Index	Mutated*	Normal*	FC	*P* value	FDR**	Probe set	Description	Gene symbol
4530	**17,7**	**71,0**	**-4,01**	**0,03420**	**0,412**	**233059_at**	**Potassium inwardly-rectifying channel, subfamily J, member 3**	***KCNJ3***
138	**32,2**	**114**	**-3,52**	**0,00063**	**0,244**	**219438_at**	**Na+/K+ transporting ATPase interacting 1**	***NKAIN1***
3114	**4,70**	**16,3**	**-3,47**	**0,02202**	**0,387**	**209988_s_at**	**Achaete-scute complex homolog 1 (Drosophila)**	***ASCL1***
5630	**8,01**	**23,3**	**-2,91**	**0,04494**	**0,436**	**207142_at**	**Potassium inwardly-rectifying channel, subfamily J, member 3**	***KCNJ3***
4210	**14,9**	**41,0**	**-2,76**	**0,03116**	**0,405**	**207141_s_at**	**Potassium inwardly-rectifying channel, subfamily J, member 3**	***KCNJ3***
967	**6,75**	**17,6**	**-2,60**	**0,00559**	**0,315**	**1552575_a_at**	**Chromosome 6 open reading frame 141**	***C6orf141***
1303	**11,7**	**30,1**	**-2,57**	**0,00775**	**0,325**	**204637_at**	**Glycoprotein hormones, alpha polypeptide**	***CGA***
3604	**16,1**	**40,3**	**-2,51**	**0,02600**	**0,394**	**206110_at**	**Histone cluster 1, H3h**	***HIST1H3H***
482	**62,0**	**154**	**-2,48**	**0,00257**	**0,289**	**213423_x_at**	**Tumor suppressor candidate 3**	***TUSC3***
1833	**15,0**	**36,6**	**-2,44**	**0,01181**	**0,351**	**219312_s_at**	**Zinc finger and BTB domain containing 10**	***ZBTB10***
715	**18,3**	**44,6**	**-2,43**	**0,00410**	**0,308**	**231729_s_at**	**Calcyphosine**	***CAPS***
4909	**4,37**	**10,5**	**-2,41**	**0,03755**	**0,418**	**209987_s_at**	**Achaete-scute complex homolog 1 (Drosophila)**	***ASCL1***
2721	**20,5**	**47,9**	**-2,34**	**0,01870**	**0,376**	**233899_x_at**	**Zinc finger and BTB domain containing 10**	***ZBTB10***
668	**53,0**	**121**	**-2,29**	**0,00384**	**0,308**	**209228_x_at**	**Tumor suppressor candidate 3**	***TUSC3***
2640	**58,6**	**133**	**-2,26**	**0,01800**	**0,373**	**228562_at**	**Zinc finger and BTB domain containing 10**	***ZBTB10***
3143	**33,2**	**74,8**	**-2,25**	**0,02230**	**0,387**	**205352_at**	**Serpin peptidase inhibitor, clade I (neuroSerpin), member 1**	***SERPINI1***
1620	**6,92**	**15,5**	**-2,24**	**0,01017**	**0,343**	**209227_at**	**Tumor suppressor candidate 3**	***TUSC3***
630	**31,0**	**67,9**	**-2,19**	**0,00357**	**0,308**	**201691_s_at**	**Tumor protein D52**	***TPD52***
5030	**8,84**	**19,3**	**-2,19**	**0,03867**	**0,420**	**206134_at**	**ADAM-like, decysin 1**	***ADAMDEC1***
2632	**4,98**	**10,8**	**-2,18**	**0,01793**	**0,372**	**241436_at**	**Sodium channel, nonvoltage-gated 1, gamma**	***SCNN1G***
290	**54,7**	**119**	**-2,17**	**0,00142**	**0,263**	**236655_at**	**Tumor protein D52**	***TPD52***
3718	**30,8**	**66,0**	**-2,14**	**0,02698**	**0,397**	**213201_s_at**	**Troponin T type 1 (skeletal, slow)**	***TNNT1***
1456	**10,0**	**21,5**	**-2,14**	**0,00890**	**0,334**	**231728_at**	**Calcyphosine**	***CAPS***
975	**31,7**	**67,0**	**-2,12**	**0,00567**	**0,315**	**203608_at**	**Aldehyde dehydrogenase 5 family, member A1**	***ALDH5A1***
696	**9,70**	**20,5**	**-2,11**	**0,00400**	**0,308**	**220936_s_at**	**H2A histone family, member J**	***H2AFJ***
2086	**11,3**	**23,6**	**-2,09**	**0,01361**	**0,356**	**222863_at**	**Zinc finger and BTB domain containing 10**	***ZBTB10***
1868	**22,7**	**47,1**	**-2,07**	**0,01207**	**0,353**	**219607_s_at**	**Membrane-spanning 4-domains, subfamily A, member 4**	***MS4A4A***
1511	**37,0**	**74,2**	**-2,00**	**0,00931**	**0,337**	**239847_at**	**cDNA clone IMAGE:6186815**	**-**
2925	30,3	60,6	-1,99	0,02051	0,383	242245_at	cDNA FLJ90705 fis, clone PLACE1007591	-
2061	12,6	25,0	-1,98	0,01344	0,356	239278_at	cDNA clone IMAGE:5301129	-
1092	20,2	39,9	-1,98	0,00641	0,319	207469_s_at	Pirin (iron-binding nuclear protein)	*PIR*
721	7,27	14,4	-1,98	0,00412	0,308	230782_at	Similar to Sorbitol dehydrogenase (L-iditol 2-dehydrogenase)	*LOC653381*
1970	8,59	17,0	-1,98	0,01287	0,355	227644_at	Regulating synaptic membrane exocytosis 4	*RIMS4*
3815	10,5	20,5	-1,95	0,02783	0,399	223565_at	Hypothetical protein MGC29506	*MGC29506*
1102	6,40	12,5	-1,95	0,00646	0,319	206214_at	2-acetyl-1-alkylglycerophosphocholine esterase	*PLA2G7*
879	44,4	86,4	-1,95	0,00509	0,313	226424_at	Calcyphosine	*CAPS*
5208	9,34	18,1	-1,93	0,04019	0,422	213906_at	v-Myb myeloblastosis viral oncogene homolog (avian)-like 1	*MYBL1*
712	23,0	44,3	-1,93	0,00409	0,308	218954_s_at	RNA polymerase III transcription initiation factor BRFU	*BRF2*
744	41,2	79,2	-1,92	0,00422	0,308	1558290_a_at	Pvt1 oncogene homolog, MYC activator (mouse)	*PVT1*
1324	14,2	27,2	-1,92	0,00793	0,327	229139_at	Junctophilin 1	*JPH1*
626	14,4	27,1	-1,89	0,00355	0,308	220016_at	AHNAK nucleoprotein	*AHNAK*
1012	37,1	69,9	-1,89	0,00586	0,316	222312_s_at	cDNA clone IMAGE:6186815	-
4227	27,5	51,7	-1,88	0,03132	0,405	214038_at	Chemokine (C-C motif) ligand 8	*CCL8*
2492	8,69	16,3	-1,87	0,01679	0,367	213768_s_at	Achaete-scute complex homolog 1 (Drosophila)	*ASCL1*
2288	9,72	18,1	-1,86	0,01520	0,363	237031_at	Full length insert cDNA clone YP08F12	-
3458	37,7	69,8	-1,85	0,02478	0,392	222731_at	Zinc finger, DHHC-type containing 2	*ZDHHC2*
2767	12,3	22,5	-1,83	0,01921	0,379	1554333_at	DnaJ (Hsp40) homolog, subfamily A, member 4	*DNAJA4*
2804	4,96	9,08	-1,83	0,01950	0,380	235801_at	-	-
1062	9,29	17,0	-1,83	0,00623	0,319	236828_at	Transcribed locus	-
112	91,1	165	-1,81	0,00050	0,240	202779_s_at	Ubiquitin-conjugating enzyme E2S	*UBE2S*
817	648	1176	-1,81	0,00467	0,312	225245_x_at	H2A histone family, member J	*H2AFJ*
3705	36,0	65,4	-1,81	0,02679	0,395	201195_s_at	Solute carrier family 7, member 5	*SLC7A5*
554	35,8	64,6	-1,81	0,00301	0,296	206066_s_at	RAD51 homolog C (S. cerevisiae)	*RAD51C*
868	111	200	-1,80	0,00502	0,313	202954_at	Ubiquitin-conjugating enzyme E2C	*UBE2C*
1761	28,1	50,5	-1,80	0,01123	0,348	221286_s_at	Hypothetical protein MGC29506	*MGC29506*
795	693	1241	-1,79	0,00454	0,311	224301_x_at	H2A histone family, member J	*H2AFJ*
5280	9,64	17,2	-1,79	0,04106	0,425	238646_at	Transcribed locus	-

Index	Mutated*	Normal*	FC	*P* value	FDR**	Probe set	Description	Gene symbol
5108	7,75	13,8	-1,79	0,03930	0,421	205697_at	Secretagogin, EF-hand calcium binding protein	*SCGN*
1008	35,2	62,9	-1,79	0,00585	0,316	204033_at	Thyroid hormone receptor interactor 13	*TRIP13*
2580	53,2	94,7	-1,78	0,01750	0,371	229796_at	SIX homeobox 4	*SIX4*
1883	21,4	37,8	-1,76	0,01223	0,355	222730_s_at	Zinc finger, DHHC-type containing 2	*ZDHHC2*
3745	3,00	5,27	-1,75	0,02724	0,397	235947_at	Similar to XP_001165016.1	-
3378	24,8	43,3	-1,75	0,02404	0,389	231069_at	Transcribed locus	-
915	371	644	-1,74	0,00527	0,313	200641_s_at	14-3-3 protein/cytosolic phospholipase A2	*YWHAZ*
1239	15,6	27,1	-1,73	0,00736	0,324	235330_at	Coiled-coil domain containing 117	*CCDC117*
822	4,90	8,47	-1,73	0,00469	0,312	238898_at	Transcribed locus	-
2457	5,97	10,3	-1,72	0,01647	0,366	209631_s_at	G protein-coupled receptor 37 (endothelin receptor type B-like)	*GPR37*
710	10,4	17,9	-1,72	0,00407	0,308	238624_at	Nemo-like kinase	*NLK*
1217	87,3	150	-1,72	0,00724	0,324	226384_at	Phosphatidic acid Phosphatase type 2 domain containing 1B	*PPAPDC1B*
1700	39,9	68,3	-1,71	0,01082	0,348	220588_at	Breast carcinoma amplified sequence 4	*BCAS4*
3691	3,56	6,07	-1,71	0,02666	0,395	1554314_at	Chromosome 6 open reading frame 141	*C6orf141*
3065	29,1	49,5	-1,70	0,02161	0,385	212314_at	KIAA0746 protein	*KIAA0746*
2204	5,88	9,96	-1,69	0,01457	0,361	1556097_at	cDNA DKFZp686A11113	-
5191	10,2	17,3	-1,69	0,03999	0,421	242338_at	Transmembrane protein 64	*TMEM64*
2284	7,04	11,9	-1,69	0,01518	0,363	236514_at	Acyl-CoA thioesterase 8	*ACOT8*
1666	23,1	39,1	-1,69	0,01053	0,345	228999_at	Chromodomain helicase DNA binding protein 2	*CHD2*
2262	70,8	120	-1,69	0,01505	0,363	212690_at	DDHD domain containing 2	*DDHD2*
2397	18,6	31,4	-1,69	0,01599	0,365	1555728_a_at	Membrane-spanning 4-domains, subfamily A, member 4	*MS4A4A*
523	350	589	-1,68	0,00279	0,291	201688_s_at	Tumor protein D52	*TPD52*
2810	57,0	95,8	-1,68	0,01955	0,380	221521_s_at	GINS complex subunit 2 (Psf2 homolog)	*GINS2*
2627	6,05	10,1	-1,68	0,01787	0,372	236105_at	Transcribed locus	-
456	53,0	88,8	-1,68	0,00244	0,288	239069_s_at	Similar to KIAA0825 protein [Pan troglodytes]	
1327	108	181	-1,67	0,00799	0,328	226568_at	Family with sequence similarity 102, member B	*FAM102B*
1024	48,9	81,8	-1,67	0,00593	0,316	1554334_a_at	DnaJ (Hsp40) homolog, subfamily A, member 4	*DNAJA4*
2085	11,0	18,4	-1,67	0,01360	0,356	214481_at	Histone cluster 1, H2am	*HIST1H2AM*
2405	77,5	129	-1,66	0,01607	0,365	218245_at	Tsukushin	*TSKU*
4633	13,9	23,1	-1,66	0,03495	0,412	213470_s_at	Heterogeneous nuclear ribonucleoprotein H1	*HNRPH1*
2685	162	269	-1,66	0,01840	0,375	210519_s_at	NAD(P)H dehydrogenase, quinone 1	*NQO1*
1606	72,0	119	-1,66	0,01006	0,342	223568_s_at	Phosphatidic acid Phosphatase type 2 domain containing 1B	*PPAPDC1B*
1302	60,3	99,7	-1,65	0,00775	0,325	218955_at	RNA polymerase III transcription initiation factor BRFU	*BRF2*
2821	14,7	24,3	-1,65	0,01969	0,381	212706_at	RAS p21 protein activator 4	*RASA4*
4835	15,2	25,0	-1,65	0,03687	0,417	213562_s_at	Squalene epoxidase	*SQLE*
3170	37,3	61,4	-1,65	0,02250	0,387	203145_at	Sperm associated antigen 5	*SPAG5*
1098	132	217	-1,65	0,00644	0,319	202431_s_at	v-Myc myelocytomatosis viral oncogene homolog (avian)	*MYC*
559	24,5	40,2	-1,64	0,00305	0,298	242304_at	Within bgcn homolog (Drosophila)	*WIBG*
3317	6,24	10,2	-1,64	0,02357	0,388	244779_at	cDNA FLJ34038 fis, clone FCBBF2005645	-
3346	170	279	-1,64	0,02376	0,388	226150_at	Phosphatidic acid Phosphatase type 2 domain containing 1B	*PPAPDC1B*
2948	18,2	29,8	-1,64	0,02068	0,384	212311_at	KIAA0746 protein	*KIAA0746*
1654	213	349	-1,64	0,01044	0,345	203381_s_at	Apolipoprotein E	*APOE*
106	361	590	-1,64	0,00043	0,217	218059_at	Zinc finger protein 706	*ZNF706*
3739	3,38	5,49	-1,63	0,02717	0,397	206757_at	Phosphodiesterase 5A, cGMP-specific	*PDE5A*
2187	16,7	27,0	-1,62	0,01449	0,361	230449_x_at	Similar toUbiquitin-conjugating enzyme E2 variant 1 isoform c	-
4174	14,5	23,4	-1,62	0,03086	0,404	239862_at	Transcribed locus	-
753	141	228	-1,62	0,00426	0,308	203382_s_at	Apolipoprotein E	*APOE*
1244	7,30	11,8	-1,61	0,00739	0,324	230361_at	Hypothetical protein KIAA1833	*KIAA1833*
2414	11,9	19,2	-1,61	0,01613	0,365	238694_at	Transcribed locus	-
1845	213	344	-1,61	0,01187	0,352	203534_at	LSM1 homolog, U6 small nuclear RNA associated (S. cerevisiae)	*LSM1*
2960	65,1	105	-1,61	0,02079	0,384	203362_s_at	MAD2 mitotic arrest deficient-like 1 (yeast)	*MAD2L1*
4603	9,86	15,9	-1,61	0,03480	0,412	1560101_at	Synapse defective 1, Rho GTPase, homolog 2 (C. elegans)	*SYDE2*
2479	110	177	-1,61	0,01670	0,367	204416_x_at	Apolipoprotein C-I	*APOC1*
1730	42,8	68,7	-1,61	0,01105	0,348	231784_s_at	WD repeats and SOF1 domain containing	*WDSOF1*
4462	42,7	68,5	-1,60	0,03352	0,411	202095_s_at	Baculoviral IAP repeat-containing 5 (survivin)	*BIRC5*
806	641	1026	-1,60	0,00460	0,311	225547_at	Small nucleolar RNA host gene (non-protein coding) 6	*SNHG6*
2891	9,33	14,9	-1,60	0,02030	0,383	223574_x_at	Protein phosphatase 2A1 B gamma subunit	*PPP2R2C*

Index	Mutated*	Normal*	FC	*P* value	FDR**	Probe set	Description	Gene symbol
1091	60,2	96,3	-1,60	0,00640	0,319	227765_at	cDNA clone IMAGE:4820809	-
371	788	1259	-1,60	0,00194	0,284	200640_at	14-3-3 protein/cytosolic phospholipase A2	*YWHAZ*
1535	52,3	83,7	-1,60	0,00951	0,337	225857_s_at	Hypothetical LOC388796	*LOC388796*
3470	14,3	22,9	-1,60	0,02486	0,392	219519_s_at	Sialic acid binding Ig-like lectin 1, sialoadhesin	*SIGLEC1*
436	13,6	21,8	-1,60	0,00230	0,288	221908_at	Transmembrane protein 118	*TMEM118*
999	412	656	-1,59	0,00578	0,316	201689_s_at	Tumor protein D52	*TPD52*
4713	32,5	51,7	-1,59	0,03566	0,413	230422_at	Formyl peptide receptor-like 2	*FPRL2*
3859	6,94	11,0	-1,59	0,02818	0,399	221345_at	Free fatty acid receptor 2	*FFAR2*
4446	4,16	6,61	-1,59	0,03340	0,411	1561817_at	cDNA FLJ35294 fis, clone PROST2008724	-
5258	222	352	-1,58	0,04077	0,424	201563_at	Sorbitol dehydrogenase	*SORD*
6067	15,5	24,6	-1,58	0,04948	0,446	228645_at	Small nucleolar RNA host gene (non-protein coding) 9	*SNHG9*
3302	18,4	28,9	-1,58	0,02351	0,388	229417_at	Transcribed locus	-
4076	112	176	-1,57	0,02989	0,401	209218_at	Squalene epoxidase	*SQLE*
3033	33,1	52,0	-1,57	0,02138	0,385	65588_at	Hypothetical LOC388796	*LOC388796*
324	12,0	18,8	-1,57	0,00161	0,272	230016_at	Chromosome 8 open reading frame 38	*C8orf38*
1292	679	1065	-1,57	0,00770	0,325	200638_s_at	14-3-3 protein/cytosolic phospholipase A2	*YWHAZ*
4604	42,0	65,8	-1,57	0,03480	0,412	227804_at	TLC domain containing 1	*TLCD1*
3849	7,38	11,6	-1,57	0,02810	0,399	204920_at	Carbamoyl-phosphate synthetase 1, mitochondrial	*CPS1*
2481	31,5	49,3	-1,57	0,01672	0,367	1554768_a_at	MAD2 mitotic arrest deficient-like 1 (yeast)	*MAD2L1*
2026	45,2	70,7	-1,57	0,01320	0,355	227132_at	Zinc finger protein 706	*ZNF706*
2298	106	165	-1,56	0,01527	0,363	216336_x_at	Metallothionein 1A	*MT1A*
4938	97,1	151	-1,56	0,03789	0,419	201467_s_at	NAD(P)H dehydrogenase, quinone 1	*NQO1*
2082	64,2	99,9	-1,56	0,01358	0,356	208002_s_at	Acyl-CoA thioesterase 7	*ACOT7*
5213	6,59	10,3	-1,56	0,04026	0,422	239752_at	cDNA FLJ38271 fis, clone FCBBF3002782	-
2013	11,1	17,3	-1,55	0,01313	0,355	228213_at	H2A histone family, member J	*H2AFJ*
3008	191	296	-1,55	0,02118	0,385	206461_x_at	Metallothionein 1H	*MT1H*
321	744	1155	-1,55	0,00161	0,272	200639_s_at	14-3-3 protein/cytosolic phospholipase A2	*YWHAZ*
5141	34,9	54,1	-1,55	0,03959	0,421	208079_s_at	Aurora kinase A	*AURKA*
2569	548	850	-1,55	0,01743	0,371	212185_x_at	Metallothionein 2A	*MT2A*
484	634	982	-1,55	0,00258	0,289	201690_s_at	Tumor protein D52	*TPD52*
433	32,2	49,8	-1,55	0,00228	0,288	221586_s_at	E2F transcription factor 5, p130-binding	*E2F5*
1889	179	277	-1,55	0,01225	0,355	225061_at	DnaJ (Hsp40) homolog, subfamily A, member 4	*DNAJA4*
5865	6,76	10,4	-1,54	0,04742	0,442	219159_s_at	SLAM family member 7	*SLAMF7*
4885	28,2	43,5	-1,54	0,03736	0,418	223253_at	Ependymin related protein 1 (zebrafish)	*EPDR1*
2664	149	230	-1,54	0,01822	0,374	235509_at	Chromosome 8 open reading frame 38	*C8orf38*
2307	19,2	29,5	-1,54	0,01532	0,363	226791_at	Kinesin family member C2	*KIFC2*
4266	57,2	87,9	-1,54	0,03174	0,406	202705_at	Cyclin B2	*CCNB2*
1450	163	249	-1,53	0,00886	0,334	202634_at	Polymerase (RNA) II (DNA directed) polypeptide K, 7.0kDa	*POLR2K*
2047	312	478	-1,53	0,01331	0,355	211456_x_at	Metallothionein 1 pseudogene 2	*MT1P2*
4171	21,4	32,8	-1,53	0,03082	0,404	217080_s_at	Homer homolog 2 (Drosophila)	*HOMER2*
2109	18,0	27,6	-1,53	0,01383	0,358	238012_at	Dipeptidyl-peptidase 7	*DPP7*
4873	43,0	65,6	-1,52	0,03720	0,417	223569_at	Phosphatidic acid Phosphatase type 2 domain containing 1B	*PPAPDC1B*
3697	79,2	121	-1,52	0,02674	0,395	226803_at	Chromatin modifying protein 4C	*CHMP4C*
1067	59,3	90,3	-1,52	0,00626	0,319	227451_s_at	Coiled-coil domain containing 90A	*CCDC90A*
1132	47,6	72,5	-1,52	0,00661	0,319	222155_s_at	G protein-coupled receptor 172A	*GPR172A*
2735	88,8	135	-1,52	0,01887	0,377	218514_at	Chromosome 17 open reading frame 71	*C17orf71*
5126	30,0	45,7	-1,52	0,03946	0,421	210117_at	Sperm associated antigen 1	*SPAG1*
3094	10,2	15,6	-1,52	0,02181	0,385	236113_at	Transcribed locus	-
1542	51,1	77,6	-1,52	0,00954	0,337	219188_s_at	MACRO domain containing 1	*MACROD1*
3580	28,4	43,1	-1,52	0,02586	0,394	221194_s_at	PTD016 protein	*LOC51136*
2352	65,1	98,7	-1,52	0,01569	0,364	201853_s_at	Cell division cycle 25 homolog B (S. pombe)	*CDC25B*
1295	8,69	13,2	-1,52	0,00771	0,325	230330_at	cDNA FLJ30011 fis, clone 3NB692000276	-
1526	22,2	33,6	-1,52	0,00943	0,337	221909_at	Transmembrane protein 118	*TMEM118*
4849	12,6	19,1	-1,52	0,03694	0,417	238818_at	KIAA1429 protein	*KIAA1429*
826	98,8	149	-1,51	0,00471	0,312	203011_at	Inositol(myo)-1(or 4)-monophosphatase 1	*IMPA1*
1796	259	392	-1,51	0,01156	0,351	202635_s_at	Polymerase (RNA) II (DNA directed) polypeptide K, 7.0kDa	*POLR2K*
1998	79,4	120	-1,51	0,01306	0,355	219363_s_at	MTERF domain containing 1	*MTERFD1*

Index	Mutated*	Normal*	FC	*P* value	FDR**	Probe set	Description	Gene symbol
2432	21,3	32,1	-1,51	0,01626	0,365	209573_s_at	Chromosome 18 open reading frame 1	*C18orf1*
4252	115	173	-1,51	0,03157	0,406	217165_x_at	Metallothionein 1F	*MT1F*
2676	5,02	7,57	-1,51	0,01831	0,374	222309_at	Chromosome 6 open reading frame 62	*C6orf62*
2941	4,19	6,31	-1,51	0,02062	0,383	213609_s_at	Seizure related 6 homolog (mouse)-like	*SEZ6L*
2636	19,5	29,3	-1,51	0,01794	0,372	210334_x_at	Baculoviral IAP repeat-containing 5 (survivin)	*BIRC5*
2741	7,79	11,7	-1,51	0,01891	0,377	219403_s_at	Heparanase	*HPSE*
4616	11,6	17,5	-1,51	0,03484	0,412	219697_at	Heparan sulfate (glucosamine) 3-O-sulfotransferase 2	*HS3ST2*
3007	45,5	68,4	-1,50	0,02117	0,385	225203_at	Protein phosphatase 1, regulatory (inhibitor) subunit 16A	*PPP1R16A*
1627	61,5	92,6	-1,50	0,01023	0,344	225378_at	Vacuolar protein sorting 37 homolog A (S. cerevisiae)	*VPS37A*
3557	108	163	-1,50	0,02565	0,394	224356_x_at	Membrane-spanning 4-domains, subfamily A, member 6A	*MS4A6A*
1096	7,40	11,1	-1,50	0,00642	0,319	1556613_s_at	Hypothetical protein LOC203107	*LOC203107*
4441	63,7	95,5	-1,50	0,03333	0,410	218009_s_at	Protein regulator of cytokinesis 1	*PRC1*
5480	77,2	116	-1,50	0,04336	0,433	235010_at	Hypothetical protein LOC729013	*LOC729013*
4289	113	169	-1,50	0,03189	0,406	201484_at	Suppressor of Ty 4 homolog 1 (S. cerevisiae)	*SUPT4H1*
583	28,2	42,1	-1,50	0,00319	0,300	227935_s_at	Polycomb group ring finger 5	*PCGF5*
1331	24,8	36,9	-1,49	0,00800	0,328	212563_at	Block of proliferation 1	*BOP1*
1482	131	195	-1,49	0,00911	0,336	200924_s_at	Solute carrier family 3, member 2	*SLC3A2*
5681	331	494	-1,49	0,04535	0,436	208581_x_at	Metallothionein 1X	*MT1X*
3589	34,3	51,0	-1,49	0,02590	0,394	228024_at	Vacuolar protein sorting 37 homolog A (S. cerevisiae)	*VPS37A*
310	7,50	11,2	-1,49	0,00150	0,265	241957_x_at	Lin-7 homolog B (C. elegans)	*LIN7B*
848	11,3	16,7	-1,48	0,00489	0,313	212619_at	KIAA0286 protein	*KIAA0286*
4312	51,2	75,9	-1,48	0,03210	0,407	226943_at	Keratin, hair, basic, 5	*KRTHB5*
1904	44,0	65,2	-1,48	0,01238	0,355	217499_x_at	Olfactory receptor, family 7, subfamily E, member 37 pseudogene	*OR7E37P*
3996	7,81	11,6	-1,48	0,02921	0,400	1555606_a_at	Glycerophosphodiester phosphodiesterase domain containing 1	*GDPD1*
2054	4,56	6,74	-1,48	0,01336	0,356	228047_at	Small nucleolar RNA, H/ACA box 72	*SNORA72*
2880	22,8	33,6	-1,48	0,02021	0,383	1555461_at	-	-
2521	54,3	80,1	-1,47	0,01701	0,369	228488_at	TBC1 domain family, member 16	*TBC1D16*
5834	145	213	-1,47	0,04713	0,442	209185_s_at	Insulin receptor substrate 2	*IRS2*
5303	689	1015	-1,47	0,04139	0,426	200800_s_at	Heat shock 70kDa protein 1A	*HSPA1A*
3389	33,6	49,6	-1,47	0,02414	0,389	202823_at	Transcription elongation factor B (SIII), polypeptide 1	*TCEB1*
308	134	198	-1,47	0,00148	0,263	218680_x_at	Huntingtin interacting protein K	*HYPK*
3659	6,09	8,97	-1,47	0,02642	0,395	239562_at	NADP-dependent methylenetetrahydrofolate dehydrogenase 2-like protein	*MTHFD2L*
3096	43,1	63,5	-1,47	0,02182	0,385	222912_at	Arrestin, beta 1	*ARRB1*
3898	14,8	21,8	-1,47	0,02848	0,399	214560_at	Formyl peptide receptor-like 2	*FPRL2*
4720	148	218	-1,47	0,03570	0,413	204745_x_at	Metallothionein 1G	*MT1G*
5517	3,53	5,18	-1,47	0,04375	0,433	217564_s_at	Carbamoyl-phosphate synthetase 1, mitochondrial	*CPS1*
2150	25,3	37,2	-1,47	0,01415	0,360	222026_at	RNA binding motif (RNP1, RRM) protein 3	*RBM3*
1615	5,69	8,34	-1,47	0,01013	0,343	217599_s_at	MyoD family inhibitor domain containing	*MDFIC*
2266	53,6	78,5	-1,47	0,01507	0,363	202481_at	Dehydrogenase/reductase (SDR family) member 3	*DHRS3*
3731	265	388	-1,47	0,02709	0,397	224447_s_at	Chromosome 17 open reading frame 37	*C17orf37*
1588	98,9	145	-1,47	0,00988	0,340	221539_at	Eukaryotic translation initiation factor 4E binding protein 1	*EIF4EBP1*
5996	92,7	136	-1,46	0,04875	0,444	209380_s_at	ATP-binding cassette, sub-family C (CFTR/MRP), member 5	*ABCC5*
1499	65,1	95,1	-1,46	0,00923	0,336	229050_s_at	Small nucleolar RNA host gene (non-protein coding) 7	*SNHG7*
1223	14,2	20,7	-1,46	0,00728	0,324	204126_s_at	CDC45 cell division cycle 45-like (S. cerevisiae)	*CDC45L*
372	130	189	-1,46	0,00195	0,284	233746_x_at	Huntingtin interacting protein K	*HYPK*
3404	6,62	9,64	-1,46	0,02428	0,390	1562904_s_at	Similar to CG7889-PA	*FLJ10661*
2242	184	268	-1,46	0,01489	0,363	201433_s_at	Phosphatidylserine synthase 1	*PTDSS1*
3183	6,40	9,30	-1,45	0,02256	0,387	210341_at	Myelin transcription factor 1	*MYT1*
4533	16,4	23,9	-1,45	0,03425	0,412	213599_at	Opa interacting protein 5	*OIP5*
2107	17,0	24,7	-1,45	0,01383	0,358	40020_at	Cadhetrin, EGF LAG seven-pass G-type receptor 3	*CELSR3*
4680	18,3	26,6	-1,45	0,03534	0,413	1552623_at	Hematopoietic SH2 domain containing	*HSH2D*
1782	27,6	40,0	-1,45	0,01137	0,349	228357_at	Unkempt homolog (Drosophila)	*UNK*
4830	62,2	89,9	-1,45	0,03679	0,416	201801_s_at	Solute carrier family 29, member 1	*SLC29A1*
2578	31,1	45,0	-1,45	0,01749	0,371	206574_s_at	Protein tyrosine phosphatase type IVA, member 3	*PTP4A3*
5119	34,1	49,3	-1,45	0,03941	0,421	204092_s_at	Aurora kinase A	*AURKA*
597	36,6	52,9	-1,44	0,00329	0,301	215030_at	G-rich RNA sequence binding factor 1	*GRSF1*
734	58,6	84,7	-1,44	0,00419	0,308	215905_s_at	WD repeat domain 57	*WDR57*

Index	Mutated*	Normal*	FC	*P* value	FDR**	Probe set	Description	Gene symbol
1246	25,7	37,2	-1,44	0,00740	0,324	205870_at	Bradykinin receptor B2	*BDKRB2*
1875	12,1	17,5	-1,44	0,01213	0,354	230454_at	Islet cell autoantigen 1,69kDa-like	*ICA1L*
1554	37,1	53,5	-1,44	0,00959	0,337	227787_s_at	Mediator complex subunit 30	*MED30*
1333	140	202	-1,44	0,00801	0,328	202433_at	Solute carrier family 35, member B1	*SLC35B1*
2791	43,3	62,5	-1,44	0,01941	0,380	202219_at	Solute carrier family 6, member 8	*SLC6A8*
2395	57,3	82,7	-1,44	0,01599	0,365	212983_at	v-HA-RAS Harvey rat sarcoma viral oncogene homolog	*HRAS*
960	22,4	32,4	-1,44	0,00554	0,315	218832_x_at	Arrestin, beta 1	*ARRB1*
1272	176	254	-1,44	0,00756	0,325	218049_s_at	Mitochondrial ribosomal protein L13	*MRPL13*
533	158	227	-1,44	0,00285	0,292	219449_s_at	Transmembrane protein 70	*TMEM70*
3565	4,68	6,75	-1,44	0,02574	0,394	1553175_s_at	Phosphodiesterase 5A, cGMP-specific	*PDE5A*
3125	26,4	38,1	-1,44	0,02214	0,387	226446_at	Hairy and enhancer of split 6 (Drosophila)	*HES6*
2369	16,6	23,8	-1,44	0,01580	0,364	209753_s_at	Thymopoietin	*TMPO*
1544	209	301	-1,44	0,00954	0,337	200661_at	Cathepsin A	*CTSA*
818	87,4	126	-1,44	0,00467	0,312	225723_at	Chromosome 6 open reading frame 129	*C6orf129*
6001	8,26	11,9	-1,44	0,04877	0,444	205692_s_at	CD38 molecule	*CD38*
3710	111	160	-1,44	0,02684	0,396	223922_x_at	Membrane-spanning 4-domains, subfamily A, member 6A	*MS4A6A*
169	17,9	25,7	-1,44	0,00078	0,244	235689_at	Mitochondrial methionyl-tRNA formyltransferase	*MTFMT*
6036	4,37	6,28	-1,44	0,04915	0,445	241412_at	Betacellulin	*BTC*
3896	67,2	96,4	-1,44	0,02846	0,399	1558703_at	Solute carrier family 46, member 1	*SLC46A1*
2546	161	231	-1,43	0,01720	0,369	226223_at	Transcribed locus	-
4549	69,1	99,0	-1,43	0,03439	0,412	209849_s_at	RAD51 homolog C (S. cerevisiae)	*RAD51C*
784	90,7	130	-1,43	0,00449	0,311	221020_s_at	Solute carrier family 25, member 32	*SLC25A32*
1856	164	235	-1,43	0,01195	0,352	223156_at	Mitochondrial ribosomal protein S23	*MRPS23*
2889	10,1	14,4	-1,43	0,02027	0,383	215731_s_at	M-phase phosphoprotein 9	*MPHOSPH9*
234	18,8	26,9	-1,43	0,00108	0,250	235015_at	Placenta Cot 25-normalized	-
3818	25,2	35,9	-1,42	0,02786	0,399	227936_at	Transmembrane protein 68	*TMEM68*
4759	62,0	88,2	-1,42	0,03608	0,414	225436_at	Family with sequence similarity 108, member C1	*FAM108C1*
4063	20,4	29,0	-1,42	0,02980	0,401	219000_s_at	Defective in sister chromatid cohesion homolog 1 (S. cerevisiae)	*DCC1*
1252	4,20	5,98	-1,42	0,00746	0,325	238566_at	Transcribed locus	-
746	83,7	119	-1,42	0,00423	0,308	202204_s_at	Autocrine motility factor receptor	*AMFR*
2005	34,8	49,4	-1,42	0,01308	0,355	221520_s_at	Cell division cycle associated 8	*CDCA8*
1912	52,3	74,3	-1,42	0,01244	0,355	202070_s_at	Isocitrate dehydrogenase 3 (NAD+) alpha	*IDH3A*
4523	80,3	114	-1,42	0,03413	0,412	226319_s_at	THO complex 4	*THOC4*
1190	118	167	-1,42	0,00703	0,322	212056_at	KIAA0182 protein	*KIAA0182*
5276	108	153	-1,42	0,04100	0,425	218187_s_at	Chromosome 8 open reading frame 33	*C8orf33*
771	154	218	-1,42	0,00442	0,311	224281_s_at	Neugrin, neurite outgrowth associated	*NGRN*
2241	113	160	-1,41	0,01489	0,363	218695_at	Exosome component 4	*EXOSC4*
230	48,1	68,1	-1,41	0,00106	0,250	218906_x_at	Kinesin light chain 2	*KLC2*
5714	180	255	-1,41	0,04574	0,438	201483_s_at	Suppressor of Ty 4 homolog 1 (S. cerevisiae)	*SUPT4H1*
4461	88,3	125	-1,41	0,03352	0,411	225374_at	Chromosome 17 open reading frame 32	*C17orf32*
900	19,1	26,9	-1,41	0,00521	0,313	1568596_a_at	Trophinin associated protein (tastin)	*TROAP*
4183	10,6	14,9	-1,41	0,03092	0,404	209924_at	Chemokine (C-C motif) ligand 18	*CCL18*
4385	31,3	44,1	-1,41	0,03267	0,407	214542_x_at	Histone cluster 1, H2ai	*HIST1H2AI*
1211	14,4	20,2	-1,41	0,00718	0,324	239699_s_at	Postmeiotic segregation increased 2-like 1	*PMS2L1*
853	13,7	19,2	-1,41	0,00491	0,313	222276_at	Transcribed locus	-
3393	335	471	-1,41	0,02419	0,390	208808_s_at	High-mobility group box 2	*HMGB2*
3930	15,6	21,9	-1,40	0,02873	0,399	206753_at	Retinol dehydrogenase 16 (all-trans)	*RDH16*
5129	7,00	9,83	-1,40	0,03946	0,421	1555216_a_at	Hypothetical LOC645722	*LOC645722*
3805	5,85	8,21	-1,40	0,02771	0,398	32128_at	Chemokine (C-C motif) ligand 18	*CCL18*
547	517	726	-1,40	0,00296	0,295	223880_x_at	Chromosome 20 open reading frame 24	*C20orf24*
2822	35,2	49,4	-1,40	0,01970	0,381	218045_x_at	Parathymosin	*PTMS*
1003	391	548	-1,40	0,00580	0,316	200078_s_at	ATPase, H+ transporting, lysosomal 21kDa, V0 subunit b	*ATP6V0B*
2470	49,2	69,0	-1,40	0,01659	0,367	200676_s_at	Ubiquitin-conjugating enzyme E2L 3	*UBE2L3*
4402	18,8	26,3	-1,40	0,03285	0,408	219751_at	SET domain containing 6	*SETD6*
671	15,6	21,8	-1,40	0,00386	0,308	1553043_a_at	CD300 molecule-like family member f	*CD300LF*
812	28,0	39,2	-1,40	0,00462	0,311	224980_at	LEM domain containing 2	*LEMD2*
3715	6,82	9,55	-1,40	0,02694	0,396	204534_at	Vitronectin	*VTN*

Index	Mutated*	Normal*	FC	*P* value	FDR**	Probe set	Description	Gene symbol
1348	33,3	46,6	-1,40	0,00809	0,328	205695_at	Serine dehydratase	*SDS*
1715	12,4	17,3	-1,40	0,01099	0,348	238780_s_at	cDNA DKFZp779F2345	-
2106	5,76	8,04	-1,40	0,01379	0,358	207746_at	Polymerase (DNA directed), theta	*POLQ*
4339	20,9	29,2	-1,39	0,03231	0,407	218521_s_at	Ubiquitin-conjugating enzyme E2W	*UBE2W*
4054	82,3	115	-1,39	0,02974	0,401	203790_s_at	Heat-responsive protein 12	*HRSP12*
2953	10,8	15,0	-1,39	0,02073	0,384	223845_at	Hypothetical protein BC001437	*LOC144305*
3448	9,48	13,2	-1,39	0,02469	0,391	1557147_a_at	Full length insert cDNA YH73H08	-
779	113	157	-1,39	0,00447	0,311	203109_at	Ubiquitin-conjugating enzyme E2M	*UBE2M*
4961	47,7	66,5	-1,39	0,03805	0,419	209408_at	Kinesin family member 2C	*KIF2C*
3037	6,19	8,62	-1,39	0,02140	0,385	1554020_at	Bicaudal D homolog 1 (Drosophila)	*BICD1*
2069	5,06	7,03	-1,39	0,01353	0,356	214874_at	Plakophilin 4	*PKP4*
813	21,8	30,2	-1,39	0,00465	0,312	215728_s_at	Acyl-CoA thioesterase 7	*ACOT7*
6034	5,34	7,41	-1,39	0,04911	0,445	220484_at	Mucolipin 3	*MCOLN3*
4409	28,9	40,1	-1,39	0,03292	0,408	201710_at	v-Myb myeloblastosis viral oncogene homolog (avian)-like 2	*MYBL2*
4546	62,4	86,5	-1,39	0,03436	0,412	202392_s_at	Phosphatidylserine decarboxylase	*PISD*
3150	174	241	-1,39	0,02235	0,387	221504_s_at	ATPase, H+ transporting, lysosomal 50/57kDa, V1 subunit H	*ATP6V1H*
2467	466	645	-1,39	0,01658	0,367	202824_s_at	Transcription elongation factor B (SIII), polypeptide 1	*TCEB1*
2367	84,4	117	-1,39	0,01579	0,364	226805_at	Chromosome 20 open reading frame 142	*C20orf142*
345	241	333	-1,39	0,00177	0,278	227291_s_at	BolA homolog 3 (E. coli)	*BOLA3*
4587	13,4	18,6	-1,38	0,03469	0,412	221638_s_at	Syntaxin 16	*STX16*
3704	4,23	5,85	-1,38	0,02679	0,395	233446_at	One cut homeobox 2	*ONECUT2*
4176	20,9	29,0	-1,38	0,03086	0,404	231952_at	Hypothetical protein LOC731450	*LOC731450*
3116	16,7	23,0	-1,38	0,02203	0,387	238728_at	Similar to KIAA0825 protein	-
4955	14,5	20,0	-1,38	0,03801	0,419	235006_at	CDKN2A interacting protein N-terminal like	*CDKN2AIPNL*
379	64,2	88,6	-1,38	0,00198	0,284	218647_s_at	YrdC domain containing (E. coli)	*YRDC*
292	11,0	15,2	-1,38	0,00143	0,263	209544_at	Receptor-interacting serine-threonine kinase 2	*RIPK2*
2472	19,9	27,4	-1,38	0,01661	0,367	221965_at	M-phase phosphoprotein 9	*MPHOSPH9*
3159	123	170	-1,38	0,02242	0,387	202353_s_at	Proteasome (prosome, macropain) 26S subunit, non-ATPase, 12	*PSMD12*
937	4,19	5,78	-1,38	0,00537	0,313	226462_at	Syntaxin binding protein 6 (amisyn)	*STXBP6*
350	60,7	83,6	-1,38	0,00179	0,278	219675_s_at	UDP-glucuronate decarboxylase 1	*UXS1*
4516	129	178	-1,38	0,03404	0,412	201266_at	Thioredoxin reductase 1	*TXNRD1*
2066	62,3	85,8	-1,38	0,01349	0,356	232662_x_at	Chromosome 10 open reading frame 58	*C10orf58*
6041	97,1	134	-1,38	0,04919	0,445	225355_at	cDNA DKFZP761M1511	-
2957	183	251	-1,37	0,02076	0,384	204426_at	Transmembrane emp24 domain trafficking protein 2	*TMED2*
4670	225	309	-1,37	0,03526	0,413	209517_s_at	Ash2 (absent, small, or homeotic)-like (Drosophila)	*ASH2L*
3296	1244	1709	-1,37	0,02349	0,388	200799_at	Heat shock 70kDa protein 1A	*HSPA1A*
2910	26,5	36,4	-1,37	0,02045	0,383	225747_at	Coenzyme Q10 homolog A (S. cerevisiae)	*COQ10A*
5005	8,83	12,1	-1,37	0,03844	0,420	222376_at	Transcribed locus	-
887	559	767	-1,37	0,00512	0,313	217835_x_at	Chromosome 20 open reading frame 24	*C20orf24*
3062	170	234	-1,37	0,02157	0,385	224743_at	Inositol monophosphatase domain containing 1	*IMPAD1*
5761	19,1	26,3	-1,37	0,04629	0,439	229106_at	Dynein, light chain, LC8-type 2	*DYNLL2*
213	6,72	9,22	-1,37	0,00096	0,244	236478_at	Interferon (alpha, beta and omega) receptor 1	*IFNAR1*
644	19,7	27,1	-1,37	0,00367	0,308	228627_at	Tousled-like kinase 2	*TLK2*
4317	11,1	15,3	-1,37	0,03215	0,407	230591_at	Hypothetical protein LOC729887	*LOC729887*
2703	115	158	-1,37	0,01854	0,375	58696_at	Exosome component 4	*EXOSC4*
3354	50,7	69,5	-1,37	0,02382	0,388	209065_at	Ubiquinol-cytochrome c reductase binding protein	*UQCRB*
4730	194	265	-1,37	0,03582	0,414	225676_s_at	WD repeats and SOF1 domain containing	*WDSOF1*
1813	304	416	-1,37	0,01169	0,351	224603_at	cDNA clone IMAGE:3831740	-
3677	172	236	-1,37	0,02657	0,395	210296_s_at	Peroxisomal membrane protein 3, 35kDa	*PXMP3*
3938	155	212	-1,37	0,02876	0,399	201584_s_at	DEAD (Asp-Glu-Ala-Asp) box polypeptide 39	*DDX39*
5579	10,3	14,1	-1,37	0,04449	0,436	1558906_a_at	cDNA clone IMAGE:5265020	-
2587	12,0	16,4	-1,37	0,01755	0,371	206109_at	Fucosyltransferase 1	*FUT1*
3902	9,30	12,7	-1,37	0,02851	0,399	212427_at	KIAA0368 protein	*KIAA0368*
2878	61,0	83,4	-1,37	0,02020	0,383	218923_at	Chitobiase, di-N-acetyl-	*CTBS*
2753	4,56	6,23	-1,37	0,01905	0,378	237246_at	Transcribed locus	-
5515	53,2	72,8	-1,37	0,04371	0,433	229444_at	Hypothetical protein LOC729776	*LOC729776*
1266	355	486	-1,37	0,00753	0,325	224376_s_at	Chromosome 20 open reading frame 24	*C20orf24*

Index	Mutated*	Normal*	FC	*P* value	FDR**	Probe set	Description	Gene symbol
5619	200	273	-1,37	0,04484	0,436	228123_s_at	Abhydrolase domain containing 12	*ABHD12*
5643	11,2	15,3	-1,36	0,04502	0,436	216985_s_at	Syntaxin 3	*STX3*
5240	30,1	41,0	-1,36	0,04059	0,423	220488_s_at	Breast carcinoma amplified sequence 3	*BCAS3*
3240	12,0	16,4	-1,36	0,02299	0,388	220233_at	F-box protein 17	*FBXO17*
5945	25,6	34,9	-1,36	0,04817	0,443	227037_at	Similar to CG12314 gene product	*LOC201164*
711	393	535	-1,36	0,00408	0,308	201923_at	Peroxiredoxin 4	*PRDX4*
4206	25,0	34,1	-1,36	0,03110	0,404	228517_at	Chromosome 1 open reading frame 149	*C1orf149*
4672	13,6	18,6	-1,36	0,03529	0,413	208033_s_at	Zinc finger homeobox 3	*ZFHX3*
4717	7,75	10,6	-1,36	0,03569	0,413	209535_s_at	-	-
3388	251	342	-1,36	0,02414	0,389	203880_at	COX17 cytochrome c oxidase assembly homolog (S. cerevisiae)	*COX17*
4625	15,2	20,7	-1,36	0,03489	0,412	202094_at	Baculoviral IAP repeat-containing 5 (survivin)	*BIRC5*
1256	18,7	25,5	-1,36	0,00748	0,325	227245_at	Chromosome 12 open reading frame 30	*C12orf30*
4806	97,0	132	-1,36	0,03648	0,415	222673_x_at	Transmembrane protein 57	*TMEM57*
5502	7,43	10,1	-1,36	0,04357	0,433	238214_at	Solute carrier family 26, member 7	*SLC26A7*
4511	38,4	52,2	-1,36	0,03401	0,412	216125_s_at	RAN binding protein 9	*RANBP9*
2285	48,0	65,3	-1,36	0,01519	0,363	218805_at	GTPase, IMAP family member 5	*GIMAP5*
6007	125	171	-1,36	0,04882	0,444	218831_s_at	Fc fragment of IgG, receptor, transporter, alpha	*FCGRT*
3038	35,1	47,7	-1,36	0,02140	0,385	217191_x_at	-	-
172	9,67	13,2	-1,36	0,00080	0,244	239067_s_at	Pannexin 2	*PANX2*
2864	34,4	46,8	-1,36	0,02011	0,383	222665_at	Family with sequence similarity 82, member B	*FAM82B*
2296	38,9	52,8	-1,36	0,01527	0,363	209695_at	Protein tyrosine phosphatase type IVA, member 3	*PTP4A3*
1607	241	327	-1,36	0,01006	0,342	219402_s_at	Der1-like domain family, member 1	*DERL1*
3606	194	263	-1,36	0,02600	0,394	224601_at	cDNA clone IMAGE:3831740	-
4359	63,6	86,4	-1,36	0,03242	0,407	226287_at	Coiled-coil domain containing 34	*CCDC34*
1561	224	304	-1,36	0,00968	0,339	217956_s_at	Enolase-phosphatase 1	*ENOPH1*
1465	251	341	-1,36	0,00897	0,334	218165_at	Chromosome 1 open reading frame 149	*C1orf149*
1537	6,94	9,42	-1,36	0,00952	0,337	205262_at	Potassium voltage-gated channel subfamily H member 2	*KCNH2*
5799	507	687	-1,36	0,04677	0,441	201577_at	Non-metastatic cells 1, protein (NM23A) expressed in	*NME1*
466	24,3	33,0	-1,36	0,00246	0,288	204817_at	Extra spindle pole bodies homolog 1 (S. cerevisiae)	*ESPL1*
4373	119	162	-1,36	0,03252	0,407	209567_at	RRS1 ribosome biogenesis regulator homolog (S. cerevisiae)	*RRS1*
2245	66,8	90,4	-1,35	0,01493	0,363	227696_at	Exosome component 6	*EXOSC6*
1990	7,42	10,0	-1,35	0,01302	0,355	1560620_at	Potassium channel, subfamily K, member 15	*KCNK15*
6103	5,74	7,77	-1,35	0,04983	0,446	222773_s_at	UDP-GalNAc:polypeptide N-acetylgalactosaminyltransferase 12	*GALNT12*
2222	21,4	29,0	-1,35	0,01476	0,363	204629_at	Parvin, beta	*PARVB*
4011	107	144	-1,35	0,02937	0,400	218447_at	Chromosome 16 open reading frame 61	*C16orf61*
3860	38,6	52,2	-1,35	0,02819	0,399	227605_at	Transcribed locus	-
266	23,7	32,0	-1,35	0,00126	0,260	229321_s_at	cDNA FLJ35002 fis, clone OCBBF2011914	-
4693	17,2	23,3	-1,35	0,03545	0,413	222218_s_at	Paired immunoglobin-like type 2 receptor alpha	*PILRA*
766	47,0	63,5	-1,35	0,00434	0,310	1558044_s_at	Exosome component 6	*EXOSC6*
831	37,2	50,2	-1,35	0,00475	0,312	222703_s_at	YrdC domain containing (E. coli)	*YRDC*
2050	52,0	70,2	-1,35	0,01332	0,355	218455_at	NFS1 nitrogen fixation 1 homolog (S. cerevisiae)	*NFS1*
2912	5,28	7,13	-1,35	0,02045	0,383	220310_at	Tubulin, alpha-like 3	*TUBAL3*
405	16,5	22,3	-1,35	0,00213	0,286	223628_at	Transmembrane protein 191A	*TMEM191A*
305	7,76	10,5	-1,35	0,00147	0,263	1563445_x_at	Cathepsin L-like 3	*CTSLL3*
386	5,23	7,06	-1,35	0,00201	0,284	227491_at	cDNA FLJ22539 fis, clone HRC13227	-
3191	288	389	-1,35	0,02262	0,387	219549_s_at	Reticulon 3	*RTN3*
1401	51,9	70,0	-1,35	0,00847	0,330	209383_at	DNA-damage-inducible transcript 3	*DDIT3*
1968	90,7	122	-1,35	0,01286	0,355	203931_s_at	Mitochondrial ribosomal protein L12	*MRPL12*
5341	71,9	97,0	-1,35	0,04184	0,428	226413_at	Hypothetical gene supported by BC047417	*LOC400027*
1505	41,4	55,8	-1,35	0,00925	0,336	218308_at	Transforming, acidic coiled-coil containing protein 3	*TACC3*
2946	118	159	-1,35	0,02065	0,383	213553_x_at	Apolipoprotein C-I	*APOC1*
5332	47,5	64,0	-1,35	0,04174	0,428	218951_s_at	PI-PLC X domain-containing protein 1	*PLCXD1*
5500	11,9	16,1	-1,35	0,04354	0,433	223874_at	Actin-related Arp11	*ARP11*
1035	15,4	20,7	-1,35	0,00601	0,318	211825_s_at	Ewing sarcoma breakpoint region 1	*EWSR1*
1084	127	170	-1,35	0,00634	0,319	229742_at	Hypothetical LOC145853	*LOC145853*
2020	174	234	-1,35	0,01317	0,355	218074_at	Family with sequence similarity 96, member B	*FAM96B*
5904	4,64	6,24	-1,35	0,04784	0,443	1554614_a_at	Polypyrimidine tract binding protein 2	*PTBP2*

Index	Mutated*	Normal*	FC	*P* value	FDR**	Probe set	Description	Gene symbol
293	13,1	17,6	-1,35	0,00144	0,263	1555943_at	Phosphoglycerate mutase family member 5	*PGAM5*
4965	7,71	10,4	-1,35	0,03810	0,419	242473_at	TNF receptor-associated factor 4	*TRAF4*
752	25,5	34,3	-1,35	0,00425	0,308	225233_at	Musashi homolog 2 (Drosophila)	*MSI2*
5228	19,9	26,8	-1,35	0,04045	0,423	203713_s_at	Lethal giant larvae homolog 2 (Drosophila)	*LLGL2*
3127	327	440	-1,34	0,02217	0,387	208836_at	ATPase, Na+/K+ transporting, beta 3 polypeptide	*ATP1B3*
476	11,8	15,8	-1,34	0,00255	0,289	238802_at	Trypsin domain containing 1	*TYSND1*
2314	98,6	132	-1,34	0,01537	0,363	200684_s_at	Ubiquitin-conjugating enzyme E2L 3	*UBE2L3*
3877	325	437	-1,34	0,02832	0,399	200708_at	Glutamic-oxaloacetic transaminase 2, mitochondrial	*GOT2*
1260	80,5	108	-1,34	0,00750	0,325	216977_x_at	Small nuclear ribonucleoprotein polypeptide A'	*SNRPA1*
3610	41,8	56,1	-1,34	0,02606	0,394	202039_at	TGFB1-induced anti-apoptotic factor 1	*TIAF1*
1529	13,5	18,1	-1,34	0,00947	0,337	244721_at	Tumor protein p53 inducible nuclear protein 1	*TP53INP1*
2123	29,4	39,4	-1,34	0,01398	0,359	38158_at	Extra spindle pole bodies homolog 1 (S. cerevisiae)	*ESPL1*
384	28,7	38,5	-1,34	0,00200	0,284	228064_at	Chromosome 22 open reading frame 36	*C22orf36*
5530	88,3	118	-1,34	0,04389	0,434	202583_s_at	RAN binding protein 9	*RANBP9*
5671	37,0	49,5	-1,34	0,04525	0,436	224753_at	Cell division cycle associated 5	*CDCA5*
5818	20,4	27,3	-1,34	0,04703	0,442	222756_s_at	Arrestin, beta 1	*ARRB1*
5521	45,0	60,2	-1,34	0,04380	0,433	219517_at	Elongation factor RNA polymerase II-like 3	*ELL3*
5205	15,2	20,3	-1,34	0,04017	0,422	1557626_at	cDNA FLJ39805 fis, clone SPLEN2007951	-
1144	5,97	7,98	-1,34	0,00670	0,320	206486_at	Lymphocyte-activation gene 3	*LAG3*
2455	143	192	-1,34	0,01646	0,366	224739_at	Pim-3 oncogene	*PIM3*
4332	6,90	9,22	-1,34	0,03225	0,407	238114_at	Protein-L-isoaspartate O-methyltransferase domain-containing protein 1	*PCMTD1*
25	9,20	12,3	-1,34	0,00011	0,201	238554_at	Cytochrome b5 type B (outer mitochondrial membrane)	*CYB5B*
70	22,6	30,2	-1,34	0,00027	0,201	213072_at	Cysteine/histidine-rich 1	*CYHR1*
2201	32,3	43,2	-1,34	0,01456	0,361	224462_s_at	Coiled-coil-helix-Coiled-coil-helix domain containing 6	*CHCHD6*
2828	186	248	-1,34	0,01973	0,381	211985_s_at	Calmodulin 1 (phosphorylase kinase, delta)	*CALM1*
693	6,09	8,13	-1,34	0,00399	0,308	229685_at	cDNA clone IMAGE:5263734	-
2550	4,95	6,61	-1,34	0,01726	0,370	228826_at	Clone IMAGE:5215917, mRNA	-
1094	332	443	-1,34	0,00641	0,319	223020_at	CLPTM1-like	*CLPTM1L*
264	159	212	-1,33	0,00126	0,260	201174_s_at	Telomeric repeat binding factor 2, interacting protein	*TERF2IP*
1781	41,8	55,8	-1,33	0,01137	0,349	214848_at	Clone 23548 mRNA sequence	-
3290	72,2	96,4	-1,33	0,02344	0,388	228787_s_at	Breast carcinoma amplified sequence 4	*BCAS4*
4960	5,19	6,92	-1,33	0,03805	0,419	1552546_a_at	Leucine zipper-EF-hand containing transmembrane protein 2	*LETM2*
991	4,76	6,35	-1,33	0,00571	0,315	1556301_at	cDNA clone IMAGE:5288145	-
5049	4,87	6,49	-1,33	0,03889	0,420	232195_at	G protein-coupled receptor 158	*GPR158*
2958	15,8	21,1	-1,33	0,02078	0,384	208776_at	Proteasome (prosome, macropain) 26S subunit, non-ATPase, 11	*PSMD11*
2019	7,20	9,59	-1,33	0,01317	0,355	228875_at	Chromosome 6 open reading frame 189	*C6orf189*
1911	62,3	83,0	-1,33	0,01244	0,355	222532_at	Signal recognition particle receptor, B subunit	*SRPRB*
2297	72,8	97,0	-1,33	0,01527	0,363	203219_s_at	Adenine phosphoribosyltransferase	*APRT*
2305	64,6	86,0	-1,33	0,01530	0,363	218607_s_at	SDA1 domain containing 1	*SDAD1*
796	127	170	-1,33	0,00455	0,311	228009_x_at	Zinc ribbon domain containing 1	*ZNRD1*
4362	27,5	36,6	-1,33	0,03245	0,407	225458_at	Hypothetical LOC25845	*LOC25845*
4798	24,0	31,9	-1,33	0,03641	0,415	209556_at	Neurochondrin	*NCDN*
2372	66,5	88,6	-1,33	0,01583	0,364	203271_s_at	Unc-119 homolog (C. elegans)	*UNC119*
3217	86,1	115	-1,33	0,02279	0,387	218919_at	Zinc finger, AN1-type domain 1	*ZFAND1*
5120	131	175	-1,33	0,03941	0,421	225051_at	Erythrocyte membrane protein band 4.1	*EPB41*
2427	63,4	84,4	-1,33	0,01623	0,365	219076_s_at	Peroxisomal membrane protein 2, 22kDa	*PXMP2*
1059	6,17	8,20	-1,33	0,00621	0,319	214536_at	Secreted LY6/PLAUR domain containing 1	*SLURP1*
1351	9,25	12,3	-1,33	0,00812	0,328	210530_s_at	Nuclear receptor subfamily 2, group C, member 1	*NR2C1*
5896	62,6	83,2	-1,33	0,04771	0,442	224368_s_at	NDRG family member 3	*NDRG3*
4889	4,33	5,75	-1,33	0,03738	0,418	242370_at	NADP-dependent methylenetetrahydrofolate dehydrogenase 2-like protein	*MTHFD2L*
4522	23,3	30,9	-1,33	0,03411	0,412	202873_at	ATPase, H+ transporting, lysosomal 42kDa, V1 subunit C1	*ATP6V1C1*
3660	54,2	71,9	-1,33	0,02644	0,395	226149_at	Chromosome 20 open reading frame 198	*C20orf198*
5504	52,5	69,7	-1,33	0,04358	0,433	218284_at	SMAD family member 3	*SMAD3*
2573	17,4	23,0	-1,33	0,01744	0,371	229572_at	Transcribed locus	-
5202	111	148	-1,33	0,04011	0,422	217749_at	Coatomer protein complex, subunit gamma	*COPG*
3779	56,9	75,5	-1,33	0,02751	0,398	213264_at	Poly(rC) binding protein 2	*PCBP2*
6061	25,5	33,8	-1,33	0,04943	0,446	225752_at	Non imprinted in Prader-Willi/Angelman syndrome 1	*NIPA1*

