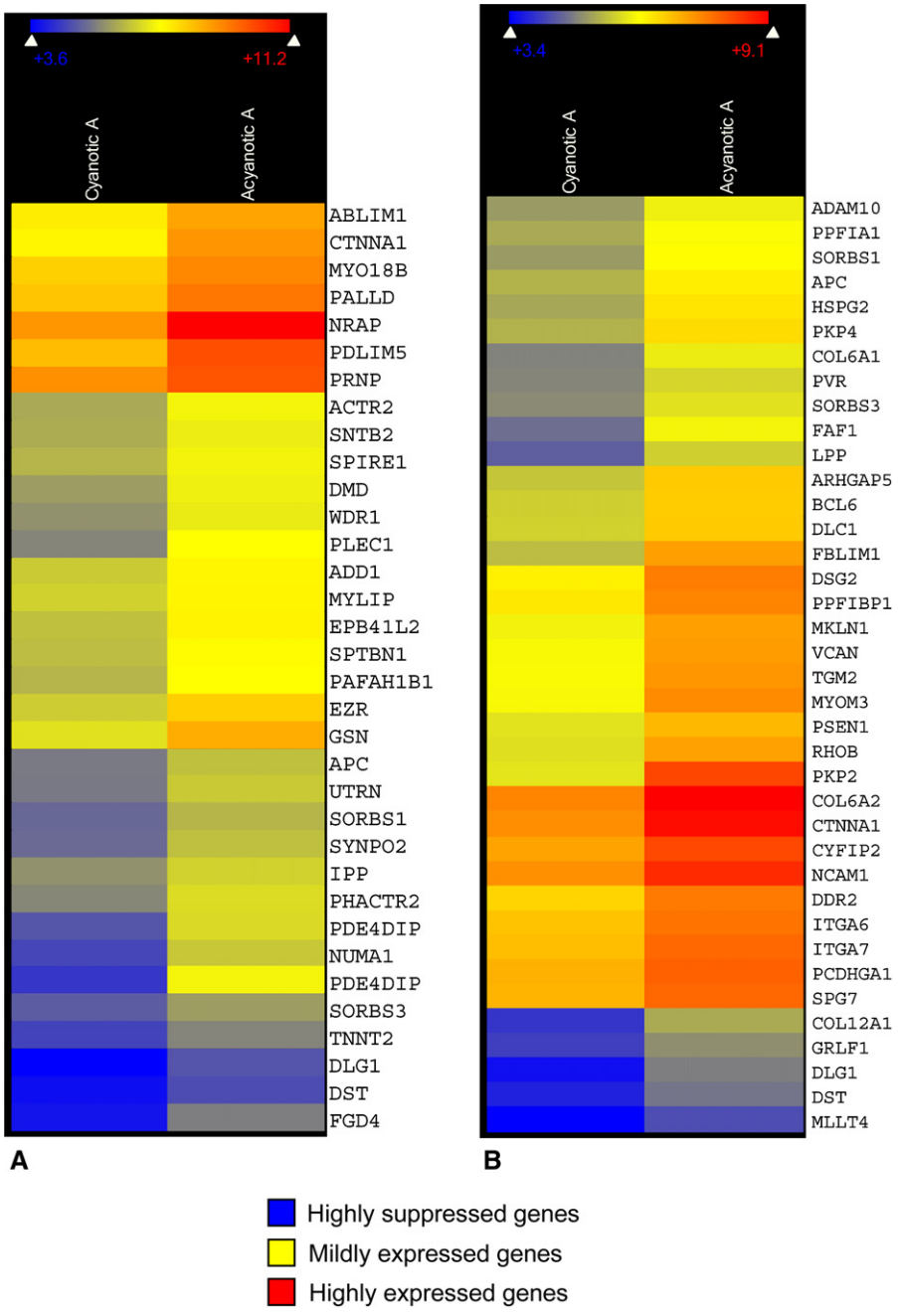

FIGURE E1. Heat Map illustrating the expression levels of contractile machinery genes. A, Cytoskeletal cluster. B, Cell adhesion cluster. Hierarchical clustering has been performed with ArrayStar software. A 3-color scale was used to illustrate expression level differences, with blue indicating low expression values, yellow indicating intermediately expressed genes, and red representing highly expressed genes.

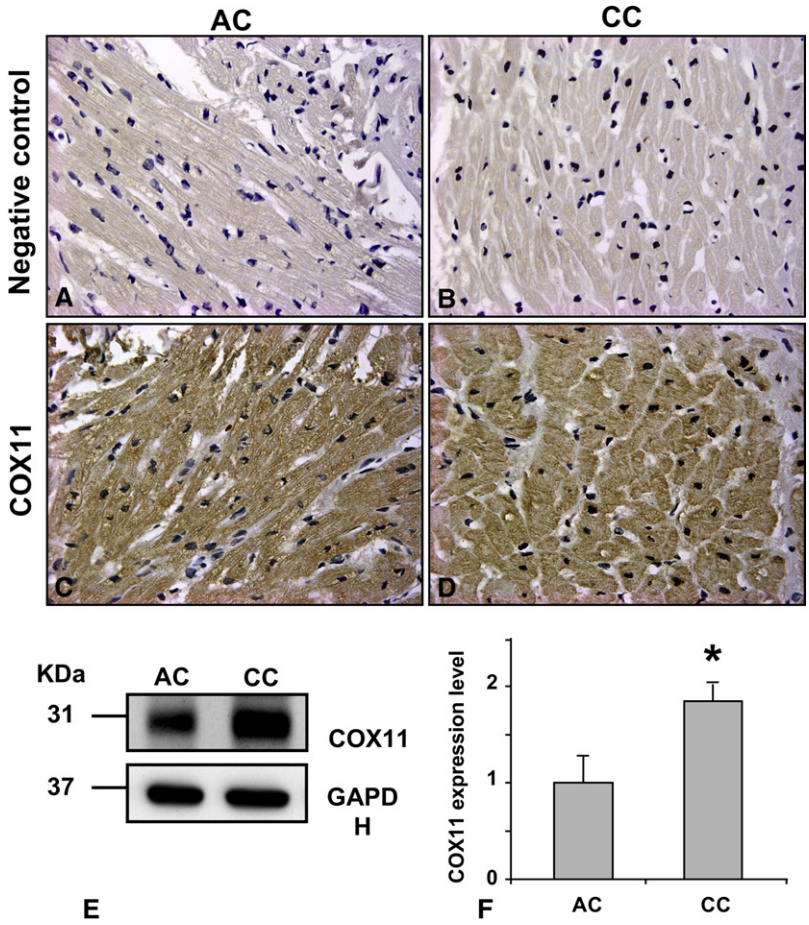

FIGURE E2. COX 11 protein immunostaining of paraffin-embedded heart tissue from acyanotic (C) and cyanotic (D) patients using COX11-specific antibody. 3,3′-Diaminobenzidine (DAB) staining (brown) reveals expression of COX11 in both tissues but not in control tissue (A and B). E and F, COX11 protein expression level in myocardium of acyanotic *(AC)* and cyanotic *(CC)* patients. Biopsy specimens were lysed to isolate protein content and Western blotting analysis was performed, probing for COX11 and glyceraldehyde-3-phosphate dehydrogenase *(GAPDH)*. COX11 was significantly upregulated in cyanotic biopsy specimens compared with that seen in acyanotic specimens. COX11 bands were normalized to glyceraldehude-3-phosphate dehydrogenase *(GAPDH)* levels. Data are presented as means ± standard errors of the mean. $*P < .05$ (n = 6).

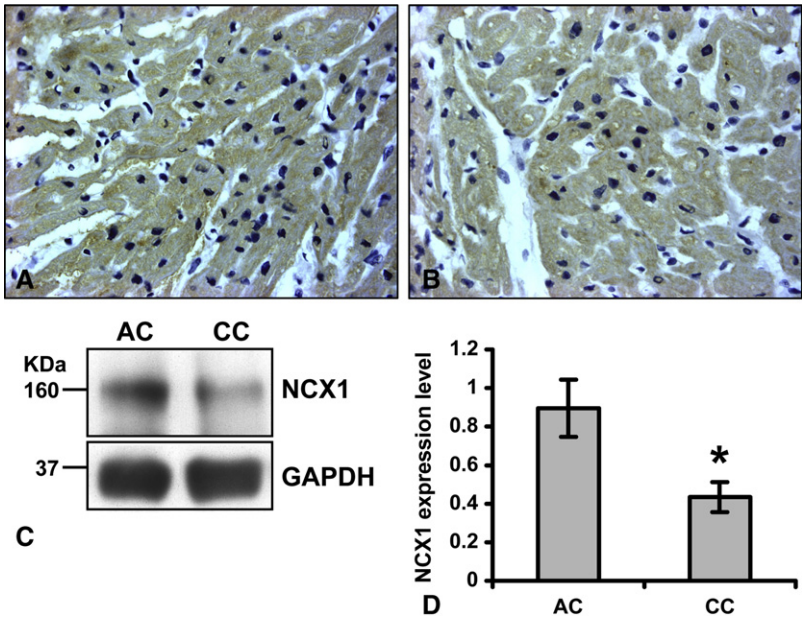

FIGURE E3. A and B, NCX1 protein immunostaining of paraffin-embedded heart tissue from acyanotic (A) and cyanotic (B) patients using NCX1-specific antibody. 3,3′-Diaminobenzidine (DAB) staining (brown) reveals expression of NCX1 in both tissues. C and D, NCX1 protein expression level in myocardium of acyanotic *(AC)* and cyanotic *(CC)* patients. Biopsy specimens were lysed to isolate protein content, and Western blotting analysis was performed, probing for NCX1 and glyceraldehude-3-phosphate dehydrogenase *(GAPDH)*. NCX1 was significantly downregulated in cyanotic biopsy specimens compared with acyanotic specimens. NCX1 bands were normalized to GAPDH levels. Data are presented as means ± standard errors of the mean. $*P < .05$ ($n = 4$).

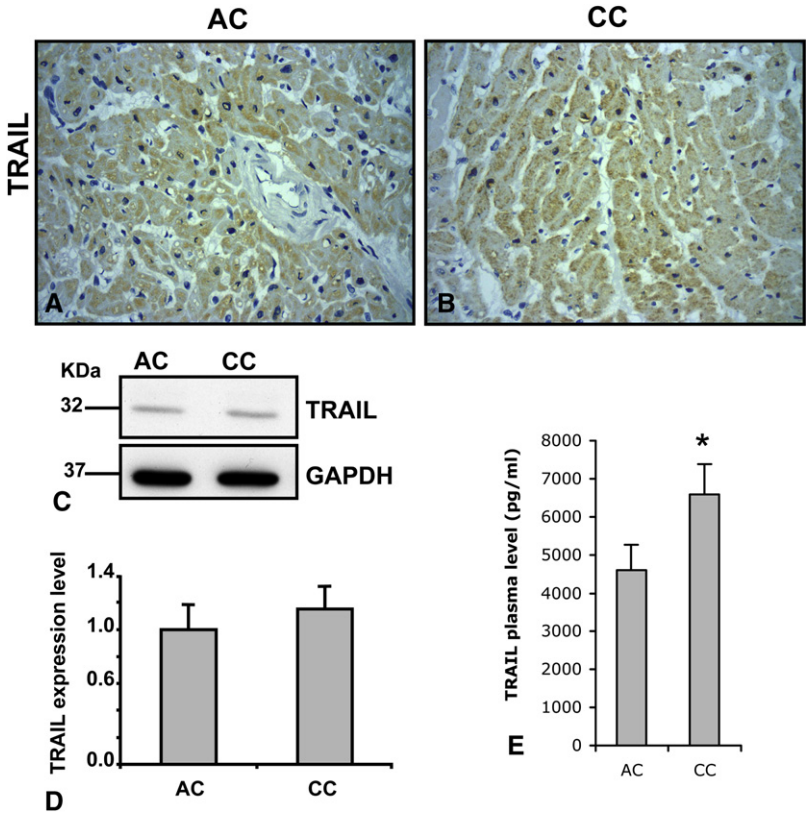

FIGURE E4. TRAIL protein immunostaining of paraffin-embedded heart tissue from acyanotic (A) and cyanotic (B) patients using TRAIL-specific antibody. 3,3′-Diaminobenzidine (DAB) staining (brown) reveals expression of TRAIL in both tissues. C and D, TRAIL protein expression level in myocardium of acyanotic *(AC)* and cyanotic *(CC)* patients. Biopsy specimens were lysed to isolate protein content, and Western blotting analysis was performed, probing for TRAIL and glyceraldehude-3-phosphate dehydrogenase (GAPDH). TRAIL was not upregulated in cyanotic biopsy specimens compared with acyanotic specimens. TRAIL bands were normalized to GAPDH levels. Data are presented as means ± standard errors of the mean (n = 6). E, Plasma levels of TRAIL in cyanotic *(CC)* and acyanotic *(AC)* children. *Solid bars* represent median protein concentration in preoperative plasma samples (in picograms per milliliter). A significantly enhanced TRAIL protein expression was observed in cyanotic samples. Data are presented as means ± standard errors of the mean. *$P < .05$ (n = 9–11).

