

Figure S1. Hierarchical clustering analysis. Figs. S1-S6 represent the genes that were often aberrantly expressed in comparison I, II, III, IV, V and VI, respectively.

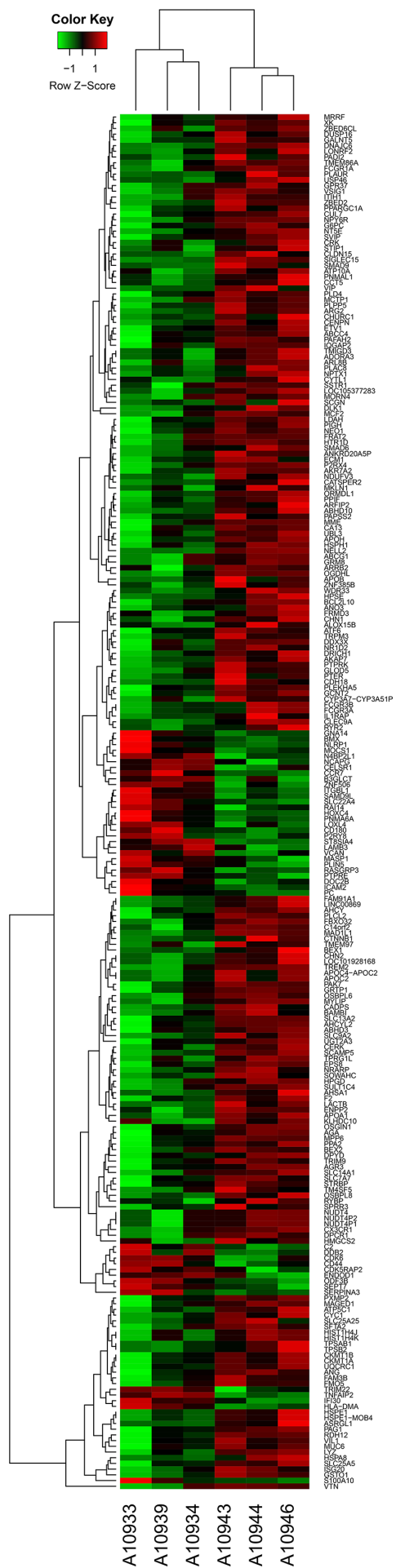


Figure S2. Hierarchical clustering analysis. Figs. S1-S6 represent the genes that were often aberrantly expressed in comparison I, II, III, IV, V and VI, respectively.

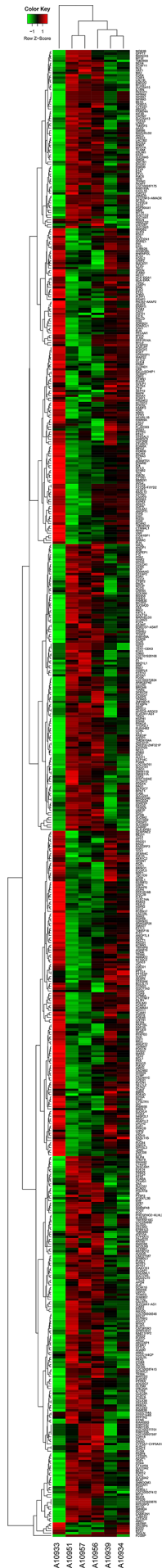




Figure S4. Hierarchical clustering analysis. Figs. S1-S6 represent the genes that were often aberrantly expressed in comparison I, II, III, IV, V and VI, respectively.

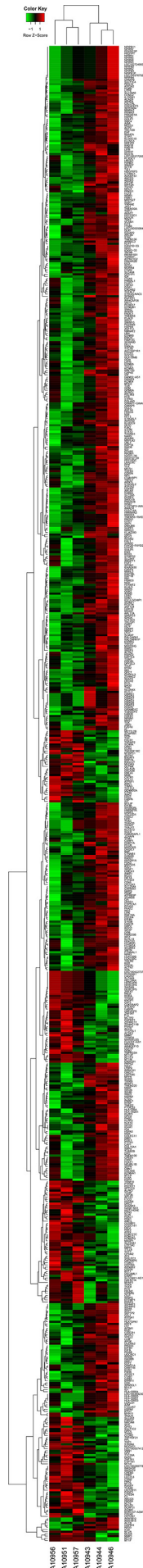


Figure S5. Hierarchical clustering analysis. Figs. S1-S6 represent the genes that were often aberrantly expressed in comparison I, II, III, IV, V and VI, respectively.

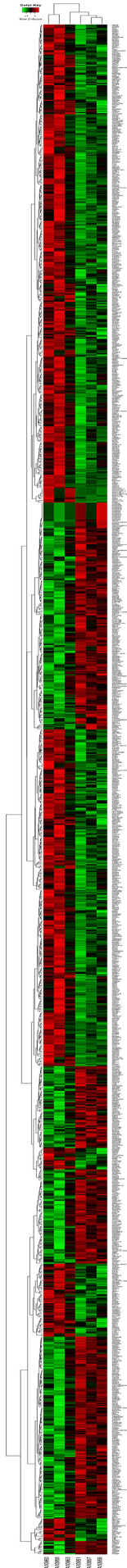


Figure S6. Hierarchical clustering analysis. Figs. S1-S6 represent the genes that were often aberrantly expressed in comparison I, II, III, IV, V and VI, respectively.

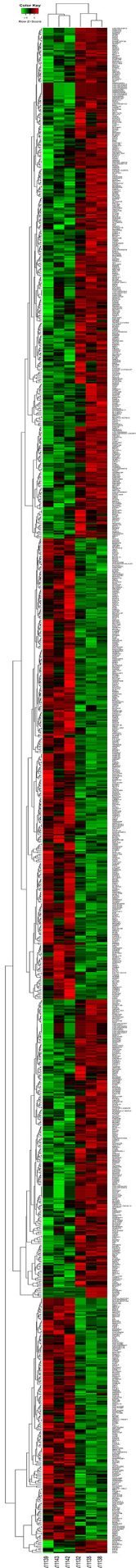


Table SI. DEGs in comparison I.

Entrez accession no.	Gene symbol	Gene name	Gall blad der wall of gall ston e (A1 093 3)	Gall blad der wall of gall ston e (A1 093 4)	Gall blad der wall of gall ston e (A1 093 9)	Gall blad der wall of chol este rol pol yps (A1 094 3)	Gall blad der wall of chol este rol pol yps (A1 094 4)	Gall blad der wall of chol este rol pol yps (A1 094 6)	Fold-ch ange	Log Fold-ch ange	Absolut e Fold-ch ange	Regul ation	P-value	False discove ry rate
6415 1	NCA PG	Non-SMC condensin I complex subunit	3.98 958	4.26 032	4.35 235	3.91 397	3.23 455	3.69 121	-1.5026 47556	-0.5875 06667	1.5026 47556	Down	0.0218 45186	0.9845 43317

		G												
9630	GNA 14	Guanine nucleotide binding protein (G protein), $\alpha$ 14	5.48 101	4.17 76	4.56 219	3.70 162	4.02 551	4.01 37	-1.7735 70485	-0.8266 56667	1.7735 70485	Down	0.0415 33501	0.9845 43317
2706 8	PPA2	Pyrophosphatase (inorganic) 2	6.87 149	7.79 937	7.69 584	8.15 868	7.96 014	8.44 246	1.6603 952	0.7315 26667	1.6603 952	Up	0.0389 65051	0.9845 43317
3697	ITIH 1	Inter- $\alpha$ -trypsin inhibitor heavy chain 1	4.53 139	5.76 317	4.63 167	6.39 866	5.80 243	5.77 947	2.0252 64027	1.0181 1	2.0252 64027	Up	0.0293 25951	0.9845 43317
7448	VTN	Vitronectin	11.4 524	12.8 472	11.7 036	13.0 509	12.9 780	12.8 385	1.9382 30298	0.9547 4	1.9382 30298	Up	0.0331 0537	0.9845 43317
8015 0	ASR GL1	Asparaginase like 1	9.17 727	9.19 058	9.22 682	9.62 751	9.53 403	10.2 263	1.5133 47533	0.5977 43333	1.5133 47533	Up	0.0260 78823	0.9845 43317
3776	CA13	Carbonic	4.37	5.47	6.05	6.59	6.21	6.49	2.2015	1.1385	2.2015	Up	0.0305	0.9845



77		anhydrase XIII	102	31	167	903	408	821	35335	1	35335		87898	43317
5534	ABH	Abhydrolase	5.29	5.60	5.43	6.13	5.97	6.56	1.7208	0.7831	1.7208	Up	0.0061	0.9845
7	D10	domain containing 10	03	036	964	952	675	334	28512	03333	28512		08075	43317
9358	ITGB	Integrin $\beta$ like 1	6.45	5.51	5.40	4.62	5.05	4.75	-1.9697	-0.9780	1.9697	Down	0.0154	0.9845
	L1		273	838	511	81	948	452	87499	4	87499		46112	43317
2322	PLCL	Phospholipase C	6.03	6.81	6.57	7.25	7.14	7.01	1.5877	0.6669	1.5877	Up	0.0235	0.9845
8	2	like 2	216	048	182	358	245	926	05498	43333	05498		74432	43317
1034	TRI	Tripartite motif	9.67	9.50	9.73	8.58	9.15	9.28	-1.5461	-0.6286	1.5461	Down	0.0234	0.9845
6	M22	containing 22	375	515	607	859	816	216	56835	86667	56835		00589	43317
4091	SMA	SMAD family	5.88	6.52	6.11	6.46	7.10	6.83	1.5435	0.6262	1.5435	Up	0.0379	0.9845
	D6	member 6	517	234	404	369	056	611	69027	7	69027		55667	43317
1648	LON	LON peptidase	4.93	5.30	4.84	5.66	5.27	5.90	1.5060	0.5908	1.5060	Up	0.0308	0.9845
32	RF2	N-terminal domain and ring finger 2	314	109	206	957	128	789	99064	16667	99064		42476	43317
1001	BCL2	BCL2-like 10	4.10	4.94	4.55	4.95	5.33	5.32	1.5916	0.6705	1.5916	Up	0.0273	0.9845

7	L10	(apoptosis facilitator)	962	207	308	373	757	503	46552	2	46552		95614	43317
1140	TRI	Tripartite motif	5.87	7.73	7.30	8.63	8.28	7.88	2.4510	1.2934	2.4510	Up	0.0352	0.9845
88	M9	containing 9	481	926	811	477	45	319	9545	26667	9545		36245	43317
2734	TME	Transmembrane	6.51	6.38	7.12	7.69	7.07	7.22	1.5723	0.6528	1.5723	Up	0.0454	0.9845
6	M97	protein 97	45	591	804	569	018	122	03798	8	03798		81147	43317
660	BMX	BMX non-receptor tyrosine kinase	5.58	4.34	4.30	3.95	3.72	4.00	-1.8021	-0.8497	1.8021	Down	0.0475	0.9845
			865	559	003	468	769	267	80275	43333	80275		10021	43317
5409	FAM	Family with	7.61	8.98	8.63	9.83	9.16	9.11	1.9466	0.9609	1.9466	Up	0.0450	0.9845
7	3B	sequence similarity 3 member B	672	351	249	82	225	514	00279	56667	00279		8553	43317
9063	N4BP	NEDD4 binding	4.53	4.49	4.20	3.54	3.96	3.93	-1.5147	-0.5991	1.5147	Down	0.0082	0.9845
4	2L1	protein 2-like 1	763	816	277	376	122	62	99307	26667	99307		47316	43317
6052	LDA	Lipid droplet	5.73	6.41	6.50	6.90	6.74	7.04	1.5996	0.6777	1.5996	Up	0.0270	0.9845
6	H	associated	39	746	732	232	859	107	61516	66667	61516		49558	43317

		hydrolase												
3914	LAM B3	Laminin subunit $\beta$ 3	5.30 498	6.21 147	5.45 485	5.22 555	3.99 354	4.39 302	-2.1730 62999	-1.1197 3	2.1730 62999	Down	0.0220 84184	0.9845 43317
1148 82	OSB PL8	Oxysterol binding protein like 8	7.38 312	7.53 895	7.84 777	8.67 02	8.17 635	9.08 359	2.0754 63173	1.0534 33333	2.0754 63173	Up	0.0059 52566	0.9845 43317
344	APO C2	Apolipoprotein C-II	6.06 565	6.58 253	5.60 903	7.88 934	6.60 426	7.64 836	2.4536 28223	1.2949 16667	2.4536 28223	Up	0.0156 3271	0.9845 43317
4731	NDU FV3	NADH:ubiquinon e oxidoreductase subunit V3	5.98 142	5.82 403	6.15 848	6.85 944	6.37 279	6.87 874	1.6422 57097	0.7156 8	1.6422 57097	Up	0.0092 6413	0.9845 43317
3158	HMG CS2	3-hydroxy-3-meth ylglutaryl-coa synthase 2 (mitochondrial)	8.40 162	7.09 511	6.42 248	9.75 264	8.05 394	8.63 892	2.8456 60068	1.5087 63333	2.8456 60068	Up	0.0452 83069	0.9845 43317
7979 9	UGT 2A3	UDP glucuronosyltrans ferase 2 family,	5.09 675	7.17 791	7.45 864	7.58 629	8.23 638	8.86 288	3.1399 68313	1.6507 5	3.1399 68313	Up	0.0436 51412	0.9845 43317

		polypeptide A3												
2115	ETV1	Ets variant 1	4.05 737	5.16 4	5.00 064	5.58 062	5.29 164	5.94 343	1.8207 84271	0.8645 6	1.8207 84271	Up	0.0354 13324	0.9845 43317
2538	G6PC	Glucose-6-phosph atase, catalytic subunit	4.75 452	5.43 539	5.53 366	5.93 609	6.14 29	5.72 377	1.6167 12709	0.6930 63333	1.6167 12709	Up	0.0272 93841	0.9845 43317
9820	CUL 7	Cullin 7	5.00 998	5.77 329	5.65 355	5.96 664	6.01 264	6.27 402	1.5214 98945	0.6054 93333	1.5214 98945	Up	0.0384 64528	0.9845 43317
4168	MCF 2	MCF.2 cell line derived transforming sequence	3.19 158	5.94 366	2.65 389	7.52 151	7.23 073	6.38 593	8.6718 91262	3.1163 46667	8.6718 91262	Up	0.0088 92106	0.9845 43317
509	ATP5 C1	ATP synthase, H+ transporting, mitochondrial F1 complex, $\gamma$ polypeptide 1	8.62 478	8.90 994	9.09 255	9.38 704	9.32 925	9.74 082	1.5262 02787	0.6099 46667	1.5262 02787	Up	0.0166 63333	0.9845 43317

2059	EPS8	Epidermal growth factor receptor pathway substrate 8	6.45	6.97	7.31	7.58	7.70	7.60	1.6449	0.7180	1.6449	Up	0.0203	0.9845
			21	625	39	526	819	306	98954	86667	98954		69704	43317
1142	LAC	Lactamase $\beta$	7.35	7.41	7.29	8.25	7.71	7.99	1.5534	0.6355	1.5534	Up	0.0101	0.9845
94	TB		344	234	355	159	489	936	7964	03333	7964		35842	43317
2338	AHC	Adenosylhomocysteinase-like 2	6.06	6.82	7.06	7.42	7.43	7.48	1.7327	0.7930	1.7327	Up	0.0230	0.9845
2	YL2		694	365	85	461	048	329	89813	96667	89813		41238	43317
2723	SUL	Sulfotransferase family 1C member 4	6.63	7.24	6.78	7.50	7.35	7.57	1.5028	0.5876	1.5028	Up	0.0231	0.9845
3	T1C4		325	64	895	725	134	298	03797	56667	03797		87931	43317
1511	ZNF3	Zinc finger protein 385B	5.11	5.10	4.06	7.29	5.58	6.14	2.9907	1.5804	2.9907	Up	0.0163	0.9845
26	85B		087	602	066	064	057	78	07187	86667	07187		89101	43317
8451	PLPP	Phospholipid phosphatase 5	4.23	4.91	4.90	5.86	5.27	5.48	1.8123	0.8578	1.8123	Up	0.0117	0.9845
3	5		119	952	17	003	631	967	56371	66667	56371		46133	43317
8003	TRP	Transient receptor potential cation	3.74	4.56	4.38	5.54	4.84	4.87	1.8083	0.8546	1.8083	Up	0.0207	0.9845
6	M3		671	447	304	264	277	288	70139	9	70139		8101	43317

		channel, subfamily M, member 3												
1089 1	PPA RGC 1A	Peroxisome proliferator-activa ted receptor $\gamma$ , coactivator 1 $\alpha$	4.13 042	5.40 051	5.18 03	6.71 609	5.50 713	6.36 366	2.4484 74776	1.2918 83333	2.4484 74776	Up	0.0219 03709	0.9845 43317
9239 9	MRR F	Mitochondrial ribosome recycling factor	4.51 916	5.10 929	5.40 633	5.55 957	5.46 269	6.06 278	1.6059 42234	0.6834 2	1.6059 42234	Up	0.0447 29776	0.9845 43317
5025	P2RX 4	Purinergic receptor P2X, ligand gated ion channel, 4	5.48 51	6.31 326	5.85 511	6.63 001	6.53 645	6.68 756	1.6626 87068	0.7335 16667	1.6626 87068	Up	0.0162 99087	0.9845 43317
5723 4	LINC 0086 9	Long intergenic non-protein coding RNA 869	6.40 799	6.69 703	6.56 82	6.93 653	7.09 127	7.44 719	1.5163 36556	0.6005 9	1.5163 36556	Up	0.0159 56414	0.9845 43317

3312	HSP A8	Heat shock protein family A (Hsp70) member 8	10.0 961 7	10.2 572 4	10.4 063 1	10.6 079 7	11.5 586 2	11.8 089 6	2.1022 63243	1.0719 43333	2.1022 63243	Up	0.0127 93567	0.9845 43317
1016	CDH 18	Cadherin 18, type 2	3.28 266	3.64 847	3.57 381	5.42 958	4.48 104	4.15 033	2.2741 64583	1.1853 36667	2.2741 64583	Up	0.0090 98318	0.9845 43317
1893	ECM 1	Extracellular matrix protein 1	5.62 869	6.21 136	6.15 15	6.83 232	6.77 343	6.23 086	1.5315 79229	0.6150 2	1.5315 79229	Up	0.0418 5254	0.9845 43317
9317	PTER	Phosphotriesteras e related	3.21 449	3.93 808	3.67 125	5.01 011	3.89 625	4.32 171	1.7428 11655	0.8014 16667	1.7428 11655	Up	0.0403 964	0.9845 43317
9975	NR1 D2	Nuclear receptor subfamily 1 group D member 2	3.63 253	4.27 309	4.70 157	4.94 998	5.28 136	4.71 676	1.7174 91946	0.7803 03333	1.7174 91946	Up	0.0339 31615	0.9845 43317
3924 65	GLO D5	Glyoxalase domain containing 5	3.28 507	4.28 237	3.48 159	5.19 657	4.35 188	4.50 226	2.0007 76476	1.0005 6	2.0007 76476	Up	0.0196 24845	0.9845 43317
7429	VIL1	Villin 1	8.13	9.27	9.39	10.1	9.53	9.75	1.8575	0.8933	1.8575	Up	0.0483	0.9845

			472	711	517	925	818	641	01445	63333	01445		71728	43317
2580	SVIP	Small	4.51	5.62	5.32	5.69	5.95	6.20	1.7339	0.7940	1.7339	Up	0.0388	0.9845
10		VCP/p97-interacting protein	47	661	393	084	1	547	0317	23333	0317		86246	43317
4311	MME	Membrane metallo-endopeptidase	4.68	6.09	5.60	6.47	6.51	6.55	2.0740	1.0524	2.0740	Up	0.0204	0.9845
			478	163	641	271	126	611	05903	2	05903		57452	43317
8470	BEX	Brain expressed X-linked 2	6.63	7.99	7.36	8.43	8.12	8.00	1.8128	0.8582	1.8128	Up	0.0448	0.9845
7	2		786	549	425	954	304	974	25425	4	25425		32913	43317
2286	NLR	NLR family, pyrin domain containing 1	5.35	4.00	4.41	3.64	3.50	3.71	-1.9565	-0.9683	1.9565	Down	0.0233	0.9845
1	P1		728	116	804	86	544	742	88002	4	88002		66963	43317
8574	AKR	Aldo-keto reductase family 7, member A2	5.60	6.03	6.06	6.66	6.45	6.45	1.5387	0.6217	1.5387	Up	0.0119	0.9845
	7A2		619	437	937	709	019	802	83217	9	83217		67809	43317
4093	SMA	SMAD family member 9	5.27	5.16	5.19	6.24	5.91	5.47	1.5885	0.6677	1.5885	Up	0.0181	0.9845
	D9		615	344	172	706	354	386	5679	16667	5679		72334	43317



5091	PC	Pyruvate carboxylase	7.44 502	5.66 709	5.73 504	5.54 43	4.80 076	4.85 207	-2.3241 01914	-1.2166 73333	2.3241 01914	Down	0.0496 73598	0.9845 43317
12	SERP INA3	Serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 3	9.56 178	6.78 279	9.90 906	5.97 187	6.73 813	6.30 431	-5.3262 00235	-2.4131 06667	5.3262 00235	Down	0.0213 91492	0.9845 43317
4884	NPT X1	Neuronal pentraxin I	4.09 585	4.41 62	4.93 406	4.89 209	5.98 764	6.29 301	2.3656 06315	1.2422 1	2.3656 06315	Up	0.0185 43546	0.9845 43317
4337	MOC S1	Molybdenum cofactor synthesis 1	5.02 087	4.21 165	4.13 603	3.61 81	3.85 993	4.01 346	-1.5429 45032	-0.6256 86667	1.5429 45032	Down	0.0460 94105	0.9845 43317
1398	CRK	V-crk avian sarcoma virus CT10 oncogene homolog	5.09 705	5.03 338	5.78 029	5.57 192	6.09 188	6.46 167	1.6681 51131	0.7382 5	1.6681 51131	Up	0.0459 81631	0.9845 43317

717	C2	Complement component 2	7.73 207	7.30 301	6.89 655	6.71 272	6.28 609	6.56 957	-1.7263 79932	-0.7877 5	1.7263 79932	Down	0.0170 73827	0.9845 43317
7977 2	MCT P1	Multiple C2 domains, transmembrane 1	4.39 319	5.29 644	4.53 471	5.53 446	5.16 04	5.39 923	1.5403 41246	0.6232 5	1.5403 41246	Up	0.0499 55569	0.9845 43317
1226 18	PLD4	Phospholipase D family member 4	4.32 07	5.20 706	4.99 39	5.71 481	5.36 243	5.46 74	1.5958 51784	0.6743 26667	1.5958 51784	Up	0.0332 54176	0.9845 43317
1706 88	NUD T4P2	Nudix hydrolase 4 pseudogene 2	7.94 991	8.72 461	7.05 272	8.70 06	9.27 632	9.22 821	2.2334 85156	1.1592 96667	2.2334 85156	Up	0.0308 78175	0.9845 43317
1008 6154 0	CYP3 A7-C YP3 A51P	CYP3A7-CYP3A51P readthrough	3.08 086	3.18 838	4.07 637	4.80 214	4.14 723	4.14 12	1.8855 51646	0.9149 86667	1.8855 51646	Up	0.0235 28165	0.9845 43317
9058	SLC1 3A2	Solute carrier family 13 (sodium-dependent dicarboxylate	5.79 316	6.90 109	7.00 095	7.60 119	7.58 437	7.59 85	2.0414 86461	1.0296 2	2.0414 86461	Up	0.0180 18592	0.9845 43317

		transporter), member 2												
9056	SLC7 A7	Solute carrier family 7 (amino acid transporter light chain, y+L system), member 7	7.44 138	8.11 803	8.22 125	8.62 044	8.63 059	8.29 888	1.5049 85931	0.5897 5	1.5049 85931	Up	0.0488 92039	0.9845 43317
1096 3	STIP 1	Stress induced phosphoprotein 1	5.16 927	4.90 964	5.63 706	5.65 051	5.68 909	6.20 934	1.5273 06911	0.6109 9	1.5273 06911	Up	0.0458 783	0.9845 43317
1019 2816 8	LOC 1019 2816 8	Uncharacterized LOC101928168	6.36 212	6.49 398	6.06 64	6.91 83	6.80 026	7.45 065	1.6805 14899	0.7489 03333	1.6805 14899	Up	0.0139 06039	0.9845 43317
2300 8	KLH DC10	Kelch domain containing 10	7.77 557	6.24 545	6.37 059	8.11 342	7.40 668	8.06 662	2.0922 23054	1.0650 36667	2.0922 23054	Up	0.0490 83003	0.9845 43317
1451	B3G	B	4.77	5.35	5.31	3.48	4.90	3.40	-2.3189	-1.2134	2.3189	Down	0.0252	0.9845

73	LCT	3-glucosyltransferase	183	961	066	851	857	464	31172	6	31172		18824	43317
3405 47	VSIG 1	V-set and immunoglobulin domain containing 1	4.09 903	5.42 272	4.50 43	5.81 982	5.65 202	5.31 323	1.8916 86914	0.9196 73333	1.8916 86914	Up	0.0346 45326	0.9845 43317
1441 10	TME M86 A	Transmembrane protein 86A	5.22 769	5.58 948	4.92 738	6.00 689	5.80 018	5.92 911	1.5843 34174	0.6638 76667	1.5843 34174	Up	0.0133 0795	0.9845 43317
1149 07	FBX O32	F-box protein 32	6.42 353	6.78 172	6.20 567	7.01 046	7.23 952	7.14 021	1.5798 1614	0.6597 56667	1.5798 1614	Up	0.0117 16424	0.9845 43317
1124	CHN 2	Chimerin 2	6.36 212	6.49 398	6.06 64	6.91 83	6.80 026	7.45 065	1.6805 14899	0.7489 03333	1.6805 14899	Up	0.0139 06039	0.9845 43317
292	SLC2 5A5	Solute carrier family 25 (mitochondrial carrier; adenine	9.96 518	10.6 068	10.6 481	10.9 515	10.8 494	11.2 186	1.5155 30969	0.5998 23333	1.5155 30969	Up	0.0341 87988	0.9845 43317

		nucleotide translocator), member 5												
2865 30	P2RY 8	Purinergic receptor P2Y, G-protein coupled, 8	6.23 21	4.64 575	6.55 598	4.28 532	4.00 296	4.91 643	-2.6568 31378	-1.4097 06667	2.6568 31378	Down	0.0319 98947	0.9845 43317
1005 2924 1	HSPE 1-MO B4	HSPE1-MOB4 readthrough	8.78 167	9.03 133	9.22 59	9.61 348	9.48 9	10.1 579	1.6707 74079	0.7405 16667	1.6707 74079	Up	0.0146 8503	0.9845 43317
2918	GRM 8	Glutamate receptor, metabotropic 8	4.82 252	6.26 7	4.27 592	5.96 9	6.71 442	6.57 392	2.4576 84969	1.2973	2.4576 84969	Up	0.0413 10061	0.9845 43317
5520 7	ARL 8B	ADP ribosylation factor like gtpase 8B	4.23 757	4.44 026	5.19 913	5.25 095	5.37 108	5.51 666	1.6863 57017	0.7539 1	1.6863 57017	Up	0.0249 3227	0.9845 43317
2292	ATF6	Activating	3.87	4.65	4.66	5.21	4.96	4.80	1.5127	0.5971	1.5127	Up	0.0479	0.9845

6		transcription factor 6	927	411	728	611	913	691	39251	63333	39251		73605	43317
29948	OSGI N1	Oxidative stress induced growth inhibitor 1	6.69 485	7.34 503	7.68 686	7.84 135	8.09 302	8.11 012	1.7083 26027	0.7725 83333	1.7083 26027	Up	0.0258 72538	0.9845 43317
441478	NRA RP	NOTCH-regulate d ankyrin repeat protein	6.71 516	7.32 901	7.07 175	7.78 116	7.95 987	7.45 671	1.6176 95417	0.6939 4	1.6176 95417	Up	0.0179 58564	0.9845 43317
3221	HOX C4	Homeobox C4	5.84 929	5.02 388	5.20 445	4.67 414	4.78 232	4.72 506	-1.5497 47668	-0.6320 33333	1.5497 47668	Down	0.0285 1125	0.9845 43317
440515	ZNF5 06	Zinc finger protein 506	4.95 326	4.38 157	5.06 736	2.93 256	4.11 428	3.21 105	-2.6052 70791	-1.3814 33333	2.6052 70791	Down	0.0052 03406	0.9845 43317
4069	LYZ	Lysozyme	6.95 675	7.94 635	9.04 6	9.75 43	10.0 746	10.4 146	4.2816 49401	2.0981 66667	4.2816 49401	Up	0.0051 69511	0.9845 43317
5791	PTPR E	Protein tyrosine phosphatase,	6.42 408	5.77 979	6.40 078	5.58 441	5.40 498	4.90 077	-1.8723 23857	-0.9048 3	1.8723 23857	Down	0.0114 5427	0.9845 43317

		receptor type, E												
4064	CD180	CD180 molecule	5.46	4.94	5.98	4.91	4.52	4.76	-1.6589	-0.7302	1.6589	Down	0.0341	0.9845
	0		33	424	171	091	33	431	18871	43333	18871		79795	43317
9032	TM4SF5	Transmembrane 4 L six family member 5	7.48	8.34	7.55	9.26	8.49	8.24	1.8258	0.8685	1.8258	Up	0.0432	0.9845
			615	996	443	35	257	014	35343	56667	35343		72415	43317
55339	WDR33	WD repeat domain 33	4.51	4.50	4.32	4.74	5.35	5.14	1.5487	0.6311	1.5487	Up	0.0112	0.9845
			882	865	977	706	941	409	5256	06667	5256		91783	43317
51233	DRIC H1	Aspartate-rich 1	3.80	4.50	4.19	4.85	4.59	5.23	1.6606	0.7317	1.6606	Up	0.0193	0.9845
			009	654	133	564	8	967	90624	83333	90624		11424	43317
335	APOA1	Apolipoprotein A-I	6.97	6.96	6.20	8.47	7.75	8.74	3.0591	1.6131	3.0591	Up	0.0021	0.9845
			141	21	648	954	603	376	1286	13333	1286		39261	43317
4888	NPY6R	Neuropeptide Y receptor Y6 (pseudogene)	5.06	5.80	5.22	6.09	6.08	6.11	1.6599	0.7311	1.6599	Up	0.0123	0.9845
			415	592	999	835	087	438	9627	8	9627		98283	43317
6281	S100A10	S100 calcium binding protein	10.9	9.59	10.0	9.44	9.42	9.18	-1.8395	-0.8793	1.8395	Down	0.0407	0.9845
			873	624	998	224	181	126	42065	46667	42065		91502	43317

		A10			1									
6485	USP4	Ubiquitin specific	5.11	4.94	5.11	5.33	5.75	5.91	1.5237	0.6076	1.5237	Up	0.0147	0.9845
4	6	peptidase 46	964	448	929	263	501	868	61033	36667	61033		71242	43317
7177	TPSA	Tryptase $\alpha/\beta$ 1	8.38	8.64	8.30	8.76	9.04	9.53	1.5925	0.6713	1.5925	Up	0.0239	0.9845
	B1		641	308	774	869	42	842	73548	6	73548		29839	43317
350	APO	Apolipoprotein H	5.17	6.05	6.06	6.77	6.59	6.97	2.0226	1.0162	2.0226	Up	0.0089	0.9845
	H	( $\beta$ -2-glycoprotein I)	747	771	636	987	211	84	96691	8	96691		76808	43317
1272	TPR	Tumor protein	6.70	6.83	7.44	7.43	7.84	7.73	1.5978	0.6761	1.5978	Up	0.0273	0.9845
62	G1L	p63 regulated 1-like	613	794	113	028	845	497	88418	66667	88418		35665	43317
8447	DOC	Double C2-like	7.26	5.92	5.76	4.67	5.28	5.62	-2.1775	-1.1226	2.1775	Down	0.0428	0.9845
	2B	domains, $\beta$	53	974	117	499	603	712	26083	9	26083		50751	43317
2305	END	Endonuclease	7.28	7.70	7.44	7.33	6.18	5.97	-1.9770	-0.9833	1.9770	Down	0.0336	0.9845
2	OD1	domain containing 1	837	881	988	576	527	591	82856	73333	82856		35992	43317
5168	ENPP	Ectonucleotide	7.49	7.35	6.95	8.06	7.82	7.84	1.5614	0.6429	1.5614	Up	0.0126	0.9845



	2	pyrophosphatase/ phosphodiesterase 2	341	066	512	32	198	276	82788	16667	82788		65517	43317
9500	MAG ED1	MAGE family member D1	8.24 641	9.28 675	8.99 486	9.39 216	9.71 645	9.54 813	1.6353 20411	0.7095 73333	1.6353 20411	Up	0.0418 27339	0.9845 43317
2147	F2	Coagulation factor II (thrombin)	6.48 685	6.93 971	7.10 44	7.54 237	7.24 188	7.67 245	1.5603 9722	0.6419 13333	1.5603 9722	Up	0.0229 47841	0.9845 43317
1159	CKM T1B	Creatine kinase, mitochondrial 1B	7.76 828	8.70 526	8.57 227	9.12 401	8.82 889	9.40 338	1.7054 54974	0.7701 56667	1.7054 54974	Up	0.0351 50218	0.9845 43317
5412	UBL 3	Ubiquitin like 3	5.43 734	5.86 081	6.36 148	6.55 774	6.61 711	7.00 531	1.7902 69358	0.8401 76667	1.7902 69358	Up	0.0179 27056	0.9845 43317
5131 6	PLA C8	Placenta specific 8	4.58 949	4.59 34	5.10 885	5.15 017	6.23 335	5.90 012	1.9962 60506	0.9973	1.9962 60506	Up	0.0153 54393	0.9845 43317
2842 66	SIGL EC15	Sialic acid binding Ig-like lectin 15	5.30 928	5.47 839	5.42 684	6.43 809	6.27 643	6.11 624	1.8303 04056	0.8720 83333	1.8303 04056	Up	0.0007 82001	0.9845 43317

1043 7	IFI30	Interferon, $\gamma$ -inducible protein 30	9.41 428	8.94 371	8.86 213	8.62 474	8.15 385	8.20 67	-1.6759 08441	-0.7449 43333	1.6759 08441	Down	0.0121 8156	0.9845 43317
1122 7	GAL NT5	Polypeptide N-acetylgalactosa minyltransferase 5	4.48 587	5.15 488	5.15 143	6.16 352	5.56 161	5.56 634	1.7815 05166	0.8330 96667	1.7815 05166	Up	0.0166 57785	0.9845 43317
1236 7	CCR 7	Chemokine (C-C motif) receptor 7	4.71 847	4.43 796	5.22 345	4.07 075	4.12 524	3.94 766	-1.6764 50633	-0.7454 1	1.6764 50633	Down	0.0098 8378	0.9845 43317
140	ADO RA3	Adenosine A3 receptor	4.55 64	4.23 61	5.03 035	5.20 362	5.55 607	6.02 88	1.9841 85167	0.9885 46667	1.9841 85167	Up	0.0111 33289	0.9845 43317
4404 82	ANK RD20 A5P	Ankyrin repeat domain 20 family member A5, pseudogene	5.87 277	6.29 94	6.13 31	7.07 794	6.70 578	6.65 589	1.6374 45247	0.7114 46667	1.6374 45247	Up	0.0083 73927	0.9845 43317
4907	NT5E	5'-nucleotidase, ecto (CD73)	4.80 951	5.59 635	4.98 493	5.71 846	6.19 203	6.25 617	1.8990 6594	0.9252 9	1.8990 6594	Up	0.0100 15137	0.9845 43317
5436	CYT	Cytokine like 1	5.21	4.66	4.57	5.48	5.56	6.43	2.0084	1.0060	2.0084	Up	0.0147	0.9845

0	L1		346	467	977	422	012	174	18613	6	18613		69156	43317
2209	FCG R1A	Fc fragment of igg, high affinity Ia, receptor (CD64)	5.02 935	5.64 109	4.73 691	5.82 116	6.06 513	5.86 193	1.7174 76073	0.7802 9	1.7174 76073	Up	0.0174 19884	0.9845 43317
6549	SLC9 A2	Solute carrier family 9, subfamily A (NHE2, cation proton antiporter 2), member 2	5.58 032	6.68 358	6.06 64	8.77 209	7.34 553	8.32 934	4.1092 82933	2.0388 86667	4.1092 82933	Up	0.0026 02688	0.9845 43317
1059 8	AHS A1	AHA1, activator of heat shock 90kda protein atpase homolog 1 (yeast)	6.91 967	6.95 717	6.80 871	7.37 942	7.25 034	7.85 035	1.5138 12649	0.5981 86667	1.5138 12649	Up	0.0196 1225	0.9845 43317
2834	CLE	C-type lectin	3.78	3.72	3.48	4.12	4.86	4.78	1.8992	0.9254	1.8992	Up	0.0042	0.9845

20	C9A	domain family 9, member A	697	959	126	436	345	632	59012	36667	59012		68823	43317
5714	PAK	P21 protein	5.37	6.86	6.32	7.53	7.30	7.19	2.2295	1.1567	2.2295	Up	0.0186	0.9845
4	7	(Cdc42/Rac)-activated kinase 7	311	432	054	321	133	371	61507	6	61507		49543	43317
1926	SCA	Secretory carrier	6.85	7.23	7.13	7.68	7.57	7.79	1.5267	0.6104	1.5267	Up	0.0081	0.9845
83	MP5	membrane protein 5	663	731	299	719	987	128	56513	7	56513		11574	43317
7384	UQC	Ubiquinol-cytochrome c reductase core protein I	7.95	8.64	8.74	9.13	8.94	9.31	1.6038	0.6815	1.6038	Up	0.0293	0.9845
	RC1		487	287	76	442	215	347	80513	66667	80513		33308	43317
2911	MYL	Myosin regulatory	6.48	7.37	5.97	7.50	8.06	8.00	2.3712	1.2456	2.3712	Up	0.0132	0.9845
6	IP	light chain interacting protein	646	281	401	726	077	213	15308	26667	15308		94069	43317
409	ARR	Arrestin, $\beta$ 2	6.21	5.98	5.25	6.63	6.49	6.35	1.6000	0.6781	1.6000	Up	0.0408	0.9845
	B2		669	742	525	804	793	784	86612	5	86612		2102	43317
5575	OGD	Oxoglutarate	5.25	5.91	4.94	6.62	6.40	6.48	2.1934	1.1332	2.1934	Up	0.0040	0.9845

3	HL	dehydrogenase-like	666	72	12	718	701	053	7764	2	7764		19479	43317
7977	GRT	Growth hormone	5.15	6.75	6.20	7.15	7.26	7.12	2.2096	1.1438	2.2096	Up	0.0233	0.9845
4	P1	regulated TBC protein 1	916	515	185	484	803	475	53262	2	53262		94585	43317
1053	LOC	Uncharacterized	4.22	4.47	3.52	4.98	5.29	5.69	2.3802	1.2510	2.3802	Up	0.0040	0.9845
7728	1053	LOC105377283	032	212	931	975	408	118	06374	86667	06374		98923	43317
3	7728													
3														
3248	HPG	Hydroxyprostagla	6.63	7.42	6.84	7.33	7.73	7.61	1.5021	0.5869	1.5021	Up	0.0491	0.9845
	D	ndin dehydrogenase 15-(NAD)	751	988	807	139	359	146	12986	93333	12986		99091	43317
1554	AGR	Anterior gradient	6.86	8.27	8.24	8.43	9.07	9.09	2.1018	1.0716	2.1018	Up	0.0398	0.9845
65	3	3, protein disulphide isomerase family	873	192	953	849	537	122	11567	33333	11567		85849	43317

		member												
1010	PPIF	Peptidylprolyl	5.18	5.47	5.85	6.06	6.20	6.66	1.7523	0.8093	1.7523	Up	0.0135	0.9845
5		isomerase F	159	868	025	359	704	779	60985		60985		97936	43317
1715	ABH	Abhydrolase	5.76	7.03	7.41	7.55	7.85	8.08	2.1267	1.0886	2.1267	Up	0.0407	0.9845
86	D3	domain	468	506	873	022	379	051	9847	83333	9847		5496	43317
		containing 3												
5582	PAG	Phosphoprotein	8.85	9.62	9.67	9.89	10.0	10.1	1.5565	0.6383	1.5565	Up	0.0390	0.9845
4	1	membrane anchor	497	518	358	239	028	736	83893	83333	83893		28654	43317
		with						9						
		glycosphingolipid												
		microdomains 1												
283	ANG	Angiogenin,	7.78	8.77	8.59	9.11	9.26	8.93	1.6505	0.7229	1.6505	Up	0.0380	0.9845
		ribonuclease,	47	871	112	508	94	885	34544	33333	34544		46933	43317
		rnase A family, 5												
4588	MUC	Mucin 6,	7.34	9.34	9.77	10.8	9.77	10.5	2.9416	1.5566	2.9416	Up	0.0495	0.9845
	6	oligomeric	869	381	914	643	399	032	38574	2	38574		92732	43317
		mucus/gel-formin						1						

		g												
5583	CEN	Centromere	4.24	4.75	4.58	5.38	4.89	5.52	1.6682	0.7383	1.6682	Up	0.0128	0.9845
9	PN	protein N	861	759	202	088	383	855	62908	46667	62908		60746	43317
6583	SLC2	Solute carrier	6.16	5.30	5.70	5.13	4.96	4.81	-1.6896	-0.7567	1.6896	Down	0.0167	0.9845
	2A4	family 22 (organic cation/zwitterion transporter), member 4	352	693	861	732	127	037	21385		21385		54863	43317
5796	PTPR	Protein tyrosine	3.71	4.22	4.02	5.00	4.55	4.59	1.6587	0.7300	1.6587	Up	0.0065	0.9845
	K	phosphatase, receptor type, K	879	215	32	567	254	609	00409	53333	00409		26247	43317
9556	C14o	Chromosome 14	6.82	7.06	6.35	7.49	7.43	7.32	1.5917	0.6705	1.5917	Up	0.0173	0.9845
	rf2	open reading frame 2	025	968	441	834	773	001	12748	8	12748		3419	43317
3336	HSPE	Heat shock	8.78	9.03	9.22	9.61	9.48	10.1	1.6707	0.7405	1.6707	Up	0.0146	0.9845
	1	protein family E	167	133	59	348	9	579	74079	16667	74079		8503	43317

		(Hsp10) member 1						7						
8618	CAD PS	Ca <sup>++</sup> -dependent secretion activator	6.13 006	6.78 967	6.54 576	7.96 276	8.22 139	7.08 978	2.4107 46578	1.2694 8	2.4107 46578	Up	0.0074 55522	0.9845 43317
2580 5	BAM BI	BMP and activin membrane-bound inhibitor	6.20 576	7.00 82	6.40 838	7.47 215	7.80 716	6.97 457	1.8367 81479	0.8771 8	1.8367 81479	Up	0.0227 04721	0.9845 43317
2861	GPR3 7	G protein-coupled receptor (endothelin receptor type B-like)	4.36 37 111	5.58 643	4.82 764	5.61 596	6.13 29	5.47 765	1.7618 73079	0.8171 1	1.7618 73079	Up	0.0496 12669	0.9845 43317
8788	DLK 1	$\Delta$ -like 1 homolog (Drosophila)	4.24 347	6.03 837	4.59 342	5.75 757	8.13 97	7.08 913	4.1040 45332	2.0370 46667	4.1040 45332	Up	0.0244 10656	0.9845 43317
1080 8	HSP H1	Heat shock protein family H (Hsp110) member	5.12 016	5.62 914	6.20 648	6.30 86	6.83 421	6.67 546	1.9374 55713	0.9541 63333	1.9374 55713	Up	0.0172 34577	0.9845 43317



		1												
3352	HTR 1D	5-hydroxytryptam ine (serotonin) receptor 1D, G protein-coupled	5.61 007	6.61 992	6.00 329	6.78 689	6.83 965	6.64 462	1.6013 55181	0.6792 93333	1.6013 55181	Up	0.0404 03688	0.9845 43317
4408 36	ODF 3B	Outer dense fiber of sperm tails 3B	8.19 928	7.65 067	8.05 663	7.47 274	7.40 625	7.22 735	-1.5158 00618	-0.6000 8	1.5158 00618	Down	0.0173 55372	0.9845 43317
9829	DNA JC6	Dnaj heat shock protein family (Hsp40) member C6	5.04 077	5.16 208	4.98 623	5.76 319	5.68 135	5.94 548	1.6628 36898	0.7336 46667	1.6628 36898	Up	0.0013 97096	0.9845 43317
2364 7	ARFI P2	ADP ribosylation factor interacting protein 2	5.33 127	5.66 05	5.77 209	6.04 439	5.85 84	6.67 085	1.5191 45443	0.6032 6	1.5191 45443	Up	0.0494 88957	0.9845 43317
7127	TNF AIP2	Tnf $\alpha$ -induced protein 2	9.41 795	9.73 77	9.87 408	8.20 627	8.62 645	8.39 12	-2.4092 82111	-1.2686 03333	2.4092 82111	Down	0.0003 5729	0.9845 43317
1537	CYC	Cytochrome c-1	8.65	9.08	8.78	9.49	9.18	9.69	1.5276	0.6113	1.5276	Up	0.0183	0.9845

	1		796	706	423	002	219	096	42187	06667	42187		53348	43317
8363	HIST 1H4J	Histone cluster 1, h4j	8.25 122	8.45 981	8.90 68	8.92 262	9.28 796	9.16 953	1.5025 64234	0.5874 26667	1.5025 64234	Up	0.0300 78133	0.9845 43317
5051	PAF AH2	Platelet-activating factor acetylhydrolase 2	3.90 226	5.09 269	5.18 461	5.74 365	5.68 691	5.37 417	1.8340 80125	0.8750 56667	1.8340 80125	Up	0.0447 57953	0.9845 43317
1524	CX3 CR1	Chemokine (C-X3-C motif) receptor 1	7.58 882	9.01 504	7.09 956	9.25 31	9.58 875	9.94 036	3.2331 26599	1.6929 3	3.2331 26599	Up	0.0119 10209	0.9845 43317
8082 4	DUS P16	Dual specificity phosphatase 16	4.75 548	5.43 046	5.19 116	5.98 651	5.44 91	5.73 978	1.5151 17834	0.5994 3	1.5151 17834	Up	0.0365 77464	0.9845 43317
2578 0	RAS GRP3	RAS guanyl releasing protein 3 (calcium and DAG-regulated)	6.21 067	5.89 315	6.53 161	5.34 429	5.65 298	5.58 651	-1.6064 58079	-0.6838 83333	1.6064 58079	Down	0.0133 24871	0.9845 43317
1654	DDX 3X	DEAD (Asp-Glu-Ala-As	4.01 362	4.45 78	4.89 755	5.02 448	5.07 236	5.10 318	1.5266 29527	0.6103 5	1.5266 29527	Up	0.0323 36386	0.9845 43317

		p) box helicase 3, X-linked												
1021	CDK 6	Cyclin-dependent kinase 6	7.08 398	6.75 83	7.10 094	6.13 997	6.20 701	6.76 063	-1.5282 38806	-0.6118 7	1.5282 38806	Down	0.0282 68843	0.9845 43317
3669	ISG2 0	Interferon stimulated exonuclease gene 20kda	9.89 465	10.9 159	10.3 568	11.7 182	11.4 472	11.0 129	2.0050 66381	1.0036 5	2.0050 66381	Up	0.0143 08039	0.9845 43317
384	ARG 2	Arginase 2	4.29 79	4.78 344	4.60 113	5.84 72	5.20 784	5.47 953	1.9328 10236	0.9507	1.9328 10236	Up	0.0034 29022	0.9845 43317
1123	CHN 1	Chimerin 1	4.25 305	4.38 322	3.89 039	4.70 842	4.56 107	5.01 682	1.5016 51464	0.5865 5	1.5016 51464	Up	0.0165 27266	0.9845 43317
5741 3	TMI GD3	Transmembrane and immunoglobulin domain containing 3	4.55 64	4.23 61	5.03 035	5.20 362	5.55 607	6.02 88	1.9841 85167	0.9885 46667	1.9841 85167	Up	0.0111 33289	0.9845 43317

960	CD44	CD44 molecule (Indian blood group)	7.17 682	6.61 615	7.24 365	5.97 766	6.32 624	6.63 804	-1.6225 09209	-0.6982 26667	1.6225 09209	Down	0.0289 6452	0.9845 43317
5485 96	CKM T1A	Creatine kinase, mitochondrial 1A	7.76 828	8.70 526	8.57 227	9.12 401	8.82 889	9.40 338	1.7054 54974	0.7701 56667	1.7054 54974	Up	0.0351 50218	0.9845 43317
9620	CELS R1	Cadherin, EGF LAG seven-pass G-type receptor 1	4.79 076	5.05 848	5.19 802	4.04 164	4.26 452	4.78 495	-1.5713 99493	-0.6520 5	1.5713 99493	Down	0.0230 06317	0.9845 43317
247	ALO X15B	Arachidonate 15-lipoxygenase, type B	4.49 345	4.06 805	4.11 029	4.63 548	5.35 302	4.73 717	1.6072 86002	0.6846 26667	1.6072 86002	Up	0.0212 4964	0.9845 43317
2570 19	FRM D3	FERM domain containing 3	4.57 856	4.17 422	4.00 787	4.60 529	4.88 08	5.08 51	1.5194 12224	0.6035 13333	1.5194 12224	Up	0.0201 08455	0.9845 43317
5283	PIGH	Phosphatidylinosi tol glycan anchor biosynthesis class H	5.62 533	6.41 631	6.25 42	6.87 696	6.58 989	6.98 102	1.6441 51604	0.7173 43333	1.6441 51604	Up	0.0239 33616	0.9845 43317

9410	ORM	ORMDL	5.36	5.74	5.85	6.19	6.21	6.51	1.5743	0.6547	1.5743	Up	0.0115	0.9845
1	DL1	sphingolipid biosynthesis regulator 1	048	794	361	995	425	201	17654	26667	17654		55215	43317
1116	NUD	Nudix hydrolase 4	7.94	8.72	7.05	8.70	9.27	9.22	2.2334	1.1592	2.2334	Up	0.0308	0.9845
3	T4		991	461	272	06	632	821	85156	96667	85156		78175	43317
8379	MAD	MAD1 mitotic arrest deficient-like 1 (yeast)	6.57	6.82	6.42	7.55	7.54	7.36	1.8441	0.8829	1.8441	Up	0.0012	0.9845
	IL1		326	234	272	68	316	723	50843	56667	50843		91689	43317
1499	CTN	Catenin $\beta$ 1	6.59	6.85	6.72	6.90	7.76	7.26	1.5043	0.5891	1.5043	Up	0.0464	0.9845
	NB1		189	124	29	552	503	294	63631	53333	63631		53649	43317
1147	SLC2	Solute carrier family (mitochondrial carrier; phosphate carrier), member	8.55	9.08	8.81	9.57	9.83	8.98	1.5653	0.6464	1.5653	Up	0.0438	0.9845
89	5A25	25	52	664	691	811	023	985	44284	8	44284		24438	43317

		25												
2330	FMO 5	Flavin containing monooxygenase 5	7.54 629	8.78 671	8.22 774	9.51 296	8.88 046	8.92 967	1.8931 42925	0.9207 83333	1.8931 42925	Up	0.0342 76122	0.9845 43317
2342 9	RYP P	RING1 and YY1 binding protein	7.93 219	7.25 988	7.86 155	8.04 929	8.76 501	8.32 033	1.6173 92694	0.6936 7	1.6173 92694	Up	0.0368 31865	0.9845 43317
1462	VCA N	Versican	5.97 797	5.78 578	4.94 017	4.36 238	4.19 191	5.06 88	-2.0377 02354	-1.0269 43333	2.0377 02354	Down	0.0219 87556	0.9845 43317
3893 76	SFTA 2	Surfactant associated 2	8.09 184	9.22 039	8.57 636	9.47 882	9.63 941	9.20 316	1.7543 46028	0.8109 33333	1.7543 46028	Up	0.0327 81368	0.9845 43317
1148 80	OSB PL6	Oxysterol binding protein like 6	6.58 653	7.49 918	6.38 885	7.81 957	7.88 434	7.56 299	1.9063 06371	0.9307 8	1.9063 06371	Up	0.0204 25989	0.9845 43317
1806	DPY D	Dihydropyrimidin e dehydrogenase	6.38 965	7.48 049	7.80 655	7.74 87	8.54 434	8.67 662	2.1400 68042	1.0976 56667	2.1400 68042	Up	0.0380 87454	0.9845 43317
7504	XK	X-linked Kx blood group	4.31 887	5.14 045	5.36 258	5.78 509	5.54 077	5.70 231	1.6648 85929	0.7354 23333	1.6648 85929	Up	0.0358 57242	0.9845 43317
3556	IL1R AP	Interleukin 1 receptor accessory	3.40 82	3.75 28	3.78 695	4.11 666	5.05 137	4.11 279	1.7143 04435	0.7776 23333	1.7143 04435	Up	0.0275 42605	0.9845 43317

		protein												
8362	HIST 1H4K	Histone cluster 1, h4k	8.25 122	8.45 981	8.90 68	8.92 262	9.28 796	9.16 953	1.5025 64234	0.5874 26667	1.5025 64234	Up	0.0300 78133	0.9845 43317
6563	SLC1 4A1	Solute carrier family 14 (urea transporter), member 1 (Kidd blood group)	6.52 426	8.22 516	6.94 562	8.28 931	8.41 077	9.06 667	2.5619 39961	1.3572 36667	2.5619 39961	Up	0.0230 64922	0.9845 43317
5329	PLA UR	Plasminogen activator, urokinase receptor	5.02 651	5.03 142	5.11 576	5.36 989	6.11 924	5.66 022	1.5784 98985	0.6585 53333	1.5784 98985	Up	0.0172 256	0.9845 43317
1005 3399 0	APO C4-A POC2	APOC4-APOC2 readthrough (NMD candidate)	6.06 565	6.58 253	5.60 903	7.88 934	6.60 426	7.64 836	2.4536 28223	1.2949 16667	2.4536 28223	Up	0.0156 3271	0.9845 43317
1188 12	MOR N4	MORN repeat containing 4	4.04 789	5.41 598	3.60 322	5.86 437	5.20 348	5.77 418	2.3921 59081	1.2583 13333	2.3921 59081	Up	0.0333 63427	0.9845 43317
1137	ZBE	ZBED6	4.68	4.88	5.61	5.76	5.66	5.89	1.6365	0.7106	1.6365	Up	0.0292	0.9845

63	D6C L	C-terminal like	741	079	605	314	057	263	94225	96667	94225		52613	43317
6262	RYR 2	Ryanodine receptor (cardiac)	3.77 091	3.92 656	3.43 009	3.96 229	4.40 075	5.04 19	1.6924 65783	0.7591 26667	1.6924 65783	Up	0.0340 15582	0.9845 43317
6751	SSTR 1	Somatostatin receptor 1	4.46 69	4.90 886	3.48 087	5.37 304	5.17 383	5.09 243	1.9020 51971	0.9275 56667	1.9020 51971	Up	0.0356 70655	0.9845 43317
1085 5	HPSE	Heparanase	4.32 842	4.46 54	4.44 368	4.67 105	5.03 964	5.31 818	1.5126 97309	0.5971 23333	1.5126 97309	Up	0.0147 48999	0.9845 43317
8417 1	LOX L4	Lysyl oxidase like 4	5.59 969	4.96 63	5.67 802	4.19 192	5.04 532	4.50 966	-1.7806 08071	-0.8323 7	1.7806 08071	Down	0.0237 99305	0.9845 43317
2214	FCG R3A	Fc fragment of igg, low affinity iiia, receptor (CD16a)	3.58 645	4.08 094	3.98 549	4.03 122	4.80 199	4.63 488	1.5210 52553	0.6050 7	1.5210 52553	Up	0.0393 30653	0.9845 43317
5534 2	STR BP	Spermatid perinuclear RNA	6.99 395	8.14 935	8.02 991	8.79 68	8.47 681	8.32 468	1.7512 19592	0.8083 6	1.7512 19592	Up	0.0472 81458	0.9845 43317



		binding protein												
5447	PLE	Pleckstrin	3.00	3.88	4.03	4.60	4.23	4.39	1.7088	0.7730	1.7088	Up	0.0293	0.9845
7	KHA 5	homology domain containing A5	045	284	248	058	541	881	31326	1	31326		52195	43317
9060	PAPS S2	3'-phosphoadenosine 5'-phosphosulfate synthase 2	5.18 235	5.78 489	5.85 456	6.71 077	5.95 796	6.19 245	1.6019 10264	0.6797 93333	1.6019 10264	Up	0.0427 97552	0.9845 43317
2651	GCN T2	Glucosaminyl (N-acetyl) transferase 2, I-branching enzyme (I blood group)	3.32 765	3.80 554	3.94 279	4.37 161	4.19 198	4.42 326	1.5550 45363	0.6369 56667	1.5550 45363	Up	0.0099 6272	0.9845 43317
9619	ABC G1	ATP binding cassette subfamily G member 1	5.44 445	6.88 116	4.89 167	6.62 536	7.22 393	7.19 237	2.4196 41539	1.2747 93333	2.4196 41539	Up	0.0414 93955	0.9845 43317

9446	GST O1	Glutathione S-transferase omega 1	9.73 155	10.1 742	9.94 167	10.6 811	10.5 349	10.4 218	1.5123 8628	0.5968 26667	1.5123 8628	Up	0.0096 48823	0.9845 43317
2414 6	CLD N15	Claudin 15	5.57 032	5.36 361	5.58 241	6.15 631	6.52 115	5.85 627	1.5937 9197	0.6724 63333	1.5937 9197	Up	0.0139 35857	0.9845 43317
1025 7	ABC C4	ATP binding cassette subfamily C member 4	3.67 291	4.87 875	5.18 755	5.48 16	5.35 537	5.97 346	2.0331 82897	1.0237 4	2.0331 82897	Up	0.0417 94918	0.9845 43317
9465	AKA P7	A-kinase anchoring protein 7	3.39 067	4.12 529	4.07 996	5.21 727	4.53 909	5.49 863	2.3289 66681	1.2196 9	2.3289 66681	Up	0.0060 1527	0.9845 43317
4406 72	NUD T4P1	Nudix hydrolase 4 pseudogene 1	7.94 991	8.72 461	7.05 272	8.70 06	9.27 632	9.22 821	2.2334 85156	1.1592 96667	2.2334 85156	Up	0.0308 78175	0.9845 43317
1577 69	FAM 91A1	Family with sequence similarity 91 member A1	6.40 799	6.69 703	6.56 82	6.93 653	7.09 127	7.44 719	1.5163 36556	0.6005 9	1.5163 36556	Up	0.0159 56414	0.9845 43317

