of lymphomas from the Emu-myc transgenic mice: the immature B stage.	52	−2.907
SAKAI_CHRONIC_HEPATITIS_VS_LIVER_CANCER_UP	Selected genes up-regulated in peripheral blood monocytes (PBMC) of patients with hepatocellular carcinoma (HCC) compared to those with chronic hepatitis.	82	−2.907
ROETH_TERT_TARGETS_UP	Genes up-regulated in T lymphocytes overexpressing TERT [GeneID = 7015] off a retrovirus vector.	14	−2.909
STARK_PREFRONTAL_CORTEX_22Q11_DELETION_UP	Genes up-regulated in prefrontal cortex (PFC) of mice carrying a hemizygotic microdeletion in the 22q11.2 region.	190	−2.911
CHIANG_LIVER_CANCER_SUBCLASS_UNANNOTATED_UP	Marker genes up-regulated in the ‘unannotated’ subclass of hepatocellular carcinoma (HCC) samples.	83	−2.918
YOSHIOKA_LIVER_CANCER_EARLY_RECURRENCE_UP	Genes up-regulated in hepatocellular carcinoma (HCC) samples from patients with early recurrence (within 2 years after surgery) after resection.	38	−2.919
VANASSE_BCL2_TARGETS_DN	Genes down-regulated in primary B lymphocytes engineered to overexpress BCL2 [GeneID = 12043].	72	−2.924
BROCKE_APOPTOSIS_REVERSED_BY_IL6	Genes changed in INA-6 cells (multiple myeloma, MM) by re-addition of IL6 [GeneID = 3569] after its initial withdrawal for 12 h.	141	−2.925
NIKOLSKY_BREAST_CANCER_8P12_P11_AMPLICON	Genes within amplicon 8p12-p11 identified in a copy number alterations study of 191 breast tumor samples.	52	−2.928
JOHNSTONE_PARVB_TARGETS_1_DN	Genes down-regulated in MDA-MB-231 cells (breast cancer) upon overexpression of PARVB [GeneID = 29780] under all three culture conditions.	61	−2.937
CLASPER_LYMPHATIC_VESSELS_DURING_METASTASIS_DN	Selected genes down-regulated during invasion of lymphatic vessels during metastasis.	36	−2.937
WORSCHECH_TUMOR_EVASION_AND_TOLEROGENICITY_UP	Selected genes with immunologic function which were reciprocally changed in evasion and tolerogenic tumor models.	30	−2.95
TURASHVILI_BREAST_DUCTAL_CARCINOMA_VS_LOBULAR_NORMAL_UP	Genes up-regulated in ductal carcinoma vs normal lobular breast cells.	72	−2.956
ZHANG_RESPONSE_TO_CANTHARIDIN_UP	Genes up-regulated in HL-60 cells (promyeloid leukemia) by cantharidin [PubChem = 6708701].	19	−2.961
KANG_GIST_WITH_PDGFRA_UP	Genes up-regulated in gastrointestinal stromal tumors (GIST) with PDGFRA [GeneID = 5156] mutations.	48	−2.965

TABLE 7-continued

Chemical Genetic Perturbations			
gs.id	gs.desc	gs.ngenes	fisherz
MARSHALL_VIRAL_INFECTION_RESPONSE_DN	Genes down-regulated in the influenza-specific CD8+ [GeneID = 925] T lymphocytes from bronchoalveolar lavage (BAL) compared to those from spleen.	29	−2.977
EHRLICH_ICF_SYNDROM_UP	Up-regulated in B lymphocytes from patients with ICF syndrome caused by mutations in DNMT3B [GeneID = 1789] compared to normals.	13	−2.981
CHIARADONNA_NEOPLASTIC_TRANSFORMATION_CDC25_UP	Genes up-regulated in reverted NIH3T3 cells (fibroblasts transformed by activated KRAS [GeneID = 3845] which then reverted to normal cells upon stable over-expression of a dominant negative form of CDC25 [GeneID = 5923]) vs normal fibroblasts.	117	−2.983
WANG_IMMORTALIZED_BY_HOXA9_AND_MEIS1_UP	Up-regulated genes in myeloid progenitors immortalized by HOXA9 [GeneID = 3205] vs those immortalized by HOXA9 and MEIS1 [GeneID = 4211].	27	−2.993
GHANDHI_BYSTANDER_IRRADIATION_UP	Genes significantly (FDR < 10%) up-regulated in IMR-90 cells (fibroblast) in response to bystander irradiation.	81	−2.993
HUANG_DASATINIB_RESISTANCE_UP	Genes whose expression positively correlated with sensitivity of breast cancer cell lines to dasatinib [PubChem = 3062316].	78	−2.998
SHIN_B_CELL_LYMPHOMA_CLUSTER_8	Cluster 8 of genes distinguishing among different B lymphocyte neoplasms.	35	−3.001
ALONSO_METASTASIS_DN	Down-regulated genes in melanoma tumors that developed metastatic disease compared to primary melanoma that did not.	25	−3.023
PLASARI_TGFB1_SIGNALING_VIA_NFIC_1HR_DN	Genes down-regulated after 1 h of TGFB1 [GeneID = 7040] stimulation in MEF cells (embryonic fibroblast) with NFIC [GeneID = 4782] knockout vs wild type MEFs.	105	−3.029
GAVIN_FOXP3_TARGETS_CLUSTER_T4	Cluster T4 of genes with similar expression profiles in thymic T lymphocytes after FOXP3 [GeneID = 50943] loss of function (LOF).	91	−3.046
GREGORY_SYNTHETIC_LETHAL_WITH_IMATINIB	Genes identified as synthetic lethal with imatinib [PubChemID = 5291] in RNAi screen in K562 cells (CML, chronic myelogenous leukemia).	135	−3.054
BHATI_G2M_ARREST_BY_2METHOXYESTRADIOL_UP	Up-regulated genes in MDA-MB-435 cells (breast cancer) undergoing G2/M arrest after treatment with 2-methoxyestradiol (2ME2)[PubChem = 1573].	114	−3.062
SASSON_RESPONSE_TO_GONADOTROPHINS_DN	Genes down-regulated in primary granulosa cells after stimulation with LH or FSH gonadotrophic hormones for 24 h.	84	−3.065
LIU_TARGETS_OF_VMYB_VS_CMYB_DN	Gene regulated in the opposite directions by v-MYB (DN) and c-MYB (UP) variants of CMYB [GeneID = 4602] overexpressed in primary monocyte cultures off adenoviral vectors.	42	−3.08

