Column ID	Symbol	p-value	FC(AI delet vs. NI)	Accession number	Description
GE83435	CFC1	0.029	-14.74	NM_032545	cripto, FRL-1, cryptic family 1
GE80256	MB	0.030	-7.60	NM_005368	myoglobin
GE593900	SOS1	0.014	-7.08	AI341328	Transcribed locus
GE61808	RERGL	0.038	-6.27	NM_024730	hypothetical protein FLJ22655
GE86790	TNC	0.006	-6.27	X78565	tenascin C (hexabrachion)
GE588622	STX18	0.026	-6.12	BX363588	syntaxin 18
GE793773	RTCD1	0.028	-5.86	BU537444	Transcribed locus, weakly similar to XP_524454.1 PREDICTED: hypothetical protein
GE765743	DKFZP451A211	0.005	-5.35	BX647655	DKFZp451A211 protein
GE770174	ONECUT2	0.007	-5.17	AV688391	CDNA FLJ42567 fis, clone BRACE3007559
GE87131	GIPC2	0.005	-4.89	NM_017655	GIPC PDZ domain containing family, member 2
GE796635	LOC283432	0.011	-4.86	BC037211	hypothetical protein LOC283432
GE80174	SLCO1C1	0.035	-4.62	NM_017435	solute carrier organic anion transporter family, member 1C1
GE59516	GPR37	0.047	-4.53	NM_005302	G protein-coupled receptor 37 (endothelin receptor type B-like)
GE80597	RDH8	0.042	-4.46	NM_015725	retinol dehydrogenase 8 (all-trans)
GE835647	SBF2	0.018	-4.45	BM665519	SET binding factor 2
GE746209	NCAM1	0.030	-4.41	BE670666	Neural cell adhesion molecule 1
GE863743	LOC100132473	0.046	-4.21	BF509363	hypothetical protein LOC100132473
GE535765	GCK	0.004	-4.19	NM_000162	glucokinase (hexokinase 4, maturity onset diabetes of the young 2)
GE619539	BCL2L1	0.046	-4.09	BI043329	BCL2-like 1
GE60399	ECE1	0.001	-4.09	BM127612	Endothelin converting enzyme 1
GE558962	DIP2C	0.016	-4.08	N92571	KIAA0934
GE797833	LOC389230	0.047	-4.01	AI286100	Hypothetical LOC389230
GE483167	MAP4K4	0.047	-4.00	BM988261	Mitogen-activated protein kinase kinase kinase kinase 4
GE85201	SLC37A1	0.030	-3.94	AK124103	CDNA FLJ42109 fis, clone TESOP2008563
GE663671	KIF26B	0.022	-3.93	AI911726	Hypothetical protein FLJ10157
GE494820	HS3ST4	0.019	-3.91	AI698706	Heparan sulfate (glucosamine) 3-O-sulfotransferase 4
GE722183	DENND5B	0.024	-3.90	BG432514	Hypothetical protein MGC24039
GE864902	RABGAP1L	0.002	-3.89	AW444900	RAB GTPase activating protein 1-like
GE57901	RAB3B	0.019	-3.89	NM_002867	RAB3B, member RAS oncogene family
GE80672	FGF19	0.044	-3.84	NM_005117	fibroblast growth factor 19
GE62557	CLCN1	0.023	-3.83	NM_000083	chloride channel 1, skeletal muscle (Thomsen disease, autosomal dominant)
GE575454	ITGBL1	0.015	-3.82	AK095102	Integrin, beta-like 1 (with EGF-like repeat domains)
GE492776	ALDH1L2	0.017	-3.81	BF802115	Aldehyde dehydrogenase 1 family, member L2
GE624065	PLCB1	0.035	-3.80	AW271221	Phospholipase C, beta 1 (phosphoinositide-specific)
GE606232	LRP1B	0.023	-3.78	CB986909	Low density lipoprotein-related protein 1B (deleted in tumors)
GE537853	PC	0.022	-3.75	AI807935	Pyruvate carboxylase
GE830886	CARS	0.035	-3.74	BF515241	Cysteinyl-tRNA synthetase
GE557636	C18ORF2	0.017	-3.66	NM_031416	chromosome 18 open reading frame 2
GE771211	IGF1R	0.006	-3.65	BU590158	Insulin-like growth factor 1 receptor
GE55572	TESC	0.009	-3.62	NM_017899	hypothetical protein FLJ20607
GE495440	UBR1	0.040	-3.56	N70681	Ubiquitin protein ligase E3 component n-recognin 1
GE87029	RTN4RL1	0.043	-3.54	AA453879	Reticulon 4 receptor-like 1
GE633198	RUNDC2C	0.029	-3.53	AA744413	MRNA; cDNA DKFZp686H0819 (from clone DKFZp686H0819)
GE54665	NECAB2	0.037	-3.52	NM_019065	EF-hand calcium binding protein 2
GE79293	CLDN3	0.008	-3.50	NM_001306	claudin 3
GE794355	DEPDC4	0.022	-3.48	NM_152317	DEP domain containing 4
GE735571	BRP44L	0.035	-3.44	T87067	Brain protein 44-like
GE781524	MS4A8B	0.005	-3.40	BE674652	Membrane-spanning 4-domains, subfamily A, member 8B

Column ID	Symbol	p-value	FC(AI delet vs. NI)	Accession number	Description
GE79426	MYL7	0.008	-3.40	NM_021223	myosin, light polypeptide 7, regulatory
GE513159	ZNF397	0.014	-3.37	AA007378	Transcribed locus, moderately similar to XP_511691.1 PREDICTED: envoplakin [Pan
GE475874	LCP1	0.007	-3.36	AI475735	lymphocyte cytosolic protein 1 (L-plastin)
GE80001	PAX9	0.012	-3.35	NM_006194	paired box gene 9
GE500231	VWF	0.038	-3.33	N65960	Von Willebrand factor
GE58254	FZD2	0.027	-3.32	NM_001466	frizzled homolog 2 (Drosophila)
GE83639	NLRP12	0.018	-3.31	NM_033297	NACHT, leucine rich repeat and PYD containing 12
GE87923	PTBP1	0.036	-3.30	X62006	polypyrimidine tract binding protein 1
GE508448	LOC144817	0.008	-3.30	AK056732	hypothetical protein LOC144817
GE614069	FLJ22536	0.027	-3.27	AI634087	Hypothetical gene supported by AK026189
GE85476	FGF14	0.009	-3.26	NM_004115	fibroblast growth factor 14
GE526055	PLEKHG1	0.014	-3.23	BU737135	Pleckstrin homology domain containing, family G (with RhoGef domain) member 1
GE813412	LOC339316	0.012	-3.22	BC043286	hypothetical protein LOC339316
GE828468	CASP8	0.041	-3.17	BG258036	Caspase 8, apoptosis-related cysteine peptidase
GE844611	RHBDD1	0.008	-3.17	AW294697	Hypothetical protein LOC84236
GE605114	ST3GAL3	0.014	-3.15	AI939358	ST3 beta-galactoside alpha-2,3-sialyltransferase 3
GE59333	EFNB3	0.006	-3.15	AK027329	ephrin-B3
GE886643	ZNF516	0.025	-3.13	BG396029	Zinc finger protein 516
GE81021	FABP1	0.034	-3.13	NM_001443	fatty acid binding protein 1, liver
GE774734	PDE11A	0.014	-3.13	AW243775	Phosphodiesterase 11A
GE521452	LPP	0.015	-3.12	BQ428740	FLJ42393 protein
GE59693	GLI1	0.029	-3.11	NM_005269	glioma-associated oncogene homolog 1 (zinc finger protein)
GE80201	RTN1	0.034	-3.10	NM_021136	reticulon 1
GE675916	HMGX3	0.038	-3.08	BE646401	KIAA0194 protein
GE624474	HEATR5A	0.042	-3.08	BX098906	Chromosome 14 open reading frame 125
GE522091	CADM2	0.025	-3.07	NM_153184	immunoglobulin superfamily, member 4D
GE525934	F2RL2	0.010	-3.04	BC043525	Coagulation factor II (thrombin) receptor-like 2
GE786844	RPAP2	0.028	-3.03	AI277314	Chromosome 1 open reading frame 82
GE833951	TDRD6	0.023	-3.03	BF057109	Phospholipase A2, group VII (platelet-activating factor acetylhydrolase, plasma)
GE782658	SOX6	0.038	-3.02	BX101216	SRY (sex determining region Y)-box 6
GE62462	KCND2	0.000	-3.01	NM_012281	potassium voltage-gated channel, Shal-related subfamily, member 2
GE525291	TMEM71	0.046	-3.00	NM_144649	transmembrane protein 71
GE493031	B3GALT1	0.045	-3.00	NM_020981	UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 1
GE539154	TLL2	0.017	-2.99	NM_012465	tolloid-like 2
GE56173	LEF1	0.015	-2.98	NM_016269	lymphoid enhancer-binding factor 1
GE61224	ATP5G2	0.030	-2.98	H83751	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit c (subunit 9),
GE59525	TLR3	0.015	-2.97	NM_003265	toll-like receptor 3
GE833078	KIAA0247	0.003	-2.97	AK127083	KIAA0247
GE554330	FLJ36644	0.035	-2.96	AK093963	hypothetical gene supported by AK093963
GE653654	MIER1	0.015	-2.96	AI702148	WD repeat domain 78
GE57323	NEUROD1	0.016	-2.96	NM_002500	neurogenic differentiation 1
GE557616	LOC729147	0.040	-2.95	AI935382	Transcribed locus
GE505658	PTCHD1	0.034	-2.95	NM_173495	patched domain containing 1
GE83802	IMPACT	0.039	-2.93	AF232229	hypothetical protein IMPACT
GE479162	FGF4	0.032	-2.92	NM_002007	fibroblast growth factor 4 (heparin secretory transforming protein 1, Kaposi sar
GE812224	NCRNA00086	0.025	-2.89	BX641629	Hypothetical protein MGC39606
GE56310	RCN1	0.026	-2.89	AI247740	LOC440135
GE835183	PARVG	0.047	-2.89	AW293504	Parvin, gamma

Column ID	Symbol	p-value	FC(AI delet vs. NI)	Accession number	Description
GE812520	C2ORF34	0.020	-2.88	BF196390	Chromosome 2 open reading frame 34
GE81351	FGF14	0.037	-2.87	NM_004115	fibroblast growth factor 14
GE525781	CDON	0.038	-2.87	AK022986	Cdon homolog (mouse)
GE56366	STAT5B	0.021	-2.87	AV723605	Signal transducer and activator of transcription 5B
GE748783	ZFHX3	0.015	-2.86	AW188568	AT-binding transcription factor 1
GE55303	SLC23A1	0.010	-2.85	NM_005847	solute carrier family 23 (nucleobase transporters), member 1
GE681995	KRAS	0.046	-2.84	AW629226	V-Ki-ras2 Kirsten rat sarcoma viral oncogene homolog
GE879159	FBXO25	0.021	-2.84	BQ647583	F-box protein 25
GE60398	RUNX3	0.013	-2.83	NM_004350	runt-related transcription factor 3
GE880225	DKFZP547K054	0.027	-2.82	BF194990	Hypothetical protein DKFZp547K054
GE818835	LIN54	0.020	-2.82	BF678497	Hypothetical protein DKFZp686L1814
GE751360	RGS10	0.046	-2.82	AA593498	Regulator of G-protein signalling 10
GE739612	LOC389493	0.042	-2.82	BX439814	Similar to Nuclear protein 1 (Protein p8) (Candidate of metastasis 1)
GE54032	TTTY2	0.019	-2.81	AF000991	testis-specific transcript, Y-linked 2
GE736147	PCDHGC3	0.038	-2.81	BF924877	Protocadherin gamma subfamily A, 12
GE59740	HOXB3	0.031	-2.80	NM_002146	homeobox B3
GE78952	HNRNPF	0.006	-2.80	NM_004966	heterogeneous nuclear ribonucleoprotein F
GE501149	COL27A1	0.021	-2.80	BC007696	collagen, type XXVII, alpha 1
GE588628	USP10	0.005	-2.79	BF915158	Ubiquitin specific peptidase 10
GE633096	SESN3	0.016	-2.78	AW978341	Sestrin 3
GE624229	BCL11B	0.028	-2.78	AA033991	B-cell CLL/lymphoma 11B (zinc finger protein)
GE845135	WDR92	0.046	-2.78	AW292857	Hypothetical protein BC014022
GE747802	DSCAM	0.024	-2.77	AI929325	Down syndrome cell adhesion molecule
GE525392	CATSPER4	0.011	-2.77	AA421134	Cation channel, sperm associated 4
GE654220	RPH3AL	0.039	-2.75	AA236651	rabphilin 3A-like (without C2 domains)
GE769024	NEDD4L	0.020	-2.75	BF477037	Neural precursor cell expressed, developmentally down-regulated 4-like
GE526180	TMEM196	0.035	-2.75	NM_152774	hypothetical protein MGC42090
GE902895	TPH1	0.044	-2.74	NM_004179	tryptophan hydroxylase 1 (tryptophan 5-monooxygenase)
GE82862	CCNJL	0.042	-2.73	BF092027	Hypothetical protein FLJ14166
GE81283	FZD5	0.015	-2.73	NM_003468	frizzled homolog 5 (Drosophila)
GE829609	C6ORF62	0.043	-2.73	BM906186	Chromosome 6 open reading frame 62
GE884238	ZFAND3	0.046	-2.72	BQ187283	Zinc finger, AN1-type domain 3
GE599378	SOCS6	0.035	-2.72	AA700753	Suppressor of cytokine signaling 6
GE494897	C1ORF62	0.044	-2.72	BX099864	Chromosome 1 open reading frame 62
GE59657	GJB1	0.014	-2.72	NM_000166	gap junction protein, beta 1, 32kDa (connexin 32, Charcot-Marie-Tooth neuropathy
GE60503	PGC	0.025	-2.72	NM_002630	progastricsin (pepsinogen C)
GE58058	GRPR	0.021	-2.72	NM_005314	gastrin-releasing peptide receptor
GE84509	CNOT7	0.007	-2.71	CA392740	CCR4-NOT transcription complex, subunit 7
GE86143	RPS6KA2	0.002	-2.71	AK027727	ribosomal protein S6 kinase, 90kDa, polypeptide 2
GE783463	HNT	0.014	-2.71	R14751	Neurotrimin
GE716639	DAPK2	0.044	-2.71	AA180810	Death-associated protein kinase 2
GE505388	CALHM2	0.027	-2.71	AI225020	Family with sequence similarity 26, member B
GE80272	SSX1	0.026	-2.71	NM_005635	synovial sarcoma, X breakpoint 1
GE848456	PPP1R12B	0.037	-2.71	BF510523	Protein phosphatase 1, regulatory (inhibitor) subunit 12B
GE59707	VIL1	0.020	-2.70	NM_007127	villin 1
GE62663	PDCD4	0.046	-2.70	NM_014456	programmed cell death 4 (neoplastic transformation inhibitor)
GE471270	ARL15	0.004	-2.70	AK026456	ADP-ribosylation factor-like 15
GE556466	WDR40B	0.046	-2.70	NM_178470	WD repeat domain 40B

Column ID	Symbol	p-value	FC(AI delet vs. NI)	Accession number	Description
GE54695	FGF18	0.045	-2.69	NM_003862	fibroblast growth factor 18
GE80087	WNT9A	0.016	-2.68	NM_003395	wingless-type MMTV integration site family, member 9A
GE746389	C11ORF49	0.034	-2.68	AI123967	MGC4707 protein
GE513392	GNAO1	0.025	-2.68	AK093105	guanine nucleotide binding protein (G protein), alpha activating activity polyp
GE581356	ARMC4	0.026	-2.67	H53792	yq85h08.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:202623
GE792017	CUL3	0.026	-2.66	BE646539	Cullin 3
GE56055	ITM2A	0.019	-2.66	NM_004867	integral membrane protein 2A
GE55395	CCHCR1	0.020	-2.66	NM_019052	coiled-coil alpha-helical rod protein 1
GE580029	LOC100132963	0.045	-2.66	AI149692	similar to hCG1808463
GE470821	IMMP2L	0.047	-2.66	BX089540	IMP2 inner mitochondrial membrane peptidase-like (S. cerevisiae)
GE879485	SCAMP1	0.034	-2.66	BF511725	Secretory carrier membrane protein 1
GE500217	LSAMP	0.031	-2.65	R49462	Transcribed locus
GE891168	C11ORF82	0.016	-2.65	NM_145018	hypothetical protein FLJ25416
GE562125	LOC342346	0.043	-2.65	XM_296817	similar to hypothetical protein DKFZp434P0316
GE611476	PTGFR	0.022	-2.65	BU534984	Prostaglandin F receptor (FP)
GE480386	LARGE	0.033	-2.64	BQ045015	like-glycosyltransferase
GE61226	RPS13	0.040	-2.64	NM_001017	ribosomal protein S13
GE517764	GTF2E1	0.001	-2.64	BX099808	General transcription factor IIE, polypeptide 1, alpha 56kDa
GE560334	COL4A3BP	0.021	-2.63	AW974465	Collagen, type IV, alpha 3 (Goodpasture antigen) binding protein
GE708909	STON2	0.046	-2.63	BI494557	Stonin 2
GE624897	SLC35F5	0.020	-2.63	AA446513	Solute carrier family 35, member F5
GE844833	DIAPH2	0.024	-2.62	AW292964	Diaphanous homolog 2 (Drosophila)
GE790256	RCSD1	0.046	-2.61	AW027501	RCSD domain containing 1
GE752862	TTC21B	0.021	-2.61	AI812049	Tetratricopeptide repeat domain 21B
GE691871	AGAP1	0.044	-2.60	BX103345	Centaurin, gamma 2
GE513001	PTPRN2	0.021	-2.60	AK093884	Protein tyrosine phosphatase, receptor type, N polypeptide 2
GE524782	C21ORF66	0.025	-2.60	BC038361	CDNA clone IMAGE:4837199
GE537904	TMEM49	0.038	-2.60	BE185268	Transmembrane protein 49
GE789470	TGIF1	0.016	-2.60	BX117081	TGFB-induced factor (TALE family homeobox)
GE497414	RRM1	0.042	-2.59	BF510839	Transcribed locus, strongly similar to NP_002897.1 radixin [Homo sapiens]
GE847994	ZNF750	0.038	-2.59	BM988168	Tubulin-specific chaperone d
GE617133	SIPA1L3	0.033	-2.59	BC000772	Signal-induced proliferation-associated 1 like 3
GE685070	ARMC9	0.036	-2.59	BF437252	Armadillo repeat containing 9
GE583888	NKX2-3	0.015	-2.58	NM_145285	NK2 transcription factor related, locus 3 (Drosophila)
GE53879	NRXN2	0.017	-2.58	NM_015080	neurexin 2
GE57660	MIF	0.007	-2.58	AW162060	Macrophage migration inhibitory factor (glycosylation-inhibiting factor)
GE59180	P2RX1	0.008	-2.58	NM_002558	purinergic receptor P2X, ligand-gated ion channel, 1
GE558478	FNDC3A	0.036	-2.57	BF771477	Fibronectin type III domain containing 3A
GE728241	HCG2036778	0.019	-2.57	AA909454	Transcribed locus
GE880824	TAF3	0.043	-2.57	BM904502	TAF3 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 140kDa
GE743043	DNAI1	0.021	-2.57	BE550140	Dynein, axonemal, intermediate polypeptide 1
GE60093	LIG3	0.044	-2.56	NM_013975	ligase III, DNA, ATP-dependent
GE581516	EGFR	0.003	-2.56	AK024321	Homo sapiens cDNA FLJ14259 fis, clone PLACE1001076.
GE511768	DNAJB8	0.009	-2.56	NM_153330	DnaJ (Hsp40) homolog, subfamily B, member 8
GE753147	NEURL	0.027	-2.56	BG008030	neuralized homolog (Drosophila)
GE526190	CCDC42	0.040	-2.55	NM_144681	coiled-coil domain containing 42
GE851667	EMCN	0.014	-2.55	AW293210	Endomucin
GE606631	CFH	0.015	-2.55	W91942	Transcribed locus