1171 55	CAT SPER 2	Cation channel, sperm associated 2	5.77 596	5.97 083	6.05 176	6.37 784	6.41 246	7.02 371	1.5930 81417	0.6718 2	1.5930 81417	Up	0.0189 03689	0.9845 43317
1643	DDB 2	Damage-specific DNA binding protein 2	7.56 483	7.38 022	6.57 705	6.44 201	6.35 419	6.64 193	-1.6184 99216	-0.6946 56667	1.6184 99216	Down	0.0430 87104	0.9845 43317
6398 2	ANO 3	Anoctamin 3	3.57 603	4.44 541	4.19 024	4.29 427	4.97 733	5.39 171	1.7619 95207	0.8172 1	1.7619 95207	Up	0.0473 89316	0.9845 43317
6449 9	TPSB 2	Tryptase $\beta$ 2 (gene/pseudogene )	8.38 641	8.64 308	8.30 774	8.76 869	9.04 42	9.53 842	1.5925 73548	0.6713 6	1.5925 73548	Up	0.0239 29839	0.9845 43317
7432	VIP	Vasoactive intestinal peptide	4.74 873	5.10 943	5.11 408	6.43 487	7.14 496	5.42 684	2.5399 67435	1.3448 1	2.5399 67435	Up	0.0162 41566	0.9845 43317
5575 5	CDK 5RAP 2	CDK5 regulatory subunit associated protein 2	8.12 642	7.66 184	7.31 053	7.33 027	6.09 621	6.93 229	-1.8834 00738	-0.9133 4	1.8834 00738	Down	0.0420 04471	0.9845 43317
8496	PNM	Paraneoplastic Ma	5.84	5.00	5.13	4.57	4.85	4.70	-1.5338	-0.6171	1.5338	Down	0.0397	0.9845

8	A6A	antigen family member 6A	986	544	469	44	442	978	20865	3	20865		5022	43317
2606	RAI1	Retinoic acid induced 14	5.96	5.42	5.70	4.72	5.23	5.34	-1.5128	-0.5973	1.5128	Down	0.0347	0.9845
4	4		464	866	721	698	424	736	93046	1	93046		15536	43317
2294	CCT5	Chaperonin containing TCP1, subunit 5 (epsilon)	5.69	5.54	5.27	5.87	6.01	6.58	1.5724	0.6530	1.5724	Up	0.0269	0.9845
8			607	967	563	926	638	476	45484	1	45484		5592	43317
1059	SCG	Secretagoin, EF-hand calcium binding protein	4.06	4.16	4.48	5.36	4.36	5.97	1.9950	0.9964	1.9950	Up	0.0415	0.9845
0	N		846	228	417	397	358	665	57047	3	57047		44666	43317
5827	PXM	Peroxisomal membrane protein 2	8.18	9.16	9.08	9.67	9.45	9.75	1.7566	0.8128	1.7566	Up	0.0259	0.9845
	P2		437	66	838	184	559	049	86399	56667	86399		53704	43317
9161	CHU	Churchill domain containing 1	4.53	4.76	4.89	5.34	4.91	5.79	1.5406	0.6235	1.5406	Up	0.0381	0.9845
2	RC1		896	417	075	646	886	912	29548	2	29548		81273	43317
989	SEPT	Septin 7	8.28	7.72	7.86	7.46	7.38	6.95	-1.6140	-0.6907	1.6140	Down	0.0184	0.9845

	7		654	346	381	412	459	3	66478		66478		76645	43317
7941	ZBE	Zinc finger,	4.32	4.96	4.70	6.34	5.71	5.65	2.3628	1.2405	2.3628	Up	0.0021	0.9845
3	D2	BED-type containing 2	272	886	157	898	006	564	20444	1	20444		93826	43317
3384	ICA	Intercellular	6.80	5.62	5.75	5.20	5.11	5.39	-1.7702	-0.8239	1.7702	Down	0.0395	0.9845
	M2	adhesion molecule 2	168	558	592	145	633	364	09365	2	09365		83186	43317
4405	PLIN	Perilipin 5	6.82	6.28	6.40	6.19	5.70	5.57	-1.6023	-0.6801	1.6023	Down	0.0236	0.9845
03	5		56	75	47	401	564	77	06342	5	06342		2611	43317
3108	HLA-	Major	9.15	8.63	8.82	8.09	8.20	8.37	-1.5658	-0.6469	1.5658	Down	0.0107	0.9845
	DMA	histocompatibility complex, class II, DM $\alpha$	296	17	767	745	279	116	83267	76667	83267		54922	43317
191	AHC	Adenosylhomocy	6.19	6.73	6.85	7.25	7.14	7.42	1.6035	0.6812	1.6035	Up	0.0169	0.9845
	Y	steinase	18	175	943	909	579	192	5444	73333	5444		81602	43317
5420	TRE	Triggering	5.84	6.73	5.72	7.10	7.13	7.30	2.1146	1.0803	2.1146	Up	0.0074	0.9845
9	M2	receptor	143	189	715	693	406	064	02754	86667	02754		74361	43317

		expressed on myeloid cells 2												
4756	NEO 1	Neogenin 1	5.68 211	6.65 759	6.30 412	7.01 046	6.71 95	6.89 183	1.5793 41692	0.6593 23333	1.5793 41692	Up	0.0441 41395	0.9845 43317
5522 8	PNM AL1	Paraneoplastic Ma antigen family-like 1	5.45 139	5.27 86	5.02 716	5.76 636	5.69 683	6.42 602	1.6365 82881	0.7106 86667	1.6365 82881	Up	0.0220 65553	0.9845 43317
6512 4	SOW AHC	Sosondowah ankyrin repeat domain family member C	6.61 208	6.87 154	7.11 912	7.92 193	7.94 469	7.28 626	1.8025 59231	0.8500 46667	1.8025 59231	Up	0.0106 76416	0.9845 43317
1078 8	IQG AP2	IQ motif containing gtpase activating protein 2	3.54 593	4.43 629	5.16 422	5.53 338	5.44 819	5.40 998	2.1165 33514	1.0817 03333	2.1165 33514	Up	0.0272 52649	0.9845 43317
4753	NEL L2	Neural EGFL like 2	5.08 122	5.11 592	5.20 055	6.54 884	6.82 198	6.85 822	3.0534 70696	1.6104 5	3.0534 70696	Up	1.9995 4E-05	0.7824 19724

1356	DPC	Diffuse	6.95	8.88	6.36	9.20	9.71	8.81	3.5902	1.8441	3.5902	Up	0.0253	0.9845
56	R1	panbronchiolitis critical region 1	642	316	644	637	227	969	97349	03333	97349		56619	43317
4289	MKL	Muskelin 1	6.16	5.93	6.59	6.55	7.26	6.74	1.5425	0.6253	1.5425	Up	0.0481	0.9845
	N1		427	577	064	546	77	359	92142	56667	92142		95535	43317
1452	RDH	Retinol	8.07	9.35	9.61	10.3	10.1	10.2	2.4121	1.2703	2.4121	Up	0.0159	0.9845
26	12	dehydrogenase 12 (all-trans/9-cis/11 -cis)	578	589	625	924	787	877	84068	4	84068		87669	43317
2340	FRA	Frequently	5.58	6.72	5.89	6.81	6.76	6.80	1.6558	0.7275	1.6558	Up	0.0463	0.9845
1	T2	rearranged in advanced T-cell lymphomas 2	156	878	285	94	487	152	05635	33333	05635		26904	43317
175	AGA	Aspartylglucosam inidase	6.26	7.52	7.67	7.83	8.25	8.16	1.9019	0.9275	1.9019	Up	0.0488	0.9845
			959	654	523	404	181	805	94841	13333	94841		67075	43317
6707	SPRR	Small proline-rich	5.59	7.14	7.49	10.1	7.66	8.33	3.9424	1.9790	3.9424	Up	0.0367	0.9845
	3	protein 3	916	978	896	885	426	242	52391	93333	52391		63708	43317

5648	MAS P1	Mannan-binding lectin serine peptidase 1 (C4/C2 activating component of Ra-reactive factor)	7.39 323	6.63 161	6.45 693	6.43 487	6.02 928	5.41 323	-1.8252 95445	-0.8681 3	1.8252 95445	Down	0.0432 35696	0.9845 43317
1124 0	PADI 2	Peptidyl arginine deiminase, type II	5.23 616	5.19 566	4.88 63	6.32 371	5.33 365	5.81 37	1.6444 97331	0.7176 46667	1.6444 97331	Up	0.0332 46961	0.9845 43317
2192 85	SAM D9L	Sterile $\alpha$ motif domain containing 9-like	6.01 471	5.36 231	5.38 228	4.68 774	5.15 74	4.90 108	-1.5922 05627	-0.6710 26667	1.5922 05627	Down	0.0236 70136	0.9845 43317
6478 1	CER K	Ceramide kinase	6.79 889	6.99 272	7.46 089	7.77 953	7.64 228	8.00 904	1.6541 805	0.7261 16667	1.6541 805	Up	0.0134 81504	0.9845 43317
5585 9	BEX 1	Brain expressed X-linked 1	6.24 49	6.28 735	6.51 006	6.81 717	7.17 424	8.31 537	2.1260 22207	1.0881 56667	2.1260 22207	Up	0.0263 30269	0.9845 43317
7903	ST8S	ST8	5.41	6.18	6.04	4.60	4.78	4.71	-2.2652	-1.1796	2.2652	Down	0.0013	0.9845



	IA4	$\alpha$ -N-acetyl-neuraminidase 4	35	019	885	625	022	698	91432	96667	91432		52058	43317
51678	MPP6	Membrane protein, palmitoylated 6	6.45751	7.53619	7.47658	8.17297	8.03417	7.97959	1.873171942	0.905483333	1.873171942	Up	0.022581586	0.984543317
338	APOB	Apolipoprotein B	4.86106	5.69068	4.77937	8.38708	5.5525	6.64636	3.367341407	1.75161	3.367341407	Up	0.042084461	0.984543317
2215	FCGR3B	Fc fragment of $\text{IgG}$ , low affinity $\text{IIIb}$ , receptor (CD16b)	3.58645	4.08094	3.98549	4.03122	4.80199	4.63488	1.521052553	0.60507	1.521052553	Up	0.039330653	0.984543317
57194	ATP10A	ATPase, class V, type 10A	5.69622	5.30231	5.03026	6.06101	5.66088	6.11239	1.517640411	0.60183	1.517640411	Up	0.032888525	0.984543317

Table SII. DEGs in comparison II.

Entrez accessi on no.	Gene symbol	Gene name	Gallb ladde r wall of gallst one (A10 933)	Gallb ladde r wall of gallst one (A10 934)	Gallb ladde r wall of gallst one (A10 939)	Gallb ladde r wall of gallbl adder adeno ma (A10 951)	Gallb ladde r wall of gallbl adder adeno ma (A10 956)	Gallb ladde r wall of gallbl adder adeno ma (A10 957)	Fold-chang e	Log fold -change	Absolute fold -change	Regulat ion	P-value	False discover y rate (FDR)
51285	RASL1 2	RAS-like, family 12	7.939 97	6.478 61	6.474 17	4.625 98	6.522 17	5.339 53	-2.7670652 54	-1.46835 6667	2.767065 254	Down	0.042621 364	0.955609 729
60481	ELOV L5	ELOVL fatty acid elongase 5	6.531 61	5.535 52	6.220 08	5.091 27	4.667 7	5.069 67	-2.2235373 93	-1.15285 6667	2.223537 393	Down	0.005258 036	0.955609 729
286530	P2RY8	Purinergic receptor P2Y, G-protein coupled, 8	6.232 1	4.645 75	6.555 98	4.158 77	4.347 08	4.489 47	-2.7885271 8	-1.47950 3333	2.788527 18	Down	0.018589 415	0.955609 729
287	ANK2	Ankyrin 2, neuronal	4.420 72	4.248 61	4.265 26	5.973 57	5.896 55	4.400 47	2.1614508 04	1.112	2.161450 804	Up	0.033062 858	0.955609 729
51705	EMCN	Endomucin	8.426 5	6.259 9	6.211 04	4.698 62	4.860 23	5.818 42	-3.5802409 07	-1.84005 6667	3.580240 907	Down	0.025342 011	0.955609 729
8379	MAD1 L1	MAD1 mitotic arrest deficient-like 1 (yeast)	6.573 26	6.822 34	6.422 72	7.210 85	7.292 1	7.665 94	1.7213295 55	0.783523 333	1.721329 555	Up	0.006388 43	0.955609 729
5238	PGM3	Phosphogluc	5.816	5.972	6.500	6.843	6.654	6.932	1.6399554	0.713656	1.639955	Up	0.015903	0.955609

5238	PGM3	Phosphogluc omutase 3	5.816 61	5.972 46	6.500 25	6.843 14	6.654 27	6.932 88	1.6399554 98	0.713656 667	1.639955 498	Up	0.015903 204	0.955609 729
253827	MSRB 3	Methionine sulfoxide reductase B3	7.535 82	6.821 31	6.423 54	4.517 76	6.814 31	4.229 34	-3.3397806 06	-1.73975 3333	3.339780 606	Down	0.042396 569	0.955609 729
3821	KLRC1	Killer cell lectin-like receptor subfamily C, member 1	4.241 77	3.674 14	3.589 05	4.83	5.456 03	5.831 27	2.9028030 01	1.537446 667	2.902803 001	Up	0.001491 72	0.955609 729
377677	CA13	Carbonic anhydrase XIII	8.321 48	9.060 56	9.180 74	10.31 298	9.791 34	10.32 038	2.4407197 77	1.287306 667	2.440719 777	Up	0.002966 312	0.955609 729
26353	HSPB8	Heat shock protein family B (small) member 8	7.414 83	5.581 62	5.567 15	4.392 64	5.266 75	4.963 73	-2.4854263 16	-1.31349 3333	2.485426 316	Down	0.044211 383	0.955609 729
29116	MYLIP	Myosin regulatory light chain interacting protein	6.596 71	7.329 22	6.504 54	7.794 51	7.539 27	7.407 54	1.7056047 17	0.770283 333	1.705604 717	Up	0.023000 971	0.955609 729
7450	VWF	Von Willebrand factor	9.934 84	7.280 22	6.771 53	4.618 27	5.342 71	6.732 01	-5.3934185 62	-2.4312	5.393418 562	Down	0.033247 688	0.955609 729
3384	ICAM2	Intercellular adhesion molecule 2	9.408 09	7.069 6	8.148 98	6.267 64	7.087 64	7.023 97	-2.6680887 69	-1.41580 6667	2.668088 769	Down	0.046061 133	0.955609 729
8436	SDPR	Serum deprivation	9.066 84	7.514 55	7.339 03	5.181 44	7.235 76	5.623 37	-3.8904849 53	-1.95995	3.890484 953	Down	0.021856 267	0.955609 729

80704	SLC19A3	Solute carrier family 19 (thiamine transporter), member 3	7.73654	6.80539	7.81923	9.38266	8.54175	8.03075	2.294214048	1.198	2.294214048	Up	0.025848971	0.955609729
127845	GOLTA	Golgi transport 1A	5.99845	6.77961	6.84567	8.17417	7.49718	7.41726	2.226781496	1.15496	2.226781496	Up	0.008673497	0.955609729
10562	OLFM4	Olfactomedin 4	3.12138	4.64452	5.00161	6.67413	5.16973	5.5311	2.899525179	1.535816667	2.899525179	Up	0.03455814	0.955609729
2321	FLT1	Fms-related tyrosine kinase 1	6.9715	5.30175	5.47977	3.96068	4.10089	4.94421	-2.994703836	-1.582413333	2.994703836	Down	0.015348392	0.955609729
10321	CRISP3	Cysteine-rich secretory protein 3	4.22429	5.16419	5.83304	8.833	7.39642	8.30312	8.596046776	3.103673333	8.596046776	Up	0.000569554	0.955609729
344	APOC2	Apolipoprotein C-II	6.06565	6.58253	5.60903	6.71307	7.13457	7.14033	1.879375483	0.910253333	1.879375483	Up	0.0153779	0.955609729
253635	GPATCH11	G-patch domain containing 11	4.3091	4.26509	4.47609	5.23274	5.19754	4.44669	1.525092414	0.608896667	1.525092414	Up	0.036127545	0.955609729
7075	TIE1	Tyrosine kinase with immunoglobulin-like and EGF-like domains 1	7.72388	5.65439	5.631	4.60895	5.19698	4.87933	-2.715723626	-1.441336667	2.715723626	Down	0.040468995	0.955609729
10141	LINC01587	Long intergenic non-protein	5.13638	6.01497	6.12998	6.74036	6.66453	6.54656	1.853227505	0.89004	1.853227505	Up	0.017391422	0.955609729

		coding RNA 1587												
5332	PLCB4	Phospholipase C $\beta$ 4	5.6053	4.38853	4.74187	3.19283	4.02253	3.74823	-2.390595434	-1.25737	2.390595434	Down	0.009872289	0.955609729
3791	KDR	Kinase insert domain receptor	7.71087	7.03969	7.32382	5.83735	6.82885	6.75879	-1.844372423	-0.88313	1.844372423	Down	0.03037232	0.955609729
57631	LRCH2	Leucine-rich repeats and calponin homology (CH) domain containing 2	4.88502	4.18055	4.22661	3.66709	3.49055	3.31906	-1.916525685	-0.938493333	1.916525685	Down	0.003585896	0.955609729
2330	FMO5	Flavin containing monooxygenase 5	7.54629	8.78671	8.22774	9.60398	8.73291	9.51425	2.138797655	1.0968	2.138797655	Up	0.023951777	0.955609729
27145	FILIP1	Filamin A interacting protein 1	6.86584	5.59357	5.31689	3.5379	5.66773	3.67478	-3.099344952	-1.631963333	3.099344952	Down	0.044167949	0.955609729
117177	RAB31P	RAB3A interacting protein	5.37832	6.66909	6.25659	7.25541	6.88418	7.27212	2.050397086	1.035903333	2.050397086	Up	0.020073506	0.955609729
114905	C1QTNF7	C1q and tumor necrosis factor related protein 7	6.48939	5.57121	5.63706	3.49797	5.76932	4.21929	-2.645780419	-1.403693333	2.645780419	Down	0.047836555	0.955609729
8566	PDXK	Pyridoxal (pyridoxine, vitamin B6)	5.98118	6.7183	6.59846	7.39628	7.01425	6.83207	1.567233347	0.64822	1.567233347	Up	0.04339205	0.955609729

		kinase												
155038	GIMA P8	Gtpase, IMAP family member 8	7.001 1	5.726 07	5.614 52	4.674 28	4.762 51	5.595 95	-2.1479841 29	-1.10298 3333	2.147984 129	Down	0.039777 024	0.955609 729
10800	CYSLT R1	Cysteinyl leukotriene receptor 1	5.010 17	4.318 17	4.495 62	3.834 07	3.669 16	4.004 54	-1.7077103 94	-0.77206 3333	1.707710 394	Down	0.007380 425	0.955609 729
2022	ENG	Endoglin	7.762 2	6.543 15	6.738 35	4.738 13	6.334 54	6.013 05	-2.4954961 3	-1.31932 6667	2.495496 13	Down	0.034335 528	0.955609 729
8824	CES2	Carboxyleste rase 2	8.503 6	9.224 69	9.311 69	9.842 45	9.497 01	9.587 93	1.5466391 81	0.629136 667	1.546639 181	Up	0.043776 43	0.955609 729
29842	TFCP2 L1	Transcriptio n factor CP2-like 1	5.044 64	6.158 48	6.588 24	7.456 33	6.655 87	7.131 62	2.2204006 18	1.15082	2.220400 618	Up	0.031153 081	0.955609 729
100506 548	LOC10 050654 8	Uncharacteri zed LOC100506 548	3.933 73	4.361 67	4.611 21	5.115 42	4.930 46	4.794 21	1.5631902 06	0.644493 333	1.563190 206	Up	0.016281 603	0.955609 729
7052	TGM2	Transglutami nase 2	4.617 98	5.185 71	4.760 85	4.302 47	4.319 59	3.633 67	-1.7048009 87	-0.76960 3333	1.704800 987	Down	0.016932 459	0.955609 729
3557	IL1RN	Interleukin 1 receptor antagonist	6.911 05	7.106 89	7.549 67	8.340 07	7.864 71	8.011 99	1.8442744 13	0.883053 333	1.844274 413	Up	0.007134 75	0.955609 729
283431	GAS2L 3	Growth arrest specific 2 like 3	5.843 76	6.656 02	6.689 61	7.031 49	7.498 87	6.892 97	1.6755638 53	0.744646 667	1.675563 853	Up	0.040334 415	0.955609 729
813	CALU	Calumenin	6.717 47	5.934 35	6.392 63	5.757 5	4.930 46	5.836 04	-1.7902362 67	-0.84015	1.790236 267	Down	0.033962 281	0.955609 729
79827	CLMP	CXADR-like membrane	5.437 74	4.872 02	4.719 77	3.997 37	4.340 12	4.429 47	-1.6866843 39	-0.75419	1.686684 339	Down	0.013438 455	0.955609 729

79827	CLMP	CXADR-like membrane protein	5.43774	4.87202	4.71977	3.99737	4.34012	4.42947	-1.686684339	-0.75419	1.686684339	Down	0.013438455	0.955609729
731	C8A	Complement component 8, $\alpha$ polypeptide	5.6679	7.07635	7.07818	7.89073	7.57384	8.0504	2.347046893	1.230846667	2.347046893	Up	0.020038289	0.955609729
9032	TM4SF5	Transmembrane 4 L six family member 5	7.48615	8.34996	7.55443	9.28158	8.79713	9.25838	2.488914492	1.315516667	2.488914492	Up	0.002700346	0.955609729
57453	DSCAML1	Down syndrome cell adhesion molecule like 1	4.8363	5.89943	5.72585	6.9493	6.16729	6.19251	1.930766009	0.949173333	1.930766009	Up	0.031834709	0.955609729
8863	PER3	Period circadian clock 3	3.71408	3.9558	4.05255	5.12874	4.34083	4.41311	1.647277182	0.720083333	1.647277182	Up	0.018539831	0.955609729
22941	SHANK2	SH3 and multiple ankyrin repeat domains 2	4.37035	5.48969	6.05202	6.61696	6.5895	6.18883	2.236242536	1.161076667	2.236242536	Up	0.029243598	0.955609729
84676	TRIM63	Tripartite motif containing 63, E3 ubiquitin protein ligase	6.09599	6.64266	6.39685	7.39201	7.70452	6.5989	1.806641182	0.85331	1.806641182	Up	0.032126879	0.955609729

3176	HNMT	Histamine N-methyltransferase	7.413 35	8.158 1	7.567 43	8.880 54	8.471 33	8.374 77	1.8182954 86	0.862586 667	1.818295 486	Up	0.012637 379	0.955609 729
112495	GTF3C6	General transcription factor IIC subunit 6	9.779 74	10.41 175	10.25 122	11.05 048	10.52 22	10.68 102	1.5195702 09	0.603663 333	1.519570 209	Up	0.035910 726	0.955609 729
3556	IL1RAP	Interleukin 1 receptor accessory protein	3.408 2	3.752 8	3.786 95	4.652 99	3.973 58	4.265 73	1.5671210 97	0.648116 667	1.567121 097	Up	0.015786 438	0.955609 729
1756	DMD	Dystrophin	8.510 23	8.996 32	8.253 55	6.793 9	8.406 29	7.200 25	-2.1732989 91	-1.11988 6667	2.173298 991	Down	0.038137 717	0.955609 729
55691	FRMD4A	FERM domain containing 4A	7.713 16	8.030 75	8.169 11	8.937 9	8.359 13	8.911 41	1.6995349 14	0.76514	1.699534 914	Up	0.013027 478	0.955609 729
25827	FBXL2	F-box and leucine-rich repeat protein 2	6.217 3	5.304 58	5.279 67	5.121 59	4.865 05	4.618 33	-1.6611626 43	-0.73219 3333	1.661162 643	Down	0.042172 116	0.955609 729
114294	LACTB	Lactamase $\beta$	7.353 44	7.412 34	7.293 55	8.457 89	8.057 28	8.103 79	1.8065159 59	0.85321	1.806515 959	Up	0.002022 108	0.955609 729
27253	PCDH17	Protocadherin 17	6.741 36	6.598 75	5.420 51	4.559 03	5.560 51	4.682 17	-2.4960324 09	-1.31963 6667	2.496032 409	Down	0.018543 892	0.955609 729
29970	SCHIP1	Schwannomin interacting protein 1	7.696 73	6.982 29	6.884 94	5.757 5	6.032 04	6.653 85	-2.0564984 72	-1.04019	2.056498 472	Down	0.014692 544	0.955609 729
2651	GCNT2	Glucosaminyl (N-acetyl) transferase 2,	3.327 65	3.805 54	3.942 79	4.637 81	3.961 58	4.419 05	1.5664369 12	0.647486 667	1.566436 912	Up	0.027908 384	0.955609 729



		I-branching enzyme (I blood group)												
254896	LOC254896	Uncharacterized LOC254896	4.80854	5.73506	5.04325	5.94503	5.84501	5.71225	1.556688194	0.63848	1.556688194	Up	0.043638733	0.955609729
140739	UBE2F	Ubiquitin conjugating enzyme E2F (putative)	6.181	6.28889	5.87162	6.74492	6.84959	6.55013	1.516813104	0.601043333	1.516813104	Up	0.014597746	0.955609729
6819	SULT1C2	Sulfotransferase family 1C member 2	6.72196	9.05175	8.68515	10.50008	9.62695	10.01383	3.716642697	1.894	3.716642697	Up	0.018104673	0.955609729
25802	LMOD1	Leiomodin 1 (smooth muscle)	5.19492	5.29232	5.05287	4.27375	4.99381	4.48647	-1.510849545	-0.59536	1.510849545	Down	0.026282094	0.955609729
84225	ZMYND15	Zinc finger, MYND-type containing 15	6.58107	6.81823	6.23839	7.19784	7.57147	6.76657	1.550496211	0.63273	1.550496211	Up	0.049225283	0.955609729
6926	TBX3	T-box 3	6.1337	4.87552	5.08924	4.10509	4.50374	4.54666	-1.97381941	-0.98099	1.97381941	Down	0.024886922	0.955609729
26255	PTTG3P	Pituitary tumor-transforming 3, pseudogene	4.93315	5.63362	5.28491	4.54147	4.87043	4.62444	-1.521098241	-0.605113333	1.521098241	Down	0.025409802	0.955609729
1265	CNN2	Calponin 2	4.01497	4.08674	4.70155	3.44111	3.94468	3.60025	-1.521759107	-0.60574	1.521759107	Down	0.032090405	0.955609729
57669	EPB41L5	Erythrocyte membrane	4.80564	5.29013	5.54639	6.3026	5.69453	5.79819	1.644580924	0.71772	1.644580924	Up	0.028697357	0.955609729

		protein band 4.1 like 5												
101059938	NPIPA7	Nuclear pore complex interacting protein family member A7	6.70725	7.99302	7.37651	8.22062	8.13039	8.1216	1.739424428	0.79861	1.739424428	Up	0.043520998	0.955609729
1272	CNTN1	Contactin 1	6.73803	5.52298	4.6665	2.72684	5.22865	3.23164	-3.767114803	-1.91346	3.767114803	Down	0.041615226	0.955609729
2118	ETV4	Ets variant 4	7.32345	9.03845	8.52	9.52311	9.29648	9.15458	2.043095536	1.030756667	2.043095536	Up	0.047399034	0.955609729
3480	IGF1R	Insulin like growth factor 1 receptor	6.00857	5.92714	5.93501	4.78577	5.65894	5.54104	-1.545767494	-0.628323333	1.545767494	Down	0.042208471	0.955609729
54843	SYTL2	Synaptotagmin like 2	7.0938	6.70177	6.87649	6.38644	6.281	5.87108	-1.637142611	-0.71118	1.637142611	Down	0.011485561	0.955609729
6167	RPL37	Ribosomal protein L37	3.93373	4.36167	4.61121	5.11542	4.93046	4.79421	1.563190206	0.644493333	1.563190206	Up	0.016281603	0.955609729
55715	DOK4	Docking protein 4	8.93015	9.71637	9.18168	10.14918	9.69306	9.84028	1.534859573	0.618106667	1.534859573	Up	0.042767586	0.955609729
11037	STON1	Stonin 1	7.88192	6.61149	6.30419	4.41444	6.56373	4.87711	-3.132772487	-1.64744	3.132772487	Down	0.039128042	0.955609729
25890	ABI3BP	ABI family member 3 binding protein	10.54479	9.74565	9.77358	9.5229	9.23296	9.05153	-1.684371068	-0.75221	1.684371068	Down	0.026617833	0.955609729
79974	CPED1	Cadherin-like and PC-esterase	5.82375	5.01713	4.26789	3.82405	4.37463	3.8681	-2.019497929	-1.013996667	2.019497929	Down	0.036534141	0.955609729

79974	CPED1	Cadherin-like and PC-esterase domain containing 1	5.82375	5.01713	4.26789	3.82405	4.37463	3.8681	-2.019497929	-1.013996667	2.019497929	Down	0.036534141	0.955609729
3148	HMGB2	High mobility group box 2	8.89441	7.78942	8.5038	6.77996	7.35421	7.36426	-2.345236367	-1.229733333	2.345236367	Down	0.007406759	0.955609729
84513	PLPP5	Phospholipid phosphatase 5	4.23119	4.91952	4.9017	5.37328	5.41148	5.17187	1.552657907	0.63474	1.552657907	Up	0.024744828	0.955609729
384	ARG2	Arginase 2	4.2979	4.78344	4.60113	5.30527	5.21602	5.18457	1.596002967	0.674463333	1.596002967	Up	0.004831871	0.955609729
136895	C7orf31	Chromosome 7 open reading frame 31	4.9425	5.01029	4.77859	5.54421	5.16326	5.96539	1.566082267	0.64716	1.566082267	Up	0.025056329	0.955609729
89122	TRIM4	Tripartite motif containing 4	3.41149	4.59812	4.36346	4.8958	4.96467	4.77823	1.687877263	0.75521	1.687877263	Up	0.043303095	0.955609729
94274	PPP1R14A	Protein phosphatase 1 regulatory inhibitor subunit 14A	10.45587	9.18509	8.8964	6.41756	9.27033	6.47619	-4.360297785	-2.124426667	4.360297785	Down	0.039001009	0.955609729
1906	EDN1	Endothelin 1	6.65554	7.08405	6.93454	7.91204	7.33735	7.32048	1.549618769	0.631913333	1.549618769	Up	0.029390674	0.955609729
258010	SVIP	Small VCP/p97-interacting protein	6.6531	7.1359	7.19398	7.65916	7.25663	7.84139	1.506708157	0.5914	1.506708157	Up	0.042292622	0.955609729

3688	ITGB1	Integrin $\beta$ 1	9.849 64	9.491 64	9.243 73	8.613 38	8.209 69	9.043 25	-1.8741416 53	-0.90623	1.874141 653	Down	0.012743 935	0.955609 729
1646	AKR1 C2	Aldo-keto reductase family 1, member C2	5.737 96	5.858 01	6.007 76	5.228 46	5.489 21	5.111 16	-1.5069518 63	-0.59163 3333	1.506951 863	Down	0.010684 943	0.955609 729
6563	SLC14 A1	Solute carrier family 14 (urea transporter), member 1 (Kidd blood group)	7.800 77	8.985 18	7.495 24	10.46 218	8.328 55	10.12 263	2.9161332 96	1.544056 667	2.916133 296	Up	0.047389 682	0.955609 729
1184	CLCN5	Chloride channel, voltage-sensi tive 5	5.770 26	6.881 18	6.491 32	7.345 52	7.229 33	6.880 08	1.7061249 8	0.770723 333	1.706124 98	Up	0.042790 82	0.955609 729
18	ABAT	4-aminobuty rate aminotransfe rase	6.213 85	6.909 8	6.152 04	7.082 76	6.799 26	7.434 79	1.6025544 02	0.680373 333	1.602554 402	Up	0.044318 313	0.955609 729
158471	PRUN E2	Prune homolog 2 (Drosophila)	7.290 53	7.080 48	7.038 87	5.913 21	7.046 1	5.469 99	-1.9910461 57	-0.99352 6667	1.991046 157	Down	0.041461 144	0.955609 729
22915	MMRN 1	Multimerin 1	9.652 41	6.382 2	6.293 8	4.489 01	5.462 21	5.474 51	-4.9276279 53	-2.30089 3333	4.927627 953	Down	0.039715 474	0.955609 729
100127 888	SLCO4 A1-AS 1	SLCO4A1 antisense RNA 1	4.170 18	4.858 7	4.793 99	7.002 98	5.381 79	6.296 23	3.0724225 99	1.619376 667	3.072422 599	Up	0.006932 207	0.955609 729
55701	ARHG	Rho guanine	6.143	6.806	6.608	7.355	7.031	7.033	1.5375357	0.62062	1.537535	Up	0.029101	0.955609

	EF40	nucleotide exchange factor (GEF) 40	29	11	19	11	19	15	97		797		318	729
9750	FAM65 B	Family with sequence similarity 65 member B	5.52047	4.07092	5.34741	3.85403	3.66189	4.22593	-2.09311271	-1.06565	2.09311271	Down	0.030867911	0.955609729
3235	HOXD9	Homeobox D9	5.34209	4.8357	4.8743	4.10841	4.69016	4.32743	-1.56052341	-0.64203	1.56052341	Down	0.021005711	0.955609729
2669	GEM	GTP binding protein overexpressed in skeletal muscle	7.36613	5.85017	5.09269	3.68372	5.25079	4.37497	-3.174442692	-1.666503333	3.174442692	Down	0.036218487	0.955609729
10550	ARL6IP5	ADP ribosylation factor like gtpase 6 interacting protein 5	10.3226	9.92641	9.48523	9.30428	9.08938	9.44007	-1.551327552	-0.633503333	1.551327552	Down	0.037114281	0.955609729
54206	ERRFI1	ERBB receptor feedback inhibitor 1	9.88726	8.77667	9.1962	8.52721	8.45321	8.66681	-1.667438248	-0.737633333	1.667438248	Down	0.040187127	0.955609729
100134934	TEN1	TEN1 CST complex subunit	6.63976	6.40313	6.80187	7.40334	7.13034	7.3433	1.599262397	0.677406667	1.599262397	Up	0.007672476	0.955609729
406	ARNTL	Aryl hydrocarbon receptor	7.18308	6.62266	6.65851	5.3651	6.33485	4.77137	-2.515729255	-1.330976667	2.515729255	Down	0.014163897	0.955609729

		nuclear translocator like												
285596	FAM153A	Family with sequence similarity 153 member A	3.68869	4.0597	3.03113	3.96192	4.77083	4.72872	1.85829988	0.893983333	1.85829988	Up	0.029300486	0.955609729
81557	MAGE D4B	Melanoma antigen family D4B	5.46145	6.50094	4.99384	6.90646	6.98994	6.87491	2.414447901	1.271693333	2.414447901	Up	0.012137053	0.955609729
2294	FOXF1	Forkhead box F1	7.22093	7.81116	7.83101	5.61615	7.29407	5.92498	-2.536138147	-1.342633333	2.536138147	Down	0.021787513	0.955609729
8857	FCGBP	Fc fragment of igg binding protein	11.1842	11.43776	13.1499	13.29505	13.17828	13.35627	2.553683977	1.35258	2.553683977	Up	0.0301196	0.955609729
1628	DBP	D site of albumin promoter (albumin D-box) binding protein	5.9074	6.78317	6.87615	8.1046	6.76394	7.93155	2.110800163	1.07779	2.110800163	Up	0.041609543	0.955609729
392465	GLOD5	Glyoxalase domain containing 5	5.00693	5.81513	5.23952	6.00501	6.20271	5.89121	1.601159097	0.679116667	1.601159097	Up	0.026499041	0.955609729
2982	GUCY1A3	Guanylate cyclase 1, soluble, $\alpha$ 3	6.05175	5.68398	5.84307	5.06444	4.27531	5.62421	-1.829707878	-0.871613333	1.829707878	Down	0.038606931	0.955609729
10631	POSTN	Periostin,	6.025	4.915	4.687	3.911	4.032	4.470	-2.1010638	-1.07112	2.101063	Down	0.022666	0.955609

10631	POSTN	Periostin, osteoblast specific factor	6.02537	4.91566	4.68719	3.91176	4.03273	4.47037	-2.101063842	-1.07112	2.101063842	Down	0.02266663	0.955609729
57144	PAK7	P21 protein (Cdc42/Rac)-activated kinase 7	5.37311	6.86432	6.32054	7.6433	6.82699	8.05523	2.501020125	1.322516667	2.501020125	Up	0.025155416	0.955609729
5142	PDE4B	Phosphodiesterase 4B	7.27315	4.17499	5.53822	3.26901	4.05672	4.11344	-3.60266207	-1.849063333	3.60266207	Down	0.041430237	0.955609729
25780	RASGRP3	RAS guanyl releasing protein 3 (calcium and DAG-regulated)	6.21067	5.89315	6.53161	5.0368	5.77098	5.60738	-1.670280033	-0.74009	1.670280033	Down	0.026707015	0.955609729
1952	CELSR2	Cadherin, EGF LAG seven-pass G-type receptor 2	4.8278	5.59241	5.44282	6.30749	5.68073	5.86834	1.585029839	0.66451	1.585029839	Up	0.042945799	0.955609729
9630	GNA14	Guanine nucleotide binding protein (G protein), $\alpha$ 14	5.48101	4.1776	4.56219	2.98759	3.95265	3.53521	-2.375860286	-1.24845	2.375860286	Down	0.014615645	0.955609729
2259	FGF14	Fibroblast growth factor 14	4.31395	4.86193	4.91523	6.35476	4.92148	6.0785	2.125609627	1.087876667	2.125609627	Up	0.02868893	0.955609729
1368	CPM	Carboxypeptidase	6.496	6.644	6.014	7.583	6.570	7.612	1.8283048	0.870506	1.828304	Up	0.036970	0.955609

63982	ANO3	Anoctamin 3	6.867 75	8.893 33	8.030 12	9.536 31	8.726 12	9.307 52	2.3942658 18	1.259583 333	2.394265 818	Up	0.044636 301	0.955609 729
2147	F2	Coagulation factor II (thrombin)	6.466 43	6.952 24	6.943 69	7.183 38	7.264 17	7.824 88	1.5547579 56	0.63669	1.554757 956	Up	0.037055 224	0.955609 729
135656	DPCR1	Diffuse panbronchiolitis critical region 1	6.956 42	8.883 16	6.366 44	9.051 11	8.678 17	9.556 37	3.2337541 49	1.69321	3.233754 149	Up	0.033804 94	0.955609 729
283377	SPRY D4	SPRY domain containing 4	6.149 15	6.896 2	6.426 47	7.014 93	7.348 58	6.917 37	1.5188927 46	0.60302	1.518892 746	Up	0.043465 866	0.955609 729
26230	TIAM2	T-cell lymphoma invasion and metastasis 2	6.066 14	6.958 17	6.293 99	7.156	6.995 97	7.007 19	1.5300936 96	0.61362	1.530093 696	Up	0.048179 562	0.955609 729
84159	ARID5 B	AT-rich interaction domain 5B	4.630 65	5.588 4	5.761 94	6.038 61	5.919 48	6.323 49	1.7015662 62	0.766863 333	1.701566 262	Up	0.047927 243	0.955609 729
642475	MROH 6	Maestro heat-like repeat family member 6	6.118 98	6.779 02	6.349 3	7.391 73	6.914 39	7.180 86	1.6777874 97	0.74656	1.677787 497	Up	0.015790 581	0.955609 729
283232	TMEM 80	Transmembrane protein 80	5.563 93	5.494 29	5.321 87	6.304 92	5.779 49	6.244 39	1.5687005 7	0.64957	1.568700 57	Up	0.013287 37	0.955609 729
5019	OXCT 1	3-oxoacid coa-transferase 1	7.196 74	5.273 36	5.036 36	3.789 1	5.010 63	4.294 45	-2.7716786 49	-1.47076	2.771678 649	Down	0.047993 631	0.955609 729
5175	PECA M1	Platelet/endothelial cell	10.68 623	8.831 93	8.832 37	7.493 24	8.002 27	8.438 6	-2.7743311 48	-1.47214	2.774331 148	Down	0.031146 665	0.955609 729



5175	PECA M1	Platelet/endo thelial cell adhesion molecule 1	10.68 623	8.831 93	8.832 37	7.493 24	8.002 27	8.438 6	-2.7743311 48	-1.47214	2.774331 148	Down	0.031146 665	0.955609 729
166348	KBTB D12	Kelch repeat and BTB (POZ) domain containing 12	4.944 59	5.291 88	4.474 9	5.280 86	5.588 82	6.374 17	1.7952191 86	0.84416	1.795219 186	Up	0.042023 686	0.955609 729
399669	ZNF32 1P	Zinc finger protein 321, pseudogene	5.425 65	6.603 86	6.313 97	7.304 41	7.404 59	6.637 12	2.0012203 11	1.00088	2.001220 311	Up	0.028817 304	0.955609 729
85480	TSLP	Thymic stromal lymphopoieti n	4.642 21	3.873 23	4.571 03	3.007 28	3.917 12	3.192 98	-1.9857674 3	-0.98969 6667	1.985767 43	Down	0.014214 436	0.955609 729
9720	CCDC 144A	Coiled-coil domain containing 144A	4.166 57	3.233 21	3.508 29	4.601 31	4.337 06	4.139 17	1.6507900 72	0.723156 667	1.650790 072	Up	0.026880 281	0.955609 729
3306	HSPA2	Heat shock protein family A (Hsp70) member 2	6.613 05	5.412 62	5.065 84	4.949 17	4.493 23	4.732 58	-1.9617982 27	-0.97217 6667	1.961798 227	Down	0.045787 785	0.955609 729
202134	FAM15 3B	Family with sequence similarity 153 member B	3.688 69	4.059 7	3.031 13	3.961 92	4.770 83	4.728 72	1.8582998 8	0.893983 333	1.858299 88	Up	0.029300 486	0.955609 729

6580	SLC22 A1	Solute carrier family 22 (organic cation transporter), member 1	5.30967	6.05123	5.59142	7.1748	6.7265	6.81397	2.385541305	1.254316667	2.385541305	Up	0.001493611	0.955609729
83661	MS4A8	Membrane-spanning 4-domains, subfamily A, member 8	6.14081	7.34354	6.97255	7.90313	7.64616	7.91508	2.003454854	1.00249	2.003454854	Up	0.016940921	0.955609729
84707	BEX2	Brain expressed X-linked 2	6.63786	7.99549	7.36425	8.41969	8.27601	8.17895	1.943984434	0.959016667	1.943984434	Up	0.026864701	0.955609729
81606	LBH	Limb bud and heart development	5.17806	5.0556	5.49202	3.87392	4.81064	4.5123	-1.79370172	-0.84294	1.79370172	Down	0.015947821	0.955609729
116159	CYYR1	Cysteine/tyrosine-rich 1	8.03254	6.17836	5.96907	4.62117	5.44168	5.55978	-2.866148447	-1.519113333	2.866148447	Down	0.034379184	0.955609729
1733	DIO1	Deiodinase, iodothyronine, type I	5.29794	6.07712	5.18107	7.58129	7.67892	7.43856	4.13402372	2.047546667	4.13402372	Up	0.000144984	0.955609729
5340	PLG	Plasminogen	4.23045	4.01421	4.60298	5.44372	4.84777	6.03869	2.235886054	1.160846667	2.235886054	Up	0.009069436	0.955609729
29094	LGALSL	Lectin, galactoside-binding-like	4.19306	3.77977	4.00931	4.96714	4.3767	4.60698	1.575955356	0.656226667	1.575955356	Up	0.01192686	0.955609729
563	AZGP1	A-2-glycoprotein 1, zinc-binding	9.25307	9.53399	9.54028	10.10918	10.01544	10.40746	1.664297487	0.734913333	1.664297487	Up	0.004879748	0.955609729

1903	S1PR3	Sphingosine-1-phosphate receptor 3	7.11302	6.41307	6.11461	4.17265	6.185	4.49489	-3.023151614	-1.596053333	3.023151614	Down	0.024359796	0.955609729
1124	CHN2	Chimerin 2	6.36212	6.49398	6.0664	7.48578	6.96308	7.84714	2.180259714	1.1245	2.180259714	Up	0.004104425	0.955609729
81889	FAHD1	Fumarylacetate hydrolase domain containing 1	6.25413	7.09605	7.03754	8.06332	7.23935	8.13271	2.022145302	1.015886667	2.022145302	Up	0.020727037	0.955609729
8404	SPARC L1	SPARC like 1	11.127	9.718	9.3434	6.20234	8.75185	8.02838	-5.285146027	-2.401943333	5.285146027	Down	0.014673519	0.955609729
116441	TM4SF18	Transmembrane 4 L six family member 18	6.82149	5.4237	5.36562	3.47865	4.54942	5.06364	-2.840936661	-1.506366667	2.840936661	Down	0.026313601	0.955609729
9099	USP2	Ubiquitin specific peptidase 2	5.79999	5.86956	5.10962	7.16723	6.14325	6.40313	1.969933142	0.978146667	1.969933142	Up	0.023009257	0.955609729
56650	CLDN D1	Claudin domain containing 1	7.72055	6.77058	6.90828	6.67668	5.85459	6.28875	-1.814782517	-0.859796667	1.814782517	Down	0.035154111	0.955609729
928	CD9	CD9 molecule	10.46311	9.34192	8.82678	7.26125	8.56255	8.33256	-2.812428982	-1.491816667	2.812428982	Down	0.022532912	0.955609729
147184	TMEM99	Transmembrane protein 99	7.6947	7.40063	7.99927	8.61261	8.21407	8.31538	1.604903626	0.682486667	1.604903626	Up	0.016788476	0.955609729
9975	NR1D2	Nuclear receptor subfamily 1 group D	4.85903	5.46269	6.11962	7.25161	5.93168	6.98962	2.368307918	1.243856667	2.368307918	Up	0.027483549	0.955609729

9975	NR1D2	Nuclear receptor subfamily 1 group D member 2	4.85903	5.46269	6.11962	7.25161	5.93168	6.98962	2.368307918	1.243856667	2.368307918	Up	0.027483549	0.955609729
100507387	LOC100507387	Uncharacterized LOC100507387	3.68869	4.0597	3.03113	3.96192	4.77083	4.72872	1.85829988	0.893983333	1.85829988	Up	0.029300486	0.955609729
55824	PAG1	Phosphoprotein membrane anchor with glycosphingolipid microdomains 1	6.39276	6.96324	7.0421	7.85755	7.23139	7.51684	1.665428403	0.735893333	1.665428403	Up	0.024654731	0.955609729
2697	GJA1	Gap junction protein $\alpha$ 1	4.52831	3.88593	4.40262	3.49652	3.85942	3.69677	-1.503213575	-0.58805	1.503213575	Down	0.021184342	0.955609729
285	ANGPT2	Angiopoietin 2	5.43242	4.39169	4.85051	4.23567	4.41553	3.70837	-1.70726065	-0.771683333	1.70726065	Down	0.040615126	0.955609729
9532	BAG2	BCL2 associated athanogene 2	6.83576	5.91758	6.54848	5.11312	5.69073	5.62249	-1.943279387	-0.958493333	1.943279387	Down	0.013434065	0.955609729
6678	SPARC	Secreted protein, acidic, cysteine-rich (osteonectin)	11.18178	8.46127	7.67109	4.62444	7.44996	7.1419	-6.49477704	-2.69928	6.49477704	Down	0.043319277	0.955609729
79924	ADM2	Adrenomedullin 2	5.39346	6.53322	6.01058	6.84164	6.71039	6.53299	1.642530318	0.71592	1.642530318	Up	0.049580221	0.955609729

4495	MT1G	Metallothionein 1G	10.14394	10.70426	10.48559	12.04633	11.76997	12.34409	3.050121402	1.608866667	3.050121402	Up	0.00019533	0.955609729
1397	CRIP2	Cysteine-rich protein 2	8.29507	7.855	8.32589	7.64456	6.96443	7.776	-1.621119003	-0.69699	1.621119003	Down	0.036913353	0.955609729
153562	MARVELD2	MARVEL domain containing 2	6.56864	8.40885	8.34554	9.40837	8.63983	9.03904	2.38623589	1.254736667	2.38623589	Up	0.0472142	0.955609729
7780	SLC30A2	Solute carrier family 30 (zinc transporter), member 2	8.71561	10.00072	9.85077	10.59677	10.4356	10.72555	2.090150269	1.063606667	2.090150269	Up	0.019267779	0.955609729
445815	PALM2-AKAP2	PALM2-AKAP2 readthrough	10.14756	8.85323	9.06801	8.56371	8.50612	8.51151	-1.776642408	-0.829153333	1.776642408	Down	0.046346954	0.955609729
84172	POLR1B	Polymerase I polypeptide B	4.75452	5.0159	5.22821	5.51181	5.92182	5.75452	1.658455153	0.72984	1.658455153	Up	0.006954787	0.955609729
80343	SEL1L2	Sel-1 suppressor of lin-12-like 2 (C. Elegans)	4.85057	4.58405	4.65116	3.73292	4.36926	3.95275	-1.598756251	-0.67695	1.598756251	Down	0.009486051	0.955609729
58494	JAM2	Junctional adhesion molecule 2	5.97316	4.51812	3.9626	3.05466	3.8649	3.67332	-2.440201021	-1.287	2.440201021	Down	0.041366636	0.955609729
9058	SLC13A2	Solute carrier family 13 (sodium-dep	9.00713	9.87465	9.31711	10.40636	10.04087	10.43	1.856750543	0.89278	1.856750543	Up	0.011123921	0.955609729

		endent dicarboxylate transporter), member 2												
79783	SUGCT	Succinyl-coa :glutarate-coa transferase	5.22474	5.70132	6.10452	4.27268	5.32878	4.83122	-1.822560451	-0.865966667	1.822560451	Down	0.036466042	0.955609729
100288332	NPIPA5	Nuclear pore complex interacting protein family member A5	6.70725	7.99302	7.37651	8.22062	8.13039	8.1216	1.739424428	0.79861	1.739424428	Up	0.043520998	0.955609729
25777	SUN2	Sad1 and UNC84 domain containing 2	5.05381	4.68023	5.0998	4.58228	4.02772	4.36094	-1.537905298	-0.620966667	1.537905298	Down	0.016731956	0.955609729
6451	SH3BGR	SH3 domain binding glutamate-rich protein like	8.38899	7.76771	7.71777	7.24389	6.87719	7.55091	-1.663428667	-0.73416	1.663428667	Down	0.029518603	0.955609729
9465	AKAP7	A-kinase anchoring protein 7	7.95662	8.90638	8.30835	9.22236	9.05386	9.59779	1.867213202	0.900886667	1.867213202	Up	0.016724219	0.955609729
10804	GJB6	Gap junction protein $\beta$ 6	5.21204	6.49664	5.94119	7.19145	6.49512	6.93984	1.989188506	0.99218	1.989188506	Up	0.028658985	0.955609729
1031	CDKN2C	Cyclin-dependent kinase inhibitor 2C (p18, inhibits	7.335	5.50613	5.46994	4.25405	5.26275	4.89503	-2.461856493	-1.299746667	2.461856493	Down	0.049905827	0.955609729

1031	CDKN2C	Cyclin-dependent kinase inhibitor 2C (p18, inhibits CDK4)	7.335	5.50613	5.46994	4.25405	5.26275	4.89503	-2.461856493	-1.299746667	2.461856493	Down	0.049905827	0.955609729
154761	LOC154761	Family with sequence similarity 115, member C pseudogene	5.92317	6.01918	6.42891	7.22699	7.08036	6.95274	1.949282696	0.962943333	1.949282696	Up	0.00194573	0.955609729
7430	EZR	Ezrin	7.69011	8.51457	8.94329	9.52088	9.08617	9.13489	1.820906275	0.864656667	1.820906275	Up	0.037544454	0.955609729
9867	PJA2	Praja ring finger 2, E3 ubiquitin protein ligase	6.33444	6.25731	6.65296	6.19944	4.99889	5.60395	-1.758253798	-0.814143333	1.758253798	Down	0.038031693	0.955609729
64853	AIDA	Axin interactor, dorsalization associated	6.40668	5.66146	5.9835	5.18312	4.90105	5.79867	-1.650534544	-0.722933333	1.650534544	Down	0.046277344	0.955609729
54346	UNC93A	Unc-93 homolog A (C. Elegans)	2.87979	3.86279	4.02048	6.28794	4.93169	4.78257	3.355156356	1.74638	3.355156356	Up	0.008516354	0.955609729
222584	FAM83B	Family with sequence similarity 83 member B	3.28266	3.80458	4.25625	4.37871	4.48636	4.56854	1.62080066	0.696706667	1.62080066	Up	0.025064437	0.955609729
29785	CYP2S1	Cytochrome P450, family	6.97988	7.8761	7.00181	8.41673	9.00599	7.91493	2.234501996	1.159953333	2.234501996	Up	0.016169285	0.955609729

388650	FAM69 A	Family with sequence similarity 69 member A	7.053 22	6.211 36	6.344 14	6.026 16	5.335 03	5.850 03	-1.7400957 18	-0.79916 6667	1.740095 718	Down	0.030864 694	0.955609 729
10268	RAMP 3	Receptor (G protein-coupled) activity modifying protein 3	8.737 1	7.098 44	7.325 49	6.274 27	7.012 32	6.542 69	-2.1593293 91	-1.11058 3333	2.159329 391	Down	0.045755 439	0.955609 729
25987	TSKU	Tsukushi, small leucine rich proteoglycan	8.583 19	8.216 82	8.852 66	7.782 1	8.332 42	7.763 3	-1.5069344 54	-0.59161 6667	1.506934 454	Down	0.049505 143	0.955609 729
54928	IMPA D1	Inositol monophosph atase domain containing 1	6.560 25	5.680 29	5.706 6	5.360 07	4.829 25	5.459 96	-1.7004933 14	-0.76595 3333	1.700493 314	Down	0.039821 347	0.955609 729
51409	HEMK 1	Hemk methyltransf erase family member 1	4.219 34	5.160 43	4.580 33	5.548 06	5.368 98	5.087	1.6035989	0.681313 333	1.603598 9	Up	0.038378 038	0.955609 729
100287 413	LOC10 028741 3	Uncharacteri zed LOC100287 413	3.603 13	4.559 84	4.164 31	4.684 19	4.962 7	4.556 9	1.5427489 72	0.625503 333	1.542748 972	Up	0.046498 198	0.955609 729
4600	MX2	MX dynamin-like gtpase 2	7.777 78	7.495 38	7.406 92	8.202 22	8.422 34	8.605 96	1.8026841 8	0.850146 667	1.802684 18	Up	0.003140 963	0.955609 729
1797	DXO	Decapping exoribonucle ase	7.898 44	7.853 6	8.260 59	6.287 2	7.482 87	6.369 53	-2.4469930 43	-1.29101	2.446993 043	Down	0.007928 414	0.955609 729



10580	SORBS1	Sorbin and SH3 domain containing 1	11.43304	9.59138	9.43059	7.5514	9.02264	8.35306	-3.586649251	-1.842636667	3.586649251	Down	0.020748544	0.955609729
7903	ST8SI A4	ST8 $\alpha$ -N-acetyl-n euraminide $\alpha$ -2,8-sialyltr ansferase 4	5.4135	6.18019	6.04885	4.08678	4.87149	5.49882	-2.087558557	-1.061816667	2.087558557	Down	0.030140968	0.955609729
64781	CERK	Ceramide kinase	6.79889	6.99272	7.46089	7.92731	7.48885	7.71974	1.545206873	0.6278	1.545206873	Up	0.030835743	0.955609729
57619	SHRO OM3	Shroom family member 3	8.82903	10.08217	10.00326	10.92889	10.41346	10.32335	1.888289544	0.91708	1.888289544	Up	0.044039197	0.955609729
80344	DCAF11	DDB1 and CUL4 associated factor 11	7.08556	7.58474	7.34787	8.05895	8.20885	8.02041	1.689597962	0.75668	1.689597962	Up	0.005252604	0.955609729
775	CACNA1C	Calcium channel, voltage-depe ndent, L type, $\alpha$ 1C subunit	5.91138	5.29592	4.66298	4.13982	4.82306	4.20215	-1.868330909	-0.90175	1.868330909	Down	0.036606075	0.955609729
101059953	NPIPA8	Nuclear pore complex interacting protein family member A8	6.70725	7.99302	7.37651	8.22062	8.13039	8.1216	1.739424428	0.79861	1.739424428	Up	0.043520998	0.955609729
4640	MYO1A	Myosin IA	7.19453	8.31363	7.35728	8.45988	8.42083	8.25692	1.690437488	0.757396667	1.690437488	Up	0.045524223	0.955609729

3751	KCND2	Potassium channel, voltage gated Shal related subfamily D, member 2	4.72799	5.22287	5.26234	5.74621	5.70666	5.73736	1.578998718	0.65901	1.578998718	Up	0.010009956	0.955609729
2634	GBP2	Guanylate binding protein 2, interferon-inducible	7.14267	6.83939	6.80187	5.34228	6.141	6.68082	-1.831818628	-0.873276667	1.831818628	Down	0.03973173	0.955609729
645954	SVILP1	Supervillin pseudogene 1	6.53557	7.12427	6.83096	5.26317	6.09226	6.24846	-1.948418158	-0.962303333	1.948418158	Down	0.017044512	0.955609729
5504	PPP1R2	Protein phosphatase 1 regulatory inhibitor subunit 2	3.78894	3.36127	3.40949	4.59208	3.95219	3.87144	1.535459011	0.61867	1.535459011	Up	0.029354265	0.955609729
84873	ADGRG7	Adhesion G protein-coupled receptor G7	3.17857	4.23839	4.45469	5.21716	4.51365	5.00258	1.937120007	0.953913333	1.937120007	Up	0.034708324	0.955609729
4629	MYH11	Myosin, heavy chain 11, smooth muscle	5.83741	6.66909	6.70445	3.60782	5.76064	4.01513	-3.843587024	-1.942453333	3.843587024	Down	0.012253837	0.955609729
9068	ANGPTL1	Angiotensin-like 1	6.75843	5.80568	5.42256	4.20536	4.5904	5.27873	-2.469227904	-1.30406	2.469227904	Down	0.016837705	0.955609729
8829	NRP1	Neuropilin 1	6.05859	5.49522	6.06472	5.26693	4.97933	5.21682	-1.645451306	-0.718483333	1.645451306	Down	0.011375334	0.955609729