TABLE 7-continued

Chemical Genetic Perturbations			
gs.id	gs.desc	gs.ngenes	fisherz
SANA_TNF_SIGNALING_UP	Genes up-regulated in five primary endothelial cell types (lung, aortic, iliac, dermal, and colon) by TNF [GeneID = 7124].	83	−3.091
SHIN_B_CELL_LYMPHOMA_CLUSTER_3	Cluster 3 of genes distinguishing among different B lymphocyte neoplasms.	27	−3.093
LU_TUMOR_ENDOTHELIAL_MARKERS_UP	Genes specifically up-regulated in tumor endothelium.	22	−3.118
XU_AKT1_TARGETS_6HR	Genes up-regulated in DU-145 cells (prostate cancer) expressing a dominant negative form of AKT1 [GeneID = 207] upon sham-treatment for 6 h (as a control for the HGF [GeneID = 3082] experiments).	27	−3.12
CROONQUIST_NRAS_SIGNALING_UP	Genes up-regulated in ANBL-6 cell line (multiple myeloma, MM) expressing a constantly active form of NRAS [GeneID = 4893] off a plasmid vector compared to those grown in the presence of IL6 [GeneID = 3569].	39	−3.127
DAUER_STAT3_TARGETS_UP	Top 50 genes up-regulated in A549 cells (lung cancer) expressing STAT3 [GeneID = 6774] off an adenovirus vector.	47	−3.127
AKL_HTLV1_INFECTION_DN	Genes down-regulated in WE17/10 cells (CD4+ [GeneID = 920] T lymphocytes) infected by HTLV1 (and thus displaying low CD7 [GeneID = 924]) compared to the uninfected (i.e., CD7+) cells.	66	−3.168
MARSON_FOXP3_CORE_DIRECT_TARGETS	Direct FOXP3 [GeneID = 50943] targets that exhibit consistent transcriptional behavior in hybridoma and in ex vivo T lymphocytes.	18	−3.18
FLOTHO_PEDIATRIC_ALL_THERAPY_RESPONSE_DN	Down-regulated genes significantly associated with positive minimal residual disease (MRD) on day 46 after chemotherapy treatment of children with acute lymphoblastic leukemia (ALL).	29	−3.19
WONG_ENDMETRIUM_CANCER_DN	Genes down-regulated in cancer endometrium samples compared to the normal endometrium.	80	−3.194
SCHEIDEREIT_IKK_INTERACTING_PROTEINS	Genes encoding IkappaB kinase (IKK) interacting proteins.	58	−3.208
BORCZUK_MALIGNANT_MESOTHELIOMA_DN	Genes down-regulated in biphasic (mixed) vs epithelial subtypes of malignant peritoneal mesothelioma.	100	−3.212
RUIZ_TNC_TARGETS_UP	Genes up-regulated in T98G cells (glioblastoma) by TNC [GeneID = 3371].	149	−3.218
PEDERSEN_METASTASIS_BY_ERBB2_ISOFORM_3	Genes regulated in MCF7 cells (breast cancer) by expression of the truncated (611-CTF) form of ERBB2 [GeneID = 2064] at both 15 h and 60 h time points.	19	−3.238
GOUYER_TATI_TARGETS_UP	Genes up-regulated in constitutively invasive HT-29 5M21 cells (colon cancer) vs those expressing functionally inactive TATI [GeneID = 6690].	10	−3.324

TABLE 7-continued

Chemical Genetic Perturbations			
gs.id	gs.desc	gs.ngenes	fisherz
ZHAN_MULTIPLE_MYELOMA_DN	Genes most significantly down-regulated in multiple myeloma samples, compared to normal bone marrow plasma cells.	39	−3.337
PUIFFE_INVASION_INHIBITED_BY_ASCITES_DN	Genes down-regulated in OV-90 cells (ovarian cancer) exposed to ascites which inhibited invasion.	143	−3.342
TONKS_TARGETS_OF_RUNX1_RUNX1T1_FUSION_GRANULOCYTE_DN	Genes down-regulated in granulocytes by RUNX1-RUNX1T1 [GeneID = 861; 862] fusion.	16	−3.343
MARSON_FOXP3_TARGETS_UP	Genes up-regulated by FOXP3 [GeneID = 50943] in both ex vivo and hybridoma cells.	65	−3.343
TING_SILENCED_BY_DICER	Epigenetically silenced genes up-regulated in HCT116 cells (colon cancer) hypomorphic for DICER1 [GeneID = 23405].	30	−3.355
HINATA_NFKB_TARGETS_KERATINOCYTE_UP	Genes up-regulated in primary keratinocytes by expression of p50 (NFKB1) and p65 (RELA) [GeneID = 4790; 5970] components of NFKB.	90	−3.364
WORSCHECH_TUMOR_EVASION_AND_TOLEROGENICITY_DN	Selected genes with immunologic function which were reciprocally changed in evasion and tolerogenic tumor models.	13	−3.404
MARSON_FOXP3_TARGETS_STIMULATED_UP	Genes with promoters bound by FOXP3 [GeneID = 50943], dependent on it, and up-regulated in hybridoma cells stimulated by PMA [PubChem = 4792] and ionomycin [PubChem = 3733].	29	−3.414
BUCKANOVICH_T_LYMPHOCYTE_HOMING_ON_TUMOR_UP	Genes up-regulated in microdissected endothelial samples from ovarian cancer tumors with tumor-infiltrating lymphocytes (TIL) vs those without TILs.	23	−3.433
LU_TUMOR_ANGIOGENESIS_UP	Up-regulated genes of putative pathways stimulated in tumor endothelial cells by papillary serous ovarian epithelial tumor cells.	25	−3.444
BERENJENO_ROCK_SIGNALING_NOT_VIA_RHOA_DN	Genes down-regulated in NIH3T3 cells (fibroblasts) after treatment with Y27632 [PubChem = 123862], an inhibitor of ROCK proteins; the changes did not depend on expression of constitutively active (Q63L) form of RHOA [GeneID = 387].	48	−3.445
HOOI_ST7_TARGETS_UP	Genes up-regulated in PC-3 cells (prostate cancer) stably expressing ST7 [GeneID = 7982] off a plasmid vector.	91	−3.447
DING_LUNG_CANCER_EXPRESSION_BY_COPY_NUMBER	The lung adenocarcinoma TSP (tumor sequencing project) genes showing strong correlation between DNA copy number variation and gene expression.	100	−3.46
CHIANG_LIVER_CANCER_SUBCLASS_PROLIFERATION_UP	Top 200 marker genes up-regulated in the 'proliferation' subclass of hepatocellular carcinoma (HCC); characterized by increased proliferation, high levels of serum AFP [GeneID = 174], and chromosomal instability.	175	−3.481