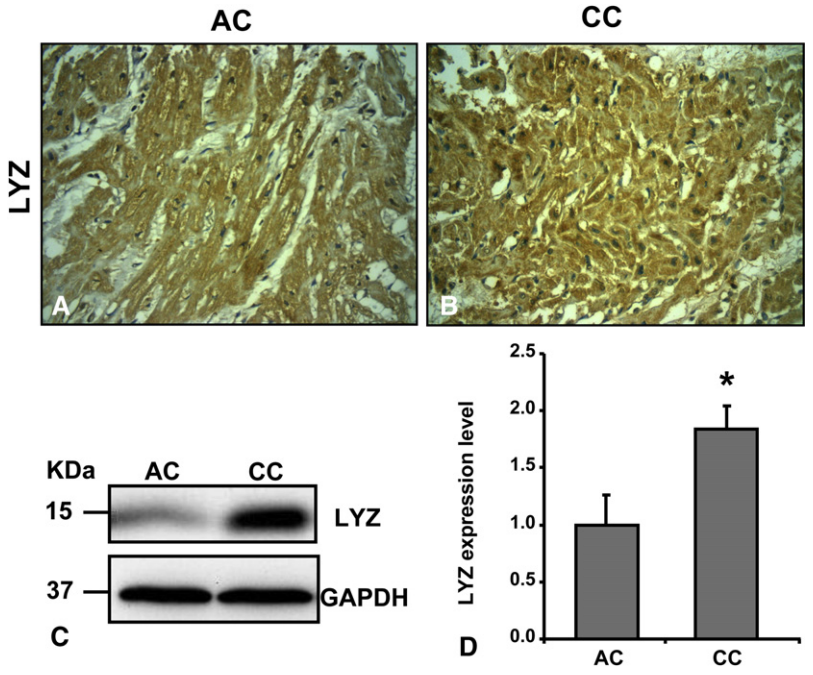

FIGURE E5. LYZ protein immunostaining of paraffin-embedded heart tissue from acyanotic (A) and cyanotic (B) patients using LYZ-specific antibody. 3,3′-Diaminobenzidine (DAB) staining (brown) reveals expression of LYZ in both tissues. C and D, LYZ protein expression level in myocardium of acyanotic *(AC)* and cyanotic *(CC)* patients. Biopsy specimens were lysed to isolate protein content, and Western blotting analysis was performed, probing for LYZ and glyceraldehude-3-phosphate dehydrogenase (GAPDH). LYZ was significantly upregulated in cyanotic biopsy specimens compared with acyanotic specimens. LYZ bands were normalized to GAPDH levels. Data are presented as means ± standard errors of the mean. $*P < .05$ (n = 6).

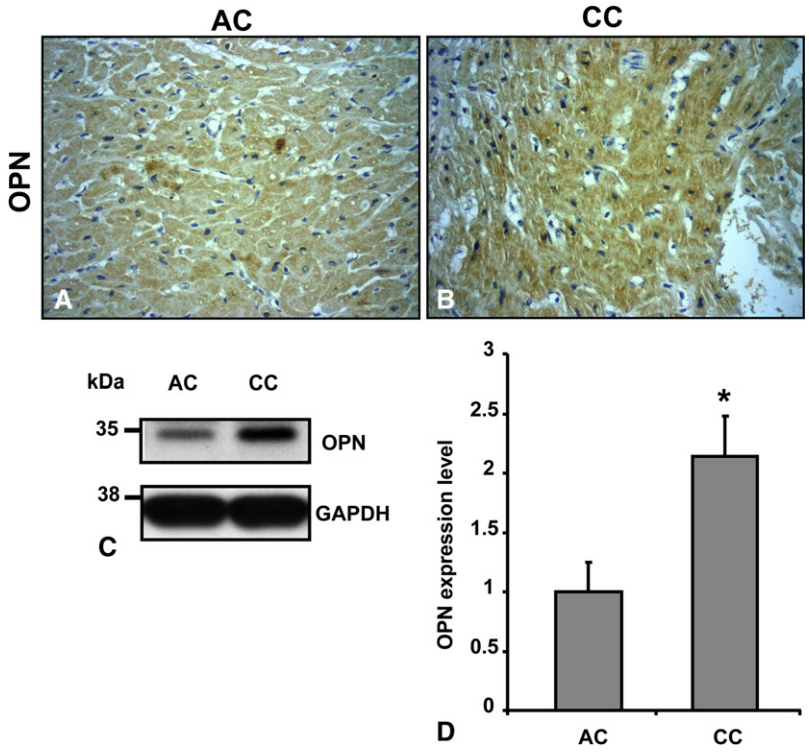

FIGURE E6. OPN protein immunostaining of paraffin-embedded heart tissue from acyanotic (A) and cyanotic (B) patients using OPN-specific antibody. 3,3′-Diaminobenzidine (DAB) staining (brown) reveals expression of OPN in both tissues. C and D, OPN protein expression level in myocardium of acyanotic *(AC)* and cyanotic *(CC)* patients. Biopsy specimens were lysed to isolate protein content, and Western blotting analysis was performed, probing for OPN and glyceraldehude-3-phosphate dehydrogenase *(GAPDH)*. OPN was significantly upregulated in cyanotic biopsy specimens compared with acyanotic specimens. OPN bands were normalized to GAPDH levels. Data are presented as means ± standard errors of the mean. *$P < .05$ (n = 6).

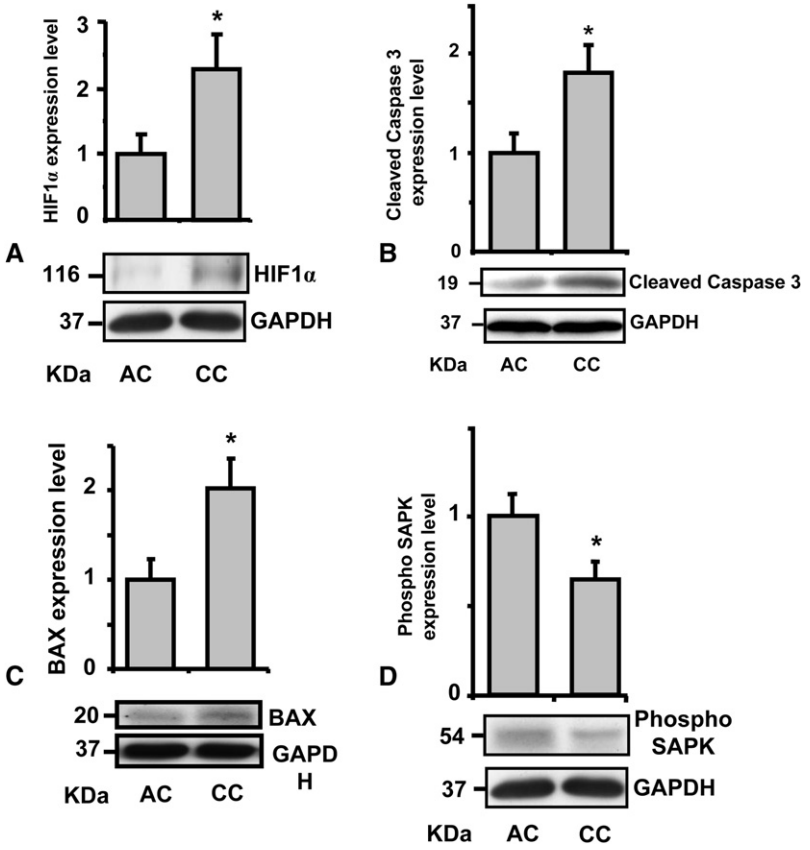

FIGURE E7. Functional validation of hypoxia-inducible factor 1 alpha, cleaved caspase-3, BAX, and phospho-SAPK protein levels in myocardium of acyanotic *(AC)* and cyanotic *(CC)* patients. Biopsy specimens were lysed to isolate protein content, and Western blotting analysis was performed, probing for HIF1α (A), cleaved caspase-3 (B), BAX (C), phospho-SAPK (D) and glyceraldehude-3-phosphate dehydrogenase *(GAPDH)*. HIF1α, cleaved caspase-3, and BAX were significantly upregulated in cyanotic compared with acyanotic biopsy specimens. Phospho-SAPK was significantly downregulated in cyanotic compared with acyanotic biopsy specimens. HIF1α, cleaved caspase-3, BAX, and phospho-SAPK bands were normalized to GAPDH levels. Data are presented as means $\pm$ standard errors of the mean. $^*P < .05$ (n = 6).

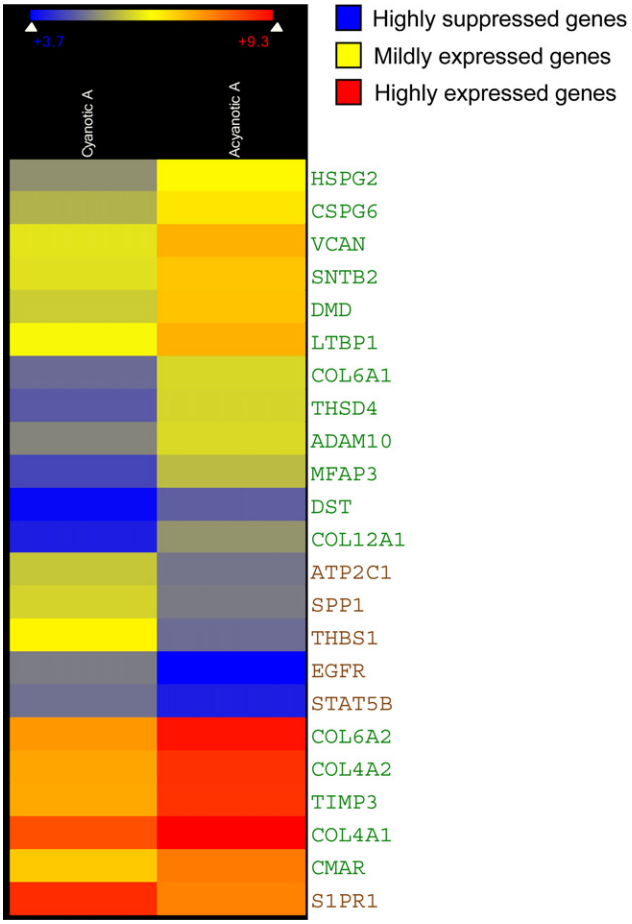

FIGURE E8. Heat Map illustrating the expression levels of the genes implicated in extracellular matrix. *Gene symbols in brown* represent transcripts that were upregulated in cyanotic patients, whereas *gene symbols in green* represent genes downregulated by means of cyanosis. Hierarchical clustering has been performed with ArrayStar software. A 3-color scale was used to illustrate expression level differences, with blue indicating low expression values, yellow indicating intermediately expressed genes, and red representing highly expressed genes.

TABLE E1. Genes exhibiting 1.8-fold or greater expression change in ventricular biopsy specimens of cyanotic versus acyanotic children (upregulated genes)

Gene title	Symbol	Fold	*P* value	Gene ID
Lysozyme	*LYZ*	5.103 up	.0112	4069
Protein phosphatase 1, catalytic subunit, beta isoform	*PPP1CB*	3.849 up	.00559	5500
Early growth response 1	*EGR1*	3.498 up	.0213	1958
RAP2C, member of RAS oncogene family	*RAP2C*	3.364 up	.0063	57826
Thrombospondin 1	*THBS1*	3.285 up	.0265	7057
Nipsnap homolog 3A	*NIPSNAP3A*	3.055 up	.0229	25934
Ubiquitin B	*UBB*	3.008 up	.00998	7314
NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 5, 13 kd	*NDUFA5*	2.984 up	.0187	4698
EF-hand calcium binding domain 2	*EFCAB2*	2.946 up	.0214	84288
Lactamase, beta 2	*LACTB2*	2.815 up	.0139	51110
Hypothetical protein DKFZp564O0523	*DKFZP564O0523*	2.769 up	.0101	84060
Beta-1,3-N-acetylgalactosaminyltransferase 1	*B3GALNT1*	2.748 up	.0355	8706
Actin-binding rho-activating protein	*ABRA*	2.711 up	.0112	137735
Eukaryotic translation initiation factor 4E	*EIF4E*	2.706 up	.0133	1977
KIAA0776	*KIAA0776*	2.694 up	.0372	23376
CDNA FLJ32626 fis, clone SYNOV1000045		2.692 up	.0448	
CDNA clone IMAGE:4820809		2.685 up	.0113	
COBW domain containing 1	*CBWD1*	2.681 up	.0212	150472
Zinc finger E-box binding homeobox 2	*ZEB2*	2.671 up	.0129	9839
Proteasome maturation protein	*POMP*	2.639 up	.0107	51371
Integral membrane protein 2A	*ITM2A*	2.631 up	.016	9452
Succinate-CoA ligase, GDP-forming, beta subunit	*SUCLG2*	2.629 up	.0443	8801
Ubiquitin-specific peptidase 28	*USP28*	2.612 up	.0124	57646
Lysophospholipase I	*LYPLA1*	2.583 up	.0109	10434
KIAA0372	*KIAA0372*	2.579 up	.0139	9652
Epidermal growth factor receptor (v-erb-b oncogene)	*EGFR*	2.553 up	.0102	1956
Family with sequence similarity 76, member B	*FAM76B*	2.552 up	.0473	143684
FYVE, RhoGEF and PH domain containing 4	*FGD4*	2.543 up	.0211	121512
Hypothetical protein FLJ13611	FLJ13611	2.534 up	.011	80006
COX11 homolog, cytochrome c oxidase assembly protein	*COX11*	2.530 up	.00736	1353
Hypothetical LOC401397	*LOC401397*	2.484 up	.0167	401397
Kelch-like 20	*KLHL20*	2.435 up	.0142	27252
FCF1 small subunit (SSU) processome component homolog	*FCF1*	2.431 up	.0163	93487
Calmodulin 3 (phosphorylase kinase, delta)	*CALM3*	2.431 up	.0205	808
Family with sequence similarity 73, member A	*FAM73A*	2.431 up	.0228	374986
CDNA clone IMAGE:5299642		2.407 up	.0432	
Proteasome (prosome, macropain) 26S subunit, ATPase, 2	*PSMC2*	2.368 up	.0135	5701
Tumor necrosis factor (ligand) superfamily, member 10	*TNFSF10*	2.363 up	.0456	8743
CDNA clone IMAGE:5267328		2.361 up	.016	
Fibroblast growth factor 7	*FGF7*	2.338 up	.0381	2252
EGF-containing fibulin-like extracellular matrix protein 1	*EFEMP1*	2.311 up	.0422	2202
Cytochrome P450, family 51, subfamily A, polypeptide 1	*CYP51A1*	2.276 up	.0113	1595
Protein phosphatase 1B (formerly 2C), magnesium-dependent, beta isoform	*PPM1B*	2.264 up	.00902	5495
Lumican	*LUM*	2.260 up	.025	4060
Serpin peptidase inhibitor, clade B (ovalbumin), member 9	*SERPINB9*	2.260 up	.0391	5272
Amyotrophic lateral sclerosis 2 (juvenile)	*ALS2*	2.256 up	.0112	57679
Rab geranylgeranyltransferase, beta subunit	*RABGGTB*	2.255 up	.00808	5876
Ubiquitin-conjugating enzyme E2D 1 (UBC4/5 homolog, yeast)	*UBE2D1*	2.243 up	.0281	7321
Hypothetical protein LOC386597	*LOC386597*	2.233 up	.0107	386597
Tubulin, epsilon 1	*TUBE1*	2.213 up	.0182	51175
COMM domain containing 8	*COMMD8*	2.204 up	.016	54951
Erythropoietin receptor	*EPOR*	2.190 up	.016	2057