100529 240	ZNF81 6-ZNF 321P	ZNF816-ZN F321P readthrough	5.425 65	6.603 86	6.313 97	7.304 41	7.404 59	6.637 12	2.0012203 11	1.00088	2.001220 311	Up	0.028817 304	0.955609 729
23704	KCNE 4	Potassium channel, voltage gated subfamily E regulatory $\beta$ subunit 4	6.379 88	6.556 21	5.545 88	3.950 05	5.708 51	4.111 83	-2.9701312 12	-1.57052 6667	2.970131 212	Down	0.019386 476	0.955609 729
54854	FAM83 E	Family with sequence similarity 83 member E	6.153 88	7.187 96	7.469 18	8.206 34	7.517 87	7.810 32	1.8762299 65	0.907836 667	1.876229 965	Up	0.047249 975	0.955609 729
6920	TCEA3	Transcriptio n elongation factor A (SII), 3	8.195 71	8.341 32	8.030 98	8.938 48	8.589 79	8.996 61	1.5716609 25	0.65229	1.571660 925	Up	0.010315 413	0.955609 729
5144	PDE4D	Phosphodiesterase 4D	4.463 53	4.523 96	4.733 49	3.219 7	4.229 95	4.136 25	-1.6377252 35	-0.71169 3333	1.637725 235	Down	0.038064	0.955609 729
9472	AKAP 6	A-kinase anchoring protein 6	5.310 08	5.779 55	6.036 95	4.692 5	4.808 03	4.684 63	-1.9731126 61	-0.98047 3333	1.973112 661	Down	0.002526 939	0.955609 729
100526 832	PHOSP HO2-K LHL23	PHOSPHO2 -KLHL23 readthrough	4.841 24	5.609 66	5.181 07	6.235 34	5.978 23	5.617 02	1.6619458	0.732873 333	1.661945 8	Up	0.026046 052	0.955609 729
389376	SFTA2	Surfactant associated 2	8.091 84	9.220 39	8.576 36	9.483 39	9.716 74	9.512 44	1.9202932 81	0.941326 667	1.920293 281	Up	0.015911 406	0.955609 729
6541	SLC7A 1	Solute carrier family 7 (cationic	4.534 43	5.054 35	4.742 47	5.338 15	5.581 97	5.602 43	1.6591373 62	0.730433 333	1.659137 362	Up	0.005637 524	0.955609 729

		amino acid transporter, y <sup>+</sup> system), member 1												
229	ALDO B	Aldolase, fructose-bisphosphate B	4.79307	6.05438	4.76424	6.17425	5.89499	6.72964	2.088397978	1.062396667	2.088397978	Up	0.035071901	0.955609729
3158	HMGCS2	3-hydroxy-3-methylglutaryl-coa synthase 2 (mitochondrial)	8.40162	7.09511	6.42248	8.74404	9.36646	9.09609	3.39276146	1.76246	3.39276146	Up	0.009638285	0.955609729
3419	IDH3A	Isocitrate dehydrogenase 3 (NAD <sup>+</sup> ) $\alpha$	5.01243	4.34273	4.55457	4.20009	3.59901	3.91464	-1.660936211	-0.731996667	1.660936211	Down	0.015632015	0.955609729
54065	SMIM11A	Small integral membrane protein 11A	5.72511	5.87277	6.12979	7.16954	6.33185	6.63989	1.746584772	0.804536667	1.746584772	Up	0.016401594	0.955609729
10136	CELA3A	Chymotrypsin like elastase family member 3A	3.34836	3.79293	3.34063	4.6902	4.41693	4.94855	2.283510357	1.191253333	2.283510357	Up	0.000531616	0.955609729
23057	NMNAT2	Nicotinamide nucleotide adenylyltransferase 2	5.90012	5.73907	5.06125	4.38705	5.10312	4.24549	-1.983790945	-0.98826	1.983790945	Down	0.016489832	0.955609729
261729	STEAP	STEAP2	6.486	6.892	7.210	7.383	7.78	7.243	1.5217063	0.60569	1.521706	Up	0.047020	0.955609

	2	metalloreductase	05	58	52	11		11	68		368		49	729
64943	NT5DC2	5'-nucleotidase domain containing 2	6.06526	4.87732	5.79045	4.02577	5.34011	4.22038	-2.068985212	-1.048923333	2.068985212	Down	0.04973934	0.955609729
5788	PTPRC	Protein tyrosine phosphatase, receptor type, C	6.92578	6.39915	6.74984	5.93716	5.8343	6.49854	-1.517387965	-0.60159	1.517387965	Down	0.044848857	0.955609729
6251	RSU1	Ras suppressor protein 1	8.60448	7.66544	8.09434	7.1465	7.35079	7.62109	-1.680192656	-0.748626667	1.680192656	Down	0.031022993	0.955609729
144501	KRT80	Keratin 80, type II	4.8351	5.41487	4.86976	6.19668	6.22749	5.13174	1.755716612	0.81206	1.755716612	Up	0.04996586	0.955609729
100533990	APOC4-APOC2	APOC4-APOC2 readthrough (NMD candidate)	6.06565	6.58253	5.60903	6.71307	7.13457	7.14033	1.879375483	0.910253333	1.879375483	Up	0.0153779	0.955609729
8618	CADPS	Ca <sup>++</sup> -dependent secretion activator	6.13006	6.78967	6.54576	7.63299	7.90191	6.66909	1.882739414	0.912833333	1.882739414	Up	0.038641807	0.955609729
552889	ATXN7L3B	Ataxin 7-like 3B	4.78688	4.34721	4.91116	5.10219	5.41352	5.31492	1.510605209	0.595126667	1.510605209	Up	0.018367039	0.955609729
8976	WASL	Wiskott-Aldrich syndrome-like	7.08237	7.32989	7.26019	7.96468	8.02108	7.73409	1.604881378	0.682466667	1.604881378	Up	0.005228809	0.955609729
4211	MEIS1	Meis	6.572	6.046	5.976	4.878	5.723	5.576	-1.7478523	-0.80558	1.747852	Down	0.026103	0.955609

		homeobox 1	15	91	42	38	77	58	68	3333	368		116	729
84632	AFAP1 L2	Actin filament associated protein 1 like 2	4.995 59	3.763 6	4.004 04	3.274 11	3.457 42	3.657 08	-1.7309211 43	-0.79154	1.730921 143	Down	0.042915 374	0.955609 729
9871	SEC24 D	SEC24 homolog D, COPII coat complex component	3.452 95	3.645 72	4.329 45	4.758 44	4.124 13	4.892 44	1.7198665 99	0.782296 667	1.719866 599	Up	0.033443 325	0.955609 729
2288	FKBP4	FK506 binding protein 4	9.003 31	9.843 81	9.566 47	10.14 486	10.12 91	10.21 02	1.6134959 99	0.69019	1.613495 999	Up	0.022745 501	0.955609 729
4154	MBNL 1	Muscleblind like splicing regulator 1	4.340 22	4.337 77	5.133 46	4.041 02	3.204 07	3.926 35	-1.8403795 53	-0.88000 3333	1.840379 553	Down	0.024599 023	0.955609 729
54716	SLC6A 20	Solute carrier family 6 (proline IMINO transporter), member 20	5.700 2	7.200 49	6.821 53	8.128 12	7.430 46	7.649 03	2.2373588 47	1.161796 667	2.237358 847	Up	0.026291 346	0.955609 729
7412	VCAM 1	Vascular cell adhesion molecule 1	6.728 9	5.119 5	6.096 12	3.821 73	4.244 58	4.580 01	-3.4012538 08	-1.76606 6667	3.401253 808	Down	0.004367 906	0.955609 729
1910	EDNR B	Endothelin receptor type B	8.220 88	5.994	5.267 78	3.997 01	5.329 59	4.514 82	-3.6818052 92	-1.88041 3333	3.681805 292	Down	0.044524 281	0.955609 729
5627	PROS1	Protein S ( $\alpha$ )	6.377	6.259	5.950	5.465	5.156	5.823	-1.6403003	-0.71396	1.640300	Down	0.016429	0.955609

			24	78	85	56	75	68	43		343		44	729
213	ALB	Albumin	4.823 65	5.648 86	6.203 53	6.160 03	6.466 48	7.553 31	2.2468855 92	1.167926 667	2.246885 592	Up	0.044086 126	0.955609 729
399948	COLC A1	Colorectal cancer associated 1	6.744 72	7.220 02	7.350 65	7.968 27	7.524 33	7.635 14	1.5200477 73	0.604116 667	1.520047 773	Up	0.033460 807	0.955609 729
28970	C11orf 54	Chromosom e 11 open reading frame 54	8.921 73	10.13 882	9.524 63	10.71 504	10.04 148	10.32 633	1.7808384 74	0.832556 667	1.780838 474	Up	0.045053 532	0.955609 729
65124	SOWA HC	Sosondowah ankyrin repeat domain family member C	6.612 08	6.871 54	7.119 12	7.919 49	7.353 67	7.629 85	1.7014404 6	0.766756 667	1.701440 46	Up	0.011351 346	0.955609 729
79822	ARHG AP28	Rho gtpase activating protein 28	6.544 85	5.417 91	5.565 56	4.207 75	5.439 7	4.806 68	-2.0345785 78	-1.02473	2.034578 578	Down	0.042059 113	0.955609 729
338	APOB	Apolipoprote in B	4.861 06	5.690 68	4.779 37	6.815 8	7.866 62	6.467 47	3.8359750 41	1.939593 333	3.835975 041	Up	0.002723 894	0.955609 729
79817	MOB3 B	MOB kinase activator 3B	7.250 18	7.888 54	7.785 76	8.602 27	7.908 01	8.570 43	1.6457478 73	0.718743 333	1.645747 873	Up	0.034899 863	0.955609 729
10117	ENAM	Enamelin	5.405 97	6.322 74	6.310 12	7.166 97	6.561 99	7.002 14	1.8627361 46	0.897423 333	1.862736 146	Up	0.023611 637	0.955609 729
59	ACTA 2	Actin, $\alpha$ 2, smooth muscle, aorta	5.149 98	4.789 71	4.425 32	3.472 35	4.482 76	3.710 24	-1.8659193 97	-0.89988 6667	1.865919 397	Down	0.022338 089	0.955609 729
3371	TNC	Tenascin C	4.986 54	3.973 07	4.983 09	2.320 94	3.876 27	2.739 14	-3.1794634 7	-1.66878 3333	3.179463 47	Down	0.008527 761	0.955609 729
122786	FRMD	FERM	8.176	5.834	6.215	4.544	5.896	5.011	-3.0134998	-1.59144	3.013499	Down	0.046906	0.955609

	6	domain containing 6	18	77	13	29		47	65		865		059	729
1582	CYP8B1	Cytochrome P450, family 8, subfamily B, polypeptide 1	4.57636	5.09878	4.68478	5.16793	5.93633	6.78776	2.261635865	1.177366667	2.261635865	Up	0.02358585	0.955609729
100861540	CYP3A7-CYP3A51P3A51P	CYP3A7-CYP3A51P readthrough	3.08086	3.18838	4.07637	4.47363	5.45531	4.1554	2.372229079	1.246243333	2.372229079	Up	0.018122813	0.955609729
4494	MT1F	Metallothionein 1F	8.83203	10.4129	9.43204	11.54488	11.15157	11.40958	3.505661422	1.809686667	3.505661422	Up	0.002675451	0.955609729
8727	CTNNAL1	Catenin $\alpha$ -like 1	8.87657	7.39041	6.92086	5.93111	5.74465	6.43131	-3.234606019	-1.69359	3.234606019	Down	0.012900981	0.955609729
126789	PUSL1	Pseudouridylate synthase-like 1	5.48041	5.82395	6.10997	6.59933	6.59426	6.21905	1.586781336	0.666103333	1.586781336	Up	0.020465187	0.955609729
9229	DLGAP1	Discs, large (Drosophila) homolog-associated protein 1	4.99257	6.08767	5.74986	6.55438	6.47989	6.46364	1.852238659	0.88927	1.852238659	Up	0.0183949	0.955609729
285382	C3orf70	Chromosome 3 open reading frame 70	7.47	6.49864	6.74308	3.99252	6.68833	5.24101	-3.024339291	-1.59662	3.024339291	Down	0.047422292	0.955609729
54825	CDHR2	Cadherin related family	5.74073	7.71201	7.0885	8.11601	8.21717	7.7985	2.292327754	1.196813333	2.292327754	Up	0.043676312	0.955609729



54825	CDHR2	Cadherin related family member 2	5.74073	7.71201	7.0885	8.11601	8.21717	7.7985	2.292327754	1.196813333	2.292327754	Up	0.043676312	0.955609729
54498	SMOX	Spermine oxidase	6.53356	7.99814	7.67351	9.06609	8.3249	8.11017	2.141542042	1.09865	2.141542042	Up	0.040722496	0.955609729
9648	GCC2	GRIP and coiled-coil domain containing 2	6.56655	7.14435	6.68362	7.91139	7.3413	7.18272	1.602469243	0.680296667	1.602469243	Up	0.036687559	0.955609729
27333	GOLIM4	Golgi integral membrane protein 4	6.91552	7.00355	6.67159	7.79589	8.11783	7.5562	1.944977321	0.959753333	1.944977321	Up	0.002557055	0.955609729
7757	ZNF208	Zinc finger protein 208	5.58708	4.74426	3.87978	3.37796	3.50657	3.80283	-2.257282004	-1.174586667	2.257282004	Down	0.024381804	0.955609729
4281	MID1	Midline 1	5.53705	4.59528	4.80372	4.10734	4.58478	3.45949	-1.902829988	-0.928146667	1.902829988	Down	0.035158125	0.955609729
694	BTG1	B-cell translocation gene 1, anti-proliferative	10.75788	10.92352	10.49335	10.13102	9.66688	9.70615	-1.85347587	-0.890233333	1.85347587	Down	0.003288077	0.955609729
5358	PLS3	Plastin 3	8.13826	7.47382	7.74666	7.00467	6.82451	7.42075	-1.627814909	-0.702936667	1.627814909	Down	0.026267159	0.955609729
171024	SYNP O2	Synaptopodin 2	9.30532	10.2311	10.66314	6.25942	9.62862	7.34002	-5.006607415	-2.323833333	5.006607415	Down	0.02923086	0.955609729
5292	PIM1	Pim-1 proto-oncogene, serine/threon	5.09268	4.08359	4.45469	4.04252	3.76066	3.8084	-1.594524944	-0.673126667	1.594524944	Down	0.036346202	0.955609729

3925	STMN1	Stathmin 1	7.28851	6.83858	6.33928	5.33479	6.43487	5.97194	-1.876776256	-0.908256667	1.876776256	Down	0.038954622	0.955609729
4493	MT1E	Metallothionein 1E	7.41296	7.67425	7.46962	8.43864	7.89771	8.49072	1.68967604	0.756746667	1.68967604	Up	0.010063473	0.955609729
3117	HLA-DQA1	Major histocompatibility complex, class II, DQ $\alpha$ 1	8.63461	8.6741	8.66085	7.22608	8.02513	8.17977	-1.797751151	-0.846193333	1.797751151	Down	0.017216186	0.955609729
5908	RAP1B	RAP1B, member of RAS oncogene family	5.51884	4.59482	4.58076	4.40312	3.56146	4.28574	-1.758932354	-0.8147	1.758932354	Down	0.045776334	0.955609729
100528007	BORCS7-ASMT	BORCS7-A SMT readthrough (NMD candidate)	6.28628	7.49762	7.16565	7.76461	7.75724	8.67592	2.118054923	1.08274	2.118054923	Up	0.029555523	0.955609729
6461	SHB	Src homology 2 domain containing adaptor protein B	6.5591	7.39475	7.45992	7.9279	7.88223	7.89316	1.697219704	0.763173333	1.697219704	Up	0.025259518	0.955609729
7453	WARS	Tryptophanyl-tRNA synthetase	5.64626	4.64709	5.03573	4.02369	4.03239	4.56688	-1.868706505	-0.90204	1.868706505	Down	0.017348087	0.955609729
92292	GLYA TL1	Glycine-N-acyltransferase	3.60313	4.55984	4.16431	4.68419	4.9627	4.5569	1.542748972	0.625503333	1.542748972	Up	0.046498198	0.955609729

		e like 1												
89870	TRIM15	Tripartite motif containing 15	6.606	7.65115	7.56353	8.31648	8.36566	7.68806	1.802301033	0.84984	1.802301033	Up	0.042727297	0.955609729
3352	HTR1D	5-hydroxytryptamine (serotonin) receptor 1D, G protein-coupled	6.19062	7.46799	6.26147	7.88426	7.24648	8.00617	2.102749025	1.072276667	2.102749025	Up	0.03154499	0.955609729
115123	MARCH3	Membrane associated ring-CH-type finger 3	7.38116	7.73124	7.691	8.62761	7.87731	8.41379	1.630261428	0.705103333	1.630261428	Up	0.022648668	0.955609729
1439	CSF2RB	Colony stimulating factor 2 receptor, $\beta$ , low-affinity (granulocyte-macrophage)	7.19561	5.66866	7.2859	5.00949	6.01663	5.4832	-2.319183005	-1.213616667	2.319183005	Down	0.042292783	0.955609729
57194	ATP10A	Atpase, class V, type 10A	5.69622	5.30231	5.03026	6.19472	6.24875	6.07518	1.777627861	0.829953333	1.777627861	Up	0.005393778	0.955609729
4496	MT1H	Metallothionein 1H	7.73298	8.5811	7.99435	10.33029	9.48095	9.95369	3.527957872	1.818833333	3.527957872	Up	0.000668336	0.955609729
8934	RAB29	RAB29, member RAS	4.69341	4.8012	5.03573	6.13394	4.93555	5.69065	1.673961871	0.743266667	1.673961871	Up	0.048330077	0.955609729

		oncogene family												
335	APOA1	Apolipoprotein A-I	6.97141	6.9621	6.20648	8.39757	6.87819	8.38574	2.256108837	1.173836667	2.256108837	Up	0.039407813	0.955609729
1047	CLGN	Calmegin	3.40735	4.58114	2.98759	4.2951	4.70776	5.94924	2.505919378	1.32534	2.505919378	Up	0.046316283	0.955609729
3320	HSP90AA1	Heat shock protein 90kDa $\alpha$ family class A member 1	8.85783	9.10029	8.77658	9.79438	9.32918	9.95485	1.718603415	0.781236667	1.718603415	Up	0.00869977	0.955609729
6555	SLC10A2	Solute carrier family 10 (sodium/bile acid cotransporter), member 2	5.83725	5.89259	6.34618	8.15236	7.90423	7.71668	3.729761379	1.899083333	3.729761379	Up	5.99474E-05	0.955609729
1266	CNN3	Calponin 3, acidic	9.48192	8.54215	8.65831	7.3953	7.57153	8.35739	-2.172545914	-1.119386667	2.172545914	Down	0.016684025	0.955609729
151230	KLHL23	Kelch like family member 23	4.84124	5.60966	5.18107	6.23534	5.97823	5.61702	1.6619458	0.732873333	1.6619458	Up	0.026046052	0.955609729
55273	TMEM100	Transmembrane protein 100	9.22438	7.19173	6.98225	6.01739	6.43213	6.56985	-2.75044172	-1.459663333	2.75044172	Down	0.043054911	0.955609729
444	ASPH	Aspartate $\beta$ -hydroxylase	7.33426	5.4384	5.72774	4.8779	4.5936	5.32266	-2.354487941	-1.235413333	2.354487941	Down	0.045174305	0.955609729
9444	QKI	QKI, KH domain	5.49132	4.15041	4.39853	3.52799	3.62563	4.19177	-1.86385548	-0.89829	1.86385548	Down	0.04745479	0.955609729

		containing, RNA binding												
27295	PDLIM 3	PDZ and LIM domain 3	7.914 63	6.132 17	6.340 39	3.199 79	5.987 57	4.173 67	-5.0702375 2	-2.34205 3333	5.070237 52	Down	0.020907 861	0.955609 729
26298	EHF	Ets homologous factor	3.829 34	4.719 21	5.077 3	5.564 64	6.094 19	5.183 36	2.1025109 78	1.072113 333	2.102510 978	Up	0.025065 598	0.955609 729
4883	NPR3	Natriuretic peptide receptor 3	9.541 68	6.759 57	6.879 62	5.828 01	6.132 19	5.666 02	-3.6088770 67	-1.85155	3.608877 067	Down	0.039376 744	0.955609 729
8548	BLZF1	Basic leucine zipper nuclear factor 1	3.958 21	4.506 05	4.739 05	5.558 79	4.737 61	5.000 08	1.6219432 4	0.697723 333	1.621943 24	Up	0.044769 964	0.955609 729
81831	NETO2	Neuropilin and tolloid like 2	3.691 21	5.325 51	5.275 6	5.933 11	5.844 95	6.454 98	2.4855641 41	1.313573 333	2.485564 141	Up	0.025580 429	0.955609 729
284422	SMIM2 4	Small integral membrane protein 24	9.247 57	11.08 461	10.91 024	11.57 432	11.38 128	11.94 046	2.3260466	1.21788	2.326046 6	Up	0.042574 392	0.955609 729
10313	RTN3	Reticulon 3	6.985 91	6.454 09	6.734 09	5.954 53	5.020 73	6.408 51	-1.9054168 69	-0.93010 6667	1.905416 869	Down	0.039956 667	0.955609 729
9663	LPIN2	Lipin 2	7.767 56	8.562 79	7.763 31	9.461 6	8.549 08	8.900 42	1.9173937 92	0.939146 667	1.917393 792	Up	0.023915 043	0.955609 729
4969	OGN	Osteoglycin	7.948 49	7.012 26	6.081 25	4.508 49	6.069 74	5.840 91	-2.9098672 41	-1.54095 3333	2.909867 241	Down	0.033885 405	0.955609 729
10217	CTDSP L	CTD small phosphatase	8.998 64	9.844 43	9.583 73	10.08 076	10.09 425	10.09 637	1.5314093 81	0.61486	1.531409 381	Up	0.036340 61	0.955609 729

		like												
23464	GCAT	Glycine C-acetyltransferase	5.90865	6.86708	6.90652	7.29571	7.3161	7.36659	1.699821592	0.765383333	1.699821592	Up	0.035050258	0.955609729
273	AMPH	Amphiphysin	5.43441	4.6922	4.81779	3.60198	4.81687	4.0505	-1.771555504	-0.825016667	1.771555504	Down	0.049552571	0.955609729
4134	MAP4	Microtubule associated protein 4	7.67193	7.03014	6.86864	6.66843	6.51883	6.61042	-1.506300907	-0.59101	1.506300907	Down	0.0446616	0.955609729
100529145	TEN1-CDK3	TEN1-CDK3 readthrough (NMD candidate)	6.63976	6.40313	6.80187	7.40334	7.13034	7.3433	1.599262397	0.677406667	1.599262397	Up	0.007672476	0.955609729
284266	SIGLEC15	Sialic acid binding Ig-like lectin 15	5.30928	5.47839	5.42684	6.39152	6.22749	6.08286	1.776601359	0.82912	1.776601359	Up	0.001321031	0.955609729
65268	WNK2	WNK lysine deficient protein kinase 2	6.47908	7.40952	6.98506	7.58772	7.65476	7.55789	1.560746972	0.642236667	1.560746972	Up	0.040389934	0.955609729
51715	RAB23	RAB23, member RAS oncogene family	6.09658	5.36572	5.59266	4.89661	4.96242	4.92441	-1.690175824	-0.757173333	1.690175824	Down	0.009456278	0.955609729
7429	VIL1	Villin 1	5.64118	6.43558	6.86837	7.42078	7.17696	6.95448	1.826434479	0.86903	1.826434479	Up	0.034886375	0.955609729
283420	CLEC9A	C-type lectin domain	3.78697	3.72959	3.48126	4.5633	4.10856	4.51958	1.660026954	0.731206667	1.660026954	Up	0.003290467	0.955609729

		family 9, member A												
91862	MARV ELD3	MARVEL domain containing 3	6.047 48	7.066 24	6.610 87	7.933 1	7.364 23	7.084 29	1.8476310 12	0.885676 667	1.847631 012	Up	0.033194 506	0.955609 729
90634	N4BP2 L1	NEDD4 binding protein 2-like 1	4.537 63	4.498 16	4.202 77	3.626 96	3.893 94	3.836 09	-1.5445536 67	-0.62719	1.544553 667	Down	0.003385 286	0.955609 729
2042	EPHA3	EPH receptor A3	7.517 83	6.258 4	5.784 12	3.715 65	5.544 08	5.142 61	-3.2928497 09	-1.71933 6667	3.292849 709	Down	0.025744 169	0.955609 729
256714	MAP7 D2	MAP7 domain containing 2	3.618 8	4.350 22	4.093 44	4.960 26	5.619 34	4.261 86	1.9004398 1	0.926333 333	1.900439 81	Up	0.039067 128	0.955609 729
9987	HNRN PDL	Heterogeneo us nuclear ribonucleopr otein D like	8.360 81	7.684 81	7.833 15	7.295 18	6.539 32	7.441 72	-1.8245196 22	-0.86751 6667	1.824519 622	Down	0.025742 011	0.955609 729
55041	PLEK HB2	Pleckstrin homology domain containing B2	5.434 72	6.491 24	6.748 91	7.585 45	7.205 65	7.456 08	2.2827454 61	1.19077	2.282745 461	Up	0.012703 987	0.955609 729
387628	KGFLP 1	Fibroblast growth factor 7 pseudogene	7.501 29	6.879 49	6.730 08	6.461 41	6.494 25	5.843 14	-1.7060816 19	-0.77068 6667	1.706081 619	Down	0.031197 641	0.955609 729
3400	ID4	Inhibitor of DNA binding 4, dominant	8.807 58	5.528 84	5.671 61	4.646 58	5.053 73	4.107 74	-4.1891571 33	-2.06666	4.189157 133	Down	0.049912 802	0.955609 729

		negative helix-loop-helix protein												
3122	HLA-DRA	Major histocompatibility complex, class II, DR $\alpha$	8.63461	8.6741	8.66085	7.22608	8.02513	8.17977	-1.797751151	-0.846193333	1.797751151	Down	0.017216186	0.955609729
2161	F12	Coagulation factor XII (Hageman factor)	6.59693	7.37518	6.98281	8.06115	7.64434	7.57151	1.710035964	0.774026667	1.710035964	Up	0.019707828	0.955609729
901	CCNG2	Cyclin G2	5.936	5.11646	5.45727	4.68819	4.48633	5.26278	-1.61418955	-0.69081	1.61418955	Down	0.04776699	0.955609729
55784	MCTP2	Multiple C2 domains, transmembrane 2	5.76443	7.31804	6.90942	7.97569	7.53406	7.65329	2.080672642	1.05705	2.080672642	Up	0.034838884	0.955609729
7102	TSPAN7	Tetraspanin 7	6.11751	4.86213	4.7495	3.94264	4.14826	4.55768	-2.03757524	-1.026853333	2.03757524	Down	0.033268171	0.955609729
79413	ZBED2	Zinc finger, BED-type containing 2	4.32272	4.96886	4.70157	5.40985	5.41216	5.36419	1.659808346	0.731016667	1.659808346	Up	0.006738927	0.955609729
90865	IL33	Interleukin 33	5.85407	3.90977	4.15754	2.72944	3.24722	3.74665	-2.637839282	-1.399356667	2.637839282	Down	0.035561786	0.955609729
55450	CAMK2N1	Calcium/calmodulin-dependent protein kinase II	9.83153	10.83764	10.23282	11.18096	10.82031	11.10972	1.66593641	0.736333333	1.66593641	Up	0.03257193	0.955609729



55450	CAMK2N1	Calcium/calmodulin-dependent protein kinase II inhibitor 1	9.83153	10.83764	10.23282	11.18096	10.82031	11.10972	1.66593641	0.736333333	1.66593641	Up	0.03257193	0.955609729
1018	CDK3	Cyclin-dependent kinase 3	6.63976	6.40313	6.80187	7.40334	7.13034	7.3433	1.599262397	0.677406667	1.599262397	Up	0.007672476	0.955609729
23022	PALLD	Palladin, cytoskeletal associated protein	10.36386	9.16236	9.0045	7.52131	9.16487	8.11978	-2.364584448	-1.241586667	2.364584448	Down	0.049168125	0.955609729
79774	GRTP1	Growth hormone regulated TBC protein 1	5.15916	6.75515	6.20185	6.96595	7.03063	7.5069	2.187232624	1.129106667	2.187232624	Up	0.029869274	0.955609729
831	CAST	Calpastatin	9.67553	9.10686	8.94728	8.69017	8.00877	8.82276	-1.665539997	-0.73599	1.665539997	Down	0.042477257	0.955609729
8611	PLPP1	Phospholipid phosphatase 1	9.51019	8.80525	8.10187	7.65097	7.95667	7.79307	-2.007685558	-1.005533333	2.007685558	Down	0.025541685	0.955609729
10232	MSLN	Mesothelin	9.47593	6.9558	7.19685	10.13834	10.0208	8.98636	3.577553479	1.838973333	3.577553479	Up	0.034944882	0.955609729
24146	CLDN15	Claudin 15	5.57032	5.36361	5.58241	7.51988	5.86847	6.27714	2.070123253	1.049716667	2.070123253	Up	0.039747936	0.955609729
960	CD44	CD44 molecule (Indian blood group)	5.90322	5.76373	6.29182	5.50703	5.08705	5.38059	-1.581580147	-0.661366667	1.581580147	Down	0.015412803	0.955609729

58191	CXCL16	Chemokine (C-X-C motif) ligand 16	8.5307	8.92471	8.51165	9.40414	9.35496	9.16623	1.572169391	0.652756667	1.572169391	Up	0.009609179	0.955609729
10979	FERMT2	Fermitin family member 2	7.08202	5.54418	5.80108	4.84471	5.00181	5.3101	-2.129065006	-1.09022	2.129065006	Down	0.032458353	0.955609729
154007	SNRN P48	Small nuclear ribonucleoprotein, U11/U12 48kda subunit	4.50275	4.72342	5.24548	5.69659	5.07438	5.57799	1.543034159	0.62577	1.543034159	Up	0.046651672	0.955609729
57509	MTUS1	Microtubule associated tumor suppressor 1	6.81485	7.5859	7.64793	8.42746	7.94742	8.14757	1.771031657	0.82459	1.771031657	Up	0.020633161	0.955609729
80150	ASRGL1	Asparaginase like 1	9.17727	9.19058	9.22682	10.60856	10.3277	9.97986	2.154196717	1.10715	2.154196717	Up	0.000883755	0.955609729
4311	MME	Membrane metallo-endopeptidase	8.59514	9.22906	8.52204	10.55378	9.6229	10.24121	2.561904445	1.357216667	2.561904445	Up	0.003374993	0.955609729
3988	LIPA	Lipase A, lysosomal acid, cholesterol esterase	7.01883	6.89773	7.20705	6.42277	5.78027	6.04418	-1.943688013	-0.958796667	1.943688013	Down	0.003194425	0.955609729
51733	UPB1	Ureidopropionase, $\beta$	4.54121	4.39138	4.94531	5.52047	5.18343	5.70352	1.793991846	0.843173333	1.793991846	Up	0.005872869	0.955609729
9371	KIF3B	Kinesin	7.623	8.201	8.205	8.917	8.470	8.640	1.5867446	0.66607	1.586744	Up	0.023786	0.955609

9371	KIF3B	Kinesin family member 3B	7.623 37	8.201 39	8.205 43	8.917 22	8.470 72	8.640 46	1.5867446 74	0.66607	1.586744 674	Up	0.023786 834	0.955609 729
8728	ADAM19	ADAM metalloproteinase domain 19	6.429 27	5.627 76	6.392	4.408 41	6.053 29	4.651 51	-2.1613609 14	-1.11194	2.161360 914	Down	0.049548 801	0.955609 729
84188	FAR1	Fatty acyl coa reductase 1	6.691 18	5.924 54	5.986 78	5.401 72	5.558 66	5.346 48	-1.6996213 05	-0.76521 3333	1.699621 305	Down	0.015904 096	0.955609 729
115361	GBP4	Guanylate binding protein 4	6.777 56	5.395 78	5.714 63	4.865 99	4.796 68	5.367 57	-1.9353260 83	-0.95257 6667	1.935326 083	Down	0.040318 578	0.955609 729
100534 612	C1QTNF3-A MACR MACR	C1QTNF3-A MACR readthrough (NMD candidate)	7.961 53	9.408 53	8.903 88	9.617 34	9.639 86	9.589 88	1.8121637 6	0.857713 333	1.812163 76	Up	0.048433 898	0.955609 729
9153	SLC28A2	Solute carrier family 28 (concentrative nucleoside transporter), member 2	5.457 74	5.839 87	7.906 53	9.638 86	9.223 74	9.326 84	7.9728747 21	2.9951	7.972874 721	Up	0.002038 587	0.955609 729
79745	CLIP4	CAP-Gly domain containing linker protein family	8.937 96	7.745 64	8.126 06	6.705 82	7.641 67	7.406 04	-2.0261064 86	-1.01871	2.026106 486	Down	0.031683 245	0.955609 729

9200	HACD1	3-hydroxyacyl-coa dehydratase 1	6.34814	5.87887	4.89686	3.62604	4.94907	4.29919	-2.669414486	-1.416523333	2.669414486	Down	0.018851811	0.955609729
9991	PTBP3	Polypyrimidine tract binding protein 3	4.56037	4.62599	5.01886	5.62979	5.37559	4.96209	1.502553819	0.587416667	1.502553819	Up	0.034847798	0.955609729
783	CACNB2	Calcium channel, voltage-dependent, $\beta$ 2 subunit	5.6053	4.84878	4.53991	3.52934	4.53991	4.12344	-1.910256894	-0.933766667	1.910256894	Down	0.033874121	0.955609729
2069	EREG	Epiregulin	4.22136	5.4679	6.33406	7.94664	5.9565	6.92028	3.031503175	1.600033333	3.031503175	Up	0.048716806	0.955609729
91614	DEPD C7	DEP domain containing 7	5.44738	6.5976	5.57358	6.68665	6.56373	6.89035	1.790947856	0.840723333	1.790947856	Up	0.036863027	0.955609729
83483	PLVAP	Plasmalemma vesicle associated protein	7.26471	6.56459	6.66133	5.3127	6.2259	5.97592	-1.988990888	-0.992036667	1.988990888	Down	0.014904685	0.955609729
10283	CWC27	CWC27 spliceosome-associated protein homolog	8.87771	8.6658	8.67641	9.8716	9.25135	9.12794	1.598800579	0.67699	1.598800579	Up	0.023353347	0.955609729
112483	SAT2	Spermidine/spermine N1-acetyltransferase family	9.77554	9.77563	9.4965	10.60044	10.46772	10.00371	1.596301686	0.674733333	1.596301686	Up	0.01447265	0.955609729

112483	SAT2	Spermidine/spermine N1-acetyltransferase family member 2	9.77554	9.77563	9.4965	10.60044	10.46772	10.00371	1.596301686	0.674733333	1.596301686	Up	0.01447265	0.955609729
5579	PRKC B	Protein kinase C, beta	4.52963	3.70943	4.6101	3.32303	3.75504	3.74051	-1.598656519	-0.67686	1.598656519	Down	0.039406601	0.955609729
54910	SEMA 4C	Sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4C	6.17627	5.7108	6.09631	5.00842	5.70249	5.34353	-1.561551337	-0.64298	1.561551337	Down	0.029360494	0.955609729
3669	ISG20	Interferon stimulated exonuclease gene 20kda	9.89465	10.9159	10.35688	11.42304	11.18711	11.32669	1.896233552	0.923136667	1.896233552	Up	0.011372522	0.955609729
54751	FBLIM 1	Filamin binding LIM protein 1	7.11302	7.71231	8.12969	9.03992	8.71773	8.37141	2.082062438	1.058013333	2.082062438	Up	0.011592833	0.955609729
54876	DCAF1 6	DDB1 and CUL4	4.94915	5.59187	5.77391	6.00597	6.02544	6.16352	1.543993487	0.626666667	1.543993487	Up	0.035675016	0.955609729

87	ACTN1	Actinin, $\alpha$ 1	6.30263	6.43514	7.00857	5.64454	6.18351	5.81875	-1.624332145	-0.699846667	1.624332145	Down	0.028020762	0.955609729
1515	CTSV	Cathepsin V	3.11098	3.70432	3.31236	3.70264	4.70021	4.29364	1.810360067	0.856276667	1.810360067	Up	0.018438263	0.955609729
10808	HSPH1	Heat shock protein family H (Hsp110) member 1	5.6348	6.3467	6.44808	7.15221	6.61315	7.03989	1.731341118	0.79189	1.731341118	Up	0.024717048	0.955609729
388561	ZNF761	Zinc finger protein 761	7.48324	7.59802	7.23701	9.35014	8.26379	9.61666	3.111132847	1.63744	3.111132847	Up	0.002949854	0.955609729
283375	SLC39A5	Solute carrier family 39 (zinc transporter), member 5	6.9773	8.50973	7.70754	9.18697	8.619	8.55574	2.078745778	1.055713333	2.078745778	Up	0.035433404	0.955609729
132014	IL17RE	Interleukin 17 receptor E	3.61724	4.25089	3.76501	4.57933	4.23799	4.6434	1.525406057	0.609193333	1.525406057	Up	0.02105628	0.955609729
9510	ADAMTS1	ADAM metalloproteinase with thrombospondin type 1 motif 1	7.95325	5.55287	5.53765	4.66797	4.97428	4.53493	-3.078434061	-1.622196667	3.078434061	Down	0.041174971	0.955609729
51776	ZAK	Sterile $\alpha$ motif and leucine zipper containing	5.1138	5.03814	4.4627	5.46296	5.55817	5.54173	1.568522981	0.649406667	1.568522981	Up	0.01615754	0.955609729

		kinase AZK												
1075	CTSC	Cathepsin C	8.109 42	7.948 94	8.067 15	7.459 45	7.261 44	7.427 72	-1.5789512 91	-0.65896 6667	1.578951 291	Down	0.004113 548	0.955609 729
10107	TRIM1 0	Tripartite motif containing 10	4.512 76	5.801 95	5.462 39	6.107 07	6.279 85	5.841 16	1.7617306 07	0.816993 333	1.761730 607	Up	0.049699 8	0.955609 729
6999	TDO2	Tryptophan 2,3-dioxygen ase	4.170 86	4.757 85	4.765 42	5.585 57	4.867 51	5.983 45	1.8844366 99	0.914133 333	1.884436 699	Up	0.025320 086	0.955609 729
51110	LACT B2	Lactamase $\beta$ 2	7.102 02	8.056 39	7.850 14	8.415 64	8.259 06	8.284 41	1.5693712 4	0.650186 667	1.569371 24	Up	0.047271 719	0.955609 729
9189	ZBED1	Zinc finger, BED-type containing 1	7.255 4	7.920 9	7.954 21	8.648 06	8.251 22	8.168 03	1.5643897 62	0.6456	1.564389 762	Up	0.039701 84	0.955609 729
6319	SCD	Stearoyl-coa desaturase ( $\Delta$ -9-desatur ase)	5.387 35	4.412 05	5.370 92	4.230 87	4.441 83	4.220 38	-1.6924110 38	-0.75908	1.692411 038	Down	0.031149 526	0.955609 729
9737	GPRA SP1	G protein-cou pled receptor associated sorting protein 1	7.279 09	6.871 27	7.000 41	6.413 41	6.773 86	6.149 4	-1.5206625 07	-0.6047	1.520662 507	Down	0.029974 192	0.955609 729
2021	ENDO G	Endonucleas e G	7.351 29	7.120 32	7.422 89	8.463 01	8.085 56	7.925 18	1.8147238 16	0.85975	1.814723 816	Up	0.004077 129	0.955609 729
79083	MLPH	Melanophili n	4.424 84	5.286 47	5.110 43	5.814 14	5.457 69	5.622 09	1.6140963 13	0.690726 667	1.614096 313	Up	0.030413 566	0.955609 729
7424	VEGF C	Vascular endothelial	8.443 95	6.331 63	6.683 81	4.407 04	6.289 82	5.601 59	-3.2950796 37	-1.72031 3333	3.295079 637	Down	0.039863 59	0.955609 729

		growth factor C												
1282	COL4A1	Collagen, type IV, alpha 1	9.21658	7.45046	6.8631	4.48193	7.22899	5.43663	-4.369687171	-2.12753	4.369687171	Down	0.040896127	0.955609729
1579	CYP4A11	Cytochrome P450, family 4, subfamily A, polypeptide 11	5.45954	5.58935	5.11509	5.71262	6.00958	6.20921	1.504353203	0.589143333	1.504353203	Up	0.025398123	0.955609729
3672	ITGA1	Integrin $\alpha$ 1	5.072	4.20139	4.13246	3.43023	4.07249	3.65824	-1.679808376	-0.748296667	1.679808376	Down	0.038929191	0.955609729
339044	PKD1P1	Polycystic kidney disease 1 (autosomal dominant) pseudogene 1	6.70725	7.99302	7.37651	8.22062	8.13039	8.1216	1.739424428	0.79861	1.739424428	Up	0.043520998	0.955609729
6549	SLC9A2	Solute carrier family 9, subfamily A (NHE2, cation proton antiporter 2), member 2	5.58032	6.68358	6.0664	8.88287	7.9624	8.49842	5.05529985	2.337796667	5.05529985	Up	0.000359415	0.955609729
1317	SLC31A1	Solute carrier family 31	5.49621	5.97224	6.59787	6.83115	6.67585	6.71292	1.644748123	0.717866667	1.644748123	Up	0.042163337	0.955609729



1317	SLC31 A1	Solute carrier family 31 (copper transporter), member 1	5.496 21	5.972 24	6.597 87	6.831 15	6.675 85	6.712 92	1.6447481 23	0.717866 667	1.644748 123	Up	0.042163 337	0.955609 729
6876	TAGLN	Transgelin	11.46 194	11.54 252	10.94 393	7.748 05	11.35 478	8.658 98	-4.1762073 19	-2.06219 3333	4.176207 319	Down	0.049402 704	0.955609 729
5350	PLN	Phospholamban	8.677 77	8.748 01	7.737 61	4.560 24	8.083 21	5.559 56	-4.9937606 22	-2.32012 6667	4.993760 622	Down	0.032346 597	0.955609 729
4162	MCAM	Melanoma cell adhesion molecule	7.409 52	5.917 22	5.897 12	4.601 73	5.759 46	5.107 85	-2.3810644 42	-1.25160 6667	2.381064 442	Down	0.038087 963	0.955609 729
10157	AASS	Aminoaldehyde synthase	7.864 31	8.590 14	7.568 87	9.070 61	9.126 61	8.293 21	1.7683085 12	0.82237	1.768308 512	Up	0.049677 955	0.955609 729
54899	PXK	PX domain containing serine/threonine kinase	5.532 47	4.776 92	5.129 03	4.450 72	4.376 32	4.764 75	-1.5321349 06	-0.61554 3333	1.532134 906	Down	0.030277 4	0.955609 729
4857	NOVA1	Neuro-oncological ventral antigen 1	7.503 35	7.123 38	7.492 87	7.165 63	6.577 78	5.943 9	-1.7541393 16	-0.81076 3333	1.754139 316	Down	0.041834 676	0.955609 729
2823	GPM6A	Glycoprotein M6A	6.584 22	6.421 13	5.772 64	2.876 81	5.680 28	3.985 32	-4.2237565 03	-2.07852 6667	4.223756 503	Down	0.018467 772	0.955609 729
51386	EIF3L	Eukaryotic translation initiation factor 3 subunit L	9.195 61	8.753 92	8.783 06	8.272 37	7.867 69	8.629 28	-1.5739794 08	-0.65441 6667	1.573979 408	Down	0.034093 693	0.955609 729

8828	NRP2	Neuropilin 2	7.667 94	7.247 47	7.062 65	6.085 46	7.002 08	6.332 29	-1.8059317 02	-0.85274 3333	1.805931 702	Down	0.023039 001	0.955609 729
129807	NEU4	Neuraminidase 4 (sialidase)	7.283 99	7.686 02	7.402 39	7.938 84	8.144 85	8.228 49	1.5654672 57	0.646593 333	1.565467 257	Up	0.010037 926	0.955609 729
51752	ERAP1	Endoplasmic reticulum aminopeptidase 1	8.206 96	8.536 25	9.122 15	7.142 51	7.133 85	8.258 24	-2.1588355 25	-1.11025 3333	2.158835 525	Down	0.024150 95	0.955609 729
6925	TCF4	Transcription factor 4	6.410 23	6.001 01	5.857 24	4.587 08	5.421 12	5.702 93	-1.8055645 52	-0.85245	1.805564 552	Down	0.033096 312	0.955609 729
7364	UGT2 B7	UDP glucuronosyl transferase 2 family, polypeptide B7	7.139 53	7.374 11	7.885 89	9.209 44	10.18 83	7.714 92	2.9711950 84	1.571043 333	2.971195 084	Up	0.035730 027	0.955609 729
196743	PAOX	Polyamine oxidase (exo-N4-amino)	6.805 67	7.071 09	6.544 44	7.732 37	7.798 3	7.224 93	1.7149105 57	0.778133 333	1.714910 557	Up	0.013039 365	0.955609 729
23158	TBC1D9	TBC1 domain family member 9	5.792 5	5.705 46	5.909 24	5.306 12	5.040 18	5.095 29	-1.5748378 95	-0.65520 3333	1.574837 895	Down	0.003847 688	0.955609 729
3685	ITGAV	Integrin $\alpha$ V	5.371 91	5.709 33	6.051 36	5.117 45	3.605 32	5.036 44	-2.1802043 02	-1.12446 3333	2.180204 302	Down	0.035352 522	0.955609 729
112616	CMTM7	CKLF-like MARVEL transmembrane domain	7.775 98	7.921 77	8.248 32	8.618 4	8.567 06	8.598 67	1.5291041 42	0.612686 667	1.529104 142	Up	0.011568 619	0.955609 729

		containing 7												
91624	NEXN	Nexilin (F actin binding protein)	6.88083	5.36262	4.59067	2.88557	4.48491	3.22068	-4.230964752	-2.080986667	4.230964752	Down	0.016231828	0.955609729
653190	ABCC6P1	ATP binding cassette subfamily C member 6 pseudogene 1 (functional)	4.35516	5.21993	4.47124	5.41079	5.63747	5.14654	1.642799788	0.716156667	1.642799788	Up	0.032292529	0.955609729
64240	ABCG5	ATP binding cassette subfamily G member 5	6.73366	7.82054	6.89366	8.77716	8.00535	8.71229	2.547319637	1.34898	2.547319637	Up	0.007255036	0.955609729
262	AMD1	Adenosylmethionine decarboxylase 1	9.34269	9.94217	10.35214	10.92224	10.74427	10.23574	1.687729076	0.755083333	1.687729076	Up	0.044921994	0.955609729
65997	RASL11B	RAS-like, family 11, member B	4.04259	4.64854	3.8462	3.41515	3.73771	3.32493	-1.609389286	-0.686513333	1.609389286	Down	0.021151406	0.955609729
5209	PFKFB3	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 3	5.1711	4.40925	5.09269	4.43444	3.87235	3.68129	-1.859592699	-0.894986667	1.859592699	Down	0.015450602	0.955609729
10352	WARS2	Tryptophanyl tRNA synthetase 2, mitochondria	7.16869	6.74533	7.00684	6.43564	6.30023	6.1404	-1.60383975	-0.68153	1.60383975	Down	0.008095487	0.955609729

		l												
5552	SRGN	Serglycin	9.958 74	7.291 54	8.480 66	6.636 61	7.023 93	7.130 84	-3.1307753 69	-1.64652	3.130775 369	Down	0.035079 479	0.955609 729
2006	ELN	Elastin	10.82 073	8.830 98	8.315 11	6.679 06	8.482 44	7.504 11	-3.4036200 59	-1.76707	3.403620 059	Down	0.047553 553	0.955609 729
350	APOH	Apolipoprotein H ( $\beta$ -2-glycoprotein I)	5.177 47	6.057 71	6.066 36	6.187 02	6.674 02	7.133 97	1.8632526 78	0.897823 333	1.863252 678	Up	0.035236 703	0.955609 729
145226	RDH12	Retinol dehydrogenase 12 (all-trans/9-cis/11-cis)	8.075 78	9.355 89	9.616 25	10.17 235	10.26 934	10.31 421	2.3554346 95	1.235993 333	2.355434 695	Up	0.017432 716	0.955609 729
957	ENTPD5	Ectonucleoside triphosphate diphosphohydrolase 5	5.599 22	6.725 75	6.285 99	6.751 2	7.476 57	6.882 58	1.7815463 28	0.83313	1.781546 328	Up	0.044764 204	0.955609 729
10018	BCL2L11	BCL2-like 11 (apoptosis facilitator)	5.694 97	5.799 12	5.351 76	4.889 94	4.598 31	5.338 35	-1.5944770 51	-0.67308 3333	1.594477 051	Down	0.024882 166	0.955609 729
3003	GZMK	Granzyme K	6.774 45	5.032 87	6.207 38	4.112 03	5.336 09	4.477 67	-2.5721414 8	-1.36297	2.572141 48	Down	0.031495 779	0.955609 729
7029	TFDP2	Transcription factor Dp-2 (E2F dimerization partner 2)	5.679 86	6.782 64	7.494 44	7.644 31	7.711 51	7.752 52	2.0711997 08	1.050466 667	2.071199 708	Up	0.047464 801	0.955609 729
347732	CATSPER3	Cation channel,	3.954 27	4.702 6	4.119 16	5.501 3	4.680 57	4.888 67	1.6991776 17	0.764836 667	1.699177 617	Up	0.031485 865	0.955609 729

		sperm associated 3												
6480	ST6GA L1	ST6 β-galactosam ide α-2,6-sialyltr anferase 1	7.286 7	6.004 08	6.803 6	5.385 28	5.322 71	6.256 06	-2.0611411 89	-1.04344 3333	2.061141 189	Down	0.035412 216	0.955609 729
202915	TMEM 184A	Transmembr ane protein 184A	5.369 82	7.082 59	6.408 87	7.126 29	7.321 25	7.392 67	1.9902872 54	0.992976 667	1.990287 254	Up	0.049854 804	0.955609 729
9724	UTP14 C	UTP14, U3 small nucleolar ribonucleopr otein, homolog C (yeast)	5.886 54	6.079 45	6.235 95	6.877 3	6.767 74	6.722 67	1.6493794 45	0.721923 333	1.649379 445	Up	0.003626 58	0.955609 729
27068	PPA2	Pyrophospha tase (inorganic) 2	6.632 36	7.397 5	6.791 15	7.797 52	7.409 64	7.728 61	1.6300542 73	0.70492	1.630054 273	Up	0.026131 86	0.955609 729
6840	SVIL	Supervillin	8.145 91	8.225 98	8.009 22	6.796 98	7.956 2	7.403 75	-1.6717896 49	-0.74139 3333	1.671789 649	Down	0.044068 979	0.955609 729
51176	LEF1	Lymphoid enhancer-bin ding factor 1	5.174 07	4.705 37	5.061 71	4.344 43	4.691 88	4.039 15	-1.5388969 92	-0.62189 6667	1.538896 992	Down	0.023920 379	0.955609 729
4756	NEO1	Neogenin 1	5.682 11	6.657 59	6.304 12	6.954 9	6.854 25	6.764 72	1.5619518 71	0.64335	1.561951 871	Up	0.047495 272	0.955609 729
284	ANGP T1	Angiopoietin 1	8.629 71	7.686 02	6.638 04	5.077 92	6.831 92	5.558 08	-3.5519632 79	-1.82861 6667	3.551963 279	Down	0.022375 555	0.955609 729
54739	XAF1	XIAP associated	7.314 44	7.537 7	7.432 91	7.675 47	7.904 19	8.494 91	1.5120508 59	0.596506 667	1.512050 859	Up	0.044470 032	0.955609 729

		factor 1												
10380	BPNT1	3'(2'), 5'-bisphosph ate nucleotidase 1	5.914 5	6.381 07	5.759 32	6.563 73	6.498 75	6.903 83	1.5552429 86	0.63714	1.555242 986	Up	0.026007 957	0.955609 729
284076	TTLL6	Tubulin tyrosine ligase like 6	5.274 99	6.366 36	5.982 93	6.458 3	6.503 06	7.082 94	1.7491734 23	0.806673 333	1.749173 423	Up	0.043226 583	0.955609 729
4735	SEPT2	Septin 2	7.216 53	6.972 6	7.411 49	6.843 36	6.246 85	6.752 35	-1.5010999 07	-0.58602	1.501099 907	Down	0.036525 152	0.955609 729
3782	KCNN 3	Potassium channel, calcium activated intermediate/ small conductance subfamily N $\alpha$ , member 3	6.581 42	5.509 89	5.976 08	4.857 61	5.449 41	4.942	-1.9178058 38	-0.93945 6667	1.917805 838	Down	0.019897 576	0.955609 729
57616	TSHZ3	Teashirt zinc finger homeobox 3	6.469 59	5.227 68	5.205 66	3.927 87	5.251 13	4.173 81	-2.2710718 25	-1.18337 3333	2.271071 825	Down	0.040537 927	0.955609 729
116255	MOGA T1	Monoacylgly cerol O-acyltransf erase 1	8.379 18	9.892 35	9.919 38	10.73 41	10.74 022	10.01 279	2.1416657 46	1.098733 333	2.141665 746	Up	0.048421 805	0.955609 729
1559	CYP2C 9	Cytochrome P450, family 2, subfamily C,	8.042 65	9.610 26	8.816 35	9.775 85	9.896 29	10.01 496	2.1032397 79	1.072613 333	2.103239 779	Up	0.026871 426	0.955609 729

		polypeptide 9												
10203	CALC RL	Calcitonin receptor like receptor	7.059 11	5.709 47	5.394 12	4.763 59	5.125 23	5.120 57	-2.0721139 37	-1.05110 3333	2.072113 937	Down	0.044805 23	0.955609 729
1644	DDC	Dopa decarboxylas e	4.354 98	4.535 79	4.879 36	5.793 01	4.945 98	5.737 36	1.8687496 81	0.902073 333	1.868749 681	Up	0.013573 457	0.955609 729
9556	C14orf 2	Chromosom e 14 open reading frame 2	4.115 64	4.984 28	5.126 47	5.711 76	5.195 14	5.620 09	1.7015701 93	0.766866 667	1.701570 193	Up	0.039321 299	0.955609 729
84329	HVCN 1	Hydrogen voltage gated channel 1	5.225 07	4.469 36	4.826 14	3.715 45	4.489 75	4.124 4	-1.6590108 63	-0.73032 3333	1.659010 863	Down	0.029308 1	0.955609 729
725	C4BPB	Complement component 4 binding protein, $\beta$	5.726 39	6.696 45	6.906 32	7.055 74	7.838 88	7.737 08	2.1448052 66	1.100846 667	2.144805 266	Up	0.021389 705	0.955609 729
115908	CTHR C1	Collagen triple helix repeat containing 1	7.406 57	5.618 14	7.100 81	4.650 32	4.953 96	4.861 73	-3.6973800 22	-1.88650 3333	3.697380 022	Down	0.004704 022	0.955609 729
573	BAG1	BCL2 associated athanogene 1	5.584 28	6.585 49	5.770 47	6.723 81	6.517 01	6.787 36	1.6199844 89	0.69598	1.619984 489	Up	0.045294 551	0.955609 729
5578	PRKC A	Protein kinase C, $\alpha$	5.543 63	6.398 28	6.445 84	7.152 59	6.740 41	6.775 66	1.6938467 26	0.760303 333	1.693846 726	Up	0.034000 155	0.955609 729
990	CDC6	Cell division cycle 6	6.332 45	7.227	7.237 96	8.246 2	8.449 17	8.501 49	2.7634745 64	1.466483 333	2.763474 564	Up	0.001361 724	0.955609 729
161882	ZFPM1	Zinc finger	8.052	9.106	8.160	9.392	9.105	9.164	1.7182619	0.78095	1.718261	Up	0.037553	0.955609

161882	ZFPM1	Zinc finger protein, FOG family member 1	8.05271	9.10699	8.16013	9.39258	9.10589	9.16421	1.718261958	0.78095	1.718261958	Up	0.037553936	0.955609729
1488	CTBP2	C-terminal binding protein 2	6.89802	7.09022	6.50434	7.81793	7.18758	7.26848	1.509220219	0.593803333	1.509220219	Up	0.049631995	0.955609729
100287175	LOC10287175	Uncharacterized LOC100287175	8.24491	8.98658	8.68898	9.7783	9.52784	8.8677	1.683102844	0.751123333	1.683102844	Up	0.043229413	0.955609729
80760	ITIH5	Inter- $\alpha$ -trypsin inhibitor heavy chain family member 5	9.0474	6.88689	6.54181	5.20002	6.6976	5.30661	-3.380625018	-1.75729	3.380625018	Down	0.047805103	0.955609729
10590	SCGN	Secretagoin, EF-hand calcium binding protein	4.06846	4.16228	4.48417	5.0137	4.74294	5.19845	1.677981333	0.746726667	1.677981333	Up	0.004656412	0.955609729
8490	RGS5	Regulator of G-protein signaling 5	7.96301	6.80106	6.76204	4.84386	5.67493	6.02431	-3.162363773	-1.661003333	3.162363773	Down	0.006881811	0.955609729
4240	MFGE8	Milk fat globule-EGF factor 8 protein	5.08738	4.57699	4.55979	4.11166	3.82555	4.24894	-1.60140328	-0.679336667	1.60140328	Down	0.011127494	0.955609729
2316	FLNA	Filamin A, $\alpha$	9.10428	9.20616	8.7028	5.78567	8.62803	6.5583	-4.038296014	-2.013746667	4.038296014	Down	0.022542987	0.955609729
23366	KIAA0	KIAA0895	2.976	3.984	3.234	4.624	3.870	4.033	1.7137895	0.77719	1.713789	Up	0.040553	0.955609



6383	SDC2	Syndecan 2	8.989 86	6.578 57	5.745 86	4.765 99	5.326 76	5.557 38	-3.7013545 41	-1.88805 3333	3.701354 541	Down	0.049177 074	0.955609 729
10398	MYL9	Myosin light chain 9	10.26 508	10.23 723	9.957 27	7.263 58	9.935 54	7.977 26	-3.3894863 64	-1.76106 6667	3.389486 364	Down	0.029383 295	0.955609 729
79152	FA2H	Fatty acid 2-hydroxylase	6.845 2	8.252 21	8.091 95	9.399 31	8.528 62	8.538 57	2.1322550 25	1.09238	2.132255 025	Up	0.041475 934	0.955609 729
94101	ORMDL1	ORMDL sphingolipid biosynthesis regulator 1	5.360 48	5.747 94	5.853 61	6.664 88	6.459 87	6.601 3	1.8938735 39	0.92134	1.893873 539	Up	0.001928 817	0.955609 729
137075	CLDN23	Claudin 23	6.124 74	7.130 16	7.137 14	8.662 26	7.304 12	8.068 88	2.3204533 06	1.214406 667	2.320453 306	Up	0.025680 041	0.955609 729
23436	CELA3B	Chymotrypsin like elastase family member 3B	3.348 36	3.792 93	3.340 63	4.690 2	4.416 93	4.948 55	2.2835103 57	1.191253 333	2.283510 357	Up	0.000531 616	0.955609 729
11227	GALNT5	Polypeptide N-acetylgalactosaminyltransferase 5	4.485 87	5.154 88	5.151 43	6.877 29	5.753 31	6.038 15	2.4489952 91	1.29219	2.448995 291	Up	0.007263 646	0.955609 729
7414	VCL	Vinculin	5.389 71	5.131 07	5.204 79	4.484 68	5.003 62	4.286 66	-1.5693893 7	-0.65020 3333	1.569389 37	Down	0.019112 54	0.955609 729
2355	FOSL2	FOS-like antigen 2	8.020 58	7.394 48	7.787 04	7.197 63	6.722 95	7.244 37	-1.6010851 1	-0.67905	1.601085 11	Down	0.026047 627	0.955609 729
8805	TRIM24	Tripartite motif containing 24	6.138 27	6.260 68	6.066 4	7.078 91	6.712 24	6.918 03	1.6793970 21	0.747943 333	1.679397 021	Up	0.003447 696	0.955609 729
5270	SERPI	Serpin	6.488	6.056	5.978	4.932	5.851	5.691	-1.6049221	-0.68250	1.604922	Down	0.049757	0.955609