TABLE 7-continued

Chemical Genetic Perturbations			
gs.id	gs.desc	gs.ngenes	fisherz
BASSO_CD40_SIGNALING_UP	Gene up-regulated by CD40 [GeneID = 958] signaling in Ramos cells (EBV negative Burkitt lymphoma).	97	−3.489
JISON_SICKLE_CELL_DISEASE_UP	Genes up-regulated in peripheral blood mononuclear cells (PBMC) from sickle cell disease patients compared to those from healthy subjects.	176	−3.5
PEDERSEN_TARGETS_OF_611CTF_ISOFORM_OF_ERBB2	Genes up-regulated in MCF7 cells (breast cancer) more than three-fold by the truncated form 611-CTF of ERBB2 [GeneID = 2064] and less than two-fold by the full-length ERBB2 [GeneID = 2064].	73	−3.533
WAMUNYOKOLI_OVARIAN_CANCER_LMP_DN	Genes down-regulated in mucinous ovarian carcinoma tumors of low malignant potential (LMP) compared to normal ovarian surface epithelium tissue.	192	−3.534
TONKS_TARGETS_OF_RUNX1_RUNX1T1_FUSION_MONOCYTE_DN	Genes down-regulated in monocytes by RUNX1-RUNX1T1 [GeneID = 861; 862] fusion.	53	−3.537
MARSON_FOXP3_TARGETS_DN	Genes down-regulated by FOXP3 [GeneID = 50943] in both ex vivo and hybridoma cells.	51	−3.54
NIKOLSKY_BREAST_CANCER_19Q13.1_AMPLICON	Genes within amplicon 19q13.1 identified in a copy number alterations study of 191 breast tumor samples.	21	−3.543
HESS_TARGETS_OF_HOXA9_AND_MEIS1_DN	Genes down-regulated in hematopoietic precursor cells conditionally expressing HOXA9 and MEIS1 [GeneID = 3205; 4211].	73	−3.554
GINESTIER_BREAST_CANCER_20Q13_AMPLIFICATION_DN	Genes down-regulated in metastatic breast cancer tumors having type 2 amplification in the 20q13 region; involves MYBL2, STK6 and ZNF217 [GeneID = 4605; 6790; 7764]	171	−3.565
LENAOUR_DENDRITIC_CELL_MATURATION_DN	Genes down-regulated during in vitro maturation of CD14+ [GeneID = 929] monocytes (day 0) into immature (day 7) and mature dendritic cells (day 14).	125	−3.586
LIU_SOX4_TARGETS_UP	Genes up-regulated in LNCaP cells (prostate cancer) by overexpression of SOX4 [GeneID = 6659] and down-regulated by its RNAi knockdown.	134	−3.611
VERHAAK_GLIOBLASTOMA_NEURAL	Genes correlated with neural type of glioblastoma multiforme tumors.	125	−3.632
ONO_AML1_TARGETS_UP	Genes up-regulated in CD4+ [GeneID = 920] T lymphocytes by expression of AML1 [GeneID = 861] off a viral vector.	24	−3.633
FERRANDO_TAL1_NEIGHBORS	Nearest neighbors of TAL1 [GeneID = 6886], based on the close agreement of their expression profiles with that of TAL1 in pediatric T cell acute lymphoblastic leukemia (T-ALL)	21	−3.645

TABLE 7-continued

Chemical Genetic Perturbations			
gs.id	gs.desc	gs.ngenes	fisherz
ZHENG_IL22_SIGNALING_UP	Genes up-regulated in ex-vivo colonic tissue after treatment with IL22 [GeneID = 50616].	53	−3.65
XU_RESPONSE_TO_TRETINOIN_AND_NSC682994_UP	Genes up-regulated synergistically in NB4 cells (acute promyelocytic leukemia, APL) by tretinoin and NSC682994 [PubChem = 444795; 388304].	17	−3.67
BROWNE_HCMV_INFECTION_4HR_UP	Genes up-regulated in primary fibroblast cell culture point after infection with HCMV (AD169 strain) at 4 h time point that were not up-regulated at the previous time point, 2 h.	54	−3.67
ZHAN_EARLY_DIFFERENTIATION_GENES_DN	B lymphocyte early differentiation genes (EDG): top genes down-regulated in tonsil B lymphocytes (TBC) compared to the tonsil plasma cells (TPC).	42	−3.679
GRANDVAUX_IRF3_TARGETS_UP	Genes up-regulated in Jurkat cells (T lymphocyte) by expression of a constitutively active form of IRF3 [GeneID = 3661].	15	−3.682
HADDAD_T_LYMPHOCYTE_AND_NK_PROGENITOR_DN	Genes down-regulated in hematopoietic progenitor cells (HPC) of T lymphocyte and NK (natural killer) lineage.	61	−3.692
BOYLAN_MULTIPLE_MYELOMA_D_DN	Genes down-regulated in group D of tumors arising from overexpression of BCL2L1 and MYC [GeneID = 598; 4609] in plasma cells.	76	−3.723
ONO_AML1_TARGETS_DN	Genes down-regulated in CD4+ [GeneID = 920] T lymphocytes by expression of AML1 [GeneID = 861] off a viral vector.	39	−3.73
MARZEC_IL2_SIGNALING_DN	Genes down-regulated by IL2 [GeneID = 3558] in cells derived from CD4+ [GeneID = 920] cutaneous T-cell lymphoma (CTCL).	34	−3.746
BILBAN_B_CLL_LPL_DN	Genes down-regulated in B-CLL (B-cell chronic leukemia) samples expressing high levels of LPL [GeneID = 4023] compared with those expressing low levels of the gene.	39	−3.749
RODRIGUES_THYROID_CARCINOMA_DN	Genes down-regulated in poorly differentiated thyroid carcinoma (PDTC) compared to anaplastic thyroid carcinoma (ATC).	76	−3.757
MARTINELLI_IMMATURE_NEUTROPHIL_DN	Neutrophil-specific genes down-regulated in comparison of immature with mature neutrophils.	11	−3.76
MORI_PLASMA_CELL_DN	Down-regulated genes in the B lymphocyte developmental signature, based on expression profiling of lymphomas from the Emu-myc transgenic mice: plasma cell.	33	−3.763
HOEBEKE_LYMPHOID_STEM_CELL_UP	Genes up-regulated in the common lymphoid progenitor (CLP, defined as CD34+CD38−CD7+ [GeneID = 947; 952; 924]) compared to a multipotent cord blood cell (defined as CD34+CD38+CD7−).	91	−3.767
STAMBOLSKY_TARGETS_OF_MUTATED_TP53_DN	Genes repressed in SKBR3 cells (breast cancer) by mutated TP53 [GeneID = 7157].	49	−3.768
DER_IFN_GAMMA_RESPONSE_UP	Genes up-regulated in HT1080 (fibrosarcoma) cells by treatment with interferon gamma for 6 h.	69	−3.782