Index	Mutated*	Normal*	FC	*P* value	FDR**	Probe set	Description	Gene symbol
5496	120	159	-1,33	0,04349	0,433	213263_s_at	Poly(rC) binding protein 2	*PCBP2*
661	25,2	33,5	-1,33	0,00382	0,308	208725_at	Eukaryotic translation initiation factor 2, subunit 2 beta, 38kDa	*EIF2S2*
1269	208	275	-1,33	0,00754	0,325	212114_at	Hypothetical LOC552889	*LOC552889*
2534	121	160	-1,33	0,01713	0,369	213892_s_at	Adenine phosphoribosyltransferase	*APRT*
4220	104	138	-1,33	0,03128	0,405	202397_at	Nuclear transport factor 2	*NUTF2*
1793	608	806	-1,33	0,01148	0,350	209066_x_at	Ubiquinol-cytochrome c reductase binding protein	*UQCRB*
2647	19,6	25,9	-1,32	0,01804	0,373	220137_at	Hypothetical protein FLJ20674	*FLJ20674*
1042	24,0	31,8	-1,32	0,00608	0,319	226156_at	v-AKT murine thymoma viral oncogene homolog 2	*AKT2*
3331	7,97	10,6	-1,32	0,02364	0,388	205495_s_at	Granulysin	*GNLY*
3768	36,5	48,3	-1,32	0,02738	0,397	225300_at	Chromosome 15 open reading frame 23	*C15orf23*
1479	10,1	13,3	-1,32	0,00907	0,335	244627_at	Dihydroxyacetone kinase 2 homolog (S. cerevisiae)	*DAK*
4488	167	221	-1,32	0,03376	0,411	202087_s_at	Cathepsin L1	*CTSL1*
3699	27,9	37,0	-1,32	0,02675	0,395	205024_s_at	RAD51 homolog (RecA homolog, E. coli) (S. cerevisiae)	*RAD51*
5104	134	178	-1,32	0,03927	0,421	209448_at	HIV-1 Tat interactive protein 2, 30kDa	*HTATIP2*
3427	26,9	35,6	-1,32	0,02452	0,391	236381_s_at	WD repeat domain 8	*WDR8*
1107	553	731	-1,32	0,00649	0,319	217722_s_at	Neugrin, neurite outgrowth associated	*NGRN*
5824	17,2	22,7	-1,32	0,04706	0,442	211519_s_at	Kinesin family member 2C	*KIF2C*
4705	6,52	8,62	-1,32	0,03558	0,413	1554508_at	Phosphoinositide-3-kinase adaptor protein 1	*PIK3AP1*
1282	55,9	73,8	-1,32	0,00764	0,325	209445_x_at	Chromosome 7 open reading frame 44	*C7orf44*
663	62,2	82,1	-1,32	0,00382	0,308	227008_at	HD domain containing 3	*HDDC3*
5763	48,4	63,9	-1,32	0,04630	0,439	208955_at	dUTP pyrophosphatase	*DUT*
3322	32,7	43,1	-1,32	0,02359	0,388	238032_at	Transcribed locus	-
4022	19,3	25,5	-1,32	0,02945	0,400	1553947_at	Exosome component 6	*EXOSC6*
4991	89,6	118	-1,32	0,03830	0,419	219071_x_at	Chromosome 8 open reading frame 30A	*C8orf30A*
3774	58,3	76,9	-1,32	0,02742	0,397	229192_s_at	Tubulin folding cofactor D	*TBCD*
6073	393	518	-1,32	0,04959	0,446	204427_s_at	Transmembrane emp24 domain trafficking protein 2	*TMED2*
1909	109	144	-1,32	0,01242	0,355	212751_at	Ubiquitin-conjugating enzyme E2N	*UBE2N*
1476	13,6	17,9	-1,32	0,00902	0,334	219154_at	RAS homolog gene family, member F (in filopodia)	*RHOF*
1056	139	183	-1,32	0,00619	0,319	201000_at	Alanyl-tRNA synthetase	*AARS*
2237	15,3	20,2	-1,32	0,01486	0,363	235389_at	PHD finger protein 20	*PHF20*
797	11,7	15,4	-1,32	0,00456	0,311	206273_at	Slowmo homolog 1 (Drosophila)	*SLMO1*
3075	35,0	46,1	-1,32	0,02169	0,385	203217_s_at	ST3 beta-galactoside alpha-2,3-sialyltransferase 5	*ST3GAL5*
2881	12,0	15,8	-1,32	0,02022	0,383	227887_at	Hypothetical LOC400236	*LOC400236*
2203	39,6	52,1	-1,32	0,01457	0,361	1554451_s_at	Cytokine induced protein 29 kDa	*CIP29*
3542	7,13	9,37	-1,31	0,02549	0,393	205920_at	Solute carrier family 6, member 6	*SLC6A6*
2310	3,99	5,25	-1,31	0,01535	0,363	237105_at	cDNA FLJ46701 fis, clone TRACH3014063	-
5337	22,9	30,1	-1,31	0,04178	0,428	238903_at	Hypothetical protein LOC137886	*LOC137886*
2244	9,26	12,2	-1,31	0,01492	0,363	231046_at	cDNA clone IMAGE:4329532	-
3753	85,9	113	-1,31	0,02729	0,397	218549_s_at	Family with sequence similarity 82, member B	*FAM82B*
2232	385	505	-1,31	0,01483	0,363	223209_s_at	Selenoprotein S	*SELS*
5733	17,1	22,5	-1,31	0,04599	0,438	214877_at	CDK5 regulatory subunit associated protein 1-like 1	*CDKAL1*
1766	7,54	9,91	-1,31	0,01126	0,348	237065_s_at	Similar to Hepatitis B virus x-interacting protein	-
2270	7,41	9,74	-1,31	0,01508	0,363	235846_at	cDNA FLJ23692 fis, clone HEP10227	-
908	11,4	14,9	-1,31	0,00524	0,313	244411_at	Similar to Syntaxin binding protein 1	-
1255	6,82	8,94	-1,31	0,00747	0,325	235814_at	Similar to Genethonin 1	-
5035	7,10	9,30	-1,31	0,03878	0,420	219502_at	Nei endonuclease VIII-like 3 (E. coli)	*NEIL3*
3520	141	185	-1,31	0,02527	0,392	217932_at	Mitochondrial ribosomal protein S7	*MRPS7*
4287	152	200	-1,31	0,03185	0,406	221637_s_at	Chromosome 11 open reading frame 48	*C11orf48*
1057	110	144	-1,31	0,00621	0,319	212884_x_at	Apolipoprotein E	*APOE*
5149	46,9	61,4	-1,31	0,03964	0,421	213592_at	Angiotensin II receptor-like 1	*AGTRL1*
4232	52,8	69,2	-1,31	0,03136	0,405	203446_s_at	Oculocerebrorenal syndrome of Lowe	*OCRL*
2128	7,74	10,1	-1,31	0,01400	0,359	214747_at	Zinc finger, BED-type containing 4	*ZBED4*
3953	18,9	24,8	-1,31	0,02888	0,399	227786_at	Mediator complex subunit 30	*MED30*
2512	9,16	12,0	-1,31	0,01690	0,368	206106_at	Mitogen-activated protein kinase 12	*MAPK12*
2435	136	178	-1,31	0,01628	0,365	225480_at	Chromosome 1 open reading frame 122	*C1orf122*
6119	5,44	7,11	-1,31	0,04996	0,446	238369_s_at	Similar to XP_001091806.1	-
3981	6,48	8,48	-1,31	0,02911	0,400	211077_s_at	Tousled-like kinase 1	*TLK1*

Index	Mutated*	Normal*	FC	*P* value	FDR**	Probe set	Description	Gene symbol
4827	3,17	4,14	-1,31	0,03675	0,416	243880_at	Golgi SNAP receptor complex member 2	*GOSR2*
704	9,94	13,0	-1,31	0,00405	0,308	236958_at	cDNA FLJ25271 fis, clone STM05584	-
3511	19,8	25,9	-1,31	0,02522	0,392	228444_at	Transcribed locus	-
3390	39,4	51,4	-1,31	0,02415	0,389	224728_at	ATP synthase mitochondrial F1 complex assembly factor 1	*ATPAF1*
3910	34,0	44,4	-1,31	0,02854	0,399	36564_at	Ring finger protein 19B	*RNF19B*
1976	138	180	-1,31	0,01291	0,355	226679_at	Solute carrier family 26, member 11	*SLC26A11*
2563	99,6	130	-1,31	0,01738	0,371	218151_x_at	G protein-coupled receptor 172A	*GPR172A*
1054	98,4	128	-1,30	0,00616	0,319	203342_at	Translocase of inner mitochondrial membrane 17 homolog B (yeast)	*TIMM17B*
1694	210	274	-1,30	0,01072	0,346	219121_s_at	RNA binding motif protein 35A	*RBM35A*
4559	7,30	9,52	-1,30	0,03445	0,412	203626_s_at	S-phase kinase-associated protein 2 (p45)	*SKP2*
1500	23,9	31,2	-1,30	0,00923	0,336	212707_s_at	RAS p21 protein activator 4	*RASA4*
2442	24,8	32,3	-1,30	0,01632	0,365	1554321_a_at	NFS1 nitrogen fixation 1 homolog (S. cerevisiae)	*NFS1*
3249	58,1	75,7	-1,30	0,02307	0,388	225779_at	Solute carrier family 27, member 4	*SLC27A4*
2535	44,6	58,1	-1,30	0,01714	0,369	204287_at	Synaptogyrin 1	*SYNGR1*
1069	15,8	20,6	-1,30	0,00628	0,319	229577_at	Transcribed locus	-
1570	8,53	11,1	-1,30	0,00976	0,340	204100_at	Thyroid hormone receptor alpha	*THRA*
5853	37,6	49,0	-1,30	0,04734	0,442	1559399_s_at	Zinc finger, CCHC domain containing 10	*ZCCHC10*
1677	6,87	8,95	-1,30	0,01058	0,345	241972_at	Hypothetical LOC401588	*LOC401588*
5577	9,47	12,3	-1,30	0,04447	0,436	205165_at	Cadhetrin, EGF LAG seven-pass G-type receptor 3 (flamingo homolog, Drosop	*CELSR3*
4999	7,12	9,26	-1,30	0,03839	0,420	233057_at	Heat shock 22kDa protein 8	*HSPB8*
5491	33,1	43,0	-1,30	0,04346	0,433	210154_at	Malic enzyme 2, NAD(+)-dependent, mitochondrial	*ME2*
5527	82,6	107	-1,30	0,04382	0,434	212090_at	Glutamate receptor, NMDA subtype, Glutamate-binding subunit	*GRINA*
3801	238	310	-1,30	0,02769	0,398	218206_x_at	SCAN domain containing 1	*SCAND1*
289	356	463	-1,30	0,00142	0,263	201698_s_at	Splicing factor, arginine/serine-rich 9	*SFRS9*
2525	364	474	-1,30	0,01704	0,369	225846_at	RNA binding motif protein 35A	*RBM35A*
5061	64,2	83,5	-1,30	0,03896	0,420	202069_s_at	Isocitrate dehydrogenase 3 (NAD+) alpha	*IDH3A*
4837	12,3	16,0	-1,30	0,03688	0,417	206612_at	Calcium channel, voltage-dependent, gamma subunit 1	*CACNG1*
893	10,2	13,3	-1,30	0,00517	0,313	239941_at	Similar to Mitochondrial ribosomal protein S23	-
5909	106	137	-1,30	0,04789	0,443	222500_at	Peptidylprolyl isomerase (cyclophilin)-like 1	*PPIL1*
3387	47,5	61,6	-1,30	0,02413	0,389	1552279_a_at	Solute carrier family 46, member 1	*SLC46A1*
4690	7,01	9,11	-1,30	0,03543	0,413	236312_at	Transcribed locus	-
1565	16,1	20,9	-1,30	0,00972	0,339	210240_s_at	Cyclin-dependent kinase inhibitor 2D	*CDKN2D*
4207	180	234	-1,30	0,03110	0,404	201212_at	Legumain	*LGMN*
4316	243	315	-1,30	0,03214	0,407	218482_at	Enhancer of yellow 2 homolog (Drosophila)	*ENY2*
1150	3,98	5,16	-1,30	0,00677	0,321	1557448_a_at	cDNA clone IMAGE:5298376	-
2710	22,3	28,9	-1,30	0,01860	0,375	205733_at	Bloom syndrome	*BLM*
2258	40,5	52,5	-1,30	0,01502	0,363	234972_at	ADP-ribosylation factor-like 16	*ARL16*
2196	6,81	8,84	-1,30	0,01452	0,361	230932_at	Transcribed locus	-
4679	128	166	-1,30	0,03533	0,413	222998_at	MAF1 homolog (S. cerevisiae)	*MAF1*
3831	24,5	31,8	-1,30	0,02798	0,399	238472_at	F-box protein 9	*FBXO9*
2539	25,6	33,2	-1,30	0,01717	0,369	205432_at	Oviductal glycoprotein 1, 120kDa (mucin 9, oviductin)	*OVGP1*
4138	33,7	43,7	-1,30	0,03052	0,403	204368_at	Solute carrier organic anion transporter family, member 2A1	*SLCO2A1*
824	204	265	-1,30	0,00470	0,312	217898_at	Chromosome 15 open reading frame 24	*C15orf24*
2422	118	153	-1,30	0,01620	0,365	221597_s_at	HSPC171 protein	*HSPC171*
4415	139	180	-1,30	0,03301	0,409	232652_x_at	SCAN domain containing 1	*SCAND1*
3135	19,5	25,2	-1,30	0,02222	0,387	221837_at	Kelch-like 22 (Drosophila)	*KLHL22*
5919	62,2	80,6	-1,30	0,04798	0,443	204278_s_at	Estrogen receptor binding site associated, antigen, 9	*EBAG9*
1257	36,2	46,8	-1,29	0,00749	0,325	204970_s_at	Basic leucine zipper transcription factor MafG	*MAFG*
1825	93,6	121	-1,29	0,01176	0,351	223107_s_at	Zinc finger, CCHC domain containing 17	*ZCCHC17*
3397	127	164	-1,29	0,02424	0,390	206055_s_at	Small nuclear ribonucleoprotein polypeptide A'	*SNRPA1*
3015	19,1	24,7	-1,29	0,02122	0,385	218727_at	Amino acid transporter	*FLJ10815*
694	46,4	60,1	-1,29	0,00400	0,308	225067_at	Unc-51-like kinase 3 (C. elegans)	*ULK3*
1375	20,1	26,0	-1,29	0,00829	0,329	226687_at	PRP40 pre-mRNA processing factor 40 homolog A (S. cerevisiae)	*PRPF40A*
2271	89,2	115	-1,29	0,01508	0,363	204565_at	Thioesterase superfamily member 2	*THEM2*
2843	29,1	37,7	-1,29	0,01988	0,382	35846_at	Thyroid hormone receptor alpha	*THRA*
2996	26,0	33,5	-1,29	0,02110	0,385	44673_at	Sialic acid binding Ig-like lectin 1, sialoadhesin	*SIGLEC1*
9	28,9	37,3	-1,29	0,00002	0,117	218415_at	Vacuolar protein sorting 33 homolog B (yeast)	*VPS33B*

Index	Mutated*	Normal*	FC	*P* value	FDR**	Probe set	Description	Gene symbol
365	5,97	7,71	-1,29	0,00190	0,284	239848_at	cDNA FLJ41316 fis, clone BRAMY2043314	-
5956	17,1	22,0	-1,29	0,04832	0,444	204887_s_at	Polo-like kinase 4 (Drosophila)	*PLK4*
4105	28,1	36,3	-1,29	0,03017	0,402	220178_at	Chromosome 19 open reading frame 28	*C19orf28*
5961	69,6	89,8	-1,29	0,04839	0,444	227527_at	Myeloid/lymphoid or mixed-lineage leukemia 2	*MLL2*
3147	629	812	-1,29	0,02234	0,387	205849_s_at	Ubiquinol-cytochrome c reductase binding protein	*UQCRB*
2246	12,5	16,1	-1,29	0,01493	0,363	228894_at	Nuclear receptor subfamily 6, group A, member 1	*NR6A1*
5296	49,6	63,9	-1,29	0,04127	0,426	205089_at	Zinc finger protein 7	*ZNF7*
5070	38,3	49,4	-1,29	0,03901	0,420	213704_at	RAB geranylgeranyltransferase, beta subunit	*RABGGTB*
4739	24,6	31,7	-1,29	0,03588	0,414	204649_at	Trophinin associated protein (tastin)	*TROAP*
5886	68,6	88,5	-1,29	0,04762	0,442	210010_s_at	Solute carrier family 25, member 1	*SLC25A1*
3130	33,0	42,5	-1,29	0,02221	0,387	203777_s_at	Ribosomal protein S6 kinase, 70kDa, polypeptide 2	*RPS6KB2*
4906	37,1	47,7	-1,29	0,03751	0,418	229453_at	Protein disulfide isomerase family A, member 3	*PDIA3*
3729	9,47	12,2	-1,29	0,02708	0,397	228828_at	Clone IMAGE:5215917, mRNA	-
4988	54,8	70,5	-1,29	0,03828	0,419	91684_g_at	Exosome component 4	*EXOSC4*
61	11,3	14,5	-1,29	0,00023	0,201	227201_at	Hypothetical protein LOC643837	*LOC643837*
1364	162	208	-1,29	0,00821	0,328	217957_at	Chromosome 16 open reading frame 80	*C16orf80*
4586	34,0	43,8	-1,29	0,03467	0,412	242790_at	SNF8, ESCRT-II complex subunit, homolog (S. cerevisiae)	*SNF8*
3716	4,16	5,36	-1,29	0,02694	0,396	215943_at	KIAA1661 protein	*KIAA1661*
4240	35,5	45,8	-1,29	0,03145	0,406	1552612_at	CDC42 small effector 2	*CDC42SE2*
1704	45,9	59,0	-1,29	0,01087	0,348	208316_s_at	Oculocerebrorenal syndrome of Lowe	*OCRL*
2148	24,6	31,6	-1,29	0,01414	0,360	217998_at	Pleckstrin homology-like domain, family A, member 1	*PHLDA1*
990	490	630	-1,29	0,00571	0,315	217962_at	Nucleolar protein family A, member 3	*NOLA3*
2686	49,9	64,1	-1,29	0,01840	0,375	215722_s_at	Small nuclear ribonucleoprotein polypeptide A'	*SNRPA1*
5308	40,3	51,7	-1,29	0,04141	0,426	225901_at	Protein tyrosine phosphatase, mitochondrial 1	*PTPMT1*
1359	10,2	13,1	-1,28	0,00819	0,328	235574_at	Guanylate binding protein 4	*GBP4*
5373	14,8	19,0	-1,28	0,04216	0,429	235625_at	Vacuolar protein sorting 41 homolog (S. cerevisiae)	*VPS41*
3092	22,2	28,6	-1,28	0,02180	0,385	223811_s_at	Chromosome 7 open reading frame 20	*C7orf20*
3966	21,3	27,4	-1,28	0,02897	0,399	216698_x_at	Olfactory receptor, family 7, subfamily E, member 47 pseudogene	*OR7E47P*
5014	29,1	37,4	-1,28	0,03856	0,420	214081_at	Plexin domain containing 1	*PLXDC1*
5941	9,56	12,3	-1,28	0,04816	0,443	207043_s_at	Solute carrier family 6, member 9	*SLC6A9*
3627	18,0	23,1	-1,28	0,02621	0,395	207458_at	Chromosome 8 open reading frame 51	*C8orf51*
3297	244	313	-1,28	0,02349	0,388	217748_at	Adiponectin receptor 1	*ADIPOR1*
161	13,0	16,7	-1,28	0,00073	0,244	238087_at	RNA terminal phosphate cyclase domain 1	*RTCD1*
3024	12,1	15,5	-1,28	0,02129	0,385	220491_at	Hepcidin antimicrobial peptide	*HAMP*
3692	6,42	8,24	-1,28	0,02666	0,395	237369_at	Transcribed locus	-
2429	40,3	51,7	-1,28	0,01624	0,365	203320_at	SH2B adaptor protein 3	*SH2B3*
1437	13,6	17,4	-1,28	0,00870	0,331	211434_s_at	Chemokine (C-C motif) receptor-like 2	*CCRL2*
4548	114	146	-1,28	0,03438	0,412	223120_at	Fucosidase, alpha-L- 2, plasma	*FUCA2*
5167	46,5	59,6	-1,28	0,03982	0,421	229232_at	Leucine rich repeat containing 57	*LRRC57*
2419	51,2	65,6	-1,28	0,01617	0,365	227456_s_at	Chromosome 6 open reading frame 136	*C6orf136*
5044	7,31	9,37	-1,28	0,03886	0,420	205581_s_at	Nitric oxide synthase 3 (endothelial cell)	*NOS3*
3287	31,0	39,8	-1,28	0,02342	0,388	204819_at	FYVE, RhoGEF and PH domain containing 1	*FGD1*
5416	404	518	-1,28	0,04256	0,430	202306_at	Polymerase (RNA) II (DNA directed) polypeptide G	*POLR2G*
5692	109	139	-1,28	0,04553	0,437	202541_at	Small inducible cytokine subfamily E, member 1	*SCYE1*
1343	15,5	19,9	-1,28	0,00806	0,328	238507_at	Transcribed locus	-
4423	95,3	122	-1,28	0,03311	0,409	224742_at	Abhydrolase domain containing 12	*ABHD12*
3057	7,37	9,44	-1,28	0,02153	0,385	239493_at	Ribosomal protein L7	*RPL7*
4503	246	315	-1,28	0,03389	0,411	212250_at	Metadherin	*MTDH*
1304	62,6	80,1	-1,28	0,00777	0,325	212434_at	GrpE-like 1, mitochondrial (E. coli)	*GRPEL1*
2374	226	290	-1,28	0,01583	0,364	224957_at	Chromosome 18 open reading frame 32	*C18orf32*
355	67,1	85,8	-1,28	0,00182	0,280	1553987_at	Chromosome 12 open reading frame 47	*C12orf47*
5508	5,47	7,00	-1,28	0,04364	0,433	221195_at	PTD016 protein	*LOC51136*
3452	11,1	14,2	-1,28	0,02471	0,391	206655_s_at	Glycoprotein Ib (platelet), beta polypeptide	*GP1BB*
4573	3,36	4,30	-1,28	0,03457	0,412	220022_at	Zinc finger protein 334	*ZNF334*
4291	5,92	7,56	-1,28	0,03190	0,406	238427_at	GrpE-like 2, mitochondrial (E. coli)	*GRPEL2*
5725	135	172	-1,28	0,04591	0,438	209397_at	Malic enzyme 2, NAD(+)-dependent, mitochondrial	*ME2*
1863	54,8	70,1	-1,28	0,01203	0,353	224804_s_at	Chromosome 15 open reading frame 17	*C15orf17*

Index	Mutated*	Normal*	FC	*P* value	FDR**	Probe set	Description	Gene symbol
424	15,3	19,5	-1,28	0,00223	0,288	209552_at	Paired box 8	*PAX8*
2303	70,9	90,4	-1,28	0,01530	0,363	1558136_s_at	Transcription initiation factor TFIID 28 kD subunit	*TAF11*
4450	16,4	21,0	-1,27	0,03343	0,411	232186_at	Chromosome 20 open reading frame 142	*C20orf142*
2212	19,1	24,3	-1,27	0,01466	0,362	220200_s_at	SET domain containing (lysine methyltransferase) 8	*SETD8*
2649	26,4	33,6	-1,27	0,01806	0,373	228566_at	Hypothetical protein FLJ10656	*P15RS*
5242	8,23	10,5	-1,27	0,04060	0,423	232422_at	Hypothetical protein BC004360	-
2971	14,0	17,8	-1,27	0,02087	0,384	220291_at	Glycerophosphodiester phosphodiesterase domain containing 2	*GDPD2*
4043	3,66	4,65	-1,27	0,02964	0,401	210447_at	Glutamate dehydrogenase 2	*GLUD2*
5593	8,17	10,4	-1,27	0,04461	0,436	205568_at	Aquaporin 9	*AQP9*
1234	7,73	9,83	-1,27	0,00734	0,324	208511_at	Pituitary tumor-transforming 3	*PTTG3*
2295	42,0	53,4	-1,27	0,01527	0,363	227093_at	Ubiquitin specific peptidase 36	*USP36*
4543	8,49	10,8	-1,27	0,03434	0,412	37145_at	Granulysin	*GNLY*
4055	183	232	-1,27	0,02975	0,401	231059_x_at	SCAN domain containing 1	*SCAND1*
3685	8,14	10,3	-1,27	0,02661	0,395	1552737_s_at	WW domain containing E3 ubiquitin protein ligase 2	*WWP2*
2803	6,08	7,72	-1,27	0,01949	0,380	210360_s_at	Metastasis suppressor 1	*MTSS1*
847	86,4	110	-1,27	0,00488	0,313	225208_s_at	Family with sequence similarity 103, member A1	*FAM103A1*
4469	78,6	99,8	-1,27	0,03357	0,411	225592_at	Nurim (nuclear envelope membrane protein)	*NRM*
598	31,8	40,3	-1,27	0,00329	0,301	225212_at	Solute carrier family 25, member 25	*SLC25A25*
4272	9,65	12,2	-1,27	0,03175	0,406	223570_at	Minichromosome maintenance complex component 10	*MCM10*
1021	54,0	68,4	-1,27	0,00591	0,316	1554553_s_at	Yip1 interacting factor homolog B (S. cerevisiae)	*YIF1B*
683	30,3	38,4	-1,27	0,00392	0,308	209777_s_at	Solute carrier family 19, member 1	*SLC19A1*
5174	59,4	75,3	-1,27	0,03985	0,421	225637_at	Differentially expressed in FDCP 8 homolog (mouse)	*DEF8*
2939	42,7	54,2	-1,27	0,02062	0,383	225699_at	Chromosome 7 open reading frame 40	*C7orf40*
5338	19,9	25,2	-1,27	0,04179	0,428	31799_at	Clone 24627 mRNA sequence	-
4259	43,9	55,6	-1,27	0,03166	0,406	202104_s_at	Spastic paraplegia 7 protein	*SPG7*
4590	122	155	-1,27	0,03472	0,412	212228_s_at	Coenzyme Q9 homolog (S. cerevisiae)	*COQ9*
2290	24,6	31,1	-1,27	0,01523	0,363	211320_s_at	Protein tyrosine phosphatase, receptor type, U	*PTPRU*
510	108	137	-1,27	0,00270	0,289	225434_at	Death effector domain containing 2	*DEDD2*
3885	7,66	9,70	-1,27	0,02837	0,399	1556227_at	Valosin containing protein (p97)/p47 complex interacting protein 1	*VCPIP1*
6012	8,25	10,4	-1,27	0,04888	0,445	239652_at	Transcribed locus	-
1478	28,3	35,8	-1,27	0,00905	0,335	227042_at	LOC150223 protein	*LOC150223*
2234	15,4	19,5	-1,26	0,01484	0,363	230039_at	-	-
1072	23,2	29,4	-1,26	0,00628	0,319	1562228_s_at	Phosphodiesterase 5A, cGMP-specific	*PDE5A*
2365	316	399	-1,26	0,01579	0,364	211984_at	Calmodulin 1 (phosphorylase kinase, delta)	*CALM1*
1490	16,6	21,0	-1,26	0,00919	0,336	205256_at	Zinc finger and BTB domain containing 39	*ZBTB39*
4769	4,96	6,27	-1,26	0,03614	0,414	206925_at	ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 4	*ST8SIA4*
3795	43,1	54,5	-1,26	0,02765	0,398	218813_s_at	SH3-domain GRB2-like endophilin B2	*SH3GLB2*
4628	6,73	8,50	-1,26	0,03490	0,412	1559051_s_at	Chromosome 6 open reading frame 150	*C6orf150*
2388	92,3	117	-1,26	0,01592	0,364	217543_s_at	Membrane-bound transcription factor peptidase, site 1	*MBTPS1*
703	37,7	47,6	-1,26	0,00403	0,308	56821_at	Amino acid transporter	*FLJ10815*
4684	94,5	119	-1,26	0,03536	0,413	221736_at	KIAA1219 protein	*KIAA1219*
4401	8,59	10,8	-1,26	0,03281	0,408	210786_s_at	Friend leukemia virus integration 1	*FLI1*
1957	29,7	37,5	-1,26	0,01279	0,355	227103_s_at	Endothelin converting enzyme 2	*ECE2*
5045	40,2	50,6	-1,26	0,03888	0,420	218821_at	Aminopeptidase-like 1	*NPEPL1*
2282	202	255	-1,26	0,01516	0,363	224748_at	WD repeat domain 68	*WDR68*
2098	16,6	21,0	-1,26	0,01375	0,358	229570_at	Laminin, alpha 5	*LAMA5*
764	39,2	49,5	-1,26	0,00432	0,309	224907_s_at	SH3-domain GRB2-like endophilin B2	*SH3GLB2*
167	16,9	21,3	-1,26	0,00078	0,244	224433_s_at	DEAD (Asp-Glu-Ala-Asp) box polypeptide 54	*DDX54*
43	93,3	118	-1,26	0,00018	0,201	221777_at	Chromosome 12 open reading frame 52	*C12orf52*
1259	106	134	-1,26	0,00750	0,325	208996_s_at	Polymerase (RNA) II (DNA directed) polypeptide C, 33kDa	*POLR2C*
918	16,0	20,1	-1,26	0,00529	0,313	213449_at	Ribonucleases P/MRP protein subunit POP1	*POP1*
2763	146	184	-1,26	0,01920	0,379	1555780_a_at	RAS homolog enriched in brain	*RHEB*
3097	71,7	90,2	-1,26	0,02187	0,386	223639_s_at	Zinc ribbon domain containing 1	*ZNRD1*
2060	68,3	85,9	-1,26	0,01344	0,356	218592_s_at	Cat eye syndrome chromosome region, candidate 5	*CECR5*
423	10,1	12,7	-1,26	0,00222	0,287	227358_at	Zinc finger and BTB domain containing 46	*ZBTB46*
4100	44,8	56,4	-1,26	0,03013	0,402	225704_at	KIAA1545 protein	*KIAA1545*
2044	5,20	6,54	-1,26	0,01329	0,355	232794_at	Hypothetical protein LOC153682	*LOC153682*

Index	Mutated*	Normal*	FC	*P* value	FDR**	Probe set	Description	Gene symbol
5506	40,8	51,4	-1,26	0,04361	0,433	208424_s_at	Cytokine induced apoptosis inhibitor 1	*CIAPIN1*
3364	58,0	72,9	-1,26	0,02390	0,388	64064_at	GTPase, IMAP family member 5	*GIMAP5*
187	11,5	14,5	-1,26	0,00087	0,244	236537_at	cDNA FLJ23896 fis, clone LNG15157	-
4932	46,6	58,6	-1,26	0,03782	0,419	202974_at	Membrane protein, palmitoylated 1, 55kDa	*MPP1*
5746	38,0	47,8	-1,26	0,04609	0,439	226793_at	Hypothetical protein LOC283267	*LOC283267*
5908	19,8	24,9	-1,26	0,04789	0,443	209052_s_at	Wolf-Hirschhorn syndrome candidate 1	*WHSC1*
5897	10,4	13,1	-1,26	0,04772	0,442	219742_at	Proline rich 7 (synaptic)	*PRR7*
1887	14,9	18,7	-1,26	0,01225	0,355	230974_at	DEAD (Asp-Glu-Ala-As) box polypeptide 19B	*DDX19B*
4696	870	1092	-1,26	0,03547	0,413	214359_s_at	Heat shock protein 90kDa alpha (cytosolic), class B member 1	*HSP90AB1*
4832	28,2	35,4	-1,26	0,03681	0,416	219491_at	Leucine rich repeat and fibronectin type III domain containing 4	*LRFN4*
298	11,2	14,1	-1,26	0,00145	0,263	230025_at	Gap junction protein, chi 1, 31.9kDa	*GJC1*
5111	43,1	54,1	-1,26	0,03934	0,421	221011_s_at	Limb bud and heart development homolog (mouse)	*LBH*
5271	51,7	64,8	-1,25	0,04096	0,425	219394_at	PhosphatidylglyceroPhosphate synthase 1	*PGS1*
173	6,22	7,81	-1,25	0,00080	0,244	1569452_at	Hypothetical locus LOC692247	*LOC692247*
1325	28,9	36,2	-1,25	0,00795	0,328	213861_s_at	Family with sequence similarity 119, member B	*FAM119B*
3786	30,2	37,9	-1,25	0,02758	0,398	227818_at	Coiled-coil domain containing 21	*CCDC21*
1380	11,6	14,5	-1,25	0,00830	0,329	232959_at	Similar to Septin 7	*LOC645513*
1356	25,1	31,4	-1,25	0,00817	0,328	228870_at	Family with sequence similarity 84, member B	*FAM84B*
2378	87,7	110	-1,25	0,01586	0,364	210153_s_at	Malic enzyme 2, NAD(+)-dependent, mitochondrial	*ME2*
3383	4,70	5,89	-1,25	0,02409	0,389	222881_at	Heparanase	*HPSE*
3472	11,0	13,8	-1,25	0,02491	0,392	206617_s_at	Renin binding protein	*RENBP*
5843	13,6	17,0	-1,25	0,04722	0,442	1553971_a_at	Opposite strand transcription unit to STAG3	*GATS*
2820	110	138	-1,25	0,01969	0,381	208848_at	Alcohol dehydrogenase 5 (class III), chi polypeptide	*ADH5*
3013	43,7	54,8	-1,25	0,02119	0,385	226063_at	VAV2 guanine nucleotide exchange factor	*VAV2*
252	5,30	6,65	-1,25	0,00117	0,254	236916_at	Serine/threonine kinase receptor associated protein	*STRAP*
2750	104	130	-1,25	0,01901	0,378	208785_s_at	Microtubule-associated protein 1 light chain 3 beta	*MAP1LC3B*
4969	35,6	44,6	-1,25	0,03812	0,419	230606_at	Gap junction protein, chi 1, 31.9kDa	*GJC1*
1991	1572	1969	-1,25	0,01302	0,355	200064_at	Heat shock protein 90kDa alpha (cytosolic), class B member 1	*HSP90AB1*
5772	7,65	9,58	-1,25	0,04639	0,439	210606_x_at	Killer cell lectin-like receptor subfamily D, member 1	*KLRD1*
5711	401	502	-1,25	0,04573	0,438	202836_s_at	Thioredoxin-like 4A	*TXNL4A*
1950	222	277	-1,25	0,01273	0,355	202483_s_at	RAN binding protein 1	*RANBP1*
2021	10,5	13,1	-1,25	0,01317	0,355	236200_at	Fas (TNFRSF6) associated factor 1	*FAF1*
4809	108	135	-1,25	0,03652	0,415	208968_s_at	Cytokine induced apoptosis inhibitor 1	*CIAPIN1*
219	45,3	56,7	-1,25	0,00100	0,250	218660_at	Dysferlin, limb girdle muscular dystrophy 2B	*DYSF*
4336	3,47	4,34	-1,25	0,03227	0,407	1559072_a_at	Leucine rich repeat containing 62	*LRRC62*
168	7,28	9,10	-1,25	0,00078	0,244	231777_at	Casein kinase 2, beta polypeptide	*CSNK2B*
5509	4,15	5,19	-1,25	0,04365	0,433	210146_x_at	Leukocyte immunoglobulin-like receptor, subfamily B member 2	*LILRB2*
4796	58,9	73,6	-1,25	0,03638	0,415	219952_s_at	Mucolipin 1	*MCOLN1*
5335	9,83	12,3	-1,25	0,04177	0,428	214775_at	Nedd4 binding protein 3	*N4BP3*
5997	4,69	5,85	-1,25	0,04875	0,444	210567_s_at	S-phase kinase-associated protein 2 (p45)	*SKP2*
1940	13,5	16,9	-1,25	0,01264	0,355	205396_at	SMAD family member 3	*SMAD3*
1755	8,07	10,1	-1,25	0,01118	0,348	214530_x_at	Erythrocyte membrane protein band 4.1	*EPB41*
4114	11,1	13,9	-1,25	0,03025	0,402	230271_at	One cut homeobox 2	*ONECUT2*
2628	34,1	42,6	-1,25	0,01790	0,372	213324_at	v-src sarcoma (Schmidt-Ruppin A-2) viral oncogene homolog (avian)	*SRC*
4095	4,00	5,00	-1,25	0,03009	0,402	208388_at	Nuclear receptor subfamily 2, group E, member 3	*NR2E3*
2233	18,1	22,6	-1,25	0,01484	0,363	219760_at	Lin-7 homolog B (C. elegans)	*LIN7B*
4468	28,5	35,6	-1,25	0,03357	0,411	229535_at	Protein tyrosine phosphatase, mitochondrial 1	*PTPMT1*
1663	9,06	11,3	-1,25	0,01050	0,345	231110_at	Transcribed locus	-
2471	33,6	41,9	-1,25	0,01660	0,367	219202_at	Rhomboid 5 homolog 2 (Drosophila)	*RHBDF2*
4496	13,4	16,8	-1,25	0,03382	0,411	215285_s_at	Putative homeodomain transcription factor 1	*PHTF1*
755	19,3	24,0	-1,25	0,00427	0,308	228364_at	Zinc finger protein 784	*ZNF784*
3211	52,0	64,8	-1,25	0,02274	0,387	209680_s_at	Kinesin family member C1	*KIFC1*
2459	6,03	7,52	-1,25	0,01651	0,367	218851_s_at	WD repeat domain 33	*WDR33*
993	52,0	64,8	-1,25	0,00572	0,315	38157_at	Dom-3 homolog Z (C. elegans)	*DOM3Z*
5988	8,38	10,4	-1,25	0,04865	0,444	1557667_at	cDNA FLJ36588 fis, clone TRACH2013991	-
740	12,9	16,1	-1,25	0,00420	0,308	219194_at	Semaphorin-4G	*SEMA4G*
2658	10,5	13,1	-1,25	0,01813	0,373	238572_at	Hypothetical protein MGC16211	*MGC16211*

Index	Mutated*	Normal*	FC	*P* value	FDR**	Probe set	Description	Gene symbol
3723	10,3	12,8	-1,24	0,02702	0,397	240297_at	Transcribed locus	-
1135	60,1	74,8	-1,24	0,00664	0,319	223954_x_at	Neuronal calcium-binding protein NECAB3	*APBA2BP*
359	73,6	91,6	-1,24	0,00184	0,281	203536_s_at	Cytosolic iron-sulfur protein assembly 1 homolog (S. cerevisiae)	*CIAO1*
33	8,19	10,2	-1,24	0,00015	0,201	227057_at	Rho GTPase activating protein 27	*ARHGAP27*
3727	253	315	-1,24	0,02706	0,397	212248_at	cDNA FLJ41088 fis, clone ASTRO2002459 (Metadherin)	*MTDH*
363	4,49	5,59	-1,24	0,00190	0,284	239184_at	Transcribed locus	-
3674	32,4	40,3	-1,24	0,02654	0,395	214955_at	Transmembrane protease, serine 6	*TMPRSS6*
3312	137	171	-1,24	0,02355	0,388	223108_s_at	Zinc finger, CCHC domain containing 17	*ZCCHC17*
5275	6,07	7,56	-1,24	0,04099	0,425	219264_s_at	Protein phosphatase 2A 48 kDa regulatory subunit	*PPP2R3B*
1184	32,0	39,8	-1,24	0,00697	0,322	216397_s_at	Block of proliferation 1	*BOP1*
1188	20,1	25,0	-1,24	0,00700	0,322	204974_at	RAB3A, member RAS oncogene family	*RAB3A*
2348	22,9	28,4	-1,24	0,01566	0,364	213520_at	RecQ protein-like 4	*RECQL4*
4474	43,0	53,5	-1,24	0,03364	0,411	207845_s_at	Anaphase promoting complex subunit 10	*ANAPC10*
309	29,9	37,1	-1,24	0,00149	0,264	217199_s_at	Signal transducer and activator of transcription 2	*STAT2*
5726	9,13	11,3	-1,24	0,04591	0,438	1558369_at	M-phase phosphoprotein 9	*MPHOSPH9*
4650	48,2	59,9	-1,24	0,03508	0,413	219214_s_at	5', 3'-nucleotidase, cytosolic	*NT5C*
4270	140	174	-1,24	0,03175	0,406	223649_s_at	Solute carrier family 25, member 39	*SLC25A39*
2661	9,47	11,8	-1,24	0,01817	0,373	229892_at	EP400 N-terminal like	*EP400NL*
3433	21,0	26,1	-1,24	0,02457	0,391	336_at	Thromboxane A2 receptor	*TBXA2R*
180	23,4	29,0	-1,24	0,00084	0,244	238628_s_at	Trafficking protein particle complex 2-like	*TRAPPC2L*
2453	65,0	80,7	-1,24	0,01645	0,366	219953_s_at	Chromosome 11 open reading frame 17	*C11orf17*
1575	6,61	8,20	-1,24	0,00979	0,340	242308_at	Mucolipin 3	*MCOLN3*
2942	40,0	49,6	-1,24	0,02062	0,383	212528_at	cDNA clone IMAGE:3878236	-
3937	586	726	-1,24	0,02876	0,399	200750_s_at	RAN, member RAS oncogene family	*RAN*
2002	10,1	12,5	-1,24	0,01307	0,355	230616_at	Similar to Laminin, beta 2 (laminin S) isoform 2	-
3260	236	292	-1,24	0,02314	0,388	202109_at	ADP-ribosylation factor interacting protein 2 (arfaptin 2)	*ARFIP2*
1650	9,55	11,8	-1,24	0,01038	0,344	238146_at	Transcribed locus	-
3000	29,3	36,2	-1,24	0,02112	0,385	232675_s_at	Uridine-cytidine kinase 1-like 1	*UCKL1*
629	28,4	35,2	-1,24	0,00356	0,308	225577_at	HLA complex group 18	*HCG18*
89	63,1	78,1	-1,24	0,00033	0,201	121_at	Paired box 8	*PAX8*
3762	7,93	9,82	-1,24	0,02735	0,397	1558123_at	Hypothetical protein FLJ35390	*FLJ35390*
1719	7,21	8,92	-1,24	0,01101	0,348	1554677_s_at	CKLF-like MARVEL transmembrane domain containing 4	*CMTM4*
2163	25,7	31,8	-1,24	0,01431	0,361	229031_at	cDNA FLJ25763 fis, clone TST06294	-
3280	7,52	9,30	-1,24	0,02336	0,388	238425_at	Transcribed locus	-
899	306	379	-1,24	0,00521	0,313	202579_x_at	High mobility group nucleosomal binding domain 4	*HMGN4*
4971	37,8	46,8	-1,24	0,03813	0,419	231808_at	Keratin associated protein 4-7	*KRTAP4-7*
1944	7,97	9,85	-1,24	0,01267	0,355	228747_at	Sec61 alpha 2 subunit (S. cerevisiae)	*SEC61A2*
3868	10,9	13,5	-1,24	0,02825	0,399	222748_s_at	Thioredoxin-like 4B	*TXNL4B*
2944	5,39	6,66	-1,24	0,02064	0,383	234211_at	cDNA FLJ21436 fis, clone COL04279	-
1828	15,8	19,5	-1,24	0,01178	0,351	229426_at	Cytochrome c oxidase subunit Va	*COX5A*
1287	7,89	9,75	-1,24	0,00765	0,325	238798_at	Transmembrane anterior posterior transformation 1	*TAPT1*
1103	115	142	-1,23	0,00646	0,319	207396_s_at	Asparagine-linked glycosylation 3 homolog	*ALG3*
2141	24,0	29,7	-1,23	0,01408	0,360	209495_at	centrosomal protein 250kDa	*CEP250*
5322	29,2	36,0	-1,23	0,04161	0,427	204857_at	MAD1 mitotic arrest deficient-like 1 (yeast)	*MAD1L1*
3842	89,7	111	-1,23	0,02805	0,399	218836_at	Ribonuclease P/MRP 21kDa subunit	*RPP21*
261	5,81	7,17	-1,23	0,00123	0,257	239856_at	Similar to XP_001175123.1	-
2808	7,16	8,83	-1,23	0,01954	0,380	1560577_at	cDNA clone IMAGE:4827370	-
2765	64,5	79,5	-1,23	0,01920	0,379	226437_at	Yip1 interacting factor homolog B (S. cerevisiae)	*YIF1B*
3436	6,44	7,94	-1,23	0,02459	0,391	1556039_s_at	G protein-coupled receptor 173	*GPR173*
490	18,6	22,9	-1,23	0,00262	0,289	202835_at	Thioredoxin-like 4A	*TXNL4A*
3984	212	262	-1,23	0,02914	0,400	201520_s_at	G-rich RNA sequence binding factor 1	*GRSF1*
1228	34,9	43,0	-1,23	0,00730	0,324	203402_at	Potassium channel shaker chain beta 2	*KCNAB2*
4254	5,96	7,34	-1,23	0,03158	0,406	1556545_at	cDNA FLJ32379 fis, clone SKMUS1000030	-
2495	13,1	16,1	-1,23	0,01682	0,367	213669_at	FCH domain only 1	*FCHO1*
1885	34,7	42,8	-1,23	0,01224	0,355	223222_at	Solute carrier family 25, member 19	*SLC25A19*
4685	35,9	44,3	-1,23	0,03537	0,413	209833_at	CASP2 and RIPK1 domain containing adaptor with death domain	*CRADD*
5652	19,4	23,9	-1,23	0,04509	0,436	208603_s_at	Mitogen-activated protein kinase 8 interacting protein 2	*MAPK8IP2*

Index	Mutated*	Normal*	FC	*P* value	FDR**	Probe set	Description	Gene symbol
414	8,71	10,7	-1,23	0,00218	0,286	1569428_at	Within bgcn homolog (Drosophila)	*WIBG*
1757	6,18	7,61	-1,23	0,01120	0,348	203578_s_at	Solute carrier family 7, member 6	*SLC7A6*
45	12,4	15,3	-1,23	0,00018	0,201	211888_x_at	Caspase 10, apoptosis-related cysteine peptidase	*CASP10*
2782	66,8	82,3	-1,23	0,01933	0,380	225593_at	LSM10, U7 small nuclear RNA associated	*LSM10*
552	24,5	30,2	-1,23	0,00299	0,296	235663_at	-	-
5526	27,5	33,8	-1,23	0,04381	0,433	224798_s_at	Chromosome 15 open reading frame 17	*C15orf17*
1317	57,2	70,4	-1,23	0,00784	0,325	212133_at	Non imprinted in Prader-Willi/Angelman syndrome 2	*NIPA2*
3904	18,1	22,3	-1,23	0,02851	0,399	224357_s_at	Membrane-spanning 4-domains, subfamily A, member 4	*MS4A4A*
4160	7,79	9,59	-1,23	0,03076	0,404	1554063_at	Chromosome 8 open reading frame 76	*C8orf76*
3654	28,3	34,8	-1,23	0,02641	0,395	232025_at	Synaptotagmin VII	*SYT7*
4020	62,6	77,1	-1,23	0,02943	0,400	200861_at	CCR4-NOT transcription complex, subunit 1	*CNOT1*
996	128	158	-1,23	0,00575	0,316	208722_s_at	Anaphase promoting complex subunit 5	*ANAPC5*
296	57,3	70,5	-1,23	0,00145	0,263	44111_at	Vacuolar protein sorting 33 homolog B (yeast)	*VPS33B*
5417	3,58	4,40	-1,23	0,04256	0,430	231797_at	SIX homeobox 4	*SIX4*
2597	42,6	52,3	-1,23	0,01765	0,371	233168_s_at	Selenoprotein O	*SELO*
3416	58,0	71,2	-1,23	0,02439	0,390	221629_x_at	Chromosome 8 open reading frame 30A	*C8orf30A*
4286	10,1	12,4	-1,23	0,03185	0,406	227055_at	Methyltransferase like 7B	*METTL7B*
2370	56,5	69,4	-1,23	0,01580	0,364	226488_at	RCC1 domain containing 1	*RCCD1*
5856	12,5	15,3	-1,23	0,04735	0,442	1565483_at	Receptor tyrosine-protein kinase erbB-1	*EGFR*
1254	7,17	8,81	-1,23	0,00747	0,325	1555617_x_at	-	-
686	24,7	30,4	-1,23	0,00393	0,308	213847_at	Peripherin	*PRPH*
2316	118	145	-1,23	0,01538	0,363	1554149_at	Claudin domain containing 1	*CLDND1*
1207	204	250	-1,23	0,00716	0,324	202529_at	Phosphoribosyl pyrophosphate synthetase-associated protein 1	*PRPSAP1*
2286	5,83	7,15	-1,23	0,01520	0,363	242941_x_at	T-box 1	*TBX1*
5469	7,69	9,44	-1,23	0,04324	0,432	205057_s_at	Iduronidase, alpha-L-	*IDUA*
1233	320	392	-1,23	0,00733	0,324	202567_at	Small nuclear ribonucleoprotein D3 polypeptide 18kDa	*SNRPD3*
1238	42,7	52,4	-1,23	0,00736	0,324	223931_s_at	Checkpoint with forkhead and ring finger domains	*CHFR*
4979	65,6	80,4	-1,23	0,03821	0,419	204247_s_at	Cyclin-dependent kinase 5	*CDK5*
614	7,84	9,60	-1,23	0,00348	0,308	223564_s_at	Guanine nucleotide binding protein (G protein), beta polypeptide 1-like	GNB1L
1631	22,0	27,0	-1,23	0,01028	0,344	238690_at	-	-
4743	551	676	-1,23	0,03593	0,414	207809_s_at	ATPase, H+ transporting, lysosomal accessory protein 1	*ATP6AP1*
2361	7,21	8,84	-1,23	0,01575	0,364	205805_s_at	Receptor tyrosine kinase-like orphan Receptor 1	*ROR1*
1515	23,5	28,8	-1,23	0,00936	0,337	218670_at	Pseudouridylate synthase 1	*PUS1*
221	28,7	35,1	-1,23	0,00102	0,250	205142_x_at	ATP-binding cassette, sub-family D (ALD), member 1	*ABCD1*
5554	12,7	15,6	-1,23	0,04421	0,435	242938_s_at	Forkhead box K2	*FOXK2*
1602	19,0	23,2	-1,22	0,00999	0,341	214228_x_at	Tumor necrosis factor receptor superfamily, member 4	*TNFRSF4*
3681	4,60	5,64	-1,22	0,02658	0,395	216959_x_at	Neuronal cell adhesion molecule	*NRCAM*
5203	57,8	70,7	-1,22	0,04013	0,422	203612_at	Bystin-like	*BYSL*
641	9,76	12,0	-1,22	0,00365	0,308	204239_s_at	Neuronatin	*NNAT*
3514	13,6	16,7	-1,22	0,02522	0,392	228525_at	Similar to Low density lipoprotein receptor-related protein 3	-
5867	103	127	-1,22	0,04742	0,442	217913_at	Vacuolar protein sorting 4 homolog A (S. cerevisiae)	*VPS4A*
3036	66,5	81,4	-1,22	0,02140	0,385	209895_at	Protein tyrosine phosphatase, non-receptor type 11	*PTPN11*
1891	168	205	-1,22	0,01228	0,355	212231_at	F-box protein 21	*FBXO21*
4631	26,1	31,9	-1,22	0,03493	0,412	222517_at	Adaptor-related protein complex 3, mu 1 subunit	*AP3M1*
969	133	163	-1,22	0,00562	0,315	217796_s_at	Nuclear protein localization 4 homolog (S. cerevisiae)	*NPLOC4*
4795	13,3	16,3	-1,22	0,03637	0,415	214755_at	UDP-N-acteylglucosamine pyrophosphorylase 1-like 1	*UAP1L1*
5447	13,8	16,9	-1,22	0,04297	0,431	206186_at	Membrane protein, palmitoylated 3	*MPP3*
4930	33,4	40,9	-1,22	0,03781	0,419	225616_at	SPRY domain containing 4	*SPRYD4*
5058	7,19	8,79	-1,22	0,03895	0,420	220577_at	GTPase, very large interferon inducible 1	*GVIN1*
3977	100	123	-1,22	0,02908	0,400	225879_at	tRNA splicing endonuclease 54 homolog (S. cerevisiae)	*TSEN54*
4817	11,6	14,2	-1,22	0,03662	0,416	221158_at	Chromosome 21 open reading frame 66	*C21orf66*
3483	276	337	-1,22	0,02501	0,392	210213_s_at	Eukaryotic translation initiation factor 6	*EIF6*
5768	10,1	12,3	-1,22	0,04634	0,439	228449_at	Similar to LOC150291 protein	-
5483	498	608	-1,22	0,04339	0,433	209046_s_at	GABA(A) receptor-associated protein-like 2	*GABARAPL2*
2848	3,91	4,77	-1,22	0,01994	0,383	222270_at	SMEK homolog 2, suppressor of mek1 (Dictyostelium)	*SMEK2*
6020	49,4	60,3	-1,22	0,04899	0,445	202111_at	Solute carrier family 4, anion exchanger, member 2	*SLC4A2*
3252	11,9	14,6	-1,22	0,02308	0,388	227876_at	KIAA1688 protein	*KIAA1688*