	NE2	peptidase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 2	01	9	88	97	37	94	67	3333	167		586	729
654	BMP6	Bone morphogenetic protein 6	4.57559	4.16257	5.29453	3.60655	4.09223	3.65174	-1.858394342	-0.894056667	1.858394342	Down	0.021633759	0.955609729
9232	PTTG1	Pituitary tumor-transforming 1	4.93315	5.63362	5.28491	4.54147	4.87043	4.62444	-1.521098241	-0.605113333	1.521098241	Down	0.025409802	0.955609729
57561	ARRDC3	Arrestin domain containing 3	7.59212	6.30397	7.38838	5.92911	4.93046	6.64694	-2.393828836	-1.25932	2.393828836	Down	0.045669144	0.955609729
4783	NFIL3	Nuclear factor, interleukin 3 regulated	8.31789	5.31043	6.29838	4.26452	5.27423	4.27174	-4.108855705	-2.038736667	4.108855705	Down	0.030342742	0.955609729
22841	RAB11FIP2	RAB11 family interacting protein 2 (class I)	4.17041	4.49963	4.09811	5.29208	4.93959	4.42513	1.547082358	0.62955	1.547082358	Up	0.037339999	0.955609729
4621	MYH3	Myosin, heavy chain 3, skeletal muscle,	4.04839	4.62444	4.36679	5.42821	5.04405	4.925	1.724143674	0.78588	1.724143674	Up	0.007549874	0.955609729

4621	MYH3	Myosin, heavy chain 3, skeletal muscle, embryonic	4.04839	4.62444	4.36679	5.42821	5.04405	4.925	1.724143674	0.78588	1.724143674	Up	0.007549874	0.955609729
348254	CCDC144CP	Coiled-coil domain containing 144C, pseudogene	4.88193	4.14682	4.17319	5.67876	5.30554	4.89543	1.856514607	0.892596667	1.856514607	Up	0.016528816	0.955609729
115207	KCTD12	Potassium channel tetramerization domain containing 12	8.07719	6.99328	7.31162	6.28256	6.57224	6.87845	-1.844138061	-0.882946667	1.844138061	Down	0.028133019	0.955609729
284047	CCDC144B	Coiled-coil domain containing 144B (pseudogene)	4.16657	3.23321	3.50829	4.60131	4.33706	4.13917	1.650790072	0.723156667	1.650790072	Up	0.026880281	0.955609729
55329	MNS1	Meiosis specific nuclear structural 1	5.06484	4.14015	4.12258	3.36732	3.52163	3.60905	-1.922775066	-0.94319	1.922775066	Down	0.009819628	0.955609729
5538	PPT1	Palmitoyl-protein thioesterase 1	6.42567	6.1348	6.31123	5.43899	5.10147	5.89363	-1.756296797	-0.812536667	1.756296797	Down	0.010999559	0.955609729
23328	SASH1	SAM and	5.968	4.616	4.665	3.939	4.215	4.360	-1.8810958	-0.91157	1.881095	Down	0.045943	0.955609

56474	CTPS2	CTP synthase 2	5.024 12	5.331 64	5.202 49	5.981 42	5.423 63	5.918 35	1.5035609 31	0.588383 333	1.503560 931	Up	0.023216 758	0.955609 729
161198	CLEC1 4A	C-type lectin domain family 14, member A	7.370 17	6.071 54	5.790 45	5.214 46	5.139 12	5.688 02	-2.0900247 11	-1.06352	2.090024 711	Down	0.041328 826	0.955609 729
5997	RGS2	Regulator of G-protein signaling 2	10.68 034	10.19 948	9.583 19	8.413 67	9.167 42	8.478 08	-2.7662789 93	-1.46794 6667	2.766278 993	Down	0.003739 484	0.955609 729
26049	FAM16 9A	Family with sequence similarity 169 member A	5.450 45	6.927 79	7.134 83	7.663 52	8.104 52	7.292 71	2.2697918 47	1.18256	2.269791 847	Up	0.041889 914	0.955609 729
401105	FLJ423 93	Uncharacterized LOC401105	6.452 16	6.781 84	7.629 48	5.524 47	4.929 6	5.204 46	-3.3287564 83	-1.73498 3333	3.328756 483	Down	0.001420 515	0.955609 729
1948	EFNB2	Ephrin-B2	8.301 94	6.383 87	6.229 1	5.352 29	5.504 72	5.685 89	-2.7460095 95	-1.45733 6667	2.746009 595	Down	0.032031 85	0.955609 729
347733	TUBB2 B	Tubulin, $\beta$ 2B class iib	7.898 44	7.853 6	8.260 59	6.287 2	7.482 87	6.369 53	-2.4469930 43	-1.29101	2.446993 043	Down	0.007928 414	0.955609 729
54492	NEUR L1B	Neuralized E3 ubiquitin protein ligase 1B	8.989 13	7.530 16	7.166 98	5.434 18	7.111 71	6.634 61	-2.8322003 66	-1.50192 3333	2.832200 366	Down	0.041369 091	0.955609 729
10418	SPON1	Spondin 1, extracellular matrix protein	6.048 35	6.353 36	6.130 05	5.047 7	5.993 17	4.977 23	-1.7874299 05	-0.83788 6667	1.787429 905	Down	0.026501 541	0.955609 729
1465	CSRP1	Cysteine and glycine rich	8.878 92	8.293 2	8.494 01	7.260 38	8.229 86	7.443 01	-1.8802962 71	-0.91096	1.880296 271	Down	0.020346 568	0.955609 729

		protein 1												
728239	MAGE D4	Melanoma antigen family D4	5.46145	6.50094	4.99384	6.90646	6.98994	6.87491	2.414447901	1.271693333	2.414447901	Up	0.012137053	0.955609729
3708	ITPR1	Inositol 1,4,5-trisphosphate receptor, type 1	8.49525	7.7138	7.84662	5.29905	7.45167	6.30042	-3.178126757	-1.668176667	3.178126757	Down	0.018029103	0.955609729
2113	ETS1	V-ets avian erythroblastosis virus E26 oncogene homolog 1	9.62691	8.02667	8.69066	6.98047	7.85948	7.96394	-2.265951004	-1.180116667	2.265951004	Down	0.037312378	0.955609729
121512	FGD4	FYVE, rhogef and PH domain containing 4	7.44034	7.59004	7.71744	8.64613	8.24619	7.7194	1.53826067	0.6213	1.53826067	Up	0.049178518	0.955609729
441386	RPS26 P3	Ribosomal protein S26 pseudogene 3	10.9709	11.15144	11.22933	12.06451	11.34135	12.07815	1.636688762	0.71078	1.636688762	Up	0.019504025	0.955609729
389384	C6orf22	Chromosome 6 open reading frame 222	4.85817	5.16779	5.34808	6.6518	6.51619	5.44909	2.115521479	1.081013333	2.115521479	Up	0.016828898	0.955609729
2526	FUT4	Fucosyltransferase 4	6.34215	7.28724	6.87802	8.78653	7.32882	7.76085	2.177888356	1.12293	2.177888356	Up	0.033490852	0.955609729
105377751	LOC10537751	Uncharacterized LOC105377	3.68869	4.0597	3.03113	3.96192	4.77083	4.72872	1.85829988	0.893983333	1.85829988	Up	0.029300486	0.955609729

		751												
642946	FLVC R1-AS 1	FLVCR1 antisense RNA 1 (head to head)	6.358 98	7.010 13	5.781 07	7.767 76	7.447 54	7.416 87	2.2356019 42	1.160663 333	2.235601 942	Up	0.009327 456	0.955609 729
10171	RCL1	RNA terminal phosphate cyclase-like 1	5.535 96	4.777 62	5.200 45	4.530 03	4.328 92	4.887 1	-1.5045443 84	-0.58932 6667	1.504544 384	Down	0.046548 285	0.955609 729
25816	TNFAI P8	TNF $\alpha$ induced protein 8	6.256 4	5.579 52	6.046 02	4.574 49	5.082 02	5.050 19	-2.0826397 88	-1.05841 3333	2.082639 788	Down	0.003368 254	0.955609 729
100507 412	LOC10 050741 2	Uncharacteri zed LOC100507 412	9.252 2	8.496 9	9.654 94	10.46 388	10.63 279	10.10 649	2.4055609 16	1.266373 333	2.405560 916	Up	0.005884 84	0.955609 729
9586	CREB5	Camp responsive element binding protein 5	7.276 57	7.220 45	6.411 18	8.240 18	7.423 58	7.702 57	1.7646433 93	0.819376 667	1.764643 393	Up	0.038413 364	0.955609 729
7010	TEK	TEK tyrosine kinase, endothelial	8.325 72	6.398 28	6.055 09	4.920 74	5.615 19	5.666 38	-2.8790509 76	-1.52559 3333	2.879050 976	Down	0.038670 045	0.955609 729
440138	ALG11	ALG11, $\alpha$ -1,2-manno syltransferas e	5.886 54	6.079 45	6.235 95	6.877 3	6.767 74	6.722 67	1.6493794 45	0.721923 333	1.649379 445	Up	0.003626 58	0.955609 729
84612	PARD6	Par-6 family	4.990	4.706	4.732	5.929	6.314	5.468	2.1351143	1.094313	2.135114	Up	0.002878	0.955609

	B	cell polarity regulator $\beta$	99	1	03	11	81	14	43	333	343		55	729
171220	DSTNP2	Destrin (actin depolymerizing factor) pseudogene 2	3.93291	4.46933	4.46515	5.14717	4.79643	4.73258	1.518797995	0.60293	1.518797995	Up	0.021699495	0.955609729
2992	GYG1	Glycogenin 1	6.13634	5.7694	6.08185	5.30251	4.86413	5.68494	-1.63807718	-0.712003333	1.63807718	Down	0.02330095	0.955609729
100505385	IQCJ-SCHIP1	IQCJ-SCHIP1 readthrough	7.69673	6.98229	6.88494	5.7575	6.03204	6.65385	-2.056498472	-1.04019	2.056498472	Down	0.014692544	0.955609729
1073	CFL2	Cofilin 2 (muscle)	6.69917	5.33674	5.20705	4.70932	4.7573	4.37108	-2.196317562	-1.135086667	2.196317562	Down	0.026625748	0.955609729
102723553	SMIM11B	Small integral membrane protein 11B	5.72511	5.87277	6.12979	7.16954	6.33185	6.63989	1.746584772	0.804536667	1.746584772	Up	0.016401594	0.955609729
84680	ACCS	1-aminocyclopropane-1-carboxylate synthase homolog (inactive)	7.19174	7.29992	6.71582	7.99614	7.37538	7.96462	1.635297741	0.709553333	1.635297741	Up	0.027607602	0.955609729
26118	WSB1	WD repeat and SOCS box containing 1	5.75815	6.36299	6.7877	5.46098	5.25211	5.82992	-1.727409346	-0.78861	1.727409346	Down	0.034828079	0.955609729
54097	FAM3B	Family with sequence	7.61672	8.98351	8.63249	9.47556	9.21536	9.13247	1.819518433	0.863556667	1.819518433	Up	0.047042436	0.955609729

		similarity 3 member B												
11217	AKAP 2	A-kinase anchoring protein 2	10.14 756	8.853 23	9.068 01	8.563 71	8.506 12	8.511 51	-1.7766424 08	-0.82915 3333	1.776642 408	Down	0.046346 954	0.955609 729
2004	ELK3	ELK3, ETS-domain protein (SRF accessory protein 2)	9.719 84	8.262 82	8.305 97	7.228 93	7.638 93	8.111 72	-2.1480337 58	-1.10301 6667	2.148033 758	Down	0.043123 29	0.955609 729
9811	CTIF	CBP80/20-d ependent translation initiation factor	6.615 64	6.547 42	6.518 71	5.560 16	6.159 97	5.354 31	-1.8265357 61	-0.86911	1.826535 761	Down	0.008157 235	0.955609 729
25932	CLIC4	Chloride intracellular channel 4	7.682 31	6.756 19	6.531 99	6.091	6.257 85	6.140 42	-1.7740827 86	-0.82707 3333	1.774082 786	Down	0.033276 327	0.955609 729
6578	SLCO2 A1	Solute carrier organic anion transporter family member 2A1	8.407 81	7.749 97	7.838 97	6.753 58	7.712 08	7.308 02	-1.6713609 49	-0.74102 3333	1.671360 949	Down	0.046069 645	0.955609 729
6335	SCN9A	Sodium channel, voltage gated, type IX $\alpha$ subunit	4.958 37	5.203 09	4.643 24	5.839 18	5.281 17	5.929 11	1.6797579 21	0.748253 333	1.679757 921	Up	0.017166 403	0.955609 729
84331	FAM19	Family with	8.244	8.986	8.688	9.778	9.527	8.867	1.6831028	0.751123	1.683102	Up	0.043229	0.955609



	5A	sequence similarity 195 member A	91	58	98	3	84	7	44	333	844		413	729
11211	FZD10	Frizzled class receptor 10	4.1975	4.07092	4.12099	3.11933	4.01621	3.21788	-1.600656049	-0.678663333	1.600656049	Down	0.026254315	0.955609729
340542	BEX5	Brain expressed X-linked 5	8.53096	9.98934	9.3434	10.72186	9.78885	10.40717	2.025193838	1.01806	2.025193838	Up	0.044299717	0.955609729
81608	FIP1L1	Factor interacting with PAPOLA and CPSF1	6.33585	7.01511	7.00022	7.80959	7.04951	7.62381	1.636458103	0.710576667	1.636458103	Up	0.043416119	0.955609729
11167	FSTL1	Follistatin like 1	7.29035	5.39675	5.1924	3.73048	4.47883	4.96855	-2.963317754	-1.567213333	2.963317754	Down	0.036329144	0.955609729
4638	MYLK	Myosin light chain kinase	9.64703	9.51765	8.71321	5.20081	8.62535	6.62087	-5.567205483	-2.476953333	5.567205483	Down	0.019856789	0.955609729
101929 876	LOC101929876	40S ribosomal protein S26	10.9709	11.15144	11.22933	12.06451	11.34135	12.07815	1.636688762	0.71078	1.636688762	Up	0.019504025	0.955609729
100533 181	FXYD6-FXYD2	FXYD6-FX YD2 readthrough	7.79421	6.94296	6.82305	4.41669	6.85592	5.85013	-2.787863644	-1.47916	2.787863644	Down	0.048251866	0.955609729
4628	MYH10	Myosin, heavy chain 10, non-muscle	5.69622	5.13881	4.91672	4.57208	4.53218	4.68122	-1.575078064	-0.655423333	1.575078064	Down	0.020709186	0.955609729
148523	CIART	Circadian associated	4.48865	5.19815	5.29833	7.51805	5.29409	7.12009	3.136234278	1.649033333	3.136234278	Up	0.026466979	0.955609729

		repressor of transcription												
5420	PODXL	Podocalyxin-like	8.37661	7.14614	7.11281	6.05223	6.39097	6.95173	-2.114343825	-1.08021	2.114343825	Down	0.033960081	0.955609729
4588	MUC6	Mucin 6, oligomeric mucus/gel-forming	7.34869	9.34381	9.77914	12.23407	10.87266	11.66247	6.801501794	2.765853333	6.801501794	Up	0.00480813	0.955609729
23197	FAF2	Fas associated factor family member 2	5.85259	6.2679	6.2759	6.84125	7.13068	6.40953	1.581934647	0.66169	1.581934647	Up	0.029831565	0.955609729
26051	PPP1R16B	Protein phosphatase 1 regulatory subunit 16B	7.35118	5.46882	6.18306	4.82963	5.02069	5.45435	-2.350221393	-1.232796667	2.350221393	Down	0.035076206	0.955609729
51701	NLK	Nemo-like kinase	7.39183	7.82219	7.30631	8.2158	8.02971	8.3544	1.616858396	0.693193333	1.616858396	Up	0.011692837	0.955609729
83539	CHST9	Carbohydrate (N-acetylglactosamine 4-O) sulfotransferase 9	4.5729	5.09961	5.03636	6.00828	5.2929	5.54602	1.638955481	0.712776667	1.638955481	Up	0.022768018	0.955609729
9391	CIAO1	Cytosolic iron-sulfur assembly component 1	5.57585	5.53502	6.62792	7.05135	6.49877	6.79912	1.827852936	0.87015	1.827852936	Up	0.036673909	0.955609729
105372824	LOC10537282	Uncharacterized protein	5.98118	6.7183	6.59846	7.39628	7.01425	6.83207	1.567233347	0.64822	1.567233347	Up	0.04339205	0.955609729

105372824	LOC105372824	Uncharacterized protein c21orf124	5.98118	6.7183	6.59846	7.39628	7.01425	6.83207	1.567233347	0.64822	1.567233347	Up	0.04339205	0.955609729
5051	PAFAH2	Platelet-activating factor acetylhydrolase 2	3.90226	5.09269	5.18461	5.91862	5.54425	5.72724	2.004881082	1.003516667	2.004881082	Up	0.026306401	0.955609729
400506	KNOP1	Lysine-rich nucleolar protein 1	6.91145	7.38662	7.19567	7.80597	8.24422	7.58578	1.640432995	0.714076667	1.640432995	Up	0.019138247	0.955609729
117854	TRIM6	Tripartite motif containing 6	5.97928	5.56221	5.28965	4.50131	5.14533	4.68342	-1.782242109	-0.833693333	1.782242109	Down	0.01295428	0.955609729
3248	HPGD	Hydroxyprostaglandin dehydrogenase 15-(NAD)	6.69485	7.7447	6.95254	7.95547	7.67204	7.93868	1.652556961	0.7247	1.652556961	Up	0.043505376	0.955609729
56907	SPIRE1	Spire-type actin nucleation factor 1	8.28223	7.70751	7.71749	6.984	7.50423	6.5806	-1.83969508	-0.879466667	1.83969508	Down	0.0204461	0.955609729
1809	DPYSL3	Dihydropyrimidinase like 3	6.13566	4.35379	4.56356	2.98759	4.18967	3.16103	-2.972286806	-1.571573333	2.972286806	Down	0.022580497	0.955609729
6231	RPS26	Ribosomal protein S26	10.9709	11.15144	11.22933	12.06451	11.34135	12.07815	1.636688762	0.71078	1.636688762	Up	0.019504025	0.955609729
5621	PRNP	Prion protein	7.66454	6.74428	7.11883	6.37644	5.84881	6.72967	-1.811992101	-0.857576667	1.811992101	Down	0.032813287	0.955609729
57462	KIAA1161	KIAA1161	5.15417	6.25507	5.76013	6.64589	6.36285	6.52543	1.726998305	0.788266667	1.726998305	Up	0.031116268	0.955609729
2273	FHL1	Four and a	10.92	7.463	7.110	4.539	6.276	6.094	-7.2813535	-2.86420	7.281353	Down	0.030200	0.955609

25825	BACE2	B-site APP-cleaving enzyme 2	7.43194	7.97497	7.81604	8.41369	8.62673	8.13321	1.569414752	0.650226667	1.569414752	Up	0.021819233	0.955609729
6591	SNAI2	Snail family zinc finger 2	7.09906	5.70062	5.65306	4.6673	5.04155	4.9466	-2.404544012	-1.265763333	2.404544012	Down	0.016712888	0.955609729
977	CD151	CD151 molecule (Raph blood group)	9.31631	9.03382	9.26503	8.57549	8.81207	8.14376	-1.618450603	-0.694613333	1.618450603	Down	0.01573791	0.955609729
101928168	LOC101928168	Uncharacterized LOC101928168	6.36212	6.49398	6.0664	7.48578	6.96308	7.84714	2.180259714	1.1245	2.180259714	Up	0.004104425	0.955609729
79056	PRRG4	Proline rich Gla (G-carboxyglutamic acid) 4 (transmembrane)	3.66165	3.92639	4.32475	4.82986	4.34133	4.74488	1.588604505	0.66776	1.588604505	Up	0.018277738	0.955609729
3115	HLA-DPB1	Major histocompatibility complex, class II, DPβ1	3.12138	2.71964	7.61231	8.27509	8.87426	7.84585	14.39294587	3.84729	14.39294587	Up	0.018542717	0.955609729
10165	SLC25A13	Solute carrier family 25 (aspartate/glutamate)	8.12546	7.89533	8.24473	8.98872	8.43533	8.63098	1.512047366	0.596503333	1.512047366	Up	0.023557621	0.955609729

10165	SLC25A13	Solute carrier family 25 (aspartate/glutamate carrier), member 13	8.12546	7.89533	8.24473	8.98872	8.43533	8.63098	1.512047366	0.596503333	1.512047366	Up	0.023557621	0.955609729
252983	STXBP4	Syntaxin binding protein 4	6.22717	6.95669	6.31353	6.88362	7.21679	7.38519	1.583082747	0.662736667	1.583082747	Up	0.036877147	0.955609729
9270	ITGB1BP1	Integrin $\beta$ 1 binding protein 1	11.23483	8.05543	6.61593	5.12057	6.02084	5.43891	-8.625591143	-3.108623333	8.625591143	Down	0.025422981	0.955609729
3822	KLRC2	Killer cell lectin-like receptor subfamily C, member 2	4.24177	3.67414	3.58905	4.83	5.45603	5.83127	2.902803001	1.537446667	2.902803001	Up	0.00149172	0.955609729
2331	FMOD	Fibromodulin	5.57379	4.78525	4.71535	3.88759	4.68611	4.08008	-1.749411885	-0.80687	1.749411885	Down	0.034060964	0.955609729
57493	HEG1	Heart development protein with EGF-like domains 1	9.3175	7.81526	7.72124	6.16524	7.52946	7.06722	-2.574026072	-1.364026667	2.574026072	Down	0.037238224	0.955609729
9342	SNAP29	Synaptosome associated protein 29kda	6.28587	6.21159	5.85019	6.83255	6.52122	6.82225	1.525684513	0.609456667	1.525684513	Up	0.01665029	0.955609729
55283	MCOLN3	Mucolipin 3	4.61899	5.97408	3.97674	6.57902	6.461	5.66197	2.597985418	1.377393333	2.597985418	Up	0.035436453	0.955609729

3778	KCNM A1	Potassium channel, calcium activated large conductance subfamily M $\alpha$ , member 1	6.119 55	6.562 8	5.872 72	3.663 07	5.276 97	3.946 03	-3.7054959 97	-1.88966 6667	3.705495 997	Down	0.003734 481	0.955609 729
653316	FAM15 3C	Family with sequence similarity 153, member C	3.688 69	4.059 7	3.031 13	3.961 92	4.770 83	4.728 72	1.8582998 8	0.893983 333	1.858299 88	Up	0.029300 486	0.955609 729
3696	ITGB8	Integrin $\beta$ 8	3.820 93	3.812 51	4.125 57	4.895 26	4.728 22	4.100 52	1.5746123 15	0.654996 667	1.574612 315	Up	0.024707 157	0.955609 729
570	BAAT	Bile acid-coa:ami no acid N-acyltransf erase	8.705 81	9.863 69	9.748 27	10.65 616	10.54 473	10.35 422	2.1127372 14	1.079113 333	2.112737 214	Up	0.013074 663	0.955609 729
8777	MPDZ	Multiple PDZ domain protein	7.971 98	6.055 21	5.863 01	3.993 36	5.593 38	4.895 03	-3.4889913	-1.80281	3.488991 3	Down	0.028293 754	0.955609 729
94122	SYTL5	Synaptotagm in like 5	4.078 12	4.858 24	4.173 43	5.841 65	5.413 84	4.959 24	2.0490852 4	1.03498	2.049085 24	Up	0.011153 461	0.955609 729
64902	AGXT 2	Alanine--gly oxylate aminotransfe rase 2	4.234 19	4.466 89	4.610 3	5.338 59	5.141 14	4.873 61	1.6028654 58	0.680653 333	1.602865 458	Up	0.006828 333	0.955609 729
8794	TNFRS F10C	Tumor necrosis	4.808 54	5.735 06	5.043 25	5.945 03	5.845 01	5.712 25	1.5566881 94	0.63848	1.556688 194	Up	0.043638 733	0.955609 729

		factor receptor superfamily member 10c, decoy without an intracellular domain												
28982	FLVCR1	Feline leukemia virus subgroup C cellular receptor 1	3.47982	4.49406	4.98428	5.57931	5.02473	5.17566	1.919211002	0.940513333	1.919211002	Up	0.045600788	0.955609729
29965	CDIP1	Cell death-inducing p53 target 1	7.56032	7.43516	7.45747	8.31783	8.41856	7.58096	1.538438387	0.621466667	1.538438387	Up	0.043772773	0.955609729
64710	NUCKS1	Nuclear casein kinase and cyclin-dependent kinase substrate 1	8.06077	7.95106	8.16921	7.64151	6.48254	7.63794	-1.748781446	-0.80635	1.748781446	Down	0.048238731	0.955609729
643752	RAP1BL	RAP1B, member of RAS oncogene family pseudogene	5.51884	4.59482	4.58076	4.40312	3.56146	4.28574	-1.758932354	-0.8147	1.758932354	Down	0.045776334	0.955609729
11126	CD160	CD160	3.897	3.685	4.441	4.964	4.469	5.034	1.7586153	0.81444	1.758615	Up	0.013774	0.955609

		molecule	43	23	82	35	11	34	91		391		421	729
6863	TAC1	Tachykinin precursor 1	7.923 99	7.912 41	8.434 53	7.630 59	6.560 68	6.755 05	-2.1557701 03	-1.10820 3333	2.155770 103	Down	0.011422 299	0.955609 729
8447	DOC2 B	Double C2-like domains, $\beta$	7.265 3	5.929 74	5.761 17	5.348 4	5.165 61	5.080 31	-2.1744190 49	-1.12063	2.174419 049	Down	0.026911 662	0.955609 729
23242	COBL	Cordon-bleu WH2 repeat protein	5.458 03	6.398 31	6.581 7	7.389 57	6.993 14	7.219 46	2.0773006 01	1.05471	2.077300 601	Up	0.013558 969	0.955609 729
3680	ITGA9	Integrin $\alpha$ 9	7.033 06	6.394 09	5.089 32	3.299 88	5.649 68	4.267 12	-3.4025035 49	-1.76659 6667	3.402503 549	Down	0.041225 075	0.955609 729
23600	AMAC R	Alpha-methylacyl-coa racemase	7.961 53	9.408 53	8.903 88	9.617 34	9.639 86	9.589 88	1.8121637 6	0.857713 333	1.812163 76	Up	0.048433 898	0.955609 729
3012	HIST1 H2AE	Histone cluster 1, h2ae	5.570 32	5.572 15	5.558 59	7.052 72	6.189 56	6.334 86	1.9435488 01	0.958693 333	1.943548 801	Up	0.006797 745	0.955609 729
654466	KGFLP 2	Keratinocyte growth factor-like protein 2	7.501 29	6.879 49	6.730 08	6.461 41	6.494 25	5.843 14	-1.7060816 19	-0.77068 6667	1.706081 619	Down	0.031197 641	0.955609 729
10231	RCAN 2	Regulator of calcineurin 2	7.533 32	7.188 74	7.228 66	4.245 73	6.031 44	6.363 92	-3.4102480 19	-1.76987 6667	3.410248 019	Down	0.013865 655	0.955609 729
285343	TCAI M	T cell activation inhibitor, mitochondria 1	7.284 7	7.910 9	7.986 87	8.680 7	8.627 1	9.028 88	2.0725448 66	1.051403 333	2.072544 866	Up	0.003841 267	0.955609 729
3249	HPN	Hepsin	8.084 85	9.214 15	8.249 24	9.511 53	9.389 48	9.331 14	1.8591416 14	0.894636 667	1.859141 614	Up	0.024194 031	0.955609 729
2568	GABR	Gamma-ami	5.613	6.727	7.986	10.06	8.661	7.730	4.1186361	2.042166	4.118636	Up	0.032541	0.955609



2568	GABRP	Gamma-aminobutyric acid (GABA) A receptor, pi	5.61357	6.72751	7.98656	10.06241	8.66135	7.73038	4.11863611	2.042166667	4.11863611	Up	0.032541353	0.955609729
8544	PIR	Pirin	7.91557	7.61911	7.86825	6.802	7.29306	7.14695	-1.647532205	-0.720306667	1.647532205	Down	0.008381054	0.955609729
2115	ETV1	Ets variant 1	7.7653	8.87137	8.54641	9.41547	8.77998	9.3692	1.733702873	0.793856667	1.733702873	Up	0.04874427	0.955609729
2230	FDX1	Ferredoxin 1	6.50231	6.85142	6.33267	7.51206	6.8406	7.08988	1.500434145	0.58538	1.500434145	Up	0.045867303	0.955609729
114880	OSBPL6	Oxysterol binding protein like 6	6.58653	7.49918	6.38885	7.79569	7.25704	8.69324	2.129433977	1.09047	2.129433977	Up	0.044647603	0.955609729
53826	FXYD6	FXYD domain containing ion transport regulator 6	7.79421	6.94296	6.82305	4.41669	6.85592	5.85013	-2.787863644	-1.47916	2.787863644	Down	0.048251866	0.955609729
1909	EDNRA	Endothelin receptor type A	7.99943	6.00156	5.70532	4.42795	5.72377	4.909	-2.92518932	-1.54853	2.92518932	Down	0.048830416	0.955609729
79814	AGMAT	Agmatinase	4.02117	4.92578	4.02589	5.19787	5.29075	4.84277	1.724506221	0.786183333	1.724506221	Up	0.027315375	0.955609729
100130933	SMIM6	Small integral membrane protein 6	7.09196	8.54744	8.17215	9.06327	8.60094	9.03994	1.950981368	0.9642	1.950981368	Up	0.041807891	0.955609729
2892	GRIA3	Glutamate receptor, ionotropic,	3.08577	3.65936	3.19875	3.67821	4.1986	4.3831	1.707647265	0.77201	1.707647265	Up	0.012880778	0.955609729

6785	ELOV L4	ELOVL fatty acid elongase 4	4.994 89	4.234 17	4.426 11	3.799 42	4.209 58	3.763 32	-1.5450105 26	-0.62761 6667	1.545010 526	Down	0.031536 766	0.955609 729
1016	CDH18	Cadherin 18, type 2	3.282 66	3.648 47	3.573 81	3.845 75	5.278 44	4.592 9	2.1004765 31	1.070716 667	2.100476 531	Up	0.018304 972	0.955609 729
11181	TREH	Trehalase	6.117 71	6.902 28	6.036 77	7.398 66	7.591 45	7.459 68	2.1901201 22	1.13101 122	2.190120 122	Up	0.003778 472	0.955609 729
7504	XK	X-linked Kx blood group	4.318 87	5.140 45	5.362 58	5.369 2	5.773 34	5.881 36	1.6632441 97	0.734	1.663244 197	Up	0.046828 081	0.955609 729
10166	SLC25 A15	Solute carrier family 25 (mitochondri al carrier; ornithine transporter) member 15	6.823 53	7.572 38	7.662 25	8.324 78	7.952 57	8.032 35	1.6823913 45	0.750513 333	1.682391 345	Up	0.026569 751	0.955609 729
84790	TUBA 1C	Tubulin, $\alpha$ 1c	10.28 378	10.78 814	10.76 163	11.38 938	11.34 549	10.98 621	1.5466820 64	0.629176 667	1.546682 064	Up	0.019076 029	0.955609 729
26503	SLC17 A5	Solute carrier family 17 (acidic sugar transporter), member 5	5.336 34	5.519 2	5.849 02	6.687 75	6.279 23	6.106 68	1.7287149 49	0.7897	1.728714 949	Up	0.010363 395	0.955609 729
26020	LRP10	LDL receptor related protein 10	4.581 9	5.490 59	5.838 26	6.162 13	6.466 48	5.849 14	1.8095947 72	0.855666 667	1.809594 772	Up	0.045124 676	0.955609 729
4907	NT5E	5'-nucleotida se, ecto	4.809 51	5.596 35	4.984 93	5.812 89	5.478 55	5.992	1.5485128 27	0.630883 333	1.548512 827	Up	0.043420 17	0.955609 729

4907	NT5E	5'-nucleotidase, ecto (CD73)	4.80951	5.59635	4.98493	5.81289	5.47855	5.992	1.548512827	0.630883333	1.548512827	Up	0.04342017	0.955609729
6932	TCF7	Transcription factor 7 (T-cell specific, HMG-box)	6.40992	5.62125	6.33267	5.47574	5.66028	5.35891	-1.540042324	-0.62297	1.540042324	Down	0.040790551	0.955609729
1838	DTNB	Dystrobrevin $\beta$	3.15089	3.87571	3.54628	4.4302	4.18564	3.8383	1.544443042	0.627086667	1.544443042	Up	0.029957886	0.955609729
7586	ZKSCAN1	Zinc finger with KRAB and SCAN domains 1	3.95243	5.13148	4.55017	6.19946	5.39242	5.6546	2.303988209	1.204133333	2.303988209	Up	0.010795501	0.955609729
4603	MYBL1	V-myb avian myeloblastosis viral oncogene homolog-like 1	5.93296	5.41232	6.45441	5.03646	5.26138	5.42684	-1.615152065	-0.69167	1.615152065	Down	0.045311731	0.955609729
196446	MYRF1	Myelin regulatory factor-like	5.3553	5.41971	5.69906	6.56001	6.8389	6.71565	2.318990109	1.213496667	2.318990109	Up	0.00025394	0.955609729
5154	PDGFA	Platelet-derived growth factor $\alpha$ polypeptide	5.35197	6.28206	5.73869	7.80274	7.02977	6.2305	2.345827074	1.230096667	2.345827074	Up	0.026097019	0.955609729
2324	FLT4	Fms-related	6.916	5.745	5.749	5.225	5.510	4.950	-1.8763686	-0.90794	1.876368	Down	0.038306	0.955609

Table SIII. DEGs in comparison III.

Entry	Gene symbol	Gene name	A10933	A10934	A10939	A10958	A10960	A10963	Fold change	logFC	absolute FC	Regulation	P-value	FDR
28673	TRAV12-2	T cell receptor $\alpha$ variable 12-2	5.54752	5.20952	4.72877	4.42279	4.67467	4.56077	-1.525406057	-0.609193333	1.525406057	Down	0.033582614	0.999940436
308	ANXA5	Annexin A5	6.85555	6.75964	6.98778	7.98821	7.29296	7.38921	1.612318391	0.689136667	1.612318391	Up	0.021117163	0.999940436
23705	CADM1	Cell adhesion molecule 1	5.99482	5.26995	5.82673	6.10244	7.37413	6.48282	1.907870611	0.931963333	1.907870611	Up	0.04474464	0.999940436
3976	LIF	Leukemia inhibitory factor	6.35804	6.18455	6.77195	7.24651	7.68051	6.64502	1.684709682	0.7525	1.684709682	Up	0.047431074	0.999940436
55125	CEP192	Centrosomal protein 192kda	7.60627	8.17279	7.42922	6.90334	6.64646	7.38164	-1.685620775	-0.75328	1.685620775	Down	0.031942132	0.999940436
257019	FRMD3	FERM domain containing 3	4.57856	4.17422	4.00787	4.96956	4.94429	5.17729	1.720959723	0.783213333	1.720959723	Up	0.00411477	0.999940436
130	COL	Collagen, type	5.1	4.8	5.1	6.6	7.1	5.4	2.59	1.37	2.59	Up	0.01	0.99

5	13A1	XIII, $\alpha$ 1	52 14	73 01	15 02	47 65	58 09	58 84	3325 566	4803 333	332 556 6		627 856 6	994 043 6
634	CEA CAM 1	Carcinoembryonic antigen-related cell adhesion molecule 1 (biliary glycoprotein)	5.3 16 62	5.2 04 05	5.7 88 18	6.6 05 74	6.1 12 19	5.8 99 18	1.70 4584 36	0.76 942	1.70 458 436	Up	0.02 131 529 2	0.99 994 043 6
747 4	WNT 5A	Wingless-type MMTV integration site family member 5A	5.3 46 78	4.8 27 17	5.3 83 79	6.3 94 54	5.7 89 42	5.9 38	1.80 8432 813	0.85 474	1.80 843 281 3	Up	0.01 051 965 5	0.99 994 043 6
559 02	ACS S2	Acyl-coa synthetase short-chain family member 2	9.2 66 84	8.6 94 4	8.7 98 17	7.9 38 29	8.2 28 59	8.4 21 15	-1.6 5151 8732	-0.7 2379 3333	1.65 151 873 2	Do wn	0.01 676 132 5	0.99 994 043 6
790 3	ST8S IA4	ST8 $\alpha$ -N-acetyl-neurami nide $\alpha$ -2,8-sialyltransfer ase 4	5.4 13 5	6.1 80 19	6.0 48 85	5.5 01 02	5.0 05 74	4.8 40 81	-1.6 9935 8219	-0.7 6499	1.69 935 821 9	Do wn	0.02 975 076 1	0.99 994 043 6
190 6	EDN 1	Endothelin 1	6.9 20 86	7.1 34 57	7.1 49 45	7.6 88 35	8.1 50 57	7.8 22 63	1.76 4048 223	0.81 889	1.76 404 822 3	Up	0.00 384 072	0.99 994 043 6
692 6	TBX 3	T-box 3	5.5 22 9	4.9 08 31	4.9 84 17	5.4 58 84	6.2 18 88	5.7 72 49	1.60 0227 104	0.67 8276 667	1.60 022 710 4	Up	0.03 984 931 1	0.99 994 043 6

604	CDH	Cadherin 26	3.9	3.8	4.5	3.4	3.7	3.2	-1.5	-0.6	1.54	Do	0.02	0.99
37	26		45	72	61	25	82	74	4995	3222	995	wn	961	994
			49	61	44	56	89	42	178	3333	178		374	043
													9	6
318	NUD	Nudix hydrolase 2	5.3	5.5	5.9	6.3	6.2	6.1	1.55	0.63	1.55	Up	0.01	0.99
	T2		22	73	09	10	86	13	2747	4823	274		555	994
			55	63	24	26	61	02	595	333	759		653	043
											5		3	6
101	LOC	Uncharacterized	3.5	3.8	3.7	4.2	4.2	4.5	1.52	0.60	1.52	Up	0.00	0.99
928	1019	LOC101928168	52	90	80	32	36	65	0086	4153	008		574	994
168	2816		12	41	03	62	85	55	407	333	640		270	043
	8										7		9	6
797	MCT	Multiple C2	4.3	5.2	4.5	6.8	6.6	4.9	2.67	1.41	2.67	Up	0.03	0.99
72	P1	domains,	93	96	34	59	66	49	0278	699	027		818	994
		transmembrane 1	19	44	71	12	34	85	098		809		239	043
											8		9	6
147	C19o	Chromosome 19	5.2	5.3	4.6	3.9	4.1	4.8	-1.6	-0.7	1.67	Do	0.03	0.99
685	rf18	open reading frame	01	08	43	26	77	09	7793	4669	793	wn	749	994
		18	57	55	24	11	57	61	8687		868		622	043
											7		3	6
573	BAG	BCL2 associated	5.5	6.5	5.7	6.6	6.6	6.7	1.60	0.68	1.60	Up	0.04	0.99
	1	athanogene 1	84	85	70	18	56	16	6305	3746	630		744	994
			28	49	47	77	03	68	906	667	590		886	043
											6		4	6
227	FHL2	Four and a half	7.6	7.8	8.3	9.2	8.5	8.5	1.77	0.82	1.77	Up	0.02	0.99
4		LIM domains 2	90	69	56	98	46	47	1821	5233	182		689	994
			13	79	65	58	44	25	579	333	157		116	043
											9			6
100	LOC	Uncharacterized	9.2	8.4	9.6	9.7	9.7	10.	1.77	0.82	1.77	Up	0.04	0.99

507	1005	LOC100507412	52	96	54	52	88	34	6441	899	644		706	994
412	0741		2	9	94	49	74	97	278		127		996	043
	2							8			8		4	6
110	KDE	KDEL	8.2	7.9	8.2	9.1	8.9	8.5	1.67	0.74	1.67	Up	0.01	0.99
15	LR3	(Lys-Asp-Glu-Leu)	87	52	23	54	76	67	5730	479	573		113	994
		endoplasmic	97	24	67	24	32	69	331		033		494	043
		reticulum protein									1		6	6
		retention receptor 3												
552	MCO	Mucolipin 3	3.7	4.4	3.9	4.2	5.4	5.2	1.91	0.93	1.91	Up	0.03	0.99
83	LN3		96	69	29	55	77	80	7655	9343	765		664	994
			73	33	22	66	58	07	187	333	518		809	043
											7		3	6
140	TCE	Transcription	6.7	7.3	7.1	8.3	7.8	7.5	1.79	0.84	1.79	Up	0.02	0.99
597	AL2	elongation factor A	25	19	75	70	23	55	3888	309	388		021	994
		(SII)-like 2	42	49	66	96	6	28	224		822		502	043
											4		8	6
114	OSB	Oxysterol binding	7.3	7.5	7.8	8.3	8.2	8.0	1.53	0.61	1.53	Up	0.01	0.99
882	PL8	protein like 8	83	38	47	73	25	10	0030	356	003		800	994
			12	95	77	69	9	93	063		006		1112	043
											3			6
800	PCN	Pecanex-like 2	4.3	4.9	4.9	5.5	5.5	5.0	1.53	0.62	1.53	Up	0.03	0.99
03	XL2	(Drosophila)	47	32	78	52	16	57	9633	2586	963		581	994
			86	47	97	92	2	94	179	667	317		743	043
											9		2	6
798	TFPI	Tissue factor	4.3	3.4	3.8	4.2	4.7	4.7	1.63	0.70	1.63	Up	0.03	0.99
0	2	pathway inhibitor 2	45	50	79	86	44	71	4867	9173	486		129	994
			73	55	08	77	54	57	067	333	706		944	043
											7		4	6
904	SPA	Sperm associated	2.8	3.8	3.8	4.7	4.0	4.3	1.79	0.84	1.79	Up	0.03	0.99

3	G9	antigen 9	51 89	70 96	62 25	12 41	07 87	93 26	3544 242	2813 333	354 424		878 200 6	994 043 6
168 002	DAC T2	Dishevelled-bindin g antagonist of β-catenin 2	5.5 32 49	6.3 24 72	5.5 08 67	4.8 32 13	4.9 29 9	5.3 41 85	-1.6 8646 2221	-0.7 54 222	1.68 646 222	Do wn	0.03 155 591 3	0.99 994 043 6
133 383	SET D9	SET domain containing 9	3.9 23 58	2.8 32 3	3.7 30 56	4.6 30 78	4.0 03 73	4.2 04 29	1.72 2041 606	0.78 412 204	1.72 204 160 6	Up	0.04 537 754 2	0.99 994 043 6
417 3	MC M4	Minichromosome maintenance complex component 4	3.6 68 1	4.2 56 5	4.1 64 31	5.2 17 09	5.3 21 5	4.2 63 53	1.87 1770 212	0.90 4403 333	1.87 177 021 2	Up	0.02 813 533 4	0.99 994 043 6
690 9	TBX 2	T-box 2	6.1 33 41	5.9 87 87	6.0 53 05	7.5 58 8	6.9 22 11	6.2 27 23	1.79 5770 934	0.84 4603 333	1.79 577 093 4	Up	0.04 294 898 2	0.99 994 043 6
557 0	PKIB	Protein kinase (camp-dependent, catalytic) inhibitor β	4.2 73 81	4.5 65 17	4.4 57 43	5.4 95 96	5.1 35 11	4.7 98 81	1.63 7116 133	0.71 1156 667	1.63 711 613 3	Up	0.01 195 321 4	0.99 994 043 6
904 27	BMF	Bcl2 modifying factor	6.6 32 79	7.4 66 28	7.4 02 53	6.3 26 85	5.8 66 69	6.4 25 11	-1.9 4663 626	-0.9 6098 3333	1.94 663 626	Do wn	0.01 404 994 2	0.99 994 043 6
953	ENT PD1	Ectonucleoside triphosphate	5.7 87	5.5 70	5.3 80	6.9 13	6.4 30	5.8 62	1.76 8455	0.82 249	1.76 845	Up	0.02 765	0.99 994



		diphosphohydrolase 1	46	32	97	57	17	48	602		560		388	043
											2		8	6
331	HSP	Heat shock protein	10.	10.	10.	10.	10.	11.	1.50	0.58	1.50	Up	0.03	0.99
2	A8	family A (Hsp70)	09	25	40	84	48	19	3560	8383	356		457	994
		member 8	61	72	63	69	64	14	931	333	093		618	043
			7	4	1	8	2	7			1		3	6
534	PLG	Plasminogen-like	4.8	4.9	4.1	4.1	4.1	3.4	-1.6	-0.7	1.67	Do	0.03	0.99
2	LB2	B2	45	22	60	80	00	03	7907	4766	907	wn	981	994
			56	27	09	8	89	24	1113	3333	1113		101	043
													6	6
491	NTR	Neurotrophic	4.5	3.7	4.1	3.4	3.8	3.2	-1.5	-0.6	1.53	Do	0.03	0.99
6	K3	tyrosine kinase,	54	37	39	68	09	92	3749	2058	749	wn	800	994
		receptor, type 3	86	36	65	15	04	94	3168		316		194	043
											8		7	6
848	AIF	Apoptosis inducing	8.2	7.5	7.4	6.9	6.8	7.0	-1.6	-0.7	1.68	Do	0.01	0.99
83	M2	factor,	43	44	50	96	99	79	8717	5461	717	wn	997	994
		mitochondria	8	58	89	37	89	17	9339	3333	933		621	043
		associated 2									9		7	6
534	PLG	Plasminogen-like	4.8	4.9	4.1	4.1	4.1	3.4	-1.6	-0.7	1.67	Do	0.03	0.99
3	LB1	B1	45	22	60	80	00	03	7907	4766	907	wn	981	994
			56	27	09	8	89	24	1113	3333	1113		101	043
													6	6
105	SCG	Secretagoin,	4.0	4.1	4.4	6.8	6.4	5.4	4.01	2.00	4.01	Up	0.00	0.99
90	N	EF-hand calcium	68	62	84	25	40	62	3293	4786	329		110	994
		binding protein	46	28	17	67	91	69	499	667	349		911	043
											9		2	6
126	NR2	Nuclear receptor	5.7	5.7	6.3	6.8	6.5	6.4	1.57	0.65	1.57	Up	0.02	0.99
382	C2A	2C2-associated	41	99	58	17	41	96	1559	2196	155		358	994
	P	protein	54	17	39	32	89	48	252	667	925		947	043

											2		7	6
729 857	RGP D2	RANBP2-like and GRIP domain containing 2	4.4 50 43	3.9 64 59	4.5 05 05	4.7 90 7	5.5 16 2	4.9 36 9	1.71 0688 007	0.77 4576 667	1.71 068 800	Up	0.01 839 120	0.99 994 043
520 9	PFKF B3	6-phosphofructo-2- kinase/fructose-2,6- biphosphatase 3	11. 38 39 3	9.8 90 92	10. 41 03	8.8 17 03	9.8 58 01	9.6 65 15	-2.1 6593 0074	-1.11 4986 667	2.16 593 007 4	Do wn	0.04 548 468 4	0.99 994 043 6
799 66	SCD 5	Stearoyl-coa desaturase 5	7.2 09 26	5.9 26 25	5.8 94 34	7.8 90 6	7.8 29 83	7.0 98 39	2.39 9926 13	1.26 299 613	2.39 992 613	Up	0.02 229 036 2	0.99 994 043 6
639 23	TNN	Tenascin N	3.7 86 97	4.4 00 4	4.0 39 33	6.0 54 92	4.4 90 33	4.8 53 31	2.08 1013 994	1.05 7286 667	2.08 101 399 4	Up	0.04 087 388 9	0.99 994 043 6
658 1	SLC2 2A3	Solute carrier family 22 (organic cation transporter), member 3	7.3 45 97	7.6 26 27	6.9 28 02	5.8 19 2	6.6 12 56	6.9 77 34	-1.7 7816 1876	-0.8 3038 6667	1.77 816 187 6	Do wn	0.04 961 496 7	0.99 994 043 6
913	CD1 E	CD1e molecule	4.3 83 04	5.0 46 94	4.8 08 97	5.9 70 49	5.7 24 05	5.2 54 3	1.87 0334 96	0.90 3296 667	1.87 033 496	Up	0.01 115 411 6	0.99 994 043 6
817 4	MAD CAM 1	Mucosal vascular addressin cell adhesion molecule 1	6.0 98 66	6.3 92 44	6.7 98 21	7.6 44 92	9.0 19 16	6.8 55 12	2.65 7304 091	1.40 9963 333	2.65 730 409 1	Up	0.03 883 353 9	0.99 994 043 6



799 60	JAD E1	Jade family PHD finger 1	8.3 89 18	8.1 89 89	8.1 83 3	9.2 23 05	9.1 78 69	8.4 04 85	1.60 3702 647	0.68 1406 667	1.60 370 264 7	Up	0.03 577 081 3	0.99 994 043 6
623 4	RPS2 8	Ribosomal protein S28	6.5 05	5.8 78 66	6.1 30 96	7.2 41 16	6.8 07 41	6.6 85 82	1.67 0087 086	0.73 9923 333	1.67 008 708 6	Up	0.01 956 437	0.99 994 043 6
485 7	NOV A1	Neuro-oncological ventral antigen 1	7.5 03 35	7.1 23 38	7.4 92 87	5.7 20 48	6.5 45 88	6.8 92 08	-1.9 8213 24	-0.9 8705 3333	1.98 213 24	Do wn	0.02 070 770 3	0.99 994 043 6
419 9	ME1	Malic enzyme 1, NADP(+)-depende nt, cytosolic	7.7 55 63	7.5 88 23	7.8 82 55	6.4 01 91	7.0 43 88	7.4 46 14	-1.7 1494 2256	-0.7 7816	1.71 494 225 6	Do wn	0.03 238 953 3	0.99 994 043 6
653 489	RGP D3	RANBP2-like and GRIP domain containing 3	4.4 50 43	3.9 64 59	4.5 05 05	4.7 90 7	5.5 16 2	4.9 36 9	1.71 0688 007	0.77 4576 667	1.71 068 800 7	Up	0.01 839 120 2	0.99 994 043 6
568 92	C8orf 4	Chromosome 8 open reading frame 4	8.1 18 15	7.3 01 55	7.2 93 07	8.5 20 94	9.7 24 17	8.1 89 64	2.36 3066 124	1.24 066	2.36 306 612 4	Up	0.03 094 809 3	0.99 994 043 6
907 6	CLD N1	Claudin 1	8.7 70 74	9.0 97 95	9.2 16 38	10. 13 66	9.7 81 62	9.2 04 71	1.60 1347 781	0.67 9286 667	1.60 134 778 1	Up	0.04 628 357	0.99 994 043 6
574	C3orf	Chromosome 3	6.6	6.3	7.0	7.5	7.5	7.2	1.74	0.80	1.74	Up	0.01	0.99

15	14	open reading frame 14	29 05	33 45	13 82	84 03	74 78	39 34	9905 078	7276 667	990 507 8		071 178 3	994 043 6
816 71	VMP 1	Vacuole membrane protein 1	8.7 99 5	8.8 76 39	10. 00 35 5	10. 38 81 2	10. 91 15 6	10. 08 67 4	2.35 4890 537	1.23 566	2.35 489 053 7	Up	0.01 719 173 6	0.99 994 043 6
619 6	RPS6 KA2	Ribosomal protein S6 kinase, 90kda, polypeptide 2	7.9 38 19	7.1 81 31	7.6 49 38	8.4 83 35	8.4 21 46	8.0 09 24	1.64 1547 694	0.71 5056 667	1.64 154 769 4	Up	0.02 769 559 3	0.99 994 043 6
798 19	WDR 78	WD repeat domain 78	4.9 85 36	5.7 83 93	5.3 85 62	4.7 00 66	4.5 68 76	4.9 09 76	-1.5 7852 4515	-0.6 5857 6667	1.57 852 451 5	Do wn	0.02 673 188 4	0.99 994 043 6
573 2	PTG ER2	Prostaglandin E receptor 2	4.7 70 91	4.0 86 22	4.3 70 29	5.5 91 36	5.5 21 94	5.0 06 25	1.95 0769 516	0.96 4043 333	1.95 076 951 6	Up	0.00 640 231 7	0.99 994 043 6
789 89	COL EC11	Collectin subfamily member 11	8.5 64 26	8.5 35 43	8.3 98 77	9.7 14 52	9.3 70 69	9.5 56 14	2.06 7131 259	1.04 763	2.06 713 125 9	Up	0.00 051 820 3	0.99 994 043 6
558 16	DOK 5	Docking protein 5	6.0 28 58	5.6 83 84	6.4 45 55	7.6 88 38	6.6 89 35	7.2 98 66	2.25 4498 682	1.17 2806 667	2.25 449 868 2	Up	0.00 936 925 7	0.99 994 043 6
315 8	HMG CS2	3-hydroxy-3-methy lglutaryl-coa	8.4 01	7.0 95	6.4 22	9.6 99	9.4 40	9.5 19	4.74 6431	2.24 6843	4.74 643	Up	0.00 302	0.99 994

		synthase (mitochondrial)	2 62	11 11	48 48	22 22	74 74	78 78	733 733	333 333	173 173		320 320	043 043
109 13	EDA R	Ectodysplasin receptor	A 5.1 47 81	5.5 38 06	5.8 29 22	6.4 07 66	6.3 85 51	5.9 53 36	1.67 4596 289	0.74 3813 333	1.67 459 628	Up 3	0.01 783 499 2	0.99 994 043 6
631 9	SCD	Stearoyl-coa desaturase ( $\Delta$ -9-desaturase)	5.3 87 35	4.4 12 05	5.3 70 92	4.0 60 2	4.0 59 1	4.6 38 72	-1.7 4605 6205	-0.8 041 620	1.74 605 620	Do wn	0.04 147 651 5	0.99 994 043 6
388	RHO B	Ras homolog family member B	6.8 57 12	6.6 34 94	6.9 57 88	7.1 84 19	7.9 78 85	7.4 00 19	1.62 9500 732	0.70 443 950	1.62 950 073	Up 2	0.02 631 392	0.99 994 043 6
162 514	TRP V3	Transient receptor potential cation channel, subfamily V, member 3	7.1 06 38	7.0 66 24	6.5 70 59	5.4 20 38	6.2 40 15	5.9 83 47	-2.0 4637 4228	-1.0 3307 422	2.04 637 422	Do wn	0.00 793 028 8	0.99 994 043 6
572 7	PTC H1	Patched 1	8.1 71 78	8.1 91 61	7.9 85 4	9.8 23 26	8.8 42 61	8.7 06 81	2.01 1070 048	1.00 7963 333	2.01 107 004	Up 8	0.01 708 523 5	0.99 994 043 6
259 04	CNO T10	CCR4-NOT transcription complex subunit 10	3.2 82 62	3.4 34 07	3.7 76 54	4.3 83 04	3.9 30 56	3.9 46 01	1.50 3988 289	0.58 8793 333	1.50 398 828	Up 9	0.01 752 652 7	0.99 994 043 6
201 8	EMX 2	Empty spiracles homeobox 2	6.6 72 1	7.6 58 53	5.2 55 12	3.9 57 33	4.4 71 95	5.5 92 92	-3.6 1630 5768	-1.8 5451 6667	3.61 630 576	Do wn	0.03 295 859	0.99 994 043

											8		6	6
793	BHL	Basic	6.1	6.4	6.6	7.5	6.8	6.9	1.61	0.68	1.61	Up	0.02	0.99
65	HE41	helix-loop-helix	78	36	6	07	47	86	1752	863	175		535	994
		family member e41	46	38		62	03	08	253		225		026	043
											3			6
440	C1orf	Chromosome 1	5.8	6.4	6.1	6.9	8.1	6.6	2.16	1.11	2.16	Up	0.03	0.99
712	186	open reading frame	58	45	59	25	92	89	5574	475	557		457	994
		186	53	53	25	56	61	39	793		479		555	043
											3		5	6
110	STM	Stathmin 2	4.5	3.4	3.0	5.9	7.1	4.4	4.54	2.18	4.54	Up	0.02	0.99
75	N2		07	64	33	05	79	75	5555	4456	555		100	994
			65	67	75	2	22	02	669	667	566		243	043
											9		6	6
211	ETS2	V-ets avian	7.6	7.0	7.4	8.1	8.4	7.6	1.59	0.67	1.59	Up	0.04	0.99
4		erythroblastosis	83	49	40	18	46	30	5483	3993	548		746	994
		virus E26 oncogene	47	82	05	08	98	26	107	333	310		425	043
		homolog 2									7		1	6
946	HAN	Heart and neural	5.2	5.2	5.3	6.7	6.3	5.4	1.84	0.88	1.84	Up	0.03	0.99
4	D2	crest derivatives	76	68	45	38	31	62	0987	048	098		314	994
		expressed 2	97	44	83	9	09	69	716		771		142	043
											6		2	6
377	KCN	Potassium channel,	7.1	8.1	8.3	9.0	8.8	8.6	1.97	0.98	1.97	Up	0.02	0.99
5	K1	two pore domain	67	14	17	76	69	01	5890	2503	589		327	994
		subfamily K,	67	4	9	49	24	75	96	333	096		995	043
		member 1											2	6
113	CHR	Cholinergic	3.3	3.3	3.6	4.1	4.9	3.7	1.78	0.83	1.78	Up	0.03	0.99
6	NA3	receptor, nicotinic	43	08	77	59	32	48	6348	7013	634		061	994
		$\alpha$ 3	1	7	93	53	37	87	214	333	821		235	043
											4		5	6

