Index	Mutated*	Normal*	FC	*P* value	FDR**	Probe set	Description	Gene symbol
113	1342	128	10,52	0,000503	0,240	202018_s_at	Lactotransferrin	*LTF*
616	362	46,7	7,76	0,003493	0,308	237395_at	Cytochrome P450, family 4, subfamily Z, polypeptide 1	*CYP4Z1*
3073	1009	142	7,10	0,021674	0,385	206378_at	Secretoglobin, family 2A, member 2	*SCGB2A2*
376	119	17,7	6,68	0,001962	0,284	214451_at	Transcription factor AP-2 beta	*TFAP2B*
578	337	60,5	5,57	0,003174	0,300	227702_at	Cytochrome P450, family 4, subfamily X, polypeptide 1	*CYP4X1*
146	210	38,4	5,47	0,000669	0,244	219768_at	V-set domain containing T cell activation inhibitor 1	*VTCN1*
86	129	24,2	5,31	0,000327	0,201	204607_at	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 2 (mitochondrial)	*HMGCS2*
2613	78,7	15,9	4,95	0,017744	0,371	205358_at	Glutamate receptor, ionotropic, AMPA 2	*GRIA2*
116	23,2	4,83	4,81	0,000513	0,240	203908_at	Solute carrier family 4, sodium bicarbonate cotransporter, member 4	*SLC4A4*
117	79,4	18,0	4,42	0,000518	0,240	239723_at	Solute carrier family 40 (iron-regulated transporter), member 1	*SLC40A1*
625	56,6	13,0	4,34	0,003549	0,308	1553394_a_a	Transcription factor AP-2 beta	*TFAP2B*
413	148	34,6	4,28	0,002175	0,286	240304_s_at	Transmembrane channel-like 5	*TMC5*
5181	216	50,9	4,25	0,039946	0,421	223864_at	Ankyrin repeat domain 30A	*ANKRD30A*
179	446	106	4,21	0,000826	0,244	223315_at	Netrin 4	*NTN4*
246	120	29,2	4,12	0,001128	0,251	210096_at	Cytochrome P450, family 4, subfamily B, polypeptide 1	*CYP4B1*
1043	312	80,2	3,89	0,006080	0,319	204041_at	Monoamine oxidase B	*MAOB*
192	44,1	11,6	3,80	0,000899	0,244	1553434_at	Cytochrome P450 4Z2 pseudogene	*CYP4Z2P*
2038	52,4	14,3	3,65	0,013273	0,355	211682_x_at	UDP glucuronosyltransferase 2 family, polypeptide B28	*UGT2B28*
819	69,6	19,6	3,54	0,004678	0,312	218963_s_at	Keratin 23 (histone deacetylase inducible)	*KRT23*
451	56,1	15,9	3,53	0,002410	0,288	230238_at	Ankyrin repeat domain 43	*ANKRD43*
177	85,8	24,3	3,52	0,000819	0,244	202888_s_at	Alanyl (membrane) aminopeptidase	*ANPEP*
1	40,9	11,9	3,43	0,000004	0,099	231227_at	Wingless-type MMTV integration site family, member 5A	*WNT5A*
1208	121	35,3	3,42	0,007161	0,324	219580_s_at	Transmembrane channel-like 5	*TMC5*
118	171	51,7	3,30	0,000526	0,240	204364_s_at	Receptor accessory protein 1	*REEP1*
680	15,2	4,62	3,29	0,003908	0,308	232277_at	Solute carrier family 28 member 3	*SLC28A3*
48	91,7	28,0	3,28	0,000195	0,201	219557_s_at	Nuclear receptor interacting protein 3	*NRIP3*
1871	339	105	3,24	0,012080	0,353	204014_at	Dual specificity phosphatase 4	*DUSP4*
1000	123	38,0	3,23	0,005782	0,316	203355_s_at	Pleckstrin and Sec7 domain containing 3	*PSD3*
521	80,7	25,4	3,18	0,002775	0,291	219630_at	PDZK1 interacting protein 1	*PDZK1IP1*
3570	73,4	23,7	3,10	0,025784	0,394	226147_s_at	Polymeric immunoglobulin receptor	*PIGR*
1001	20,8	6,75	3,08	0,005791	0,316	238133_at	Netrin G1	*NTNG1*
2553	1238	402	3,08	0,017275	0,370	219197_s_at	Signal peptide, CUB domain, EGF-like 2	*SCUBE2*
6088	237	77,6	3,06	0,049699	0,446	229764_at	Tumor protein p63 regulated 1	*TPRG1*
133	66,1	21,7	3,05	0,000589	0,240	230316_at	SEC14-like 2 (S. cerevisiae)	*SEC14L2*
102	79,0	26,1	3,03	0,000402	0,216	204541_at	SEC14-like 2 (S. cerevisiae)	*SEC14L2*
53	19,2	6,32	3,03	0,000205	0,201	209292_at	Inhibitor of DNA binding 4, dominant negative helix-loop-helix	*ID4*
98	28,1	9,36	3,00	0,000382	0,213	204855_at	Serpin peptidase inhibitor, clade B (ovalbumin), member 5	*SERPINB5*
150	1110	371	2,99	0,000691	0,244	227556_at	Nucleoside diphosphate kinase 7	*NME7*
4302	326	110	2,97	0,032016	0,407	212774_at	Zinc finger protein 238	*ZNF238*
1484	65,9	22,2	2,97	0,009119	0,336	220177_s_at	Transmembrane protease, serine 3	*TMPRSS3*
15	129	43,4	2,96	0,000054	0,191	209291_at	Inhibitor of DNA binding 4, dominant negative helix-loop-helix	*ID4*
268	204	68,9	2,96	0,001277	0,260	217966_s_at	Family with sequence similarity 129, member A	*FAM129A*
55	110	37,1	2,96	0,000212	0,201	212325_at	LIM and calponin homology domains 1	*LIMCH1*
987	113	38,1	2,96	0,005695	0,315	222904_s_at	Transmembrane channel-like 5	*TMC5*
227	40,0	13,6	2,93	0,001050	0,250	222862_s_at	Adenylate kinase 5	*AK5*
284	177	60,7	2,92	0,001390	0,263	222288_at	Hypothetical protein FLJ20489	-
392	211	72,6	2,91	0,002058	0,285	227182_at	Sushi domain containing 3	*SUSD3*
389	45,7	15,8	2,89	0,002023	0,284	223949_at	Transmembrane protease, serine 3	*TMPRSS3*
194	26,6	9,28	2,87	0,000900	0,244	205513_at	Transcobalamin I (vitamin B12 binding protein, R binder family)	*TCN1*
1174	283	99,0	2,86	0,006896	0,321	204015_s_at	Dual specificity phosphatase 4	*DUSP4*
555	78,8	27,6	2,85	0,003021	0,296	1553589_a_a	PDZK1 interacting protein 1	*PDZK1IP1*
28	121	42,5	2,84	0,000131	0,201	205990_s_at	Wingless-type MMTV integration site family, member 5A	*WNT5A*
364	83,8	29,7	2,82	0,001899	0,284	203354_s_at	Pleckstrin and Sec7 domain containing 3	*PSD3*
100	144	51,0	2,82	0,000390	0,213	206401_s_at	Microtubule-associated protein tau	*MAPT*
72	46,1	16,4	2,81	0,000277	0,201	213425_at	Wingless-type MMTV integration site family, member 5A	*WNT5A*
27	1769	641	2,76	0,000127	0,201	201242_s_at	ATPase, Na+/K+ transporting, beta 1 polypeptide	*ATP1B1*
2139	167	61,4	2,72	0,014063	0,359	225728_at	Sorbin and SH3 domain containing 2	*SORBS2*

Index	Mutated*	Normal*	FC	*P* value	FDR**	Probe set	Description	Gene symbol
204	183	67,2	2,72	0,000935	0,244	228481_at	Periostin, osteoblast specific factor	*POSTN*
56	873	322	2,71	0,000216	0,201	201243_s_at	ATPase, Na+/K+ transporting, beta 1 polypeptide	*ATP1B1*
280	27,5	10,2	2,71	0,001368	0,263	219308_s_at	Adenylate kinase 5	*AK5*
1117	21,9	8,12	2,70	0,006533	0,319	204455_at	Dystonin	*DST*
548	23,9	8,88	2,69	0,002964	0,295	1563367_at	Hypothetical protein LOC100128977	*LOC100128977*
3020	54,5	20,2	2,69	0,021271	0,385	207981_s_at	Estrogen-related receptor gamma	*ESRRG*
19	273	101	2,69	0,000081	0,201	212328_at	LIM and calponin homology domains 1	*LIMCH1*
1231	188	70,0	2,69	0,007320	0,324	204288_s_at	Sorbin and SH3 domain containing 2	*SORBS2*
1794	144	54,5	2,64	0,011486	0,350	203130_s_at	Kinesin family member 5C	*KIF5C*
714	63,3	24,1	2,63	0,004096	0,308	227154_at	Immunoglobin superfamily, member 21	*IGSF21*
1524	47,2	18,0	2,62	0,009416	0,337	231098_at	Transcribed locus	-
375	43,6	16,7	2,61	0,001960	0,284	226847_at	Follistatin	*FST*
590	59,4	22,9	2,59	0,003254	0,301	243806_at	ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 6	*SIAT8F*
4089	55,1	21,3	2,58	0,030066	0,402	209480_at	Major histocompatibility complex, class II, DQ beta 1	*HLA-DQB1*
2399	588	228	2,58	0,015996	0,365	207847_s_at	Mucin 1, cell surface associated	*MUC1*
1299	85,1	33,4	2,55	0,007740	0,325	219440_at	Retinoic acid induced 2	*RAI2*
256	57,6	22,6	2,55	0,001196	0,255	222900_at	Nuclear receptor interacting protein 3	*NRIP3*
1455	103	40,5	2,53	0,008896	0,334	211000_s_at	Interleukin 6 signal transducer (gp130, oncostatin M receptor)	*IL6ST*
5348	61,6	24,4	2,52	0,041927	0,429	209351_at	Keratin 14	*KRT14*
196	44,4	17,8	2,50	0,000908	0,244	226029_at	Vang-like 2 (van gogh, Drosophila)	*VANGL2*
166	193	77,3	2,49	0,000777	0,244	212327_at	LIM and calponin homology domains 1	*LIMCH1*
141	86,0	34,5	2,49	0,000645	0,244	243030_at	Mitogen-activated protein kinase kinase kinase 1	*MAP3K1*
90	242	97,2	2,49	0,000332	0,201	202149_at	Neural precursor cell expressed, developmentally down-regulated 9	*NEDD9*
1591	1263	509	2,48	0,009901	0,340	201667_at	Gap junction protein, alpha 1, 43kDa	*GJA1*
1408	62,9	25,5	2,47	0,008513	0,330	224358_s_at	Membrane-spanning 4-domains, subfamily A, member 7	*MS4A7*
5145	52,1	21,1	2,46	0,039615	0,421	213695_at	Paraoxonase 3	*PON3*
1310	426	173	2,46	0,007819	0,325	217967_s_at	Family with sequence similarity 129, member A	*FAM129A*
8	359	146	2,46	0,000015	0,099	212240_s_at	Phosphoinositide-3-kinase, regulatory subunit 1 (p85 alpha)	*PIK3R1*
658	41,6	17,1	2,43	0,003814	0,308	239907_at	Transcribed locus	-
2749	794	327	2,43	0,019005	0,378	202357_s_at	Complement factor B	*CFB*
4852	55,2	22,8	2,42	0,036972	0,417	229030_at	Calpain 8	*CAPN8*
2562	48,7	20,1	2,42	0,017375	0,371	209369_at	Annexin A3	*ANXA3*
4	168	69,6	2,41	0,000011	0,099	203407_at	Periplakin	*PPL*
1198	49,1	20,3	2,41	0,007070	0,323	202037_s_at	Secreted frizzled-related protein 1	*SFRP1*
3864	30,6	12,7	2,41	0,028229	0,399	226884_at	Leucine rich repeat neuronal 1	*LRRN1*
2945	125	52,0	2,41	0,020642	0,383	203021_at	Secretory leukocyte peptidase inhibitor	*SLPI*
450	144	60,4	2,38	0,002404	0,288	203928_x_at	Microtubule-associated protein tau	*MAPT*
1985	561	236	2,37	0,012957	0,355	204320_at	Collagen, type XI, alpha 1	*COL11A1*
3267	738	312	2,37	0,023215	0,388	37892_at	Collagen, type XI, alpha 1	*COL11A1*
4326	257	109	2,37	0,032194	0,407	226034_at	cDNA clone IMAGE:3881549	-
101	108	45,5	2,36	0,000401	0,216	229518_at	Family with sequence similarity 46, member B	*FAM46B*
1352	56,7	24,0	2,36	0,008118	0,328	235651_at	-	-
1318	39,3	16,7	2,36	0,007843	0,325	213060_s_at	Chitinase 3-like 2	*CHI3L2*
1191	87,5	37,3	2,35	0,007032	0,322	203240_at	FC fragment of IgG binding protein	*FCGBP*
66	59,8	25,5	2,35	0,000251	0,201	241459_at	LIM and calponin homology domains 1	*LIMCH1*
2729	121	51,6	2,34	0,018795	0,377	225871_at	Six transmembrane epithelial antigen of the prostate 2	*STEAP2*
1053	74,8	32,0	2,34	0,006149	0,319	1555497_a_a	Cytochrome P450, family 4, subfamily B, polypeptide 1	*CYP4B1*
49	101	43,2	2,34	0,000195	0,201	212249_at	Phosphoinositide-3-kinase, regulatory subunit 1 (p85 alpha)	*PIK3R1*
1336	124	53,1	2,33	0,008019	0,328	228648_at	Leucine-rich alpha-2-glycoprotein 1	*LRG1*
1772	94,8	40,7	2,33	0,011296	0,348	218613_at	Pleckstrin and Sec7 domain containing 3	*PSD3*
154	251	108	2,32	0,000703	0,244	206385_s_at	Ankyrin 3, node of Ranvier (ankyrin G)	*ANK3*
1550	110	47,4	2,31	0,009560	0,337	204863_s_at	Interleukin 6 signal transducer (oncostatin M receptor)	*IL6ST*
1876	284	123	2,31	0,012131	0,354	204284_at	Protein phosphatase 1, regulatory (inhibitor) subunit 3C	*PPP1R3C*
2291	11,7	5,10	2,30	0,015235	0,363	244623_at	Potassium voltage-gated channel, KQT-like subfamily, member 5	*KCNQ5*
631	261	114	2,30	0,003570	0,308	226597_at	Receptor accessory protein 6	*REEP6*
2117	101	44,3	2,29	0,013891	0,359	233123_at	Solute carrier family 40 (iron-regulated transporter), member 1	*SLC40A1*
5206	57,5	25,1	2,29	0,040172	0,422	203485_at	Reticulon 1	*RTN1*

Index	Mutated*	Normal*	FC	*P* value	FDR**	Probe set	Description	Gene symbol
857	26,6	11,7	2,28	0,004948	0,313	209900_s_at	Solute carrier family 16, member 1	*SLC16A1*
1366	338	149	2,27	0,008221	0,328	232458_at	Collagen, type III, alpha 1	*COL3A1*
2300	1064	468	2,27	0,015280	0,363	213693_s_at	Mucin 1, cell surface associated	*MUC1*
579	119	52,4	2,27	0,003176	0,300	203929_s_at	Microtubule-associated protein tau	*MAPT*
1376	307	136	2,27	0,008295	0,329	229218_at	Collagen, type I, alpha 2	*COL1A2*
745	141	62,3	2,27	0,004223	0,308	213110_s_at	Collagen, type IV, alpha 5	*COL4A5*
1138	991	438	2,26	0,006647	0,319	223044_at	Solute carrier family 40 (iron-regulated transporter), member 1	*SLC40A1*
933	257	114	2,25	0,005358	0,313	235371_at	Glycosyltransferase 8 domain containing 4	*GLT8D4*
5445	36,7	16,3	2,25	0,042949	0,431	222853_at	Fibronectin leucine rich transmembrane protein 3	*FLRT3*
3180	161	71,7	2,24	0,022552	0,387	203058_s_at	3'-phosphoadenosine 5'-phosphosulfate synthase 2	*PAPSS2*
835	376	168	2,24	0,004769	0,312	223343_at	Membrane-spanning 4-domains, subfamily A, member 7	*MS4A7*
431	29,8	13,3	2,24	0,002272	0,288	211828_s_at	TRAF2 and NCK interacting kinase	*TNIK*
93	27,7	12,4	2,23	0,000347	0,204	229994_at	Glyceronephosphate O-acyltransferase	*GNPAT*
563	122	54,9	2,23	0,003070	0,298	204365_s_at	Receptor accessory protein 1	*REEP1*
3763	189	84,7	2,23	0,027356	0,397	239435_x_at	Shroom family member 1	*SHROOM1*
1093	86,2	38,7	2,23	0,006408	0,319	226992_at	Nitric oxide synthase trafficker	*NOSTRIN*
4697	16,0	7,21	2,23	0,035470	0,413	235763_at	Solute carrier family 44, member 5	*SLC44A5*
203	442	199	2,22	0,000934	0,244	225464_at	FERM domain containing 6	*FRMD6*
18	439	199	2,21	0,000076	0,201	222450_at	Transmembrane, prostate androgen induced RNA	*TMEPAI*
1763	316	143	2,21	0,011236	0,348	209459_s_at	4-aminobutyrate aminotransferase	*ABAT*
134	105	47,9	2,20	0,000589	0,240	203887_s_at	Thrombomodulin	*THBD*
220	399	181	2,20	0,001017	0,250	225481_at	FERM domain containing 6	*FRMD6*
1431	32,4	14,7	2,20	0,008679	0,331	213680_at	Keratin 6B	*KRT6B*
890	287	131	2,20	0,005141	0,313	227811_at	FYVE, RhoGEF and PH domain containing 3	*FGD3*
3541	47,0	21,4	2,20	0,025480	0,393	229659_s_at	Polymeric immunoglobulin receptor	*PIGR*
85	182	83,0	2,19	0,000327	0,201	204446_s_at	Arachidonate 5-lipoxygenase	*ALOX5*
1937	43,7	19,9	2,19	0,012616	0,355	227019_at	Chromosome 1 open reading frame 226	*C1orf226*
4745	12,9	5,89	2,19	0,035948	0,414	213992_at	Collagen, type IV, alpha 6	*COL4A6*
199	14,0	6,40	2,19	0,000924	0,244	243952_at	TPTE pseudogene	*psiTPTE22*
44	49,0	22,4	2,18	0,000181	0,201	211965_at	Zinc finger protein 36, C3H type-like 1	*ZFP36L1*
10	66,8	30,6	2,18	0,000035	0,180	212762_s_at	Transcription factor 7-like 2 (T-cell specific, HMG-box)	*TCF7L2*
343	17,2	7,89	2,18	0,001740	0,277	1558048_x_a	-	-
5803	89,3	41,0	2,18	0,046848	0,441	204864_s_at	Interleukin 6 signal transducer (gp130, oncostatin M receptor)	*IL6ST*
594	54,4	25,0	2,18	0,003271	0,301	1558686_at	cDNA clone YP99D02	-
3682	81,1	37,3	2,17	0,026584	0,395	205542_at	Six transmembrane epithelial antigen of the prostate 1	*STEAP1*
235	53,6	24,7	2,17	0,001089	0,250	210319_x_at	MSH homeobox 2	*MSX2*
732	429	198	2,17	0,004183	0,308	217771_at	Golgi membrane protein 1	*GOLM1*
5833	1106	510	2,17	0,047131	0,442	214440_at	N-acetyltransferase 1 (arylamine N-acetyltransferase)	*NAT1*
7	86,9	40,2	2,16	0,000014	0,099	216511_s_at	Transcription factor 7-like 2 (T-cell specific, HMG-box)	*TCF7L2*
902	93,1	43,0	2,16	0,005222	0,313	213506_at	Coagulation factor II (thrombin) receptor-like 1	*F2RL1*
1696	311	144	2,15	0,010779	0,347	209460_at	4-aminobutyrate aminotransferase	*ABAT*
136	19,3	8,95	2,15	0,000608	0,244	244181_at	Phosphoinositide-3-kinase, regulatory subunit 1 (p85 alpha)	*PIK3R1*
3408	903	419	2,15	0,024308	0,390	214428_x_at	Complement component 4A (Rodgers blood group	*C4A*
3093	164	76,2	2,15	0,021805	0,385	212551_at	CAP, adenylate cyclase-associated protein, 2 (yeast)	*CAP2*
122	47,9	22,3	2,15	0,000566	0,240	219232_s_at	EGL nine homolog 3 (C. elegans)	*EGLN3*
2972	26,5	12,3	2,15	0,020878	0,384	226492_at	Semaphorin 6D	*SEMA6D*
412	63,4	29,6	2,15	0,002172	0,286	240690_at	Homolog of rat pragma of Rnd2	*PRAGMIN*
391	17,8	8,30	2,14	0,002028	0,284	214981_at	Periostin, osteoblast specific factor	*POSTN*
1850	712	334	2,14	0,011902	0,352	222453_at	Cytochrome b reductase 1	*CYBRD1*
258	19,2	8,98	2,13	0,001208	0,256	237839_at	Ankyrin 3, node of Ranvier (ankyrin G)	*ANK3*
441	6,14	2,88	2,13	0,002341	0,288	210738_s_at	Solute carrier family 4, sodium bicarbonate cotransporter, member 4	*SLC4A4*
51	21,0	9,84	2,13	0,000198	0,201	209598_at	Paraneoplastic antigen MA2	*PNMA2*
463	15,4	7,24	2,13	0,002458	0,288	211494_s_at	Solute carrier family 4, sodium bicarbonate cotransporter, member 4	*SLC4A4*
92	251	118	2,13	0,000343	0,204	224975_at	Nuclear factor I/A	*NFIA*
725	83,5	39,3	2,13	0,004146	0,308	221958_s_at	G protein-coupled receptor 177	*GPR177*
1340	316	149	2,12	0,008051	0,328	223344_s_at	Membrane-spanning 4-domains, subfamily A, member 7	*MS4A7*
393	47,6	22,5	2,12	0,002074	0,285	230763_at	Spermatogenesis associated 17	*SPATA17*

Index	Mutated*	Normal*	FC	*P* value	FDR**	Probe set	Description	Gene symbol
325	**14,5**	**6,85**	**2,12**	**0,001626**	**0,272**	**240024_at**	**SEC14-like 2 (S. cerevisiae)**	***SEC14L2***
3988	**93,1**	**44,0**	**2,12**	**0,029178**	**0,400**	**209706_at**	**NK3 homeobox 1**	***NKX3-1***
439	**14,6**	**6,90**	**2,12**	**0,002329**	**0,288**	**204933_s_at**	**Tumor necrosis factor receptor superfamily, member 11b**	***TNFRSF11B***
205	**7,77**	**3,67**	**2,12**	**0,000948**	**0,244**	**204932_at**	**Tumor necrosis factor receptor superfamily, member 11b**	***TNFRSF11B***
4197	**1672**	**791**	**2,11**	**0,031024**	**0,404**	**208451_s_at**	**Complement component 4A (Rodgers blood group)**	***C4A***
435	**207**	**98,1**	**2,11**	**0,002300**	**0,288**	**221584_s_at**	**Calcium-activated potassium channel subunit alpha-1**	***KCNMA1***
2064	**192**	**91,6**	**2,10**	**0,013476**	**0,356**	**224996_at**	**Aspartate beta-hydroxylase**	***ASPH***
5766	**95,5**	**45,6**	**2,10**	**0,046334**	**0,439**	**204400_at**	**Embryonal Fyn-associated substrate**	***EFS***
866	**512**	**245**	**2,09**	**0,005012**	**0,313**	**221666_s_at**	**PYD and CARD domain containing**	***PYCARD***
5597	**55,2**	**26,4**	**2,09**	**0,044640**	**0,436**	**206224_at**	**Cystatin SN**	***CST1***
410	**17,2**	**8,21**	**2,09**	**0,002158**	**0,286**	**227051_at**	**cDNA clone IMAGE:4393354**	**-**
2670	**15,2**	**7,27**	**2,09**	**0,018260**	**0,374**	**221933_at**	**Neuroligin 4, X-linked**	***NLGN4X***
1077	**117**	**56,0**	**2,08**	**0,006317**	**0,319**	**215073_s_at**	**Nuclear receptor subfamily 2, group F, member 2**	***NR2F2***
5	**121**	**58,3**	**2,08**	**0,000012**	**0,099**	**216035_x_at**	**Transcription factor 7-like 2 (T-cell specific, HMG-box)**	***TCF7L2***
2491	**76,8**	**37,0**	**2,08**	**0,016787**	**0,367**	**211695_x_at**	**Mucin 1, cell surface associated**	***MUC1***
2197	**58,5**	**28,3**	**2,07**	**0,014525**	**0,361**	**219412_at**	**RAB38, member RAS oncogene family**	***RAB38***
679	**28,2**	**13,6**	**2,07**	**0,003899**	**0,308**	**231929_at**	**IKAROS family zinc finger 2 (Helios)**	***IKZF2***
3566	**24,6**	**11,9**	**2,07**	**0,025741**	**0,394**	**1564241_at**	**ATPase, Na+/K+ transporting, alpha 4 polypeptide**	***ATP1A4***
1412	**42,1**	**20,3**	**2,07**	**0,008532**	**0,330**	**205541_s_at**	**G1 to S phase transition 2**	***GSPT2***
1543	**22,6**	**11,0**	**2,06**	**0,009541**	**0,337**	**229510_at**	**Membrane-spanning 4-domains, subfamily A, member 14**	***MS4A14***
323	**132**	**64,1**	**2,05**	**0,001612**	**0,272**	**214761_at**	**Zinc finger protein 423**	***ZNF423***
1226	**9,02**	**4,39**	**2,05**	**0,007288**	**0,324**	**206522_at**	**Maltase-glucoamylase (alpha-glucosidase)**	***MGAM***
909	**66,2**	**32,3**	**2,05**	**0,005249**	**0,313**	**242874_at**	**cDNA FLJ37931 fis, clone CTONG2004397**	**-**
297	**46,5**	**22,7**	**2,05**	**0,001451**	**0,263**	**203780_at**	**Myelin protein zero-like 2**	***MPZL2***
1332	**27,6**	**13,5**	**2,05**	**0,008004**	**0,328**	**227444_at**	**Armadillo repeat containing, X-linked 4**	***ARMCX4***
30	**45,9**	**22,6**	**2,03**	**0,000138**	**0,201**	**222027_at**	**Nuclear casein kinase and cyclin-dependent kinase substrate 1**	***NUCKS1***
184	**33,8**	**16,7**	**2,03**	**0,000854**	**0,244**	**232968_at**	**Fibronectin type III and ankyrin repeat domains 1**	***FANK1***
5840	**56,5**	**27,9**	**2,03**	**0,047191**	**0,442**	**210222_s_at**	**Reticulon 1**	***RTN1***
63	**355**	**175**	**2,02**	**0,000237**	**0,201**	**222449_at**	**Transmembrane, prostate androgen induced RNA**	***TMEPAI***
271	**240**	**119**	**2,02**	**0,001298**	**0,261**	**235085_at**	**Homolog of rat pragma of Rnd2**	***PRAGMIN***
3919	**16,5**	**8,17**	**2,02**	**0,028625**	**0,399**	**220625_s_at**	**E74-like factor 5 (ets domain transcription factor)**	***ELF5***
5086	**68,5**	**33,9**	**2,02**	**0,039151**	**0,420**	**208228_s_at**	**Fibroblast growth factor receptor 2**	***FGFR2***
130	**360**	**179**	**2,02**	**0,000581**	**0,240**	**226806_s_at**	**Nuclear factor I/A**	***NFIA***
2273	**146**	**72,6**	**2,02**	**0,015097**	**0,363**	**204285_s_at**	**Phorbol-12-myristate-13-acetate-induced protein 1**	***PMAIP1***
2318	**75,1**	**37,3**	**2,01**	**0,015395**	**0,363**	**202236_s_at**	**Solute carrier family 16, member 1**	***SLC16A1***
115	**222**	**110**	**2,01**	**0,000512**	**0,240**	**212239_at**	**Phosphoinositide-3-kinase, regulatory subunit 1 (p85 alpha)**	***PIK3R1***
888	**69,3**	**34,4**	**2,01**	**0,005128**	**0,313**	**204463_s_at**	**Endothelin receptor type A**	***EDNRA***
34	**46,6**	**23,2**	**2,01**	**0,000146**	**0,201**	**201340_s_at**	**Ectodermal-neural cortex (with BTB-like domain)**	***ENC1***
2665	**17,9**	**8,91**	**2,01**	**0,018221**	**0,374**	**232124_at**	**Family with sequence similarity 198, member A**	***C3orf41***
842	**447**	**223**	**2,01**	**0,004825**	**0,313**	**223125_s_at**	**Chromosome 1 open reading frame 21**	***C1orf21***
4412	**321**	**160**	**2,01**	**0,032952**	**0,408**	**203060_s_at**	**3'-phosphoadenosine 5'-phosphosulfate synthase 2**	***PAPSS2***
3319	**98,2**	**48,9**	**2,01**	**0,023586**	**0,388**	**225123_at**	**Sestrin 3**	***SESN3***
593	**128**	**63,9**	**2,00**	**0,003271**	**0,301**	**227514_at**	**Inositol 1,4,5-triphosphate receptor interacting protein-like 2**	***ITPRIPL2***
3074	**84,4**	**42,2**	**2,00**	**0,021681**	**0,385**	**230364_at**	**Choline phosphotransferase 1**	***CHPT1***
864	**45,6**	**22,8**	**2,00**	**0,004994**	**0,313**	**204363_at**	**Coagulation factor III (thromboplastin, tissue factor)**	***F3***
4951	14,7	7,35	1,99	0,037975	0,419	1552767_a_a	Heparan sulfate 6-O-sulfotransferase 2	*HS6ST2*
785	115	57,8	1,99	0,004493	0,311	212915_at	PDZ domain containing RING finger 3	*PDZRN3*
197	26,3	13,2	1,99	0,000911	0,244	242903_at	Interferon gamma receptor 1	*IFNGR1*
1802	15,1	7,55	1,99	0,011600	0,351	202234_s_at	Solute carrier family 16, member 1	*SLC16A1*
157	44,0	22,1	1,99	0,000708	0,244	222847_s_at	EGL nine homolog 3 (C. elegans)	*EGLN3*
5541	110	55,4	1,99	0,044049	0,435	223278_at	Gap junction protein, beta 2, 26kDa	*GJB2*
148	12,6	6,36	1,99	0,000682	0,244	235952_at	Transcribed locus	-
5819	36,2	18,2	1,98	0,047031	0,442	233814_at	Ephrin-A5	*EFNA5*
336	536	271	1,98	0,001715	0,277	209121_x_at	Nuclear receptor subfamily 2, group F, member 2	*NR2F2*
326	371	188	1,98	0,001629	0,272	230958_s_at	Glyceronephosphate O-acyltransferase	*GNPAT*
1007	51,4	26,0	1,97	0,005834	0,316	230788_at	I beta-1,6-N-acetylglucosaminyltransferase	*GCNT2*
574	40,4	20,5	1,97	0,003154	0,300	1569607_s_a	Ankyrin repeat domain 20 family, member A1	*ANKRD20A1*

Index	Mutated*	Normal*	FC	*P* value	FDR**	Probe set	Description	Gene symbol
206	278	141	1,97	0,000950	0,244	202709_at	Fibromodulin	*FMOD*
327	133	67,8	1,96	0,001630	0,272	226084_at	Microtubule-associated protein 1B	*MAP1B*
4066	254	129	1,96	0,029819	0,401	231766_s_at	Collagen, type XII, alpha 1	*COL12A1*
274	21,8	11,1	1,96	0,001313	0,262	244026_at	Elongation factor, RNA polymerase II, 2	*ELL2*
126	21,6	11,0	1,96	0,000574	0,240	226885_at	Transcribed locus	-
5995	83,6	42,7	1,96	0,048745	0,444	225008_at	Aspartate beta-hydroxylase	*ASPH*
638	162	82,8	1,96	0,003626	0,308	209522_s_at	Carnitine acetyltransferase	*CRAT*
2964	817	418	1,96	0,020824	0,384	209875_s_at	Secreted phosphoprotein 1	*SPP1*
4037	19,6	10,0	1,96	0,029579	0,401	1564358_at	cDNA FLJ22631 fis, clone HSI06451	-
1339	46,5	23,8	1,95	0,008044	0,328	213107_at	TRAF2 and NCK interacting kinase	*TNIK*
67	190	97,1	1,95	0,000252	0,201	224976_at	Nuclear factor I/A	*NFIA*
2711	13,9	7,09	1,95	0,018609	0,375	205044_at	Gamma-aminobutyric acid (GABA) A receptor, pi	*GABRP*
4813	273	140	1,95	0,036577	0,416	203917_at	Coxsackie virus and adenovirus receptor	*CXADR*
211	44,3	22,7	1,95	0,000957	0,244	203888_at	Thrombomodulin	*THBD*
756	160	82,1	1,94	0,004275	0,308	225379_at	Microtubule-associated protein tau	*MAPT*
706	46,6	24,0	1,94	0,004054	0,308	227082_at	cDNA DKFZp586K1922	-
3238	708	365	1,94	0,022982	0,388	212196_at	Interleukin 6 signal transducer (oncostatin M receptor)	*IL6ST*
3165	45,8	23,6	1,94	0,022459	0,387	228221_at	Solute carrier family 44, member 3	*SLC44A3*
4851	11,6	6,01	1,94	0,036961	0,417	204591_at	Cell adhesion molecule L1-like	*CHL1*
1765	23,4	12,1	1,94	0,011260	0,348	205157_s_at	Keratin 17	*KRT17*
162	408	211	1,93	0,000746	0,244	224970_at	Nuclear factor I/A	*NFIA*
556	22,1	11,4	1,93	0,003024	0,296	239768_x_at	G patch domain containing 2	*GPATCH2*
1280	63,7	33,0	1,93	0,007616	0,325	1556126_s_a	G patch domain containing 2	*GPATCH2*
353	49,4	25,6	1,93	0,001807	0,279	233442_at	PDZ domain containing ring finger 3	*PDZRN3*
4192	135	70,0	1,93	0,030967	0,404	212554_at	CAP, adenylate cyclase-associated protein, 2 (yeast)	*CAP2*
654	826	428	1,93	0,003769	0,308	228297_at	Calponin 3, acidic	*CNN3*
418	59,2	30,7	1,93	0,002193	0,286	214807_at	cDNA DKFZp564O0862	-
2379	63,4	32,9	1,93	0,015858	0,364	232113_at	Hypothetical protein LOC399959	*LOC399959*
193	43,0	22,3	1,93	0,000899	0,244	210021_s_at	Cyclin O	*CCNO*
537	12,0	6,22	1,93	0,002890	0,293	1569208_a_a	LIM and calponin homology domains 1	*LIMCH1*
1674	16,5	8,56	1,92	0,010559	0,345	219250_s_at	Fibronectin leucine rich transmembrane protein 3	*FLRT3*
17	364	190	1,92	0,000068	0,201	212761_at	Transcription factor 7-like 2 (T-cell specific, HMG-box)	*TCF7L2*
1044	38,3	20,0	1,92	0,006098	0,319	228949_at	G protein-coupled receptor 177	*GPR177*
3550	157	81,8	1,92	0,025564	0,394	221841_s_at	Kruppel-like factor 4 (gut)	*KLF4*
1792	8,09	4,23	1,91	0,011482	0,350	1569344_a_a	cDNA clone IMAGE:4044872	-
3614	6,01	3,16	1,90	0,026086	0,395	214601_at	Tryptophan hydroxylase 1 (tryptophan 5-monooxygenase)	*TPH1*
1028	61,6	32,4	1,90	0,005949	0,316	215856_at	Sialic acid binding Ig-like lectin 15	*SIGLEC15*
3961	101	53,5	1,90	0,028941	0,399	224221_s_at	Vav 3 guanine nucleotide exchange factor	*VAV3*
1467	48,6	25,7	1,90	0,008976	0,334	206483_at	Leucine rich repeat containing 6	*LRRC6*
68	66,6	35,2	1,90	0,000259	0,201	242829_x_at	F-box and leucine-rich repeat protein 3	*FBXL3*
245	55,1	29,1	1,89	0,001128	0,251	243963_at	Serologically defined colon cancer antigen 8	*SDCCAG8*
3417	65,9	34,8	1,89	0,024406	0,391	205948_at	Protein tyrosine phosphatase, receptor type, T	*PTPRT*
1418	22,2	11,7	1,89	0,008595	0,331	219890_at	C-type lectin domain family 5, member A	*CLEC5A*
5018	530	280	1,89	0,038593	0,420	219087_at	Asporin	*ASPN*
139	42,2	22,4	1,89	0,000631	0,244	239392_s_at	Pogo transposable element with KRAB domain	*POGK*
1447	80,2	42,5	1,89	0,008803	0,333	222529_at	Solute carrier family 25, member 37	*SLC25A37*
2680	128	68,0	1,88	0,018347	0,374	223126_s_at	Chromosome 1 open reading frame 21	*C1orf21*
36	36,6	19,5	1,88	0,000149	0,201	239476_at	Phosphoinositide-3-kinase, regulatory subunit 1 (p85 alpha)	*PIK3R1*
2551	11,5	6,13	1,88	0,017269	0,370	237183_at	Polypeptide N-acetylgalactosaminyltransferase 5	*GALNT5*
1443	21,7	11,6	1,87	0,008776	0,332	1554712_a_a	Glycine-N-acyltransferase-like 2	*GLYATL2*
4613	2309	1236	1,87	0,034825	0,412	202286_s_at	Tumor-associated calcium signal transducer 2	*TACSTD2*
716	81,8	43,9	1,86	0,004115	0,308	226985_at	FYVE, RhoGEF and PH domain containing 5	*FGD5*
3035	53,9	29,0	1,86	0,021394	0,385	209493_at	PDZ domain containing 2	*PDZD2*
1284	65,4	35,1	1,86	0,007646	0,325	241769_at	Vitronectin receptor subunit alpha (antigen CD51)	*ITGAV*
1213	73,7	39,6	1,86	0,007201	0,324	226909_at	KIAA1729 protein	*KIAA1729*
11	115	61,9	1,86	0,000037	0,180	216037_x_at	Transcription factor 7-like 2 (T-cell specific, HMG-box)	*TCF7L2*
123	8,86	4,78	1,86	0,000566	0,240	240361_at	-	-