TABLE 7-continued

Chemical Genetic Perturbations			
gs.id	gs.desc	gs.ngenes	fisherz
TAVOR_CEBPA_TARGETS_UP	Genes up-regulated in KCL22 cells (chronic myelogenous leukemia, CML, with BCR-ABL1 [GeneID = 613; 25] fusion) by expression of CEBPA [GeneID = 1050].	47	−3.824
FOSTER_TOLERANT_MACROPHAGE_UP	Class T (tolerizeable) genes: induced during the first LPS stimulation and either not re-induced or induced to a much lesser degree in tolerant macrophages.	149	−3.841
NEMETH_INFLAMMATORY_RESPONSE_LPS_UP	Genes up-regulated in RAW 264.7 cells (macrophage) 3 hr after stimulation with bacterial lipopolysaccharide (LPS).	83	−3.858
SEKI_INFLAMMATORY_RESPONSE_LPS_UP	Genes up-regulated in hepatic stellar cells after stimulation with bacterial lipopolysacharide (LPS).	75	−3.877
ANASTASSIOU_CANCER_MESENCHYMAL_TRANSITION_SIGNATURE	Genes in the ‘mesenchymal transition signature’ common to all invasive cancer types.	64	−3.881
GEISS_RESPONSE_TO_DSRNA_UP	Genes up-pregulated by dsRNA in GRE cells (glioma; no interferon system).	37	−3.905
DUTTA_APOPTOSIS_VIA_NFKB	NF-kB target genes involved in the regulation of programmed cell death.	33	−3.925
DACOSTA_UV_RESPONSE_VIA_ERCC3_TTD_DN	Genes exclusively down-regulated in fibroblasts expressing the TTD mutant form of ERCC3 [GeneID = 2071], after UVC irradiation.	84	−3.945
GAZDA_DIAMOND_BLACKFAN_ANEMIA_PROGENITOR_UP	Genes up-regulated in common hematopoietic progenitor cells isolated from bone marrow of patients with Diamond-Blackfan anemia (DBA) and mutated RPS19 [GeneID = 6223].	39	−3.999
GENTLES_LEUKEMIC_STEM_CELL_UP	Genes up-regulated in LSC (leukemic stem) cells compared to LPC (leukemia progenitor) cells from AML (acute myeloid leukemia) tumor samples.	29	−4.016
VALK_AML_CLUSTER_5	Top 40 genes from cluster 5 of acute myeloid leukemia (AML) expression profile; 96% of the samples are FAB M4 or M5 subtype.	32	−4.024
GAVIN_PDE3B_TARGETS	Genes changed in peripheral regulatory T lymphocytes that depend on PDE3B [GeneID = 5140].	21	−4.046
SU_THYMUS	Genes up-regulated specifically in human thymus.	20	−4.093
BENNETT_SYSTEMIC_LUPUS_ERYTHEMATOSUS	Genes significantly up-regulated in the blood mononuclear cells from patients with systemic lupus erythematosus compared to those from healthy persons.	28	−4.116
TAKEDA_TARGETS_OF_NUP98_HOXA9_FUSION_10D_UP	Genes up-regulated in CD34+ [GeneID = 947] hematopoetic cells by expression of NUP98-HOXA9 fusion [GeneID = 4928; 3205] off a retroviral vector at 10 days after transduction.	188	−4.128

TABLE 7-continued

Chemical Genetic Perturbations			
gs.id	gs.desc	gs.ngenes	fisherz
WUNDER_INFLAMMATORY_RESPONSE_AND_CHOLESTEROL_UP	Genes up-regulated in gastric mucosal tissue of mice on 2% cholesterol [PubChem = 5997] diet and infected with H. pylori vs those infected with H. pylori while on 0% cholesterol diet.	56	−4.145
IKEDA_MIR30_TARGETS_UP	Genes up-regulated in hypertrophic hearts (due to expression of constitutively active form of PPP3CA [GeneID = 5530]) and predicted to be targets of miR-30 microRNA.	115	−4.171
CHIANG_LIVER_CANCER_SUBCLASS_CTNNB1_DN	Top 200 marker genes down-regulated in the ‘CTNNB1’ subclass of hepatocellular carcinoma (HCC); characterized by activated CTNNB1 [GeneID = 1499].	168	−4.178
TAKEDA_TARGETS_OF_NUP98_HOXA9_FUSION_16D_UP	Genes up-regulated in CD34+ [GeneID = 947] hematopoetic cells by expression of NUP98-HOXA9 fusion [GeneID = 4928; 3205] off a retroviral vector at 16 days after transduction.	167	−4.179
NAKAJIMA_EOSINOPHIL	Top 30 increased eosinophil specific transcripts.	29	−4.191
WANG_CLIM2_TARGETS_DN	Genes down-regulated in MCF7 cells (breast cancer) engineered to conditionally express a dominant negative form of CLIM2 [GeneID = 8861] by a Tet Off system.	177	−4.192
MORI_LARGE_PRE_BII_LYMPHOCYTE_DN	Down-regulated genes in the B lymphocyte developmental signature, based on expression profiling of lymphomas from the Emu-myc transgenic mice: the Large Pre-BII stage.	58	−4.196
GRAHAM_CML_DIVIDING_VS_NORMAL_QUIESCENT_DN	Genes down-regulated in quiescent CD34+ [GeneID = 8842] cells isolated from peripheral blood of normal donors compared to the dividing cells from CML (chronic myeloid leukemia) patients.	93	−4.204
GRAHAM_NORMAL_QUIESCENT_VS_NORMAL_DIVIDING_UP	Genes up-regulated in quiescent vs dividing CD34+ [GeneID = 8842] cells isolated from peripheral blood of normal donors.	65	−4.215
KIM_GLIS2_TARGETS_UP	Partial list of genes up-regulated in the kidney of GLIS2 [GeneID = 84662] knockout mice compared to the wild type.	82	−4.247
LINDSTEDT_DENDRITIC_CELL_MATURATION_C	Maturation of monocyte-derived dendritic cells (DC) in response to inflammatory stimuli: genes up-regulated only at 48 hr after the stimulation (cluster C).	68	−4.252
GAURNIER_PSMD4_TARGETS	Inflammatory cytokines, chemokines and their cognate receptors up-regulated in THP-1 cells (monocyte) after treatment with PSMD4 [GeneID = 5710].	67	−4.255
RADAEVA_RESPONSE_TO_IFNA1_UP	Genes up-regulated in primary hepatocytes and Hep3B (hepatocyte) cells in response to IFNA [GeneID = 3439].	51	−4.259