836	MS4	Membrane-spanning	6.1	7.3	6.9	8.9	7.5	8.0	2.59	1.37	2.59	Up	0.02	0.99
61	A8	g 4-domains, subfamily A, member 8	40	43	72	98	62	22	5057	5766	505		242	994
			81	54	55	88	38	94	79	667	779		577	043
													2	6
135	CPA3	Carboxypeptidase	8.1	7.9	7.1	9.1	8.3	8.7	1.99	0.99	1.99	Up	0.02	0.99
9		A3 (mast cell)	78	35	84	81	77	22	2477	4563	247		200	994
			32	36	43	95	53	32	363	333	736		227	043
											3		2	6
717	TPM	Tropomyosin 4	6.6	6.8	7.3	9.0	7.8	7.8	2.49	1.31	2.49	Up	0.01	0.99
1	4		04	73	58	40	52	97	2787	776	278		208	994
			7	84	04	23	59	04	666		766		776	043
											6		5	6
417	MC	Minichromosome	3.6	3.9	4.3	4.9	5.1	4.4	1.82	0.86	1.82	Up	0.01	0.99
1	M2	maintenance	91	46	38	47	78	55	5713	846	571		128	994
		complex	21	28	69	17	96	43	009		300		140	043
		component 2									9		8	6
253	RICT	RPTOR	3.9	4.4	4.7	3.5	3.7	3.8	-1.5	-0.6	1.59	Do	0.02	0.99
260	OR	independent	38	09	74	37	25	43	9345	7216	345	wn	196	994
		companion of	57	25	67	23	7	08	6903		690		053	043
		MTOR, complex 2									3		5	6
102	MSL	Mesothelin	9.4	6.9	7.1	10.	9.6	9.8	4.24	2.08	4.24	Up	0.01	0.99
32	N		75	55	96	39	89	01	1986	474	198		958	994
			93	8	85	21	09	56	413		641		899	043
						5					3		4	6
205	EPH	Epoxide hydrolase	8.7	8.7	8.6	7.0	8.0	8.2	-1.9	-0.9	1.90	Do	0.03	0.99
2	X1	1, microsomal	82	33	20	34	33	84	0231	2775	231	wn	024	994
		(xenobiotic)	49	39	6	96	96	3	1275	3333	127		646	043
											5			6
841	SLIT	SLIT and NTRK	3.9	5.0	4.4	6.0	5.9	5.2	2.41	1.27	2.41	Up	0.00	0.99



89	RK6	like family member 6	63 66	13 67	54 15	31 49	82 95	41 89	9904 309	495	990 430 9		795 743 9	994 043 6
360 6	IL18	Interleukin 18	4.1 15 8	5.7 68 01	5.2 63 87	7.2 13 38	6.4 94 99	5.8 02 84	2.74 0634 617	1.45 451	2.74 063 461 7	Up	0.02 938 843 3	0.99 994 043 6
510 66	SSU H2	Ssu-2 homolog ( <i>C. Elegans</i> )	4.7 12 15	5.1 63 49	4.8 98 04	5.0 63 83	5.8 25 74	6.0 46 59	1.64 8126 143	0.72 0826	1.64 812 614 3	Up	0.04 211 211	0.99 994 043 6
400 966	RGP D1	RANBP2-like and GRIP domain containing 1	4.4 50 43	3.9 64 59	4.5 05 05	4.7 90 7	5.5 16 2	4.9 36 9	1.71 0688 007	0.77 4576 667	1.71 068 800 7	Up	0.01 839 120 2	0.99 994 043 6
648 54	USP4 6	Ubiquitin specific peptidase 46	5.1 19 64	4.9 44 48	5.1 19 29	5.9 93 84	5.6 27 1	5.4 94 59	1.56 2699 087	0.64 404	1.56 269 908 7	Up	0.00 958 619 6	0.99 994 043 6
644 99	TPSB 2	Tryptase $\beta$ 2 (gene/pseudogene)	8.3 86 41	8.6 43 08	8.3 07 74	9.5 04 69	8.6 09 74	9.3 28 77	1.62 6747 12	0.70 199	1.62 674 712	Up	0.03 781 360 2	0.99 994 043 6
750 4	XK	X-linked Kx blood group	4.3 18 87	5.1 40 45	5.3 62 58	5.8 53 24	5.8 69 94	5.6 52 19	1.80 3946 642	0.85 1156 667	1.80 394 664 2	Up	0.02 267 806 6	0.99 994 043 6
458 8	MUC 6	Mucin 6, oligomeric	7.3 48	9.3 43	9.7 79	11. 54	11. 02	10. 87	5.01 1236	2.32 5166	5.01 123	Up	0.00 901	0.99 994

		mucus/gel-forming	69	81	14	04	71	95	642	667	664		707	043
						2	7	5			2		1	6
796	ACS	Acyl-coa	4.8	4.9	4.7	3.8	3.7	4.7	-1.6	-0.7	1.65	Do	0.03	0.99
11	S3	synthetase	06	95	30	62	81	16	5169	2394	169	wn	212	994
		short-chain family	21	76	04	6	19	38	4269	6667	426		907	043
		member 3									9		6	6
743	VIP	Vasoactive	4.2	4.3	5.1	4.8	6.3	5.8	2.13	1.09	2.13	Up	0.04	0.99
2		intestinal peptide	64	82	70	47	56	96	5361	448	536		339	994
			71	15	01	47	34	5	015		101		989	043
											5		3	6
761	CA3	Carbonic anhydrase	5.4	5.7	5.6	4.4	4.3	5.4	-1.7	-0.8	1.78	Do	0.03	0.99
		III	48	04	07	32	56	74	8027	3209	027	wn	625	994
			09	69	42	85	11	95	0748	6667	074		149	043
											8		8	6
125	ADH	Alcohol	11.	11.	11.	10.	10.	11.	-2.2	-1.1	2.26	Do	0.01	0.99
	1B	dehydrogenase 1B	91	63	58	13	12	33	6197	7758	197	wn	429	994
		(class I), $\beta$	64	23	25	49	81	54	5547	3333	554		337	043
		polypeptide	1	4	6	9	5	2			7		2	6
151	CTS	Cathepsin V	3.1	3.7	3.3	4.1	4.4	3.6	1.64	0.71	1.64	Up	0.02	0.99
5	V		10	04	12	91	66	16	2238	5663	223		908	994
			98	32	36	92	04	69	125	333	812		876	043
											5		6	6
548	RET	Retinol saturase	10.	10.	9.4	9.1	9.3	9.2	-1.7	-0.7	1.72	Do	0.04	0.99
84	SAT	(all-trans-retinol	67	02	82	98	61	67	2235	8438	235	wn	118	994
		13,14-reductase)	80	02	44	49	28	8	9936	6667	993		036	043
			5	4							6		6	6
286	LUR	Leucine rich	6.9	6.9	7.3	8.1	8.3	7.3	1.78	0.83	1.78	Up	0.02	0.99
343	APIL	adaptor protein	61	64	55	10	42	32	4149	5236	414		878	994
		1-like	13	15	34	51	88	94	695	667	969		073	043

											5		1	6
131 6	KLF6 6	Kruppel-like factor 6	6.1 63 62	5.1 11 91	5.8 34 95	7.0 37 6	7.2 27 62	6.2 05 38	2.17 3529 987	1.12 004	2.17 352 998 7	Up	0.02 261 142	0.99 994 043 6
552 28	PNM AL1	Paraneoplastic Ma antigen family-like 1	5.4 51 39	5.2 78 6	5.0 27 16	6.9 33 86	6.4 73 88	5.5 16 89	2.07 8909 084	1.05 5826 667	2.07 890 908 4	Up	0.02 660 648 1	0.99 994 043 6
241 47	FJX1	Four jointed box 1	5.3 38 15	4.4 81 88	4.6 09 5	6.7 68 77	5.7 93 37	5.3 60 64	2.24 1425 684	1.16 4416 667	2.24 142 568 4	Up	0.02 778 751 7	0.99 994 043 6
549 79	HRA SLS2	HRAS-like suppressor 2	3.3 33 63	3.8 45 83	3.5 63 63	4.1 91 92	4.3 24 67	4.1 94 23	1.57 5609 477	0.65 591	1.57 560 947 7	Up	0.00 407 706 9	0.99 994 043 6
536 6	PMA IP1	Phorbol-12-myrista te-13-acetate-induc ed protein 1	4.3 85 84	3.8 97 95	4.8 46 65	4.7 99 8	5.3 62 92	5.1 62 95	1.66 0644 58	0.73 1743 333	1.66 064 458	Up	0.03 546 543 5	0.99 994 043 6
510 02	TPR KB	TP53RK binding protein	4.4 02 68	4.9 76 58	4.6 04 12	3.6 72 3	4.0 07 87	4.0 77 14	-1.6 7251 985	-0.7 4202 3333	1.67 251 985	Do wn	0.00 736 906 3	0.99 994 043 6
570 02	YAE 1D1	Yae1 domain containing 1	6.3 00 32	6.4 39 66	6.0 29 68	6.8 71 2	6.9 43 77	6.7 19 2	1.50 3338 614	0.58 817	1.50 333 861 4	Up	0.01 354 664 3	0.99 994 043 6

966	CD59	CD59 molecule, complement regulatory protein	5.1 17 25	5.7 88 48	5.4 72 72	6.4 45 95	6.2 02 96	5.8 78 83	1.64 3111 063	0.71 643 3111	1.64 063	Up	0.02 248 407 4	0.99 994 043 6
556 12	FER MT1	Fermitin family member 1	6.1 73 67	7.6 95 13	6.5 40 56	8.6 12 33	7.8 20 68	7.5 21 56	2.26 8496 866	1.18 1736 667	2.26 849 686 6	Up	0.04 211 516 7	0.99 994 043 6
127 700	OSC P1	Organic solute carrier partner 1	4.8 46 06	4.8 64 43	4.6 56 28	4.0 55 57	4.0 78 75	4.4 31 45	-1.5 1606 6812	-0.6 0033 3333	1.51 606 681 2	Do wn	0.00 615 407 2	0.99 994 043 6
229 43	DKK 1	Dickkopf WNT signaling pathway inhibitor 1	5.3 76 92	5.7 79 27	4.8 99 29	8.9 94 87	7.1 05 49	5.9 37 6	3.98 3840 81	1.99 416 081	3.98 384 081	Up	0.03 478 911 4	0.99 994 043 6
190 8	EDN 3	Endothelin 3	3.2 45 29	3.8 05 74	3.3 83 56	4.9 26 11	5.1 82 37	3.6 88 71	2.17 4775 78	1.12 0866 667	2.17 477 578	Up	0.02 892 000 8	0.99 994 043 6
871 78	PNP T1	Polyribonucleotide nucleotidyltransferase 1	4.2 37 82	4.4 30 35	4.9 59 75	5.2 69 4	5.0 50 09	5.1 26 31	1.52 1991 182	0.60 596 118 2	1.52 199 118 2	Up	0.02 588 592 5	0.99 994 043 6
602	BCL 3	B-cell CLL/lymphoma 3	8.4 22 12	8.2 22 06	8.5 43 43	7.7 69 93	7.5 27 59	7.5 04 96	-1.7 3512 9491	-0.7 9504 3333	1.73 512 949 1	Do wn	0.00 293 777	0.99 994 043 6
147	PRO	Protein interacting	5.3	5.5	5.1	5.0	4.5	4.4	-1.6	-0.6	1.60	Do	0.01	0.99

011	CA1	with cyclin A1	90 67	22 37	73 66	09 98	59 42	73 39	0358 7785	8130 3333	358 778 5	wn	099 789 3	994 043 6
510	ST8S	ST8	3.1	3.4	3.8	4.0	4.8	4.2	1.82	0.87	1.82	Up	0.01	0.99
46	IA3	$\alpha$ -N-acetyl-neurami nide $\alpha$ -2,8-sialyltransfer ase 3	69 3	87 19	00 32	52 47	11 98	03 21	8021 874	0283 333	802 187 4		178 697 6	994 043 6
758	ZKS	Zinc finger with	3.9	5.1	4.5	5.5	5.4	5.5	1.92	0.94	1.92	Up	0.01	0.99
6	CAN	KRAB and SCAN	52	31	50	41	27	04	7245	654	724		669	994
	1	domains 1	43	48	17	56	99	15	02		502		856 6	043 6
845	PLPP	Phospholipid	4.2	4.9	4.9	5.6	5.4	5.1	1.65	0.72	1.65	Up	0.02	0.99
13	5	phosphatase 5	31	19	01	87	00	45	5205	701	520		392	994
			19	52	7	66	26	52	105		510 5		779 9	043 6
555	HES6	Hes family bhlh	5.6	6.5	6.5	7.1	6.9	6.9	1.73	0.79	1.73	Up	0.02	0.99
02		transcription factor	68	12	45	58	82	70	5498	535	549		375	994
		6	41	21	08	89	11	75	358		835 8		047 2	043 6
531	PKP2	Plakophilin 2	3.6	4.6	4.3	6.1	4.7	5.0	2.13	1.09	2.13	Up	0.04	0.99
8			06	74	87	58	59	33	4773	4083	477		385	994
			99	22	4	48	11	27	982	333	398 2		326 7	043 6
108	HSP	Heat shock protein	8.5	8.9	9.0	9.2	9.6	9.7	1.60	0.68	1.60	Up	0.01	0.99
08	H1	family H (Hsp110)	38	45	87	86	06	31	6818	4206	681		774	994
		member 1	57	38	76	21	64	48	154	667	815 4		150 2	043 6
379	KCN	Potassium	4.5	4.0	4.3	7.0	6.2	4.7	3.19	1.67	3.19	Up	0.02	0.99

0	S3	voltage-gated channel, modifier subfamily S, member 3	65 12	86 11	13 95	11 25	55 64	23 36	3245 191	5023 333	324 519 1		206 362 9	994 043 6
112 4	CHN 2	Chimerin 2	3.5 52 12	3.8 90 41	3.7 80 03	4.2 32 62	4.2 36 85	4.5 65 55	1.52 0086 407	0.60 4153 333	1.52 008 640 7	Up	0.00 574 270 9	0.99 994 043 6
191	AHC Y	Adenosylhomocysteinase	6.1 91 8	6.7 31 75	6.8 59 43	7.6 90 84	7.2 09 82	7.5 31 37	1.84 4227 541	0.88 3016 667	1.84 422 754 1	Up	0.00 931 756 6	0.99 994 043 6
259 87	TSK U	Tsukushi, small leucine rich proteoglycan	8.5 83 19	8.2 16 82	8.8 52 66	7.7 08 54	7.5 77 69	7.5 50 91	-1.9 1654 7826	-0.9 3851 782	1.91 654 782 6	Down	0.00 319 146 6	0.99 994 043 6
988 6	RHO BTB 1	Rho-related BTB domain containing 1	6.0 10 95	5.8 84 69	5.9 00 16	7.0 76 52	6.3 19 56	6.3 08 22	1.55 4194 075	0.63 6166 667	1.55 419 407 5	Up	0.03 803 878 6	0.99 994 043 6
112 21	DUS P10	Dual specificity phosphatase 10	4.4 21 26	4.5 35 93	4.4 67 13	4.9 50 95	4.9 90 52	5.3 22 42	1.52 9637 715	0.61 319 771	1.52 963 771 5	Up	0.00 491 328 7	0.99 994 043 6
406 991	MIR2 1	Microrna 21	8.7 99 5	8.8 76 39	10. 00 35 5	10. 38 81 2	10. 91 15 6	10. 08 67 4	2.35 4890 537	1.23 566 053 7	2.35 489 053 7	Up	0.01 719 173 6	0.99 994 043 6
556	TRM	Trna	4.8	5.0	5.3	4.3	4.5	4.1	-1.6	-0.7	1.62	Do	0.00	0.99

87	U	5-methylaminomethyl-2-thiouridylate methyltransferase	68 7	16 64	44 91	95 93	25 82	95 05	2956 0972	0448 3333	956 097 2	wn	568 582 6	994 043 6
717 7	TPS AB1	Tryptase $\alpha/\beta$ 1	8.3 86 41	8.6 43 08	8.3 07 74	9.5 04 69	8.6 09 74	9.3 28 77	1.62 6747 12	0.70 199 712	1.62 674 712	Up	0.03 781 360 2	0.99 994 043 6
258 30	SULT 4A1	Sulfotransferase family 4A member 1	4.1 80 49	4.3 95 74	3.9 57 1	5.3 49 43	4.8 80 41	4.5 79 91	1.69 2090 424	0.75 8806 667	1.69 209 042 4	Up	0.01 457 793 4	0.99 994 043 6
105 376 948	LOC 1053 7694 8	Uncharacterized LOC105376948	4.7 12 15	5.1 63 49	4.8 98 04	5.0 63 83	5.8 25 74	6.0 46 59	1.64 8126 143	0.72 0826 667	1.64 812 614 3	Up	0.04 211 211	0.99 994 043 6
657 1	SLC1 8A2	Solute carrier family 18 (vesicular monoamine transporter), member 2	4.4 94 33	4.7 13 54	4.1 32 41	5.7 21 21	4.8 29 26	5.3 55 3	1.80 8963 544	0.85 5163 333	1.80 896 354 4	Up	0.01 759 625 6	0.99 994 043 6
126	ADH 1C	Alcohol dehydrogenase 1C (class I), gamma polypeptide	10. 18 18 3	11. 14 67 4	10. 92 37 2	9.0 93 93	9.2 14 67	10. 39 43 7	-2.2 7065 208	-1.1 8310 6667	2.27 065 208	Do wn	0.02 938 095 2	0.99 994 043 6
213	ALB	Albumin	3.5 96 21	4.8 90 43	4.9 47 8	7.7 64 61	5.4 09 09	7.5 13 49	5.34 2753 043	2.41 7583 333	5.34 275 304 3	Up	0.01 224 227 3	0.99 994 043 6

595	CCN D1	Cyclin D1	5.1 98 32	5.7 00 83	6.0 17 48	6.4 61 38	6.1 22 22	6.4 39 57	1.62 6961 374	0.70 218	1.62 696 137 4	Up	0.02 713 905 1	0.99 994 043 6
204 3	EPH A4	EPH receptor A4	5.3 07	4.8 11 22	4.1 55 31	5.2 88 73	6.6 34 93	5.7 25 94	2.18 1554 728	1.12 5356 667	2.18 155 472 8	Up	0.03 692 242 2	0.99 994 043 6
231 42	DCU N1D 4	DCN1, defective in cullin neddylation 1, domain containing 4	7.3 48 96	7.0 57 19	6.8 45 67	6.6 63 78	6.1 81 85	6.4 95 43	-1.5 5500 5842	-0.6 3692 584 2	1.55 500 584 2	Do wn	0.02 178 663 9	0.99 994 043 6
101 02	TSF M	Ts translation elongation factor, mitochondrial	4.2 40 12	4.3 40 01	4.4 30 2	5.7 86 6	4.6 20 49	4.9 36 5	1.71 4458 916	0.77 7753 333	1.71 445 891 6	Up	0.03 848 719 4	0.99 994 043 6
31	ACA CA	Acetyl-coa carboxylase $\alpha$	8.2 69 7	8.0 21 24	8.7 16 3	7.9 61 06	7.4 11 4	7.5 68 7	-1.61 1823 009	-0.6 8869 3333	1.61 182 300 9	Do wn	0.03 035 100 1	0.99 994 043 6
234 23	TME D3	Transmembrane p24 trafficking protein 3	6.8 77 01	7.4 99 08	7.5 45 64	8.2 80 82	7.9 81 9	7.9 59 2	1.70 1409 011	0.76 673	1.70 140 901 1	Up	0.01 557 076 3	0.99 994 043 6
633 8	SCN N1B	Sodium channel, non-voltage gated 1 $\beta$ subunit	6.5 19 74	5.1 19 75	5.0 87 81	4.5 07 53	4.3 76 24	4.6 32 8	-2.0 9978 75	-1.0 7024 3333	2.09 978 75	Do wn	0.03 327 064 2	0.99 994 043 6
544	KRT	Keratin 20, type I	4.3	4.7	4.1	7.5	8.2	5.1	6.02	2.59	6.02	Up	0.01	0.99



74	20		54 85	01 41	40 48	79 98	64 09	27 37	7528 915	1566 667	752 891 5		426 279 7	994 043 6
517 51	HIG D1B	HIG1 hypoxia inducible domain family member 1B	6.1 37 9	6.2 44 73	6.2 91 82	7.2 94 17	7.7 38 63	6.4 77 8	1.92 5700 489	0.94 5383 333	1.92 570 048 9	Up	0.02 513 291 3	0.99 994 043 6
678	ZFP3 6L2	ZFP36 ring finger protein-like 2	6.8 99 48	8.1 21 74	7.8 49 35	8.7 08 85	8.8 22 65	8.0 76 8	1.88 2404 49	0.91 2576 667	1.88 240 449	Up	0.04 751 536 3	0.99 994 043 6
100 131 541	LOC 1001 3154 1	Uncharacterized LOC100131541	5.4 13 89	5.5 72 68	5.5 18 27	7.4 19 43	6.1 97 09	5.9 58 73	2.03 2802 423	1.02 347 242 3	2.03 280 242 3	Up	0.03 503 358 6	0.99 994 043 6
585 13	EPS1 5L1	Epidermal growth factor receptor pathway substrate 15-like 1	4.5 09 93	4.4 69 33	4.3 83 5	5.4 01 69	5.0 99 18	4.7 50 15	1.54 6942 958	0.62 942 295 8	1.54 694 295 8	Up	0.01 369 506 9	0.99 994 043 6
558 59	BEX 1	Brain expressed X-linked 1	6.2 44 9	6.2 87 35	6.5 10 06	6.8 20 24	7.9 40 3	7.7 11 26	2.20 8647 73	1.14 3163 333	2.20 864 773	Up	0.00 922 806 6	0.99 994 043 6
916 12	CHU RC1	Churchill domain containing 1	4.5 38 96	4.7 64 17	4.8 90 75	5.8 24 8	4.9 88 68	5.5 33 28	1.64 4474 534	0.71 7626 667	1.64 447 453 4	Up	0.02 274 448 5	0.99 994 043 6

Table SIV. DEGs in comparison IV.

En try	Gene symb ol	Gene name	A 10	A 10	A 10	A 10	A 10	A 10	Fol d-c han ge	log FC	abs olu teFC	Re gu lat ion	P-v alu e	FD R
87	TNF	Tumor necrosis	4.	3.	5.	5.	6.	5.	2.2	1.1	2.2	U	0.0	0.9
94	RSF1	factor receptor	97	82	28	68	56	33	472	681	47	p	28	30
	OC	superfamily	00	37	72	33	35	86	594	666	25		85	85
		member 10c, decoy	8	6	1	4	9	2	05	67	94		02	92
		without an intracellular domain									05		44	11
74	WNT	Wingless-type	5.	5.	5.	4.	5.	4.	-1.	-0.	1.5	D	0.0	0.9
74	5A	MMTV integration	78	31	49	79	02	79	579	659	79	o	04	30
		site family member	53	26	28	51	47	36	119	12	11	w	75	85
		5A	5	7	7	7	6		115		91	n	38	92
											15		32	11
17	DM	Dystrophin	7.	9.	9.	6.	8.	7.	-2.	-1.	2.6	D	0.0	0.9
56	D		95	00	69	79	40	20	673	418	73	o	27	30
			20	84	69	39	62	02	976	986	97	w	79	85
			2	7	1		9	5	278	667	62	n	09	92
											78		66	11
10	SUB	SUB1 homolog,	4.	5.	5.	4.	4.	4.	-1.	-0.	1.6	D	0.0	0.9
92	1	transcriptional	88	27	89	68	44	73	657	729	57	o	21	30
3		regulator	14	38	22	42	24	25	945	396	94	w	41	85
				8	5	9	7	8	596	667	55	n	54	92
											96		8	11
34	APO	Apolipoprotein C-I	10	9.	9.	7.	8.	9.	-2.	-1.1	2.1	D	0.0	0.9

1	C1		.1	44	37	87	67	12	162	125	62	o	13	30
			83	24	33	09	03	00	329	866	32	w	01	85
			32	6	4	7	3	6	929	67	99	n	94	92
											29		39	11
62	CFB	Complement factor	7.	8.	8.	6.	6.	7.	-2.	-1.	2.1	D	0.0	0.9
9		B	82	19	20	78	70	48	120	084	20	o	02	30
			76	56	57	03	83	64	821	623	82	w	10	85
			6	6	5	9	9	2	695	333	16	n	07	92
											95		91	11
31	HLA	Major	8.	8.	8.	7.	8.	8.	-1.	-0.	1.6	D	0.0	0.9
22	-DR	histocompatibility	33	36	95	22	02	17	669	739	69	o	34	30
	A	complex, class II,	24	48	06	60	51	97	022	003	02	w	17	85
		DR $\alpha$	2	8	9	8	3	7	419	333	24	n	87	92
											19		05	11
23	TBC	TBC1 domain	4.	4.	4.	3.	3.	3.	-1.	-0.	1.5	D	0.0	0.9
21	1D1	family member 1	30	30	57	92	63	85	504	589	04	o	02	30
6			82	62	10	86	02	75	937	703	93	w	94	85
			4	9	5	8	8	1	25	333	72	n	35	92
											5		22	11
10	UBE	Ubiquitin	7.	6.	7.	8.	7.	7.	1.6	0.7	1.6	U	0.0	0.9
08	2CP5	conjugating	31	82	15	23	69	64	979	637	97	p	07	30
74		enzyme E2C	08	56	15	83	52	57	178	666	91		92	85
26		pseudogene 5	4	3	9	5	5	6	59	67	78		17	92
0											59		61	11
23	CEL	Chymotrypsin like	4.	3.	3.	4.	4.	4.	1.8	0.8	1.8	U	0.0	0.9
43	A3B	elastase family	04	43	87	69	41	94	657	997	65	p	02	30
6		member 3B	43	44	75	02	69	85	857	833	78		40	85
			5	5	3		3	5	55	33	57		97	92
											55		76	11

13	CRE	Camp responsive	4.	4.	4.	3.	3.	3.	-1.	-0.	1.5	D	0.0	0.9
85	B1	element binding	05	60	32	64	95	59	510	595	10	o	09	30
		protein 1	52	43	15	63	26	60	894	403	89	w	51	85
			9	9	9	5	5	6	926	333	49	n	43	92
											26		56	11
28	LGA	Lectin,	6.	6.	7.	5.	6.	6.	-1.	-0.	1.5	D	0.0	0.9
41	LS9	galactoside-binding	98	93	16	90	66	73	507	592	07	o	38	30
94	B	, soluble, 9B	30	51	41	81	25	45	700	35	70	w	33	85
			7	9	1	9	8	5	636		06	n	51	92
											36		89	11
55	UTP	UTP6 small	5.	5.	5.	5.	4.	5.	-1.	-0.	1.5	D	0.0	0.9
81	6	subunit processome	24	79	80	20	64	21	506	591	06	o	32	30
3		component	24	46	00	08	62	58	704	396	70	w	99	85
			3		6	1	2	7	676	667	46	n	03	92
											76		6	11
34	IGH	Immunoglobulin	8.	9.	8.	7.	8.	7.	-1.	-0.	1.9	D	0.0	0.9
92		heavy locus	29	48	88	93	11	70	958	969	58	o	111	30
			12	48	50	20	57	46	265	576	26	w	20	85
			4	6	7	4	9	1	892	667	58	n	09	92
											92		9	11
11	FZD	Frizzled class	4.	3.	4.	3.	4.	3.	-1.	-0.	1.6	D	0.0	0.9
21	10	receptor 10	17	93	37	11	01	21	635	709	35	o	21	30
1			57	32	23	93	62	78	029	316	02	w	24	85
			6	8	3	3	1	8	501	667	95	n	82	92
											01		81	11
17	SYN	Synaptopodin 2	6.	8.	7.	4.	7.	5.	-3.	-1.	3.6	D	0.0	0.9
10	PO2		72	00	79	52	15	22	656	870	56	o	22	30
24			31	14	08	10	97	34	263	37	26	w	10	85
				4		2	9	2	382		33	n	78	92

												82		47	11
25 80 0	SLC 39A6	Solute carrier family 39 (zinc transporter), member 6	5. 10 2 6	5. 66 12 8	6. 05 53 8	4. 83 78 6	4. 72 71 8	5. 27 51 8	-1. 579 505 908	-0. 659 473 333	1.5 79 50 59	D o w n	0.0 38 91 31	0.9 30 85 92	
12 64 32	RIN L	Ras and Rab interactor like	5. 29 09 1	5. 02 80 1	4. 64 24 9	5. 87 28 9	5. 33 31 2	5. 51 24 2	1.5 007 392 5	0.5 856 733 33	1.5 00 73 92 5	U p	0.0 28 35 79 09	0.9 30 85 92 11	
65 36 35	WAS H7P	WAS protein family homolog 7 pseudogene	7. 80 77 1	7. 50 08 5	7. 00 97 2	8. 94 64 6	8. 50 34 6	8. 07 44 4	2.0 975 327 45	1.0 686 933 33	2.0 97 53 27 45	U p	0.0 05 38 14 06	0.9 30 85 92 11	
68 40	SVIL	Supervillin	6. 57 89 6	7. 38 74 5	8. 13 84 3	5. 89 43 8	6. 81 28 8	6. 51 40 8	-1. 946 919 635	-0. 961 193 333	1.9 46 91 96 35	D o w n	0.0 45 36 91 39	0.9 30 85 92 11	
11 61 59	CYY R1	Cysteine/tyrosine-r ich 1	5. 75 15 9	6. 26 39 3	6. 53 93 5	4. 62 11 7	5. 44 16 8	5. 55 97 8	-1. 968 932 064	-0. 977 413 333	1.9 68 93 20 64	D o w n	0.0 12 39 06 41	0.9 30 85 92 11	
43 11	MM E	Membrane metallo-endopeptid ase	3. 80 88	3. 56 77	3. 39 99	4. 87 21	4. 02 09	4. 42 28	1.7 981 084	0.8 464 8	1.7 98 10	U p	0.0 05 65	0.9 30 85	

			5		1	3		7	04		84		09	92
											04		12	11
27	FILI	Filamin A	4.	5.	6.	3.	5.	3.	-2.	-1.	2.8	D	0.0	0.9
14	P1	interacting protein	96	87	62	53	66	67	887	529	87	o	40	30
5		1	15	89	89	79	77	47	184	663	18	w	53	85
			8	2			3	8	56	333	45	n	79	92
											6		5	11
79	CPE	Cadherin-like and	7.	8.	8.	5.	7.	6.	-2.	-1.	2.6	D	0.0	0.9
97	D1	PC-esterase	03	04	33	49	46	27	624	391	24	o	29	30
4		domain containing	72	35	23	76	5	50	113	83	11	w	13	85
		1	5	8	4	5		3	279		32	n	42	92
											79		2	11
64	SVIL	Supervillin	6.	6.	7.	5.	6.	6.	-1.	-0.	1.8	D	0.0	0.9
59	P1	pseudogene 1	13	72	48	26	09	24	885	915	85	o	45	30
54			68	36	93	31	22	84	987	32	98	w	34	85
			8	2	5	7	6	6	351		73	n	38	92
											51		89	11
29	SCHI	Schwannomin	4.	5.	4.	4.	4.	4.	-1.	-0.	1.6	D	0.0	0.9
97	P1	interacting protein	55	25	92	02	25	39	607	684	07	o	09	30
0		1	75	84	18	64	97	80	230	576	23	w	85	85
			6	1	8	1		1	299	667	02	n	40	92
											99		85	11
44	MT1	Metallothionein 1E	7.	7.	7.	8.	7.	8.	1.7	0.7	1.7	U	0.0	0.9
93	E		94	51	04	43	89	49	109	748	10	p	19	30
			03	53	7	86	77	07	686	133	96		76	85
			2	1		4	1	2	59	33	86		93	92
											59		4	11
80	CEP	Centrosomal	6.	6.	6.	7.	7.	6.	1.5	0.6	1.5	U	0.0	0.9
32	70	protein 70kda	87	35	54	63	22	73	216	056	21	p	45	30

1			01 8	87 6	85 9	20 8	96 1	28 8	958 2	8	69 58 2		07 60 9	85 92 11
40 13 87	LRR D1	Leucine-rich repeats and death domain containing 1	6. 82 62 7	6. 38 18 6	7. 46 44 4	6. 20 27 6	5. 68 49 4	6. 53 61 5	-1. 681 295 526	-0. 749 573 333	1.6 81 29 55 26	D o w n	0.0 47 63 27 03	0.9 30 85 92 11
72 99 93	SHIS A9	Shisa family member 9	7. 13 93 3	6. 74 95 8	6. 56 14 1	7. 41 61 8	7. 60 66 2	7. 32 09 3	1.5 487 847 65	0.6 311 366 67	1.5 48 78 47 65	U p	0.0 10 80 32 2	0.9 30 85 92 11
84 83	CILP	Cartilage intermediate layer protein	4. 01 86 7	6. 59 39 2	5. 14 13 8	6. 89 51 6	7. 22 79 7	9. 20 58 7	5.7 556 811 26	2.5 249 866 67	5.7 55 68 11 26	U p	0.0 11 48 42 6	0.9 30 85 92 11
44 96	MT1 H	Metallothionein 1H	9. 56 62 8	7. 26 63 3	6. 22 33 7	10 .3 30 29	9. 48 09 5	9. 95 36 9	4.7 119 252 96	2.2 363 166 67	4.7 11 92 52 96	U p	0.0 18 26 06 89	0.9 30 85 92 11
37 2	ARC N1	Archain 1	5. 76 74 8	6. 03 91 8	6. 19 08 6	5. 56 67 7	5. 12 17 6	5. 54 88 6	-1. 501 838 832	-0. 586 73 88	1.5 01 83 88 32	D o w n	0.0 15 26 56 24	0.9 30 85 92 11
63	PRD	PR domain	5.	6.	6.	5.	5.	5.	-1.	-0.	1.7	D	0.0	0.9

9	M1	containing 1, with ZNF domain	88 30 2	18 64 5	57 33 8	07 57 5	55 16 5	54 89 7	768 071 56	822 176 667	68 07 15 6	o w n	07 02 43 51	30 85 92 11
16 54	DDX 3X	DEAD (Asp-Glu-Ala-Asp) box helicase 3, X-linked	5. 02 44 8	5. 07 23 6	5. 10 31 8	4. 72 38 7	3. 95 26 5	4. 17 26 4	-1. 721 444 895	-0. 783 62 48 95	1.7 21 44 48 95	D o w n	0.0 05 15 66 63	0.9 30 85 92 11
54 46 9	ZFA ND6	Zinc finger, AN1-type domain 6	7. 00 63 8	7. 03 75 1	7. 34 07 6	6. 72 69 8	5. 87 27 6	6. 75 87 6	-1. 597 021 055	-0. 675 383 333	1.5 97 02 10 55	D o w n	0.0 32 54 27 83	0.9 30 85 92 11
84 23 0	LRR C8C	Leucine-rich repeat containing 8 family member C	5. 98 32 9	6. 46 11 8	6. 55 77 8	5. 55 09 4	6. 02 14 7	5. 15 55 2	-1. 691 238 354	-0. 758 08 354	1.6 91 23 83 54	D o w n	0.0 19 56 23 22	0.9 30 85 92 11
29 11 6	MYL IP	Myosin regulatory light chain interacting protein	7. 50 72 6	8. 06 07 7	8. 00 21 3	7. 41 04 4	6. 70 04 2	7. 50 98 9	-1. 568 954 303	-0. 649 803 333	1.5 68 95 43 03	D o w n	0.0 37 12 21 66	0.9 30 85 92 11
63 35	SCN 9A	Sodium channel, voltage gated, type IX $\alpha$ subunit	5. 18 41 5	4. 56 08 2	4. 52 95 7	5. 83 91 8	5. 28 11 7	5. 92 91 1	1.8 986 491 47	0.9 249 733 33	1.8 98 64 91 47	U p	0.0 06 05 48 37	0.9 30 85 92 11



37 91	KDR	Kinase insert domain receptor	7. 15 37 3	6. 96 77 1	7. 49 39 1	5. 83 73 5	6. 82 88 5	6. 75 87 9	-1. 658 777 059	-0. 730 12 70	1.6 58 77 70	D o w n	0.0 36 31 97	0.9 30 85 92
23 21	FLT1	Fms-related tyrosine kinase 1	5. 23 60 4	5. 21 36 5	6. 02 82 8	3. 96 06 8	4. 10 08 9	4. 94 42 1	-2. 230 504 409	-1. 157 37 44	2.2 30 50 44	D o w n	0.0 07 18 05	0.9 30 85 92
11 33 1	PHB 2	Prohibitin 2	8. 33 69 4	8. 67 42 9	9. 04 05 6	8. 04 72 8	7. 70 99 4	8. 45 08 3	-1. 531 112 192	-0. 614 58 19	1.5 311 12 19	D o w n	0.0 38 70 20	0.9 30 85 92
74 12	VCA M1	Vascular cell adhesion molecule 1	5. 57 69 5	5. 23 89 5	5. 75 01 2	3. 82 17 3	4. 24 45 8	4. 58 00 1	-2. 473 521 889	-1. 306 566 667	2.4 73 52 18	D o w n	0.0 00 48 96	0.9 30 85 92
49 73	OLR 1	Oxidized low density lipoprotein (lectin-like) receptor 1	6. 03 98 8	7. 08 64 9	6. 28 81 6	5. 23 60 1	5. 47 94 5	6. 19 11 1	-1. 785 077 445	-0. 835 986 667	1.7 85 07 74	D o w n	0.0 38 69 24	0.9 30 85 92
57 60 2	USP 36	Ubiquitin specific peptidase 36	5. 88 86	5. 67 31 5	4. 90 71 1	6. 75 76 6	6. 47 87 8	5. 74 42 8	1.7 866 866 88	0.8 372 866 67	1.7 86 68 66	U p	0.0 37 76 18	0.9 30 85 92

												88		8	11
98	CEP	Centrosomal	5.	4.	4.	5.	6.	5.	2.0	1.0	2.0	U	0.0	0.9	
57	350	protein 350kda	81	92	41	51	80	85	128	092	12	p	46	30	
			62	18	78	94	47	95	644	5	86		86	85	
			9	1	6	4	5	2	2		44		41	92	
											2		81	11	
57	ZNF	Zinc finger,	7.	6.	6.	7.	7.	7.	1.5	0.6	1.5	U	0.0	0.9	
16	X1	NFX1-type	17	93	29	40	73	11	307	142	30	p	49	30	
9		containing 1	13	48	87	03	38	34	832	7	78		22	85	
				4	7	9	5	8	29		32		45	92	
											29		79	11	
10	LOC	Uncharacterized	10	8.	8.	10	10	10	2.3	1.2	2.3	U	0.0	0.9	
05	1005	LOC100507412	.4	84	21	.4	.6	.1	585	378	58	p	40	30	
07	0741		32	04	69	63	32	06	333	9	53		94	85	
41	2		04	7	8	88	79	49	48		33		85	92	
2											48		57	11	
90	KLH	Kelch like family	7.	7.	7.	5.	6.	6.	-2.	-1.	2.0	D	0.0	0.9	
29	L13	member 13	07	30	44	66	80	30	026	019	26	o	07	30	
3			82	78	09	14	35	50	523	006	52	w	59	85	
			8	8		6	5	3	165	667	31	n	23	92	
											65		29	11	
55	CDK	CDK5 regulatory	7.	6.	6.	7.	8.	7.	2.0	1.0	2.0	U	0.0	0.9	
75	5RA	subunit associated	33	09	93	81	18	40	248	177	24	p	17	30	
5	P2	protein 2	02	62	22	45	78	97	055	833	80		12	85	
			7	1	9	3	5	4	03	33	55		39	92	
											03		16	11	
10	FER	Fermitin family	4.	4.	5.	3.	4.	3.	-1.	-0.	1.6	D	0.0	0.9	
97	MT2	member 2	11	70	42	93	10	93	689	756	89	o	36	30	
9			09	87	45	43	08	90	543	633	54	w	27	85	

				3	5	4	9	5	31	333	33	n	65	92
											1		01	11
60	MRP	Mitochondrial	7.	7.	7.	7.	6.	7.	-1.	-0.	1.5	D	0.0	0.9
48	S35	ribosomal protein	38	33	81	05	56	02	544	627	44	o	16	30
8		S35	45	05	24	97	42	13	771	393	77	w	48	85
			5	9	2	7	5	6	372	333	13	n	85	92
											72		5	11
25	SDH	Succinate	9.	9.	10	9.	9.	9.	-1.	-0.	1.5	D	0.0	0.9
58	AP1	dehydrogenase	64	91	.0	48	02	14	571	652	71	o	06	30
12		complex subunit A,	26	69	53	21	82	54	737	36	73	w	23	85
		flavoprotein	8	4	34	6	7	5	185		71	n	94	92
		pseudogene 1									85		1	11
84	ZNF	Zinc finger protein	7.	6.	7.	8.	7.	7.	1.6	0.7	1.6	U	0.0	0.9
91	587	587	31	82	15	23	69	64	979	637	97	p	07	30
4			08	56	15	83	52	57	178	666	91		92	85
			4	3	9	5	5	6	59	67	78		17	92
											59		61	11
65	SLC	Solute carrier	6.	7.	7.	4.	7.	5.	-3.	-1.	3.2	D	0.0	0.9
46	8A1	family 8	55	56	69	17	21	34	239	695	39	o	44	30
		(sodium/calcium	35	97	82	87	04	50	482	763	48	w	05	85
		exchanger),	3	9	3	9	1	6	431	333	24	n	09	92
		member 1									31		91	11
34	APO	Apolipoprotein E	9.	9.	9.	8.	8.	9.	-2.	-1.	2.0	D	0.0	0.9
8	E		71	79	85	08	98	08	098	069	98	o	03	30
			51	48	65	91	35	59	473	34	47	w	67	85
			5	6	8	1	1	5	144		31	n	53	92
											44		86	11
78	COL	Collectin subfamily	8.	8.	9.	6.	8.	7.	-2.	-1.	2.6	D	0.0	0.9
98	EC11	member 11	73	84	37	99	73	08	604	381	04	o	16	30

9			80 9	68 7	41 4	67 7	84 4	05 1	717 06	126 667	71 70 6	w n	63 99	85 92 11
74 32	VIP	Vasoactive intestinal peptide	6. 43 48 7	7. 14 49 6	5. 42 68 4	4. 39 45 5	5. 38 10 9	4. 29 33 7	-3. 129 401 282	-1. 645 886 667	3.1 29 40 12 82	D o w n	0.0 07 64 31 14	0.9 30 85 92 11
25 70 19	FRM D3	FERM domain containing 3	4. 60 52 9	4. 88 08 9	5. 08 51 2	4. 29 26 2	4. 26 43 8	4. 07 43 8	-1. 566 049 702	-0. 647 13 97	1.5 66 04 97 02	D o w n	0.0 03 82 68 46	0.9 30 85 92 11
23 48	FOL R1	Folate receptor 1 (adult)	4. 73 40 4	4. 83 47 5	4. 56 69 7	5. 79 50 7	5. 43 32 8	5. 01 05 8	1.6 256 650 08	0.7 010 3 08	1.6 25 66 50 08	U p	0.0 11 35 75 03	0.9 30 85 92 11
63 57	CCL 13	Chemokine (C-C motif) ligand 13	3. 92 64 4	3. 92 85 8	3. 74 06 2	4. 19 72 7	4. 63 38 7	4. 58 22 1	1.5 219 314 02	0.6 059 033 33	1.5 21 93 14 02	U p	0.0 04 29 30 55	0.9 30 85 92 11
65 25	SMT N	Smoothelin	6. 41 53	6. 71 89 1	7. 72 32 6	5. 57 87 6	6. 44 38 7	5. 74 90 9	-2. 040 020 053	-1. 028 583 333	2.0 40 02 00 53	D o w n	0.0 24 68 95 22	0.9 30 85 92 11
79	ZDH	Zinc finger,	6.	7.	6.	8.	7.	7.	2.0	1.0	2.0	U	0.0	0.9

84	HC1	DHHC-type	91	05	68	66	61	44	350	250	35	p	12	30
4	1	containing 11	36	02	32	03	54	65	769	833	07		07	85
			3	3		4	6	1	31	33	69		18	92
											31		84	11
98	POM	POM121	6.	6.	6.	6.	7.	7.	1.5	0.6	1.5	U	0.0	0.9
83	121	transmembrane	93	35	04	85	32	06	534	354	53	p	35	30
		nucleoporin	23	22	64	11	10	53	473	733	44		44	85
			9	1	9	3	3	5	36	33	73		52	92
											36		56	11
53	PKM	Pyruvate kinase,	8.	8.	9.	8.	7.	7.	-1.	-0.	1.9	D	0.0	0.9
15		muscle	68	21	26	13	34	81	938	954	38	o	14	30
			50	72	38	63	86	70	145	676	14	w	08	85
			1		9	7	3	7	213	667	52	n	81	92
											13		26	11
54	GRA	GRAM domain	4.	4.	4.	3.	3.	3.	-1.	-0.	1.6	D	0.0	0.9
76	MD1	containing 1C	07	33	28	59	11	94	602	680	02	o	12	30
2	C		71	33	72	08	63	89	746	546	74	w	28	85
			4	7	5	6	1	5	954	667	69	n	50	92
											54		25	11
46	NAR	Asparaginyl-trna	6.	6.	7.	5.	5.	5.	-2.	-1.	2.1	D	0.0	0.9
77	S	synthetase	24	52	14	88	03	67	151	105	51	o	06	30
			57	98	17	77	43	98	088	066	08	w	41	85
				2	1	8	6	9	18	667	81	n	00	92
											8		16	11
48	NPY	Neuropeptide Y	6.	6.	7.	5.	6.	5.	-2.	-1.	2.2	D	0.0	0.9
52			84	56	13	45	06	53	242	165	42	o	00	30
			77	34	45	48	34	16	746	266	74	w	97	85
			6	1	7	3	3	8	665	667	66	n	62	92
											65		05	11

77 1	CA1 2	Carbonic anhydrase XII	7. 56 62 5	6. 47 46 2	6. 29 00 1	7. 46 37 1	7. 97 11 5	7. 58 65 6	1.8 619 917 32	0.8 968 466 67	1.8 61 99 17 32	U p	0.0 29 21 51 29	0.9 30 85 92 11
90 42 7	BMF	Bcl2 modifying factor	6. 96 49 9	7. 93 22 6	7. 13 02 4	6. 12 56 6	6. 99 02 1	6. 59 20 2	-1. 709 056 391	-0. 773 2 63 91	1.7 09 05 63 91	D o w n	0.0 38 92 02 25	0.9 30 85 92 11
39 77	LIFR	Leukemia inhibitory factor receptor $\alpha$	6. 09 06 3	6. 29 96 4	5. 55 71 7	5. 36 69 8	4. 75 16 4	5. 01 13 2	-1. 917 420 373	-0. 939 166 667	1.9 17 42 03 73	D o w n	0.0 05 06 96 53	0.9 30 85 92 11
22 09 65	FAM 13C	Family with sequence similarity 13 member C	5. 24 94	6. 35 05 3	6. 53 23 5	4. 17 58 7	4. 37 47 8	5. 40 12 4	-2. 627 085 826	-1. 393 463 333	2.6 27 08 58 26	D o w n	0.0 11 21 52 4	0.9 30 85 92 11
51 71 9	CAB 39	Calcium binding protein 39	3. 91 62 3	4. 02 84 8	4. 76 25 4	3. 88 71 2	2. 79 25 8	3. 66 67 2	-1. 725 414 916	-0. 786 943 333	1.7 25 41 49 16	D o w n	0.0 42 91 92 25	0.9 30 85 92 11
40 6	ARN TL	Aryl hydrocarbon receptor nuclear translocator like	6. 83 68 6	7. 01 19 4	6. 59 32 5	5. 36 51 5	6. 33 48 5	4. 77 13 7	-2. 502 858 39	-1. 323 576 667	2.5 02 85 83	D o w n	0.0 07 37 75	0.9 30 85 92

											9		48	11
51 05 0	PI15	Peptidase inhibitor 15	3. 87 49 3	4. 08 72 3	5. 61 02 3	3. 19 85 2	3. 86 2	3. 46 19 2	-2. 023 215 507	-1. 016 65	2.0 23 21 55 07	D o w n	0.0 47 98 89 88	0.9 30 85 92 11
23 16	FLN A	Filamin A, $\alpha$	8. 12 92 2	8. 99 41 9	9. 44 57 9	5. 78 56 7	8. 62 80 3	6. 55 83	-3. 644 531 408	-1. 865 733 333	3.6 44 53 14 08	D o w n	0.0 27 68 70 15	0.9 30 85 92 11
79 79 9	UGT 2A3	UDP glucuronosyltransf erases 2 family, polypeptide A3	7. 58 62 9	8. 23 63 8	8. 86 28 8	7. 46 82 5	5. 63 02 2	6. 70 59	-3. 088 828 99	-1. 627 06	3.0 88 82 89 9	D o w n	0.0 10 94 32 13	0.9 30 85 92 11
60 48 1	ELO VL5	ELOVL fatty acid elongase 5	5. 59 84 3	5. 70 58 3	6. 38 10 7	5. 09 12 7	4. 66 77	5. 06 96 7	-1. 934 861 098	-0. 952 23	1.9 34 86 10 98	D o w n	0.0 04 46 50 3	0.9 30 85 92 11
85 48 0	TSL P	Thymic stromal lymphopoietin	4. 08 52 1	4. 73 80 9	5. 44 15 6	3. 00 72 8	3. 91 71 2	3. 19 29 8	-2. 607 185 68	-1. 382 493 333	2.6 07 18 56 8	D o w n	0.0 05 63 31 8	0.9 30 85 92 11
44 03 66	HER C2P8	Hect domain and RLD 2 pseudogene 8	7. 13 93	6. 74 95	6. 56 14	7. 41 61	7. 60 66	7. 32 09	1.5 487 847	0.6 311 366	1.5 48 78	U p	0.0 10 80	0.9 30 85

			3	8	1	8	2	3	65	67	47		32	92
											65		2	11
65	HLT	Helicase-like	4.	4.	5.	3.	3.	4.	-1.	-0.	1.5	D	0.0	0.9
96	F	transcription factor	20	54	00	96	43	35	584	663	84	o	45	30
			27	70	22	82	42	79	348	89	34	w	16	85
			1	4	9	1	4	2	817		88	n	59	92
											17		43	11
22	PDC	Programmed cell	5.	5.	5.	6.	6.	5.	1.5	0.6	1.5	U	0.0	0.9
98	D11	death 11	79	47	49	13	51	92	205	046	20	p	15	30
4			15	56	86	76	44	76	606	033	56		12	85
			3	7	8	4	3	2	2	33	06		23	92
											2		8	11
23	FOS	FOS-like antigen 2	7.	7.	7.	7.	6.	7.	-1.	-0.	1.5	D	0.0	0.9
55	L2		33	99	76	19	72	24	561	643	61	o	22	30
			32	82	34	76	29	43	908	31	90	w	42	85
			3	3	2	3	5	7	565		85	n	33	92
											65		32	11
84	RGS	Regulator of	6.	6.	7.	4.	5.	6.	-3.	-1.	3.0	D	0.0	0.9
90	5	G-protein signaling	83	84	73	84	67	02	081	623	81	o	02	30
		5	50	04	87	38	49	43	672	713	67	w	19	85
			9	4	1	6	3	1	038	333	20	n	44	92
											38		33	11
10	HER	Hect domain and	7.	6.	6.	7.	7.	7.	1.5	0.6	1.5	U	0.0	0.9
02	C2P4	RLD 2 pseudogene	13	74	56	41	60	32	487	311	48	p	10	30
89		4	93	95	14	61	66	09	847	366	78		80	85
57			3	8	1	8	2	3	65	67	47		32	92
4											65		2	11
25	QPC	Glutaminyl-peptide	4.	4.	4.	3.	3.	3.	-1.	-0.	1.7	D	0.0	0.9
79	T	cyclotransferase	26	49	74	60	75	85	702	767	02	o	01	30



7			57 1	76 4	67 5	17 3	26	24 1	655 623	786 667	65 56 23	w n	21 02 37	85 92 11
71 50	TOP 1	Topoisomerase (DNA) I	9. 71 98 6	9. 57 03 5	8. 83 66 1	10 .2 00 24	10 .0 13 09	9. 80 00 1	1.5 463 211 73	0.6 288 4 11 73	1.5 46 32 11 73	U p	0.0 33 47 19 96	0.9 30 85 92 11
55 78 4	MCT P2	Multiple C2 domains, transmembrane 2	7. 17 42 4	6. 89 99 8	7. 00 00 5	7. 97 56 9	7. 53 40 6	7. 65 32 9	1.6 202 951 85	0.6 962 566 67	1.6 20 29 51 85	U p	0.0 03 80 24 47	0.9 30 85 92 11
88 35	SOC S2	Suppressor of cytokine signaling 2	5. 47 5	6. 08 11 3	6. 66 06 7	4. 41 94 5	5. 19 30 9	5. 59 61	-2. 003 774 277	-1. 002 72	2.0 03 77 42 77	D o w n	0.0 29 28 76 02	0.9 30 85 92 11
22 02	EFE MP1	EGF containing fibulin-like extracellular matrix protein 1	4. 33 99 1	6. 55 95 8	5. 98 50 9	6. 45 19 5	7. 78 91 8	8. 59 29 7	3.9 536 175 87	1.9 831 733 33	3.9 53 61 75 87	U p	0.0 19 67 95 55	0.9 30 85 92 11
25 80 2	LMO D1	Leiomodin 1 (smooth muscle)	4. 82 34 9	5. 20 92 1	5. 60 57 9	4. 27 37 5	4. 99 38 1	4. 48 64 7	-1. 545 585 359	-0. 628 153 333	1.5 45 58 53 59	D o w n	0.0 40 06 31 65	0.9 30 85 92 11
12	KLH	Kelch domain	6.	6.	6.	5.	5.	6.	-1.	-0.	1.5	D	0.0	0.9

68	DC9	containing 9	34	42	33	69	40	05	572	653	72	o	09	30
23			78	53	91	50	48	19	954	476	95	w	19	85
			2	8	3	4	8	8	203	667	42	n	82	92
											03		8	11
70	TEK	TEK tyrosine	5.	6.	6.	4.	5.	5.	-1.	-0.	1.9	D	0.0	0.9
10		kinase, endothelial	72	35	93	92	61	66	914	937	14	o	24	30
			29	16	91	07	51	63	741	15	74	w	24	85
			4	3	9	4	9	8	986		19	n	28	92
											86		63	11
63	SDC	Syndecan 2	5.	5.	6.	4.	4.	5.	-2.	-1.	2.0	D	0.0	0.9
83	2		01	98	14	23	70	06	063	045	63	o	14	30
			67	59	63	71	77	91	414	033	41	w	71	85
			1	9	6		3	3	033	333	40	n	87	92
											33		39	11
14	PRI	Proline rich	5.	5.	5.	4.	4.	5.	-1.	-0.	1.5	D	0.0	0.9
52	MA1	membrane anchor	39	81	76	68	83	56	548	631	48	o	37	30
70	1		86	39	63	81	73	01	698	056	69	w	04	85
			3	2	6	9	9	6	885	667	88	n	16	92
											85		25	11
23	RYB	RING1 and YY1	8.	8.	8.	8.	7.	7.	-1.	-0.	1.5	D	0.0	0.9
42	P	binding protein	04	76	32	00	35	98	511	596	11	o	44	30
9			92	50	03	32	81	49	652	126	65	w	89	85
			9	1	3	2		3	644	667	26	n	55	92
											44		57	11
10	TUB	Tubulin, $\gamma$ complex	3.	4.	4.	3.	3.	3.	-1.	-0.	1.5	D	0.0	0.9
42	GCP	associated protein	79	20	45	84	41	41	507	592	07	o	18	30
6	3	3	97	07	72	95	86	28	554	21	55	w	89	85
			4	3	4	3	9	6	335		43	n	90	92
											35		54	11

90 1	CCN G2	Cyclin G2	5. 36 01 8	5. 62 05 7	5. 57 78 9	4. 68 81 9	4. 48 63 3	5. 26 27 8	-1. 632 534 334	-0. 707 113 333	1.6 32 53 43 34	D o w n	0.0 12 10 25 54	0.9 30 85 92 11
10 84 1	FTC D	Formimidoyltransf erases cyclodeaminase	6. 04 31	4. 99 39	5. 37 32	5. 90 56 6	6. 12 32 7	6. 35 13 4	1.5 764 615 69	0.6 566 9 69	1.5 76 46 15 69	U p	0.0 44 40 74 86	0.9 30 85 92 11
60	ACT B	Actin, $\beta$	11 .2 13 43	11 .6 69 84	11 .9 42 89	11 .3 59 16	10 .6 52 28	10 .9 31 7	-1. 545 071 212	-0. 627 673 333	1.5 45 07 12 12	D o w n	0.0 30 54 53 59	0.9 30 85 92 11
18 2	JAG 1	Jagged 1	4. 65 96 1	5. 05 46	5. 51 03 5	4. 39 05 7	3. 95 26 5	4. 76 60 4	-1. 630 257 662	-0. 705 1 662	1.6 30 25 76 62	D o w n	0.0 33 24 68 57	0.9 30 85 92 11
72 84 11	GUS BP1	Glucuronidase, $\beta$ pseudogene 1	6. 54 03	6. 28 58 2	6. 15 84 1	6. 77 27 8	7. 35 11	6. 74 81 8	1.5 466 820 64	0.6 291 766 67	1.5 46 68 20 64	U p	0.0 18 01 60 71	0.9 30 85 92 11
31 76	HN MT	Histamine N-methyltransferase	8. 23 05 4	8. 03 93 7	7. 56 62 7	8. 88 05 4	8. 47 13 3	8. 37 47 7	1.5 477 294 81	0.6 301 533 33	1.5 47 72 94	U p	0.0 21 92 81	0.9 30 85 92

												81		44	11
48	NRC	Neuronal cell	8.	8.	9.	9.	9.	9.	1.5	0.6	1.5	U	0.0	0.9	
97	AM	adhesion molecule	56	46	00	62	09	13	252	09	25	p	19	30	
			36	67	14	1	92	84	016		20		82	85	
				1	5		9	7	53		16		91	92	
											53		36	11	
10	MYL	Myosin light chain	9.	10	10	7.	9.	7.	-3.	-1.	3.4	D	0.0	0.9	
39	9	9	63	.0	.8	26	93	97	479	798	79	o	25	30	
8			38	43	95	35	55	72	709	966	70	w	41	85	
			1	5	97	8	4	6	012	667	90	n	90	92	
											12		33	11	
41	MBN	Muscleblind like	4.	4.	5.	4.	3.	3.	-2.	-1.	2.0	D	0.0	0.9	
54	L1	splicing regulator 1	23	69	24	04	20	92	005	004	05	o	11	30	
			79	70	88	10	40	63	752	143	75	w	44	85	
			9	6	2	2	7	5	136	333	21	n	70	92	
											36		38	11	
44	AKR	Aldo-keto	11	11	11	10	10	11	-1.	-0.	1.6	D	0.0	0.9	
12	1B15	reductase family 1,	.6	.2	.8	.5	.8	.1	610	687	10	o	09	30	
82		member B15	06	89	29	69	98	94	806	783	80	w	67	85	
			77	22	75	48	64	27	65	333	66	n	63	92	
											5		43	11	
54	RNF	Ring finger protein	4.	3.	4.	4.	4.	4.	1.5	0.5	1.5	U	0.0	0.9	
89	43	43	07	68	20	79	42	49	000	850	00	p	10	30	
4			02	62	30	49	58	39	979	566	09		93	85	
			1	9	5	6	4	2	09	67	79		06	92	
											09		56	11	
21	FBL	Fibulin 2	5.	7.	6.	7.	7.	8.	2.5	1.3	2.5	U	0.0	0.9	
99	N2		47	24	19	01	60	36	660	595	66	p	24	30	
			24	25	01	54	13	68	097	266	00		39	85	