Index	Mutated*	Normal*	FC	*P* value	FDR**	Probe set	Description	Gene symbol
32	12,6	15,3	-1,22	0,00014	0,201	230169_at	THAP domain containing 6	*THAP6*
5635	21,1	25,7	-1,22	0,04498	0,436	226564_at	ZFAT zinc finger 1	*ZFAT1*
4508	13,1	16,0	-1,22	0,03397	0,412	228676_at	Oral cancer overexpressed 1	*ORAOV1*
1506	5,62	6,85	-1,22	0,00927	0,336	238782_at	cDNA FLJ41633 fis, clone FCBBF3003435	-
2428	32,0	39,0	-1,22	0,01623	0,365	217924_at	Chromosome 6 open reading frame 106	*C6orf106*
2373	180	220	-1,22	0,01583	0,364	226935_s_at	CLPTM1-like	*CLPTM1L*
6107	20,7	25,2	-1,22	0,04985	0,446	236989_at	Transcribed locus	-
5613	48,5	59,1	-1,22	0,04477	0,436	218927_s_at	Carbohydrate (chondroitin 4) sulfotransferase 12	*CHST12*
1248	11,5	14,1	-1,22	0,00741	0,324	227901_at	Hypothetical LOC648987	*LOC648987*
4632	31,8	38,8	-1,22	0,03494	0,412	213688_at	Calmodulin 1 (phosphorylase kinase, delta)	*CALM1*
2660	11,5	14,0	-1,22	0,01816	0,373	230293_at	MSTP088 (MST088)	-
2065	14,3	17,4	-1,22	0,01348	0,356	214819_at	IQ motif and Sec7 domain 2	*IQSEC2*
483	11,8	14,4	-1,22	0,00258	0,289	1554616_at	Serpin peptidase inhibitor, clade B (ovalbumin), member 8	*SERPINB8*
5187	14,6	17,8	-1,22	0,03997	0,421	217124_at	IQ motif containing E	*IQCE*
5544	6,35	7,75	-1,22	0,04407	0,435	208253_at	Sialic acid binding Ig-like lectin 8	*SIGLEC8*
4978	69,0	84,1	-1,22	0,03820	0,419	209217_s_at	WD repeat domain 45	*WDR45*
2211	9,47	11,5	-1,22	0,01465	0,362	227726_at	Ring finger protein 166	*RNF166*
4096	8,28	10,1	-1,22	0,03010	0,402	228641_at	Caspase recruitment domain family, member 8	*CARD8*
5821	31,5	38,3	-1,22	0,04704	0,442	229741_at	Hypothetical protein MGC3260	*MGC3260*
2543	16,1	19,6	-1,22	0,01719	0,369	227799_at	Myosin IG	*MYO1G*
4198	58,3	70,9	-1,22	0,03103	0,404	202407_s_at	PRP31 pre-mRNA processing factor 31 homolog (S. cerevisiae)	*PRPF31*
3789	25,9	31,5	-1,22	0,02759	0,398	229121_at	cDNA FLJ44441 fis, clone UTERU2020242	-
3525	14,3	17,4	-1,22	0,02529	0,392	241640_at	B-cell receptor-associated protein 29	*BCAP29*
132	6,48	7,89	-1,22	0,00059	0,240	220138_at	Heart and neural crest derivatives expressed 1	*HAND1*
3368	5,77	7,02	-1,22	0,02393	0,388	235291_s_at	Hypothetical protein LOC643977	*FLJ32255*
4611	10,1	12,3	-1,22	0,03482	0,412	215938_s_at	Phospholipase A2, group VI (cytosolic, calcium-independent)	*PLA2G6*
4766	45,4	55,3	-1,22	0,03611	0,414	221752_at	Slingshot homolog 1 (Drosophila)	*SSH1*
6115	45,3	55,1	-1,22	0,04992	0,446	227815_at	Transcribed locus	-
183	4,12	5,02	-1,22	0,00085	0,244	207226_at	Histone cluster 1, H2bn	*HIST1H2BN*
5398	5,43	6,60	-1,22	0,04234	0,429	239696_at	Transcribed locus	-
2638	6,80	8,26	-1,22	0,01798	0,373	216929_x_at	ABO blood group	*ABO*
145	6,30	7,66	-1,22	0,00066	0,244	207510_at	Bradykinin receptor B1	*BDKRB1*
3641	774	940	-1,22	0,02633	0,395	208689_s_at	Ribophorin II	*RPN2*
856	6,71	8,15	-1,22	0,00494	0,313	243017_at	Transcribed locus	-
3443	35,0	42,5	-1,21	0,02463	0,391	205448_s_at	Mitogen-activated protein kinase kinase kinase 12	*MAP3K12*
1038	15,1	18,3	-1,21	0,00604	0,318	218457_s_at	DNA (cytosine-5-)-methyltransferase 3 alpha	*DNMT3A*
1848	23,7	28,8	-1,21	0,01190	0,352	238760_at	Tyrosyl-tRNA synthetase	*YARS*
107	57,7	70,1	-1,21	0,00043	0,217	225271_at	Transmembrane protein 63B	*TMEM63B*
2681	13,5	16,3	-1,21	0,01836	0,374	226442_at	Ankyrin repeat and BTB (POZ) domain containing 1	*ABTB1*
799	28,3	34,3	-1,21	0,00456	0,311	1553015_a_at	RecQ protein-like 4	*RECQL4*
2594	42,2	51,2	-1,21	0,01765	0,371	210647_x_at	Phospholipase A2, group VI (cytosolic, calcium-independent)	*PLA2G6*
538	19,7	23,9	-1,21	0,00289	0,293	229408_at	Histone deacetylase 5	*HDAC5*
3467	10,9	13,3	-1,21	0,02484	0,392	235614_at	Transmembrane protein 151	*TMEM151*
2684	94,0	114	-1,21	0,01839	0,375	200913_at	Protein phosphatase 2, catalytic subunit, gamma isoform	*PPM1G*
634	5,51	6,69	-1,21	0,00361	0,308	236787_at	cDNA FLJ35091 fis, clone PLACE6005786	-
5036	16,4	19,9	-1,21	0,03880	0,420	231003_at	Solute carrier family 35, member B3	*SLC35B3*
2956	20,4	24,8	-1,21	0,02076	0,384	215283_at	Hypothetical gene supported by BC041875	*LOC400642*
4242	47,7	57,9	-1,21	0,03148	0,406	215982_s_at	Dom-3 homolog Z (C. elegans)	*DOM3Z*
404	11,4	13,8	-1,21	0,00213	0,286	1570156_s_at	Formin 1	*FMN1*
777	7,80	9,46	-1,21	0,00445	0,311	244707_at	Transcribed locus	-
3372	21,7	26,3	-1,21	0,02399	0,389	204947_at	E2F transcription factor 1	*E2F1*
3918	154	186	-1,21	0,02861	0,399	218132_s_at	tRNA splicing endonuclease 34 homolog (S. cerevisiae)	*TSEN34*
1031	6,42	7,78	-1,21	0,00597	0,317	238829_at	Transcribed locus	-
367	27,5	33,3	-1,21	0,00191	0,284	218725_at	Solute carrier family 25, member 22	*SLC25A22*
5981	340	412	-1,21	0,04856	0,444	201011_at	Ribophorin I	*RPN1*
2674	62,8	76,1	-1,21	0,01828	0,374	90265_at	Centaurin, alpha 1	*CENTA1*
1626	12,4	15,0	-1,21	0,01023	0,344	205484_at	Signaling threshold regulating transmembrane adaptor 1	*SIT1*

Index	Mutated*	Normal*	FC	*P* value	FDR**	Probe set	Description	Gene symbol
5172	124	150	-1,21	0,03984	0,421	1564207_at	Hypothetical protein FLJ35390	*FLJ35390*
5460	28,8	34,9	-1,21	0,04313	0,432	221991_at	Neurexophilin 3	*NXPH3*
5226	5,52	6,69	-1,21	0,04043	0,423	224525_s_at	Obg-like ATPase 1	*OLA1*
5309	40,6	49,1	-1,21	0,04143	0,426	212871_at	Mitogen-activated protein kinase-activated protein kinase 5	*MAPKAPK5*
1090	6,00	7,27	-1,21	0,00640	0,319	212272_at	Lipin 1	*LPIN1*
3932	5,02	6,08	-1,21	0,02874	0,399	238598_s_at	cDNA FLJ44201 fis, clone THYMU3000841	-
4119	9,99	12,1	-1,21	0,03028	0,402	211210_x_at	SH2 domain protein 1A, Duncan's disease	*SH2D1A*
2349	3,89	4,70	-1,21	0,01567	0,364	244224_x_at	Ly6/neurotoxin 1	*LYNX1*
3855	163	198	-1,21	0,02815	0,399	212361_s_at	ATPase, Ca++ transporting, cardiac muscle, slow twitch 2	*ATP2A2*
4086	8,51	10,3	-1,21	0,03002	0,402	1553568_a_at	Histone cluster 1, H1t	*HIST1H1T*
1750	13,2	16,0	-1,21	0,01117	0,348	217187_at	Mucin 5AC, oligomeric mucus/gel-forming	*MUC5AC*
5004	1493	1805	-1,21	0,03843	0,420	200925_at	Cytochrome c oxidase subunit VIa polypeptide 1	*COX6A1*
4982	299	362	-1,21	0,03822	0,419	211759_x_at	Tubulin folding cofactor B	*TBCB*
1897	10,3	12,5	-1,21	0,01233	0,355	239484_at	cDNA clone IMAGE:4795796	-
3823	15,9	19,2	-1,21	0,02790	0,399	242048_at	Prefoldin subunit 6	*PFDN6*
892	10,8	13,0	-1,21	0,00516	0,313	220730_at	Hypothetical protein FLJ12986	*FLJ12986*
4654	28,9	34,9	-1,21	0,03515	0,413	221634_at	Ribosomal protein L23a pseudogene 7	*RPL23AP7*
1275	23,2	28,0	-1,21	0,00759	0,325	228419_at	cDNA FLJ32491 fis, clone SKNSH1000308	-
4525	41,3	49,9	-1,21	0,03414	0,412	203099_s_at	Chromodomain protein, Y-like	*CDYL*
267	8,65	10,4	-1,21	0,00127	0,260	210659_at	Chemokine-like receptor 1	*CMKLR1*
3884	12,0	14,5	-1,21	0,02836	0,399	205865_at	AT rich interactive domain 3A (BRIGHT-like)	*ARID3A*
4843	22,4	27,0	-1,21	0,03692	0,417	230334_at	cDNA clone IMAGE:40078968	-
678	19,3	23,3	-1,21	0,00390	0,308	222648_at	TBC1 domain family, member 16	*TBC1D16*
6066	19,9	24,0	-1,21	0,04948	0,446	203036_s_at	Metastasis suppressor 1	*MTSS1*
3367	10,1	12,2	-1,21	0,02392	0,388	234955_at	Similar to Zinc-alpha-2-glycoprotein precursor	*LOC401393*
1601	5,70	6,88	-1,21	0,00998	0,341	222019_at	Prefoldin subunit 6	*PFDN6*
1489	495	597	-1,21	0,00918	0,336	201527_at	ATPase, H+ transporting, lysosomal 14kDa, V1 subunit F	*ATP6V1F*
1277	4,22	5,09	-1,21	0,00760	0,325	215149_at	cDNA clone IMAGE:5260262	-
5053	37,2	44,9	-1,21	0,03893	0,420	218777_at	Receptor accessory protein 4	*REEP4*
3867	13,0	15,6	-1,21	0,02824	0,399	228753_at	Similar to XP_001148836.1	-
2915	8,37	10,1	-1,21	0,02047	0,383	240295_at	Transcribed locus	-
1504	176	212	-1,21	0,00924	0,336	201050_at	Phospholipase D family, member 3	*PLD3*
5021	10,8	13,0	-1,21	0,03862	0,420	207697_x_at	Leukocyte immunoglobulin-like receptor, subfamily B member 2	*LILRB2*
546	30,8	37,1	-1,20	0,00295	0,295	220036_s_at	Limb region 1 homolog (mouse)-like	*LMBR1L*
20	5,29	6,37	-1,20	0,00008	0,201	239198_at	Enhancer of zeste homolog 1 (Drosophila)	*EZH1*
2579	11,3	13,6	-1,20	0,01750	0,371	222087_at	Pvt1 oncogene homolog, MYC activator (mouse)	*PVT1*
71	8,38	10,1	-1,20	0,00028	0,201	1552887_at	Chromosome 10 open reading frame 27	*C10orf27*
4620	12,5	15,0	-1,20	0,03485	0,412	227342_s_at	Myeloma overexpressed gene (hypothetical protein LOC26579)	*MYEOV*
1882	31,2	37,6	-1,20	0,01222	0,355	227907_at	cDNA clone IMAGE:6470300	-
3055	5,25	6,32	-1,20	0,02152	0,385	204714_s_at	Coagulation factor V (proaccelerin, labile factor)	*F5*
4354	16,1	19,3	-1,20	0,03241	0,407	213884_s_at	Tripartite motif-containing 3	*TRIM3*
430	15,4	18,5	-1,20	0,00227	0,288	211693_at	Immunoglobulin heavy constant alpha 1	*IGHA1*
2847	8,43	10,1	-1,20	0,01992	0,383	227704_at	Chromosome 19 open reading frame 12	*C19orf12*
768	401	482	-1,20	0,00437	0,311	223026_s_at	Vacuolar protein sorting 29 homolog (S. cerevisiae)	*VPS29*
2115	145	174	-1,20	0,01387	0,359	222460_s_at	NEFA-interacting nuclear protein NIP30	*NIP30*
5131	7,50	9,02	-1,20	0,03949	0,421	207795_s_at	Killer cell lectin-like receptor subfamily D, member 1	*KLRD1*
402	10,2	12,2	-1,20	0,00211	0,286	217017_at	Oxysterol binding protein-like 10	*OSBPL10*
2993	19,2	23,1	-1,20	0,02109	0,385	221293_s_at	Differentially expressed in FDCP 6 homolog (mouse)	*DEF6*
254	6,60	7,93	-1,20	0,00118	0,254	221331_x_at	Cytotoxic T-lymphocyte-associated protein 4	*CTLA4*
4983	15,0	18,1	-1,20	0,03823	0,419	214957_at	Actin-like 8	*ACTL8*
6078	15,0	18,0	-1,20	0,04962	0,446	230139_at	cDNA FLJ43345 fis, clone NT2RI3008228	-
3497	5,05	6,07	-1,20	0,02514	0,392	232965_at	Hypothetical gene supported by BC000922	*LOC400684*
2938	4,39	5,27	-1,20	0,02060	0,383	235607_at	Similar to Heterogeneous nuclear ribonucleoprotein D0	-
3620	46,8	56,3	-1,20	0,02614	0,395	219447_s_at	Solute carrier family 35, member C2	*SLC35C2*
5659	7,52	9,03	-1,20	0,04514	0,436	1562953_s_at	Chromosome 4 open reading frame 12	*C4orf12*
515	11,8	14,2	-1,20	0,00275	0,291	224805_s_at	Chromosome 15 open reading frame 17	*C15orf17*
2023	53,0	63,6	-1,20	0,01320	0,355	225287_s_at	Transmembrane protein 55B	*TMEM55B*

Index	Mutated*	Normal*	FC	*P* value	FDR**	Probe set	Description	Gene symbol
6003	21,9	26,2	-1,20	0,04879	0,444	241792_x_at	cDNA FLJ33355 fis, clone BRACE2005151	-
3510	2053	2465	-1,20	0,02522	0,392	213187_x_at	Ferritin, light polypeptide	*FTL*
2330	7,20	8,64	-1,20	0,01553	0,364	215195_at	Protein kinase C, alpha	*PRKCA*
4260	77,9	93,5	-1,20	0,03166	0,406	217427_s_at	HIR histone cell cycle regulation defective homolog A	*HIRA*
4481	8,01	9,61	-1,20	0,03370	0,411	217486_s_at	Zinc finger, DHHC-type containing 17	*ZDHHC17*
5750	51,3	61,5	-1,20	0,04614	0,439	1558304_s_at	tRNA splicing endonuclease 54 homolog (S. cerevisiae)	*TSEN54*
2668	20,7	24,9	-1,20	0,01825	0,374	218939_at	Leucine zipper-EF-hand containing transmembrane protein 1	*LETM1*
1264	6,94	8,33	-1,20	0,00752	0,325	235686_at	Chromosome 2 open reading frame 60	*C2orf60*
4253	15,3	18,3	-1,20	0,03157	0,406	201808_s_at	Endoglin (Osler-Rendu-Weber syndrome 1)	*ENG*
4658	306	367	-1,20	0,03518	0,413	201804_x_at	Tubulin folding cofactor B	*TBCB*
4689	201	241	-1,20	0,03541	0,413	213404_s_at	RAS homolog enriched in brain	*RHEB*
2799	7,16	8,59	-1,20	0,01944	0,380	219873_at	Collectin sub-family member 11	*COLEC11*
22	11,7	14,1	-1,20	0,00009	0,201	219246_s_at	2-oxoglutarate and iron-dependent oxygenase domain-containing protein 2	*OGFOD2*
1935	30,3	36,3	-1,20	0,01261	0,355	215873_x_at	ATP-binding cassette, sub-family C (CFTR/MRP), member 10	*ABCC10*
4281	10,3	12,3	-1,20	0,03181	0,406	229112_at	Hypothetical protein LOC285813	*LOC285813*
1071	6,74	8,08	-1,20	0,00628	0,319	234668_at	cDNA FLJ23175 fis, clone LNG10438	-
1557	7,39	8,85	-1,20	0,00961	0,337	239366_at	Transcribed locus	-
621	7,00	8,39	-1,20	0,00352	0,308	240761_at	Transcribed locus	-
4208	12,9	15,5	-1,20	0,03111	0,404	205243_at	Solute carrier family 13, member 3	*SLC13A3*
2833	19,3	23,1	-1,20	0,01977	0,381	203507_at	CD68 molecule	*CD68*
709	3,56	4,27	-1,20	0,00407	0,308	211006_s_at	Potassium voltage-gated channel subfamily B member 1	*KCNB1*
804	4,30	5,15	-1,20	0,00459	0,311	239588_s_at	-	-
151	5,07	6,07	-1,20	0,00069	0,244	1552915_at	Interleukin 28A (Interferon, lambda 2)	*IL28A*
265	6,24	7,47	-1,20	0,00126	0,260	207778_at	Regenerating islet-derived 1 pseudogene	*REGL*
4407	96,5	116	-1,20	0,03290	0,408	222451_s_at	Zinc finger, DHHC-type containing 9	*ZDHHC9*
1691	15,7	18,8	-1,20	0,01070	0,346	222304_x_at	Olfactory receptor, family 7, subfamily E, member 47 pseudogene	*OR7E47P*
1780	16,0	19,2	-1,20	0,01135	0,349	226232_at	cDNA FLJ33772 fis, clone BRSSN2000175	-
718	11,4	13,6	-1,20	0,00412	0,308	220671_at	CCR4 carbon catabolite repression 4-like (S. cerevisiae)	*CCRN4L*
3558	35,7	42,7	-1,20	0,02568	0,394	218907_s_at	Leucine rich repeat containing 61	*LRRC61*
5057	14,1	16,9	-1,20	0,03895	0,420	239324_at	cDNA clone IMAGE:2960540	-
611	13,8	16,5	-1,20	0,00346	0,308	219907_at	Fibroblast growth factor receptor substrate 3	*FRS3*
3717	80,1	95,8	-1,20	0,02695	0,396	224735_at	Cytochrome b, ascorbate dependent 3	*CYBASC3*
2425	44,6	53,4	-1,20	0,01622	0,365	204706_at	Inositol polyphosphate-5-phosphatase, 72 kDa	*INPP5E*
5877	461	552	-1,20	0,04749	0,442	205353_s_at	Phosphatidylethanolamine binding protein 1	*PEBP1*
26	3,16	3,78	-1,20	0,00012	0,201	1568656_at	cDNA clone IMAGE:5265210	-
3540	374	447	-1,20	0,02547	0,393	224779_s_at	Family with sequence similarity 96, member A	*FAM96A*
861	12,0	14,4	-1,20	0,00497	0,313	210264_at	G protein-coupled receptor 35	*GPR35*
2215	5,36	6,41	-1,20	0,01467	0,362	231025_at	Transcribed locus	-
2713	6,77	8,10	-1,20	0,01862	0,375	224399_at	Programmed cell death 1 ligand 2	*PDCD1LG2*
808	39,6	47,3	-1,20	0,00461	0,311	220762_s_at	Guanine nucleotide binding protein (G protein), beta polypeptide 1-like	*GNB1L*
3351	301	359	-1,20	0,02380	0,388	226177_at	Glycolipid transfer protein	*GLTP*
3827	86,4	103	-1,20	0,02793	0,399	215631_s_at	Breast cancer metastasis suppressor 1	*BRMS1*
3056	4,64	5,54	-1,20	0,02152	0,385	239470_at	Hypothetical protein LOC644809	*FLJ38596*
4179	56,9	68,0	-1,20	0,03089	0,404	205061_s_at	Exosome component 9	*EXOSC9*
6033	26,2	31,3	-1,19	0,04910	0,445	206351_s_at	Peroxisome biogenesis factor 10	*PEX10*
3903	14,6	17,5	-1,19	0,02851	0,399	210821_x_at	Centromere protein A	*CENPA*
2137	21,2	25,3	-1,19	0,01405	0,359	64432_at	Chromosome 12 open reading frame 47	*C12orf47*
5435	9,41	11,2	-1,19	0,04283	0,431	221640_s_at	Leucine-rich repeats and death domain containing	*LRDD*
964	4,87	5,82	-1,19	0,00559	0,315	239041_at	Histone cluster 1, H2ak	*HIST1H2AK*
3539	41,3	49,3	-1,19	0,02547	0,393	1554721_a_at	Transcription initiation factor TFIID 150 kDa subunit	*TAF2*
1477	4,36	5,20	-1,19	0,00905	0,335	232827_at	Clone L50 polyadenylated HERV LTR sequence	-
3632	12,4	14,8	-1,19	0,02626	0,395	207873_x_at	Seizure related 6 homolog (mouse)-like	*SEZ6L*
1625	32,0	38,2	-1,19	0,01022	0,344	202879_s_at	Pleckstrin homology, Sec7 and coiled-coil domains 1	*PSCD1*
3328	31,7	37,8	-1,19	0,02363	0,388	227146_at	Quiescin Q6 sulfhydryl oxidase 2	*QSOX2*
42	4,19	5,00	-1,19	0,00017	0,201	214248_s_at	Tripartite motif-containing 2	*TRIM2*
5913	272	324	-1,19	0,04794	0,443	218462_at	Brix domain containing 5	*BXDC5*
595	39,9	47,6	-1,19	0,00328	0,301	221686_s_at	RecQ protein-like 5	*RECQL5*

Index	Mutated*	Normal*	FC	*P* value	FDR**	Probe set	Description	Gene symbol
3375	14,4	17,1	-1,19	0,02402	0,389	212844_at	Ribosomal RNA processing 1 homolog B (S. cerevisiae)	*RRP1B*
2112	362	432	-1,19	0,01385	0,358	224129_s_at	Dpy-30-like protein	*HDPY-30*
5836	5,80	6,92	-1,19	0,04715	0,442	240615_at	cDNA FLJ34894 fis, clone NT2NE2017982	-
2916	4,76	5,68	-1,19	0,02047	0,383	206004_at	Transglutaminase 3	*TGM3*
1422	20,6	24,6	-1,19	0,00862	0,331	1564031_a_at	RELT-like 2	*RELL2*
5326	138	165	-1,19	0,04163	0,427	202084_s_at	SEC14-like 1 (S. cerevisiae)	*SEC14L1*
948	42,2	50,3	-1,19	0,00544	0,313	210225_x_at	Leukocyte immunoglobulin-like receptor, subfamily B member 3	*LILRB3*
5209	9,87	11,8	-1,19	0,04020	0,422	231312_at	Transcribed locus	-
4856	4,82	5,75	-1,19	0,03703	0,417	244074_at	Full-length cDNA clone CS0DI026YO05	-
5493	5,75	6,85	-1,19	0,04348	0,433	209776_s_at	Solute carrier family 19, member 1	*SLC19A1*
2732	18,1	21,5	-1,19	0,01884	0,377	204522_at	Dom-3 homolog Z (C. elegans)	*DOM3Z*
5814	15,8	18,8	-1,19	0,04698	0,442	206818_s_at	Cyclin M2	*CNNM2*
233	6,48	7,71	-1,19	0,00108	0,250	1554367_at	Family with sequence similarity 26, member C	*FAM26C*
3645	7,12	8,48	-1,19	0,02634	0,395	228395_at	Glycosyltransferase 8 domain containing 1	*GLT8D1*
1947	17,7	21,1	-1,19	0,01272	0,355	203977_at	Tafazzin	*TAZ*
4280	12,9	15,4	-1,19	0,03180	0,406	241427_x_at	cDNA DKFZP434I0714	-
841	7,89	9,40	-1,19	0,00482	0,313	1557532_at	NADH-ubiquinone oxidoreductase subunit B14.5a	*NDUFA7*
2536	6,43	7,65	-1,19	0,01715	0,369	227321_at	Opposite strand transcription unit to STAG3	*GATS*
4499	8,71	10,4	-1,19	0,03384	0,411	216253_s_at	Parvin, beta	*PARVB*
4714	47,5	56,6	-1,19	0,03567	0,413	213473_at	BRCA1 associated protein	*BRAP*
4248	14,0	16,6	-1,19	0,03154	0,406	241839_at	Transcribed locus	-
260	18,4	21,9	-1,19	0,00123	0,257	1566775_at	Dynein, axonemal, heavy chain 1	*DNAH1*
3032	13,2	15,8	-1,19	0,02137	0,385	227965_at	Full-length cDNA clone CS0DJ011YE02	-
2611	6,53	7,77	-1,19	0,01773	0,371	229052_at	Ankyrin repeat domain 39	*ANKRD39*
1558	23,4	27,8	-1,19	0,00964	0,338	230062_at	KIAA1666 protein	*KIAA1666*
3793	7,07	8,41	-1,19	0,02762	0,398	228646_at	Protein phosphatase 1, regulatory (inhibitor) subunit 1C	*PPP1R1C*
1168	7,70	9,16	-1,19	0,00687	0,321	1568706_s_at	Advillin	*AVIL*
3838	12,4	14,8	-1,19	0,02804	0,399	210008_s_at	Mitochondrial ribosomal protein S12	*MRPS12*
1977	3,09	3,67	-1,19	0,01291	0,355	1556776_a_at	Full length insert cDNA YN57B01	-
5459	357	424	-1,19	0,04312	0,432	201013_s_at	Multifunctional protein ADE2	*PAICS*
5479	16,4	19,5	-1,19	0,04335	0,433	235359_at	Leucine rich repeat containing 33	*LRRC33*
3105	7,43	8,84	-1,19	0,02192	0,386	226205_at	Ankyrin repeat domain 13 family, member D	*ANKRD13D*
3200	13,8	16,3	-1,19	0,02266	0,387	211894_x_at	Seizure related 6 homolog (mouse)-like	*SEZ6L*
6021	78,9	93,8	-1,19	0,04901	0,445	224807_at	GRAM domain containing 1A	*GRAMD1A*
5123	28,6	34,0	-1,19	0,03944	0,421	225094_at	SET domain containing (lysine methyltransferase) 8	*SETD8*
882	6,50	7,73	-1,19	0,00510	0,313	221336_at	Atonal homolog 1 (Drosophila)	*ATOH1*
914	10,4	12,4	-1,19	0,00526	0,313	1552348_at	Protease, serine, 33	*PRSS33*
5928	12,5	14,8	-1,19	0,04804	0,443	211082_x_at	MAP/microtubule affinity-regulating kinase 2	*MARK2*
2687	12,0	14,3	-1,19	0,01841	0,375	207671_s_at	Bestrophin 1	*BEST1*
2081	9,73	11,6	-1,19	0,01358	0,356	1553540_a_at	Solute carrier family 29, member 2	*SLC29A2*
108	7,41	8,81	-1,19	0,00043	0,217	223779_at	Hypothetical protein MGC10981	*MGC10981*
5861	11,4	13,5	-1,19	0,04739	0,442	207509_s_at	Leukocyte-associated immunoglobulin-like receptor 2	*LAIR2*
3444	17,5	20,7	-1,19	0,02465	0,391	229612_at	Transcribed locus	-
4787	30,6	36,4	-1,19	0,03631	0,415	221809_at	RAN binding protein 10	*RANBP10*
156	9,15	10,9	-1,19	0,00071	0,244	206938_at	Steroid-5-alpha-reductase, alpha polypeptide 2	*SRD5A2*
2842	4,25	5,05	-1,19	0,01987	0,382	230776_at	cDNA FLJ36181 fis, clone TESTI2026794	-
2274	5,73	6,81	-1,19	0,01511	0,363	1559509_at	cDNA FLJ35328 fis, clone PROST2013531	-
335	5,18	6,15	-1,19	0,00170	0,277	220437_at	Hepatocellular carcinoma-associated gene TD26	*LOC55908*
2340	247	293	-1,19	0,01562	0,364	221984_s_at	Family with sequence similarity 134, member A	*FAM134A*
1108	10,1	12,0	-1,19	0,00649	0,319	211096_at	Pre-B-cell leukemia homeobox 2	*PBX2*
1614	82,3	97,6	-1,19	0,01012	0,343	202264_s_at	Translocase of outer mitochondrial membrane 40 homolog (yeast)	*TOMM40*
3323	11,7	13,9	-1,19	0,02360	0,388	232476_at	cDNA FLJ21452 fis, clone COL04505	-
5980	170	202	-1,19	0,04856	0,444	224615_x_at	Histocompatibility (minor) 13	*HM13*
3409	23,0	27,3	-1,19	0,02433	0,390	211037_s_at	Leukocyte receptor cluster (LRC) member 4	*LENG4*
4028	9,28	11,0	-1,19	0,02951	0,400	215989_at	Chromobox homolog 2 (Pc class homolog, Drosophila)	*CBX2*
509	18,2	21,6	-1,19	0,00269	0,289	233939_at	REX1, RNA exonuclease 1 homolog (S. cerevisiae)	*REXO1*
2633	97,3	115	-1,19	0,01793	0,372	201933_at	Chromatin modifying protein 1A	*CHMP1A*

Index	Mutated*	Normal*	FC	*P* value	FDR**	Probe set	Description	Gene symbol
5190	16,5	19,6	-1,19	0,03998	0,421	2028_s_at	E2F transcription factor 1	*E2F1*
2331	45,5	54,0	-1,19	0,01556	0,364	1552473_at	Guanidinoacetate N-methyltransferase	*GAMT*
5663	175	207	-1,19	0,04519	0,436	209786_at	High mobility group nucleosomal binding domain 4	*HMGN4*
4989	9,57	11,3	-1,19	0,03829	0,419	235528_at	Guanylate cyclase activator 1B (retina)	*GUCA1B*
1175	3,41	4,04	-1,18	0,00690	0,321	207793_s_at	Erythrocyte membrane protein band 4.1	*EPB41*
338	6,56	7,77	-1,18	0,00173	0,277	232320_at	cDNA FLJ22706 fis, clone HSI13163	-
4283	19,2	22,7	-1,18	0,03182	0,406	219817_at	Chromosome 12 open reading frame 47	*C12orf47*
2992	26,1	30,9	-1,18	0,02105	0,385	227633_at	RAS homolog enriched in brain	*RHEB*
3528	5,48	6,48	-1,18	0,02535	0,393	239016_at	Transcribed locus	-
5330	22,8	27,0	-1,18	0,04169	0,428	225476_at	HLA-B associated transcript 4	*BAT4*
3230	9,28	11,0	-1,18	0,02291	0,388	229855_at	Ring finger protein 34	*RNF34*
1966	23,5	27,9	-1,18	0,01285	0,355	213402_at	Zinc finger protein 787	*ZNF787*
2240	9,04	10,7	-1,18	0,01489	0,363	238072_at	cDNA FLJ38016 fis, clone CTONG2012724	-
5144	4,97	5,89	-1,18	0,03961	0,421	240869_at	Full length insert cDNA clone ZE05A03	-
684	22,6	26,8	-1,18	0,00392	0,308	209957_s_at	Natriuretic peptide precursor A	*NPPA*
689	10,9	12,9	-1,18	0,00395	0,308	232922_s_at	Chromosome 20 open reading frame 59	*C20orf59*
836	18,1	21,4	-1,18	0,00478	0,312	211173_at	Cholecystokinin A receptor	*CCKAR*
833	4,96	5,87	-1,18	0,00476	0,312	1555377_at	Olfactory receptor, family 4, subfamily D, member 2	*OR4D2*
306	5,36	6,34	-1,18	0,00148	0,263	237827_at	-	-
5411	50,3	59,6	-1,18	0,04251	0,430	229758_at	Tigger transposable element derived 5	*TIGD5*
2012	12,4	14,7	-1,18	0,01311	0,355	205575_at	Complement component 1, q subcomponent-like 1	*C1QL1*
78	7,13	8,44	-1,18	0,00030	0,201	224001_at	Family with sequence similarity 135, member B	*FAM135B*
5993	5,43	6,43	-1,18	0,04874	0,444	223573_s_at	Protein phosphatase 2A1 B gamma subunit	*PPP2R2C*
3585	4,14	4,90	-1,18	0,02588	0,394	211303_x_at	Growth-inhibiting protein 26	*PSMAL*
1941	28,3	33,5	-1,18	0,01266	0,355	237257_at	RAB4B, member RAS oncogene family	*RAB4B*
301	28,4	33,6	-1,18	0,00146	0,263	220659_s_at	Chromosome 7 open reading frame 43	*C7orf43*
604	4,81	5,69	-1,18	0,00335	0,303	216065_at	Similar to XP_530916.1	-
5715	293	346	-1,18	0,04575	0,438	208799_at	Proteasome (prosome, macropain) subunit, beta type, 5	*PSMB5*
2773	17,7	20,9	-1,18	0,01924	0,379	229864_at	Transmembrane protein 103	*TMEM103*
5329	11,1	13,2	-1,18	0,04167	0,428	237186_at	cDNA DKFZp779F2345	-
3468	10,2	12,0	-1,18	0,02485	0,392	235194_at	Two pore segment channel 2	*TPCN2*
1740	11,9	14,1	-1,18	0,01111	0,348	219996_at	Ankyrin repeat and SOCS box-containing 7	*ASB7*
4692	23,5	27,8	-1,18	0,03544	0,413	228405_at	Rhophilin, Rho GTPase binding protein 1	*RHPN1*
674	16,1	19,0	-1,18	0,00386	0,308	229637_at	Synembryn-B	*RIC8B*
5139	7,49	8,85	-1,18	0,03958	0,421	237220_at	Transcribed locus	-
1548	7,21	8,52	-1,18	0,00956	0,337	220130_x_at	Leukotriene B4 receptor 2	*LTB4R2*
2497	29,6	34,9	-1,18	0,01682	0,367	1554050_at	Sphingomyelin phosphodiesterase, acid-like 3B	*SMPDL3B*
2717	27,1	32,0	-1,18	0,01867	0,376	213098_at	RCD1 required for cell differentiation1 homolog (S. pombe)	*RQCD1*
243	4,37	5,16	-1,18	0,00111	0,250	215882_at	Centrosomal protein 152kDa	*CEP152*
2935	24,8	29,2	-1,18	0,02059	0,383	1570402_at	Kinesin light chain 3	*KLC3*
1171	7,72	9,12	-1,18	0,00688	0,321	241644_at	BolA homolog 2 (E. coli)	*BOLA2*
4985	25,9	30,6	-1,18	0,03826	0,419	223055_s_at	Exportin 5	*XPO5*
5868	76,2	89,9	-1,18	0,04743	0,442	202281_at	Cyclin G associated kinase	*GAK*
569	15,2	18,0	-1,18	0,00311	0,299	236863_at	Chromosome 17 open reading frame 67	*C17orf67*
37	28,2	33,3	-1,18	0,00015	0,201	216678_at	Intraflagellar transport 122 homolog (Chlamydomonas)	*IFT122*
121	3914	4618	-1,18	0,00056	0,240	200062_s_at	Ribosomal protein L30	*RPL30*
3736	62,7	74,0	-1,18	0,02713	0,397	221821_s_at	Chromosome 12 open reading frame 41	*C12orf41*
4636	4,14	4,88	-1,18	0,03497	0,412	217651_at	Transcribed locus	-
6079	4,52	5,33	-1,18	0,04963	0,446	1569190_at	Sodium channel and clathrin linker 1	*SCLT1*
188	115	135	-1,18	0,00087	0,244	200070_at	Chromosome 2 open reading frame 24	*C2orf24*
1860	8,51	10,0	-1,18	0,01199	0,353	228912_at	Villin 1	*VIL1*
165	19,6	23,1	-1,18	0,00076	0,244	237367_x_at	CASP8 and FADD-like apoptosis regulator	*CFLAR*
1898	20,2	23,8	-1,18	0,01234	0,355	202571_s_at	Discs, large (Drosophila) homolog-associated protein 4	*DLGAP4*
5816	586	691	-1,18	0,04698	0,442	202857_at	Transmembrane protein 4	*TMEM4*
2317	20,5	24,1	-1,18	0,01539	0,363	224079_at	Interleukin 17C	*IL17C*
4862	951	1120	-1,18	0,03710	0,417	208628_s_at	Y box binding protein 1	*YBX1*
1718	65,7	77,4	-1,18	0,01101	0,348	225789_at	Centaurin, gamma 3	*CENTG3*

Index	Mutated*	Normal*	FC	*P* value	FDR**	Probe set	Description	Gene symbol
3289	40,3	47,5	-1,18	0,02342	0,388	225437_s_at	Chromosome 7 open reading frame 27	*C7orf27*
351	4,02	4,74	-1,18	0,00179	0,278	224004_at	Zinc finger protein 226	*ZNF226*
1253	16,0	18,8	-1,18	0,00746	0,325	239592_at	Transcribed locus	-
2934	43,1	50,8	-1,18	0,02058	0,383	219611_s_at	Coiled-coil domain containing 21	*CCDC21*
2794	48,8	57,5	-1,18	0,01942	0,380	1564208_x_at	Hypothetical protein FLJ35390	*FLJ35390*
1829	6,88	8,10	-1,18	0,01179	0,351	1559064_at	Nucleoporin 153kDa	*NUP153*
1867	26,6	31,4	-1,18	0,01206	0,353	211135_x_at	Leukocyte immunoglobulin-like receptor, subfamily B member 3	*LILRB3*
1124	386	455	-1,18	0,00657	0,319	211036_x_at	Anaphase promoting complex subunit 5	*ANAPC5*
3059	5,15	6,06	-1,18	0,02153	0,385	220448_at	Potassium channel, subfamily K, member 12	*KCNK12*
659	17,5	20,6	-1,18	0,00382	0,308	217324_at	cDNA DKFZp434B1521	-
2574	38,2	45,0	-1,18	0,01745	0,371	216008_s_at	Ariadne homolog 2 (Drosophila)	*ARIH2*
59	3,71	4,37	-1,18	0,00022	0,201	241654_at	Transcribed locus	-
897	11,9	14,0	-1,18	0,00519	0,313	222094_at	Sulfotransferase family, cytosolic, 1A, phenol-preferring, member 3	*SULT1A3*
5852	24,2	28,5	-1,18	0,04733	0,442	53987_at	RAN binding protein 10	*RANBP10*
2254	40,1	47,3	-1,18	0,01500	0,363	219149_x_at	Debranching enzyme homolog 1 (S. cerevisiae)	*DBR1*
2339	7,31	8,60	-1,18	0,01561	0,364	230847_at	Werner helicase interacting protein 1	*WRNIP1*
1247	19,1	22,5	-1,18	0,00741	0,324	207408_at	Solute carrier family 22, member 14	*SLC22A14*
525	3,89	4,58	-1,18	0,00280	0,291	1553533_at	Junctophilin 1	*JPH1*
956	4,11	4,83	-1,18	0,00552	0,315	243804_at	Myotubularin related protein 7	*MTMR7*
2747	8,20	9,65	-1,18	0,01900	0,378	1554095_at	RNA binding motif protein 33	*RBM33*
931	23,9	28,1	-1,18	0,00535	0,313	211773_s_at	Zinc finger with KRAB and SCAN domains 3	*ZKSCAN3*
1498	12,7	15,0	-1,18	0,00922	0,336	223812_at	Hypothetical protein LOC51252	*LOC51252*
727	5,74	6,75	-1,18	0,00415	0,308	244709_at	Clone IMAGE:5200887, mRNA	-
5632	14,7	17,3	-1,18	0,04496	0,436	240379_at	Transcribed locus	-
74	4,88	5,74	-1,18	0,00028	0,201	206843_at	Crystallin, beta A4	*CRYBA4*
1582	118	139	-1,18	0,00985	0,340	218037_at	Family with sequence similarity 134, member A	*FAM134A*
5399	110	130	-1,18	0,04234	0,429	218126_at	Family with sequence similarity 82, member C	*FAM82C*
2959	6,53	7,68	-1,18	0,02079	0,384	242618_at	Tripartite motif-containing 26	*TRIM26*
4241	10,9	12,8	-1,18	0,03148	0,406	238226_at	Family with sequence similarity 70, member B	*FAM70B*
2162	5,16	6,06	-1,18	0,01429	0,361	235992_s_at	Hypothetical protein LOC606495	*LOC606495*
4863	6,68	7,85	-1,18	0,03710	0,417	1561595_x_at	Full length insert cDNA YN57B01	-
508	4,39	5,16	-1,18	0,00269	0,289	211614_at	C33.6 unnamed HERV-H protein	-
5664	26,7	31,4	-1,18	0,04519	0,436	212735_at	KIAA0226 protein	*KIAA0226*
1319	15,8	18,6	-1,18	0,00786	0,326	242885_at	-	-
1555	8,53	10,0	-1,18	0,00960	0,337	1559121_s_at	Ariadne homolog 2 (Drosophila)	*ARIH2*
4682	7,60	8,93	-1,18	0,03535	0,413	243680_at	Similar to XP_001152474.1	-
3624	44,6	52,4	-1,18	0,02616	0,395	212059_s_at	TNF-receptor ubiquitous scaffolding/signaling protein	*TRPC4AP*
5415	18,7	21,9	-1,17	0,04256	0,430	204795_at	Proline rich 3	*PRR3*
3326	6,55	7,69	-1,17	0,02362	0,388	220692_at	HSPC047 protein	-
2651	10,1	11,9	-1,17	0,01808	0,373	243774_at	Mucin 20, cell surface associated	*MUC20*
4964	15,2	17,9	-1,17	0,03808	0,419	244765_at	Transcribed locus	-
1768	28,7	33,7	-1,17	0,01127	0,348	208947_s_at	UPF1 regulator of nonsense transcripts homolog (yeast)	*UPF1*
3725	4,83	5,67	-1,17	0,02704	0,397	1554356_at	GINS complex subunit 4 (Sld5 homolog)	*GINS4*
5353	903	1061	-1,17	0,04200	0,429	221619_s_at	Mitochondrial carrier homolog 1 (C. elegans)	*MTCH1*
1670	6,52	7,66	-1,17	0,01054	0,345	220961_s_at	Transforming growth factor beta regulator 4	*TBRG4*
2057	13,2	15,5	-1,17	0,01340	0,356	206650_at	IQ motif containing C	*IQCC*
4900	6,57	7,71	-1,17	0,03749	0,418	210359_at	Metastasis suppressor 1	*MTSS1*
927	36,3	42,6	-1,17	0,00533	0,313	210651_s_at	EPH receptor B2	*EPHB2*
2070	4,63	5,44	-1,17	0,01353	0,356	1555868_at	Hypothetical protein LOC729070	*LOC729070*
5318	60,0	70,5	-1,17	0,04151	0,427	219022_at	Chromosome 12 open reading frame 43	*C12orf43*
4356	6,07	7,13	-1,17	0,03241	0,407	227844_at	Formin-like 3	*FMNL3*
1381	6,48	7,61	-1,17	0,00831	0,329	240257_at	Synaptojanin 2	*SYNJ2*
3852	18,1	21,3	-1,17	0,02814	0,399	212618_at	Zinc finger protein 609	*ZNF609*
178	6,04	7,09	-1,17	0,00082	0,244	1560410_at	Clone IMAGE:5241870, mRNA sequence	-
5334	6,88	8,07	-1,17	0,04176	0,428	216150_at	cDNA FLJ11547 fis, clone HEMBA1002934	-
2795	22,2	26,1	-1,17	0,01943	0,380	224064_s_at	Dehydrodolichyl diphosphate synthase	*DHDDS*
4340	47,5	55,7	-1,17	0,03233	0,407	228257_at	Ankyrin repeat domain 52	*ANKRD52*

Index	Mutated*	Normal*	FC	*P* value	FDR**	Probe set	Description	Gene symbol
2826	6,73	7,89	-1,17	0,01973	0,381	231232_at	Transcribed locus	-
5082	31,6	37,1	-1,17	0,03911	0,420	235181_at	Chromosome 2 open reading frame 60	*C2orf60*
31	4,09	4,79	-1,17	0,00014	0,201	219724_s_at	KIAA0748 protein	*KIAA0748*
3202	72,9	85,5	-1,17	0,02268	0,387	1554093_a_at	Small nuclear RNA activating complex, polypeptide 5, 19kDa	*SNAPC5*
1913	9,70	11,4	-1,17	0,01247	0,355	210100_s_at	ATP-binding cassette, sub-family A (ABC1), member 2	*ABCA2*
5444	25,0	29,3	-1,17	0,04294	0,431	1556340_at	Mitogen-activated protein kinase 12	*MAPK12*
6092	33,4	39,2	-1,17	0,04973	0,446	44065_at	Chromosome 12 open reading frame 52	*C12orf52*
5935	9,29	10,9	-1,17	0,04812	0,443	205881_at	Zinc finger protein 74	*ZNF74*
1391	12,1	14,2	-1,17	0,00841	0,330	240443_at	Transcribed locus	-
2694	109	127	-1,17	0,01848	0,375	232209_x_at	Histocompatibility (minor) 13	*HM13*
5972	21,5	25,2	-1,17	0,04849	0,444	213615_at	Membrane bound O-acyltransferase domain containing 5	*MBOAT5*
5118	119	139	-1,17	0,03940	0,421	212034_s_at	Exocyst complex component 7	*EXOC7*
3862	13,1	15,4	-1,17	0,02822	0,399	228522_at	Hypothetical protein LOC642031	*LOC642031*
417	22,0	25,8	-1,17	0,00219	0,286	209588_at	EPH receptor B2	*EPHB2*
2051	9,44	11,1	-1,17	0,01333	0,355	217349_s_at	LIM domain only 6	*LMO6*
4998	18,7	21,9	-1,17	0,03839	0,420	232106_s_at	Coiled-coil domain containing 123	*CCDC123*
237	548	642	-1,17	0,00110	0,250	208736_at	Actin related protein 2/3 complex, subunit 3, 21kDa	*ARPC3*
895	3,40	3,98	-1,17	0,00518	0,313	238361_s_at	Transcribed locus	-
4255	7,20	8,43	-1,17	0,03161	0,406	237611_at	Transcribed locus	-
5906	104	122	-1,17	0,04785	0,443	219162_s_at	Mitochondrial ribosomal protein L11	*MRPL11*
932	17,0	20,0	-1,17	0,00536	0,313	1568718_at	Chromosome 6 open reading frame 85	*C6orf85*
5511	14,0	16,4	-1,17	0,04366	0,433	216047_x_at	Seizure related 6 homolog (mouse)-like	*SEZ6L*
2473	6,19	7,25	-1,17	0,01662	0,367	208059_at	Chemokine (C-C motif) receptor 8	*CCR8*
496	6,15	7,20	-1,17	0,00265	0,289	1559754_at	Lymphotoxin beta (TNF superfamily, member 3)	*LTB*
1402	4,67	5,47	-1,17	0,00847	0,330	243220_at	Transcribed locus	-
2786	18,2	21,4	-1,17	0,01935	0,380	238627_at	Trafficking protein particle complex 2-like	*TRAPPC2L*
3264	104	121	-1,17	0,02317	0,388	223420_at	DnaJ (Hsp40) homolog, subfamily C, member 14	*DNAJC14*
460	9,63	11,3	-1,17	0,00245	0,288	231637_at	Transcribed locus	-
2184	6,47	7,58	-1,17	0,01447	0,361	244890_at	-	-
760	21,5	25,2	-1,17	0,00429	0,308	1553657_at	von Willebrand factor A domain containing 3A	*VWA3A*
4410	20,0	23,4	-1,17	0,03294	0,408	218933_at	Spermatogenesis associated 5-like 1	*SPATA5L1*
2287	18,9	22,1	-1,17	0,01520	0,363	1559870_at	Clone IMAGE:5225645, mRNA	-
1717	5,31	6,22	-1,17	0,01101	0,348	230572_at	Chromosome 4 open reading frame 38	*C4orf38*
5134	32,6	38,2	-1,17	0,03950	0,421	221846_s_at	CASK interacting protein 2	*CASKIN2*
3787	8,70	10,2	-1,17	0,02758	0,398	1556555_at	cDNA clone IMAGE:4825327	-
4004	95,5	112	-1,17	0,02930	0,400	212861_at	Major facilitator superfamily domain containing 5	*MFSD5*
2327	4,72	5,52	-1,17	0,01549	0,364	231095_at	cDNA FLJ42857 fis, clone BRHIP2009340	-
1954	115	134	-1,17	0,01276	0,355	221983_at	Family with sequence similarity 134, member A	*FAM134A*
3307	22,2	26,0	-1,17	0,02352	0,388	239368_at	Family with sequence similarity 111, member A	*FAM111A*
5535	12,0	14,0	-1,17	0,04394	0,434	215919_s_at	Mitochondrial ribosomal protein S11	*MRPS11*
4520	131	153	-1,17	0,03406	0,412	213604_at	Transcription elongation factor B (SIII), polypeptide 3	*TCEB3*
5081	38,7	45,2	-1,17	0,03910	0,420	225587_at	Transmembrane protein 129	*TMEM129*
4836	3,92	4,58	-1,17	0,03688	0,417	238977_at	Minichromosome maintenance complex component 6	*MCM6*
1128	9,05	10,6	-1,17	0,00659	0,319	237735_at	cDNA clone IMAGE:5296164	-
3271	20,4	23,8	-1,17	0,02326	0,388	227841_at	Cementum protein 1	*CEMP1*
5395	6,58	7,70	-1,17	0,04231	0,429	1554465_s_at	Zinc finger protein 673	*ZNF673*
2364	127	148	-1,17	0,01578	0,364	31837_at	Transmembrane protein 112B	*TMEM112B*
5528	65,5	76,6	-1,17	0,04384	0,434	203855_at	WD repeat domain 47	*WDR47*
5688	102	119	-1,17	0,04542	0,437	214263_x_at	Polymerase (RNA) II (DNA directed) polypeptide C, 33kDa	*POLR2C*
5268	10,4	12,1	-1,17	0,04091	0,425	229952_at	Similar to Spectrin, beta, non-erythrocytic 1 isoform 4	-
2796	9,32	10,9	-1,17	0,01943	0,380	228705_at	Calpain 12	*CAPN12*
4239	98,4	115	-1,17	0,03141	0,405	215293_s_at	FGF receptor activating protein 1	*FRAG1*
5492	3,85	4,50	-1,17	0,04347	0,433	1552897_a_at	Potassium voltage-gated channel, subfamily G, member 3	*KCNG3*
2772	19,3	22,6	-1,17	0,01924	0,379	235525_at	cDNA FLJ39926 fis, clone SPLEN2021157	-
2385	50,7	59,3	-1,17	0,01590	0,364	229164_s_at	Ankyrin repeat and BTB (POZ) domain containing 1	*ABTB1*
517	4,61	5,39	-1,17	0,00275	0,291	220447_at	Histamine receptor H3	*HRH3*
2650	7,19	8,41	-1,17	0,01807	0,373	233530_at	(clone 33) macronuclear mRNA	-

Index	Mutated*	Normal*	FC	*P* value	FDR**	Probe set	Description	Gene symbol
1711	24,0	28,0	-1,17	0,01095	0,348	1557450_s_at	Clone IMAGE:241447, mRNA sequence	-
4617	44,4	51,9	-1,17	0,03484	0,412	222732_at	Tripartite motif-containing 39	*TRIM39*
1050	10,6	12,4	-1,17	0,00614	0,319	234113_at	cDNA DKFZp313A1612	-
3422	50,8	59,4	-1,17	0,02447	0,391	218427_at	Serologically defined colon cancer antigen 3	*SDCCAG3*
3960	48,9	57,2	-1,17	0,02892	0,399	204300_at	PET112-like (yeast)	*PET112L*
5950	17,7	20,7	-1,17	0,04826	0,443	243731_at	Similar to Solute carrier family 27, member 5	-
2733	11,0	12,9	-1,17	0,01884	0,377	208544_at	Adrenergic, alpha-2B-, receptor	*ADRA2B*
493	13,8	16,1	-1,17	0,00264	0,289	205387_s_at	Chorionic gonadotropin, beta polypeptide	*CGB*
2108	4,48	5,23	-1,17	0,01383	0,358	1560021_at	cDNA FLJ37333 fis, clone BRAMY2020106	-
5273	582	679	-1,17	0,04098	0,425	200675_at	CD81 molecule	*CD81*
3193	444	518	-1,17	0,02262	0,387	223857_x_at	Transmembrane protein 85	*TMEM85*
1296	56,2	65,7	-1,17	0,00772	0,325	204189_at	Retinoic acid receptor, gamma	*RARG*
6101	7,39	8,63	-1,17	0,04981	0,446	230818_at	Transcribed locus	-
5595	3,62	4,22	-1,17	0,04461	0,436	214540_at	Histone cluster 1, H2bo	*HIST1H2BO*
5164	48,5	56,7	-1,17	0,03980	0,421	212170_at	RNA binding motif protein 12	*RBM12*
2143	62,5	73,0	-1,17	0,01411	0,360	221708_s_at	Unc-45 homolog A (C. elegans)	*UNC45A*
4880	15,9	18,6	-1,17	0,03732	0,418	237044_s_at	-	-
905	12,8	14,9	-1,17	0,00523	0,313	239785_at	DAZ interacting protein 1-like	*DZIP1L*
545	3,45	4,03	-1,17	0,00294	0,295	207874_s_at	Complement factor H-related 4	*CFHR4*
1530	29,2	34,1	-1,17	0,00947	0,337	1570197_at	Clone IMAGE:5111803, mRNA	-
3245	7,67	8,95	-1,17	0,02301	0,388	226570_at	ATPase, Na+/K+ transporting, beta 3 polypeptide	*ATP1B3*
1311	18,6	21,7	-1,17	0,00782	0,325	221981_s_at	WD repeat domain 59	*WDR59*
467	16,0	18,6	-1,17	0,00246	0,288	231723_at	Sorting nexin 12	*SNX12*
945	5,62	6,56	-1,17	0,00543	0,313	1558758_s_at	cDNA FLJ23791 fis, clone HEP21711	-
1010	24,7	28,8	-1,17	0,00586	0,316	1557105_a_at	cDNA DKFZp686P1116	-
3662	60,8	70,9	-1,17	0,02648	0,395	1552615_at	Acetyl-Coenzyme A carboxylase beta	*ACACB*
2914	3,78	4,41	-1,17	0,02047	0,383	233688_at	Kv channel interacting protein 3, calsenilin	*KCNIP3*
739	10,1	11,8	-1,17	0,00420	0,308	240763_at	Transcribed locus	-
1289	44,1	51,4	-1,17	0,00767	0,325	203677_s_at	TAR (HIV-1) RNA binding protein 2	*TARBP2*
998	6,74	7,86	-1,17	0,00576	0,316	243156_at	Transcribed locus	-
541	7,87	9,17	-1,17	0,00290	0,293	236998_at	Coiled-coil domain containing 56	*CCDC56*
3411	6,42	7,49	-1,17	0,02434	0,390	208087_s_at	Z-DNA binding protein 1	*ZBP1*
946	15,6	18,2	-1,17	0,00543	0,313	233694_at	Heat shock 70kDa protein 1-like	*HSPA1L*
299	5,70	6,64	-1,17	0,00145	0,263	230806_s_at	Family with sequence similarity 65, member A	*FAM65A*
453	8,54	9,95	-1,17	0,00243	0,288	220057_at	X antigen family, member 1D	*XAGE1D*
2997	14,9	17,4	-1,17	0,02111	0,385	235239_at	Quiescin Q6 sulfhydryl oxidase 2	*QSOX2*
3428	42,2	49,2	-1,17	0,02454	0,391	204691_x_at	Phospholipase A2, group VI (cytosolic, calcium-independent)	*PLA2G6*
1760	17,3	20,2	-1,17	0,01122	0,348	1554523_a_at	Cyclin M2	*CNNM2*
40	4,68	5,45	-1,17	0,00017	0,201	1557879_at	Coiled-coil domain containing 108	*CCDC108*
645	14,3	16,7	-1,17	0,00367	0,308	243266_at	Transcribed locus	-
1629	7,28	8,49	-1,17	0,01026	0,344	234133_s_at	Hypothetical protein LOC728543	*LOC728543*
891	17,5	20,4	-1,17	0,00515	0,313	219707_at	Copine VII	*CPNE7*
2461	21,0	24,5	-1,16	0,01652	0,367	219986_s_at	Acyl-Coenzyme A dehydrogenase family, member 10	*ACAD10*
5457	26,4	30,7	-1,16	0,04312	0,432	218141_at	Ubiquitin-conjugating enzyme E2O	*UBE2O*
5783	10,3	12,0	-1,16	0,04656	0,440	215660_s_at	Microtubule associated serine/threonine kinase 2	*MAST2*
613	6,71	7,81	-1,16	0,00346	0,308	217376_at	Similar to Signal-regulatory protein gamma precursor	*LOC441938*
5914	14,8	17,3	-1,16	0,04794	0,443	224406_s_at	Fc receptor-like 5	*FCRL5*
901	69,2	80,6	-1,16	0,00522	0,313	218083_at	Prostaglandin E synthase 2	*PTGES2*
3231	6,33	7,37	-1,16	0,02291	0,388	215087_at	Chromosome 15 open reading frame 39	*C15orf39*
255	7,50	8,73	-1,16	0,00119	0,254	232430_at	Hypothetical LOC148696	*LOC148696*
3337	45,3	52,7	-1,16	0,02368	0,388	212035_s_at	Exocyst complex component 7	*EXOC7*
2789	370	430	-1,16	0,01939	0,380	200098_s_at	Anaphase promoting complex subunit 5	*ANAPC5*
608	19,3	22,4	-1,16	0,00340	0,306	1567166_at	-	-
1595	5,42	6,30	-1,16	0,00992	0,340	210746_s_at	Erythrocyte membrane protein band 4.2	*EPB42*
1251	15,7	18,3	-1,16	0,00744	0,325	207366_at	Potassium voltage-gated channel subfamily S member 1	*KCNS1*
4576	99,3	115	-1,16	0,03459	0,412	203694_s_at	DEAH (Asp-Glu-Ala-His) box polypeptide 16	*DHX16*
2151	6,43	7,49	-1,16	0,01417	0,360	1565254_s_at	Elongation factor RNA polymerase II	*ELL*