Column ID	Symbol	p-value	FC(AI delet vs. NI)	Accession number	Description
GE883383	TMEM196	0.027	-2.55	BX647256	hypothetical protein MGC42090
GE835642	TGFBR3	0.040	-2.55	BF509889	Transforming growth factor, beta receptor III (betaglycan, 300kDa)
GE742952	NGLY1	0.039	-2.55	AI425043	N-glycanase 1
GE716674	CSMD2	0.040	-2.55	AA805541	High-mobility group box 4
GE480459	FAM111B	0.009	-2.55	NM_198947	cancer-associated nucleoprotein
GE84677	ANKH	0.028	-2.55	W02417	Ankylosis, progressive homolog (mouse)
GE733189	COL11A1	0.023	-2.54	AK022035	Collagen, type XI, alpha 1
GE496650	TRIM67	0.009	-2.54	BE465331	Hypothetical protein FLJ30430
GE537757	SIRPB2	0.031	-2.54	BG539998	Protein tyrosine phosphatase, non-receptor type substrate 1-like 3
GE821046	NCRNA00153	0.035	-2.53	BQ187306	Chromosome 20 open reading frame 19
GE59665	LALBA	0.048	-2.53	NM_002289	lactalbumin, alpha-
GE782075	CDH13	0.042	-2.53	AF088013	Cadherin 13, H-cadherin (heart)
GE897537	NCAM2	0.008	-2.53	AK021495	Neural cell adhesion molecule 2
GE833485	PSMG4	0.044	-2.52	AK126623	hypothetical LOC389362
GE495765	LOC100129869	0.023	-2.52	AK128005	unnamed protein product; Homo sapiens cDNA FLJ46124 fis, clone TESTI2040372.
GE57571	HMGCL	0.041	-2.51	NM_000191	3-hydroxymethyl-3-methylglutaryl-Coenzyme A lyase (hydroxymethylglutaricaciduria
GE855844	TRAF3IP2	0.024	-2.51	AW138021	TRAF3 interacting protein 2
GE53516	PKN3	0.034	-2.51	NM_013355	protein kinase N3
GE83267	KCNA7	0.049	-2.50	NM_031886	potassium voltage-gated channel, shaker-related subfamily, member 7
GE632575	SHROOM1	0.049	-2.50	AI828458	Apical protein 2
GE786167	FAM107B	0.043	-2.50	AA203497	Chromosome 10 open reading frame 45
GE749824	EPX	0.045	-2.50	BE222258	Eosinophil peroxidase
GE85378	SLC35D3	0.017	-2.50	AI306597	Solute carrier family 35, member D3
GE741024	C10ORF114	0.041	-2.50	CB409529	Chromosome 10 open reading frame 114
GE60460	TNFRSF11B	0.048	-2.49	NM_002546	tumor necrosis factor receptor superfamily, member 11b (osteoprotegerin)
GE80182	PCDHB4	0.047	-2.48	NM_018938	protocadherin beta 4
GE905225	TAAR1	0.026	-2.48	NM_138327	trace amine associated receptor 1
GE662738	TYW3	0.042	-2.48	CA446960	Chromosome 1 open reading frame 171
GE644990	HOXC6	0.039	-2.48	BX113221	Hypothetical gene supported by AK022887; AK056417
GE57766	HTR6	0.045	-2.47	NM_000871	5-hydroxytryptamine (serotonin) receptor 6
GE62969	FFAR2	0.045	-2.47	NM_005306	G protein-coupled receptor 43
GE786149	EMP1	0.044	-2.47	AI446224	Epithelial membrane protein 1
GE719460	ZEB1	0.045	-2.47	BQ329735	Transcription factor 8 (represses interleukin 2 expression)
GE589466	LARP1	0.027	-2.47	AA972120	La ribonucleoprotein domain family, member 1
GE719466	MYT1L	0.024	-2.47	BF110303	Myelin transcription factor 1-like
GE62642	MYBPC3	0.002	-2.46	NM_000256	myosin binding protein C, cardiac
GE796784	ADAM10	0.023	-2.46	BF751109	ADAM metallopeptidase domain 10
GE687167	MSRA	0.049	-2.46	CB068665	Methionine sulfoxide reductase A
GE660733	RBMS3	0.006	-2.46	AA425671	RNA binding motif, single stranded interacting protein
GE81638	DRAP1	0.008	-2.46	NM_006442	DR1-associated protein 1 (negative cofactor 2 alpha)
GE59756	HIVEP1	0.013	-2.45	NM_002114	human immunodeficiency virus type I enhancer binding protein 1
GE86433	BTG1	0.044	-2.45	BC009050	B-cell translocation gene 1, anti-proliferative
GE570886	C18ORF19	0.046	-2.45	NM_152352	chromosome 18 open reading frame 19
GE86022	RAP1A	0.026	-2.45	AU126086	RAP1A, member of RAS oncogene family
GE483166	LTF	0.022	-2.45	W86820	Lactotransferrin
GE654270	FBP1	0.042	-2.45	AI052624	Fructose-1,6-bisphosphatase 1
GE53263	ST18	0.021	-2.44	NM_014682	suppression of tumorigenicity 18 (breast carcinoma) (zinc finger protein)
GE60019	FAM12A	0.032	-2.44	NM_006683	family with sequence similarity 12, member A

Column ID	Symbol	p-value	FC(AI delet vs. NI)	Accession number	Description
GE714590	WDR1	0.031	-2.44	AI247365	WD repeat domain 1
GE59129	MAP2K6	0.036	-2.44	NM_002758	mitogen-activated protein kinase kinase 6
GE53254	WSCD1	0.033	-2.43	BE766697	KIAA0523 protein
GE517496	CARD14	0.033	-2.43	NM_024110	caspase recruitment domain family, member 14
GE522142	IREB2	0.027	-2.43	AI283837	Iron-responsive element binding protein 2
GE58059	PRPH2	0.042	-2.43	NM_000322	retinal degeneration, slow
GE886395	LOC145783	0.028	-2.42	BF972343	hypothetical LOC145783
GE763215	IQCH	0.047	-2.42	BI022639	Full-length cDNA clone CS0DC021YJ09 of Neuroblastoma Cot 25-normalized of Homo s
GE579121	LOC439957	0.013	-2.42	AI654903	Similar to Ig kappa chain V region (Z4) - human
GE791697	MTSS1	0.014	-2.42	W02191	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 9, 22kDa
GE511971	CASC2	0.006	-2.42	NM_178816	cancer susceptibility candidate 2
GE80437	C13ORF28	0.021	-2.41	NM_145248	LOC122258
GE777598	STAM	0.007	-2.41	AW852409	Signal transducing adaptor molecule (SH3 domain and ITAM motif) 1
GE622884	PSMB7	0.002	-2.41	BX113527	Myeloproliferative disease associated tumor antigen 5
GE533121	MUC7	0.005	-2.40	NM_152291	mucin 7, salivary
GE475806	MYADML	0.039	-2.40	BC031088	myeloid-associated differentiation marker-like
GE526938	CBX6	0.033	-2.40	NM_014292	chromobox homolog 6
GE56553	GLTSCR2	0.044	-2.40	NM_015710	glioma tumor suppressor candidate region gene 2
GE481254	DKFZP547K054	0.008	-2.39	BX110656	Hypothetical protein DKFZp547K054
GE54134	CDH16	0.000	-2.39	NM_004062	cadherin 16, KSP-cadherin
GE88234	LOC146429	0.009	-2.39	AL137382	hypothetical protein LOC146429
GE848911	KCNJ5	0.048	-2.38	AA506997	MRNA; cDNA DKFZp779F2345 (from clone DKFZp779F2345)
GE777120	FAM40B	0.023	-2.38	AW028153	Family with sequence similarity 40, member B
GE592353	NCOA2	0.043	-2.38	AW979075	Nuclear receptor coactivator 2
GE515574	LOC729897	0.018	-2.38	BE244176	Hypothetical LOC200475
GE765929	FLJ42709	0.019	-2.37	AW022410	Hypothetical gene supported by AK124699
GE567884	UNC45B	0.027	-2.37	NM_173167	unc-45 homolog B (C. elegans)
GE581421	LOC440981	0.047	-2.37	BG214950	Similar to CG32056-PA
GE544076	CD300LG	0.013	-2.36	NM_145273	CD300 antigen like family member G
GE818605	THUMPD1	0.044	-2.36	BG166339	THUMP domain containing 1
GE59319	RPL3L	0.043	-2.36	NM_005061	ribosomal protein L3-like
GE57091	CREM	0.025	-2.35	NM_182717	cAMP responsive element modulator
GE80774	FAM181A	0.020	-2.35	NM_138344	chromosome 14 open reading frame 152
GE903194	TPR	0.013	-2.34	AI332534	Translocated promoter region (to activated MET oncogene)
GE816230	RORA	0.019	-2.34	T90468	RAR-related orphan receptor A
GE529951	LOC100132624	0.043	-2.34	CB050297	KLK16 mRNA, partial sequence
GE848179	PHF14	0.012	-2.34	BQ027674	PHD finger protein 14
GE57467	GP1BA	0.049	-2.34	NM_000173	glycoprotein Ib (platelet), alpha polypeptide
GE585328	PPP1R16B	0.039	-2.34	AL833255	Protein phosphatase 1, regulatory (inhibitor) subunit 16B
GE517767	FLJ39061	0.022	-2.33	AK096380	hypothetical protein FLJ39061
GE81440	OTOF	0.041	-2.33	NM_004802	otoferlin
GE61471	KRT83	0.022	-2.33	NM_002282	keratin, hair, basic, 3
GE58777	RCVRN	0.011	-2.31	NM_002903	recoverin
GE60551	C7ORF28A	0.030	-2.31	AA558437	Chromosome 7 open reading frame 28B
GE87197	MAPKAP1	0.008	-2.31	AI629026	Mitogen-activated protein kinase associated protein 1
GE56133	SH3BGRL2	0.016	-2.31	NM_031469	SH3 domain binding glutamic acid-rich protein like 2
GE62639	ABCC2	0.044	-2.31	NM_000392	ATP-binding cassette, sub-family C (CFTR/MRP), member 2
GE618665	HELLS	0.020	-2.31	AW273055	Helicase, lymphoid-specific

Column ID	Symbol	p-value	FC(AI delet vs. NI)	Accession number	Description
GE675811	IQCH	0.021	-2.30	AA203355	IQ motif containing H
GE53484	SNF1LK2	0.019	-2.30	AB096248	SNF1-like kinase 2
GE755852	PDCD4	0.037	-2.30	BX507202	Programmed cell death 4 (neoplastic transformation inhibitor)
GE805982	FAT3	0.038	-2.30	CA426935	FAT tumor suppressor homolog 3 (Drosophila)
GE891568	MRPL43	0.040	-2.30	NM_176792	mitochondrial ribosomal protein L43
GE644283	ADH5	0.019	-2.29	AA700426	Alcohol dehydrogenase 5 (class III), chi polypeptide
GE85094	C7ORF44	0.007	-2.29	AK024861	Homo sapiens cDNA: FLJ21208 fis, clone COL00363.
GE756165	PTK2	0.028	-2.28	AW977253	PTK2 protein tyrosine kinase 2
GE58627	APIP	0.006	-2.28	NM_015957	APAF1 interacting protein
GE716337	KLF12	0.030	-2.27	BX109619	Kruppel-like factor 12
GE83133	RGS5	0.035	-2.27	CD677889	Regulator of G-protein signalling 5
GE56675	ATPAF1	0.045	-2.27	AI908678	ATP synthase mitochondrial F1 complex assembly factor 1
GE597285	EEA1	0.036	-2.27	AW975982	Early endosome antigen 1, 162kD
GE58293	SELP	0.028	-2.27	NM_003005	selectin P (granule membrane protein 140kDa, antigen CD62)
GE85814	RPL13A	0.048	-2.27	BC000514	ribosomal protein L13a
GE484762	CCDC146	0.036	-2.27	BI042346	coiled-coil domain containing 146
GE81380	ALK	0.017	-2.26	NM_004304	anaplastic lymphoma kinase (Ki-1)
GE520935	SNX30	0.009	-2.26	BE764638	Sorting nexin family member 30
GE53068	NRCAM	0.021	-2.26	NM_005010	neuronal cell adhesion molecule
GE80474	SLC22A17	0.021	-2.26	NM_016609	solute carrier family 22 (organic cation transporter), member 17
GE523513	NXPH3	0.026	-2.26	NM_007225	neurexophilin 3
GE826474	ZNF346	0.034	-2.26	BF529156	Zinc finger protein 346
GE59093	PTK7	0.020	-2.25	NM_002821	PTK7 protein tyrosine kinase 7
GE87868	ALG9	0.046	-2.25	NM_024740	asparagine-linked glycosylation 9 homolog (yeast, alpha 1,2 mannosyltransferase)
GE799491	KCNJ12	0.033	-2.25	BG338507	Potassium inwardly-rectifying channel, subfamily J, member 12
GE58465	SERGEF	0.037	-2.25	NM_012139	deafness locus associated putative guanine nucleotide exchange factor
GE844404	CASQ1	0.012	-2.25	BM467196	calsequestrin 1 (fast-twitch, skeletal muscle)
GE85482	ETF1	0.029	-2.24	M75715	eukaryotic translation termination factor 1
GE852404	LOC727869	0.002	-2.24	AW015982	Transcribed locus
GE61697	MAGED4B	0.009	-2.24	NM_030801	melanoma antigen family D, 4
GE59654	G6PD	0.021	-2.23	NM_000402	glucose-6-phosphate dehydrogenase
GE680494	PDE10A	0.037	-2.23	R37728	Phosphodiesterase 10A
GE744385	SLC47A1	0.009	-2.23	AI638691	Hypothetical protein FLJ10847
GE555090	LOC286370	0.012	-2.23	BC039331	hypothetical protein LOC286370
GE81892	ZBTB44	0.032	-2.23	NM_014155	BTB (POZ) domain containing 15
GE874492	PNLIPRP3	0.024	-2.23	BG033763	Pancreatic lipase-related protein 3
GE585308	PLEKHA2	0.037	-2.23	AA911673	pleckstrin homology domain containing, family A (phosphoinositide binding speci
GE669869	DSCAML1	0.015	-2.22	AA010973	Down syndrome cell adhesion molecule like 1
GE548004	BICD1	0.021	-2.22	BQ181282	Bicaudal D homolog 1 (Drosophila)
GE56967	ARMC7	0.043	-2.22	N64394	Armadillo repeat containing 7
GE849284	FAM65C	0.032	-2.22	BQ011791	family with sequence similarity 65, member C
GE765386	NFAT5	0.041	-2.21	AW859722	Nuclear factor of activated T-cells 5, tonicity-responsive
GE824447	RSBN1	0.028	-2.21	BQ429614	Round spermatid basic protein 1
GE749522	ZRANB3	0.017	-2.21	AI065106	Zinc finger, RAN-binding domain containing 3
GE501251	LOC121952	0.033	-2.21	AF339833	Hypothetical protein LOC121952
GE54339	HTATIP2	0.029	-2.21	NM_006410	HIV-1 Tat interactive protein 2, 30kDa
GE62350	HSD17B12	0.005	-2.20	NM_016142	hydroxysteroid (17-beta) dehydrogenase 12
GE629023	SH3RF1	0.050	-2.20	AA393551	Transcribed locus