TABLE E1. Continued

Gene title	Symbol	Fold	*P* value	Gene ID
Adaptor-related protein complex 1, sigma 2 subunit	*AP1S2*	2.186 up	.0454	8905
Striatin, calmodulin binding protein 3	*STRN3*	2.186 up	.0243	29966
Phosphatase and actin regulator 2	*PHACTR2*	2.181 up	.0203	9749
Zinc-binding alcohol dehydrogenase, domain containing 1	*ZADH1*	2.162 up	.0266	145482
Tetraspanin 12	*TSPAN12*	2.159 up	.036	23554
Transcribed locus		2.157 up	.0121	
Ankyrin 1, erythrocytic	*ANK1*	2.148 up	.0298	286
Adenosine kinase	*ADK*	2.143 up	.0113	132
Chromosome 18 open reading frame 55	*C18orf55*	2.140 up	.0169	29090
Solute carrier family 22, member 25	*UST6*	2.130 up	.0242	387601
Glycine amidinotransferase (L-arginine:glycine amidinotransferase)	*GATM*	2.130 up	.0343	2628
Arginyltransferase 1	*ATE1*	2.130 up	.0291	11101
Serum deprivation response (phosphatidylserine-binding protein)	*SDPR*	2.128 up	.0391	8436
Calponin 3, acidic	*CNN3*	2.125 up	.0407	1266
Hypothetical protein LOC285708	*LOC285708*	2.110 up	.0154	285708
		2.106 up	.0368	
Chromosome 10 open reading frame 110	*C10orf110*	2.102 up	.0482	55853
Stomatin (EPB72)–like 1	*STOML1*	2.099 up	.011	9399
Heterogeneous nuclear ribonucleoprotein H1 (H)	*HNRPH1*	2.092 up	.0254	3187
Solute carrier family 2 (facilitated glucose transporter), member 13	*SLC2A13*	2.092 up	.0237	114134
Pallidin homolog (mouse)	*PLDN*	2.087 up	.0138	26258
Trinucleotide repeat containing 6B	*TNRC6B*	2.079 up	.0357	23112
Ubiquitin-conjugating enzyme E2D 1 (UBC4/5 homolog, yeast)	*UBE2D1*	2.075 up	.0342	7321
Nuclear factor of activated T cells, cytoplasmic, calcineurin-dependent 2 interacting protein	*NFATC2IP*	2.075 up	.0136	84901
Syntaxin-binding protein 3	*STXBP3*	2.073 up	.0115	6814
Transcription elongation factor B (SIII), polypeptide 1 (15 kd, elongin C)	*TCEB1*	2.071 up	.0243	6921
EF-hand domain family, member A2	*EFHA2*	2.064 up	.0142	286097
Lyrm7 homolog (mouse)	*LYRM7*	2.052 up	.0481	90624
ARP3 actin-related protein 3 homolog (yeast)	*ACTR3*	2.048 up	.0298	10096
Short coiled-coil protein	*SCOC*	2.047 up	.0213	60592
Ribosomal protein L15///similar to ribosomal protein L15	*RPL15*	2.047 up	.0212	728088
Hypothetical LOC441642	*LOC441642*	2.046 up	.0159	441642
CDNA clone IMAGE:4794011		2.043 up	.0237	
Homo sapiens, clone IMAGE:4480721, mRNA		2.043 up	.0448	
Chromosome 8 open reading frame 4	*C8orf4*	2.042 up	.0388	56892
Polymerase (RNA) II (DNA directed) polypeptide K, 7.0 kd	*POLR2K*	2.042 up	.0176	5440
PRO1268 protein	*PRO1268*	2.040 up	.0237	29006
Sarcolemma-associated protein	*SLMAP*	2.038 up	.0169	7871
Glyceraldehyde-3-phosphate dehydrogenase–like 19///similar to glyceraldehyde-3-phosphate dehydrogenase (GAPDH)	*GAPDHL19/// LOC732268*	2.036 up	.0153	442262/// 732268
Eukaryotic translation initiation factor 4E	*EIF4E*	2.033 up	.0264	1977
WD repeat and SOCS box–containing 2	*WSB2*	2.031 up	.0371	55884
CDNA FLJ32691 fis, clone TESTI2000221		2.022 up	.00678	
COMM domain containing 10	*COMMD10*	2.020 up	.0196	51397
Zinc finger protein, X-linked	*ZFX*	2.014 up	.0112	7543
Ribosomal protein L23a pseudogene 7	*RPL23AP7*	2.011 up	.0106	118433
SH3 domain–binding glutamic acid–rich protein like	*SH3BGRL*	2.004 up	.0214	6451
p21 (CDKN1A)–activated kinase 2	*PAK2*	2.002 up	.0114	5062
Copine IV	*CPNE4*	2.000 up	.0172	131034

TABLE E1. Continued

Gene title	Symbol	Fold	*P* value	Gene ID
NLR family, pyrin domain containing 1	*NLRP1*	1.999 up	.0303	22861
X-prolyl aminopeptidase (aminopeptidase P) 3, putative	*XPNPEP3*	1.998 up	.0379	63929
Ribosomal protein L37a	*RPL37A*	1.997 up	.035	6168
Protein tyrosine phosphatase type IVA, member 1	*PTP4A1*	1.989 up	.0175	7803
CDNA FLJ30565 fis, clone BRAWH2005008		1.988 up	.0169	
Basic leucine zipper nuclear factor 1 (JEM-1)	*BLZF1*	1.987 up	.0405	8548
Karyopherin alpha 2 (RAG cohort 1, importin alpha 1)	*KPNA2*	1.986 up	.0242	3838
Transcribed locus		1.982 up	.0437	
Insulin-like growth factor binding protein 7	*IGFBP7*	1.981 up	.0404	3490
Centrosomal protein 170 kd	*CEP170*	1.977 up	.0458	9859
B-cell chronic lymphocytic leukemia/lymphoma 10	*BCL10*	1.964 up	.0237	8915
Poly(A) binding protein interacting protein 1	*PAIP1*	1.962 up	.0347	10605
Mediterranean fever	*MEFV*	1.957 up	.0137	4210
Similar to 60S ribosomal protein L35	*LOC643653*	1.957 up	.0222	643653
Annexin A7	*ANXA7*	1.955 up	.012	310
Folliculin	*FLCN*	1.952 up	.0255	201163
Septin 7	*SEPT7*	1.948 up	.0483	989
TM2 domain containing 1	*TM2D1*	1.945 up	.0157	83941
CD8a molecule	*CD8A*	1.942 up	.0186	925
Secreted phosphoprotein 1 (osteopontin, bone sialoprotein I, early T-lymphocyte activation 1)	*SPP1*	1.941 up	.0115	6696
Selenoprotein P, plasma, 1	*SEPP1*	1.937 up	.0206	6414
Transmembrane protein 123	*TMEM123*	1.935 up	.011	114908
CDNA clone IMAGE:5273964		1.935 up	.0483	
Src kinase–associated phosphoprotein 2	*SKAP2*	1.934 up	.0406	8935
Cyclin-dependent kinase inhibitor 2C (p18, inhibits CDK4)	*CDKN2C*	1.933 up	.0125	1031
		1.927 up	.024	
Transcribed locus		1.926 up	.0221	
Spermidine/spermine N1-acetyltransferase 1	*SAT1*	1.925 up	.0162	6303
THAP domain containing 5	*THAP5*	1.924 up	.0113	168451
Actin-like 6A	*ACTL6A*	1.923 up	.0182	86
SMT3 suppressor of mif two 3 homolog 1 (*S cerevisiae*)	*SUMO1*	1.922 up	.00972	7341
MAD2 mitotic arrest deficient–like 1 (yeast)	*MAD2L1*	1.922 up	.0114	4085
MANSC domain containing 1	*MANSC1*	1.921 up	.0232	54682
Endothelial differentiation, sphingolipid G protein–coupled receptor, 1	*EDG1*	1.915 up	.0242	1901
Wingless-type MMTV integration site family, member 6	*WNT6*	1.914 up	.0387	7475
Carboxypeptidase E	*CPE*	1.914 up	.0236	1363
Transcribed locus		1.909 up	.0315	
Interleukin 33	*IL33*	1.901 up	.0456	90865
OMA1 homolog, zinc metallopeptidase (*S cerevisiae*)	*OMA1*	1.899 up	.0263	115209
Calreticulin	*CALR*	1.898 up	.0443	811
Clone 114 tumor rejection antigen		1.895 up	.0405	
Solute carrier family 12 (sodium/potassium/chloride transporters), member 2	*SLC12A2*	1.893 up	.0158	6558
		1.893 up	.0217	
EF-hand domain family, member A1	*EFHA1*	1.892 up	.0243	221154
Ribosomal protein L38	*RPL38*	1.890 up	.0253	6169
Homo sapiens, clone IMAGE:5440917, mRNA		1.889 up	.0374	
Yip1 domain family, member 4	*YIPF4*	1.887 up	.0146	84272
Guanine nucleotide binding protein (G protein), gamma 10///hypothetical protein LOC552891	*GNG10///LOC552891*	1.884 up	.0224	2790///552891
Peroxisomal biogenesis factor 7	*PEX7*	1.881 up	.0135	5191
Signal transducer and activator of transcription 5B	*STAT5B*	1.881 up	.0195	6777
3′(2′), 5′-Bisphosphate nucleotidase 1	*BPNT1*	1.876 up	.0281	10380