Index	Mutated*	Normal*	FC	*P* value	FDR**	Probe set	Description	Gene symbol
1699	9,19	10,7	-1,16	0,01082	0,348	222080_s_at	cDNA clone IMAGE:4865340	-
2487	3,57	4,15	-1,16	0,01677	0,367	208382_s_at	DMC1 dosage suppressor of mck1 homolog	*DMC1*
1405	5,63	6,55	-1,16	0,00849	0,330	238023_at	-	-
3152	12,3	14,4	-1,16	0,02237	0,387	220805_at	Histamine receptor H2	*HRH2*
4678	6,72	7,82	-1,16	0,03532	0,413	207495_at	RAB28, member RAS oncogene family	*RAB28*
1942	3,04	3,54	-1,16	0,01266	0,355	214586_at	G protein-coupled receptor 37 (endothelin receptor type B-like)	*GPR37*
5552	17,7	20,6	-1,16	0,04418	0,435	1555083_at	Ribosomal protein L13A pseudogene	*MGC34774*
3318	60,0	69,8	-1,16	0,02358	0,388	225620_at	RAB35, member RAS oncogene family	*RAB35*
14	3,64	4,23	-1,16	0,00005	0,191	1553447_at	ATP/GTP binding protein-like 1	*AGBL1*
5363	3,79	4,41	-1,16	0,04208	0,429	244313_at	Complement component (3b/4b) receptor 1 (Knops blood group)	*CR1*
5287	116	135	-1,16	0,04113	0,425	218089_at	Chromosome 20 open reading frame 4	*C20orf4*
2400	35,4	41,1	-1,16	0,01600	0,365	202099_s_at	DiGeorge syndrome critical region gene 2	*DGCR2*
1137	5,46	6,35	-1,16	0,00664	0,319	1553044_at	Connexin 62	*CX62*
3811	36,3	42,2	-1,16	0,02777	0,398	221250_s_at	MAX dimerization protein 3	*MXD3*
195	6,87	7,99	-1,16	0,00090	0,244	220645_at	Family with sequence similarity 55, member D	*FAM55D*
2872	11,6	13,5	-1,16	0,02018	0,383	214340_at	Arachidonate 12-lipoxygenase pseudogene 2	*ALOX12P2*
342	15,6	18,1	-1,16	0,00174	0,277	227832_at	Methyl-CpG binding domain protein 6	*MBD6*
5372	6,80	7,90	-1,16	0,04216	0,429	244294_at	cDNA FLJ26260 fis, clone DMC05193	-
374	6,54	7,60	-1,16	0,00196	0,284	216825_s_at	Myeloproliferative leukemia virus oncogene	*MPL*
3226	5,40	6,27	-1,16	0,02286	0,387	238945_at	-	-
4726	24,6	28,6	-1,16	0,03576	0,414	202385_s_at	Treacher Collins-Franceschetti syndrome 1	*TCOF1*
4125	30,1	35,0	-1,16	0,03034	0,402	236667_at	Transmembrane protein 120B	*TMEM120B*
536	6,29	7,31	-1,16	0,00286	0,292	230325_at	cDNA clone IMAGE:4393471	-
2004	5,48	6,37	-1,16	0,01308	0,355	1557196_a_at	cDNA DKFZp547B198	-
1074	7,69	8,92	-1,16	0,00630	0,319	207260_at	FEV (ETS oncogene family)	*FEV*
2875	9,86	11,5	-1,16	0,02019	0,383	231958_at	Chromosome 3 open reading frame 31	*C3orf31*
4574	16,0	18,6	-1,16	0,03457	0,412	1558529_s_at	Clone IMAGE:4778855, mRNA	-
5793	11,3	13,1	-1,16	0,04672	0,441	204465_s_at	Internexin neuronal Intermediate filament protein, alpha	*INA*
2700	17,3	20,1	-1,16	0,01852	0,375	211521_s_at	Pleckstrin homology, Sec7 and coiled-coil domains 4	*PSCD4*
4582	7,79	9,04	-1,16	0,03461	0,412	209697_at	Protein phosphatase 2B, catalytic subunit, gamma isoform	*PPP3CC*
3975	11,3	13,1	-1,16	0,02906	0,400	235939_at	cDNA FLJ36815 fis, clone ASTRO2003740	-
6075	13,3	15,4	-1,16	0,04959	0,446	213200_at	Synaptophysin	*SYP*
2869	6,34	7,36	-1,16	0,02014	0,383	236257_at	CD2-associated protein	*CD2AP*
3336	4,35	5,04	-1,16	0,02367	0,388	242183_at	cDNA FLJ38849 fis, clone MESAN2008936	-
4421	9,37	10,9	-1,16	0,03310	0,409	213078_x_at	1-acylglycerol-3-phosphate O-acyltransferase 7 (lysophosphatidic acid acyltra	*AGPAT7*
1355	7,95	9,22	-1,16	0,00814	0,328	216409_at	Acyl-CoA synthetase long-chain family member 6	*ACSL6*
954	5,47	6,34	-1,16	0,00549	0,314	1560255_at	Chromosome 10 open reading frame 31	*C10orf31*
5922	4,99	5,79	-1,16	0,04799	0,443	205955_at	-	-
5522	9,97	11,6	-1,16	0,04381	0,433	241671_x_at	Hypothetical locus LOC401237	*FLJ22536*
903	3,62	4,20	-1,16	0,00523	0,313	207433_at	Interleukin 10	*IL10*
2846	12,3	14,2	-1,16	0,01992	0,383	1554332_a_at	mRNA similar to LOC149651	-
4529	314	364	-1,16	0,03419	0,412	203462_x_at	Eukaryotic translation initiation factor 3, subunit B	*EIF3B*
1552	14,7	17,0	-1,16	0,00957	0,337	231189_at	Hypothetical protein MGC40574	*MGC40574*
4649	21,0	24,3	-1,16	0,03508	0,413	234465_at	Essential meiotic endonuclease 1 homolog 1 (S. pombe)	*EME1*
2248	9,12	10,6	-1,16	0,01494	0,363	210039_s_at	Protein kinase C, theta	*PRKCQ*
5192	10,2	11,8	-1,16	0,04001	0,421	214300_s_at	Topoisomerase (DNA) III alpha	*TOP3A*
2279	7,85	9,10	-1,16	0,01515	0,363	231664_at	Solute carrier family 25, member 29	*SLC25A29*
4234	48,5	56,2	-1,16	0,03139	0,405	218758_s_at	Ribosomal RNA processing 1 homolog (S. cerevisiae)	*RRP1*
3134	26,1	30,2	-1,16	0,02222	0,387	211133_x_at	Leukocyte immunoglobulin-like receptor, subfamily B member 3	*LILRB3*
3780	14,2	16,4	-1,16	0,02752	0,398	239933_x_at	-	-
35	4,89	5,66	-1,16	0,00015	0,201	1563743_at	Chromosome 1 open reading frame 180	*C1orf180*
1617	6,95	8,06	-1,16	0,01014	0,343	206119_at	Betaine-homocysteine methyltransferase	*BHMT*
951	8,71	10,1	-1,16	0,00545	0,314	227867_at	Hypothetical protein LOC129293	*LOC129293*
5052	9,96	11,5	-1,16	0,03892	0,420	224088_at	Neuromedin U receptor 2	*NMUR2*
4972	33,1	38,3	-1,16	0,03816	0,419	205333_s_at	RCE1 homolog, prenyl protein peptidase (S. cerevisiae)	*RCE1*
4706	29,8	34,5	-1,16	0,03558	0,413	226369_at	Hypothetical locus LOC338799	*LOC338799*
2092	4,28	4,96	-1,16	0,01367	0,357	1554086_at	Tubulin, gamma complex associated protein 3	*TUBGCP3*

Index	Mutated*	Normal*	FC	*P* value	FDR**	Probe set	Description	Gene symbol
3224	6,48	7,51	-1,16	0,02284	0,387	207600_at	Potassium voltage-gated channel subfamily C member 3	*KCNC3*
632	5,88	6,81	-1,16	0,00357	0,308	207064_s_at	Amine oxidase, copper containing 2 (retina-specific)	*AOC2*
2113	5,37	6,22	-1,16	0,01385	0,358	228022_at	Coiled-coil domain containing 18	*CCDC18*
2332	9,35	10,8	-1,16	0,01556	0,364	1557729_at	G protein-coupled receptor kinase 5	*GRK5*
1678	14,6	16,9	-1,16	0,01059	0,345	238473_at	cDNA clone IMAGE:4432160	-
1164	17,0	19,7	-1,16	0,00685	0,321	240607_at	Myocardial infarction associated transcript	*MIAT*
1014	18,6	21,6	-1,16	0,00587	0,316	238789_at	Ankyrin repeat domain 15	*ANKRD15*
5665	21,5	24,9	-1,16	0,04520	0,436	218855_at	G protein-coupled receptor 175	*GPR175*
1441	3,89	4,50	-1,16	0,00876	0,332	1562458_at	Ubiquitin-conjugating enzyme E2W	*UBE2W*
2600	6,70	7,75	-1,16	0,01766	0,371	242437_at	Similar to XP_529777.1	-
269	7,07	8,19	-1,16	0,00128	0,260	242757_at	MAM domain containing glycosylphosphatidylinositol anchor 1	*MDGA1*
1762	4,89	5,66	-1,16	0,01123	0,348	206341_at	Interleukin 2 receptor, alpha	*IL2RA*
5872	3,52	4,08	-1,16	0,04744	0,442	243689_s_at	Chromosome 20 open reading frame 80	*C20orf80*
845	5,01	5,80	-1,16	0,00485	0,313	210451_at	Pyruvate kinase, liver and RBC	*PKLR*
2133	12,5	14,5	-1,16	0,01402	0,359	205944_s_at	Clathrin, heavy chain-like 1	*CLTCL1*
5696	10,7	12,3	-1,16	0,04559	0,438	230936_at	DnaJ (Hsp40) related, subfamily B, member 13	*DNAJB13*
1665	13,5	15,6	-1,16	0,01053	0,345	232550_at	Abhydrolase domain containing 1	*ABHD1*
2043	52,9	61,2	-1,16	0,01329	0,355	34225_at	Wolf-Hirschhorn syndrome candidate 2	*WHSC2*
4947	316	365	-1,16	0,03797	0,419	208688_x_at	Eukaryotic translation initiation factor 3, subunit B	*EIF3B*
446	19,5	22,6	-1,16	0,00238	0,288	1555215_a_at	Histamine receptor H3	*HRH3*
329	8,12	9,39	-1,16	0,00164	0,272	234698_at	N-6 adenine-specific DNA methyltransferase 1 (putative)	*N6AMT1*
4367	51,3	59,3	-1,16	0,03248	0,407	201945_at	Furin (paired basic amino acid cleaving enzyme)	*FURIN*
1195	64,4	74,5	-1,16	0,00705	0,323	1552749_a_at	Kinesin light chain 3	*KLC3*
5012	7,39	8,55	-1,16	0,03852	0,420	207440_at	Solute carrier family 35, member A2	*SLC35A2*
4914	15,6	18,1	-1,16	0,03762	0,418	232134_at	cDNA FLJ11652 fis, clone HEMBA1004461	-
531	21,7	25,0	-1,16	0,00284	0,292	237630_s_at	Clone PP1195 unknown mRNA	-
1695	7,06	8,17	-1,16	0,01077	0,347	214558_at	G protein-coupled receptor 12	*GPR12*
3142	60,2	69,6	-1,16	0,02229	0,387	209490_s_at	Palmitoyl-protein thioesterase 2	*PPT2*
5510	146	168	-1,16	0,04366	0,433	211630_s_at	Glutathione synthetase	*GSS*
4737	21,7	25,1	-1,16	0,03585	0,414	1563318_s_at	MAGI family member, X-linked	*MAGIX*
4944	10,2	11,8	-1,16	0,03793	0,419	208352_x_at	Ankyrin 1, erythrocytic	*ANK1*
5231	13,3	15,4	-1,16	0,04047	0,423	205813_s_at	Methionine adenosyltransferase I, alpha	*MAT1A*
2110	5,89	6,81	-1,16	0,01384	0,358	1553789_a_at	Chromosome 21 open reading frame 58	*C21orf58*
724	4,85	5,60	-1,16	0,00414	0,308	232139_s_at	KIAA1919 protein	*KIAA1919*
4413	13,9	16,1	-1,16	0,03300	0,409	232274_at	Cyclin L2	*CCNL2*
2430	6,98	8,07	-1,16	0,01625	0,365	239800_at	Transcribed locus	-
366	13,9	16,1	-1,16	0,00191	0,284	231306_at	Lysozyme-like 4	*LYZL4*
4093	6,02	6,96	-1,16	0,03009	0,402	236242_at	-	-
2568	12,7	14,7	-1,16	0,01742	0,371	223563_at	Guanine nucleotide binding protein (G protein), beta polypeptide 1-like	*GNB1L*
1400	5,01	5,79	-1,16	0,00846	0,330	240620_at	Transcribed locus	-
4888	9,31	10,8	-1,16	0,03737	0,418	236132_at	-	-
4145	19,8	22,9	-1,16	0,03059	0,403	1556797_at	Hypothetical protein LOC386597	*LOC386597*
3031	16,0	18,5	-1,15	0,02136	0,385	236073_at	EPH receptor A10	*EPHA10*
153	7,77	8,97	-1,15	0,00070	0,244	241087_at	-	-
2144	7,56	8,73	-1,15	0,01412	0,360	204330_s_at	Mitochondrial ribosomal protein S12	*MRPS12*
4857	22,5	26,0	-1,15	0,03704	0,417	206827_s_at	Transient receptor potential cation channel subfamily V member 6	*TRPV6*
1459	7,09	8,19	-1,15	0,00891	0,334	228388_at	Nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, b	*NFKBIB*
1193	13,6	15,7	-1,15	0,00703	0,322	208128_x_at	Kinesin family member 25	*KIF25*
5235	12,3	14,2	-1,15	0,04051	0,423	209767_s_at	Glycoprotein Ib (platelet), beta polypeptide	*GP1BB*
3970	8,35	9,64	-1,15	0,02900	0,399	204696_s_at	Cell division cycle 25 homolog A (S. pombe)	*CDC25A*
3285	8,08	9,33	-1,15	0,02341	0,388	1554646_at	Oxysterol binding protein-like 1A	*OSBPL1A*
733	8,61	9,94	-1,15	0,00419	0,308	233196_at	cDNA FLJ11777 fis, clone HEMBA1005909	-
5402	117	135	-1,15	0,04238	0,429	213203_at	Small nuclear RNA activating complex, polypeptide 5, 19kDa	*SNAPC5*
3124	4,31	4,98	-1,15	0,02214	0,387	215056_at	Clone 23695 mRNA sequence	-
3923	4,11	4,75	-1,15	0,02868	0,399	1569315_s_at	Hypothetical protein FLJ44451	*FLJ44451*
3303	12,3	14,2	-1,15	0,02351	0,388	213870_at	Collagen, type XI, alpha 2	*COL11A2*
5333	13,3	15,4	-1,15	0,04175	0,428	230439_at	Hypothetical gene supported by BC031661	*LOC389458*

Index	Mutated*	Normal*	FC	*P* value	FDR**	Probe set	Description	Gene symbol
5217	50,1	57,8	-1,15	0,04031	0,422	203412_at	Leucine-zipper-like transcription regulator 1	*LZTR1*
3573	59,0	68,1	-1,15	0,02580	0,394	226428_at	Transportin 2 (importin 3, karyopherin beta 2b)	*TNPO2*
4667	24,2	27,9	-1,15	0,03524	0,413	227060_at	RELT tumor necrosis factor receptor	*RELT*
2678	9,52	11,0	-1,15	0,01832	0,374	233138_at	Chromosome 18 open reading frame 1	*C18orf1*
770	6,49	7,49	-1,15	0,00442	0,311	215511_at	Transcription factor 20	*TCF20*
2355	20,5	23,7	-1,15	0,01572	0,364	208242_at	Retina and anterior neural fold homeobox	*RAX*
253	5,04	5,82	-1,15	0,00117	0,254	208553_at	Histone cluster 1, H1e	*HIST1H1E*
1039	15,9	18,3	-1,15	0,00604	0,318	211231_x_at	Cytochrome P450, family 4, subfamily A, polypeptide 11	*CYP4A11*
259	7,38	8,52	-1,15	0,00122	0,257	232708_at	Galactose-1-phosphate uridylyltransferase	*GALT*
94	7,50	8,65	-1,15	0,00035	0,206	237726_at	Transcribed locus	-
1716	7,82	9,02	-1,15	0,01100	0,348	236482_at	Transmembrane channel-like 6	*TMC6*
1167	7,75	8,94	-1,15	0,00687	0,321	1565879_at	Full length insert cDNA clone YQ73D03	-
5124	30,7	35,4	-1,15	0,03944	0,421	226514_at	Zinc finger protein 71	*ZNF71*
13	4,13	4,76	-1,15	0,00005	0,191	241819_at	Tumor necrosis factor (ligand) superfamily, member 8	*TNFSF8*
1621	6,29	7,26	-1,15	0,01018	0,343	238416_x_at	Conserved nuclear protein NHN1	*NHN1*
2034	11,9	13,8	-1,15	0,01324	0,355	204095_s_at	Elongation factor RNA polymerase II	*ELL*
1613	5,37	6,19	-1,15	0,01011	0,343	1552833_at	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 6	*B3GNT6*
4601	13,7	15,8	-1,15	0,03480	0,412	219883_at	Potassium channel, subfamily K, member 4	*KCNK4*
1861	16,8	19,3	-1,15	0,01201	0,353	1555998_at	ATP synthase D chain, mitochondrial	*ATP5H*
240	5,81	6,69	-1,15	0,00111	0,250	236061_at	PR domain containing 15	*PRDM15*
114	3,63	4,19	-1,15	0,00051	0,240	241085_at	Similar to Adrenergic, alpha-1A-, receptor	-
39	9,63	11,1	-1,15	0,00016	0,201	236392_at	p53-associated parkin-like cytoplasmic protein	*PARC*
3545	13,9	16,0	-1,15	0,02550	0,393	205950_s_at	Carbonic anhydrase I	*CA1*
5839	11,9	13,7	-1,15	0,04718	0,442	209334_s_at	Proteasome (prosome, macropain) 26S subunit, non-ATPase, 9	*PSMD9*
5481	183	211	-1,15	0,04338	0,433	201342_at	Small nuclear ribonucleoprotein polypeptide C	*SNRPC*
322	4,97	5,73	-1,15	0,00161	0,272	1561916_at	GA binding protein transcription factor, alpha subunit pseudogene	*GABPAP*
3184	8,38	9,67	-1,15	0,02257	0,387	228800_x_at	Aurora kinase A interacting protein 1	*AURKAIP1*
816	25,7	29,6	-1,15	0,00466	0,312	1555478_at	Chromosome 17 open reading frame 82	*C17orf82*
2712	7,07	8,15	-1,15	0,01861	0,375	205468_s_at	Interferon regulatory factor 5	*IRF5*
5717	59,9	69,0	-1,15	0,04578	0,438	227951_s_at	Family with sequence similarity 98, member C	*FAM98C*
1063	6,88	7,93	-1,15	0,00624	0,319	223929_s_at	-	-
920	6,68	7,69	-1,15	0,00530	0,313	232590_at	cDNA FLJ33454 fis, clone BRAMY2000231	-
852	13,1	15,1	-1,15	0,00490	0,313	231151_at	Discs, large (Drosophila) homolog-associated protein 3	*DLGAP3*
232	7,56	8,70	-1,15	0,00108	0,250	211848_s_at	Carcinoembryonic antigen-related cell adhesion molecule 7	*CEACAM7*
5983	6,03	6,94	-1,15	0,04859	0,444	1555953_at	Collagen, type XVIII, alpha 1	*COL18A1*
4137	18,8	21,6	-1,15	0,03049	0,403	219620_x_at	Chromosome 9 open reading frame 167	*C9orf167*
2841	11,3	13,0	-1,15	0,01984	0,382	241825_at	Chromosome 2 open reading frame 60	*C2orf60*
4825	376	433	-1,15	0,03670	0,416	200055_at	Transcription initiation factor TFIID 30 kD subunit	*TAF10*
340	30,6	35,3	-1,15	0,00173	0,277	239607_at	G protein-coupled receptor 156	*GPR156*
1145	14,7	16,9	-1,15	0,00671	0,321	207685_at	Crystallin, beta B3	*CRYBB3*
735	7,99	9,20	-1,15	0,00419	0,308	220971_at	Interleukin 25	*IL25*
470	10,7	12,3	-1,15	0,00251	0,289	1552652_at	Hermansky-Pudlak syndrome 4	*HPS4*
2451	20,4	23,5	-1,15	0,01641	0,366	204371_s_at	KH-type splicing regulatory protein (FUSE binding protein 2)	*KHSRP*
3498	7,70	8,87	-1,15	0,02514	0,392	211211_x_at	SH2 domain protein 1A, Duncan's disease	*SH2D1A*
3597	19,9	22,9	-1,15	0,02595	0,394	207188_at	Cyclin-dependent kinase 3	*CDK3*
834	7,30	8,41	-1,15	0,00476	0,312	240818_at	Similar to Ovochymase 1	-
3381	16,7	19,2	-1,15	0,02406	0,389	217058_at	GNAS complex locus	*GNAS*
1841	8,35	9,61	-1,15	0,01183	0,351	208602_x_at	CD6 molecule	*CD6*
2210	19,1	21,9	-1,15	0,01464	0,362	230756_at	Zinc finger protein 683	*ZNF683*
3291	9,44	10,9	-1,15	0,02344	0,388	211469_s_at	Chemokine (C-X-C motif) receptor 6	*CXCR6*
3334	7,81	8,99	-1,15	0,02366	0,388	223600_s_at	KIAA1683 protein	*KIAA1683*
1724	14,5	16,6	-1,15	0,01104	0,348	227743_at	Myosin XVB pseudogene	*MYO15B*
1276	12,2	14,0	-1,15	0,00759	0,325	241166_at	Transcribed locus	-
3646	56,2	64,7	-1,15	0,02634	0,395	239053_at	Cytosolic iron-sulfur protein assembly 1 homolog (S. cerevisiae)	*CIAO1*
2231	8,12	9,34	-1,15	0,01482	0,363	224273_at	Chromosome 3 open reading frame 20	*C3orf20*
4120	30,0	34,6	-1,15	0,03028	0,402	219019_at	-	-
2523	3,41	3,92	-1,15	0,01702	0,369	232026_at	Hect domain and RLD 4	*HERC4*

Index	Mutated*	Normal*	FC	*P* value	FDR**	Probe set	Description	Gene symbol
5279	18,0	20,7	-1,15	0,04105	0,425	224466_s_at	Basic leucine zipper transcription factor MafG	*MAFG*
4990	8,96	10,3	-1,15	0,03830	0,419	216014_s_at	Zinc finger, X-linked, duplicated A	*ZXDA*
3360	5,58	6,42	-1,15	0,02384	0,388	1557567_a_at	Hypothetical protein LOC148987	*LOC148987*
815	10,7	12,3	-1,15	0,00466	0,312	1566821_at	cDNA FLJ32664 fis, clone TESTI1000088	-
1776	30,1	34,6	-1,15	0,01130	0,348	1554170_a_at	Similar to Hypothetical protein MGC49416	*LOC255374*
1438	8,82	10,1	-1,15	0,00871	0,331	221454_at	BCL2-related ovarian killer	*BOK*
3327	9,00	10,3	-1,15	0,02363	0,388	203806_s_at	Fanconi anemia, complementation group A	*FANCA*
3675	7,83	9,00	-1,15	0,02656	0,395	239248_at	(clone 33) macronuclear mRNA	-
1384	9,38	10,8	-1,15	0,00833	0,329	238655_at	Acyl-Coenzyme A dehydrogenase family, member 10	*ACAD10*
129	6,19	7,12	-1,15	0,00058	0,240	235624_at	High density lipoprotein binding protein (vigilin)	*HDLBP*
862	30,0	34,4	-1,15	0,00497	0,313	204046_at	Phospholipase C, beta 2	*PLCB2*
5820	5,66	6,51	-1,15	0,04703	0,442	229992_at	Hypothetical LOC149837	*LOC149837*
5452	10,5	12,1	-1,15	0,04301	0,431	1556422_at	cDNA FLJ33357 fis, clone BRACE2005189	-
3168	15,6	17,9	-1,15	0,02248	0,387	208594_x_at	Leukocyte immunoglobulin-like receptor subfamily A member 6	*LILRA6*
3895	8,94	10,3	-1,15	0,02846	0,399	215491_at	Myc-related gene from lung cancer	*MYCL1*
702	18,7	21,5	-1,15	0,00403	0,308	208397_x_at	Potassium inwardly-rectifying channel, subfamily J, member 5	*KCNJ5*
4027	16,8	19,3	-1,15	0,02951	0,400	214339_s_at	Mitogen-activated protein kinase kinase kinase kinase 1	*MAP4K1*
5163	16,8	19,4	-1,15	0,03978	0,421	204856_at	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 3	*B3GNT3*
1497	39,3	45,2	-1,15	0,00921	0,336	1554442_at	Bestrophin 1	*BEST1*
1019	15,8	18,2	-1,15	0,00590	0,316	221162_at	HERV-H LTR-associating 1	*HHLA1*
2968	23,3	26,8	-1,15	0,02085	0,384	218964_at	AT rich interactive domain 3B (BRIGHT-like)	*ARID3B*
1872	6,31	7,25	-1,15	0,01210	0,353	238822_at	Transcribed locus	-
2075	6,34	7,28	-1,15	0,01356	0,356	209999_x_at	Suppressor of cytokine signaling 1	*SOCS1*
2353	5,43	6,24	-1,15	0,01569	0,364	216914_at	Cell division cycle 25 homolog C (S. pombe)	*CDC25C*
4683	3,67	4,22	-1,15	0,03535	0,413	1569736_at	cDNA clone IMAGE:5264099	-
3423	10,5	12,0	-1,15	0,02447	0,391	211165_x_at	EPH receptor B2	*EPHB2*
1306	7,52	8,64	-1,15	0,00778	0,325	240784_at	Chromosome 7 open reading frame 52	*C7orf52*
5813	27,4	31,5	-1,15	0,04696	0,442	226530_at	BCL2 modifying factor	*BMF*
328	10,9	12,5	-1,15	0,00163	0,272	240664_at	Transcribed locus	-
4182	6,94	7,97	-1,15	0,03091	0,404	228626_at	Transcribed locus	-
5010	1959	2249	-1,15	0,03848	0,420	201090_x_at	Tubulin, alpha 1b	*TUBA1B*
1578	17,4	20,0	-1,15	0,00981	0,340	231378_at	Similar to XP_001095369.1	-
3395	13,7	15,7	-1,15	0,02419	0,390	235483_at	cDNA FLJ30906 fis, clone FEBRA2006055	-
1647	4,54	5,21	-1,15	0,01037	0,344	238872_at	cDNA FLJ43312 fis, clone NT2RI2012659	-
4408	12,1	13,9	-1,15	0,03290	0,408	244808_at	GRAM domain containing 1A	*GRAMD1A*
477	12,3	14,2	-1,15	0,00256	0,289	235135_at	Transcription initiation factor TFIID 30 kD subunit	*TAF10*
3678	3,32	3,82	-1,15	0,02658	0,395	215767_at	Zinc finger protein 804A	*ZNF804A*
1286	5,17	5,93	-1,15	0,00765	0,325	1564822_at	cDNA DKFZp434J2111	-
2194	3,93	4,51	-1,15	0,01452	0,361	220545_s_at	Testis-specific kinase substrate	*TSKS*
3764	3767	4324	-1,15	0,02736	0,397	212788_x_at	Ferritin, light polypeptide	*FTL*
276	4,98	5,71	-1,15	0,00133	0,263	210472_at	Metallothionein 1G	*MT1G*
1926	20,6	23,6	-1,15	0,01253	0,355	211222_s_at	huntingtin-associated protein 1 (neuroan 1)	*HAP1*
1312	5,96	6,83	-1,15	0,00782	0,325	238442_at	Hexamethylene bis-acetamide inducible 1	*HEXIM1*
2771	9,07	10,4	-1,15	0,01923	0,379	207096_at	Serum amyloid A4, constitutive	*SAA4*
4823	6,88	7,89	-1,15	0,03668	0,416	214556_at	Somatostatin receptor 4	*SSTR4*
5691	32,3	37,0	-1,15	0,04552	0,437	215903_s_at	Microtubule associated serine/threonine kinase 2	*MAST2*
5471	6,66	7,65	-1,15	0,04325	0,432	206804_at	CD3g molecule, gamma (CD3-TCR complex)	*CD3G*
858	4,43	5,08	-1,15	0,00496	0,313	1569681_at	cDNA clone IMAGE:5209417	-
135	5,54	6,35	-1,15	0,00060	0,244	1555339_at	RAP1A, member of RAS oncogene family	*RAP1A*
1116	21,7	24,9	-1,15	0,00653	0,319	37796_at	Leucine rich repeat neuronal 4	*LRCH4*
3548	5,31	6,10	-1,15	0,02552	0,393	214245_at	Ribosomal protein S14	*RPS14*
1315	9,12	10,5	-1,15	0,00783	0,325	237188_x_at	Sperm associated antigen 4-like	*SPAG4L*
5106	6,66	7,63	-1,15	0,03929	0,421	1570007_at	Leucine rich repeat containing 8 family, member C	*LRRC8C*
64	5,29	6,07	-1,15	0,00025	0,201	1561705_at	cDNA clone IMAGE:5272626	-
1955	4,48	5,13	-1,15	0,01277	0,355	207008_at	Interleukin 8 receptor, beta	*IL8RB*
3374	5,79	6,64	-1,15	0,02402	0,389	222944_s_at	MAGI family member, X-linked	*MAGIX*
1753	7,82	8,96	-1,15	0,01118	0,348	220560_at	Chromosome 11 open reading frame 21	*C11orf21*

Index	Mutated*	Normal*	FC	*P* value	FDR**	Probe set	Description	Gene symbol
4878	4,63	5,31	-1,15	0,03724	0,417	1560058_at	Hypothetical gene supported by AK093779	*LOC399900*
976	11,4	13,1	-1,15	0,00567	0,315	204311_at	ATPase, Na+/K+ transporting, beta 2 polypeptide	*ATP1B2*
602	7,41	8,49	-1,15	0,00335	0,303	204551_s_at	Alpha-2-HS-glycoprotein	*AHSG*
3149	201	231	-1,15	0,02235	0,387	213153_at	SET domain containing 1B	*SETD1B*
2387	37,8	43,3	-1,15	0,01591	0,364	1556748_x_at	cDNA FLJ39784 fis, clone SPLEN2002314	-
2375	11,9	13,6	-1,15	0,01584	0,364	231619_at	Transcribed locus	-
774	6,48	7,43	-1,15	0,00443	0,311	208321_s_at	Calcium binding protein 1	*CABP1*
2571	6,82	7,82	-1,15	0,01743	0,371	240358_at	Transcribed locus	-
4473	5,03	5,76	-1,15	0,03362	0,411	236213_at	Similar to Proteasome 26S subunit, non-ATPase, 14	-
2724	5,00	5,72	-1,15	0,01871	0,376	1556471_at	Sex comb on midleg-like 4 (Drosophila)	*SCML4*
1539	12,1	13,9	-1,15	0,00953	0,337	1569426_at	cDNA clone IMAGE:4822128	-
881	4,20	4,82	-1,15	0,00510	0,313	243396_at	Transcribed locus	-
4758	455	522	-1,15	0,03608	0,414	62987_r_at	Calcium channel, voltage-dependent, gamma subunit 4	*CACNG4*
437	4,48	5,14	-1,15	0,00231	0,288	221084_at	5-hydroxytryptamine (serotonin) receptor 3B	*HTR3B*
1587	5,44	6,23	-1,15	0,00987	0,340	234362_s_at	Cytotoxic T-lymphocyte-associated protein 4	*CTLA4*
3603	7,26	8,32	-1,15	0,02599	0,394	241314_at	Transcribed locus	-
3651	21,9	25,1	-1,15	0,02639	0,395	206220_s_at	RAS p21 protein activator 3	*RASA3*
2175	4,58	5,24	-1,15	0,01439	0,361	237513_at	Trypsin X3	*TRY1*
3639	24,1	27,6	-1,15	0,02633	0,395	226798_at	BCL2-like 13 (apoptosis facilitator)	*BCL2L13*
941	11,8	13,5	-1,15	0,00538	0,313	217184_s_at	Leukocyte tyrosine kinase	*LTK*
1888	42,6	48,8	-1,15	0,01225	0,355	1556042_s_at	Hypothetical locus LOC338799	*LOC338799*
1933	6,74	7,72	-1,15	0,01261	0,355	224547_at	Surfactant protein B-binding protein	-
110	3,31	3,79	-1,15	0,00044	0,221	216277_at	BUB1 budding uninhibited by benzimidazoles 1 homolog (yeast)	*BUB1*
3419	7,22	8,27	-1,15	0,02443	0,391	222930_s_at	Agmatine ureohydrolase (agmatinase)	*AGMAT*
1162	7,46	8,55	-1,15	0,00685	0,321	1561446_at	cDNA clone IMAGE:4829179	-
4651	8,27	9,48	-1,15	0,03510	0,413	207087_x_at	Ankyrin 1, erythrocytic	*ANK1*
2185	10,0	11,5	-1,15	0,01448	0,361	229562_at	Ribosomal protein L10a	*RPL10A*
1480	11,7	13,4	-1,15	0,00907	0,335	232933_at	KIAA1656 protein	*KIAA1656*
3110	18,6	21,3	-1,14	0,02197	0,386	221578_at	RAS association (RalGDS/AF-6) domain family 4	*RASSF4*
3201	19,5	22,4	-1,14	0,02266	0,387	220510_at	Rh family, B glycoprotein	*RHBG*
2834	6,81	7,79	-1,14	0,01979	0,382	236876_at	H1 histone family, member N, testis-specific	*H1FNT*
1410	7,52	8,61	-1,14	0,00852	0,330	1556962_at	cDNA FLJ90125 fis, clone HEMBA1007291	-
1369	8,28	9,48	-1,14	0,00823	0,328	232223_at	Clone 24863 mRNA sequence	-
1099	8,61	9,86	-1,14	0,00644	0,319	1560472_at	Hypothetical protein LOC338588	*LOC338588*
4451	5,88	6,73	-1,14	0,03343	0,411	234894_at	Inter-alpha (globulin) inhibitor H5-like	*ITIH5L*
5745	58,3	66,7	-1,14	0,04609	0,439	219538_at	WD repeat domain 5B	*WDR5B*
2078	4,58	5,24	-1,14	0,01357	0,356	233731_at	cDNA DKFZp564D123	-
4032	11,6	13,3	-1,14	0,02954	0,401	229452_at	Transmembrane protein 88	*TMEM88*
5791	6,28	7,19	-1,14	0,04668	0,441	1562247_at	Hypothetical protein LOC286058	*LOC286058*
1686	37,5	42,9	-1,14	0,01066	0,345	218475_at	HpaII tiny fragments locus 9C	*HTF9C*
3324	31,4	36,0	-1,14	0,02362	0,388	219068_x_at	ATPase family, AAA domain containing 3A	*ATAD3A*
2738	9,99	11,4	-1,14	0,01889	0,377	222245_s_at	Fer-1-like 4 (C. elegans)	*FER1L4*
5381	33,3	38,1	-1,14	0,04219	0,429	209346_s_at	Phosphatidylinositol 4-kinase type 2 alpha	*PI4K2A*
5965	4,87	5,57	-1,14	0,04844	0,444	215035_at	Immunoglobulin lambda variable 6-57	*IGLV6-57*
6083	2505	2865	-1,14	0,04966	0,446	213646_x_at	Tubulin, alpha 1b	*TUBA1B*
73	11,2	12,8	-1,14	0,00028	0,201	236719_at	Similar to XP_001086437.1	-
2441	23,6	27,0	-1,14	0,01632	0,365	238150_at	-	-
2131	32,5	37,1	-1,14	0,01401	0,359	239026_x_at	Centaurin, gamma 3	*CENTG3*
487	3,30	3,77	-1,14	0,00259	0,289	1563169_at	Clone IMAGE:4499056, mRNA	-
6023	9,88	11,3	-1,14	0,04901	0,445	207129_at	Carbonic anhydrase VB, mitochondrial	*CA5B*
2812	18,6	21,2	-1,14	0,01961	0,381	212545_s_at	Zinc fingers and homeoboxes 3	*ZHX3*
2892	11,1	12,7	-1,14	0,02030	0,383	220714_at	PR domain containing 14	*PRDM14*
2024	11,2	12,9	-1,14	0,01320	0,355	238180_at	Transcribed locus	-
3900	48,6	55,6	-1,14	0,02849	0,399	223607_x_at	Zinc finger, SWIM-type containing 1	*ZSWIM1*
5879	36,9	42,2	-1,14	0,04753	0,442	1569834_at	cDNA clone IMAGE:5295705	-
3251	10,1	11,5	-1,14	0,02308	0,388	244701_at	cDNA FLJ33712 fis, clone BRAWH2008255	-
1973	48,0	54,9	-1,14	0,01291	0,355	227237_x_at	ATPase family, AAA domain containing 3B	*ATAD3B*

Index	Mutated*	Normal*	FC	*P* value	FDR**	Probe set	Description	Gene symbol
1572	8,99	10,3	-1,14	0,00977	0,340	222712_s_at	Mucin 13, cell surface associated	*MUC13*
5900	6,76	7,73	-1,14	0,04780	0,443	242288_s_at	Elastin microfibril interfacer 2	*EMILIN2*
1023	4,93	5,64	-1,14	0,00593	0,316	228712_at	WNK lysine deficient protein kinase 1	*WNK1*
708	8,59	9,81	-1,14	0,00406	0,308	234376_at	v-Myc myelocytomatosis viral related oncogene, neuroblastoma derived (avia	*MYCN*
4395	9,31	10,6	-1,14	0,03276	0,407	1569206_at	T-complex 11 (mouse)-like 2	*TCP11L2*
647	3,92	4,49	-1,14	0,00368	0,308	217259_at	cDNA DKFZp586H0123	-
2634	7,76	8,87	-1,14	0,01794	0,372	230080_at	Homeobox A4	*HOXA4*
5682	32,6	37,2	-1,14	0,04536	0,436	1569949_at	G protein-coupled receptor kinase 5	*GRK5*
5742	21,0	24,0	-1,14	0,04607	0,439	218786_at	5'-nucleotidase domain containing 3	*NT5DC3*
2987	22,7	26,0	-1,14	0,02101	0,384	213633_at	SH3-domain binding protein 1	*SH3BP1*
878	11,4	13,1	-1,14	0,00509	0,313	234688_x_at	Centrobin, centrosomal BRCA2 interacting protein	*CNTROB*
1439	8,88	10,2	-1,14	0,00876	0,332	237036_at	F-box protein 10	*FBXO10*
765	13,3	15,2	-1,14	0,00433	0,309	243912_x_at	DNA dC->dU-editing enzyme APOBEC-3F	*APOBEC3F*
3083	5,14	5,87	-1,14	0,02173	0,385	243114_at	Transcribed locus	-
2592	9,88	11,3	-1,14	0,01760	0,371	223635_s_at	Single stranded DNA binding protein 3	*SSBP3*
2292	14,2	16,2	-1,14	0,01524	0,363	208224_at	Homeobox B1	*HOXB1*
1279	7,85	8,98	-1,14	0,00761	0,325	233467_s_at	Tetraspanin 32	*TSPAN32*
5615	12,1	13,8	-1,14	0,04479	0,436	234130_at	LIM domain binding 3	*LDB3*
1430	23,7	27,1	-1,14	0,00867	0,331	214335_at	Ribosomal protein L18	*RPL18*
1095	30,5	34,9	-1,14	0,00642	0,319	206911_at	Tripartite motif-containing 25	*TRIM25*
3987	1677	1915	-1,14	0,02915	0,400	211750_x_at	Tubulin, alpha 1c	*TUBA1C*
47	7,10	8,12	-1,14	0,00019	0,201	230725_at	-	-
953	6,81	7,79	-1,14	0,00549	0,314	233217_at	HSPC102 protein	-
104	4,20	4,80	-1,14	0,00042	0,217	241449_at	Similar to XP_001174538.1	-
4070	14,6	16,7	-1,14	0,02986	0,401	233846_at	Coiled-coil domain containing 85A	*CCDC85A*
2191	15,0	17,1	-1,14	0,01451	0,361	235799_at	Kinetochore-associated protein NSL1 homolog	*NSL1*
3643	4,92	5,62	-1,14	0,02634	0,395	239668_at	Transcribed locus	-
5778	13,2	15,1	-1,14	0,04652	0,440	220427_at	Obscurin, cytoskeletal calmodulin and titin-interacting RhoGEF	*OBSCN*
4034	14,1	16,1	-1,14	0,02955	0,401	220747_at	HSPC072 protein	*HSPC072*
4187	11,5	13,2	-1,14	0,03095	0,404	217373_x_at	Mdm2 p53 binding protein homolog (mouse)	*MDM2*
526	2,68	3,06	-1,14	0,00281	0,291	1552430_at	WD repeat domain 17	*WDR17*
1680	14,9	17,0	-1,14	0,01060	0,345	233679_at	TGF-beta-activated kinase 1-binding protein 1	*MAP3K7IP1*
1428	6,99	7,99	-1,14	0,00867	0,331	223967_at	Angiopoietin-like 6	*ANGPTL6*
3814	9,92	11,3	-1,14	0,02779	0,398	211266_s_at	G protein-coupled receptor 4	*GPR4*
3450	17,8	20,4	-1,14	0,02470	0,391	221687_s_at	Family with sequence similarity 125, member B	*FAM125B*
3744	12,2	14,0	-1,14	0,02724	0,397	207921_x_at	Paired box 8	*PAX8*
1285	8,02	9,16	-1,14	0,00765	0,325	207457_s_at	Lymphocyte antigen 6 complex, locus G6D	*LY6G6D*
1748	10,8	12,3	-1,14	0,01116	0,348	1570239_a_at	Mast cell immunoreceptor signal transducer	*MIST*
125	3,57	4,07	-1,14	0,00057	0,240	1565780_at	ATP-binding cassette, sub-family A (ABC1), member 8	*ABCA8*
2213	13,4	15,3	-1,14	0,01466	0,362	234506_at	cDNA DKFZp564M163	-
5269	24,0	27,4	-1,14	0,04093	0,425	205247_at	Notch homolog 4 (Drosophila)	*NOTCH4*
4622	12,1	13,9	-1,14	0,03488	0,412	211660_at	POU class 2 homeobox 2	*POU2F2*
2391	12,2	14,0	-1,14	0,01595	0,365	211554_s_at	Apoptotic peptidase activating factor 1	*APAF1*
3628	4,76	5,43	-1,14	0,02621	0,395	205359_at	A kinase (PRKA) anchor protein 6	*AKAP6*
2448	6,38	7,28	-1,14	0,01640	0,366	239165_at	Transcribed locus	-
952	12,7	14,5	-1,14	0,00547	0,314	232310_at	Hypothetical LOC388889	*LOC388889*
5573	16,7	19,1	-1,14	0,04439	0,435	241201_at	KIAA1530 protein	*KIAA1530*
3637	7,62	8,69	-1,14	0,02629	0,395	227343_at	Myeloma overexpressed gene (hypothetical protein LOC26579)	*MYEOV*
1367	9,41	10,7	-1,14	0,00822	0,328	241490_s_at	PiggyBac transposable element derived 2	*PGBD2*
5409	4,00	4,57	-1,14	0,04249	0,429	1558452_at	Transmembrane protein 144	*TMEM144*
1434	5,36	6,12	-1,14	0,00869	0,331	239909_at	ADAMTS-like 1	*ADAMTSL1*
3	3,29	3,76	-1,14	0,00001	0,099	243460_at	Transcribed locus	-
4106	23,5	26,8	-1,14	0,03018	0,402	216694_at	-	-
876	15,3	17,5	-1,14	0,00505	0,313	240305_at	cDNA clone IMAGE:5285563	-
6045	6,05	6,90	-1,14	0,04924	0,445	1554376_s_at	Protein-tyrosine phosphatase-like member A	*PTPLA*
535	12,2	13,9	-1,14	0,00286	0,292	220490_at	-	-
2619	12,6	14,3	-1,14	0,01780	0,371	239157_at	Zinc finger and SCAN domain containing 12-like 1	*ZSCAN12L1*

Index	Mutated*	Normal*	FC	*P* value	FDR**	Probe set	Description	Gene symbol
105	5886	6713	-1,14	0,00042	0,217	1553569_at	Phosphatidylinositol glycan anchor biosynthesis, class F	*PIGF*
2855	5,55	6,33	-1,14	0,02003	0,383	231415_at	Williams Beuren syndrome chromosome region 22	*WBSCR22*
3239	22,3	25,4	-1,14	0,02298	0,388	244157_x_at	-	-
751	5,21	5,94	-1,14	0,00425	0,308	238817_at	RIMS binding protein 2	*RIMBP2*
1580	5,66	6,45	-1,14	0,00983	0,340	206225_at	Zinc finger protein 507	*ZNF507*
775	5,42	6,18	-1,14	0,00443	0,311	241241_at	Ribosomal protein S14	*RPS14*
5214	26,5	30,2	-1,14	0,04027	0,422	234471_s_at	Nuclear receptor coactivator 5	*NCOA5*
4924	36,4	41,5	-1,14	0,03775	0,419	211512_s_at	Opioid growth factor receptor	*OGFR*
673	8,48	9,67	-1,14	0,00386	0,308	217658_at	THAP domain containing, apoptosis associated protein 3	*THAP3*
1840	11,5	13,1	-1,14	0,01183	0,351	229148_at	-	-
2381	5,51	6,28	-1,14	0,01587	0,364	205605_at	Homeobox D9	*HOXD9*
622	18,7	21,3	-1,14	0,00353	0,308	1561019_at	Full length insert cDNA clone ZD95A07	-
3061	4,99	5,69	-1,14	0,02154	0,385	204830_x_at	Pregnancy specific beta-1-glycoprotein 5	*PSG5*
1344	8,55	9,75	-1,14	0,00806	0,328	237595_at	LIM homeobox transcription factor 1, alpha	*LMX1A*
1778	17,7	20,2	-1,14	0,01132	0,348	206467_x_at	Tumor necrosis factor receptor superfamily, member 6b, decoy	*TNFRSF6B*
226	3,65	4,16	-1,14	0,00105	0,250	1565306_a_at	Solute carrier family 8, member 1	*SLC8A1*
1549	17,9	20,3	-1,14	0,00956	0,337	234647_at	Kv channel interacting protein 3, calsenilin	*KCNIP3*
3770	7,29	8,31	-1,14	0,02739	0,397	215449_at	Benzodiazapine receptor (peripheral)-like 1	*BZRPL1*
2346	9,66	11,0	-1,14	0,01566	0,364	205589_at	Myosin, light chain 3, alkali; ventricular, skeletal, slow	*MYL3*
4887	5,92	6,74	-1,14	0,03737	0,418	208360_s_at	-	-
3076	8,66	9,86	-1,14	0,02169	0,385	220684_at	T-box 21	*TBX21*
432	4,44	5,06	-1,14	0,00228	0,288	1558995_at	Zinc finger protein 547	*ZNF547*
1104	6,56	7,47	-1,14	0,00646	0,319	243344_at	Clone IMAGE:5194137, mRNA	-
3115	97,5	111	-1,14	0,02203	0,387	53912_at	Sorting nexin 11	*SNX11*
189	3,12	3,56	-1,14	0,00088	0,244	211491_at	Adrenergic, alpha-1A-, receptor	*ADRA1A*
741	7,09	8,08	-1,14	0,00421	0,308	229224_x_at	Hypothetical LOC643085	*LOC643085*
1662	7,24	8,25	-1,14	0,01049	0,345	220727_at	Potassium channel, subfamily K, member 10	*KCNK10*
791	11,9	13,6	-1,14	0,00452	0,311	206798_x_at	Deleted in lung and esophageal cancer 1	*DLEC1*
224	11,6	13,2	-1,14	0,00104	0,250	220379_at	Fascin homolog 3, actin-bundling protein, testicular	*FSCN3*
2235	8,64	9,84	-1,14	0,01485	0,363	233137_at	Clone IMAGE:121687 mRNA sequence	-
1997	4,54	5,17	-1,14	0,01306	0,355	217677_at	Pleckstrin homology domain-containing family A member 2	*PLEKHA2*
2003	19,8	22,6	-1,14	0,01307	0,355	1555359_at	Phosphatidylinositol glycan anchor biosynthesis, class Q	*PIGQ*
2146	5,76	6,56	-1,14	0,01412	0,360	229993_at	Zinc finger, CCHC domain containing 3	*ZCCHC3*
428	8,07	9,19	-1,14	0,00226	0,288	232577_at	Hypothetical protein LOC145945	*LOC145945*
222	8,62	9,81	-1,14	0,00103	0,250	231893_at	KIAA1755 protein	*KIAA1755*
2040	4,57	5,20	-1,14	0,01328	0,355	209738_x_at	Pregnancy specific beta-1-glycoprotein 6	*PSG6*
1453	4,04	4,60	-1,14	0,00889	0,334	1570650_at	Cysteine conjugate-beta lyase; cytoplasmic	*CCBL1*
1609	5,99	6,82	-1,14	0,01008	0,342	234811_at	Centromere protein N	*CENPN*
5638	50,6	57,6	-1,14	0,04499	0,436	202140_s_at	CDC-like kinase 3	*CLK3*
1120	27,8	31,6	-1,14	0,00654	0,319	239720_at	Similar to RIKEN cDNA B230118G17 gene	*MGC19604*
1361	10,3	11,7	-1,14	0,00820	0,328	234499_at	cDNA DKFZp566K203	-
2790	10,2	11,6	-1,14	0,01940	0,380	220476_s_at	Chromosome 1 open reading frame 183	*C1orf183*
867	16,6	18,9	-1,14	0,00501	0,313	231743_at	Wingless-type MMTV integration site family, member 3	*WNT3*
2088	5,61	6,38	-1,14	0,01362	0,356	237324_s_at	Hexokinase domain containing 1	*HKDC1*
2099	6,05	6,88	-1,14	0,01375	0,358	236852_at	F-box protein 43	*FBXO43*
1820	23,9	27,1	-1,14	0,01172	0,351	1555754_s_at	Atrophin 1	*ATN1*
3299	6,02	6,85	-1,14	0,02350	0,388	231877_at	RNA (guanine-9-) methyltransferase domain containing 2	*RG9MTD2*
6037	8,06	9,17	-1,14	0,04915	0,445	234696_at	Similar to Testicular serine protease 2	*LOC138652*
3380	3,55	4,04	-1,14	0,02405	0,389	210531_at	Nuclear receptor subfamily 2, group C, member 1	*NR2C1*
4122	6,96	7,92	-1,14	0,03031	0,402	229548_at	Similar to UNC-84 homolog B	-
889	5,48	6,24	-1,14	0,00513	0,313	237599_at	Similar to Finger protein 286	-
2599	11,8	13,5	-1,14	0,01765	0,371	1561133_at	Full length insert cDNA clone ZD60A10	-
1048	11,8	13,5	-1,14	0,00612	0,319	1562256_at	NLR family, pyrin domain containing 1	*NLRP1*
3848	163	185	-1,14	0,02810	0,399	201805_at	Protein kinase, AMP-activated, gamma 1 non-catalytic subunit	*PRKAG1*
3009	10,1	11,5	-1,14	0,02118	0,385	241820_at	RAP1 interacting factor homolog (yeast)	*RIF1*
2456	10,6	12,0	-1,14	0,01647	0,366	224498_x_at	Axin 2 (conductin, axil)	*AXIN2*
1822	11,0	12,5	-1,14	0,01173	0,351	232400_at	SEC14-like 2 (S. cerevisiae)	*SEC14L2*

Index	Mutated*	Normal*	FC	*P* value	FDR**	Probe set	Description	Gene symbol
3335	39,3	44,7	-1,14	0,02366	0,388	201796_s_at	Valyl-tRNA synthetase	*VARS*
4505	3,16	3,59	-1,14	0,03391	0,412	236575_at	cDNA clone IMAGE:4823793	-
1406	4,46	5,07	-1,14	0,00850	0,330	1556536_at	HCG2044152 protein	-
786	6,18	7,03	-1,14	0,00449	0,311	1565580_s_at	TatD DNase domain containing 2	*TATDN2*
163	26,1	29,7	-1,14	0,00075	0,244	210043_at	FERM domain containing 8	*FRMD8*
1378	19,2	21,9	-1,14	0,00830	0,329	240587_x_at	Transcribed locus	-
4110	5,61	6,38	-1,14	0,03021	0,402	223987_at	Chordin-like 2	*CHRDL2*
1830	4,63	5,26	-1,14	0,01179	0,351	231051_at	Full length insert cDNA clone ZD51E06	-
4802	40,6	46,2	-1,14	0,03644	0,415	89476_r_at	Aminopeptidase-like 1	*NPEPL1*
4975	9,94	11,3	-1,14	0,03818	0,419	211900_x_at	CD6 molecule	*CD6*
1779	30,8	35,0	-1,14	0,01134	0,349	241918_at	Transmembrane protein 16G	*TMEM16G*
758	6,49	7,37	-1,14	0,00428	0,308	243058_at	-	-
3244	8,02	9,11	-1,14	0,02300	0,388	222301_at	Chromosome 1 open reading frame 61	*C1orf61*
3203	8,26	9,39	-1,14	0,02268	0,387	1554382_at	Hypothetical protein LOC200261	*LOC200261*
5713	8,05	9,15	-1,14	0,04574	0,438	235863_at	Junctional sarcoplasmic reticulum protein 1	*JSRP1*
1522	6,54	7,44	-1,14	0,00940	0,337	239947_at	Transcribed locus	-
124	7,37	8,37	-1,14	0,00057	0,240	242651_at	Transcribed locus	-
2167	4,35	4,94	-1,14	0,01434	0,361	219393_s_at	v-AKT murine thymoma viral oncogene homolog	*AKT3*
5401	5,34	6,07	-1,14	0,04236	0,429	230170_at	Oncostatin M	*OSM*
3594	58,0	65,9	-1,14	0,02592	0,394	202958_at	Protein tyrosine phosphatase, non-receptor type 9	*PTPN9*
1987	4,28	4,87	-1,14	0,01298	0,355	1555626_a_at	Signaling lymphocytic activation molecule family member 1	*SLAMF1*
1417	3,57	4,06	-1,14	0,00858	0,331	223550_s_at	Carbonic anhydrase X	*CA10*
776	4,59	5,22	-1,14	0,00443	0,311	216471_x_at	Synovial sarcoma, X breakpoint 2	*SSX2*
3233	7,37	8,38	-1,14	0,02291	0,388	1561960_at	Hypothetical gene supported by AB067507	*LOC390627*
3722	25,2	28,7	-1,14	0,02702	0,397	221306_at	G protein-coupled receptor 27	*GPR27*
2216	7,68	8,73	-1,14	0,01468	0,362	1570133_at	Clone IMAGE:5172579, mRNA	-
811	11,0	12,5	-1,14	0,00462	0,311	241437_s_at	EP400 N-terminal like	*EP400NL*
1839	4,57	5,19	-1,14	0,01183	0,351	231589_at	-	-
3060	16,5	18,8	-1,14	0,02154	0,385	207004_at	B-cell CLL/lymphoma 2	*BCL2*
2042	17,0	19,3	-1,14	0,01328	0,355	1559629_at	Clone IMAGE:5744974, mRNA	-
782	17,7	20,1	-1,14	0,00448	0,311	1559461_at	Clone IMAGE:3852236, mRNA	-
491	3,43	3,89	-1,14	0,00262	0,289	1569746_s_at	cDNA clone IMAGE:5265020	-
3803	14,8	16,9	-1,14	0,02770	0,398	1568743_at	ATPase, Class V, type 10A	*ATP10A*
1659	6,12	6,96	-1,14	0,01048	0,345	1553757_at	IQ motif containing G	*IQCG*
3447	35,2	40,0	-1,14	0,02467	0,391	1556479_at	cDNA FLJ40474 fis, clone TESTI2042928	-
3560	4,90	5,57	-1,14	0,02570	0,394	222520_s_at	Intraflagellar transport 57 homolog (Chlamydomonas)	*IFT57*
728	4,43	5,03	-1,14	0,00416	0,308	1561221_x_at	Hypothetical protein LOC728099	*LOC728099*
3476	7,27	8,25	-1,14	0,02496	0,392	206353_at	Cytochrome c oxidase subunit VIa polypeptide 2	*COX6A2*
2091	6,50	7,39	-1,14	0,01365	0,357	240590_at	Hypothetical protein LOC348761	*LOC348761*
503	4,79	5,44	-1,14	0,00267	0,289	239308_at	Dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 1A	*DYRK1A*
2102	33,6	38,1	-1,14	0,01378	0,358	213323_s_at	Zinc finger CCCH-type containing 7B	*ZC3H7B*
5239	7,25	8,23	-1,14	0,04059	0,423	229622_at	Family with sequence similarity 132, member B	*FAM132B*
1134	17,3	19,7	-1,14	0,00663	0,319	1568667_s_at	Lipid storage droplet protein 5	*LSDP5*
3490	3,98	4,51	-1,14	0,02509	0,392	244489_at	-	-
4609	7,10	8,06	-1,14	0,03482	0,412	232464_at	Tripartite motif-containing pseudogene 1	*TRIMP1*
527	5,26	5,97	-1,14	0,00281	0,291	220227_at	Cadhetrin 4, type 1, R-Cadhetrin (retinal)	*CDH4*
5627	7,76	8,80	-1,14	0,04492	0,436	223510_at	Neuropilin 2	*NRP2*
677	5,88	6,67	-1,14	0,00389	0,308	220343_at	Phosphodiesterase 7B	*PDE7B*
2389	12,4	14,1	-1,13	0,01592	0,364	210442_at	Interleukin 1 receptor-like 1	*IL1RL1*
2336	5,19	5,89	-1,13	0,01559	0,364	216747_at	Amyloid beta precursor protein-binding, family B, member 2	*APBB2*
4225	9,61	10,9	-1,13	0,03132	0,405	1564373_a_at	Hypothetical protein LOC283887	*LOC283887*
5184	4,51	5,12	-1,13	0,03996	0,421	235325_at	Spastic paraplegia 7 protein	*SPG7*
382	2,90	3,29	-1,13	0,00199	0,284	1552765_x_at	Transmembrane protein 67	*TMEM67*
5259	24,4	27,7	-1,13	0,04080	0,424	206926_s_at	Interleukin 11	*IL11*
5893	51,7	58,7	-1,13	0,04767	0,442	227035_x_at	Retinitis pigmentosa 9 pseudogene	*LOC441212*
5140	6,07	6,89	-1,13	0,03958	0,421	216327_s_at	Sialic acid binding Ig-like lectin 8	*SIGLEC8*
5583	3,18	3,60	-1,13	0,04452	0,436	235230_at	cDNA FLJ34317 fis, clone FEBRA2008475	-