Column ID	Symbol	p-value	FC(AI delet vs. NI)	Accession number	Description
GE80233	TRPC7	0.025	-2.20	NM_020389	transient receptor potential cation channel, subfamily C, member 7
GE57330	NPAT	0.048	-2.20	NM_002519	nuclear protein, ataxia-telangiectasia locus
GE474321	EPB41L1	0.027	-2.20	BM971731	Erythrocyte membrane protein band 4.1-like 1
GE852806	ADARB2	0.014	-2.19	AW293835	Adenosine deaminase, RNA-specific, B2 (RED2 homolog rat)
GE87223	GPR110	0.023	-2.19	NM_153840	G protein-coupled receptor 110
GE54361	LILRA4	0.043	-2.19	NM_012276	leukocyte immunoglobulin-like receptor, subfamily A (with TM domain), member 4
GE85571	GPT2	0.032	-2.19	NM_133443	glutamic pyruvate transaminase (alanine aminotransferase) 2
GE88552	CPO	0.008	-2.19	NM_173077	carboxypeptidase O
GE750407	ATP12A	0.032	-2.19	BC035268	ATPase, H+/K+ transporting, nongastric, alpha polypeptide
GE763044	FAM59A	0.012	-2.19	H84097	Family with sequence similarity 59, member A
GE640629	BDH1	0.011	-2.19	W86052	LOC442100
GE746499	DNAH5	0.049	-2.19	AI927879	Dynein, axonemal, heavy polypeptide 5
GE854563	MLL3	0.027	-2.19	BQ720078	Myeloid/lymphoid or mixed-lineage leukemia 3
GE555790	LOXL1	0.017	-2.19	AK056885	lysyl oxidase-like 1
GE602927	KIF6	0.002	-2.18	N74402	Kinesin family member 6
GE768589	CEP164	0.040	-2.18	BU159474	Similar to hypothetical protein FLJ36492
GE518429	FLJ43663	0.028	-2.18	AW084563	hypothetical LOC378805
GE767150	CSDA	0.050	-2.18	AI222658	Cold shock domain protein A
GE57342	MAML1	0.036	-2.17	NM_014757	mastermind-like 1 (Drosophila)
GE80000	CD300C	0.034	-2.17	NM_006678	CD300C antigen
GE729964	SLC1A2	0.039	-2.17	AI124744	Solute carrier family 1 (glial high affinity glutamate transporter), member 2
GE87454	SGK269	0.015	-2.17	BI869593	KIAA2002 protein
GE524660	LOC202451	0.045	-2.17	BC022980	hypothetical protein LOC202451
GE569634	SLIT3	0.048	-2.17	BF509794	Transcribed locus
GE828459	CDC26	0.024	-2.17	AA399531	Solute carrier family 31 (copper transporters), member 1
GE88240	BBS12	0.044	-2.16	NM_152618	hypothetical protein FLJ35630
GE57940	PRKACB	0.028	-2.16	NM_002731	protein kinase, cAMP-dependent, catalytic, beta
GE61257	EMR3	0.008	-2.16	NM_032571	egf-like module containing, mucin-like, hormone receptor-like 3
GE832527	NRP2	0.029	-2.16	BU738899	Neuropilin 2
GE56181	LHCGR	0.044	-2.16	AL049443	TFIIA-alpha/beta-like factor
GE508119	CCDC108	0.037	-2.16	AK092605	Hypothetical protein DKFZp434O0527
GE577479	WDR88	0.016	-2.15	NM_173479	hypothetical protein LOC126248
GE88331	SDK1	0.017	-2.15	NM_152744	sidekick homolog 1 (chicken)
GE79771	PPAPDC1B	0.011	-2.15	NM_032483	phosphatidic acid phosphatase type 2 domain containing 1B
GE478173	POLR1E	0.031	-2.14	AI652887	Polymerase (RNA) I associated factor 1
GE609747	UBE3A	0.012	-2.14	AI280028	ubiquitin protein ligase E3A
GE726212	KIF6	0.016	-2.14	N58267	Kinesin family member 6
GE83256	NRIP2	0.032	-2.14	NM_031474	nuclear receptor interacting protein 2
GE685216	INO80	0.013	-2.14	AI682281	INO80 homolog (S. cerevisiae)
GE653969	CCNJL	0.043	-2.14	BE328090	Hypothetical protein FLJ14166
GE697209	PPTC7	0.043	-2.13	AA805719	T-cell activation protein phosphatase 2C
GE722961	ITGB6	0.036	-2.13	BG191465	Transcribed locus
GE814676	DKFZP434G179	0.034	-2.13	AL137337	hypothetical protein DKFZp434G179
GE734379	UBE2H	0.009	-2.13	AW968686	Ubiquitin-conjugating enzyme E2H (UBC8 homolog, yeast)
GE822311	HPGD	0.007	-2.13	BG619134	Hydroxyprostaglandin dehydrogenase 15-(NAD)
GE745147	MED13L	0.018	-2.13	BF055521	mediator complex subunit 13-like
GE625099	LOC647323	0.033	-2.12	AI271617	hypothetical protein LOC647323
GE81344	CDKN1B	0.029	-2.12	NM_004064	cyclin-dependent kinase inhibitor 1B (p27, Kip1)

Column ID	Symbol	p-value	FC(AI delet vs. NI)	Accession number	Description
GE54895	SLC16A8	0.020	-2.12	AF132611	solute carrier 16 (monocarboxylic acid transporters), member 8
GE518833	UNQ6975	0.041	-2.12	BQ020437	NGNL6975
GE84596	AARS2	0.012	-2.12	AB033096	alanyl-tRNA synthetase like
GE529732	HCG2042779	0.007	-2.12	BU738825	hCG2042779
GE53806	AMIGO1	0.014	-2.12	W88515	Adhesion molecule with Ig-like domain 1
GE581211	CLYBL	0.030	-2.11	AI419840	Citrate lyase beta like
GE501576	C15ORF43	0.020	-2.10	NM_152448	hypothetical protein MGC33951
GE707690	CPNE2	0.044	-2.10	AI660863	Copine II
GE519791	BACH2(includesEG:60468)	0.001	-2.10	AW978120	BTB and CNC homology 1, basic leucine zipper transcription factor 2
GE749628	MMP21	0.008	-2.10	NM_147191	matrix metallopeptidase 21
GE605811	RIMS1	0.008	-2.10	BE673740	Regulating synaptic membrane exocytosis 1
GE805234	C6ORF154	0.007	-2.09	BM128735	Chromosome 6 open reading frame 154
GE82595	CD209	0.033	-2.09	NM_021155	CD209 antigen
GE84742	SH2D6	0.022	-2.08	NM_198482	similar to B-cell linker; B cell linker protein
GE478609	VN1R2	0.012	-2.08	NM_173856	vomeronasal 1 receptor 2
GE862854	IFIT2	0.028	-2.08	BF511134	Interferon-induced protein with tetratricopeptide repeats 2
GE755129	APBA1	0.024	-2.07	AA121632	amyloid beta (A4) precursor protein-binding, family A, member 1
GE54060	CDON	0.024	-2.06	NM_016952	Cdon homolog (mouse)
GE698541	SPAG16	0.041	-2.06	BQ102344	Sperm associated antigen 16
GE81474	MED13	0.039	-2.06	NM_005121	thyroid hormone receptor associated protein 1
GE82966	MAGIX	0.017	-2.06	NM_024859	PDZ domain containing, X chromosome
GE721877	CCDC40	0.022	-2.06	AI191633	Coiled-coil domain containing 40
GE621039	TSPAN8	0.010	-2.06	AI475154	Tetraspanin 8
GE662098	GEM	0.018	-2.05	BX112717	GTP binding protein overexpressed in skeletal muscle
GE596368	LRRC39	0.009	-2.05	BF060753	Leucine rich repeat containing 39
GE60025	NUCB2	0.048	-2.05	NM_005013	nucleobindin 2
GE517049	PHACTR3	0.045	-2.05	AL832577	Phosphatase and actin regulator 3
GE675190	LOC100129965	0.007	-2.05	BM711811	PR domain containing 11
GE57831	CYP11A1	0.005	-2.05	NM_000781	cytochrome P450, family 11, subfamily A, polypeptide 1
GE867446	TM7SF3	0.026	-2.05	AW452923	Transmembrane 7 superfamily member 3
GE484443	NFKBID	0.046	-2.05	AK126825	T-cell activation NFKB-like protein
GE85385	MAML3	0.045	-2.04	NM_018717	mastermind-like 3 (Drosophila)
GE82109	H19	0.030	-2.04	BF996346	H19, imprinted maternally expressed untranslated mRNA
GE82804	C11ORF49	0.002	-2.04	NM_024113	MGC4707 protein
GE79945	ZFPM2	0.034	-2.04	NM_012082	zinc finger protein, multitype 2
GE79817	INHBE	0.010	-2.04	NM_031479	inhibin, beta E
GE776646	PUS10	0.038	-2.04	AW172503	Hypothetical protein FLJ32312
GE601874	RWDD3	0.031	-2.04	AI480240	RWD domain containing 3
GE567161	TAS2R39	0.029	-2.04	NM_176881	taste receptor, type 2, member 39
GE82408	GABRQ	0.029	-2.03	NM_018558	gamma-aminobutyric acid (GABA) receptor, theta
GE59709	MYBL2	0.033	-2.03	NM_002466	v-myb myeloblastosis viral oncogene homolog (avian)-like 2
GE53431	NOL4	0.020	-2.03	NM_003787	nucleolar protein 4
GE582937	MRRF	0.024	-2.03	C15527	Mitochondrial ribosome recycling factor
GE723220	PUS3	0.039	-2.03	BU567489	pseudouridylate synthase 3
GE59708	DAO	0.047	-2.03	NM_001917	D-amino-acid oxidase
GE726210	FNDC3B	0.001	-2.03	AW438419	Fibronectin type III domain containing 3B
GE81797	RPL13A	0.025	-2.03	NM_012423	ribosomal protein L13a
GE526607	PTTG1IP	0.024	-2.03	AL603150	Integrin, beta 2 (antigen CD18 (p95), lymphocyte function-associated antigen 1;

Column ID	Symbol	p-value	FC(AI delet vs. NI)	Accession number	Description
GE833631	PPP2R5C	0.027	-2.02	AI350654	protein phosphatase 2, regulatory subunit B', gamma isoform
GE630605	ZC3H11A	0.015	-2.02	BM789135	Zinc finger CCCH-type containing 11A
GE710362	M6PRBP1	0.033	-2.02	BM974065	Mannose-6-phosphate receptor binding protein 1
GE80056	MPPED2	0.001	-2.02	NM_001584	metallophosphoesterase domain containing 2
GE544920	LOC100129460	0.005	-2.02	AK026768	dpy-19-like 1 pseudogene 1 (C. elegans)
GE775756	LOC285547	0.028	-2.01	AK096368	hypothetical protein LOC285547
GE600991	MAL2	0.029	-2.00	AA912839	Mal, T-cell differentiation protein 2
GE83790	DCN	0.032	-2.00	AI990925	Decorin
GE59569	GABRE	0.037	-2.00	NM_004961	gamma-aminobutyric acid (GABA) A receptor, epsilon
GE62594	C11ORF58	0.005	-2.00	NM_014267	small acidic protein
GE56587	ASXL3	0.038	-2.00	AL133050	KIAA1713
GE58366	GNE	0.024	-2.00	NM_005476	glucosamine (UDP-N-acetyl)-2-epimerase/N-acetylmannosamine kinase
GE83168	FCRL2	0.043	-2.00	NM_030764	Fc receptor-like 2
GE569300	LOC100132005	0.043	-1.99	BQ876865	hypothetical LOC100132005
GE512891	LOC400238	0.030	-1.99	BX090735	Hypothetical gene supported by AK093266
GE482180	EXT2	0.018	-1.99	AV718935	exostoses (multiple) 2
GE525301	NRXN3	0.021	-1.99	BX248745	Full-length cDNA 5-PRIME end of clone CS0CAP002YE20 of Thymus of Homo sapiens (h
GE661622	GOLSYN	0.021	-1.99	AA741565	Hypothetical protein FLJ20366
GE58844	PLK1	0.032	-1.99	NM_005030	polo-like kinase 1 (Drosophila)
GE628980	GRIN2B	0.047	-1.99	AA167284	Glutamate receptor, ionotropic, N-methyl D-aspartate 2B
GE782793	TAF15	0.040	-1.99	AI821243	TAF15 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 68kDa
GE62563	EPHB4	0.006	-1.98	AW579301	CKLF-like MARVEL transmembrane domain containing 6
GE598156	CADPS	0.010	-1.98	BC029460	Ca2+-dependent secretion activator
GE887127	C2ORF74	0.007	-1.98	BF673400	Hypothetical gene supported by AK075484; BC014578
GE789484	XRCC2	0.028	-1.97	BG494177	X-ray repair complementing defective repair in Chinese hamster cells 2
GE481130	ASZ1	0.012	-1.97	NM_130768	ankyrin repeat, SAM and basic leucine zipper domain containing 1
GE669527	LRCH1	0.031	-1.97	AA211791	Leucine-rich repeats and calponin homology (CH) domain containing 1
GE53638	RPH3A	0.022	-1.97	NM_014954	rabphilin 3A homolog (mouse)
GE82136	TMEM216	0.047	-1.97	NM_016499	HSPC244
GE79570	GYLTL1B	0.038	-1.97	NM_152312	glycosyltransferase-like 1B
GE679215	LOC100133219	0.013	-1.96	AI798232	hypothetical protein LOC100133219
GE791348	RAB4B	0.025	-1.96	BC040374	RAB4B, member RAS oncogene family
GE800001	PDE7B	0.043	-1.96	AK000141	Phosphodiesterase 7B
GE62927	PTBP2	0.023	-1.96	NM_021190	polypyrimidine tract binding protein 2
GE607838	CPXM2	0.018	-1.95	BI826310	Carboxypeptidase X (M14 family), member 2
GE702391	FYN	0.039	-1.95	AV661514	FYN oncogene related to SRC, FGR, YES
GE85747	OR8B4	0.009	-1.95	XM_210186	synonyms: OR8B4P, OR11-315; olfactory receptor, family 8, subfamily B, member 4
GE623550	RAP1B	0.044	-1.95	AI400344	RAP1B, member of RAS oncogene family
GE892802	RUNDC2B	0.008	-1.95	AA865087	Similar to FLJ12363 protein
GE903141	LOC283697	0.044	-1.95	AK096061	hypothetical protein LOC283697
GE61564	ALPL	0.040	-1.94	NM_000478	alkaline phosphatase, liver/bone/kidney
GE765670	MBNL1	0.034	-1.94	BG942732	Muscleblind-like (Drosophila)
GE671345	PRAGMIN	0.039	-1.94	AA608841	Hypothetical protein DKFZp761P0423
GE803371	IMPAD1	0.047	-1.93	R71416	Inositol monophosphatase domain containing 1
GE549804	EIF3M	0.002	-1.93	CA414434	Dendritic cell protein
GE79495	TMEM125	0.049	-1.93	NM_144626	hypothetical protein MGC17299
GE476680	STK39	0.032	-1.93	BU664651	Serine threonine kinase 39 (STE20/SPS1 homolog, yeast)
GE832160	PLEKHG1	0.043	-1.92	BU753068	pleckstrin homology domain containing, family G (with RhoGef domain) member 1

Column ID	Symbol	p-value	FC(AI delet vs. NI)	Accession number	Description
GE56511	DLC1	0.039	-1.92	NM_006094	deleted in liver cancer 1
GE686302	BRWD1	0.028	-1.92	BX103387	Bromodomain and WD repeat domain containing 1
GE53960	KCNT1	0.046	-1.92	AB037843	potassium channel, subfamily T, member 1
GE56656	COPB1	0.016	-1.92	NM_016451	coatomer protein complex, subunit beta
GE507358	WNT4	0.040	-1.91	W72348	Wingless-type MMTV integration site family, member 4
GE899954	CD200	0.015	-1.91	BF368117	CD200 antigen
GE80534	CLDN17	0.002	-1.91	NM_012131	claudin 17
GE841944	SMYD3	0.032	-1.91	BF515527	SET and MYND domain containing 3
GE572585	FAM47A	0.028	-1.91	BC026171	family with sequence similarity 47, member A
GE80975	HCG1640785	0.031	-1.91	F28158	ribosomal protein S25 pseudogene
GE705190	PBX3	0.041	-1.91	AA521307	Pre-B-cell leukemia transcription factor 3
GE487008	CACNG5	0.008	-1.91	NM_014404	calcium channel, voltage-dependent, gamma subunit 5
GE499342	FAM160A1	0.029	-1.91	AA021503	Similar to RIKEN cDNA 9930021J17
GE60029	ACVR2B	0.021	-1.90	NM_001106	activin A receptor, type IIB
GE85242	C1GALT1	0.026	-1.90	BX496307	Core 1 synthase, glycoprotein-N-acetylgalactosamine 3-beta-galactosyltransferase
GE746085	AIDA	0.028	-1.90	AI873250	axin interactor, dorsalization associated
GE711341	FANCM	0.022	-1.90	BE350003	Fanconi anemia, complementation group M
GE665321	LOC100132644	0.041	-1.90	AA159978	Transcribed locus
GE552711	ZNF292	0.038	-1.89	H02806	Zinc finger protein 292
GE577021	CERKL	0.043	-1.89	BC020465	Homo sapiens cDNA clone IMAGE:3870103.
GE585809	FAM83G	0.024	-1.89	AI365243	family with sequence similarity 83, member G
GE55783	PRMT6	0.014	-1.88	NM_018137	HMT1 hnRNP methyltransferase-like 6 (S. cerevisiae)
GE53530	CAMTA1	0.016	-1.88	AI267687	Calmodulin binding transcription activator 1
GE836273	PACSIN3	0.024	-1.88	BF939328	Protein kinase C and casein kinase substrate in neurons 3
GE86233	NAMPT	0.024	-1.88	BF095282	Pre-B-cell colony enhancing factor 1
GE79155	RPS3	0.010	-1.88	CB126340	Ribosomal protein S3
GE832977	GPR153	0.032	-1.88	AW138499	G protein-coupled receptor 153
GE88158	BAT4	0.030	-1.88	NM_033177	HLA-B associated transcript 4
GE87873	WARS2	0.021	-1.88	BM854501	Tryptophanyl tRNA synthetase 2 (mitochondrial)
GE480710	RNF169	0.009	-1.88	BE676540	Similar to ribosomal protein L31
GE87482	RDH10	0.048	-1.88	NM_172037	retinol dehydrogenase 10 (all-trans)
GE529431	RPP30	0.015	-1.88	AK095810	hypothetical protein LOC283012
GE875279	CTD-2514C3.1	0.036	-1.87	BF038828	hypothetical LOC100134868
GE675434	VTI1A	0.046	-1.87	NM_145206	vesicle transport through interaction with t-SNAREs homolog 1A (yeast)
GE561708	PAQR4	0.035	-1.87	NM_152341	progestin and adipoQ receptor family member IV
GE86327	HIST1H2BH	0.039	-1.86	BX507388	Histone 1, H2bh
GE53363	KIAA0652	0.000	-1.86	NM_014741	KIAA0652
GE497758	ZDBF2	0.031	-1.86	AK002005	KIAA1571 protein
GE57479	VDR	0.040	-1.86	NM_000376	vitamin D (1,25- dihydroxyvitamin D3) receptor
GE57501	CCL4	0.044	-1.86	NM_002984	chemokine (C-C motif) ligand 4
GE879086	GTPBP1	0.010	-1.86	BF514555	GTP binding protein 1
GE59772	ERCC2	0.017	-1.86	NM_000400	excision repair cross-complementing rodent repair deficiency, complementation gr
GE688225	AKAP13	0.029	-1.86	AW973471	A kinase (PRKA) anchor protein 13
GE757151	SEC22B	0.046	-1.85	AK023270	SEC22 vesicle trafficking protein-like 1 (S. cerevisiae)
GE84594	NAP1L1	0.028	-1.85	BC002387	nucleosome assembly protein 1-like 1
GE630971	LIMCH1	0.016	-1.85	AI351179	DKFZP686A01247 hypothetical protein
GE898884	ZDHHC16	0.019	-1.85	AA350398	zinc finger, DHHC-type containing 16
GE81295	HIST1H2BF	0.031	-1.85	NM_003522	histone 1, H2bf