TABLE 7-continued

Chemical Genetic Perturbations			
gs.id	gs.desc	gs.ngenes	fisherz
GAVIN_FOXP3_TARGETS_CLUSTER_P3	Cluster P3 of genes with similar expression profiles in peripheral T lymphocytes after FOXP3 [GeneID = 50943] loss of function (LOF).	154	−4.291
DAZARD_UV_RESPONSE_CLUSTER_G6	Cluster G6: genes increasingly down-regulated in NHEK cells (normal keratinocyte) after UV-B irradiation.	151	−4.326
CASORELLI_APL_SECONDARY_VS_DE_NOVO_UP	Genes up-regulated in secondary APL (acute promyelocytic leukemia) compared to the de novo tumors.	39	−4.348
BOHN_PRIMARY_IMMUNODEFICIENCY_SYNDROM_DN	Genes down-regulated in B lymphocytes from patients with primary immunodefiency syndrome.	39	−4.362
TIEN_INTESTINE_PROBIOTICS_2HR_DN	Genes down-regulated in Caco-2 cells (intestinal epithelium) after coculture with the probiotic bacteria L. casei for 2 h.	86	−4.38
SWEET_KRAS_TARGETS_UP	Genes upregulated in KRAS [GeneID = 3845] knockdown vs control in a human cell line.	81	−4.407
WORSCHECH_TUMOR_REJECTION_UP	Up-regulated genes defining rejection of mammary carcinoma (MMC) tumors.	55	−4.409
LEE_NAIVE_T_LYMPHOCYTE	Genes enriched in the naive circulating T lymphocytes compared to the earlier differentiation stages.	18	−4.445
DUNNE_TARGETS_OF_AML1_MTG8_FUSION_UP	Genes up-regulated in Kasumi-1 cells (acute myeloid leukaemia (AML) with the t(8; 21) translocation) after knockdown of the AML1 MTG8 fusion [GeneID = 861; 862] by RNAi.	48	−4.447
RAGHAVACHARI_PLATELET_SPECIFIC_GENES	Genes in this set correspond to the most abuntant transcripts that are also specific to platelets.	68	−4.459
RHEIN_ALL_GLUCOCORTICOID_THERAPY_UP	Genes up-regulated in ALL (acute lymphoblastic leukemia) blasts after 1 week of treatment with glucocorticoids.	75	−4.463
BILD_CTNNB1_ONCOGENIC_SIGNATURE	Genes selected in supervised analyses to discriminate cells expressing activated beta-catenin (CTNNB1) [GeneID = 1499] oncogene from control cells expressing GFP.	80	−4.496
KAMIKUBO_MYELOID_CEBPA_NETWORK	Network of differentially expressed myeloid genes centered around CEBPA [GeneID = 1050].	28	−4.511
FINETTI_BREAST_CANCER_KINOME_GREEN	Genes in the green cluster of protein kinases distinguishing between luminal A and basal breast cancer subtypes.	16	−4.52
EINAV_INTERFERON_SIGNATURE_IN_CANCER	A gene expression signature found in a subset of cancer patients suggestive of a deregulated immune or inflammatory response.	27	−4.532
SEITZ_NEOPLASTIC_TRANSFORMATION_BY_8P_DELETION_UP	Genes up-regulated in CT60/4 cells (breast cancer reverted to normal by transfer of chromosome 8p region) vs parental MDA-MB-231 cells (deleted chromosome 8p).	68	−4.55
TIEN_INTESTINE_PROBIOTICS_6HR_DN	Genes down-regulated in Caco-2 cells (intestinal epithelium) after coculture with the probiotic bacteria L. casei for 6 h.	161	−4.565

TABLE 7-continued

Chemical Genetic Perturbations			
gs.id	gs.desc	gs.ngenes	fisherz
SENGUPTA_EBNA1_ANTICORRELATED	Genes whose reduced expression in nasopharyngeal carinoma (NPC) correlated most with the increased expression of EBNA1 [GeneID = 3783774], a latent gene of Epstein-Barr virus (EBV).	161	−4.565
ZHU_CMV_8_HR_UP	Up-regulated at 8 h following infection of primary human foreskin fibroblasts with CMV	46	−4.566
KUROZUMI_RESPONSE_TO_ONCOCYTIC_VIRUS_AND_CYCLIC_RGD	Inflammatory cytokines and their receptors moduated in brain tumors in response to treatment with cyclic RGD peptide prior to the oncocytic virus therapy.	21	−4.577
MORI_PRE_BI_LYMPHOCYTE_DN	Down-regulated genes in the B lymphocyte developmental signature, based on expression profiling of lymphomas from the Emu-myc transgenic mice: the Pre-BI stage.	76	−4.592
WIELAND_UP_BY_HBV_INFECTION	Genes induced in the liver during hepatitis B (HBV) viral clearance in chimpanzees.	96	−4.641
LIU_VAV3_PROSTATE_CARCINOGENESIS_UP	Selected genes up-regulated in prostate tumors developed by transgenic mice overexpressing VAV3 [GeneID = 10451] in prostate epithelium.	88	−4.649
TONKS_TARGETS_OF_RUNX1_RUNX1T1_FUSION_HSC_DN	Genes down-regulated in normal hematopoietic progenitors by RUNX1-RUNX1T1 [GeneID = 861; 862] fusion.	181	−4.692
ODONNELL_TARGETS_OF_MYC_AND_TFRC_UP	Genes down-regulated in P493-6 cells (B lymphocyte, Burkitt's lymphoma model) by MYC [GeneID = 4609] and up-regulated by RNAi knockdown of TFRC [GeneID = 7037].	82	−4.732
KRASNOSELSKAYA_ILF3_TARGETS_UP	Up-regulated in GHOST(3)CXCR4 cells (osteosarcoma) upon ectopic expression of ILF3 [GeneID = 3609].	38	−4.82
GAVIN_FOXP3_TARGETS_CLUSTER_P4	Cluster P4 of genes with similar expression profiles in peripheral T lymphocytes after FOXP3 [GeneID = 50943] loss of function (LOF).	99	−4.832
DAZARD_RESPONSE_TO_UV_SCC_DN	Genes down-regulated in SCC12B2 cells (squamous cell carcinoma) by UV-B irradiation.	121	−4.833
LINDSTEDT_DENDRITIC_CELL_MATURATION_B	Maturation of monocyte-derived dendritic cells (DC) in response to inflammatory stimuli: genes up-regulated both at 8 hr and 48 hr after the stimulation (cluster B).	50	−4.835
MORI_MATURE_B_LYMPHOCYTE_UP	Up-regulated genes in the B lymphocyte developmental signature, based on expression profiling of lymphomas from the Emu-myc transgenic mice: the mature B	88	−4.87
NAKAYAMA_SOFT_TISSUE_TUMORS_PCA1_UP	Top 100 probe sets contributing to the positive side of the 1st principal component; predominantly associated with spindle cell and pleomorphic sarcoma samples.	70	−4.902