Index	Mutated*	Normal*	FC	*P* value	FDR**	Probe set	Description	Gene symbol
646	49,9	26,9	1,85	0,003673	0,308	1557527_at	Runt-related transcription factor 1 (aml1 oncogene)	*RUNX1*
2659	52,9	28,6	1,85	0,018154	0,373	243729_at	cDNA FLJ37931 fis, clone CTONG2004397	-
886	78,4	42,4	1,85	0,005117	0,313	212736_at	Chromosome 16 open reading frame 45	*C16orf45*
3172	333	180	1,85	0,022504	0,387	232615_at	Phosphodiesterase 4D interacting protein	*PDE4DIP*
5474	99,5	53,9	1,85	0,043272	0,432	204286_s_at	Phorbol-12-myristate-13-acetate-induced protein 1	*PMAIP1*
128	99,8	54,1	1,85	0,000575	0,240	225265_at	RNA binding motif, single stranded interacting protein 1	*RBMS1*
4993	107	58,1	1,85	0,038307	0,419	205613_at	Synaptotagmin XVII	*SYT17*
1130	14,0	7,62	1,84	0,006590	0,319	220428_at	CD207 molecule, langerin	*CD207*
3771	59,7	32,4	1,84	0,027388	0,397	227812_at	Tumor necrosis factor receptor superfamily, member 19	*TNFRSF19*
742	390	212	1,84	0,004216	0,308	209120_at	Nuclear receptor subfamily 2, group F, member 2	*NR2F2*
4224	126	68,4	1,84	0,031311	0,405	202986_at	Aryl-hydrocarbon receptor nuclear translocator 2	*ARNT2*
96	13,4	7,31	1,84	0,000374	0,212	232125_at	cDNA FLJ12166 fis, clone MAMMA1000616	-
54	266	145	1,84	0,000212	0,201	212614_at	AT rich interactive domain 5B (MRF1-like)	*ARID5B*
2905	908	495	1,83	0,020424	0,383	217763_s_at	RAB31, member RAS oncogene family	*RAB31*
2615	15,8	8,59	1,83	0,017764	0,371	232459_at	Cytochrome b reductase 1	*CYBRD1*
627	35,4	19,3	1,83	0,003559	0,308	240038_at	Elongation factor, RNA polymerase II, 2	*ELL2*
2476	147	80,4	1,83	0,016668	0,367	1553132_a_a	Tandem C2 domains, nuclear	*TC2N*
880	129	70,5	1,83	0,005093	0,313	223519_at	Sterile alpha motif and leucine zipper containing kinase AZK	*ZAK*
380	49,6	27,2	1,83	0,001979	0,284	202150_s_at	Neural precursor cell expressed, developmentally down-regulated 9	*NEDD9*
1414	73,7	40,4	1,83	0,008557	0,331	238447_at	RNA binding motif, single stranded interacting protein	*RBMS3*
1583	16,2	8,86	1,82	0,009862	0,340	39549_at	Neuronal PAS domain protein 2	*NPAS2*
1906	5,29	2,90	1,82	0,012388	0,355	223810_at	Kelch-like 1 (Drosophila)	*KLHL1*
4915	34,1	18,7	1,82	0,037625	0,418	235629_at	Fibronectin 1	*FN1*
1388	19,6	10,7	1,82	0,008374	0,330	211734_s_at	FC fragment of IgE, high affinity I, receptor for; alpha polypeptide	*FCER1A*
950	123	67,7	1,82	0,005442	0,313	219572_at	Ca2+-dependent activator protein for secretion 2	*CADPS2*
3300	100	55,1	1,82	0,023506	0,388	228256_s_at	Erythrocyte membrane protein band 4.1 like 4A	*EPB41L4A*
1726	11,3	6,23	1,82	0,011045	0,348	1566764_at	Metastasis associated in colon cancer 1	*MACC1*
917	144	78,9	1,82	0,005282	0,313	227224_at	Ral GEF with PH domain and SH3 binding motif 2	*RALGPS2*
175	54,7	30,1	1,82	0,000803	0,244	219771_at	TBC1 domain family, member 8B (with GRAM domain)	*TBC1D8B*
499	55,8	30,7	1,82	0,002656	0,289	222075_s_at	Ornithine decarboxylase antizyme 3	*OAZ3*
825	55,9	30,8	1,81	0,004708	0,312	222549_at	Claudin 1	*CLDN1*
1651	35,5	19,6	1,81	0,010394	0,344	232151_at	Metastasis associated in colon cancer 1	*MACC1*
5915	147	81,3	1,81	0,047945	0,443	229872_s_at	Hypothetical protein LOC730257	*LOC730257*
400	30,9	17,0	1,81	0,002090	0,285	233223_at	Neural precursor cell expressed, developmentally down-regulated 9	*NEDD9*
1708	51,8	28,7	1,81	0,010916	0,348	228950_s_at	G protein-coupled receptor 177	*GPR177*
1308	68,0	37,7	1,81	0,007787	0,325	203518_at	Lysosomal trafficking regulator	*LYST*
341	140	77,3	1,80	0,001733	0,277	229943_at	Tripartite motif-containing 13	*TRIM13*
511	171	94,7	1,80	0,002714	0,290	1558080_s_a	DnaJ (Hsp40) homolog, subfamily C, member 3	*DNAJC3*
291	241	134	1,80	0,001423	0,263	231897_at	Leukotriene B4 12-hydroxydehydrogenase	*LTB4DH*
1541	44,6	24,7	1,80	0,009536	0,337	204735_at	Phosphodiesterase 4A, cAMP-specific	*PDE4A*
3117	63,0	35,0	1,80	0,022048	0,387	235733_at	Transcribed locus	-
449	49,0	27,3	1,80	0,002394	0,288	226439_s_at	Neurobeachin	*NBEA*
2159	36,1	20,1	1,80	0,014225	0,360	238455_at	Plexin domain containing 2	*PLXDC2*
4482	46,8	26,1	1,80	0,033716	0,411	201820_at	Keratin 5	*KRT5*
62	31,1	17,3	1,80	0,000228	0,201	212649_at	DEAH (Asp-Glu-Ala-His) box polypeptide 29	*DHX29*
3451	6,99	3,89	1,79	0,024701	0,391	210576_at	Cytochrome P450, family 4, subfamily F, polypeptide 8	*CYP4F8*
717	116	64,8	1,79	0,004116	0,308	205011_at	Loss of heterozygosity, 11, chromosomal region 2, gene A	*LOH11CR2A*
191	67,2	37,6	1,79	0,000891	0,244	207836_s_at	RNA binding protein with multiple splicing	*RBPMS*
719	33,2	18,6	1,79	0,004119	0,308	205555_s_at	MSH homeobox 2	*MSX2*
3724	40,0	22,4	1,79	0,027028	0,397	1555407_s_a	FYVE, RhoGEF and PH domain containing 3	*FGD3*
1216	10,0	5,62	1,79	0,007240	0,324	1556190_s_a	Prion protein (p27-30) (Creutzfeldt-Jakob disease)	*PRNP*
273	49,2	27,6	1,78	0,001310	0,262	203542_s_at	Kruppel-like factor 9	*KLF9*
2055	40,5	22,7	1,78	0,013369	0,356	236114_at	Runt-related transcription factor 1 (aml1 oncogene)	*RUNX1*
4358	14,1	7,90	1,78	0,032416	0,407	206091_at	Matrilin 3	*MATN3*
387	147	82,4	1,78	0,002008	0,284	203120_at	Tumor protein p53 binding protein, 2	*TP53BP2*
700	37,5	21,1	1,78	0,004011	0,308	215536_at	Major histocompatibility complex, class II, DQ beta 2	*HLA-DQB2*
968	20,1	11,3	1,78	0,005615	0,315	241872_at	SH3-domain GRB2-like (endophilin) interacting protein 1	*SGIP1*

Index	Mutated*	Normal*	FC	*P* value	FDR**	Probe set	Description	Gene symbol
236	49,2	27,7	1,78	0,001101	0,250	209632_at	Protein phosphatase 2 (formerly 2A), regulatory subunit B'', alpha	*PPP2R3A*
1112	132	74,2	1,78	0,006509	0,319	205097_at	Solute carrier family 26 (sulfate transporter), member 2	*SLC26A2*
1660	35,4	20,0	1,77	0,010480	0,345	206191_at	Ectonucleoside triphosphate diphosphohydrolase 3	*ENTPD3*
1278	52,6	29,7	1,77	0,007609	0,325	209655_s_at	Transmembrane protein 47	*TMEM47*
2770	30,6	17,3	1,77	0,019221	0,379	1558612_a_a	ATPase, Na+/K+ transporting, alpha 4 polypeptide	*ATP1A4*
495	87,7	49,6	1,77	0,002640	0,289	230906_at	N-acetylgalactosaminyltransferase 10	*GALNT10*
4515	49,9	28,2	1,77	0,034036	0,412	218857_s_at	Asparaginase like 1	*ASRGL1*
4569	220	125	1,77	0,034553	0,412	202464_s_at	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 3	*PFKFB3*
4703	108	60,9	1,77	0,035548	0,413	214295_at	KIAA0485 protein	*KIAA0485*
4151	247	140	1,77	0,030628	0,403	227384_s_at	Hypothetical protein LOC727820	*LOC727820*
1011	413	234	1,76	0,005857	0,316	226085_at	Chromobox homolog 5 (HP1 alpha homolog, Drosophila)	*CBX5*
5489	344	195	1,76	0,043445	0,433	214329_x_at	Tumor necrosis factor (ligand) superfamily, member 10	*TNFSF10*
5094	54,3	30,8	1,76	0,039195	0,420	229744_at	Sperm specific antigen 2	*SSFA2*
871	200	113	1,76	0,005028	0,313	227740_at	U2AF homology motif (UHM) kinase 1	*UHMK1*
1202	5,58	3,17	1,76	0,007111	0,323	1554027_a_a	Solute carrier family 4, sodium bicarbonate cotransporter, member 4	*SLC4A4*
637	124	70,1	1,76	0,003620	0,308	235003_at	U2AF homology motif (UHM) kinase 1	*UHMK1*
358	45,0	25,5	1,76	0,001833	0,280	222314_x_at	Eosinophil granule ontogeny transcript (non-protein coding)	*EGOT*
896	65,7	37,3	1,76	0,005182	0,313	218451_at	CUB domain containing protein 1	*CDCP1*
270	36,4	20,7	1,76	0,001291	0,261	213462_at	Neuronal PAS domain protein 2	*NPAS2*
1516	19,5	11,1	1,76	0,009365	0,337	243546_at	Sestrin 3	*SESN3*
566	72,1	41,1	1,75	0,003093	0,299	213342_at	Yes-associated protein 1, 65kDa	*YAP1*
4981	35,1	20,0	1,75	0,038216	0,419	205907_s_at	Osteomodulin	*OMD*
390	123	70,2	1,75	0,002025	0,284	226065_at	Prickle homolog 1 (Drosophila)	*PRICKLE1*
200	81,2	46,4	1,75	0,000925	0,244	222734_at	Tryptophanyl tRNA synthetase 2, mitochondrial	*WARS2*
1683	22,8	13,0	1,75	0,010637	0,345	242458_at	Ral GEF with PH domain and SH3 binding motif 2	*RALGPS2*
929	36,0	20,6	1,75	0,005334	0,313	207300_s_at	Coagulation factor VII (serum prothrombin conversion accelerator)	*F7*
3019	22,2	12,7	1,75	0,021268	0,385	1564064_a_a	ATPase, Class VI, type 11B	*ATP11B*
1538	31,6	18,1	1,75	0,009523	0,337	235592_at	Elongation factor, RNA polymerase II, 2	*ELL2*
2	635	364	1,75	0,000007	0,099	211962_s_at	Zinc finger protein 36, C3H type-like 1	*ZFP36L1*
1433	182	104	1,75	0,008691	0,331	201730_s_at	Translocated promoter region (to activated MET oncogene)	*TPR*
697	35,5	20,4	1,74	0,004003	0,308	214269_at	Major facilitator superfamily domain containing 7	*MFSD7*
1636	36,5	21,0	1,74	0,010311	0,344	205729_at	Oncostatin M receptor	*OSMR*
5311	64,8	37,2	1,74	0,041436	0,426	235924_at	cDNA FLJ42287 fis, clone TLIVE2005866	-
1245	371	213	1,74	0,007398	0,324	1568619_s_a	Hypothetical protein LOC162073	*LOC162073*
1605	21,7	12,5	1,74	0,010038	0,342	241837_at	AT rich interactive domain 5B (MRF1-like)	*ARID5B*
1807	162	93,3	1,74	0,011634	0,351	234970_at	Tandem C2 domains, nuclear	*TC2N*
2000	60,8	35,0	1,74	0,013064	0,355	232797_at	Vitronectin receptor subunit alpha (antigen CD51)	*ITGAV*
5188	19,7	11,3	1,74	0,039978	0,421	206595_at	Cystatin E/M	*CST6*
2657	36,9	21,2	1,74	0,018124	0,373	229105_at	G protein-coupled receptor 39	*GPR39*
1640	77,8	45,0	1,73	0,010338	0,344	229530_at	Guanylate cyclase 1, soluble, alpha 3	*GUCY1A3*
894	124	72,0	1,73	0,005167	0,313	226621_at	Fibrinogen gamma chain	*FGG*
3129	72,6	42,0	1,73	0,022184	0,387	236179_at	Cadherin 11, type 2, OB-cadherin (osteoblast)	*CDH11*
2351	66,3	38,4	1,73	0,015686	0,364	229307_at	Ankyrin repeat domain 28	*ANKRD28*
1475	24,6	14,3	1,73	0,009014	0,334	241864_x_at	Transcribed locus	-
1653	15,2	8,80	1,72	0,010426	0,345	241310_at	Transcribed locus	-
2025	13,9	8,07	1,72	0,013199	0,355	240120_at	Sorbin and SH3 domain containing 2	*SORBS2*
142	225	130	1,72	0,000645	0,244	218788_s_at	SET and MYND domain containing 3	*SMYD3*
479	16,4	9,54	1,72	0,002563	0,289	213109_at	TRAF2 and NCK interacting kinase	*TNIK*
1915	1281	743	1,72	0,012500	0,355	212195_at	Interleukin 6 signal transducer (gp130, oncostatin M receptor)	*IL6ST*
1965	15,7	9,10	1,72	0,012849	0,355	225660_at	Semaphorin 6A-1	*SEMA6A*
408	154	89,2	1,72	0,002147	0,286	228824_s_at	Prostaglandin reductase 1	*PTGR1*
1826	7,45	4,33	1,72	0,011762	0,351	204913_s_at	SRY (sex determining region Y)-box 11	*SOX11*
1398	63,2	36,7	1,72	0,008450	0,330	228141_at	Glutathione peroxidase 8 (putative)	*GPX8*
300	87,4	50,8	1,72	0,001461	0,263	207749_s_at	Protein phosphatase 2 (formerly 2A), regulatory subunit B'', alpha	*PPP2R3A*
979	33,5	19,5	1,72	0,005682	0,315	235834_at	Caldesmon 1	*CALD1*
528	11,1	6,45	1,72	0,002818	0,292	221583_s_at	Calcium-activated potassium channel subunit alpha-1	*KCNMA1*
3025	20,1	11,7	1,72	0,021294	0,385	235957_at	Glutamate receptor interacting protein 1	*GRIP1*

Index	Mutated*	Normal*	FC	*P* value	FDR**	Probe set	Description	Gene symbol
1495	19,3	11,3	1,72	0,009209	0,336	242736_at	Sorbin and SH3 domain containing 1	*SORBS1*
549	78,7	45,8	1,72	0,002972	0,295	214734_at	Exophilin 5	*EXPH5*
41	18,8	11,0	1,72	0,000172	0,201	228602_at	Sarcoglycan, delta (35kDa dystrophin-associated glycoprotein)	*SGCD*
488	23,7	13,8	1,72	0,002619	0,289	242931_at	LON peptidase N-terminal domain and ring finger 3	*LONRF3*
2585	92,2	53,8	1,71	0,017536	0,371	206994_at	Cystatin S	*CST4*
231	52,2	30,5	1,71	0,001070	0,250	244533_at	Protein tyrosine phosphatase, non-receptor type 14	*PTPN14*
2554	68,4	40,0	1,71	0,017283	0,370	239597_at	Poly(A) specific ribonuclease subunit homolog (S. cerevisiae)	*PAN3*
3485	55,3	32,3	1,71	0,025017	0,392	223948_s_at	Transmembrane protease, serine 3	*TMPRSS3*
2090	23,9	14,0	1,71	0,013626	0,356	235278_at	MACRO domain containing 2	*MACROD2*
3800	76,6	44,8	1,71	0,027683	0,398	217867_x_at	Beta-site APP-cleaving enzyme 2	*BACE2*
2153	14,8	8,68	1,71	0,014179	0,360	230472_at	Iroquois homeobox 1	*IRX1*
2716	68,1	39,9	1,71	0,018663	0,376	243296_at	Pre-B-cell colony enhancing factor 1	*PBEF1*
3543	848	497	1,71	0,025495	0,393	217762_s_at	RAB31, member RAS oncogene family	*RAB31*
3587	65,1	38,2	1,71	0,025885	0,394	204157_s_at	KIAA0999 protein	*KIAA0999*
940	49,7	29,2	1,70	0,005379	0,313	236561_at	Transforming growth factor, beta receptor I	*TGFBR1*
1771	25,1	14,7	1,70	0,011292	0,348	213929_at	Exophilin 5	*EXPH5*
2056	170	100	1,70	0,013390	0,356	227533_at	Transcribed locus	-
2326	65,8	38,7	1,70	0,015473	0,364	232138_at	Muscleblind-like 2 (Drosophila)	*MBNL2*
1513	9,22	5,42	1,70	0,009319	0,337	220117_at	Zinc finger protein 659	*ZNF659*
4051	61,2	36,0	1,70	0,029701	0,401	241897_at	RNA binding protein with multiple splicing	*RBPMS*
4115	299	176	1,70	0,030261	0,402	228993_s_at	Non-protein coding RNA 81	*NCRNA00081*
6074	7,90	4,65	1,70	0,049585	0,446	231626_at	Tryptophan hydroxylase 1	*TPH1*
3370	128	75,4	1,70	0,023966	0,389	227232_at	Enah/Vasp-like	*EVL*
5709	249	147	1,70	0,045713	0,438	202506_at	Sperm specific antigen 2	*SSFA2*
624	108	63,7	1,70	0,003541	0,308	202962_at	Kinesin family member 13B	*KIF13B*
851	59,2	34,9	1,69	0,004897	0,313	242281_at	Glutamate-ammonia ligase (glutamine synthetase)	*GLUL*
4994	15,4	9,09	1,69	0,038316	0,419	205908_s_at	Osteomodulin	*OMD*
198	14,2	8,38	1,69	0,000917	0,244	233286_at	PDZ domain containing ring finger 3	*PDZRN3*
904	82,7	48,9	1,69	0,005233	0,313	204948_s_at	Follistatin	*FST*
1075	90,7	53,7	1,69	0,006305	0,319	201369_s_at	Zinc finger protein 36, C3H type-like 2	*ZFP36L2*
1741	27,2	16,1	1,69	0,011126	0,348	232112_at	Ral GEF with PH domain and SH3 binding motif 2	*RALGPS2*
1509	308	183	1,69	0,009303	0,337	202820_at	Aryl hydrocarbon receptor	*AHR*
1052	322	191	1,69	0,006147	0,319	218694_at	Armadillo repeat containing, X-linked 1	*ARMCX1*
3488	85,4	50,6	1,69	0,025069	0,392	227997_at	Interleukin 17 receptor D	*IL17RD*
2408	7,59	4,50	1,69	0,016095	0,365	220014_at	Proline rich 16	*PRR16*
388	27,0	16,0	1,69	0,002012	0,284	214366_s_at	Arachidonate 5-lipoxygenase	*ALOX5*
2306	669	397	1,69	0,015300	0,363	1555812_a_a	Rho GDP dissociation inhibitor (GDI) beta	*ARHGDIB*
2407	156	92,5	1,69	0,016084	0,365	241879_at	Transcribed locus	-
3050	86,1	51,1	1,68	0,021466	0,385	223349_s_at	BCL2-related ovarian killer	*BOK*
313	51,8	30,8	1,68	0,001577	0,272	213826_s_at	H3 histone, family 3A	*H3F3A*
3936	79,2	47,1	1,68	0,028758	0,399	203642_s_at	COBL-like 1	*COBLL1*
792	19,8	11,7	1,68	0,004531	0,311	239726_at	Ankyrin 3, node of Ranvier (ankyrin G)	*ANK3*
69	85,7	50,9	1,68	0,000266	0,201	221503_s_at	Karyopherin alpha 3 (importin alpha 4)	*KPNA3*
3832	27,0	16,1	1,68	0,028005	0,399	220266_s_at	Kruppel-like factor 4 (gut)	*KLF4*
1100	42,7	25,4	1,68	0,006453	0,319	209442_x_at	Ankyrin 3, node of Ranvier (ankyrin G)	*ANK3*
287	10,3	6,13	1,68	0,001403	0,263	224463_s_at	Chromosome 11 open reading frame 70	*C11orf70*
723	267	159	1,68	0,004143	0,308	224894_at	Yes-associated protein 1, 65kDa	*YAP1*
1675	89,5	53,4	1,68	0,010563	0,345	205107_s_at	Ephrin-A4	*EFNA4*
147	18,0	10,8	1,68	0,000677	0,244	1557242_at	Similar to Fibroblast growth factor receptor 3 precursor (FGFR-3)	*LOC442200*
514	35,0	21,0	1,67	0,002747	0,291	220272_at	Basonuclin 2	*BNC2*
1795	14,2	8,52	1,67	0,011533	0,351	215047_at	Tripartite motif-containing 58	*TRIM58*
2624	523	314	1,67	0,017825	0,371	206116_s_at	Tropomyosin 1 (alpha)	*TPM1*
3012	302	181	1,67	0,021190	0,385	225496_s_at	Synaptotagmin-like 2	*SYTL2*
2856	368	221	1,67	0,020049	0,383	226534_at	KIT ligand	*KITLG*
3004	720	432	1,67	0,021137	0,385	217202_s_at	Glutamate-ammonia ligase (glutamine synthetase)	*GLUL*
4456	40,4	24,3	1,67	0,033478	0,411	209167_at	Glycoprotein M6B	*GPM6B*
2517	13,6	8,20	1,66	0,016975	0,369	230970_at	Slingshot homolog 2 (Drosophila)	*SSH2*

Index	Mutated*	Normal*	FC	*P* value	FDR**	Probe set	Description	Gene symbol
5930	41,1	24,7	1,66	0,048060	0,443	229125_at	Ankyrin repeat domain 38	*ANKRD38*
2552	135	81,1	1,66	0,017275	0,370	236251_at	Vitronectin receptor subunit alpha (antigen CD51)	*ITGAV*
3330	43,5	26,2	1,66	0,023639	0,388	203641_s_at	COBL-like 1	*COBLL1*
3626	40,4	24,3	1,66	0,026198	0,395	226069_at	Prickle homolog 1 (Drosophila)	*PRICKLE1*
1720	17,3	10,4	1,66	0,011019	0,348	236237_at	KIAA1370 protein	*KIAA1370*
916	26,9	16,2	1,66	0,005275	0,313	222735_at	Transmembrane protein 38B	*TMEM38B*
5056	160	96,2	1,66	0,038950	0,420	202990_at	Phosphorylase, glycogen	*PYGL*
4610	334	201	1,66	0,034821	0,412	212560_at	Sortilin-related receptor, L(DLR class) A repeats-containing	*SORL1*
1623	47,7	28,8	1,66	0,010197	0,344	221207_s_at	Neurobeachin	*NBEA*
352	17,8	10,8	1,66	0,001793	0,278	242321_at	cDNA clone ZE03F06	-
427	106	63,7	1,66	0,002256	0,288	222158_s_at	PPPDE peptidase domain containing 1	*PPPDE1*
571	22,1	13,4	1,66	0,003140	0,300	244571_s_at	Tetratricopeptide repeat domain 12	*TTC12*
1783	67,5	40,8	1,66	0,011373	0,349	232369_at	Muscleblind-like 2 (Drosophila)	*MBNL2*
769	247	149	1,65	0,004380	0,311	201911_s_at	FERM, RhoGEF (ARHGEF) and pleckstrin domain protein 1	*FARP1*
1810	17,0	10,3	1,65	0,011676	0,351	206556_at	Clusterin-like 1 (retinal)	*CLUL1*
160	37,3	22,6	1,65	0,000722	0,244	217875_s_at	Transmembrane, prostate androgen induced RNA	*TMEPAI*
4882	18,1	10,9	1,65	0,037333	0,418	233231_at	Methylcrotonoyl-Coenzyme A carboxylase 2 (beta)	*MCCC2*
6022	315	191	1,65	0,049010	0,445	226279_at	Protease, serine, 23	*PRSS23*
5608	12,0	7,29	1,65	0,044721	0,436	243722_at	PYD (pyrin domain) containing 1	*PYDC1*
558	95,9	58,2	1,65	0,003025	0,296	226252_at	cDNA FLJ34585 fis, clone KIDNE2008758	-
5168	18,2	11,1	1,65	0,039820	0,421	208006_at	Forkhead box I1	*FOXI1*
4305	11,9	7,22	1,65	0,032037	0,407	215506_s_at	DIRAS family, GTP-binding RAS-like 3	*DIRAS3*
543	7,96	4,83	1,65	0,002920	0,294	226933_s_at	Inhibitor of DNA binding 4, dominant negative helix-loop-helix protein	*ID4*
2125	33,1	20,1	1,65	0,013990	0,359	243598_at	Glycerol-3-phosphate dehydrogenase 2 (mitochondrial)	*GPD2*
1798	60,3	36,7	1,65	0,011576	0,351	238465_at	Chromosome 5 open reading frame 35	*C5orf35*
539	53,9	32,8	1,64	0,002895	0,293	223530_at	Tudor and KH domain containing	*TDRKH*
1961	49,3	30,0	1,64	0,012816	0,355	201983_s_at	Avian erythroblastic leukemia viral (v-erb-b) oncogene homolog	*EGFR*
207	464	283	1,64	0,000954	0,244	212294_at	Guanine nucleotide binding protein (G protein), gamma 12	*GNG12*
2263	85,4	52,0	1,64	0,015052	0,363	204036_at	Lysophosphatidic acid receptor 1	*EDG2*
1017	174	106	1,64	0,005886	0,316	213158_at	cDNA clone IMAGE:4214654	-
1242	13,5	8,25	1,64	0,007382	0,324	218772_x_at	Transmembrane protein 38B	*TMEM38B*
3350	84,8	51,7	1,64	0,023787	0,388	212236_x_at	Keratin 17	*KRT17*
1546	750	458	1,64	0,009548	0,337	210139_s_at	Peripheral myelin protein 22	*PMP22*
2437	14,3	8,75	1,64	0,016289	0,365	204914_s_at	SRY (sex determining region Y)-box 11	*SOX11*
4191	33,1	20,2	1,64	0,030965	0,404	226676_at	Zinc finger protein 521	*ZNF521*
3909	96,6	59,1	1,64	0,028531	0,399	202932_at	v-yes-1 Yamaguchi sarcoma viral oncogene homolog 1	*YES1*
4056	50,9	31,1	1,63	0,029751	0,401	238478_at	Basonuclin 2	*BNC2*
3396	11,0	6,76	1,63	0,024222	0,390	220475_at	Solute carrier family 28 member 3	*SLC28A3*
1727	29,9	18,3	1,63	0,011046	0,348	230730_at	Sarcoglycan, delta (35kDa dystrophin-associated glycoprotein)	*SGCD*
498	5,79	3,54	1,63	0,002651	0,289	237134_at	Transcribed locus	-
1194	18,6	11,4	1,63	0,007041	0,322	203930_s_at	Microtubule-associated protein tau	*MAPT*
4495	81,3	49,8	1,63	0,033807	0,411	213135_at	T-cell lymphoma invasion and metastasis 1	*TIAM1*
1473	10,4	6,39	1,63	0,008999	0,334	241762_at	F-box protein 32	*FBXO32*
242	9,93	6,09	1,63	0,001111	0,250	232116_at	Grainyhead-like 3 (Drosophila)	*GRHL3*
4067	53,6	32,9	1,63	0,029824	0,401	230722_at	Basonuclin 2	*BNC2*
5604	93,4	57,3	1,63	0,044711	0,436	211368_s_at	Caspase 1, apoptosis-related cysteine peptidase	*CASP1*
3349	81,3	49,9	1,63	0,023785	0,388	230712_at	Neuroblastoma breakpoint family, member 1	*NBPF1*
2503	13,1	8,04	1,63	0,016843	0,367	209863_s_at	Tumor protein p63	*TP63*
1842	14,5	8,87	1,63	0,011844	0,351	214321_at	Nephroblastoma overexpressed gene	*NOV*
2879	180	111	1,63	0,020209	0,383	209030_s_at	Cell adhesion molecule 1	*CADM1*
3054	137	83,8	1,63	0,021510	0,385	222446_s_at	Beta-site APP-cleaving enzyme 2	*BACE2*
959	30,0	18,4	1,63	0,005539	0,315	241359_at	cDNA FLJ20031 fis, clone ADSU02180	-
4483	44,4	27,3	1,63	0,033718	0,411	202672_s_at	Activating transcription factor 3	*ATF3*
1046	461	283	1,63	0,006113	0,319	227856_at	Chromosome 4 open reading frame 32	*C4orf32*
2988	11,7	7,19	1,63	0,021007	0,384	202859_x_at	Interleukin 8	*IL8*
448	716	440	1,63	0,002392	0,288	201368_at	Zinc finger protein 36, C3H type-like 2	*ZFP36L2*
278	164	101	1,63	0,001357	0,263	226282_at	cDNA clone ZE03F06	-

Index	Mutated*	Normal*	FC	*P* value	FDR**	Probe set	Description	Gene symbol
640	54,8	33,7	1,63	0,003639	0,308	202191_s_at	Growth arrest-specific 7	*GAS7*
1394	1346	827	1,63	0,008433	0,330	208683_at	Calpain 2, (m/II) large subunit	*CAPN2*
1754	388	239	1,63	0,011177	0,348	203509_at	Sortilin-related receptor, L(DLR class) A repeats-containing	*SORL1*
75	116	71,2	1,63	0,000291	0,201	219625_s_at	Collagen, type IV, alpha 3 (Goodpasture antigen) binding protein	*COL4A3BP*
57	21,5	13,2	1,63	0,000216	0,201	214212_x_at	Pleckstrin homology domain containing, family C member 1	*PLEKHC1*
4292	560	345	1,62	0,031900	0,406	227404_s_at	Early growth response 1	*EGR1*
3754	132	81,4	1,62	0,027290	0,397	227628_at	Glutathione peroxidase 8 (putative)	*GPX8*
1577	41,5	25,5	1,62	0,009798	0,340	203543_s_at	Kruppel-like factor 9	*KLF9*
1517	97,6	60,2	1,62	0,009366	0,337	212382_at	Transcription factor 4	*TCF4*
3851	130	80,6	1,62	0,028109	0,399	239246_at	FERM, RhoGEF (ARHGEF) and pleckstrin domain protein 1	*FARP1*
3194	98,0	60,6	1,62	0,022634	0,387	242343_x_at	Zinc finger protein 518A	*ZNF518*
1032	11,1	6,89	1,62	0,005999	0,318	222320_at	Hyperparathyroidism 2 protein	*CDC73*
5328	6,75	4,17	1,62	0,041669	0,428	235831_at	Transcribed locus	-
1109	27,1	16,8	1,62	0,006492	0,319	238909_at	S100 calcium binding protein A10	*S100A10*
319	118	73,2	1,62	0,001596	0,272	214724_at	DIX domain containing 1	*DIXDC1*
5542	130	80,3	1,62	0,044061	0,435	209031_at	Cell adhesion molecule 1	*CADM1*
6046	190	118	1,62	0,049264	0,445	213350_at	Ribosomal protein S11	*RPS11*
480	62,5	38,7	1,61	0,002568	0,289	221042_s_at	Calmin (calponin-like, transmembrane)	*CLMN*
3160	14,2	8,82	1,61	0,022427	0,387	242396_at	Hypothetical protein LOC644192	*LOC644192*
4465	458	284	1,61	0,033537	0,411	232914_s_at	Synaptotagmin-like 2	*SYTL2*
4748	48,0	29,7	1,61	0,035988	0,414	213790_at	ADAM metallopeptidase domain 12	*ADAM12*
3516	178	110	1,61	0,025248	0,392	235501_at	FERM, RhoGEF (ARHGEF) and pleckstrin domain protein 1	*FARP1*
5609	26,4	16,4	1,61	0,044732	0,436	215483_at	A kinase (PRKA) anchor protein (yotiao) 9	*AKAP9*
288	72,6	45,0	1,61	0,001412	0,263	225041_at	M-phase phosphoprotein, mpp8	*HSMPP8*
4729	18,0	11,2	1,61	0,035816	0,414	233109_at	Collagen, type XII, alpha 1	*COL12A1*
5028	296	184	1,61	0,038663	0,420	218806_s_at	Vav 3 guanine nucleotide exchange factor	*VAV3*
2581	70,6	43,9	1,61	0,017505	0,371	213156_at	cDNA clone IMAGE:4214654	-
3269	23,9	14,9	1,61	0,023248	0,388	212177_at	Splicing factor, arginine/serine-rich 18	*SFRS18*
4322	36,4	22,6	1,61	0,032177	0,407	236225_at	Gamma-glutamyltransferase 6 homolog (rat)	*GGT6*
181	1203	748	1,61	0,000838	0,244	208949_s_at	Lectin, galactoside-binding, soluble, 3	*LGALS3*
5636	129	80,0	1,61	0,044981	0,436	214927_at	Integrin, beta-like 1 (with EGF-like repeat domains)	*ITGBL1*
1896	229	143	1,61	0,012326	0,355	228188_at	FOS-like antigen 2	*FOSL2*
3270	53,1	33,1	1,61	0,023250	0,388	220940_at	KIAA1641 protein	*KIAA1641*
5432	117	72,8	1,60	0,042790	0,431	209656_s_at	Transmembrane protein 47	*TMEM47*
5826	80,2	50,0	1,60	0,047075	0,442	229704_at	Androgen-induced proliferation inhibitor	*PDS5B*
691	10,4	6,48	1,60	0,003971	0,308	238067_at	TBC1 domain family, member 8B (with GRAM domain)	*TBC1D8B*
3406	140	87,0	1,60	0,024301	0,390	221824_s_at	Membrane-associated ring finger (C3HC4) 8	*MARCH8*
520	121	75,8	1,60	0,002767	0,291	209633_at	Protein phosphatase 2 (formerly 2A), regulatory subunit B'', alpha	*PPP2R3A*
103	28,7	17,9	1,60	0,000413	0,217	230518_at	Myelin protein zero-like 2	*MPZL2*
214	273	170	1,60	0,000961	0,244	219221_at	Zinc finger and BTB domain containing 38	*ZBTB38*
2322	127	79,2	1,60	0,015439	0,364	222746_s_at	B-box and SPRY domain containing	*BSPRY*
584	187	117	1,60	0,003220	0,301	206061_s_at	Dicer1, Dcr-1 homolog (Drosophila)	*DICER1*
2119	24,9	15,6	1,60	0,013906	0,359	237456_at	RING1 and YY1 binding protein	*RYBP*
395	35,6	22,3	1,60	0,002084	0,285	219469_at	Dynein, cytoplasmic 2, heavy chain 1	*DYNC2H1*
4428	28,1	17,6	1,60	0,033159	0,409	239587_at	Transcribed locus	-
5232	184	115	1,60	0,040493	0,423	200824_at	Glutathione S-transferase pi	*GSTP1*
4845	23,5	14,8	1,59	0,036920	0,417	236587_at	Transcribed locus	-
971	547	343	1,59	0,005626	0,315	212386_at	Transcription factor 4	*TCF4*
1702	159	100,0	1,59	0,010844	0,348	226117_at	TRAF-interacting protein with a forkhead-associated domain	*TIFA*
1881	10,9	6,88	1,59	0,012201	0,355	210739_x_at	Solute carrier family 4, sodium bicarbonate cotransporter, member 4	*SLC4A4*
1464	114	71,4	1,59	0,008959	0,334	229499_at	Calpain 13	*CAPN13*
5622	504	317	1,59	0,044890	0,436	228708_at	RAB27B, member RAS oncogene family	*RAB27B*
529	33,9	21,3	1,59	0,002827	0,292	213239_at	Family with sequence similarity 162, member A	*FAM162A*
2654	94,3	59,3	1,59	0,018094	0,373	212233_at	Microtubule-associated protein 1B	*MAP1B*
5716	32,4	20,4	1,59	0,045772	0,438	206271_at	Toll-like receptor 3	*TLR3*
3487	53,9	33,9	1,59	0,025032	0,392	220751_s_at	Chromosome 5 open reading frame 4	*C5orf4*
279	972	612	1,59	0,001364	0,263	210835_s_at	C-terminal binding protein 2	*CTBP2*

Index	Mutated*	Normal*	FC	*P* value	FDR**	Probe set	Description	Gene symbol
3688	152	95,6	1,59	0,026634	0,395	202933_s_at	v-yes-1 Yamaguchi sarcoma viral oncogene homolog 1	*YES1*
4949	100	63,3	1,59	0,037968	0,419	226225_at	Mutated in colorectal cancers	*MCC*
1397	175	111	1,59	0,008437	0,330	218792_s_at	B-box and SPRY domain containing	*BSPRY*
1914	169	107	1,59	0,012472	0,355	221942_s_at	Guanylate cyclase 1, soluble, alpha 3	*GUCY1A3*
3777	44,8	28,2	1,59	0,027458	0,397	218273_s_at	Protein phosphatase 2C, magnesium-dependent, catalytic subunit	*PPM2C*
567	51,8	32,6	1,59	0,003099	0,299	241233_x_at	Chromosome 21 open reading frame 81	*C21orf81*
4540	26,3	16,6	1,59	0,034300	0,412	210538_s_at	Baculoviral IAP repeat-containing 3	*BIRC3*
1851	10,3	6,49	1,59	0,011917	0,352	233819_s_at	Zinc finger protein 294	*ZNF294*
149	48,4	30,6	1,58	0,000689	0,244	1554106_at	Neurobeachin-like 1	*ALS2CR16*
5389	47,6	30,0	1,58	0,042253	0,429	242920_at	SIK family kinase 3	*SIK3*
1205	53,7	33,9	1,58	0,007132	0,324	214149_s_at	ATPase, H+ transporting, lysosomal 9kDa, V0 subunit e1	*ATP6V0E1*
368	22,8	14,4	1,58	0,001918	0,284	230071_at	Septin 11	*SEPT11*
80	11,4	7,21	1,58	0,000301	0,201	231149_s_at	Unc-51-like kinase 4 (C. elegans)	*ULK4*
961	232	147	1,58	0,005559	0,315	224895_at	Yes-associated protein 1, 65kDa	*YAP1*
3087	489	309	1,58	0,021766	0,385	202336_s_at	Peptidylglycine alpha-amidating monooxygenase	*PAM*
2616	9,71	6,14	1,58	0,017773	0,371	206548_at	Hypothetical protein FLJ23556	*FKJ23556*
426	70,3	44,4	1,58	0,002253	0,288	233540_s_at	CDK5 regulatory subunit associated protein 2	*CDK5RAP2*
1493	66,3	41,9	1,58	0,009199	0,336	222834_s_at	Guanine nucleotide binding protein (G protein), gamma 12	*GNG12*
2438	300	189	1,58	0,016292	0,365	228153_at	Ring finger 144B	*RNF144B*
3034	28,8	18,2	1,58	0,021381	0,385	209318_x_at	Pleiomorphic adenoma gene-like 1	*PLAGL1*
5283	85,1	53,8	1,58	0,041092	0,425	225806_at	Jub, ajuba homolog (Xenopus laevis)	*JUB*
2570	10,7	6,78	1,58	0,017428	0,371	215686_x_at	Transcription factor AP-2 beta	*TFAP2B*
2936	20,4	12,9	1,58	0,020591	0,383	240146_at	Capping protein (actin filament) muscle Z-line, alpha 2	*CAPZA2*
4946	38,9	24,6	1,58	0,037943	0,419	244246_at	Mirror-image polydactyly 1	*MIPOL1*
3365	69,1	43,7	1,58	0,023903	0,388	237064_x_at	Dynein, axonemal, heavy chain 14	*DNAH14*
2219	849	537	1,58	0,014710	0,362	227792_at	Inositol 1,4,5-triphosphate receptor interacting protein-like 2	*ITPRIPL2*
754	149	94,1	1,58	0,004270	0,308	212256_at	N-acetylgalactosaminyltransferase 10	*GALNT10*
1020	71,2	45,1	1,58	0,005898	0,316	241722_x_at	Transcribed locus	-
370	88,4	56,0	1,58	0,001941	0,284	225957_at	Adult retina protein	*LOC153222*
962	253	160	1,58	0,005570	0,315	204373_s_at	Centrosomal protein 350kDa	*CEP350*
4808	30,2	19,1	1,58	0,036508	0,415	222528_s_at	Solute carrier family 25, member 37	*SLC25A37*
4102	30,7	19,5	1,58	0,030147	0,402	229817_at	Zinc finger protein 608	*ZNF608*
1710	27,6	17,5	1,58	0,010940	0,348	239393_at	Poly(A) specific ribonuclease subunit homolog (S. cerevisiae)	*PAN3*
2784	10,3	6,50	1,58	0,019340	0,380	1552405_at	NLR family, pyrin domain containing 5	*NLRP5*
1835	29,5	18,7	1,58	0,011814	0,351	239619_at	Zinc finger protein 395	*ZNF395*
2590	16,7	10,6	1,58	0,017573	0,371	218610_s_at	Hypothetical protein FLJ11151	*FLJ11151*
2114	49,8	31,6	1,58	0,013870	0,359	221276_s_at	Syncoilin, intermediate filament 1	*SYNC1*
2447	10,5	6,66	1,58	0,016391	0,366	202036_s_at	Secreted frizzled-related protein 1	*SFRP1*
3707	28,7	18,2	1,57	0,026801	0,395	236297_at	cDNA FLJ45742 fis, clone KIDNE2016327	-
4440	8,42	5,35	1,57	0,033335	0,410	202235_at	Solute carrier family 16, member 1	*SLC16A1*
2324	57,4	36,5	1,57	0,015461	0,364	233924_s_at	Exocyst complex component 6	*EXOC6*
1733	75,6	48,0	1,57	0,011083	0,348	215338_s_at	Natural killer-tumor recognition sequence	*NKTR*
2631	32,4	20,6	1,57	0,017907	0,372	243395_at	CD55 molecule, decay accelerating factor for complement	*CD55*
5002	27,9	17,7	1,57	0,038404	0,420	244075_at	Hydroxysteroid (17-beta) dehydrogenase 7 pseudogene 2	*HSD17B7P2*
1673	16,5	10,5	1,57	0,010558	0,345	243233_at	Poly(A) specific ribonuclease subunit homolog (S. cerevisiae)	*PAN3*
4275	87,0	55,3	1,57	0,031776	0,406	218344_s_at	REST corepressor 3	*RCOR3*
565	418	266	1,57	0,003091	0,299	202822_at	LIM domain containing preferred translocation partner in lipoma	*LPP*
5220	35,3	22,5	1,57	0,040360	0,423	227816_at	Netrin 1	*NTN1*
4090	24,7	15,8	1,57	0,030069	0,402	243704_at	G patch domain containing 2	*GPATCH2*
2161	41,2	26,2	1,57	0,014281	0,361	207565_s_at	Major histocompatibility complex, class I-related	*MR1*
1951	25,4	16,2	1,57	0,012736	0,355	239296_at	Zinc finger homeobox 1b	*ZFHX1B*
229	11,0	6,99	1,57	0,001058	0,250	238303_at	Oligosaccharyl transferase subunit STT3B	*STT3B*
1747	31,9	20,3	1,57	0,011154	0,348	206527_at	4-aminobutyrate aminotransferase	*ABAT*
2769	54,5	34,8	1,57	0,019219	0,379	238520_at	Transcriptional regulating factor 1	*TRERF1*
2344	31,9	20,3	1,57	0,015645	0,364	1556277_a_a	PAP associated domain containing 4	*PAPD4*
457	11,6	7,43	1,57	0,002445	0,288	240016_at	SUMO1/sentrin specific peptidase 6	*SENP6*
81	45,3	28,9	1,57	0,000306	0,201	222239_s_at	Integrator complex subunit 6	*INTS6*