Column ID	Symbol	p-value	FC(AI delet vs. NI)	Accession number	Description
GE58519	SNX11	0.048	-1.85	NM_013323	sorting nexin 11
GE793196	PAX1	0.030	-1.85	AI027131	Paired box gene 1
GE62790	TSHB	0.017	-1.85	AI366963	Transcribed locus, strongly similar to XP_575014.1 PREDICTED: similar to RIKEN c
GE487850	C21ORF58	0.031	-1.85	AY039243	chromosome 21 open reading frame 58
GE546078	GLIPR1L2	0.005	-1.85	NM_152436	hypothetical protein MGC39497
GE81015	DNAH8	0.048	-1.85	NM_001371	dynein, axonemal, heavy polypeptide 8
GE56899	PLA2G12A	0.048	-1.85	H28612	Full-length cDNA clone CS0DF027YF17 of Fetal brain of Homo sapiens (human)
GE469953	CALHM1	0.007	-1.85	BC036208	family with sequence similarity 26, member C
GE551139	SPHKAP	0.020	-1.85	AI290868	SPHK1 (sphingosine kinase type 1) interacting protein
GE584891	SEC31A	0.017	-1.84	BX110326	SEC31-like 1 (S. cerevisiae)
GE610283	DAZAP1	0.034	-1.84	AW664787	DAZ associated protein 1
GE572293	FLJ12547	0.023	-1.84	AI678116	hypothetical protein FLJ12547
GE772355	UTP14C	0.019	-1.84	R64064	Similar to hypothetical protein B230397C21
GE873396	CPNE8	0.034	-1.84	BQ924206	Copine VIII
GE82899	E2F8	0.045	-1.84	NM_024680	E2F transcription factor 8
GE678262	MICAL3	0.015	-1.84	AA769428	Microtubule associated monoxygenase, calponin and LIM domain containing 3
GE59015	LSS	0.042	-1.83	NM_002340	lanosterol synthase (2,3-oxidosqualene-lanosterol cyclase)
GE876472	KLHL31	0.024	-1.83	BF694569	Transcribed locus, moderately similar to NP_536845.1 cytochrome c oxidase subuni
GE545565	KRTAP9-2	0.022	-1.83	NM_031961	keratin associated protein 9-2
GE80489	ASB4	0.001	-1.83	NM_016116	ankyrin repeat and SOCS box-containing 4
GE607884	ATAD3A	0.050	-1.83	BX114825	Transcribed locus
GE83996	SIGLEC15	0.049	-1.83	AK095432	CD33 antigen-like 3
GE88508	RPL28	0.026	-1.83	NM_000991	ribosomal protein L28
GE623041	ANKH	0.030	-1.83	BX119305	Ankylosis, progressive homolog (mouse)
GE60069	HTR5A	0.018	-1.83	NM_024012	5-hydroxytryptamine (serotonin) receptor 5A
GE799775	KIAA1432	0.023	-1.83	BX104718	KIAA1432
GE56202	PDCD4	0.024	-1.82	NM_014456	programmed cell death 4 (neoplastic transformation inhibitor)
GE57241	HDAC1	0.004	-1.82	NM_004964	histone deacetylase 1
GE884445	CCDC67	0.047	-1.82	BG492295	Hypothetical protein FLJ25393
GE55212	CLDN9	0.015	-1.82	NM_020982	claudin 9
GE837414	CDH13	0.041	-1.82	AW297466	Cadherin 13, H-cadherin (heart)
GE471434	CD44	0.025	-1.82	AL702902	CD44 antigen (homing function and Indian blood group system)
GE765148	TASP1	0.007	-1.82	BI496961	Taspase, threonine aspartase, 1
GE82299	KBTBD4	0.004	-1.81	AK001312	kelch repeat and BTB (POZ) domain containing 4
GE591944	WDR27	0.048	-1.81	AI033599	WD repeat domain 27
GE653339	CPNE5	0.006	-1.81	BX118391	Copine V
GE62179	FIGNL1	0.027	-1.81	AL834387	fidgetin-like 1
GE63235	EPPK1	0.032	-1.81	AB051895	epiplakin 1
GE789856	PDE4B	0.043	-1.81	N36873	Transcribed locus, weakly similar to XP_517655.1 PREDICTED: similar to KIAA0825
GE521480	C19ORF16	0.042	-1.81	BC031875	chromosome 19 open reading frame 16
GE62372	ICA1	0.016	-1.80	AA838019	Islet cell autoantigen 1, 69kDa
GE829712	LOXL1	0.045	-1.80	BF512044	Lysyl oxidase-like 1
GE838614	TTLL11	0.036	-1.80	BQ027232	Tubulin tyrosine ligase-like family, member 11
GE589776	ELF1	0.037	-1.80	H80081	E74-like factor 1 (ets domain transcription factor)
GE56657	TWF2	0.029	-1.79	NM_007284	PTK9L protein tyrosine kinase 9-like (A6-related protein)
GE85997	ATP5L	0.045	-1.79	NM_006476	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit g
GE62107	ZFYVE9	0.002	-1.79	NM_004799	zinc finger, FYVE domain containing 9
GE586118	COBLL1	0.015	-1.79	AI186265	COBL-like 1

Column ID	Symbol	p-value	FC(AI delet vs. NI)	Accession number	Description
GE787068	MAP3K5(includesEG:4217)	0.041	-1.79	AV710568	mitogen-activated protein kinase kinase kinase 5
GE82249	CCDC109B	0.024	-1.78	NM_017918	hypothetical protein FLJ20647
GE792954	PCSK2	0.025	-1.78	CA773152	Proprotein convertase subtilisin/kexin type 2
GE85827	PNLIPRP3	0.035	-1.78	AL833418	pancreatic lipase-related protein 3
GE83496	PLCD4	0.037	-1.78	NM_032726	phospholipase C, delta 4
GE530584	PVRIG	0.038	-1.78	AA923161	Opposite strand transcription unit to STAG3
GE62098	GPR27	0.045	-1.78	NM_018971	G protein-coupled receptor 27
GE485904	EIF4E3	0.021	-1.78	AI652910	Eukaryotic translation initiation factor 4E member 3
GE499204	LOC220980	0.031	-1.78	BX378393	Hypothetical protein LOC220980
GE564061	ANO5	0.033	-1.78	AL832374	transmembrane protein 16E
GE85608	PVRIG	0.032	-1.78	CF455431	Stromal antigen 3
GE749133	ASH1L	0.036	-1.78	AW593839	POU domain, class 6, transcription factor 1
GE79750	GOLM1	0.008	-1.78	NM_016548	golgi phosphoprotein 2
GE82478	CCBL2	0.019	-1.78	BQ373191	RNA binding motif protein, X-linked-like 1
GE53605	CORO2B	0.041	-1.77	NM_006091	coronin, actin binding protein, 2B
GE750029	LOC283089	0.047	-1.77	AK094649	hypothetical protein LOC283089
GE473371	TNRC18	0.045	-1.77	BU950138	KIAA1856 protein
GE817529	C3	0.027	-1.77	H75739	Complement component 3
GE650985	LOC200772	0.049	-1.77	BU682871	Similar to KIAA0445 protein
GE781678	LRCH1	0.036	-1.77	N75768	leucine-rich repeats and calponin homology (CH) domain containing 1
GE55076	TRAF3	0.047	-1.77	AA644442	TNF receptor-associated factor 3
GE79604	EIF4EBP1	0.019	-1.77	NM_004095	eukaryotic translation initiation factor 4E binding protein 1
GE861693	LOC729620	0.049	-1.76	BX117828	hypothetical LOC729620
GE78981	ZNF581	0.047	-1.76	AW250591	Zinc finger protein 581
GE58166	GTF2H1	0.002	-1.76	NM_005316	general transcription factor IIH, polypeptide 1, 62kDa
GE895185	ZNF37B	0.016	-1.76	AK026980	zinc finger protein 37b (KOX 21)
GE85852	DMWD	0.004	-1.76	AA400004	Dystrophia myotonica-containing WD repeat motif
GE57701	EDC4	0.033	-1.76	NM_014329	autoantigen
GE870303	PTPN3	0.031	-1.76	AW014624	Protein tyrosine phosphatase, non-receptor type 3
GE87755	LYG2	0.002	-1.76	NM_175735	lysozyme-like
GE82708	GPR135	0.012	-1.76	NM_022571	G protein-coupled receptor 135
GE604352	SNX21	0.040	-1.76	AW970898	Chromosome 20 open reading frame 161
GE57218	CKAP5	0.002	-1.76	NM_014756	cytoskeleton associated protein 5
GE80370	KSR1	0.021	-1.75	BC035488	Kinase suppressor of ras 1
GE847439	ATP5S	0.037	-1.75	AW450915	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit s (factor B)
GE58898	SLC1A1	0.008	-1.75	NM_004170	solute carrier family 1 (neuronal/epithelial high affinity glutamate transporter
GE469916	TACC2	0.046	-1.75	BX111019	transforming, acidic coiled-coil containing protein 2
GE590663	NKAIN2	0.046	-1.75	AA984073	T-cell lymphoma breakpoint associated target 1
GE62837	MAPK8IP1	0.008	-1.75	NM_005456	mitogen-activated protein kinase 8 interacting protein 1
GE53192	HS2ST1	0.027	-1.75	NM_012262	heparan sulfate 2-O-sulfotransferase 1
GE570139	LOC729376	0.028	-1.75	CF528549	CDNA FLJ43945 fis, clone TESTI4014445
GE721358	AADACL1	0.027	-1.75	AW083937	Arylacetamide deacetylase-like 1
GE55964	FBXO3	0.013	-1.75	NM_012175	F-box protein 3
GE85086	IFT122	0.036	-1.74	R97233	Intraflagellar transport 122 homolog (Chlamydomonas)
GE501186	FLJ36166	0.047	-1.74	N34516	Hypothetical protein FLJ36166
GE88165	RPS16	0.046	-1.74	AI749553	Ribosomal protein S16
GE82736	NT5DC2	0.046	-1.74	AW580268	Hypothetical protein FLJ12442
GE61120	ENTPD4	0.010	-1.74	CA412561	Ectonucleoside triphosphate diphosphohydrolase 4

Column ID	Symbol	p-value	FC(AI delet vs. NI)	Accession number	Description
GE702466	CAPS2	0.009	-1.74	BE465261	calcyphosine 2
GE828728	SBF2	0.022	-1.74	BQ022721	SET binding factor 2
GE601688	CTNNA3	0.046	-1.74	AW975030	Catenin (cadherin-associated protein), alpha 3
GE85506	DOCK7	0.035	-1.74	AK125049	dedicator of cytokinesis 7
GE603785	IL28RA	0.045	-1.73	AI832093	Interleukin 28 receptor, alpha (interferon, lambda receptor)
GE582873	RASA3	0.048	-1.73	AW172526	RAS p21 protein activator 3
GE898723	XAGE5	0.045	-1.73	NM_130775	X antigen family, member 5
GE59231	ARFIP2	0.025	-1.73	NM_012402	ADP-ribosylation factor interacting protein 2 (arfaptin 2)
GE61909	HIPK3	0.016	-1.73	AA805539	Homeodomain interacting protein kinase 3
GE85937	RPS9	0.031	-1.73	NM_001013	ribosomal protein S9
GE813074	OSBPL9	0.030	-1.73	AW968210	oxysterol binding protein-like 9
GE79735	HIPK3	0.045	-1.73	NM_005734	homeodomain interacting protein kinase 3
GE628878	HCG2045614	0.032	-1.72	BX412503	hCG2045614
GE59479	TSG101	0.009	-1.72	NM_006292	tumor susceptibility gene 101
GE56704	C15ORF55	0.018	-1.72	BX117628	Nuclear protein in testis
GE740874	ASB4	0.021	-1.72	AI457276	Ankyrin repeat and SOCS box-containing 4
GE495153	LOC100130988	0.038	-1.72	BQ420400	Hypothetical LOC392670
GE546379	DENND2C	0.007	-1.72	NM_198459	DENN/MADD domain containing 2C
GE88765	CPA4	0.029	-1.72	BE156039	Carboxypeptidase A4
GE471415	LOC400456	0.013	-1.72	BC040875	hypothetical gene supported by BC040875
GE707785	DTWD2	0.041	-1.72	H29590	ym61a05.s1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:52642 3', mRNA
GE558951	C11ORF46	0.008	-1.72	NM_152316	chromosome 11 open reading frame 46
GE662608	BHLHB8	0.040	-1.72	AI434186	basic helix-loop-helix domain containing, class B, 8
GE55821	PLEKHA5	0.025	-1.71	NM_019012	pleckstrin homology domain containing, family A member 5
GE86316	GAL3ST4	0.007	-1.71	NM_024637	galactose-3-O-sulfotransferase 4
GE603405	NFE2L3	0.028	-1.71	AA534197	nuclear factor (erythroid-derived 2)-like 3
GE56532	TAF3	0.023	-1.71	BQ441483	TAF3 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 140kDa
GE661640	GIPC3	0.029	-1.71	AK098244	CDNA FLJ40925 fis, clone UTERU2006486
GE87615	ZCCHC7	0.002	-1.71	NM_032226	zinc finger, CCHC domain containing 7
GE774968	ATP8B3	0.048	-1.71	BC033179	ATPase, Class I, type 8B, member 3
GE898045	C8ORF46	0.048	-1.71	NM_152765	chromosome 8 open reading frame 46
GE79868	EEF1A1	0.004	-1.71	BF170701	Eukaryotic translation elongation factor 1 alpha 1
GE53082	NACAD	0.041	-1.71	BU543827	KIAA0363 protein
GE503894	ST8SIA6	0.029	-1.71	AW002415	ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 6
GE789836	ARFGEF2	0.011	-1.70	AI343519	ADP-ribosylation factor guanine nucleotide-exchange factor 2 (brefeldin A-inhibi
GE580123	SYT9	0.048	-1.70	BM553771	Synaptotagmin IX
GE62288	GPR68	0.036	-1.70	NM_003485	G protein-coupled receptor 68
GE80282	L2HGDH	0.032	-1.70	NM_024884	L-2-hydroxyglutarate dehydrogenase
GE57425	CTDSPL	0.030	-1.70	NM_005808	CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) small phosphatas
GE61961	AGPAT4	0.036	-1.70	NM_020133	1-acylglycerol-3-phosphate O-acyltransferase 4 (lysophosphatidic acid acyltransf
GE88595	DGKH	0.023	-1.70	AA722077	Diacylglycerol kinase, eta
GE86442	TTC17	0.016	-1.70	NM_018259	tetratricopeptide repeat domain 17
GE57559	CYP4A11	0.011	-1.70	NM_000778	cytochrome P450, family 4, subfamily A, polypeptide 11
GE54338	CREBL2	0.011	-1.70	NM_001310	cAMP responsive element binding protein-like 2
GE571158	FAM151A	0.039	-1.70	NM_176782	chromosome 1 open reading frame 179
GE79433	C12ORF53	0.028	-1.70	NM_153685	hypothetical protein DKFZp547D2210
GE56755	ZBED5	0.009	-1.69	NM_021211	transposon-derived Buster1 transposase-like protein gene
GE86065	RBM33	0.019	-1.69	AL137724	proline rich 8

Column ID	Symbol	p-value	FC(AI delet vs. NI)	Accession number	Description
GE631533	MAML3	0.019	-1.69	AK124941	Mastermind-like 3 (Drosophila)
GE55454	WDR40A	0.006	-1.69	NM_015397	WD repeat domain 40A
GE84191	LOC132241	0.037	-1.69	AL117606	hypothetical protein LOC132241
GE82062	UBE2J1	0.016	-1.69	NM_016021	ubiquitin-conjugating enzyme E2, J1 (UBC6 homolog, yeast)
GE748175	MACF1	0.028	-1.68	BF994533	Microtubule-actin crosslinking factor 1
GE687965	INVS	0.012	-1.68	AI371988	Inversin
GE721094	ALKBH3	0.024	-1.68	AV763865	Hypothetical protein LOC221120
GE60253	NUP88	0.017	-1.68	NM_002532	nucleoporin 88kDa
GE86029	SFTPB	0.025	-1.68	NM_000542	surfactant, pulmonary-associated protein B
GE83213	HNRNPA1	0.016	-1.68	NM_002136	heterogeneous nuclear ribonucleoprotein A1
GE59362	FUBP3	0.021	-1.68	U69127	far upstream element (FUSE) binding protein 3
GE532986	TRPC1	0.046	-1.68	BF949171	Transient receptor potential cation channel, subfamily C, member 1
GE58976	SLC1A6	0.047	-1.68	NM_005071	solute carrier family 1 (high affinity aspartate/glutamate transporter), member
GE56485	DNAJC27	0.027	-1.68	NM_016544	Ras-associated protein Rap1
GE488651	DIDO1	0.043	-1.68	NM_022105	death inducer-obliterator 1
GE56549	RASSF8	0.024	-1.67	CF455785	Ras association (RalGDS/AF-6) domain family 8
GE59245	GPR19	0.024	-1.67	NM_006143	G protein-coupled receptor 19
GE59137	PDE1C	0.034	-1.67	NM_005020	phosphodiesterase 1C, calmodulin-dependent 70kDa
GE54580	PSIP1	0.003	-1.67	NM_033222	PC4 and SFRS1 interacting protein 1
GE705695	TNFRSF21	0.019	-1.67	AI922677	Tumor necrosis factor receptor superfamily, member 21
GE56062	RPL3	0.025	-1.67	CD686625	Full-length cDNA clone CS0DK002YP16 of HeLa cells Cot 25-normalized of Homo sapi
GE53145	SOCS6	0.029	-1.67	NM_004232	suppressor of cytokine signaling 6
GE79354	OMA1	0.013	-1.67	NM_145243	OMA1 homolog, zinc metallopeptidase (S. cerevisiae)
GE55630	APBB1IP	0.030	-1.67	NM_019043	amyloid beta (A4) precursor protein-binding, family B, member 1 interacting prot
GE79890	GDI2	0.009	-1.67	NM_001494	GDP dissociation inhibitor 2
GE886197	DUSP8	0.050	-1.67	BG254553	Dual specificity phosphatase 8
GE804880	ARID5B	0.022	-1.67	AL832681	AT rich interactive domain 5B (MRF1-like)
GE725201	XIST	0.039	-1.66	BQ369419	X (inactive)-specific transcript
GE776426	EPHA10	0.003	-1.66	BC041360	EPH receptor A10
GE61380	RPS5	0.046	-1.66	NM_001009	ribosomal protein S5
GE88596	FCN1	0.005	-1.66	BX644928	Ficolin (collagen/fibrinogen domain containing) 1
GE795573	SHB	0.036	-1.66	AK055947	hypothetical protein LOC158230
GE54070	CDK2AP1	0.032	-1.66	NM_004642	CDK2-associated protein 1
GE84031	PDE9A	0.031	-1.66	AB017602	phosphodiesterase 9A
GE484897	UBQLN3	0.020	-1.66	NM_017481	ubiquilin 3
GE80669	CRYBA4	0.043	-1.65	NM_001886	crystallin, beta A4
GE84383	TUBB1	0.030	-1.65	AA402364	Tubulin, beta 1
GE53121	SOCS7	0.043	-1.65	BX105723	Suppressor of cytokine signaling 7
GE518563	FLJ44087	0.027	-1.65	AI147392	Hypothetical protein LOC284263
GE63225	CCBL2	0.044	-1.65	R48038	RNA binding motif protein, X-linked-like 1
GE80919	FUT2	0.028	-1.65	D87942	fucosyltransferase 2 (secretor status included)
GE674318	DLEU2	0.040	-1.65	AA648984	Deleted in lymphocytic leukemia, 2
GE58881	SLC4A3	0.041	-1.65	NM_005070	solute carrier family 4, anion exchanger, member 3
GE85851	KIFC3	0.028	-1.65	AV654547	AV654547 GLC Homo sapiens cDNA clone GLCDXA02 3', mRNA sequence.
GE57736	GCLM	0.007	-1.65	NM_002061	glutamate-cysteine ligase, modifier subunit
GE849549	LONRF2	0.001	-1.64	BM675650	Transcribed locus
GE810779	C6ORF199	0.039	-1.64	NM_145025	chromosome 6 open reading frame 199
GE815456	HS2ST1	0.046	-1.64	W45350	CDNA FLJ46011 fis, clone SPLEN2007314