			2	2	7	6	8	5	76	67	97		73	92
											76		18	11
15	CBW	COBW domain	4.	3.	4.	3.	3.	3.	-1.	-0.	1.6	D	0.0	0.9
04	D2	containing 2	45	86	15	71	32	19	674	744	74	o	05	30
72			21	23	27	57	17	77	812		81	w	34	85
			2	7	1	4	2	4	975		29	n	61	92
											75		82	11
44	MT1	Metallothionein 1F	11	9.	8.	11	11	11	3.2	1.7	3.2	U	0.0	0.9
94	F		.0	27	70	.5	.1	.4	510	008	51	p	12	30
			27	08	54	44	51	09	145	9	01		64	85
			06	8	2	88	57	58	21		45		23	92
											21		3	11
33	HSP	Heat shock protein	5.	6.	5.	4.	4.	4.	-1.	-0.	1.9	D	0.0	0.9
06	A2	family A (Hsp70)	08	11	88	94	49	73	956	968	56	o	08	30
		member 2	11	40	50	91	32	25	678	406	67	w	47	85
				4	6	7	3	8	417	667	84	n	53	92
											17		91	11
64	SEL	Selectin P	6.	6.	7.	5.	5.	6.	-1.	-0.	1.7	D	0.0	0.9
03	P		38	99	19	54	97	55	784	835	84	o	26	30
			62	91	57	35	74	45	112	206	11	w	85	85
			5	9	2		6	8	595	667	25	n	52	92
											95		32	11
10	SPO	Spondin 1,	6.	6.	7.	3.	6.	4.	-3.	-1.	3.3	D	0.0	0.9
41	N1	extracellular matrix	32	90	80	95	89	88	399	765	99	o	39	30
8		protein	21	54	2	37	19	77	658	39	65	w	86	85
			9	1		2	4	7	893		88	n	71	92
											93		79	11
10	OLF	Olfactomedin 4	3.	3.	5.	6.	5.	5.	3.3	1.7	3.3	U	0.0	0.9
56	M4		99	00	20	67	16	53	045	244	04	p	18	30

2			01 6	60 4	53 6	41 3	97 3	11	794 15	666 67	57 94 15		57 00 13	85 92 11
22 73	FHL 1	Four and a half LIM domains 1	6. 15 91 1	7. 26 17 2	7. 60 13 7	4. 53 93 2	6. 27 62 4	6. 09 41 9	-2. 586 169 2	-1. 370 816 667	2.5 86 16 92	D o w n	0.0 32 51 73 23	0.9 30 85 92 11
16 11 98	CLE C14 A	C-type lectin domain family 14, member A	5. 90 59 6	6. 17 50 3	6. 24 88 5	5. 21 44 6	5. 13 91 2	5. 68 80 2	-1. 696 717 838	-0. 762 746 667	1.6 96 71 78 38	D o w n	0.0 04 77 13 72	0.9 30 85 92 11
28 39 70	PDX DC2 P	Pyridoxal-depende nt decarboxylase domain containing 2, pseudogene	5. 15 31	5. 57 97 5	6. 33 36 7	4. 89 51 7	4. 32 09	5. 20 72 5	-1. 841 706 712	-0. 881 043 333	1.8 41 70 67 12	D o w n	0.0 31 97 36 18	0.9 30 85 92 11
12 42 22	PAQ R4	Progesterin and adipoq receptor family member IV	7. 26 42 9	7. 23 02 2	7. 51 48 7	8. 99 00 7	7. 73 40 9	8. 13 28	1.9 308 240 03	0.9 492 166 67	1.9 30 82 40 03	U p	0.0 14 96 13 29	0.9 30 85 92 11
56 55	KLK 10	Kallikrein related peptidase 10	8. 71 14 6	8. 57 99 4	8. 91 96 8	7. 72 68 8	8. 08 35 6	8. 38 70 1	-1. 592 407 973	-0. 671 21 79	1.5 92 40 79 73	D o w n	0.0 10 18 89 19	0.9 30 85 92 11
25	FUT	Fucosyltransferase	4.	5.	5.	4.	4.	4.	-1.	-0.	1.5	D	0.0	0.9

30	8	8 (α (1,6) fucosyltransferase)	84 75 3	23 61 5	51 10 2	69 09 3	41 53 6	61 09 9	543 073 376	625 806 667	43 07 33 76	o w n	12 26 17 19	30 85 92 11
10 05 27 97 8	TME M56- RWD D3	TMEM56-RWDD3 readthrough	5. 89 43 1	5. 86 80 1	6. 65 24 5	5. 37 69 9	5. 04 31 1	5. 84 50 5	-1. 643 236 349	-0. 716 54 63 49	1.6 43 23 63 49	D o w n	0.0 36 14 35 53	0.9 30 85 92 11
85 47 7	SCIN	Scinderin	5. 46 97 4	6. 05 81 1	5. 95 79 1	6. 97 31 2	6. 18 37 5	6. 53 15 14	1.6 634 594 14	0.7 341 866 67	1.6 63 45 94 14	U p	0.0 19 28 09 9	0.9 30 85 92 11
23 19 3	GAN AB	Glucosidase, α; neutral AB	7. 53 74 9	7. 28 85 6	6. 91 90 3	6. 86 20 5	6. 45 20 9	6. 61 98 9	-1. 520 325 251	-0. 604 38 52 51	1.5 20 32 52 51	D o w n	0.0 18 51 78 25	0.9 30 85 92 11
10 23 1	RCA N2	Regulator of calcineurin 2	6. 26 56	7. 58 97	7. 70 95	4. 24 57 5	6. 03 14 3	6. 36 39 4 2	-3.1 193 670 75	-1. 641 253 333	3.1 19 36 70 75	D o w n	0.0 26 33 67 71	0.9 30 85 92 11
38 8	RHO B	Ras homolog family member B	6. 05 48 4	7. 98 13 5	6. 76 43 5	6. 07 89 5	5. 63 72 5	5. 94 72 5	-2. 064 386 832	-1. 045 713 333	2.0 64 38 68 32	D o w n	0.0 45 71 32 93	0.9 30 85 92 11

10	NPIP	Nuclear pore	5.	5.	6.	4.	4.	5.	-1.	-0.	1.8	D	0.0	0.9
10	A7	complex	15	57	33	89	32	20	841	881	41	o	31	30
59		interacting protein	31	97	36	51	09	72	706	043	70	w	97	85
93		family member A7		5		7		5	712	333	67	n	36	92
8											12		18	11
90	CLD	Claudin 2	9.	7.	9.	10	9.	9.	2.2	1.1	2.2	U	0.0	0.9
75	N2		50	60	19	.2	99	58	452	668	45	p	37	30
			76	25	75	29	57	28	353	666	23		46	85
			3		1	57	8	9	31	67	53		11	92
											31		52	11
86	EIF3	Eukaryotic	8.	9.	9.	8.	7.	8.	-1.	-0.	1.6	D	0.0	0.9
67	H	translation	60	04	38	53	68	65	644	718	44	o	45	30
		initiation factor 3	24	29	65	82	70	26	915	013	91	w	41	85
		subunit H	9	7	6		9	9	34	333	53	n	47	92
											4		9	11
31	HLA	Major	9.	9.	10	8.	9.	9.	-1.	-0.	1.5	D	0.0	0.9
13	-DPA	histocompatibility	45	71	.4	80	36	44	573	653	73	o	48	30
	1	complex, class II,	46	72	07	2	73	86	270	766	27	w	02	85
		DP $\alpha$ 1	3		45		5	3	418	667	04	n	86	92
											18		31	11
38	ZNF	Zinc finger protein	6.	7.	7.	9.	8.	9.	2.8	1.5	2.8	U	0.0	0.9
85	761	761	91	91	83	35	26	61	743	232	74	p	05	30
61			89	12	07	01	37	66	053	133	30		50	85
			7	1	7	4	9	6	49	33	53		54	92
											49		8	11
23	AM	A-methylacyl-coa	6.	6.	6.	5.	5.	5.	-1.	-0.	1.7	D	0.0	0.9
60	ACR	racemase	29	20	52	76	12	71	749	807	49	o	05	30
0			64	38	27	15	54	42	925	293	92	w	17	85
			7	5	6	6		4	294	333	52	n	56	92



											94		18	11
54 12	UBL 3	Ubiquitin like 3	6. 55 77 4	6. 61 71 1	7. 00 53 1	6. 18 08 7	5. 12 83	6. 37 45 6	-1. 780 328 335	-0. 832 143 333	1.7 80 32 83 35	D o w n	0.0 35 27 93 73	0.9 30 85 92 11
66 52	SOR D	Sorbitol dehydrogenase	8. 31 27 6	8. 32 56 5	8. 34 15 1	7. 02 44 5	7. 52 06 1	7. 24 20 3	-2. 091 121 178	-1. 064 276 667	2.0 91 12 11 78	D o w n	0.0 00 22 78 9	0.9 30 85 92 11
28 61	GPR 37	G protein-coupled receptor (endothelin receptor type B-like)	5. 61 59 6	6. 13 29	5. 47 76 5	5. 09 07 5	4. 81 41 4	5. 48 44 2	-1. 528 800 335	-0. 612 4 335	1.5 28 80 03 35	D o w n	0.0 34 09 61 93	0.9 30 85 92 11
27 34 1	RRP 7A	Ribosomal RNA processing homolog A	4. 40 87 8	4. 15 81 3	4. 12 62 4	4. 77 98 3	4. 70 75 8	5. 00 03 8	1.5 138 406 3	0.5 982 133 33	1.5 13 84 06 3	U p	0.0 03 47 86 35	0.9 30 85 92 11
40 92	SMA D7	SMAD family member 7	4. 96 27 6	5. 74 94 1	5. 91 82	4. 01 87 2	4. 91 78	4. 77 06 7	-1. 964 814 8	-0. 974 393 333	1.9 64 81 48	D o w n	0.0 16 28 01 12	0.9 30 85 92 11
94 72	AKA P6	A-kinase anchoring protein 6	5. 53 44	5. 72 25	6. 27 10	4. 69 25	4. 80 80	4. 68 46	-2. 164 889	-1.1 142 933	2.1 64 88	D o w	0.0 00 71	0.9 30 85

			6	6	2		3	3	416	33	94	n	58	92
											16		68	11
18	DPY	Dihydropyrimidina	3.	5.	5.	2.	4.	3.	-2.	-1.	2.6	D	0.0	0.9
09	SL3	se like 3	94	05	47	98	18	16	600	378	00	o	14	30
			27	79	41	75	96	10	579	833	57	w	97	85
			1		8	9	7	3	845	333	98	n	67	92
											45		68	11
15	CYP	Cytochrome P450,	6.	6.	7.	6.	5.	6.	-1.	-0.	1.6	D	0.0	0.9
95	51A1	family 51,	82	38	46	20	68	53	681	749	81	o	47	30
		subfamily A,	62	18	44	27	49	61	295	573	29	w	63	85
		polypeptide 1	7	6	4	6	4	5	526	333	55	n	27	92
											26		03	11
74	EIF4	Eukaryotic	6.	7.	7.	6.	5.	6.	-1.	-0.	1.9	D	0.0	0.9
58	H	translation	68	31	31	76	55	20	908	932	08	o	21	30
		initiation factor 4H	40	47	69	28	43	09	620	53	62	w	35	85
			4	2	1	5		3	138		01	n	25	92
											38		3	11
28	TCA	T cell activation	8.	7.	7.	8.	8.	9.	1.8	0.8	1.8	U	0.0	0.9
53	IM	inhibitor,	13	64	99	68	62	02	122	578	12	p	01	30
43		mitochondrial	01	20	11	07	71	88	768	033	27		93	85
			3	3	1			8	12	33	68		10	92
											12		1	11
51	LUC	LUC7-like 3	7.	8.	7.	8.	9.	8.	1.8	0.8	1.8	U	0.0	0.9
74	7L3	pre-mrna splicing	87	19	35	67	10	20	060	528	06	p	18	30
7		factor	93	70	63	96	87	29	527	4	05		99	85
			9	2	3	2	3	1	12		27		11	92
											12		22	11
19	PAO	Polyamine oxidase	7.	6.	6.	7.	7.	7.	1.6	0.6	1.6	U	0.0	0.9
67	X	(exo-N4-amino)	24	79	63	73	79	22	169	932	16	p	16	30

43			96 9	56 6	04 1	23 7	83	49 3	555 28	8	95 55 28		78 36 77	85 92 11
95 32	BAG 2	BCL2 associated athanogene 2	4. 05 30 3	4. 07 71 4	5. 16 44 1	2. 99 71 3	3. 65 67 3	3. 83 60 9	-1. 911 727 198	-0. 934 876 667	1.9 11 72 71 98	D o w n	0.0 25 86 61 61	0.9 30 85 92 11
27 29	GCL C	Glutamate-cysteine ligase, catalytic subunit	6. 11 08 8	6. 29 77 1	6. 51 14 3	5. 46 14 8	5. 82 10 2	5. 85 13 5	-1. 510 880 963	-0. 595 39 09 63	1.5 10 88 09 63	D o w n	0.0 11 20 31 31	0.9 30 85 92 11
49 8	ATP5 A1	ATP synthase, H <sup>+</sup> transporting, mitochondrial F1 complex, $\alpha$ subunit 1, cardiac muscle	9. 54 74 6	9. 85 71 6	10 .3 91 94	9. 32 10 2	8. 61 42 5	9. 21 59 2	-1. 842 660 134	-0. 881 79 01 34	1.8 42 66 01 34	D o w n	0.0 11 31 73 35	0.9 30 85 92 11
27 29 5	PDL1 M3	PDZ and LIM domain 3	5. 72 42 8	6. 44 26 6	7. 40 17 1	3. 19 97 9	5. 98 75 7	4. 17 36 7	-4. 196 558 426	-2. 069 206 667	4.1 96 55 84 26	D o w n	0.0 19 32 74 09	0.9 30 85 92 11
87	ACT N1	Actinin, $\alpha$ 1	6. 94 63 5	7. 30 88 2	7. 89 57 4	6. 44 60 3	6. 76 41 6	6. 54 00 9	-1. 741 354 581	-0. 800 21 45 81	1.7 41 35 45 81	D o w n	0.0 12 97 45 87	0.9 30 85 92 11
11	KCT	Potassium channel	7.	7.	8.	6.	6.	7.	-1.	-0.	1.7	D	0.0	0.9

52	D12	tetramerization	12	91	03	31	90	43	747	804	47	o	46	30
07		domain containing	24	99	41	74	42	99	081	946	08	w	36	85
		12	2		6	4	3	7	205	667	12	n	16	92
											05		73	11
96	ARH	Rho guanine	6.	6.	6.	7.	6.	6.	1.6	0.7	1.6	U	0.0	0.9
39	GEF	nucleotide	24	62	49	77	87	88	499	224	49	p	27	30
	10	exchange factor 10	66	01	98	79	03	55	702	4	97		42	85
			2		1	8	1	6	36		02		78	92
											36			11
10	LOC	NP1P-like protein 1	5.	5.	6.	4.	4.	5.	-1.	-0.	1.8	D	0.0	0.9
27	1027		15	57	33	89	32	20	841	881	41	o	31	30
24	2499		31	97	36	51	09	72	706	043	70	w	97	85
99	3			5		7		5	712	333	67	n	36	92
3											12		18	11
22	SHA	SH3 and multiple	6.	5.	5.	6.	6.	6.	1.5	0.5	1.5	U	0.0	0.9
94	NK2	ankyrin repeat	07	55	98	61	58	18	110	955	11	p	19	30
1		domains 2	46	29	11	69	95	88	031	066	00		20	85
			7	5	5	6		3	48	67	31		44	92
											48		18	11
60	SCO	Short coiled-coil	4.	5.	6.	4.	3.	4.	-1.	-0.	1.7	D	0.0	0.9
59	C	protein	96	30	02	94	88	92	799	847	99	o	47	30
2			60	81	53	61	68	31	795	833	79	w	82	85
			7	8	3	2	4	2	927	333	59	n	49	92
											27		15	11
84	TCH	Trichoplein, keratin	5.	6.	5.	6.	6.	6.	1.7	0.8	1.7	U	0.0	0.9
26	P	filament binding	57	08	21	38	92	07	864	370	86	p	20	30
0			62	77	46	93	20	84	142	666	41		45	85
			6		8	9	1	4	53	67	42		72	92
											53		32	11

87 26	EED	Embryonic ectoderm development	5. 06 62 6	5. 22 25 7	6. 00 32 7	5. 09 55 9	4. 28 00 5	4. 82 69 1	-1. 620 587 218	-0. 696 516 667	1.6 20 58 72 18	D o w n	0.0 49 28 57 71	0.9 30 85 92 11
25 38	G6P C	Glucose-6-phospha tase, catalytic subunit	7. 35 58 6	7. 23 07 3	6. 07 43 1	5. 44 40 7	6. 13 12 8	5. 60 02 6	-2. 237 307 153	-1. 161 763 333	2.2 37 30 71 53	D o w n	0.0 12 35 93 24	0.9 30 85 92 11
71 48	TNX B	Tenascin XB	6. 00 12 4	7. 84 30 2	6. 71 67 3	7. 33 29 3	8. 09 13 4	8. 46 33 6	2.1 567 814 6	1.1 088 8 6	2.1 56 78 14 6	U p	0.0 49 27 88 26	0.9 30 85 92 11
57 12 4	CD2 48	CD248 molecule, endosialin	7. 00 10 2	7. 73 35 7	7. 80 94 7	7. 68 36 4	8. 55 77 6	8. 50 39 9	1.6 629 867 42	0.7 337 766 67	1.6 62 98 67 42	U p	0.0 43 89 55 46	0.9 30 85 92 11
22 87 3	DZIP 1	DAZ interacting zinc finger protein 1	4. 58 28	5. 33 20 4	5. 75 94 8	3. 70 23 7	4. 87 18 2	4. 17 95 3	-1. 963 643 91	-0. 973 533 333	1.9 63 64 39 1	D o w n	0.0 30 95 64 63	0.9 30 85 92 11
47 7	ATP1 A2	Atpase, Na <sup>+</sup> /K <sup>+</sup> transporting, $\alpha$ 2 polypeptide	6. 10 17	7. 00 16 8	7. 00 8 7	4. 58 71 7	6. 28 57 9	5. 29 87 7	-2. 484 949 73	-1. 313 216 667	2.4 84 94 97	D o w n	0.0 18 11 94	0.9 30 85 92

											3		41	11
51	PDE	Phosphodiesterase	4.	4.	5.	3.	4.	4.	-1.	-0.	1.8	D	0.0	0.9
44	4D	4D	37	64	22	21	22	13	848	886	48	o	23	30
			89	66	04	97	99	62	989	736	98	w	34	85
			8	7	6		5	5	032	667	90	n	57	92
											32		17	11
40	DUO	Dual oxidase	9.	10	9.	7.	9.	9.	-2.	-1.	2.3	D	0.0	0.9
57	XA2	maturation factor 2	55	.1	87	41	46	05	302	203	02	o	38	30
53			96	07	30	39	13	49	934	473	93	w	63	85
			3	92	8	1	3	7	428	333	44	n	14	92
											28		3	11
57	PSP	Phosphoserine	7.	8.	8.	7.	7.	4.	-3.	-1.	3.8	D	0.0	0.9
23	H	phosphatase	83	49	72	75	13	30	863	950	63	o	42	30
			03	35	14	28	33	90	825	03	82	w	68	85
			4	3	7		9	6	661		56	n	71	92
											61		82	11
95	ENT	Ectonucleoside	5.	5.	6.	4.	5.	4.	-1.	-0.	1.9	D	0.0	0.9
3	PD1	triphosphate	41	74	16	03	66	81	913	936	13	o	46	30
		diphosphohydrolase 1	05	52	40	70	29	04	866	49	86	w	75	85
			7	6	7	5	8		235		62	n	88	92
											35		7	11
51	KLH	Kelch like family	4.	4.	5.	3.	4.	4.	-1.	-0.	1.5	D	0.0	0.9
08	L5	member 5	25	71	00	74	02	29	554	636	54	o	22	30
8			07	55	99	79	62	30	330	293	33	w	92	85
			3		8	9	6	8	537	333	05	n	45	92
											37		57	11
33	PKD	Polycystic kidney	5.	5.	6.	4.	4.	5.	-1.	-0.	1.8	D	0.0	0.9
90	1P1	disease 1	15	57	33	89	32	20	841	881	41	o	31	30
44		(autosomal	31	97	36	51	09	72	706	043	70	w	97	85

		dominant) pseudogene 1		5		7		5	712	333	67	n	36	92
											12		18	11
78	PTP4	Protein tyrosine	6.	7.	7.	7.	5.	6.	-2.	-1.	2.0	D	0.0	0.9
03	A1	phosphatase type IVA, member 1	71	72	84	00	73	38	077	054	77	o	29	30
			70	55	37	75	12	39	022	516	02	w	34	85
			6	5	4	8	7	5	244	667	22	n	64	92
											44		66	11
12	CCR	Chemokine (C-C	5.	4.	4.	5.	5.	5.	1.5	0.6	1.5	U	0.0	0.9
35	6	motif) receptor 6	01	62	77	03	39	85	428	255	42	p	25	30
			42	70	04	46	57	80	452	933	84		68	85
			3	6	3	9	5	6	17	33	52		65	92
											17		3	11
10	NBR	Neighbor of	6.	6.	5.	6.	6.	7.	1.6	0.6	1.6	U	0.0	0.9
23	2	BRCA1 gene 2	49	11	84	45	86	17	041	817	04	p	23	30
0		(non-protein coding)	26	40	73	72	53	67	065	7	10		40	85
				4	5		7	3	79		65		44	92
											79		17	11
74	VTN	Vitronectin	13	12	12	11	12	12	-1.	-0.	1.5	D	0.0	0.9
48			.0	.9	.8	.9	.3	.6	548	631	48	o	11	30
			50	78	38	10	76	86	802	153	80	w	85	85
			95	01	56	43	9	73	658	333	26	n	25	92
											58		04	11
10	PDC	Programmed cell	5.	5.	5.	6.	5.	6.	1.5	0.6	1.5	U	0.0	0.9
01	D6	death 6	89	77	26	30	89	68	723	529	72	p	33	30
6			71	28	47	84	91	59	510	233	35		40	85
			9	8	6	9	8	3	25	33	10		53	92
											25		89	11
90	DIR	DIRAS family,	5.	6.	6.	4.	5.	4.	-2.	-1.	2.6	D	0.0	0.9
77	AS3	GTP-binding	17	33	74	02	72	24	677	420	77	o	29	30

		RAS-like 3	26 7	41 7	56 1	89 2	07 1	00 7	555 848	916 667	55 58 48	w n	14 30 13	85 92 11
28 89 6	IGK V1D- 33	Immunoglobulin $\kappa$ variable 1D-33	4. 84 29 2	5. 68 69 1	5. 56 01 6	4. 43 06 2	4. 01 58 8	4. 39 53 2	-2.1 180 304 54	-1. 082 723 333	2.1 18 03 04 54	D o w n	0.0 02 39 96 6	0.9 30 85 92 11
50 96	PCC B	Propionyl-coa carboxylase $\beta$ subunit	7. 87 44 5	7. 31 66 6	7. 93 18 1	6. 97 76 6	6. 85 40 1	7. 37 95 1	-1. 555 357 978	-0. 637 246 667	1.5 55 35 79 78	D o w n	0.0 22 31 33 68	0.9 30 85 92 11
50 61 8	ITSN 2	Intersectin 2	8. 24 08 6	7. 94 47 5	7. 28 24 5	8. 87 98 5	8. 96 69 9	8. 02 18 9	1.7 413 344 64	0.8 001 933 33	1.7 41 33 44 64	U p	0.0 40 26 57 59	0.9 30 85 92 11
52 12	VIT	Vitrin	3. 36 08 2	3. 96 37 7	3. 30 01 7	3. 77 25 7	5. 08 41 7	5. 75 78 3	2.5 139 570 46	1.3 299 6 70 46	2.5 13 95 70 46	U p	0.0 21 55 60 95	0.9 30 85 92 11
40 82	MAR CKS	Myristoylated alanine-rich protein kinase C substrate	7. 07 27 7	7. 70 80 3	7. 46 62 4	6. 43 59 4	6. 87 56 2	7. 02 80 2	-1. 553 813 481	-0. 635 813 333	1.5 53 81 34 81	D o w n	0.0 23 93 00 34	0.9 30 85 92 11
64	AID	Axin interactor,	5.	5.	6.	5.	4.	5.	-1.	-0.	1.7	D	0.0	0.9



85	A	dorsalization	68	98	24	36	76	28	784	835	84	o	05	30
3		associated	93	98	04	55	46	40	001	116	00	w	63	85
			3	1	8	8	1	8	3	667	13	n	02	92
													2	11
33	HSP	Heat shock protein	10	11	11	10	9.	10	-2.	-1.	2.5	D	0.0	0.9
12	A8	family A (Hsp70)	.6	.5	.8	.1	22	.5	546	348	46	o	111	30
		member 8	07	58	08	33	47	72	225	36	22	w	88	85
			97	62	96	2	8	49	158		51	n	50	92
											58		8	11
36	IRS1	Insulin receptor	6.	6.	6.	5.	5.	6.	-1.	-0.	1.5	D	0.0	0.9
67		substrate 1	28	45	80	71	77	22	525	609	25	o	19	30
			43	37	52	39	24	87	635	41	63	w	98	85
			3	7	4		6	5	162		51	n	50	92
											62		73	11
33	ID3	Inhibitor of DNA	6.	7.	7.	5.	5.	5.	-3.	-1.	3.5	D	0.0	0.9
99		binding 3,	78	75	12	57	48	15	523	817	23	o	00	30
		dominant negative	35	66	48	23	58	54	884	166	88	w	14	85
		helix-loop-helix	9	7	9	1	5	9	568	667	45	n	78	92
		protein									68		84	11
23	KCN	Potassium channel,	5.	6.	6.	3.	5.	4.	-3.	-1.	3.0	D	0.0	0.9
70	E4	voltage gated	11	75	71	95	70	11	036	602	36	o	25	30
4		subfamily E	09	56	10	00	85	18	494	406	49	w	49	85
		regulatory $\beta$	4	1	6	5	1	3	312	667	43	n	83	92
		subunit 4									12		83	11
10	NDR	N-myc downstream	5.	6.	6.	5.	4.	5.	-1.	-0.	1.9	D	0.0	0.9
39	G1	regulated 1	79	31	25	87	47	14	941	956	41	o	24	30
7			25	04	77	33	30	34	183	936	18	w	14	85
				1	7	3	9	5	721	667	37	n	64	92
											21		74	11

59	PLE	Pleckstrin	7.	6.	6.	7.	7.	7.	1.5	0.6	1.5	U	0.0	0.9
33	KHA	homology domain	13	74	56	41	60	32	487	311	48	p	10	30
8	1	containing A1	93	95	14	61	66	09	847	366	78		80	85
			3	8	1	8	2	3	65	67	47		32	92
											65		2	11
72	C4BP	Complement	3.	3.	3.	3.	4.	4.	1.7	0.7	1.7	U	0.0	0.9
2	A	component 4	62	66	38	75	88	35	078	721	07	p	20	30
		binding protein, $\alpha$	93	70	13	21	98	23	484	8	84		93	85
			5	9	4		3	9	98		84		51	92
											98		23	11
79	ARH	Rho gtpase	5.	5.	6.	4.	5.	4.	-1.	-0.	1.8	D	0.0	0.9
82	GAP	activating protein	33	61	19	20	43	80	860	896	60	o	31	30
2	28	28	20	67	34	77	97	66	959	046	95	w	10	85
			9	8		5		8	511	667	95	n	12	92
											11		53	11
48	NNA	Neuronatin	7.	8.	8.	6.	7.	6.	-1.	-0.	1.8	D	0.0	0.9
26	T		44	41	20	71	60	98	891	919	91	o	19	30
			58	44	52	77	02	97	105	23	10	w	56	85
			2	5	3	6	8	7	697		56	n	02	92
											97		8	11
23	MRP	Mitochondrial	4.	5.	5.	4.	4.	4.	-1.	-0.	1.5	D	0.0	0.9
10	S27	ribosomal protein	89	32	69	88	37	87	508	592	08	o	39	30
7		S27	63	51	21	64	22	66	101	733	10	w	63	85
			6	1	1	8	3	7	295	333	12	n	07	92
											95		75	11
11	FKB	FK506 binding	3.	3.	4.	3.	3.	3.	-1.	-0.	1.5	D	0.0	0.9
32	P9	protein 9	93	73	07	29	05	61	506	591	06	o	08	30
8			28	56	20	01	72	94	548	246	54	w	06	85
			7	5	8	7	7	2	029	667	80	n	75	92

												29		11	11
22	POM	POM121 and ZP3	6.	6.	6.	6.	7.	7.	1.5	0.6	1.5	U	0.0	0.9	
93	ZP3	fusion	93	35	04	85	32	06	534	354	53	p	35	30	
2			23	22	64	11	10	53	473	733	44		44	85	
			9	1	9	3	3	5	36	33	73		52	92	
											36		56	11	
48	ATP2	Atpase, Ca <sup>++</sup>	5.	5.	5.	5.	4.	5.	-1.	-0.	1.5	D	0.0	0.9	
8	A2	transporting,	53	36	73	12	58	14	504	589	04	o	17	30	
		cardiac muscle,	20	49	17	31	96	77	655	433	65	w	89	85	
		slow twitch 2	9	4	8	4	4	3	628	333	56	n	86	92	
											28		93	11	
52	PHF	PHD finger protein	6.	6.	5.	6.	7.	6.	1.5	0.6	1.5	U	0.0	0.9	
53	2	2	49	09	55	64	14	36	919	707	91	p	49	30	
			05	48	57	57	31	45	223	7	92		57	85	
			1	2	7	1	1	9	87		23		98	92	
											87		31	11	
19	EEF2	Eukaryotic	8.	9.	8.	8.	8.	8.	-1.	-0.	1.5	D	0.0	0.9	
38		translation	80	20	59	22	08	48	518	602	18	o	16	30	
		elongation factor 2	61	56	7	86	94	33	320	476	32	w	15	85	
			8	9		5	6	3	824	667	08	n	74	92	
											24		97	11	
34	IGFB	Insulin like growth	5.	7.	6.	7.	7.	9.	3.3	1.7	3.3	U	0.0	0.9	
89	P6	factor binding	14	88	30	66	76	16	672	515	67	p	35	30	
		protein 6	87	31	73	34	95	09	636	766	26		07	85	
			2	6			7	4	06	67	36		41	92	
											06		66	11	
95	ADA	ADAM	4.	6.	5.	4.	4.	4.	-1.	-0.	1.7	D	0.0	0.9	
10	MTS	metallopeptidase	82	00	71	66	97	53	727	789	27	o	31	30	
	1	with	75	65	03	79	42	49	996	1	99	w	08	85	

		thrombospondin type 1 motif 1	6	5	7	7	8	3	146		61	n	26	92
											46		13	11
30	CD2	CD209 molecule	4.	5.	4.	4.	7.	6.	2.6	1.3	2.6	U	0.0	0.9
83	09		59	35	78	82	34	71	028	800	02	p	48	30
5			57	62	54	28	20	28	340	833	83		16	85
			7		8	1	5	4	52	33	40		35	92
											52		32	11
57	PTP	Protein tyrosine	5.	5.	4.	6.	6.	5.	1.7	0.7	1.7	U	0.0	0.9
91	RE	phosphatase, receptor type, E	58	40	90	04	29	91	250	865	25	p	06	30
			44	49	07	61	14	23	003	966	00		43	85
			1	8	7	9	5	1	64	67	03		23	92
											64		42	11
34	TUB	Tubulin, $\beta$ 2B class	7.	7.	8.	6.	7.	6.	-2.	-1.	2.1	D	0.0	0.9
77	B2B	iib	43	63	36	28	48	36	140	097	40	o	18	30
33			71	00	60	72	28	95	433	903	43	w	87	85
			8	7	6		7	3	974	333	39	n	29	92
											74		42	11
10	BOR	BORCS7-ASMT	7.	7.	7.	7.	7.	8.	1.5	0.6	1.5	U	0.0	0.9
05	CS7-	readthrough (NMD	59	62	60	88	94	79	172	014	17	p	42	30
28	ASM	candidate)	26	67	36	34	92	47	792	866	27		18	85
00	T				1	1	5	1	85	67	92		65	92
7											85		67	11
55	CBW	COBW domain	4.	3.	4.	3.	3.	3.	-1.	-0.	1.6	D	0.0	0.9
87	D1	containing 1	45	86	15	71	32	19	674	744	74	o	05	30
1			21	23	27	57	17	77	812		81	w	34	85
			2	7	1	4	2	4	975		29	n	61	92
											75		82	11
57	PLX	Plexin domain	5.	5.	5.	4.	5.	4.	-1.	-0.	1.5	D	0.0	0.9
12	DC1	containing 1	00	23	45	17	13	55	525	609	25	o	43	30

5			82 9	61 5	17 7	67 7	62 4	41 9	910 135	67	91 01 35	w n	34 56 06	85 92 11
65 00	SKP 1	S-phase kinase-associated protein 1	9. 73 73 7	9. 68 45 1	9. 90 28 9	9. 09 12	8. 73 65	9. 50 14	-1. 585 813 743	-0. 665 223 333	1.5 85 81 37 43	D o w n	0.0 11 99 60 31	0.9 30 85 92 11
27 23 3	SUL T1C4	Sulfotransferase family 1C member 4	5. 70 97 1	5. 61 68 8	5. 79 95 9	4. 95 93 8	4. 72 82 2	5. 15 79 1	-1. 693 752 802	-0. 760 223 333	1.6 93 75 28 02	D o w n	0.0 01 52 89 7	0.9 30 85 92 11
28 40 76	TTL L6	Tubulin tyrosine ligase like 6	6. 02 83 3	5. 89 98 5	6. 00 29 6	6. 45 83 6	6. 50 30 6	7. 08 29 4	1.6 294 517 88	0.7 043 866 67	1.6 29 45 17 88	U p	0.0 07 96 19 09	0.9 30 85 92 11
18 45	DUS P3	Dual specificity phosphatase 3	5. 96 76 1	5. 94 55 3	6. 28 41 3	5. 58 07 5	5. 32 26 5	5. 50 80 9	-1. 510 744 825	-0. 595 26	1.5 10 74 48 25	D o w n	0.0 06 55 31 7	0.9 30 85 92 11
10 96 3	STIP 1	Stress induced phosphoprotein 1	5. 65 05 1	5. 68 90 9	6. 20 93 4	5. 21 37 3	4. 26 91 6	5. 37 72 8	-1. 861 230 413	-0. 896 256 667	1.8 61 23 04 13	D o w n	0.0 20 87 49 07	0.9 30 85 92 11
64	SH3	SH3 domain	7.	7.	8.	7.	6.	7.	-1.	-0.	1.6	D	0.0	0.9

51	BGR	binding	45	92	17	21	53	56	677	746	77	o	37	30
	L	glutamate-rich	17	00	90	06	16	85	907	663	90	w	81	85
		protein like	4	1	4	1	1	8	673	333	76	n	95	92
											73		34	11
35	CXC	Chemokine (C-X-C	4.	4.	3.	4.	5.	4.	1.6	0.7	1.6	U	0.0	0.9
77	R1	motif) receptor 1	00	09	87	53	00	61	516	239	51	p	01	30
			60	43	71	75	10	08	751	3	67		94	85
			3	9	6	2	4	1	88		51		15	92
											88		88	11
84	FND	Fibronectin type III	5.	5.	6.	4.	5.	4.	-1.	-0.	1.7	D	0.0	0.9
62	C1	domain containing	85	23	11	62	27	82	772	825	72	o	15	30
4		1	26	70	94	44	84	83	681	933	68	w	50	85
			3	8	1	4	9	9	481	333	14	n	99	92
											81		22	11
87	SNX	Sorting nexin 3	7.	8.	8.	7.	7.	7.	-1.	-0.	1.7	D	0.0	0.9
24	3		83	24	61	47	06	85	704	769	04	o	20	30
			89	87	74	53	16	88	994	766	99	w	72	85
			3	9	2	4	2	8	005	667	40	n	68	92
											05		66	11
96	KIA	KIAA0430	4.	5.	5.	4.	3.	4.	-1.	-0.	1.6	D	0.0	0.9
65	A043		61	04	19	33	88	36	692	758	92	o	06	30
	0		42	58	46	50	16	16	082	8	08	w	22	85
			5	5	4	5	2	7	604		26	n	98	92
											04		93	11
94	HAN	Heart and neural	5.	5.	5.	4.	5.	4.	-1.	-0.	1.5	D	0.0	0.9
21	D1	crest derivatives	15	47	46	51	02	72	529	613	29	o	09	30
		expressed 1	43	91	67	14	2	74	563	12	56	w	60	85
			8	9	2	6		7	498		34	n	29	92
											98		99	11

92	COP	Coatomer protein	5.	6.	6.	5.	5.	5.	-1.	-0.	1.6	D	0.0	0.9
76	B2	complex subunit $\beta$	87	14	36	47	12	56	670	740	70	o	05	30
		2 ( $\beta$ prime)	78	41	23	50	32	45	797	536	79	w	07	85
			9	5	7	5	4	1	241	667	72	n	88	92
											41		36	11
71	TNX	Tenascin XA	6.	7.	6.	7.	8.	8.	2.1	1.1	2.1	U	0.0	0.9
46	A	(pseudogene)	00	84	71	33	09	46	567	088	56	p	49	30
			12	30	67	29	13	33	814	8	78		27	85
			4	2	3	3	4	6	6		14		88	92
											6		26	11
84	LTV	LTV1 ribosome	4.	4.	5.	4.	3.	3.	-1.	-0.	1.8	D	0.0	0.9
94	1	biogenesis factor	07	55	03	08	04	87	846	884	46	o	26	30
6			34	08	45	39	99	11	239	59	23	w	12	85
			5		5	4	8	1	863		98	n	36	92
											63		99	11
59	RAP	RAP1A, member	6.	6.	7.	5.	5.	6.	-1.	-0.	1.6	D	0.0	0.9
06	1A	of RAS oncogene	14	49	12	99	36	22	655	727	55	o	46	30
		family	88	51	29	01	58	88	641	39	64	w	96	85
			9	5	8	1	9	5	137		11	n	00	92
											37		98	11
67	STA	SH3 and cysteine	5.	5.	5.	4.	3.	4.	-1.	-0.	1.9	D	0.0	0.9
69	C	rich domain	27	34	39	61	67	92	913	936	13	o	14	30
			13	94	68	16	17	52	600	29	60	w	71	85
					2	8		7	936		09	n	13	92
											36		67	11
63	SDH	Succinate	7.	8.	8.	7.	7.	7.	-1.	-0.	1.7	D	0.0	0.9
92	D	dehydrogenase	89	22	76	66	07	78	724	786	24	o	21	30
		complex subunit D,	26	39	44	36	53	27	805	433	80	w	66	85
		integral membrane	7	2	9	9	2	7	081	333	50	n	08	92

		protein									81		74	11
12	CLT	Clathrin, heavy	9.	9.	10	9.	8.	9.	-1.	-0.	1.6	D	0.0	0.9
13	C	chain (Hc)	46	65	2	23	56	43	642	715	42	o	37	30
			72	50	71	86	94	83	454	853	45	w	06	85
			5	2	78	9	1	9	418	333	44	n	57	92
											18		06	11
37	KCN	Potassium channel,	5.	6.	6.	4.	5.	4.	-1.	-0.	1.9	D	0.0	0.9
82	N3	calcium activated	17	75	24	85	44	94	969	977	69	o	36	30
		intermediate/small	74	90	52	76	94	2	186	6	18	w	02	85
		conductance	8	6	8	1	1		836		68	n	50	92
		subfamily N $\alpha$ , member 3									36		6	11
58	ABC	ATP binding	5.	5.	5.	4.	4.	4.	-1.	-0.	1.6	D	0.0	0.9
25	D3	cassette subfamily	28	63	59	99	69	71	626	701	26	o	02	30
		D member 3	62	45	35	68	9	28	608	866	60	w	76	85
			3	3	9	6		9	059	667	80	n	53	92
											59		19	11
22	FKB	FK506 binding	8.	7.	7.	7.	6.	7.	-1.	-0.	1.5	D	0.0	0.9
80	P1A	protein 1A	13	27	83	01	99	25	581	661	81	o	21	30
			21	90	22	03	13	66	927	683	92	w	67	85
			4	5	4	3	9	6	337	333	73	n	04	92
											37		83	11
51	TAF	TATA-box binding	4.	5.	5.	4.	3.	4.	-1.	-0.	1.8	D	0.0	0.9
61	9B	protein associated	62	32	57	58	91	38	844	882	44	o	13	30
6		factor 9b	65	87	71	30	97	10	044	873	04	w	40	85
			6	8	8	9	9	2	324	333	43	n	46	92
											24		98	11
74	VBP	Von Hippel-Lindau	5.	5.	6.	5.	5.	5.	-1.	-0.	1.6	D	0.0	0.9
11	1	binding protein 1	67	69	58	28	08	39	655	727	55	o	24	30



			14	23	10	64	44	14	759	493	75	w	45	85
			7	1	9	4	6	9	727	333	97	n	01	92
											27		93	11
11	TRI	Tripartite motif	8.	8.	7.	7.	7.	7.	-1.	-0.	1.6	D	0.0	0.9
40	M9	containing 9	63	28	88	21	82	61	642	716	42	o	18	30
88			47	45	31	45	65	25	898	243	89	w	25	85
			7		9	8	7	8	479	333	84	n	22	92
											79		44	11
27	GNG	Guanine nucleotide	7.	8.	8.	6.	7.	7.	-1.	-0.	1.7	D	0.0	0.9
91	11	binding protein (G	72	42	52	98	77	57	713	777	13	o	24	30
		protein), $\gamma$ 11	85	43	04	99	75	40	884	27	88	w	76	85
			8		2	2	2	5	633		46	n	58	92
											33		91	11
10	C1Q	C1QTNF3-AMAC	6.	6.	6.	5.	5.	5.	-1.	-0.	1.7	D	0.0	0.9
05	TNF	R readthrough	29	20	52	76	12	71	749	807	49	o	05	30
34	3-A	(NMD candidate)	64	38	27	15	54	42	925	293	92	w	17	85
61	MAC		7	5	6	6		4	294	333	52	n	56	92
2	R										94		18	11
89	SKA	Src kinase	4.	4.	4.	3.	3.	4.	-1.	-0.	1.5	D	0.0	0.9
35	P2	associated	05	09	70	28	69	08	513	597	13	o	44	30
		phosphoprotein 2	74	72	36	07	67	75	420	813	42	w	01	85
			7	3	9		5		963	333	09	n	71	92
											63		8	11
55	SPT	Serine	5.	5.	5.	6.	6.	5.	1.5	0.5	1.5	U	0.0	0.9
30	LC3	palmitoyltransferas	43	37	64	35	14	71	011	861	01	p	18	30
4		e, long chain base	47	08	63	41	60	00	831		18		97	85
		subunit 3	9	6	7	7	9	6	48		31		00	92
											48		08	11
61	RPS5	Ribosomal protein	11	12	12	11	10	11	-1.	-0.	1.6	D	0.0	0.9

93		S5	.6 89 81	.0 09 01	.3 62 23	.2 21 73	.9 78 84	.8 06 77	607 222 872	684 57	07 22 28 72	o w n	25 45 12 03	30 85 92 11
20 53	EPH X2	Epoxide hydrolase 2, cytoplasmic	6. 71 42 1	6. 74 27 8	7. 04 66 8	6. 18 30 2	6. 12 97 7	6. 35 97 7	-1. 526 650 69	-0. 610 37	1.5 26 65 06 9	D o w n	0.0 05 52 97 51	0.9 30 85 92 11
77 84	ZP3	Zona pellucida glycoprotein 3 (sperm receptor)	5. 34 23 1	5. 39 73 4	5. 38 75 8	5. 66 74 7	6. 99 16 9	7. 27 34 8	2.4 090 594 56	1.2 684 7	2.4 09 05 94 56	U p	0.0 11 25 64 15	0.9 30 85 92 11
57 48 4	RNF 150	Ring finger protein 150	6. 73 94 1	6. 06 37 8	5. 99 98 9	4. 20 86 1	6. 11 44 8	4. 86 53 8	-2. 305 207 577	-1. 204 896 667	2.3 05 20 75 77	D o w n	0.0 31 45 70 76	0.9 30 85 92 11
41 79	CD4 6	CD46 molecule, complement regulatory protein	7. 04 58 1	7. 55 04 3	8. 04 22 1	7. 07 53 8	5. 27 69 7	6. 88 01 7	-2. 196 657 585	-1. 135 31	2.1 96 65 75 85	D o w n	0.0 47 23 15 83	0.9 30 85 92 11
11 23	CHN 1	Chimerin 1	4. 70 84 2	4. 56 10 7	5. 01 68 2	3. 93 97 6	3. 93 74 1	4. 63 34 6	-1. 507 223 468	-0. 591 893 333	1.5 07 22 34 68	D o w n	0.0 30 31 31 52	0.9 30 85 92 11

12 64	CNN 1	Calponin 1, basic, smooth muscle	7. 82 78 4	8. 80 96 9	9. 14 23 9	4. 88 84 6	8. 36 55 2	5. 38 20 3	-5. 209 963 746	-2. 381 273 333	5.2 09 96 37 46	D o w n	0.0 23 97 62 88	0.9 30 85 92 11
64 26	SRS F1	Serine/arginine-ric h splicing factor 1	7. 01 08 4	7. 54 78 2	7. 79 51 7	6. 88 77 2	6. 14 36 9	6. 96 17 8	-1. 725 339 173	-0. 786 88 91 73	1.7 25 33 91 73	D o w n	0.0 25 43 59 46	0.9 30 85 92 11
48 83	NPR 3	Natriuretic peptide receptor 3	6. 45 43	7. 51 93 5	7. 59 51 1	5. 82 80 1	6. 13 21 9	5. 66 60 2	-2. 486 609 564	-1. 314 18 95 64	2.4 86 60 95 64	D o w n	0.0 03 35 64 9	0.9 30 85 92 11
57 53 8	ALP K3	A kinase 3	5. 52 25 7	5. 29 69 9	5. 46 26 9	6. 58 46 6	5. 82 90 3	5. 87 62 6	1.5 902 607 44	0.6 692 633 33	1.5 90 26 07 44	U p	0.0 18 41 72 55	0.9 30 85 92 11
55 22 8	PNM AL1	Paraneoplastic Ma antigen family-like 1	5. 76 63 6	5. 69 68 3	6. 42 60 2	3. 46 11 3	5. 55 25 1	3. 91 70 1	-3. 144 556 738	-1. 652 856 667	3.1 44 55 67 38	D o w n	0.0 12 08 97 01	0.9 30 85 92 11
92 8	CD9	CD9 molecule	8. 63 24 1	9. 38 12 1	9. 88 01 8	7. 26 12 5	8. 56 25 5	8. 33 25 6	-2. 371 522 134	-1. 245 813 333	2.3 71 52 21	D o w n	0.0 17 04 72	0.9 30 85 92

											34		02	11
58 49 4	JAM 2	Junctional adhesion molecule 2	3. 68 76 5	4. 64 65 4	4. 48 99 9	3. 05 46 6	3. 86 49 2	3. 67 33 2	-1. 674 542 122	-0. 743 766 667	1.6 74 54 21 22	D o w n	0.0 37 51 26 88	0.9 30 85 92 11
15 43	CYP 1A1	Cytochrome P450, family 1, subfamily A, polypeptide 1	7. 94 26 4	9. 51 39 4	7. 35 82 9	10 .9 90 9	8. 89 16 3	9. 73 73 57	3.0 349 091 57	1.6 016 533 33	3.0 34 90 91 57	U p	0.0 41 31 25 15	0.9 30 85 92 11
34 94	IGH A2	Immunoglobulin heavy constant $\alpha$ 2 (A2m marker)	8. 29 12 4	9. 48 48 6	8. 88 50 7	7. 93 20 4	8. 11 57 9	7. 70 46 1	-1. 958 265 892	-0. 969 576 667	1.9 58 26 58 92	D o w n	0.0 111 20 09 9	0.9 30 85 92 11
38 56	KRT 8	Keratin 8, type II	9. 71 6	10 .3 32 54	9. 64 00 6	9. 25 83 2	8. 47 07 2	9. 03 51 2	-1. 965 386 884	-0. 974 813 333	1.9 65 38 68 84	D o w n	0.0 06 10 73 33	0.9 30 85 92 11
79 80 4	HAN D2-A S1	HAND2 antisense RNA 1 (head to head)	5. 35 46 4	6. 61 99 8	6. 76 95 4	4. 05 78 8	5. 95 25 6	4. 38 73 2	-2. 729 808 978	-1. 448 8 978	2.7 29 80 89 78	D o w n	0.0 31 01 93 33	0.9 30 85 92 11
29 92	GYG 1	Glycogenin 1	5. 59 04	5. 89 02	6. 76 06	5. 30 25	4. 86 41	5. 68 49	-1. 736 982	-0. 796 583	1.7 36 98	D o w	0.0 44 95	0.9 30 85

			8	2	3	1	3	4	638	333	26	n	09	92
											38		37	11
26	GEM	GTP binding	4.	6.	6.	3.	5.	4.	-2.	-1.	2.5	D	0.0	0.9
69		protein	73	52	10	68	25	37	555	353	55	o	34	30
		overexpressed in	70	94	46	37	07	49	962	866	96	w	18	85
		skeletal muscle	7		1	2	9	7	494	667	24	n	98	92
											94		13	11
58	RAD	RAD21 cohesin	7.	7.	7.	6.	6.	6.	-1.	-0.	1.5	D	0.0	0.9
85	21	complex	45	16	04	72	50	60	527	611	27	o	06	30
		component	54	33	72	69	15	27	977	623	97	w	22	85
			8	8	8	8	6	3	536	333	75	n	15	92
											36		33	11
72	TXN	Thioredoxin	6.	6.	7.	5.	5.	5.	-2.	-1.	2.1	D	0.0	0.9
96	RD1	reductase 1	42	40	32	79	26	72	179	123	79	o	04	30
			31	38	77	08	39	89	040	693	04	w	56	85
			9	7	1		1	8	987	333	09	n	50	92
											87		93	11
55	AIM	Absent in	5.	4.	5.	7.	7.	5.	2.8	1.4	2.8	U	0.0	0.9
05	1L	melanoma 1-like	63	90	32	53	50	31	267	991	26	p	31	30
7			22	33	60	63	83	43	350	366	73		48	85
			2	6	4		9	4	52	67	50		10	92
											52		94	11
26	EHF	Ets homologous	5.	5.	6.	5.	4.	5.	-1.	-0.	1.5	D	0.0	0.9
29		factor	54	68	07	48	61	29	556	638	56	o	38	30
8			22	99	09	11	47	15	806	59	80	w	17	85
			9		8	2	7	1	89		68	n	83	92
											9		43	11
57	AS3	Arsenite	7.	7.	7.	7.	7.	8.	1.5	0.6	1.5	U	0.0	0.9
41	MT	methyltransferase	59	62	60	88	94	79	172	014	17	p	42	30

2			26	67	36	34	92	47	792	866	27		18	85
					1	1	5	1	85	67	92		65	92
											85		67	11
44	MT1	Metallothionein	6.	5.	5.	7.	7.	7.	2.4	1.3	2.4	U	0.0	0.9
99	M	1M	98	73	72	76	01	62	945	187	94	p	08	30
			67	73	47	90	23	38	449	766	54		00	85
			9	6	2	6	2	2	51	67	49		88	92
											51		79	11
79	MA	Mannosidase,	5.	5.	6.	5.	4.	5.	-1.	-0.	1.7	D	0.0	0.9
69	NEA	endo- $\alpha$	54	75	22	28	52	30	742	801	42	o	18	30
4			78	01	91	50	88	84	984	56	98	w	18	85
			3	6		3	9	9	814		48	n	09	92
											14		29	11
64	ERA	Endoplasmic	4.	5.	7.	7.	6.	8.	3.1	1.6	3.1	U	0.0	0.9
16	P2	reticulum	88	34	40	25	90	47	751	668	75	p	39	30
7		aminopeptidase 2	65	79	01	76	10	64	688	333	16		26	85
			1	8	9	4	6	8	93	33	88		04	92
											93		57	11
84	SPA	SPARC like 1	8.	9.	10	6.	8.	8.	-3.	-1.	3.5	D	0.0	0.9
04	RCL		70	73	.0	20	75	02	570	836	70	o	21	30
	1		99	11	50	23	18	83	823	256	82	w	18	85
			6	8	2	4	5	8	107	667	31	n	03	92
											07		45	11
36	ITG	Integrin $\alpha$ 9	5.	5.	6.	3.	5.	4.	-3.	-1.	3.0	D	0.0	0.9
80	A9		47	94	60	29	64	26	039	603	39	o	22	30
			66	54	55	98	96	71	140	663	14	w	44	85
			2	7	8	8	8	2	418	333	04	n	04	92
											18		58	11
27	TIN	Tubulointerstitial	4.	3.	3.	4.	5.	3.	1.9	0.9	1.9	U	0.0	0.9



68	SUL	Sulfotransferase	9.	9.	8.	10	9.	10	1.7	0.8	1.7	U	0.0	0.9
19	T1C2	family 1C member 2	73	03	87	.5	62	.0	821	336	82	p	21	30
			75	07	17	00	69	13	638	3	16		51	85
			3	2	2	08	5	83	71		38		84	92
											71		42	11
29	SLC	Solute carrier	6.	6.	7.	6.	5.	6.	-1.	-0.	1.7	D	0.0	0.9
1	25A4	family 25 (mitochondrial carrier; adenine nucleotide translocator), member 4	75	95	51	56	95	32	728	789	28	o	13	30
			64	81	05	86	96	81	507	526	50	w	04	85
				2	5	5	5	9	264	667	72	n	88	92
											64		39	11
2	A2M	A-2-macroglobulin	10	10	11	9.	10	10	-1.	-0.	1.9	D	0.0	0.9
			.7	.7	.2	05	.6	.1	942	957	42	o	36	30
			93	89	03	23	66	94	251	73	25	w	02	85
			45	26	52	9	27	38	465		14	n	41	92
											65		52	11
57	ARR	Arrestin domain	4.	5.	5.	4.	4.	4.	-1.	-0.	1.5	D	0.0	0.9
56	DC3	containing 3	87	28	13	41	31	71	532	615	32	o	07	30
1			36	43	08	29	14	78	099	51	09	w	27	85
				3	3	2	7	4	506		95	n	73	92
											06		58	11
30	HAB	Hyaluronan	7.	8.	8.	7.	6.	7.	-1.	-0.	1.7	D	0.0	0.9
26	P2	binding protein 2	46	08	16	07	86	32	761	817	61	o	07	30
			63	13	53	41	56	19	901	133	90	w	30	85
			8	5	1		1	3	575	333	15	n	67	92
											75		61	11
65	SLC	Solute carrier	6.	6.	5.	7.	6.	6.	1.8	0.8	1.8	U	0.0	0.9
80	22A1	family 22 (organic	10	12	84	17	72	81	402	799	40	p	01	30



		cation transporter), member 1	44 1	30 8	80 3	48	65	39 7	69	166 67	26 9		22 23 89	85 92 11
40 13	VWA 5A	Von Willebrand factor A domain containing 5A	5. 71 44 1	5. 84 81 3	6. 10 33 6	5. 05 75 6	5. 45 21 9	5. 37 09 9	-1. 510 507 485	-0. 595 033 333	1.5 10 50 74 85	D o w n	0.0 09 99 34 91	0.9 30 85 92 11
10 01 27 88 8	SLC O4A 1-AS 1	SLCO4A1 antisense RNA 1	5. 39 29 2	4. 41 67 5	4. 58 93 9	7. 00 29 8	5. 38 17 9	6. 29 62 3	2.6 894 540 37	1.4 273 133 33	2.6 89 45 40 37	U p	0.0 10 48 40 6	0.9 30 85 92 11
31 23	HLA -DR B1	Major histocompatibility complex, class II, DR $\beta$ 1	10 .1 20 15	10 .2 33 12	11 .0 53 67	9. 24 28 4	10 .0 67 13	9. 22 63 2	-1. 941 111 961	-0. 956 883 333	1.9 411 11 96 1	D o w n	0.0 16 70 42 06	0.9 30 85 92 11
34 93	IGH A1	Immunoglobulin heavy constant $\alpha$ 1	8. 29 12 4	9. 48 48 6	8. 88 50 7	7. 93 20 4	8. 11 57 9	7. 70 46 1	-1. 958 265 892	-0. 969 576 667	1.9 58 26 58 92	D o w n	0.0 111 20 09 9	0.9 30 85 92 11
46 38	MYL K	Myosin light chain kinase	8. 05 89 7	9. 21 15 2	10 .1 84	5. 20 08 1	8. 62 53 5	6. 62 08 7	-5. 048 378 221	-2. 335 82	5.0 48 37 82 21	D o w n	0.0 27 07 11 76	0.9 30 85 92 11
57	SCU	Signal peptide,	6.	6.	7.	5.	6.	5.	-2.	-1.	2.1	D	0.0	0.9