Index	Mutated*	Normal*	FC	*P* value	FDR**	Probe set	Description	Gene symbol
3523	137	87,2	1,57	0,025286	0,392	226865_at	cDNA DKFZp564O0862	-
809	48,5	30,9	1,57	0,004615	0,311	228315_at	cDNA clone IMAGE:5261213	-
1594	97,5	62,2	1,57	0,009923	0,340	238706_at	PAP associated domain containing 4	*PAPD4*
781	68,0	43,5	1,57	0,004474	0,311	223412_at	Kelch repeat and BTB (POZ) domain containing 7	*KBTBD7*
1457	37,7	24,1	1,57	0,008909	0,334	1558105_a_a	Similar to LOC169932, clone IMAGE:4499203	-
247	28,3	18,1	1,57	0,001140	0,251	223465_at	Collagen, type IV, alpha 3 (Goodpasture antigen) binding protein	*COL4A3BP*
3772	21,4	13,7	1,56	0,027401	0,397	207417_s_at	Zinc finger protein 177	*ZNF177*
109	44,5	28,5	1,56	0,000439	0,220	219278_at	Mitogen-activated protein kinase kinase kinase 6	*MAP3K6*
2032	33,1	21,2	1,56	0,013238	0,355	230708_at	Prickle homolog 1 (Drosophila)	*PRICKLE1*
1049	1657	1060	1,56	0,006138	0,319	210986_s_at	tropomyosin 1 (alpha)	*TPM1*
5310	228	146	1,56	0,041427	0,426	211423_s_at	C-5 sterol desaturase	*SC5DL*
1604	242	155	1,56	0,009995	0,341	202555_s_at	Myosin, light chain kinase	*MYLK*
3552	8,49	5,44	1,56	0,025614	0,394	1568574_x_a	Secreted phosphoprotein 1	*SPP1*
4760	82,7	53,0	1,56	0,036079	0,414	235103_at	Mannosidase, alpha, class 2A, member 1	*MAN2A1*
1512	25,3	16,2	1,56	0,009313	0,337	215314_at	Ankyrin 3, node of Ranvier (ankyrin G)	*ANK3*
344	33,2	21,3	1,56	0,001763	0,278	203263_s_at	Cdc42 guanine nucleotide exchange factor (GEF) 9	*ARHGEF9*
3979	16,0	10,2	1,56	0,029089	0,400	237128_at	Hypothetical protein FLJ20184	*LOC54848*
2991	55,6	35,6	1,56	0,021037	0,385	209209_s_at	Fermitin family homolog 2 (Drosophila)	*FERMT2*
4185	629	403	1,56	0,030945	0,404	201311_s_at	SH3 domain binding glutamic acid-rich protein like	*SH3BGRL*
1788	118	75,6	1,56	0,011446	0,350	224933_s_at	Jumonji domain containing 1C	*JMJD1C*
2887	17,6	11,3	1,56	0,020249	0,383	1563209_a_a	MACRO domain containing 2	*MACROD2*
119	117	75,2	1,56	0,000531	0,240	218819_at	Integrator complex subunit 6	*INTS6*
5040	27,6	17,7	1,56	0,038849	0,420	228427_at	F-box protein 16	*FBXO16*
4673	392	251	1,56	0,035294	0,413	225927_at	Mitogen-activated protein kinase kinase kinase 1	*MAP3K1*
1567	20,8	13,3	1,56	0,009741	0,340	230892_at	Transcribed locus	-
675	235	151	1,56	0,003866	0,308	214352_s_at	v-Ki-ras2 Kirsten rat sarcoma viral oncogene homolog	*KRAS*
1790	25,9	16,6	1,56	0,011463	0,350	230424_at	Chromosome 5 open reading frame 13	*C5orf13*
334	398	256	1,56	0,001676	0,274	209360_s_at	Runt-related transcription factor 1 (aml1 oncogene)	*RUNX1*
316	18,1	11,6	1,56	0,001588	0,272	1559957_a_a	Hypothetical protein LOC642852	*LOC642852*
1981	132	84,8	1,56	0,012927	0,355	222798_at	Phosphotriesterase related	*PTER*
407	5,58	3,59	1,56	0,002145	0,286	1566772_at	Schwannomin interacting protein 1	*SCHIP1*
4875	76,6	49,2	1,56	0,037222	0,417	222513_s_at	Sorbin and SH3 domain containing 1	*SORBS1*
1386	12,0	7,72	1,55	0,008329	0,329	1556770_a_a	Leucine rich repeat containing 17	*LRRC17*
3030	362	233	1,55	0,021326	0,385	212958_x_at	Peptidylglycine alpha-amidating monooxygenase	*PAM*
1952	126	81,1	1,55	0,012748	0,355	202124_s_at	Trafficking protein, kinesin binding 2	*TRAK2*
209	333	214	1,55	0,000955	0,244	209226_s_at	Transportin 1	*TNPO1*
1337	46,7	30,1	1,55	0,008024	0,328	205076_s_at	Myotubularin related protein 11	*MTMR11*
422	124	80,2	1,55	0,002210	0,286	226259_at	Exocyst complex component 6	*EXOC6*
3454	930	599	1,55	0,024746	0,392	210987_x_at	tropomyosin 1 (alpha)	*TPM1*
1709	10,3	6,63	1,55	0,010940	0,348	244443_at	Chromodomain helicase DNA binding protein 2	*CHD2*
2558	86,6	55,8	1,55	0,017356	0,371	231862_at	chromobox homolog 5 (HP1 alpha homolog, Drosophila)	*CBX5*
4052	29,7	19,1	1,55	0,029708	0,401	241838_at	Transcribed locus	-
2518	32,5	20,9	1,55	0,016986	0,369	1566766_a_a	Metastasis associated in colon cancer 1	*MACC1*
2506	41,2	26,6	1,55	0,016850	0,367	228121_at	Transforming growth factor, beta 2	*TGFB2*
1047	23,8	15,3	1,55	0,006120	0,319	236953_s_at	NHL repeat containing 3	*NHLRC3*
1930	28,1	18,1	1,55	0,012581	0,355	214153_at	ELOVL family member 5, elongation of long chain fatty acids	*ELOVL5*
5288	1110	717	1,55	0,041144	0,425	221731_x_at	Versican	*VCAN*
2894	42,3	27,3	1,55	0,020332	0,383	210102_at	Loss of heterozygosity, 11, chromosomal region 2, gene A	*LOH11CR2A*
3108	73,5	47,4	1,55	0,021946	0,386	230229_at	Discs, large homolog 1 (Drosophila)	*DLG1*
23	23,5	15,2	1,55	0,000099	0,201	226688_at	Chromosome 3 open reading frame 23	*C3orf23*
4571	51,9	33,5	1,55	0,034563	0,412	204689_at	Hematopoietically expressed homeobox	*HHEX*
803	21,7	14,0	1,55	0,004579	0,311	208022_s_at	CDC14 cell division cycle 14 homolog B (S. cerevisiae)	*CDC14B*
1632	161	104	1,55	0,010284	0,344	209485_s_at	Oxysterol binding protein-like 1A	*OSBPL1A*
540	225	145	1,55	0,002897	0,293	201960_s_at	MYC binding protein 2	*MYCBP2*
140	117	76,0	1,55	0,000635	0,244	223466_x_at	Collagen, type IV, alpha 3 (Goodpasture antigen) binding protein	*COL4A3BP*
2595	71,9	46,5	1,55	0,017646	0,371	201367_s_at	Zinc finger protein 36, C3H type-like 2	*ZFP36L2*
159	25,0	16,2	1,55	0,000715	0,244	240436_at	Similar to FRAS1 related extracellular matrix protein 2	*LOC729697*

Index	Mutated*	Normal*	FC	*P* value	FDR**	Probe set	Description	Gene symbol
3258	21,7	14,1	1,54	0,023139	0,388	207029_at	KIT ligand	*KITLG*
550	212	137	1,54	0,002973	0,295	214430_at	Galactosidase, alpha	*GLA*
1371	76,0	49,3	1,54	0,008235	0,328	226550_at	Similar to LOC169932	*LOC169932*
474	213	138	1,54	0,002518	0,289	225269_s_at	RNA binding motif, single stranded interacting protein 1	*RBMS1*
1273	880	571	1,54	0,007578	0,325	202371_at	Transcription elongation factor A (SII)-like 4	*TCEAL4*
1374	600	390	1,54	0,008283	0,329	214722_at	Notch homolog 2 (Drosophila) N-terminal like	*NOTCH2NL*
994	119	77,0	1,54	0,005727	0,315	212263_at	Quaking homolog, KH domain RNA binding (mouse)	*QKI*
3347	108	70,1	1,54	0,023768	0,388	222757_s_at	Sterile alpha motif and leucine zipper containing kinase AZK	*ZAK*
3778	159	103	1,54	0,027465	0,397	208935_s_at	Lectin, galactoside-binding, soluble, 8 (galectin 8)	*LGALS8*
1004	225	146	1,54	0,005809	0,316	201959_s_at	MYC binding protein 2	*MYCBP2*
649	82,9	53,9	1,54	0,003689	0,308	223178_s_at	5'-nucleotidase domain containing 1	*NT5DC1*
3306	14,0	9,13	1,54	0,023513	0,388	214375_at	PTPRF interacting protein, binding protein 1 (liprin beta 1)	*PPFIBP1*
2416	302	196	1,54	0,016133	0,365	228487_s_at	RAS responsive element binding protein 1	*RREB1*
2193	34,8	22,6	1,54	0,014511	0,361	225759_x_at	Calmin (calponin-like, transmembrane)	*CLMN*
361	1022	665	1,54	0,001870	0,283	221829_s_at	Transportin 1	*TNPO1*
216	67,9	44,2	1,54	0,000967	0,244	221215_s_at	Receptor-interacting serine-threonine kinase 4	*RIPK4*
5979	65,0	42,3	1,54	0,048543	0,444	242110_at	Rho GTPase activating protein 5	*ARHGAP5*
2195	106	69,2	1,54	0,014516	0,361	242558_at	Catenin (cadherin-associated protein), beta 1, 88kDa	*CTNNB1*
238	170	111	1,53	0,001103	0,250	202304_at	Fibronectin type III domain containing 3A	*FNDC3A*
3486	23,2	15,1	1,53	0,025021	0,392	210172_at	Splicing factor 1	*SF1*
176	67,6	44,1	1,53	0,000804	0,244	224943_at	BTB (POZ) domain containing 7	*BTBD7*
4600	11,2	7,28	1,53	0,034786	0,412	232568_at	hypothetical protein MGC24103	*MGC24103*
4694	1136	741	1,53	0,035453	0,413	200648_s_at	Glutamate-ammonia ligase (glutamine synthetase)	*GLUL*
2121	103	67,5	1,53	0,013913	0,359	212526_at	Spastic paraplegia 20	*SPG20*
4073	253	165	1,53	0,029870	0,401	203753_at	Transcription factor 4	*TCF4*
519	89,5	58,4	1,53	0,002761	0,291	238430_x_at	Schlafen family member 5	*SLFN5*
127	212	139	1,53	0,000574	0,240	215464_s_at	Tax1 (human T-cell leukemia virus type I) binding protein 3	*TAX1BP3*
4526	33,4	21,8	1,53	0,034161	0,412	205525_at	Caldesmon 1	*CALD1*
2172	67,9	44,3	1,53	0,014360	0,361	1566342_at	Superoxide dismutase 2, mitochondrial	*SOD2*
1734	17,6	11,5	1,53	0,011085	0,348	242737_at	RAD51-like 1 (S. cerevisiae)	*RAD51L1*
5855	174	114	1,53	0,047341	0,442	204352_at	TNF receptor-associated factor 5	*TRAF5*
722	62,4	40,8	1,53	0,004137	0,308	235341_at	DnaJ (Hsp40) homolog, subfamily C, member 3	*DNAJC3*
1921	15,4	10,0	1,53	0,012516	0,355	233106_at	Chromosome 14 open reading frame 82	*C14orf82*
5150	68,1	44,5	1,53	0,039641	0,421	218775_s_at	WW and C2 domain containing 2	*WWC2*
3237	22,2	14,5	1,53	0,022975	0,388	238563_at	Spectrin SH3 domain binding protein 1	*SSH3BP1*
516	261	171	1,53	0,002753	0,291	212265_at	Quaking homolog, KH domain RNA binding (mouse)	*QKI*
4799	31,2	20,5	1,53	0,036413	0,415	205529_s_at	Runt-related transcription factor 1; translocated to, 1 (cyclin D-related)	*RUNX1T1*
1592	22,2	14,5	1,53	0,009902	0,340	210325_at	CD1a molecule	*CD1A*
2268	18,2	11,9	1,53	0,015078	0,363	207018_s_at	RAB27B, member RAS oncogene family	*RAB27B*
3292	414	272	1,52	0,023445	0,388	201160_s_at	Cold shock domain protein A	*CSDA*
1119	169	111	1,52	0,006535	0,319	222413_s_at	Myeloid/lymphoid or mixed-lineage leukemia 3	*MLL3*
2989	52,0	34,1	1,52	0,021015	0,384	214720_x_at	Septin 10	*SEPT10*
4480	39,6	26,0	1,52	0,033694	0,411	202504_at	Tripartite motif-containing 29	*TRIM29*
1922	44,9	29,5	1,52	0,012516	0,355	235457_at	Mastermind-like 2 (Drosophila)	*MAML2*
925	10,1	6,62	1,52	0,005329	0,313	1558101_at	Nuclear factor I/A	*NFIA*
3933	48,3	31,7	1,52	0,028740	0,399	1553764_a_a	Jub, ajuba homolog (Xenopus laevis)	*JUB*
332	124	81,2	1,52	0,001654	0,272	222810_s_at	RAS protein activator like 2	*RASAL2*
5466	8,91	5,86	1,52	0,043170	0,432	215028_at	Semaphorin 6A-1	*SEMA6A*
1221	42,6	28,0	1,52	0,007263	0,324	243908_at	Zinc finger protein 638	*ZNF638*
934	31,6	20,8	1,52	0,005358	0,313	204761_at	USP6 N-terminal like	*USP6NL*
6004	57,9	38,1	1,52	0,048789	0,444	235775_at	Transmembrane and tetratricopeptide repeat containing 2	*TMTC2*
1258	174	115	1,52	0,007490	0,325	209488_s_at	RNA binding protein with multiple splicing	*RBPMS*
1200	38,0	25,0	1,52	0,007086	0,323	206734_at	Jerky homolog-like (mouse)	*JRKL*
1243	84,7	55,8	1,52	0,007383	0,324	207357_s_at	N-acetylgalactosaminyltransferase 10	*GALNT10*
2692	131	86,1	1,52	0,018450	0,375	203215_s_at	Myosin VI	*MYO6*
3802	18,7	12,3	1,52	0,027689	0,398	219683_at	Frizzled homolog 3 (Drosophila)	*FZD3*
3162	1052	694	1,52	0,022438	0,387	201288_at	Rho GDP dissociation inhibitor (GDI) beta	*ARHGDIB*

Index	Mutated*	Normal*	FC	*P* value	FDR**	Probe set	Description	Gene symbol
2035	269	177	1,52	0,013254	0,355	222605_at	REST corepressor 3	*RCOR3*
3178	105	69,4	1,51	0,022544	0,387	201656_at	Integrin, alpha 6	*ITGA6*
3078	161	107	1,51	0,021702	0,385	203143_s_at	KIAA0040 protein	*KIAA0040*
202	11,0	7,30	1,51	0,000929	0,244	220302_at	Male germ cell-associated kinase	*MAK*
522	1045	691	1,51	0,002786	0,291	223193_x_at	Family with sequence similarity 162, member A	*FAM162A*
3186	208	137	1,51	0,022596	0,387	224793_s_at	Transforming growth factor, beta receptor I	*TGFBR1*
3441	15,5	10,2	1,51	0,024630	0,391	233364_s_at	Hypothetical protein LOC399959	*LOC399959*
6	158	105	1,51	0,000013	0,099	212402_at	Zinc finger CCCH-type containing 13	*ZC3H13*
2501	14,2	9,38	1,51	0,016838	0,367	208859_s_at	Alpha thalassemia/mental retardation syndrome X-linked	*ATRX*
1801	11,2	7,42	1,51	0,011596	0,351	215164_at	Transcription factor 4	*TCF4*
1330	132	87,7	1,51	0,008001	0,328	217550_at	Activating transcription factor 6	*ATF6*
2080	7,30	4,84	1,51	0,013580	0,356	239301_at	RAS p21 protein activator (GTPase activating protein) 1	*RASA1*
46	66,0	43,7	1,51	0,000186	0,201	235687_at	Zinc finger protein 626	*ZNF626*
263	16,8	11,1	1,51	0,001259	0,260	210255_at	RAD51-like 1 (S. cerevisiae)	*RAD51L1*
1832	22,7	15,1	1,51	0,011798	0,351	221556_at	CDC14 cell division cycle 14 homolog B (S. cerevisiae)	*CDC14B*
2982	59,2	39,3	1,51	0,020965	0,384	238884_at	Catenin (cadherin-associated protein), delta 1	*CTNND1*
1404	11,6	7,70	1,51	0,008477	0,330	1552269_at	Spermatogenesis associated 17	*SPATA17*
6027	280	185	1,51	0,049027	0,445	202887_s_at	DNA-damage-inducible transcript 4	*DDIT4*
1739	140	93,0	1,51	0,011100	0,348	213015_at	Bobby sox homolog (Drosophila)	*BBX*
411	1115	739	1,51	0,002170	0,286	201220_x_at	C-terminal binding protein 2	*CTBP2*
5494	31,2	20,7	1,51	0,043485	0,433	233824_at	cDNA FLJ21428 fis, clone COL04203	-
1026	25,3	16,8	1,51	0,005942	0,316	243709_at	Solute carrier family 38, member 9	*SLC38A9*
95	23,9	15,8	1,51	0,000362	0,208	206636_at	RAS p21 protein activator 2	*RASA2*
2629	8,57	5,69	1,51	0,017897	0,372	213456_at	Sclerostin domain containing 1	*SOSTDC1*
445	26,2	17,4	1,51	0,002370	0,288	206928_at	Zinc finger protein 124	*ZNF124*
5403	138	91,7	1,51	0,042400	0,429	243768_at	SUMO1/sentrin specific peptidase 6	*SENP6*
4363	214	142	1,51	0,032453	0,407	227034_at	Ankyrin repeat domain 57	*ANKRD57*
5379	37,4	24,8	1,51	0,042181	0,429	224851_at	Cyclin-dependent kinase 6	*CDK6*
5690	40,9	27,2	1,50	0,045512	0,437	204624_at	ATPase, Cu++ transporting, beta polypeptide	*ATP7B*
1938	273	182	1,50	0,012623	0,355	235308_at	Zinc finger and BTB domain containing 20	*ZBTB20*
670	838	557	1,50	0,003849	0,308	224345_x_at	Family with sequence similarity 162, member A	*FAM162A*
244	1011	672	1,50	0,001123	0,251	209154_at	Tax1 (human T-cell leukemia virus type I) binding protein 3	*TAX1BP3*
210	44,7	29,7	1,50	0,000956	0,244	230192_at	Tripartite motif-containing 13	*TRIM13*
2728	806	536	1,50	0,018778	0,376	221896_s_at	HIG1 domain family, member 1A	*HIGD1A*
458	23,5	15,7	1,50	0,002449	0,288	239247_at	Hypothetical protein LOC401577	*LOC401577*
1131	86,2	57,4	1,50	0,006605	0,319	210223_s_at	Major histocompatibility complex, class I-related	*MR1*
730	113	75,3	1,50	0,004173	0,308	213528_at	Chromosome 1 open reading frame 156	*C1orf156*
76	484	323	1,50	0,000291	0,201	225132_at	F-box and leucine-rich repeat protein 3	*FBXL3*
2908	56,0	37,3	1,50	0,020442	0,383	1566785_x_a	N-ethylmaleimide-sensitive factor	*NSF*
1210	224	149	1,50	0,007173	0,324	224937_at	Prostaglandin F2 receptor negative regulator	*PTGFRN*
311	45,0	30,0	1,50	0,001536	0,270	1558733_at	Zinc finger and BTB domain containing 38	*ZBTB38*
2811	99,2	66,2	1,50	0,019599	0,381	227276_at	Plexin domain containing 2	*PLXDC2*
79	34,0	22,7	1,50	0,000297	0,201	210943_s_at	Lysosomal trafficking regulator	*LYST*
823	236	158	1,50	0,004700	0,312	209487_at	RNA binding protein with multiple splicing	*RBPMS*
859	32,8	21,9	1,50	0,004964	0,313	219455_at	Chromosome 7 open reading frame 63	*C7orf63*
4623	15,0	9,99	1,50	0,034877	0,412	239487_at	Family with sequence similarity 98, member A	*FAM98A*
790	55,1	36,8	1,50	0,004521	0,311	228825_at	prostaglandin reductase 1	*PTGR1*
5066	103	68,9	1,50	0,038994	0,420	242467_at	Casein kinase 1, alpha 1	*CSNK1A1*
3812	187	125	1,50	0,027781	0,398	200965_s_at	Actin binding LIM protein 1	*ABLIM1*
5281	31,4	21,0	1,50	0,041086	0,425	1554195_a_a	Chromosome 5 open reading frame 46	*C5orf46*
2063	147	98,4	1,50	0,013447	0,356	204633_s_at	Ribosomal protein S6 kinase, 90kDa, polypeptide 5	*RPS6KA5*
3438	16,0	10,7	1,49	0,024617	0,391	240861_at	-	-
5710	7,42	4,96	1,49	0,045721	0,438	238877_at	Eyes absent homolog 4 (Drosophila)	*EYA4*
1712	96,6	64,6	1,49	0,010957	0,348	204072_s_at	Furry homolog (Drosophila)	*FRY*
416	103	69,2	1,49	0,002189	0,286	225623_at	KIAA1737 protein	*KIAA1737*
318	291	195	1,49	0,001592	0,272	208908_s_at	Calpastatin	*CAST*
2103	31,4	21,0	1,49	0,013784	0,358	243851_at	RAB3 GTPase activating protein subunit 2 (non-catalytic)	*RAB3GAP2*

Index	Mutated*	Normal*	FC	*P* value	FDR**	Probe set	Description	Gene symbol
5197	45,0	30,2	1,49	0,040056	0,421	1555370_a_a	Calmodulin binding transcription activator 1	*CAMTA1*
4740	153	103	1,49	0,035879	0,414	218967_s_at	Phosphotriesterase related	*PTER*
2755	54,2	36,3	1,49	0,019071	0,378	1553186_x_a	RAS and EF-hand domain containing	*RASEF*
981	136	91,2	1,49	0,005689	0,315	223177_at	5'-nucleotidase domain containing 1	*NT5DC1*
272	77,2	51,8	1,49	0,001298	0,261	203128_at	Serine palmitoyltransferase, long chain base subunit 2	*SPTLC2*
3929	134	89,8	1,49	0,028733	0,399	209750_at	Nuclear receptor subfamily 1, group D, member 2	*NR1D2*
1158	29,2	19,6	1,49	0,006810	0,321	229603_at	Bardet-Biedl syndrome 12	*BBS12*
21	484	325	1,49	0,000088	0,201	223287_s_at	Forkhead box P1	*FOXP1*
1527	9,65	6,48	1,49	0,009430	0,337	244860_at	SIK family kinase 3	*SIK3*
2315	29,3	19,7	1,49	0,015371	0,363	234604_at	cDNA FLJ21228 fis, clone COL00739	-
5476	70,8	47,6	1,49	0,043292	0,432	239082_at	cDNA clone IMAGE:5311370	-
3100	51,0	34,3	1,49	0,021899	0,386	219033_at	Poly (ADP-ribose) polymerase family, member 8	*PARP8*
5516	28,8	19,4	1,49	0,043749	0,433	210653_s_at	Branched chain keto acid dehydrogenase E1, beta polypeptide	*BCKDHB*
2096	23,7	16,0	1,49	0,013733	0,358	226984_at	FYVE, RhoGEF and PH domain containing 5	*FGD5*
532	102	68,4	1,49	0,002845	0,292	226977_at	Similar to bovine IgA regulatory protein	*LOC492311*
5792	405	272	1,49	0,046712	0,441	222258_s_at	SH3-domain binding protein 4	*SH3BP4*
801	73,9	49,7	1,49	0,004571	0,311	217813_s_at	Spindlin 1	*SPIN1*
5075	99,6	67,0	1,49	0,039043	0,420	203706_s_at	Frizzled homolog 7 (Drosophila)	*FZD7*
3434	547	368	1,49	0,024581	0,391	200907_s_at	Palladin, cytoskeletal associated protein	*PALLD*
4098	97,4	65,6	1,48	0,030117	0,402	226246_at	Potassium channel tetramerisation domain containing 1	*KCTD1*
425	159	107	1,48	0,002236	0,288	214041_x_at	Ribosomal protein L37a	*RPL37A*
2494	137	92,5	1,48	0,016801	0,367	203319_s_at	Zinc finger protein 148	*ZNF148*
4335	81,9	55,2	1,48	0,032270	0,407	207604_s_at	Solute carrier family 4, sodium bicarbonate cotransporter, member 7	*SLC4A7*
1573	34,4	23,2	1,48	0,009768	0,340	206117_at	Tropomyosin 1 (alpha)	*TPM1*
2179	18,5	12,5	1,48	0,014410	0,361	219885_at	schlafen family member 12	*SLFN12*
5482	125	84,5	1,48	0,043380	0,433	203266_s_at	Mitogen-activated protein kinase kinase 4	*MAP2K4*
1036	77,9	52,5	1,48	0,006019	0,318	226722_at	Family with sequence similarity 20, member C	*FAM20C*
2849	448	302	1,48	0,019937	0,383	201324_at	Epithelial membrane protein 1	*EMP1*
4784	10,7	7,20	1,48	0,036271	0,414	210282_at	Zinc finger, MYM-type 2	*ZMYM2*
2269	61,9	41,7	1,48	0,015078	0,363	219390_at	FK506 binding protein 14, 22 kDa	*FKBP14*
1466	135	91,4	1,48	0,008970	0,334	230669_at	RAS p21 protein activator 2	*RASA2*
1932	480	324	1,48	0,012601	0,355	221943_x_at	Ribosomal protein L38	*RPL38*
3784	159	107	1,48	0,027562	0,398	226582_at	Hypothetical gene supported by BC009385	*LOC400043*
3905	1286	869	1,48	0,028521	0,399	200872_at	S100 calcium binding protein A10	*S100A10*
643	271	183	1,48	0,003668	0,308	212698_s_at	Septin 10	*SEPT10*
250	25,5	17,2	1,48	0,001148	0,251	206587_at	Chaperonin containing TCP1, subunit 6B (zeta 2)	*CCT6B*
4710	40,3	27,2	1,48	0,035639	0,413	221826_at	Angel homolog 2 (Drosophila)	*ANGEL2*
4637	48,9	33,1	1,48	0,034974	0,412	201996_s_at	Spen homolog, transcriptional regulator (Drosophila)	*SPEN*
6085	330	223	1,48	0,049690	0,446	225064_at	Rabaptin, RAB GTPase binding effector protein 1	*RABEP1*
1241	286	193	1,48	0,007365	0,324	215127_s_at	RNA binding motif, single stranded interacting protein 1	*RBMS1*
2522	77,8	52,7	1,48	0,017014	0,369	227701_at	Chromosome 10 open reading frame 118	*C10orf118*
3120	59,2	40,0	1,48	0,022086	0,387	228852_at	Endosulfine alpha	*ENSA*
1746	183	124	1,48	0,011149	0,348	208663_s_at	Tetratricopeptide repeat domain 3	*TTC3*
4036	9,30	6,29	1,48	0,029576	0,401	211124_s_at	KIT ligand	*KITLG*
5724	50,6	34,3	1,48	0,045873	0,438	230337_at	SON of sevenless homolog 1 (Drosophila)	*SOS1*
4448	27,8	18,8	1,48	0,033401	0,411	235408_x_at	Zinc finger protein 117	*ZNF117*
2653	11,4	7,69	1,48	0,018089	0,373	241789_at	RNA binding motif, single stranded interacting protein	*RBMS3*
793	15,2	10,3	1,48	0,004532	0,311	244023_at	Spleen tyrosine kinase	*SYK*
471	82,7	56,0	1,48	0,002509	0,289	222632_s_at	Leucine zipper transcription factor-like 1	*LZTFL1*
3809	63,1	42,7	1,48	0,027752	0,398	223134_at	Bobby sox homolog (Drosophila)	*BBX*
2560	39,3	26,6	1,48	0,017359	0,371	219204_s_at	serine racemase	*SRR*
3752	119	81,0	1,48	0,027281	0,397	211783_s_at	Metastasis associated 1	*MTA1*
1865	531	360	1,48	0,012051	0,353	213229_at	Dicer1, Dcr-1 homolog (Drosophila)	*DICER1*
1141	59,4	40,3	1,47	0,006692	0,320	238444_at	Zinc finger protein 618	*ZNF618*
2250	5,69	3,86	1,47	0,014951	0,363	1554557_at	ATPase, Class VI, type 11B	*ATP11B*
4777	280	190	1,47	0,036218	0,414	202133_at	WW domain containing transcription regulator 1	*WWTR1*
4107	31,0	21,0	1,47	0,030190	0,402	219501_at	Ecto-NOX disulfide-thiol exchanger 1	*ENOX1*

Index	Mutated*	Normal*	FC	*P* value	FDR**	Probe set	Description	Gene symbol
1736	40,8	27,7	1,47	0,011097	0,348	228772_at	Histamine N-methyltransferase	*HNMT*
5917	43,5	29,6	1,47	0,047951	0,443	227415_at	Hypothetical protein LOC283508	*LOC283508*
2251	71,0	48,2	1,47	0,014960	0,363	201151_s_at	Muscleblind-like (Drosophila)	*MBNL1*
2871	113	76,8	1,47	0,020167	0,383	211110_s_at	Androgen receptor	*AR*
1560	200	136	1,47	0,009649	0,338	218595_s_at	HEAT repeat containing 1	*HEATR1*
2299	12,3	8,38	1,47	0,015275	0,363	207017_at	RAB27B, member RAS oncogene family	*RAB27B*
2975	114	77,4	1,47	0,020917	0,384	218721_s_at	Chromosome 1 open reading frame 27	*C1orf27*
3546	269	183	1,47	0,025502	0,393	218084_x_at	FXYD domain containing ion transport regulator 5	*FXYD5*
701	45,0	30,6	1,47	0,004023	0,308	1555913_at	Gon-4-like (C. elegans)	*GON4L*
349	21,8	14,9	1,47	0,001778	0,278	238044_at	Tripartite motif-containing 8	*TRIM8*
3366	7,10	4,83	1,47	0,023903	0,388	209866_s_at	Latrophilin 3	*LPHN3*
4591	19,5	13,3	1,47	0,034720	0,412	238575_at	Oxysterol binding protein-like 6	*OSBPL6*
1358	329	224	1,47	0,008193	0,328	224811_at	cDNA FLJ30652 fis, clone DFNES2000011	-
1425	27,2	18,5	1,47	0,008633	0,331	232522_at	Transcription factor 7-like 2 (T-cell specific, HMG-box)	*TCF7L2*
3084	34,7	23,6	1,47	0,021728	0,385	227785_at	Serologically defined colon cancer antigen 8	*SDCCAG8*
2156	24,9	17,0	1,47	0,014207	0,360	240145_at	Transcribed locus	-
2166	85,7	58,4	1,47	0,014337	0,361	1553185_at	RAS and EF-hand domain containing	*RASEF*
3227	110	74,7	1,47	0,022857	0,387	224829_at	Cytoplasmic polyadenylation element binding protein 4	*CPEB4*
3272	181	124	1,47	0,023277	0,388	224252_s_at	FXYD domain containing ion transport regulator 5	*FXYD5*
4202	90,2	61,5	1,47	0,031079	0,404	214620_x_at	Peptidylglycine alpha-amidating monooxygenase	*PAM*
137	71,4	48,7	1,47	0,000619	0,244	209648_x_at	Suppressor of cytokine signaling 5	*SOCS5*
4500	90,0	61,4	1,47	0,033844	0,411	206848_at	Homeobox A7	*HOXA7*
1309	158	108	1,47	0,007815	0,325	206453_s_at	NDRG family member 2	*NDRG2*
4606	264	180	1,47	0,034808	0,412	208936_x_at	Lectin, galactoside-binding, soluble, 8 (galectin 8)	*LGALS8*
4755	463	316	1,46	0,036026	0,414	224694_at	Anthrax toxin receptor 1	*ANTXR1*
1357	549	375	1,46	0,008184	0,328	221478_at	BCL2/adenovirus E1B 19kDa interacting protein 3-like	*BNIP3L*
1857	65,1	44,5	1,46	0,011965	0,352	1555480_a_a	Filamin binding LIM protein 1	*FBLIM1*
599	136	93,0	1,46	0,003295	0,301	207956_x_at	PDS5, regulator of cohesion maintenance, homolog B (S. cerevisiae)	*PDS5B*
1154	55,3	37,8	1,46	0,006778	0,321	231002_s_at	Rabaptin, RAB GTPase binding effector protein 1	*RABEP1*
4334	136	93,0	1,46	0,032264	0,407	224726_at	Mindbomb homolog 1 (Drosophila)	*MIB1*
3027	59,4	40,6	1,46	0,021305	0,385	216202_s_at	Serine palmitoyltransferase, long chain base subunit 2	*SPTLC2*
928	18,4	12,6	1,46	0,005332	0,313	214052_x_at	BAT2 domain containing 1	*BAT2D1*
2334	9,58	6,55	1,46	0,015569	0,364	236558_at	Muscleblind-like (Drosophila)	*MBNL1*
464	322	220	1,46	0,002459	0,288	207657_x_at	Transportin 1	*TNPO1*
530	808	553	1,46	0,002835	0,292	229353_s_at	Nuclear casein kinase and cyclin-dependent kinase substrate 1	*NUCKS1*
2927	18,5	12,7	1,46	0,020511	0,383	1552627_a_a	Rho GTPase activating protein 5	*ARHGAP5*
1971	169	115	1,46	0,012883	0,355	202421_at	Immunoglobulin superfamily, member 3	*IGSF3*
1454	13,4	9,19	1,46	0,008893	0,334	219523_s_at	Odz, odd Oz/ten-m homolog 3 (Drosophila)	*ODZ3*
452	358	245	1,46	0,002417	0,288	207467_x_at	Calpastatin	*CAST*
1169	15,4	10,5	1,46	0,006876	0,321	236446_at	Transcribed locus	-
1419	25,4	17,4	1,46	0,008598	0,331	222237_s_at	Zinc finger protein 228	*ZNF228*
810	297	204	1,46	0,004618	0,311	222619_at	Zinc finger protein 281	*ZNF281*
1345	350	240	1,46	0,008066	0,328	221479_s_at	BCL2/adenovirus E1B 19kDa interacting protein 3-like	*BNIP3L*
4319	76,6	52,5	1,46	0,032160	0,407	1562836_at	DEAD (Asp-Glu-Ala-Asp) box polypeptide 6	*DDX6*
5787	147	101	1,46	0,046602	0,440	228067_at	Chromosome 2 open reading frame 55	*C2orf55*
3941	297	204	1,46	0,028773	0,399	208933_s_at	Lectin, galactoside-binding, soluble, 8 (galectin 8)	*LGALS8*
2691	197	135	1,46	0,018447	0,375	228545_at	Zinc finger protein 148	*ZNF148*
4372	94,4	64,8	1,46	0,032522	0,407	230085_at	Pyruvate dehydrogenase kinase, isozyme 3	*PDK3*
850	9,70	6,66	1,46	0,004893	0,313	236862_at	Golgi associated PDZ and coiled-coil motif containing	*GOPC*
2706	48,7	33,5	1,46	0,018554	0,375	1556373_a_a	Family with sequence similarity 185, member A	*FAM185A*
4563	14,5	9,96	1,46	0,034487	0,412	1557432_at	RAS protein activator like 2	*RASAL2*
883	453	311	1,45	0,005109	0,313	204517_at	Peptidylprolyl isomerase C (cyclophilin C)	*PPIC*
2126	24,2	16,7	1,45	0,013994	0,359	204964_s_at	Sarcospan (Kras oncogene-associated gene)	*SSPN*
942	40,8	28,1	1,45	0,005401	0,313	234912_at	Hypothetical protein LOC651964	*LOC651964*
1393	66,2	45,6	1,45	0,008424	0,330	219542_at	NIMA (never in mitosis gene a)- related kinase 11	*NEK11*
3112	180	124	1,45	0,021978	0,386	202379_s_at	Natural killer-tumor recognition sequence	*NKTR*
3412	1619	1115	1,45	0,024339	0,390	208788_at	ELOVL family member 5, elongation of long chain fatty acids	*ELOVL5*

Index	Mutated*	Normal*	FC	*P* value	FDR**	Probe set	Description	Gene symbol
3279	44,8	30,9	1,45	0,023353	0,388	204255_s_at	Vitamin D (1,25- dihydroxyvitamin D3) receptor	*VDR*
3857	11,4	7,87	1,45	0,028161	0,399	237733_at	KIAA0564 protein	*KIAA0564*
1925	10,9	7,52	1,45	0,012527	0,355	243582_at	SH3 domain containing ring finger 2	*SH3RF2*
5230	386	266	1,45	0,040466	0,423	214433_s_at	Selenium binding protein 1	*SELENBP1*
5807	8,43	5,81	1,45	0,046861	0,441	232541_at	Avian erythroblastic leukemia viral (v-erb-b) oncogene homolog	*EGFR*
3622	17,9	12,4	1,45	0,026148	0,395	215248_at	Growth factor receptor-bound protein 10	*GRB10*
573	696	480	1,45	0,003149	0,300	201218_at	C-terminal binding protein 2	*CTBP2*
303	129	88,9	1,45	0,001465	0,263	210596_at	Magnesium transporter 1	*MAGT1*
1177	156	108	1,45	0,006912	0,321	225295_at	Solute carrier family 39 (zinc transporter), member 10	*SLC39A10*
4695	55,5	38,3	1,45	0,035459	0,413	225178_at	Tetratricopeptide repeat domain 14	*TTC14*
2714	1094	755	1,45	0,018626	0,375	217845_x_at	HIG1 domain family, member 1A	*HIGD1A*
2454	36,6	25,3	1,45	0,016453	0,366	216682_s_at	Family with sequence similarity 48, member A	*FAM48A*
3126	92,1	63,6	1,45	0,022169	0,387	207233_s_at	Microphthalmia-associated transcription factor	*MITF*
5193	9,78	6,75	1,45	0,040022	0,421	226210_s_at	Maternally expressed 3	*MEG3*
174	5,84	4,03	1,45	0,000800	0,244	237951_at	Zinc finger protein 2 homlog (mouse)	*ZFP2*
4005	14,7	10,2	1,45	0,029314	0,400	1566442_at	Chromosome 1 open reading frame 21	*C1orf21*
1389	70,3	48,5	1,45	0,008388	0,330	214056_at	Myeloid cell leukemia sequence 1 (BCL2-related)	*MCL1*
6077	57,6	39,8	1,45	0,049587	0,446	228806_at	RAR-related orphan receptor C	*RORC*
4958	107	74,1	1,45	0,038042	0,419	226245_at	Potassium channel tetramerisation domain containing 1	*KCTD1*
3313	98,6	68,2	1,45	0,023552	0,388	213593_s_at	Transformer-2 alpha	*TRA2A*
2760	309	213	1,45	0,019155	0,379	211202_s_at	Jumonji, AT rich interactive domain 1B	*JARID1B*
4380	11,8	8,16	1,45	0,032570	0,407	209792_s_at	Kallikrein-related peptidase 10	*KLK10*
312	10,6	7,35	1,45	0,001564	0,272	214422_at	RAD23 homolog B (S. cerevisiae)	*RAD23B*
3023	71,5	49,5	1,44	0,021277	0,385	213956_at	Centrosomal protein 350kDa	*CEP350*
4094	263	182	1,44	0,030088	0,402	201616_s_at	Caldesmon 1	*CALD1*
2028	24,1	16,7	1,44	0,013220	0,355	208499_s_at	DnaJ (Hsp40) homolog, subfamily C, member 3	*DNAJC3*
131	52,4	36,3	1,44	0,000586	0,240	218849_s_at	Protein phosphatase 1, regulatory (inhibitor) subunit 13 like	*PPP1R13L*
1809	25,5	17,7	1,44	0,011666	0,351	232776_at	PDZ domain containing ring finger 3	*PDZRN3*
3596	41,8	28,9	1,44	0,025928	0,394	232333_at	Mastermind-like 2 (Drosophila)	*MAML2*
2815	122	84,6	1,44	0,019632	0,381	202321_at	Geranylgeranyl diphosphate synthase 1	*GGPS1*
1585	101	69,8	1,44	0,009867	0,340	202514_at	Discs, large homolog 1 (Drosophila)	*DLG1*
3131	77,0	53,4	1,44	0,022212	0,387	225968_at	Prickle homolog 2 (Drosophila)	*PRICKLE2*
4388	288	200	1,44	0,032699	0,407	201549_x_at	Jumonji, AT rich interactive domain 1B	*JARID1B*
6056	251	174	1,44	0,049403	0,446	226538_at	Mannosidase, alpha, class 2A, member 1	*MAN2A1*
551	109	75,5	1,44	0,002974	0,295	203127_s_at	Serine palmitoyltransferase, long chain base subunit 2	*SPTLC2*
3561	12,7	8,84	1,44	0,025700	0,394	239784_at	SET and MYND domain containing 3	*SMYD3*
1656	325	226	1,44	0,010451	0,345	221816_s_at	PHD finger protein 11	*PHF11*
248	157	109	1,44	0,001141	0,251	225192_at	Chromosome 10 open reading frame 46	*C10orf46*
3394	55,6	38,6	1,44	0,024189	0,390	228173_at	GNAS complex locus	*GNAS*
1556	57,8	40,1	1,44	0,009606	0,337	222679_s_at	DCUN1 domain-containing protein 1	*DCUN1D1*
2832	86,8	60,3	1,44	0,019764	0,381	223380_s_at	LATS, large tumor suppressor, homolog 2 (Drosophila)	*LATS2*
158	346	241	1,44	0,000714	0,244	201152_s_at	Muscleblind-like (Drosophila)	*MBNL1*
2929	69,2	48,1	1,44	0,020535	0,383	222850_s_at	DnaJ (Hsp40) homolog, subfamily B, member 14	*DNAJB14*
2475	103	71,2	1,44	0,016666	0,367	204345_at	Collagen, type XVI, alpha 1	*COL16A1*
3913	48,2	33,5	1,44	0,028564	0,399	229689_s_at	Discs, large homolog 5 (Drosophila)	*DLG5*
6064	35,0	24,3	1,44	0,049456	0,446	235000_at	cDNA FLJ30652 fis, clone DFNES2000011	-
208	57,8	40,2	1,44	0,000955	0,244	214001_x_at	Family with sequence similarity 110, member A	*FAM110A*
3939	187	130	1,44	0,028764	0,399	212387_at	Transcription factor 4	*TCF4*
980	6,13	4,27	1,44	0,005688	0,315	242664_at	-	-
217	754	525	1,44	0,000970	0,244	224596_at	Solute carrier family 44, member 1	*SLC44A1*
4053	10,6	7,37	1,44	0,029723	0,401	243140_at	Actin, alpha 2, smooth muscle, aorta	*ACTA2*
2311	208	145	1,44	0,015361	0,363	227322_s_at	BRCA2 and CDKN1A interacting protein	*BCCIP*
1721	76,0	52,9	1,44	0,011024	0,348	225988_at	Hect domain and RLD 4	*HERC4*
4899	10,5	7,28	1,44	0,037488	0,418	1563022_at	Coiled-coil domain containing 160	*CCDC160*
5926	187	130	1,44	0,048015	0,443	208934_s_at	Lectin, galactoside-binding, soluble, 8 (galectin 8)	*LGALS8*
3044	47,5	33,1	1,44	0,021431	0,385	1565639_a_a	Peripheral myelin protein 22	*PMP22*
2920	53,5	37,2	1,44	0,020492	0,383	212634_at	KIAA0776 protein	*KIAA0776*