TABLE E1. Continued

Gene title	Symbol	Fold	*P* value	Gene ID
Inhibitor of DNA binding 2, dominant negative helix-loop-helix protein///inhibitor of DNA binding 2B, dominant negative helix-loop-helix protein	*ID2///ID2B*	1.875 up	.0448	3398///84099
Eukaryotic translation initiation factor 1A, X-linked	*EIF1AX*	1.866 up	.0317	1964
OTU domain containing 6B	*OTUD6B*	1.865 up	.0325	51633
RAB12, member RAS oncogene family	*RAB12*	1.864 up	.024	201475
Late cornified envelope 1E	*LCE1E*	1.862 up	.00469	353135
RNA binding motif (RNP1, RRM) protein 3	*RBM3*	1.862 up	.0125	5935
Thiopurine S-methyltransferase	*TPMT*	1.858 up	.0232	7172
Mitochondrial ribosomal protein L50	*MRPL50*	1.856 up	.0389	54534
Hydroxysteroid dehydrogenase like 2	*HSDL2*	1.853 up	.0352	84263
CDNA clone IMAGE:4830861		1.849 up	.0181	
Methylenetetrahydrofolate dehydrogenase ($NADP^+$ dependent) 2–like	*MTHFD2L*	1.847 up	.0293	441024
Jagged 1 (Alagille syndrome)	*JAG1*	1.847 up	.0319	182
		1.847 up	.0111	
Myozenin 2	*MYOZ2*	1.843 up	.032	51778
Family with sequence similarity 115, member A	*FAM115A*	1.842 up	.0368	9747
Cysteine and histidine–rich domain (CHORD)–containing 1	*CHORDC1*	1.841 up	.0109	26973
ATPase, Ca^{++} transporting, type 2C, member 1	*ATP2C1*	1.841 up	.0435	27032
Copine IV	*CPNE4*	1.841 up	.0149	131034
NLR family, pyrin domain containing 1	*NLRP1*	1.834 up	.0241	22861
Basic transcription factor 3	*BTF3*	1.834 up	.0104	689
Golgi transport 1 homolog B *(S cerevisiae)*	*GOLT1B*	1.833 up	.0312	51026
Transcribed locus		1.832 up	.0171	
Hypothetical protein FLJ22222	*FLJ22222*	1.829 up	.0115	79701
Dihydropyrimidine dehydrogenase	*DPYD*	1.826 up	.0395	1806
Chromosome 5 open reading frame 33	*C5orf33*	1.825 up	.0109	133686
Epidermal growth factor receptor (erythroblastic leukemia viral (v-erb-b) oncogene homolog, avian)	*EGFR*	1.824 up	.0152	1956
Jerky homolog–like (mouse)	*JRKL*	1.824 up	.0387	8690
Sphingomyelin synthase 1	*SGMS1*	1.824 up	.0109	259230
Zinc finger protein 654	*ZNF654*	1.823 up	.0367	55279
Transcribed locus (serine/threonine kinase 17B) (apoptosis-inducing)	*STK17B*	1.819 up	.0236	
Gap junction protein, beta 4, 30.3 kd	*GJB4*	1.814 up	.032	127534
Sp3 transcription factor	*SP3*	1.813 up	.0124	6670
Leucine-rich repeat containing 25	*LRRC25*	1.813 up	.028	126364
Transmembrane and tetratricopeptide repeat containing 3	*TMTC3*	1.813 up	.0209	160418
Nucleosome assembly protein 1–like 1	*NAP1L1*	1.812 up	.0266	4673
Fibrinogen-like 2	*FGL2*	1.812 up	.0191	10875
Zinc finger protein 552	*ZNF552*	1.808 up	.0125	79818
Hypothetical gene supported by AK023501	FLJ13439	1.808 up	.0206	399876
Full-length insert cDNA clone ZD82B02		1.807 up	.0197	
Mesenchymal stem cell protein DSC96		1.805 up	.034	
Apolipoprotein B mRNA editing enzyme, catalytic polypeptide–like 3G	*APOBEC3G*	1.803 up	.0176	60489
Eukaryotic translation initiation factor 1A, X-linked///eukaryotic translation initiation factor 1A pseudogene 1	*EIF1AP1///EIF1AX*	1.803 up	.0298	1964///280661
GULP, engulfment adaptor PTB domain containing 1	*GULP1*	1.801 up	.0437	51454

TABLE E2. Genes exhibiting 1.8-fold or greater expression change in ventricular biopsy specimens of cyanotic versus acyanotic children (downregulated genes)

Gene title	Symbol	Fold	*P* value	Gene ID
Oxoglutarate (alpha-ketoglutarate) dehydrogenase (lipoamide)	*OGDH*	6.227 down	.0218	4967
Nebulin-related anchoring protein	*NRAP*	5.878 down	.0154	4892
Plakophilin 2	*PKP2*	5.058 down	.0124	5318
Mitofusin 2	*MFN2*	4.453 down	.0216	9927
Glucosamine (N-acetyl)-6-sulfatase	*GNS*	4.439 down	.0136	2799
AHNAK nucleoprotein	*AHNAK*	4.417 down	.011	79026
Solute carrier family 8 (sodium/calcium exchanger), member 1	*SLC8A1*	4.284 down	.00929	6546
Coatomer protein complex, subunit alpha	*COPA*	4.221 down	.0222	1314
Cardiomyopathy-associated 5	*CMYA5*	4.185 down	.0118	202333
Phosphodiesterase 4D–interacting protein (myomegalin)	*PDE4DIP*	3.875 down	.0114	9659
Nuclear mitotic apparatus protein 1	*NUMA1*	3.768 down	.0116	4926
SET domain containing 5	*SETD5*	3.652 down	.0124	55209
Forkhead box O3	*FOXO3*	3.606 down	.0271	2309
Solute carrier family 39 (zinc transporter), member 14	*SLC39A14*	3.589 down	.0199	23516
Plectin 1, intermediate filament binding protein 500 kd	*PLEC1*	3.542 down	.0228	5339
Zinc finger protein 36, C3H type–like 2	*ZFP36L2*	3.495 down	.0347	678
Homeodomain interacting protein kinase 3	*HIPK3*	3.485 down	.0121	10114
Chromosome 19 open reading frame 6	*C19orf6*	3.457 down	.0113	91304
Filamin binding LIM protein 1	*FBLIM1*	3.429 down	.0314	54751
Interleukin 6 signal transducer (gp130, oncostatin M receptor)	*IL6ST*	3.397 down	.0114	3572
YTH domain family, member 3	*YTHDF3*	3.396 down	.0146	253943
DEAD (Asp-Glu-Ala-Asp) box polypeptide 42	*DDX42*	3.385 down	.0124	11325
AF4/FMR2 family, member 4	*AFF4*	3.372 down	.0136	27125
DEAH (Asp-Glu-Ala-His) box polypeptide 9	*DHX9*	3.350 down	.011	1660
WD repeat domain 68	*WDR68*	3.246 down	.0131	10238
ATPase type 13A3	*ATP13A3*	3.204 down	.00672	79572
Sec61 alpha 1 subunit *(S cerevisiae)*	*SEC61A1*	3.183 down	.0175	29927
Chaperone, ABC1 activity of bc1 complex homolog	*CABC1*	3.182 down	.0219	56997
Signal-induced proliferation-associated 1 like 2	*SIPA1L2*	3.164 down	.0183	57568
Gelsolin (amyloidosis, Finnish type)	*GSN*	3.155 down	.0125	2934
A kinase (PRKA) anchor protein 6	*AKAP6*	3.123 down	.00579	9472
Peroxisome proliferator–activated receptor alpha	*PPARA*	3.107 down	.03	5465
PDZ and LIM domain 5	*PDLIM5*	3.101 down	.0125	10611
Tetratricopeptide repeat domain 3	*TTC3*	3.088 down	.0109	7267
Sp1 transcription factor	*SP1*	3.080 down	.0146	6667
Trafficking protein, kinesin binding 1	*TRAK1*	3.074 down	.0224	22906
Inositol polyphosphate-5-phosphatase, 40 kd	*INPP5A*	3.072 down	.0145	3632
Phosphodiesterase 3A, cGMP-inhibited	*PDE3A*	3.069 down	.00601	5139
Suppressor of Ty 16 homolog *(S cerevisiae)*	*SUPT16H*	3.057 down	.0187	11198
Nucleoporin 62 kd	*NUP62*	3.054 down	.0161	23636
Proteasome (prosome, macropain) activator subunit 4	*PSME4*	3.047 down	.0113	23198
FYVE, RhoGEF and PH domain containing 4	*FGD4*	3.043 down	.00671	121512
ELKS/RAB6-interacting/CAST family member 1	*ERC1*	3.033 down	.0219	23085
PRP6 pre-mRNA processing factor 6 homolog	*PRPF6*	3.029 down	.0125	24148
Collagen, type VI, alpha 1	*COL6A1*	3.000 down	.00664	1291
Myotubularin related protein 1	*MTMR1*	2.983 down	.00996	8776
CDNA FLJ38472 fis, clone FEBRA2022148		2.981 down	.0437	
Transformation/transcription domain–associated protein	*TRRAP*	2.973 down	.0136	8295
Ubiquitination factor E4B (UFD2 homolog, yeast)	*UBE4B*	2.970 down	.0116	10277
Myeloid cell leukemia sequence 1 (BCL2-related)	*MCL1*	2.967 down	.0218	4170
ATPase, Ca^{++} transporting, plasma membrane 4	*ATP2B4*	2.957 down	.0121	493

TABLE E2. Continued

Gene title	Symbol	Fold	*P* value	Gene ID
Filamin A interacting protein 1	*FILIP1*	2.950 down	.0066	27145
Ribosomal protein S23	*RPS23*	2.945 down	.0156	6228
Carboxypeptidase D	*CPD*	2.937 down	.0137	1362
F-box and WD repeat domain containing 11	*FBXW11*	2.925 down	.0112	23291
LAG1 homolog, ceramide synthase 6	*LASS6*	2.914 down	.0366	253782
SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 2	*SMARCA2*	2.905 down	.0111	6595
Sorbin and SH3 domain containing 1	*SORBS1*	2.894 down	.0176	10580
Guanine nucleotide binding protein (G protein), alpha 13	*GNA13*	2.865 down	.0241	10672
SCY1-like 2 *(S cerevisiae)*	*SCYL2*	2.852 down	.0119	55681
Fas (TNFRSF6) associated factor 1	*FAF1*	2.819 down	.0139	11124
Ezrin	*EZR*	2.818 down	.0295	7430
Zinc finger protein 672	*ZNF672*	2.814 down	.0144	79894
GATA binding protein 4	*GATA4*	2.805 down	.0212	2626
Phosphodiesterase 1C, calmodulin-dependent 70 kd	*PDE1C*	2.803 down	.0109	5137
Fibroblast growth factor receptor 1	*FGFR1*	2.800 down	.0132	2260
Muscleblind-like 2 *(Drosophila)*	*MBNL2*	2.780 down	.0244	10150
Ubiquitin protein ligase E3 component n-recognin 1	*UBR1*	2.771 down	.0253	197131
Sodium channel, voltage-gated, type VII, alpha	*SCN7A*	2.769 down	.0113	6332
Collagen, type VI, alpha 2	*COL6A2*	2.742 down	.0112	1292
Myelin basic protein	*MBP*	2.742 down	.0103	4155
Eukaryotic translation initiation factor 4 gamma, 1	*EIF4G1*	2.740 down	.0125	1981
Exportin 7	*XPO7*	2.736 down	.0112	23039
Endothelial PAS domain protein 1	*EPAS1*	2.725 down	.0232	2034
MutS homolog 6 *(E coli)*	*MSH6*	2.724 down	.0129	2956
Transforming growth factor, beta receptor II (70/80 kd)	*TGFBR2*	2.715 down	.0124	7048
Gamma-aminobutyric acid (GABA) A receptor, beta 1	*GABRB1*	2.710 down	.0311	2560
Pleckstrin homology–like domain, family B, member 2	*PHLDB2*	2.706 down	.0174	90102
Catenin (cadherin-associated protein), alpha 1, 102 kd	*CTNNA1*	2.703 down	.0228	1495
Carboxyl ester lipase (bile salt–stimulated lipase)	*CEL*	2.700 down	.0449	1056
Prune homolog	*PRUNE*	2.678 down	.0233	58497
BCL2-like 1	*BCL2L1*	2.674 down	.0329	598
Solute carrier family 16, member 1 (monocarboxylic acid transporter 1)	*SLC16A1*	2.672 down	.0128	6566
CDNA FLJ38048 fis, clone CTONG2014264///CDNA FLJ39067 fis, clone NT2RP7014910		2.668 down	.0154	
ADP-ribosylation factor guanine nucleotide-exchange factor 2	*ARFGEF2*	2.654 down	.0168	10564
Chromosome 9 open reading frame 5	*C9orf5*	2.650 down	.01	23731
Zinc finger, MYND domain containing 11	*ZMYND11*	2.635 down	.011	10771
Ras homolog gene family, member B	*RHOB*	2.634 down	.0488	388
Kringle containing transmembrane protein 1	*KREMEN1*	2.620 down	.0448	83999
F-box protein 38	*FBXO38*	2.617 down	.0125	81545
Secretory carrier membrane protein 1	*SCAMP1*	2.616 down	.011	9522
Putative homeodomain transcription factor 2	*PHTF2*	2.605 down	.0178	57157
Spastic paraplegia 7	*SPG7*	2.598 down	.0451	6687
Membrane protein, palmitoylated 5 (MAGUK p55 subfamily member 5)	*MPP5*	2.595 down	.0103	64398
BCL2-associated transcription factor 1	*BCLAF1*	2.585 down	.0138	9774
Nuclear receptor coactivator 2	*NCOA2*	2.580 down	.0116	10499
Myomesin family, member 3	*MYOM3*	2.579 down	.0346	127294
Forkhead box N3	*FOXN3*	2.573 down	.0118	1112
Blood vessel epicardial substance	*BVES*	2.570 down	.0295	11149
Family with sequence similarity 62 (C2 domain containing) member B	*FAM62B*	2.569 down	.0134	57488