Index	Mutated*	Normal*	FC	*P* value	FDR**	Probe set	Description	Gene symbol
2921	5,29	6,01	-1,13	0,02049	0,383	220095_at	Chromosome 9 open reading frame 39	*C9orf39*
1893	6,19	7,02	-1,13	0,01231	0,355	216117_at	Exosome component 2	*EXOSC2*
4976	12,0	13,6	-1,13	0,03819	0,419	239415_at	Microtubule-associated protein 9	*MAP9*
3491	8,49	9,63	-1,13	0,02510	0,392	243083_at	Hypothetical gene supported by BC040831	*LOC401351*
2356	6,55	7,43	-1,13	0,01572	0,364	238014_at	-	-
4853	12,0	13,6	-1,13	0,03698	0,417	1567257_at	Olfactory receptor, family 1, subfamily J, member 2	*OR1J2*
2932	11,0	12,5	-1,13	0,02056	0,383	234099_at	cDNA FLJ13494 fis, clone PLACE1004384	-
1679	7,80	8,84	-1,13	0,01060	0,345	235865_at	CUG triplet repeat, RNA binding protein 1	*CUGBP1*
3161	14,0	15,9	-1,13	0,02243	0,387	232988_at	KIAA0182 protein	*KIAA0182*
3158	7,53	8,54	-1,13	0,02241	0,387	206178_at	Phospholipase A2, group V	*PLA2G5*
2559	7,22	8,19	-1,13	0,01736	0,371	1556453_at	cDNA FLJ35971 fis, clone TESTI2013257	-
507	6,99	7,93	-1,13	0,00269	0,289	1562818_at	Nicotinamide nucleotide adenylyltransferase 2	*NMNAT2*
164	10,7	12,2	-1,13	0,00076	0,244	1554759_at	SNAP25-interacting protein	*SNIP*
1444	12,5	14,2	-1,13	0,00878	0,332	217622_at	Rhomboid domain containing 3	*RHBDD3*
2604	10,5	11,9	-1,13	0,01768	0,371	206802_at	Paired box 5	*PAX5*
4881	18,1	20,5	-1,13	0,03733	0,418	229668_at	Hypothetical protein LOC90393	*LOC90393*
3968	4,04	4,58	-1,13	0,02898	0,399	236660_at	cDNA FLJ45600 fis, clone BRTHA3020369	-
3515	23,2	26,3	-1,13	0,02525	0,392	1553444_a_at	Chromosome 1 open reading frame 127	*C1orf127*
4829	66,3	75,1	-1,13	0,03679	0,416	221956_at	Leucine rich repeat neuronal 4	*LRCH4*
1274	6,11	6,93	-1,13	0,00758	0,325	1553936_a_at	Hypothetical protein MGC2848	*MGC2848*
5177	10,7	12,1	-1,13	0,03990	0,421	218600_at	LIM domain containing 2	*LIMD2*
1127	20,4	23,1	-1,13	0,00657	0,319	242145_at	Transcribed locus	-
635	3,10	3,52	-1,13	0,00361	0,308	240138_at	Transcribed locus	-
650	6,66	7,55	-1,13	0,00369	0,308	1565559_at	MAGI family member, X-linked	*MAGIX*
1817	5,90	6,69	-1,13	0,01171	0,351	1563045_at	cDNA clone IMAGE:4827232	-
1347	17,5	19,8	-1,13	0,00807	0,328	211791_s_at	Potassium channel shaker chain beta 2	*KCNAB2*
2499	4,80	5,44	-1,13	0,01684	0,367	243238_at	Phosphorylase, glycogen; brain	*PYGB*
4554	6,32	7,16	-1,13	0,03442	0,412	230827_at	Similar to HBxAg transactivated protein 2 isoform 5	-
4774	7,27	8,23	-1,13	0,03621	0,414	207346_at	Syntaxin 2	*STX2*
1353	5,82	6,59	-1,13	0,00812	0,328	221380_at	Mahlavu hepatocellular carcinoma	*HHCM*
12	2,95	3,34	-1,13	0,00004	0,180	242682_at	-	-
415	3,55	4,02	-1,13	0,00219	0,286	230910_s_at	Lymphocyte antigen 6 complex, locus K	*LY6K*
3430	34,9	39,5	-1,13	0,02455	0,391	223462_at	Transmembrane protein 175	*TMEM175*
1804	12,4	14,0	-1,13	0,01162	0,351	208489_at	Gap junction protein, alpha 8, 50kDa	*GJA8*
3706	10,3	11,6	-1,13	0,02680	0,395	206892_at	Anti-Mullerian hormone receptor, type II	*AMHR2*
3757	23,0	26,0	-1,13	0,02731	0,397	224125_at	Pleckstrin homology domain containing, family N member 1	*PLEKHN1*
1002	4,93	5,58	-1,13	0,00579	0,316	1560862_at	cDNA DKFZp434I235	-
1731	6,98	7,91	-1,13	0,01105	0,348	241725_at	E2F transcription factor 7	*E2F7*
1671	20,5	23,2	-1,13	0,01055	0,345	209559_at	Huntingtin interacting protein 1 related	*HIP1R*
2726	13,1	14,8	-1,13	0,01874	0,376	231360_at	Chromosome 20 open reading frame 141	*C20orf141*
348	11,1	12,5	-1,13	0,00178	0,278	244152_at	Transcribed locus	-
2402	6,36	7,20	-1,13	0,01602	0,365	211195_s_at	Tumor protein p63	*TP63*
4341	7,62	8,63	-1,13	0,03233	0,407	208191_x_at	Pregnancy specific beta-1-glycoprotein 4	*PSG4*
5431	33,2	37,6	-1,13	0,04279	0,431	219997_s_at	COP9 constitutive photomorphogenic homolog subunit 7B	*COPS7B*
4154	10,8	12,2	-1,13	0,03064	0,403	216892_at	Immunoglobulin heavy constant gamma 1 (G1m marker)	*IGHG1*
295	3,73	4,23	-1,13	0,00144	0,263	1562983_at	Hypothetical gene supported by BC039667	*LOC441025*
4048	7,17	8,12	-1,13	0,02967	0,401	206154_at	Retinaldehyde binding protein 1	*RLBP1*
652	3,43	3,88	-1,13	0,00371	0,308	235777_at	Ankyrin repeat domain 44	*ANKRD44*
2943	7,51	8,50	-1,13	0,02063	0,383	243429_at	Transcribed locus	-
1372	4,07	4,61	-1,13	0,00824	0,328	243073_at	Transcribed locus	-
5354	161	183	-1,13	0,04201	0,429	215399_s_at	Amplified in osteosarcoma	*OS9*
2337	6,34	7,17	-1,13	0,01560	0,364	237715_at	AT-hook transcription factor	*AKNA*
1122	5,16	5,84	-1,13	0,00655	0,319	236171_at	ATPase, Ca++ transporting, type 2C, member 2	*ATP2C2*
759	8,24	9,32	-1,13	0,00429	0,308	219144_at	Dual specificity phosphatase 26 (putative)	*DUSP26*
83	4,35	4,92	-1,13	0,00031	0,201	229791_at	Acyltransferase like 1	*AYTL1*
1468	7,96	9,01	-1,13	0,00898	0,334	237151_s_at	Similar to Hypothetical protein	*MGC33657*
2413	26,3	29,8	-1,13	0,01612	0,365	230345_at	Transcribed locus	-

Index	Mutated*	Normal*	FC	*P* value	FDR**	Probe set	Description	Gene symbol
1368	7,93	8,97	-1,13	0,00823	0,328	232813_s_at	Golgin-like protein	*GOLGA*
5321	34,0	38,4	-1,13	0,04158	0,427	1552863_a_at	Calcium channel, voltage-dependent, gamma subunit 6	*CACNG6*
1373	3,55	4,01	-1,13	0,00825	0,329	220834_at	Membrane-spanning 4-domains, subfamily A, member 12	*MS4A12*
377	4,99	5,65	-1,13	0,00196	0,284	1561472_at	Hypothetical protein LOC728805	*LOC728805*
3017	18,4	20,8	-1,13	0,02126	0,385	47105_at	Dihydrouridine synthase 2-like, SMM1 homolog (S. cerevisiae)	*DUS2L*
2513	18,4	20,8	-1,13	0,01691	0,368	220573_at	Kallikrein-related peptidase 14	*KLK14*
3684	13,0	14,7	-1,13	0,02660	0,395	1552845_at	Claudin 15	*CLDN15*
3333	39,4	44,6	-1,13	0,02366	0,388	205021_s_at	Forkhead box N3	*FOXN3*
787	25,5	28,8	-1,13	0,00450	0,311	1561355_at	Hypothetical locus LOC692247	*LOC692247*
5441	16,5	18,7	-1,13	0,04288	0,431	206807_s_at	Adducin 2 (beta)	*ADD2*
1224	9,22	10,4	-1,13	0,00729	0,324	211873_s_at	¨Protocadherin gamma subfamily A, 9	*PCDHGA9*
985	26,2	29,6	-1,13	0,00569	0,315	234956_at	Hypothetical protein LOC93444	*LOC93444*
1649	4,83	5,47	-1,13	0,01037	0,344	221360_s_at	Growth hormone secretagogue receptor	*GHSR*
38	3,48	3,93	-1,13	0,00015	0,201	1561353_at	cDNA clone IMAGE:4816369	-
1142	17,4	19,6	-1,13	0,00669	0,320	233378_at	Hypothetical protein LOC731419	*LOC731419*
1946	8,06	9,11	-1,13	0,01272	0,355	228689_at	NADH-ubiquinone oxidoreductase subunit B14.7	*NDUFA11*
4565	28,0	31,7	-1,13	0,03451	0,412	205331_s_at	Receptor accessory protein 2	*REEP2*
2198	5,26	5,95	-1,13	0,01453	0,361	215124_at	Zinc finger protein 550	*ZNF550*
2431	5,27	5,96	-1,13	0,01625	0,365	243043_at	Transcribed locus	-
3304	5,66	6,39	-1,13	0,02351	0,388	241516_at	-	-
5564	10,9	12,3	-1,13	0,04430	0,435	211263_s_at	Proprotein convertase subtilisin/kexin type 6	*PCSK6*
2893	5,38	6,08	-1,13	0,02031	0,383	237913_at	Transcribed locus	-
3735	3,46	3,92	-1,13	0,02712	0,397	1561430_s_at	Chromosome 3 open reading frame 15	*C3orf15*
3262	8,92	10,1	-1,13	0,02316	0,388	232787_at	PPAR-alpha-interacting complex protein 285	*PRIC285*
2149	24,2	27,3	-1,13	0,01415	0,360	1563273_at	Full length insert cDNA clone ZA89G05	-
4309	24,6	27,8	-1,13	0,03208	0,407	215670_s_at	SCAN domain containing 2	*SCAND2*
4876	5,21	5,89	-1,13	0,03723	0,417	234965_at	Apoptosis related protein APR-4	-
4071	16,3	18,4	-1,13	0,02986	0,401	231255_at	Myosin phosphatase-Rho interacting protein	*M-RIP*
1403	19,0	21,5	-1,13	0,00847	0,330	206444_at	Phosphodiesterase 1B, calmodulin-dependent	*PDE1B*
3429	10,8	12,2	-1,13	0,02455	0,391	222515_x_at	Transmembrane protein 165	*TMEM165*
1979	7,86	8,89	-1,13	0,01292	0,355	221083_at	Potassium voltage-gated channel, KQT-like subfamily, member 4	*KCNQ4*
65	4,03	4,55	-1,13	0,00025	0,201	1566500_at	-	-
5802	17,6	19,9	-1,13	0,04682	0,441	226469_s_at	Gamma-glutamyltransferase-like 3	*GGTL3*
2301	10,1	11,4	-1,13	0,01528	0,363	241849_at	Transcribed locus	-
5414	8,16	9,22	-1,13	0,04255	0,430	238887_at	Clone IMAGE:3901628, mRNA	-
2319	17,8	20,1	-1,13	0,01541	0,363	1553399_a_at	Chromosome 17 open reading frame 69	*C17orf69*
502	3,31	3,74	-1,13	0,00267	0,289	235906_at	Transcription initiation factor TFIID 30 kD subunit	*TAF10*
1514	4,44	5,01	-1,13	0,00936	0,337	240540_at	-	-
283	7,67	8,66	-1,13	0,00139	0,263	230801_at	Chromosome 20 open reading frame 77	*C20orf77*
1199	11,4	12,9	-1,13	0,00708	0,323	214896_at	mRNA full length insert cDNA clone EUROIMAGE 29222	-
1738	4,53	5,12	-1,13	0,01110	0,348	1558021_at	RAB9 effector protein with kelch motifs	*RABEPK*
275	6,30	7,12	-1,13	0,00132	0,262	1562689_at	Hypothetical protein LOC151484	*LOC151484*
5817	14,1	15,9	-1,13	0,04701	0,442	1570295_at	Clone IMAGE:6059689, mRNA	-
3612	5,72	6,46	-1,13	0,02607	0,394	230924_at	Tubulin tyrosine ligase-like family, member 6	*TTLL6*
2529	10,4	11,8	-1,13	0,01708	0,369	1554219_at	-	-
5394	2100	2371	-1,13	0,04230	0,429	212639_x_at	Tubulin, alpha 1b	*TUBA1B*
762	4,02	4,54	-1,13	0,00430	0,308	220288_at	Myosin XVA	*MYO15A*
1111	17,1	19,3	-1,13	0,00650	0,319	243138_at	Transcribed locus	-
3086	7,72	8,72	-1,13	0,02176	0,385	236568_at	Coiled-coil and C2 domain containing 1B	*CC2D1B*
1869	13,5	15,2	-1,13	0,01207	0,353	233761_at	cDNA DKFZp762F0616	-
4352	37,3	42,1	-1,13	0,03241	0,407	223153_x_at	Transmembrane and ubiquitin-like domain containing 1	*TMUB1*
2844	4,67	5,28	-1,13	0,01989	0,382	233069_at	Protein phosphatase 4, regulatory subunit 1-like	*PPP4R1L*
4750	9,37	10,6	-1,13	0,03600	0,414	241326_at	Adenylate kinase 7	*AK7*
1945	6,66	7,52	-1,13	0,01267	0,355	240347_at	Transcribed locus	-
373	5,12	5,78	-1,13	0,00196	0,284	233188_at	Polypeptide GalNAc transferase-like protein 4	*GALNTL4*
3098	8,06	9,10	-1,13	0,02187	0,386	230662_at	Ring finger protein 187	*RNF187*
50	5984	6754	-1,13	0,00020	0,201	1553570_x_at	Phosphatidylinositol glycan anchor biosynthesis, class F	*PIGF*

Index	Mutated*	Normal*	FC	*P* value	FDR**	Probe set	Description	Gene symbol
5974	69,4	78,3	-1,13	0,04852	0,444	202556_s_at	Microspherule protein 1	*MCRS1*
562	5,03	5,67	-1,13	0,00306	0,298	1564203_at	Hypothetical protein LOC147004	*LOC147004*
285	3,37	3,80	-1,13	0,00139	0,263	1566734_at	Hypothetical protein LOC283454	*LOC283454*
2009	6,88	7,77	-1,13	0,01310	0,355	1560513_at	Hypothetical LOC400568	*LOC400568*
4422	9,17	10,3	-1,13	0,03310	0,409	232435_at	Chromosome X open reading frame 45	*CXorf45*
3343	18,7	21,1	-1,13	0,02374	0,388	229445_at	Cytochrome b-245, alpha polypeptide	*CYBA*
4521	8,93	10,1	-1,13	0,03410	0,412	1570531_at	cDNA clone IMAGE:4344985	-
1290	32,2	36,3	-1,13	0,00769	0,325	1565611_at	Dynein, light chain, roadblock-type 1	*DYNLRB1*
3064	35,9	40,5	-1,13	0,02160	0,385	205313_at	Transcription factor 2, hepatic; LF-B3	*TCF2*
4634	15,1	17,1	-1,13	0,03495	0,412	214311_at	Zinc finger protein-like 1	*ZFPL1*
1151	4,75	5,36	-1,13	0,00677	0,321	238273_at	Solute carrier family 13, member 4	*SLC13A4*
144	23,8	26,9	-1,13	0,00065	0,244	1553136_at	Potassium channel tetramerisation domain containing 18	*KCTD18*
2312	7,86	8,86	-1,13	0,01536	0,363	234914_at	Zinc finger protein 7	*ZNF7*
5889	16,1	18,1	-1,13	0,04764	0,442	243261_at	Hypothetical protein LOC154822	*LOC154822*
5072	8,06	9,10	-1,13	0,03903	0,420	230297_x_at	Synaptic Ras GTPase activating protein 1 homolog (rat)	*SYNGAP1*
5532	8,39	9,46	-1,13	0,04392	0,434	208240_s_at	Fibroblast growth factor 1 (acidic)	*FGF1*
3026	33,0	37,2	-1,13	0,02129	0,385	55583_at	Dedicator of cytokinesis 6	*DOCK6*
5970	2563	2891	-1,13	0,04848	0,444	211058_x_at	Tubulin, alpha 1b	*TUBA1B*
1948	4,52	5,09	-1,13	0,01272	0,355	236183_at	Dynein, cytoplasmic 1, heavy chain 1	*DYNC1H1*
2990	5,05	5,69	-1,13	0,02102	0,384	206162_x_at	Synaptotagmin V	*SYT5*
1153	16,6	18,7	-1,13	0,00678	0,321	1557723_at	Hypothetical protein LOC285847	*LOC285847*
4891	4,61	5,20	-1,13	0,03738	0,418	223951_at	Chromosome 21 open reading frame 116	*C21orf116*
4262	7,59	8,56	-1,13	0,03168	0,406	210197_at	Inositol 1,3,4-triphosphate 5/6 kinase	*ITPK1*
5135	6,45	7,28	-1,13	0,03950	0,421	222797_at	Dihydropyrimidinase-like 5	*DPYSL5*
2591	64,4	72,6	-1,13	0,01758	0,371	1562022_s_at	RAD9 homolog A (S. pombe)	*RAD9A*
906	14,0	15,7	-1,13	0,00524	0,313	239838_at	Zinc finger protein 776	*ZNF776*
1688	4,28	4,83	-1,13	0,01067	0,345	208514_at	Potassium voltage-gated channel, Isk-related family, member 1	*KCNE1*
585	6,09	6,86	-1,13	0,00323	0,301	230983_at	Family with sequence similarity 129, member C	*FAM129C*
2814	6,50	7,33	-1,13	0,01963	0,381	213777_s_at	-	-
4605	39,6	44,6	-1,13	0,03480	0,412	225360_at	TraB domain containing	*TRABD*
5606	1750	1973	-1,13	0,04471	0,436	209251_x_at	Tubulin, alpha 1c	*TUBA1C*
1215	4,61	5,20	-1,13	0,00722	0,324	234931_at	AYP1 pseudogene 1	*AYP1p1*
3353	7,60	8,57	-1,13	0,02382	0,388	211403_x_at	Variable charge, Y-linked	*VCY*
4403	3,81	4,30	-1,13	0,03287	0,408	1552518_s_at	MDM2 (mouse double minute 2)-binding protein, 104kD	*MTBP*
619	6,95	7,83	-1,13	0,00350	0,308	1556994_at	cDNA clone IMAGE:5296604	-
5835	12,6	14,2	-1,13	0,04714	0,442	220207_at	Hypothetical protein LOC541469	*LOC541469*
5694	14,5	16,3	-1,13	0,04556	0,437	210752_s_at	MAX-like protein X	*MLX*
1424	3,96	4,46	-1,13	0,00863	0,331	207285_x_at	Chorionic somatomammotropin hormone-like 1	*CSHL1*
2350	3,89	4,38	-1,13	0,01568	0,364	216569_at	-	-
1432	4,82	5,43	-1,13	0,00868	0,331	234553_at	cDNA FLJ20012 fis, clone ADKA03438	-
4368	15,1	17,0	-1,13	0,03249	0,407	230853_at	Similar to XP_529987.1	-
4485	11,4	12,8	-1,13	0,03374	0,411	229489_at	Transcribed locus	-
4235	13,3	15,0	-1,13	0,03139	0,405	239821_at	Hypothetical protein LOC644975	*FLJ30064*
1030	5,61	6,32	-1,13	0,00597	0,317	206760_s_at	Fc fragment of IgE, low affinity II, receptor for (CD23)	*FCER2*
1365	3,91	4,40	-1,13	0,00822	0,328	211108_s_at	Janus kinase 3 (a protein tyrosine kinase, leukocyte)	*JAK3*
2052	9,27	10,4	-1,13	0,01334	0,355	1553248_at	Coiled-coil domain containing 57	*CCDC57*
5676	107	121	-1,13	0,04530	0,436	201640_x_at	Cleft lip and palate associated transmembrane protein 1	*CLPTM1*
2208	7,47	8,41	-1,13	0,01461	0,362	1553168_at	Glutamate receptor, ionotropic, kainate 5	*GRIK5*
1975	8,04	9,05	-1,13	0,01291	0,355	220571_at	PR domain containing 11	*PRDM11*
4476	4,74	5,34	-1,13	0,03365	0,411	1553478_at	Proline rich 10	*PRR10*
5830	10,1	11,3	-1,13	0,04712	0,442	232042_at	Tweety homolog 2 (Drosophila)	*TTYH2*
3282	13,4	15,0	-1,13	0,02339	0,388	231922_at	Zinc finger protein 276	*ZNF276*
3068	5,71	6,43	-1,13	0,02165	0,385	243719_at	Serine/threonine kinase 19	*STK19*
5257	13,3	14,9	-1,13	0,04075	0,424	235375_x_at	Tetratricopeptide repeat domain 9B	*TTC9B*
505	4,25	4,79	-1,13	0,00268	0,289	206803_at	Prodynorphin	*PDYN*
1147	12,8	14,4	-1,13	0,00674	0,321	1556727_at	Progressive rod-cone degeneration	*PRCD*
3870	9,54	10,7	-1,13	0,02828	0,399	239074_at	GRB2-related adaptor protein-like	*LOC400581*

Index	Mutated*	Normal*	FC	*P* value	FDR**	Probe set	Description	Gene symbol
1349	5,95	6,70	-1,13	0,00810	0,328	234328_at	-	-
5876	9,87	11,1	-1,13	0,04747	0,442	237092_at	Transcribed locus	-
3210	5,16	5,81	-1,13	0,02273	0,387	1555039_a_at	ATP-binding cassette, sub-family C (CFTR/MRP), member 4	*ABCC4*
5032	10,9	12,2	-1,13	0,03868	0,420	216789_at	cDNA FLJ22786 fis, clone KAIA2150	-
2253	25,9	29,1	-1,13	0,01500	0,363	232892_at	Chromosome 20 open reading frame 166	*C20orf166*
5484	408	459	-1,13	0,04340	0,433	200714_x_at	Amplified in osteosarcoma	*OS9*
3014	7,56	8,51	-1,13	0,02121	0,385	229474_at	Flavoprotein oxidoreductase MICAL3	*MICAL3*
3956	5,87	6,61	-1,13	0,02889	0,399	240406_at	Similar to Ubiquitin specific protease 16 isoform a	-
1029	10,1	11,4	-1,13	0,00596	0,317	224543_at	Selectin-like osteoblast-derived protein	*SVEP1*
657	7,81	8,79	-1,13	0,00380	0,308	214233_at	ADP-ribosylation factor-binding protein GGA2	*GGA2*
4405	87,3	98,3	-1,13	0,03288	0,408	396_f_at	Erythropoietin receptor	*EPOR*
4931	4,78	5,38	-1,13	0,03782	0,419	1557720_s_at	Myosin XVI	*MYO16*
1235	3,49	3,93	-1,13	0,00734	0,324	203170_at	KIAA0409 protein	*KIAA0409*
4702	15,0	16,8	-1,13	0,03550	0,413	1567255_at	Olfactory receptor, family 10, subfamily D, member 1 pseudogene	*OR10D1P*
2293	7,98	8,98	-1,13	0,01524	0,363	233143_at	Chromosome 20 open reading frame 173	*C20orf173*
2048	4,82	5,42	-1,13	0,01331	0,355	211743_s_at	Proteoglycan 2, bone marrow	*PRG2*
757	3,91	4,40	-1,13	0,00428	0,308	228715_at	Zinc finger, CCHC domain containing 12	*ZCCHC12*
1204	5,38	6,05	-1,13	0,00713	0,324	222007_s_at	FK506 binding protein 8, 38kDa	*FKBP8*
5756	4,45	5,01	-1,13	0,04621	0,439	220399_at	Hypothetical protein FLJ22639	*FLJ22639*
936	11,2	12,6	-1,13	0,00536	0,313	1552602_at	Calcium channel, voltage-dependent, gamma subunit 5	*CACNG5*
5844	2473	2783	-1,13	0,04722	0,442	211072_x_at	Tubulin, alpha 1b	*TUBA1B*
1870	4,69	5,27	-1,13	0,01208	0,353	1562830_at	Methyltransferase 5 domain containing 1	*METT5D1*
4389	8,37	9,41	-1,13	0,03270	0,407	208223_s_at	Activin A receptor, type IB	*ACVR1B*
1735	8,94	10,1	-1,13	0,01109	0,348	1560059_at	Vacuolar protein sorting 37 homolog C (S. cerevisiae)	*VPS37C*
1110	7,56	8,51	-1,13	0,00650	0,319	223919_at	p53-regulated apoptosis-inducing protein 1	*P53AIP1*
3992	10,2	11,5	-1,12	0,02919	0,400	214479_at	GDNF family receptor alpha 3	*GFRA3*
4828	11,1	12,4	-1,12	0,03676	0,416	208414_s_at	Homeobox B3	*HOXB3*
1669	114	128	-1,12	0,01054	0,345	218381_s_at	U2 small nuclear RNA auxiliary factor 2	*U2AF2*
3506	5,13	5,78	-1,12	0,02518	0,392	220871_at	-	-
1496	7,15	8,05	-1,12	0,00921	0,336	222374_at	Beta-transducin repeat containing	*BTRC*
2979	24,7	27,7	-1,12	0,02095	0,384	220989_s_at	Amnionless homolog (mouse)	*AMN*
743	30,3	34,1	-1,12	0,00422	0,308	224555_x_at	Interleukin 1 family, member 7 (zeta)	*IL1F7*
877	4,56	5,12	-1,12	0,00506	0,313	224006_at	cDNA clone IMAGE:3831123	-
1079	29,1	32,7	-1,12	0,00632	0,319	206437_at	Endothelial differentiation G-protein coupled receptor 6	*EDG6*
4164	7,99	8,98	-1,12	0,03077	0,404	232462_s_at	BC040926	*FLJ23569*
1697	30,2	33,9	-1,12	0,01079	0,348	1570362_at	cDNA clone IMAGE:5749586	-
705	14,8	16,6	-1,12	0,00405	0,308	1561538_at	cDNA clone IMAGE:5271875	-
2994	6,56	7,38	-1,12	0,02109	0,385	210182_at	Cortistatin	*CORT*
3656	4,48	5,04	-1,12	0,02641	0,395	241444_at	Transcribed locus	-
676	8,37	9,41	-1,12	0,00387	0,308	207967_at	Vacuolar protein sorting 45 homolog (S. cerevisiae)	*VPS45*
1338	5,88	6,61	-1,12	0,00804	0,328	1553505_at	Alpha-2-macroglobulin-like 1	*A2ML1*
3667	6,19	6,96	-1,12	0,02651	0,395	1570336_at	3-hydroxybutyrate dehydrogenase, type 1	*BDH1*
3235	7,97	8,96	-1,12	0,02293	0,388	1557569_at	Mannose-P-dolichol utilization defect 1	*MPDU1*
4858	8,36	9,40	-1,12	0,03707	0,417	211484_s_at	Down syndrome cell adhesion molecule	*DSCAM*
3599	4,74	5,32	-1,12	0,02596	0,394	1559926_at	Hypothetical protein LOC728353	*LOC728353*
874	8,26	9,29	-1,12	0,00505	0,313	241361_at	Transcribed locus	-
4648	22,4	25,2	-1,12	0,03505	0,412	214699_x_at	WD repeat domain, phosphoinositide interacting 2	*WIPI2*
2544	9,10	10,2	-1,12	0,01720	0,369	236424_at	Centrosomal protein 250kDa	*CEP250*
2498	14,4	16,2	-1,12	0,01683	0,367	231401_s_at	-	-
2896	12,8	14,3	-1,12	0,02034	0,383	216143_at	cDNA DKFZp434L092	-
2906	4,48	5,04	-1,12	0,02042	0,383	234444_at	cDNA DKFZp434B0735	-
2341	9,93	11,2	-1,12	0,01562	0,364	241540_at	-	-
2275	6,19	6,95	-1,12	0,01513	0,363	1561944_at	cDNA clone IMAGE:5287444	-
356	4,17	4,69	-1,12	0,00183	0,280	207448_at	Protein O-fucosyltransferase 2	*POFUT2*
2831	4,54	5,10	-1,12	0,01976	0,381	213371_at	LIM domain binding 3	*LDB3*
5029	12,1	13,6	-1,12	0,03866	0,420	243045_at	SET and MYND domain containing 1	*SMYD1*
5301	31,4	35,3	-1,12	0,04138	0,426	37424_at	Coiled-coil alpha-helical rod protein 1	*CCHCR1*

Index	Mutated*	Normal*	FC	*P* value	FDR**	Probe set	Description	Gene symbol
6008	13,5	15,2	-1,12	0,04883	0,444	1553162_x_at	Chromosome 19 open reading frame 55	*C19orf55*
1016	5,44	6,11	-1,12	0,00588	0,316	221362_at	5-hydroxytryptamine (serotonin) receptor 5A	*HTR5A*
1055	10,3	11,5	-1,12	0,00618	0,319	1556586_x_at	cDNA clone IMAGE:5310697	-
3459	20,0	22,5	-1,12	0,02478	0,392	1563632_at	Hypothetical protein LOC220980	*LOC220980*
3951	4,41	4,96	-1,12	0,02887	0,399	233277_at	Deleted in lymphocytic leukemia, 7	*DLEU7*
2557	6,24	7,01	-1,12	0,01731	0,370	239187_at	Chromosome 4 open reading frame 30	*C4orf30*
4081	12,4	14,0	-1,12	0,02995	0,401	238266_at	Transcribed locus	-
2825	7,32	8,23	-1,12	0,01972	0,381	1555196_at	cDNA clone IMAGE:4825558	-
5391	11,4	12,8	-1,12	0,04227	0,429	231226_at	Hypothetical protein LOC728142	*LOC728142*
1616	4,70	5,28	-1,12	0,01013	0,343	240805_at	Transcribed locus	-
3732	21,6	24,3	-1,12	0,02709	0,397	221099_at	-	-
2818	4,20	4,72	-1,12	0,01967	0,381	240958_at	Unc-5 homolog C (C. elegans)	*UNC5C*
2886	8,08	9,08	-1,12	0,02024	0,383	228890_at	Atonal homolog 8 (Drosophila)	*ATOH8*
1423	6,13	6,89	-1,12	0,00863	0,331	1559948_at	cDNA FLJ20447 fis, clone KAT05276	-
4660	23,1	25,9	-1,12	0,03518	0,413	231228_at	BCL2-like 1	*BCL2L1*
5686	3,91	4,39	-1,12	0,04539	0,436	206930_at	Glycine-N-acyltransferase	*GLYAT*
5083	114	128	-1,12	0,03913	0,420	202495_at	Tubulin folding cofactor C	*TBCC*
4285	20,1	22,6	-1,12	0,03184	0,406	240508_at	-	-
1749	5,50	6,18	-1,12	0,01117	0,348	222345_at	Transcribed locus	-
1481	5,40	6,06	-1,12	0,00909	0,335	232241_at	-	-
3449	18,4	20,7	-1,12	0,02469	0,391	234214_at	cDNA FLJ39333 fis, clone OCBBF2017306	-
2524	7,84	8,80	-1,12	0,01704	0,369	214546_s_at	Purinergic receptor P2Y, G-protein coupled, 11	*P2RY11*
4763	7,50	8,42	-1,12	0,03610	0,414	207742_s_at	Nuclear receptor subfamily 6, group A, member 1	*NR6A1*
1448	15,6	17,5	-1,12	0,00881	0,333	1569361_a_at	Similar to Serine/arginine repetitive matrix 1	-
485	3,67	4,12	-1,12	0,00259	0,289	244001_at	Nucleosome assembly protein 1-like 4	*NAP1L4*
5633	10,2	11,4	-1,12	0,04497	0,436	242497_at	TRAF-type zinc finger domain containing 1	*TRAFD1*
5074	11,4	12,8	-1,12	0,03904	0,420	242684_at	Zinc finger protein 425	*ZNF425*
5079	13,7	15,3	-1,12	0,03907	0,420	210431_at	Alkaline phosphatase, placental-like 2	*ALPPL2*
6016	5,61	6,30	-1,12	0,04896	0,445	210015_s_at	Microtubule-associated protein 2	*MAP2*
3101	7,89	8,86	-1,12	0,02190	0,386	206610_s_at	Coagulation factor XI (plasma thromboplastin antecedent)	*F11*
314	3,82	4,29	-1,12	0,00159	0,272	231515_at	Transcribed locus	-
687	5,56	6,24	-1,12	0,00393	0,308	239584_at	cDNA FLJ35805 fis, clone TESTI2005982	-
738	3,88	4,36	-1,12	0,00420	0,308	243230_at	-	-
1335	8,30	9,32	-1,12	0,00802	0,328	1560068_a_at	Clone IMAGE:5762932, mRNA	-
3980	7,82	8,78	-1,12	0,02910	0,400	232243_at	Microcephaly, primary autosomal recessive 1	*MCPH1*
2368	9,16	10,3	-1,12	0,01580	0,364	230796_at	Hypothetical LOC440900	*LOC440900*
5712	7,44	8,34	-1,12	0,04574	0,438	234024_at	Cerebellin 4 precursor	*CBLN4*
2637	27,2	30,5	-1,12	0,01798	0,373	224923_at	Tetratricopeptide repeat domain 7A	*TTC7A*
1263	31,6	35,5	-1,12	0,00752	0,325	219333_s_at	Calpain 10	*CAPN10*
1180	4,72	5,30	-1,12	0,00693	0,321	240976_at	Transcribed locus	-
4942	5,48	6,15	-1,12	0,03793	0,419	234439_at	cDNA FLJ10235 fis, clone HEMBB1000339	-
838	4,22	4,73	-1,12	0,00480	0,313	214863_at	Full length insert cDNA clone ZC35F11	-
3935	4,27	4,79	-1,12	0,02875	0,399	238365_s_at	Hypothetical LOC339541	*MGC33556*
3338	6,18	6,94	-1,12	0,02369	0,388	217603_at	ATPase, H+ transporting, lysosomal V0 subunit a2	*ATP6V0A2*
1126	3,72	4,17	-1,12	0,00657	0,319	1564539_at	Hypothetical protein LOC647323	*LOC647323*
2504	5,16	5,79	-1,12	0,01685	0,367	237679_at	Tripartite motif-containing 66	*TRIM66*
698	3,46	3,88	-1,12	0,00401	0,308	243972_at	Transcribed locus	-
3208	8,16	9,15	-1,12	0,02272	0,387	229102_at	HIV-1 Tat interactive protein 2, 30kDa	*HTATIP2*
5561	6,42	7,20	-1,12	0,04429	0,435	220634_at	T-box 4	*TBX4*
2746	5,64	6,32	-1,12	0,01899	0,378	208376_at	Chemokine (C-C motif) receptor 4	*CCR4*
4841	10,2	11,5	-1,12	0,03690	0,417	233983_at	Transglutaminase 6	*TGM6*
2366	12,4	13,9	-1,12	0,01579	0,364	243576_at	-	-
1598	4,10	4,60	-1,12	0,00997	0,341	238308_at	Transcribed locus	-
576	3,77	4,23	-1,12	0,00316	0,300	207592_s_at	Brain cyclic nucleotide gated channel 2	*HCN2*
2130	5,37	6,03	-1,12	0,01401	0,359	237098_at	Chromosome 1 open reading frame 21	*C1orf21*
6090	12,8	14,3	-1,12	0,04972	0,446	1568719_s_at	Chromosome 6 open reading frame 85	*C6orf85*
3642	5,18	5,81	-1,12	0,02633	0,395	1553809_a_at	Chromosome 9 open reading frame 71	*C9orf71*

Index	Mutated*	Normal*	FC	*P* value	FDR**	Probe set	Description	Gene symbol
4992	7,36	8,25	-1,12	0,03831	0,419	233909_at	cDNA DKFZp564C0962	-
5994	4,31	4,84	-1,12	0,04874	0,444	207514_s_at	Guanine nucleotide binding protein (G protein), alpha transducing activity pol	*GNAT1*
3756	9,41	10,6	-1,12	0,02730	0,397	1569419_at	Clone IMAGE:4994945, mRNA	-
1237	6,87	7,70	-1,12	0,00736	0,324	240227_at	Mesoderm induction early response 1 homolog (Xenopus laevis)	*MIER1*
1487	7,26	8,15	-1,12	0,00916	0,336	221368_at	Sialidase 2 (cytosolic sialidase)	*NEU2*
58	3,08	3,45	-1,12	0,00022	0,201	1562699_at	Neural cell adhesion molecule 1	*NCAM1*
2058	5,69	6,38	-1,12	0,01343	0,356	1559867_at	cDNA FLJ32420 fis, clone SKMUS2000898	-
5080	9,01	10,1	-1,12	0,03908	0,420	1559522_at	cDNA FLJ40173 fis, clone TESTI2016922	-
2095	4,19	4,70	-1,12	0,01373	0,358	239126_at	Chromosome 19 open reading frame 23	*C19orf23*
381	4,15	4,65	-1,12	0,00199	0,284	207617_at	DEAD (Asp-Glu-Ala-Asp) box polypeptide 3, X-linked	*DDX3X*
4429	22,0	24,7	-1,12	0,03316	0,409	1566207_at	Transcription elongation factor A (SII), 1	*TCEA1*
4937	5,15	5,78	-1,12	0,03789	0,419	240672_at	-	-
4144	6,39	7,16	-1,12	0,03057	0,403	1561273_at	-	-
5366	12,0	13,5	-1,12	0,04212	0,429	241568_at	Transcribed locus	-
6116	11,3	12,7	-1,12	0,04993	0,446	216760_at	HRAS-like suppressor 2	*HRASLS2*
3113	5,11	5,73	-1,12	0,02199	0,386	1560589_a_at	Clone IMAGE:4657243, mRNA	-
4645	12,2	13,7	-1,12	0,03505	0,412	243435_at	KCNQ1 overlapping transcript 1	*KCNQ1OT1*
1770	7,40	8,29	-1,12	0,01129	0,348	213240_s_at	Keratin 4	*KRT4*
4838	8,41	9,42	-1,12	0,03689	0,417	228984_at	KIAA1394 protein	*KIAA1394*
4246	7,08	7,94	-1,12	0,03151	0,406	233445_at	Transcribed locus	-
5278	17,6	19,8	-1,12	0,04104	0,425	224203_at	Suppressor of fused homolog (Drosophila)	*SUFU*
1170	9,75	10,9	-1,12	0,00688	0,321	208354_s_at	Solute carrier family 12, member 3	*SLC12A3*
2010	7,62	8,54	-1,12	0,01311	0,355	236008_at	Chromosome 9 open reading frame 73	*C9orf73*
2838	9,44	10,6	-1,12	0,01981	0,382	211410_x_at	Killer cell immunoglobulin-like receptor 2DL5A	*KIR2DL5A*
5992	11,3	12,6	-1,12	0,04873	0,444	237507_at	Keratin 73	*KRT73*
2074	9,60	10,8	-1,12	0,01356	0,356	235495_at	Coiled-coil domain containing 97	*CCDC97*
5462	44,6	50,0	-1,12	0,04314	0,432	232581_x_at	Human immunodeficiency virus type I enhancer binding protein 3	*HIVEP3*
1661	3,45	3,86	-1,12	0,01049	0,345	1565838_at	cDNA FLJ35990 fis, clone TESTI2014415	-
2561	6,77	7,58	-1,12	0,01737	0,371	1553802_a_at	SRY (sex determining region Y)-box 3	*SOX3*
1589	7,64	8,56	-1,12	0,00988	0,340	237730_at	cDNA clone IMAGE:5269981	-
1411	7,97	8,93	-1,12	0,00852	0,330	206008_at	Transglutaminase 1	*TGM1*
4080	4,67	5,23	-1,12	0,02994	0,401	214498_at	Agouti signaling protein, nonagouti homolog (mouse)	*ASIP*
3748	6,16	6,90	-1,12	0,02725	0,397	240917_at	-	-
1547	4,33	4,86	-1,12	0,00955	0,337	1566680_at	cDNA FLJ37017 fis, clone BRACE2010642	-
1862	10,4	11,7	-1,12	0,01202	0,353	219748_at	Triggering receptor expressed on myeloid cells-like 2	*TREML2*
3822	12,7	14,2	-1,12	0,02789	0,399	1555650_at	Kelch-like 17 (Drosophila)	*KLHL17*
3689	6,09	6,82	-1,12	0,02665	0,395	224457_at	Hypothetical protein MGC12982	*MGC12982*
3205	6,93	7,76	-1,12	0,02269	0,387	209937_at	Transmembrane 4 L six family member 4	*TM4SF4*
3376	6,37	7,14	-1,12	0,02404	0,389	1568248_x_at	Small nucleolar RNA, H/ACA box 71B	*SNORA71B*
3195	4,62	5,17	-1,12	0,02264	0,387	1556505_at	cDNA clone IMAGE:4826545	-
2500	6,24	6,99	-1,12	0,01684	0,367	215340_at	Adenylate cyclase 1 (brain)	*ADCY1*
2354	38,8	43,4	-1,12	0,01571	0,364	219640_at	Claudin 15	*CLDN15*
5863	10,6	11,9	-1,12	0,04741	0,442	1558174_at	Family with sequence similarity 43, member A	*FAM43A*
5127	5,09	5,70	-1,12	0,03946	0,421	1556879_at	cDNA FLJ39461 fis, clone PROST2011660	-
3377	11,7	13,1	-1,12	0,02404	0,389	230887_at	CDC14 cell division cycle 14 homolog B (S. cerevisiae)	*CDC14B*
1165	8,54	9,56	-1,12	0,00685	0,321	231006_at	Spermatogenesis associated 8	*SPATA8*
729	7,41	8,30	-1,12	0,00417	0,308	221165_s_at	Interleukin 22	*IL22*
1596	15,0	16,8	-1,12	0,00995	0,341	234882_at	-	-
978	5,91	6,62	-1,12	0,00567	0,315	244309_at	Transcribed locus	-
5529	4,13	4,62	-1,12	0,04387	0,434	244879_at	-	-
6084	19,3	21,6	-1,12	0,04967	0,446	217159_x_at	Sialic acid binding Ig-like lectin 7	*SIGLEC7*
3712	5,02	5,62	-1,12	0,02691	0,396	220534_at	Tripartite motif-containing 48	*TRIM48*
2445	7,33	8,21	-1,12	0,01635	0,366	234246_at	-	-
2617	7,37	8,25	-1,12	0,01778	0,371	233395_at	cDNA FLJ12353 fis, clone MAMMA1002322	-
1729	11,4	12,7	-1,12	0,01105	0,348	1569212_at	Scavenger receptor protein family member	*LOC619207*
1849	4,46	4,99	-1,12	0,01190	0,352	207251_at	Meprin A, beta	*MEP1B*
1866	14,5	16,3	-1,12	0,01205	0,353	213337_s_at	Suppressor of cytokine signaling 1	*SOCS1*

Index	Mutated*	Normal*	FC	*P* value	FDR**	Probe set	Description	Gene symbol
1458	39,6	44,4	-1,12	0,00891	0,334	1553361_x_at	F-box and leucine-rich repeat protein 18	*FBXL18*
2596	6,03	6,75	-1,12	0,01765	0,371	240760_at	CMT1A duplicated region transcript 15	*CDRT15*
506	9,60	10,8	-1,12	0,00269	0,289	239608_at	1-acylglycerol-3-phosphate O-acyltransferase 7 (lysophosphatidic acid acyltra	*AGPAT7*
5898	6,02	6,73	-1,12	0,04775	0,443	242554_at	Two pore segment channel 2	*TPCN2*
1838	78,3	87,7	-1,12	0,01183	0,351	202513_s_at	Protein phosphatase 2, regulatory subunit B', delta isoform	*PPP2R5D*
3529	10,8	12,1	-1,12	0,02536	0,393	206064_s_at	Peptidylprolyl isomerase (cyclophilin)-like 2	*PPIL2*
3403	6,41	7,17	-1,12	0,02428	0,390	237757_at	Transcribed locus	-
4736	6,94	7,76	-1,12	0,03585	0,414	227885_at	Hypothetical LOC400236	*LOC400236*
3053	4,03	4,51	-1,12	0,02148	0,385	235809_at	Lin-54 homolog (C. elegans)	*LIN54*
3863	4,26	4,77	-1,12	0,02822	0,399	1559222_at	cDNA FLJ30725 fis, clone FCBBF4000415	-
5233	3,63	4,07	-1,12	0,04049	0,423	244459_at	Transcribed locus	-
3986	10,1	11,4	-1,12	0,02914	0,400	241276_at	-	-
2068	3,69	4,13	-1,12	0,01352	0,356	215746_at	(clone B3B3E13) chromosome 4p16.3 DNA fragment	-
1758	11,8	13,2	-1,12	0,01121	0,348	208539_x_at	Small proline-rich protein 2B	*SPRR2B*
4859	6,70	7,50	-1,12	0,03707	0,417	217471_at	cDNA DKFZp586B1324	-
4925	9,76	10,9	-1,12	0,03777	0,419	230268_at	Transcribed locus	-
3028	5,74	6,42	-1,12	0,02131	0,385	239323_at	cDNA clone IMAGE:5302680	-
5110	14,5	16,2	-1,12	0,03931	0,421	242933_at	Transcribed locus	-
3578	11,4	12,8	-1,12	0,02583	0,394	229972_at	Transcribed locus	-
1574	4,88	5,47	-1,12	0,00978	0,340	1561557_at	Lipase A, lysosomal acid, cholesterol esterase	*LIPA*
3437	6,91	7,73	-1,12	0,02460	0,391	243881_at	cDNA FLJ45325 fis, clone BRHIP3006717	-
5454	37,1	41,5	-1,12	0,04304	0,432	238594_x_at	Dual specificity phosphatase 8	*DUSP8*
1494	5,63	6,29	-1,12	0,00920	0,336	228085_at	cDNA clone IMAGE:4818335	-
1160	6,58	7,36	-1,12	0,00682	0,321	236190_at	Xylosyltransferase I	*XYLT1*
6042	10,3	11,5	-1,12	0,04921	0,445	216911_s_at	Hypermethylated in cancer 2	*HIC2*
4874	7,27	8,13	-1,12	0,03722	0,417	216597_at	Similar to Cationic trypsin III precursor (Pretrypsinogen III)	*LOC642150*
2995	14,0	15,7	-1,12	0,02110	0,385	1563485_at	cDNA DKFZp451D039	-
2598	4,76	5,33	-1,12	0,01765	0,371	231625_at	Solute carrier family 22, member 9	*SLC22A9*
403	3,67	4,11	-1,12	0,00212	0,286	244465_at	Hypothetical protein LOC283033	*LOC283033*
1060	7,32	8,19	-1,12	0,00621	0,319	1558230_at	Splicing factor 3b, subunit 2, 145kDa	*SF3B2*
737	5,02	5,62	-1,12	0,00420	0,308	1555834_at	Ubiquitin carboxyl-terminal esterase L1	*UCHL1*
5832	29,5	33,0	-1,12	0,04713	0,442	223663_at	Coiled-coil domain containing 88B	*CCDC88B*
3329	80,3	89,8	-1,12	0,02364	0,388	212431_at	KIAA0194 protein	*KIAA0194*
5089	5,95	6,66	-1,12	0,03917	0,420	1562045_at	cDNA FLJ34133 fis, clone FCBBF3010601	-
5133	12,3	13,8	-1,12	0,03950	0,421	233696_at	cDNA FLJ21357 fis, clone COL02835	-
3850	13,2	14,7	-1,12	0,02810	0,399	239707_at	Solute carrier family 5, member 10	*SLC5A10*
277	4,26	4,76	-1,12	0,00135	0,263	216622_at	Laminin, beta 4	*LAMB4*
6014	4,75	5,31	-1,12	0,04891	0,445	1562719_at	cDNA clone IMAGE:5297905	-
5404	58,7	65,7	-1,12	0,04241	0,429	212156_at	Vacuolar protein sorting 39 homolog (S. cerevisiae)	*VPS39*
2160	7,57	8,46	-1,12	0,01424	0,360	229929_at	SplA/ryanodine receptor domain and SOCS box containing 4	*SPSB4*
651	8,92	9,97	-1,12	0,00370	0,308	1563405_at	ATPase, H+/K+ exchanging, beta polypeptide	*ATP4B*
3002	3,77	4,21	-1,12	0,02113	0,385	1558601_at	Hypothetical protein LOC285194	*LOC285194*
3281	5,70	6,37	-1,12	0,02337	0,388	205124_at	Myocyte enhancer factor 2B	*MEF2B*
4417	4,92	5,50	-1,12	0,03305	0,409	206017_at	KIAA0319 protein	*KIAA0319*
1664	12,0	13,4	-1,12	0,01051	0,345	233782_at	WD repeat domain 68	*WDR68*
3308	14,2	15,9	-1,12	0,02353	0,388	241054_at	Transcribed locus	-
4734	5,61	6,27	-1,12	0,03583	0,414	1570541_s_at	Similar to Guanylate binding protein 3	*LOC729936*
4752	87,0	97,2	-1,12	0,03600	0,414	1569105_at	SET domain containing 5	*SETD5*
4295	17,7	19,8	-1,12	0,03193	0,406	210200_at	WW domain containing E3 ubiquitin protein ligase 2	*WWP2*
1553	3,55	3,97	-1,12	0,00958	0,337	216901_s_at	IKAROS family zinc finger 1 (Ikaros)	*IKZF1*
1076	7,31	8,17	-1,12	0,00632	0,319	1564319_at	Chromosome 19 open reading frame 16	*C19orf16*
5455	5,13	5,73	-1,12	0,04305	0,432	219139_s_at	KIAA1922 protein	*KIAA1922*
1707	7,02	7,85	-1,12	0,01091	0,348	211364_at	Methylthioadenosine phosphorylase	*MTAP*
6104	6,90	7,71	-1,12	0,04983	0,446	220902_at	Hypothetical LOC196707	*FLJ12616*
2669	21,5	24,1	-1,12	0,01825	0,374	229507_at	Chromosome 3 open reading frame 54	*C3orf54*
4177	6,91	7,72	-1,12	0,03088	0,404	236709_at	Similar to XP_529699.1	-
3703	12,1	13,5	-1,12	0,02678	0,395	220320_at	Docking protein 3	*DOK3*

Index	Mutated*	Normal*	FC	*P* value	FDR**	Probe set	Description	Gene symbol
1133	5,10	5,70	-1,12	0,00662	0,319	217242_at	Zinc finger protein 154	*ZNF154*
2545	12,6	14,1	-1,12	0,01720	0,369	239676_x_at	Hypothetical protein LOC642031	*LOC642031*
3266	14,4	16,1	-1,12	0,02321	0,388	1559204_x_at	v-KI-Ras2 Kirsten rat sarcoma viral oncogene homolog	*KRAS*
4243	11,1	12,4	-1,12	0,03148	0,406	230107_at	Transcribed locus	-
3442	16,3	18,2	-1,12	0,02463	0,391	239256_at	Transcribed locus	-
949	5,74	6,41	-1,12	0,00544	0,313	1559257_a_at	Membrane associated guanylate kinase inverted-1	*MAGI1*
1123	6,11	6,83	-1,12	0,00655	0,319	231621_at	Transcribed locus	-
4129	8,85	9,88	-1,12	0,03040	0,402	208888_s_at	Nuclear receptor co-repressor 2	*NCOR2*
3466	4,74	5,30	-1,12	0,02484	0,392	230749_s_at	Calcium/calmodulin-dependent protein kinase II delta	*CAMK2D*
5649	11,7	13,0	-1,12	0,04507	0,436	223884_at	Opticin	*OPTC*
3359	12,2	13,6	-1,12	0,02384	0,388	239396_at	cDNA clone IMAGE:4150640	-
2247	23,1	25,8	-1,12	0,01493	0,363	226737_at	Solute carrier family 25, member 42	*SLC25A42*
570	6,17	6,89	-1,12	0,00312	0,300	1560631_at	Calcium binding and coiled-coil domain 2	*CALCOCO2*
4572	6,02	6,72	-1,12	0,03457	0,412	206223_at	Lemur tyrosine kinase 2	*LMTK2*
2076	8,84	9,87	-1,12	0,01357	0,356	214064_at	Transferrin	*TF*
1395	5,17	5,77	-1,12	0,00843	0,330	1553673_at	Serine/threonine kinase 35	*STK35*
5520	16,2	18,0	-1,12	0,04379	0,433	221350_at	Homeobox C8	*HOXC8*
3526	22,7	25,3	-1,12	0,02532	0,393	225015_s_at	Serine/threonine kinase 40	*STK40*
4006	10,8	12,0	-1,12	0,02932	0,400	240623_at	Transcribed locus	-
4155	5,89	6,57	-1,12	0,03065	0,403	236865_at	Transcribed locus	-
1041	3,39	3,79	-1,12	0,00605	0,318	1563277_at	Full length insert cDNA YQ02E12	-
504	3,18	3,55	-1,12	0,00268	0,289	1561288_at	cDNA clone IMAGE:4838258	-
989	5,09	5,68	-1,12	0,00570	0,315	236786_at	Family with sequence similarity 135, member B	*FAM135B*
4132	3,51	3,92	-1,12	0,03041	0,402	242779_at	Transcribed locus	-
2466	17,4	19,5	-1,12	0,01657	0,367	216537_s_at	Sialic acid binding Ig-like lectin 7	*SIGLEC7*
1681	6,65	7,42	-1,12	0,01061	0,345	240809_at	Chromosome 21 open reading frame 121	*C21orf121*
5612	8,59	9,58	-1,12	0,04477	0,436	234287_at	mRNA partial cDNA sequence from cDNA selection, DCR1-8.0	-
3636	7,16	7,99	-1,12	0,02629	0,395	241454_at	Transcribed locus	-
512	45,5	50,7	-1,12	0,00273	0,291	33768_at	Dystrophia myotonica, WD repeat containing	*DMWD*
1161	11,5	12,8	-1,12	0,00683	0,321	217365_at	Similar to PRAME family member 6	*LOC729343*
5387	9,21	10,3	-1,12	0,04224	0,429	232764_at	Cyclin B2	*CCNB2*
1271	7,61	8,49	-1,12	0,00755	0,325	207940_x_at	Cannabinoid receptor 1 (brain)	*CNR1*
3701	5,94	6,63	-1,12	0,02677	0,395	215194_at	Protein kinase C, alpha	*PRKCA*
5427	9,47	10,6	-1,12	0,04270	0,430	240372_at	Transcribed locus	-
401	6,43	7,17	-1,12	0,00209	0,285	244863_at	Transcribed locus	-
3679	5,51	6,15	-1,12	0,02658	0,395	224258_at	Endozepine-like protein type 1 mutant	-
1173	5,18	5,78	-1,12	0,00689	0,321	1560856_at	Clone IMAGE:5742065, mRNA	-
4148	16,4	18,3	-1,12	0,03061	0,403	232091_s_at	Zinc finger, DHHC-type containing 24	*ZDHHC24*
5439	18,5	20,6	-1,12	0,04287	0,431	239628_at	Transcribed locus	-
152	3,19	3,56	-1,12	0,00070	0,244	208481_at	Ankyrin repeat and SOCS box-containing 4	*ASB4*
4072	6,43	7,17	-1,12	0,02986	0,401	234187_at	cDNA FLJ22754 fis, clone KAIA0615	-
2403	10,3	11,5	-1,12	0,01603	0,365	234037_s_at	cDNA FLJ22846 fis, clone KAIA555	-
1823	3,48	3,88	-1,12	0,01174	0,351	237050_at	Similar to Potassium channel tetramerisation domain containing 17 isoform 2	-
1586	15,1	16,9	-1,12	0,00987	0,340	222012_at	Hypothetical protein BC002926	*LOC90379*
4644	17,0	18,9	-1,12	0,03503	0,412	229496_at	CLP1, cleavage and polyadenylation factor I subunit, homolog (S. cerevisiae)	*CLP1*
2202	9,62	10,7	-1,12	0,01457	0,361	239257_at	Mov10l1, Moloney leukemia virus 10-like 1, homolog (mouse)	*MOV10L1*
4688	3,19	3,56	-1,12	0,03540	0,413	214554_at	Histone cluster 1, H2ak	*HIST1H2AK*
557	10,2	11,4	-1,12	0,00302	0,296	1553115_at	Naked cuticle homolog 1 (Drosophila)	*NKD1*
4195	14,6	16,3	-1,12	0,03098	0,404	238276_at	Transcribed locus	-
3875	13,4	15,0	-1,12	0,02829	0,399	230453_s_at	ATPase, Ca++ transporting, ubiquitous	*ATP2A3*
1610	6,58	7,34	-1,12	0,01009	0,342	244438_at	Similar to N-myc proto-oncogene protein	-
1189	4,79	5,34	-1,12	0,00703	0,322	240646_at	GTPase, IMAP family member 8	*GIMAP8*
2157	3,24	3,61	-1,12	0,01422	0,360	230673_at	Polycystic kidney and hepatic disease-like 1	*PKHD1L1*
3121	11,6	13,0	-1,12	0,02209	0,387	1557590_at	Hypothetical protein LOC147299	*LOC147299*
5179	12,1	13,5	-1,12	0,03991	0,421	242341_x_at	Glycerate kinase	*GLYCTK*
2639	4,78	5,33	-1,12	0,01799	0,373	243035_at	Transcribed locus	-
4454	7,00	7,81	-1,12	0,03345	0,411	213978_at	Actin-bundling protein with BAIAP2 homology	*ABBA-1*