Index	Mutated*	Normal*	FC	*P* value	FDR**	Probe set	Description	Gene symbol
84	109	75,7	1,44	0,000313	0,201	208127_s_at	Suppressor of cytokine signaling 5	*SOCS5*
726	5,63	3,92	1,44	0,004148	0,308	1555573_at	Chromosome 10 open reading frame 93	*C10orf93*
963	227	158	1,43	0,005572	0,315	218501_at	Rho guanine nucleotide exchange factor (GEF) 3	*ARHGEF3*
1634	7,77	5,42	1,43	0,010310	0,344	240110_at	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 2 (mitochondrial)	*HMGCS2*
699	146	102	1,43	0,004009	0,308	222424_s_at	Nuclear casein kinase and cyclin-dependent kinase substrate 1	*NUCKS1*
1812	70,7	49,3	1,43	0,011684	0,351	215281_x_at	Pogo transposable element with ZNF domain	*POGZ*
4311	23,9	16,7	1,43	0,032096	0,407	242144_at	PAP associated domain containing 4	*PAPD4*
440	7,19	5,01	1,43	0,002338	0,288	231247_s_at	Hypothetical protein LOC730257	*LOC730257*
2016	523	364	1,43	0,013150	0,355	212586_at	Calpastatin	*CAST*
5620	19,3	13,5	1,43	0,044865	0,436	235121_at	Zinc finger protein 542	*ZNF542*
3522	71,0	49,5	1,43	0,025277	0,392	227931_at	INO80 complex subunit D	*INO80D*
5642	213	149	1,43	0,045018	0,436	201694_s_at	Early growth response 1	*EGR1*
3223	30,0	20,9	1,43	0,022835	0,387	1569353_at	CP110 protein	*CP110*
1196	133	92,8	1,43	0,007063	0,323	207266_x_at	RNA binding motif, single stranded interacting protein 1	*RBMS1*
2186	22,3	15,6	1,43	0,014484	0,361	210281_s_at	Zinc finger, MYM-type 2	*ZMYM2*
3386	1537	1073	1,43	0,024121	0,389	201312_s_at	SH3 domain binding glutamic acid-rich protein like	*SH3BGRL*
77	66,7	46,5	1,43	0,000292	0,201	212746_s_at	Centrosomal protein 170kDa	*CEP170*
4892	169	118	1,43	0,037385	0,418	223681_s_at	InaD-like (Drosophila)	*INADL*
2394	287	200	1,43	0,015979	0,365	206555_s_at	THUMP domain containing 1	*THUMPD1*
5374	13,4	9,33	1,43	0,042164	0,429	205559_s_at	Proprotein convertase subtilisin/kexin type 5	*PCSK5*
1725	145	101	1,43	0,011045	0,348	218149_s_at	Zinc finger protein 395	*ZNF395*
3225	15,0	10,5	1,43	0,022842	0,387	1565566_a_a	Syntaxin 7	*STX7*
1446	156	109	1,43	0,008790	0,332	201917_s_at	Solute carrier family 25, member 36	*SLC25A36*
2077	50,8	35,5	1,43	0,013569	0,356	220296_at	N-acetylgalactosaminyltransferase 10	*GALNT10*
397	482	337	1,43	0,002086	0,285	211967_at	Transmembrane protein 123	*TMEM123*
1803	179	125	1,43	0,011612	0,351	224889_at	Forkhead box O3	*FOXO3*
4435	116	81,2	1,43	0,033215	0,409	227561_at	Discoidin domain receptor family, member 2	*DDR2*
419	297	207	1,43	0,002195	0,286	201846_s_at	RING1 and YY1 binding protein	*RYBP*
286	449	314	1,43	0,001399	0,263	225010_at	Coiled-coil domain containing 6	*CCDC6*
3402	79,1	55,3	1,43	0,024278	0,390	226876_at	Family with sequence similarity 101, member B	*FAM101B*
5495	14,3	10,0	1,43	0,043490	0,433	205006_s_at	N-myristoyltransferase 2	*NMT2*
3530	37,5	26,3	1,43	0,025361	0,393	232994_s_at	Rho-guanine nucleotide exchange factor	*RGNEF*
873	250	175	1,43	0,005045	0,313	202184_s_at	Nucleoporin 133kDa	*NUP133*
855	20,8	14,6	1,43	0,004930	0,313	222565_s_at	Protein kinase D3	*PRKD3*
5158	87,2	61,0	1,43	0,039715	0,421	226899_at	Unc-5 homolog B (C. elegans)	*UNC5B*
2116	13,9	9,70	1,43	0,013875	0,359	236417_at	cDNA clone YI40G07	*MFN1*
2502	46,6	32,6	1,43	0,016840	0,367	214395_x_at	Eukaryotic translation elongation factor 1 delta	*EEF1D*
2688	87,6	61,3	1,43	0,018424	0,375	1568678_s_a	FGFR1 oncogene partner	*FGFR1OP*
5285	510	357	1,43	0,041112	0,425	209684_at	RAS and RAB interactor 2	*RIN2*
1903	171	120	1,43	0,012376	0,355	204290_s_at	Aldehyde dehydrogenase 6 family, member A1	*ALDH6A1*
4282	14,6	10,2	1,43	0,031816	0,406	233607_at	Bicaudal C homolog 1 (Drosophila)	*BICC1*
5555	13,4	9,37	1,43	0,044219	0,435	236322_at	Ring finger protein 145	*RNF145*
5073	338	237	1,43	0,039041	0,420	212492_s_at	Jumonji domain containing 2B	*JMJD2B*
1962	112	78,5	1,43	0,012819	0,355	201219_at	C-terminal binding protein 2	*CTBP2*
1033	942	661	1,43	0,006002	0,318	220942_x_at	Family with sequence similarity 162, member A	*FAM162A*
4593	493	345	1,43	0,034757	0,412	214709_s_at	Kinectin 1 (kinesin receptor)	*KTN1*
465	157	110	1,43	0,002459	0,288	224736_at	Cell division cycle and apoptosis regulator 1	*CCAR1*
2132	15,7	11,0	1,43	0,014015	0,359	221986_s_at	Kelch-like 24 (Drosophila)	*KLHL24*
2509	28,5	20,0	1,43	0,016870	0,368	235959_at	AT rich interactive domain 4B (RBP1-like)	*ARID4B*
346	132	92,8	1,43	0,001775	0,278	218491_s_at	Thymocyte nuclear protein 1	*THYN1*
5567	20,8	14,6	1,43	0,044315	0,435	204324_s_at	Golgi integral membrane protein 4	*GOLIM4*
4869	125	87,8	1,43	0,037158	0,417	217738_at	Pre-B-cell colony enhancing factor 1	*PBEF1*
5587	54,6	38,3	1,42	0,044562	0,436	222592_s_at	Acyl-CoA synthetase long-chain family member 5	*ACSL5*
3532	29,2	20,5	1,42	0,025384	0,393	238493_at	Zinc finger protein 506	*ZNF506*
3174	79,7	56,0	1,42	0,022511	0,387	229732_at	Zinc finger protein 823	*ZNF823*
1953	97,2	68,2	1,42	0,012763	0,355	219553_at	Nucleoside diphosphate kinase 7	*NME7*
1421	533	375	1,42	0,008609	0,331	208661_s_at	Tetratricopeptide repeat domain 3	*TTC3*

Index	Mutated*	Normal*	FC	*P* value	FDR**	Probe set	Description	Gene symbol
5589	69,2	48,7	1,42	0,044579	0,436	223201_s_at	Transmembrane protein 164	*TMEM164*
52	9,29	6,54	1,42	0,000201	0,201	207068_at	Zinc finger protein 37 homolog (mouse)	*ZFP37*
1980	26,2	18,5	1,42	0,012920	0,355	1556049_at	Reticulon 4	*RTN4*
1622	538	379	1,42	0,010180	0,343	201008_s_at	Thioredoxin interacting protein	*TXNIP*
692	6,73	4,74	1,42	0,003985	0,308	1559706_at	Rho-guanine nucleotide exchange factor	*RGNEF*
2777	272	192	1,42	0,019296	0,380	208158_s_at	Oxysterol binding protein-like 1A	*OSBPL1A*
2220	17,5	12,3	1,42	0,014713	0,362	236600_at	Spastic paraplegia 20	*SPG20*
1471	179	126	1,42	0,008991	0,334	221588_x_at	Aldehyde dehydrogenase 6 family, member A1	*ALDH6A1*
2743	28,2	19,9	1,42	0,018927	0,377	1565149_at	Dynein, cytoplasmic 2, heavy chain 1	*DYNC2H1*
4116	55,9	39,4	1,42	0,030270	0,402	205588_s_at	FGFR1 oncogene partner	*FGFR1OP*
3141	105	74,1	1,42	0,022294	0,387	227121_at	cDNA DKFZp586K1922	-
339	43,9	30,9	1,42	0,001733	0,277	227056_at	KIAA0141 protein	*KIAA0141*
846	76,7	54,1	1,42	0,004873	0,313	235889_at	Transcribed locus	-
2170	50,0	35,3	1,42	0,014349	0,361	205786_s_at	Integrin, alpha M (complement component 3 receptor 3 subunit)	*ITGAM*
4642	7,31	5,15	1,42	0,035008	0,412	206713_at	Netrin G1	*NTNG1*
5241	248	175	1,42	0,040595	0,423	218435_at	DnaJ (Hsp40) homolog, subfamily C, member 15	*DNAJC15*
4112	41,3	29,2	1,42	0,030216	0,402	208555_x_at	Cystatin SA	*CST2*
2819	73,3	51,8	1,42	0,019671	0,381	214499_s_at	BCL2-associated transcription factor 1	*BCLAF1*
5122	47,0	33,2	1,41	0,039430	0,421	209781_s_at	KH domain containing, RNA binding, signal transduction associated 3	*KHDRBS3*
4580	17,1	12,1	1,41	0,034614	0,412	239486_at	Transcribed locus	-
4560	25,8	18,3	1,41	0,034463	0,412	229276_at	Immunoglobulin superfamily, member 9	*IGSF9*
302	84,9	60,0	1,41	0,001464	0,263	223711_s_at	Thymocyte nuclear protein 1	*THYN1*
3502	210	148	1,41	0,025172	0,392	209210_s_at	Fermitin family homolog 2 (Drosophila)	*FERMT2*
4599	96,6	68,4	1,41	0,034777	0,412	229238_at	Chromosome 17 open reading frame 97	*C17orf97*
5304	41,6	29,5	1,41	0,041386	0,426	244674_at	RNA binding motif protein 6	*RBM6*
1491	148	105	1,41	0,009194	0,336	219622_at	RAB20, member RAS oncogene family	*RAB20*
4669	37,1	26,3	1,41	0,035252	0,413	234785_at	-	-
5957	231	164	1,41	0,048343	0,444	210480_s_at	Myosin VI	*MYO6*
3602	117	83,1	1,41	0,025977	0,394	225956_at	Adult retina protein	*LOC153222*
1879	24,8	17,6	1,41	0,012162	0,354	204037_at	Lysophosphatidic acid receptor 1	*EDG2*
2477	769	545	1,41	0,016675	0,367	222433_at	Enabled homolog (Drosophila)	*ENAH*
444	10,6	7,52	1,41	0,002366	0,288	212079_s_at	Myeloid/lymphoid or mixed-lineage leukemia	*MLL*
6051	88,0	62,4	1,41	0,049301	0,445	1553575_at	Mitochondrially encoded NADH dehydrogenase 6	*MTND6*
2145	13,2	9,35	1,41	0,014119	0,360	1559361_at	Metastasis associated in colon cancer 1	*MACC1*
4382	19,5	13,8	1,41	0,032602	0,407	227752_at	Serine palmitoyltransferase, long chain base subunit 3	*SPTLC3*
2588	23,7	16,8	1,41	0,017550	0,371	209293_x_at	Inhibitor of DNA binding 4, dominant negative helix-loop-helix protein	*ID4*
3045	43,0	30,5	1,41	0,021431	0,385	239515_at	Sperm autoantigenic protein 17	*SPA17*
3630	15,5	11,0	1,41	0,026233	0,395	231235_at	Natural killer-tumor recognition sequence	*NKTR*
1066	79,8	56,7	1,41	0,006255	0,319	211711_s_at	Phosphatase and tensin homolog	*PTEN*
3382	150	106	1,41	0,024073	0,389	214055_x_at	BAT2 domain containing 1	*BAT2D1*
3040	36,9	26,2	1,41	0,021426	0,385	230179_at	Hypothetical protein LOC285812	*LOC285812*
1009	13,0	9,24	1,41	0,005855	0,316	239606_at	I beta-1,6-N-acetylglucosaminyltransferase	*GCNT2*
1703	10,1	7,18	1,41	0,010860	0,348	232978_at	Muscleblind-like 2 (Drosophila)	*MBNL2*
489	16,7	11,9	1,41	0,002620	0,289	238723_at	Ataxin 3	*ATXN3*
5497	142	101	1,41	0,043511	0,433	213224_s_at	Non-protein coding RNA 81	*NCRNA00081*
3635	12,8	9,10	1,41	0,026290	0,395	236562_at	Zinc finger protein 439	*ZNF439*
2548	236	168	1,41	0,017216	0,369	203318_s_at	Zinc finger protein 148	*ZNF148*
2745	216	154	1,41	0,018992	0,378	205383_s_at	Zinc finger and BTB domain containing 20	*ZBTB20*
1956	246	175	1,41	0,012781	0,355	203640_at	Muscleblind-like 2 (Drosophila)	*MBNL2*
3690	234	166	1,41	0,026655	0,395	225258_at	Filamin binding LIM protein 1	*FBLIM1*
5090	6,45	4,59	1,41	0,039171	0,420	1556125_at	G patch domain containing 2	*GPATCH2*
5851	19,9	14,1	1,41	0,047333	0,442	237107_at	Protein kinase, interferon-inducible double stranded RNA dependent	*PRKRA*
2904	53,9	38,3	1,41	0,020424	0,383	232693_s_at	Zinc finger protein 395	*ZNF395*
111	204	145	1,41	0,000471	0,232	209225_x_at	Transportin 1	*TNPO1*
2067	102	72,3	1,41	0,013504	0,356	231873_at	Bone morphogenetic protein receptor, type II	*BMPR2*
1799	17,8	12,6	1,40	0,011579	0,351	1561181_at	AT rich interactive domain 5B (MRF1-like)	*ARID5B*
2541	441	314	1,40	0,017180	0,369	202028_s_at	Ribosomal protein L38	*RPL38*

Index	Mutated*	Normal*	FC	*P* value	FDR**	Probe set	Description	Gene symbol
5112	66,8	47,6	1,40	0,039357	0,421	200841_s_at	Glutamyl-prolyl-tRNA synthetase	*EPRS*
4709	164	117	1,40	0,035626	0,413	209348_s_at	v-maf musculoaponeurotic fibrosarcoma oncogene homolog (avian)	*MAF*
1013	17,1	12,2	1,40	0,005865	0,316	238693_at	Polyhomeotic homolog 3 (Drosophila)	*PHC3*
4426	21,0	15,0	1,40	0,033150	0,409	240758_at	ArfGAP with GTPase domain, ankyrin repeat and PH domain 1	*AGAP1*
2382	24,8	17,7	1,40	0,015884	0,364	222693_at	Fibronectin type III domain containing 3B	*FNDC3B*
1999	188	134	1,40	0,013063	0,355	203232_s_at	Ataxin 1	*ATXN1*
1584	18,5	13,2	1,40	0,009866	0,340	242814_at	Serpin peptidase inhibitor, clade B (ovalbumin), member 9	*SERPINB9*
1847	150	107	1,40	0,011890	0,352	209868_s_at	RNA binding motif, single stranded interacting protein 1	*RBMS1*
5339	177	126	1,40	0,041804	0,428	224595_at	Solute carrier family 44, member 1	*SLC44A1*
3361	41,4	29,6	1,40	0,023885	0,388	216235_s_at	Endothelin receptor type A	*EDNRA*
4038	4,99	3,56	1,40	0,029589	0,401	221008_s_at	Alanine-glyoxylate aminotransferase 2-like 1	*AGXT2L1*
5566	60,3	43,1	1,40	0,044312	0,435	229694_at	Bromodomain and WD repeat domain containing 2	*BRWD2*
601	147	105	1,40	0,003343	0,303	203656_at	FIG4 homolog (S. cerevisiae)	*FIG4*
3464	68,2	48,7	1,40	0,024821	0,392	218401_s_at	Zinc finger protein 281	*ZNF281*
347	105	75,2	1,40	0,001777	0,278	212604_at	Mitochondrial ribosomal protein S31	*MRPS31*
837	840	601	1,40	0,004801	0,313	210554_s_at	C-terminal binding protein 2	*CTBP2*
4431	7,34	5,24	1,40	0,033187	0,409	205871_at	Plasminogen-like B2	*PLGLB2*
2690	15,8	11,3	1,40	0,018445	0,375	228686_at	Hypothetical protein LOC644873	*FLJ33630*
1146	9,76	6,98	1,40	0,006731	0,321	207264_at	KDEL endoplasmic reticulum protein retention receptor 3	*KDELR3*
2641	57,0	40,7	1,40	0,018009	0,373	213056_at	FERM domain containing 4B	*FRMD4B*
5170	21,1	15,1	1,40	0,039831	0,421	209446_s_at	Chromosome 7 open reading frame 44	*C7orf44*
120	5,60	4,01	1,40	0,000550	0,240	239605_x_at	Transforming growth factor, beta receptor 1	*TGFBR1*
690	111	79,1	1,40	0,003949	0,308	212946_at	KIAA0564 protein	*KIAA0564*
6011	174	124	1,40	0,048880	0,445	214077_x_at	Meis homeobox 3 pseudogene 1	*MEIS3P1*
251	78,9	56,5	1,40	0,001161	0,253	1556000_s_a	BTB (POZ) domain containing 7	*BTBD7*
2806	20,7	14,8	1,40	0,019517	0,380	220638_s_at	Cas-Br-M (murine) ecotropic retroviral transforming sequence c	*CBLC*
4163	35,5	25,4	1,40	0,030772	0,404	217608_at	P18SRP protein	*P18SRP*
1106	163	117	1,40	0,006469	0,319	225243_s_at	Sarcolemma associated protein	*SLMAP*
2181	343	246	1,40	0,014427	0,361	204112_s_at	Histamine N-methyltransferase	*HNMT*
5523	437	313	1,40	0,043808	0,433	201259_s_at	Synaptophysin-like 1	*SYPL1*
2333	165	118	1,40	0,015567	0,364	229420_at	cDNA FLJ37566 fis, clone BRCOC2002085	-
3185	88,5	63,5	1,39	0,022587	0,387	223261_at	Polymerase (DNA directed) kappa	*POLK*
542	405	290	1,39	0,002907	0,293	203044_at	Carbohydrate (chondroitin) synthase 1	*CHSY1*
4327	74,5	53,4	1,39	0,032204	0,407	221123_x_at	Zinc finger protein 395	*ZNF395*
5949	17,3	12,4	1,39	0,048203	0,443	239449_at	Ankylosis, progressive homolog (mouse)	*ANKH*
2526	91,4	65,6	1,39	0,017053	0,369	206854_s_at	Mitogen-activated protein kinase kinase kinase 7	*MAP3K7*
3840	78,4	56,3	1,39	0,028045	0,399	223216_x_at	Huntington's disease gene regulatory region-binding protein 2	*PBF*
1603	57,5	41,3	1,39	0,009994	0,341	202984_s_at	BCL2-associated athanogene 5	*BAG5*
4531	181	130	1,39	0,034211	0,412	225093_at	Utrophin	*UTRN*
1176	670	481	1,39	0,006912	0,321	208991_at	Signal transducer and activator of transcription 3	*STAT3*
3256	18,2	13,1	1,39	0,023114	0,388	242405_at	Mastermind-like 2 (Drosophila)	*MAML2*
501	47,8	34,3	1,39	0,002664	0,289	226267_at	Jun dimerization protein 2	*JDP2*
4057	15,7	11,3	1,39	0,029765	0,401	242384_at	Cytoplasmic polyadenylation element binding protein 4	*CPEB4*
1149	125	90,1	1,39	0,006758	0,321	204716_at	Coiled-coil domain containing 6	*CCDC6*
5384	18,5	13,3	1,39	0,042241	0,429	222844_s_at	Serine racemase	*SRR*
3164	70,8	50,9	1,39	0,022458	0,387	212398_at	Radixin	*RDX*
3874	23,0	16,5	1,39	0,028290	0,399	231183_s_at	Jagged 1 (Alagille syndrome)	*JAG1*
4754	315	226	1,39	0,036020	0,414	206662_at	Glutaredoxin (thioltransferase)	*GLRX*
3413	60,7	43,7	1,39	0,024370	0,390	226682_at	RAR-related orphan receptor A	*RORA*
972	20,5	14,8	1,39	0,005641	0,315	205187_at	SMAD family member 5	*SMAD5*
3926	34,8	25,0	1,39	0,028702	0,399	211621_at	Androgen receptor	*AR*
2783	12,3	8,88	1,39	0,019334	0,380	240498_at	Ets variant 6	*ETV6*
2836	15,9	11,4	1,39	0,019798	0,382	239173_at	InaD-like (Drosophila)	*INADL*
2396	132	95,1	1,39	0,015987	0,365	224950_at	Prostaglandin F2 receptor negative regulator	*PTGFRN*
5359	786	566	1,39	0,042020	0,429	200897_s_at	Palladin, cytoskeletal associated protein	*PALLD*
2192	38,5	27,8	1,39	0,014508	0,361	224963_at	Solute carrier family 26 (sulfate transporter), member 2	*SLC26A2*
911	14,5	10,4	1,39	0,005250	0,313	241336_at	Transcribed locus	-

Index	Mutated*	Normal*	FC	*P* value	FDR**	Probe set	Description	Gene symbol
1562	160	115	1,39	0,009692	0,339	203748_x_at	RNA binding motif, single stranded interacting protein 1	*RBMS1*
805	507	365	1,39	0,004594	0,311	201260_s_at	Synaptophysin-like 1	*SYPL1*
5789	30,0	21,6	1,39	0,046653	0,441	235122_at	Immunodeficiency virus type I enhancer binding protein 3	*HIVEP3*
2540	78,1	56,3	1,39	0,017179	0,369	221045_s_at	Period homolog 3 (Drosophila)	*PER3*
1682	123	88,5	1,39	0,010633	0,345	203774_at	5-methyltetrahydrofolate-homocysteine methyltransferase	*MTR*
513	846	610	1,39	0,002737	0,291	200985_s_at	CD59 molecule, complement regulatory protein	*CD59*
4265	11,2	8,04	1,39	0,031737	0,406	1558447_at	Hypothetical protein LOC100128439	*LOC100128439*
610	8,38	6,04	1,39	0,003449	0,308	241360_at	Coiled-coil domain containing 15	*CCDC15*
1668	9,33	6,72	1,39	0,010537	0,345	229110_at	cDNA clone IMAGE:4794876	-
6071	18,3	13,2	1,39	0,049559	0,446	236696_at	U2-associated SR140 protein	*SR140*
4493	348	251	1,39	0,033779	0,411	202023_at	Ephrin-A1	*EFNA1*
2781	205	148	1,39	0,019305	0,380	204142_at	Enolase superfamily member 1	*ENOSF1*
3649	12,2	8,79	1,39	0,026377	0,395	1556935_at	Laminin, alpha 4	*LAMA4*
1427	96,8	69,8	1,39	0,008650	0,331	1558142_at	Trinucleotide repeat containing 6B	*TNRC6B*
628	164	118	1,39	0,003560	0,308	209106_at	Nuclear receptor coactivator 1	*NCOA1*
5034	169	122	1,39	0,038743	0,420	217739_s_at	Pre-B-cell colony enhancing factor 1	*PBEF1*
2788	29,6	21,4	1,39	0,019385	0,380	228482_at	CMT1A duplicated region transcript 4	*CDRT4*
2895	26,0	18,8	1,39	0,020334	0,383	229541_at	Homeobox containing 1	*HMBOX1*
642	877	633	1,39	0,003657	0,308	201009_s_at	Thioredoxin interacting protein	*TXNIP*
4514	28,4	20,5	1,38	0,034018	0,412	244310_at	RAR-related orphan receptor A	*RORA*
443	47,7	34,5	1,38	0,002360	0,288	213813_x_at	Ferritin, light polypeptide-like 1	*FTL*
3016	57,3	41,4	1,38	0,021240	0,385	223540_at	Poliovirus receptor-related 4	*PVRL4*
4378	166	120	1,38	0,032564	0,407	202211_at	ADP-ribosylation factor GTPase activating protein 3	*ARFGAP3*
4879	654	472	1,38	0,037272	0,418	200915_x_at	Kinectin 1 (kinesin receptor)	*KTN1*
2542	213	154	1,38	0,017180	0,369	211015_s_at	Heat shock 70kDa protein 4	*HSPA4*
4393	196	142	1,38	0,032723	0,407	201548_s_at	Jumonji, AT rich interactive domain 1B	*JARID1B*
4436	35,2	25,4	1,38	0,033216	0,409	233004_x_at	Nuclear factor I/A	*NFIA*
596	4,95	3,58	1,38	0,003281	0,301	240921_at	-	-
3005	104	75,3	1,38	0,021154	0,385	222633_at	Transducin (beta)-like 1X-linked receptor 1	*TBL1XR1*
4236	63,9	46,2	1,38	0,031397	0,405	219138_at	Ribosomal protein L14	*RPL14*
3088	48,4	35,0	1,38	0,021776	0,385	210224_at	Major histocompatibility complex, class I-related	*MR1*
5942	185	134	1,38	0,048160	0,443	225640_at	Hypothetical gene supported by AK091718	*LOC401504*
5624	8,13	5,88	1,38	0,044913	0,436	233720_at	Sorbin and SH3 domain containing 2	*SORBS2*
5267	22,1	16,0	1,38	0,040913	0,425	1569519_at	Neuroblastoma breakpoint family, member 1	*NBPF1*
4723	548	397	1,38	0,035729	0,414	203216_s_at	Myosin VI	*MYO6*
3198	106	76,6	1,38	0,022652	0,387	230618_s_at	HLA-B associated transcript 2-like 2	*BAT2L2*
3583	15,9	11,5	1,38	0,025869	0,394	1552309_a_a	Nexilin (F actin binding protein)	*NEXN*
3332	31,4	22,7	1,38	0,023657	0,388	226765_at	Spectrin, beta, non-erythrocytic 1	*SPTBN1*
2605	354	257	1,38	0,017689	0,371	204131_s_at	Forkhead box O3	*FOXO3*
2970	8,04	5,82	1,38	0,020866	0,384	238317_x_at	RNA binding motif, single stranded interacting protein 1	*RBMS1*
4135	134	96,9	1,38	0,030466	0,403	210621_s_at	RAS p21 protein activator (GTPase activating protein) 1	*RASA1*
2720	140	102	1,38	0,018682	0,376	212798_s_at	Ankyrin repeat and MYND domain containing 2	*ANKMY2*
1744	29,6	21,5	1,38	0,011145	0,348	205415_s_at	Ataxin 3	*ATXN3*
2321	10,6	7,67	1,38	0,015417	0,363	230375_at	Splicing factor, arginine/serine-rich 18	*SFRS18*
1563	14,5	10,5	1,38	0,009712	0,339	232710_at	cDNA FLJ11415 fis, clone HEMBA1000942	-
5546	26,5	19,3	1,38	0,044099	0,435	238311_at	KIAA0776 protein	*KIAA0776*
2238	98,8	71,7	1,38	0,014878	0,363	222692_s_at	Fibronectin type III domain containing 3B	*FNDC3B*
1294	231	167	1,38	0,007702	0,325	204616_at	Ubiquitin carboxyl-terminal esterase L3 (ubiquitin thiolesterase)	*UCHL3*
3501	110	79,9	1,38	0,025158	0,392	218693_at	Tetraspanin 15	*TSPAN15*
24	19,0	13,8	1,38	0,000100	0,201	205215_at	Ring finger protein 2	*RNF2*
600	154	112	1,38	0,003336	0,303	224827_at	Ubiquitin domain containing 2	*UBTD2*
2410	22,9	16,6	1,37	0,016102	0,365	229397_s_at	Glucocorticoid receptor DNA binding factor 1	*GRLF1*
218	11,9	8,67	1,37	0,000978	0,245	235567_at	RAR-related orphan receptor A	*RORA*
1806	56,2	40,9	1,37	0,011624	0,351	1555910_at	Pentatricopeptide repeat domain 2	*PTCD2*
2276	51,1	37,2	1,37	0,015132	0,363	231075_x_at	RAS association (RalGDS/AF-6) and pleckstrin homology domains 1	*RAPH1*
1209	185	135	1,37	0,007164	0,324	209817_at	Protein phosphatase 3 (formerly 2B), catalytic subunit, beta isoform	*PPP3CB*
5442	24,0	17,5	1,37	0,042909	0,431	205578_at	Receptor tyrosine kinase-like orphan receptor 2	*ROR2*

Index	Mutated*	Normal*	FC	*P* value	FDR**	Probe set	Description	Gene symbol
3421	23,0	16,7	1,37	0,024465	0,391	1555240_s_a	Guanine nucleotide binding protein (G protein), gamma 12	*GNG12*
1895	256	186	1,37	0,012316	0,355	212410_at	EF-hand domain family, member A1	*EFHA1*
4419	132	96,0	1,37	0,033065	0,409	212917_x_at	RecQ protein-like (DNA helicase Q1-like)	*RECQL*
5017	4,89	3,56	1,37	0,038592	0,420	238103_at	CDNA FLJ37936 fis, clone CTONG2005468	-
4475	38,6	28,1	1,37	0,033648	0,411	234192_s_at	G kinase anchoring protein 1	*GKAP1*
1568	20,5	14,9	1,37	0,009751	0,340	1554004_a_a	Rho-guanine nucleotide exchange factor	*RGNEF*
656	116	84,5	1,37	0,003784	0,308	212936_at	Family with sequence similarity 172, member A	*C5orf21*
2754	138	100	1,37	0,019070	0,378	225674_at	B-cell receptor-associated protein 29	*BCAP29*
4778	107	78,2	1,37	0,036230	0,414	204518_s_at	Peptidylprolyl isomerase C (cyclophilin C)	*PPIC*
5939	21,8	15,9	1,37	0,048147	0,443	1569142_at	Tripartite motif-containing 13	*TRIM13*
2759	256	187	1,37	0,019144	0,379	225273_at	WWC family member 3	*WWC3*
2564	49,8	36,3	1,37	0,017391	0,371	227733_at	Transmembrane protein 63C	*TMEM63C*
750	117	85,4	1,37	0,004249	0,308	209647_s_at	Suppressor of cytokine signaling 5	*SOCS5*
4800	20,2	14,7	1,37	0,036425	0,415	230102_at	Ets variant gene 5 (ets-related molecule)	*ETV5*
2008	693	506	1,37	0,013093	0,355	212600_s_at	Ubiquinol-cytochrome c reductase core protein II	*UQCRC2*
1097	208	152	1,37	0,006432	0,319	204690_at	Syntaxin 8	*STX8*
4510	17,2	12,5	1,37	0,034001	0,412	242188_at	Protein tyrosine phosphatase, receptor type, G	*PTPRG*
636	7,59	5,54	1,37	0,003619	0,308	231109_at	CUG triplet repeat, RNA binding protein 2	*CUGBP2*
4277	26,9	19,6	1,37	0,031784	0,406	237383_at	Transcribed locus	-
2601	25,3	18,4	1,37	0,017665	0,371	214493_s_at	InaD-like (Drosophila)	*INADL*
4303	24,4	17,8	1,37	0,032033	0,407	1554919_s_a	Chromosome 7 open reading frame 63	*C7orf63*
4025	38,5	28,1	1,37	0,029474	0,400	203836_s_at	Mitogen-activated protein kinase kinase kinase 5	*MAP3K5*
2252	32,0	23,4	1,37	0,014997	0,363	236754_at	Protein phosphatase 1, regulatory (inhibitor) subunit 2	*PPP1R2*
333	307	225	1,37	0,001675	0,274	202808_at	Chromosome 10 open reading frame 26	*C10orf26*
4121	30,5	22,3	1,37	0,030300	0,402	205395_s_at	MRE11 meiotic recombination 11 homolog A (S. cerevisiae)	*MRE11A*
5320	423	309	1,37	0,041550	0,427	217869_at	Hydroxysteroid (17-beta) dehydrogenase 12	*HSD17B12*
1136	60,8	44,5	1,37	0,006643	0,319	226787_at	Zinc finger protein 18	*ZNF18*
3265	156	114	1,37	0,023193	0,388	218594_at	HEAT repeat containing 1	*HEATR1*
5827	30,2	22,0	1,37	0,047078	0,442	222858_s_at	Dual adaptor of phosphotyrosine and 3-phosphoinositides	*DAPP1*
4001	113	82,6	1,37	0,029287	0,400	221763_at	Jumonji domain containing 1C	*JMJD1C*
5244	159	116	1,37	0,040599	0,423	212397_at	Radixin	*RDX*
4425	18,7	13,7	1,37	0,033119	0,409	244464_at	Ubiquitin-conjugating enzyme E2E 2 (UBC4/5 homolog, yeast)	*UBE2E2*
2053	14,4	10,5	1,37	0,013345	0,355	242243_at	TATA element modulatory factor 1	*TMF1*
3940	92,2	67,5	1,37	0,028764	0,399	219757_s_at	Chromosome 14 open reading frame 101	*C14orf101*
3295	203	149	1,37	0,023478	0,388	212420_at	E74-like factor 1 (ets domain transcription factor)	*ELF1*
3157	31,6	23,1	1,37	0,022409	0,387	204225_at	Histone deacetylase 4	*HDAC4*
3310	42,9	31,4	1,37	0,023546	0,388	238476_at	Adult retina protein	*C5orf41*
1984	27,4	20,1	1,37	0,012953	0,355	215239_x_at	Zinc finger protein 273	*ZNF273*
5934	6,53	4,78	1,37	0,048111	0,443	241708_at	Dedicator of cytokinesis 1	*DOCK1*
1101	97,1	71,1	1,37	0,006456	0,319	1557370_s_a	MYC binding protein 2	*MYCBP2*
5386	39,2	28,7	1,37	0,042245	0,429	226380_at	Protein tyrosine phosphatase, non-receptor type 21	*PTPN21*
5136	412	302	1,37	0,039515	0,421	200883_at	Ubiquinol-cytochrome c reductase core protein II	*UQCRC2*
5428	12,4	9,11	1,37	0,042706	0,430	1554741_s_a	Fibroblast growth factor 7 (keratinocyte growth factor)	*FGF7*
4147	45,9	33,7	1,37	0,030601	0,403	228251_at	UBX domain containing 1	*UBXD1*
1387	258	189	1,36	0,008348	0,329	217858_s_at	Armadillo repeat containing, X-linked 3	*ARMCX3*
2272	11,1	8,17	1,36	0,015090	0,363	1558184_s_a	Zinc finger protein 17	*ZNF17*
1460	96,0	70,4	1,36	0,008919	0,334	204703_at	Intraflagellar transport 88 homolog (Chlamydomonas)	*IFT88*
4159	72,9	53,5	1,36	0,030734	0,404	211944_at	BAT2 domain containing 1	*BAT2D1*
2174	61,0	44,8	1,36	0,014364	0,361	226203_at	cDNA clone IMAGE:5299888	-
5582	121	88,8	1,36	0,044509	0,436	206695_x_at	Zinc finger protein 43	*ZNF43*
5116	49,3	36,2	1,36	0,039390	0,421	227405_s_at	Frizzled homolog 8 (Drosophila)	*FZD8*
3582	63,8	46,9	1,36	0,025868	0,394	216905_s_at	Suppression of tumorigenicity 14 (colon carcinoma)	*ST14*
2652	20,8	15,3	1,36	0,018082	0,373	227987_at	Vacuolar protein sorting 13 homolog A (S. cerevisiae)	*VPS13A*
60	504	370	1,36	0,000226	0,201	224837_at	Forkhead box P1	*FOXP1*
5701	39,3	28,8	1,36	0,045646	0,438	209119_x_at	Nuclear receptor subfamily 2, group F, member 2	*NR2F2*
667	24,2	17,8	1,36	0,003838	0,308	244813_at	RAD51-like 1 (S. cerevisiae)	*RAD51L1*
6094	220	161	1,36	0,049743	0,446	209444_at	RAP1, GTP-GDP dissociation stimulator 1	*RAP1GDS1*