Column ID	Symbol	p-value	FC(AI delet vs. NI)	Accession number	Description
GE54459	RAB6A	0.014	-1.64	NM_002869	RAB6A, member RAS oncogene family
GE83485	SUV420H2	0.002	-1.64	NM_032701	suppressor of variegation 4-20 homolog 2 (Drosophila)
GE482434	KALRN	0.033	-1.64	AI275610	Kalirin, RhoGEF kinase
GE723695	EPS15	0.024	-1.64	BX093454	Epidermal growth factor receptor pathway substrate 15
GE81768	EIF2C1	0.024	-1.64	NM_012199	eukaryotic translation initiation factor 2C, 1
GE474773	SH2D6	0.047	-1.64	NM_198482	similar to B-cell linker; B cell linker protein
GE497938	CXORF48	0.023	-1.64	AW295025	chromosome X open reading frame 48
GE59728	ACP2	0.014	-1.63	NM_001610	acid phosphatase 2, lysosomal
GE834484	TIAM1	0.030	-1.63	BQ024652	T-cell lymphoma invasion and metastasis 1
GE808538	LOC339298	0.040	-1.63	BC043002	hypothetical protein LOC339298
GE524452	NKAIN2	0.017	-1.63	BX115655	Na+/K+ transporting ATPase interacting 2
GE485502	C12ORF60	0.042	-1.63	NM_175874	hypothetical protein MGC47869
GE541217	HM13	0.028	-1.63	AA570696	Histocompatibility (minor) 13
GE80154	TTC6	0.025	-1.63	BX161415	tetratricopeptide repeat domain 6
GE844649	MGRN1	0.026	-1.63	BU742896	Mahogunin, ring finger 1
GE491531	RYR2	0.038	-1.62	AA719296	Ryanodine receptor 2 (cardiac)
GE54440	15-Sep	0.017	-1.62	NM_004261	15 kDa selenoprotein
GE87299	TPRG1L	0.004	-1.62	NM_182752	family with sequence similarity 79, member A
GE495865	ZAK	0.033	-1.62	AI283196	Hypothetical protein LOC339751
GE473289	MRVI1	0.006	-1.62	AI150346	Murine retrovirus integration site 1 homolog
GE617069	TEAD2	0.047	-1.62	CB049347	TEA domain family member 2
GE78955	RPS15A	0.025	-1.61	AA010849	Chromosome 20 open reading frame 19
GE55991	C3ORF59	0.033	-1.61	NM_178496	similar to BcDNA:GH11415 gene product
GE87813	AGK	0.004	-1.61	BE694349	Multiple substrate lipid kinase
GE611594	SLC2A9	0.042	-1.61	AK025887	solute carrier family 2 (facilitated glucose transporter), member 9
GE56221	PIK3C2A	0.025	-1.61	D62281	Phosphoinositide-3-kinase, class 2, alpha polypeptide
GE578880	ANKRD43	0.020	-1.61	NM_175873	ankyrin repeat domain 43
GE82717	C1ORF149	0.036	-1.61	NM_022756	chromosome 1 open reading frame 149
GE885455	F8A1	0.023	-1.61	BM722299	Coagulation factor VIII-associated (intronic transcript) 1
GE61363	EEF1G	0.007	-1.60	AA225828	Eukaryotic translation elongation factor 1 gamma
GE85099	IARS	0.021	-1.60	W03062	Isoleucine-tRNA synthetase
GE53425	FZD1	0.015	-1.60	NM_003505	frizzled homolog 1 (Drosophila)
GE528433	C9ORF163	0.021	-1.60	NM_152571	hypothetical protein FLJ36779
GE83441	SPINK7	0.008	-1.60	NM_032566	esophagus cancer-related gene-2
GE54017	HNRNPR	0.019	-1.60	NM_005826	heterogeneous nuclear ribonucleoprotein R
GE82355	RSBN1	0.013	-1.60	NM_018364	round spermatid basic protein 1
GE623510	EEF1G	0.009	-1.60	BI489517	Coiled-coil-helix-coiled-coil-helix domain containing 3
GE813317	ITFG1	0.047	-1.59	BX114982	Transcribed locus, weakly similar to XP_528662.1 PREDICTED: similar to Immunoglo
GE842776	GNA12	0.017	-1.59	BF515137	Guanine nucleotide binding protein (G protein) alpha 12
GE81658	API5	0.004	-1.59	NM_006595	apoptosis inhibitor 5
GE79756	NUP160	0.004	-1.59	BF968999	Nucleoporin 160kDa
GE837902	ZNF605	0.023	-1.59	BQ003590	Zinc finger protein 605
GE60153	ZNF74	0.032	-1.59	NM_003426	zinc finger protein 74 (Cos52)
GE56237	RSBN1	0.041	-1.59	D61092	Round spermatid basic protein 1
GE652276	UBE2U	0.041	-1.59	BX116499	Ubiquitin-conjugating enzyme E2U (putative)
GE887158	SEC24C(includesEG:9632)	0.017	-1.59	BE737711	SEC24 family, member C (S. cerevisiae)
GE61315	RPL5	0.032	-1.59	AA814425	Similar to ribosomal protein L5; 60S ribosomal protein L5
GE88640	SAP130	0.027	-1.59	NM_024545	mSin3A-associated protein 130

Column ID	Symbol	p-value	FC(AI delet vs. NI)	Accession number	Description
GE55229	NXF1	0.032	-1.59	NM_006362	nuclear RNA export factor 1
GE55376	FBXL5	0.030	-1.58	NM_012161	F-box and leucine-rich repeat protein 5
GE53567	KIAA0895	0.012	-1.58	BI260221	KIAA0895 protein
GE58315	SOCS2	0.040	-1.58	NM_003877	suppressor of cytokine signaling 2
GE81110	GNAQ	0.001	-1.58	CD644251	Guanine nucleotide binding protein (G protein), q polypeptide
GE504590	PEAR1	0.034	-1.58	AK074121	platelet endothelial aggregation receptor 1
GE57951	XRCC1	0.011	-1.58	NM_006297	X-ray repair complementing defective repair in Chinese hamster cells 1
GE55097	CMIP	0.046	-1.58	R05960	C-Maf-inducing protein
GE497098	FCRL3	0.006	-1.58	AI376616	Fc receptor-like 3
GE615394	GPC3	0.017	-1.57	R94486	glypican 3
GE87033	C9ORF45	0.034	-1.57	NM_030814	chromosome 9 open reading frame 45
GE801862	FAM40B	0.020	-1.57	CA389993	Family with sequence similarity 40, member B
GE81887	FLJ35390	0.021	-1.57	AV743061	Hypothetical protein FLJ35390
GE83085	IFT74	0.038	-1.57	NM_025103	intraflagellar transport 74 homolog (Chlamydomonas)
GE515480	BMPR1A	0.025	-1.57	NM_004329	bone morphogenetic protein receptor, type IA
GE839787	AGFG2	0.042	-1.57	BF512495	Insulin receptor substrate 3-like
GE777701	SBF1	0.023	-1.57	CF142366	SET binding factor 1
GE495671	DR1	0.019	-1.56	AI887658	down-regulator of transcription 1, TBP-binding (negative cofactor 2)
GE79925	RPL7	0.039	-1.56	NM_000971	ribosomal protein L7
GE886128	CD81	0.033	-1.56	BM908449	CD81 antigen (target of antiproliferative antibody 1)
GE80563	EPHA7	0.005	-1.56	NM_004440	EPH receptor A7
GE628244	FMNL2	0.043	-1.56	BX108588	Formin-like 2
GE88845	OR52D1	0.031	-1.56	AC087380	Homo sapiens chromosome 11, clone RP11-454O22, complete sequence.
GE884498	C14ORF179	0.039	-1.56	BQ924814	MGC16028 similar to RIKEN cDNA 1700019E19 gene
GE844576	FCHSD2	0.028	-1.56	AA875908	FCH and double SH3 domains 2
GE82466	RHOF	0.038	-1.56	NM_019034	ras homolog gene family, member F (in filopodia)
GE83363	FYTTD1	0.029	-1.55	NM_032288	forty-two-three domain containing 1
GE87075	UEVLD	0.016	-1.55	NM_018314	ubiquitin-conjugating enzyme E2-like
GE750714	CYP2R1	0.022	-1.55	BF869225	Cytochrome P450, family 2, subfamily R, polypeptide 1
GE890135	EEF1G	0.045	-1.55	BE394491	Coiled-coil-helix-coiled-coil-helix domain containing 3
GE470947	RPL38	0.019	-1.55	BC007982	hypothetical protein MGC16275
GE526314	ZNF518A	0.049	-1.55	BU075986	Zinc finger protein 518
GE54559	ZNF205	0.049	-1.55	NM_003456	zinc finger protein 205
GE59624	HCCA2	0.008	-1.55	NM_053005	HCCA2 protein
GE61957	FKBP9L	0.031	-1.54	BX283612	FK506 binding protein 9-like
GE54829	TRIM33	0.014	-1.54	NM_015906	tripartite motif-containing 33
GE508275	RPL11	0.032	-1.54	BE934844	RC2-LT0007-300800-013-c09 LT0007 Homo sapiens cDNA, mRNA sequence.
GE56037	STRBP	0.006	-1.54	NM_018387	spermatid perinuclear RNA binding protein
GE62867	GNA12	0.005	-1.54	BE389395	Guanine nucleotide binding protein (G protein) alpha 12
GE79512	ETS2	0.043	-1.54	NM_005239	v-ets erythroblastosis virus E26 oncogene homolog 2 (avian)
GE59820	PNPLA2	0.014	-1.54	AA764777	Patatin-like phospholipase domain containing 2
GE671576	LOC149401	0.021	-1.54	AI652864	Similar to SLIT-ROBO Rho GTPase activating protein 2
GE87760	METTL9	0.044	-1.54	NM_016025	DORA reverse strand protein 1
GE85185	EYA3	0.039	-1.53	AA449710	eyes absent homolog 3 (Drosophila)
GE825382	EIF4EBP2	0.042	-1.53	BM450361	Eukaryotic translation initiation factor 4E binding protein 2
GE58923	C11ORF41	0.049	-1.53	U10991	chromosome 11 open reading frame 41
GE777422	FLJ45537	0.012	-1.53	BX097894	FLJ45537 protein
GE80227	WHSC1	0.045	-1.53	NM_133334	Wolf-Hirschhorn syndrome candidate 1

Column ID	Symbol	p-value	FC(AI delet vs. NI)	Accession number	Description
GE580588	KRT37	0.006	-1.53	NM_003770	keratin, hair, acidic, 7
GE796638	TRIM37	0.031	-1.53	AI792525	Tripartite motif-containing 37
GE81574	MC5R	0.039	-1.53	NM_005913	melanocortin 5 receptor
GE744809	MYLK4	0.050	-1.53	AK096893	Homo sapiens cDNA FLJ39574 fis, clone SKMUS2002693.
GE765146	APP	0.002	-1.53	CB053621	Amyloid beta (A4) precursor protein (peptidase nexin-II, Alzheimer disease)
GE55205	PHTF1	0.038	-1.53	NM_006608	putative homeodomain transcription factor 1
GE86694	SBDS	0.021	-1.52	AW853976	Shwachman-Bodian-Diamond syndrome
GE58443	MAN1B1	0.014	-1.52	NM_007230	synonym: MANA-ER; endoplasmic reticulum alpha-mannosidase 1; endoplasmic reticul
GE56491	RPRD1B	0.047	-1.52	NM_021215	chromosome 20 open reading frame 77
GE81602	NEUROG1	0.004	-1.52	NM_006161	neurogenin 1
GE58814	INA	0.032	-1.52	NM_032727	internexin neuronal intermediate filament protein, alpha
GE527682	IFLTD1	0.013	-1.52	NM_152590	likely ortholog of mouse Pas1 candidate 1
GE79640	VCP	0.020	-1.51	BM853854	Valosin-containing protein
GE53755	WBP11	0.042	-1.51	NM_016312	WW domain binding protein 11
GE58938	GABPA	0.028	-1.51	NM_002040	GA binding protein transcription factor, alpha subunit 60kDa
GE82706	C14ORF135	0.037	-1.51	NM_022495	chromosome 14 open reading frame 135
GE61175	EIF3H	0.032	-1.51	NM_003756	eukaryotic translation initiation factor 3, subunit 3 gamma, 40kDa
GE510120	C17ORF66	0.027	-1.51	NM_152781	chromosome 17 open reading frame 66
GE88449	HSF1	0.003	-1.51	BG983163	Heat shock transcription factor 1
GE472290	FBXL4	0.033	-1.51	AK055220	F-box and leucine-rich repeat protein 4
GE62332	ADAMTS8	0.032	-1.51	NM_007037	ADAM metallopeptidase with thrombospondin type 1 motif, 8
GE59063	METAP2	0.007	-1.51	NM_006838	methionyl aminopeptidase 2
GE769330	ASCC1	0.040	-1.50	AA632993	nq11h09.s1 NCI_CGAP_Thy1 Homo sapiens cDNA clone IMAGE:1143617 similar to contai
GE56185	TM9SF4	0.000	-1.50	NM_014742	transmembrane 9 superfamily protein member 4
GE55406	TASP1	0.005	-1.50	NM_017714	taspase, threonine aspartase, 1
GE866382	PTK2	0.022	-1.50	BF509623	PTK2 protein tyrosine kinase 2
GE79894	EFNA3	0.038	1.50	NM_004952	ephrin-A3
GE80240	ZNF558	0.020	1.50	NM_144693	zinc finger protein 558
GE83432	NT5DC1	0.026	1.50	NM_032519	synonyms: LP2642, C6orf200, MGC24302, MGC131837; chromosome 6 open reading frame
GE83501	LMNB2	0.038	1.50	NM_032737	lamin B2
GE59645	ADA	0.028	1.50	NM_000022	adenosine deaminase
GE81591	TNIP1	0.026	1.51	NM_006058	TNFAIP3 interacting protein 1
GE83513	KPNA4	0.003	1.51	NM_002268	karyopherin alpha 4 (importin alpha 3)
GE62221	MAPKAPK3	0.036	1.51	NM_004635	mitogen-activated protein kinase-activated protein kinase 3
GE81165	NFYA	0.017	1.51	NM_002505	nuclear transcription factor Y, alpha
GE54320	STX6	0.043	1.51	BE766470	Syntaxin 6
GE54657	FAM172A	0.030	1.51	NM_032042	hypothetical protein DKFZp564D172
GE789668	STXBP5	0.031	1.51	BX116201	CDNA FLJ43226 fis, clone HCASM2009588
GE487925	LOC100128434	0.040	1.51	AK091251	CDNA FLJ33932 fis, clone CTONG2017798
GE57805	NR3C1	0.006	1.51	BF055517	Nuclear receptor subfamily 3, group C, member 1 (glucocorticoid receptor)
GE753302	LIPA	0.046	1.52	BC040833	Lipase A, lysosomal acid, cholesterol esterase (Wolman disease)
GE62186	RRAGD	0.021	1.52	NM_021244	Ras-related GTP binding D
GE86450	UNKL	0.024	1.52	NM_023076	chromosome 16 open reading frame 28
GE624984	SATB1	0.038	1.52	AK124253	SATB homeobox 1
GE478916	MIER3	0.038	1.52	AW780232	DKFZP781I1119 hypothetical protein
GE57204	GPD1L	0.018	1.52	NM_015141	glycerol-3-phosphate dehydrogenase 1-like
GE847026	RRAGD	0.043	1.52	BQ030086	Ras-related GTP binding D
GE513651	ZNF431	0.015	1.53	NM_133473	zinc finger protein 431