TABLE E2. Continued

Gene title	Symbol	Fold	*P* value	Gene ID
Procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), beta polypeptide	*P4HB*	2.564 down	.0384	5034
Ubiquitin-specific peptidase 2	*USP2*	2.544 down	.00576	9099
Zinc finger, FYVE domain containing 1	*ZFYVE1*	2.540 down	.0149	53349
General transcription factor II, i	*GTF2I*	2.539 down	.0135	2969
Son of sevenless homolog 2	*SOS2*	2.539 down	.0211	6655
Thrombospondin, type I, domain containing 4	*THSD4*	2.536 down	.0177	79875
Jumonji domain containing 1C	*JMJD1C*	2.533 down	.0098	221037
Ring finger protein 38	*RNF38*	2.532 down	.00664	152006
Muscleblind-like	*MBNL1*	2.517 down	.0418	4154
Coiled-coil domain containing 93	*CCDC93*	2.515 down	.0102	54520
Cleft lip and palate associated transmembrane protein 1	*CLPTM1*	2.505 down	.0301	1209
HECT domain containing 1	*HECTD1*	2.502 down	.0133	25831
Transmembrane protein 168	*TMEM168*	2.500 down	.00924	64418
ST6 beta-galactosamide alpha-2,6-sialyltranferase 1	*ST6GAL1*	2.495 down	.0306	6480
Glutamate-ammonia ligase (glutamine synthetase)	*GLUL*	2.493 down	.0239	2752
WD repeat domain 1	*WDR1*	2.490 down	.0212	9948
UBX domain containing 7	*UBXD7*	2.483 down	.0233	26043
Dihydrolipoamide branched chain transacylase E2	*DBT*	2.482 down	.0161	1629
Zinc finger, BED-type containing 1	*ZBED1*	2.478 down	.0168	9189
Solute carrier family 29 (nucleoside transporters), member 1	*SLC29A1*	2.476 down	.0163	2030
Mitogen-activated protein kinase 14	*MAPK14*	2.472 down	.0205	1432
GRB2-associated binding protein 1	*GAB1*	2.465 down	.00951	2549
Coiled-coil domain containing 22	*CCDC22*	2.461 down	.0137	28952
Latent transforming growth factor beta binding protein 3	*LTBP3*	2.459 down	.0169	4054
Replication initiator 1	*REPIN1*	2.455 down	.0256	29803
Utrophin	*UTRN*	2.452 down	.0111	7402
Signal recognition particle receptor ("docking protein")	*SRPR*	2.451 down	.0181	6734
Forkhead box J3	*FOXJ3*	2.450 down	.0142	22887
Collagen, type XII, alpha 1	*COL12A1*	2.446 down	.0109	1303
TIMP metallopeptidase inhibitor 3 (Sorsby fundus dystrophy, pseudoinflammatory)	*TIMP3*	2.445 down	.0338	7078
Sperm associated antigen 9	*SPAG9*	2.445 down	.0109	9043
Zinc finger protein 395	*ZNF395*	2.441 down	.0264	55893
A kinase (PRKA) anchor protein 1	*AKAP1*	2.437 down	.0226	8165
Activating transcription factor 2	*ATF2*	2.434 down	.0145	1386
Collagen, type IV, alpha 2	*COL4A2*	2.431 down	.0277	1284
Myelin basic protein	*MBP*	2.427 down	.00494	4155
Golgi associated PDZ and coiled-coil motif containing	*GOPC*	2.424 down	.00952	57120
Microfibrillar-associated protein 3	*MFAP3*	2.423 down	.0171	4238
UBX domain containing 2	*UBXD2*	2.420 down	.0136	23190
Heparan sulfate proteoglycan 2	*HSPG2*	2.415 down	.0109	3339
Desmoglein 2	*DSG2*	2.411 down	.0203	1829
Exocyst complex component 4	*EXOC4*	2.410 down	.019	60412
Chloride intracellular channel 4	*CLIC4*	2.410 down	.0207	25932
RAN binding protein 2	*RANBP2*	2.405 down	.0116	5903
Ring finger and CCCH-type zinc finger domains 2	*RC3H2*	2.405 down	.0119	54542
ATP-binding cassette, sub-family C (CFTR/MRP), member 9	*ABCC9*	2.402 down	.0066	10060
LSM14B, SCD6 homolog B *(S cerevisiae)*	*LSM14B*	2.396 down	.0118	149986
Synaptopodin 2	*SYNPO2*	2.395 down	.0246	171024
Tripeptidyl peptidase I	*TPP1*	2.391 down	.0215	1200
Sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6D	*SEMA6D*	2.386 down	.0442	80031
Discs, large homolog 1 *(Drosophila)*	*DLG1*	2.382 down	.0197	1739

TABLE E2. Continued

Gene title	Symbol	Fold	*P* value	Gene ID
Obscurin-like 1	*OBSL1*	2.381 down	.0441	23363
Ubiquitination factor E4B (UFD2 homolog, yeast)	*UBE4B*	2.377 down	.0108	10277
LIM domain containing preferred translocation partner in lipoma	*LPP*	2.372 down	.0134	4026
Plakophilin 4	*PKP4*	2.366 down	.00687	8502
Dual specificity phosphatase 3 (vaccinia virus phosphatase VH1-related)	*DUSP3*	2.361 down	.0233	1845
Phosphatase and actin regulator 2	*PHACTR2*	2.361 down	.0158	9749
DEAD (Asp-Glu-Ala-Asp) box polypeptide 3, X-linked	*DDX3X*	2.357 down	.0208	1654
Protein tyrosine phosphatase, nonreceptor type 11 (Noonan syndrome 1)	*PTPN11*	2.351 down	.0112	5781
Chromosome 6 open reading frame 106	*C6orf106*	2.348 down	.012	64771
Rho GTPase activating protein 5	*ARHGAP5*	2.348 down	.0103	394
Runt-related transcription factor 1; translocated to, 1 (cyclin D-related)	*RUNX1T1*	2.348 down	.0119	862
Phosphoinositide-3-kinase, class 2, alpha polypeptide	*PIK3C2A*	2.347 down	.0169	5286
Phospholipase D1, phosphatidylcholine-specific	*PLD1*	2.347 down	.0256	5337
Dystrophin (muscular dystrophy, Duchenne and Becker types)	*DMD*	2.344 down	.00618	1756
Ankyrin 2, neuronal	*ANK2*	2.343 down	.00798	287
Janus kinase 1 (a protein tyrosine kinase)	*JAK1*	2.340 down	.0227	3716
Lamin A/C	*LMNA*	2.335 down	.0134	4000
Bromodomain containing 4	*BRD4*	2.334 down	.039	23476
Ubiquitin specific peptidase 42	*USP42*	2.321 down	.0166	84132
Methyl CpG binding protein 2 (Rett syndrome)	*MECP2*	2.320 down	.0479	4204
Transglutaminase 2 (C polypeptide, protein-glutamine-gamma-glutamyltransferase)	*TGM2*	2.319 down	.0206	7052
Ankylosis, progressive homolog (mouse)	*ANKH*	2.312 down	.0205	56172
Muskelin 1, intracellular mediator containing kelch motifs	*MKLN1*	2.311 down	.0249	4289
Lysosomal-associated membrane protein 1	*LAMP1*	2.311 down	.0274	3916
CUG triplet repeat, RNA binding protein 1	*CUGBP1*	2.309 down	.0112	10658
Secretory carrier membrane protein 1	*SCAMP1*	2.308 down	.0113	9522
WD repeat domain 68	*WDR68*	2.307 down	.0172	10238
Ribosomal protein S6 kinase, 90 kd, polypeptide 2	*RPS6KA2*	2.304 down	.0354	6196
Junctional adhesion molecule 3	*JAM3*	2.303 down	.0158	83700
Bromodomain containing 2	*BRD2*	2.294 down	.022	6046
Phosphatidylinositol 4-kinase, catalytic, beta	*PI4KB*	2.292 down	.0128	5298
Jun D proto-oncogene	*JUND*	2.289 down	.0242	3727
Microtubule associated serine/threonine kinase family member 4	*MAST4*	2.285 down	.0448	375449
Utrophin	*UTRN*	2.284 down	.011	7402
Chromosome 11 open reading frame 30	*C11orf30*	2.284 down	.0433	56946
RAB6A, member RAS oncogene family	*RAB6A*	2.283 down	.0134	5870
Chromosome 4 open reading frame 18	*C4orf18*	2.283 down	.0142	51313
Protein tyrosine phosphatase, non-receptor type 11 (Noonan syndrome 1)	*PTPN11*	2.283 down	.00661	5781
Upstream binding transcription factor, RNA polymerase I	*UBTF*	2.281 down	.0101	7343
Collagen, type VI, alpha 1	*COL6A1*	2.280 down	.0169	1291
Calcium channel, voltage-dependent, beta 2 subunit	*CACNB2*	2.280 down	.0449	783
Corin, serine peptidase	*CORIN*	2.277 down	.0284	10699
Spire homolog 1 *(Drosophila)*	*SPIRE1*	2.276 down	.0311	56907
Collagen, type VI, alpha 1	*COL6A1*	2.273 down	.00933	1291
Angiopoietin-like 2	*ANGPTL2*	2.272 down	.0125	23452
Sortilin 1	*SORT1*	2.271 down	.0214	6272
Vacuolar protein sorting 35 homolog *(S cerevisiae)*	*VPS35*	2.269 down	.0219	55737
ADAM metallopeptidase domain 9 (meltrin gamma)	*ADAM9*	2.269 down	.016	8754
Palladin, cytoskeletal associated protein	*PALLD*	2.266 down	.0127	23022

TABLE E2. Continued

Gene title	Symbol	Fold	*P* value	Gene ID
Tumor necrosis factor receptor superfamily, member 19	*TNFRSF19*	2.258 down	.0218	55504
Zinc finger protein, X-linked///zinc finger protein, Y-linked	*ZFX///ZFY*	2.256 down	.0216	7543///7544
Oxoglutarate (alpha-ketoglutarate) dehydrogenase (lipoamide)	*OGDH*	2.251 down	.0124	4967
CDV3 homolog (mouse)	*CDV3*	2.251 down	.0111	55573
Meningioma expressed antigen 5 (hyaluronidase)	*MGEA5*	2.245 down	.0113	10724
Solute carrier family 7 (cationic amino acid transporter, y+ system), member 6	*SLC7A6*	2.245 down	.0455	9057
Component of oligomeric Golgi complex 3	*COG3*	2.241 down	.0125	83548
Protein tyrosine phosphatase, non-receptor type 21	*PTPN21*	2.239 down	.0199	11099
Obscurin-like 1	*OBSL1*	2.238 down	.0324	23363
Phosphorylase kinase, gamma 1 (muscle)	*PHKG1*	2.236 down	.0239	5260
LanC lantibiotic synthetase component C-like 1 (bacterial)	*LANCL1*	2.234 down	.0183	10314
Obscurin-like 1	*OBSL1*	2.229 down	.0282	23363
Ubiquitin specific peptidase 47	*USP47*	2.227 down	.00285	55031
Structural maintenance of chromosomes 3	*SMC3*	2.226 down	.0134	9126
Ankyrin repeat and KH domain containing 1	*ANKHD1*	2.225 down	.0259	404734
Kelch repeat and BTB (POZ) domain containing 2	*KBTBD2*	2.225 down	.0116	25948
Arginine-glutamic acid dipeptide (RE) repeats	*RERE*	2.224 down	.0448	473
Nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 2 interacting protein	*NFATC2IP*	2.223 down	.0151	84901
Spire homolog 1 *(Drosophila)*	*SPIRE1*	2.217 down	.0146	56907
Protein phosphatase 1, regulatory (inhibitor) subunit 3B	*PPP1R3B*	2.217 down	.0234	79660
Versican	*VCAN*	2.212 down	.0487	1462
Mitogen-activated protein kinase 14	*MAPK14*	2.210 down	.0377	1432
ARP2 actin-related protein 2 homolog (yeast)	*ACTR2*	2.205 down	.0088	10097
Sorbin and SH3 domain containing 1	*SORBS1*	2.205 down	.0112	10580
Son of sevenless homolog 2 *(Drosophila)*	*SOS2*	2.204 down	.0404	6655
Mitogen-activated protein kinase 14	*MAPK14*	2.201 down	.0111	1432
Glucosaminyl (N-acetyl) transferase 2, I-branching enzyme (I blood group)	*GCNT2*	2.194 down	.0255	2651
MRNA; cDNA DKFZp451B209 (from clone DKFZp451B209)		2.193 down	.028	
ARP2 actin-related protein 2 homolog (yeast)	*ACTR2*	2.193 down	.0167	10097
Syntaxin 16	*STX16*	2.192 down	.0145	8675
Non-POU domain containing, octamer-binding	*NONO*	2.190 down	.0255	4841
Jumonji, AT rich interactive domain 1B	*JARID1B*	2.189 down	.0274	10765
Replication protein A1, 70 kd	*RPA1*	2.185 down	.0103	6117
Sorting nexin 13	*SNX13*	2.183 down	.0124	23161
Neural cell adhesion molecule 1	*NCAM1*	2.177 down	.0119	4684
Ubiquitin protein ligase E3B	*UBE3B*	2.177 down	.012	89910
Endoplasmic reticulum aminopeptidase 2	*ERAP2*	2.172 down	.0346	64167
Mitogen-activated protein kinase kinase kinase kinase 5	*MAP4K5*	2.171 down	.0111	11183
Chromosome 6 open reading frame 166	*C6orf166*	2.168 down	.0171	55122
Prickle homolog 1 *(Drosophila)*	*PRICKLE1*	2.168 down	.0424	144165
Erythrocyte membrane protein band 4.1-like 2	*EPB41L2*	2.168 down	.0116	2037
Platelet-activating factor acetylhydrolase, isoform Ib, alpha subunit 45 kd	*PAFAH1B1*	2.165 down	.0262	5048
Chromosome 1 open reading frame 55	*C1orf55*	2.164 down	.0169	163859
v-erb-b2 erythroblastic leukemia viral oncogene homolog 2, neuro/glioblastoma derived oncogene homolog (avian)	*ERBB2*	2.163 down	.0132	2064
DnaJ (Hsp40) homolog, subfamily C, member 14	*DNAJC14*	2.163 down	.0253	85406
Family with sequence similarity 115, member A///family with sequence similarity 115, member B	*FAM115A/// FAM115B*	2.162 down	.011	653199///9747
Trans-Golgi network protein 2	*TGOLN2*	2.160 down	.0212	10618
Presenilin 1 (Alzheimer disease 3)	*PSEN1*	2.160 down	.0142	5663