TABLE 7-continued

Chemical Genetic Perturbations			
gs.id	gs.desc	gs.ngenes	fisherz
ICHIBA_GRAFT_VERSUS_HOST_DISEASE_35D_UP	Hepatic graft versus host disease (GVHD), day 35: genes up-regulated in allogeneic vs syngeneic bone marrow transplant.	127	−4.903
BERTUCCI_MEDULLARY_VS_DUCTAL_BREAST_CANCER_UP	Genes up-regulated in medullary breast cancer (MBC) relative to ductal breast cancer (DBD).	197	−4.942
TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_LOBULAR_NORMAL_DN	Genes down-regulated in lobular carcinoma vs normal lobular breast cells.	73	−4.994
DER_IFN_BETA_RESPONSE_UP	Genes up-regulated in HT1080 (fibrosarcoma) cells by treatment with interferon beta for 6 h.	100	−5.009
CHAN_INTERFERON_PRODUCING_DENDRITIC_CELL	Genes up-regulated in spleen interferon-producing dendritic cells (IKDC) compared to plasmacytoid dendritic cells (PDC) and conventional dendritic cells (cDC).	10	−5.027
KIM_GERMINAL_CENTER_T_HELPER_UP	Genes up-regulated in germinal center T helper cells compared to other CD4+ [GeneID = 920] T lymphocyte types.	65	−5.041
HAHTOLA_SEZARY_SYNDROM_UP	Genes up-regulated in monocytes isolated from peripheral blood samples of Sezary syndrome patients compared to those from healthy normal donors.	96	−5.05
BOYLAN_MULTIPLE_MYELOMA_PCA1_UP	Top up-regulated genes from principal component 1 (PCA1) which captures variation between normal plasma cells and tumors arising from aberrant expression of BCL2L1 and MYC [GeneID = 598; 4609].	98	−5.089
GAVIN_FOXP3_TARGETS_CLUSTER_P7	Cluster P7 of genes with similar expression profiles in peripheral T lymphocytes after FOXP3 [GeneID = 50943] loss of function (LOF).	89	−5.099
ZHANG_INTERFERON_RESPONSE	Interferon-inducible genes up-regulated in A549 cells (lung cancer) infected with a respiratory syncytial virus (RSV) that had its NS1 [GeneID = 1494468] gene knocked down by RNAi.	22	−5.1
LU_IL4_SIGNALING	Genes up-regulated in peripheral B lymphocytes after incubation with IL4 [GeneID = 3565] for 4 h.	91	−5.159
HAHTOLA_CTCL_PATHOGENESIS	Differentially expressed genes relevant to pathogenesis of cutaneous T cell lymphoma (CTCL).	16	−5.221
DIAZ_CHRONIC_MEYLOGENOUS_LEUKEMIA_DN	Genes down-regulated in CD34+ [GeneID = 947] cells isolated from bone marrow of CML (chronic myelogenous leukemia) patients, compared to those from normal donors.	106	−5.234
ONO_FOXP3_TARGETS_DN	Genes down-regulated in CD4+ [GeneID = 920] T lymphocytes transduced with FOXP3 [GeneID = 50943].	41	−5.235
TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_DUCTAL_NORMAL_UP	Genes up-regulated in lobular carcinoma vs normal ductal breast cells.	68	−5.314

TABLE 7-continued

Chemical Genetic Perturbations			
gs.id	gs.desc	gs.ngenes	fisherz
ZHENG_FOXP3_TARGETS_IN_T_LYMPHOCYTE_DN	Genes with promoters bound by FOXP3 [GeneID = 50943] and which are down-regulated only in mature (peripheral blood) regulatory CD4+ [GeneID = 920] T lymphocytes.	36	−5.329
IKEDA_MIR133_TARGETS_UP	Genes up-regulated in hypertrophic hearts (due to expression of constitutively active form of PPP3CA [GeneID = 5530]) and predicted to be targets of miR-133 microRNA.	43	−5.33
HUANG_GATA2_TARGETS_UP	Genes up-regulated in G1ME cells (megakaryocyte/erythroid progenitor lacking GATA1 [GeneID = 2623]) upon knockdown of GATA2 [GeneID = 2624] by RNAi.	141	−5.337
VECCHI_GASTRIC_CANCER_ADVANCED_VS_EARLY_UP	Up-regulated genes distinguishing between two subtypes of gastric cancer: advanced (AGC) and early (EGC).	172	−5.379
BOWIE_RESPONSE_TO_TAMOXIFEN	Genes up-regulated by tamoxifen [PubChem = 5376] in HMEC-E6 cells (mammary epithelial cells damaged by expression of HPV-16 E6 [GeneID = 1489078]).	18	−5.393
TAKEDA_TARGETS_OF_NUP98_HOXA9_FUSION_3D_UP	Genes up-regulated in CD34+ [GeneID = 947] hematopoetic cells by expression of NUP98-HOXA9 fusion [GeneID = 4928; 3205] off a retroviral vector at 3 days after transduction.	178	−5.46
SMIRNOV_RESPONSE_TO_IR_6HR_DN	Genes down-regulated in B lymphocytes at 6 h after exprosure to 10 Gy dose of ionizing radiation.	113	−5.489
WINTER_HYPOXIA_DN	Genes down-regulated in head and neck tumor samples which clustered around known hypoxia genes.	52	−5.505
HAHTOLA_SEZARY_SYNDROM_DN	Genes down-regulated in monocytes isolated from peripheral blood samples of Sezary syndrome patients compared to those from healthy normal donors.	38	−5.539
ROSS_AML_WITH_CBFB_MYH11_FUSION	Top 63 probe sets for pediatric acute myeloid leukemia (AML) subtype inv(16); has a CBFB-MYH11 fusion [GeneID = 865; 4629].	50	−5.565
WATANABE_ULCERATIVE_COLITIS_WITH_CANCER_DN	Genes down-regulated in non-neoplastic rectal mucosa samples from patients having cancer associated with ulcerative collitis, compared to those who did not have the cancer.	14	−5.575
BOSCO_ALLERGEN_INDUCED_TH2_ASSOCIATED_MODULE	Genes representing a co-expression network in atopic CD4 [GeneID = 920] T lymphocyte responses.	143	−5.688
DER_IFN_ALPHA_RESPONSE_UP	Genes up-regulated in HT1080 cells (fibrosarcoma) by treatment with interferon alpha for 6 h.	73	−5.851
DAUER_STAT3_TARGETS_DN	Top 50 genes down-regulated in A549 cells (lung cancer) expressing STAT3 [GeneID = 6774] off an adenovirus vector.	49	−5.852