Column ID	Symbol	p-value	FC(AI delet vs. NI)	Accession number	Description
GE61524	NEDD8	0.025	1.53	BG826796	Neural precursor cell expressed, developmentally down-regulated 8
GE718609	ACTR1B	0.005	1.53	BX119702	ARP1 actin-related protein 1 homolog B, centractin beta (yeast)
GE635882	TUBB2A	0.048	1.53	AI864693	Tubulin, beta 2A
GE88694	C1ORF216	0.050	1.53	NM_152374	hypothetical protein FLJ38984
GE83456	GTPBP3	0.046	1.53	NM_032620	GTP binding protein 3 (mitochondrial)
GE62446	POLQ	0.026	1.53	NM_006596	polymerase (DNA directed), theta
GE59614	PGK1	0.035	1.53	NM_000291	phosphoglycerate kinase 1
GE684260	DMTF1	0.021	1.54	H29027	Hypothetical LOC401385
GE651707	UHRF1BP1L	0.022	1.54	R39803	KIAA0701 protein
GE79571	MAP4K2	0.025	1.54	NM_004579	mitogen-activated protein kinase kinase kinase kinase 2
GE59544	BTN3A1	0.010	1.54	NM_007048	butyrophilin, subfamily 3, member A1
GE806822	LOC645212	0.042	1.54	BU150787	Transcribed locus
GE54621	NIT1	0.001	1.54	NM_005600	nitrilase 1
GE490349	C3ORF17	0.012	1.54	AA436214	Chromosome 3 open reading frame 17
GE551600	WDR90	0.029	1.54	NM_145294	similar to RIKEN cDNA 3230401M21 [Mus musculus]
GE57308	KNTC1	0.006	1.54	NM_014708	kinetochore associated 1
GE59733	ODC1	0.039	1.55	NM_002539	ornithine decarboxylase 1
GE80915	UBE3A	0.028	1.55	NM_000462	ubiquitin protein ligase E3A (human papilloma virus E6-associated protein, Angel
GE53268	MGRN1	0.045	1.55	D30926	Mahogunin, ring finger 1
GE58513	ANKRD11	0.039	1.55	BG108845	Ankyrin repeat domain 11
GE833939	ARHGAP26	0.022	1.55	BQ011167	Rho GTPase activating protein 26
GE62404	C7ORF27	0.016	1.55	NM_152743	chromosome 7 open reading frame 27
GE61197	ATP6V0C	0.042	1.55	BM822797	ATPase, H+ transporting, lysosomal 16kDa, V0 subunit c
GE53907	FAM44A	0.005	1.56	W68261	KIAA1327 protein
GE58907	JAK3	0.020	1.56	NM_000215	Janus kinase 3 (a protein tyrosine kinase, leukocyte)
GE80351	NARFL	0.036	1.56	NM_022493	nuclear prelamin A recognition factor-like
GE62286	UXS1	0.037	1.56	NM_025076	UDP-glucuronate decarboxylase 1
GE892360	ZNF714	0.008	1.56	BC050468	hypothetical protein LOC148206
GE56453	TJAP1	0.009	1.56	NM_080604	tight junction associated protein 1 (peripheral)
GE57490	FDXR	0.030	1.56	NM_004110	ferredoxin reductase
GE58555	ATAD2	0.034	1.57	NM_014109	ATPase family, AAA domain containing 2
GE591164	ZNF530	0.020	1.57	BX106478	zinc finger protein 530
GE87448	PANK3	0.032	1.57	NM_024594	pantothenate kinase 3
GE81922	LAT	0.002	1.57	NM_014387	linker for activation of T cells
GE57992	NFKB1	0.007	1.58	NM_003998	nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (p105)
GE87089	USP36	0.020	1.58	AI766835	Ubiquitin specific peptidase 36
GE60200	POLG	0.002	1.58	AI890083	KIAA1794
GE564215	IDH3A	0.023	1.58	AA769577	isocitrate dehydrogenase 3 (NAD+) alpha
GE81070	CDK2	0.043	1.58	NM_001798	cyclin-dependent kinase 2
GE59469	SNRPN	0.043	1.58	BX090300	Small nuclear ribonucleoprotein polypeptide N
GE737071	PLXNC1	0.045	1.58	AI829674	Plexin C1
GE82118	NOP16	0.037	1.58	NM_016391	hypothetical protein HSPC111
GE83571	ATG4D	0.026	1.59	N39115	Hypothetical protein FLJ12949
GE85645	TOMM40L	0.027	1.59	NM_032174	translocase of outer mitochondrial membrane 40 homolog-like (yeast)
GE888220	NUFIP2	0.043	1.59	BF796642	82-kD FMRP Interacting Protein
GE789114	C16ORF88	0.000	1.59	F34272	Similar to TSG118.1
GE753937	SREBF2	0.027	1.59	AI991305	Sterol regulatory element binding transcription factor 2
GE85691	RAVER2	0.012	1.59	AB046799	hypothetical protein FLJ10770

Column ID	Symbol	p-value	FC(AI delet vs. NI)	Accession number	Description
GE499816	MYL6	0.018	1.59	NM_021019	myosin, light polypeptide 6, alkali, smooth muscle and non-muscle
GE53110	PSMD12	0.025	1.60	NM_002816	proteasome (prosome, macropain) 26S subunit, non-ATPase, 12
GE53756	HSF4	0.003	1.60	D87673	heat shock transcription factor 4
GE85381	INTS2	0.013	1.60	NM_020748	KIAA1287
GE61469	ZNF700	0.010	1.60	AI924688	Zinc finger protein 700
GE82431	MARK1	0.004	1.60	NM_018650	MAP/microtubule affinity-regulating kinase 1
GE62298	GLS	0.008	1.60	NM_014905	glutaminase
GE59173	RAB9A	0.002	1.61	NM_004251	RAB9A, member RAS oncogene family
GE82617	ELK4	0.030	1.61	NM_001973	ELK4, ETS-domain protein (SRF accessory protein 1)
GE53132	HDAC4	0.033	1.61	NM_006037	histone deacetylase 4
GE886331	MCTS1	0.047	1.61	AW386292	C1GALT1-specific chaperone 1
GE82055	MRPL4	0.045	1.61	NM_015956	mitochondrial ribosomal protein L4
GE59856	CSK	0.025	1.61	NM_004383	c-src tyrosine kinase
GE841830	INMT	0.023	1.61	NM_006774	indolethylamine N-methyltransferase
GE84016	CALCOCO1	0.029	1.61	BQ711854	Calcium binding and coiled-coil domain 1
GE719636	TRIO	0.048	1.61	BX093523	Triple functional domain (PTPRF interacting)
GE88656	MSL3	0.045	1.61	NM_006800	male-specific lethal 3-like 1 (Drosophila)
GE82142	SIRT7	0.001	1.62	NM_016538	sirtuin (silent mating type information regulation 2 homolog) 7 (S. cerevisiae)
GE769325	UNKL	0.025	1.62	AW382204	Chromosome 16 open reading frame 28
GE512985	ARSH	0.035	1.62	XM_293401	synonym: sulfatase; go_function: sulfuric ester hydrolase activity [goid 0008484
GE531346	MYEF2	0.028	1.62	AI572493	Solute carrier family 24, member 5
GE58352	NDUFA5	0.028	1.62	NM_005000	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 5, 13kDa
GE822595	C19ORF44	0.042	1.62	BE878259	chromosome 19 open reading frame 44
GE633042	RPL35A	0.043	1.63	AI306578	Ribosomal protein L35a
GE59136	CDKN2D	0.037	1.63	NM_001800	cyclin-dependent kinase inhibitor 2D (p19, inhibits CDK4)
GE504557	OR3A2	0.021	1.63	NM_002551	olfactory receptor, family 3, subfamily A, member 2
GE79322	GIPC1	0.028	1.63	NM_005716	GIPC PDZ domain containing family, member 1
GE59801	CKS1B	0.046	1.63	NM_001826	CDC28 protein kinase regulatory subunit 1B
GE87559	KIAA1467	0.023	1.63	C18454	KIAA1467 protein
GE85700	SAPS2	0.047	1.64	N45732	SAPS domain family, member 2
GE58304	HIST1H4C	0.031	1.64	NM_003542	histone 1, H4c
GE587455	ZZEF1	0.047	1.64	AI732604	Zinc finger, ZZ-type with EF-hand domain 1
GE488070	C10ORF51	0.022	1.64	AK128027	chromosome 10 open reading frame 51
GE59925	PCTK1	0.027	1.64	NM_006201	PCTAIRE protein kinase 1
GE86885	RPS27L	0.049	1.64	BC047648	ribosomal protein S27-like
GE796431	PHOX2A	0.047	1.65	NM_005169	paired-like (aristaless) homeobox 2a
GE592302	PTEN	0.029	1.65	AI917390	Phosphatase and tensin homolog (mutated in multiple advanced cancers 1)
GE55886	CCDC25	0.042	1.65	NM_018246	coiled-coil domain containing 25
GE57455	GAS2L3	0.005	1.65	NM_174942	growth arrest-specific 2 like 3
GE81085	CTNNA1	0.032	1.66	NM_001903	catenin (cadherin-associated protein), alpha 1, 102kDa
GE87513	LYPLAL1	0.046	1.66	BM714914	Lysophospholipase-like 1
GE552994	DKFZP781N1041	0.047	1.66	AW340603	Similar to RIKEN cDNA 6430537H07 gene
GE733458	CD99	0.014	1.66	CB130113	CD99 antigen
GE687007	B4GALNT4	0.039	1.66	NM_178537	beta1,4-N-acetylgalactosaminyltransferases IV
GE56468	KCTD9	0.046	1.67	NM_017634	potassium channel tetramerisation domain containing 9
GE591298	NSMCE2	0.050	1.67	AI082823	Chromosome 8 open reading frame 36
GE84139	PFDN2	0.042	1.67	BG542161	Prefoldin 2
GE549080	OR7D2	0.030	1.67	AK095468	olfactory receptor, family 7, subfamily D, member 2

Column ID	Symbol	p-value	FC(AI delet vs. NI)	Accession number	Description
GE57033	PNPT1	0.000	1.67	NM_033109	polyribonucleotide nucleotidyltransferase 1
GE55260	SLC19A2	0.024	1.67	NM_006996	solute carrier family 19 (thiamine transporter), member 2
GE775043	C6ORF222	0.039	1.67	BX648558	hypothetical protein DKFZp779B1540
GE473534	NLN	0.023	1.68	NM_020726	neurolysin (metallopeptidase M3 family)
GE815694	HK1	0.038	1.68	AI972312	Hexokinase 1
GE852866	DIDO1	0.020	1.68	BM987066	Death inducer-obliterator 1
GE63277	PCDHB9	0.013	1.68	NM_019119	protocadherin beta 9
GE843609	FBP2	0.016	1.69	BF514199	Fructose-1,6-bisphosphatase 2
GE588065	ITGB3BP	0.035	1.69	BX091255	Integrin beta 3 binding protein (beta3-endonexin)
GE83566	KIAA1984	0.041	1.69	BM511494	Chromosome 9 open reading frame 86
GE80956	GNRH1	0.026	1.69	NM_000825	gonadotropin-releasing hormone 1 (luteinizing-releasing hormone)
GE506550	GABPB2	0.008	1.69	NM_144618	hypothetical protein MGC29891
GE625819	WWOX	0.038	1.69	BM716547	WW domain containing oxidoreductase
GE54725	ERO1L	0.006	1.70	NM_014584	ERO1-like (S. cerevisiae)
GE890401	NFKBID	0.041	1.70	NM_032721	T-cell activation NFKB-like protein
GE85297	SMARCAL1	0.006	1.70	AI797084	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subf
GE88495	GPR108	0.023	1.70	BG987489	G protein-coupled receptor 108
GE81242	STRN	0.049	1.70	NM_003162	striatin, calmodulin binding protein
GE88555	PIK3CA	0.004	1.70	BX341752	Phosphoinositide-3-kinase, catalytic, alpha polypeptide
GE888638	PMPCB	0.024	1.71	BM722628	Peptidase (mitochondrial processing) beta
GE83395	CCDC77	0.005	1.71	NM_032358	hypothetical protein MGC13183
GE867238	ZNF600	0.044	1.71	AA723897	Zinc finger protein 600
GE662578	RGS3	0.002	1.71	AW151660	regulator of G-protein signaling 3
GE85599	ZNF80	0.017	1.71	X65233	zinc finger protein 80 (pT17)
GE498773	MRS2	0.018	1.71	BQ721189	MRS2-like, magnesium homeostasis factor (S. cerevisiae)
GE55471	RPP25	0.033	1.71	NM_017793	ribonuclease P 25kDa subunit
GE87326	CTHRC1	0.038	1.71	NM_138455	collagen triple helix repeat containing 1
GE572531	HIST1H4D	0.045	1.71	NM_003539	histone 1, H4d
GE81468	TLE3	0.048	1.72	NM_005078	transducin-like enhancer of split 3 (E(sp1) homolog, Drosophila)
GE62464	USF1	0.013	1.72	NM_007122	upstream transcription factor 1
GE860286	ARHGAP26	0.013	1.72	BU754312	Rho GTPase activating protein 26
GE756208	NRXN1	0.038	1.72	AA174070	Neurexin 1
GE56782	C19ORF66	0.042	1.73	NM_018381	hypothetical protein FLJ11286
GE57352	DNAJB1	0.026	1.73	NM_006145	DnaJ (Hsp40) homolog, subfamily B, member 1
GE600869	ITFG1	0.032	1.73	BC015844	T-cell immunomodulatory protein
GE701062	CTNNBL1	0.032	1.74	AA693872	Catenin, beta like 1
GE571843	RHEBL1	0.033	1.74	NM_144593	Ras homolog enriched in brain like 1
GE81504	PTPN14	0.026	1.74	CA397830	Protein tyrosine phosphatase, non-receptor type 14
GE481202	PRRT3	0.024	1.75	AI807687	proline-rich transmembrane protein 3
GE801438	LOC339666	0.009	1.75	BC041349	hypothetical protein LOC339666
GE86195	THBS1	0.023	1.75	BU959813	Thrombospondin 1
GE522927	RP11-49G10.8	0.029	1.75	NM_173859	breast cancer and salivary gland expression gene
GE86364	SLC41A1	0.015	1.75	NM_173854	solute carrier family 41, member 1
GE574644	LYN	0.036	1.76	BU607424	V-yes-1 Yamaguchi sarcoma viral related oncogene homolog
GE86359	GSTK1	0.039	1.76	AK055103	glutathione S-transferase kappa 1
GE786902	IFNGR1	0.042	1.76	CA771718	Interferon gamma receptor 1
GE56665	UHMK1	0.016	1.76	AA261924	U2AF homology motif (UHM) kinase 1
GE56161	LOC730101	0.019	1.76	N90633	Hypothetical protein LOC221362

Column ID	Symbol	p-value	FC(AI delet vs. NI)	Accession number	Description
GE600439	DLEU7	0.026	1.77	AI659523	deleted in lymphocytic leukemia, 7
GE518189	SMARCA4	0.044	1.77	BX097298	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subf
GE81986	ZZEF1	0.010	1.77	NM_015113	zinc finger, ZZ-type with EF-hand domain 1
GE55266	RPGR	0.029	1.77	NM_000328	retinitis pigmentosa GTPase regulator
GE793334	FLJ46419	0.047	1.77	BU193672	FLJ46419 protein
GE831115	LITAF	0.030	1.77	AW291049	Lipopolysaccharide-induced TNF factor
GE622590	POLR3H	0.043	1.78	AA196481	Aconitase 2, mitochondrial
GE53264	NBEAL2	0.008	1.78	BU429796	Neurobeachin-like 2
GE88071	SF4	0.040	1.78	NM_021164	splicing factor 4
GE55171	TRPC6	0.031	1.78	NM_004621	transient receptor potential cation channel, subfamily C, member 6
GE81563	ZNF443	0.011	1.78	BC032753	zinc finger protein 443
GE649833	DZIP1	0.038	1.78	AI765929	Claudin 10
GE84637	ATP2A3	0.027	1.79	BI031652	ATPase, Ca++ transporting, ubiquitous
GE733432	RG9MTD2	0.021	1.79	AL564528	RNA (guanine-9-) methyltransferase domain containing 2
GE59542	BTN3A3	0.013	1.79	NM_006994	butyrophilin, subfamily 3, member A3
GE544221	LPCAT4	0.026	1.79	NM_153613	1-acylglycerol-3-phosphate O-acyltransferase 7 (lysophosphatidic acid acyltransf
GE80135	ATP6AP2	0.024	1.79	NM_005765	ATPase, H+ transporting, lysosomal accessory protein 2
GE81309	SORBS2	0.045	1.79	NM_003603	sorbin and SH3 domain containing 2
GE88304	LOC375010	0.035	1.79	U79301	hypothetical LOC375010
GE676136	NPAL2	0.030	1.79	AA814011	NIPA-like domain containing 2
GE633524	PIK3R1	0.006	1.80	AI379149	Phosphoinositide-3-kinase, regulatory subunit 1 (p85 alpha)
GE583261	SLC19A2	0.043	1.80	AK093612	Solute carrier family 19 (thiamine transporter), member 2
GE58207	ENG	0.010	1.80	NM_000118	endoglin (Osler-Rendu-Weber syndrome 1)
GE765853	TRPM3	0.026	1.80	AW022053	Transient receptor potential cation channel, subfamily M, member 3
GE905935	MCCC2	0.028	1.80	AF086534	Methylcrotonoyl-Coenzyme A carboxylase 2 (beta)
GE83128	SPTBN4	0.020	1.80	NM_020971	spectrin, beta, non-erythrocytic 4
GE785534	NEURL	0.020	1.81	BX335392	neuralized homolog (Drosophila)
GE58184	CD36	0.038	1.81	NM_000072	CD36 antigen (collagen type I receptor, thrombospondin receptor)
GE768406	NAT5	0.012	1.81	AA724829	N-acetyltransferase 5 (ARD1 homolog, S. cerevisiae)
GE88813	GLT25D1	0.026	1.81	NM_024656	glycosyltransferase 25 domain containing 1
GE54543	ESRRG	0.049	1.82	NM_001438	estrogen-related receptor gamma
GE876989	C3ORF23	0.043	1.82	BG493222	Chromosome 3 open reading frame 23
GE56689	LOC54492	0.037	1.82	CD677650	Hypothetical protein DKFZP761M1511
GE87532	LOC653506	0.034	1.83	AF086149	Ubiquitin C
GE56089	CLCN7	0.009	1.83	NM_001287	chloride channel 7
GE535968	ADAMTS6	0.031	1.83	NM_197941	ADAM metallopeptidase with thrombospondin type 1 motif, 6
GE484981	UNC5CL	0.035	1.83	NM_173561	unc-5 homolog C (C. elegans)-like
GE906547	C2ORF27	0.013	1.83	BG575991	chromosome 2 open reading frame 27
GE740229	COMMD10	0.039	1.83	CA773690	COMM domain containing 10
GE494547	KIAA1377	0.034	1.84	AK095004	KIAA1377 protein
GE772434	ITGB1BP1	0.022	1.84	BX113943	Integrin beta 1 binding protein 1
GE59587	WDR68	0.011	1.84	NM_005828	WD repeat domain 68
GE547975	RNF215	0.023	1.84	AI494102	KIAA1656 protein
GE85868	ATP6V0A1	0.015	1.84	T27157	ATPase, H+ transporting, lysosomal V0 subunit a isoform 1
GE58013	NFIA	0.003	1.84	NM_181504	phosphoinositide-3-kinase, regulatory subunit 1 (p85 alpha)
GE649923	EDAR	0.022	1.84	AI732569	Ectodysplasin A receptor
GE487405	DKFZP686I15217	0.041	1.84	AI190029	Hypothetical protein DKFZp686I15217
GE62820	THOC4	0.007	1.85	NM_005782	THO complex 4