TABLE E2. Continued

Gene title	Symbol	Fold	*P* value	Gene ID
Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain, 2	*CITED2*	2.160 down	.0323	10370
Ubiquitin-like modifier activating enzyme 1	*UBA1*	2.159 down	.0234	7317
Phosphatidylinositol-4-phosphate 5-kinase, type I, alpha	*PIP5K1A*	2.157 down	.0366	8394
B-cell chronic lymphocytic leukemia/lymphoma 6 (zinc finger protein 51)	*BCL6*	2.156 down	.0463	604
Zinc finger protein 317	*ZNF317*	2.155 down	.0206	57693
Sorting nexin 13	*SNX13*	2.153 down	.0236	23161
SUMO1/sentrin/SMT3 specific peptidase 3	*SENP3*	2.150 down	.0127	26168
Structural maintenance of chromosomes 3	*SMC3*	2.149 down	.0115	9126
Methionine adenosyltransferase II, alpha	*MAT2A*	2.148 down	.0187	4144
Polymerase (DNA-directed), delta interacting protein 3	*POLDIP3*	2.145 down	.0133	84271
Receptor interacting protein kinase 5	*RIPK5*	2.139 down	.012	25778
Retinoic acid receptor, beta	*RARB*	2.137 down	.0307	5915
O-linked N-acetylglucosamine (GlcNAc) transferase (UDP-N-acetylglucosamine:polypeptide-N-acetylglucosaminyl transferase)	*OGT*	2.136 down	.0154	8473
PTPRF interacting protein, binding protein 1 (liprin beta 1)	*PPFIBP1*	2.136 down	.012	8496
Trinucleotide repeat containing 6C	*TNRC6C*	2.136 down	.0124	57690
FRY-like	*FRYL*	2.134 down	.0128	285527
Ankyrin repeat and FYVE domain containing 1	*ANKFY1*	2.134 down	.0125	51479
DIP2 disco-interacting protein 2 homolog C *(Drosophila)*	*DIP2C*	2.134 down	.0113	22982
ARP2 actin-related protein 2 homolog (yeast)	*ACTR2*	2.133 down	.015	10097
Deleted in liver cancer 1	*DLC1*	2.132 down	.0206	10395
ets variant gene 1	*ETV1*	2.131 down	.0239	2115
Translocated promoter region (to activated MET oncogene)	*TPR*	2.131 down	.0243	7175
Signal transducer and activator of transcription 3 (acute-phase response factor)	*STAT3*	2.130 down	.0187	6774
Calcium binding protein 39	*CAB39*	2.129 down	.0217	51719
Glutamine and serine rich 1	*QSER1*	2.129 down	.0119	79832
Actin binding LIM protein 1	*ABLIM1*	2.127 down	.017	3983
Zinc finger protein 36, C3H type-like 2	*ZFP36L2*	2.125 down	.0394	678
Junctional adhesion molecule 3	*JAM3*	2.122 down	.00921	83700
Golgi autoantigen, golgin subfamily a, 2	*GOLGA2*	2.121 down	.0272	2801
Nuclear factor I/A	*NFIA*	2.121 down	.0102	4774
Cholinergic receptor, muscarinic 2	*CHRM2*	2.120 down	.0355	1129
Ankyrin 3, node of Ranvier (ankyrin G)	*ANK3*	2.120 down	.0365	288
Neuroblastoma breakpoint family, member 1	*NBPF1*	2.117 down	.0114	149013
FRY-like	*FRYL*	2.115 down	.0254	285527
UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 2 (GalNAc-T2)	*GALNT2*	2.113 down	.0158	2590
MAP/microtubule affinity-regulating kinase 2	*MARK2*	2.113 down	.0376	2011
Transmembrane 9 superfamily protein member 4	*TM9SF4*	2.113 down	.0212	9777
Nucleobindin 1	*NUCB1*	2.109 down	.0258	4924
Rho GTPase activating protein 26	*ARHGAP26*	2.109 down	.0228	23092
Dynactin 1 (p150, glued homolog, *Drosophila*)	*DCTN1*	2.109 down	.0157	1639
Ubiquitin specific peptidase 10	*USP10*	2.106 down	.0209	9100
Squamous cell carcinoma antigen recognized by T cells 3	*SART3*	2.105 down	.0113	9733
Importin 8	*IPO8*	2.104 down	.0137	10526
Hepatocyte growth factor-regulated tyrosine kinase substrate	*HGS*	2.103 down	.0206	9146
Solute carrier family 8 (sodium/calcium exchanger), member 1	*SLC8A1*	2.102 down	.0122	6546
Protein tyrosine phosphatase, non-receptor type 12	*PTPN12*	2.102 down	.041	5782
Chloride intracellular channel 4	*CLIC4*	2.100 down	.026	25932
FK506 binding protein 15, 133 kd	*FKBP15*	2.099 down	.0249	23307
Insulin-like growth factor binding protein 5	*IGFBP5*	2.097 down	.0263	3488

TABLE E2. Continued

Gene title	Symbol	Fold	*P* value	Gene ID
ATPase, H^+ transporting, lysosomal 70 kd, V1 subunit A	*ATP6V1A*	2.097 down	.0143	523
Neighbor of BRCA1 gene 1///similar to neighbor of BRCA1 gene 1	*LOC727732/// NBR1*	2.096 down	.0126	4077///727732
TEA domain family member 2	*TEAD2*	2.096 down	.0399	8463
Cytokine-like nuclear factor n-pac	*N-PAC*	2.095 down	.0225	84656
CCR4-NOT transcription complex, subunit 1	*CNOT1*	2.093 down	.0122	23019
Myosin XVIIIB	*MYO18B*	2.090 down	.0218	84700
Leucine-rich repeats and immunoglobulin-like domains 1	*LRIG1*	2.090 down	.0134	26018
Zinc finger protein 514	*ZNF514*	2.090 down	.0335	84874
Apolipoprotein E	*APOE*	2.088 down	.0284	348
Minichromosome maintenance complex component 7	*MCM7*	2.086 down	.0258	4176
Arsenate resistance protein 2	*ARS2*	2.082 down	.0209	51593
N-acetyltransferase 11	*NAT11*	2.081 down	.0317	79829
GM2 ganglioside activator	*GM2A*	2.079 down	.0372	2760
Jun D proto-oncogene	*JUND*	2.079 down	.0218	3727
Mitogen-activated protein kinase kinase kinase 2	*MAP3K2*	2.077 down	.00667	10746
Karyopherin alpha 1 (importin alpha 5)	*KPNA1*	2.076 down	.0169	3836
YY1 transcription factor	*YY1*	2.075 down	.048	7528
KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 1	*KDELR1*	2.074 down	.0175	10945
Prolyl endopeptidase-like	*PREPL*	2.072 down	.0113	9581
O-linked N-acetylglucosamine (GlcNAc) transferase (UDP-N-acetylglucosamine:polypeptide-N-acetylglucosaminyl transferase)	*OGT*	2.072 down	.0136	8473
Insulin-like growth factor 2 receptor	*IGF2R*	2.072 down	.0102	3482
Zinc finger protein 275	*ZNF275*	2.070 down	.0462	10838
Zinc finger, MYM-type 2	*ZMYM2*	2.069 down	.0255	7750
GTPase activating protein (SH3 domain) binding protein 2	*G3BP2*	2.069 down	.0134	9908
CDNA FLJ33081 fis, clone TRACH2000321		2.069 down	.0287	
KIAA0430	*KIAA0430*	2.068 down	.0136	9665
ets variant gene 1	*ETV1*	2.068 down	.0125	2115
Leucine rich repeat (in FLII) interacting protein 2	*LRRFIP2*	2.067 down	.0162	9209
Endothelial differentiation, lysophosphatidic acid G-protein-coupled receptor, 7	*EDG7*	2.066 down	.0437	23566
Obscurin-like 1	*OBSL1*	2.066 down	.0243	23363
Retinoblastoma-like 2 (p130)	*RBL2*	2.065 down	.0175	5934
Ubiquitin-conjugating enzyme E2G 2 (UBC7 homolog, yeast)	*UBE2G2*	2.065 down	.0125	7327
Calcium channel, voltage-dependent, alpha 2/delta subunit 1	*CACNA2D1*	2.062 down	.0237	781
Uridine-cytidine kinase 1-like 1	*UCKL1*	2.062 down	.0344	54963
Bromodomain containing 2	*BRD2*	2.059 down	.0473	6046
Tripartite motif-containing 56	*TRIM56*	2.059 down	.0129	81844
AF4/FMR2 family, member 4	*AFF4*	2.059 down	.0442	27125
Ubiquitously transcribed tetratricopeptide repeat, X chromosome	*UTX*	2.058 down	.0299	7403
Spectrin, beta, nonerythrocytic 1	*SPTBN1*	2.057 down	.017	6711
Striatin, calmodulin binding protein	*STRN*	2.057 down	.0113	6801
Uridine-cytidine kinase 1	*UCK1*	2.056 down	.0281	83549
Solute carrier family 2 (facilitated glucose transporter), member 11	*SLC2A11*	2.055 down	.0197	66035
Hypothetical LOC552889	*LOC552889*	2.053 down	.0136	552889
Peroxisome proliferator-activated receptor alpha	*PPARA*	2.051 down	.0151	5465
Chromosome 10 open reading frame 46	*C10orf46*	2.051 down	.0163	143384

TABLE E2. Continued

Gene title	Symbol	Fold	*P* value	Gene ID
Outer dense fiber of sperm tails 2	*ODF2*	2.049 down	.0114	4957
O-linked N-acetylglucosamine (GlcNAc) transferase (UDP-N-acetylglucosamine:polypeptide-N-acetylglucosaminyl transferase)	*OGT*	2.048 down	.016	8473
Janus kinase 1 (a protein tyrosine kinase)	*JAK1*	2.047 down	.0312	3716
Structure specific recognition protein 1	*SSRP1*	2.047 down	.0211	6749
Glutamyl-prolyl-tRNA synthetase	*EPRS*	2.047 down	.0149	2058
Karyopherin alpha 4 (importin alpha 3)	*KPNA4*	2.045 down	.0126	3840
MAD1 mitotic arrest deficient-like 1 (yeast)	*MAD1L1*	2.045 down	.0331	8379
Zinc finger CCCH-type containing 11A	*ZC3H11A*	2.045 down	.0113	9877
Ubiquitin specific peptidase 25	*USP25*	2.044 down	.0103	29761
Tribbles homolog 2 *(Drosophila)*	*TRIB2*	2.044 down	.00966	28951
Adenomatous polyposis coli	*APC*	2.043 down	.0111	324
Centrosomal protein 68 kd	*CEP68*	2.040 down	.0174	23177
Protein phosphatase 1, regulatory (inhibitor) subunit 12B	*PPP1R12B*	2.040 down	.012	4660
v-crk sarcoma virus CT10 oncogene homolog (avian)	*CRK*	2.037 down	.022	1398
Protein phosphatase 2, regulatory subunit B′, delta isoform	*PPP2R5D*	2.034 down	.0319	5528
GATA zinc finger domain containing 1	*GATAD1*	2.033 down	.0295	57798
Dipeptidyl-peptidase 8	*DPP8*	2.031 down	.0442	54878
Mitochondrial tumor suppressor 1	*MTUS1*	2.030 down	.0258	57509
Ubiquitination factor E4B (UFD2 homolog, yeast)	*UBE4B*	2.028 down	.0118	10277
Fusion (involved in t(12;16) in malignant liposarcoma)	*FUS*	2.027 down	.0394	2521
Hippocalcin-like 1	*HPCAL1*	2.027 down	.0449	3241
ATP-binding cassette, sub-family C (CFTR/MRP), member 9	*ABCC9*	2.027 down	.0125	10060
Protein tyrosine phosphatase, non-receptor type 21	*PTPN21*	2.025 down	.0234	11099
Ubiquitin specific peptidase 34	*USP34*	2.024 down	.0159	9736
DEAD (Asp-Glu-Ala-Asp) box polypeptide 3, X-linked	*DDX3X*	2.024 down	.0203	1654
Phosphatidylinositol binding clathrin assembly protein	*PICALM*	2.023 down	.0158	8301
Transportin 3	*TNPO3*	2.022 down	.0166	23534
Non-POU domain containing, octamer-binding	*NONO*	2.022 down	.0192	4841
ORM1-like 3 *(S cerevisiae)*	*ORMDL3*	2.021 down	.014	94103
Mitogen-activated protein kinase kinase kinase kinase 4	*MAP4K4*	2.021 down	.0371	9448
Tribbles homolog 1 *(Drosophila)*	*TRIB1*	2.021 down	.0206	10221
WD repeat domain 6	*WDR6*	2.020 down	.0135	11180
Aspartate beta-hydroxylase	*ASPH*	2.020 down	.00586	444
Zinc finger protein 45	*ZNF45*	2.019 down	.0125	7596
SET domain containing 5	*SETD5*	2.019 down	.0266	55209
Eukaryotic translation initiation factor 4E nuclear import factor 1	*EIF4ENIF1*	2.017 down	.0142	56478
High-density lipoprotein binding protein (vigilin)	*HDLBP*	2.013 down	.0162	3069
Mannosyl (alpha-1,3-)-glycoprotein beta-1, 4-N-acetylglucosaminyltransferase, isozyme B	*MGAT4B*	2.012 down	.0175	11282
AT rich interactive domain 1A (SWI-like)	*ARID1A*	2.012 down	.0426	8289
Alkylglycerone phosphate synthase	*AGPS*	2.011 down	.00981	8540
MLCK protein	*MLCK*	2.010 down	.0158	91807
FYVE, RhoGEF and PH domain containing 6	*FGD6*	2.009 down	.0163	55785
Cytoplasmic FMR1 interacting protein 2	*CYFIP2*	2.007 down	.0392	26999
Acyl-CoA thioesterase 11	*ACOT11*	2.003 down	.0417	26027
Ubiquitin specific peptidase 11	*USP11*	2.001 down	.0306	8237
Zinc finger protein 395///F-box protein 16	*FBXO16///ZNF395*	2.000 down	.035	157574///55893
Adrenergic, alpha-1A-, receptor	*ADRA1A*	1.998 down	.0404	148
M-phase phosphoprotein 9	*MPHOSPH9*	1.996 down	.0239	10198
Nudix (nucleoside diphosphate linked moiety X)-type motif 21	*NUDT21*	1.995 down	.0167	11051
Kruppel-like factor 3 (basic)	*KLF3*	1.993 down	.0169	51274
Synovial sarcoma translocation, chromosome 18	*SS18*	1.992 down	.0185	6760