75	BE2	CUB domain,	77	86	63	44	81	79	107	075	07	o	23	30
8		EGF-like 2	70	59	37	24	50	22	642	63	64	w	43	85
			9	2	1	8	9	6	242		22	n	71	92
											42		28	11
64	ABC	ATP binding	7.	7.	7.	8.	8.	8.	1.7	0.8	1.7	U	0.0	0.9
24	G5	cassette subfamily	49	96	53	77	00	71	847	357	84	p	09	30
0		G member 5	34	21	21	71	53	22	351	1	73		63	85
			1	2	4	6	5	9	52		51		10	92
											52		64	11
34	RSP	R-spondin 2	4.	4.	5.	3.	4.	3.	-1.	-0.	1.7	D	0.0	0.9
04	O2		00	75	11	47	44	48	771	825	71	o	46	30
19			94	09	56	12	27	67	666	106	66	w	53	85
			5	5	3		6	5	023	667	60	n	70	92
											23		01	11
45	MT1	Metallothionein 1X	8.	7.	7.	8.	8.	9.	2.0	1.0	2.0	U	0.0	0.9
01	X		49	74	26	91	56	15	616	438	61	p	10	30
			34	04	91	00	56	87	508		65		87	85
			5	9	9	9	6	8	12		08		92	92
											12		73	11
10	HEL	HELLP associated	7.	6.	6.	7.	7.	7.	1.5	0.6	1.5	U	0.0	0.9
11	LPA	long non-coding	13	74	56	41	60	32	487	311	48	p	10	30
01	R	RNA	93	95	14	61	66	09	847	366	78		80	85
69			3	8	1	8	2	3	65	67	47		32	92
2											65		2	11
54	PGP	Pyroglutamyl-pepti	7.	7.	6.	7.	7.	7.	1.5	0.6	1.5	U	0.0	0.9
85	EP1	dase I	41	09	92	88	90	46	192	033	19	p	15	30
8			47	89	69	52	39	15	472	566	24		57	85
			8	8	6	5	7	7	35	67	72		55	92
											35		06	11

31 09	HLA -DM B	Major histocompatibility complex, class II, DM $\beta$	5. 77 12 9	5. 71 15 6	6. 39 42 2	4. 19 19 2	5. 13 40 2	5. 55 05 5	-2. 000 268 035	-1. 000 193 333	2.0 00 26 80 35	D o w n	0.0 23 57 34 46	0.9 30 85 92 11
51 5	ATP5 F1	ATP synthase, H <sup>+</sup> transporting, mitochondrial Fo complex subunit B1	3. 23 48 7	3. 89 18 5	3. 93 43 5	4. 45 38 4	4. 54 78 9	3. 82 80 7	1.5 048 051 24	0.5 895 766 67	1.5 04 80 51 24	U p	0.0 49 38 86 73	0.9 30 85 92 11
10 95 7	PNR C1	Proline rich nuclear receptor coactivator 1	7. 62 48 7	8. 36 57 6	8. 10 04 8	7. 61 62 8	6. 79 73 4	7. 64 78 6	-1. 598 305 657	-0. 676 543 333	1.5 98 30 56 57	D o w n	0.0 46 56 72 12	0.9 30 85 92 11
83 45 0	DRC 3	Dynein regulatory complex subunit 3	5. 81 50 7	5. 99 29 1	6. 01 41 5	6. 64 05 5	6. 99 16 8	6. 05 19 8	1.5 376 139 53	0.6 206 933 33	1.5 37 61 39 53	U p	0.0 34 69 87 15	0.9 30 85 92 11
22 99 8	LIM CH1	LIM and calponin homology domains 1	7. 20 93	7. 64 25	7. 39 38	6. 77 05 7	6. 02 10 4	7. 18 74 9	-1. 688 243 887	-0. 755 523 333	1.6 88 24 38 87	D o w n	0.0 34 22 95 56	0.9 30 85 92 11
56 84 9	TCE AL7	Transcription elongation factor A (SII)-like 7	4. 73 29 1	5. 69 8	6. 19 57 1	3. 31 70 6	4. 95 41 7	4. 39 47 5	-2. 497 030 31	-1. 320 213 333	2.4 97 03 03	D o w n	0.0 26 60 02	0.9 30 85 92

											1		57	11
57	TSH	Teashirt zinc finger	5.	5.	5.	4.	5.	4.	-1.	-0.	1.5	D	0.0	0.9
61	Z3	homeobox 3	34	41	73	72	41	56	508	593	08	o	41	30
6			04	02	88	80	84	29	787	39	78	w	78	85
			8	5	8	6	6	2	888		78	n	75	92
											88		48	11
45	MT2	Metallothionein 2A	12	11	10	12	12	12	1.9	0.9	1.9	U	0.0	0.9
02	A		.0	.4	.6	.0	.3	.7	666	757	66	p	22	30
			72	28	81	25	51	31	178	166	61		07	85
			33	48	39	74	8	81	83	67	78		13	92
											83		65	11
31	HLA	Major	10	10	11	9.	10	9.	-1.	-0.	1.9	D	0.0	0.9
25	-DR	histocompatibility	.1	.2	.0	24	.0	22	941	956	411	o	16	30
	B3	complex, class II,	20	33	53	28	67	63	111	883	11	w	70	85
		DR β 3	15	12	67	4	13	2	961	333	96	n	42	92
											1		06	11
94	AKA	A-kinase anchoring	5.	4.	5.	4.	4.	4.	-1.	-0.	1.5	D	0.0	0.9
65	P7	protein 7	21	53	49	79	26	32	543	626	43	o	47	30
			72	90	86	06	31	12	975	65	97	w	59	85
			7	9	3	9	2	3	65		56	n	15	92
											5		99	11
10	TME	Transmembrane	8.	8.	8.	7.	6.	8.	-1.	-0.	1.7	D	0.0	0.9
95	D2	p24 trafficking	05	17	70	73	72	03	758	814	58	o	47	30
9		protein 2	80	33	65	78	36	22	960	723	96	w	44	85
			5	3	5	9	6	1	802	333	08	n	31	92
											02		4	11
50	P4H	Prolyl	9.	9.	9.	9.	8.	9.	-1.	-0.	1.5	D	0.0	0.9
34	B	4-hydroxylase, β	58	38	52	17	33	06	557	639	57	o	24	30
		polypeptide	19	47	54	99	09	37	368	11	36	w	83	85

					2	8	2	9	121		81	n	19	92
											21		47	11
22	PI16	Peptidase inhibitor	5.	7.	6.	7.	7.	8.	2.5	1.3	2.5	U	0.0	0.9
14		16	99	53	48	14	98	86	119	287	11	p	31	30
76			58	74	21	85	78	53	249	933	92		21	85
			1	7	1	6	3	8	02	33	49		61	92
											02		61	11
57	VAT	Vesicle amine	5.	5.	6.	4.	5.	4.	-1.	-0.	1.9	D	0.0	0.9
68	1L	transport 1-like	76	68	26	29	87	65	949	962	49	o	411	30
7			06	94	36	34	92	24	242	913	24	w	17	85
			6	6	6	2		2	162	333	21	n	40	92
											62		5	11
19	EFN	Ephrin-B2	5.	6.	6.	5.	5.	5.	-1.	-0.	1.6	D	0.0	0.9
48	B2		75	40	50	35	50	68	633	707	33	o	14	30
			66	08	85	22	47	58	224	723	22	w	45	85
			6	5	6	9	2	9	748	333	47	n	14	92
											48		79	11
38	YPE	Yippee like 2	9.	9.	9.	8.	8.	8.	-1.	-0.	1.5	D	0.0	0.9
84	L2		61	48	06	56	96	87	502	587	02	o	15	30
03			30	65	99	50	84	32	710	566	71	w	38	85
			2	6	1	8	5	6	051	667	00	n	78	92
											51		45	11
25	GAP	Growth associated	6.	5.	5.	4.	5.	4.	-2.	-1.	2.0	D	0.0	0.9
96	43	protein 43	25	61	54	26	28	73	060	042	60	o	08	30
			92	43	01	16	83	49	374	906	37	w	75	85
			1	2	5	8	3	5	61	667	46	n	36	92
											1		66	11
23	PDZ	PDZ domain	5.	5.	6.	4.	5.	5.	-1.	-0.	1.9	D	0.0	0.9
02	RN3	containing ring	13	97	64	47	27	11	951	964	51	o	37	30

4		finger 3	53 8	73 8	91 9	92 7	18 6	75 5	283 409	423 333	28 34 09	w n	65 72	85 92 11
22 09 88	HNR NPA 3	Heterogeneous nuclear ribonucleoprotein A3	5. 58 43	6. 26 13 1	6. 40 40 7	5. 45 97 5	4. 90 27 1	5. 74 04 9	-1. 642 139 474	-0. 715 576 667	1.6 42 13 94 74	D o w n	0.0 38 24 27 46	0.9 30 85 92 11
55 38	PPT1	Palmitoyl-protein thioesterase 1	5. 96 61 6	6. 50 63 8	7. 00 51 3	5. 43 89 9	5. 10 14 7	5. 89 36 3	-2. 020 239 964	-1. 014 526 667	2.0 20 23 99 64	D o w n	0.0 10 82 43 97	0.9 30 85 92 11
36 85	ITGA V	Integrin $\alpha$ V	5. 38 63 4	5. 83 11 5	6. 29 82 4	5. 11 74 5	3. 60 53 2	5. 03 64 4	-2. 381 999 868	-1. 252 173 333	2.3 81 99 98 68	D o w n	0.0 18 97 97 12	0.9 30 85 92 11
62 51	RSU 1	Ras suppressor protein 1	7. 65 16 5	7. 97 98 5	8. 25 04 1	7. 14 65 9	7. 35 07 9	7. 62 10 9	-1. 502 998 254	-0. 587 843 333	1.5 02 99 82 54	D o w n	0.0 21 52 32 64	0.9 30 85 92 11
66 78	SPA RC	Secreted protein, acidic, cysteine-rich (osteonectin)	6. 44 59 4	6. 97 95 9	7. 57 73	4. 01 87 2	6. 14 02	6. 05 19 8	-3. 025 786 092	-1. 597 31	3.0 25 78 60 92	D o w n	0.0 24 33 45 95	0.9 30 85 92 11
57	CCD	Coiled-coil domain	6.	6.	6.	6.	7.	6.	1.5	0.6	1.5	U	0.0	0.9

82	C181	containing 181	35	25	00	97	07	51	686	494	68	p	111	30
1			36	58	59	86	00	52	208	966	62		71	85
			9	6	7	8	6	7	33	67	08		37	92
											33			11
64	SMI	Small integral	4.	6.	6.	4.	4.	4.	-2.	-1.	2.4	D	0.0	0.9
45	M10	membrane protein	98	24	45	27	89	68	425	278	25	o	10	30
38		10	62	73	11	53	19	31	137	066	13	w	31	85
				8	3	8	4	9	701	667	77	n	05	92
											01		59	11
10	MBN	Muscleblind-like	4.	4.	4.	4.	3.	4.	-1.	-0.	1.5	D	0.0	0.9
15	L2	splicing regulator 2	57	79	75	33	80	19	512	596	12	o	07	30
0			80	11	98	72	76	37	368	81	36	w	43	85
			6	2	7	8		4	808		88	n	29	92
											08		65	11
27	PCD	Protocadherin 17	5.	5.	6.	4.	5.	4.	-2.	-1.	2.0	D	0.0	0.9
25	H17		75	86	34	55	56	68	075	053	75	o	07	30
3			22	94	01	90	05	21	348	353	34	w	43	85
			6		1	3	1	7	089	333	80	n	43	92
											89		63	11
14	TTC	Tetratricopeptide	6.	5.	6.	5.	5.	5.	-1.	-0.	1.5	D	0.0	0.9
55	7B	repeat domain 7B	15	99	35	05	96	58	549	632	49	o	32	30
67			12	87	22	57	67	35	815	096	81	w	52	85
			6	5	5	1	6		703	667	57	n	97	92
											03		61	11
23	GAB	GABA(A)	7.	7.	7.	7.	7.	6.	-1.	-0.	1.5	D	0.0	0.9
71	ARA	receptor-associated	57	91	84	24	13	93	595	673	95	o	03	30
0	PL1	protein like 1	42	49	25	04	72	30	107	653	10	w	49	85
			2	8	7	5	7	9	144	333	71	n	06	92
											44		56	11

70	TIE1	Tyrosine kinase	5.	5.	6.	4.	5.	4.	-1.	-0.	1.6	D	0.0	0.9
75		with	00	65	17	60	19	87	643	716	43	o	46	30
		immunoglobulin-li	42	30	74	89	69	93	186	496	18	w	22	85
		ke and EGF-like	1	8	6	5	8	3	993	667	69	n	58	92
		domains 1									93		78	11
13	C4orf32	Chromosome 4 open reading frame 32	7.	6.	6.	7.	7.	7.	1.5	0.6	1.5	U	0.0	0.9
27			13	74	56	41	60	32	487	311	48	p	10	30
20			93	95	14	61	66	09	847	366	78		80	85
			3	8	1	8	2	3	65	67	47		32	92
											65		2	11
10	CDC42EP23	CDC42 effector protein (Rho gtpase binding) 3	5.	5.	5.	4.	5.	5.	-1.	-0.	1.5	D	0.0	0.9
60			17	70	82	68	02	20	511	595	11	o	27	30
2			48	32	36	56	47	46	083	583	08	w	79	85
			4	8	7	4	3	7	447	333	34	n	20	92
											47		5	11
91	FCGR2C	Fc fragment of igg, low affinity iiic, receptor for (CD32) (gene/pseudogene)	6.	6.	6.	5.	6.	6.	-1.	-0.	1.6	D	0.0	0.9
03			86	75	81	45	71	13	637	711	37	o	44	30
			53	45	51	44	51	16	210	24	21	w	11	85
			4	1	2	8	2	5	699		06	n	55	92
											99		06	11
14	MT1P3	Metallothionein 1 pseudogene 3	6.	6.	5.	7.	7.	7.	2.0	1.0	2.0	U	0.0	0.9
08			88	34	75	59	27	30	933	657	93	p	05	30
51			56	36	38	9	87	27	013	8	30		70	85
			6	9	1		3	7	27		13		41	92
											27		4	11
40	LYZ	Lysozyme	9.	10	10	9.	8.	8.	-2.	-1.	2.6	D	0.0	0.9
69			75	.0	.4	06	48	54	614	386	14	o	00	30
			43	74	14	19	18	04	400	48	40	w	32	85
				64	66	5	1		202		02	n	29	92



											02		54	11
37 08	ITPR 1	Inositol 1,4,5-trisphosphate receptor, type 1	6. 88 89 2	7. 90 50 3	8. 17 77 2	5. 29 90 5	7. 45 16 7	6. 30 04 2	-2. 473 996 284	-1. 306 843 333	2.4 73 99 62 84	D o w n	0.0 45 83 68 73	0.9 30 85 92 11
47 83	NFIL 3	Nuclear factor, interleukin 3 regulated	5. 68 98 5	5. 96 37 7	5. 53 93 8	4. 26 45 2	5. 27 42 3	4. 27 17 4	-2. 184 803 202	-1. 127 503 333	2.1 84 80 32 02	D o w n	0.0 04 76 13 64	0.9 30 85 92 11
40 11 05	FLJ4 2393	Uncharacterized LOC401105	6. 65 10 5	6. 86 47 3	6. 42 09 7	5. 52 44 7	4. 92 96 6	5. 20 44 6	-2. 687 099 978	-1. 426 05 99	2.6 87 09 99 78	D o w n	0.0 00 13 50 84	0.9 30 85 92 11
19 03	S1PR 3	Sphingosine-1-pho sphate receptor 3	5. 84 29 8	6. 35 26 9	7. 70 58 9	4. 17 26 5	6. 18 5 9	4. 49 48 9	-3. 210 964 393	-1. 683 006 667	3.2 10 96 43 93	D o w n	0.0 27 56 08 11	0.9 30 85 92 11
34 26	CFI	Complement factor I	6. 80 89 2	7. 12 93 1	7. 20 39 3	6. 59 88 9	5. 50 25 3	6. 62 10 4	-1. 749 044 101	-0. 806 566 667	1.7 49 04 41 01	D o w n	0.0 32 95 79 47	0.9 30 85 92 11
11 69 85	ARA P1	Arfgap with rhogap domain, ankyrin repeat and PH	8. 46 08	8. 33 98	8. 01 66	7. 67 48	7. 46 5	7. 40 67	-1. 689 855	-0. 756 9	1.6 89 85	D o w	0.0 02 27	0.9 30 85

		domain 1	6	1	5	4		8	633		56	n	67	92
											33		16	11
70	TGM	Transglutaminase 2	4.	4.	4.	3.	3.	3.	-1.	-0.	1.7	D	0.0	0.9
52	2		19	29	79	44	96	33	799	847	99	o	05	30
			73	43	10	49	48	02	446	553	44	w	19	85
			8		1	3	5	5	654	333	66	n	89	92
											54		57	11
86	PLPP	Phospholipid	8.	8.	8.	7.	7.	8.	-1.	-0.	1.5	D	0.0	0.9
13	3	phosphatase 3	24	56	82	64	77	44	509	594	09	o	45	30
			88	03	95	15	37	05	753	313	75	w	62	85
			6	9	1	4	8		83	333	38	n	26	92
											3		29	11
38	HER	Hect domain and	7.	6.	6.	7.	7.	7.	1.5	0.6	1.5	U	0.0	0.9
82	C2P5	RLD 2 pseudogene	13	74	56	41	60	32	487	311	48	p	10	30
54		5	93	95	14	61	66	09	847	366	78		80	85
			3	8	1	8	2	3	65	67	47		32	92
											65		2	11
22	RIM	Regulating	4.	4.	4.	3.	3.	3.	-1.	-0.	1.5	D	0.0	0.9
99	S1	synaptic membrane	19	83	43	99	97	66	524	608	24	o	12	30
9		exocytosis 1	36	58	58	37	76	95	310	156	31	w	60	85
			9	5	1	5	2	1	351	667	03	n	60	92
											51		44	11
79	GAL	Polypeptide	5.	4.	5.	6.	5.	5.	1.8	0.9	1.8	U	0.0	0.9
62	NT1	N-acetylgalactosa	48	48	12	29	90	62	807	112	80	p	13	30
3	4	minyltransferase 14	01	71	77	89	54	45	133	8	71		15	85
			4	9	3	6	4		81		33		63	92
											81		65	11
55	PGM	Phosphoglucomuta	5.	5.	5.	5.	4.	5.	-1.	-0.	1.5	D	0.0	0.9
27	2	se 2	38	21	80	04	38	01	576	656	76	o	25	30

6			45 4	59 9	90 8	82 9	04 9	14 1	224 83	473 333	22 48 3	w n	12 01 16	85 92 11
80 76	MFA P5	Microfibrillar associated protein 5	3. 22 50 9	5. 60 77 7	3. 20 48 4	6. 23 79	7. 12 75 8	8. 66 21	10. 055 828 19	3.3 299 6	10. 05 58 28 19	U p	0.0 03 13 19 4	0.9 30 85 92 11
11 00 5	SPIN K5	Serine peptidase inhibitor, Kazal type 5	6. 23 78 1	5. 01 26	4. 51 58 4	3. 30 18 6	4. 47 22 4	4. 42 41 5	-2. 280 473 386	-1. 189 333 333	2.2 80 47 33 86	D o w n	0.0 38 65 98 57	0.9 30 85 92 11
23 05 2	END OD1	Endonuclease domain containing 1	7. 33 57 6	6. 18 52 7	5. 97 59 1	8. 22 05 9	7. 78 43 4	7. 52 90 4	2.5 414 937 21	1.3 456 766 67	2.5 41 49 37 21	U p	0.0 06 53 19 21	0.9 30 85 92 11
81 60 7	PVR L4	Poliovirus receptor-related 4	7. 00 24	7. 21 18	7. 40 76 9	8. 00 31 7	7. 73 06 7	7. 67 47 1	1.5 110 520 26	0.5 955 533 33	1.5 11 05 20 26	U p	0.0 08 56 15 07	0.9 30 85 92 11
85 7	CAV 1	Caveolin 1	8. 02 64 6	9. 05 34 9	9. 03 89 5	6. 44 52 2	8. 11 23 6	7. 74 81 6	-2. 413 377 055	-1. 271 053 333	2.4 13 37 70 55	D o w n	0.0 25 50 42 43	0.9 30 85 92 11
66	SNA	Small nuclear RNA	4.	4.	4.	4.	3.	4.	-1.	-0.	1.5	D	0.0	0.9

19	PC3	activating complex polypeptide 3	39 96 2	55 72 2	89 46 2	26 45 8	77 66 9	00 31 2	518 194 538	602 356 667	18 19 45 38	o w n	11 41 19 23	30 85 92 11
60 04	RGS 16	Regulator of G-protein signaling 16	5. 54 36 8	6. 53 11 2	5. 59 29	4. 83 76 8	5. 01 41 8	4. 98 05 3	-1. 925 326 783	-0. 945 103 333	1.9 25 32 67 83	D o w n	0.0 08 28 83 56	0.9 30 85 92 11
93 58	ITG BL1	Integrin $\beta$ like 1	5. 38 66 7	5. 86 96 1	5. 08 43 4	6. 12 08 8	7. 71 02 1	5. 89 92 37	2.1 884 205 37	1.1 298 9 37	2.1 88 42 05 37	U p	0.0 42 29 58 35	0.9 30 85 92 11
51 38 6	EIF3 L	Eukaryotic translation initiation factor 3 subunit L	8. 79 09 7	9. 18 76 8	9. 68 02 7	8. 27 23 7	7. 86 76 9	8. 62 92 8	-1. 949 620 51	-0. 963 193 333	1.9 49 62 05 1	D o w n	0.0 08 40 12 8	0.9 30 85 92 11
72 79 56	SDH AP2	Succinate dehydrogenase complex subunit A, flavoprotein pseudogene 2	9. 64 26 8	9. 91 69 4	10 .0 53 34	9. 48 21 6	9. 02 82 7	9. 14 54 5	-1. 571 737 185	-0. 652 36 71 85	1.5 71 73 71 85	D o w n	0.0 06 23 94 1	0.9 30 85 92 11
22 52	FGF 7	Fibroblast growth factor 7	6. 71 67 3	7. 03 45 8	7. 78 47 8	3. 64 22 5	7. 01 75 4	5. 13 42 2	-3. 768 525 096	-1. 914 525 096	3.7 68 52 50 96	D o w n	0.0 36 44 23 82	0.9 30 85 92 11

10 63 1	POS TN	Periostin, osteoblast specific factor	4. 99 23 1	5. 14 36 9	4. 89 14 6	3. 91 17 6	4. 03 27 3	4. 47 03 7	-1. 828 735 806	-0. 870 846 667	1.8 28 73 58 06	D o w n	0.0 01 23 24 21	0.9 30 85 92 11
71 36	TNN I2	Troponin I type 2 (skeletal, fast)	9. 37 26 7	8. 80 62 6	8. 72 66 3	10 .4 62 82	10 .4 67 36	9. 38 01 7	2.1 960 790 71	1.1 349 3 90 71	2.1 96 07 90 71	U p	0.0 08 39 96 32	0.9 30 85 92 11
62 75	S100 A4	S100 calcium binding protein A4	9. 67 65 9	9. 93 60 1	9. 31 38 4	9. 75 74 3	10 .4 76 57	10 .5 95 14	1.5 521 127 18	0.6 342 333 33	1.5 52 11 27 18	U p	0.0 39 59 32 63	0.9 30 85 92 11
51 32 6	ARL 17A	ADP-ribosylation factor like gtpase 17A	4. 80 13 1	4. 51 23 2	4. 51 53 1	3. 79 43 6	3. 57 36 5	4. 46 30 7	-1. 586 616 363	-0. 665 953 333	1.5 86 61 63 63	D o w n	0.0 21 74 66 41	0.9 30 85 92 11
10 10 5	PPIF	Peptidylprolyl isomerase F	6. 06 35 9	6. 20 70 4	6. 66 77 9	5. 90 23 1	5. 68 54 8	5. 44 75 9	-1. 552 234 652	-0. 634 346 667	1.5 52 23 46 52	D o w n	0.0 16 78 60 59	0.9 30 85 92 11
84 06	SRP X	Sushi-repeat containing protein, X-linked	7. 00 44 3	8. 30 52 5	8. 57 88 6	5. 89 90 5	7. 34 62 4	7. 03 64 7	-2. 300 998 431	-1. 202 26 84	2.3 00 99 84	D o w n	0.0 41 75 79	0.9 30 85 92

												31		53	11
71	TNF	TNF $\alpha$ induced	5.	4.	4.	5.	5.	5.	5.	1.6	0.6	1.6	U	0.0	0.9
27	AIP2	protein 2	11	94	53	52	94	21	193	954	19	p	17	30	
			37	76	96	83	17	73	932	533	39		82	85	
			2		5		3		1	33	32		76	92	
											1		87	11	
44	MT1	Metallothionein 1J,	6.	6.	5.	7.	7.	7.	2.0	1.0	2.0	U	0.0	0.9	
98	JP	pseudogene	88	34	75	59	27	30	933	657	93	p	05	30	
			56	36	38	9	87	27	013	8	30		70	85	
			6	9	1		3	7	27		13		41	92	
											27		4	11	
43	MM	Matrix	10	9.	10	11	10	10	1.7	0.8	1.7	U	0.0	0.9	
12	P1	metallopeptidase 1	.4	20	.7	.1	.8	.9	935	427	93	p	48	30	
			36	65	03	66	07	00	110	866	51		53	85	
			78	3	03	61	26	83	91	67	10		65	92	
											91		14	11	
35	IGK	Immunoglobulin $\kappa$	4.	5.	5.	4.	4.	4.	-2.1	-1.	2.1	D	0.0	0.9	
14	C	constant	84	68	56	43	01	39	180	082	18	o	02	30	
			29	69	01	06	58	53	304	723	03	w	39	85	
			2	1	6	2	8	2	54	333	04	n	96	92	
											54		6	11	
25	GAP	Glyceraldehyde-3-	12	11	12	11	11	11	-1.	-0.	1.5	D	0.0	0.9	
97	DH	phosphate	.1	.8	.1	.3	.2	.6	529	612	29	o	03	30	
		dehydrogenase	12	61	71	52	69	85	199	776	19	w	96	85	
			78	74	12	74	05	52	535	667	95	n	21	92	
											35		29	11	
46	NAP	Nucleosome	3.	4.	5.	3.	3.	3.	-1.	-0.	1.7	D	0.0	0.9	
75	1L3	assembly protein	75	52	10	30	97	62	769	823	69	o	39	30	
		1-like 3	00	16	54	77	33	7	093	01	09	w	90	85	

			9	2	2	2	8		133		31	n	47	92
											33		26	11
28	GPM	Glycoprotein M6A	4.	6.	7.	2.	5.	3.	-4.	-2.	4.0	D	0.0	0.9
23	6A		75	75	13	87	68	98	092	033	92	o	37	30
			03	74	38	68	02	53	786	083	78	w	29	85
			2	6	8	1	8	2	281	333	62	n	38	92
											81		14	11
10	EDIL	EGF-like repeats	8.	8.	9.	6.	8.	6.	-2.	-1.	2.8	D	0.0	0.9
08	3	and discoidin I-like	04	75	10	80	42	15	840	506	40	o	27	30
5		domains 3	56	17	24	21	90	01	536	163	53	w	66	85
			8	7	4	6	6	8	287	333	62	n	24	92
											87		37	11
26	RAL	Ral gtpase	4.	4.	4.	4.	3.	3.	-1.	-0.	1.6	D	0.0	0.9
13	GAP	activating protein,	20	95	66	20	37	96	691	758	91	o	20	30
4	A1P	$\alpha$ subunit 1	14	49	12	16	79	37	246	086	24	w	59	85
		(catalytic)	2	8	9	8	6	9	17	667	61	n	73	92
		pseudogene									7		06	11
10	LOC	WAS protein	7.	7.	7.	8.	8.	8.	2.0	1.0	2.0	U	0.0	0.9
02	1002	family homolog 1	80	50	00	94	50	07	975	686	97	p	05	30
88	8877	pseudogene	77	08	97	64	34	44	327	933	53		38	85
77	8		1	5	2	6	6	4	45	33	27		14	92
8											45		06	11
10	FXY	FXYD6-FXYD2	6.	7.	7.	4.	6.	5.	-2.	-1.	2.7	D	0.0	0.9
05	D6-F	readthrough	34	23	97	41	85	85	780	475	80	o	48	30
33	XYD		29	23	33	66	59	01	401	293	40	w	83	85
18	2		3	7	2	9	2	3	702	333	17	n	12	92
1											02		46	11
65	SLC	Solute carrier	9.	8.	9.	10	9.	9.	1.5	0.6	1.5	U	0.0	0.9
13	2A1	family 2	08	89	07	.2	48	17	303	138	30	p	46	30

		(facilitated glucose transporter), member 1	42 6	05 5	73	30 69	62 6	67 1	376 49	5	33 76 49		58 23 73	85 92 11
50 48	PAF AH1 B1	Platelet activating factor acetylhydrolase 1b regulatory subunit 1	4. 38 83 5	5. 13 07 9	5. 52 52	4. 66 16 2	3. 93 01 2	4. 29 54 6	-1. 646 093 936	-0. 719 046 667	1.6 46 09 39 36	D o w n	0.0 49 15 17 58	0.9 30 85 92 11
73 64	UGT 2B7	UDP glucuronosyltransferase 2 family, polypeptide B7	5. 94 60 9	6. 55 34 3	8. 66 62	9. 20 94 4	10 .1 88 3	7. 71 49 2	3.9 512 615 12	1.9 823 133 33	3.9 51 26 15 12	U p	0.0 40 16 58 38	0.9 30 85 92 11
10 04 9	DNA JB6	Dnaj heat shock protein family (Hsp40) member B6	5. 56 35	6. 14 44 9	6. 90 13	5. 50 69 5	4. 98 48 8	5. 34 71 2	-1. 896 645 432	-0. 923 45	1.8 96 64 54 32	D o w n	0.0 23 87 07 09	0.9 30 85 92 11
68 76	TAG LN	Transgelin	10 .6 10 81	11 .3 27 5	11 .5 60 5	7. 74 80 5	11 .3 54 78	8. 65 89 8	-3. 763 739 209	-1. 912 166 667	3.7 63 73 92 09	D o w n	0.0 49 38 04 31	0.9 30 85 92 11
90 79	LDB 2	LIM domain binding 2	4. 54 17 4	5. 01 24 8	5. 17 61 3	3. 97 62 6	3. 81 58 9	4. 74 76 1	-1. 658 865 211	-0. 730 196 667	1.6 58 86 52 11	D o w n	0.0 29 65 99 48	0.9 30 85 92 11
35	JCH	Joining chain of	7.	7.	7.	7.	7.	6.	-1.	-0.	1.5	D	0.0	0.9



12	AIN	multimeric iga and igm	17 37 8	83 73 1	80 76 6	01 91 9	11 55 2	92 23 6	502 355 949	587 226 667	02 35 59 49	o w n	22 74 34 09	30 85 92 11
13 06	COL 15A1	Collagen, type XV, $\alpha$ 1	7. 29 63 4	8. 11 17 7	8. 21 13 1	5. 95 84 5	7. 44 28 1	7. 23 57 2	-1. 991 901 996	-0. 994 146 667	1.9 91 90 19 96	D o w n	0.0 45 64 23 42	0.9 30 85 92 11
33 97	ID1	Inhibitor of DNA binding 1, dominant negative helix-loop-helix protein	9. 00 30 9	10 .7 40 28	9. 37 94 9	8. 65 61 9	7. 06 94 4	7. 22 70 9	-4. 160 287 797	-2. 056 683 333	4.1 60 28 77 97	D o w n	0.0 05 82 32 87	0.9 30 85 92 11
60 95	ROR A	RAR-related orphan receptor A	7. 29 36 4	6. 94 18 1	6. 17 26 7	7. 67 37 8	7. 45 88 8	7. 53 85 2	1.6 868 441 26	0.7 543 266 67	1.6 86 84 41 26	U p	0.0 26 89 57 54	0.9 30 85 92 11
35 97	IL13 RA1	Interleukin 13 receptor, $\alpha$ 1	5. 34 64 3	5. 39 40 4	5. 58 65 3	4. 79 14 7	4. 51 11 6	5. 22 39 6	-1. 515 881 172	-0. 600 156 667	1.5 15 88 11 72	D o w n	0.0 18 21 72 66	0.9 30 85 92 11
57 18 7	THO C2	THO complex 2	7. 18 99 7	6. 88 07 9	6. 30 22 6	7. 61 67 5	7. 54 63 2	7. 28 08 2	1.6 136 003 85	0.6 902 833 33	1.6 13 60 03 85	U p	0.0 21 72 24 8	0.9 30 85 92 11

58	RAB	RAB6A, member	6.	6.	6.	5.	5.	5.	-1.	-0.	1.5	D	0.0	0.9
70	6A	RAS oncogene	03	01	26	55	07	76	558	64	58	o	15	30
		family	78	41	91	74	60	75	329		32	w	03	85
			9			6	7	6	159		91	n	14	92
											59		2	11
10	NPIP	Nuclear pore	5.	5.	6.	4.	4.	5.	-1.	-0.	1.8	D	0.0	0.9
10	A8	complex	15	57	33	89	32	20	841	881	41	o	31	30
59		interacting protein	31	97	36	51	09	72	706	043	70	w	97	85
95		family member A8		5		7		5	712	333	67	n	36	92
3											12		18	11
87	CTN	Catenin $\alpha$ -like 1	6.	7.	7.	5.	5.	6.	-2.	-1.1	2.1	D	0.0	0.9
27	NAL		62	18	62	93	74	43	158	103	58	o	05	30
	1		98	41	41	11	46	13	990	566	99	w	24	85
			2	6	6	1	5	1	158	67	01	n	23	92
											58		42	11
99	HNR	Heterogeneous	7.	8.	8.	7.	6.	7.	-1.	-0.	1.7	D	0.0	0.9
87	NPD	nuclear	29	06	17	15	48	48	742	801	42	o	37	30
	L	ribonucleoprotein	79	44	29	91	49	72	739	356	73	w	66	85
		D like	8	3	6	1		9	175	667	91	n	89	92
											75		82	11
55	EPN	Epsin 3	5.	5.	5.	6.	5.	6.	1.5	0.6	1.5	U	0.0	0.9
04	3		75	66	70	92	97	14	603	418	60	p	34	30
0			65	26	65	95	57	62	755	933	37		60	85
			8	9	6	9		2	89	33	55		72	92
											89		29	11
53	PLN	Phospholamban	5.	7.	7.	3.	6.	3.	-3.	-1.	3.9	D	0.0	0.9
50			52	28	34	67	61	92	947	980	47	o	42	30
			60	76	41	54	11	89	073	783	07	w	98	85
			9	8	1	2	4	7	36	333	33	n	06	92

											6		24	11
64	ST6	ST6	5.	6.	6.	5.	5.	6.	-1.	-0.	1.7	D	0.0	0.9
80	GAL	$\beta$ -galactosamide	87	58	91	38	32	25	746	804	46	o	45	30
	1	$\alpha$ -2,6-sialyltransferase 1	6	32	92	52	27	60	935	826	93	w	92	85
				8	5	8	1	6	893	667	58	n	14	92
											93		55	11
51	MPP	Membrane protein,	8.	8.	7.	7.	7.	7.	-1.	-0.	1.5	D	0.0	0.9
67	6	palmitoylated 6	17	03	97	08	52	73	531	614	31	o	13	30
8			29	41	95	04	87	26	536	98	53	w	55	85
			7	7	9	2		7	765		67	n	34	92
											65		94	11
88	TSC	TSC22 domain	7.	8.	8.	7.	6.	7.	-1.	-0.	1.7	D	0.0	0.9
48	22D1	family member 1	41	03	18	04	73	32	791	841	91	o	09	30
			15	07	91	7	66	38	696	326	69	w	92	85
			9	2	4		6	1	985	667	69	n	62	92
											85		43	11
27	PDC	Programmed cell	6.	7.	7.	6.	5.	6.	-1.	-0.	1.7	D	0.0	0.9
25	D4	death 4 (neoplastic	73	33	03	66	71	40	708	772	08	o	23	30
0		transformation	87	17	23	80	68	02	329	586	32	w	23	85
		inhibitor)	3	3	8	3	1	4	974	667	99	n	18	92
											74		91	11
19	ACS	Acyl-coa	6.	7.	7.	7.	8.	7.	1.8	0.8	1.8	U	0.0	0.9
73	F3	synthetase family	54	70	04	95	15	83	492	869	49	p	14	30
22		member 3	17	11	72	37	79	93	667	533	26		70	85
			7	2	8	5	3	5	37	33	67		41	92
											37		02	11
64	NPIP	Nuclear pore	5.	5.	6.	4.	4.	5.	-1.	-0.	1.8	D	0.0	0.9
27	A3	complex	15	57	33	89	32	20	841	881	41	o	31	30
78		interacting protein	31	97	36	51	09	72	706	043	70	w	97	85

		family member A3		5		7		5	712	333	67	n	36	92
											12		18	11
74	WAR	Tryptophanyl-trna	4.	4.	5.	4.	4.	4.	-1.	-0.	1.6	D	0.0	0.9
53	S	synthetase	68	72	48	02	03	56	691	758	91	o	18	30
			48	73	59	36	23	68	582	373	58	w	81	85
			8			9	9	8	257	333	22	n	36	92
											57		5	11
48	NN	Nicotinamide	6.	6.	7.	7.	8.	7.	2.2	1.1	2.2	U	0.0	0.9
37	MT	N-methyltransferas	61	91	03	75	69	70	918	965	91	p	03	30
		e	20	25	56	32	20	45	987	433	89		07	85
			7	2		2	7	3	85	33	87		65	92
											85		75	11
10	GPC	Glypican 6	8.	8.	8.	7.	7.	7.	-1.	-0.	1.6	D	0.0	0.9
08	6		16	27	83	77	86	52	630	705	30	o	10	30
2			53	72	89	42	87	34	223	07	22	w	51	85
			4	8	7	5		3	762		37	n	52	92
											62		22	11
79	WLS	Wntless Wnt ligand	6.	7.	7.	6.	5.	6.	-1.	-0.	1.7	D	0.0	0.9
97		secretion mediator	43	11	37	48	73	28	758	813	58	o	24	30
1			98	80	76	11	13	11	014	946	01	w	29	85
			7	8	1	7	9	6	131	667	41	n	57	92
											31		8	11
59	RB1	Retinoblastoma 1	4.	4.	5.	4.	3.	4.	-1.	-0.	1.6	D	0.0	0.9
25			63	65	43	35	95	13	692	758	92	o	13	30
			07	55	94	97	26	64	266	956	26	w	67	85
			3	7	7	8	5	7	363	667	63	n	23	92
											63		74	11
94	LY86	Lymphocyte	6.	6.	6.	5.	6.	6.	-1.	-0.	1.6	D	0.0	0.9
50		antigen 86	53	63	99	59	02	50	603	680	03	o	28	30

			37	77	11	29	08	60	176	933	17	w	30	85
			5	7	5	6	4	7	575	333	65	n	34	92
											75		05	11
54	POD	Podocalyxin-like	7.	6.	7.	6.	6.	6.	-1.	-0.	1.5	D	0.0	0.9
20	XL		00	86	48	05	39	95	574	654	74	o	41	30
			60	38	93	22	09	17	357	763	35	w	81	85
			4	3	5	3	7	3	667	333	76	n	77	92
											67		63	11
57	LRC	Leucine-rich	3.	4.	4.	3.	3.	3.	-1.	-0.	1.6	D	0.0	0.9
63	H2	repeats and	78	16	71	38	34	73	661	732	61	o	15	30
1		calponin homology	15	43	69	34	99	13	734	69	73	w	72	85
		(CH) domain	4	8		6	9		619		46	n	28	92
		containing 2									19		02	11
55	GIM	Gtpase, IMAP	6.	6.	6.	5.	5.	6.	-1.	-0.	1.6	D	0.0	0.9
34	AP5	family member 5	16	20	81	11	78	11	652	724	52	o	40	30
0			31	81	84	41	36	75	656	786	65	w	03	85
			8	1		9	3	1	238	667	62	n	95	92
											38		58	11
56	ADC	Aarf domain	5.	5.	5.	4.	4.	4.	-1.	-0.	1.7	D	0.0	0.9
99	K3	containing kinase 3	32	81	52	68	66	90	747	805	47	o	01	30
7			33	55	62	31	36	2	650	416	65	w	62	85
			1		6	9	3		46	667	04	n	46	92
											6		9	11
53	ACP	Acid phosphatase	5.	6.	6.	5.	5.	5.	-1.	-0.	1.5	D	0.0	0.9
2		2, lysosomal	55	02	09	35	11	45	500	585	00	o	16	30
			84	60	71	14	94	36	784	716	78	w	12	85
			8	6	5	4	7	3	327	667	43	n	66	92
											27		65	11
70	THY	Thy-1 cell surface	5.	6.	6.	6.	7.	6.	1.8	0.9	1.8	U	0.0	0.9

70	1	antigen	34	41	08	27	36	94	830	130	83	p	32	30
			64	44	35	71	48	17	613	8	06		23	85
			6	4	8	4	8		45		13		43	92
											45		36	11
10	PTG	Prostaglandin E	7.	8.	8.	7.	6.	7.	-1.	-0.	1.8	D	0.0	0.9
72	ES3	synthase 3	85	31	65	68	49	95	867	900	67	o	49	30
8			91	61	92	25	93	05	014	733	01	w	07	85
			9		7	1	4	1	76	333	47	n	96	92
											6		24	11
10	SMC	Structural	5.	5.	6.	5.	4.	5.	-1.	-0.	1.5	D	0.0	0.9
05	4	maintenance of	52	87	07	45	80	36	532	615	32	o	28	30
1		chromosomes 4	18	40	73	90	24	48	241	643	24	w	11	85
			8	5	4	6	5	3	109	333	11	n	91	92
											09		13	11
84	LTB	Latent	7.	8.	8.	7.	7.	7.	-1.	-0.	1.6	D	0.0	0.9
25	P4	transforming	45	28	32	01	50	48	612	689	12	o	33	30
		growth factor $\beta$	84	43	98	86	34	17	843	606	84	w	71	85
		binding protein 4	3	4	6	4	5	2	736	667	37	n	46	92
											36		64	11
26	HSP	Heat shock protein	5.	6.	6.	4.	5.	4.	-2.	-1.	2.1	D	0.0	0.9
35	B8	family B (small)	12	09	72	39	26	96	153	106	53	o	26	30
3		member 8	54	18	62	26	67	37	689	81	68	w	93	85
			5	1	9	4	5	3	097		90	n	40	92
											97		48	11
72	NPIP	Nuclear pore	5.	5.	6.	4.	4.	5.	-1.	-0.	1.8	D	0.0	0.9
88	B11	complex	15	57	33	89	32	20	841	881	41	o	31	30
88		interacting protein	31	97	36	51	09	72	706	043	70	w	97	85
		family member		5		7		5	712	333	67	n	36	92
		B11									12		18	11

11 60 39	OSR 2	Odd-skipped related transcription factor 2	4. 40 67 2	4. 79 66 9	5. 36 32	4. 10 97 2	4. 00 27 2	4. 36 34 9	-1. 621 010 385	-0. 696 893 333	1.6 21 01 03 85	D o w n	0.0 21 74 92 17	0.9 30 85 92 11
54 6	ATR X	A thalassemia/mental retardation syndrome X-linked	6. 39 84 7	6. 62 03 5	5. 55 07 7	7. 25 43 8	7. 35 22 1	6. 63 97 4	1.8 560 642 69	0.8 922 466 67	1.8 56 06 42 69	U p	0.0 23 00 92 18	0.9 30 85 92 11
23 08 9	PEG 10	Paternally expressed 10	5. 60 49 7	5. 55 79 5	5. 75 18 1	4. 85 55 9	4. 74 53 5	4. 96 3 054	-1. 721 417 054	-0. 783 596 667	1.7 21 41 70 54	D o w n	0.0 00 55 06 92	0.9 30 85 92 11
63 87 4	ABH D4	Abhydrolase domain containing 4	5. 24 33 5	5. 42 69 8	5. 60 51 2	4. 43 93 3	4. 75 68 3	5. 28 37 2	-1. 514 165 953	-0. 598 523 333	1.5 14 16 59 53	D o w n	0.0 32 08 05 62	0.9 30 85 92 11
85 45 8	DIX DC1	DIX domain containing 1	7. 01 27 2	7. 70 90 6	7. 61 72 7	6. 10 30 5	6. 93 85 8	6. 67 56 7	-1. 832 631 429	-0. 873 916 667	1.8 32 63 14 29	D o w n	0.0 13 08 68 26	0.9 30 85 92 11
23 57 6	DDA H1	Dimethylarginine dimethylaminohydr olase 1	4. 32 04 3	4. 69 70 6	5. 26 37 1	4. 23 80 5	3. 29 35 7	3. 73 18 5	-2. 008 209 804	-1. 005 91 000	2.0 08 20 98	D o w n	0.0 10 71 36	0.9 30 85 92

											04		2	11
22	PXD	PX domain	7.	7.	7.	8.	8.	8.	1.5	0.6	1.5	U	0.0	0.9
17	C1	containing 1	66	89	58	97	00	18	937	723	93	p	32	30
49			07	19	79	17	24	38	183	966	71		40	85
			8	9	8	1	3		23	67	83		67	92
											23		52	11
14	CTN	Catenin $\beta$ 1	6.	7.	7.	6.	6.	6.	-1.	-0.	1.7	D	0.0	0.9
99	NB1		90	76	26	22	42	76	787	837	87	o	10	30
			55	50	29	84	45	77	037	57	03	w	80	85
			2	3	4	5	9	4	613		76	n	63	92
											13		54	11
23	NPIP	Nuclear pore	5.	5.	6.	4.	4.	5.	-1.	-0.	1.8	D	0.0	0.9
11	B3	complex	15	57	33	89	32	20	841	881	41	o	31	30
7		interacting protein	31	97	36	51	09	72	706	043	70	w	97	85
		family, member B3		5		7		5	712	333	67	n	36	92
											12		18	11
92	NPIP	Nuclear pore	5.	5.	6.	4.	4.	5.	-1.	-0.	1.8	D	0.0	0.9
84	A1	complex	15	57	33	89	32	20	841	881	41	o	31	30
		interacting protein	31	97	36	51	09	72	706	043	70	w	97	85
		family member A1		5		7		5	712	333	67	n	36	92
											12		18	11
23	FAF2	Fas associated	6.	6.	5.	6.	7.	6.	1.5	0.6	1.5	U	0.0	0.9
19		factor family	59	13	74	84	13	40	548	367	54	p	46	30
7		member 2	43	30	38	12	06	95	226	5	82		30	85
			6	1	4	5	8	3	18		26		06	92
											18		07	11
15	ATP8	Atpase, class I,	7.	7.	7.	6.	5.	6.	-1.	-0.	1.5	D	0.0	0.9
83	B5P	type 8B, member 5,	00	03	34	72	87	75	597	675	97	o	32	30
81		pseudogene	63	75	07	69	27	87	021	383	02	w	54	85



			8	1	6	8	6	6	055	333	10	n	27	92
											55		83	11
54	NEU	Neuralized E3	6.	7.	8.	5.	7.	6.	-2.	-1.	2.4	D	0.0	0.9
49	RL1	ubiquitin protein	76	88	48	43	11	63	490	316	90	o	39	30
2	B	ligase 1B	12	73	16	41	17	46	778	596	77	w	37	85
			1	9	9	8	1	1	388	667	83	n	94	92
											88		2	11
49	OGN	Osteoglycin	6.	6.	6.	4.	5.	5.	-2.	-1.	2.3	D	0.0	0.9
69			13	35	20	01	34	59	372	246	72	o	12	30
			13	18	64	08	57	29	996	71	99	w	11	85
				4	8	4	5		545		65	n	93	92
											45		35	11
63	TNN	Tenascin N	4.	3.	4.	3.	4.	3.	-1.	-0.	1.5	D	0.0	0.9
92			81	97	90	81	21	77	551	633	51	o	41	30
3			36	78	85	28	1	59	223	406	22	w	88	85
			8	5	5	7		9	61	667	36	n	57	92
											1		33	11
72	NPIP	Nuclear pore	5.	5.	6.	4.	4.	5.	-1.	-0.	1.8	D	0.0	0.9
96	B1P	complex	15	57	33	89	32	20	841	881	41	o	31	30
02		interacting protein	31	97	36	51	09	72	706	043	70	w	97	85
		family member B1,		5		7		5	712	333	67	n	36	92
		pseudogene									12		18	11
50	HDG	Hepatoma-derived	5.	5.	5.	4.	5.	4.	-1.	-0.	1.5	D	0.0	0.9
81	FRP3	growth factor,	12	43	90	71	11	81	526	610	26	o	26	30
0		related protein 3	77	79	89	38	36	65	506	233	50	w	60	85
			9	9	7	9		6	077	333	60	n	28	92
											77		78	11
10	CWC	CWC27	8.	8.	8.	9.	9.	9.	1.6	0.6	1.6	U	0.0	0.9
28	27	spliceosome-associ	87	63	69	87	25	12	036	813	03	p	12	30

3		ated protein homolog	90 1	35 1	44 1	16	13 5	79 4	063 11	2	60 63 11		89 15 49	85 92 11
11	ADC	Adenylate cyclase	5.	6.	6.	4.	5.	5.	-1.	-0.	1.5	D	0.0	0.9
7	YAP	activating	80	41	13	97	82	70	532	615	32	o	48	30
	1R1	polypeptide 1 (pituitary) receptor type I	99 3	24 6	54 6	95 4	90 3	24 2	216 328	62	21 63 28	w n	98 36 53	85 92 11
20	STO	Stomatin	5.	6.	6.	5.	5.	5.	-1.	-0.	1.6	D	0.0	0.9
40	M		84 63 6	31 65 1	79 98 7	97 89 1	22 75 9	71 00 6	604 429 058	682 06	04 42 90 58	o w n	45 86 34 4	30 85 92 11
51	ARM	Armadillo repeat	7.	8.	8.	6.	7.	7.	-1.	-0.	1.5	D	0.0	0.9
30	CX1	containing,	42	23	01	93	26	64	527	610	27	o	49	30
9		X-linked 1	65 5	88 8	52 6	63 9	67 4	49 4	183 407	873 333	18 34 07	w n	89 69 96	85 92 11
78	SLM	Sarcolemma	4.	4.	5.	3.	3.	3.	-1.	-0.	1.6	D	0.0	0.9
71	AP	associated protein	09 88 3	20 24 3	09 17 3	99 51 4	55 45 4	64 39 4	662 222 297	733 113 333	62 22 22 97	o w n	27 11 64 13	30 85 92 11
59	RAP	RAP1B, member	4.	4.	5.	4.	3.	4.	-1.	-0.	1.6	D	0.0	0.9
08	1B	of RAS oncogene family	58 07 6	65 86 9	24 06 7	40 31 2	56 14 6	28 57 4	673 961 871	743 266 667	73 96 18 71	o w n	24 86 34 96	30 85 92 11
15	SH3	SH3 domain	6.	6.	6.	5.	5.	5.	-1.	-0.	1.5	D	0.0	0.9

25	D19	containing 19	02	04	48	55	34	84	516	600	16	o	17	30
03			06	02	98	88	85	23	087	353	08	w	72	85
			9	2	1	4	1	1	829	333	78	n	56	92
											29		81	11
51	CES	Carboxylesterase 1	5.	6.	5.	3.	3.	5.	-3.	-1.	3.5	D	0.0	0.9
71	IP1	pseudogene 1	99	71	75	81	71	41	579	839	79	o	04	30
6			37	48	33	69	49	05	570	786	57	w	69	85
			1		1		7	9	928	667	09	n	37	92
											28		4	11
53	FXD	FXD domain	6.	7.	7.	4.	6.	5.	-2.	-1.	2.7	D	0.0	0.9
82	D6	containing ion	34	23	97	41	85	85	780	475	80	o	48	30
6		transport regulator	29	23	33	66	59	01	401	293	40	w	83	85
		6	3	7	2	9	2	3	702	333	17	n	12	92
											02		46	11
33	HSP	Heat shock protein	8.	8.	8.	7.	7.	7.	-1.	-0.	1.5	D	0.0	0.9
13	A9	family A (Hsp70)	07	13	45	82	24	75	530	614	30	o	16	30
		member 9	45	40	76	05	70	56	864	346	86	w	53	85
			4	7	1	6	2		579	667	45	n	28	92
											79		91	11
36	ITG	Integrin $\beta$ 1	8.	9.	9.	8.	8.	9.	-1.	-0.	1.7	D	0.0	0.9
88	B1		97	53	70	61	20	04	724	785	24	o	18	30
			99	60	82	33	96	32	251	97	25	w	71	85
			3	8	2	8	9	5	235		12	n	38	92
											35		06	11
17	DLA	Dihydrolipoamide	5.	5.	5.	4.	4.	4.	-1.	-0.	1.5	D	0.0	0.9
37	T	S-acetyltransferase	17	11	40	92	23	68	533	616	33	o	15	30
			30	13	99	27	79	43	062	416	06	w	49	85
			5		8	4	9	5	662	667	26	n	80	92
											62		7	11

44 95	MT1 G	Metallothionein 1G	11 .9 28 11	9. 02 56 3	8. 27 65 8	12 .0 46 33	11 .7 69 97	12 .3 44 09	4.9 589 110 02	2.3 100 233 33	4.9 58 91 10 02	U p	0.0 24 06 04 91	0.9 30 85 92 11
54 20 6	ERR FII 1	ERBB receptor feedback inhibitor 1	8. 66 74 6	10 .0 52 74	9. 31 91 2	8. 52 72 1	8. 45 32 1	8. 66 68 1	-1. 737 922 333	-0. 797 363 2	1.7 37 92 2	D o w n	0.0 37 28 08 72	0.9 30 85 92 11
93 78	NRX N1	Neurexin 1	4. 27 42 3	4. 40 92 9	4. 13 28 6	3. 67 31 3	3. 75 53 2	3. 61 40 2	-1. 506 607 204	-0. 591 303 333	1.5 06 60 72 04	D o w n	0.0 01 28 91 26	0.9 30 85 92 11
15 24	CX3 CR1	Chemokine (C-X3-C motif) receptor 1	9. 25 31	9. 58 87 5	9. 94 03 6	8. 19 67 2	8. 92 09 6	9. 40 12 9	-1. 686 945 463	-0. 754 413 333	1.6 86 94 54 63	D o w n	0.0 44 57 40 85	0.9 30 85 92 11
51 20 1	ZDH HC2	Zinc finger, DHHC-type containing 2	4. 08 37 8	4. 20 00 9	4. 72 62 4	3. 54 88 4	3. 53 12 6	4. 13 64 7	-1. 513 441 943	-0. 597 833 333	1.5 13 44 19 43	D o w n	0.0 31 35 16 53	0.9 30 85 92 11
14 65	CSR P1	Cysteine and glycine rich protein 1	7. 37 25	7. 62 53 5	7. 87 90 9	6. 60 63 4	7. 50 71	6. 84 28 2	-1. 558 574 013	-0. 640 226 667	1.5 58 57 40	D o w n	0.0 38 58 72	0.9 30 85 92

											13		56	11
82 1	CAN X	Calnexin	9. 09 13 7	9. 28 20 7	9. 59 34	8. 79 88 3	8. 24 24 5	8. 94 03 1	-1. 582 000 439	-0. 661 75	1.5 82 00 04 39	D o w n	0.0 18 39 20 48	0.9 30 85 92 11
11 59 08	CTH RC1	Collagen triple helix repeat containing 1	5. 02 94 1	5. 80 81 1	5. 80 25 3	4. 65 03 2	4. 95 39 6	4. 86 17 3	-1. 652 534 052	-0. 724 68	1.6 52 53 40 52	D o w n	0.0 15 35 43 62	0.9 30 85 92 11
68 3	BST 1	Bone marrow stromal cell antigen 1	4. 05 17 9	5. 32 45 1	5. 75 01 1	6. 81 31 4	6. 22 16 1	6. 59 81 9	2.8 327 042 81	1.5 021 8	2.8 32 70 42 81	U p	0.0 07 02 19 3	0.9 30 85 92 11
11 31 46	AHN AK2	AHNAK nucleoprotein 2	4. 37 38 8	5. 52 91 2	5. 49 26 5	5. 43 32 5	6. 38 60 6	6. 63 59 3	2.0 277 268 64	1.0 198 633 33	2.0 27 72 68 64	U p	0.0 36 54 87 85	0.9 30 85 92 11
71 68	TPM 1	Tropomyosin 1 ( $\alpha$ )	7. 58 71 7	7. 70 45 1	8. 07 18 1	7. 00 51 1	7. 40 95 2	6. 80 19 6	-1. 642 200 182	-0. 715 63	1.6 42 20 01 82	D o w n	0.0 09 99 61 8	0.9 30 85 92 11
88 05	TRI M24	Tripartite motif containing 24	6. 89 03	6. 75 18	6. 95 36	7. 83 57	7. 46 5	7. 25 39	1.5 724 055	0.6 529 733	1.5 72 40	U p	0.0 07 95	0.9 30 85

				5		5		2	2	33	55		88	92
											2		25	11
58	QAR	Glutaminyl-trna synthetase	6.	7.	7.	6.	6.	6.	-1.	-0.	1.5	D	0.0	0.9
59	S		62	07	32	58	11	45	537	620	37	o	24	30
			21	59	05	42	95	25	645	723	64	w	13	85
			1		5	6	5	8	928	333	59	n	85	92
											28		99	11
72	CBW	COBW domain containing 7	4.	3.	4.	3.	3.	3.	-1.	-0.	1.6	D	0.0	0.9
80	D7		45	86	15	71	32	19	674	744	74	o	05	30
13			21	23	27	57	17	77	812		81	w	34	85
			2	7	1	4	2	4	975		29	n	61	92
											75		82	11
33	HSP	Heat shock protein family A (Hsp70) member 5	8.	8.	9.	8.	7.	8.	-1.	-0.	1.9	D	0.0	0.9
09	A5		23	88	21	20	01	17	972	979	72	o	31	30
			67	38	29	75	23	42	214	816	21	w	76	85
			1	6	8	8	2		77	667	47	n	00	92
											7		93	11
56	PRO	Protein S ( $\alpha$ )	5.	5.	6.	5.	5.	5.	-1.	-0.	1.5	D	0.0	0.9
27	S1		90	91	62	46	15	82	587	666	87	o	33	30
			22	85	52	55	67	36	430	693	43	w	06	85
			2	9	6	6	5	8	394	333	03	n	68	92
											94		23	11
11	SCR	Stimulator of chondrogenesis 1	6.	6.	7.	3.	6.	4.	-4.	-2.1	4.3	D	0.0	0.9
34	G1		07	67	42	25	56	00	342	186	42	o	29	30
1			58	91	85	43	35	95	964	8	96	w	03	85
				1	6	1	5	7	018		40	n	85	92
											18		89	11
37	KCN	Potassium channel, calcium activated	7.	8.	8.	4.	8.	6.	-3.	-1.	3.5	D	0.0	0.9
78	MA1		41	59	68	98	23	03	514	813	14	o	46	30

		large conductance subfamily M $\alpha$ , member 1	35 2	06 7	61 9	01 1	01 2	98 3	793 668	44	79 36 68	w n	77 38 15	85 92 11
28 51 4	DLL 1	$\Delta$ -like ( <i>Drosophila</i> )	1 5. 46 12	5. 5. 76 58	6. 6. 20 34	4. 4. 88 72	5. 5. 47 14	5. 5. 10 64	-1. -0. 574 739	-0. -0. 655 113	1.5 1.5 74 73	D o w	0.0 0.0 25 01	0.9 30 85
81 87 6	RAB 1B	RAB1B, member RAS oncogene family	6. 12 7	5. 95 06	5. 60 56	5. 27 50	4. 93 54	5. 31 74	-1. 645 398	-0. 718 436	1.6 45 39	D o w	0.0 05 82	0.9 30 85
				2	2	2	7	4	082	667	80	n	23	92
											82		44	11
31 27	HLA -DR	Major histocompatibility complex, class II, DR $\beta$ 5	10 .1 20 15	10 .2 33 12	11 .0 53 67	9. 24 28 4	10 .0 67 13	9. 22 63 2	-1. 941 111 961	-0. 956 883 333	1.9 1.9 11 96 1	D o w n	0.0 16 70 42	0.9 30 85 92
71 02	TSP AN7	Tetraspanin 7	4. 38 33 3	5. 27 92 2	5. 89 00 3	3. 94 26 4	4. 14 82 6	4. 55 76 8	-1. 956 126 947	-0. 968	1.9 56 12 69 47	D o w n	0.0 29 32 97 59	0.9 30 85 92 11
55 32 9	MNS 1	Meiosis specific nuclear structural 1	3. 77 03 5	4. 53 52 8	4. 18 24 2	3. 36 73 2	3. 52 16 3	3. 60 90 5	-1. 583 755 907	-0. 663 35	1.5 83 75 59 07	D o w n	0.0 09 87 03 3	0.9 30 85 92 11
31	HLA	Major	8.	8.	8.	7.	8.	8.	-1.	-0.	1.6	D	0.0	0.9