Column ID	Symbol	p-value	FC(AI delet vs. NI)	Accession number	Description
GE882682	C9ORF117	0.044	1.85	BF338273	Chromosome 9 open reading frame 117
GE61522	BPNT1	0.018	1.85	NM_006085	3'(2'), 5'-bisphosphate nucleotidase 1
GE57935	LSP1	0.017	1.85	NM_002339	lymphocyte-specific protein 1
GE60089	NEB	0.009	1.85	NM_004543	nebulin
GE733097	FLJ39739	0.019	1.85	AK097058	FLJ39739 protein
GE57493	ITGAM	0.040	1.86	NM_000632	integrin, alpha M (complement component receptor 3, alpha; also known as CD11b (
GE61055	UAP1L1	0.016	1.86	BM044040	UDP-N-acteylglucosamine pyrophosphorylase 1-like 1
GE87560	SNX18	0.032	1.86	AA504570	Sorting nexin associated golgi protein 1
GE774158	METT5D1	0.043	1.86	AW117704	xe34e12.x1 NCI_CGAP_Ut1 Homo sapiens cDNA clone IMAGE:2609038 3' similar to cont
GE83217	ZNF93	0.018	1.86	AK022550	zinc finger protein 505
GE57664	VLDLR	0.031	1.87	NM_003383	very low density lipoprotein receptor
GE82201	NDE1	0.009	1.87	NM_017668	nudE nuclear distribution gene E homolog 1 (A. nidulans)
GE61297	APOBEC3B	0.019	1.87	NM_004900	apolipoprotein B mRNA editing enzyme, catalytic polypeptide-like 3B
GE83885	C21ORF29	0.032	1.87	NM_144991	chromosome 21 open reading frame 29
GE85553	SCAF1	0.022	1.87	NM_021228	serine arginine-rich pre-mRNA splicing factor SR-A1
GE57299	UCK2	0.009	1.87	NM_012474	uridine-cytidine kinase 2
GE83493	NFKBID	0.025	1.88	NM_032721	T-cell activation NFKB-like protein
GE53850	ASAP1	0.028	1.88	BF058310	DDEF1 intronic transcript 1
GE86716	TFDP2	0.020	1.88	BX647881	Transcription factor Dp-2 (E2F dimerization partner 2)
GE86069	EMB	0.044	1.88	NM_198449	embigin homolog (mouse)
GE511138	MAGI1	0.040	1.88	AK130632	membrane associated guanylate kinase, WW and PDZ domain containing 1
GE81669	MMP24	0.015	1.88	NM_006690	matrix metallopeptidase 24 (membrane-inserted)
GE528325	RGS5	0.016	1.88	AA229652	Regulator of G-protein signalling 5
GE86044	SLC25A39	0.033	1.88	BF317223	CGI-69 protein
GE81392	DDX12	0.013	1.89	AA385297	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 12 (CHL1-like helicase homolog, S.
GE514327	PNLDC1	0.035	1.90	NM_173516	poly(A)-specific ribonuclease (PARN)-like domain containing 1
GE700641	FRMD4A	0.028	1.90	AA917972	FERM domain containing 4A
GE609580	ZNF766	0.034	1.90	AU160820	Hypothetical protein LOC90321
GE597704	SRI	0.038	1.90	BE551081	Sorcin
GE54481	CROT	0.001	1.90	NM_021151	carnitine O-octanoyltransferase
GE84013	C1ORF192	0.002	1.91	AK023394	Chromosome 1 open reading frame 192
GE56486	KIF20B	0.044	1.91	NM_016195	M-phase phosphoprotein 1
GE490200	MRPL55	0.036	1.91	AK094778	mitochondrial ribosomal protein L55
GE61543	IARS2	0.014	1.91	NM_018060	isoleucine-tRNA synthetase 2, mitochondrial
GE649929	MED24	0.041	1.91	AW516080	Thyroid hormone receptor associated protein 4
GE87171	UNC13D	0.024	1.91	T83023	Unc-13 homolog D (C. elegans)
GE81642	SPAG5	0.013	1.91	NM_006461	sperm associated antigen 5
GE54699	CHRD	0.032	1.91	NM_003741	chordin
GE494016	LOC389043	0.005	1.91	AK125982	Hypothetical gene supported by AK125982; BC042817
GE54944	IER5	0.029	1.92	NM_016545	immediate early response 5
GE481095	C18ORF24	0.004	1.92	NM_145060	chromosome 18 open reading frame 24
GE848907	UBE2E2	0.025	1.92	BQ002494	Ubiquitin-conjugating enzyme E2E 2 (UBC4/5 homolog, yeast)
GE709150	PRPF18	0.031	1.92	BM788348	PRP18 pre-mRNA processing factor 18 homolog (yeast)
GE88341	PFKFB2	0.006	1.92	AB044805	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 2
GE53021	SOCS1	0.027	1.92	NM_003745	suppressor of cytokine signaling 1
GE55660	LOC286272	0.013	1.92	AK000939	hypothetical protein LOC286272
GE833861	STK38L	0.034	1.93	AW444572	Serine/threonine kinase 38 like
GE512449	FAF1	0.036	1.93	AV655330	Fas (TNFRSF6) associated factor 1

Column ID	Symbol	p-value	FC(AI delet vs. NI)	Accession number	Description
GE59309	BRCA1	0.049	1.93	NM_007296	breast cancer 1, early onset
GE81666	CCL27	0.008	1.93	NM_006664	chemokine (C-C motif) ligand 27
GE763425	TBC1D16	0.023	1.93	AU253627	AU253627 human unfavorable neuroblastoma cDNA Homo sapiens cDNA clone Nbla10286
GE710170	LOC728606	0.031	1.93	AK056805	CDNA FLJ32243 fis, clone PROST1000039
GE83188	C14ORF93	0.016	1.93	BC045740	Chromosome 14 open reading frame 93
GE81716	BTN3A1	0.013	1.94	NM_007048	butyrophilin, subfamily 3, member A1
GE506792	ME3	0.046	1.94	AW015176	malic enzyme 3, NADP(+)-dependent, mitochondrial
GE85128	HIBCH	0.043	1.94	AW104464	3-hydroxyisobutyryl-Coenzyme A hydrolase
GE59892	FBN1	0.027	1.94	NM_000138	fibrillin 1 (Marfan syndrome)
GE657015	CDH11	0.029	1.95	AI291310	Cadherin 11, type 2, OB-cadherin (osteoblast)
GE500145	LOC152586	0.046	1.95	BQ428631	Similar to RIKEN cDNA 4933434I20
GE715872	RERE	0.045	1.95	AW235269	arginine-glutamic acid dipeptide (RE) repeats
GE81991	RCOR1	0.034	1.95	NM_015156	REST corepressor 1
GE81688	SPINK5	0.001	1.96	NM_006846	serine peptidase inhibitor, Kazal type 5
GE517478	DOCK2	0.041	1.96	NM_004946	dedicator of cytokinesis 2
GE58734	DTL	0.046	1.96	NM_016448	denticleless homolog (Drosophila)
GE87462	SMARCD2	0.001	1.96	NM_003077	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subf
GE55640	C19ORF60	0.042	1.96	NM_017967	hypothetical protein FLJ20850
GE60197	RAD54L	0.011	1.97	NM_003579	RAD54-like (S. cerevisiae)
GE865501	DNAH10	0.048	1.97	BU741872	Dynein, axonemal, heavy polypeptide 10
GE782884	STXBP6	0.043	1.97	AI669586	Syntaxin binding protein 6 (amisyn)
GE62068	KLHL12	0.004	1.97	NM_021633	kelch-like 12 (Drosophila)
GE84183	FLJ14186	0.037	1.97	AF086554	Hypothetical gene supported by AK024248; AL137733
GE87732	GDPD3	0.049	1.98	NM_024307	glycerophosphodiester phosphodiesterase domain containing 3
GE671817	ZDHHC1	0.028	1.98	C14858	C14858 Clontech human aorta polyA+ mRNA (#6572) Homo sapiens cDNA clone 093E04 3
GE84903	OCIAD1	0.010	1.98	BU854406	OCIA domain containing 1
GE56586	INTS7	0.031	1.99	AA418221	Chromosome 1 open reading frame 73
GE84734	UBE3A	0.042	1.99	BU659774	Small nuclear ribonucleoprotein polypeptide N
GE729467	STK32B	0.044	2.00	BE503322	Serine/threonine kinase 32B
GE819111	TUBE1	0.000	2.00	AK126191	Tubulin, epsilon 1
GE863397	SLFN5	0.031	2.00	N43973	schlafen family member 5
GE82388	ASAP1	0.028	2.01	BF094007	DDEF1 intronic transcript 1
GE619667	SHH	0.015	2.01	NM_000193	sonic hedgehog homolog (Drosophila)
GE62917	FCGR3A	0.028	2.01	NM_000569	Fc fragment of IgG, low affinity IIIa, receptor (CD16a)
GE596018	NR3C1	0.019	2.01	R62551	Nuclear receptor subfamily 3, group C, member 1 (glucocorticoid receptor)
GE59644	TGFB1	0.019	2.02	NM_000660	transforming growth factor, beta 1 (Camurati-Engelmann disease)
GE56305	CASP4	0.041	2.02	W39601	Caspase 4, apoptosis-related cysteine peptidase
GE53331	UPB1	0.028	2.02	NM_016327	ureidopropionase, beta
GE894671	ZNF321	0.006	2.02	BQ007859	Transcribed locus, weakly similar to XP_517655.1 PREDICTED: similar to KIAA0825
GE88297	TMEM81	0.005	2.02	AY359081	similar to RIKEN cDNA 4930429O20
GE55217	SLC25A10	0.014	2.02	NM_012140	solute carrier family 25 (mitochondrial carrier; dicarboxylate transporter), mem
GE87212	GTDC1	0.012	2.03	NM_024659	glycosyltransferase-like domain containing 1
GE60547	BTN3A2	0.004	2.03	AA310176	Butyrophilin, subfamily 3, member A2
GE62210	B3GNT5	0.025	2.03	NM_032047	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 5
GE56253	EMILIN1	0.009	2.04	NM_007046	elastin microfibril interfacer 1
GE57441	FSTL1	0.007	2.04	NM_007085	follistatin-like 1
GE58045	DRD5	0.014	2.05	NM_000798	dopamine receptor D5
GE483991	WIPI1	0.016	2.05	BM664718	WD repeat domain, phosphoinositide interacting 1

Column ID	Symbol	p-value	FC(AI delet vs. NI)	Accession number	Description
GE56177	TTC22	0.020	2.05	BM919426	Tetratricopeptide repeat domain 22
GE888171	MXD3	0.034	2.05	BQ053282	MAX dimerization protein 3
GE81249	TFRC	0.039	2.06	NM_003234	transferrin receptor (p90, CD71)
GE712156	LPCAT4	0.026	2.06	AI679759	lysophosphatidylcholine acyltransferase 4
GE663037	LOC728531	0.018	2.07	AI561175	hypothetical LOC728531
GE83345	ANKRD20A1	0.027	2.07	AL136793	ankyrin repeat domain 20 family, member A1
GE61778	GLT8D2	0.041	2.07	NM_031302	glycosyltransferase 8 domain containing 2
GE55804	GNL3L	0.032	2.08	NM_019067	guanine nucleotide binding protein-like 3 (nucleolar)-like
GE59426	RAPGEF4	0.038	2.08	NM_007023	Rap guanine nucleotide exchange factor (GEF) 4
GE87753	REEP4	0.003	2.09	NM_025232	chromosome 8 open reading frame 20
GE59715	IRF1	0.003	2.09	NM_002198	interferon regulatory factor 1
GE80003	GNA13	0.021	2.09	NM_006572	guanine nucleotide binding protein (G protein), alpha 13
GE79364	B2M	0.001	2.10	NM_004048	beta-2-microglobulin
GE694755	CD1C	0.037	2.10	AW024273	Transcribed locus
GE63154	MAP3K11	0.007	2.11	AI738536	Mitogen-activated protein kinase kinase kinase 11
GE55120	TCF19	0.035	2.11	AI989809	POU domain, class 5, transcription factor 1
GE56789	ECT2	0.015	2.11	NM_018098	epithelial cell transforming sequence 2 oncogene
GE834142	LOC284890	0.044	2.11	AW291007	Similar to RIKEN cDNA 4930583C14
GE54147	NDC80	0.039	2.11	NM_006101	kinetochore associated 2
GE820751	PPM1H	0.001	2.11	BM721901	Protein phosphatase 1H (PP2C domain containing)
GE470813	SCHIP1	0.017	2.11	BF111903	Schwannomin interacting protein 1
GE82569	PCDHB16	0.013	2.12	NM_020957	protocadherin beta 16
GE481319	ZNF57	0.019	2.12	NM_173480	hypothetical protein LOC126295
GE53936	ARRDC3	0.028	2.12	NM_020801	arrestin domain containing 3
GE572630	FLJ20464	0.005	2.13	NM_017834	hypothetical protein FLJ20464
GE53242	CCL26	0.035	2.13	NM_006072	chemokine (C-C motif) ligand 26
GE59795	TYK2	0.034	2.13	NM_003331	tyrosine kinase 2
GE54230	RGS12	0.023	2.14	NM_002926	regulator of G-protein signalling 12
GE608195	EXPH5	0.008	2.14	AK000786	Exophilin 5
GE57498	TOP2A	0.003	2.14	NM_001067	topoisomerase (DNA) II alpha 170kDa
GE85962	PIK3R1	0.014	2.14	NM_181504	phosphoinositide-3-kinase, regulatory subunit 1 (p85 alpha)
GE474661	FLJ90723	0.046	2.14	BC046188	Homo sapiens, clone IMAGE:5092955
GE736690	CDCA2	0.003	2.14	AA278504	Cell division cycle associated 2
GE62259	MICB	0.002	2.15	NM_005931	MHC class I polypeptide-related sequence B
GE781278	TRIM37	0.041	2.15	AA460710	Tripartite motif-containing 37
GE808724	C21ORF90	0.039	2.16	BE549688	Chromosome 21 open reading frame 90
GE57024	SH3RF1	0.041	2.16	NM_020870	SH3 multiple domains 2
GE60098	RBBP5	0.008	2.16	NM_005057	retinoblastoma binding protein 5
GE52951	BCL6B	0.042	2.17	NM_181844	B-cell CLL/lymphoma 6, member B (zinc finger protein)
GE554574	LOC149643	0.005	2.17	BM559359	Hypothetical LOC149643
GE59759	CCNA2	0.010	2.17	CF139543	Cyclin A2
GE83306	MND1	0.034	2.18	NM_032117	GAJ protein
GE617543	UCK2	0.009	2.19	BP431917	LOC440701
GE81622	IFI30	0.005	2.19	NM_006332	interferon, gamma-inducible protein 30
GE79012	ESPL1	0.020	2.19	NM_012291	extra spindle poles like 1 (S. cerevisiae)
GE80790	C22ORF25	0.011	2.20	BE708875	Non-metastatic cells 2, protein (NM23B) expressed in
GE56483	ULK3	0.027	2.20	NM_015518	unc-51-like kinase 3 (C. elegans)
GE63200	DNPEP	0.016	2.20	BE671707	Aspartyl aminopeptidase

Column ID	Symbol	p-value	FC(AI delet vs. NI)	Accession number	Description
GE59170	BMP4	0.023	2.21	NM_001202	bone morphogenetic protein 4
GE478996	CDCA5	0.019	2.21	NM_080668	cell division cycle associated 5
GE590054	E2F5	0.011	2.21	AI277955	qm51c01.x1 Soares_placenta_8to9weeks_2NbHP8to9W Homo sapiens cDNA clone IMAGE:18
GE57617	ENPEP	0.027	2.21	NM_001977	glutamyl aminopeptidase (aminopeptidase A)
GE88347	KLHL29	0.037	2.22	AL589210	Kelch repeat and BTB (POZ) domain containing 9
GE55780	CEP55	0.005	2.22	NM_018131	centrosomal protein 55kDa
GE709079	LSR	0.034	2.22	AA527172	Lipolysis stimulated lipoprotein receptor
GE83335	NLRC5	0.045	2.24	BF365509	Nucleotide-binding oligomerization domains 27
GE906759	LOC100129837	0.045	2.24	AK092197	similar to ZNF124 protein
GE57140	ADAM8	0.012	2.24	NM_001109	ADAM metallopeptidase domain 8
GE711932	ITGAV	0.046	2.24	AA558704	Integrin, alpha V (vitronectin receptor, alpha polypeptide, antigen CD51)
GE61581	GLIPR1	0.012	2.24	BU675991	GLI pathogenesis-related 1 (glioma)
GE858059	CHSY3	0.022	2.25	BQ182928	Chondroitin sulfate synthase 3
GE79181	TAP1	0.004	2.25	NM_000593	transporter 1, ATP-binding cassette, sub-family B (MDR/TAP)
GE80599	KCNC2	0.029	2.26	NM_139136	potassium voltage-gated channel, Shaw-related subfamily, member 2
GE785548	PLXNC1	0.006	2.27	AI290473	Plexin C1
GE657869	FBXO43	0.012	2.27	AA740602	F-box protein 43
GE623989	SLC25A28	0.006	2.28	AK094405	Solute carrier family 25, member 28
GE79766	NXT2	0.015	2.28	NM_018698	nuclear transport factor 2-like export factor 2
GE81042	CYR61	0.023	2.28	NM_001554	cysteine-rich, angiogenic inducer, 61
GE55180	RP2	0.000	2.29	NM_006915	retinitis pigmentosa 2 (X-linked recessive)
GE588846	LOC148203	0.017	2.29	AW303287	Hypothetical protein LOC148203
GE54510	3-Mar	0.019	2.29	NM_178450	membrane-associated ring finger (C3HC4) 3
GE83121	ZNF430	0.000	2.30	NM_025189	zinc finger protein 430
GE57827	PROS1	0.050	2.30	NM_000313	protein S (alpha)
GE54586	SMTN	0.029	2.30	NM_006932	smoothelin
GE79183	IGF2	0.039	2.31	NM_000612	insulin-like growth factor 2 (somatomedin A)
GE81571	TRAIP	0.005	2.31	NM_005879	TRAF interacting protein
GE81088	CFD	0.031	2.32	NM_001928	D component of complement (adipsin)
GE632956	DAZAP1	0.006	2.32	AI023688	DAZ associated protein 1
GE80147	GULP1	0.016	2.33	NM_016315	GULP, engulfment adaptor PTB domain containing 1
GE53603	KIAA0922	0.035	2.34	NM_015196	KIAA0922 protein
GE905456	KLHL18	0.022	2.34	NM_025010	kelch-like 18 (Drosophila)
GE57194	E2F3	0.032	2.35	NM_001949	E2F transcription factor 3
GE80356	FLJ25006	0.035	2.35	NM_144610	hypothetical protein FLJ25006
GE62031	TINAGL1	0.033	2.37	NM_022164	tubulointerstitial nephritis antigen-like 1
GE57064	DLGAP5	0.001	2.37	NM_014750	discs, large homolog 7 (Drosophila)
GE890536	DNM3	0.036	2.37	AK021543	Dynamin 3
GE840013	GABRB2	0.028	2.37	BX118696	Gamma-aminobutyric acid (GABA) A receptor, beta 2
GE59843	CD46	0.040	2.37	NM_153826	membrane cofactor protein (CD46, trophoblast-lymphocyte cross-reactive antigen)
GE521024	LOC344595	0.016	2.38	BC045680	Hypothetical LOC344595
GE57004	PRSS23	0.001	2.38	NM_007173	protease, serine, 23
GE87123	RPS6KL1	0.040	2.38	AL390152	ribosomal protein S6 kinase-like 1
GE79130	APOD	0.003	2.38	NM_001647	apolipoprotein D
GE677575	ARID1B	0.014	2.39	BE502024	AT rich interactive domain 1B (SWI1-like)
GE53017	TRAF5	0.025	2.40	NM_004619	TNF receptor-associated factor 5
GE836003	LOC100134716	0.032	2.40	AK125429	CDNA FLJ43440 fis, clone OCBBF2030517
GE59197	CHRNB4	0.013	2.40	NM_000750	cholinergic receptor, nicotinic, beta polypeptide 4