TABLE E2. Continued

Gene title	Symbol	Fold	*P* value	Gene ID
Exocyst complex component 5	*EXOC5*	1.991 down	.016	10640
Rabaptin, RAB GTPase binding effector protein 1	*RABEP1*	1.990 down	.0482	9135
PRP4 pre-mRNA processing factor 4 homolog (yeast)	*PRPF4*	1.990 down	.0206	9128
CDNA FLJ10151 fis, clone HEMBA1003402		1.986 down	.0136	
CDNA clone IMAGE:5263531		1.986 down	.0114	
SH3-domain GRB2-like endophilin B2	*SH3GLB2*	1.985 down	.0301	56904
Serologically defined colon cancer antigen 1	*SDCCAG1*	1.985 down	.0111	9147
Zinc finger protein 398	*ZNF398*	1.981 down	.0365	57541
Cytochrome b reductase 1	*CYBRD1*	1.980 down	.0237	79901
Transformation/transcription domain-associated protein	*TRRAP*	1.977 down	.0235	8295
SON DNA binding protein	*SON*	1.975 down	.0125	6651
Nucleoporin 133 kd	*NUP133*	1.975 down	.0187	55746
Discoidin domain receptor family, member 2	*DDR2*	1.973 down	.0112	4921
A kinase (PRKA) anchor protein 8-like	*AKAP8L*	1.971 down	.0291	26993
Lanosterol synthase (2,3-oxidosqualene-lanosterol cyclase)	*LSS*	1.971 down	.0347	4047
dpy-19-like 1 *(C elegans)*	*DPY19L1*	1.968 down	.0174	23333
Dystonin	*DST*	1.967 down	.00579	667
Splicing factor, arginine/serine-rich 8 (suppressor-of-white-apricot homolog, *Drosophila*)	*SFRS8*	1.967 down	.0239	6433
NGFI-A binding protein 1 (EGR1 binding protein 1)	*NAB1*	1.965 down	.0132	4664
Exocyst complex component 7	*EXOC7*	1.963 down	.0278	23265
Syntrophin, beta 2 (dystrophin-associated protein A1, 59 kd, basic component 2)	*SNTB2*	1.962 down	.0196	6645
SEC63 homolog *(S cerevisiae)*	*SEC63*	1.961 down	.0142	11231
SHC (Src homology 2 domain containing) transforming protein 1	*SHC1*	1.960 down	.0129	6464
Engulfment and cell motility 2	*ELMO2*	1.960 down	.021	63916
Chromosome 1 open reading frame 25	*C1orf25*	1.959 down	.0309	81627
Glutamate-ammonia ligase (glutamine synthetase)	*GLUL*	1.958 down	.0355	2752
MYST histone acetyltransferase (monocytic leukemia) 4	*MYST4*	1.957 down	.0229	23522
FOS-like antigen 2	*FOSL2*	1.957 down	.0326	2355
KIAA0692	*KIAA0692*	1.957 down	.025	23141
Potassium channel tetramerization domain containing 20	*KCTD20*	1.955 down	.028	222658
WD repeat domain 26	*WDR26*	1.955 down	.0125	80232
Senataxin	*SETX*	1.953 down	.0121	23064
Trinucleotide repeat containing 6B	*TNRC6B*	1.951 down	.00655	23112
Transmembrane 9 superfamily member 1	*TM9SF1*	1.951 down	.0301	10548
Family with sequence similarity 108, member B1	*FAM108B1*	1.948 down	.0404	51104
Transmembrane protein 30A	*TMEM30A*	1.948 down	.0137	55754
CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) small phosphatase like 2	*CTDSPL2*	1.948 down	.0238	51496
Zinc finger protein 24	*ZNF24*	1.947 down	.011	7572
HLA-B associated transcript 3	*BAT3*	1.947 down	.0299	7917
Chromosome 21 open reading frame 33	*C21orf33*	1.946 down	.0321	8209
Protein kinase C substrate 80K-H	*PRKCSH*	1.945 down	.0205	5589
Pleckstrin homology, Sec7 and coiled-coil domains 3	*PSCD3*	1.943 down	.0134	9265
BCL2-antagonist of cell death	*BAD*	1.941 down	.0326	572
A kinase (PRKA) anchor protein 10	*AKAP10*	1.941 down	.0355	11216
Sorbin and SH3 domain containing 3	*SORBS3*	1.939 down	.0162	10174
v-akt murine thymoma viral oncogene homolog 2	*AKT2*	1.939 down	.035	208
Myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, *Drosophila*)	*MLL*	1.939 down	.0264	4297
Integrin, alpha 7	*ITGA7*	1.938 down	.0256	3679
Ankyrin repeat and KH domain containing 1///ANKHD1-EIF4EBP3	*ANKHD1/// ANKHD1-EIF4EBP3*	1.938 down	.0401	404734/// 54882

TABLE E2. Continued

Gene title	Symbol	Fold	*P* value	Gene ID
CCR4-NOT transcription complex, subunit 4	*CNOT4*	1.937 down	.0261	4850
CDNA FLJ38461 fis, clone FEBRA2020977		1.935 down	.0168	
Membrane-associated ring finger (C3HC4) 6	*7-Mar*	1.935 down	.00973	10299
Zinc finger protein 540	*ZNF540*	1.934 down	.024	163255
Solute carrier family 30 (zinc transporter), member 5	*SLC30A5*	1.934 down	.00814	64924
Ral guanine nucleotide dissociation stimulator	*RALGDS*	1.934 down	.0212	5900
Mitogen-activated protein kinase 1	*MAPK1*	1.933 down	.0124	5594
Small G protein signaling modulator 3	*SGSM3*	1.932 down	.0354	27352
Intracisternal A particle-promoted polypeptide	*IPP*	1.932 down	.0337	3652
Mediator complex subunit 23	*MED23*	1.931 down	.0242	9439
Bone morphogenetic protein receptor, type II (serine/threonine kinase)	*BMPR2*	1.929 down	.0111	659
MOCO sulphurase C-terminal domain containing 2	*MOSC2*	1.928 down	.00932	54996
Myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, *Drosophila*)	*MLL*	1.927 down	.0172	4297
Troponin T type 2 (cardiac)	*TNNT2*	1.926 down	.0352	7139
ATPase, H^+ transporting, lysosomal V0 subunit a1	*ATP6V0A1*	1.925 down	.0372	535
RAD23 homolog A *(S cerevisiae)*	*RAD23A*	1.924 down	.0205	5886
Nuclear receptor coactivator 3	*NCOA3*	1.924 down	.0496	8202
Myelin basic protein	*MBP*	1.924 down	.0167	4155
Solute carrier family 33 (acetyl-CoA transporter), member 1	*SLC33A1*	1.923 down	.0112	9197
T-box 5	*TBX5*	1.923 down	.0203	6910
DEAH (Asp-Glu-Ala-His) box polypeptide 9	*DHX9*	1.923 down	.0112	1660
Intraflagellar transport 122 homolog *(Chlamydomonas)*	*IFT122*	1.922 down	.0247	55764
Calnexin	*CANX*	1.921 down	.0103	821
Rab and DnaJ domain containing	*RBJ*	1.921 down	.03	51277
Hydroxyacyl-coenzyme A dehydrogenase/3-ketoacyl-coenzyme A thiolase/enoyl-coenzyme A hydratase (trifunctional protein), alpha subunit	*HADHA*	1.921 down	.0375	3030
Dystonin	*DST*	1.919 down	.0112	667
Phosphoinositide-3-kinase, class 2, alpha polypeptide	*PIK3C2A*	1.919 down	.0216	5286
ADAM metallopeptidase domain 10	*ADAM10*	1.918 down	.0433	102
Fibronectin type III domain containing 3A	*FNDC3A*	1.918 down	.00672	22862
Spire homolog 1 *(Drosophila)*	*SPIRE1*	1.917 down	.0109	56907
RAS and EF-hand domain containing	*RASEF*	1.917 down	.0401	158158
Phosphodiesterase 1C, calmodulin-dependent 70 kd	*PDE1C*	1.916 down	.0136	5137
Ring finger protein 19A	*RNF19A*	1.916 down	.0112	25897
alkB, alkylation repair homolog 5 *(E coli)*	*ALKBH5*	1.916 down	.0208	54890
zer-1 homolog *(C elegans)*	*ZER1*	1.915 down	.0125	10444
Obscurin, cytoskeletal calmodulin and titin-interacting RhoGEF	*OBSCN*	1.914 down	.0387	84033
Zinc finger with KRAB and SCAN domains 1	*ZKSCAN1*	1.914 down	.0142	7586
Chloride intracellular channel 5	*CLIC5*	1.913 down	.0391	53405
WW domain containing adaptor with coiled-coil	*WAC*	1.913 down	.00669	51322
Wolfram syndrome 1 (wolframin)	*WFS1*	1.912 down	.0492	7466
Son of sevenless homolog 1 *(Drosophila)*	*SOS1*	1.911 down	.0448	6654
Cytoskeleton associated protein 5	*CKAP5*	1.909 down	.0109	9793
Cullin 4B	*CUL4B*	1.909 down	.0204	8450
Paired related homeobox 1	*PRRX1*	1.908 down	.0262	5396
Minichromosome maintenance complex component 3 associated protein	*MCM3AP*	1.907 down	.0424	8888
Sp1 transcription factor	*SP1*	1.906 down	.0327	6667
Nuclear transcription factor Y, gamma	*NFYC*	1.904 down	.0239	4802

TABLE E2. Continued

Gene title	Symbol	Fold	*P* value	Gene ID
v-rel reticuloendotheliosis viral oncogene homolog A, nuclear factor of kappa light polypeptide gene enhancer in B-cells 3, p65 (avian)	*RELA*	1.904 down	.0498	5970
Chromosome 5 open reading frame 22	*C5orf22*	1.903 down	.0126	55322
MYST histone acetyltransferase (monocytic leukemia) 4	*MYST4*	1.903 down	.0135	23522
Iroquois homeobox 5	*IRX5*	1.903 down	.0313	10265
Epoxide hydrolase 1, microsomal (xenobiotic)	*EPHX1*	1.903 down	.0158	2052
Microtubule associated monoxygenase, calponin and LIM domain containing 3///similar to Protein MICAL-3	*LOC731210 ///MICAL3*	1.903 down	.0487	57553/// 731210
Putative homeodomain transcription factor 2	*PHTF2*	1.902 down	.04	57157
Mitogen-activated protein kinase kinase kinase 3	*MAP3K3*	1.901 down	.0458	4215
Zinc finger protein 227	*ZNF227*	1.900 down	.0262	7770
Membrane associated guanylate kinase, WW and PDZ domain containing 2	*MAGI2*	1.900 down	.035	9863
Bicaudal D homolog 2 *(Drosophila)*	*BICD2*	1.900 down	.0232	23299
Adducin 1 (alpha)	*ADD1*	1.900 down	.0136	118
Plexin B1	*PLXNB1*	1.900 down	.034	5364
Adenylate cyclase 9	*ADCY9*	1.899 down	.0163	115
Zinc finger CCCH-type containing 7A	*ZC3H7A*	1.899 down	.0118	29066
TOX high mobility group box family member 4///similar to Epidermal Langerhans cell protein LCP1	*LOC285412 ///TOX4*	1.899 down	.0263	285412/// 9878
Nucleoporin 98 kd	*NUP98*	1.898 down	.0212	4928
Platelet derived growth factor C	*PDGFC*	1.897 down	.0461	56034
Block of proliferation 1///similar to block of proliferation 1	*BOP1/// LOC727967*	1.897 down	.0448	23246/// 727967
Obscurin, cytoskeletal calmodulin and titin-interacting RhoGEF	*OBSCN*	1.896 down	.0392	84033
guanine nucleotide binding protein (G protein), beta 5	*GNB5*	1.894 down	.0396	10681
Protein tyrosine phosphatase, nonreceptor type 21	*PTPN21*	1.894 down	.0278	11099
Adaptor-related protein complex 3, delta 1 subunit	*AP3D1*	1.890 down	.0112	8943
v-akt murine thymoma viral oncogene homolog 2	*AKT2*	1.889 down	.0174	208
Solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 6	*SLC25A6*	1.889 down	.0291	293
Zinc finger, DHHC-type containing 5	*ZDHHC5*	1.888 down	.0136	25921
Latent transforming growth factor beta binding protein 1	*LTBP1*	1.888 down	.0126	4052
Rho GTPase activating protein 26	*ARHGAP26*	1.887 down	.0245	23092
ATPase, class I, type 8B, member 2	*ATP8B2*	1.885 down	.0109	57198
Tuberous sclerosis 2	*TSC2*	1.885 down	.0281	7249
ATPase, class VI, type 11A	*ATP11A*	1.884 down	.0107	23250
RIO kinase 3 (yeast)	*RIOK3*	1.883 down	.0238	8780
Golgi apparatus protein 1	*GLG1*	1.882 down	.0234	2734
Nicotinamide nucleotide transhydrogenase	*NNT*	1.880 down	.0106	23530
Chromosome 19 open reading frame 6	*C19orf6*	1.879 down	.0125	91304
Bromodomain containing 2	*BRD2*	1.879 down	.0228	6046
Purine-rich element binding protein B	*PURB*	1.879 down	.0281	5814
Glutathione reductase	*GSR*	1.879 down	.00928	2936
ADP-ribosylation factor guanine nucleotide-exchange factor 1 (brefeldin A-inhibited)	*ARFGEF1*	1.877 down	.00671	10565
ADP-ribosylation factor interacting protein 1 (arfaptin 1)	*ARFIP1*	1.877 down	.0116	27236
Rhotekin	*RTKN*	1.876 down	.0109	6242
Jumonji domain containing 3, histone lysine demethylase	*JMJD3*	1.875 down	.0102	23135
Zinc finger and SCAN domain containing 18	*ZSCAN18*	1.874 down	.0223	65982
Kelch repeat and BTB (POZ) domain containing 4	*KBTBD4*	1.873 down	.044	55709
PRP6 pre-mRNA processing factor 6 homolog *(S cerevisiae)*	*PRPF6*	1.872 down	.0132	24148
CCR4-NOT transcription complex, subunit 3	*CNOT3*	1.871 down	.0226	4849