Index	Mutated*	Normal*	FC	*P* value	FDR**	Probe set	Description	Gene symbol
4939	60,7	44,6	1,36	0,037891	0,419	241425_at	Nucleoporin like 1	*NUPL1*
4818	211	155	1,36	0,036618	0,416	212423_at	Zinc finger, CCHC domain containing 24	*ZCCHC24*
3505	58,8	43,2	1,36	0,025182	0,392	242669_at	Ubiquitin-fold modifier 1	*UFM1*
3029	66,7	49,0	1,36	0,021321	0,385	204635_at	Ribosomal protein S6 kinase, 90kDa, polypeptide 5	*RPS6KA5*
447	29,5	21,7	1,36	0,002391	0,288	221555_x_at	CDC14 cell division cycle 14 homolog B (S. cerevisiae)	*CDC14B*
4245	14,1	10,4	1,36	0,031505	0,406	205222_at	L-3-hydroxyacyl-CoA dehydrogenase	*EHHADH*
5360	9,21	6,78	1,36	0,042032	0,429	243041_s_at	RNA binding motif, single stranded interacting protein	*RBMS3*
1874	29,3	21,6	1,36	0,012125	0,354	242878_at	-	-
4558	30,0	22,1	1,36	0,034449	0,412	229654_at	Zinc finger protein 44	*ZNF44*
1532	141	104	1,36	0,009477	0,337	221787_at	Chromosome 6 open reading frame 120	*C6orf120*
3965	42,0	30,9	1,36	0,028965	0,399	230886_at	Transcribed locus	-
88	11,8	8,65	1,36	0,000330	0,201	236849_at	Vesicle transport through interaction with t-SNAREs homolog 1A	*VTI1A*
3132	39,2	28,9	1,36	0,022214	0,387	33494_at	Electron-transferring-flavoprotein dehydrogenase	*ETFDH*
4790	35,7	26,3	1,36	0,036330	0,415	202669_s_at	Ephrin-B2	*EFNB2*
317	236	174	1,36	0,001588	0,272	203704_s_at	RAS responsive element binding protein 1	*RREB1*
5952	20,4	15,0	1,36	0,048288	0,444	220840_s_at	Chromosome 1 open reading frame 112	*C1orf112*
688	35,9	26,5	1,36	0,003940	0,308	208876_s_at	p21 (CDKN1A)-activated kinase 2	*PAK2*
2682	21,3	15,7	1,36	0,018363	0,374	242722_at	LIM domain 7	*LMO7*
798	12,0	8,87	1,36	0,004555	0,311	243469_at	E74-like factor 2 (ets domain transcription factor)	*ELF2*
3478	6,79	5,00	1,36	0,024976	0,392	240866_at	LIM domain containing preferred translocation partner in lipoma	*LPP*
1214	29,9	22,0	1,36	0,007213	0,324	243772_at	Serologically defined colon cancer antigen 8	*SDCCAG8*
789	43,9	32,4	1,36	0,004507	0,311	1554003_at	Rho-guanine nucleotide exchange factor	*RGNEF*
3221	5,28	3,89	1,36	0,022830	0,387	239370_at	cDNA clone ZE01A04	-
4855	22,4	16,5	1,36	0,037023	0,417	242431_at	Ubiquitin-conjugating enzyme E2-binding protein 1	*ARIH1*
2485	56,8	41,9	1,36	0,016748	0,367	209105_at	Nuclear receptor coactivator 1	*NCOA1*
2033	82,9	61,1	1,36	0,013238	0,355	201746_at	Tumor protein p53 (Li-Fraumeni syndrome)	*TP53*
3111	415	306	1,36	0,021974	0,386	202743_at	Phosphoinositide-3-kinase, regulatory subunit 3 (p55, gamma)	*PIK3R3*
3605	26,9	19,8	1,36	0,026000	0,394	233977_at	Growth regulation by estrogen in breast cancer-like	*KIAA1772*
2465	136	100	1,36	0,016563	0,367	218379_at	RNA binding motif protein 7	*RBM7*
5161	69,2	51,0	1,36	0,039739	0,421	207606_s_at	Rho GTPase activating protein 12	*ARHGAP12*
773	139	103	1,36	0,004427	0,311	202305_s_at	Fasciculation and elongation protein zeta 2 (zygin II)	*FEZ2*
239	162	119	1,36	0,001109	0,250	203614_at	UTP14, U3 small nucleolar ribonucleoprotein, homolog C (yeast)	*UTP14C*
4390	87,1	64,3	1,36	0,032708	0,407	1569057_s_a	Melanoma inhibitory activity family, member 3	*MIA3*
617	14,3	10,6	1,36	0,003494	0,308	241709_s_at	Dedicator of cytokinesis 1	*DOCK1*
5599	63,4	46,8	1,35	0,044658	0,436	221946_at	Chromosome 9 open reading frame 116	*C9orf116*
1488	138	102	1,35	0,009179	0,336	233952_s_at	Zinc finger protein 295	*ZNF295*
4219	26,3	19,4	1,35	0,031255	0,405	231403_at	Triple functional domain (PTPRF interacting)	*TRIO*
4627	21,7	16,1	1,35	0,034900	0,412	213623_at	Kinesin family member 3A	*KIF3A*
865	309	228	1,35	0,004995	0,313	218229_s_at	Pogo transposable element with KRAB domain	*POGK*
4290	558	412	1,35	0,031890	0,406	202351_at	Vitronectin receptor subunit alpha (antigen CD51)	*ITGAV*
1905	130	96,3	1,35	0,012386	0,355	201918_at	Solute carrier family 25, member 36	*SLC25A36*
2854	11,9	8,76	1,35	0,020010	0,383	232110_at	Polypeptide N-acetylgalactosaminyltransferase 5	*GALNT5*
4200	12,1	8,93	1,35	0,031059	0,404	233087_at	F-box and leucine-rich repeat protein 17	*FBXL17*
3455	66,4	49,1	1,35	0,024747	0,392	212858_at	Progestin and adipoQ receptor family member IV	*PAQR4*
5883	150	111	1,35	0,047590	0,442	201325_s_at	Epithelial membrane protein 1	*EMP1*
2304	72,5	53,6	1,35	0,015297	0,363	233936_s_at	Gametogenetin binding protein 2	*GGNBP2*
2480	98,6	73,0	1,35	0,016719	0,367	227413_at	Ubiquitin-like domain containing CTD phosphatase 1	*UBLCP1*
3273	78,5	58,1	1,35	0,023279	0,388	1554351_a_a	TIP41, TOR signaling pathway regulator-like (S. cerevisiae)	*TIPRL*
2985	45,0	33,3	1,35	0,020986	0,384	214175_x_at	PDZ and LIM domain 4	*PDLIM4*
623	84,1	62,3	1,35	0,003529	0,308	229009_at	SIX homeobox 5	*SIX5*
1463	9,71	7,19	1,35	0,008945	0,334	1569796_s_a	Attractin-like 1	*ATRNL1*
6114	407	301	1,35	0,049896	0,446	201876_at	Paraoxonase 2	*PON2*
1786	256	189	1,35	0,011410	0,349	209579_s_at	Methyl-CpG binding domain protein 4	*MBD4*
5600	106	78,6	1,35	0,044661	0,436	213025_at	THUMP domain containing 1	*THUMPD1*
5173	84,2	62,4	1,35	0,039846	0,421	226647_at	Transmembrane protein 25	*TMEM25*
2358	9,54	7,07	1,35	0,015729	0,364	216147_at	Septin 11	*SEPT11*
2122	19,6	14,6	1,35	0,013955	0,359	207950_s_at	Ankyrin 3, node of Ranvier (ankyrin G)	*ANK3*

Index	Mutated*	Normal*	FC	*P* value	FDR**	Probe set	Description	Gene symbol
4721	96,1	71,3	1,35	0,035710	0,413	226541_at	F-box protein 30	*FBXO30*
1300	471	349	1,35	0,007742	0,325	200984_s_at	CD59 molecule, complement regulatory protein	*CD59*
1086	220	163	1,35	0,006364	0,319	209107_x_at	Nuclear receptor coactivator 1	*NCOA1*
2328	163	121	1,35	0,015505	0,364	226247_at	Pleckstrin homology domain containing, family A member 1	*PLEKHA1*
3595	21,0	15,6	1,35	0,025928	0,394	222354_at	F11 receptor	*FR11*
4848	54,7	40,6	1,35	0,036936	0,417	229173_at	KIAA1715 protein	*KIAA1715*
2586	217	161	1,35	0,017543	0,371	224955_at	TEA domain family member 1 (SV40 transcriptional enhancer factor)	*TEAD1*
2420	7,43	5,52	1,35	0,016179	0,365	1553672_at	Enabled homolog (Drosophila)	*ENAH*
5114	24,5	18,2	1,35	0,039378	0,421	220918_at	Chromosome 21 open reading frame 96	*C21orf96*
2644	42,7	31,7	1,35	0,018026	0,373	218006_s_at	Zinc finger protein 22 (KOX 15)	*ZNF22*
3670	13,0	9,64	1,35	0,026522	0,395	233224_at	Karyopherin alpha 3 (importin alpha 4)	*KPNA3*
3755	23,7	17,6	1,34	0,027293	0,397	218833_at	sterile alpha motif and leucine zipper containing kinase AZK	*ZAK*
930	25,0	18,6	1,34	0,005346	0,313	223713_at	Radial spoke head 3 homolog (Chlamydomonas)	*RSPH3*
2608	185	138	1,34	0,017707	0,371	203173_s_at	Esophageal cancer associated protein	*MGC16824*
4214	190	141	1,34	0,031226	0,405	201910_at	FERM, RhoGEF (ARHGEF) and pleckstrin domain protein 1	*FARP1*
4653	54,4	40,5	1,34	0,035147	0,413	206240_s_at	Zinc finger protein 136	*ZNF136*
473	106	78,9	1,34	0,002514	0,289	1553103_at	Nuclear transcription factor, X-box binding 1	*NFX1*
4139	111	82,5	1,34	0,030549	0,403	217952_x_at	PHD finger protein 3	*PHF3*
3243	82,9	61,7	1,34	0,022996	0,388	205405_at	Semaphorin 5A	*SEMA5A*
3398	605	451	1,34	0,024247	0,390	202442_at	Adaptor-related protein complex 3, sigma 1 subunit	*AP3S1*
1593	2123	1581	1,34	0,009902	0,340	215001_s_at	Glutamate-ammonia ligase (glutamine synthetase)	*GLUL*
2027	435	324	1,34	0,013216	0,355	208992_s_at	Signal transducer and activator of transcription 3	*STAT3*
3484	268	200	1,34	0,025016	0,392	200842_s_at	Glutamyl-prolyl-tRNA synthetase	*EPRS*
4810	38,9	29,0	1,34	0,036541	0,415	218766_s_at	Tryptophanyl tRNA synthetase 2, mitochondrial	*WARS2*
4762	221	165	1,34	0,036100	0,414	211948_x_at	BAT2 domain containing 1	*BAT2D1*
3254	178	133	1,34	0,023110	0,388	202180_s_at	Major vault protein	*MVP*
582	205	153	1,34	0,003194	0,300	212742_at	Zinc finger protein 364	*ZNF364*
4699	10,1	7,57	1,34	0,035478	0,413	222180_at	v-yes-1 Yamaguchi sarcoma viral oncogene homolog 1	*YES1*
3257	73,2	54,6	1,34	0,023129	0,388	201083_s_at	BCL2-associated transcription factor 1	*BCLAF1*
2508	144	108	1,34	0,016854	0,367	203238_s_at	Notch homolog 3 (Drosophila)	*NOTCH3*
1383	49,5	36,9	1,34	0,008328	0,329	227438_at	Alpha-kinase 1	*ALPK1*
360	55,7	41,5	1,34	0,001852	0,281	219362_at	MAK10 homolog, amino-acid N-acetyltransferase subunit, (S.	*MAK10*
2176	28,9	21,5	1,34	0,014396	0,361	1568594_s_a	Tripartite motif-containing 52	*TRIM52*
5472	7,55	5,63	1,34	0,043265	0,432	214524_at	Growth hormone releasing hormone	*GHRH*
3943	139	104	1,34	0,028790	0,399	221761_at	Adenylosuccinate synthase	*ADSS*
4459	13,3	9,95	1,34	0,033508	0,411	236704_at	Phosphodiesterase 4D interacting protein	*PDE4DIP*
1564	50,8	37,9	1,34	0,009715	0,339	221496_s_at	Transducer of ERBB2, 2	*TOB2*
5315	6,67	4,98	1,34	0,041471	0,427	207120_at	Zinc finger protein 667	*ZNF667*
2701	11,9	8,91	1,34	0,018527	0,375	1558815_at	Sorbin and SH3 domain containing 2	*SORBS2*
5371	58,1	43,4	1,34	0,042156	0,429	201888_s_at	Interleukin 13 receptor, alpha 1	*IL13RA1*
662	9,18	6,86	1,34	0,003823	0,308	1556235_at	cDNA FLJ34369 fis, clone FEBRA2017098	-
2171	186	139	1,34	0,014359	0,361	221664_s_at	F11 receptor	*F11R*
1808	445	333	1,34	0,011663	0,351	201413_at	Hydroxysteroid (17-beta) dehydrogenase 4	*HSD17B4*
3720	83,0	62,0	1,34	0,027005	0,397	219156_at	synaptojanin 2 binding protein	*SYNJ2BP*
3931	87,3	65,2	1,34	0,028738	0,399	206829_x_at	Zinc finger protein 430	*ZNF430*
5020	28,4	21,2	1,34	0,038621	0,420	223730_at	Glypican 6	*GPC6*
4715	1502	1123	1,34	0,035668	0,413	201666_at	TIMP metallopeptidase inhibitor 1	*TIMP1*
4621	46,9	35,1	1,34	0,034870	0,412	202516_s_at	Discs, large homolog 1 (Drosophila)	*DLG1*
4264	14,3	10,7	1,34	0,031728	0,406	236983_at	Transmembrane channel-like 5	*TMC5*
4698	226	169	1,34	0,035476	0,413	202656_s_at	SERTA domain containing 2	*SERTAD2*
2022	523	391	1,34	0,013188	0,355	224891_at	Forkhead box O3	*FOXO3*
2602	27,2	20,3	1,34	0,017666	0,371	212027_at	RNA binding motif protein 25	*RBM25*
6098	207	155	1,34	0,049784	0,446	223272_s_at	Chromosome 1 open reading frame 57	*C1orf57*
4477	242	181	1,34	0,033671	0,411	223223_at	ARV1 homolog (S. cerevisiae)	*ARV1*
6069	28,2	21,1	1,34	0,049529	0,446	243759_at	Splicing factor, arginine/serine-rich 15	*SFRS15*
620	16,2	12,1	1,34	0,003506	0,308	232206_at	Unc-51-like kinase 4 (C. elegans)	*ULK4*
2362	61,9	46,4	1,34	0,015765	0,364	206554_x_at	SET domain and mariner transposase fusion gene	*SETMAR*

Index	Mutated*	Normal*	FC	*P* value	FDR**	Probe set	Description	Gene symbol
4060	83,6	62,6	1,34	0,029796	0,401	229810_at	Transcribed locus	-
2189	39,4	29,5	1,34	0,014493	0,361	213494_s_at	YY1 transcription factor	*YY1*
2223	77,6	58,1	1,34	0,014765	0,363	240044_x_at	Trinucleotide repeat containing 6B	*TNRC6B*
4626	6,06	4,54	1,34	0,034891	0,412	235547_at	NEDD4 binding protein 2-like 2	*N4BP2L2*
3473	84,8	63,5	1,34	0,024915	0,392	214264_s_at	Chromosome 14 open reading frame 143	*C14orf143*
1197	34,4	25,7	1,33	0,007066	0,323	204180_s_at	Zinc finger and BTB domain containing 43	*ZBTB43*
1157	182	137	1,33	0,006801	0,321	224857_s_at	Polymerase (RNA) I polypeptide D, 16kDa	*POLR1D*
1212	305	228	1,33	0,007185	0,324	201133_s_at	Praja 2, RING-H2 motif containing	*PJA2*
281	93,4	70,0	1,33	0,001372	0,263	54632_at	Thyroid adenoma associated	*THADA*
4820	136	102	1,33	0,036650	0,416	202052_s_at	Retinoic acid induced 14	*RAI14*
4026	208	156	1,33	0,029485	0,400	214693_x_at	Neuroblastoma breakpoint family, member 14	*NBPF14*
2097	30,6	22,9	1,33	0,013739	0,358	232097_at	TOX high mobility group box family member 4	*TOX4*
6000	49,1	36,8	1,33	0,048771	0,444	216835_s_at	Docking protein 1, 62kDa (downstream of tyrosine kinase 1)	*DOK1*
2874	52,8	39,6	1,33	0,020184	0,383	207688_s_at	Inhibin, beta C	*INHBC*
4127	49,9	37,4	1,33	0,030364	0,402	235938_at	Transcribed locus	-
4366	114	85,5	1,33	0,032479	0,407	213341_at	Fem-1 homolog c (C. elegans)	*FEM1C*
3385	131	98,4	1,33	0,024097	0,389	218578_at	Hyperparathyroidism 2 protein	*CDC73*
1576	23,2	17,4	1,33	0,009792	0,340	206429_at	Coagulation factor II (thrombin) receptor-like 1	*F2RL1*
3524	11,9	8,96	1,33	0,025289	0,392	210365_at	Runt-related transcription factor 1 (aml1 oncogene)	*RUNX1*
5571	99,3	74,5	1,33	0,044377	0,435	217985_s_at	Bromodomain adjacent to zinc finger domain, 1A	*BAZ1A*
5667	212	159	1,33	0,045223	0,436	214305_s_at	Splicing factor 3b, subunit 1, 155kDa	*SF3B1*
2017	36,0	27,0	1,33	0,013160	0,355	202972_s_at	Family with sequence similarity 13, member A1	*FAM13A1*
1624	318	239	1,33	0,010206	0,344	212463_at	CD59 molecule, complement regulatory protein	*CD59*
1005	520	391	1,33	0,005813	0,316	201251_at	Pyruvate kinase, muscle	*PKM2*
2183	105	78,6	1,33	0,014447	0,361	222754_at	tRNA nucleotidyl transferase, CCA-adding, 1	*TRNT1*
5305	1046	786	1,33	0,041390	0,426	201403_s_at	Microsomal glutathione S-transferase 3	*MGST3*
4047	69,0	51,8	1,33	0,029663	0,401	221277_s_at	Pseudouridylate synthase 3	*PUS3*
442	335	252	1,33	0,002345	0,288	214170_x_at	Fumarate hydratase	*FH*
3949	69,1	52,0	1,33	0,028839	0,399	1559038_at	Septin 2	*SEPT2*
357	83,5	62,8	1,33	0,001832	0,280	225757_s_at	Calmin (calponin-like, transmembrane)	*CLMN*
1884	4,78	3,59	1,33	0,012232	0,355	242033_at	Ring finger protein 180	*RNF180*
420	203	152	1,33	0,002205	0,286	218198_at	DEAH (Asp-Glu-Ala-His) box polypeptide 32	*DHX32*
1015	225	169	1,33	0,005873	0,316	204313_s_at	cAMP responsive element binding protein 1	*CREB1*
2338	46,9	35,3	1,33	0,015605	0,364	231016_s_at	Aryl hydrocarbon receptor nuclear translocator	*ARNT*
3400	124	93,6	1,33	0,024254	0,390	222667_s_at	Ash1 (absent, small, or homeotic)-like (Drosophila)	*ASH1L*
3648	55,8	42,0	1,33	0,026358	0,395	230734_x_at	Striatin, calmodulin binding protein	*STRN*
3298	118	88,6	1,33	0,023502	0,388	216246_at	Ribosomal protein S20	*RPS20*
5196	11,1	8,32	1,33	0,040056	0,421	237491_at	Myosin, heavy chain 10, non-muscle	*MYH10*
3673	159	120	1,33	0,026526	0,395	221589_s_at	Aldehyde dehydrogenase 6 family, member A1	*ALDH6A1*
4968	14,8	11,2	1,33	0,038109	0,419	208200_at	Interleukin 1, alpha	*IL1A*
241	529	398	1,33	0,001111	0,250	224838_at	Forkhead box P1	*FOXP1*
4215	58,5	44,0	1,33	0,031226	0,405	204085_s_at	Ceroid-lipofuscinosis, neuronal 5	*CLN5*
1121	36,6	27,6	1,33	0,006545	0,319	222599_s_at	Neuron navigator 2	*NAV2*
2190	29,8	22,4	1,33	0,014502	0,361	243790_at	Zinc finger protein 585A	*ZNF585A*
4744	28,7	21,6	1,33	0,035936	0,414	205809_s_at	Wiskott-Aldrich syndrome-like	*WASL*
5223	55,4	41,8	1,33	0,040397	0,423	228466_at	GA binding protein transcription factor, beta subunit 2	*GABPB2*
5051	121	91,5	1,33	0,038920	0,420	209515_s_at	RAB27A, member RAS oncogene family	*RAB27A*
1901	71,3	53,8	1,33	0,012362	0,355	203329_at	Protein tyrosine phosphatase, receptor type, M	*PTPRM*
1996	9,36	7,06	1,33	0,013038	0,355	237133_at	Sterile alpha motif and leucine zipper containing kinase AZK	*ZAK*
4347	118	89,1	1,33	0,032377	0,407	238002_at	Golgi integral membrane protein 4	*GOLIM4*
4166	160	121	1,33	0,030780	0,404	202040_s_at	Jumonji, AT rich interactive domain 1A	*JARID1A*
653	91,7	69,2	1,32	0,003728	0,308	221771_s_at	M-phase phosphoprotein, mpp8	*HSMPP8*
1534	63,7	48,1	1,32	0,009505	0,337	219348_at	SNARE-like tail-anchored protein 1 homolog	*USE1*
5194	197	149	1,32	0,040040	0,421	212044_s_at	Ribosomal protein L27a	*RPL27A*
3509	209	158	1,32	0,025212	0,392	226447_at	Ash1 (absent, small, or homeotic)-like (Drosophila)	*ASH1L*
228	73,2	55,3	1,32	0,001054	0,250	220212_s_at	Thyroid adenoma associated	*THADA*
1579	95,6	72,2	1,32	0,009820	0,340	225769_at	Component of oligomeric golgi complex 6	*COG6*

Index	Mutated*	Normal*	FC	*P* value	FDR**	Probe set	Description	Gene symbol
1185	42,8	32,3	1,32	0,006976	0,322	215153_at	Nitric oxide synthase 1 (neuronal) adaptor protein	*NOS1AP*
2519	35,1	26,5	1,32	0,016999	0,369	213575_at	Transformer-2 alpha	*TRA2A*
4716	6,36	4,81	1,32	0,035671	0,413	1569348_at	TPTE pseudogene	*psiTPTE22*
1461	95,4	72,1	1,32	0,008929	0,334	225507_at	Splicing factor, arginine/serine-rich 18	*SFRS18*
1156	9,67	7,31	1,32	0,006789	0,321	227766_at	Ligase IV, DNA, ATP-dependent	*LIG4*
4911	69,4	52,4	1,32	0,037558	0,418	215221_at	Forkhead box P1	*FOXP1*
2493	8,83	6,68	1,32	0,016799	0,367	241026_at	ADAM metallopeptidase domain 12	*ADAM12*
3175	149	113	1,32	0,022527	0,387	222763_s_at	WD repeat domain 33	*WDR33*
3837	91,7	69,3	1,32	0,028033	0,399	204312_x_at	cAMP responsive element binding protein 1	*CREB1*
3553	59,2	44,8	1,32	0,025615	0,394	243931_at	CD58 molecule	*CD58*
3066	42,4	32,1	1,32	0,021616	0,385	222487_s_at	Ribosomal protein S27-like	*RPS27L*
4162	10,4	7,88	1,32	0,030770	0,404	1560171_at	SNF2 histone linker PHD RING helicase	*SHPRH*
4674	22,8	17,3	1,32	0,035295	0,413	1554438_at	KIAA1217 protein	*KIAA1217*
783	28,0	21,2	1,32	0,004489	0,311	224023_s_at	Chromosome 3 open reading frame 10	*C3orf10*
5765	41,4	31,4	1,32	0,046330	0,439	216521_s_at	BRCA1/BRCA2-containing complex, subunit 3	*BRCC3*
1288	134	101	1,32	0,007671	0,325	218204_s_at	FYVE and coiled-coil domain containing 1	*FYCO1*
4728	128	97,1	1,32	0,035787	0,414	213642_at	Ribosomal protein L27	*RPL27*
4583	9,00	6,82	1,32	0,034643	0,412	207345_at	Follistatin	*FST*
2129	60,4	45,8	1,32	0,014003	0,359	214513_s_at	cAMP responsive element binding protein 1	*CREB1*
1218	121	92,0	1,32	0,007243	0,324	230440_at	Zinc finger protein 469	*ZNF469*
3325	822	623	1,32	0,023623	0,388	208662_s_at	Tetratricopeptide repeat domain 3	*TTC3*
182	6,02	4,56	1,32	0,000839	0,244	239539_at	NIMA (never in mitosis gene a)-related kinase 3	*NEK3*
1181	15,0	11,3	1,32	0,006957	0,322	1561689_at	cDNA DKFZp547G1518	-
2977	20,0	15,2	1,32	0,020921	0,384	243050_at	Peripheral myelin protein 22	*PMP22*
5448	51,0	38,6	1,32	0,042968	0,431	204645_at	Cyclin T2	*CCNT2*
1928	838	636	1,32	0,012570	0,355	218205_s_at	MAP kinase interacting serine/threonine kinase 2	*MKNK2*
4237	13,5	10,3	1,32	0,031402	0,405	242576_x_at	NEDD4 binding protein 2-like 2	*N4BP2L2*
3856	322	244	1,32	0,028153	0,399	218242_s_at	suppressor of variegation 4-20 homolog 1 (Drosophila)	*SUV420H1*
609	14,1	10,7	1,32	0,003435	0,308	236557_at	Zinc finger and BTB domain containing 38	*ZBTB38*
3342	6,90	5,24	1,32	0,023724	0,388	236930_at	Numb homolog (Drosophila)	*NUMB*
3069	7,22	5,48	1,32	0,021663	0,385	1558199_at	Fibronectin 1	*FN1*
4675	65,0	49,3	1,32	0,035307	0,413	202699_s_at	Transmembrane protein 63A	*TMEM63A*
6047	122	92,8	1,32	0,049281	0,445	227447_at	Superkiller viralicidic activity 2-like 2 (S. cerevisiae)	*SKIV2L2*
544	1223	928	1,32	0,002926	0,294	217802_s_at	Nuclear casein kinase and cyclin-dependent kinase substrate 1	*NUCKS1*
4833	239	181	1,32	0,036829	0,417	218618_s_at	Fibronectin type III domain containing 3B	*FNDC3B*
4430	24,1	18,3	1,32	0,033173	0,409	232716_at	cDNA FLJ11971 fis, clone HEMBB1001208	-
2011	1441	1094	1,32	0,013111	0,355	228222_at	Protein phosphatase 1, catalytic subunit, beta isoform	*PPP1CB*
1268	364	277	1,32	0,007544	0,325	224571_at	Interferon regulatory factor 2 binding protein 2	*IRF2BP2*
2999	34,2	26,0	1,32	0,021113	0,385	230395_at	Methyltransferase like 9	*METTL9*
3021	178	135	1,32	0,021274	0,385	214004_s_at	Vestigial like 4 (Drosophila)	*VGLL4*
3861	116	88,3	1,32	0,028187	0,399	202778_s_at	Zinc finger, MYM-type 2	*ZMYM2*
320	169	129	1,31	0,001600	0,272	225695_at	Chromosome 2 open reading frame 18	*C2orf18*
2708	10,9	8,26	1,31	0,018567	0,375	238967_at	Claudin 1	*CLDN1*
3709	137	104	1,31	0,026822	0,395	225181_at	AT rich interactive domain 1B (SWI1-like)	*ARID1B*
3507	64,4	49,0	1,31	0,025199	0,392	220992_s_at	Chromosome 1 open reading frame 25	*C1orf25*
3776	139	106	1,31	0,027447	0,397	224097_s_at	F11 receptor	*F11R*
2006	84,0	63,9	1,31	0,013086	0,355	223211_at	2-hydroxyacyl-CoA lyase 1	*HACL1*
2845	74,9	57,1	1,31	0,019914	0,383	232902_s_at	Arginyl-tRNA synthetase 2, mitochondrial (putative)	*RARS2*
3263	52,0	39,6	1,31	0,023162	0,388	236160_at	Thyroid hormone receptor interactor 11	*TRIP11*
2225	77,6	59,1	1,31	0,014790	0,363	218092_s_at	HIV-1 Rev binding protein	*HRB*
4676	73,8	56,2	1,31	0,035307	0,413	205084_at	B-cell receptor-associated protein 29	*BCAP29*
780	10,0	7,63	1,31	0,004474	0,311	232599_at	Exocyst complex component 6	*EXOC6*
4588	63,9	48,8	1,31	0,034690	0,412	230619_at	Aryl hydrocarbon receptor nuclear translocator	*ARNT*
2705	15,3	11,6	1,31	0,018551	0,375	210290_at	Zinc finger protein 174	*ZNF174*
1858	32,8	25,0	1,31	0,011974	0,352	214057_at	Myeloid cell leukemia sequence 1 (BCL2-related)	*MCL1*
2041	151	115	1,31	0,013276	0,355	208772_at	Ankyrin repeat and KH domain containing 1	*ANKHD1*
5921	8,31	6,34	1,31	0,047993	0,443	228577_x_at	Outer dense fiber of sperm tails 2-like	*ODF2L*

Index	Mutated*	Normal*	FC	*P* value	FDR**	Probe set	Description	Gene symbol
3463	50,1	38,3	1,31	0,024811	0,392	204167_at	Biotinidase	*BTD*
794	57,5	43,9	1,31	0,004535	0,311	205340_at	Zinc finger and BTB domain containing 24	*ZBTB24*
3534	19,5	14,9	1,31	0,025404	0,393	236094_at	Transcription factor 7-like 2 (T-cell specific, HMG-box)	*TCF7L2*
3199	26,7	20,4	1,31	0,022658	0,387	228184_at	Dispatched homolog 1 (Drosophila)	*DISP1*
4811	11,9	9,05	1,31	0,036542	0,415	222242_s_at	Kallikrein-related peptidase 5	*KLK5*
4173	75,7	57,8	1,31	0,030852	0,404	202440_s_at	Suppression of tumorigenicity 5	*ST5*
2829	67,6	51,6	1,31	0,019735	0,381	226981_at	Myeloid/lymphoid or mixed-lineage leukemia	*MLL*
3278	86,0	65,7	1,31	0,023351	0,388	218713_at	NMDA receptor regulated 2	*NARG2*
984	169	129	1,31	0,005692	0,315	203156_at	A kinase (PRKA) anchor protein 11	*AKAP11*
4681	27,3	20,9	1,31	0,035344	0,413	238028_at	Chromosome 6 open reading frame 132	*C6orf132*
5093	223	171	1,31	0,039187	0,420	202373_s_at	RAB3 GTPase activating protein subunit 2 (non-catalytic)	*RAB3GAP2*
4180	230	176	1,31	0,030902	0,404	212418_at	E74-like factor 1 (ets domain transcription factor)	*ELF1*
2049	221	169	1,31	0,013309	0,355	214594_x_at	ATPase, Class I, type 8B, member 1	*ATP8B1*
5159	51,8	39,6	1,31	0,039732	0,421	217653_x_at	-	-
3750	155	119	1,31	0,027267	0,397	218323_at	RAS homolog gene family, member T1	*RHOT1*
605	36,1	27,6	1,31	0,003356	0,303	235240_at	Ataxin 3	*ATXN3*
3666	1006	770	1,31	0,026498	0,395	223000_s_at	F11 receptor	*F11R*
2383	9,37	7,16	1,31	0,015893	0,364	244286_at	Formin binding protein 1	*FNBP1*
3106	262	201	1,31	0,021931	0,386	203137_at	Wilms tumor 1 associated protein	*WTAP*
4662	28,7	22,0	1,31	0,035198	0,413	243492_at	Thioesterase superfamily member 4	*THEM4*
5207	37,1	28,4	1,31	0,040181	0,422	1552656_s_a	U2AF homology motif (UHM) kinase 1	*UHMK1*
4844	87,7	67,1	1,31	0,036919	0,417	203883_s_at	RAB11 family interacting protein 2 (class I)	*RAB11FIP2*
4564	96,7	74,0	1,31	0,034503	0,412	202165_at	Protein phosphatase 1, regulatory (inhibitor) subunit 2	*PPP1R2*
223	16,1	12,3	1,31	0,001029	0,250	238841_at	Protein tyrosine phosphatase domain containing 1	*PTPDC1*
4893	372	285	1,31	0,037386	0,418	1554241_at	Coagulation factor C homolog, cochlin	*COCH*
912	78,1	59,8	1,31	0,005252	0,313	203187_at	Dedicator of cytokinesis 1	*DOCK1*
3399	60,0	45,9	1,31	0,024249	0,390	203375_s_at	Tripeptidyl peptidase II	*TPP2*
4012	71,5	54,7	1,31	0,029386	0,400	215698_at	Jumonji, AT rich interactive domain 1A	*JARID1A*
1399	290	222	1,31	0,008450	0,330	200931_s_at	Vinculin	*VCL*
5854	23,6	18,1	1,31	0,047338	0,442	222736_s_at	Transmembrane protein 38B	*TMEM38B*
3942	20,0	15,4	1,31	0,028788	0,399	222134_at	D-aspartate oxidase	*DDO*
4973	9,85	7,54	1,31	0,038156	0,419	203699_s_at	Deiodinase, iodothyronine, type II	*DIO2*
1676	83,0	63,6	1,31	0,010574	0,345	215136_s_at	Exosome component 8	*EXOSC8*
5658	60,8	46,6	1,31	0,045133	0,436	218503_at	KIAA1797 protein	*KIAA1797*
5842	113	86,5	1,31	0,047213	0,442	215450_at	Small nuclear ribonucleoprotein polypeptide E	*SNRPE*
6038	45,6	34,9	1,31	0,049156	0,445	219687_at	Hedgehog acyltransferase	*HHAT*
2762	76,0	58,2	1,30	0,019163	0,379	220925_at	N(alpha)-acetyltransferase 35, NatC auxiliary subunit	*MAK10*
1081	179	137	1,30	0,006326	0,319	223028_s_at	Sorting nexin 9	*SNX9*
5977	46,9	35,9	1,30	0,048541	0,444	232046_at	KIAA1217 protein	*KIAA1217*
1250	911	699	1,30	0,007424	0,325	224569_s_at	Interferon regulatory factor 2 binding protein 2	*IRF2BP2*
5137	6,22	4,77	1,30	0,039544	0,421	241885_at	68 kDa TATA-binding protein-associated factor	*TAF15*
3741	45,3	34,7	1,30	0,027224	0,397	214221_at	Alstrom syndrome 1	*ALMS1*
2673	37,0	28,4	1,30	0,018275	0,374	1558996_at	Forkhead box P1	*FOXP1*
3890	76,6	58,8	1,30	0,028433	0,399	213788_s_at	Non-protein coding RNA 94	*FLJ35348*
2907	80,3	61,6	1,30	0,020432	0,383	203971_at	Solute carrier family 31 (copper transporters), member 1	*SLC31A1*
171	106	81,4	1,30	0,000791	0,244	227026_at	M-phase phosphoprotein, mpp8	*HSMPP8*
3214	11,4	8,76	1,30	0,022771	0,387	244669_at	Small nucleolar RNA, C/D box 50A	*SNHG5*
1321	8,87	6,81	1,30	0,007877	0,326	238859_at	Family with sequence similarity 149, member B1	*FAM149B1*
1407	180	138	1,30	0,008500	0,330	219083_at	SHQ1 homolog (S. cerevisiae)	*SHQ1*
4929	44,4	34,1	1,30	0,037797	0,419	227891_s_at	68 kDa TATA-binding protein-associated factor	*TAF15*
1396	151	116	1,30	0,008434	0,330	203132_at	Retinoblastoma 1 (including osteosarcoma)	*RB1*
4807	38,5	29,6	1,30	0,036495	0,415	212366_at	Zinc finger protein 292	*ZNF292*
3640	168	129	1,30	0,026326	0,395	223189_x_at	Myeloid/lymphoid or mixed-lineage leukemia 5	*MLL5*
3711	266	205	1,30	0,026866	0,396	208815_x_at	Heat shock 70kDa protein 4	*HSPA4*
1118	292	224	1,30	0,006533	0,319	202181_at	KIAA0247 protein	*KIAA0247*
1958	186	143	1,30	0,012798	0,355	202515_at	Discs, large homolog 1 (Drosophila)	*DLG1*
1969	32,6	25,0	1,30	0,012861	0,355	201905_s_at	CTD small phosphatase-like protein	*CTDSPL*

Index	Mutated*	Normal*	FC	*P* value	FDR**	Probe set	Description	Gene symbol
2555	94,7	72,8	1,30	0,017292	0,370	212923_s_at	Chromosome 6 open reading frame 145	*C6orf145*
5628	240	185	1,30	0,044933	0,436	208999_at	Septin 8	*SEPT8*
1483	23,4	18,0	1,30	0,009115	0,336	243350_at	Chromosome 5 open reading frame 15	*C5orf15*
2226	21,6	16,6	1,30	0,014798	0,363	231995_at	Chromosome 9 open reading frame 82	*C9orf82*
2496	488	375	1,30	0,016821	0,367	229394_s_at	Glucocorticoid receptor DNA binding factor 1	*GRLF1*
5666	114	87,7	1,30	0,045208	0,436	220419_s_at	Ubiquitin specific peptidase 25	*USP25*
4315	4,43	3,41	1,30	0,032137	0,407	242906_at	cDNA DKFZp313B1017	-
2484	204	157	1,30	0,016747	0,367	204314_s_at	cAMP responsive element binding protein 1	*CREB1*
1222	12,1	9,33	1,30	0,007269	0,324	201335_s_at	Rho guanine nucleotide exchange factor (GEF) 12	*ARHGEF12*
4492	111	85,7	1,30	0,033777	0,411	201883_s_at	UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, polypeptide 1	*B4GALT1*
2376	74,8	57,6	1,30	0,015843	0,364	205606_at	Low density lipoprotein receptor-related protein 6	*LRP6*
1089	26,2	20,2	1,30	0,006385	0,319	212759_s_at	Transcription factor 7-like 2 (T-cell specific, HMG-box)	*TCF7L2*
2488	10,3	7,93	1,30	0,016766	0,367	225807_at	Jub, ajuba homolog (Xenopus laevis)	*JUB*
91	134	103	1,30	0,000335	0,201	220355_s_at	Polybromo 1	*PBRM1*
4153	46,5	35,8	1,30	0,030632	0,403	224631_at	Zinc finger protein 91 homolog (mouse)	*ZFP91*
2045	15,9	12,3	1,30	0,013297	0,355	231933_at	Membrane-associated ring finger (C3HC4) 8	*MARCH8*
3284	206	159	1,30	0,023406	0,388	223190_s_at	Myeloid/lymphoid or mixed-lineage leukemia 5	*MLL5*
3796	209	161	1,30	0,027652	0,398	212888_at	Dicer1, Dcr-1 homolog (Drosophila)	*DICER1*
4995	98,1	75,5	1,30	0,038339	0,420	225954_s_at	Midnolin	*MIDN*
2218	9,64	7,43	1,30	0,014709	0,362	217951_s_at	PHD finger protein 3	*PHF3*
2105	11,5	8,89	1,30	0,013791	0,358	239930_at	UDP-GalNAc:polypeptide N-acetylgalactosaminyltransferase 2	*GALNT2*
4101	253	195	1,30	0,030146	0,402	202271_at	F-box protein 28	*FBXO28*
603	22,8	17,6	1,30	0,003349	0,303	205135_s_at	nuclear fragile X mental retardation protein interacting protein 1	*NUFIP1*
5735	101	78,1	1,30	0,046000	0,438	234491_s_at	Salvador homolog 1 (Drosophila)	*SAV1*
6113	4633	3570	1,30	0,049881	0,446	215076_s_at	Collagen, type III, alpha 1	*COL3A1*
5249	287	221	1,30	0,040640	0,423	228785_at	Zinc finger protein 281	*ZNF281*
5708	140	108	1,30	0,045701	0,438	205178_s_at	Retinoblastoma binding protein 6	*RBBP6*
5775	78,8	60,8	1,30	0,046449	0,440	204066_s_at	Centaurin, gamma 2	*CENTG2*
3555	755	582	1,30	0,025641	0,394	200983_x_at	CD59 molecule, complement regulatory protein	*CD59*
5524	13,0	10,0	1,30	0,043811	0,433	230126_s_at	Jumonji domain containing 2B	*JMJD2B*
3999	123	95,0	1,30	0,029269	0,400	228980_at	Ring finger and FYVE-like domain containing 1	*RFFL*
1420	58,5	45,2	1,30	0,008606	0,331	235728_at	Zinc finger protein 3 homolog (mouse)	*ZFP3*
2468	46,1	35,6	1,30	0,016587	0,367	239035_at	5,10-methylenetetrahydrofolate reductase (NADPH)	*MTHFR*
1229	294	227	1,29	0,007311	0,324	201302_at	Annexin A4	*ANXA4*
4333	187	144	1,29	0,032255	0,407	214177_s_at	Pre-B-cell leukemia homeobox interacting protein 1	*PBXIP1*
2280	240	186	1,29	0,015155	0,363	225629_s_at	Zinc finger and BTB domain containing 4	*ZBTB4*
2530	185	143	1,29	0,017088	0,369	202372_at	RAB3 GTPase activating protein subunit 2 (non-catalytic)	*RAB3GAP2*
5392	195	151	1,29	0,042279	0,429	225334_at	Chromosome 10 open reading frame 32	*C10orf32*
2135	5,02	3,88	1,29	0,014029	0,359	1564699_at	cDNA clone IMAGE:4297077	-
2589	80,1	61,9	1,29	0,017551	0,371	202414_at	DNA excision repair protein ERCC-5	*ERCC5*
2257	24,7	19,1	1,29	0,015020	0,363	229298_at	Kelch repeat and BTB (POZ) domain containing 7	*KBTBD7*
1390	195	150	1,29	0,008404	0,330	210249_s_at	Nuclear receptor coactivator 1	*NCOA1*
2761	20,1	15,5	1,29	0,019156	0,379	230937_at	Hypothetical protein LOC285835	*LOC285835*
982	307	237	1,29	0,005690	0,315	211503_s_at	RAB14, member RAS oncogene family	*RAB14*
1713	4,34	3,36	1,29	0,010984	0,348	221805_at	neurofilament, light polypeptide 68kDa	*NEFL*
4539	170	132	1,29	0,034291	0,412	212648_at	DEAH (Asp-Glu-Ala-His) box polypeptide 29	*DHX29*
4157	108	83,4	1,29	0,030721	0,404	218802_at	Coiled-coil domain containing 109B	*CCDC109B*
4212	298	231	1,29	0,031187	0,405	213233_s_at	Kelch-like 9 (Drosophila)	*KLHL9*
5340	334	259	1,29	0,041822	0,428	201015_s_at	Junction plakoglobin	*JUP*
4249	281	218	1,29	0,031552	0,406	202593_s_at	Membrane interacting protein of RGS16	*MIR16*
5621	61,7	47,8	1,29	0,044867	0,436	218644_at	Pleckstrin 2	*PLEK2*
2345	28,6	22,2	1,29	0,015647	0,364	207492_at	N-glycanase 1	*NGLY1*
1967	1471	1140	1,29	0,012857	0,355	226880_at	Nuclear casein kinase and cyclin-dependent kinase substrate 1	*NUCKS1*
1630	6,92	5,36	1,29	0,010280	0,344	235133_at	Zinc finger, DHHC domain containing 14	*ZDHHC14*
1179	13,7	10,6	1,29	0,006930	0,321	244536_at	Tumor protein p53 binding protein, 2	*TP53BP2*
5096	57,9	44,9	1,29	0,039207	0,420	210731_s_at	Lectin, galactoside-binding, soluble, 8 (galectin 8)	*LGALS8*
1068	333	258	1,29	0,006266	0,319	203033_x_at	Fumarate hydratase	*FH*