Index	Mutated*	Normal*	FC	*P* value	FDR**	Probe set	Description	Gene symbol
4518	4,46	4,98	-1,12	0,03406	0,412	240209_at	Chromosome 16 open reading frame 78	*C16orf78*
829	4,42	4,93	-1,12	0,00474	0,312	215345_x_at	T cell receptor gamma variable 7	*TRGV7*
4954	6,36	7,10	-1,12	0,03800	0,419	217633_at	URB1 ribosome biogenesis 1 homolog (S. cerevisiae)	*URB1*
1140	4,48	4,99	-1,12	0,00668	0,320	1561706_at	cDNA DKFZp547N0516	-
2452	6,07	6,77	-1,12	0,01645	0,366	221186_at	cDNA FLJ12781 fis, clone NT2RP2001861	-
1692	5,22	5,82	-1,11	0,01071	0,346	233523_at	Chromosome 20 open reading frame 186	*C20orf186*
4386	5,46	6,09	-1,11	0,03268	0,407	213949_s_at	Deoxyhypusine hydroxylase/monooxygenase	*DOHH*
2101	8,91	9,93	-1,11	0,01378	0,358	207311_at	Double C2-like domains, beta	*DOC2B*
5892	17,8	19,9	-1,11	0,04766	0,442	223994_s_at	Solute carrier family 12, member 9	*SLC12A9*
4186	5,71	6,37	-1,11	0,03095	0,404	241398_at	Metallophosphoesterase domain containing 1	*MPPED1*
2308	4,52	5,04	-1,11	0,01532	0,363	232352_at	ISL LIM homeobox 2	*ISL2*
1416	5,10	5,69	-1,11	0,00858	0,331	221289_at	Distal-less homeobox 6	*DLX6*
3967	12,3	13,7	-1,11	0,02898	0,399	1554175_at	CD300 molecule-like family member b	*CD300LB*
4058	23,8	26,5	-1,11	0,02977	0,401	1563808_at	MCF.2 cell line derived transforming sequence-like	*MCF2L*
2227	39,4	43,9	-1,11	0,01480	0,363	218551_at	Invasion inhibitory protein 45	*MIIP*
863	4,90	5,46	-1,11	0,00497	0,313	215740_at	cDNA FLJ12573 fis, clone NT2RM4000979	-
5270	4,06	4,52	-1,11	0,04093	0,425	205289_at	Bone morphogenetic protein 2	*BMP2*
4331	5,66	6,31	-1,11	0,03224	0,407	210508_s_at	Potassium voltage-gated channel, KQT-like subfamily, member 2	*KCNQ2*
5823	6,97	7,77	-1,11	0,04705	0,442	1553544_at	G protein-coupled receptor 101	*GPR101*
3785	4,22	4,71	-1,11	0,02757	0,398	217177_s_at	cDNA FLJ13658 fis, clone PLACE1011567	-
4467	6,78	7,56	-1,11	0,03355	0,411	240891_at	Follistatin-like 1	*FSTL1*
5773	11,3	12,6	-1,11	0,04639	0,439	241747_s_at	Cullin 7	*CUL7*
5229	6,31	7,04	-1,11	0,04046	0,423	1570282_at	-	-
1040	4,81	5,36	-1,11	0,00605	0,318	1559568_at	cDNA DKFZp313C0731	-
3177	8,53	9,50	-1,11	0,02254	0,387	244520_at	Transcribed locus	-
1611	4,95	5,52	-1,11	0,01009	0,342	219839_x_at	T-cell leukemia/lymphoma 6	*TCL6*
3829	6,10	6,80	-1,11	0,02795	0,399	239094_at	Hypothetical protein LOC730961	*LOC730961*
3222	15,4	17,1	-1,11	0,02283	0,387	1552995_at	Interleukin 27	*IL27*
5355	7,25	8,08	-1,11	0,04201	0,429	205874_at	Inositol 1,4,5-trisphosphate 3-kinase A	*ITPKA*
4801	23,7	26,5	-1,11	0,03643	0,415	231305_at	Transcribed locus	-
2567	7,11	7,93	-1,11	0,01740	0,371	1555542_at	Actin filament associated protein 1-like 1	*AFAP1L1*
2514	3,78	4,21	-1,11	0,01693	0,368	1563092_at	mRNA full length insert cDNA clone EUROIMAGE 712308	-
5660	14,2	15,9	-1,11	0,04515	0,436	217095_x_at	Natural cytotoxicity triggering receptor 1	*NCR1*
589	4,74	5,29	-1,11	0,00325	0,301	216729_at	cDNA FLJ21735 fis, clone COLF3350	-
4199	22,8	25,4	-1,11	0,03104	0,404	1554516_at	Hypothetical protein LOC203274	*LOC203274*
1992	3,99	4,44	-1,11	0,01303	0,355	240732_at	Transcribed locus	-
4370	11,6	12,9	-1,11	0,03252	0,407	201269_s_at	NudC domain containing 3	*NUDCD3*
6009	6,13	6,83	-1,11	0,04883	0,444	204499_at	ATP/GTP binding protein 1	*AGTPBP1*
4420	45,7	50,8	-1,11	0,03309	0,409	221890_at	Zinc finger protein 335	*ZNF335*
4082	4,85	5,40	-1,11	0,02998	0,402	222055_at	Fumarylacetoacetate hydrolase domain containing 2A	*FAHD2A*
3373	22,6	25,2	-1,11	0,02400	0,389	231355_at	cDNA FLJ30598 fis, clone BRAWH2009263	-
939	3,98	4,44	-1,11	0,00538	0,313	222189_at	Hypothetical LOC646649	*LOC646649*
3432	7,88	8,77	-1,11	0,02457	0,391	231428_at	Transcribed locus	-
5519	24,9	27,8	-1,11	0,04379	0,433	216551_x_at	Phospholipase C, gamma 1	*PLCG1*
3928	5,86	6,52	-1,11	0,02873	0,399	238405_at	Transcribed locus	-
2954	12,7	14,1	-1,11	0,02074	0,384	244182_at	Clone IMAGE:5756056, mRNA	-
3481	16,8	18,7	-1,11	0,02499	0,392	207892_at	CD40 ligand (TNF superfamily, member 5, hyper-IgM syndrome)	*CD40LG*
2779	8,18	9,11	-1,11	0,01930	0,380	1560618_at	Clone IMAGE:5186867, mRNA	-
3886	21,8	24,3	-1,11	0,02838	0,399	223733_s_at	Protein phosphatase 4, regulatory subunit 1-like	*PPP4R1L*
612	4,30	4,79	-1,11	0,00346	0,308	231373_at	Ring finger protein 133	*RNF133*
3769	8,16	9,09	-1,11	0,02738	0,397	223508_at	Notch homolog 1, translocation-associated (Drosophila)	*NOTCH1*
4338	17,1	19,0	-1,11	0,03229	0,407	1561403_at	Spermatogenesis and oogenesis specific basic helix-loop-helix 1	*SOHLH1*
748	2,98	3,31	-1,11	0,00424	0,308	237551_at	URB1 ribosome biogenesis 1 homolog (S. cerevisiae)	*URB1*
5171	9,30	10,4	-1,11	0,03983	0,421	203673_at	Thyroglobulin	*TG*
5759	6,11	6,80	-1,11	0,04626	0,439	211380_s_at	Protein kinase, cGMP-dependent, type I	*PRKG1*
369	3,21	3,57	-1,11	0,00194	0,284	233886_at	cDNA DKFZp564F172	-
5905	26,5	29,5	-1,11	0,04784	0,443	209415_at	fizzy/cell division cycle 20 related 1 (Drosophila)	*FZR1*

Index	Mutated*	Normal*	FC	*P* value	FDR**	Probe set	Description	Gene symbol
5236	13,4	14,9	-1,11	0,04051	0,423	217490_at	cDNA DKFZp564P073	-
3556	4,75	5,29	-1,11	0,02565	0,394	223756_at	Hypothetical protein FLJ10081	*FLJ10081*
2961	8,61	9,59	-1,11	0,02081	0,384	204801_s_at	Dehydrogenase/reductase (SDR family) member 12	*DHRS12*
1225	11,2	12,4	-1,11	0,00729	0,324	223536_at	Pleckstrin and Sec7 domain containing 2	*PSD2*
907	4,37	4,87	-1,11	0,00524	0,313	1562116_at	Clone IMAGE:5191738, mRNA	-
1350	5,04	5,61	-1,11	0,00811	0,328	231150_at	Transcribed locus	-
5558	19,1	21,3	-1,11	0,04425	0,435	232907_at	Ubiquitin protein ligase E3 component n-recognin 4	*UBR4*
633	14,6	16,2	-1,11	0,00361	0,308	1566268_at	Full length insert cDNA YR25G06	-
2731	30,8	34,3	-1,11	0,01881	0,377	89948_at	Chromosome 20 open reading frame 67	*C20orf67*
4411	5,56	6,18	-1,11	0,03294	0,408	1569264_at	Hypothetical gene supported by BC013370	*LOC400655*
4181	9,43	10,5	-1,11	0,03091	0,404	235541_at	LAS1-like (S. cerevisiae)	*LAS1L*
2207	41,0	45,6	-1,11	0,01459	0,361	632_at	Glycogen synthase kinase 3 alpha	*GSK3A*
3133	5,95	6,62	-1,11	0,02222	0,387	217702_at	Interleukin 27 receptor, alpha	*IL27RA*
5776	10,7	11,9	-1,11	0,04647	0,440	1559478_at	cDNA clone IMAGE:5270289	-
5336	3,38	3,76	-1,11	0,04178	0,428	231449_at	Transcribed locus	-
5396	7,22	8,03	-1,11	0,04231	0,429	207792_at	Opioid receptor, delta 1	*OPRD1*
923	3,30	3,67	-1,11	0,00532	0,313	1562216_at	-	-
5805	19,4	21,6	-1,11	0,04685	0,441	223726_at	Potassium voltage-gated channel, subfamily H member 3	*KCNH3*
3680	11,4	12,7	-1,11	0,02658	0,395	1556669_a_at	Full length insert cDNA clone YR71G12	-
1886	5,12	5,70	-1,11	0,01224	0,355	231066_s_at	Chloride channel 4	*CLCN4*
307	3,13	3,48	-1,11	0,00148	0,263	237240_at	Transcribed locus	-
2169	24,2	26,9	-1,11	0,01435	0,361	1562981_at	Hemoglobin, beta	*HBB*
639	5,85	6,51	-1,11	0,00363	0,308	242867_x_at	Transcribed locus	-
1125	4,96	5,52	-1,11	0,00657	0,319	243441_at	Transcribed locus	-
3246	5,28	5,87	-1,11	0,02303	0,388	206417_at	Cyclic nucleotide gated channel alpha 1	*CNGA1*
1362	4,03	4,48	-1,11	0,00820	0,328	231742_at	Cone-rod homeobox	*CRX*
3908	38,9	43,3	-1,11	0,02853	0,399	204692_at	Leucine rich repeat neuronal 4	*LRCH4*
2538	3,30	3,67	-1,11	0,01717	0,369	1561678_at	cDNA clone IMAGE:5266579	-
3616	12,1	13,4	-1,11	0,02611	0,395	212389_at	SET binding factor 1	*SBF1*
4773	26,1	29,0	-1,11	0,03620	0,414	231553_s_at	Flavoprotein oxidoreductase MICAL3	*MICAL3*
2036	4,15	4,61	-1,11	0,01326	0,355	228872_at	Family with sequence similarity 108, member B1	*FAM108B1*
974	3,56	3,96	-1,11	0,00566	0,315	1564209_at	Hypothetical protein LOC282980	*LOC282980*
2805	8,54	9,50	-1,11	0,01952	0,380	207644_at	Forkhead box H1	*FOXH1*
3095	4,32	4,81	-1,11	0,02182	0,385	228659_at	-	-
3847	24,9	27,6	-1,11	0,02808	0,399	1557656_at	Hypothetical gene supported by AK093266	*LOC400238*
3369	11,1	12,3	-1,11	0,02396	0,389	234397_at	-	-
1518	5,12	5,69	-1,11	0,00938	0,337	210107_at	Chloride channel, calcium activated, family member 1	*CLCA1*
5550	14,0	15,5	-1,11	0,04413	0,435	1557630_s_at	cDNA clone IMAGE:5273415	-
2709	6,79	7,54	-1,11	0,01860	0,375	1559578_at	cDNA FLJ31857 fis, clone NT2RP7001156	-
3978	8,16	9,07	-1,11	0,02908	0,400	206986_at	Hypothetical protein LOC728985	*LOC728985*
6122	4,86	5,40	-1,11	0,04998	0,446	229332_at	4-hydroxyphenylpyruvate dioxygenase-like	*HPDL*
225	3,36	3,73	-1,11	0,00104	0,250	1570263_at	-	-
1354	5,01	5,57	-1,11	0,00813	0,328	1557693_at	cDNA clone IMAGE:5303580	-
4624	9,48	10,5	-1,11	0,03488	0,412	234575_at	Zinc finger protein 71	*ZNF71*
5128	3,67	4,08	-1,11	0,03946	0,421	223796_at	Contactin associated protein-like 3	*CNTNAP3*
2663	4,96	5,51	-1,11	0,01819	0,374	207359_at	Calcium/calmodulin-dependent protein kinase kinase 2, beta	*CAMKK2*
3215	6,51	7,24	-1,11	0,02277	0,387	238373_at	H1 histone family, member N, testis-specific	*H1FNT*
3392	5,11	5,68	-1,11	0,02416	0,389	1560153_at	Fraser syndrome 1	*FRAS1*
3535	32,1	35,7	-1,11	0,02543	0,393	1563315_s_at	Glutamate-rich 1	*ERICH1*
5537	4,15	4,61	-1,11	0,04396	0,434	224195_at	Testis-specific transcript, Y-linked 12	*TTTY12*
4545	8,33	9,25	-1,11	0,03436	0,412	228079_at	Chromosome 3 open reading frame 58	*C3orf58*
3206	8,56	9,51	-1,11	0,02270	0,387	243343_at	Transcribed locus	-
2582	14,6	16,2	-1,11	0,01752	0,371	221328_at	Claudin 17	*CLDN17*
5971	9,32	10,4	-1,11	0,04849	0,444	216019_x_at	Pleckstrin homology-like domain, family B, member 1	*PHLDB1*
1732	5,65	6,28	-1,11	0,01105	0,348	216226_at	Transcription initiation factor TFIID 105 kDa subunit	*TAF4B*
4257	7,46	8,28	-1,11	0,03163	0,406	233733_at	cDNA DKFZp434E1920	-
2625	5167	5741	-1,11	0,01784	0,372	1553551_s_at	-	-

Index	Mutated*	Normal*	FC	*P* value	FDR**	Probe set	Description	Gene symbol
5064	7,61	8,45	-1,11	0,03897	0,420	243987_at	Similar to XP_001136680.1	-
4394	5,75	6,39	-1,11	0,03275	0,407	1554115_at	Hypothetical gene LOC133874	*LOC133874*
2392	4,27	4,74	-1,11	0,01596	0,365	237275_at	Similar to Otoconin 90	-
82	3,71	4,12	-1,11	0,00031	0,201	241055_at	Endothelial PAS domain protein 1	*EPAS1*
1931	15,7	17,4	-1,11	0,01258	0,355	1555742_at	-	-
3085	5,96	6,62	-1,11	0,02174	0,385	234456_at	Trafficking protein particle complex 4	*TRAPPC4*
5574	4,61	5,13	-1,11	0,04439	0,435	1560399_a_at	OTU domain containing 7A	*OTUD7A*
4479	6,95	7,73	-1,11	0,03369	0,411	240169_at	Full length insert cDNA clone YO64F11	-
586	7,85	8,72	-1,11	0,00324	0,301	235909_at	Hypothetical gene supported by BC040598	*LOC400960*
5815	4,59	5,10	-1,11	0,04698	0,442	221323_at	UL16 binding protein 1	*ULBP1*
1525	3,71	4,13	-1,11	0,00942	0,337	1558534_at	Hypothetical gene LOC283846	-
2384	6,11	6,79	-1,11	0,01589	0,364	1557908_at	cDNA FLJ37090 fis, clone BRACE2017587	-
5297	6,29	6,99	-1,11	0,04127	0,426	228807_at	-	-
3063	11,4	12,6	-1,11	0,02159	0,385	215420_at	Indian hedgehog homolog (Drosophila)	*IHH*
3446	18,0	20,0	-1,11	0,02466	0,391	1558211_s_at	v-src sarcoma (Schmidt-Ruppin A-2) viral oncogene homolog (avian)	*SRC*
1916	7,71	8,56	-1,11	0,01250	0,355	241892_at	Transcribed locus	-
1440	5,79	6,43	-1,11	0,00876	0,332	222285_at	immunoglobulin heavy constant delta	*IGHD*
3293	8,92	9,91	-1,11	0,02345	0,388	235087_at	Unkempt homolog (Drosophila)-like	*UNKL*
3893	11,2	12,4	-1,11	0,02844	0,399	1555021_a_at	Scavenger receptor class F, member 1	*SCARF1*
1265	20,2	22,4	-1,11	0,00753	0,325	211350_s_at	Chromosome 6 open reading frame 54	*C6orf54*
2898	24,7	27,4	-1,11	0,02035	0,383	223525_at	Delta-like 4 (Drosophila)	*DLL4*
832	3,55	3,95	-1,11	0,00475	0,312	1566279_at	-	-
695	2,91	3,23	-1,11	0,00400	0,308	1562443_at	Retinaldehyde binding protein 1-like 2	*RLBP1L2*
6082	7,91	8,78	-1,11	0,04966	0,446	231454_at	Placenta-specific 4	*PLAC4*
2730	12,2	13,6	-1,11	0,01881	0,377	214898_x_at	Mucin 3B, cell surface associated	*MUC3B*
5849	8,97	9,96	-1,11	0,04730	0,442	1555063_at	Ubiquitin specific peptidase 6	*USP6*
4870	8,19	9,09	-1,11	0,03718	0,417	222695_s_at	Axin 2 (conductin, axil)	*AXIN2*
2675	4,97	5,52	-1,11	0,01830	0,374	237558_at	Transcribed locus	-
2323	4,16	4,61	-1,11	0,01546	0,364	1562965_at	Clone IMAGE:5744268, mRNA	-
5115	16,8	18,7	-1,11	0,03938	0,421	233486_at	Hypothetical protein LOC729940	*LOC729940*
5383	6,03	6,70	-1,11	0,04221	0,429	243376_at	TRAF family member-associated NFKB activator	*TANK*
4561	4,30	4,77	-1,11	0,03446	0,412	206078_at	Kalirin, RhoGEF kinase	*KALRN*
4443	30,3	33,7	-1,11	0,03338	0,411	210737_at	Tubby homolog (mouse)	*TUB*
1687	4,27	4,74	-1,11	0,01066	0,345	207913_at	Similar to Cytochrome P450, family 2, subfamily F, polypeptide 1	*LOC731992*
4188	5,38	5,97	-1,11	0,03096	0,404	240283_at	-	-
5443	14,5	16,1	-1,11	0,04293	0,431	214968_at	DEAD (Asp-Glu-Ala-Asp) box polypeptide 51	*DDX51*
5456	7,50	8,33	-1,11	0,04308	0,432	206839_at	Chromosome 22 open reading frame 31	*C22orf31*
4014	6,71	7,45	-1,11	0,02939	0,400	244577_at	Transcribed locus	-
2837	4,83	5,36	-1,11	0,01980	0,382	224086_at	-	-
4251	18,6	20,6	-1,11	0,03157	0,406	211624_s_at	Dopamine receptor D2	*DRD2*
4663	21,8	24,2	-1,11	0,03520	0,413	216481_at	Glutamate receptor interacting protein 2	*GRIP2*
869	3,70	4,11	-1,11	0,00502	0,313	231501_at	Similar to XP_001141902.1	-
763	5,84	6,49	-1,11	0,00430	0,308	1567540_at	Sperm associated antigen 10	*SPAG10*
4854	24,8	27,5	-1,11	0,03701	0,417	210226_at	Nuclear receptor subfamily 4, group A, member 1	*NR4A1*
3702	6,14	6,82	-1,11	0,02677	0,395	234671_at	Keratin associated protein 4-2	*KRTAP4-2*
438	4,18	4,63	-1,11	0,00232	0,288	240640_at	-	-
3197	7,32	8,13	-1,11	0,02265	0,387	244127_at	Transcribed locus	-
5985	3,81	4,22	-1,11	0,04861	0,444	210492_at	Microfibrillar-associated protein 3-like	*MFAP3L*
2752	10,0	11,1	-1,11	0,01905	0,378	244421_at	Transcribed locus	-
4131	6,27	6,96	-1,11	0,03041	0,402	237207_at	Transcribed locus	-
4268	7,32	8,12	-1,11	0,03174	0,406	1557279_at	intersectin 1 (SH3 domain protein)	*ITSN1*
5590	13,8	15,3	-1,11	0,04458	0,436	210457_x_at	High mobility group AT-hook 1	*HMGA1*
294	3,80	4,22	-1,11	0,00144	0,263	210921_at	-	-
4814	15,1	16,8	-1,11	0,03659	0,416	216183_at	Transglutaminase 2	*TGM2*
3519	4,71	5,23	-1,11	0,02526	0,392	1564443_at	Deleted in lymphocytic leukemia, 2	*DLEU2*
429	6,27	6,96	-1,11	0,00226	0,288	207385_at	Transcription factor Dp family, member 3	*TFDP3*
4035	4,71	5,22	-1,11	0,02956	0,401	214599_at	Involucrin	*IVL*

Index	Mutated*	Normal*	FC	*P* value	FDR**	Probe set	Description	Gene symbol
2173	8,64	9,58	-1,11	0,01436	0,361	240497_at	-	-
5327	8,36	9,28	-1,11	0,04164	0,427	240001_at	-	-
2206	7,64	8,48	-1,11	0,01459	0,361	217077_s_at	Gamma-aminobutyric acid (GABA) B receptor, 2	*GABBR2*
4134	20,9	23,2	-1,11	0,03043	0,402	236441_at	Transcribed locus	-
840	5,31	5,89	-1,11	0,00481	0,313	1554372_at	-	-
3579	3,94	4,37	-1,11	0,02584	0,394	236638_at	Transcribed locus	-
1377	3,76	4,17	-1,11	0,00830	0,329	234603_at	cDNA DKFZp566E213	-
5284	4,36	4,84	-1,11	0,04110	0,425	230480_at	Piwi-like 4 (Drosophila)	*PIWIL4*
2029	4,05	4,50	-1,11	0,01323	0,355	1569283_at	HCG1646157 protein	-
660	12,8	14,2	-1,11	0,00382	0,308	244307_s_at	Synaptotagmin XV	*SYT15*
5260	6,34	7,03	-1,11	0,04085	0,425	240565_at	Zinc finger protein 28 homolog (mouse)	*ZFP28*
3315	3,51	3,89	-1,11	0,02356	0,388	1556476_at	Hypothetical protein LOC283485	*LOC283485*
1206	3,46	3,83	-1,11	0,00715	0,324	231160_at	Transcribed locus	-
2255	6,10	6,77	-1,11	0,01501	0,363	234239_at	cDNA FLJ21668 fis, clone COL08982	-
4204	5,94	6,59	-1,11	0,03109	0,404	1554583_a_at	Hypothetical protein MGC50559	*MGC50559*
4977	5,09	5,64	-1,11	0,03819	0,419	210602_s_at	Cadhetrin 6, type 2, K-Cadhetrin (fetal kidney)	*CDH6*
3693	18,4	20,4	-1,11	0,02668	0,395	208347_at	-	-
1645	3,64	4,04	-1,11	0,01036	0,344	1562712_at	Clone IMAGE:5165425, mRNA	-
4785	13,3	14,8	-1,11	0,03628	0,414	203937_s_at	Transcription initiation factor SL1/TIF-IB subunit C	*TAF1C*
1892	5,82	6,46	-1,11	0,01228	0,355	1553031_at	G protein-coupled receptor 115	*GPR115*
561	3,85	4,27	-1,11	0,00306	0,298	233283_at	cDNA FLJ14025 fis, clone HEMBA1003667	-
910	4,96	5,50	-1,11	0,00525	0,313	208563_x_at	POU class 3 homeobox 3	*POU3F3*
3440	9,16	10,2	-1,11	0,02463	0,391	1556107_at	cDNA DKFZp667C1617	-
5008	64,9	72,0	-1,11	0,03847	0,420	206635_at	Cholinergic receptor, nicotinic, beta 2 (neuronal)	*CHRNB2*
2556	4,81	5,33	-1,11	0,01729	0,370	1563171_at	cDNA clone IMAGE:5165280	-
2277	6,83	7,58	-1,11	0,01514	0,363	215594_at	PTR2 mRNA for repetitive sequence	-
4551	8,32	9,23	-1,11	0,03441	0,412	232913_at	Transmembrane emp24 protein transport domain containing 8	*TMED8*
2671	9,45	10,5	-1,11	0,01826	0,374	231224_x_at	Protein kinase, AMP-activated, gamma 2 non-catalytic subunit	*PRKAG2*
5505	126	140	-1,11	0,04359	0,433	1569522_at	Clone IMAGE:4424208, mRNA	-
1159	9,02	10,0	-1,11	0,00681	0,321	221112_at	Interleukin 1 receptor accessory protein-like 2	*IL1RAPL2*
6070	20,6	22,9	-1,11	0,04955	0,446	1566954_at	cDNA FLJ20891 fis, clone ADKA03345	-
4445	8,76	9,72	-1,11	0,03340	0,411	211147_s_at	Purinergic receptor P2X-like 1, orphan receptor	*P2RXL1*
943	6,47	7,18	-1,11	0,00541	0,313	1558770_a_at	Chromosome 17 open reading frame 38	*C17orf38*
4556	8,79	9,75	-1,11	0,03444	0,412	1559977_a_at	Solute carrier family 25, member 34	*SLC25A34*
5871	29,8	33,0	-1,11	0,04744	0,442	204056_s_at	Mevalonate kinase (mevalonic aciduria)	*MVK*
3321	8,18	9,07	-1,11	0,02359	0,388	1563842_at	Phosphatidylinositol glycan anchor biosynthesis, class G	*PIGG*
1600	5,35	5,93	-1,11	0,00998	0,341	220908_at	Coiled-coil domain containing 33	*CCDC33*
983	3,29	3,64	-1,11	0,00569	0,315	244240_at	-	-
935	6,09	6,75	-1,11	0,00536	0,313	236320_at	Coiled-coil domain containing 17	*CCDC17*
3993	6,68	7,40	-1,11	0,02920	0,400	1562641_at	Family with sequence similarity 122C	*FAM122C*
2695	98,5	109	-1,11	0,01848	0,375	1556507_at	cDNA clone IMAGE:5267328	-
3891	11,5	12,8	-1,11	0,02844	0,399	240744_at	Carboxypeptidase A5	*CPA5*
2505	30,4	33,7	-1,11	0,01685	0,367	221180_at	Yeast Sps1/Ste20-related kinase 4 (S. cerevisiae)	*YSK4*
3920	16,5	18,3	-1,11	0,02863	0,399	1559402_a_at	Chromosome 1 open reading frame 61	*C1orf61*
1983	19,1	21,2	-1,11	0,01295	0,355	227090_at	PHD finger protein 21A	*PHF21A*
3569	10,5	11,6	-1,11	0,02577	0,394	207187_at	Janus kinase 3 (a protein tyrosine kinase, leukocyte)	*JAK3*
2136	61,2	67,8	-1,11	0,01404	0,359	31861_at	Immunoglobulin mu binding protein 2	*IGHMBP2*
5183	5,00	5,54	-1,11	0,03995	0,421	1554940_a_at	Hypothetical LOC388882	*LOC388882*
3320	5,80	6,43	-1,11	0,02359	0,388	1552917_at	Interleukin 29 (Interferon, lambda 1)	*IL29*
5653	14,4	16,0	-1,11	0,04510	0,436	1562434_at	Unkempt homolog (Drosophila)	*UNK*
3839	8,31	9,21	-1,11	0,02804	0,399	1562674_at	Clone IMAGE:5165176, mRNA	-
3407	3,96	4,39	-1,11	0,02430	0,390	215409_at	1-acylglycerol-3-phosphate O-acyltransferase 7 (lysophosphatidic acid acyltra	*AGPAT7*
4009	6,30	6,98	-1,11	0,02934	0,400	242535_at	Transcribed locus	-
2256	8,02	8,89	-1,11	0,01502	0,363	206913_at	Bile acid Coenzyme A: amino acid N-acyltransferase	*BAAT*
2722	5,84	6,47	-1,11	0,01871	0,376	238321_at	TEA domain family member 2	*TEAD2*
1608	4,87	5,40	-1,11	0,01007	0,342	1556999_at	Hypothetical protein LOC285045	*LOC285045*
4041	6,63	7,35	-1,11	0,02962	0,401	234534_at	cDNA FLJ20100 fis, clone COL04648	-

Index	Mutated*	Normal*	FC	*P* value	FDR**	Probe set	Description	Gene symbol
5796	7,09	7,85	-1,11	0,04675	0,441	240157_at	Transcribed locus	-
421	3,11	3,45	-1,11	0,00221	0,286	234581_at	cDNA FLJ21257 fis, clone COL01407	-
5091	10,4	11,5	-1,11	0,03917	0,420	1552646_at	Interleukin 11 receptor, alpha	*IL11RA*
2885	8,54	9,46	-1,11	0,02024	0,383	1567298_at	Olfactory receptor, family 13, subfamily C, member 4	*OR13C4*
1978	3,97	4,39	-1,11	0,01292	0,355	233887_at	G protein-coupled receptor 126	*GPR126*
494	6,31	6,99	-1,11	0,00264	0,289	230138_at	Frequenin homolog (Drosophila)	*FREQ*
3608	5,04	5,58	-1,11	0,02603	0,394	223881_at	Islet cell autoantigen 1,69kDa-like	*ICA1L*
1827	4,01	4,44	-1,11	0,01177	0,351	1562384_at	Chromosome 21 mRNA sequence	-
2867	9,09	10,1	-1,11	0,02011	0,383	219672_at	Erythroid associated factor	*ERAF*
5234	30,1	33,4	-1,11	0,04050	0,423	216791_at	Transmembrane protein 92	*TMEM92*
3892	6,11	6,77	-1,11	0,02844	0,399	217459_at	cDNA DKFZp434L1016	-
4203	25,5	28,3	-1,11	0,03108	0,404	214444_s_at	Poliovirus receptor	*PVR*
2289	6,62	7,33	-1,11	0,01521	0,363	206844_at	Fructose-1,6-bisphosphatase 2	*FBP2*
3414	12,0	13,2	-1,11	0,02437	0,390	215875_at	cDNA FLJ23167 fis, clone LNG09902	-
5000	18,6	20,6	-1,11	0,03839	0,420	217033_x_at	Neurotrophic tyrosine kinase, receptor, type 3	*NTRK3*
3997	15,7	17,4	-1,11	0,02927	0,400	237736_at	Transcribed locus	-
1061	31,3	34,7	-1,11	0,00623	0,319	202523_s_at	SPARC/osteonectin, CWCV, and Kazal-like domains proteoglycan 2	*SPOCK2*
4310	4,82	5,34	-1,11	0,03209	0,407	232920_at	Hypothetical LOC550631	*LOC550631*
3294	6,09	6,75	-1,11	0,02345	0,388	1555051_at	Chromosome 10 open reading frame 53	*C10orf53*
1689	5,32	5,89	-1,11	0,01067	0,345	241046_at	Transcribed locus	-
1775	11,5	12,7	-1,11	0,01130	0,348	206455_s_at	Rhodopsin (opsin 2, rod pigment)	*RHO*
4782	14,5	16,0	-1,11	0,03627	0,414	1555343_at	Multiple EGF-like-domains 10	*MEGF10*
2697	5,00	5,54	-1,11	0,01850	0,375	233752_s_at	Zinc finger homeobox 3	*ZFHX3*
736	18,4	20,4	-1,11	0,00420	0,308	1561171_a_at	FLJ40198 protein	*FLJ36131*
3457	5,19	5,74	-1,11	0,02477	0,392	241013_at	Family with sequence similarity 124A	*FAM124A*
3144	6,61	7,32	-1,11	0,02231	0,387	215476_at	Clone 23726 mRNA sequence	-
2200	4,32	4,79	-1,11	0,01454	0,361	214576_at	Keratin 36	*KRT36*
4984	13,5	15,0	-1,11	0,03825	0,419	230253_at	Signal peptide, CUB domain, EGF-like 3	*SCUBE3*
1155	7,25	8,03	-1,11	0,00678	0,321	239327_at	Transcribed locus	-
4953	9,92	11,0	-1,11	0,03799	0,419	1566484_at	cDNA DKFZp666K2010	-
4349	5,40	5,98	-1,11	0,03239	0,407	216779_at	Cylicin, basic protein of sperm head cytoskeleton 1	*CYLC1*
1326	4,34	4,80	-1,11	0,00798	0,328	1556645_s_at	Clone IMAGE:6016214, mRNA	-
1113	6,59	7,29	-1,11	0,00651	0,319	234206_at	cDNA FLJ21271 fis, clone COL01751	-
1619	6,15	6,81	-1,11	0,01017	0,343	1556914_at	cDNA clone IMAGE:4838482	-
5806	5,43	6,01	-1,11	0,04686	0,441	206454_s_at	Rhodopsin (opsin 2, rod pigment)	*RHO*
3982	3,47	3,84	-1,11	0,02913	0,400	1566140_at	Homeodomain-only protein	*HOP*
1722	4,40	4,87	-1,11	0,01103	0,348	240722_at	Transcribed locus	-
5180	36,1	40,0	-1,11	0,03993	0,421	36888_at	KIAA0841 protein	*KIAA0841*
2261	5,27	5,84	-1,11	0,01505	0,363	230975_at	Transcribed locus	-
3894	7,74	8,56	-1,11	0,02845	0,399	207969_x_at	Acrosomal vesicle protein 1	*ACRV1*
3915	3,52	3,89	-1,11	0,02860	0,399	232562_at	cDNA FLJ11554 fis, clone HEMBA1003037	-
564	5,21	5,77	-1,11	0,00309	0,299	234027_at	Coiled-coil domain containing 129	*CCDC129*
2434	6,26	6,93	-1,11	0,01627	0,365	1559354_a_at	Full length insert cDNA YQ09C04	-
828	3,63	4,02	-1,11	0,00472	0,312	1560298_at	cDNA clone IMAGE:4814133	-
4659	17,3	19,1	-1,11	0,03518	0,413	206998_x_at	Proline-rich protein BstNI subfamily 1	*PRB1*
3934	6,25	6,91	-1,11	0,02874	0,399	1569219_at	Clone IMAGE:4655360, mRNA	-
2464	9,58	10,6	-1,11	0,01654	0,367	214256_at	ATPase, Class V, type 10A	*ATP10A*
4059	9,55	10,6	-1,11	0,02978	0,401	1562239_at	Small G protein signaling modulator 1	*SGSM1*
5001	16,7	18,4	-1,11	0,03840	0,420	208277_at	Paired-like homeodomain 3	*PITX3*
1706	13,4	14,8	-1,11	0,01089	0,348	220045_at	Neurogenic differentiation 6	*NEUROD6*
2320	3,80	4,20	-1,11	0,01541	0,363	230478_at	Oncoprotein induced transcript 3	*OIT3*
2758	5,94	6,57	-1,11	0,01914	0,379	243322_at	Transcribed locus	-
2911	13,1	14,5	-1,11	0,02045	0,383	1566994_at	Clone GCRG114 mRNA sequence	-
5753	8,31	9,19	-1,11	0,04618	0,439	1562681_at	Keratin associated protein 5-2	*KRTAP5-2*
524	3,42	3,79	-1,11	0,00279	0,291	234852_at	Hypothetical protein LOC648859	*LOC648859*
4010	5,53	6,12	-1,11	0,02936	0,400	236148_at	Full length insert cDNA clone YA80A03	-
3140	6,14	6,79	-1,11	0,02227	0,387	243079_x_at	Transcribed locus	-

Index	Mutated*	Normal*	FC	*P* value	FDR**	Probe set	Description	Gene symbol
1178	5,96	6,59	-1,11	0,00692	0,321	236127_at	Transcribed locus	-
2793	4,90	5,42	-1,11	0,01941	0,380	236291_at	Retinol dehydrogenase 5 (11-cis/9-cis)	*RDH5*
2862	12,9	14,3	-1,11	0,02010	0,383	234356_at	cDNA DKFZP434K028	-
2900	7,70	8,52	-1,11	0,02036	0,383	232863_at	Zinc finger protein 815	*ZNF815*
4013	6,55	7,24	-1,11	0,02939	0,400	1560149_at	Solute carrier family 29, member 2	*SLC29A2*
4768	19,1	21,1	-1,11	0,03614	0,414	237378_at	FLJ46321 protein	*FLJ46321*
3922	5,99	6,62	-1,11	0,02864	0,399	237765_at	Chromosome 14 open reading frame 68	*C14orf68*
4099	6,13	6,78	-1,11	0,03013	0,402	231611_at	Similar to XP_001104477.1	-
2030	4,75	5,25	-1,11	0,01323	0,355	236343_at	Transcribed locus	-
1964	8,04	8,89	-1,11	0,01284	0,355	206812_at	Adrenergic, beta-3-, receptor	*ADRB3*
170	3,25	3,59	-1,11	0,00079	0,244	236618_at	Chromosome 20 open reading frame 132	*C20orf132*
5148	4,04	4,47	-1,11	0,03964	0,421	242723_at	Transcribed locus	-
5358	9,15	10,1	-1,11	0,04201	0,429	241053_at	Hypothetical protein LOC730184	*LOC730184*
2865	5,33	5,89	-1,11	0,02011	0,383	206775_at	Cubilin (intrinsic factor-cobalamin receptor)	*CUBN*
459	2,95	3,26	-1,11	0,00245	0,288	237514_at	cDNA clone IMAGE:5267328	-
1220	3,30	3,65	-1,11	0,00726	0,324	1560284_at	cDNA clone IMAGE:5271145	-
1148	18,6	20,6	-1,11	0,00675	0,321	230157_at	Cadhetrin-like 24	*CDH24*
190	2,89	3,20	-1,11	0,00088	0,244	206676_at	Carcinoembryonic antigen-related cell adhesion molecule 8	*CEACAM8*
1129	3,76	4,15	-1,11	0,00659	0,319	224209_s_at	Guanine deaminase	*GDA*
2118	5,70	6,30	-1,11	0,01389	0,359	1554974_at	Aspartoacylase (aminocyclase) 3	*ACY3*
3588	11,0	12,2	-1,11	0,02589	0,394	242848_x_at	Transcribed locus	-
2093	4,57	5,05	-1,11	0,01367	0,357	1562327_at	cDNA clone IMAGE:4794893	-
3758	6,10	6,74	-1,11	0,02731	0,397	1566232_at	cDNA DKFZp667I0318	-
4585	5,00	5,52	-1,11	0,03465	0,412	230859_at	Transcribed locus	-
3813	13,2	14,6	-1,11	0,02779	0,398	208034_s_at	Protein Z, vitamin K-dependent plasma glycoProtein	*PROZ*
767	14,3	15,8	-1,11	0,00437	0,311	1554580_a_at	WW domain containing E3 ubiquitin protein ligase 2	*WWP2*
1528	3,09	3,41	-1,11	0,00945	0,337	1568755_a_at	cDNA clone IMAGE:5267015	-
669	3,68	4,06	-1,11	0,00384	0,308	1560895_at	Hypothetical LOC645188	*LOC645188*
761	5,07	5,60	-1,11	0,00430	0,308	224539_s_at	Protocadherin alpha subfamily C, 2	*PCDHAC2*
3609	57,3	63,3	-1,11	0,02605	0,394	1553359_at	F-box and leucine-rich repeat protein 18	*FBXL18*
1612	3,69	4,08	-1,11	0,01010	0,343	231642_at	Chromosome 6 open reading frame 201	*C6orf201*
3219	7,36	8,13	-1,11	0,02281	0,387	220776_at	Potassium inwardly-rectifying channel, subfamily J, member 14	*KCNJ14*
4861	12,3	13,6	-1,10	0,03709	0,417	244711_at	Transcribed locus	-
4497	6,89	7,62	-1,10	0,03383	0,411	207316_at	Hyaluronan synthase 1	*HAS1*
3983	4,06	4,48	-1,10	0,02914	0,400	1559033_at	Hypothetical protein LOC255167	*LOC255167*
4369	4,25	4,69	-1,10	0,03251	0,407	1561693_at	Hypothetical gene supported by BC030596	*LOC400794*
1986	12,6	13,9	-1,10	0,01297	0,355	232880_at	cDNA DKFZp434E145	-
1536	4,55	5,03	-1,10	0,00951	0,337	240534_at	Transcribed locus	-
5937	23,4	25,9	-1,10	0,04814	0,443	1553572_a_at	Cytoglobin	*CYGB*
2986	3,34	3,69	-1,10	0,02100	0,384	237268_at	Down syndrome cell adhesion molecule	*DSCAM*
5147	12,4	13,7	-1,10	0,03962	0,421	216145_at	Velo-cardio-facial syndrome 22q11 region mRNA sequence	
3176	24,4	27,0	-1,10	0,02253	0,387	1556722_a_at	Hypothetical protein FLJ33706	*FLJ33706*
5588	17,7	19,6	-1,10	0,04457	0,436	1553656_at	Tectorin beta	*TECTB*
4791	5,98	6,60	-1,10	0,03633	0,415	207072_at	Interleukin 18 receptor accessory protein	*IL18RAP*
5451	8,30	9,17	-1,10	0,04300	0,431	234768_at	cDNA FLJ20865 fis, clone ADKA01850	-
1078	9,17	10,1	-1,10	0,00632	0,319	207228_at	Protein kinase, cAMP-dependent, catalytic, gamma	*PRKACG*
1073	4,08	4,51	-1,10	0,00629	0,319	243393_at	Transcribed locus	-
4418	20,6	22,7	-1,10	0,03306	0,409	208568_at	Melanocortin 2 receptor (adrenocorticotropic hormone)	*MC2R*
2863	5,87	6,48	-1,10	0,02010	0,383	210632_s_at	Sarcoglycan, alpha (50kDa dystrophin-associated glycoprotein)	*SGCA*
4024	10,5	11,6	-1,10	0,02946	0,400	1569461_at	-	-
3959	3,15	3,47	-1,10	0,02891	0,399	206177_s_at	Arginase, liver	*ARG1*
1917	3,71	4,09	-1,10	0,01251	0,355	244091_at	Transcribed locus	-
1492	3,79	4,18	-1,10	0,00919	0,336	231122_x_at	Zinc finger, DHHC-type containing 19	*ZDHHC19*
5862	24,7	27,3	-1,10	0,04740	0,442	206817_x_at	Trinucleotide repeat containing 4	*TNRC4*
1737	5,28	5,83	-1,10	0,01110	0,348	236052_at	Hypothetical LOC388610	*LOC388610*
3574	4,06	4,48	-1,10	0,02581	0,394	216015_s_at	NLR family, pyrin domain containing 3	*NLRP3*
4007	4,99	5,51	-1,10	0,02932	0,400	206465_at	Acyl-CoA synthetase bubblegum family member 1	*ACSBG1*

Index	Mutated*	Normal*	FC	*P* value	FDR**	Probe set	Description	Gene symbol
3286	4,27	4,72	-1,10	0,02341	0,388	1556641_at	Hypothetical protein FLJ37228	*FLJ37228*
3621	12,5	13,8	-1,10	0,02614	0,395	237266_at	Similar to Kv channel interacting protein 2 isoform 4	-
4963	5,29	5,84	-1,10	0,03807	0,419	230693_at	ATPase, Ca++ transporting, cardiac muscle, fast twitch 1	*ATP2A1*
1824	3,25	3,59	-1,10	0,01176	0,351	1561278_at	cDNA clone IMAGE:4829538	-
5121	9,66	10,7	-1,10	0,03942	0,421	233623_at	Clone FLB3107 mRNA sequence	-
2446	8,72	9,63	-1,10	0,01637	0,366	1568734_a_at	HCLS1 binding protein 3	*HS1BP3*
4149	4,20	4,63	-1,10	0,03061	0,403	220064_at	Tetratricopeptide repeat domain 21B	*TTC21B*
3352	5,56	6,14	-1,10	0,02380	0,388	221097_s_at	Calcium-activated potassium channel subunit beta-2	*KCNMB2*
3274	5,44	6,00	-1,10	0,02329	0,388	1553555_at	Taste receptor, type 2, member 38	*TAS2R38*
3474	7,21	7,96	-1,10	0,02493	0,392	243769_at	-	-
3479	19,3	21,3	-1,10	0,02498	0,392	207205_at	Carcinoembryonic antigen-related cell adhesion molecule 4	*CEACAM4*
3146	114	126	-1,10	0,02232	0,387	229356_x_at	INO80 complex homolog 1 (S. cerevisiae)	*INOC1*
3873	6,86	7,57	-1,10	0,02829	0,399	207421_at	Carbonic anhydrase VA, mitochondrial	*CA5A*
4987	9,62	10,6	-1,10	0,03827	0,419	1553900_s_at	POM121-like protein	-
2572	15,1	16,7	-1,10	0,01744	0,371	229561_at	Chromosome 14 open reading frame 121	*C14orf121*
4940	4,23	4,67	-1,10	0,03791	0,419	216085_at	cDNA DKFZP434C153	-
844	3,88	4,28	-1,10	0,00484	0,313	1553059_at	Peptidoglycan recognition protein 3	*PGLYRP3*
5107	11,3	12,5	-1,10	0,03929	0,421	234586_at	Sarcosine dehydrogenase	*SARDH*
4647	10,3	11,4	-1,10	0,03505	0,412	1555550_at	ligand-gated ion channel, zinc activated 1	*LGICZ1*
4320	4,57	5,04	-1,10	0,03216	0,407	223372_at	DnaJ (Hsp40) homolog, subfamily C, member 4	*DNAJC4*
2737	5,66	6,25	-1,10	0,01889	0,377	236151_at	KIAA1853 protein	*KIAA1853*
5737	10,5	11,6	-1,10	0,04601	0,438	210155_at	Myocilin	*MYOC*
4375	17,3	19,1	-1,10	0,03256	0,407	241800_x_at	-	-
5453	33,2	36,6	-1,10	0,04302	0,431	206901_at	Chromosome 19 open reading frame 57	*C19orf57*
4353	5,06	5,58	-1,10	0,03241	0,407	211132_at	-	-
5037	4,68	5,17	-1,10	0,03880	0,420	240611_at	-	-
4700	13,9	15,3	-1,10	0,03549	0,413	1554613_a_at	KIAA0226 protein	*KIAA0226*
5263	6,00	6,62	-1,10	0,04089	0,425	233368_s_at	RAB and DnaJ domain containing	*RBJ*
4457	22,7	25,0	-1,10	0,03348	0,411	237401_at	Actinin, alpha 1	*ACTN1*
3773	8,60	9,49	-1,10	0,02741	0,397	1559426_at	cDNA FLJ39210 fis, clone OCBBF2006154	-
2792	5,78	6,38	-1,10	0,01941	0,380	231998_at	-	-
5377	20,1	22,2	-1,10	0,04217	0,429	206883_x_at	Glycoprotein IX (platelet)	*GP9*
2084	3,81	4,21	-1,10	0,01360	0,356	241197_at	Transcribed locus	-
4314	11,4	12,6	-1,10	0,03211	0,407	207770_x_at	Chorionic somatomammotropin hormone 2	*CSH2*
4223	21,6	23,8	-1,10	0,03129	0,405	1554749_s_at	Chloride channel Kb	*CLCNKB*
2224	3,15	3,47	-1,10	0,01477	0,363	243923_at	Similar to XP_529637.1	-
3358	4,82	5,31	-1,10	0,02384	0,388	220381_at	Rho GTPase activating protein 28	*ARHGAP28*
5998	8,00	8,82	-1,10	0,04877	0,444	243891_at	Transcribed locus	-
4504	12,3	13,5	-1,10	0,03390	0,412	214750_at	Placenta-specific 4	*PLAC4*
5683	15,5	17,1	-1,10	0,04537	0,436	244580_at	Clone IMAGE:4871993, mRNA	-
1114	3,41	3,76	-1,10	0,00652	0,319	233043_at	Hypothetical protein LOC221814	*LOC221814*
2715	3,76	4,15	-1,10	0,01865	0,376	240953_at	Transcribed locus	-
5361	3,65	4,02	-1,10	0,04205	0,429	235960_at	Full length insert cDNA YI38B04	-
4364	4,03	4,44	-1,10	0,03245	0,407	1569782_at	cDNA clone IMAGE:5259303	-
185	2,71	2,99	-1,10	0,00086	0,244	1560174_at	Sperm associated antigen 16	*SPAG16*
5178	9,20	10,1	-1,10	0,03990	0,421	1563228_x_at	Hypothetical protein MGC15523	*MGC15523*
5923	5,11	5,63	-1,10	0,04799	0,443	1562099_at	cDNA clone IMAGE:5425336	-
4557	11,0	12,2	-1,10	0,03445	0,412	221382_at	-	-
2418	5,31	5,86	-1,10	0,01617	0,365	1557369_a_at	Hypothetical protein LOC285401	*LOC285401*
4355	4,83	5,33	-1,10	0,03241	0,407	207636_at	Serpin peptidase inhibitor, clade I (pancpin), member 2	*SERPINI2*
3869	4,77	5,26	-1,10	0,02826	0,399	234526_at	Olfactory receptor, family 51, subfamily B, member 6	*OR51B6*
1034	3,63	4,00	-1,10	0,00601	0,318	1566277_at	Olfactory receptor, family 5, subfamily E, member 1 pseudogene	*OR5E1P*
3533	4,94	5,45	-1,10	0,02540	0,393	234460_at	-	-
6059	33,9	37,4	-1,10	0,04941	0,446	226173_at	TBC1 domain family, member 25	*TBC1D25*
1334	3,47	3,83	-1,10	0,00801	0,328	1562163_at	Full length insert cDNA clone YR43F03	-
4274	5,74	6,33	-1,10	0,03177	0,406	223935_at	Long transient receptor potential channel 5	*TRPM5*
4433	6,67	7,35	-1,10	0,03321	0,409	237434_x_at	Hypothetical gene supported by BC043530	*LOC345222*

Index	Mutated*	Normal*	FC	*P* value	FDR**	Probe set	Description	Gene symbol
4233	3,30	3,64	-1,10	0,03138	0,405	235178_x_at	Establishment of cohesion 1 homolog 2 (S. cerevisiae)	*ESCO2*
2609	5,69	6,27	-1,10	0,01772	0,371	237089_at	-	-
4935	5,43	5,99	-1,10	0,03786	0,419	231756_at	Zona pellucida glycoprotein 4	*ZP4*
1485	5,98	6,59	-1,10	0,00912	0,336	202482_x_at	RAN binding protein 1	*RANBP1*
3563	4,15	4,58	-1,10	0,02570	0,394	1555368_x_at	Zinc finger protein 479	*ZNF479*
5365	8,10	8,93	-1,10	0,04211	0,429	1557258_a_at	B-cell CLL/lymphoma 10	*BCL10*
3708	6,34	6,98	-1,10	0,02681	0,395	238275_at	Huntingtin-associated protein 1 (neuroan 1)	*HAP1*
1918	4,83	5,32	-1,10	0,01251	0,355	236056_s_at	Membrane-associated ring finger (C3HC4) 8	
5976	20,5	22,6	-1,10	0,04854	0,444	222960_at	Calcium channel, voltage-dependent, T type, alpha 1H subunit	*CACNA1H*
2411	5,28	5,82	-1,10	0,01610	0,365	1562549_at	cDNA clone IMAGE:5270889	-
2768	4,27	4,71	-1,10	0,01921	0,379	231685_at	-	-
2940	6,86	7,57	-1,10	0,02062	0,383	234441_at	cDNA DKFZp434F1872	-
4438	5,59	6,17	-1,10	0,03324	0,410	206484_s_at	X-prolyl aminopeptidase (aminopeptidase P) 2, membrane-bound	*XPNPEP2*
2623	4,06	4,48	-1,10	0,01782	0,371	238691_at	Small nucleolar RNA host gene (non-protein coding) 10	*SNHG10*
4997	5,25	5,78	-1,10	0,03837	0,420	234530_s_at	Chromosome 6 open reading frame 12	*C6orf12*
5920	6,42	7,07	-1,10	0,04798	0,443	216175_at	cDNA FLJ21623 fis, clone COL07915	-
1087	8,40	9,26	-1,10	0,00637	0,319	1557660_s_at	Hypothetical protein LOC728883	*LOC728883*
2672	97,3	107	-1,10	0,01827	0,374	224429_x_at	Pseudogene MGC10997	*MGC10997*
5054	8,99	9,90	-1,10	0,03893	0,420	244652_at	Transcribed locus	-
4406	23,1	25,4	-1,10	0,03288	0,408	206047_at	Guanine nucleotide binding protein (G protein), beta polypeptide 3	*GNB3*
4732	5,61	6,18	-1,10	0,03583	0,414	229048_at	Full length insert cDNA clone ZD86A03	-
2704	8,22	9,06	-1,10	0,01854	0,375	242632_at	FYVE, RhoGEF and PH domain containing 2	*FGD2*
5962	17,5	19,3	-1,10	0,04841	0,444	240393_at	Transcribed locus	-
4189	21,5	23,7	-1,10	0,03096	0,404	1553839_at	cDNA DKFZp761B107	-
2917	4,05	4,46	-1,10	0,02048	0,383	221361_at	Olfactory marker protein	*OMP*
5449	50,0	55,1	-1,10	0,04298	0,431	1560439_at	HCG2040376 protein	-
5794	13,2	14,6	-1,10	0,04674	0,441	1558590_at	Methyltransferase 11 domain containing 1	*METT11D1*
4974	21,5	23,7	-1,10	0,03816	0,419	227142_at	Pleckstrin homology domain containing family G member 5	*PLEKHG5*
4687	4,51	4,97	-1,10	0,03538	0,413	1554537_at	Transmembrane protein 126B	*TMEM126B*
5748	4,87	5,36	-1,10	0,04612	0,439	1570138_at	Clone IMAGE:5115854, mRNA	-
947	4,21	4,63	-1,10	0,00543	0,313	1561389_at	cDNA clone IMAGE:4825217	-
4506	5,52	6,08	-1,10	0,03393	0,412	207662_at	T-box 1	*TBX1*
3726	5,87	6,46	-1,10	0,02705	0,397	231126_at	Hypothetical protein LOC339778	*LOC339778*
4712	5,51	6,07	-1,10	0,03565	0,413	1563608_a_at	Potassium channel, subfamily T, member 1	*KCNT1*
4901	4,60	5,07	-1,10	0,03750	0,418	1566844_at	Period 4 pseudogene	*PER4*
4414	3,41	3,76	-1,10	0,03300	0,409	1559633_a_at	Cholinergic receptor, muscarinic 3	*CHRM3*
3362	26,2	28,9	-1,10	0,02389	0,388	224243_at	Apolipoprotein A-V	*APOA5*
3102	6,61	7,28	-1,10	0,02191	0,386	1569911_at	Clone IMAGE:3884408, mRNA	-
4427	13,1	14,4	-1,10	0,03316	0,409	210925_at	Class II, major histocompatibility complex, transactivator	*CIITA*
1972	8,04	8,86	-1,10	0,01289	0,355	240455_at	Transcribed locus	-
3301	5,05	5,56	-1,10	0,02351	0,388	1566228_at	cDNA clone IMAGE:2988896	-
3845	9,03	9,95	-1,10	0,02806	0,399	237643_at	Transcribed locus	-
5841	55,2	60,8	-1,10	0,04720	0,442	223617_x_at	ATPase family, AAA domain containing 3B	*ATAD3B*
1314	5,73	6,31	-1,10	0,00783	0,325	240671_at	Full-length cDNA clone CS0DM007YH16	-
4146	6,90	7,60	-1,10	0,03060	0,403	214229_at	Dynein, axonemal, heavy chain 17	*DNAH17*
2531	4,39	4,84	-1,10	0,01710	0,369	242459_at	Transcribed locus	-
1070	3,26	3,58	-1,10	0,00628	0,319	221146_at	-	-
4050	4,75	5,23	-1,10	0,02968	0,401	210770_s_at	Calcium channel, voltage-dependent, P/Q type, alpha 1A subunit	*CACNA1A*
1637	4,05	4,46	-1,10	0,01031	0,344	1555098_a_at	Calcium channel, voltage-dependent, beta 2 subunit	*CACNB2*
6080	5,86	6,45	-1,10	0,04964	0,446	1558378_a_at	AHNAK nucleoprotein 2	*AHNAK2*
362	3,16	3,48	-1,10	0,00189	0,284	1568802_at	Clone IMAGE:3912773, mRNA sequence	-
5068	49,4	54,4	-1,10	0,03901	0,420	1559638_at	Chromosome 1 open reading frame 200	*C1orf200*
2719	4,52	4,98	-1,10	0,01868	0,376	234121_at	cDNA FLJ20486 fis, clone KAT08039	-
3051	8,42	9,27	-1,10	0,02147	0,385	237922_at	Transcribed locus	-
3791	8,29	9,12	-1,10	0,02761	0,398	1569268_at	Glutamate receptor, ionotropic, N-methyl D-aspartate 2C	*GRIN2C*
3363	6,16	6,78	-1,10	0,02389	0,388	236566_at	Transcribed locus	-
4256	5,23	5,76	-1,10	0,03163	0,406	233178_at	TGFB-induced factor homeobox 2-like, Y-linked	*TGIF2LY*