TABLE 7-continued

Chemical Genetic Perturbations			
gs.id	gs.desc	gs.ngenes	fisherz
UROSEVIC_RESPONSE_TO_IMIQUIMOD	Interferon cluster genes up-regulated in skin tumors treated with imiquimod [PubChem = 57469].	23	−5.914
ICHIBA_GRAFT_VERSUS_HOST_DISEASE_D7_UP	Hepatic graft versus host disease (GVHD), day 7: up-regulated in allogeneic vs syngeneic bone marrow transplant.	101	−6.048
LIANG_SILENCED_BY_METHYLATION_2	Genes up-regulated in T24 cells (bladder carcinoma) after treatment with decitabine (5-aza-2'-deoxycytidine) [PubChem = 451668].	51	−6.1
ZHAN_MULTIPLE_MYELOMA_LB_DN	Top 50 down-regulated genes in cluster LB of multiple myeloma samples belonging to the low bone disease group.	39	−6.128
SMIRNOV_RESPONSE_TO_IR_2HR_DN	Genes down-regulated in B lymphocytes at 2 h after exprosure to 10 Gy dose of ionizing radiation.	55	−6.131
PASQUALUCCI_LYMPHOMA_BY_GC_STAGE_DN	Genes down-regulated in post-GC, BCL6 [GeneID = 604] dependent B cell non-Hodgkin's lymphoma (B-NHL) vs MYC [GeneID = 4609] driven pre-GC lymphoma.	161	−6.177
TARTE_PLASMA_CELL_VS_B_LYMPHOCYTE_DN	Genes down-regulated in plasma cells compared with B lymphocytes.	38	−6.207
BOWIE_RESPONSE_TO_EXTRACELLULAR_MATRIX	Genes up-regulated by growing HMEC-E6 cells (mammary epithelial cells damaged by expression of HPV-16 E6 [GeneID = 1489078]) in extracellular matrix (ECM).	17	−6.209
SMIRNOV_CIRCULATING_ENDOTHELIOCYTES_IN_CANCER_UP	Genes up-regulated in circulating endothelial cells (CEC) from cancer patients compared to those from healthy donors.	155	−6.213
GRANDVAUX_IFN_RESPONSE_NOT_VIA_IRF3	Genes up-regulated in Jurkat cells (T lymphocyte) by IFN1@, and IFNB1 [GeneID = 3438; 3456] but not by overexpression of a constitutively active form of IRF3 [GeneID = 3661].	13	−6.218
KUROZUMI_RESPONSE_TO_ONCOCYTIC_VIRUS	Inflammatory cytokines and their receptors modulated in brain tumors after treatment with an oncocytic virus, a potential anticancer therapy.	43	−6.354
TAKEDA_TARGETS_OF_NUP98_HOXA9_FUSION_16D_DN	Genes down-regulated in CD34+ [GeneID = 947] hematopoetic cells by expression of NUP98-HOXA9 fusion [GeneID = 4928; 3205] off a retroviral vector at 16 days after transduction.	130	−6.365
BROWN_MYELOID_CELL_DEVELOPMENT_UP	Genes defining differentiation potential of the bipotential myeloid cell line FDB.	158	−6.503
TAKEDA_TARGETS_OF_NUP98_HOXA9_FUSION_10D_DN	Genes down-regulated in CD34+ [GeneID = 947] hematopoetic cells by expression of NUP98-HOXA9 fusion [GeneID = 4928; 3205] off a retroviral vector at 10 days after transduction.	139	−6.513
VILIMAS_NOTCH1_TARGETS_UP	Genes up-regulated in bone marrow progenitors by constitutively active NOTCH1 [GeneID = 4851].	51	−6.594

TABLE 7-continued

Chemical Genetic Perturbations			
gs.id	gs.desc	gs.ngenes	fisherz
SANA_RESPONSE_TO_IFNG_UP	Genes up-regulated in five primary endothelial cell types (lung, aortic, iliac, dermal, and colon) by IFNG [GeneID = 3458].	75	−6.598
BOSCO_INTERFERON_INDUCED_ANTIVIRAL_MODULE	Genes representing interferon-induced antiviral module in sputum during asthma exacerbations.	75	−6.911
BOSCO_TH1_CYTOTOXIC_MODULE	Genes representing Th1/cytotoxic module in sputum during asthma exacerbations.	107	−6.961
CHUNG_BLISTER_CYTOTOXICITY_DN	Genes down-regulated in blister cells from patients with adverse drug reactions (ADR).	44	−7.116
FARMER_BREAST_CANCER_CLUSTER_1	Cluster 1: interferon, T and B lymphocyte genes clustered together across breast cancer samples.	42	−7.281
MOSERLE_IFNA_RESPONSE	Top 50 genes up-regulated in ovarian cancer progenitor cells (also known as side population, SP, cells) in response to interferon alpha (IFNA).	30	−7.46
ZHENG_FOXP3_TARGETS_IN_THYMUS_UP	Genes with promoters bound by FOXP3 [GeneID = 50943] and which are up-regulated only in developing (located in the thymus) regulatory CD4+ [GeneID = 920] T lymphocytes.	187	−7.485
ALTEMEIER_RESPONSE_TO_LPS_WITH_MECHANICAL_VENTILATION	Genes up-regulated in lung tissue upon LPS aspiration with mechanical ventilation (MV) compared to control (PBS aspiration without MV).	117	−7.638
FLECHNER_BIOPSY_KIDNEY_TRANSPLANT_REJECTED_VS_OK_UP	Genes up-regulated in kidney biopsies from patients with acute transplant rejection compared to the biopsies from patients with well functioning kidneys more than 1-year post transplant.	83	−7.809
HECKER_IFNB1_TARGETS	Genes transcriptionally modulated in the blood of multiple sclerosis patients in response to subcutaneous treatment with recombinant IFNB1 [GeneID = 3456].	92	−7.956
TAKEDA_TARGETS_OF_NUP98_HOXA9_FUSION_8D_DN	Genes down-regulated in CD34+ [GeneID = 947] hematopoetic cells by expression of NUP98-HOXA9 fusion [GeneID = 4928; 3205] off a retroviral vector at 8 days after transduction.	198	−9.058
BROWNE_INTERFERON_RESPONSIVE_GENES	Genes up-regulated in primary fibroblast culture after treatment with interferon alpha for 6 h.	67	−9.279
LEE_EARLY_T_LYMPHOCYTE_DN	Genes down-regulated at early stages of progenitor T lymphocyte maturation compared to the late stages.	55	−9.974
LEE_DIFFERENTIATING_T_LYMPHOCYTE	Genes enriched at every T lymphocyte differentiation stage compared to the early passage fetal thymic stromal cultures (TSC).	192	−10.833

[0081] Table 8 shows the Number of Data Sets

TABLE 8

Number of Data Sets

Age-group	No. of datasets	No. of samples
11-12	13	47
12-13	9	35
13-14	8	29
14-15	8	27
15-16	10	27
16-17	10	51
17-18	14	74
18-19	17	56
19-20	13	33
20-21	14	40
21-22	16	49
22-23	17	43
23-24	14	49
24-25	19	61
25-26	19	51
26-27	18	55
27-28	17	61
28-29	13	53
29-30	15	50
30-31	18	49
31-32	17	48
32-33	17	60
33-34	18	73
34-35	17	64
35-36	20	73
36-37	21	78
37-38	20	57
38-39	17	46
39-40	20	65
40-41	22	94
41-42	18	79
42-43	19	68
43-44	17	69
44-45	23	63
45-46	20	63
46-47	17	55
47-48	20	67
48-49	22	82
49-50	26	89

[0082] Thus, in certain embodiments, as shown herein, samples are sorted by age, and then hierarchical clustering can be performed to identify sets of genes that are most correlated with older and thus deleterious effects, and younger. These genes are candidate biomarkers for reproductive status.