Index	Mutated*	Normal*	FC	*P* value	FDR**	Probe set	Description	Gene symbol
1436	6,50	5,04	1,29	0,008701	0,331	222936_s_at	PPPDE peptidase domain containing 1	*PPPDE1*
4562	5,57	4,32	1,29	0,034472	0,412	1559360_at	Ephrin-A5	*EFNA5*
3460	8,20	6,36	1,29	0,024786	0,392	1559343_at	Small nuclear ribonucleoprotein polypeptide N	*SNRPN*
2575	273	212	1,29	0,017479	0,371	203045_at	Ninjurin 1	*NINJ1*
385	245	190	1,29	0,002005	0,284	223238_s_at	Polybromo 1	*PBRM1*
4238	23,7	18,4	1,29	0,031402	0,405	1555082_a_a	NIMA (never in mitosis gene a)- related kinase 11	*NEK11*
1599	22,5	17,5	1,29	0,009976	0,341	224375_at	-	-
1385	15,4	12,0	1,29	0,008329	0,329	1558755_x_a	Zinc finger protein 763	*ZNF763*
2978	48,7	37,8	1,29	0,020942	0,384	221985_at	Kelch-like 24 (Drosophila)	*KLHL24*
4865	11,1	8,63	1,29	0,037107	0,417	1556423_at	Vasohibin 1	*VASH1*
5215	164	127	1,29	0,040292	0,422	225399_at	Chromosome 1 open reading frame 19	*C1orf19*
2283	443	344	1,29	0,015178	0,363	201816_s_at	Glioblastoma amplified sequence	*GBAS*
1219	23,7	18,4	1,29	0,007250	0,324	241874_at	Chromosome 5 open reading frame 53	*C5orf53*
6086	285	222	1,29	0,049690	0,446	206989_s_at	Splicing factor, arginine/serine-rich 2, interacting protein	*SFRS2IP*
5857	90,8	70,7	1,29	0,047366	0,442	58780_s_at	Hypothetical protein FLJ10357	*FLJ10357*
1082	175	136	1,29	0,006332	0,319	212104_s_at	RNA binding motif protein 9	*RBM9*
5890	25,8	20,1	1,29	0,047638	0,442	236109_at	RNA pseudouridylate synthase domain containing 4	*RPUSD4*
3537	94,5	73,6	1,29	0,025444	0,393	210028_s_at	Origin recognition complex, subunit 3-like (yeast)	*ORC3L*
2918	43,8	34,1	1,28	0,020483	0,383	234660_s_at	DIS3 mitotic control homolog (S. cerevisiae)	*DIS3*
3039	105	81,9	1,28	0,021421	0,385	218298_s_at	Chromosome 14 open reading frame 159	*C14orf159*
492	73,8	57,5	1,28	0,002634	0,289	230623_x_at	Ubiquitin specific peptidase 28	*USP28*
4337	36,7	28,6	1,28	0,032273	0,407	219307_at	Prenyl (decaprenyl) diphosphate synthase, subunit 2	*PDSS2*
2969	626	488	1,28	0,020864	0,384	212773_s_at	Translocase of outer mitochondrial membrane 20 homolog (yeast)	*TOMM20*
1667	132	103	1,28	0,010536	0,345	212676_at	Neurofibromin 1	*NF1*
4377	80,7	62,9	1,28	0,032561	0,407	223679_at	Catenin (cadherin-associated protein), beta 1, 88kDa	*CTNNB1*
2813	123	95,6	1,28	0,019620	0,381	202005_at	Suppression of tumorigenicity 14 (colon carcinoma)	*ST14*
29	4,61	3,60	1,28	0,000134	0,201	234330_at	cDNA FLJ14081 fis, clone HEMBB1002280	-
4967	17,2	13,4	1,28	0,038108	0,419	210251_s_at	RUN and FYVE domain containing 3	*RUFY3*
2127	169	132	1,28	0,013995	0,359	201411_s_at	Pleckstrin homology domain-containing family B member 2	*PLEKHB2*
4029	52,3	40,8	1,28	0,029509	0,400	213271_s_at	Dopey family member 1	*DOPEY1*
5237	62,9	49,0	1,28	0,040542	0,423	204831_at	Cyclin-dependent kinase 8	*CDK8*
2335	27,4	21,4	1,28	0,015586	0,364	213298_at	Nuclear factor I/C (CCAAT-binding transcription factor)	*NFIC*
4434	89,9	70,2	1,28	0,033210	0,409	241993_x_at	Forkhead box P1	*FOXP1*
4908	395	308	1,28	0,037540	0,418	226128_at	Chromosome 1 open reading frame 58	*C1orf58*
3568	18,7	14,6	1,28	0,025750	0,394	228748_at	CD59 molecule, complement regulatory protein	*CD59*
3586	87,3	68,2	1,28	0,025882	0,394	1553677_a_a	TIP41, TOR signaling pathway regulator-like (S. cerevisiae)	*TIPRL*
2621	2180	1702	1,28	0,017810	0,371	217807_s_at	Glioma tumor suppressor candidate region gene 2	*GLTSCR2*
4536	172	134	1,28	0,034269	0,412	217954_s_at	PHD finger protein 3	*PHF3*
5798	53,9	42,1	1,28	0,046770	0,441	242750_at	Methylmalonic aciduria (cobalamin deficiency) cblA type	*MMAA*
3493	10,0	7,85	1,28	0,025104	0,392	224044_at	RAS homolog gene family, member T1	*RHOT1*
5800	14,2	11,1	1,28	0,046781	0,441	206448_at	Zinc finger protein 365	*ZNF365*
4907	5,77	4,51	1,28	0,037524	0,418	1557961_s_a	N-terminal EF-hand calcium binding protein 1	*NECAB1*
1811	10,5	8,23	1,28	0,011679	0,351	244272_s_at	Membrane targeting (tandem) C2 domain containing 1	*MTAC2D1*
1064	62,4	48,8	1,28	0,006244	0,319	227895_at	Family with sequence similarity 120B	*FAM120B*
4008	93,5	73,1	1,28	0,029322	0,400	223021_x_at	Vps20-associated 1 homolog (S. cerevisiae)	*VTA1*
5687	34,5	27,0	1,28	0,045389	0,436	239364_at	Ets variant 6	*ETV6*
5847	12,8	9,97	1,28	0,047281	0,442	228948_at	EPH receptor A4	*EPHA4*
3872	210	164	1,28	0,028285	0,399	223151_at	DCUN1 domain-containing protein 5	*DCUN1D5*
486	205	160	1,28	0,002589	0,289	223329_x_at	SGT1, suppressor of G2 allele of SKP1 (S. cerevisiae)	*SUGT1*
1743	13,1	10,2	1,28	0,011131	0,348	1569020_at	Neural precursor cell expressed, developmentally down-regulated 9	*NEDD9*
2449	110	85,9	1,28	0,016399	0,366	226277_at	Collagen, type IV, alpha 3 (Goodpasture antigen) binding protein	*COL4A3BP*
3232	90,8	71,0	1,28	0,022914	0,388	225838_at	Enhancer of polycomb homolog 2 (Drosophila)	*EPC2*
938	42,2	33,0	1,28	0,005368	0,313	204786_s_at	Interferon (alpha, beta and omega) receptor 2	*IFNAR2*
5498	98,2	76,8	1,28	0,043512	0,433	235196_at	Hyperparathyroidism 2 protein	*CDC73*
1329	266	208	1,28	0,007999	0,328	217885_at	Importin 9	*IPO9*
1370	10,8	8,42	1,28	0,008234	0,328	205460_at	neuronal PAS domain protein 2	*NPAS2*
5016	5,70	4,46	1,28	0,038592	0,420	206032_at	Desmocollin 3	*DSC3*

Index	Mutated*	Normal*	FC	*P* value	FDR**	Probe set	Description	Gene symbol
1006	24,5	19,2	1,28	0,005833	0,316	217230_at	Villin 2 (ezrin)	*VIL2*
5307	6,06	4,74	1,28	0,041399	0,426	1557895_at	FLJ35934 protein	*FLJ35934*
577	7,63	5,98	1,28	0,003171	0,300	217538_at	Small G protein signaling modulator 2	*SGSM2*
3138	105	82,6	1,28	0,022259	0,387	210776_x_at	Transcription factor 3	*TCF3*
6105	106	83,2	1,28	0,049843	0,446	223304_at	Solute carrier family 37 member 3	*SLC37A3*
5891	27,4	21,4	1,28	0,047647	0,442	230759_at	Sorting nexin 14	*SNX14*
2267	48,1	37,7	1,28	0,015072	0,363	240166_x_at	RNA (guanine-9-) methyltransferase domain containing 3	*RG9MTD3*
5963	7,83	6,13	1,28	0,048431	0,444	241198_s_at	Chromosome 11 open reading frame 70	*C11orf70*
3865	60,8	47,7	1,28	0,028230	0,399	225539_at	Zinc finger protein 295	*ZNF295*
3527	74,1	58,0	1,28	0,025327	0,393	209798_at	Nuclear protein, ataxia-telangiectasia locus	*NPAT*
2689	123	96,5	1,28	0,018430	0,375	238761_at	Mediator complex subunit 28	*MED28*
2565	11,8	9,27	1,28	0,017400	0,371	236149_at	THO complex 3	*THOC3*
4541	60,7	47,6	1,28	0,034311	0,412	219303_at	Chromosome 13 open reading frame 7	*C13orf7*
97	5,86	4,60	1,28	0,000377	0,212	1560776_at	Family with sequence similarity 18, member B2	*FAM18B2*
681	153	120	1,28	0,003912	0,308	224309_s_at	SGT1, suppressor of G2 allele of SKP1 (S. cerevisiae)	*SUGT1*
5349	359	282	1,28	0,041933	0,429	202322_s_at	Geranylgeranyl diphosphate synthase 1	*GGPS1*
747	5,76	4,52	1,28	0,004234	0,308	37170_at	BMP2 inducible kinase	*BMP2K*
4602	24,9	19,5	1,28	0,034797	0,412	236268_at	SEC22 vesicle trafficking protein homolog C (S. cerevisiae)	*SEC22C*
5570	6,29	4,93	1,28	0,044354	0,435	232885_at	Non-protein coding RNA 81	*NCRNA00081*
3163	59,1	46,4	1,28	0,022450	0,387	222607_s_at	DIS3 mitotic control homolog (S. cerevisiae)	*DIS3*
5397	101	79,3	1,28	0,042322	0,429	210285_x_at	Wilms tumor 1 associated protein	*WTAP*
5559	30,4	23,9	1,27	0,044255	0,435	219011_at	Pleckstrin homology domain-containing family A member 4	*PLEKHA4*
3471	140	110	1,27	0,024902	0,392	231807_at	KIAA1217 protein	*KIAA1217*
1166	18,7	14,6	1,27	0,006860	0,321	242136_x_at	Hypothetical protein LOC403340	*MGC70870*
1342	7,76	6,09	1,27	0,008057	0,328	240465_at	Chromosome 4 open reading frame 32	*C4orf32*
820	178	140	1,27	0,004683	0,312	207643_s_at	Tumor necrosis factor receptor superfamily, member 1A	*TNFRSF1A*
1519	67,7	53,1	1,27	0,009389	0,337	213463_s_at	Family with sequence similarity 149, member B1	*FAM149B1*
3664	342	269	1,27	0,026486	0,395	202677_at	RAS p21 protein activator (GTPase activating protein) 1	*RASA1*
5076	13,7	10,8	1,27	0,039052	0,420	232279_at	PHD finger protein 15	*PHF15*
2154	62,3	48,9	1,27	0,014186	0,360	212076_at	Myeloid/lymphoid or mixed-lineage leukemia	*MLL*
2549	139	110	1,27	0,017262	0,370	227569_at	Ligand of numb-protein X 2	*LNX2*
4470	220	173	1,27	0,033588	0,411	202790_at	Claudin 7	*CLDN7*
4216	4,20	3,30	1,27	0,031239	0,405	235075_at	Desmoglein 3 (pemphigus vulgaris antigen)	*DSG3*
6044	78,0	61,3	1,27	0,049239	0,445	225504_at	Homeobox containing 1	*HMBOX1*
2630	38,4	30,2	1,27	0,017905	0,372	204838_s_at	MUTL homolog 3 (E. coli)	*MLH3*
3657	60,0	47,2	1,27	0,026413	0,395	209378_s_at	KIAA1128 protein	*KIAA1128*
1745	12,0	9,44	1,27	0,011145	0,348	232457_at	LIM and calponin homology domains 1	*LIMCH1*
5850	47,5	37,3	1,27	0,047331	0,442	226783_at	Alanine-glyoxylate aminotransferase 2-like 2	*AGXT2L2*
2785	10,0	7,89	1,27	0,019343	0,380	237262_at	Family with sequence similarity 59, member A	*FAM59A*
4049	26,4	20,7	1,27	0,029667	0,401	204054_at	Phosphatase and tensin homolog	*PTEN*
4278	91,3	71,8	1,27	0,031792	0,406	222136_x_at	Zinc finger protein 43	*ZNF43*
5169	23,7	18,7	1,27	0,039825	0,421	222364_at	Solute carrier family 44, member 1	*SLC44A1*
4042	30,0	23,6	1,27	0,029635	0,401	228091_at	Syntaxin 17	*STX17*
3593	632	497	1,27	0,025913	0,394	201334_s_at	Rho guanine nucleotide exchange factor (GEF) 12	*ARHGEF12*
3047	176	138	1,27	0,021453	0,385	224703_at	WD repeat domain 22	*WDR22*
4156	170	134	1,27	0,030678	0,404	225080_at	Myosin IC	*MYO1C*
4575	18,8	14,8	1,27	0,034585	0,412	205180_s_at	ADAM metallopeptidase domain 8	*ADAM8*
3906	116	91,0	1,27	0,028522	0,399	218244_at	Nucleolar protein 8	*NOL8*
3854	6,52	5,13	1,27	0,028142	0,399	1556650_at	Autism susceptibility candidate 2	*AUTS2*
6065	77,8	61,3	1,27	0,049473	0,446	240277_at	Solute carrier family 30 (zinc transporter), member 7	*SLC30A7*
814	10,4	8,23	1,27	0,004655	0,312	222438_at	Mediator complex subunit 4	*MED4*
4399	12,1	9,55	1,27	0,032786	0,407	238342_at	Hypothetical protein LOC283846	*LOC283846*
1183	4,53	3,57	1,27	0,006957	0,322	1557036_at	Zinc finger and BTB domain containing 1	*ZBTB1*
3006	11,1	8,77	1,27	0,021167	0,385	230542_at	Zinc finger protein 597	*ZNF597*
3925	11,3	8,87	1,27	0,028693	0,399	206652_at	Zinc finger, MYM-type 5	*ZMYM5*
6055	144	113	1,27	0,049379	0,446	213026_at	ATG12 autophagy related 12 homolog (S. cerevisiae)	*ATG12*
2800	67,8	53,4	1,27	0,019466	0,380	219024_at	Pleckstrin homology domain containing, family A member 1	*PLEKHA1*

Index	Mutated*	Normal*	FC	*P* value	FDR**	Probe set	Description	Gene symbol
4196	20,6	16,3	1,27	0,030996	0,404	240723_at	Enah/Vasp-like	*EVL*
3499	136	107	1,27	0,025144	0,392	214773_x_at	TIP41, TOR signaling pathway regulator-like (S. cerevisiae)	*TIPRL*
5810	374	295	1,27	0,046927	0,442	226214_at	Membrane interacting protein of RGS16	*MIR16*
1635	6,21	4,90	1,27	0,010310	0,344	240829_at	Peroxisomal biogenesis factor 3	*PEX3*
4342	30,1	23,8	1,27	0,032332	0,407	206348_s_at	Pyruvate dehydrogenase kinase, isozyme 3	*PDK3*
2342	78,3	61,8	1,27	0,015631	0,364	225398_at	RNA pseudouridylate synthase domain containing 4	*RPUSD4*
1283	161	127	1,27	0,007640	0,325	218243_at	RUN and FYVE domain containing 1	*RUFY1*
1924	129	102	1,27	0,012518	0,355	224945_at	BTB (POZ) domain containing 7	*BTBD7*
3439	143	113	1,27	0,024624	0,391	222414_at	Myeloid/lymphoid or mixed-lineage leukemia 3	*MLL3*
5755	23,3	18,4	1,27	0,046191	0,439	230164_at	Zinc finger protein 621	*ZNF621*
4724	78,3	61,8	1,27	0,035738	0,414	215616_s_at	Jumonji domain containing 2B	*JMJD2B*
3536	18,9	14,9	1,27	0,025437	0,393	216621_at	Rho-associated, coiled-coil containing protein kinase 1	*ROCK1*
4735	69,8	55,1	1,27	0,035844	0,414	203481_at	Chromosome 10 open reading frame 6	*C10orf6*
3314	7,15	5,65	1,27	0,023558	0,388	243555_at	Endothelin receptor type A	*EDNRA*
1291	12,7	10,1	1,27	0,007697	0,325	211094_s_at	Neurofibromin 1	*NF1*
4313	144	114	1,27	0,032102	0,407	209024_s_at	Synaptotagmin binding, cytoplasmic RNA interacting protein	*SYNCRIP*
3782	6,86	5,42	1,26	0,027532	0,398	1559697_a_a	cDNA clone YW24B11	-
3072	148	117	1,26	0,021670	0,385	234950_s_at	Ring finger and WD repeat domain 2	*RFWD2*
2142	170	135	1,26	0,014101	0,360	202386_s_at	KIAA0430 protein	*KIAA0430*
3765	35,0	27,7	1,26	0,027366	0,397	213100_at	Unc-5 homolog B (C. elegans)	*UNC5B*
3948	77,1	60,9	1,26	0,028828	0,399	217496_s_at	Insulin-degrading enzyme	*IDE*
5317	79,5	62,9	1,26	0,041490	0,427	204084_s_at	Ceroid-lipofuscinosis, neuronal 5	*CLN5*
5368	39,4	31,2	1,26	0,042143	0,429	219565_at	Cytochrome P450, family 20, subfamily A, polypeptide 1	*CYP20A1*
454	352	278	1,26	0,002430	0,288	222389_s_at	WW domain containing adaptor with coiled-coil	*WAC*
1018	74,9	59,3	1,26	0,005886	0,316	63009_at	SHQ1 homolog (S. cerevisiae)	*SHQ1*
3631	45,3	35,9	1,26	0,026255	0,395	214220_s_at	Alstrom syndrome 1	*ALMS1*
4269	44,1	34,9	1,26	0,031745	0,406	1556034_s_a	Myotubularin related protein 11	*MTMR11*
1027	301	238	1,26	0,005943	0,316	217836_s_at	YY1 associated protein 1	*YY1AP1*
2901	152	121	1,26	0,020371	0,383	201613_s_at	Adaptor-related protein complex 1, gamma 2 subunit	*AP1G2*
4898	22,3	17,7	1,26	0,037472	0,418	204742_s_at	PDS5, regulator of cohesion maintenance, homolog B (S. cerevisiae)	*PDS5B*
4831	35,8	28,4	1,26	0,036802	0,416	219610_at	Rho-guanine nucleotide exchange factor	*RGNEF*
3881	323	256	1,26	0,028341	0,399	209102_s_at	HMG-box transcription factor 1	*HBP1*
5677	82,9	65,7	1,26	0,045324	0,436	203972_s_at	Peroxisomal biogenesis factor 3	*PEX3*
3958	104	82,4	1,26	0,028901	0,399	203035_s_at	Protein inhibitor of activated STAT, 3	*PIAS3*
472	11,8	9,34	1,26	0,002513	0,289	241152_at	Family with sequence similarity 120B	*FAM120B*
6017	11,7	9,29	1,26	0,048969	0,445	213067_at	Myosin, heavy chain 10, non-muscle	*MYH10*
3964	308	244	1,26	0,028956	0,399	201132_at	Heterogeneous nuclear ribonucleoprotein H2	*HNRPH2*
2462	354	281	1,26	0,016522	0,367	201301_s_at	Annexin A4	*ANXA4*
3089	329	261	1,26	0,021783	0,385	201153_s_at	Muscleblind-like (Drosophila)	*MBNL1*
4614	286	227	1,26	0,034830	0,412	224570_s_at	Interferon regulatory factor 2 binding protein 2	*IRF2BP2*
2072	285	227	1,26	0,013542	0,356	234969_s_at	Enhancer of polycomb homolog 1 (Drosophila)	*EPC1*
3853	9,22	7,32	1,26	0,028139	0,399	235784_at	Mitochondrial transcription termination factor	*MTERF*
2482	7,45	5,91	1,26	0,016728	0,367	206010_at	Hyaluronan binding protein 2	*HABP2*
4742	226	179	1,26	0,035914	0,414	225284_at	DnaJ (Hsp40) homolog, subfamily C, member 3	*DNAJC3*
4449	56,4	44,8	1,26	0,033417	0,411	200702_s_at	DEAD (Asp-Glu-Ala-Asp) box polypeptide 24	*DDX24*
4491	559	445	1,26	0,033777	0,411	212952_at	Calreticulin	*CALR*
5063	6,69	5,32	1,26	0,038964	0,420	242007_at	Primary neuroblastoma cDNA, clone:Nbla03526, full insert sequence	-
3834	833	662	1,26	0,028012	0,399	200810_s_at	Cold inducible RNA binding protein	*CIRBP*
5563	14,7	11,7	1,26	0,044296	0,435	226637_at	Ubiquitin-conjugating enzyme E2H (UBC8 homolog, yeast)	*UBE2H*
1821	7,77	6,18	1,26	0,011725	0,351	219834_at	Calcium-response factor	*ALS2CR8*
3897	25,0	19,9	1,26	0,028465	0,399	238722_x_at	N-acyl-phosphatidylethanolamine-hydrolyzing phospholipase D	*NAPE-PLD*
1618	128	102	1,26	0,010167	0,343	203530_s_at	Syntaxin 4	*STX4*
4158	808	643	1,26	0,030724	0,404	201121_s_at	Progesterone receptor membrane component 1	*PGRMC1*
4707	137	109	1,26	0,035583	0,413	201529_s_at	Replication protein A1, 70kDa	*RPA1*
2443	157	125	1,26	0,016345	0,366	224834_at	Ubiquitin domain containing 2	*UBTD2*
2177	5,74	4,57	1,26	0,014405	0,361	242985_x_at	Ring finger protein 180	*RNF180*
1831	12,2	9,71	1,26	0,011795	0,351	1565620_at	Centaurin, gamma-like family, member 1	*CTGLF1*

Index	Mutated*	Normal*	FC	*P* value	FDR**	Probe set	Description	Gene symbol
5478	9,00	7,17	1,26	0,043318	0,432	229669_at	Hypothetical gene supported by BC072410	*LOC440416*
3255	152	121	1,26	0,023112	0,388	227864_s_at	Family with sequence similarity 125, member A	*FAM125A*
5185	71,5	57,0	1,25	0,039966	0,421	212840_at	UBX domain containing 7	*UBXD7*
1262	8,22	6,55	1,25	0,007513	0,325	232722_at	Ribonuclease T2	*RNASET2*
5693	39,0	31,1	1,25	0,045552	0,437	238783_at	Transmembrane protein 161B	*TMEM161B*
5157	365	291	1,25	0,039709	0,421	201887_at	Interleukin 13 receptor, alpha 1	*IL13RA1*
5105	15,4	12,3	1,25	0,039278	0,421	223400_s_at	Polybromo 1	*PBRM1*
5138	285	227	1,25	0,039549	0,421	223306_at	Emopamil binding protein-like	*EBPL*
2239	176	140	1,25	0,014886	0,363	218142_s_at	Cereblon	*CRBN*
3167	8,58	6,85	1,25	0,022473	0,387	1560026_at	Hypothetical protein LOC149402	*LOC149401*
6013	25,4	20,3	1,25	0,048892	0,445	213252_at	SH3 and PX domains 2A	*SH3PXD2A*
921	4,73	3,77	1,25	0,005307	0,313	206033_s_at	Desmocollin 3	*DSC3*
3601	43,8	35,0	1,25	0,025975	0,394	204423_at	Muskelin 1, intracellular mediator containing kelch motifs	*MKLN1*
4371	168	134	1,25	0,032522	0,407	218528_s_at	Ring finger protein 38	*RNF38*
3305	117	93,5	1,25	0,023512	0,388	209175_at	SEC23 interacting protein	*SEC23IP*
4247	192	153	1,25	0,031536	0,406	225264_at	Arginyl-tRNA synthetase 2, mitochondrial (putative)	*RARS2*
5378	6,05	4,83	1,25	0,042175	0,429	216683_at	Tubulin folding cofactor A	*TBCA*
4170	12,3	9,82	1,25	0,030811	0,404	235471_at	Chromosome 10 open reading frame 72	*C10orf72*
4143	19,4	15,5	1,25	0,030568	0,403	243659_at	Elongation factor, RNA polymerase II, 2	*ELL2*
5324	611	488	1,25	0,041620	0,427	208623_s_at	Villin 2 (ezrin)	*VIL2*
749	30,1	24,0	1,25	0,004248	0,308	1556067_a_a	Jumonji domain containing 3	*JMJD3*
4584	71,5	57,2	1,25	0,034644	0,412	226323_at	Coiled-coil domain containing 16	*CCDC16*
3041	170	136	1,25	0,021427	0,385	201813_s_at	TBC1 domain family, member 5	*TBC1D5*
1639	247	197	1,25	0,010332	0,344	203250_at	RNA binding motif protein 16	*RBM16*
2736	7,87	6,29	1,25	0,018875	0,377	237208_at	WD repeat domain 61	*WDR61*
5216	12,0	9,60	1,25	0,040304	0,422	239957_at	SET domain containing 5	*SETD5*
143	9,42	7,53	1,25	0,000653	0,244	244168_s_at	Unc-51-like kinase 4 (C. elegans)	*ULK4*
5760	68,9	55,1	1,25	0,046272	0,439	209533_s_at	Phospholipase A2-activating protein	*PLAA*
3204	288	230	1,25	0,022686	0,387	225032_at	Fibronectin type III domain containing 3B	*FNDC3B*
1163	11,0	8,83	1,25	0,006851	0,321	242280_x_at	Cytoplasmic polyadenylation element binding protein 4	*CPEB4*
3494	10,7	8,52	1,25	0,025115	0,392	1565567_at	Syntaxin 7	*STX7*
5572	179	143	1,25	0,044389	0,435	209432_s_at	cAMP responsive element binding protein 3	*CREB3*
5423	279	223	1,25	0,042677	0,430	212287_at	Suppressor of zeste 12 homolog (Drosophila)	*SUZ12*
4941	70,1	56,0	1,25	0,037913	0,419	219530_at	Partner and localizer of BRCA2	*PALB2*
5722	186	149	1,25	0,045857	0,438	221825_at	Angel homolog 2 (Drosophila)	*ANGEL2*
5645	62,1	49,7	1,25	0,045052	0,436	213412_at	Tight junction protein 3 (zona occludens 3)	*TJP3*
3830	102	81,5	1,25	0,027976	0,399	226073_at	Transmembrane protein 218	*TMEM218*
282	14,3	11,4	1,25	0,001387	0,263	220171_x_at	KIAA1704 protein	*KIAA1704*
1902	195	156	1,25	0,012370	0,355	218082_s_at	Upstream binding protein 1 (LBP-1a)	*UBP1*
518	249	199	1,25	0,002756	0,291	202122_s_at	Mannose-6-phosphate receptor binding protein 1	*M6PRBP1*
5092	154	123	1,25	0,039177	0,420	222148_s_at	RAS homolog gene family, member T1	*RHOT1*
2577	77,8	62,3	1,25	0,017485	0,371	201085_s_at	SON DNA binding protein	*SON*
2866	21,9	17,5	1,25	0,020114	0,383	204501_at	Nephroblastoma overexpressed gene	*NOV*
2147	9,32	7,46	1,25	0,014131	0,360	205503_at	Protein tyrosine phosphatase, non-receptor type 14	*PTPN14*
4916	104	82,9	1,25	0,037628	0,418	226155_at	Family with sequence similarity 160, member B1	*FAM161B1*
4103	27,7	22,2	1,25	0,030150	0,402	205205_at	V-rel reticuloendotheliosis viral oncogene homolog B	*RELB*
3480	88,8	71,1	1,25	0,024981	0,392	202725_at	Polymerase (RNA) II (DNA directed) polypeptide A, 220kDa	*POLR2A*
6029	23,2	18,6	1,25	0,049057	0,445	230592_at	NSL1, MIND kinetochore complex component, homolog (S. cerevisiae)	*NSL1*
6035	14,3	11,4	1,25	0,049118	0,445	229794_at	Zinc finger protein 585A	*ZNF585A*
5721	83,6	67,0	1,25	0,045828	0,438	235056_at	Ets variant gene 6 (TEL oncogene)	*ETV6*
2884	231	185	1,25	0,020237	0,383	209484_s_at	NSL1, MIND kinetochore complex component, homolog (S. cerevisiae)	*NSL1*
434	9,57	7,67	1,25	0,002286	0,288	238851_at	Ankyrin repeat domain 13A	*ANKRD13A*
5670	384	308	1,25	0,045249	0,436	213455_at	Family with sequence similarity 114, member A1	*FAM114A1*
3465	182	146	1,25	0,024833	0,392	231968_at	UDP-glucose glycoprotein glucosyltransferase 1	*UGCGL1*
4133	74,1	59,4	1,25	0,030413	0,402	218221_at	Aryl hydrocarbon receptor nuclear translocator	*ARNT*
3415	6,87	5,51	1,25	0,024385	0,390	1569512_at	Supervillin	*SVIL*
2739	218	175	1,25	0,018899	0,377	200596_s_at	Eukaryotic translation initiation factor 3, subunit A	*EIF3A*

Index	Mutated*	Normal*	FC	*P* value	FDR**	Probe set	Description	Gene symbol
3821	10,8	8,66	1,25	0,027890	0,399	234151_at	CUG triplet repeat, RNA binding protein 2	*CUGBP2*
4321	66,2	53,1	1,25	0,032173	0,407	238653_at	Leucine-rich repeats and immunoglobulin-like domains 2	*LRIG2*
4595	105	84,4	1,25	0,034766	0,412	225317_at	Acyl-Coenzyme A binding domain containing 6	*ACBD6*
3899	14,7	11,8	1,25	0,028482	0,399	226627_at	Septin 8	*SEPT8*
4922	39,2	31,4	1,25	0,037708	0,419	206853_s_at	Mitogen-activated protein kinase kinase kinase 7	*MAP3K7*
4023	117	94,0	1,25	0,029457	0,400	239891_x_at	RAB12, member RAS oncogene family	*RAB12*
4229	12,5	10,1	1,25	0,031335	0,405	238243_at	cDNA clone YI43B12	-
4324	299	240	1,25	0,032183	0,407	202038_at	Ubiquitination factor E4A (UFD2 homolog, yeast)	*UBE4A*
2037	6,11	4,91	1,25	0,013271	0,355	223867_at	Tektin 3	*TEKT3*
1045	121	97,4	1,25	0,006113	0,319	201473_at	Jun B proto-oncogene	*JUNB*
5222	1013	814	1,24	0,040381	0,423	201170_s_at	Basic helix-loop-helix domain containing, class B, 2	*BHLHB2*
5426	564	453	1,24	0,042688	0,430	200760_s_at	ADP-ribosylation-like factor 6 interacting protein 5	*ARL6IP5*
3500	82,7	66,4	1,24	0,025153	0,392	203723_at	Inositol 1,4,5-trisphosphate 3-kinase B	*ITPKB*
5907	123	99,0	1,24	0,047874	0,443	212538_at	Dedicator of cytokinesis 9	*DOCK9*
1652	341	274	1,24	0,010398	0,344	215088_s_at	Succinate dehydrogenase cytochrome b560 subunit, mitochondrial	*SDHC*
5003	261	210	1,24	0,038419	0,420	201845_s_at	RING1 and YY1 binding protein	*RYBP*
553	5,31	4,27	1,24	0,003007	0,296	239571_at	Myocyte enhancer factor 2A	*MEF2A*
462	253	204	1,24	0,002457	0,288	212086_x_at	Lamin A/C	*LMNA*
1322	8,33	6,70	1,24	0,007893	0,326	39548_at	Neuronal PAS domain protein 2	*NPAS2*
3453	116	93,6	1,24	0,024725	0,391	221786_at	Chromosome 6 open reading frame 120	*C6orf120*
4039	123	98,6	1,24	0,029594	0,401	225050_at	Zinc finger protein 512	*ZNF512*
5410	189	152	1,24	0,042490	0,429	226126_at	TBC1 domain containing kinase	*TBCK*
5637	94,9	76,3	1,24	0,044983	0,436	226178_at	Suppressor of cytokine signaling 4	*SOCS4*
5777	103	82,5	1,24	0,046501	0,440	223269_at	Polymerase (RNA) III (DNA directed) polypeptide G (32kD)-like	*POLR3GL*
3445	104	83,8	1,24	0,024655	0,391	212603_at	Mitochondrial ribosomal protein S31	*MRPS31*
1270	58,8	47,3	1,24	0,007545	0,325	204711_at	KIAA0753 protein	*KIAA0753*
3431	93,5	75,3	1,24	0,024567	0,391	214429_at	Myotubularin related protein 6	*MTMR6*
2015	58,6	47,2	1,24	0,013146	0,355	222955_s_at	Family with sequence similarity 45, member A	*FAM45A*
5198	137	110	1,24	0,040105	0,422	223007_s_at	Chromosome 9 open reading frame 5	*C9orf5*
1305	13,4	10,8	1,24	0,007774	0,325	221854_at	Plakophilin 1	*PKP1*
3236	113	90,7	1,24	0,022942	0,388	207513_s_at	Zinc finger protein 189	*ZNF189*
4701	9,74	7,85	1,24	0,035496	0,413	207016_s_at	Aldehyde dehydrogenase 1 family, member A2	*ALDH1A2*
2474	16,0	12,9	1,24	0,016644	0,367	228913_at	Hypothetical protein LOC100190939	*LOC100190939*
2357	216	174	1,24	0,015726	0,364	203338_at	Protein phosphatase 2, regulatory subunit B', epsilon isoform	*PPP2R5E*
5704	134	108	1,24	0,045657	0,438	204771_s_at	Transcription termination factor, RNA polymerase I	*TTF1*
3182	181	146	1,24	0,022556	0,387	224445_s_at	Zinc finger, FYVE domain containing 21	*ZFYVE21*
3887	92,3	74,4	1,24	0,028395	0,399	1555789_s_a	Nucleoporin 98kDa	*NUP98*
1152	4,69	3,78	1,24	0,006776	0,321	1553894_at	Coiled-coil domain containing 122	*CCDC122*
3173	79,3	64,0	1,24	0,022506	0,387	213940_s_at	Formin binding protein 1	*FNBP1*
2775	109	87,6	1,24	0,019266	0,380	205917_at	Zinc finger protein 264	*ZNF264*
5607	79,7	64,3	1,24	0,044717	0,436	223221_at	SCO cytochrome oxidase deficient homolog 1 (yeast)	*SCO1*
606	8,30	6,70	1,24	0,003362	0,303	215428_at	tight junction protein 1 (zona occludens 1)	*TJP1*
2511	73,0	58,9	1,24	0,016885	0,368	209073_s_at	Numb homolog (Drosophila)	*NUMB*
478	9,72	7,85	1,24	0,002562	0,289	227226_at	Chromosome 6 open reading frame 117	*C6orf117*
4797	41,6	33,6	1,24	0,036388	0,415	224304_x_at	Ninein (GSK3B interacting protein)	*NIN*
4789	47,4	38,3	1,24	0,036311	0,415	1554762_a_a	WW and C2 domain containing 2	*WWC2*
497	24,2	19,5	1,24	0,002648	0,289	240095_at	Transcribed locus	-
4442	96,7	78,0	1,24	0,033367	0,411	204908_s_at	B-cell CLL/lymphoma 3	*BCL3*
3792	153	123	1,24	0,027619	0,398	213123_at	Microfibrillar-associated protein 3	*MFAP3*
4118	234	189	1,24	0,030275	0,402	224572_s_at	Interferon regulatory factor 2 binding protein 2	*IRF2BP2*
5973	17,0	13,7	1,24	0,048503	0,444	227839_at	Methyl-CpG binding domain protein 5	*MBD5*
1834	4,51	3,65	1,24	0,011808	0,351	232958_at	phosphorylase, glycogen	*PYGL*
4512	135	109	1,24	0,034012	0,412	219276_x_at	Chromosome 9 open reading frame 82	*C9orf82*
4553	493	398	1,24	0,034415	0,412	200765_x_at	Catenin (cadherin-associated protein), alpha 1, 102kDa	*CTNNA1*
5084	51,1	41,3	1,24	0,039131	0,420	213736_at	Cytochrome c oxidase subunit Vb	*COX5B*
2666	12,0	9,70	1,24	0,018229	0,374	239162_at	Death-associated protein kinase 1	*DAPK1*
5673	236	191	1,24	0,045279	0,436	228992_at	Mediator complex subunit 28	*MED28*