Index	Mutated*	Normal*	FC	*P* value	FDR**	Probe set	Description	Gene symbol
3288	5,38	5,92	-1,10	0,02342	0,388	1561785_at	Mucin 4, cell surface associated	*MUC4*
5751	3,57	3,93	-1,10	0,04615	0,439	1568634_a_at	Similar to Hypothetical protein MGC38937	*LOC339977*
5132	7,58	8,34	-1,10	0,03950	0,421	216492_at	Killer cell immunoglobulin-like receptor, three domains, X1	*KIR3DX1*
5085	8,80	9,68	-1,10	0,03914	0,420	244833_at	Coiled-coil domain containing 63	*CCDC63*
1230	3,86	4,25	-1,10	0,00731	0,324	1569624_at	Clone IMAGE:4248008, mRNA	-
2087	3,52	3,88	-1,10	0,01362	0,356	1556487_a_at	Chromosome 3 open reading frame 15	*C3orf15*
4298	34,1	37,5	-1,10	0,03198	0,407	1568704_a_at	Calcium homeostasis endoplasmic reticulum protein	*CHERP*
2974	3,13	3,45	-1,10	0,02090	0,384	1561543_at	cDNA clone IMAGE:5299981	-
5182	18,7	20,6	-1,10	0,03995	0,421	1559924_at	cDNA clone IMAGE:5303182	-
5525	12,0	13,2	-1,10	0,04381	0,433	241939_at	IQ motif containing GTPase activating protein 3	*IQGAP3*
1474	6,99	7,69	-1,10	0,00900	0,334	216759_at	HRAS-like suppressor 2	*HRASLS2*
1705	10,9	12,0	-1,10	0,01088	0,348	1563090_at	Coiled-coil domain containing 33	*CCDC33*
3070	3,67	4,04	-1,10	0,02166	0,385	209816_at	Patched homolog 1 (Drosophila)	*PTCH1*
3077	3,99	4,39	-1,10	0,02169	0,385	215534_at	cDNA DKFZp586C1923	-
2046	2,73	3,01	-1,10	0,01330	0,355	242502_at	Potassium voltage-gated channel, subfamily H member 5	*KCNH5*
3496	4,07	4,47	-1,10	0,02514	0,392	1560891_a_at	Full length insert cDNA clone YY75G10	-
4957	9,71	10,7	-1,10	0,03802	0,419	221464_at	Olfactory receptor, family 1, subfamily D, member 2	*OR1D2*
4343	10,6	11,7	-1,10	0,03233	0,407	1552768_at	Calcium/calmodulin-dependent protein kinase kinase 1, alpha	*CAMKK1*
4950	26,4	29,0	-1,10	0,03797	0,419	208052_x_at	Carcinoembryonic antigen-related cell adhesion molecule 3	*CEACAM3*
5467	16,3	18,0	-1,10	0,04318	0,432	219899_x_at	NADPH dependent diflavin oxidoreductase 1	*NDOR1*
3547	5,06	5,56	-1,10	0,02551	0,393	244588_at	-	-
2281	8,01	8,81	-1,10	0,01516	0,363	1558340_at	DIX domain containing 1	*DIXDC1*
992	3,16	3,47	-1,10	0,00571	0,315	1555591_at	PIF1 5'-to-3' DNA helicase homolog (S. cerevisiae)	*PIF1*
5470	10,2	11,3	-1,10	0,04324	0,432	243569_at	Transmembrane protein 174	*TMEM174*
3384	8,95	9,84	-1,10	0,02410	0,389	220635_at	Psoriasis susceptibility 1 candidate 2	*PSORS1C2*
3340	6,12	6,73	-1,10	0,02371	0,388	231477_at	Transcribed locus	-
4015	9,30	10,2	-1,10	0,02939	0,400	1561683_at	cDNA clone IMAGE:5270641	-
2089	3,50	3,85	-1,10	0,01363	0,356	1564029_at	Ubiquitin specific peptidase 49	*USP49*
5251	16,5	18,2	-1,10	0,04067	0,423	230041_at	cDNA FLJ14057 fis, clone HEMBB1000337	-
2158	5,33	5,86	-1,10	0,01423	0,360	233145_at	CUB and Sushi multiple domains 2	*CSMD2*
2458	8,58	9,44	-1,10	0,01650	0,367	222323_at	-	-
3652	4,75	5,23	-1,10	0,02640	0,395	237461_at	NLR family, pyrin domain containing 7	*NLRP7*
5156	8,69	9,55	-1,10	0,03970	0,421	244798_at	Similar to XP_001099403.1	-
1816	5,85	6,43	-1,10	0,01171	0,351	1553347_s_at	Potassium voltage-gated channel subfamily A member 6	*KCNA6*
4928	5,23	5,75	-1,10	0,03779	0,419	1561097_at	cDNA clone IMAGE:5270855	-
1025	3,11	3,42	-1,10	0,00593	0,316	232084_at	Small glutamine rich protein with tetratricopeptide repeats 2	*SGTB*
3379	9,28	10,2	-1,10	0,02405	0,389	228447_at	Splicing factor, arginine/serine-rich 17A	*SFRS17A*
6099	2994	3292	-1,10	0,04979	0,446	202029_x_at	Ribosomal protein L38	*RPL38*
1819	4,50	4,95	-1,10	0,01172	0,351	1555245_s_at	Retinitis pigmentosa 1-like 1	*RP1L1*
5782	7,21	7,93	-1,10	0,04656	0,440	224042_at	Ureidopropionase, beta	*UPB1*
3880	3,95	4,34	-1,10	0,02834	0,399	240212_at	cDNA clone IMAGE:5267797	-
1451	5,23	5,74	-1,10	0,00887	0,334	240005_at	Transcribed locus	-
1240	15,9	17,5	-1,10	0,00736	0,324	206477_s_at	Neuro-oncological ventral antigen 2	*NOVA2*
3944	4,84	5,32	-1,10	0,02879	0,399	211171_s_at	Phosphodiesterase 10A	*PDE10A*
2947	4,06	4,46	-1,10	0,02065	0,383	208162_s_at	Hypothetical protein FLJ10232	*FLJ10232*
3220	4,46	4,90	-1,10	0,02283	0,387	1557389_at	cDNA FLJ32222 fis, clone PLACE6004101	-
3551	5,63	6,19	-1,10	0,02559	0,394	1554978_at	Chromosome 8 open reading frame 68	*C8orf68*
4793	6,89	7,58	-1,10	0,03634	0,415	220585_at	Hexokinase domain containing 1	*HKDC1*
5629	5,17	5,68	-1,10	0,04493	0,436	238888_at	Transcribed locus	-
5878	8,66	9,52	-1,10	0,04753	0,442	241847_at	-	-
6050	13,1	14,3	-1,10	0,04930	0,445	243269_s_at	Chromosome 9 open reading frame 144	*C9orf144*
2919	7,41	8,14	-1,10	0,02049	0,383	234048_s_at	KIAA1632 protein	*KIAA1632*
6010	8,81	9,68	-1,10	0,04884	0,444	227714_s_at	-	-
4731	7,31	8,03	-1,10	0,03583	0,414	219776_s_at	-	-
2230	8,81	9,68	-1,10	0,01482	0,363	236501_at	Sal-like 4 (Drosophila)	*SALL4*
3817	3,51	3,85	-1,10	0,02786	0,399	240415_at	Transcribed locus	-
5644	6,44	7,08	-1,10	0,04504	0,436	224551_s_at	Spectrin, beta, non-erythrocytic 4	*SPTBN4*

Index	Mutated*	Normal*	FC	*P* value	FDR**	Probe set	Description	Gene symbol
2801	4,19	4,60	-1,10	0,01947	0,380	234869_at	-	-
5514	9,82	10,8	-1,10	0,04367	0,433	1564251_at	EMI domain containing 1	*EMID1*
965	3,13	3,44	-1,10	0,00559	0,315	1555454_at	Lipopolysaccharide-induced TNF factor	*LITAF*
5804	4,73	5,19	-1,10	0,04685	0,441	207395_at	Butyrophilin, subfamily 1, member A1	*BTN1A1*
1297	4,94	5,43	-1,10	0,00772	0,325	1564138_at	F-box and WD repeat domain containing 12	*FBXW12*
2873	4,30	4,72	-1,10	0,02018	0,383	1555488_at	-	-
6054	36,8	40,4	-1,10	0,04938	0,446	231629_x_at	Kallikrein-related peptidase 3	*KLK3*
3733	6,28	6,90	-1,10	0,02710	0,397	224244_s_at	Apolipoprotein A-V	*APOA5*
3216	24,3	26,7	-1,10	0,02279	0,387	1569986_x_at	Troponin T type 3 (skeletal, fast)	*TNNT3*
3655	5,98	6,57	-1,10	0,02641	0,395	233777_at	cDNA FLJ12075 fis, clone HEMBB1002425	-
3572	6,14	6,75	-1,10	0,02580	0,394	237840_at	Hypothetical gene supported by BC062774	*LOC388948*
4824	9,48	10,4	-1,10	0,03670	0,416	1554989_at	KIAA0317 protein	*KIAA0317*
4959	10,1	11,1	-1,10	0,03804	0,419	230184_at	cDNA FLJ39179 fis, clone OCBBF2004147	-
4657	8,31	9,12	-1,10	0,03516	0,413	237021_at	Hypothetical protein LOC144486	*LOC144486*
5023	3,49	3,84	-1,10	0,03863	0,420	1560946_at	cDNA FLJ32698 fis, clone TESTI2000427	-
5282	6,08	6,68	-1,10	0,04109	0,425	240264_at	-	-
1789	7,13	7,83	-1,10	0,01146	0,350	240350_at	Transcribed locus	-
5130	6,90	7,58	-1,10	0,03948	0,421	227659_at	Pleckstrin homology domain-containing family A member 3	*PLEKHA3*
5669	5,58	6,13	-1,10	0,04524	0,436	223885_at	Calneuron 1	*CALN1*
1501	7,78	8,55	-1,10	0,00923	0,336	1552872_at	Chromosome X and Y open reading frame 2	*CXYorf2*
1844	4,42	4,86	-1,10	0,01186	0,352	214379_at	Transcribed locus	-
5266	7,75	8,51	-1,10	0,04090	0,425	224135_at	WD repeat domain 87	*WDR87*
720	4,14	4,55	-1,10	0,00412	0,308	222247_at	Putative X-linked retinopathy protein	*DXS542*
5369	4,44	4,87	-1,10	0,04214	0,429	244746_at	Semaphorin-4D	*SEMA6D*
2371	13,8	15,2	-1,10	0,01582	0,364	221292_at	Patched homolog 2 (Drosophila)	*PTCH2*
5412	8,07	8,87	-1,10	0,04253	0,430	231231_at	Formin-like 3	*FMNL3*
2404	4,97	5,46	-1,10	0,01606	0,365	236743_at	1-acylglycerol-3-phosphate O-acyltransferase 6 (lysophosphatidic acid acyltra	*AGPAT6*
1767	3,90	4,28	-1,10	0,01127	0,348	1560011_at	Prostate stem cell antigen	*PSCA*
2635	3,89	4,27	-1,10	0,01794	0,372	216748_at	Pyrin and HIN domain family, member 1	*PYHIN1*
4884	7,40	8,13	-1,10	0,03734	0,418	215974_at	HLA complex group 4 pseudogene 6	*HCG4P6*
1742	4,93	5,41	-1,10	0,01113	0,348	1566032_at	cDNA DKFZp686J0929	-
3990	6,56	7,21	-1,10	0,02918	0,400	232479_at	Chromosome 20 open reading frame 42	*C20orf42*
1201	4,24	4,65	-1,10	0,00710	0,323	1569832_at	cDNA clone IMAGE:5264841	-
5758	15,3	16,8	-1,10	0,04624	0,439	222107_x_at	Leucine zipper, putative tumor suppressor 1	*LZTS1*
4834	5,50	6,03	-1,10	0,03686	0,417	239310_at	Transcribed locus	-
6112	4,64	5,09	-1,10	0,04988	0,446	243687_at	Transcribed locus	-
5289	5,47	6,01	-1,10	0,04115	0,425	1553644_at	Chromosome 14 open reading frame 49	*C14orf49*
3049	3,93	4,31	-1,10	0,02146	0,385	240371_at	Hypothetical protein LOC647107	*LOC647107*
1728	9,37	10,3	-1,10	0,01105	0,348	237431_at	Hypothetical protein LOC731851	*LOC731851*
468	3,15	3,45	-1,10	0,00247	0,288	1554784_at	Contactin 1	*CNTN1*
5065	8,65	9,49	-1,10	0,03898	0,420	1557848_at	cDNA clone IMAGE:5272084	-
2398	7,11	7,80	-1,10	0,01600	0,365	1565783_at	cDNA FLJ36796 fis, clone ADRGL2006817	-
2870	4,94	5,42	-1,10	0,02014	0,383	241341_at	-	-
1540	3,74	4,11	-1,10	0,00953	0,337	220191_at	Gastrokine 1	*GKN1*
2412	4,71	5,17	-1,10	0,01612	0,365	236848_s_at	Testis expressed 13A	*TEX13A*
731	3,71	4,07	-1,10	0,00418	0,308	241290_at	Hypothetical protein LOC729766	*LOC729766*
973	13,7	15,0	-1,10	0,00565	0,315	1559989_at	Tropomyosin 4	*TPM4*
3613	7,97	8,75	-1,10	0,02607	0,394	1568981_at	cDNA clone IMAGE:5277449	-
500	3,34	3,67	-1,10	0,00266	0,289	1555433_at	Solute carrier family 39, member 14	*SLC39A14*
1531	5,24	5,75	-1,10	0,00948	0,337	1567027_at	SH3-domain GRB2-like pseudogene 2	*SH3GLP2*
4258	10,0	11,0	-1,10	0,03164	0,406	208303_s_at	Cytokine receptor-like factor 2	*CRLF2*
2094	7,41	8,12	-1,10	0,01370	0,358	235582_at	E2F transcription factor 2	*E2F2*
2645	10,9	12,0	-1,10	0,01804	0,373	228911_at	ADAM metallopeptidase with thrombospondin type 1 motif, 7	*ADAMTS7*
2823	4,13	4,53	-1,10	0,01971	0,381	231323_at	Proteasome (prosome, macropain) subunit, beta type, 2	*PSMB2*
1293	3,91	4,29	-1,10	0,00770	0,325	215998_at	Clone 24533 mRNA sequence	-
3212	5,22	5,73	-1,10	0,02274	0,387	235357_at	D4, zinc and double PHD fingers, family 3	*DPF3*
2950	23,0	25,2	-1,10	0,02071	0,384	215822_x_at	Myelin transcription factor 1	*MYT1*

Index	Mutated*	Normal*	FC	*P* value	FDR**	Probe set	Description	Gene symbol
1341	2,92	3,20	-1,10	0,00805	0,328	1552458_at	Methyl-CpG binding domain protein 3-like 1	*MBD3L1*
3123	12,3	13,4	-1,10	0,02211	0,387	235455_at	Family with sequence similarity 131, member C	*FAM131C*
4767	5,14	5,63	-1,10	0,03611	0,414	1555799_at	Fc receptor-like 5	*FCRL5*
2164	5,84	6,40	-1,10	0,01432	0,361	231390_at	Hypothetical protein LOC730116	*LOC730116*
1751	4,42	4,84	-1,10	0,01117	0,348	237260_at	cDNA clone IMAGE:4838968	-
4641	10,5	11,5	-1,10	0,03499	0,412	227513_s_at	Leucine rich repeat (in FLII) interacting protein 1	*LRRFIP1*
4490	7,78	8,53	-1,10	0,03377	0,411	216992_s_at	Glutamate receptor, metabotropic 8	*GRM8*
5580	5,46	5,99	-1,10	0,04449	0,436	1566486_at	cDNA DKFZp547M116	-
5503	3,98	4,37	-1,10	0,04357	0,433	237820_at	Transcribed locus	-
3644	10,4	11,4	-1,10	0,02634	0,395	206887_at	Chemokine binding protein 2	*CCBP2*
2902	6,23	6,84	-1,10	0,02040	0,383	229922_at	G protein regulated inducer of neurite outgrowth 1	*GPRIN1*
4228	10,2	11,1	-1,10	0,03133	0,405	1562263_at	Lysyl oxidase-like 2	*LOXL2*
1559	8,20	8,99	-1,10	0,00964	0,338	1561270_at	cDNA clone IMAGE:5271318	-
469	7,18	7,87	-1,10	0,00249	0,289	241074_at	Similar to Ig heavy chain V region M315 precursor	-
4640	6,41	7,03	-1,10	0,03499	0,412	1561611_at	Full length insert cDNA clone ZD67H01	-
4230	10,0	11,0	-1,10	0,03134	0,405	1554475_a_at	Chromosome 19 open reading frame 47	*C19orf47*
958	4,30	4,71	-1,10	0,00553	0,315	233033_at	Zinc finger E-box binding homeobox 2	*ZEB2*
3766	3,12	3,42	-1,10	0,02737	0,397	1552875_a_at	CD200 receptor 1	*CD200R1*
3672	4,26	4,67	-1,10	0,02652	0,395	1553796_at	Hypothetical locus FLJ30594	*FLJ30594*
6117	11,5	12,6	-1,10	0,04995	0,446	215055_at	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase-like 1	*B3GNTL1*
5967	7,50	8,22	-1,10	0,04846	0,444	221990_at	Paired box 8	*PAX8*
1182	3,95	4,33	-1,10	0,00696	0,322	1567250_at	Olfactory receptor, family 10, subfamily A, member 3	*OR10A3*
3022	4,21	4,62	-1,10	0,02128	0,385	234174_at	-	-
4905	6,79	7,45	-1,10	0,03751	0,418	207960_at	-	-
2626	3,71	4,07	-1,10	0,01787	0,372	216328_at	Sialic acid binding Ig-like lectin 8	*SIGLEC8*
1320	3,41	3,74	-1,10	0,00787	0,326	1561604_at	cDNA clone IMAGE:4796102	-
4519	7,04	7,72	-1,10	0,03406	0,412	239976_at	Acyl-Coenzyme A dehydrogenase family, member 9	*ACAD9*
4065	5,41	5,93	-1,10	0,02982	0,401	234766_at	Olfactory receptor, family 8, subfamily D, member 2	*OR8D2*
5406	12,5	13,7	-1,10	0,04243	0,429	1560001_at	Similar to 40S ribosomal protein S3a	*LOC649314*
4471	3,36	3,68	-1,10	0,03359	0,411	233753_at	Splicing factor, arginine/serine-rich 15	*SFRS15*
5732	4,69	5,14	-1,10	0,04598	0,438	1555738_at	CKLF-like MARVEL transmembrane domain containing 1	*CMTM1*
3917	7,70	8,44	-1,10	0,02861	0,399	1555308_at	Caspase recruitment domain family, member 14	*CARD14*
5461	8,30	9,09	-1,10	0,04313	0,432	231583_at	Keratin 74	*KRT74*
2265	4,51	4,95	-1,10	0,01506	0,363	1562865_at	Clone IMAGE:4279626, mRNA	-
4704	13,0	14,2	-1,10	0,03557	0,413	204356_at	LIM domain kinase 1	*LIMK1*
4392	5,47	5,99	-1,10	0,03272	0,407	228017_s_at	Chromosome 20 open reading frame 58	*C20orf58*
5247	47,5	52,1	-1,10	0,04062	0,423	235817_at	Transmembrane protein 184A	*TMEM184A*
3921	5,19	5,68	-1,10	0,02863	0,399	211018_at	Lanosterol synthase (2,3-oxidosqualene-lanosterol cyclase)	*LSS*
5291	39,4	43,2	-1,10	0,04119	0,426	1553262_a_at	Urotensin 2 receptor	*UTS2R*
6068	4,47	4,90	-1,10	0,04951	0,446	239989_at	Transcribed locus	-
4444	5,64	6,18	-1,10	0,03339	0,411	1563539_at	cDNA DKFZp762C115	-
1415	3,55	3,88	-1,10	0,00856	0,331	233830_at	Hypothetical protein LOC90246	*LOC90246*
2007	3,65	4,00	-1,10	0,01309	0,355	237905_at	Keratin 25	*KRT25*
5611	8,83	9,67	-1,10	0,04474	0,436	233726_at	cDNA DKFZp586C1523	-
3276	5,46	5,98	-1,10	0,02333	0,388	233361_at	Ankyrin repeat domain 44	*ANKRD44*
4895	2,86	3,14	-1,10	0,03741	0,418	216703_at	-	-
5548	8,73	9,57	-1,10	0,04411	0,435	1552503_at	Fraser syndrome 1	*FRAS1*
2693	4,05	4,43	-1,10	0,01847	0,375	239988_at	Transcribed locus	-
3947	9,37	10,3	-1,10	0,02882	0,399	233991_at	Clone 24894 mRNA sequence	-
2566	4,17	4,56	-1,10	0,01740	0,371	240011_at	Tau tubulin kinase 2	*TTBK2*
5153	6,28	6,88	-1,10	0,03965	0,421	1566097_at	cDNA DKFZp761K02121	-
2984	3,51	3,85	-1,10	0,02097	0,384	1558652_at	Hypothetical protein FLJ10081	*FLJ10081*
3629	6,11	6,69	-1,10	0,02623	0,395	217128_s_at	Calcium/calmodulin-dependent protein kinase IG	*CAMK1G*
3976	8,32	9,11	-1,10	0,02907	0,400	222928_s_at	Retinoic acid induced 16	*RAI16*
4550	10,6	11,7	-1,10	0,03440	0,412	216739_at	cDNA FLJ20874 fis, clone ADKA02818	-
3846	6,59	7,21	-1,09	0,02807	0,399	220528_at	Vanin 3	*VNN3*
2079	2,99	3,27	-1,09	0,01358	0,356	1553736_at	Coiled-coil domain containing 131	*CCDC131*

Index	Mutated*	Normal*	FC	*P* value	FDR**	Probe set	Description	Gene symbol
6024	4,17	4,57	-1,09	0,04901	0,445	243822_at	Transcribed locus	-
4877	5,49	6,01	-1,09	0,03724	0,417	223893_at	Enamelin	*ENAM*
3912	8,32	9,11	-1,09	0,02856	0,399	206981_at	Sodium channel, voltage-gated, type IV, alpha subunit	*SCN4A*
5067	12,3	13,5	-1,09	0,03900	0,420	1566474_at	cDNA DKFZp451O1018	-
3737	10,7	11,7	-1,09	0,02713	0,397	1563816_at	GRB2-associated binding protein family, member 4	*GAB4*
3348	10,1	11,0	-1,09	0,02378	0,388	240767_x_at	Vacuolar protein sorting 13 homolog A (S. cerevisiae)	*VPS13A*
2852	3,62	3,96	-1,09	0,02000	0,383	238410_x_at	Transcribed locus	-
2924	4,13	4,53	-1,09	0,02050	0,383	216886_at	Cholinergic receptor, nicotinic, alpha 4	*CHRNA4*
5788	2,97	3,25	-1,09	0,04660	0,440	201062_at	Stomatin	*STOM*
4383	11,5	12,5	-1,09	0,03265	0,407	230488_s_at	BPR	*LOC138948*
4952	91,4	100	-1,09	0,03799	0,419	179_at	Postmeiotic segregation increased 2-like 11	*PMS2L11*
682	4,59	5,02	-1,09	0,00391	0,308	243468_at	Expressed in prostate and testis	*PATE*
2031	5,15	5,64	-1,09	0,01323	0,355	234743_at	LIM domains containing 1	*LIMD1*
4104	25,7	28,1	-1,09	0,03016	0,402	234241_at	-	-
1115	4,89	5,35	-1,09	0,00653	0,319	214979_at	ATP-binding cassette, sub-family C (CFTR/MRP), member 3	*ABCC3*
6108	16,8	18,4	-1,09	0,04986	0,446	232192_at	Hypothetical protein LOC153811	*LOC153811*
4267	4,13	4,52	-1,09	0,03174	0,406	235995_at	-	-
2642	4,24	4,64	-1,09	0,01801	0,373	240396_at	Interleukin 20 receptor, alpha	*IL20RA*
2683	3,91	4,28	-1,09	0,01837	0,374	215762_at	Transcribed locus	-
1642	3,27	3,57	-1,09	0,01035	0,344	223835_x_at	Orthopedia homeobox	*OTP*
5199	14,0	15,3	-1,09	0,04011	0,422	1552419_s_at	Tubulin tyrosine ligase-like family, member 10	*TTLL10*
5859	17,4	19,0	-1,09	0,04737	0,442	243411_at	Polymerase (DNA-directed), delta interacting protein 3	*POLDIP3*
5512	9,92	10,9	-1,09	0,04366	0,433	244858_at	TGFB-induced factor homeobox 1	*TGIF1*
4936	4,77	5,22	-1,09	0,03786	0,419	237669_at	-	-
5754	4,33	4,74	-1,09	0,04619	0,439	1557682_a_at	Hypothetical protein LOC284688	-
3592	33,5	36,7	-1,09	0,02591	0,394	206508_at	CD70 molecule	*CD70*
2483	3,24	3,55	-1,09	0,01673	0,367	224533_s_at	Chromosome 6 open reading frame 142	*C6orf142*
475	3,02	3,30	-1,09	0,00253	0,289	208288_at	ATP-binding cassette, sub-family B (MDR/TAP), member 11	*ABCB11*
2646	5,00	5,47	-1,09	0,01804	0,373	221442_at	Melanocortin 3 receptor	*MC3R*
2976	4,67	5,11	-1,09	0,02092	0,384	229967_at	CKLF-like MARVEL transmembrane domain containing 2	*CMTM2*
5882	9,04	9,89	-1,09	0,04759	0,442	216018_at	Ring finger protein 5	*RNF5*
3513	4,11	4,50	-1,09	0,02522	0,392	242821_at	Chromosome 9 open reading frame 93	*C9orf93*
5598	8,65	9,46	-1,09	0,04464	0,436	1556620_at	Full length insert cDNA clone YT69G03	-
3665	5,34	5,84	-1,09	0,02649	0,395	239030_at	-	-
4083	3,42	3,74	-1,09	0,02999	0,402	230719_at	Transcribed locus	-
3671	4,54	4,97	-1,09	0,02652	0,395	1560896_a_at	Full length insert cDNA clone ZD42A09	-
4084	7,40	8,09	-1,09	0,02999	0,402	237323_at	Hexokinase domain containing 1	*HKDC1*
5419	4,62	5,05	-1,09	0,04258	0,430	1558300_at	EF-hand calcium binding domain 5	*EFCAB5*
5984	9,53	10,4	-1,09	0,04860	0,444	240023_at	Transcribed locus	-
957	3,11	3,40	-1,09	0,00552	0,315	243335_at	-	-
4209	3,38	3,70	-1,09	0,03114	0,404	234839_at	cDNA DKFZp564I103	-
5408	5,33	5,83	-1,09	0,04248	0,429	203784_s_at	DEAD (Asp-Glu-Ala-Asp) box polypeptide 28	*DDX28*
3261	15,3	16,7	-1,09	0,02315	0,388	1557666_s_at	Chromosome 9 open reading frame 98	*C9orf98*
5700	11,0	12,0	-1,09	0,04564	0,438	1561542_at	-	-
5418	4,58	5,01	-1,09	0,04258	0,430	1560870_a_at	Full length insert cDNA clone ZD45F06	-
885	2,75	3,01	-1,09	0,00511	0,313	1552732_at	Actin-binding Rho activating protein	*ABRA*
2909	3,75	4,10	-1,09	0,02045	0,383	216120_s_at	ATPase, Ca++ transporting, plasma membrane 2	*ATP2B2*
5189	6,57	7,18	-1,09	0,03998	0,421	244199_at	Twinfilin, actin-binding protein, homolog 1 (Drosophila)	*TWF1*
3760	6,60	7,22	-1,09	0,02734	0,397	1561293_at	cDNA clone IMAGE:5296640	-
5437	4,16	4,55	-1,09	0,04284	0,431	236747_at	-	-
4751	4,57	5,00	-1,09	0,03600	0,414	1562984_at	Clone IMAGE:5171167, mRNA	-
6110	7,65	8,37	-1,09	0,04987	0,446	228978_at	Hypothetical LOC645722	*LOC645722*
2937	2,88	3,15	-1,09	0,02060	0,383	210498_at	Clathrin, heavy chain (Hc)	*CLTC*
5224	3,70	4,04	-1,09	0,04040	0,423	243368_at	Transcribed locus	-
6002	9,61	10,5	-1,09	0,04877	0,444	244713_at	Transcribed locus	-
1859	35,3	38,6	-1,09	0,01198	0,352	1556900_at	Hypothetical protein LOC149773	*LOC149773*
2243	3,51	3,84	-1,09	0,01492	0,363	238236_at	Transcribed locus	-

Index	Mutated*	Normal*	FC	*P* value	FDR**	Probe set	Description	Gene symbol
5243	3,96	4,33	-1,09	0,04060	0,423	1558845_at	cDNA FLJ40376 fis, clone TESTI2035121	-
5940	4,09	4,47	-1,09	0,04815	0,443	217624_at	PDGFA associated protein 1	*PDAP1*
315	3,13	3,43	-1,09	0,00159	0,272	217345_at	-	-
4772	3,90	4,27	-1,09	0,03619	0,414	1560905_at	Full length insert cDNA clone YB65G12	-
4046	4,57	4,99	-1,09	0,02965	0,401	207637_at	WSC domain containing 2	*WSCD2*
3686	4,24	4,63	-1,09	0,02662	0,395	1565896_at	cDNA clone IMAGE:5266332	-
3607	5,13	5,61	-1,09	0,02603	0,394	217484_at	Complement component (3b/4b) receptor 1 (Knops blood group)	*CR1*
4821	3,92	4,29	-1,09	0,03667	0,416	237590_at	-	-
666	3,81	4,17	-1,09	0,00384	0,308	1557886_at	Coiled-coil domain containing 46	*CCDC46*
2677	4,04	4,42	-1,09	0,01832	0,374	1563018_at	T-box 5	*TBX5*
1088	3,73	4,08	-1,09	0,00637	0,319	233338_at	Similar to Nucleosome-binding protein 1	*LOC653135*
4130	6,35	6,94	-1,09	0,03040	0,402	221415_s_at	Gap junction protein, alpha 10, 59kDa	*GJA10*
6089	5,71	6,24	-1,09	0,04971	0,446	226904_at	Solute carrier family 6, member 10	*SLC6A10P*
5499	4,20	4,59	-1,09	0,04353	0,433	241258_at	Transcribed locus	-
3658	3,86	4,22	-1,09	0,02641	0,395	211690_at	Ribosomal protein S6	*RPS6*
5769	11,6	12,7	-1,09	0,04635	0,439	207609_s_at	Cytochrome P450, family 1, subfamily A, polypeptide 2	*CYP1A2*
3916	4,41	4,82	-1,09	0,02860	0,399	1556578_a_at	Hypothetical gene supported by AK056507	*FLJ31945*
1051	5,43	5,93	-1,09	0,00614	0,319	1560181_at	Clone IMAGE:5752728, mRNA	-
3118	4,47	4,88	-1,09	0,02205	0,387	234618_at	cDNA DKFZp586M151	-
3878	5,36	5,86	-1,09	0,02833	0,399	237468_at	Transcribed locus	-
2390	31,2	34,0	-1,09	0,01594	0,365	213442_x_at	SAM pointed domain containing ets transcription factor	*SPDEF*
4211	4,96	5,42	-1,09	0,03117	0,405	1555792_a_at	Coiled-coil domain containing 116	*CCDC116*
3562	7,33	8,01	-1,09	0,02570	0,394	215816_at	Glucuronidase, beta/immunoglobulin lambda-like polypeptide 1 pseudogene	*LOC91316*
4033	4,20	4,59	-1,09	0,02955	0,401	240678_at	Transcribed locus	-
1037	4,03	4,41	-1,09	0,00602	0,318	208434_at	Myelodysplasia syndrome 1	*MDS1*
4463	3,53	3,86	-1,09	0,03352	0,411	220025_at	T-box, brain, 1	*TBR1*
4447	3,06	3,34	-1,09	0,03340	0,411	206835_at	Statherin	*STATH*
1638	3,96	4,33	-1,09	0,01032	0,344	1569418_at	cDNA clone IMAGE:4894320	-
6121	4,83	5,27	-1,09	0,04998	0,446	1556907_at	Zinc finger protein 474	*ZNF474*
1648	7,68	8,39	-1,09	0,01037	0,344	1553637_s_at	Transmembrane and coiled-coil domains 5	*TMCO5*
4847	4,57	4,99	-1,09	0,03693	0,417	205152_at	Solute carrier family 6, member 1	*SLC6A1*
5929	9,12	9,96	-1,09	0,04806	0,443	1556355_x_at	Ral guanine nucleotide dissociation stimulator-like 3	*RGL3*
5290	15,8	17,3	-1,09	0,04116	0,425	227381_at	Cerebral endothelial cell adhesion molecule 1	*CEECAM1*
5264	17,8	19,4	-1,09	0,04089	0,425	217219_at	cDNA DKFZP434A062	-
2584	4,42	4,83	-1,09	0,01753	0,371	240935_at	-	-
3668	27,3	29,8	-1,09	0,02652	0,395	1560300_a_at	DMRT-like family C1	*DMRTC1*
5698	6,98	7,63	-1,09	0,04560	0,438	242155_x_at	Transcribed locus	-
2104	3,95	4,31	-1,09	0,01379	0,358	240177_at	Transcribed locus	-
5071	6,02	6,57	-1,09	0,03903	0,420	1565772_at	p21/Cdc42/Rac1-activated kinase 1 (STE20 homolog, yeast)	*PAK1*
2417	3,61	3,94	-1,09	0,01617	0,365	216201_at	cDNA FLJ21586 fis, clone COL06920	-
5543	32,7	35,7	-1,09	0,04407	0,435	242151_at	Transcribed locus	-
2439	9,82	10,7	-1,09	0,01630	0,365	239702_x_at	-	-
5989	4,79	5,23	-1,09	0,04866	0,444	240783_at	Transcribed locus	-
1462	3,42	3,73	-1,09	0,00894	0,334	1568647_at	cDNA clone IMAGE:4426835	-
5576	4,60	5,02	-1,09	0,04443	0,436	240650_at	Calcium channel, voltage-dependent, R type, alpha 1E subunit	*CACNA1E*
3081	5,71	6,23	-1,09	0,02171	0,385	237824_at	Transcribed locus	-
884	4,87	5,31	-1,09	0,00511	0,313	1552842_at	Heparan sulfate 6-O-sulfotransferase 3	*HS6ST3*
4357	5,61	6,13	-1,09	0,03241	0,407	207894_s_at	T-cell leukemia/lymphoma 6	*TCL6*
4756	3,90	4,26	-1,09	0,03605	0,414	232655_at	UDP glucuronosyltransferase 1 family, polypeptide A6	*UGT1A6*
3843	14,9	16,3	-1,09	0,02806	0,399	240114_s_at	Transmembrane protein 174	*TMEM174*
1873	3,23	3,52	-1,09	0,01212	0,354	240986_at	Transcribed locus	-
1307	4,08	4,46	-1,09	0,00779	0,325	236374_at	Cortexin 3	*CTXN3*
2965	3,74	4,08	-1,09	0,02083	0,384	1563502_at	Zinc finger, DHHC-type containing 2	*ZDHHC2*
2840	4,43	4,83	-1,09	0,01982	0,382	1553534_at	NLR family, pyrin domain containing 10	*NLRP10*
4296	4,30	4,70	-1,09	0,03194	0,407	1561018_at	Full length insert cDNA clone ZD44H09	-
4607	4,21	4,59	-1,09	0,03481	0,412	231364_at	cDNA clone IMAGE:4796864	-
5809	4,61	5,03	-1,09	0,04690	0,441	240346_at	Hypothetical LOC644222	*LOC644222*

Index	Mutated*	Normal*	FC	*P* value	FDR**	Probe set	Description	Gene symbol
3952	7,21	7,87	-1,09	0,02888	0,399	1563805_a_at	Family with sequence similarity 83, member C	*FAM83C*
5536	5,97	6,51	-1,09	0,04395	0,434	221072_at	Chromosome 9 open reading frame 31	*C9orf31*
1784	4,11	4,49	-1,09	0,01139	0,349	1562066_at	Hypothetical protein LOC286144	*LOC286144*
5221	7,73	8,44	-1,09	0,04037	0,423	221346_at	Olfactory receptor, family 10, subfamily J, member 1	*OR10J1*
2798	4,34	4,74	-1,09	0,01944	0,380	221347_at	Cholinergic receptor, muscarinic 5	*CHRM5*
4218	8,32	9,08	-1,09	0,03125	0,405	205973_at	Fasciculation and elongation protein zeta 1 (zygin I)	*FEZ1*
1105	3,76	4,10	-1,09	0,00646	0,319	AFFX-ThrX-5_a	-	-
1959	2,85	3,12	-1,09	0,01281	0,355	204721_s_at	DnaJ (Hsp40) homolog, subfamily C, member 6	*DNAJC6*
919	3,01	3,28	-1,09	0,00529	0,313	230517_at	Similar to GLI-Kruppel family member HKR1	*tcag7.1196*
5651	6,60	7,21	-1,09	0,04507	0,436	1561060_at	cDNA clone IMAGE:5298862	-
5678	4,00	4,37	-1,09	0,04533	0,436	237889_s_at	Hypothetical LOC553137	*LOC553137*
5487	4,83	5,27	-1,09	0,04343	0,433	1559674_at	Zinc finger protein 333	*ZNF333*
3633	10,7	11,7	-1,09	0,02627	0,395	219746_at	D4, zinc and double PHD fingers, family 3	*DPF3*
5436	5,30	5,78	-1,09	0,04283	0,431	241383_at	Similar to Hypothetical protein A930006D11	*LOC201181*
1413	18,0	19,7	-1,09	0,00854	0,330	204626_s_at	Integrin, beta 3 (platelet glycoprotein IIIa, antigen CD61)	*ITGB3*
4913	4,39	4,79	-1,09	0,03757	0,418	219621_at	Claspin homolog (Xenopus laevis)	*CLSPN*
4031	8,04	8,77	-1,09	0,02952	0,400	231651_at	cDNA FLJ36110 fis, clone TESTI2021939	-
4923	3,81	4,15	-1,09	0,03772	0,419	211319_at	-	-
3973	3,84	4,19	-1,09	0,02904	0,400	1556084_at	Heterogeneous nuclear ribonucleoprotein M	*HNRPM*
3099	2,78	3,03	-1,09	0,02188	0,386	207523_at	Chromosome 6 open reading frame 10	*C6orf10*
926	3,06	3,33	-1,09	0,00533	0,313	241072_s_at	-	-
3985	3,82	4,16	-1,09	0,02914	0,400	241297_at	-	-
4489	11,5	12,6	-1,09	0,03377	0,411	217711_at	TEK tyrosine kinase, endothelial	*TEK*
2547	3,77	4,11	-1,09	0,01721	0,369	1569680_at	cDNA clone IMAGE:4288701	-
3799	3,76	4,10	-1,09	0,02767	0,398	207315_at	CD226 molecule	*CD226*
2409	3,72	4,06	-1,09	0,01610	0,365	231675_s_at	Alcohol dehydrogenase 4 (class II), pi polypeptide	*ADH4*
2725	13,9	15,2	-1,09	0,01872	0,376	239076_at	Septin 13	*SEPT13*
4956	7,05	7,69	-1,09	0,03802	0,419	243883_at	Matrix metallopeptidase 15 (membrane-inserted)	*MMP15*
2923	5,63	6,14	-1,09	0,02050	0,383	242421_at	Transcribed locus	-
591	3,07	3,35	-1,09	0,00327	0,301	1557802_at	Clone IMAGE:5547568, mRNA	-
3924	3,97	4,33	-1,09	0,02868	0,399	233447_at	Chromosome 6 open reading frame 86	*C6orf86*
3804	35,2	38,4	-1,09	0,02770	0,398	1557371_a_at	Hypothetical protein LOC158376	*LOC158376*
5578	11,3	12,3	-1,09	0,04447	0,436	204397_at	Echinoderm microtubule associated protein like 2	*EML2*
4552	4,60	5,02	-1,09	0,03441	0,412	215297_at	Hypothetical locus LOC441204	*LOC441204*
4400	3,39	3,69	-1,09	0,03280	0,408	237462_at	Transcribed locus	-
4840	7,14	7,79	-1,09	0,03690	0,417	215841_at	Guanylate cyclase activator 1B (retina)	*GUCA1B*
5781	5,84	6,37	-1,09	0,04654	0,440	1563324_at	Hypothetical protein LOC389457	*LOC389457*
3841	4,94	5,39	-1,09	0,02805	0,399	211803_at	Cyclin-dependent kinase 2	*CDK2*
1655	4,76	5,19	-1,09	0,01045	0,345	215110_at	Mannose-binding lectin (protein A) 1, pseudogene 1	*MBL1P1*
2983	3,70	4,03	-1,09	0,02097	0,384	237150_at	Transcribed locus	-
1379	4,67	5,10	-1,09	0,00830	0,329	1552854_a_at	Hypothetical protein FLJ32784	*FLJ32784*
3356	4,55	4,96	-1,09	0,02383	0,388	241259_at	GRB2-associated binding protein 3	*GAB3*
4532	4,42	4,82	-1,09	0,03421	0,412	229565_x_at	T-box 3 (ulnar mammary syndrome)	*TBX3*
1080	5,58	6,08	-1,09	0,00632	0,319	1557702_at	cDNA clone IMAGE:5265308	-
3781	4,42	4,82	-1,09	0,02752	0,398	231314_at	Similar to XP_530643.1	-
615	6,80	7,41	-1,09	0,00348	0,308	1561976_at	Chromosome 1 open reading frame 167	*C1orf167*
4062	9,24	10,1	-1,09	0,02980	0,401	242373_at	Transcribed locus	-
2809	5,24	5,71	-1,09	0,01954	0,380	238248_at	Uromodulin (uromucoid, Tamm-Horsfall glycoprotein)	*UMOD*
3751	3,46	3,77	-1,09	0,02728	0,397	224238_at	-	-
1392	2,62	2,85	-1,09	0,00842	0,330	1557030_at	GRB2-associated binding protein 1	*GAB1*
2302	3,79	4,13	-1,09	0,01529	0,363	232506_s_at	Chromosome 15 open reading frame 41	*C15orf41*
1449	6,68	7,28	-1,09	0,00883	0,333	217450_at	-	-
2059	23,7	25,8	-1,09	0,01343	0,356	1562026_at	WNK lysine deficient protein kinase 2	*WNK2*
4718	4,18	4,55	-1,09	0,03570	0,413	1566123_at	Fatty acid binding protein 6, ileal (gastrotropin)	*FABP6*
2018	4,44	4,84	-1,09	0,01317	0,355	238088_at	cDNA clone IMAGE:5259414	-
4244	4,50	4,91	-1,09	0,03149	0,406	239356_at	Clone IMAGE:1257951, mRNA sequence	-
5880	3,66	3,99	-1,09	0,04754	0,442	243517_at	-	-

Index	Mutated*	Normal*	FC	*P* value	FDR**	Probe set	Description	Gene symbol
3018	4,22	4,60	-1,09	0,02127	0,385	1563316_at	Clone IMAGE:5748207, mRNA	-
4466	4,40	4,79	-1,09	0,03355	0,411	207213_s_at	Ubiquitin specific peptidase 2	*USP2*
3889	6,84	7,45	-1,09	0,02843	0,399	230059_at	Deformed epidermal autoregulatory factor 1 (Drosophila)	*DEAF1*
4478	5,68	6,19	-1,09	0,03367	0,411	243975_at	Clone IMAGE:5763888, mRNA	-
2221	4,52	4,92	-1,09	0,01474	0,363	208046_at	Histone cluster 1, H4a	*HIST1H4A*
4804	6,32	6,88	-1,09	0,03647	0,415	1566622_at	cDNA DKFZp667F0113	-
2612	4,28	4,66	-1,09	0,01774	0,371	242179_s_at	Tetraspanin 16	*TSPAN16*
5911	6,26	6,82	-1,09	0,04793	0,443	221105_at	-	-
5146	14,0	15,2	-1,09	0,03962	0,421	224100_s_at	Dihydropyrimidinase-like 5	*DPYSL5*
1929	3,93	4,28	-1,09	0,01257	0,355	1555729_a_at	CD209 molecule	*CD209*
1943	5,16	5,62	-1,09	0,01267	0,355	210753_s_at	EPH receptor B1	*EPHB1*
4172	3,36	3,66	-1,09	0,03084	0,404	221886_at	DENN/MADD domain containing 2A	*DENND2A*
6063	5,67	6,17	-1,09	0,04944	0,446	221707_s_at	Vacuolar protein sorting 53 homolog (S. cerevisiae)	*VPS53*
3911	5,58	6,08	-1,09	0,02855	0,399	1566039_a_at	Hypothetical gene supported by BC036933	*LOC401220*
3179	5,68	6,18	-1,09	0,02254	0,387	1565671_a_at	Hypothetical gene supported by NM_001531	*LOC391142*
3435	6,73	7,33	-1,09	0,02458	0,391	1560935_s_at	Hypothetical protein LOC284669	*LOC284669*
3181	4,24	4,62	-1,09	0,02255	0,387	1555988_a_at	Hypothetical protein LOC126536	*LOC126536*
5166	2,85	3,10	-1,09	0,03981	0,421	1565833_at	-	-
3311	11,0	12,0	-1,09	0,02355	0,388	215487_x_at	Hypothetical gene supported by BC042812	*LOC728882*
1846	3,01	3,28	-1,09	0,01189	0,352	206884_s_at	Sciellin	*SCEL*
2620	3,96	4,32	-1,09	0,01781	0,371	244606_at	ATPase, Na+/K+ transporting, alpha 1 polypeptide	*ATP1A1*
5367	3,59	3,91	-1,09	0,04214	0,429	241121_at	Transcribed locus	-
5720	3,21	3,50	-1,09	0,04580	0,438	224045_x_at	Chromosome 18 open reading frame 2	*C18orf2*
4374	3,55	3,86	-1,09	0,03253	0,407	237805_at	Hypothetical protein LOC729296	*LOC729296*
2756	3,54	3,86	-1,09	0,01910	0,379	237375_at	Similar to XP_530528.1	-
3482	5,25	5,71	-1,09	0,02500	0,392	207990_x_at	Acrosomal vesicle protein 1	*ACRV1*
2062	3,39	3,69	-1,09	0,01345	0,356	1562941_at	cDNA clone IMAGE:5288253	-
2830	3,87	4,21	-1,09	0,01974	0,381	206603_at	Solute carrier family 2, member 4	*SLC2A4*
3048	3,12	3,40	-1,09	0,02146	0,385	1570284_x_at	Clone IMAGE:4696056, mRNA	-
3683	31,2	34,0	-1,09	0,02659	0,395	231792_at	Myosin light chain kinase 2, skeletal muscle	*MYLK2*
5729	5,32	5,79	-1,09	0,04595	0,438	1563255_at	Hypothetical protein LOC728883	*LOC728883*
5117	9,53	10,4	-1,09	0,03940	0,421	207185_at	Solute carrier family 10, member 1	*SLC10A1*
6019	4,33	4,71	-1,09	0,04899	0,445	243425_at	Transcribed locus	-
5100	3,91	4,25	-1,09	0,03923	0,420	241048_at	Transcribed locus	-
3591	3,99	4,34	-1,09	0,02591	0,394	206244_at	Complement component (3b/4b) receptor 1 (Knops blood group)	*CR1*
3250	20,0	21,7	-1,09	0,02307	0,388	1556747_a_at	cDNA FLJ39784 fis, clone SPLEN2002314	-
5286	4,52	4,92	-1,09	0,04112	0,425	231668_x_at	Immunoglobulin heavy constant gamma 1 (G1m marker)	*IGHG1*
5201	8,31	9,05	-1,09	0,04011	0,422	1561336_at	Deoxyribonuclease I-like 3	*DNASE1L3*
5797	24,2	26,4	-1,09	0,04677	0,441	1557964_at	Eukaryotic translation initiation factor 4 gamma, 2	*EIF4G2*
2120	3,70	4,03	-1,09	0,01391	0,359	230953_at	cDNA clone IMAGE:4824446	-
4753	6,22	6,77	-1,09	0,03602	0,414	1562433_at	Hypothetical protein FLJ10489	*FLJ10489*
4064	3,89	4,23	-1,09	0,02981	0,401	1570653_at	Similar to v-Myb myeloblastosis viral oncogene homolog (avian)	-
2478	7,01	7,63	-1,09	0,01669	0,367	234195_at	cDNA FLJ22426 fis, clone HRC08780	-
3283	4,04	4,40	-1,09	0,02339	0,388	1568913_at	NOL1/NOP2/Sun domain family, member 3	*NSUN3*
3128	3,35	3,64	-1,09	0,02218	0,387	1567078_x_at	-	-
1843	4,08	4,44	-1,09	0,01185	0,351	1555000_at	OK/SW-CL.36	-
4152	4,41	4,80	-1,09	0,03063	0,403	1556426_at	Hexosaminidase A (alpha polypeptide)	*HEXA*
5501	3,63	3,95	-1,09	0,04354	0,433	1564491_at	Chromosome X open reading frame 18	*CXorf18*
1759	3,18	3,46	-1,09	0,01122	0,348	236729_at	Caspase 3, apoptosis-related cysteine peptidase	*CASP3*
4598	4,37	4,75	-1,09	0,03477	0,412	235813_at	cDNA FLJ46701 fis, clone TRACH3014063	-
5902	7,87	8,56	-1,09	0,04783	0,443	238194_at	Transcribed locus	-
944	4,37	4,75	-1,09	0,00542	0,313	1562943_at	Clone IMAGE:5742085, mRNA	-
6081	5,83	6,34	-1,09	0,04965	0,446	219845_at	BARX homeobox 1	*BARX1*
4117	15,7	17,1	-1,09	0,03027	0,402	1556397_at	cDNA FLJ37122 fis, clone BRACE2022448	-
966	3,23	3,52	-1,09	0,00559	0,315	1562432_at	cDNA clone IMAGE:4794272	-
3189	3,76	4,09	-1,09	0,02260	0,387	217359_s_at	Neural cell adhesion molecule 1	*NCAM1*
3625	4,12	4,48	-1,09	0,02617	0,395	240790_at	Transcribed locus	-

Index	Mutated*	Normal*	FC	*P* value	FDR**	Probe set	Description	Gene symbol
3229	5,48	5,96	-1,09	0,02290	0,388	239929_at	Hypothetical protein FLJ32569	*FLJ32569*
6049	4,93	5,36	-1,09	0,04929	0,445	1553323_a_at	Cation channel, sperm associated 2	*CATSPER2*
5024	4,06	4,41	-1,09	0,03863	0,420	1570049_at	Clone IMAGE:5176619, mRNA	-
2998	3,70	4,02	-1,09	0,02111	0,385	1553241_at	-	-
5680	11,3	12,3	-1,09	0,04535	0,436	207784_at	Arylsulfatase D	*ARSD*
3647	20,2	21,9	-1,09	0,02635	0,395	1566502_at	cDNA DKFZp434B049	-
5468	5,10	5,55	-1,09	0,04320	0,432	240872_at	Transcribed locus	-
2406	4,88	5,31	-1,09	0,01608	0,365	1560509_at	cDNA DKFZp547H194	-
3824	8,66	9,41	-1,09	0,02792	0,399	234549_at	cDNA DKFZp586G1917	-
4921	11,7	12,7	-1,09	0,03770	0,419	1557342_a_at	Hypothetical protein LOC150381	*LOC150381*
4396	53,3	57,9	-1,09	0,03277	0,407	1556291_at	cDNA DKFZp564N2472	-
1853	3,05	3,32	-1,09	0,01194	0,352	229935_s_at	-	-
4661	41,4	45,0	-1,09	0,03519	0,413	91920_at	Brevican	*BCAN*
6053	5,31	5,77	-1,09	0,04937	0,446	1566476_at	-	-
5959	3,73	4,05	-1,09	0,04837	0,444	1564051_at	-	-
2278	4,01	4,36	-1,09	0,01515	0,363	230594_at	Transcribed locus	-
2516	3,13	3,40	-1,09	0,01695	0,368	1553299_at	Hypothetical protein FLJ31401	-
5858	4,06	4,41	-1,09	0,04737	0,442	216245_at	Interleukin 1 receptor antagonist	*IL1RN*
5407	3,47	3,77	-1,09	0,04244	0,429	244837_at	-	-
5757	3,80	4,13	-1,09	0,04622	0,439	1557446_x_at	Triggering receptor expressed on myeloid cells-like 3	*TREML3*
4494	3,60	3,91	-1,09	0,03380	0,411	241190_at	Transcribed locus	-
4538	3,66	3,98	-1,09	0,03429	0,412	236842_at	cDNA FLJ36110 fis, clone TESTI2021939	-
2386	3,43	3,73	-1,09	0,01591	0,364	1560309_s_at	Full length insert cDNA clone YP59A09	-
922	3,91	4,25	-1,09	0,00531	0,313	210384_at	Protein arginine methyltransferase 2	*PRMT2*
4597	12,8	13,9	-1,09	0,03477	0,412	206657_s_at	Myogenic differentiation 1	*MYOD1*
4150	5,21	5,66	-1,09	0,03062	0,403	227831_at	Chromosome 9 open reading frame 5	*C9orf5*
3554	4,06	4,41	-1,09	0,02562	0,394	231344_at	Transcribed locus	-
1919	3,67	3,99	-1,09	0,01251	0,355	233671_at	cDNA FLJ11179 fis, clone PLACE1007450	-
1551	3,59	3,90	-1,09	0,00956	0,337	211349_at	Solute carrier family 15, member 1	*SLC15A1*
3052	4,45	4,84	-1,09	0,02148	0,385	1569849_at	cDNA clone IMAGE:4838370	-
6005	6,85	7,44	-1,09	0,04880	0,444	234708_at	Single-strand-selective monofunctional uracil-DNA glycosylase 1	*SMUG1*
6028	4,36	4,74	-1,09	0,04903	0,445	238270_x_at	-	-
1672	3,89	4,23	-1,09	0,01055	0,345	1561143_at	Full length insert cDNA clone ZD46F01	-
5601	14,7	15,9	-1,09	0,04468	0,436	216439_at	Tyrosine kinase, non-receptor, 2	*TNK2*
4566	12,4	13,4	-1,09	0,03452	0,412	238201_at	Transcribed locus	-
3946	3,63	3,94	-1,09	0,02882	0,399	240796_at	Transcribed locus	-
2780	3,25	3,53	-1,09	0,01930	0,380	1560810_at	Clone IMAGE:5745158, mRNA	-
2614	4,17	4,53	-1,09	0,01775	0,371	1554030_at	Arylsulfatase B	*ARSB*
5699	3,45	3,75	-1,09	0,04564	0,438	237912_at	-	-
5899	10,8	11,7	-1,09	0,04776	0,443	206152_at	Centaurin, gamma 1	*CENTG1*
4589	4,15	4,50	-1,09	0,03471	0,412	232829_at	Olfactory receptor, family 52, subfamily K, member 3 pseudogene	*OR52K3P*
3492	3,93	4,27	-1,09	0,02510	0,392	239206_at	Complement component (3b/4b) receptor 1-like	*CR1L*
5565	4,41	4,78	-1,09	0,04430	0,435	217433_at	Transforming, acidic coiled-coil containing protein 1	*TACC1*
5450	5,71	6,20	-1,09	0,04299	0,431	1561218_s_at	Hypothetical protein LOC728099	*LOC728099*
3767	4,53	4,91	-1,09	0,02737	0,397	1566737_at	HCG2036596 protein	-
5958	3,91	4,24	-1,09	0,04835	0,444	1564202_at	cDNA FLJ38820 fis, clone LIVER2008473	-
5175	3,69	4,01	-1,09	0,03987	0,421	1560698_a_at	Hypothetical protein LOC283392	*LOC283392*
4276	4,14	4,50	-1,09	0,03178	0,406	1555603_at	B melanoma antigen	*BAGE*
5705	5,34	5,79	-1,09	0,04569	0,438	230969_at	LOC374973 protein	*LOC374973*
5912	4,89	5,31	-1,09	0,04794	0,443	234744_x_at	-	-
2931	6,31	6,85	-1,09	0,02055	0,383	214571_at	Fibroblast growth factor 3	*FGF3*
5113	6,33	6,88	-1,09	0,03937	0,421	211389_x_at	Killer cell immunoglobulin-like receptor 3DS1	*KIR3DS1*
5382	8,32	9,03	-1,09	0,04219	0,429	243670_at	Transcribed locus	-
4348	4,02	4,36	-1,09	0,03238	0,407	237721_s_at	Ankyrin repeat and SOCS box-containing 4	*ASB4*
1426	3,39	3,68	-1,09	0,00865	0,331	206285_at	Nephronophthisis 1 (juvenile)	*NPHP1*
3495	3,60	3,91	-1,09	0,02513	0,392	238073_at	-	-
2727	4,67	5,07	-1,09	0,01877	0,376	241037_at	-	-