[0083] In certain embodiments, predictors of reproductive success can be verified as follows: The genes most associated with pregnancy outcome (both positive and negative) can be tested on a separate sample set prior to IVF treatment to verify predictive power of the gene set. Two approaches can be used: one with individual qRT-PCR primers for each gene, and a second with the entire set of primers.

[0084] In a non-limiting Example, the diagnostic application can be implemented as follows: A blood sample from a patient is collected, RT-PCR performed using the diagnostic primer set, and the profile results matched using Pearson correlation to the reproductive age profile. For example, a 32-year old patient might have a blood profile that best matches that of a 38 year old, indicating that she is reproductively aged relative to her chronological age, and thus might not want to delay childbearing much longer. Under current guidelines, older patients might be denied IVF or other ART treatment, but the tests herein could show that a chronologically 43-year old patient might best match that of an average 38 year old, and thus would still be a viable candidate for IVF or other assisted reproductive techniques. Thus, a diagnostic that easily and accurately correlates a key set of biomarkers with reproductive capacity can be useful for several applications.

[0085] In certain embodiments, the methods herein may be directed to the measure or determination of oocyte quality based on a combination of two or more any of the markers discussed herein. For example, a determination of characteristics of two or more of the genes or pathways discussed herein can, in certain embodiments, provide a more accurate set of data regarding a subject's oocyte quality and thus her likelihood of conceiving, than would be the case with only a single gene or pathway.

[0086] In certain embodiments, the technology herein contemplates methods or kits that comprise a binding molecule, for example, a binding composition that specifically binds to any protein produced by a biomarker gene discussed herein and may be conjugated to another molecule, for example, an enzyme or a molecule that provides a visual indication of oocyte quality of some other detected characteristic of the cell.

[0087] Although the present technology has been described in relation to particular embodiments thereof, these embodiments and examples are merely exemplary and not intended to be limiting. Many other variations and modifications and other uses will become apparent to those skilled in the art. The present technology should, therefore, not be limited by the specific disclosure herein, and may be embodied in other forms not explicitly described here, without departing from the spirit thereof

I claim:

1. A method of determining the quality of an oocyte in the body of a human without disturbing or destroying the oocyte, the method comprising:

(a) obtaining a cell sample from a female subject, wherein the cell sample does not include the oocyte;

(b) measuring a characteristic of a gene or pathway indicative of oocyte quality in the cell sample; and

(c) predicting or determining the quality of the oocyte based on the characteristic of the gene or pathway.

2. The method of claim **1**, wherein step (b) comprises measuring a gene expression value of the cell sample through an RT-PCR assay, an ELISA assay or a colorometric test.

3. The method of claim **2**, wherein step (b) further comprises comparing the measured gene expression values to a known gene expression value of an oocyte with Pearson correlation, or by matching the measured gene expression values to a known gene expression profile from a library of genes as markers of oocyte quality.

4. The method of claim **1**, wherein the cell sample is extracted from blood, skin, hair, urine, saliva, sweat or vaginal secretion.

5. The method of claim **1**, wherein the gene or pathway is chosen from SERPINB2 (serpin peptidase inhibitor, clade B, member 2, also known as PAI-2); IGFIR (insulin-like growth factor 1 receptor); PIK3CB (phosphoinositide-3-kinase, catalytic, beta polypeptide), IRS2 (insulin receptor substrate 2), HSPA8, HSPD1, HSP60, TGF-β and insulin/IGF-1 (IIS) signaling pathway.

6. A method of predicting the quality of an oocyte in the body of a mammal without disturbing or destroying the oocyte, the method comprising the steps of:

(a) obtaining a cell sample from the mammal, wherein the cell sample does not include the oocyte;

(b) conducting an RT-PCR assay or an ELISA assay on the cell sample using a primer for a gene known to be correlated with aging, and comparing the result with a known value obtained from a library of genes known to be correlated with decreased oocyte quality; and

(d) predicting the likelihood of oocyte viability based on (b).

7. A kit for predicting a woman's oocyte quality without the need for disturbing or destroying an oocyte, the kit comprising:

(a) a collection container for collecting a cell sample obtained from the woman's body, wherein the cell sample does not include an oocyte;

(b) a testing assay comprising RT-PCR or ELISA, wherein the testing assay measures a characteristic of a gene, pathway or transcriptional profile characteristic of the cell sample, and wherein the characteristic indicates the likely quality of an oocyte; and

(c) a visual indicator visible to the woman, the visual indicator providing information regarding the predicted quality of the oocyte.

8. The kit of claim **7**, wherein the gene or pathway is chosen from SERPINB2 (serpin peptidase inhibitor, clade B, member 2, also known as PAI-2); IGFIR (insulin-like growth factor 1 receptor); PIK3CB (phosphoinositide-3-kinase, catalytic, beta polypeptide), IRS2 (insulin receptor substrate 2), HSPA8, HSPD1, HSP60, TGF-β and insulin/IGF-1 (IIS) signaling pathway.

9. A method of producing a library of genes as markers of oocyte quality, the method comprising the steps of:

(a) gathering expression data from cells of women in a particular age range;

(b) calculating an average gene expression for each gene at each age in the range by averaging the expression for that gene in a window of a given period of time;

(c) comparing the average gene expression of (b) to an "age vector" to indicate which genes change most with age; and

(d) calculating a FisherZ score, thereby identifying the genes at the tail ends of the distribution as indicators of biological age.

10. The method of claim **9**, wherein for one or more of the genes identified in step (d), the Spearmann correlation of the average gene expression to the age vector was determined, and then sorted by the FisherZ score.

11. The method of claim **10**, wherein the genes for which a score above 2 (top 5%) was calculated were added to a set of significantly changed age-dependent genes to comprise the library of genes.

12. The method of claim **9**, further comprising any of the following steps: correlating a test gene with a quantitative and measured characteristic of oocyte quality; listing the correlation in the library; comparing a measured characteristic of a gene provided by a patient with that listed in the library; and determining the quality of an oocyte of a patient based on the comparison.

13. A method of developing a reproductive aging gene expression profile and one or more candidate markers of reproductive success or oocyte quality, the method comprising the steps of claim **9**.

14. The method of claim **1**, wherein the characteristic measured in the cell sample is assigned a score that conveys the expected oocyte viability.

15. The method of claim **14**, wherein the score conveys the expected oocyte viability compared to an average for women of the same age as the female subject.

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专利名称(译)	卵母细胞质量的生物标志物		
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摘要(译)

本技术涉及卵母细胞质量和卵母细胞质量下降的生物标志物，以及与这些生物标志物有关的方法，包括确定卵母细胞质量的方法，用于其的试剂盒，以及文库，生殖衰老基因表达谱和谱集 与相同的信息。