Index	Mutated*	Normal*	FC	*P* value	FDR**	Probe set	Description	Gene symbol
1641	202	163	1,24	0,010340	0,344	221699_s_at	DEAD (Asp-Glu-Ala-Asp) box polypeptide 50	*DDX50*
3391	57,7	46,7	1,24	0,024157	0,389	214672_at	Tubulin tyrosine ligase-like family, member 5	*TTLL5*
1836	143	115	1,24	0,011814	0,351	218572_at	Chromatin modifying protein 4A	*CHMP4A*
5475	33,0	26,7	1,24	0,043287	0,432	232724_at	Membrane-spanning 4-domains, subfamily A, member 6A	*MS4A6A*
2922	30,5	24,7	1,24	0,020495	0,383	216174_at	Hepatocellular carcinoma-related HCRP1	*HCRP1*
4656	172	139	1,24	0,035159	0,413	203447_at	Proteasome (prosome, macropain) 26S subunit, non-ATPase, 5	*PSMD5*
5885	33,0	26,7	1,24	0,047614	0,442	241348_at	Zinc finger protein 654	*ZNF654*
2860	92,4	74,7	1,24	0,020095	0,383	223182_s_at	1-acylglycerol-3-phosphate O-acyltransferase 3	*AGPAT3*
5331	9,85	7,97	1,24	0,041741	0,428	1560112_at	WD repeat and FYVE domain containing 2	*WDFY2*
3794	95,6	77,4	1,24	0,027639	0,398	220326_s_at	Hypothetical protein FLJ10357	*FLJ10357*
5186	21,6	17,5	1,24	0,039970	0,421	239266_at	Small nucleolar RNA host gene 5 (non-protein coding)	*SNHG5*
3512	26,2	21,2	1,23	0,025218	0,392	226220_at	Methyltransferase like 9	*METTL9*
665	32,1	26,0	1,23	0,003832	0,308	227411_at	Wilms tumor 1 interacting protein	*WTIP*
788	5,27	4,27	1,23	0,004507	0,311	239661_at	AF4/FMR2 family, member 1	*AFF1*
3974	879	712	1,23	0,029043	0,400	210844_x_at	Catenin (cadherin-associated protein), alpha 1, 102kDa	*CTNNA1*
5046	179	145	1,23	0,038889	0,420	212694_s_at	Propionyl Coenzyme A carboxylase, beta polypeptide	*PCCB*
186	38,8	31,5	1,23	0,000862	0,244	223401_at	Chromosome 17 open reading frame 48	*C17orf48*
3259	128	104	1,23	0,023143	0,388	222531_s_at	Chromosome 14 open reading frame 108	*C14orf108*
1864	7,63	6,19	1,23	0,012028	0,353	243826_at	Nuclear receptor coactivator 1	*NCOA1*
6043	126	102	1,23	0,049222	0,445	225159_s_at	Mediator complex subunit 28	*MED28*
3517	133	108	1,23	0,025251	0,392	218616_at	Integrator complex subunit 12	*INTS12*
1815	227	184	1,23	0,011710	0,351	226347_at	Fucosyltransferase 11 (alpha (1,3) fucosyltransferase)	*FUT11*
2933	44,5	36,1	1,23	0,020572	0,383	219169_s_at	Transcription factor B1, mitochondrial	*TFB1M*
2883	867	703	1,23	0,020225	0,383	200797_s_at	Myeloid cell leukemia sequence 1 (BCL2-related)	*MCL1*
2962	795	645	1,23	0,020812	0,384	224731_at	High-mobility group box 1	*HMGB1*
4318	137	111	1,23	0,032157	0,407	203719_at	DNA excision repair protein ERCC-1	*ERCC1*
1261	187	152	1,23	0,007505	0,325	202225_at	v-crk sarcoma virus CT10 oncogene homolog	*CRK*
3559	130	105	1,23	0,025693	0,394	212264_s_at	Wings apart-like homolog (Drosophila)	*WAPAL*
4360	63,7	51,8	1,23	0,032427	0,407	218873_at	Gon-4-like (C. elegans)	*GON4L*
3971	23,8	19,3	1,23	0,029015	0,399	212758_s_at	Zinc finger E-box binding homeobox 1	*ZEB1*
5250	41,7	33,9	1,23	0,040672	0,423	203254_s_at	Talin 1	*TLN1*
1800	27,0	22,0	1,23	0,011584	0,351	204136_at	Collagen, type VII, alpha 1	*COL7A1*
1022	12,7	10,4	1,23	0,005924	0,316	230305_at	Transcribed locus	-
2360	40,8	33,2	1,23	0,015746	0,364	213728_at	Lysosomal-associated membrane protein 1	*LAMP1*
4805	7,07	5,75	1,23	0,036468	0,415	1555123_at	ST6 beta-galactosamide alpha-2,6-sialyltranferase 2	*ST6GAL2*
3728	14,3	11,6	1,23	0,027064	0,397	1558445_at	cDNA clone IMAGE:5277883	-
3783	118	95,6	1,23	0,027558	0,398	201624_at	Aspartyl-tRNA synthetase	*DARS*
4781	223	181	1,23	0,036268	0,414	212066_s_at	Ubiquitin specific peptidase 34	*USP34*
3538	253	206	1,23	0,025451	0,393	225144_at	Bone morphogenetic protein receptor, type II	*BMPR2*
6120	446	362	1,23	0,049977	0,446	222431_at	Spindlin 1	*SPIN1*
3590	6,34	5,16	1,23	0,025896	0,394	242856_at	cDNA FLJ10247 fis, clone HEMBB1000705	-
4579	43,9	35,7	1,23	0,034610	0,412	203592_s_at	Follistatin-like 3 (secreted glycoprotein)	*FSTL3*
2618	5,28	4,30	1,23	0,017785	0,371	206983_at	Chemokine (C-C motif) receptor 6	*CCR6*
1429	7,96	6,48	1,23	0,008672	0,331	243648_at	Zinc finger CCCH-type containing 11A	*ZC3H11A*
6025	468	381	1,23	0,049022	0,445	200798_x_at	Myeloid cell leukemia sequence 1 (BCL2-related)	*MCL1*
5744	89,6	72,9	1,23	0,046078	0,439	213063_at	Zinc finger CCCH-type containing 14	*ZC3H14*
1470	4,76	3,88	1,23	0,008989	0,334	233139_at	Ataxin 2-binding protein 1	*A2BP1*
383	300	245	1,23	0,001992	0,284	218571_s_at	Chromatin modifying protein 4A	*CHMP4A*
2740	57,2	46,6	1,23	0,018900	0,377	220935_s_at	CDK5 regulatory subunit associated protein 2	*CDK5RAP2*
4962	185	151	1,23	0,038055	0,419	218139_s_at	Chromosome 14 open reading frame 108	*C14orf108*
3746	24,9	20,3	1,23	0,027243	0,397	232637_at	Septin 2	*SEPT2*
6057	642	523	1,23	0,049408	0,446	208636_at	Actinin, alpha 1	*ACTN1*
5176	27,7	22,5	1,23	0,039888	0,421	209203_s_at	Bicaudal D homolog 2 (Drosophila)	*BICD2*
2876	9,83	8,01	1,23	0,020194	0,383	231471_at	zinc finger protein 638	*ZNF638*
5960	247	201	1,23	0,048384	0,444	225336_at	Splicing factor, arginine/serine-rich 2, interacting protein	*SFRS2IP*
997	4,72	3,85	1,23	0,005755	0,316	238297_at	Phosphatase and actin regulator 1	*PHACTR1*
572	212	173	1,23	0,003144	0,300	243_g_at	Microtubule-associated protein 4	*MAP4*

Index	Mutated*	Normal*	FC	*P* value	FDR**	Probe set	Description	Gene symbol
3109	405	330	1,23	0,021947	0,386	215096_s_at	Esterase D/formylglutathione hydrolase	*ESD*
1805	23,5	19,1	1,23	0,011624	0,351	227587_at	KRI1 homolog (S. cerevisiae)	*KRI1*
4398	16,5	13,4	1,23	0,032783	0,407	232890_at	-	-
5741	40,4	33,0	1,23	0,046067	0,439	210210_at	Myelin protein zero-like 1	*MPZL1*
2899	83,4	68,1	1,23	0,020348	0,383	223356_s_at	Mitochondrial translational initiation factor 3	*MTIF3*
2757	97,3	79,4	1,23	0,019126	0,379	208878_s_at	p21 (CDKN1A)-activated kinase 2	*PAK2*
5088	26,6	21,7	1,23	0,039159	0,420	241460_at	Ribosomal protein S6 kinase, 90 kDa, polypeptide 3	*RPS6KA2*
2723	7,24	5,91	1,23	0,018710	0,376	232964_at	Williams Beuren syndrome chromosome region 19	*WBSCR19*
2469	390	318	1,23	0,016588	0,367	208631_s_at	3-ketoacyl-Coenzyme A (CoA) thiolase, alpha subunit	*HADHA*
3653	695	567	1,22	0,026402	0,395	208684_at	Coatomer protein complex, subunit alpha	*COPA*
4860	11,4	9,35	1,22	0,037078	0,417	236808_at	FGFR1 oncogene partner 2	*FGFR1OP2*
4381	9,21	7,52	1,22	0,032594	0,407	217655_at	FXYD domain containing ion transport regulator 5	*FXYD5*
3567	5,39	4,40	1,22	0,025744	0,394	216563_at	Ankyrin repeat domain 12	*ANKRD12*
830	4,40	3,59	1,22	0,004743	0,312	239788_at	Suppressor of mec-8 and unc-52 homolog (C. elegans)	*SMU1*
2313	327	268	1,22	0,015366	0,363	202232_s_at	Eukaryotic translation initiation factor 3, subunit M	*EIF3M*
2309	96,1	78,5	1,22	0,015326	0,363	218153_at	Cysteinyl-tRNA synthetase 2, mitochondrial (putative)	*CARS2*
4306	6,00	4,90	1,22	0,032039	0,407	1560201_at	Zinc finger protein 713	*ZNF713*
800	24,3	19,9	1,22	0,004560	0,311	1553286_at	Zinc finger protein 555	*ZNF555*
924	472	386	1,22	0,005324	0,313	205480_s_at	UDP-glucose pyrophosphorylase 2	*UGP2*
3461	329	269	1,22	0,024790	0,392	212377_s_at	Notch homolog 2 (Drosophila)	*NOTCH2*
1452	538	440	1,22	0,008870	0,334	201007_at	Hydroxyacyl-Coenzyme A (CoA) dehydrogenase, beta subunit	*HADHB*
5668	54,6	44,7	1,22	0,045235	0,436	226251_at	Additional sex combs like 2 (Drosophila)	*ASXL2*
5314	93,1	76,2	1,22	0,041467	0,427	229650_s_at	Chromosome 19 open reading frame 42	*C19orf42*
5055	144	118	1,22	0,038950	0,420	225477_s_at	Nuclear receptor subfamily 2, group C, member 2	*NR2C2*
607	5,87	4,81	1,22	0,003400	0,306	1570165_at	carbohydrate (chondroitin 4) sulfotransferase 11	*CHST11*
5954	263	216	1,22	0,048297	0,444	200764_s_at	Catenin (cadherin-associated protein), alpha 1, 102kDa	*CTNNA1*
3694	13,5	11,1	1,22	0,026711	0,395	237398_at	Transcribed locus	-
4578	65,8	53,9	1,22	0,034604	0,412	218588_s_at	Chromosome 5 open reading frame 3	*C5orf3*
5027	22,7	18,6	1,22	0,038646	0,420	213328_at	NIMA (never in mitosis gene a)-related kinase 1	*NEK1*
5740	62,8	51,5	1,22	0,046057	0,439	220720_x_at	Family with sequence similarity 128, member B	*FAM128B*
5634	9,47	7,76	1,22	0,044977	0,436	1552261_at	WAP four-disulfide core domain 2	*WFDC2*
4577	122	100	1,22	0,034602	0,412	243916_x_at	Ubiquitin-like domain containing CTD phosphatase 1	*UBLCP1*
4284	63,5	52,0	1,22	0,031841	0,406	235013_at	Solute carrier family 31 (copper transporters), member 1	*SLC31A1*
5313	21,1	17,3	1,22	0,041461	0,427	242167_at	Chromosome 10 open reading frame 119	*C10orf119*
3420	83,0	68,1	1,22	0,024456	0,391	203822_s_at	E74-like factor 2 (ets domain transcription factor)	*ELF2*
4231	6,49	5,33	1,22	0,031356	0,405	235761_at	Tyrosylprotein sulfotransferase 2	*TPST2*
249	7,53	6,18	1,22	0,001142	0,251	231698_at	Hypothetical protein LOC647115	*FLJ36848*
4547	63,3	52,0	1,22	0,034366	0,412	213302_at	Phosphoribosylformylglycinamidine synthase	*PFAS*
1328	7,41	6,08	1,22	0,007996	0,328	233817_at	Neuroblastoma breakpoint family, member 10	*NBPF10*
4109	6,14	5,05	1,22	0,030199	0,402	232924_at	Leucine rich repeat containing 17	*LRRC17*
3833	34,5	28,3	1,22	0,028012	0,399	205665_at	Tetraspanin 9	*TSPAN9*
5125	98,2	80,8	1,22	0,039444	0,421	203334_at	DEAH (Asp-Glu-Ala-His) box polypeptide 8	*DHX8*
3888	30,8	25,4	1,22	0,028397	0,399	242981_at	Cytochrome P450, family 3, subfamily A, polypeptide 5	*CYP3A5*
2152	64,5	53,1	1,22	0,014179	0,360	228075_x_at	Transcription factor B1, mitochondrial	*TFB1M*
1442	14,1	11,6	1,22	0,008770	0,332	227575_s_at	Chromosome 14 open reading frame 102	*C14orf102*
5728	34,9	28,7	1,22	0,045939	0,438	37462_i_at	Splicing factor 3a, subunit 2, 66kDa	*SF3A2*
2861	345	284	1,22	0,020096	0,383	213531_s_at	RAB3 GTPase activating protein subunit 1 (catalytic)	*RAB3GAP1*
843	8,48	6,98	1,21	0,004829	0,313	233689_at	Transcription factor 7-like 2 (T-cell specific, HMG-box)	*TCF7L2*
4416	314	259	1,21	0,033028	0,409	218659_at	Additional sex combs like 2 (Drosophila)	*ASXL2*
2380	62,4	51,4	1,21	0,015858	0,364	217579_x_at	Atlastin GTPase 2	*ATL2*
3759	75,9	62,6	1,21	0,027317	0,397	226958_s_at	Mediator complex subunit 11	*MED11*
4896	265	219	1,21	0,037418	0,418	202160_at	CREB binding protein	*CREBBP*
5767	42,4	35,0	1,21	0,046339	0,439	218489_s_at	Aminolevulinate, delta-, dehydratase	*ALAD*
4822	45,9	37,8	1,21	0,036674	0,416	223330_s_at	SGT1, suppressor of G2 allele of SKP1 (S. cerevisiae)	*SUGT1*
3721	7,26	5,98	1,21	0,027006	0,397	1552536_at	Vesicle transport v-SNARE protein Vti1-like 2	*VTI1A*
2537	23,4	19,3	1,21	0,017162	0,369	216751_at	cDNA FLJ21226 fis, clone COL00721	-
5966	13,7	11,3	1,21	0,048449	0,444	211002_s_at	Tripartite motif-containing 29	*TRIM29*

Index	Mutated*	Normal*	FC	*P* value	FDR**	Probe set	Description	Gene symbol
5212	143	118	1,21	0,040252	0,422	226339_at	TruB pseudouridine (psi) synthase homolog 1 (E. coli)	*TRUB1*
4567	584	481	1,21	0,034549	0,412	209009_at	Esterase D/formylglutathione hydrolase	*ESD*
4217	12,4	10,2	1,21	0,031244	0,405	1558469_at	LIM domain containing preferred translocation partner in lipoma	*LPP*
3154	48,8	40,2	1,21	0,022373	0,387	205652_s_at	Tubulin tyrosine ligase-like family, member 1	*TTLL1*
2359	6,84	5,64	1,21	0,015733	0,364	227136_s_at	Chromosome 10 open reading frame 46	*C10orf46*
1814	6,52	5,38	1,21	0,011689	0,351	220623_s_at	Testis specific, 10	*TSGA10*
4391	185	153	1,21	0,032717	0,407	207196_s_at	TNFAIP3 interacting protein 1	*TNIP1*
2450	7,66	6,32	1,21	0,016409	0,366	214319_at	Furry homolog (Drosophila)	*FRY*
5253	46,6	38,5	1,21	0,040706	0,424	227335_at	Death inducer-obliterator 1	*DIDO1*
5641	105	86,7	1,21	0,045014	0,436	209367_at	Syntaxin binding protein 2	*STXBP2*
4775	509	420	1,21	0,036211	0,414	202004_x_at	Succinate dehydrogenase cytochrome b560 subunit, mitochondrial	*SDHC*
3819	172	142	1,21	0,027872	0,399	201573_s_at	Eukaryotic translation termination factor 1	*ETF1*
3669	139	115	1,21	0,026520	0,395	202930_s_at	Succinate-CoA ligase, ADP-forming, beta subunit	*SUCLA2*
3549	5,01	4,14	1,21	0,025535	0,393	206862_at	Zinc finger protein 254	*ZNF254*
3268	59,9	49,5	1,21	0,023220	0,388	221822_at	Coiled-coil domain containing 101	*CCDC101*
5743	113	93,3	1,21	0,046078	0,439	224768_at	IWS1 homolog (S. cerevisiae)	*IWS1*
4780	174	143	1,21	0,036246	0,414	229322_at	Protein phosphatase 2, regulatory subunit B', epsilon isoform	*PPP2R5E*
3991	12,2	10,0	1,21	0,029187	0,400	1563512_at	Nitric oxide synthase 1 (neuronal) adaptor protein	*NOS1AP*
6018	6,08	5,02	1,21	0,048981	0,445	238185_at	RNA binding motif, single stranded interacting protein 1	*RBMS1*
6040	42,9	35,5	1,21	0,049189	0,445	212786_at	C-type lectin domain family 16, member A	*CLEC16A*
5274	9,48	7,84	1,21	0,040984	0,425	1565811_at	Protein phosphatase 2B regulatory subunit 1	*PPP3R1*
5706	181	150	1,21	0,045693	0,438	201706_s_at	Peroxisomal biogenesis factor 19	*PEX19*
5440	53,3	44,1	1,21	0,042880	0,431	223555_at	Gon-4-like (C. elegans)	*GON4L*
3828	76,4	63,2	1,21	0,027934	0,399	217843_s_at	Mediator complex subunit 4	*MED4*
5033	8,24	6,81	1,21	0,038702	0,420	234036_x_at	cDNA FLJ21384 fis, clone COL03354	-
2124	17,6	14,6	1,21	0,013985	0,359	235654_at	Transcribed locus	-
2963	5,74	4,75	1,21	0,020822	0,384	1553646_at	Highly divergent homeobox	*HDX*
970	69,3	57,4	1,21	0,005625	0,315	204568_at	KIAA0831 protein	*KIAA0831*
4527	91,7	75,9	1,21	0,034174	0,412	221006_s_at	sorting nexin family member 27	*SNX27*
3749	9,58	7,94	1,21	0,027264	0,397	242171_at	Platelet derived growth factor C	*PDGFC*
1787	9,78	8,10	1,21	0,011441	0,350	237026_at	Sorbin and SH3 domain containing 1	*SORBS1*
1227	122	101	1,21	0,007294	0,324	226054_at	Bromodomain containing 4	*BRD4*
2510	27,4	22,7	1,21	0,016885	0,368	227215_at	Golgi associated PDZ and coiled-coil motif containing	*GOPC*
4629	7,04	5,83	1,21	0,034913	0,412	222924_at	Sarcolemma associated protein	*SLMAP*
5539	62,3	51,6	1,21	0,044020	0,435	221256_s_at	Haloacid dehalogenase-like hydrolase domain containing 3	*HDHD3*
3462	635	527	1,21	0,024800	0,392	225312_at	COMM domain containing 6	*COMMD6*
2001	164	136	1,21	0,013067	0,355	224699_s_at	Extended synaptotagmin-like protein 2	*ESYT2*
5770	281	233	1,21	0,046353	0,439	202026_at	Succinate dehydrogenase complex subunit D	*SDHD*
4250	132	109	1,21	0,031565	0,406	202102_s_at	Bromodomain containing 4	*BRD4*
6048	40,4	33,5	1,21	0,049281	0,445	227579_at	-	-
4534	435	361	1,21	0,034252	0,412	223006_s_at	Chromosome 9 open reading frame 5	*C9orf5*
4655	229	190	1,21	0,035159	0,413	225229_at	AF4/FMR2 family, member 4	*AFF4*
3969	68,8	57,1	1,21	0,029000	0,399	203328_x_at	Insulin-degrading enzyme	*IDE*
2877	150	124	1,20	0,020196	0,383	226468_at	Zinc finger protein 364	*ZNF364*
3858	6,30	5,23	1,20	0,028173	0,399	205560_at	Proprotein convertase subtilisin/kexin type 5	*PCSK5*
3738	115	95,1	1,20	0,027140	0,397	218102_at	2-deoxyribose-5-phosphate aldolase homolog (C. elegans)	*DERA*
1633	11,2	9,31	1,20	0,010290	0,344	231366_at	MGC44478	*FDPSL2A*
5569	234	194	1,20	0,044333	0,435	225519_at	Protein phosphatase 4, regulatory subunit 2	*PPP4R2*
3945	4,14	3,44	1,20	0,028807	0,399	220666_at	-	-
4846	9,82	8,16	1,20	0,036920	0,417	220273_at	Interleukin 17B	*IL17B*
3600	10,2	8,51	1,20	0,025962	0,394	231167_at	Solute carrier family 44, member 1	*SLC44A1*
1900	77,6	64,4	1,20	0,012354	0,355	204812_at	ZW10, kinetochore associated, homolog (Drosophila)	*ZW10*
3955	155	129	1,20	0,028895	0,399	225417_at	Enhancer of polycomb homolog 1 (Drosophila)	*EPC1*
4074	6,33	5,26	1,20	0,029882	0,401	232427_at	Zinc finger protein 224	*ZNF224*
2807	9,30	7,73	1,20	0,019529	0,380	231369_at	Zinc finger protein 333	*ZNF333*
5838	63,8	53,1	1,20	0,047180	0,442	206782_s_at	DnaJ (Hsp40) homolog, subfamily C, member 4	*DNAJC4*
2155	5,24	4,36	1,20	0,014200	0,360	237248_at	Phosphodiesterase 11A	*PDE11A*

Index	Mutated*	Normal*	FC	*P* value	FDR**	Probe set	Description	Gene symbol
16	3,66	3,04	1,20	0,000056	0,191	239129_at	Transforming growth factor, beta receptor 1	*TGFBR1*
5011	5,59	4,65	1,20	0,038515	0,420	1557113_at	Hypothetical protein LOC283588	*LOC283588*
575	12,7	10,6	1,20	0,003159	0,300	236199_at	Arachidonate 5-lipoxygenase	*ALOX5*
3011	21,6	18,0	1,20	0,021185	0,385	214757_at	Postmeiotic segregation increased 2-like 2 pseudogene	*PMS2L2*
2520	67,0	55,8	1,20	0,017004	0,369	213349_at	Transmembrane and coiled-coil domain family 1	*TMCC1*
4872	90,3	75,2	1,20	0,037190	0,417	212080_at	Myeloid/lymphoid or mixed-lineage leukemia	*MLL*
1899	126	105	1,20	0,012352	0,355	219526_at	Chromosome 14 open reading frame 169	*C14orf169*
4927	14,5	12,1	1,20	0,037792	0,419	216685_s_at	Methylthioadenosine phosphorylase	*MTAP*
2593	5,01	4,18	1,20	0,017627	0,371	237376_at	Cullin 3	*CUL3*
4945	24,8	20,7	1,20	0,037937	0,419	201333_s_at	Rho guanine nucleotide exchange factor (GEF) 12	*ARHGEF12*
4764	57,7	48,1	1,20	0,036108	0,414	227541_at	WD repeat domain 20	*WDR20*
2199	181	151	1,20	0,014533	0,361	223081_at	PHD finger protein 23	*PHF23*
1769	9,42	7,86	1,20	0,011275	0,348	240176_at	Hypothetical protein LOC541471	*LOC541471*
913	7,10	5,93	1,20	0,005256	0,313	232930_at	Dedicator of cytokinesis 1	*DOCK1*
5848	5,98	4,99	1,20	0,047290	0,442	243352_at	Alpha-kinase 1	*ALPK1*
3213	13,6	11,3	1,20	0,022767	0,387	232940_s_at	Myeloid/lymphoid or mixed-lineage leukemia 3	*MLL3*
5227	24,0	20,0	1,20	0,040437	0,423	1559249_at	Ataxin 1	*ATXN1*
3577	16,9	14,1	1,20	0,025825	0,394	243201_at	Heterogeneous nuclear ribonucleoprotein H2	*HNRPH2*
262	5,23	4,37	1,20	0,001237	0,258	227939_s_at	Transformer-2 alpha	*TRA2A*
5262	5,05	4,22	1,20	0,040873	0,425	232303_at	Zinc finger protein 608	*ZNF608*
3807	23,0	19,2	1,20	0,027721	0,398	219075_at	Yip1 domain family, member 2	*YIPF2*
4592	4,61	3,86	1,20	0,034744	0,412	238811_at	ATPase, Class VI, type 11B	*ATP11B*
4664	9,19	7,69	1,20	0,035223	0,413	1554867_a_a	Proline rich 16	*PRR16*
3836	9,18	7,68	1,20	0,028032	0,399	238865_at	Similar to poly(A) binding protein, cytoplasmic 4 (inducible form)	*LOC132430*
5007	4,69	3,92	1,20	0,038469	0,420	219936_s_at	G protein-coupled receptor 87	*GPR87*
4652	60,4	50,5	1,19	0,035132	0,413	202584_at	Nuclear transcription factor, X-box binding 1	*NFX1*
2858	39,5	33,1	1,19	0,020070	0,383	228917_at	Zinc finger protein 510	*ZNF510*
2209	10,5	8,83	1,19	0,014633	0,362	237418_at	CDK5 regulatory subunit associated protein 2	*CDK5RAP2*
6123	10,7	8,98	1,19	0,049992	0,446	205894_at	Arylsulfatase E (chondrodysplasia punctata 1)	*ARSE*
5618	190	159	1,19	0,044833	0,436	201877_s_at	Protein phosphatase 2, regulatory subunit B', gamma isoform	*PPP2R5C*
5999	338	283	1,19	0,048771	0,444	201528_at	Replication protein A1, 70kDa	*RPA1*
2816	16,9	14,2	1,19	0,019638	0,381	212650_at	EH domain binding protein 1	*EHBP1*
3151	13,9	11,7	1,19	0,022368	0,387	237252_at	Thrombomodulin	*THBD*
3615	207	173	1,19	0,026088	0,395	221502_at	Karyopherin alpha 3 (importin alpha 4)	*KPNA3*
5039	17,3	14,5	1,19	0,038830	0,420	238827_at	SH3 domain containing ring finger 2	*SH3RF2*
5477	5,79	4,85	1,19	0,043305	0,432	214967_at	cDNA FLJ12055 fis, clone HEMBB1002049	-
4325	7,41	6,21	1,19	0,032186	0,407	238614_x_at	Zinc finger protein 430	*ZNF430*
5292	8,31	6,97	1,19	0,041199	0,426	1553216_at	Zinc finger protein 41	*ZNF41*
4361	7,35	6,16	1,19	0,032432	0,407	1557797_a_a	Zinc finger E-box binding homeobox 2	*ZEB2*
4307	46,5	39,0	1,19	0,032045	0,407	214783_s_at	Annexin A11	*ANXA11*
2742	64,4	54,0	1,19	0,018920	0,377	204928_s_at	Solute carrier family 10, member 3	*SLC10A3*
2702	5,18	4,35	1,19	0,018540	0,375	1566825_at	Rho GTPase activating protein 24	*ARHGAP24*
4424	62,2	52,2	1,19	0,033118	0,409	225234_at	Cas-Br-M (murine) ecotropic retroviral transforming sequence	*CBL*
4108	504	423	1,19	0,030195	0,402	206200_s_at	Annexin A11	*ANXA11*
3883	52,9	44,4	1,19	0,028348	0,399	237868_x_at	FK506 binding protein 15, 133kDa	*FKBP15*
5964	65,7	55,2	1,19	0,048437	0,444	233775_x_at	cDNA FLJ13242 fis, clone OVARC1000578	-
5388	8,98	7,55	1,19	0,042252	0,429	236241_at	Mediator complex subunit 31	*MED31*
2606	162	137	1,19	0,017699	0,371	235142_at	Zinc finger and BTB domain containing 8	*ZBTB8*
3241	497	418	1,19	0,022991	0,388	224936_at	Eukaryotic translation initiation factor 2, subunit 3 gamma	*EIF2S3*
4003	41,2	34,7	1,19	0,029304	0,400	238510_at	Zinc finger protein 720	*ZNF720*
5831	90,2	75,9	1,19	0,047123	0,442	214902_x_at	Hypothetical protein FLJ42393	*FLJ42393*
1533	31,0	26,1	1,19	0,009503	0,337	212078_s_at	Myeloid/lymphoid or mixed-lineage leukemia	*MLL*
1058	4,61	3,88	1,19	0,006206	0,319	232332_at	KIAA1210 protein	*RP13-347D8.3*
3424	46,6	39,2	1,19	0,024470	0,391	244406_at	Zinc finger protein 20	*ZNF20*
4088	5,15	4,33	1,19	0,030065	0,402	241242_at	Family with sequence similarity 120A	*FAM120A*
4019	13,1	11,1	1,19	0,029426	0,400	239023_at	CDC42 small effector 1	*CDC42SE1*
4919	49,2	41,4	1,19	0,037662	0,419	236027_at	Chromosome 10 open reading frame 78	*C10orf78*

Index	Mutated*	Normal*	FC	*P* value	FDR**	Probe set	Description	Gene symbol
3508	82,8	69,8	1,19	0,025201	0,392	205745_x_at	ADAM metallopeptidase domain 17	*ADAM17*
2718	5,75	4,85	1,19	0,018671	0,376	244655_at	Hypothetical protein LOC644192	*LOC644192*
3998	24,2	20,4	1,19	0,029266	0,400	203348_s_at	Ets variant gene 5 (ets-related molecule)	*ETV5*
2111	525	443	1,19	0,013848	0,358	202231_at	Eukaryotic translation initiation factor 3, subunit M	*EIF3M*
2787	120	102	1,19	0,019363	0,380	218147_s_at	Glycosyltransferase 8 domain containing 1	*GLT8D1*
5540	1104	931	1,19	0,044029	0,435	200761_s_at	ADP-ribosylation-like factor 6 interacting protein 5	*ARL6IP5*
4894	7,25	6,11	1,19	0,037400	0,418	1569538_at	Clone FLB8310 PRO2225	-
5975	20,2	17,1	1,19	0,048531	0,444	242297_at	RAS responsive element binding protein 1	*RREB1*
4141	9,44	7,97	1,18	0,030562	0,403	1558306_at	Thyroid adenoma associated	*THADA*
2138	44,7	37,7	1,18	0,014054	0,359	218466_at	TBC1 domain family, member 17	*TBC1D17*
5364	11,7	9,87	1,18	0,042082	0,429	232588_at	Stromal antigen 1	*STAG1*
4458	9,99	8,43	1,18	0,033495	0,411	227913_at	Exosome component 3	*EXOSC3*
3687	791	668	1,18	0,026627	0,395	211938_at	Eukaryotic translation initiation factor 4B	*EIF4B*
2490	10,8	9,10	1,18	0,016784	0,367	214605_x_at	G protein-coupled receptor 1	*GPR1*
988	8,17	6,90	1,18	0,005696	0,315	230790_x_at	Forkhead box N3	*FOXN3*
560	4,96	4,19	1,18	0,003054	0,298	234605_at	CDC14 cell division cycle 14 homolog B (S. cerevisiae)	*CDC14B*
5951	655	553	1,18	0,048273	0,444	226801_s_at	Axin interactor, dorsalization associated	*AIDA*
4161	10,7	9,04	1,18	0,030766	0,404	232428_at	Monoacylglycerol O-acyltransferase 2	*MOGAT2*
4085	10,6	8,97	1,18	0,030000	0,402	238027_at	Hypothetical protein LOC202051	*LOC202051*
5421	633	535	1,18	0,042622	0,430	208942_s_at	Translocation protein 1	*TLOC1*
2463	94,4	79,8	1,18	0,016526	0,367	204765_at	Rho guanine nucleotide exchange factor (GEF) 5	*ARHGEF5*
1503	459	388	1,18	0,009241	0,336	217874_at	succinate-CoA ligase, GDP-forming, alpha subunit	*SUCLG1*
4124	296	250	1,18	0,030332	0,402	224777_s_at	PAF acetylhydrolase 30 kDa subunit	*PAFAH1B2*
1172	6,82	5,77	1,18	0,006886	0,321	1557158_s_a	Myeloid/lymphoid or mixed-lineage leukemia 3	*MLL3*
1545	5,52	4,68	1,18	0,009545	0,337	1558754_at	Zinc finger protein 763	*ZNF763*
1855	9,53	8,07	1,18	0,011950	0,352	232465_at	Transcription factor 7-like 2 (T-cell specific, HMG-box)	*TCF7L2*
3122	5,95	5,04	1,18	0,022089	0,387	1567044_s_a	LSM14A, SCD6 homolog A (S. cerevisiae)	*LSM14A*
3357	9,84	8,34	1,18	0,023837	0,388	229274_at	GNAS complex locus	*GNAS*
6039	75,5	64,0	1,18	0,049159	0,445	225565_at	cAMP responsive element binding protein 1	*CREB1*
3531	5,44	4,61	1,18	0,025382	0,393	1565638_at	Peripheral myelin protein 22	*PMP22*
2698	11,4	9,64	1,18	0,018502	0,375	214000_s_at	Regulator of G-protein signalling 10	*RGS10*
1486	4,29	3,64	1,18	0,009150	0,336	220328_at	Polyhomeotic homolog 3 (Drosophila)	*PHC3*
1301	3738	3169	1,18	0,007743	0,325	211940_x_at	H3 histone, family 3A	*H3F3A*
5534	171	145	1,18	0,043938	0,434	204028_s_at	RAB GTPase activating protein 1	*RABGAP1*
664	286	243	1,18	0,003828	0,308	226052_at	Bromodomain containing 4	*BRD4*
6102	17,4	14,8	1,18	0,049810	0,446	226890_at	WD repeat domain 35	*WDR35*
2426	7,69	6,53	1,18	0,016220	0,365	1562059_at	Transmembrane 9 superfamily member 3	*TM9SF3*
5646	31,3	26,6	1,18	0,045055	0,436	213896_x_at	Family with sequence similarity 149, member B1	*FAM149B1*
5779	153	130	1,18	0,046525	0,440	202537_s_at	Chromatin modifying protein 2B	*CHMP2B*
1785	10,5	8,93	1,18	0,011402	0,349	203969_at	Peroxisomal biogenesis factor 3	*PEX3*
5151	30,0	25,4	1,18	0,039647	0,421	215718_s_at	PHD finger protein 3	*PHF3*
2377	6,55	5,56	1,18	0,015844	0,364	230258_at	GLIS family zinc finger 3	*GLIS3*
4691	204	173	1,18	0,035438	0,413	201434_at	Tetratricopeptide repeat domain 1	*TTC1*
2622	8,58	7,29	1,18	0,017816	0,371	235283_at	Integrator complex subunit 6	*INTS6*
4087	11,8	10,1	1,18	0,030029	0,402	232621_at	Ubiquitin specific peptidase 48	*USP48*
4970	96,7	82,2	1,18	0,038124	0,419	206551_x_at	Kelch-like 24 (Drosophila)	*KLHL24*
3119	12,9	11,0	1,18	0,022053	0,387	244698_at	CMT1A duplicated region transcript 4	*CDRT4*
1894	5,37	4,57	1,18	0,012314	0,355	214829_at	Aminoadipate-semialdehyde synthase	*AASS*
331	4,70	4,00	1,18	0,001647	0,272	242258_at	Zinc finger and BTB domain containing 1	*ZBTB1*
3676	27,6	23,5	1,18	0,026571	0,395	1557690_x_a	Neuronal PAS domain protein 2	*NPAS2*
5293	6,26	5,32	1,18	0,041222	0,426	242006_at	Leber congenital amaurosis 5	*LCA5*
5916	4,12	3,51	1,18	0,047949	0,443	206543_at	ATP-dependent helicase SMARCA2	*SMARCA2*
1756	5,67	4,83	1,18	0,011197	0,348	1562815_at	EF-hand calcium binding domain 6	*EFCAB6*
2440	5,29	4,50	1,17	0,016309	0,365	210697_at	Zinc finger protein 257	*ZNF257*
4902	76,0	64,7	1,17	0,037505	0,418	214316_x_at	Calreticulin	*CALR*
4075	3,44	2,93	1,17	0,029884	0,401	240292_x_at	Ankyrin repeat and sterile alpha motif domain containing 1B	*ANKS1B*
2607	5,75	4,89	1,17	0,017706	0,371	244691_at	SET domain containing 5	*SETD5*

Index	Mutated*	Normal*	FC	*P* value	FDR**	Probe set	Description	Gene symbol
4213	920	784	1,17	0,031202	0,405	217768_at	Chromosome 14 open reading frame 166	*C14orf166*
4021	6,36	5,42	1,17	0,029430	0,400	233253_at	cDNA FLJ14147 fis, clone MAMMA1002973	-
977	57,5	49,0	1,17	0,005671	0,315	235828_at	PRELI domain containing 2	*PRELID2*
3426	5,12	4,36	1,17	0,024496	0,391	243361_at	Splicing factor, arginine/serine-rich 12	*SFRS12*
2744	18,6	15,8	1,17	0,018935	0,377	219172_at	Ubiquitin domain containing 1	*UBTD1*
2930	19,8	16,8	1,17	0,020548	0,383	219380_x_at	Polymerase (DNA directed), eta	*POLH*
4920	257	219	1,17	0,037673	0,419	219598_s_at	RWD domain containing 1	*RWDD1*
2528	10,9	9,30	1,17	0,017077	0,369	214980_at	Ubiquitin protein ligase E3A	*UBE3A*
1963	4,35	3,71	1,17	0,012834	0,355	1558560_s_a	Basic leucine zipper nuclear factor 1 (JEM-1)	*BLZF1*
4040	19,6	16,7	1,17	0,029597	0,401	203945_at	Arginase, type II	*ARG2*
3747	5,82	4,96	1,17	0,027245	0,397	242456_at	MRE11 meiotic recombination 11 homolog A (S. cerevisiae)	*MRE11A*
5924	6,41	5,47	1,17	0,047997	0,443	239889_at	Chromosome 13 open reading frame 21	*C13orf21*
5488	84,2	71,8	1,17	0,043438	0,433	207268_x_at	Abl interactor 2	*ABI2*
5943	98,4	83,9	1,17	0,048165	0,443	1558511_s_a	Extended synaptotagmin-like protein 2	*ESYT2*
592	1152	984	1,17	0,003269	0,301	200677_at	Pituitary tumor-transforming 1 interacting protein	*PTTG1IP*
5042	35,6	30,4	1,17	0,038856	0,420	219247_s_at	Zinc finger, DHHC-type containing 14	*ZDHHC14*
1837	5,16	4,41	1,17	0,011815	0,351	1567457_at	RAS-related C3 botulinum toxin substrate 1	*RAC1*
5102	5,67	4,84	1,17	0,039232	0,420	208268_at	ADAM metallopeptidase domain 28	*ADAM28*
1502	49,6	42,4	1,17	0,009238	0,336	222195_s_at	Chromosome 9 open reading frame 156	*C9orf156*
5050	10,6	9,08	1,17	0,038907	0,420	214008_at	Twinfilin, actin-binding protein, homolog 1 (Drosophila)	*TWF1*
5357	132	113	1,17	0,042012	0,429	203057_s_at	PR domain containing 2, with ZNF domain	*PRDM2*
3043	28,3	24,2	1,17	0,021428	0,385	214028_x_at	Tudor domain containing 3	*TDRD3*
406	7,45	6,38	1,17	0,002133	0,286	214031_s_at	Keratin 7	*KRT7*
588	190	163	1,17	0,003249	0,301	1555945_s_a	Family with sequence similarity 120A	*FAM120A*
1701	51,4	44,0	1,17	0,010831	0,348	222492_at	Pyridoxal (pyridoxine, vitamin B6) kinase	*PDXK*
875	4,17	3,57	1,17	0,005050	0,313	236409_at	Lysophospholipase-like 1	*LYPLAL1*
5931	25,5	21,9	1,17	0,048084	0,443	209920_at	Bone morphogenetic protein receptor, type II	*BMPR2*
5947	211	181	1,17	0,048195	0,443	212399_s_at	Vestigial like 4 (Drosophila)	*VGLL4*
3277	523	448	1,17	0,023346	0,388	201807_at	Vacuolar protein sorting 26 homolog A (S. pombe)	*VPS26A*
455	4,29	3,68	1,17	0,002434	0,288	240485_at	Tetratricopeptide repeat domain 8	*TTC8*
4996	261	224	1,16	0,038359	0,420	202985_s_at	BCL2-associated athanogene 5	*BAG5*
4030	18,6	15,9	1,16	0,029511	0,400	231548_at	Forkhead box O3	*FOXO3*
5675	5,36	4,61	1,16	0,045287	0,436	205092_x_at	Zinc finger and BTB domain containing 1	*ZBTB1*
4167	46,6	40,0	1,16	0,030793	0,404	222649_at	Exportin 4	*XPO4*
4816	33,8	29,0	1,16	0,036601	0,416	220938_s_at	Glucocorticoid modulatory element binding protein 1	*GMEB1*
2424	2177	1871	1,16	0,016211	0,365	214938_x_at	High-mobility group box 1	*HMGB1*
1281	4,74	4,07	1,16	0,007629	0,325	1562775_at	Nudix (nucleoside diphosphate linked moiety X)-type motif 12	*NUDT12*
3798	5,25	4,51	1,16	0,027669	0,398	1557553_at	Protein phosphatase 1, regulatory (inhibitor) subunit 12B	*PPP1R12B*
4344	5,23	4,49	1,16	0,032339	0,407	239461_at	Polypeptide N-acetylgalactosaminyltransferase-like protein 2	*GALNTL2*
3188	27,0	23,3	1,16	0,022597	0,387	209126_x_at	Keratin 6B	*KRT6B*
4273	11,7	10,0	1,16	0,031762	0,406	228132_at	Actin binding LIM protein family, member 2	*ABLIM2*
3148	4,94	4,25	1,16	0,022347	0,387	202035_s_at	Secreted frizzled-related protein 1	*SFRP1*
1777	16,2	14,0	1,16	0,011306	0,348	213863_s_at	Ornithine decarboxylase antizyme 3	*OAZ3*
587	6,19	5,33	1,16	0,003244	0,301	1565628_at	Leucine-rich repeat kinase 1	*LRRK1*
2868	52,4	45,1	1,16	0,020138	0,383	221192_x_at	Major facilitator superfamily domain containing 11	*MFSD11*
3079	7,67	6,60	1,16	0,021704	0,385	230392_at	cDNA FLJ31096 fis, clone IMR321000207	-
5933	122	105	1,16	0,048100	0,443	221564_at	Protein arginine methyltransferase 2	*PRMT2*
5695	7,34	6,33	1,16	0,045566	0,437	209800_at	Keratin 16	*KRT16*
1685	53,7	46,2	1,16	0,010651	0,345	47530_at	Chromosome 9 open reading frame 156	*C9orf156*
3477	7,37	6,35	1,16	0,024971	0,392	1563947_a_a	ELKS/RAB6-interacting/CAST family member 1	*ERC1*
4866	30,7	26,4	1,16	0,037112	0,417	232867_at	Serine palmitoyltransferase, long chain base subunit 2	*SPTLC2*
3866	190	164	1,16	0,028243	0,399	212245_at	Multiple coagulation factor deficiency 2	*MCFD2*
2415	15,6	13,5	1,16	0,016131	0,365	205203_at	Phospholipase D1, phosphatidylcholine-specific	*PLD1*
5422	1707	1473	1,16	0,042629	0,430	200680_x_at	High-mobility group box 1	*HMGB1*
2393	8,96	7,72	1,16	0,015975	0,365	241701_at	Rho GTPase activating protein 21	*ARHGAP21*
3169	36,3	31,3	1,16	0,022488	0,387	214253_s_at	Dystrobrevin, beta	*DTNB*
3719	6,79	5,87	1,16	0,026999	0,397	237173_at	Similar to phosphodiesterase 4D interacting protein isoform 1	*LOC647500*