TABLE E2. Continued

Gene title	Symbol	Fold	*P* value	Gene ID
Zinc finger, RAN-binding domain containing 1	*ZRANB1*	1.870 down	.0289	54764
Glucosidase, alpha; neutral AB	*GANAB*	1.870 down	.0149	23193
Protein tyrosine phosphatase, receptor type, f polypeptide (PTPRF), interacting protein (liprin), alpha 1	*PPFIA1*	1.870 down	.0281	8500
Vitamin K epoxide reductase complex, subunit 1-like 1	*VKORC1L1*	1.869 down	.0114	154807
Ring finger and CCCH-type zinc finger domains 2	*RC3H2*	1.869 down	.0112	54542
F-box and leucine-rich repeat protein 15	*FBXL15*	1.869 down	.0287	79176
Zinc finger, FYVE domain containing 9	*ZFYVE9*	1.869 down	.0129	9372
Transcribed locus		1.867 down	.0217	
Trinucleotide repeat containing 6B	*TNRC6B*	1.867 down	.0128	23112
Anterior pharynx defective 1 homolog A *(C elegans)*	*APH1A*	1.867 down	.0317	51107
Protein phosphatase 5, catalytic subunit	*PPP5C*	1.866 down	.0448	5536
Zinc finger protein 289, ID1 regulated	*ZNF289*	1.866 down	.0462	84364
UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 2 (GalNAc-T2)	*GALNT2*	1.865 down	.0191	2590
Solute carrier family 25, member 30	*SLC25A30*	1.864 down	.0372	253512
Kelch-like 23 *(Drosophila)*	*KLHL23*	1.864 down	.0281	151230
RAB3 GTPase activating protein subunit 2 (non-catalytic)	*RAB3GAP2*	1.862 down	.0129	25782
Ring finger and CCCH-type zinc finger domains 2	*RC3H2*	1.861 down	.0128	54542
Phospholipase C, beta 4	*PLCB4*	1.859 down	.016	5332
Glucosidase, beta (bile acid) 2	*GBA2*	1.858 down	.0134	57704
Cyclin-dependent kinase inhibitor 1C (p57, Kip2)	*CDKN1C*	1.858 down	.0266	1028
WWC family member 3	*WWC3*	1.857 down	.0109	55841
Tripeptidyl peptidase I	*TPP1*	1.856 down	.0294	1200
CD99 molecule-like 2	*CD99L2*	1.855 down	.0203	83692
Zinc finger protein 655	*ZNF655*	1.853 down	.0226	79027
Actin filament associated protein 1-like 1	*AFAP1L1*	1.853 down	.016	134265
Eukaryotic translation initiation factor 4B	*EIF4B*	1.852 down	.0112	1975
p21 (CDKN1A)-activated kinase 2	*PAK2*	1.852 down	.0125	5062
Poliovirus receptor	*PVR*	1.852 down	.00712	5817
RAB3 GTPase activating protein subunit 1 (catalytic)	*RAB3GAP1*	1.852 down	.0274	22930
Interleukin enhancer binding factor 3, 90 kd	*ILF3*	1.851 down	.0116	3609
Chromosome 6 open reading frame 106	*C6orf106*	1.850 down	.03	64771
Purine-rich element binding protein A	*PURA*	1.850 down	.0384	5813
Wolf-Hirschhorn syndrome candidate 1-like 1	*WHSC1L1*	1.849 down	.0167	54904
Fem-1 homolog b *(C elegans)*	*FEM1B*	1.849 down	.0214	10116
Jun oncogene	*JUN*	1.848 down	.0243	3725
NDRG family member 2	*NDRG2*	1.848 down	.0415	57447
Protocadherin gamma subfamily A, 1	*PCDHGA1*	1.847 down	.0112	9708
Solute carrier family 6 (neurotransmitter transporter, creatine), member 8	*SLC6A8*	1.847 down	.0266	6535
Upstream binding transcription factor, RNA polymerase I	*UBTF*	1.847 down	.0227	7343
Zer-1 homolog *(C elegans)*	*ZER1*	1.846 down	.0166	10444
Prion protein (p27-30) (Creutzfeldt-Jakob disease, Gerstmann-Strausler-Scheinker syndrome, fatal familial insomnia)	*PRNP*	1.845 down	.0168	5621
General transcription factor IIIC, polypeptide 1, alpha 220 kd	*GTF3C1*	1.844 down	.0274	2975
Pumilio homolog 1 *(Drosophila)*	*PUM1*	1.843 down	.0257	9698
Splicing factor, arginine/serine-rich 1 (splicing factor 2, alternate splicing factor)	*SFRS1*	1.842 down	.0158	6426
Kelch repeat and BTB (POZ) domain containing 2	*KBTBD2*	1.842 down	.0124	25948
Translocase of inner mitochondrial membrane 44 homolog (yeast)	*TIMM44*	1.841 down	.0241	10469
1-Acylglycerol-3-phosphate O-acyltransferase 3	*AGPAT3*	1.841 down	.011	56894

TABLE E2. Continued

Gene title	Symbol	Fold	*P* value	Gene ID
Ezrin	*EZR*	1.840 down	.0279	7430
Down syndrome critical region gene 3	*DSCR3*	1.840 down	.0355	10311
v-ets erythroblastosis virus E26 oncogene homolog 1 (avian)	*ETS1*	1.839 down	.0347	2113
Ubiquitin-conjugating enzyme E2S///similar to ubiquitin-conjugating enzyme E2S (Ubiquitin-conjugating enzyme E2-24 kd) (Ubiquitin-protein ligase) (Ubiquitin carrier protein) (E2-EPF5)	*LOC731049 ///UBE2S*	1.839 down	.049	27338/// 731049
Solute carrier family 6 (neurotransmitter transporter, creatine), member 8	*SLC6A8*	1.837 down	.0172	6535
Minichromosome maintenance complex component 3 associated protein	*MCM3AP*	1.835 down	.017	8888
Glucocorticoid receptor DNA binding factor 1	*GRLF1*	1.834 down	.0218	2909
Aryl hydrocarbon receptor nuclear translocator	*ARNT*	1.832 down	.0179	405
Integrin, alpha 6	*ITGA6*	1.832 down	.0394	3655
La ribonucleoprotein domain family, member 5	*LARP5*	1.831 down	.0238	23185
Heat shock transcription factor 1	*HSF1*	1.831 down	.0255	3297
DCP1 decapping enzyme homolog A *(S cerevisiae)*	*DCP1A*	1.829 down	.0142	55802
Sterile alpha motif domain containing 4A	*SAMD4A*	1.829 down	.0121	23034
Desmin	*DES*	1.829 down	.0484	1674
KIAA1826	*KIAA1826*	1.828 down	.0423	84437
Microtubule associated serine/threonine kinase family member 4	*MAST4*	1.828 down	.0448	375449
Nuclear factor I/C (CCAAT-binding transcription factor)	*NFIC*	1.828 down	.0119	4782
Heat shock 70 kd protein 4	*HSPA4*	1.828 down	.0167	3308
Forkhead box O3	*FOXO3*	1.827 down	.024	2309
Core-binding factor, beta subunit	*CBFB*	1.825 down	.0121	865
Mitogen-activated protein kinase kinase 2	*MAP2K2*	1.822 down	.0295	5605
RRN3 RNA polymerase I transcription factor homolog *(S cerevisiae)*///RRN3 RNA polymerase I transcription factor homolog *(S cerevisiae)* pseudogene	*LOC653390/// LOC730092 ///RRN3*	1.822 down	.0307	54700/// 653390/// 730092
GCN1 general control of amino-acid synthesis 1-like 1 (yeast)	*GCN1L1*	1.822 down	.0242	10985
Cullin 5	*CUL5*	1.821 down	.0119	8065
CDNA FLJ34585 fis, clone KIDNE2008758		1.821 down	.0142	
Related RAS viral (r-ras) oncogene homolog 2	*RRAS2*	1.820 down	.0206	22800
MAX dimerization protein 4	*MXD4*	1.820 down	.0161	10608
Transglutaminase 2 (C polypeptide, protein-glutamine-gamma-glutamyltransferase)	*TGM2*	1.820 down	.0419	7052
Collagen, type IV, alpha 1	*COL4A1*	1.820 down	.0216	1282
Polymerase I and transcript release factor	*PTRF*	1.819 down	.0286	284119
Methyl-CpG binding domain protein 1	*MBD1*	1.819 down	.0245	4152
BTG family, member 2	*BTG2*	1.819 down	.0337	7832
G protein–coupled receptor kinase 5	*GRK5*	1.819 down	.0452	2869
Protein associated with topoisomerase II homolog 1 (yeast)	*PATL1*	1.818 down	.0147	219988
Interleukin enhancer binding factor 3, 90 kd	*ILF3*	1.818 down	.0328	3609
Ras homolog gene family, member J	*RHOJ*	1.817 down	.0278	57381
Chromosome 10 open reading frame 18	*C10orf18*	1.817 down	.0136	54906
NMDA receptor regulated 2	*NARG2*	1.817 down	.0424	79664
Transcription factor 25 (basic helix-loop-helix)	*TCF25*	1.817 down	.0142	22980
Spastic paraplegia 7 (pure and complicated autosomal recessive)	*SPG7*	1.817 down	.0368	6687
Heterogeneous nuclear ribonucleoprotein M	*HNRPM*	1.815 down	.0206	4670
Fidgetin	*FIGN*	1.814 down	.0484	55137
Chromosome 5 open reading frame 41	*C5orf41*	1.814 down	.049	153222
SMAD specific E3 ubiquitin protein ligase 1	*SMURF1*	1.812 down	.0237	57154
Cold inducible RNA binding protein	*CIRBP*	1.812 down	.04	1153

TABLE E2. Continued

Gene title	Symbol	Fold	*P* value	Gene ID
SLAIN motif family, member 2	*SLAIN2*	1.812 down	.0309	57606
Required for meiotic nuclear division 5 homolog A *(S cerevisiae)*	*RMND5A*	1.811 down	.0383	64795
SH3 domain protein D19	*SH3D19*	1.811 down	.0445	152503
Pericentriolar material 1	*PCM1*	1.810 down	.00823	5108
Quaking homolog, KH domain RNA binding (mouse)	*QKI*	1.810 down	.0266	9444
Insulin-degrading enzyme	*IDE*	1.809 down	.0192	3416
zinc finger, HIT type 4	*ZNHIT4*	1.808 down	.018	83444
T-box 5	*TBX5*	1.808 down	.0128	6910
Myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, *Drosophila*); translocated to, 4	*MLLT4*	1.807 down	.0283	4301
Myosin regulatory light chain interacting protein	*MYLIP*	1.807 down	.031	29116
Phosphate cytidylyltransferase 1, choline, alpha	*PCYT1A*	1.806 down	.0208	5130
RNA binding motif protein 8A	*RBM8A*	1.805 down	.0339	9939
Protein kinase C and casein kinase substrate in neurons 2	*PACSIN2*	1.804 down	.0284	11252
Polymerase (RNA) II (DNA directed) polypeptide E, 25 kd	*POLR2E*	1.804 down	.0356	5434
Stromal antigen 2	*STAG2*	1.804 down	.0203	10735
Chromosome 1 open reading frame 71	*C1orf71*	1.803 down	.0187	163882
Transmembrane protein 127	*TMEM127*	1.803 down	.0244	55654
Valyl-tRNA synthetase	*VARS*	1.802 down	.0291	7407
prosaposin (variant Gaucher disease and variant metachromatic leukodystrophy)	*PSAP*	1.801 down	.0324	5660
Zinc finger protein 12	*ZNF12*	1.800 down	.0384	7559