Index	Mutated*	Normal*	FC	*P* value	FDR**	Probe set	Description	Gene symbol
3826	6,05	6,56	-1,09	0,02793	0,399	233781_s_at	RAP1 interacting factor homolog (yeast)	*RIF1*
4783	54,5	59,2	-1,09	0,03627	0,414	220962_s_at	Peptidyl arginine deiminase, type I	*PADI1*
4513	14,7	15,9	-1,09	0,03402	0,412	1559675_at	-	-
6030	12,5	13,6	-1,09	0,04906	0,445	1557022_at	cDNA clone IMAGE:5298883	-
5986	5,36	5,82	-1,09	0,04863	0,444	1553350_at	Family with sequence similarity 123C	*FAM123C*
2436	2,69	2,92	-1,09	0,01628	0,365	1568840_at	WD repeats and SOF1 domain containing	*WDSOF1*
3187	4,31	4,68	-1,09	0,02260	0,387	1558856_at	DMRT-like family A2	*DMRTA2*
5586	5,57	6,04	-1,08	0,04455	0,436	220515_at	Dual specificity phosphatase 21	*DUSP21*
461	3,00	3,26	-1,08	0,00245	0,288	1565840_at	cDNA FLJ35990 fis, clone TESTI2014415	-
5703	4,50	4,88	-1,08	0,04565	0,438	208275_x_at	Undifferentiated embryonic cell transcription factor 1	*UTF1*
5352	4,25	4,61	-1,08	0,04198	0,429	241007_at	Transcribed locus	-
1646	3,69	4,00	-1,08	0,01036	0,344	1566739_at	Phospholipase C, epsilon 1	*PLCE1*
3740	3,77	4,09	-1,08	0,02722	0,397	243727_at	Copine VIII	*CPNE8*
4194	5,85	6,35	-1,08	0,03098	0,404	230010_at	KIAA1853 protein	*KIAA1853*
5560	8,10	8,79	-1,08	0,04426	0,435	244012_x_at	-	-
6076	5,31	5,76	-1,08	0,04959	0,446	230574_at	-	-
2655	3,10	3,36	-1,08	0,01811	0,373	215663_at	Muscleblind-like (Drosophila)	*MBNL1*
1993	3,59	3,89	-1,08	0,01303	0,355	1560771_at	cDNA FLJ36254 fis, clone THYMU2002157	-
4792	5,02	5,45	-1,08	0,03633	0,415	1552991_at	Olfactory receptor, family 5, subfamily P, member 2	*OR5P2*
5277	4,54	4,93	-1,08	0,04102	0,425	206281_at	Adenylate cyclase activating polypeptide 1 (pituitary)	*ADCYAP1*
1249	3,26	3,54	-1,08	0,00741	0,325	211341_at	POU class 4 homeobox 1	*POU4F1*
5584	4,36	4,72	-1,08	0,04452	0,436	224181_at	Chromosome 18 open reading frame 2	*C18orf2*
4190	3,60	3,90	-1,08	0,03096	0,404	1555353_at	Low density lipoprotein-related protein 1	*LRP1*
4288	4,10	4,44	-1,08	0,03185	0,406	216217_at	Phospholipase C-like 2	*PLCL2*
5393	4,01	4,35	-1,08	0,04229	0,429	1556456_at	Hypothetical FLJ39739	*FLJ39739*
5927	6,12	6,63	-1,08	0,04803	0,443	238216_at	Clone IMAGE:4340526, mRNA	-
3743	4,40	4,77	-1,08	0,02723	0,397	221271_at	Interleukin 21	*IL21*
3623	3,23	3,51	-1,08	0,02616	0,395	217470_at	cDNA DKFZp434F1011	-
4612	17,0	18,4	-1,08	0,03483	0,412	216371_at	-	-
3153	3,28	3,55	-1,08	0,02237	0,387	239192_at	Par-3 partitioning defective 3 homolog B (C. elegans)	*PARD3B*
5591	12,1	13,1	-1,08	0,04458	0,436	1553865_a_at	cDNA DKFZp761H2121	-
2751	3,75	4,07	-1,08	0,01903	0,378	1562923_at	cDNA clone IMAGE:4838328	-
827	4,41	4,78	-1,08	0,00472	0,312	1562974_at	cDNA clone IMAGE:5302821	-
1083	2,81	3,05	-1,08	0,00634	0,319	1563392_at	Chromosome 21, Down syndrome critical region transcript	-
5009	10,8	11,7	-1,08	0,03848	0,420	217341_at	-	-
2507	3,51	3,81	-1,08	0,01685	0,367	231483_at	Similar to XP_001149380.1	-
3611	31,4	34,1	-1,08	0,02606	0,394	1556718_s_at	cDNA FLJ35483 fis, clone SMINT2008277	-
5603	4,00	4,33	-1,08	0,04471	0,436	1556490_a_at	Hypothetical LOC388946	*LOC388946*
394	2,89	3,13	-1,08	0,00208	0,285	1570486_at	SRY (sex determining region Y)-box 6	*SOX6*
1203	7,40	8,02	-1,08	0,00712	0,323	1553863_at	Chromosome 10 open reading frame 64	*C10orf64*
3871	3,99	4,32	-1,08	0,02828	0,399	1559065_a_at	C-type lectin superfamily 4, member G	*CLEC4G*
4738	5,52	5,98	-1,08	0,03586	0,414	1565583_at	Zinc finger and SCAN domain containing 5	*ZSCAN5*
4594	4,66	5,05	-1,08	0,03476	0,412	1564444_at	cDNA FLJ40178 fis, clone TESTI2017932	-
5350	4,62	5,01	-1,08	0,04196	0,429	1555048_a_at	Chromosome 21 open reading frame 29	*C21orf29*
4293	7,76	8,41	-1,08	0,03192	0,406	1566535_at	cDNA FLJ40701 fis, clone THYMU2025909	-
4725	4,58	4,96	-1,08	0,03576	0,414	1555085_at	-	-
986	3,60	3,90	-1,08	0,00569	0,315	1555116_s_at	Solute carrier family 11, member 1	*SLC11A1*
5901	8,98	9,73	-1,08	0,04780	0,443	1560409_at	Clone IMAGE:5211852, mRNA	-
2460	3,98	4,32	-1,08	0,01652	0,367	1565801_at	cDNA clone IMAGE:4796818	-
3957	3,84	4,16	-1,08	0,02890	0,399	1561099_at	Hypothetical LOC642757	*FLJ32756*
4850	4,33	4,69	-1,08	0,03695	0,417	217507_at	Solute carrier family 11, member 1	*SLC11A1*
5655	5,54	6,00	-1,08	0,04510	0,436	235367_at	Myopalladin	*MYPN*
3469	13,4	14,5	-1,08	0,02485	0,392	1564431_a_at	FLJ45224 protein	*FLJ45224*
872	3,18	3,44	-1,08	0,00504	0,313	207477_at	-	-
5822	27,6	29,9	-1,08	0,04704	0,442	1569679_at	Cadhetrin-like 22	*CDH22*
3107	6,35	6,88	-1,08	0,02193	0,386	237203_at	Clone IMAGE:4214313, mRNA	-
5048	3,98	4,31	-1,08	0,03889	0,420	241679_at	-	-

Index	Mutated*	Normal*	FC	*P* value	FDR**	Probe set	Description	Gene symbol
2827	4,86	5,27	-1,08	0,01973	0,381	1556502_at	cDNA clone IMAGE:4825100	-
3963	5,60	6,07	-1,08	0,02895	0,399	216790_at	cDNA FLJ22812 fis, clone KAIA2955	-
5162	4,99	5,41	-1,08	0,03978	0,421	207665_at	ADAM metallopeptidase domain 21	*ADAM21*
4502	4,86	5,27	-1,08	0,03388	0,411	1560832_at	Clone IMAGE:4063532, mRNA	-
3196	9,86	10,7	-1,08	0,02265	0,387	220996_s_at	Chromosome 1 open reading frame 14	*C1orf14*
2903	2,96	3,21	-1,08	0,02041	0,383	234454_at	-	-
4618	3,94	4,26	-1,08	0,03485	0,412	1556200_a_at	Chromosome 10 open reading frame 90	*C10orf90*
4328	17,8	19,3	-1,08	0,03221	0,407	1558705_at	Atonal homolog 8 (Drosophila)	*ATOH8*
4397	4,77	5,17	-1,08	0,03278	0,407	233606_at	cDNA FLJ11424 fis, clone HEMBA1001026	-
5719	7,79	8,44	-1,08	0,04580	0,438	1566602_at	RNA pseudouridylate synthase domain containing 3	*RPUSD3*
672	2,63	2,85	-1,08	0,00386	0,308	231613_at	MAP/microtubule affinity-regulating kinase 1	*MARK1*
6031	3,72	4,03	-1,08	0,04909	0,445	230631_s_at	Full-length cDNA clone CS0DI051YA02	-
2928	3,47	3,76	-1,08	0,02053	0,383	220984_s_at	Solute carrier organic anion transporter family, member 5A1	*SLCO5A1*
3634	3,48	3,77	-1,08	0,02628	0,395	1566339_at	Small nucleolar RNA, C/D box 8	*SNORD8*
2857	4,90	5,30	-1,08	0,02006	0,383	207924_x_at	Paired box 8	*PAX8*
1920	6,80	7,37	-1,08	0,01251	0,355	1569887_a_at	Hypothetical protein LOC286135	*LOC286135*
1469	3,30	3,58	-1,08	0,00898	0,334	217380_s_at	Clone DT1P1A11 Mrna	-
1923	3,86	4,18	-1,08	0,01252	0,355	1559559_at	Chromosome 9 open reading frame 79	*C9orf79*
5513	5,14	5,56	-1,08	0,04367	0,433	207503_at	T-complex 10 (mouse)	*TCP10*
5155	4,31	4,67	-1,08	0,03969	0,421	234357_at	cDNA FLJ13578 fis, clone PLACE1008757	-
1628	3,24	3,51	-1,08	0,01025	0,344	244602_at	Transcribed locus	-
2679	3,62	3,92	-1,08	0,01833	0,374	1564337_at	cDNA FLJ35701 fis, clone SPLEN2020007	-
3339	6,59	7,13	-1,08	0,02371	0,388	243095_at	Transcribed locus	-
2421	5,87	6,35	-1,08	0,01618	0,365	1555545_at	Kallikrein-related peptidase 2	*KLK2*
5294	6,23	6,74	-1,08	0,04123	0,426	229621_x_at	Early B-cell factor 3	*EBF3*
2329	8,39	9,08	-1,08	0,01551	0,364	1553837_at	Phosphoglycerate mutase family member 5	*PGAM5*
4646	10,3	11,1	-1,08	0,03505	0,412	217637_at	Full length insert cDNA clone ZE05A03	-
1974	3,70	4,00	-1,08	0,01291	0,355	231105_at	Similar to XP_001132401.1	-
2699	3,50	3,78	-1,08	0,01851	0,375	244138_at	Hypothetical protein LOC728904	*LOC728904*
4635	8,21	8,89	-1,08	0,03496	0,412	229239_x_at	Solute carrier organic anion transporter family, member 4A1	*SLCO4A1*
5662	2,88	3,12	-1,08	0,04519	0,436	217443_at	cDNA DKFZp434F104	-
5346	5,77	6,24	-1,08	0,04191	0,429	241476_at	Similar to XP_001130933.1	-
2343	5,28	5,72	-1,08	0,01564	0,364	222965_at	Hypothetical protein PRO2214	*PRO2214*
4387	3,16	3,42	-1,08	0,03268	0,407	214382_at	Unc-93 homolog A (C. elegans)	*UNC93A*
4912	4,13	4,47	-1,08	0,03757	0,418	1556960_a_at	HCG2007354 protein	-
2835	9,22	9,98	-1,08	0,01979	0,382	1554065_at	Family with sequence similarity 125, member B	*FAM125B*
5918	6,39	6,91	-1,08	0,04797	0,443	216059_at	Paired box 3	*PAX3*
4630	4,45	4,81	-1,08	0,03491	0,412	208247_at	Chromosome 3 open reading frame 51	*C3orf51*
2967	3,79	4,10	-1,08	0,02085	0,384	206446_s_at	Elastase 2A	*ELA2A*
5556	4,01	4,34	-1,08	0,04423	0,435	216223_at	Carboxypeptidase N, polypeptide 2	*CPN2*
3521	8,25	8,93	-1,08	0,02527	0,392	207500_at	Caspase 5, apoptosis-related cysteine peptidase	*CASP5*
4544	6,39	6,91	-1,08	0,03434	0,412	214242_at	Mannosidase, alpha, class 1A, member 2	*MAN1A2*
5351	3,57	3,86	-1,08	0,04198	0,429	215249_at	Ribosomal protein L35a	*RPL35A*
5463	8,66	9,37	-1,08	0,04314	0,432	240500_at	-	-
5295	4,59	4,96	-1,08	0,04124	0,426	1567358_at	Neuron navigator 2	*NAV2*
3650	5,95	6,43	-1,08	0,02638	0,395	240716_at	Tetratricopeptide repeat domain 23	*TTC23*
2532	4,48	4,85	-1,08	0,01711	0,369	1566181_at	cDNA FLJ20881 fis, clone ADKA03177	-
5614	9,43	10,2	-1,08	0,04478	0,436	1553688_at	Methyltransferase like 6	*METTL6*
2981	5,18	5,60	-1,08	0,02096	0,384	1555237_at	cDNA clone IMAGE:4336144	-
4140	3,58	3,87	-1,08	0,03056	0,403	224136_at	Mitogen-activated protein kinase 1	*p41*
4178	3,64	3,93	-1,08	0,03089	0,404	237767_at	FERM, RhoGEF (ARHGEF) and pleckstrin domain protein 1	*FARP1*
5869	5,93	6,41	-1,08	0,04743	0,442	243553_x_at	Transcribed locus	-
5866	3,92	4,24	-1,08	0,04742	0,442	216946_at	Major histocompatibility complex, class II, DO alpha	*HLA-DOA*
2797	2,92	3,15	-1,08	0,01943	0,380	1557739_at	cDNA clone IMAGE:5298947	-
5458	5,16	5,58	-1,08	0,04312	0,432	1559049_a_at	BAH domain and coiled-coil containing 1	*BAHCC1*
5718	4,40	4,76	-1,08	0,04580	0,438	232232_s_at	Solute carrier family 22, member 16	*SLC22A16*
3456	3,20	3,45	-1,08	0,02475	0,392	215958_at	cDNA FLJ12003 fis, clone HEMBB1001537	-

Index	Mutated*	Normal*	FC	*P* value	FDR**	Probe set	Description	Gene symbol
5881	13,6	14,7	-1,08	0,04758	0,442	1553163_at	ADP-ribosylhydrolase like 1	*ADPRHL1*
4376	3,45	3,73	-1,08	0,03256	0,407	1561485_at	IQ motif containing with AAA domain	*IQCA*
5795	4,59	4,96	-1,08	0,04675	0,441	233738_at	cDNA DKFZp566E1346	-
4883	3,33	3,59	-1,08	0,03734	0,418	1567076_at	-	-
5874	4,51	4,88	-1,08	0,04745	0,442	1569750_at	cDNA clone IMAGE:4822123	-
4002	3,32	3,58	-1,08	0,02930	0,400	1570101_at	cDNA clone IMAGE:5269204	-
2527	2,71	2,93	-1,08	0,01707	0,369	207901_at	Interleukin 12B	*IL12B*
707	3,23	3,49	-1,08	0,00406	0,308	1569064_at	Hypothetical LOC643338	*LOC643338*
3136	3,53	3,82	-1,08	0,02223	0,387	1552929_at	G protein-coupled receptor kinase 7	*GRK7*
4581	3,23	3,49	-1,08	0,03461	0,412	244446_at	cDNA clone IMAGE:5266114	-
1764	2,79	3,01	-1,08	0,01124	0,348	222966_at	-	-
5736	3,67	3,97	-1,08	0,04601	0,438	1560262_at	Clone IMAGE:5751523, mRNA	-
2264	3,55	3,83	-1,08	0,01505	0,363	240431_at	-	-
5323	5,29	5,71	-1,08	0,04162	0,427	243094_at	Chromosome 13 open reading frame 21	*C13orf21*
3410	3,95	4,27	-1,08	0,02433	0,390	240477_at	Transcribed locus	-
995	3,01	3,25	-1,08	0,00573	0,315	216313_at	Protocadherin beta 17 pseudogene	*PCDHB17*
4746	2,97	3,20	-1,08	0,03595	0,414	1563524_a_at	Chromosome 14 open reading frame 85	*C14orf85*
4472	5,73	6,19	-1,08	0,03360	0,411	217005_at	Low density lipoprotein receptor	*LDLR*
4464	4,70	5,07	-1,08	0,03354	0,411	1560455_at	Hypothetical protein LOC339166	*LOC339166*
1791	3,48	3,76	-1,08	0,01147	0,350	1567270_at	-	-
6058	3,65	3,94	-1,08	0,04941	0,446	220115_s_at	Cadhetrin 10, type 2 (T2-Cadhetrin)	*CDH10*
3503	3,74	4,04	-1,08	0,02517	0,392	202493_x_at	Chorionic somatomammotropin hormone 1	*CSH1*
5485	5,28	5,70	-1,08	0,04341	0,433	232526_at	Inositol 1,4,5-trisphosphate 3-kinase B	*ITPKB*
5356	3,56	3,85	-1,08	0,04201	0,429	1566861_at	Hypothetical protein LOC145663	*LOC145663*
4765	12,8	13,8	-1,08	0,03611	0,414	1554752_a_at	cDNA clone IMAGE:3528357	-
5616	6,13	6,62	-1,08	0,04482	0,436	241515_at	-	-
4886	3,48	3,75	-1,08	0,03737	0,418	1566693_at	cDNA FLJ20947 fis, clone ADSE01841	-
5433	4,83	5,22	-1,08	0,04281	0,431	1555624_a_at	Slingshot homolog 1 (Drosophila)	*SSH1*
4638	2,89	3,12	-1,08	0,03498	0,412	231781_s_at	Leucine rich repeat containing 2	*LRRC2*
3844	3,09	3,34	-1,08	0,02806	0,399	1553120_at	Claspin homolog (Xenopus laevis)	*CLSPN*
5762	4,44	4,79	-1,08	0,04629	0,439	1559561_at	F-box protein, helicase, 18	*FBXO18*
4786	4,34	4,69	-1,08	0,03629	0,415	1553844_a_at	Chromosome 10 open reading frame 67	*C10orf67*
5955	3,49	3,77	-1,08	0,04831	0,444	211617_at	Aldolase A, fructose-bisphosphate pseudogene 2	*ALDOAP2*
1934	3,29	3,55	-1,08	0,01261	0,355	220854_at	-	-
6006	12,9	14,0	-1,08	0,04881	0,444	217557_s_at	Carboxypeptidase M	*CPM*
6111	3,28	3,54	-1,08	0,04987	0,446	1556081_at	cDNA FLJ33441 fis, clone BRACE2021932	-
3618	4,73	5,10	-1,08	0,02612	0,395	1559777_at	cDNA FLJ32866 fis, clone TESTI2003718	-
1995	3,22	3,47	-1,08	0,01304	0,355	241238_at	Transcribed locus	-
3576	3,07	3,31	-1,08	0,02582	0,394	1561009_at	Monoamine oxidase B	*MAOB*
5385	3,99	4,30	-1,08	0,04224	0,429	1568864_at	Hypothetical protein MGC2752	*MGC2752*
5825	5,77	6,22	-1,08	0,04706	0,442	233745_at	cDNA FLJ34894 fis, clone NT2NE2017982	-
4643	3,98	4,29	-1,08	0,03501	0,412	217632_at	Guanine nucleotide binding protein-like 3 (nucleolar)-like	*GNL3L*
3581	12,5	13,5	-1,08	0,02586	0,394	1553917_at	Phosphatidylinositol-3-phosphate 5-kinase type III	*PIP5K3*
2228	5,90	6,37	-1,08	0,01480	0,363	1563488_at	Transmembrane protein 132B	*TMEM132B*
1752	2,83	3,05	-1,08	0,01117	0,348	1566266_at	Full length insert cDNA YQ80D07	-
3344	3,19	3,44	-1,08	0,02375	0,388	207870_at	A kinase (PRKA) anchor protein (yotiao) 9	*AKAP9*
5078	7,12	7,68	-1,08	0,03906	0,420	1561702_at	cDNA clone IMAGE:5268043	-
5978	3,94	4,25	-1,08	0,04854	0,444	222298_at	cDNA FLJ41644 fis, clone FEBRA2009362	-
5420	4,40	4,75	-1,08	0,04261	0,430	1563612_at	-	-
5764	4,38	4,72	-1,08	0,04631	0,439	222177_s_at	SCAN domain containing 2	*SCAND2*
5486	4,86	5,24	-1,08	0,04341	0,433	207615_s_at	Chromosome 16 open reading frame 3	*C16orf3*
2951	3,15	3,39	-1,08	0,02072	0,384	235622_at	Transcribed locus	-
1085	3,29	3,54	-1,08	0,00636	0,319	239460_at	Cytochrome P450, family 19, subfamily A, polypeptide 1	*CYP19A1*
5672	4,42	4,76	-1,08	0,04527	0,436	1562691_at	Clone IMAGE:5723690, mRNA	-
5165	28,6	30,9	-1,08	0,03980	0,421	204292_x_at	Serine/threonine kinase 11	*STK11*
5218	4,07	4,39	-1,08	0,04034	0,423	214648_at	Glutathione peroxidase 5	*GPX5*
5808	3,88	4,18	-1,08	0,04689	0,441	1561455_at	Hypothetical protein LOC284294	*LOC284294*

Index	Mutated*	Normal*	FC	*P* value	FDR**	Probe set	Description	Gene symbol
5298	7,28	7,84	-1,08	0,04127	0,426	240584_at	-	-
1797	4,05	4,37	-1,08	0,01156	0,351	1553446_at	Hypothetical protein FLJ37396	*FLJ37396*
4910	4,74	5,11	-1,08	0,03755	0,418	1563143_at	Clone IMAGE:5172510, mRNA	-
4113	3,26	3,52	-1,08	0,03023	0,402	1559970_at	Hypothetical protein LOC730034	*LOC730034*
5062	4,08	4,40	-1,08	0,03896	0,420	1564595_at	Clone IMAGE:5745181, mRNA	-
5152	5,68	6,12	-1,08	0,03965	0,421	235403_at	Transcribed locus	-
3090	7,43	8,01	-1,08	0,02179	0,385	211827_s_at	Potassium voltage-gated channel subfamily D member 3	*KCND3*
4165	4,03	4,34	-1,08	0,03078	0,404	219841_at	Activation-induced cytidine deaminase	*AICDA*
5790	3,83	4,12	-1,08	0,04667	0,441	215830_at	SH3 and multiple ankyrin repeat domains 2	*SHANK2*
1890	4,05	4,37	-1,08	0,01225	0,355	215872_at	-	-
5154	5,27	5,67	-1,08	0,03967	0,421	205753_at	C-reactive protein, pentraxin-related	*CRP*
3700	10,5	11,3	-1,08	0,02676	0,395	1563641_a_at	Selectin ligand interactor cytoplasmic-1	*SLIC1*
4537	3,63	3,91	-1,08	0,03429	0,412	233581_at	Clone 24850 mRNA sequence	-
2980	3,02	3,25	-1,08	0,02096	0,384	240122_at	DIRAS family, GTP-binding RAS-like 2	*DIRAS2*
4761	3,24	3,49	-1,08	0,03609	0,414	206810_at	Zinc finger protein 44	*ZNF44*
4323	6,31	6,80	-1,08	0,03218	0,407	1557981_at	Ribosomal protein S9	*RPS9*
655	3,40	3,66	-1,08	0,00377	0,308	241421_at	Transcribed locus	-
3139	3,22	3,46	-1,08	0,02226	0,387	1562750_at	cDNA clone IMAGE:4751528	-
5780	15,5	16,7	-1,08	0,04653	0,440	229832_x_at	SH3 domain and tetratricopeptide repeats 1	*SH3TC1*
2643	3,73	4,01	-1,08	0,01802	0,373	1557314_at	cDNA clone IMAGE:5303069	-
5888	5,26	5,66	-1,08	0,04763	0,442	208000_at	GPI anchored molecule like protein	*GML*
5265	6,62	7,13	-1,08	0,04089	0,425	1556369_a_at	Phosphorylase kinase, gamma 2 (testis)	*PHKG2*
4779	3,21	3,46	-1,08	0,03623	0,414	217083_at	Mitogen-activated protein kinase-activated protein kinase 5	*MAPKAPK5*
4017	10,6	11,4	-1,08	0,02942	0,400	214818_at	Coiled-coil domain containing 57	*CCDC57*
2325	4,11	4,42	-1,08	0,01547	0,364	237949_at	Transcribed locus	-
4168	4,33	4,67	-1,08	0,03080	0,404	1560750_at	Hypothetical protein LOC151121	*LOC151121*
3571	2,62	2,82	-1,08	0,02580	0,394	1552522_at	Tigger transposable element derived 4	*TIGD4*
3730	3,07	3,31	-1,08	0,02708	0,397	1554887_at	-	-
5739	8,88	9,56	-1,08	0,04603	0,439	1562411_at	MLCK protein	*MLCK*
5430	12,1	13,1	-1,08	0,04274	0,430	216337_at	(clone Z146) retinal mRNA, 3' end and repeat region	-
4330	4,40	4,73	-1,08	0,03224	0,407	1558177_at	Chromosome 14 open reading frame 83	*C14orf83*
5968	10,5	11,3	-1,08	0,04847	0,444	1569496_s_at	Spondin 2, extracellular matrix protein	*SPON2*
5987	4,41	4,75	-1,08	0,04865	0,444	1562687_x_at	cDNA FLJ20158 fis, clone COL08935	-
2259	3,13	3,37	-1,08	0,01504	0,363	207672_at	-	-
5142	5,29	5,69	-1,08	0,03959	0,421	1556477_a_at	Hypothetical protein LOC283485	*LOC283485*
1988	2,92	3,14	-1,08	0,01301	0,355	1553329_at	Chromosome 7 open reading frame 45	*C7orf45*
2168	3,27	3,52	-1,08	0,01434	0,361	234179_at	cDNA FLJ23200 fis, clone KAIA38871	-
3734	3,21	3,45	-1,08	0,02712	0,397	240581_at	Hypothetical LOC644135	*LOC644135*
5594	5,55	5,97	-1,08	0,04461	0,436	1554322_a_at	Histone deacetylase 4	*HDAC4*
5200	3,59	3,86	-1,08	0,04011	0,422	238713_at	Transcribed locus	-
2662	3,91	4,21	-1,08	0,01818	0,373	1560590_s_at	Clone IMAGE:2905626, mRNA	-
5343	8,37	9,00	-1,08	0,04188	0,429	1553890_s_at	Hypothetical protein BC018697	*LOC126147*
2648	3,83	4,12	-1,08	0,01804	0,373	1562541_at	Hypothetical protein LOC285928	*LOC285928*
4903	2,96	3,18	-1,08	0,03750	0,418	1569407_at	cDNA clone IMAGE:4825059	-
3082	3,48	3,74	-1,08	0,02172	0,385	1559661_at	Odz, odd Oz/ten-m homolog 3 (Drosophila)	*ODZ3*
4926	4,14	4,45	-1,08	0,03779	0,419	1557404_at	cDNA clone IMAGE:5266464	-
5674	3,25	3,50	-1,08	0,04528	0,436	1563376_at	Clone IMAGE:4469683, mRNA	-
3234	3,44	3,70	-1,08	0,02293	0,388	1570394_at	5'-3' exoribonuclease 1	*XRN1*
5936	5,37	5,77	-1,08	0,04814	0,443	233125_at	cDNA FLJ11686 fis, clone HEMBA1004944	-
4747	2,92	3,14	-1,08	0,03596	0,414	1554781_at	Hypothetical protein MGC32805	*MGC32805*
4501	2,98	3,20	-1,08	0,03388	0,411	1552394_a_at	ENTH domain containing 1	*ENTHD1*
778	3,23	3,48	-1,07	0,00446	0,311	1563085_at	-	-
5657	2,80	3,02	-1,07	0,04512	0,436	241986_at	BMP binding endothelial regulator	*BMPER*
3071	3,42	3,68	-1,07	0,02166	0,385	1552453_a_at	WD repeat domain 88	*WDR88*
4948	4,60	4,95	-1,07	0,03797	0,419	1557697_at	cDNA clone IMAGE:5311511	-
4966	2,95	3,17	-1,07	0,03810	0,419	241461_at	Transcribed locus	-
1445	4,20	4,51	-1,07	0,00879	0,332	243066_at	N-acetylneuraminate pyruvate lyase	*NPL*

Index	Mutated*	Normal*	FC	*P* value	FDR**	Probe set	Description	Gene symbol
5464	2,59	2,78	-1,07	0,04316	0,432	1554921_a_at	Sciellin	*SCEL*
5884	3,96	4,26	-1,07	0,04761	0,442	221439_at	Retinoblastoma binding protein 9	*RBBP9*
4890	9,19	9,87	-1,07	0,03738	0,418	1561371_at	Hypothetical gene supported by AK096399	*FLJ39080*
5302	2,84	3,05	-1,07	0,04138	0,426	1553497_at	Chromosome 12 open reading frame 37	*C12orf37*
3994	4,53	4,87	-1,07	0,02921	0,400	1565858_at	Small nucleolar RNA, H/ACA box 71A	*SNORA71A*
4169	3,72	4,00	-1,07	0,03081	0,404	1569257_at	Formin-like 1	*FMNL1*
4142	3,35	3,60	-1,07	0,03056	0,403	1562642_at	cDNA clone IMAGE:5288897	-
3137	3,78	4,06	-1,07	0,02225	0,387	1555430_at	Chromosome 9 open reading frame 97	*C9orf97*
3835	4,31	4,63	-1,07	0,02802	0,399	234933_at	KIAA1345 protein	*KIAA1345*
3248	2,93	3,15	-1,07	0,02307	0,388	211239_s_at	ADAM metallopeptidase domain 7	*ADAM7*
1714	2,73	2,93	-1,07	0,01099	0,348	240251_at	Intraflagellar transport 80 homolog (Chlamydomonas)	*IFT80*
5248	3,23	3,47	-1,07	0,04064	0,423	224126_at	Solute carrier family 10, member 7	*SLC10A7*
4432	3,39	3,64	-1,07	0,03320	0,409	1554965_at	Filamin A interacting protein 1-like	*FILIP1L*
5059	5,43	5,83	-1,07	0,03895	0,420	215366_at	Sorting nexin 13	*SNX13*
4299	8,50	9,13	-1,07	0,03201	0,407	36742_at	Tripartite motif-containing 15	*TRIM15*
4261	4,13	4,44	-1,07	0,03168	0,406	1563822_at	cDNA FLJ37602 fis, clone BRCOC2009380	-
4794	3,32	3,57	-1,07	0,03635	0,415	207544_s_at	Alcohol dehydrogenase 6 (class V)	*ADH6*
3190	3,01	3,23	-1,07	0,02262	0,387	236074_at	cDNA FLJ31443 fis, clone NT2NE2000808	-
5873	7,33	7,87	-1,07	0,04745	0,442	1554591_at	Gene differentially expressed in prostate	*GDEP*
4917	45,1	48,5	-1,07	0,03763	0,418	233307_x_at	cDNA FLJ20066 fis, clone COL01632	-
5518	3,92	4,21	-1,07	0,04378	0,433	220517_at	Vacuolar protein sorting 13 homolog C (S. cerevisiae)	*VPS13C*
5507	7,57	8,13	-1,07	0,04362	0,433	234557_at	Similar to COMM domain containing 4	*LOC440292*
2249	2,85	3,06	-1,07	0,01494	0,363	1554871_at	-	-
5903	3,14	3,38	-1,07	0,04783	0,443	207033_at	Gastric intrinsic factor (vitamin B synthesis)	*GIF*
5738	6,71	7,20	-1,07	0,04601	0,438	236726_at	cDNA FLJ43552 fis, clone PROST2017972	-
3995	3,21	3,45	-1,07	0,02921	0,400	224289_s_at	FKSG83	*FKSG83*
1569	3,27	3,51	-1,07	0,00975	0,340	234622_at	cDNA FLJ21514 fis, clone COL05780	-
5325	4,46	4,79	-1,07	0,04162	0,427	210348_at	Septin 4	*SEPT4*
4068	3,00	3,22	-1,07	0,02983	0,401	241678_at	Transcribed locus	-
2888	3,01	3,23	-1,07	0,02025	0,383	220697_at	cDNA clone IMAGE:40003562	-
5895	5,14	5,52	-1,07	0,04768	0,442	228344_s_at	T-box 3 (ulnar mammary syndrome)	*TBX3*
5099	13,3	14,3	-1,07	0,03922	0,420	230562_at	cDNA FLJ25042 fis, clone CBL03351	-
1382	2,83	3,04	-1,07	0,00832	0,329	1564628_at	cDNA DKFZp564A136	-
5013	3,69	3,96	-1,07	0,03855	0,420	1553785_at	RasGEF domain family, member 1B	*RASGEF1B*
3504	2,71	2,90	-1,07	0,02517	0,392	217400_at	Similar to Proliferating cell nuclear antigen (PCNA) (Cyclin)	*LOC392454*
3564	2,93	3,15	-1,07	0,02572	0,394	1553134_s_at	Chromosome 9 open reading frame 72	*C9orf72*
2576	4,29	4,60	-1,07	0,01748	0,371	1560212_a_at	Transcribed locus	-
3489	4,37	4,68	-1,07	0,02509	0,392	211369_at	PRO2168	-
5723	6,60	7,07	-1,07	0,04586	0,438	1569516_at	Clone IMAGE:5585187, mRNA	-
5640	3,14	3,37	-1,07	0,04500	0,436	232999_at	cDNA DKFZp564M1563	-
807	3,56	3,82	-1,07	0,00460	0,311	231315_at	Transcribed locus	-
4897	2,93	3,14	-1,07	0,03744	0,418	239479_x_at	Transcribed locus	-
3341	3,35	3,59	-1,07	0,02372	0,388	233778_at	Uncharacterized gastric protein ZG16P	
5617	3,92	4,21	-1,07	0,04483	0,436	1557767_at	Nanos homolog 2 (Drosophila)	*NANOS2*
4016	3,31	3,55	-1,07	0,02941	0,400	241620_at	Structural maintenance of chromosomes flexible hinge domain containing 1	*SMCHD1*
4452	5,69	6,10	-1,07	0,03344	0,411	237811_at	Transcribed locus	-
1927	2,76	2,96	-1,07	0,01255	0,355	237978_at	Transcribed locus	-
4297	3,65	3,91	-1,07	0,03195	0,407	243427_at	Transcribed locus	-
1507	2,96	3,18	-1,07	0,00927	0,336	1562520_at	cDNA FLJ37868 fis, clone BRSSN2017297	-
5575	4,11	4,41	-1,07	0,04442	0,436	229406_at	Hypothetical protein LOC146713	*HRNBP3*
5860	4,52	4,85	-1,07	0,04738	0,442	1554842_at	Solute carrier family 12, member 1	*SLC12A1*
2444	3,12	3,34	-1,07	0,01635	0,366	1552715_a_at	Relaxin/insulin-like family peptide receptor 1	*RXFP1*
3663	3,97	4,26	-1,07	0,02648	0,395	1555671_at	Islet cell autoantigen 1,69kDa-like	*ICA1L*
1994	2,75	2,95	-1,07	0,01303	0,355	237987_x_at	-	-
4757	3,88	4,16	-1,07	0,03607	0,414	1554716_s_at	Chromosome 15 open reading frame 50	*C15orf50*
5109	5,58	5,98	-1,07	0,03930	0,421	1564559_at	Hypothetical protein LOC728073	*LOC728073*
4749	3,79	4,06	-1,07	0,03599	0,414	1567139_at	TTY2 gene, clone TTY2L12A	

Index	Mutated*	Normal*	FC	*P* value	FDR**	Probe set	Description	Gene symbol
1877	2,75	2,95	-1,07	0,01214	0,354	1563754_at	Glutamate receptor, ionotropic, kainate 2	*GRIK2*
5684	4,07	4,36	-1,07	0,04538	0,436	239820_at	Ring finger protein 7	*RNF7*
5727	7,30	7,82	-1,07	0,04592	0,438	1570068_at	Clone IMAGE:4294479, mRNA	-
4018	3,25	3,48	-1,07	0,02942	0,400	242047_at	Pleckstrin homology domain containing, family K member 1	*PLEKHK1*
5400	13,2	14,2	-1,07	0,04235	0,429	207488_at	-	-
2748	3,27	3,50	-1,07	0,01900	0,378	209990_s_at	Gamma-aminobutyric acid (GABA) B receptor, 2	*GABBR2*
4069	3,41	3,65	-1,07	0,02984	0,401	216477_at	-	-
1409	3,65	3,91	-1,07	0,00851	0,330	235251_at	cDNA FLJ42786 fis, clone BRAWH3006761	-
5254	3,03	3,25	-1,07	0,04072	0,424	1562850_at	cDNA clone IMAGE:5742601	-
2778	13,7	14,7	-1,07	0,01930	0,380	1563425_at	Clone IMAGE:429302, mRNA sequence	-
2073	3,08	3,30	-1,07	0,01355	0,356	1555345_at	Solute carrier family 38, member 4	*SLC38A4*
5047	3,49	3,73	-1,07	0,03889	0,420	1566219_at	Hypothetical protein LOC338651	*LOC338651*
4294	3,63	3,88	-1,07	0,03193	0,406	1570234_at	Clone IMAGE:5169759, mRNA	-
5300	3,14	3,36	-1,07	0,04131	0,426	240073_at	-	-
2603	10,7	11,5	-1,07	0,01767	0,371	1569300_at	Chromosome 1 open reading frame 148	*C1orf148*
2401	3,53	3,78	-1,07	0,01601	0,365	1553472_at	Hypothetical protein FLJ32955	*FLJ32955*
3950	4,90	5,25	-1,07	0,02884	0,399	217439_at	-	-
5022	5,54	5,93	-1,07	0,03862	0,420	243674_at	-	-
5245	4,81	5,14	-1,07	0,04061	0,423	233556_at	cDNA clone IMAGE:5274560	-
5319	7,29	7,80	-1,07	0,04151	0,427	240567_at	cDNA clone IMAGE:4096591	-
2926	3,91	4,19	-1,07	0,02051	0,383	1555135_at	-	-
4453	3,78	4,04	-1,07	0,03344	0,411	215964_at	EST clone 22453 mariner transposon Hsmar1 sequence	-
5944	2,99	3,20	-1,07	0,04817	0,443	233050_at	Chromosome 6 open reading frame 174	*C6orf174*
3575	3,58	3,83	-1,07	0,02581	0,394	203820_s_at	Insulin-like growth factor 2 mRNA binding protein 3	*IGF2BP3*
4904	4,18	4,47	-1,07	0,03751	0,418	1564084_at	CAD trifunctional protein	*CAD*
3661	3,48	3,73	-1,07	0,02647	0,395	235818_at	v-Set and transmembrane domain containing 1	*VSTM1*
4175	4,13	4,42	-1,07	0,03086	0,404	1565882_at	cDNA FLJ12064 fis, clone HEMBB1002232	-
6015	4,36	4,66	-1,07	0,04894	0,445	228265_at	cDNA clone IMAGE:6214748	-
4346	3,31	3,54	-1,07	0,03237	0,407	1559732_at	Negative regulator of ubiquitin-like proteins 1	*NUB1*
4061	3,39	3,62	-1,07	0,02980	0,401	1569721_at	cDNA clone IMAGE:4838541	-
4986	4,63	4,95	-1,07	0,03827	0,419	238857_at	Arginyltransferase 1	*ATE1*
2897	3,55	3,80	-1,07	0,02034	0,383	1566505_at	cDNA FLJ34475 fis, clone HLUNG2003716	-
6118	3,14	3,36	-1,07	0,04996	0,446	220551_at	Solute carrier family 17, member 6	*SLC17A6*
4201	3,25	3,47	-1,07	0,03108	0,404	231127_at	Transcribed locus	-
5252	4,57	4,89	-1,07	0,04068	0,423	1557056_at	Hypothetical protein LOC133491	*LOC133491*
3761	3,00	3,21	-1,07	0,02734	0,397	1566481_at	cDNA DKFZp313L2229	-
1690	2,90	3,10	-1,07	0,01069	0,346	1560063_a_at	cDNA DKFZp667J114	-
2433	3,52	3,77	-1,07	0,01626	0,365	AFFX-LysX-M_	-	-
2610	3,23	3,45	-1,07	0,01773	0,371	231308_at	Similar to Ankyrin repeat and FYVE domain containing 1 isoform 1	-
5031	3,54	3,79	-1,07	0,03867	0,420	1559069_at	mRNA full length insert cDNA clone EUROIMAGE 240968	-
2824	4,17	4,46	-1,07	0,01972	0,381	1568931_at	cDNA clone IMAGE:4799464	-
2217	2,88	3,08	-1,07	0,01469	0,362	232314_at	Mitochondrial fission regulator 1	*MTFR1*
2853	75,1	80,2	-1,07	0,02001	0,383	38447_at	Ankyrin repeat domain 13 family, member D	*ANKRD13D*
2776	3,05	3,26	-1,07	0,01928	0,380	215542_at	-	-
5019	5,75	6,14	-1,07	0,03861	0,420	1565918_a_at	mRNA from chromosome 5q21-22, clone:LI26	-
1236	5,71	6,10	-1,07	0,00735	0,324	1561392_at	cDNA clone IMAGE:3877950	-
5774	6,67	7,13	-1,07	0,04642	0,440	243248_at	Transcribed locus	-
5639	4,63	4,95	-1,07	0,04499	0,436	217512_at	-	-
5785	4,10	4,39	-1,07	0,04659	0,440	216160_at	cDNA FLJ14169 fis, clone NT2RP2002056	-
2851	3,26	3,49	-1,07	0,01997	0,383	224379_at	Ferritin, heavy polypeptide-like 17	*FTHL17*
3046	3,16	3,38	-1,07	0,02145	0,385	220860_at	Purine-rich element binding protein G	*PURG*
4128	3,77	4,03	-1,07	0,03038	0,402	215463_at	Olfactory receptor, family 7, subfamily E, member 24	*OR7E24*
5910	4,10	4,38	-1,07	0,04792	0,443	224128_at	Chromosome 20 open reading frame 43	*C20orf43*
5697	4,61	4,92	-1,07	0,04559	0,438	220461_at	Pecanex-like 2 (Drosophila)	*PCNXL2*
2766	4,20	4,49	-1,07	0,01921	0,379	1561407_at	Centaurin, delta 1	*CENTD1*
5413	2,98	3,18	-1,07	0,04253	0,430	1559651_at	Similar to Casein kinase I alpha	*LOC161635*
3808	6,33	6,76	-1,07	0,02774	0,398	1565612_at	Dynein, light chain, roadblock-type 1	*DYNLRB1*

Index	Mutated*	Normal*	FC	*P* value	FDR**	Probe set	Description	Gene symbol
5316	4,41	4,71	-1,07	0,04148	0,427	1552459_a_at	Methyl-CpG binding domain protein 3-like 1	*MBD3L1*
4826	3,12	3,33	-1,07	0,03674	0,416	241553_at	Germ cell associated 1	*GSG1*
5101	3,71	3,97	-1,07	0,03923	0,420	238239_at	WD repeat domain 27	*WDR27*
5533	3,38	3,61	-1,07	0,04393	0,434	231335_at	Membrane-spanning 4-domains, subfamily A, member 6E	*MS4A6E*
5272	4,00	4,27	-1,07	0,04096	0,425	214515_at	Olfactory receptor, family 1, subfamily E, member 1	*OR1E1*
3207	3,15	3,37	-1,07	0,02270	0,387	1569585_at	cDNA clone IMAGE:3959751	-
5306	2,80	2,99	-1,07	0,04140	0,426	240050_s_at	Transcribed locus	-
1590	3,11	3,32	-1,07	0,00988	0,340	242964_at	Transcribed locus	-
5837	4,06	4,34	-1,07	0,04717	0,442	1561732_at	Clone IMAGE:5547271, mRNA	-
6109	4,38	4,68	-1,07	0,04987	0,446	241254_at	Transcribed locus	-
1698	3,17	3,38	-1,07	0,01080	0,348	1562193_at	Clone IMAGE:5744109, mRNA	-
5219	3,83	4,09	-1,07	0,04036	0,423	223678_s_at	Surfactant, pulmonary-associated protein A1B	*SFTPA1B*
4308	4,63	4,95	-1,07	0,03208	0,407	207817_at	Interferon, omega 1	*IFNW1*
4487	3,71	3,96	-1,07	0,03375	0,411	224154_at	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 2	*B3GNT2*
5549	4,70	5,02	-1,07	0,04413	0,435	221401_at	Calcium channel, voltage-dependent, gamma subunit 5	*CACNG5*
4839	3,23	3,45	-1,07	0,03689	0,417	241651_at	Transcribed locus	-
5390	5,86	6,25	-1,07	0,04227	0,429	1556003_a_at	Transcribed locus	-
5596	4,47	4,77	-1,07	0,04462	0,436	1553818_x_at	POM121-like protein	-
4535	4,57	4,88	-1,07	0,03427	0,412	1555666_at	Protein tyrosine phosphatase, receptor type, S	*PTPRS*
5689	3,20	3,41	-1,07	0,04548	0,437	1556297_a_at	cDNA clone IMAGE:5295605	-
3275	2,94	3,13	-1,07	0,02331	0,388	1569929_at	-	-
5828	4,30	4,58	-1,07	0,04710	0,442	1557287_at	cDNA clone IMAGE:4837072	-
1581	2,44	2,60	-1,07	0,00984	0,340	1568925_at	MLCK protein	*MLCK*
4842	3,60	3,83	-1,07	0,03691	0,417	1565920_at	mRNA from chromosome 5q21-22, clone:LI26	-
5210	5,18	5,52	-1,07	0,04021	0,422	1558855_at	FERM, RhoGEF and pleckstrin domain protein 2	*FARP2*
4111	3,00	3,20	-1,07	0,03022	0,402	243652_at	Transcribed locus	-
2294	3,03	3,23	-1,07	0,01525	0,363	244225_x_at	-	-
5026	3,22	3,43	-1,07	0,03864	0,420	235262_at	Zinc finger protein 585B	*ZNF585B*
2014	3,43	3,66	-1,07	0,01314	0,355	241543_at	-	-
2913	3,40	3,63	-1,07	0,02046	0,383	206909_at	-	-
5829	3,69	3,93	-1,07	0,04711	0,442	1553861_at	T-complex 11 (mouse)-like 2	*TCP11L2*
5097	4,73	5,04	-1,07	0,03922	0,420	209847_at	Cadhetrin 17, LI Cadhetrin (liver-intestine)	*CDH17*
4864	2,97	3,17	-1,06	0,03710	0,417	1559229_at	cDNA clone IMAGE:3621839	-
5370	2,85	3,04	-1,06	0,04215	0,429	211119_at	Estrogen receptor 2 (ER beta)	*ESR2*
5538	23,7	25,2	-1,06	0,04401	0,434	234481_at	-	-
3695	2,92	3,11	-1,06	0,02673	0,395	1560940_at	cDNA FLJ32834 fis, clone TESTI2003236	-
870	3,09	3,29	-1,06	0,00502	0,313	1561445_at	cDNA clone IMAGE:4821940	-
4615	2,99	3,19	-1,06	0,03484	0,412	242291_at	Eukaryotic translation initiation factor 4E nuclear import factor 1	*EIF4ENIF1*
5702	4,06	4,32	-1,06	0,04565	0,438	1557451_at	DiGeorge syndrome critical region gene 10	*DGCR10*
4812	5,88	6,27	-1,06	0,03656	0,415	1562034_at	Chromosome 21 open reading frame 134	*C21orf134*
3790	3,32	3,54	-1,06	0,02760	0,398	210436_at	Chaperonin containing TCP1, subunit 8 (theta)	*CCT8*
5969	3,46	3,68	-1,06	0,04848	0,444	1562424_at	Hypothetical protein LOC285889	*LOC285889*
5581	2,95	3,14	-1,06	0,04450	0,436	234679_at	Keratin associated protein 9-3	*KRTAP9-3*
5982	3,76	4,00	-1,06	0,04856	0,444	1555476_at	Iron-responsive element binding protein 2	*IREB2*
3010	2,73	2,90	-1,06	0,02118	0,385	1560404_a_at	ATP binding domain 4	*ATPBD4*
3418	2,88	3,07	-1,06	0,02442	0,391	1564392_at	Chromosome 21 open reading frame 131	*C21orf131*
4384	3,07	3,27	-1,06	0,03265	0,407	236888_at	Capping protein (actin filament) muscle Z-line, alpha 3	*CAPZA3*
5069	3,14	3,34	-1,06	0,03901	0,420	1564235_at	HCG1994895 protein	-
5547	3,17	3,37	-1,06	0,04410	0,435	215448_at	Clone 23638 mRNA sequence	-
1139	3,55	3,78	-1,06	0,00666	0,320	234309_at	Testis-specific transcript, Y-linked 7	*TTTY7*
5625	4,18	4,45	-1,06	0,04492	0,436	1564590_a_at	Orofacial cleft 1 candidate 1	*OFCC1*
5545	3,66	3,89	-1,06	0,04408	0,435	220978_at	Keratin associated protein 1-3	*KRTAP1-3*
5811	2,77	2,95	-1,06	0,04694	0,442	1561703_at	cDNA clone IMAGE:5269594	-
2260	2,79	2,97	-1,06	0,01505	0,363	240952_at	Transcribed locus	-
3698	4,30	4,57	-1,06	0,02674	0,395	234427_at	T cell receptor alpha locus	*TRA@*
4671	2,89	3,07	-1,06	0,03526	0,413	215704_at	Filaggrin	*FLG*
5375	3,90	4,14	-1,06	0,04217	0,429	1562597_at	Clone IMAGE:5742729, mRNA	-

Index	Mutated*	Normal*	FC	*P* value	FDR**	Probe set	Description	Gene symbol
4350	3,37	3,58	-1,06	0,03239	0,407	1557672_s_at	cDNA clone IMAGE:5297153	-
5438	4,21	4,47	-1,06	0,04287	0,431	1552414_at	WAP four-disulfide core domain 9	*WFDC9*
2489	2,73	2,90	-1,06	0,01678	0,367	229478_x_at	Basic, immunoglobulin-like variable motif containing	*BIVM*
1989	3,09	3,28	-1,06	0,01301	0,355	210521_s_at	Fetuin B	*FETUB*
5160	2,75	2,92	-1,06	0,03973	0,421	216672_s_at	Myelin transcription factor 1-like	*MYT1L*
5098	3,48	3,70	-1,06	0,03922	0,420	239950_at	Homeo box A11, antisense	*HOXA11S*
2966	3,11	3,30	-1,06	0,02084	0,384	233312_at	Ropporin 1-like	*ROPN1L*
3696	2,73	2,90	-1,06	0,02674	0,395	217452_s_at	UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 2	*B3GALT2*
4329	4,80	5,09	-1,06	0,03221	0,407	234416_at	Immunoglobulin lambda variable 2-14	*IGLV2-14*
1880	2,80	2,98	-1,06	0,01219	0,355	243725_at	Transcribed locus	-
1510	2,57	2,73	-1,06	0,00931	0,337	241291_at	cDNA FLJ36657 fis, clone UTERU2001876	-
6032	7,59	8,05	-1,06	0,04910	0,445	231141_at	cDNA clone IMAGE:4838568	-
4608	4,15	4,40	-1,06	0,03481	0,412	241128_at	-	-
5605	3,54	3,76	-1,06	0,04471	0,436	231529_at	Maternally expressed 3	*MEG3*
4263	3,18	3,37	-1,06	0,03171	0,406	1567612_at	Transcript ch132	-
4091	4,22	4,47	-1,06	0,03008	0,402	241056_at	Zinc finger CCCH-type containing 3	*ZC3H3*
3145	2,75	2,91	-1,06	0,02231	0,387	240474_x_at	Transcribed locus	-
3598	2,62	2,78	-1,06	0,02595	0,394	1557206_at	Hypothetical protein FLJ35848	*FLJ35848*
3001	2,77	2,94	-1,06	0,02113	0,385	1568898_at	Clone IMAGE:3921535, mRNA	-
4486	2,70	2,86	-1,06	0,03375	0,411	233295_at	Pheromone receptor (PHRET) pseudogene	-
5551	3,70	3,92	-1,06	0,04414	0,435	220527_at	Mitochondrial ribosomal protein L20	*MRPL20*
3901	2,88	3,05	-1,06	0,02851	0,399	1562640_at	Hypothetical protein LOC285943	*LOC285943*
4351	2,80	2,96	-1,06	0,03240	0,407	231665_at	Arginase, liver	*ARG1*
4126	3,14	3,32	-1,06	0,03036	0,402	1558813_at	Transmembrane emp24 protein transport domain containing 5	*TMED5*
4097	2,69	2,85	-1,06	0,03011	0,402	1556877_at	cDNA clone IMAGE:4799788	-
3218	2,73	2,89	-1,06	0,02280	0,387	237996_at	-	-
4788	2,75	2,90	-1,06	0,03631	0,415	1562313_at	BCL6 co-repressor-like 2	*BCORL2*
2839	2,78	2,94	-1,06	0,01981	0,382	1568711_a_at	cDNA clone IMAGE:4829846	-
5752	3,55	3,75	-1,06	0,04616	0,439	1555369_at	B melanoma antigen	*BAGE*
4460	2,75	2,91	-1,06	0,03351	0,411	241569_at	Transcribed locus	-
3192	3,30	3,48	-1,06	0,02262	0,387	234616_at	cDNA FLJ21341 fis, clone COL02653	-
4719	3,16	3,33	-1,05	0,03570	0,413	1558645_at	Mindbomb homolog 1 (Drosophila)	*MIB1*
4498	3,04	3,21	-1,05	0,03384	0,411	1553022_at	Zinc finger, imprinted 3	*ZIM3*
5405	2,98	3,14	-1,05	0,04243	0,429	1562418_at	Clone IMAGE:5227164, mRNA	-
5043	2,75	2,89	-1,05	0,03886	0,420	234209_at	cDNA FLJ21495 fis, clone COL05614	-
2952	2,46	2,59	-1,05	0,02072	0,384	1569591_at	Coagulation factor XI (plasma thromboplastin antecedent)	*F11*
5845	2,96	3,11	-1,05	0,04722	0,442	1570517_at	Four and a half LIM domains 5	*FHL5*
5434	3,16	3,31	-1,05	0,04281	0,431	1558846_at	Pancreatic lipase-related protein 3	*PNLIPRP3*
5344	2,73	2,86	-1,05	0,04189	0,429	236735_at	-	-
1658	2,58	2,71	-1,05	0,01047	0,345	241557_x_at	Transcribed locus	-
3954	2,80	2,93	-1,05	0,02889	0,399	1563680_at	Hypothetical protein LOC284950	*LOC284950*
5195	2,78	2,91	-1,05	0,04006	0,421	215944_at	-	-
4568	2,59	2,72	-1,05	0,03455	0,412	243281_at	Transcribed locus	-
2214	2,41	2,53	-1,05	0,01467	0,362	241961_at	Steroid 5 alpha-reductase 2-like 2	*SRD5A2L2*
4044	3,16	3,31	-1,05	0,02965	0,401	232817_at	cDNA FLJ13415 fis, clone PLACE1001799	-
5095	2,98	3,12	-1,05	0,03920	0,420	207674_at	Fc fragment of IgA, receptor for	*FCAR*
3914	2,62	2,74	-1,05	0,02858	0,399	1557717_at	Hypothetical protein LOC338862	*LOC338862*
4045	2,65	2,77	-1,05	0,02965	0,401	1561437_at	Hypothetical gene LOC728012	*LOC728012*
5255	2,94	3,07	-1,04	0,04073	0,424	1560989_at	Full length insert cDNA clone YY93H10	-
5771	2,87	2,99	-1,04	0,04637	0,439	1570194_x_at	Clone IMAGE:4480721, mRNA	-
4741	3,30	3,43	-1,04	0,03591	0,414	237938_at	Transcribed locus	-
5256	2,58	2,68	-1,04	0,04075	0,424	1561959_x_at	Full length insert cDNA clone YR17E12	-

*** Geometric mean of intensities**

**** False Discovery Rate**