Index	Mutated*	Normal*	FC	*P* value	FDR**	Probe set	Description	Gene symbol
4279	3,90	3,37	1,16	0,031801	0,406	232980_at	LMBR1 domain containing 1	*LMBRD1*
1644	9,14	7,89	1,16	0,010357	0,344	239769_at	Cadherin 11, type 2, OB-cadherin (osteoblast)	*CDH11*
5531	31,1	26,9	1,16	0,043887	0,434	227823_at	Retrotransposon gag domain containing 4	*RGAG4*
3475	6,13	5,30	1,16	0,024960	0,392	1565887_at	Transient receptor potential cation channel, subfamily M, member 7	*TRPM7*
5425	21,0	18,1	1,16	0,042688	0,430	243656_at	Hypothetical protein LOC642852	*LOC642852*
4555	6,00	5,18	1,16	0,034440	0,412	231061_at	La ribonucleoprotein domain family, member 7	*LARP7*
2134	5,38	4,65	1,16	0,014029	0,359	221697_at	Microtubule-associated protein 1 light chain 3 gamma	*MAP1LC3C*
1520	12,8	11,0	1,16	0,009394	0,337	1555752_at	Saitohin	*STH*
5650	1931	1671	1,16	0,045067	0,436	208646_at	Ribosomal protein S14	*RPS14*
2178	8,96	7,75	1,16	0,014409	0,361	241627_x_at	Hypothetical protein FLJ10357	*FLJ10357*
1521	59,8	51,7	1,16	0,009399	0,337	202640_s_at	RAN binding protein 3	*RANBP3*
2802	5,17	4,48	1,15	0,019474	0,380	1553300_a_a	Diacylglycerol kinase, eta	*DGKH*
5623	3,99	3,46	1,15	0,044911	0,436	204748_at	Prostaglandin-endoperoxide synthase 2	*PTGS2*
6096	80,8	70,0	1,15	0,049756	0,446	203291_at	CCR4-NOT transcription complex, subunit 4	*CNOT4*
955	10,6	9,16	1,15	0,005504	0,315	210535_at	B9 protein	*EPPB9*
5015	19,2	16,6	1,15	0,038580	0,420	1570078_a_a	Dedicator of cytokinesis 5	*DOCK5*
1323	3,68	3,19	1,15	0,007915	0,327	215339_at	Natural killer-tumor recognition sequence	*NKTR*
409	6,64	5,76	1,15	0,002148	0,286	1558874_a_a	cDNA clone YP97H11	-
3103	4,08	3,54	1,15	0,021909	0,386	216997_x_at	Transducin-like enhancer of split 4 (E(sp1) homolog, Drosophila)	*TLE4*
618	8,68	7,52	1,15	0,003500	0,308	232878_at	Hypothetical protein LOC644192	*LOC644192*
1657	4330	3757	1,15	0,010453	0,345	213828_x_at	H3 histone, family 3A	*H3F3A*
5731	22,9	19,9	1,15	0,045976	0,438	241757_x_at	Dynein, cytoplasmic 2, light intermediate chain 1	*DYNC2LI1*
4639	6,10	5,29	1,15	0,034982	0,412	241776_at	Transcribed locus	-
3907	5,79	5,02	1,15	0,028526	0,399	244755_at	Xenotropic and polytropic retrovirus receptor	*XPR1*
3617	26,0	22,6	1,15	0,026116	0,395	220215_at	Zinc finger protein 669	*ZNF669*
1878	6,59	5,72	1,15	0,012155	0,354	235492_at	Ring finger protein 217	*RNF217*
304	9,32	8,10	1,15	0,001467	0,263	1563283_at	cDNA clone IMAGE:4828909	-
1643	5,61	4,88	1,15	0,010350	0,344	1553211_at	Ankyrin-repeat and fibronectin type III domain containing 1	*ANKFN1*
5568	5,38	4,68	1,15	0,044332	0,435	237622_at	Transcribed locus	-
5870	4,16	3,62	1,15	0,047434	0,442	235575_at	Succinate dehydrogenase complex, subunit A, flavoprotein	*SDHALP2*
1571	8,63	7,51	1,15	0,009762	0,340	204680_s_at	Rap guanine nucleotide exchange factor (GEF) 5	*RAPGEF5*
3713	209	182	1,15	0,026924	0,396	219097_x_at	Chromosome 19 open reading frame 42	*C19orf42*
1267	4345	3782	1,15	0,007544	0,325	208755_x_at	H3 histone, family 3A	*H3F3A*
4437	5,33	4,64	1,15	0,033242	0,410	242916_at	Centrosomal protein 110kDa	*CEP110*
4868	6,57	5,73	1,15	0,037156	0,417	230451_at	DISC1 disrupted in schizophrenia 1	*DISC1*
399	6,36	5,54	1,15	0,002090	0,285	236306_at	KIAA2026 protein	*KIAA2026*
5557	14,7	12,8	1,15	0,044236	0,435	232566_at	Nucleolar protein family 6 (RNA-associated)	*NOL6*
3042	22,5	19,6	1,15	0,021428	0,385	240494_at	CTD small phosphatase-like protein	*CTDSPL*
1523	19,6	17,1	1,15	0,009416	0,337	233065_at	Ring finger protein 207	*RNF207*
4301	8,35	7,29	1,15	0,032011	0,407	238608_at	Laminin, beta 1	*LAMB1*
4455	5,15	4,50	1,15	0,033465	0,411	206035_at	v-rel reticuloendotheliosis viral oncogene homolog (avian)	*REL*
4727	6,16	5,38	1,15	0,035769	0,414	236678_at	Jagged 1 (Alagille syndrome)	*JAG1*
4000	12,4	10,8	1,15	0,029274	0,400	227225_at	Hypothetical gene supported by AK125693	*LOC439985*
5801	18,9	16,5	1,14	0,046784	0,441	219617_at	Chromosome 2 open reading frame 34	*C2orf34*
4365	9,04	7,90	1,14	0,032466	0,407	209359_x_at	Runt-related transcription factor 1 (aml1 oncogene)	*RUNX1*
6095	5,42	4,73	1,14	0,049745	0,446	235540_at	Gonadotropin-releasing hormone 1	*GNRH1*
4077	17,1	15,0	1,14	0,029919	0,401	240134_at	WWC family member 3	*WWC3*
5424	5,20	4,54	1,14	0,042684	0,430	220842_at	Abelson helper integration site 1	*AHI1*
5730	1453	1271	1,14	0,045972	0,438	222229_x_at	Similar to 60S ribosomal protein L26	*LOC392501*
1566	5,21	4,56	1,14	0,009729	0,340	1556113_at	cDNA DKFZp451A211 protein	*DKFZp451A211*
3788	8,76	7,66	1,14	0,027581	0,398	215415_s_at	Lysosomal trafficking regulator	*LYST*
5685	157	138	1,14	0,045379	0,436	222207_x_at	Williams Beuren syndrome chromosome region 19 pseudogene	*LOC389517*
5041	19,7	17,2	1,14	0,038851	0,420	236629_at	Chromosome 1 open reading frame 69	*C1orf69*
2188	5,56	4,86	1,14	0,014490	0,361	244340_x_at	-	-
3242	4,96	4,34	1,14	0,022993	0,388	219685_at	Transmembrane protein 35	*TMEM35*
3058	6,77	5,93	1,14	0,021531	0,385	228656_at	Prospero homeobox 1	*PROX1*
330	3,65	3,20	1,14	0,001639	0,272	1558920_at	Solute carrier family 8 (sodium/calcium exchanger), member 1	*SCL8A1*

Index	Mutated*	Normal*	FC	*P* value	FDR**	Probe set	Description	Gene symbol
5553	16,5	14,5	1,14	0,044202	0,435	229392_s_at	Phosphoinositide-3-kinase, regulatory subunit 2 (p85 beta)	*PIK3R2*
5946	44,1	38,6	1,14	0,048181	0,443	201213_at	Protein phosphatase 1, regulatory (inhibitor) subunit 7	*PPP1R7*
6097	3,64	3,19	1,14	0,049760	0,446	220474_at	Solute carrier family 25 member 21	*SLC25A21*
2656	6,25	5,47	1,14	0,018114	0,373	204110_at	Histamine N-methyltransferase	*HNMT*
5060	9,64	8,45	1,14	0,038956	0,420	214600_at	TEA domain family member 1 (SV40 transcriptional enhancer factor)	*TEAD1*
4507	4,66	4,09	1,14	0,033953	0,412	234020_x_at	Copper metabolism (Murr1) domain containing 1	*COMMD1*
3518	9,93	8,71	1,14	0,025254	0,392	239306_at	Chromosome 14 open reading frame 93	*C14orf93*
4404	318	279	1,14	0,032875	0,408	223060_at	Chromosome 14 open reading frame 119	*C14orf119*
2100	4,12	3,61	1,14	0,013760	0,358	237963_x_at	KIAA1529 protein	*KIAA1529*
898	5,51	4,83	1,14	0,005203	0,313	232858_at	Sex comb on midleg homolog 1 (Drosophila)	*SCMH1*
2973	5,53	4,85	1,14	0,020879	0,384	1560332_at	Carbohydrate (chondroitin) sulfotransferase 11	*CHST11*
3797	3843	3374	1,14	0,027660	0,398	200012_x_at	Ribosomal protein L21	*RPL21*
3156	7,97	7,00	1,14	0,022400	0,387	205783_at	Kallikrein-related peptidase 13	*KLK13*
1298	4,16	3,66	1,14	0,007724	0,325	222172_at	Neuronal PAS domain protein 3	*NPAS3*
1818	4,02	3,53	1,14	0,011714	0,351	209125_at	Keratin 6A	*KRT6A*
5661	8,37	7,36	1,14	0,045180	0,436	205520_at	Striatin, calmodulin binding protein	*STRN*
5006	27,6	24,3	1,14	0,038454	0,420	1556066_at	Jumonji domain containing 3	*JMJD3*
2039	24,9	21,9	1,14	0,013274	0,355	1556014_at	Mesoderm posterior 2 homolog (mouse)	*MESP2*
6072	197	173	1,14	0,049585	0,446	203043_at	Zinc finger, BED-type containing 1	*ZBED1*
4770	10,3	9,02	1,14	0,036157	0,414	233117_at	Microtubule-associated protein tau	*MAPT*
3927	236	207	1,14	0,028727	0,399	226024_at	Copper metabolism (Murr1) domain containing 1	*COMMD1*
6100	14,6	12,8	1,14	0,049799	0,446	211993_at	WNK lysine deficient protein kinase 1	*WNK1*
1065	4,65	4,09	1,14	0,006246	0,319	239980_at	Chromosome 22 open reading frame 28	*C22orf28*
4509	4,84	4,27	1,14	0,033981	0,412	220986_s_at	Tigger transposable element derived 6	*TIGD6*
5948	4,33	3,81	1,14	0,048197	0,443	236277_at	p21 protein (Cdc42/Rac)-activated kinase 3	*PAK3*
1186	7,05	6,21	1,14	0,006976	0,322	207552_at	ATP synthase proteolipid P2	*ATP5G2*
2182	11,6	10,2	1,13	0,014441	0,361	1558484_s_a	Leucine rich repeat containing 27	*LRRC27*
5647	15,2	13,4	1,13	0,045057	0,436	214492_at	Sarcoglycan, delta (35kDa dystrophin-associated glycoprotein)	*SGCD*
4733	3,55	3,13	1,13	0,035831	0,414	237825_x_at	Transcribed locus	-
4379	5,24	4,62	1,13	0,032568	0,407	1559394_a_a	Receptor tyrosine kinase-like orphan receptor 1	*ROR1*
4943	5,25	4,63	1,13	0,037929	0,419	242636_at	Prolylcarboxypeptidase (angiotensinase C)	*PRCP*
2667	4,33	3,82	1,13	0,018241	0,374	232538_at	FLJ23573 fis, clone LNG12520	-
648	4,60	4,06	1,13	0,003681	0,308	215635_at	Phosphodiesterase 8A	*PDE8A*
5602	11,8	10,4	1,13	0,044708	0,436	1556229_at	Carboxylate kinase-like	*CARLK*
5585	6,75	5,97	1,13	0,044528	0,436	230067_at	Family with sequence similarity 124A	*FAM124A*
5103	5,21	4,61	1,13	0,039244	0,420	241041_at	Solute carrier family 8 (sodium/calcium exchanger), member 1	*SLC8A1*
2533	24,5	21,7	1,13	0,017131	0,369	226836_at	SFT2 domain containing 1	*SFT2D1*
3962	311	275	1,13	0,028950	0,399	1555948_s_a	Family with sequence similarity 120A	*FAM120A*
4092	43,6	38,6	1,13	0,030080	0,402	219128_at	Chromosome 2 open reading frame 42	*C2orf42*
3619	5,35	4,74	1,13	0,026136	0,395	221625_at	cDNA FLJ46609 fis, clone TKIDN2010200	-
398	3,84	3,41	1,13	0,002087	0,285	1554413_s_a	RUN domain containing 2B	*RUNDC2B*
1773	5868	5198	1,13	0,011296	0,348	206559_x_at	Eukaryotic translation elongation factor 1 alpha 1	*EEF1A1*
4078	11,6	10,2	1,13	0,029924	0,401	209327_s_at	NOP16 nucleolar protein homolog (yeast)	*NOP16*
4722	42,3	37,5	1,13	0,035711	0,413	217142_at	Eukaryotic translation elongation factor 1 alpha 1	*EEF1A1*
5143	13,0	11,5	1,13	0,039594	0,421	231658_x_at	Ribosomal protein L36	*RPL36*
4222	19,9	17,6	1,13	0,031290	0,405	228663_x_at	FLT3-interacting zinc finger 1	*FIZ1*
3825	5,00	4,44	1,13	0,027925	0,399	236354_at	Zinc finger, MYND domain containing 17	*ZMYND17*
4776	8,93	7,92	1,13	0,036212	0,414	229859_at	Intercellular adhesion molecule 3	*ICAM3*
6052	6,45	5,72	1,13	0,049331	0,446	1569608_x_a	Similar to ankyrin repeat domain 20A	*LOC643187*
2140	7,37	6,55	1,13	0,014073	0,360	214401_at	Paired box 1	*PAX1*
1360	4,63	4,11	1,13	0,008199	0,328	1560230_at	Supervillin	*SVIL*
5465	228	203	1,13	0,043161	0,432	202469_s_at	Cleavage and polyadenylation specific factor 6, 68kDa	*CPSF6*
4918	95,9	85,2	1,13	0,037660	0,419	200767_s_at	Family with sequence similarity 120A	*FAM120A*
1852	3,70	3,29	1,13	0,011938	0,352	236999_at	Peptidylprolyl isomerase domain and WD repeat containing 1	*PPWD1*
3405	9,70	8,62	1,13	0,024293	0,390	1553169_at	Chromosome 20 open reading frame 75	*C20orf75*
5786	31,4	27,9	1,13	0,046596	0,440	220411_x_at	Podocan-like 1	*PODNL1*
1192	6,06	5,38	1,13	0,007032	0,322	214445_at	Elongation factor, RNA polymerase II, 2	*ELL2*

Index	Mutated*	Normal*	FC	*P* value	FDR**	Probe set	Description	Gene symbol
5894	5,66	5,03	1,13	0,047683	0,442	237671_at	RAD51-like 1 (S. cerevisiae)	*RAD51L1*
5038	19,4	17,2	1,13	0,038809	0,420	214525_x_at	MutL homolog 3 (E. coli)	*MLH3*
3155	6,96	6,19	1,13	0,022379	0,387	229188_s_at	Zinc and ring finger 2	*ZNRF2*
2882	7,89	7,02	1,12	0,020225	0,383	206012_at	Left-right determination factor 2	*LEFTY2*
1316	4303	3828	1,12	0,007836	0,325	213347_x_at	Ribosomal protein S4, X-linked	*RPS4X*
2363	575	511	1,12	0,015774	0,364	207988_s_at	Actin related protein 2/3 complex, subunit 2, 34kDa	*ARPC2*
4226	5340	4753	1,12	0,031322	0,405	216520_s_at	Tumor protein, translationally-controlled 1	*TPT1*
215	3,91	3,48	1,12	0,000963	0,244	214034_at	Endoplasmic reticulum aminopeptidase 1	*ARTS-1*
3345	7,84	6,99	1,12	0,023759	0,388	236688_at	FERM and PDZ domain containing 3	*FRMPD3*
5938	13,8	12,3	1,12	0,048146	0,443	1563529_at	Hydrocephalus inducing homolog 2 (mouse)	*HYDIN2*
4184	6,51	5,80	1,12	0,030944	0,404	241494_at	Serine incorporator 5	*SERINC5*
2583	3,86	3,44	1,12	0,017527	0,371	241913_at	Kelch-like 8 (Drosophila)	*KLHL8*
534	5,12	4,57	1,12	0,002857	0,292	238786_at	Transcribed locus	-
5490	6,77	6,04	1,12	0,043450	0,433	236779_at	Mitochondrial ribosomal protein S5	*MRPS5*
99	3,49	3,12	1,12	0,000386	0,213	208054_at	Hect domain and RLD 4	*HERC4*
6060	6,42	5,73	1,12	0,049414	0,446	234697_x_at	Chromosome 3 open reading frame 31	*C3orf31*
3228	8,41	7,52	1,12	0,022897	0,388	236869_at	Transcribed locus	-
4300	12,7	11,3	1,12	0,032007	0,407	1553346_a_a	Trinucleotide repeat containing 6A	*TNRC6A*
1949	4,07	3,64	1,12	0,012725	0,355	219195_at	PPAR-gamma coactivator 1-alpha	*PPARGC1A*
772	3,70	3,31	1,12	0,004423	0,311	1563389_at	cDNA clone IMAGE:4836780	-
839	4,06	3,63	1,12	0,004807	0,313	1557275_a_a	cDNA FLJ20031 fis, clone ADSU02180	-
3879	5,03	4,50	1,12	0,028335	0,399	244206_at	AN1, ubiquitin-like, homolog (Xenopus laevis)	*ANUBL1*
1774	11,6	10,4	1,12	0,011299	0,348	219674_s_at	High density lipoprotein binding protein (vigilin)	*HDLBP*
4871	6,08	5,44	1,12	0,037185	0,417	207653_at	Forkhead box D2	*FOXD2*
3876	4,81	4,31	1,12	0,028314	0,399	211086_x_at	NIMA (never in mitosis gene a)-related kinase 1	*NEK1*
5238	4,09	3,67	1,12	0,040574	0,423	217057_s_at	GNAS complex locus	*GNAS*
1982	3,45	3,09	1,12	0,012935	0,355	1566787_at	Similar to poly (ADP-ribose) glycohydrolase	*PARG*
4711	10,2	9,13	1,12	0,035646	0,413	177_at	Phospholipase D1, phosphatidylcholine-specific	*PLD1*
2696	7138	6404	1,11	0,018486	0,375	204892_x_at	Eukaryotic translation elongation factor 1 alpha 1	*EEF1A1*
3253	4,23	3,80	1,11	0,023081	0,388	243008_at	RAS homolog enriched in brain	*RHEB*
2949	14,9	13,4	1,11	0,020711	0,384	219626_at	MAP7 domain containing 3	*MAP7D3*
2859	4,55	4,09	1,11	0,020072	0,383	236944_at	Transcribed locus	-
481	4,28	3,85	1,11	0,002572	0,289	1556800_a_a	Glutamate receptor, metabotropic 8	*GRM8*
1684	3,91	3,51	1,11	0,010646	0,345	1558964_at	FAT tumor suppressor homolog 3 (Drosophila)	*FAT3*
5087	5,80	5,21	1,11	0,039159	0,420	229311_at	G kinase anchoring protein 1	*GKAP1*
821	3,96	3,56	1,11	0,004689	0,312	1553630_at	Chromosome 10 open reading frame 107	*C10orf107*
2205	5,54	4,99	1,11	0,014575	0,361	222337_at	Oxysterol binding protein-like 9	*OSBPL9*
257	3,17	2,86	1,11	0,001202	0,256	215647_at	RNA binding motif protein 26	*RBM26*
2774	6,94	6,25	1,11	0,019258	0,380	234079_at	Rho-guanine nucleotide exchange factor	*RGNEF*
1908	3,78	3,40	1,11	0,012416	0,355	230081_at	Phosphatidylinositol-specific phospholipase C, X domain containing 3	*PLCXD3*
4815	4,00	3,60	1,11	0,036593	0,416	220719_at	Hypothetical protein FLJ13769	*FLJ13769*
1363	3,57	3,22	1,11	0,008207	0,328	1567527_at	Ubiquitin B (UBB) mRNA, 3' UTR and genetic suppressor element	-
354	6207	5593	1,11	0,001808	0,279	212869_x_at	Tumor protein, translationally-controlled 1	*TPT1*
5376	10,1	9,07	1,11	0,042168	0,429	224458_at	Chromosome 9 open reading frame 125	*C9orf125*
3544	415	374	1,11	0,025498	0,393	200829_x_at	Zinc finger protein 207	*ZNF207*
3742	10,1	9,08	1,11	0,027228	0,397	233862_at	cDNA clone IMAGE:4698949	-
5626	24,0	21,6	1,11	0,044919	0,436	243860_at	Ataxin 1	*ATXN1*
2180	5,19	4,68	1,11	0,014410	0,361	237628_at	Tryptophanyl tRNA synthetase 2, mitochondrial	*WARS2*
580	4,96	4,48	1,11	0,003183	0,300	233240_at	cDNA FLJ10255 fis, clone HEMBB1000852	-
5846	4,32	3,90	1,11	0,047265	0,442	238279_x_at	Collagen, type IV, alpha 3 (Goodpasture antigen) binding protein	*COL4A3BP*
6091	5114	4616	1,11	0,049719	0,446	224594_x_at	Actin, beta	*ACTB*
581	3,30	2,98	1,11	0,003186	0,300	242642_at	NudE nuclear distribution gene E homolog (A. nidulans)-like 1	*NDEL1*
5747	5,56	5,02	1,11	0,046116	0,439	217201_at	RAS protein activator like 2	*RASAL2*
1960	11,4	10,3	1,11	0,012812	0,355	237331_s_at	Hypothetical protein LOC100128977	*LOC100128977*
4867	7,21	6,51	1,11	0,037151	0,417	239701_at	Ectonucleoside triphosphate diphosphohydrolase 1	*ENTPD1*
3247	3,59	3,24	1,11	0,023061	0,388	232945_at	pseudouridylate synthase 10	*PUS10*
4528	5,53	5,00	1,11	0,034179	0,412	241711_at	Transducin (beta)-like 1 X-linked receptor 1	*TBL1XR1*

Index	Mutated*	Normal*	FC	*P* value	FDR**	Probe set	Description	Gene symbol
4439	5,07	4,58	1,11	0,033326	0,410	1559672_a_a	Chromosome 9 open reading frame 93	*C9orf93*
1143	3,42	3,09	1,11	0,006695	0,320	1558107_at	FSHD region gene 1 family, member B	*FRG1B*
3425	47,2	42,7	1,11	0,024487	0,391	209547_s_at	Splicing factor 4	*SF4*
87	3,61	3,27	1,10	0,000328	0,201	234588_at	-	-
854	5215	4721	1,10	0,004916	0,313	211943_x_at	Tumor protein, translationally-controlled 1	*TPT1*
201	5945	5384	1,10	0,000925	0,244	212284_x_at	Tumor protein, translationally-controlled 1	*TPT1*
3171	3,66	3,31	1,10	0,022504	0,387	231925_at	CDNA FLJ23006 fis, clone LNG00414	-
5925	4,65	4,21	1,10	0,048007	0,443	237322_at	Myocardial infarction associated transcript (non-protein coding)	*MIAT*
1910	4,54	4,12	1,10	0,012436	0,355	231610_at	Tau tubulin kinase 2	*TTBK2*
3584	5,81	5,26	1,10	0,025871	0,394	1566609_at	cDNA FLJ25907 fis, clone CBR04607	-
2423	3,70	3,36	1,10	0,016202	0,365	220729_at	-	-
5592	4,13	3,75	1,10	0,044609	0,436	234243_at	Brix domain containing 5	*BXDC5*
4345	10,6	9,63	1,10	0,032356	0,407	201205_at	Ribosome binding protein 1 homolog 180kDa	*RRBP1*
1435	4,22	3,83	1,10	0,008700	0,331	241228_at	Transcribed locus	-
6093	7,75	7,04	1,10	0,049730	0,446	1562946_at	cDNA clone IMAGE:3503939	-
5299	4,02	3,65	1,10	0,041287	0,426	1568777_at	Echinoderm microtubule associated protein like 5	*EML5*
849	3,93	3,57	1,10	0,004889	0,313	1556925_at	Structural maintenance of chromosomes 3	*SMC3*
5446	3,82	3,47	1,10	0,042957	0,431	1560264_at	Mastermind-like 3 (Drosophila)	*MAML3*
4271	4,08	3,71	1,10	0,031749	0,406	211022_s_at	Alpha thalassemia/mental retardation syndrome X-linked	*ATRX*
3816	4684	4261	1,10	0,027829	0,399	200781_s_at	Ribosomal protein S15a	*RPS15A*
1723	4,47	4,07	1,10	0,011039	0,348	1561106_at	Chromosome 6 open reading frame 217	*C6orf217*
4542	5,12	4,66	1,10	0,034324	0,412	1555151_s_a	L-threonine dehydrogenase	*TDH*
1939	6,27	5,71	1,10	0,012633	0,355	206248_at	Protein kinase C, epsilon	*PRKCE*
2707	14,3	13,0	1,10	0,018561	0,375	227879_at	AlkB, alkylation repair homolog 7 (E. coli)	*ALKBH7*
5211	3,34	3,05	1,10	0,040226	0,422	233945_at	UDP-glucose ceramide glucosyltransferase-like 2	*UGCGL2*
2890	5,84	5,32	1,10	0,020289	0,383	1553506_at	Carboxypeptidase O	*CPO*
2817	3,84	3,50	1,10	0,019664	0,381	234805_at	ATPase family, AAA domain containing 1	*ATAD1*
3316	7,61	6,95	1,10	0,023566	0,388	223953_s_at	Zinc finger and BTB domain containing 37	*ZBTB37*
2955	5,01	4,57	1,10	0,020746	0,384	239690_at	Transcribed locus	-
2734	5,23	4,77	1,10	0,018849	0,377	206962_x_at	Zinc finger protein 638	*ZNF638*
4686	4622	4218	1,10	0,035378	0,413	213583_x_at	Eukaryotic translation elongation factor 1 alpha 1	*EEF1A1*
4205	4,13	3,77	1,10	0,031091	0,404	1566106_at	Mitofusin 2	*MFN2*
5887	16,5	15,0	1,10	0,047624	0,442	239381_at	Kallikrein-related peptidase 7	*KLK7*
1232	5,30	4,84	1,10	0,007329	0,324	228926_s_at	ATP-dependent helicase SMARCA2	*SMARCA2*
5025	7,92	7,24	1,09	0,038639	0,420	242624_at	Actin binding LIM protein family, member 2	*ABLIM2*
568	2167	1981	1,09	0,003107	0,299	214327_x_at	Tumor protein, translationally-controlled 1	*TPT1*
1472	3,23	2,96	1,09	0,008998	0,334	221057_at	Spermatogenesis associated 1	*SPATA1*
685	3,27	2,99	1,09	0,003927	0,308	239712_at	Chromosome 9 open reading frame 93	*C9orf93*
2083	4,30	3,93	1,09	0,013595	0,356	1558518_at	TGF-beta activated kinase 1/MAP3K7 binding protein 3	*MAP3K7IP3*
3882	5272	4827	1,09	0,028346	0,399	213614_x_at	Eukaryotic translation elongation factor 1 alpha 1	*EEF1A1*
5225	3,83	3,52	1,09	0,040414	0,423	244275_at	Transcribed locus	-
4677	4,21	3,86	1,09	0,035310	0,413	1559695_a_a	DLGAP1, Discs, large (Drosophila) homolog-associated protein 1	*DLGAP1*
5864	5,00	4,59	1,09	0,047415	0,442	1561631_at	Spermatogenesis associated, serine-rich 2-like	*SPATS2L*
4079	3,72	3,41	1,09	0,029936	0,401	240990_at	RAB5A, member RAS oncogene family	*RAB5A*
2236	3,57	3,28	1,09	0,014852	0,363	243316_x_at	Vacuolar protein sorting 26 homolog A (S. pombe)	*VPS26A*
2071	4,21	3,86	1,09	0,013541	0,356	229171_at	CENPB DNA-binding domains containing 1	*CENPBD1*
1346	4,46	4,09	1,09	0,008069	0,328	233227_at	KIAA1109 protein	*KIAA1109*
5380	10,6	9,73	1,09	0,042186	0,429	204250_s_at	Centrosomal protein 164kDa	*CEP164*
2165	3,79	3,49	1,09	0,014334	0,361	244146_at	DTW domain containing 1	*DTWD1*
5990	3,50	3,21	1,09	0,048718	0,444	216595_at	DnaJ (Hsp40) homolog, subfamily C, member 22	*DNAJC22*
6026	3,63	3,34	1,09	0,049024	0,445	231930_at	ELMO/CED-12 domain containing 1	*ELMOD1*
5749	3,73	3,43	1,09	0,046135	0,439	1559369_at	Chromosome 5 open reading frame 44	*C5orf44*
4484	4,35	4,01	1,09	0,033740	0,411	1556323_at	CUG triplet repeat, RNA binding protein 2	*CUGBP2*
2486	5,03	4,63	1,09	0,016751	0,367	216536_at	Olfactory receptor, family 7, subfamily E, member 19 pseudogene	*OR7E19P*
3003	9,32	8,59	1,09	0,021133	0,385	239085_at	Jun dimerization protein 2	*JDP2*
6124	3701	3412	1,08	0,049993	0,446	229563_s_at	Ribosomal protein L10a	*RPL10A*
713	3,01	2,77	1,08	0,004092	0,308	1558667_at	Spermatogenesis associated 22	*SPATA22*

Index	Mutated*	Normal*	FC	*P* value	FDR**	Probe set	Description	Gene symbol
3638	3,86	3,56	1,08	0,026309	0,395	235380_at	Arachidonate 5-lipoxygenase	*ALOX5*
5347	3,59	3,31	1,08	0,041919	0,429	1555038_at	Erythrocyte membrane protein band 4.1 like 4A	*EPB41L4A*
396	3,17	2,93	1,08	0,002086	0,285	238203_at	-	-
3355	4,68	4,32	1,08	0,023825	0,388	232953_at	Chromosome 20 open reading frame 69	*C20orf69*
4708	3,94	3,65	1,08	0,035603	0,413	217571_at	-	-
3810	4,82	4,46	1,08	0,027763	0,398	211347_at	CDC14 cell division cycle 14 homolog B (S. cerevisiae)	*CDC14B*
3067	6,32	5,85	1,08	0,021654	0,385	1563098_at	EEF1A2 binding protein	*EEF1A2BP1*
378	2,82	2,61	1,08	0,001972	0,284	1554072_s_a	Coiled-coil domain containing 67	*CCDC67*
212	3,11	2,88	1,08	0,000958	0,244	240768_x_at	UBX domain protein 4	*UBXD2*
2515	4,92	4,56	1,08	0,016944	0,368	1566040_at	cDNA DKFZp667F083	-
5473	3,15	2,92	1,08	0,043268	0,432	1568916_at	Spire homolog 2 (Drosophila)	*SPIRE2*
3989	4,08	3,78	1,08	0,029178	0,400	210500_at	Ubiquitin associated protein 2-like	*UBAP2L*
802	3,24	3,01	1,08	0,004575	0,311	231391_at	Cortexin 3	*CTXN3*
5631	3,83	3,55	1,08	0,044947	0,436	239770_at	Family with sequence similarity 62 (C2 domain containing), member C	*FAM62C*
4980	3,30	3,06	1,08	0,038210	0,419	217175_at	UDP glucuronosyltransferase 2 family, polypeptide B15	*UGT2B15*
4819	5425	5039	1,08	0,036637	0,416	200933_x_at	Ribosomal protein S4, X-linked	*RPS4X*
5429	10,8	10,0	1,08	0,042726	0,430	241203_at	-	-
5654	4,69	4,36	1,07	0,045099	0,436	232179_at	Hypothetical protein LOC158863	*LOC158863*
1508	3,62	3,37	1,07	0,009285	0,337	233393_at	Methionine sulfoxide reductase A	*MSRA*
4517	4,06	3,78	1,07	0,034044	0,412	1563044_at	cDNA clone IMAGE:5164837	-
5648	3,69	3,43	1,07	0,045065	0,436	240034_at	Transcribed locus	-
6106	6,57	6,13	1,07	0,049851	0,446	210760_x_at	Thyroid hormone receptor interactor 11	*TRIP11*
3309	3,30	3,07	1,07	0,023531	0,388	222246_at	Syntaxin binding protein 3	*STXBP3*
5679	3,00	2,79	1,07	0,045343	0,436	1560775_at	cDNA FLJ25185 fis, clone CBR09429	-
337	2,84	2,64	1,07	0,001719	0,277	234432_at	Metastasis related protein (MB2)	-
1597	5094	4754	1,07	0,009955	0,341	207783_x_at	HECT, UBA and WWE domain containing 1	*HUWE1*
4933	4,96	4,63	1,07	0,037824	0,419	242038_at	Leucine rich repeat containing 8 family, member B	*LRRC8B*
155	2,66	2,49	1,07	0,000705	0,244	1569810_at	cDNA clone IMAGE:5271710	-
5362	8,52	7,96	1,07	0,042063	0,429	215500_at	Similar to RIKEN cDNA 4933437K13	*LOC92017*
5656	3,11	2,91	1,07	0,045103	0,436	1561362_at	cDNA FLJ36285 fis, clone THYMU2003470	-
5953	5,29	4,94	1,07	0,048296	0,444	217004_s_at	MCF.2 cell line derived transforming sequence	*MCF2*
860	3,08	2,88	1,07	0,004964	0,313	1563053_at	Coiled-coil domain containing 13	*CCDC13*
6087	3,07	2,87	1,07	0,049696	0,446	243262_at	-	-
3714	5,01	4,69	1,07	0,026935	0,396	240641_at	Transcribed locus	-
1936	3,25	3,05	1,07	0,012615	0,355	1564273_at	Jelch domain containing 1	*KLHDC1*
5077	3,16	2,96	1,07	0,039053	0,420	237830_at	-	-
5312	3,51	3,29	1,07	0,041437	0,426	1557869_at	Mitochondrial ribosomal protein L55	*MRPL55*
1693	3,68	3,45	1,07	0,010710	0,346	1562139_a_a	Forkhead box P2	*FOXP2*
4619	3,79	3,55	1,07	0,034847	0,412	241264_at	WD repeat domain 7	*WDR7*
2347	3,58	3,35	1,07	0,015661	0,364	1566867_at	Ataxin 2-binding protein 1	*A2BP1*
4666	2,97	2,78	1,07	0,035242	0,413	244817_at	Inhibitor of growth family, member 1	*ING1*
3166	2,88	2,70	1,07	0,022463	0,387	216097_at	PHD finger protein 14	*PHF14*
1313	2,79	2,62	1,07	0,007827	0,325	1561331_at	Chromosome 1 open reading frame 99	*C1orf99*
5246	3,97	3,73	1,07	0,040612	0,423	1568826_at	Hypothetical protein LOC389372	*LOC389372*
3371	3,35	3,15	1,06	0,023978	0,389	219962_at	Angiotensin I converting enzyme (peptidyl-dipeptidase A) 2	*ACE2*
5812	3,75	3,53	1,06	0,046940	0,442	209638_x_at	Regulator of G-protein signaling 12	*RGS12*
3820	4,17	3,92	1,06	0,027890	0,399	234893_s_at	Dynein, axonemal, heavy chain 6	*DNHL1*
3401	3,27	3,07	1,06	0,024260	0,390	216619_at	GTP-binding protein 10 (putative)	*GTPBP10*
5610	3,45	3,24	1,06	0,044735	0,436	1570408_at	cDNA clone pp9953	-
4668	3,99	3,76	1,06	0,035244	0,413	1559109_a_a	Vacuolar protein sorting 53 homolog (S. cerevisiae)	*VPS53*
3775	3,80	3,57	1,06	0,027438	0,397	1568932_at	cDNA clone IMAGE:4830452	-
5932	3,34	3,15	1,06	0,048096	0,443	239905_at	YTH domain containing 1	*YTHDC1*
4193	6,73	6,35	1,06	0,030973	0,404	1561579_at	Hypothetical protein LOC728445	*LOC728445*
5734	3,04	2,87	1,06	0,045997	0,438	1569669_at	Forkhead box R2	*FOXR2*
1907	2,98	2,81	1,06	0,012409	0,355	244412_at	-	-
5261	3,34	3,15	1,06	0,040870	0,425	234765_at	Brain-specific angiogenesis inhibitor 3	*BAI3*
1187	3,01	2,84	1,06	0,006997	0,322	1565877_at	Nucleoporin 153kDa	*NUP153*

Index	Mutated*	Normal*	FC	*P* value	FDR**	Probe set	Description	Gene symbol
4934	3,95	3,73	1,06	0,037845	0,419	242904_x_at	Transmembrane protein 66	*TMEM66*
4136	3,39	3,20	1,06	0,030482	0,403	1570111_at	Chromosome 14 open reading frame 48	*C14orf48*
5875	3,32	3,13	1,06	0,047461	0,442	1555284_at	Amyotrophic lateral sclerosis 2 (juvenile)	*ALS2*
4570	3,01	2,84	1,06	0,034557	0,412	236220_at	Transcribed locus	-
3806	2,94	2,78	1,06	0,027714	0,398	1559035_a_a	Aryl hydrocarbon receptor	*ARH*
1854	3,00	2,84	1,06	0,011943	0,352	1562860_at	cDNA clone IMAGE:5744121	-
2229	3,08	2,91	1,06	0,014807	0,363	1569823_at	hypothetical protein LOC440346	*LOC440346*
5204	3,44	3,25	1,06	0,040145	0,422	216632_at	Neuron navigator 3	*NAV3*
3104	3,49	3,30	1,06	0,021916	0,386	1552851_at	Zinc finger and SCAN domain containing 4	*ZSCAN4*
4771	2,98	2,82	1,06	0,036158	0,414	1570103_at	Golgi autoantigen, golgin subfamily a, 6-like 9	*GOLGA6L9*
5784	3,18	3,01	1,06	0,046585	0,440	1566899_at	Succinate dehydrogenase flavoprotein subunit	*HSSUCCDH*
5345	3,32	3,14	1,06	0,041904	0,429	240992_at	Transcribed locus	-
3972	2,61	2,47	1,06	0,029040	0,400	1564631_at	EF-hand calcium binding domain 3	*EFCAB3*
3091	2,73	2,58	1,06	0,021795	0,385	241909_at	Tankyrase, TRF1-interacting ankyrin-related ADP-ribose polymerase 2	*TNKS2*
4524	3,05	2,89	1,06	0,034133	0,412	1561737_at	cDNA DKFZp667L064	-
2764	3,17	3,00	1,05	0,019197	0,379	1555839_a_a	Chromosome 3 open reading frame 79	*C3orf79*
3080	3,11	2,95	1,05	0,021707	0,385	1566632_at	cDNA clone IMAGE:3950788	-
6062	3,69	3,50	1,05	0,049435	0,446	232585_at	Tousled-like kinase 2	*TLK2*
5342	2,99	2,84	1,05	0,041860	0,428	207879_at	-	-
3209	4,04	3,84	1,05	0,022721	0,387	1560358_at	Phosphorylase kinase, alpha 2	*PHKA2*
2850	2,79	2,65	1,05	0,019957	0,383	1566202_at	Protein phosphatase 3 (formerly 2B), catalytic subunit, alpha isoform	*PPP3CA*
4803	3,02	2,88	1,05	0,036455	0,415	1560516_at	Transmembrane protein 26	*TMEM26*
4304	2,74	2,61	1,05	0,032035	0,407	242198_at	Transcribed locus	-
4123	2,83	2,70	1,05	0,030324	0,402	215112_x_at	MCF.2 cell line derived transforming sequence-like 2	*MCF2L2*
4221	2,81	2,69	1,05	0,031284	0,405	1556873_at	Mex-3 homolog C (C. elegans)	*MEX3C*
5562	2,68	2,57	1,04	0,044295	0,435	234779_at	-	-
4596	2,85	2,73	1,04	0,034768	0,412	1567878_at	Defensin, beta 114	*DEFB114*
4665	2,72	2,61	1,04	0,035228	0,413	1554507_at	N-acetylated alpha-linked acidic dipeptidase 2	*NAALAD2*
5991	2,70	2,59	1,04	0,048724	0,444	1563040_s_a	cDNA clone IMAGE:5170410	-
5707	2,71	2,61	1,04	0,045697	0,438	1566930_at	Transcription factor B2, mitochondrial	*TFB2M*

*** Geometric mean of intensities**

**** False Discovery Rate**