Column ID	Symbol	p-value	FC(AI delet vs. NI)	Accession number	Description
GE59949	PELO	0.019	2.41	BG182768	Pelota homolog (Drosophila)
GE53894	KIAA1303	0.043	2.42	NM_020761	raptor
GE80759	KRTAP4-12	0.009	2.42	NM_031854	keratin associated protein 4-12
GE62465	KIF11	0.006	2.42	NM_004523	kinesin family member 11
GE81715	BTN3A2	0.042	2.42	NM_007047	butyrophilin, subfamily 3, member A2
GE84296	RAB40B	0.034	2.42	BM928140	RAB40B, member RAS oncogene family
GE82943	FAM124B	0.031	2.43	NM_024785	hypothetical protein FLJ22746
GE523639	UNC84A	0.014	2.44	BM677609	Unc-84 homolog A (C. elegans)
GE645838	ALOX12	0.030	2.45	AK074580	CDNA FLJ90099 fis, clone HEMBA1006016
GE56084	NXT2	0.022	2.45	NM_018698	nuclear transport factor 2-like export factor 2
GE62878	KCNE3	0.047	2.46	CB267074	Potassium voltage-gated channel, Isk-related family, member 3
GE490488	AMBRA1	0.031	2.47	BF086681	Hypothetical protein FLJ20294
GE60045	CTGF	0.040	2.48	NM_001901	connective tissue growth factor
GE87023	FAM43A	0.029	2.49	NM_153690	family with sequence similarity 43, member A
GE62318	IGSF8	0.035	2.49	NM_052868	immunoglobulin superfamily, member 8
GE626484	MIPOL1	0.048	2.49	BC031615	Mirror-image polydactyly 1
GE85319	C21ORF63	0.029	2.49	BM997748	Hypothetical protein LOC442092
GE57534	NPY	0.012	2.51	NM_000905	neuropeptide Y
GE81174	PLAGL1	0.038	2.51	NM_002656	pleiomorphic adenoma gene-like 1
GE85066	SLC12A4	0.043	2.51	BG977660	Solute carrier family 12 (potassium/chloride transporters), member 4
GE80964	MGP	0.023	2.52	NM_000900	matrix Gla protein
GE62838	BTN2A2	0.022	2.52	NM_006995	butyrophilin, subfamily 2, member A2
GE479853	ABCA12	0.018	2.53	NM_015657	ATP-binding cassette, sub-family A (ABC1), member 12
GE57345	FCGBP	0.028	2.53	NM_003890	Fc fragment of IgG binding protein
GE746940	INHBA	0.047	2.54	CB140207	Inhibin, beta A (activin A, activin AB alpha polypeptide)
GE53669	TPX2	0.003	2.55	NM_012112	TPX2, microtubule-associated, homolog (Xenopus laevis)
GE60482	VLDLR	0.001	2.56	NM_003383	very low density lipoprotein receptor
GE80300	RACGAP1	0.001	2.56	NM_013277	Rac GTPase activating protein 1
GE80529	PLAUR	0.041	2.58	NM_002659	plasminogen activator, urokinase receptor
GE523275	LOC100127996	0.034	2.59	BX097452	Transcribed locus
GE561268	FOXD4L3	0.002	2.59	NM_199135	FOXD4-like 2
GE799300	SSH2	0.048	2.60	NM_033389	slingshot homolog 2 (Drosophila)
GE867785	LOC400027	0.009	2.60	BQ027566	hypothetical gene supported by BC047417
GE57137	KIF14	0.044	2.60	NM_014875	kinesin family member 14
GE87422	APLN	0.045	2.60	BX118770	Apelin, AGTRL1 ligand
GE82666	CENPK	0.007	2.62	NM_022145	leucine zipper protein FKSG14
GE58077	SPR	0.010	2.63	NM_003124	sepiapterin reductase (7,8-dihydrobiopterin:NADP+ oxidoreductase)
GE53690	DBF4	0.001	2.63	NM_006716	DBF4 homolog (S. cerevisiae)
GE60459	KIAA0040	0.034	2.64	NM_014656	KIAA0040
GE469698	C5ORF13	0.039	2.64	R42039	chromosome 5 open reading frame 13
GE792732	GGT1	0.046	2.64	M24903	gamma-glutamyltransferase 1
GE624182	KIF18B	0.014	2.64	BM999069	Hypothetical protein LOC146909
GE61110	IL32	0.037	2.65	NM_004221	interleukin 32
GE79835	MMP2	0.030	2.65	NM_004530	matrix metallopeptidase 2 (gelatinase A, 72kDa gelatinase, 72kDa type IV collage
GE767989	TIFA	0.001	2.66	NM_052864	TRAF-interacting protein with a forkhead-associated domain
GE82247	C12ORF48	0.005	2.67	NM_017915	hypothetical protein FLJ20641
GE846640	LOC375010	0.032	2.67	BQ574149	hypothetical LOC375010
GE734721	TSPAN18	0.005	2.69	BC033368	tetraspanin 18

Column ID	Symbol	p-value	FC(AI delet vs. NI)	Accession number	Description
GE59688	ITIH2	0.023	2.70	NM_002216	inter-alpha (globulin) inhibitor H2
GE53544	LMO7	0.008	2.71	NM_005358	LIM domain 7
GE56382	COL6A2	0.009	2.71	NM_001849	collagen, type VI, alpha 2
GE516913	ERVWE1	0.020	2.72	NM_014590	endogenous retroviral family W, env(C7), member 1 (syncytin)
GE79827	OLFML2B	0.021	2.74	N25353	Olfactomedin-like 2B
GE59302	KIF2C	0.003	2.76	NM_006845	kinesin family member 2C
GE79587	COL4A1	0.014	2.76	NM_001845	collagen, type IV, alpha 1
GE79508	ENPEP	0.005	2.77	NM_001977	glutamyl aminopeptidase (aminopeptidase A)
GE79889	MXD3	0.047	2.77	NM_031300	MAX dimerization protein 3
GE532754	CCDC70	0.034	2.78	NM_031290	hypothetical protein DKFZp434K1172
GE534426	FN1	0.041	2.78	NM_002026	fibronectin 1
GE61391	SNAI2	0.011	2.79	NM_003068	snail homolog 2 (Drosophila)
GE62647	ARHGAP26	0.027	2.80	NM_015071	Rho GTPase activating protein 26
GE62200	DNMT3A	0.002	2.81	NM_022552	DNA (cytosine-5-)-methyltransferase 3 alpha
GE55801	ASF1B	0.000	2.81	NM_018154	ASF1 anti-silencing function 1 homolog B (S. cerevisiae)
GE59802	CKS2	0.010	2.82	NM_001827	CDC28 protein kinase regulatory subunit 2
GE61971	COL6A1	0.040	2.84	BE062797	Collagen, type VI, alpha 1
GE59115	TNFSF10	0.025	2.86	NM_003810	tumor necrosis factor (ligand) superfamily, member 10
GE57538	TK1	0.022	2.87	NM_003258	thymidine kinase 1, soluble
GE79600	NOG	0.014	2.90	NM_005450	noggin
GE61151	FAP	0.037	2.90	BG208151	Fibroblast activation protein, alpha
GE682522	RYR2	0.029	2.92	AI474085	Ryanodine receptor 2 (cardiac)
GE59846	RRM2	0.009	2.94	NM_001034	ribonucleotide reductase M2 polypeptide
GE57381	PXDN	0.008	2.95	AA179761	Peroxidasin homolog (Drosophila)
GE635247	LIFR	0.046	2.96	BE466688	Leukemia inhibitory factor receptor
GE79044	IL6R	0.034	2.96	NM_000565	interleukin 6 receptor
GE541396	C5ORF47	0.049	2.97	BX116313	Hypothetical protein LOC133491
GE836403	PSMA1	0.042	2.98	BF508466	Proteasome (prosome, macropain) subunit, alpha type, 1
GE56120	SERTAD4	0.007	2.98	N40495	SERTA domain containing 4
GE63002	CDC2	0.001	2.98	NM_001786	cell division cycle 2, G1 to S and G2 to M
GE53197	SRGAP2	0.016	2.98	BI497146	SLIT-ROBO Rho GTPase activating protein 2
GE85420	CASC5	0.001	3.04	AA662240	Cancer susceptibility candidate 5
GE53732	SULF1	0.020	3.06	NM_015170	sulfatase 1
GE80890	COL5A1	0.017	3.06	NM_000093	collagen, type V, alpha 1
GE735552	UBE3A	0.022	3.07	AW057554	Ubiquitin protein ligase E3A (human papilloma virus E6-associated protein, Angel
GE88232	HTR5B	0.000	3.08	BX113754	5-hydroxytryptamine (serotonin) receptor 5B
GE57886	CCNB1	0.016	3.09	NM_031966	cyclin B1
GE81247	TEC	0.004	3.12	NM_003215	tec protein tyrosine kinase
GE86945	ELOVL7	0.030	3.12	AL137506	ELOVL family member 7, elongation of long chain fatty acids (yeast)
GE814771	IFT88	0.047	3.13	AF088052	Intraflagellar transport 88 homolog (Chlamydomonas)
GE58318	PRC1	0.003	3.14	NM_003981	protein regulator of cytokinesis 1
GE57082	KIAA0101	0.005	3.14	NM_014736	KIAA0101
GE56866	HJURP	0.008	3.15	NM_018410	hypothetical protein DKFZp762E1312
GE57486	INHBA	0.023	3.15	NM_002192	inhibin, beta A (activin A, activin AB alpha polypeptide)
GE538804	TXK	0.014	3.16	AA747923	TXK tyrosine kinase
GE741471	LOC147343	0.000	3.16	BF343036	Hypothetical protein LOC147343
GE609106	NRXN1	0.008	3.18	BI494455	Neurexin 1
GE52999	LRRC8C	0.034	3.18	BE222289	Leucine rich repeat containing 8 family, member C

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GE476053	LOC340508	0.013	3.18	BC043374	hypothetical protein LOC340508
GE83237	NUF2	0.038	3.19	NM_031423	cell division cycle associated 1
GE61338	TAGLN	0.004	3.19	H26843	transgelin
GE621318	SMARCA4	0.012	3.22	BF750200	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subf
GE59766	COL6A3	0.002	3.25	NM_004369	collagen, type VI, alpha 3
GE62111	BCO2	0.046	3.26	NM_031938	beta-carotene dioxygenase 2
GE61153	LDLR	0.017	3.26	NM_000527	low density lipoprotein receptor (familial hypercholesterolemia)
GE60354	CENPE	0.000	3.31	NM_001813	centromere protein E, 312kDa
GE59373	ZMYND10	0.023	3.33	NM_015896	zinc finger, MYND-type containing 10
GE62933	RHOBTB3	0.005	3.36	NM_014899	Rho-related BTB domain containing 3
GE81805	HMMR	0.022	3.40	NM_012484	hyaluronan-mediated motility receptor (RHAMM)
GE78964	CCNB2	0.021	3.43	NM_004701	cyclin B2
GE58267	CENPA	0.001	3.45	NM_001809	centromere protein A, 17kDa
GE56450	MCF2	0.002	3.45	NM_005369	MCF.2 cell line derived transforming sequence
GE57938	CDC25C	0.039	3.51	NM_001790	cell division cycle 25C
GE62415	P2RY1	0.004	3.54	AK026659	purinergic receptor P2Y, G-protein coupled, 1
GE779950	RALYL	0.011	3.54	AI791127	Hypothetical protein LOC138046
GE55803	ANLN	0.000	3.56	NM_018685	anillin, actin binding protein (scraps homolog, Drosophila)
GE87885	LOC388279	0.037	3.57	AV725613	Hypothetical gene supported by AF275804
GE54754	TSPAN9	0.033	3.68	NM_006675	tetraspanin 9
GE88593	GNA11	0.006	3.70	AL110227	guanine nucleotide binding protein (G protein), alpha 11 (Gq class)
GE560143	ZNF488	0.047	3.71	NM_153034	zinc finger protein 488
GE546951	HRNBP3	0.031	3.72	BF222375	Similar to ataxin 2-binding protein 1 isoform 4; hexaribonucleotide binding prot
GE59670	COL4A2	0.025	3.73	NM_001846	collagen, type IV, alpha 2
GE82389	PBK	0.001	3.77	NM_018492	PDZ binding kinase
GE81449	GDF15	0.009	3.79	NM_004864	growth differentiation factor 15
GE84281	SETBP1	0.031	3.80	AK023905	Homo sapiens cDNA FLJ13843 fis, clone THYRO1000796.
GE57549	COL7A1	0.043	3.82	NM_000094	collagen, type VII, alpha 1 (epidermolysis bullosa, dystrophic, dominant and rec
GE80871	ARHGAP11A	0.006	3.82	NM_014783	Rho GTPase activating protein 11A
GE562082	PAK2	0.003	3.86	NM_002577	p21 (CDKN1A)-activated kinase 2
GE574933	E2F2	0.013	3.87	NM_004091	E2F transcription factor 2
GE471816	LOC375010	0.048	3.88	BC035915	Hypothetical LOC375010
GE558313	TBC1D8	0.041	3.89	BM970493	TBC1 domain family, member 8 (with GRAM domain)
GE57964	CEL	0.016	3.91	NM_001807	carboxyl ester lipase (bile salt-stimulated lipase)
GE59386	UBE2C	0.015	3.93	NM_007019	ubiquitin-conjugating enzyme E2C
GE62547	AURKB	0.000	3.95	NM_004217	aurora kinase B
GE79659	ANGPTL1	0.035	3.99	NM_004673	angiopoietin-like 1
GE54551	PLK2	0.005	4.00	NM_006622	polo-like kinase 2 (Drosophila)
GE82558	SPC25	0.001	4.00	NM_020675	spindle pole body component 25 homolog (S. cerevisiae)
GE55708	DEPDC1B	0.002	4.03	NM_018369	DEP domain containing 1B
GE87517	CENPM	0.003	4.10	NM_024053	chromosome 22 open reading frame 18
GE81252	THBS1	0.013	4.10	NM_003246	thrombospondin 1
GE79793	KIF15	0.001	4.12	NM_020242	kinesin family member 15
GE479776	HOXB5	0.050	4.14	NM_002147	homeobox B5
GE54996	SPOCK1	0.007	4.18	NM_004598	sparc/osteonectin, cwcv and kazal-like domains proteoglycan (testican) 1
GE85491	LOX	0.003	4.27	CD678960	Lysyl oxidase
GE81745	PLA2R1	0.011	4.36	NM_007366	phospholipase A2 receptor 1, 180kDa
GE753422	FNDC1	0.000	4.38	H88455	Fibronectin type III domain containing 1

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GE672411	THOC7	0.016	4.46	AI274553	qv62b06.x1 NCI_CGAP_Ut1 Homo sapiens cDNA clone IMAGE:1986131 3', mRNA sequence.
GE58567	UBE2T	0.008	4.47	NM_014176	ubiquitin-conjugating enzyme E2T (putative)
GE87317	HTRA3	0.004	4.48	NM_053044	HtrA serine peptidase 3
GE82539	XAGE1D	0.009	4.49	NM_020411	X antigen family, member 1
GE62777	PLA2R1	0.025	4.51	NM_007366	phospholipase A2 receptor 1, 180kDa
GE566099	CTAG2	0.005	4.67	NM_020994	cancer/testis antigen 2
GE59394	BIRC5	0.016	4.70	NM_001168	baculoviral IAP repeat-containing 5 (survivin)
GE58498	SPON2	0.041	5.01	AA149494	Spondin 2, extracellular matrix protein
GE61118	LTBP1	0.007	5.14	NM_000627	latent transforming growth factor beta binding protein 1
GE57824	SERPINE1	0.004	5.22	NM_000602	serpin peptidase inhibitor, clade E (nexin, plasminogen activator inhibitor type
GE768333	GCUD2	0.010	5.34	AI630319	Family with sequence similarity 72, member A
GE490464	LOC647946	0.024	5.47	AK090603	CDNA FLJ33284 fis, clone ASTRO2009458
GE629415	LOC285965	0.000	5.50	AL833583	hypothetical protein LOC285965
GE79081	COL3A1	0.010	5.90	NM_000090	collagen, type III, alpha 1 (Ehlers-Danlos syndrome type IV, autosomal dominant)
GE59276	NCRNA00084	0.024	6.09	BF094597	Trophoblast-derived noncoding RNA
GE83343	C2ORF14	0.049	6.27	AL136789	chromosome 2 open reading frame 14
GE80570	MSTN	0.048	6.77	NM_005259	growth differentiation factor 8
GE782559	IGF2	0.029	6.83	AF318382	chromosome 11 open reading frame 43
GE55782	ASPM	0.022	6.86	NM_018136	asp (abnormal spindle)-like, microcephaly associated (Drosophila)
GE80888	COL1A1	0.015	6.90	NM_000088	collagen, type I, alpha 1
GE527787	MAGEC1	0.048	7.04	NM_005462	melanoma antigen family C, 1
GE62449	NEK2	0.005	7.84	NM_002497	NIMA (never in mitosis gene a)-related kinase 2
GE57073	POSTN	0.019	12.61	NM_006475	periostin, osteoblast specific factor