17	-DQ	histocompatibility	33	36	95	22	02	17	669	739	69	o	34	30
	A1	complex, class II,	24	48	06	60	51	97	022	003	02	w	17	85
		DQ $\alpha$ 1	2	8	9	8	3	7	419	333	24	n	87	92
											19		05	11
25	RAL	Ral gtpase	4.	4.	4.	4.	3.	3.	-1.	-0.	1.6	D	0.0	0.9
39	GAP	activating protein,	20	95	66	20	37	96	691	758	91	o	20	30
59	A1	$\alpha$ subunit 1	14	49	12	16	79	37	246	086	24	w	59	85
		(catalytic)	2	8	9	8	6	9	17	667	61	n	73	92
											7		06	11
64	SRS	Serine/arginine-ric	4.	5.	5.	4.	3.	4.	-2.	-1.	2.2	D	0.0	0.9
30	F5	h splicing factor 5	00	55	40	33	06	09	231	158	31	o	39	30
			78	25	63	01	37	87	478		47	w	81	85
			7			6	8	3	645		86	n	00	92
											45		41	11
23	TBC	TBC1 domain	5.	6.	5.	5.	5.	5.	-1.	-0.	1.6	D	0.0	0.9
15	1D9	family member 9	71	01	99	30	04	09	692	758	92	o	01	30
8			10	23	48	61	01	52	188	89	18	w	44	85
			7	8	1	2	8	9	165		81	n	64	92
											65		91	11
10	CEL	Chymotrypsin like	4.	3.	3.	4.	4.	4.	1.8	0.8	1.8	U	0.0	0.9
13	A3A	elastase family	04	43	87	69	41	94	657	997	65	p	02	30
6		member 3A	43	44	75	02	69	85	857	833	78		40	85
			5	5	3		3	5	55	33	57		97	92
											55		76	11
25	RNF	Ring finger protein	6.	6.	7.	6.	5.	6.	-1.	-0.	1.5	D	0.0	0.9
89	19A	19A, RBR E3	36	79	07	58	79	03	519	603	19	o	49	30
7		ubiquitin protein	61	02	07	11	82	66	626	716	62	w	81	85
		ligase	9	6	2	7	5		385	667	63	n	84	92
											85		93	11



28 13	GP2	Glycoprotein 2 (zymogen granule membrane)	8. 37 85 4	7. 58 38 6	8. 09 43 9	9. 37 07 4	8. 31 54 5	9. 98 32 7	2.3 041 319 43	1.2 042 233 33	2.3 04 13 19 43	U p	0.0 19 71 05 27	0.9 30 85 92 11
25 84 2	ASF 1A	Anti-silencing function 1A histone chaperone	6. 22 84 1	6. 06 92 5	6. 59 13 6	5. 49 80 2	5. 60 34 1	6. 02 82 2	-1. 501 554 32	-0. 586 456 667	1.5 01 55 43 2	D o w n	0.0 23 46 37 83	0.9 30 85 92 11
34 00	ID4	Inhibitor of DNA binding 4, dominant negative helix-loop-helix protein	5. 87 14	7. 28 09 6	6. 23 38 9	4. 29 69 1	3. 69 40 6	3. 86 51 3	-5. 696 398 201	-2. 510 05 82	5.6 96 39 82 01	D o w n	0.0 00 13 22 82	0.9 30 85 92 11
65 06 69	GAS 6-AS 1	GAS6 antisense RNA 1	5. 72 01 2	5. 08 71 3	6. 12 16 2	6. 74 31 1	6. 86 89 6	6. 05 49 6	1.8 825 654 2	0.9 127 56 54 2	1.8 82 56 54 2	U p	0.0 20 53 74 09	0.9 30 85 92 11
54 93	PPL	Periplakin	9. 27 74 3	9. 66 64 3	9. 32 48 3	10. .4 97 08	9. 82 55 4	10. .1 90 89	1.6 797 928 51	0.7 482 833 33	1.6 79 79 28 51	U p	0.0 06 34 70 73	0.9 30 85 92 11
53 34	PLC L1	Phospholipase C like 1	5. 14 41 1	4. 18 98 9	4. 13 04 3	3. 45 88 9	4. 25 30 8	3. 23 19	-1. 790 281 767	-0. 840 186 667	1.7 90 28 17	D o w n	0.0 41 27 37	0.9 30 85 92

											67		58	11
84 98 1	MIR 22H G	MIR22 host gene	3. 96 67 9	5. 09 26 9	4. 44 37 4	3. 90 50 6	3. 82 77 5	3. 90 26 5	-1. 539 650 966	-0. 622 603 333	1.5 39 65 09 66	D o w n	0.0 44 50 78 08	0.9 30 85 92 11
28 98 4	RGC C	Regulator of cell cycle	7. 03 38 1	7. 06 18 9	7. 30 43 4	5. 28 30 6	5. 89 48 5	6. 41 22 1	-2. 411 571 08	-1. 269 973 333	2.4 11 57 10 8	D o w n	0.0 02 03 98 42	0.9 30 85 92 11
55 73	PRK AR1 A	Protein kinase, camp-dependent, regulatory subunit type I $\alpha$	5. 18 73 4	6. 20 91 2	5. 96 51 7	5. 23 40 9	4. 36 42 2	5. 13 42 2	-1. 836 560 811	-0. 877 006 667	1.8 36 56 08 11	D o w n	0.0 27 98 98 4	0.9 30 85 92 11
86 11	PLPP 1	Phospholipid phosphatase 1	8. 12 36 2	8. 81 16 6	9. 35 39 2	7. 65 09 7	7. 95 66 7	7. 79 30 7	-1. 949 129 573	-0. 962 83 743	1.9 49 12 95 73	D o w n	0.0 11 84 24 88	0.9 30 85 92 11
72 86 22	SKP 1P2	S-phase kinase-associated protein 1 pseudogene 2	9. 73 73 7	9. 68 45 1	9. 90 28 9	9. 09 12 65	8. 73 65 14	9. 50 14 743	-1. 585 813 743	-0. 665 223 333	1.5 85 81 37 43	D o w n	0.0 11 99 60 31	0.9 30 85 92 11
10 04 22	LOC 1004 2273	Uncharacterized LOC100422737	7. 13 93	6. 74 95	6. 56 14	7. 41 61	7. 60 66	7. 32 09	1.5 487 847	0.6 311 366	1.5 48 78	U p	0.0 10 80	0.9 30 85

73	7		3	8	1	8	2	3	65	67	47		32	92
7											65		2	11
39	LIPA	Lipase A,	6.	7.	7.	6.	5.	6.	-1.	-0.	1.8	D	0.0	0.9
88		lysosomal acid,	55	04	38	42	78	04	880	910	80	o	07	30
		cholesterol esterase	70	16	11	27	02	41	174	866	17	w	95	85
			5	2	5	7	7	8	632	667	46	n	97	92
											32		73	11
64	MRO	Maestro heat-like	6.	6.	6.	7.	6.	7.	1.6	0.6	1.6	U	0.0	0.9
24	H6	repeat family	51	53	39	39	91	18	033	810	03	p	03	30
75		member 6	43	04	89	17	43	08	284	7	32		87	85
			9	1	7	3	9	6	51		84		33	92
											51		38	11
27	B3G	B-1,3-glucuronyltr	4.	4.	4.	5.	4.	5.	1.6	0.7	1.6	U	0.0	0.9
08	AT1	ansferase 1	40	40	20	30	57	27	428	162	42	p	10	30
7			21	54	39	99	80	22	491		84		46	85
			7	6	7	3	6	1	33		91		78	92
											33		48	11
10	CFL	Cofilin 1	9.	9.	10	8.	9.	9.	-1.	-0.	1.5	D	0.0	0.9
72	1	(non-muscle)	63	56	.0	95	08	23	568	649	68	o	04	30
			66	69	24	99	25	77	584	463	58	w	80	85
			8	2	93	4			591	333	45	n	71	92
											91		01	11
46	MYB	Myosin binding	4.	4.	5.	4.	6.	6.	2.2	1.1	2.2	U	0.0	0.9
04	PC1	protein C, slow	29	30	13	80	08	32	418	646	41	p	23	30
		type	27	04	29	98	54	47	141	666	81		99	85
			4	6	2	8	8	6	27	67	41		61	92
											27		22	11
11	C12o	Chromosome 12	10	10	10	9.	10	10	-1.	-0.	1.5	D	0.0	0.9
32	rf57	open reading frame	.6	.5	.8	72	.0	.4	506	591	06	o	15	30

46		57	03 78	29 06	00 3	77 4	07 08	23 38	965 79	646 667	96 57 9	w n	74 31 82	85 92 11
10 53 76 75 2	LOC 1053 7675 2	NPIP-like protein 1	5. 15 31	5. 57 97	6. 33 36	4. 89 51	4. 32 09	5. 20 72	-1. 841 706	-0. 881 043	1.8 41 70	D o w n	0.0 31 97 36 18	0.9 30 85 92 11
25 95 0	RWD D3	RWD domain containing 3	5. 89 43 1	5. 86 80 1	6. 65 24 5	5. 37 69 9	5. 04 31 1	5. 84 50 5	-1. 643 236 349	-0. 716 54	1.6 43 23 63 49	D o w n	0.0 36 14 35 53	0.9 30 85 92 11
23 40 1	FRA T2	Frequently rearranged in advanced T-cell lymphomas 2	6. 81 94	6. 76 48 7	6. 80 15 2	5. 96 80 5	5. 96 30 7	6. 57 37 6	-1. 544 318 153	-0. 626 97	1.5 44 31 81 53	D o w n	0.0 13 71 08	0.9 30 85 92 11
22 89 0	ZBT B1	Zinc finger and BTB domain containing 1	4. 39 24 6	4. 35 28 3	4. 63 36 1	5. 48 73 9	4. 62 91 3	5. 10 08 3	1.5 292 313 34	0.6 128 066 67	1.5 29 23 13 34	U p	0.0 26 29 07 72	0.9 30 85 92 11
23 32	FMR 1	Fragile X mental retardation 1	4. 70 97 9	5. 04 85 2	5. 69 06 5	4. 63 88 9	4. 28 3 9	4. 59 85 3	-1. 561 407 026	-0. 642 846 667	1.5 61 40 70 26	D o w n	0.0 35 67 27 93	0.9 30 85 92 11
27	TNF	Tumor necrosis	9.	9.	9.	10	9.	9.	1.5	0.5	1.5	U	0.0	0.9

24	RSF2	factor receptor	64	46	48	.4	98	95	111	956	111	p	07	30
2	1	superfamily	75	49	91	48	80	17	812	766	81		83	85
		member 21	4	8	6	92	5	4	08	67	20		75	92
											8		09	11
55	SRG	Serglycin	7.	8.	7.	6.	7.	7.	-2.	-1.	2.2	D	0.0	0.9
52	N		44	81	97	63	02	13	212	145	12	o	09	30
			18	16	40	66	39	08	038	376	03	w	64	85
			5	5	1	1	3	4	762	667	87	n	58	92
											62		41	11
87	ADA	ADAM	6.	6.	7.	6.	5.	6.	-1.	-0.	1.6	D	0.0	0.9
54	M9	metallopeptidase	62	53	20	23	61	24	693	760	93	o	17	30
		domain 9	47	94	63	51	03	43	764	233	76	w	41	85
				5	4	3	1	5	542	333	45	n	51	92
											42		34	11
20	ENG	Endoglin	6.	6.	7.	4.	6.	6.	-2.	-1.	2.1	D	0.0	0.9
22			26	64	42	73	33	01	121	085	21	o	43	30
			98	57	56	81	45	30	620	166	62	w	97	85
				3	9	3	4	5	568	667	05	n	10	92
											68		27	11
78	CAC	Calcium channel,	4.	5.	5.	3.	4.	4.	-2.	-1.	2.2	D	0.0	0.9
3	NB2	voltage-dependent,	81	33	61	52	53	12	286	192	86	o	04	30
		$\beta$ 2 subunit	55	75	80	93	99	34	007	83	00	w	12	85
			8	7	3	4	1	4	283		72	n	64	92
											83		59	11
42	MEI	Meis homeobox 1	5.	6.	6.	4.	5.	5.	-1.	-0.	1.7	D	0.0	0.9
11	S1		66	07	84	87	72	57	748	805	48	o	46	30
			76	91	94	83	37	65	171	846	17	w	50	85
			8	2	7	8	7	8	431	667	14	n	13	92
											31		82	11

10	LOC	HLA class II	10	10	11	9.	10	9.	-1.	-0.	1.9	D	0.0	0.9
53	1053	histocompatibility	.1	.2	.0	24	.0	22	941	956	411	o	16	30
69	6923	antigen, DRB1-7 $\beta$	20	33	53	28	67	63	111	883	11	w	70	85
23	0	chain	15	12	67	4	13	2	961	333	96	n	42	92
0											1		06	11
83	TMT	Transmembrane	6.	6.	6.	5.	6.	5.	-1.	-0.	1.7	D	0.0	0.9
85	C1	and	45	55	72	31	46	58	731	791	31	o	26	30
7		tetratricopeptide	74	95	42	79	64	18	073	666	07	w	64	85
		repeat containing 1	8	2	8	2	8	8	122	667	31	n	59	92
											22		68	11
23	EPB	Erythrocyte	4.	4.	5.	3.	3.	4.	-1.	-0.	1.7	D	0.0	0.9
13	41L3	membrane protein	16	30	21	59	60	09	732	792	32	o	25	30
6		band 4.1-like 3	11	19	45	42	66	79	549	896	54	w	84	85
			5	5	2	7	8	8	614	667	96	n	90	92
											14		23	11
94	MED	Mediator complex	5.	5.	6.	5.	4.	5.	-1.	-0.	1.5	D	0.0	0.9
12	21	subunit 21	76	82	29	52	93	60	524	608	24	o	32	30
			63	97	47	97	16	33	881	696	88	w	67	85
			6	2	7	4	4	8	006	667	10	n	98	92
											06		78	11
47	GIM	Gtpase, IMAP	5.	5.	5.	4.	4.	5.	-1.	-0.	1.6	D	0.0	0.9
43	AP6	family member 6	40	37	99	62	53	51	619	695	19	o	48	30
44			14	02	23	75	77	27	262	336	26	w	14	85
			6	8	5	8	1	9	259	667	22	n	68	92
											59		02	11
55	PRK	Protein kinase,	5.	5.	5.	4.	5.	3.	-1.	-0.	1.8	D	0.0	0.9
92	G1	cgmp-dependent,	37	70	40	71	25	93	815	860	15	o	26	30
		type I	10	30	99	23	58	35	990	756	99	w	05	85
			4	3	8	7	4	7	514	667	05	n	34	92

											14		38	11
78 05	LAP TM5	Lysosomal protein transmembrane 5	8. 11 75 1	8. 30 44	8. 30 53	6. 85 67 3	7. 64 51 6	7. 82 60 4	-1. 740 811 509	-0. 799 76	1.7 40 81 15 09	D o w n	0.0 14 37 85 69	0.9 30 85 92 11
51 70 5	EMC N	Endomucin	5. 46 15 9	6. 41 48 1	6. 86 92 2	4. 69 86 2	4. 86 02 3	5. 81 84 2	-2. 177 666 96	-1. 122 783 333	2.1 77 66 69 6	D o w n	0.0 27 62 33 74	0.9 30 85 92 11
64 29 46	FLV CR1- AS1	FLVCR1 antisense RNA 1 (head to head)	6. 39 43 3	6. 73 09 4	6. 65 45 4	7. 76 77 6	7. 44 75 4	7. 41 68 7	1.9 329 263 48	0.9 507 866 67	1.9 32 92 63 48	U p	0.0 00 59 76 36	0.9 30 85 92 11
10 78 8	IQG AP2	IQ motif containing gtpase activating protein 2	5. 53 33 8	5. 44 81 9	5. 40 99 8	4. 89 31 9	3. 93 15 8	4. 76 03 5	-1. 912 522 429	-0. 935 476 667	1.9 12 52 24 29	D o w n	0.0 06 20 95 45	0.9 30 85 92 11
55 75 4	TME M30 A	Transmembrane protein 30A	4. 99 57 7	4. 91 99 3	5. 77 98 9	4. 84 85 9	4. 05 56 7	4. 32 33 9	-1. 768 647 655	-0. 822 646 667	1.7 68 64 76 55	D o w n	0.0 21 67 39 19	0.9 30 85 92 11
55 18	PPP2 R1A	Protein phosphatase 2 regulatory subunit	6. 83 72	7. 40 90	7. 37 50	6. 77 48	6. 32 43	6. 72 81	-1. 513 672	-0. 598 053	1.5 13 67	D o w	0.0 24 23	0.9 30 85

		A, $\alpha$	8	3	8	1		2	749	333	27	n	69	92
											49		49	11
26	GBP	Guanylate binding	6.	7.	6.	5.	6.	6.	-1.	-0.	1.8	D	0.0	0.9
34	2	protein 2,	98	19	66	34	14	68	860	895	60	o	27	30
		interferon-inducibl	99	15	99	22	1	08	611	776	61	w	49	85
		e	9		4	8		2	265	667	12	n	85	92
											65		52	11
28	ACA	Acyl-coa	5.	5.	5.	4.	4.	5.	-1.	-0.	1.5	D	0.0	0.9
97	D9	dehydrogenase	34	36	48	68	65	02	528	612	28	o	04	30
6		family member 9	69	69	91	43	95	30	404	026	40	w	08	85
			2	8	9	6	6	9	771	667	47	n	75	92
											71		42	11
51	UPB	Ureidopropionase,	5.	4.	3.	5.	5.	5.	2.0	1.0	2.0	U	0.0	0.9
73	1	$\beta$	09	32	94	52	18	70	218	157	21	p	09	30
3			26	42	34	04	34	35	883	033	88		27	85
			9		2	7	3	2	51	33	83		73	92
											51		43	11
79	FA2	Fatty acid	8.	8.	8.	9.	8.	8.	1.5	0.6	1.5	U	0.0	0.9
15	H	2-hydroxylase	41	00	18	39	52	53	407	236	40	p	42	30
2			05	41	08	93	86	85	754	566	77		54	85
			3	9	1	1	2	7	99	67	54		32	92
											99		31	11
19	EDN	Endothelin receptor	5.	6.	6.	4.	5.	4.	-2.	-1.	2.3	D	0.0	0.9
09	RA	type A	77	33	73	42	72	90	393	259	93	o	09	30
			38	44	03	79	37	9	817	313	81	w	13	85
			6	2	8	5	7		774	333	77	n	36	92
											74		99	11
16	CITE	Cbp/p300-interacti	7.	7.	7.	8.	7.	8.	1.5	0.6	1.5	U	0.0	0.9
37	D4	ng transactivator,	62	70	70	74	84	25	236	075	23	p	29	30



32		with Glu/Asp rich carboxy-terminal domain, 4	22 5	36	18 2	70 5	62 5	70 5	800 6	6 6	68 00 6		31 03 66	85 92 11
73	UQC	Ubiquinol-cytochro	9.	8.	9.	8.	8.	8.	-1.	-0.	1.6	D	0.0	0.9
84	RC1	me c reductase core protein I	13 44 2	94 21 5	31 34 7	51 87 1	08 97 8	60 96 8	651 705 718	723 956 667	51 70 57	o w n	04 77 63	30 85 92 11
26	STE	STEAP2	7.	6.	7.	7.	7.	7.	1.5	0.5	1.5	U	0.0	0.9
17	AP2	metalloreductase	00	49	15	38	78	24	007	857	00	p	33	30
29			50 8	19 4	20 6	31 1		31 1	808 59	133 33	78 08 59		41 92 8	85 92 11
48	NOV	Nephroblastoma	4.	4.	4.	4.	4.	3.	-1.	-0.	1.5	D	0.0	0.9
56		overexpressed	53 88 1	52 96	94 09 3	02 49 2	28 44 4	86 36 8	528 482 463	612 1	28 48 24 63	o w n	07 74 99 07	30 85 92 11
64	NPIP	Nuclear pore	5.	5.	6.	4.	4.	5.	-1.	-0.	1.8	D	0.0	0.9
27	A2	complex	15	57	33	89	32	20	841	881	41	o	31	30
99		interacting protein family member A2	31 5	97 5	36 7	51 7	09 7	72 5	706 712	043 333	70 67	w n	97 36	85 92 11
86	SLC	Solute carrier	4.	5.	6.	5.	3.	4.	-2.	-1.	2.4	D	0.0	0.9
71	4A4	family 4 (sodium bicarbonate cotransporter), member 4	72 67	91 45 9	18 92 9	32 86 3	51 23 1	19 22 9	404 577 347	265 783 333	04 57 73 47	o w n	41 55 36 93	30 85 92 11
79	MM	Multimerin 2	5.	5.	6.	4.	5.	5.	-1.	-0.	1.5	D	0.0	0.9

81	RN2		55	60	11	67	17	52	553	635	53	o	38	30
2			32	53	75	05	91	02	382	413	38	w	54	85
			1	7	1			5	732	333	27	n	09	92
											32		85	11
14	CTN	Cystinosin,	4.	4.	3.	4.	5.	4.	1.6	0.7	1.6	U	0.0	0.9
97	S	lysosomal cystine	91	11	69	97	15	73	379	118	37	p	43	30
		transporter	13	59	79	38	44	25	030	5	90		76	85
			6	9	5	5	2	8	91		30		09	92
											91		05	11
23	NM	Nicotinamide	5.	5.	6.	4.	5.	4.	-2.	-1.	2.3	D	0.0	0.9
05	NAT	nucleotide	04	82	55	38	10	24	349	232	49	o	14	30
7	2	adenyltransferase	73	60	93	70	31	54	483	343	48	w	26	85
		2	4	5		5	2	9	007	333	30	n	92	92
											07		99	11
62	RYR	Ryanodine receptor	3.	4.	5.	2.	4.	3.	-2.	-1.	2.1	D	0.0	0.9
62	2	2 (cardiac)	96	40	04	66	12	21	187	129	87	o	22	30
			22	07	19	94	79	96	556	32	55	w	40	85
			9	5		1	3	4	077		60	n	03	92
											77		42	11
69	BTG	B-cell translocation	10	11	10	10	9.	9.	-1.	-0.	1.8	D	0.0	0.9
4	1	gene 1,	.9	.0	.1	.1	66	70	855	891	55	o	08	30
		anti-proliferative	86	27	64	31	68	61	361	7	36	w	73	85
			63	83	69	02	8	5	101		11	n	87	92
											01		78	11
10	NPIP	Nuclear pore	5.	5.	6.	4.	4.	5.	-1.	-0.	1.8	D	0.0	0.9
02	A5	complex	15	57	33	89	32	20	841	881	41	o	31	30
88		interacting protein	31	97	36	51	09	72	706	043	70	w	97	85
33		family member A5		5		7		5	712	333	67	n	36	92
2											12		18	11

17 97	DXO	Decapping exoribonuclease	7. 43 71 8	7. 63 00 7	8. 36 60 6	6. 28 72 7	7. 48 28 7	6. 36 95 3	-2. 140 433 974	-1. 097 903 333	2.1 40 43 39 74	D o w n	0.0 18 87 29 42	0.9 30 85 92 11
99 48	WD R1	WD repeat domain 1	4. 96 08 8	5. 14 35 6	5. 67 30 2	4. 52 31 7	4. 42 19 2	4. 56 29 2	-1. 689 367 654	-0. 756 483 333	1.6 89 36 76 54	D o w n	0.0 05 37 06 45	0.9 30 85 92 11
28 73 8	TRA J17	T cell receptor $\alpha$ joining 17	7. 52 97 9	7. 71 63 8	7. 94 6 3	6. 34 80 3	6. 65 49 6	7. 71 79 6	-1. 769 988 516	-0. 823 74 85	1.7 69 98 85 16	D o w n	0.0 42 37 23 06	0.9 30 85 92 11
49 53	ODC 1	Ornithine decarboxylase 1	8. 51 78 9	9. 09 98 2	9. 02 15 1	8. 44 52 1	7. 85 45 8	8. 37 17 2	-1. 575 602 197	-0. 655 903 333	1.5 75 60 21 97	D o w n	0.0 20 19 26 42	0.9 30 85 92 11
40 05 06	KNO P1	Lysine-rich nucleolar protein 1	7. 70 46 3	6. 92 66 1	6. 44 79 4	7. 80 59 7	8. 24 42 2	7. 58 57 8	1.8 053 309 5	0.8 522 633 33	1.8 05 33 09 5	U p	0.0 32 26 50 6	0.9 30 85 92 11
11 95 87	CPX M2	Carboxypeptidase X (M14 family), member 2	5. 39 76 7	6. 24 69 7	5. 19 84 1	6. 38 26 5	7. 18 76 4	7. 20 47 7	2.4 805 671 29	1.3 106 7 71	2.4 80 56 71	U p	0.0 04 65 11	0.9 30 85 92

											29		81	11
89 10	SGC E	Sarcoglycan epsilon	7. 51 90 4	8. 06 96 1	7. 84 76 2	6. 99 54 4	7. 16 72 9	7. 26 62 3	-1. 590 084 388	-0. 669 103 333	1.5 90 08 43 88	D o w n	0.0 06 68 34 13	0.9 30 85 92 11
19 75	EIF4 B	Eukaryotic translation initiation factor 4B	7. 51 15 7	7. 79 91 8	8. 08 21 6	7. 34 11 4	6. 52 97 8	7. 38 57 6	-1. 638 160 447	-0. 712 076 667	1.6 38 16 04 47	D o w n	0.0 29 62 06 64	0.9 30 85 92 11
88 39	WIS P2	WNT1 inducible signaling pathway protein 2	4. 45 58 9	6. 03 00 7	4. 83 91 5	6. 99 35 4	6. 94 56 1	8. 36 27 1	5.0 126 841 53	2.3 255 833 33	5.0 12 68 41 53	U p	0.0 01 83 66 36	0.9 30 85 92 11
23 00 8	KLH DC1 0	Kelch domain containing 10	5. 50 37 2	5. 58 61 7	6. 07 83 1	5. 25 25 5	4. 33 29 3	5. 08 22 3	-1. 782 011 524	-0. 833 506 667	1.7 82 01 15 24	D o w n	0.0 16 50 08 02	0.9 30 85 92 11
10 13 0	PDI A6	Protein disulfide isomerase family A member 6	9. 08 64 8	8. 92 01 5	9. 38 62 2	8. 48 86 3	8. 26 76 3	8. 84 63 5	-1. 512 312 9	-0. 596 756 667	1.5 12 31 29	D o w n	0.0 17 42 17 07	0.9 30 85 92 11
81 84 9	ST6 GAL NAC	ST6 ( $\alpha$ -N-acetyl-neura minyl-2,3- $\beta$ -galact	3. 90 54	5. 60 07	6. 12 84	3. 54 69	4. 47 68	3. 66 65	-2. 487 649	-1. 314 783	2.4 87 64	D o w	0.0 42 88	0.9 30 85

	5	osyl-1,3)-N-acetylgl alactosaminide $\alpha$ -2,6-sialyltransfer ase 5	8	9	3	7		8	679	333	96	n	11	92
											79		61	11
40	LUM	Lumican	9.	9.	9.	7.	9.	9.	-1.	-0.	1.8	D	0.0	0.9
60			75	83	77	94	40	30	867	900	67	o	38	30
			53	51	13	61	99	32	088	79	08	w	65	85
				9	2	8	7	9	095		80	n	27	92
											95		86	11
22	FBN	Fibrillin 1	3.	3.	2.	3.	5.	4.	2.5	1.3	2.5	U	0.0	0.9
00	1		78	34	78	87	73	36	493	501	49	p	21	30
			69	65	42	27	37	16	274	166	32		08	85
			7	5	7	3	4	7	03	67	74		37	92
											03		98	11
21	ESR	Estrogen-related	4.	4.	4.	3.	3.	3.	-1.	-0.	1.8	D	0.0	0.9
04	RG	receptor $\gamma$	34	68	63	77	51	80	811	857	11	o	00	30
			25	99	09	28	76	13	514	196	51	w	42	85
			2	8	2	9	3	1	893	667	48	n	61	92
											93		58	11
40	CAP	Cell cycle	6.	6.	7.	6.	5.	6.	-1.	-0.	1.5	D	0.0	0.9
76	RIN1	associated protein	63	84	36	51	94	53	533	617	33	o	38	30
		1	94	26	28	33	03	93	969	27	96	w	84	85
			5	2	1	3	6	8	715		97	n	99	92
											15		8	11
22	FOX	Forkhead box F1	6.	7.	8.	5.	7.	5.	-2.	-1.	2.6	D	0.0	0.9
94	F1		82	99	22	61	29	92	644	403	44	o	25	30
			05	76	60	61	40	49	594	046	59	w	36	85
			9	6	9	5	7	8	753	667	47	n	44	92
											53		09	11

12	CNT	Contactin	6.	5.	5.	6.	7.	7.	2.2	1.1	2.2	U	0.0	0.9	
96	NAP	associated	35	46	25	00	39	22	690	820	69	p	23	30	
84	5	protein-like 5	25	26	70	71	01	12	525	9	05		72	85	
			8	9	4	3	6	9	16		25		53	92	
											16		85	11	
18	ECM	Extracellular	9.	9.	9.	7.	8.	7.	-2.	-1.1	2.1	D	0.0	0.9	
93	1	matrix protein 1	33	17	40	84	77	96	166	151	66	o	02	30	
			74	91	90	39	42	19	165	433	16	w	29	85	
				1	8	6	7	3	291	33	52	n	78	92	
											91		89	11	
45	MUC	Mucin	6,	10	9.	10	12	10	11	2.3	1.2	2.3	U	0.0	0.9
88	6	oligomeric	.8	77	.5	.2	.8	.6	121	092	12	p	14	30	
		mucus/gel-forming	64	39	03	34	72	62	473	333	14		28	85	
			3	9	21	07	66	47	36	33	73		43	92	
											36		57	11	
36	ITG	Integrin $\beta$ 6	5.	5.	5.	5.	4.	4.	-1.	-0.	1.5	D	0.0	0.9	
94	B6		46	29	39	14	32	89	514	598	14	o	25	30	
			15	89	03	01	01	50	151	51	15	w	53	85	
			5		8	5	2	3	959		19	n	91	92	
											59		17	11	
14	LAY	Layilin	5.	6.	6.	4.	5.	4.	-1.	-0.	1.9	D	0.0	0.9	
39	N		54	05	76	72	96	84	929	948	29	o	48	30	
03			87	76	80	47	27	27	272	056	27	w	70	85	
			7	1	3	6	1	7	146	667	21	n	36	92	
											46		73	11	
64	CBW	COBW domain	4.	3.	4.	3.	3.	3.	-1.	-0.	1.6	D	0.0	0.9	
40	D6	containing 6	45	86	15	71	32	19	674	744	74	o	05	30	
19			21	23	27	57	17	77	812		81	w	34	85	
			2	7	1	4	2	4	975		29	n	61	92	

											75		82	11
11 49 07	FBX O32	F-box protein 32	7. 01 04 6	7. 23 95 2	7. 14 02 1	5. 32 86 3	6. 92 66 2	6. 26 29 1	-1. 941 730 979	-0. 957 343 333	1.9 41 73 09 79	D o w n	0.0 31 29 26 14	0.9 30 85 92 11
38 90 15	SLC 9A4	Solute carrier family 9, subfamily A (NHE4, cation proton antiporter 4), member 4	7. 13 93 3	6. 74 95 8	6. 56 14 1	7. 41 61 8	7. 60 66 2	7. 32 09 3	1.5 487 847 65	0.6 311 366 67 65	1.5 48 78 47 65	U p	0.0 10 80 32 2	0.9 30 85 92 11
14 51 73	B3G LCT	B 3-glucosyltransferase	3. 99 84 5	5. 18 74 2	4. 63 01 9	5. 40 16 2	5. 16 28 2	5. 36 57 6	1.6 298 207 84	0.7 047 133 33 84	1.6 29 82 07 84	U p	0.0 37 88 72 79	0.9 30 85 92 11
55 77	PRK AR2 B	Protein kinase, camp-dependent, regulatory subunit type II $\beta$	4. 76 03 9	4. 93 86 5	5. 63 41 1	4. 17 92 5	4. 34 60 5	4. 02 54 1	-1. 901 964 08	-0. 927 49 08	1.9 01 96 40 8	D o w n	0.0 04 56 05 4	0.9 30 85 92 11
69 26	TBX 3	T-box 3	5. 45 14	5. 22 24 9	5. 42 91 7	4. 10 50 9	4. 50 37 4	4. 54 66 6	-1. 975 918 351	-0. 982 523 333	1.9 75 91 83 51	D o w n	0.0 00 39 69 75	0.9 30 85 92 11
27 14 7	DEN ND2 A	DENN/MADD domain containing 2A	4. 31 95	4. 17 40	3. 81 34	4. 88 64	5. 05 21	4. 23 56	1.5 394 126	0.6 223 8	1.5 39 41	U p	0.0 31 85	0.9 30 85

			5	7	8	8	5	1	42		26		66	92
											42		71	11
72	TUB	Tubby bipartite	5.	6.	6.	3.	5.	4.	-2.	-1.	2.6	D	0.0	0.9
75		transcription factor	04	02	58	66	33	50	606	381	06	o	24	30
			32	21	58	01	66	83	282	993	28	w	58	85
				6	4	9	7	6	255	333	22	n	81	92
											55		2	11
84	SDP	Serum deprivation	6.	8.	8.	5.	7.	5.	-3.	-1.	3.7	D	0.0	0.9
36	R	response	98	31	45	18	23	62	748	906	48	o	11	30
			87	73	34	14	57	33	499	313	49	w	84	85
			7	3	1	4	6	7	821	333	98	n	27	92
											21		21	11
69	TCF	Transcription	4.	4.	3.	4.	5.	4.	1.7	0.8	1.7	U	0.0	0.9
34	7L2	factor 7-like 2	48	26	47	80	53	35	659	204	65	p	48	30
		(T-cell specific,	55	21	84	09	02	62	608	533	96		76	85
		HMG-box)	3	8		7	7	3	17	33	08		68	92
											17		08	11
55	PPP1	Protein	6.	6.	6.	5.	5.	5.	-1.	-0.	1.8	D	0.0	0.9
07	R3C	phosphatase 1	11	23	87	38	82	33	858	893	58	o	06	30
		regulatory subunit	40	95	92	39	90	85	063	8	06	w	80	85
		3C	4	9	9	8	3	1	748		37	n	49	92
											48		33	11
55	PRK	Protein kinase,	5.	6.	6.	5.	5.	5.	-1.	-0.	1.5	D	0.0	0.9
67	ACB	camp-dependent, $\beta$	86	14	46	35	39	85	541	624	41	o	20	30
		catalytic subunit	81	10	88	27	99	18	672	496	67	w	32	85
				8	5	3	2	9	866	667	28	n	20	92
											66		4	11
31	HLA	Major	9.	8.	9.	9.	7.	6.	-3.	-1.	3.0	D	0.0	0.9
26	-DR	histocompatibility	45	74	99	31	37	65	061	614	61	o	38	30



	B4	complex, class II, DR $\beta$ 4	38 1	29 9	44 7	63 1	92 7	24 5	870 642	413 333	87 06 42	w n	12 75 3	85 92 11
21 61	F12	Coagulation factor XII (Hageman factor)	7. 43 2	6. 86 90 5	7. 02 12	8. 06 11	7. 64 43	7. 57 15 1	1.5 708 695	0.6 515 633 33	1.5 70 86 95	U p	0.0 14 87 08 14	0.9 30 85 92 11
55 06 3	ZCW PW1	Zinc finger, CW type with PWWP domain 1	5. 06 90 4	5. 33 49 8	4. 78 82	6. 00 78 5	5. 64 96 8	5. 41 62 7	1.5 445 358 24	0.6 271 733 33	1.5 44 53 58 24	U p	0.0 18 49 11 49	0.9 30 85 92 11
55 79 8	MET TL2 B	Methyltransferase like 2B	5. 03 49 3	5. 16 44 7	4. 89 32 7	5. 94 63 2	5. 59 18 6	5. 67 34 9	1.6 316 519 35	0.7 063 333 33	1.6 31 65 19 35	U p	0.0 02 30 90 83	0.9 30 85 92 11
84 93 5	MED AG	Mesenteric estrogen-dependent adipogenesis	4. 12 21 9	4. 68 01 7	4. 28 11 4	4. 65 06 3	5. 22 14	6. 15 84 3	1.9 756 398 85	0.9 823 2 85	1.9 75 63 98 85	U p	0.0 27 12 68 94	0.9 30 85 92 11
54 20 9	TRE M2	Triggering receptor expressed on myeloid cells 2	7. 10 69 3	7. 13 40 6	7. 30 06 4	6. 15 46 3	6. 68 66 5	6. 55 63 9	-1. 641 088 831	-0. 714 653 333	1.6 41 08 88 31	D o w n	0.0 04 47 49 81	0.9 30 85 92 11
65	ZDH	Zinc finger,	6.	7.	6.	8.	7.	7.	2.0	1.0	2.0	U	0.0	0.9

30	HC1	DHHC-type	91	05	68	66	61	44	350	250	35	p	12	30
82	1B	containing 11B	36	02	32	03	54	65	769	833	07		07	85
			3	3		4	6	1	31	33	69		18	92
											31		84	11
30	HIF1	Hypoxia inducible	6.	7.	7.	6.	5.	6.	-1.	-0.	1.7	D	0.0	0.9
91	A	factor 1, $\alpha$ subunit	73	42	86	99	99	57	764	819	64	o	44	30
		(basic	74	54	09	33	86	39	557	306	55	w	72	85
		helix-loop-helix	3	5	5	3	4	4	774	667	77	n	73	92
		transcription									74		24	11
		factor)												
28	ANG	Angiopoietin 1	6.	8.	7.	5.	6.	5.	-2.	-1.	2.6	D	0.0	0.9
4	PT1		15	03	57	07	83	55	698	432	98	o	38	30
			71	44	28	79	19	80	566	193	56	w	41	85
			9	2	9	2	2	8	675	333	66	n	54	92
											75		98	11
44	NPIP	Nuclear pore	5.	5.	6.	4.	4.	5.	-1.	-0.	1.8	D	0.0	0.9
03	B4	complex	15	57	33	89	32	20	841	881	41	o	31	30
45		interacting protein	31	97	36	51	09	72	706	043	70	w	97	85
		family member B4		5		7		5	712	333	67	n	36	92
											12		18	11
10	LOC	Uncharacterized	5.	5.	5.	5.	4.	4.	-1.	-0.	1.5	D	0.0	0.9
05	1005	LOC100505984	46	29	39	14	32	89	514	598	14	o	25	30
05	0598		15	89	03	01	01	50	151	51	15	w	53	85
98	4		5		8	5	2	3	959		19	n	91	92
4											59		17	11
52	PGD	Phosphogluconate	9.	9.	9.	8.	8.	9.	-1.	-0.	1.5	D	0.0	0.9
26		dehydrogenase	27	40	52	50	77	02	555	637	55	o	05	30
			88	95	3	22	56	06	717	58	71	w	76	85
				2		3	9	6	384		73	n	84	92

											84		19	11
80	DCA	DDB1 and CUL4	7.	7.	7.	8.	8.	8.	1.5	0.6	1.5	U	0.0	0.9
34	F11	associated factor 11	66	33	26	05	20	02	971	755	97	p	03	30
4			13	49	53	89	88	04	538	033	15		16	85
			8	6	6	5	5	1	97	33	38		73	92
											97		1	11
22	CBW	COBW domain	4.	3.	4.	3.	3.	3.	-1.	-0.	1.6	D	0.0	0.9
08	D5	containing 5	45	86	15	71	32	19	674	744	74	o	05	30
69			21	23	27	57	17	77	812		81	w	34	85
			2	7	1	4	2	4	975		29	n	61	92
											75		82	11
28	CDH	Cadherin 19, type 2	5.	5.	4.	3.	4.	3.	-2.	-1.	2.0	D	0.0	0.9
51	19		25	09	87	80	35	98	039	028	39	o	00	30
3			84	22	52	54	22	29	793	423	79	w	54	85
			2		9	2	9	3	82	333	38	n	27	92
											2		41	11
37	WAS	WAS protein	7.	7.	7.	8.	8.	8.	2.0	1.0	2.0	U	0.0	0.9
46	H3P	family homolog 3	80	50	00	94	50	07	975	686	97	p	05	30
66		pseudogene	77	08	97	64	34	44	327	933	53		38	85
			1	5	2	6	6	4	45	33	27		14	92
											45		06	11
58	MS4	Membrane-spanning	4.	4.	4.	3.	4.	4.	-1.	-0.	1.6	D	0.0	0.9
47	A7	g 4-domains,	81	96	90	92	49	08	653	725	53	o	03	30
5		subfamily A,	35	75	37	61	87	46	053	133	05	w	00	85
		member 7	8		9	3	3	1	404	333	34	n	23	92
											04		22	11
58	RAB	RAB1A, member	6.	5.	5.	5.	4.	5.	-1.	-0.	1.6	D	0.0	0.9
61	1A	RAS oncogene	12	95	60	27	93	31	645	718	45	o	05	30
		family	7	06	56	50	54	74	398	436	39	w	82	85

				2	2	2	7	4	082	667	80	n	23	92
											82		44	11
10	CAL	Calcitonin receptor	5.	5.	6.	4.	5.	5.	-1.	-0.	1.5	D	0.0	0.9
20	CRL	like receptor	38	56	04	76	12	12	581	661	81	o	13	30
3			99	11	32	35	52	05	883	643	88	w	66	85
			2	6	4	9	3	7	477	333	34	n	32	92
											77		2	11
28	TRD	T cell receptor Δ	7.	7.	7.	6.	6.	7.	-1.	-0.	1.7	D	0.0	0.9
51	V2	variable 2	52	71	94	34	65	71	769	823	69	o	42	30
7			97	63	6	80	49	79	988	74	98	w	37	85
			9	8		3	6	6	516		85	n	23	92
											16		06	11
83	CAS	Caspase 3	4.	4.	5.	4.	3.	4.	-1.	-0.	1.5	D	0.0	0.9
6	P3		44	96	07	34	69	41	598	676	98	o	24	30
			88	30	64	63	86	27	630	836	63	w	85	85
			4	1	4	9	2	7	663	667	06	n	37	92
											63		41	11
10	GIM	GIMAP1-GIMAP5	6.	6.	6.	5.	5.	6.	-1.	-0.	1.6	D	0.0	0.9
05	AP1-	readthrough	16	20	81	11	78	11	652	724	52	o	40	30
27	GIM		31	81	84	41	36	75	656	786	65	w	03	85
94	AP5		8	1		9	3	1	238	667	62	n	95	92
9											38		58	11
28	IGK	Immunoglobulin κ	4.	5.	5.	4.	4.	4.	-2.1	-1.	2.1	D	0.0	0.9
93	V1-3	variable 1-33	84	68	56	43	01	39	180	082	18	o	02	30
3	3		29	69	01	06	58	53	304	723	03	w	39	85
			2	1	6	2	8	2	54	333	04	n	96	92
											54		6	11
21	F3	Coagulation factor	7.	7.	7.	8.	8.	8.	1.6	0.6	1.6	U	0.0	0.9
52		III (thromboplastin,	54	75	70	52	22	32	137	904	13	p	01	30

		tissue factor)	10 1	27 9	71 2	58 3	14 3	48 9	420 63	1	74 20 63		82 14 02	85 92 11
10 69 9	COR IN	Corin, serine peptidase	6. 55 34 4	6. 18 45 1	7. 15 62 5	4. 99 42 9	5. 63 52 7	5. 71 46 1	-2. 271 024 6	-1. 183 343 333	2.2 71 02 46	D o w n	0.0 04 20 04 85	0.9 30 85 92 11
18 03	DPP 4	Dipeptidyl-peptida se 4	9. 39 07 4	9. 07 15	8. 68 48 6	9. 96 15 1	9. 37 15 7	9. 89 36 9	1.6 198 085 8	0.6 958 233 33	1.6 19 80 85 8	U p	0.0 18 01 96 75	0.9 30 85 92 11
95 86	CRE B5	Camp responsive element binding protein 5	8. 26 44 8	7. 98 73 7	7. 43 65 4	9. 23 87 6	8. 54 73 9	8. 49 52 5	1.8 205 024 3	0.8 643 366 67	1.8 20 50 24 3	U p	0.0 14 92 11 94	0.9 30 85 92 11
83 87 5	BCO 2	B-carotene oxygenase 2	7. 72 97 2	8. 09 52	7. 68 86	7. 49 63 8	6. 15 91	7. 06 85 6	-1. 905 047 099	-0. 929 826 667	1.9 05 04 70 99	D o w n	0.0 22 72 95 87	0.9 30 85 92 11
54 60 2	NDF IP2 2	Nedd4 family interacting protein 2	5. 78 91 8	5. 65 98 4	5. 87 67 4	5. 58 77 6	4. 48 09 5	5. 25 17 3	-1. 589 353 455	-0. 668 44	1.5 89 35 34 55	D o w n	0.0 41 13 65 44	0.9 30 85 92 11
64	CHS	Carbohydrate	6.	7.	6.	5.	5.	6.	-1.	-0.	1.7	D	0.0	0.9

37	T8	(N-acetylgalactosa	45	35	77	85	80	45	767	821	67	o	19	30
7		mine 4-0)	37	68	27	07	86	83	740	906	74	w	03	85
		sulfotransferase 8	6		8		2		697	667	06	n	30	92
											97		49	11
16	DDB	Damage-specific	6.	6.	6.	7.	7.	6.	1.6	0.7	1.6	U	0.0	0.9
43	2	DNA binding	44	35	64	44	76	50	920	588	92	p	41	30
		protein 2	20	41	19	34	49	61	943	1	09		06	85
			1	9	3	4	6	6	33		43		32	92
											33		6	11
56	PRN	Prion protein	6.	6.	7.	6.	5.	6.	-1.	-0.	1.7	D	0.0	0.9
21	P		76	90	58	37	84	72	700	766	00	o	31	30
			79	01	55	64	88	96	803	216	80	w	60	85
			4	1	2	4	1	7	731	667	37	n	35	92
											31		07	11
97	UTP	UTP14, U3 small	6.	6.	5.	6.	6.	6.	1.5	0.6	1.5	U	0.0	0.9
24	14C	nucleolar	16	41	66	97	62	49	259	097	25	p	31	30
		ribonucleoprotein,	94	99	85	56	13	01	453	033	94		36	85
		homolog C (yeast)	7		4			2	91	33	53		94	92
											91		15	11
28	GPX	Glutathione	9.	8.	8.	8.	9.	9.	1.8	0.9	1.8	U	0.0	0.9
78	3	peroxidase 3	05	83	06	73	94	99	696	027	69	p	49	30
			82	87	45	59	38	01	652	8	66		68	85
			6	2	6	6		2	64		52		89	92
											64		17	11
26	WSB	WD repeat and	5.	6.	6.	5.	5.	5.	-1.	-0.	1.6	D	0.0	0.9
11	1	SOCS box	95	34	40	46	25	82	648	721	48	o	08	30
8		containing 1	64	91	20	09	21	99	971	566	97	w	46	85
			5	8	8	8	1	2	731	667	17	n	76	92
											31		53	11

85	AKR	Aldo-keto	6.	6.	6.	5.	5.	6.	-1.	-0.	1.6	D	0.0	0.9
74	7A2	reductase family 7, member A2	66	45	45	84	42	22	616	693	16	o	14	30
			70	01	80	18	53	86	824	163	82	w	06	85
			9	9	2		9	2	775	333	47	n	24	92
											75		32	11
37	KCN	Potassium channel	5.	5.	6.	4.	5.	4.	-1.	-0.	1.8	D	0.0	0.9
79	MB1	subfamily M	35	81	35	62	40	72	899	925	99	o	16	30
		regulatory $\beta$	51	13	75	12	04	59	311	476	31	w	32	85
		subunit 1	4	7	7	9	1	5	671	667	16	n	29	92
											71		72	11
51	PDK	Pyruvate	6.	5.	5.	7.	6.	6.	2.0	1.0	2.0	U	0.0	0.9
63	1	dehydrogenase	27	24	95	48	54	51	300	215	30	p	19	30
		kinase, isozyme 1	66	49	16	46	19	11	660	266	06		24	85
				1	2		2	9	49	67	60		91	92
											49		7	11
34	IDH3	Isocitrate	8.	8.	9.	8.	7.	8.	-1.	-0.	1.5	D	0.0	0.9
20	B	dehydrogenase 3	88	80	07	41	89	56	548	630	48	o	14	30
		(NAD+) $\beta$	18	94	73	23	54	94	033	436	03	w	19	85
			1	2		5	5	2	473	667	34	n	94	92
											73		62	11
57	TWF	Twinfilin actin	4.	4.	5.	4.	3.	4.	-1.	-0.	1.6	D	0.0	0.9
56	1	binding protein 1	96	78	61	82	97	47	626	701	26	o	37	30
			82	91	42	07	10	50	266	563	26	w	94	85
			4		5	8	4	8	093	333	60	n	00	92
											93		01	11
87	MPD	Multiple PDZ	5.	6.	6.	3.	5.	4.	-2.	-1.	2.2	D	0.0	0.9
77	Z	domain protein	15	29	58	99	59	89	269	182	69	o	40	30
			10	28	53	33	33	50	624	453	62	w	07	85
			1		2	6	8	3	034	333	40	n	59	92

											34		63	11
21 99 02	TME M13 6	Transmembrane protein 136	5. 28 62 3	5. 26 09 9	4. 93 04 6	4. 59 49 3	4. 50 01 3	4. 61 31 8	-1. 505 052 8	-0. 589 813 333	1.5 05 05 2	D o w n	0.0 04 10 00	0.9 30 85 92
12 72	CNT N1	Contactin 1	4. 94 72 7	6. 07 35 6	6. 07 96 6	2. 72 68 4	5. 22 86 5	3. 23 16 4	-3. 920 669 412	-1. 971 1 412	3.9 20 66 94 12	D o w n	0.0 14 69 77 8	0.9 30 85 92 11
30 12	HIST 1H2 AE	Histone cluster 1, h2ae	6. 07 23 1	5. 96 80 4	5. 68 58 4	7. 05 27 2	6. 18 95 6	6. 33 48 6	1.5 336 649 42	0.6 169 833 33	1.5 33 66 49 42	U p	0.0 38 86 65 8	0.9 30 85 92 11
57 27	PTC H1	Patched 1	8. 15 72 8	8. 68 66 4	9. 21 92 4	6. 93 25 1	8. 06 36 8	7. 65 95 8	-2. 197 419 02	-1. 135 81 02	2.1 97 41 90 2	D o w n	0.0 12 53 49 83	0.9 30 85 92 11
56 64 9	TMP RSS4	Transmembrane protease, serine 4	6. 31 74 5	6. 68 84 2	6. 57 19 4	7. 04 78 1	7. 76 05 4	7. 32 22 3	1.8 036 549 06	0.8 509 233 33	1.8 03 65 49 06	U p	0.0 04 47 15 57	0.9 30 85 92 11
28 97 7	MRP L42	Mitochondrial ribosomal protein L42	6. 45 96	6. 59 66	6. 93 49	6. 31 16	5. 46 71	6. 21 71	-1. 585 689	-0. 665 11	1.5 85 68	D o w	0.0 32 44	0.9 30 85



			7	5			8	1	171		91	n	21	92
											71		19	11
51	PLA	Placenta specific 8	5.	6.	5.	4.	5.	4.	-2.	-1.	2.0	D	0.0	0.9
31	C8		15	23	90	31	00	92	016	012	16	o	11	30
6			01	33	01	55	26	93	788	06	78	w	61	85
			7	5	2			6	784		87	n	60	92
											84		23	11
64	RAP	RAP1B, member of RAS oncogene family pseudogene	4.	4.	5.	4.	3.	4.	-1.	-0.	1.6	D	0.0	0.9
37	IBL		58	65	24	40	56	28	673	743	73	o	24	30
52			07	86	06	31	14	57	961	266	96	w	86	85
			6	9	7	2	6	4	871	667	18	n	34	92
											71		96	11
49	NSF	N-ethylmaleimide- sensitive factor	5.	6.	6.	5.	5.	6.	-1.	-0.	1.6	D	0.0	0.9
05			79	30	73	45	16	06	646	719	46	o	46	30
			66	79	49	06	90	17	455	363	45	w	47	85
				9	7	9	3	5	287	333	52	n	39	92
											87		33	11
97	TOX	Thymocyte selection associated high mobility group box	3.	4.	4.	3.	4.	3.	-1.	-0.	1.5	D	0.0	0.9
60			99	48	50	31	05	73	545	628	45	o	22	30
			83	95	54	62	58	55	999	54	99	w	78	85
			3	4		7	5	3	658		96	n	21	92
											58		83	11
55	TME	Transmembrane protein 100	7.	7.	8.	6.	6.	6.	-3.	-1.	3.4	D	0.0	0.9
27	M10		79	66	85	01	43	56	401	766	011	o	00	30
3	0		80	38	55	73	21	98	112	006	12	w	73	85
			1	6	2	9	3	5	357	667	35	n	18	92
											7		38	11
55	ARL	ADP ribosylation factor like gtpase	5.	5.	5.	5.	3.	4.	-1.	-0.	1.7	D	0.0	0.9
20	8B		25	37	51	06	79	88	736	795	36	o	37	30

7		8B	09 5	10 8	66 6	83 1	87 4	39 9	140 053	883 333	14 00 53	w n	15 83 59	85 92 11
65 43 46	LGA LS9 C	Lectin, galactoside-binding , soluble, 9C	6. 98 30 7	6. 93 51 9	7. 16 41 1	5. 90 81 9	6. 66 25 8	6. 73 45 5	-1. 507 700 636	-0. 592 35 06	1.5 07 70 06 36	D o w n	0.0 38 33 51 89	0.9 30 85 92 11
70 43	TGF B3	Transforming growth factor $\beta$ 3	5. 91 43 5	6. 34 89 8	6. 97 71 7	4. 94 33 6	6. 26 39 3	5. 34 57 9	-1. 860 649 956	-0. 895 806 667	1.8 60 64 99 56	D o w n	0.0 49 21 52 61	0.9 30 85 92 11
28 66 3	TRA V20	T cell receptor $\alpha$ variable 20	7. 52 97 9	7. 71 63 8	7. 94 6 3	6. 34 80 3	6. 65 49 6	7. 71 79 6	-1. 769 988 516	-0. 823 74 85	1.7 69 98 85 16	D o w n	0.0 42 37 23 06	0.9 30 85 92 11
81 60 6	LBH	Limb bud and heart development	5. 31 48 6	5. 60 77 7	6. 85 00 5	3. 87 39 2	4. 81 06 4	4. 51 23 4	-2. 878 412 453	-1. 525 273 333	2.8 78 41 24 53	D o w n	0.0 06 72 56 61	0.9 30 85 92 11
15 81 58	RAS EF	RAS and EF-hand domain containing	8. 36 60 9	7. 99 50 4	7. 57 59 6	8. 67 20 2	8. 62 33 4	8. 82 22 7	1.6 550 177 23	0.7 268 466 67	1.6 55 01 77 23	U p	0.0 09 29 9	0.9 30 85 92 11
93	KL	Klotho	4.	3.	4.	3.	3.	3.	-1.	-0.	1.6	D	0.0	0.9

65			26	94	26	18	79	31	651	723	51	o	04	30
			39	94	00	78	67	74	602	866	60	w	47	85
			9	8	7	2		2	682	667	26	n	33	92
											82		91	11
10	TRI	Tripartite motif	5.	5.	5.	6.	6.	5.	1.5	0.6	1.5	U	0.0	0.9
10	M10	containing 10	60	47	17	10	27	84	757	560	75	p	07	30
7			75	52	71	70	98	11	478	366	74		73	85
			3	9	5	7	5	6	2	67	78		19	92
											2		3	11
38	TME	Transmembrane	8.	7.	8.	7.	7.	7.	-1.	-0.	1.5	D	0.0	0.9
83	M22	protein 220	21	82	11	52	71	11	514	598	14	o	17	30
35	0		21	05	10	33	35	07	333	683	33	w	92	85
			7	5	1	4	9	5	888	333	38	n	60	92
											88		98	11
75	YW	Tyrosine	4.	5.	5.	4.	3.	4.	-1.	-0.	1.8	D	0.0	0.9
31	HAE	3-monooxygenase/t	95	06	84	58	83	81	835	876	35	o	25	30
		ryptophan	65	35	37	35	97	16	652	293	65	w	41	85
		5-monooxygenase		7	6	2	5	8	957	333	29	n	68	92
		activation protein,									57		07	11
		epsilon												
26	FBX	F-box protein 3	5.	6.	6.	5.	5.	5.	-1.	-0.	1.6	D	0.0	0.9
27	O3		86	35	73	62	19	86	684	752	84	o	23	30
3			34	14	03	55	18	98	896	66	89	w	06	85
			5	3	8	5	9	4	533		65	n	24	92
											33		87	11
80	SEM	Sema domain,	5.	5.	6.	4.	5.	5.	-1.	-0.	1.6	D	0.0	0.9
03	A6D	transmembrane	55	85	25	80	66	14	608	685	08	o	33	30
1		domain (TM), and	49	26	37	30	05	16	129	383	12	w	59	85
		cytoplasmic	5	8	8	8	3	5	215	333	92	n	37	92

		domain, (semaphorin) 6D									15		21	11
65 91	SNA I2	Snail family zinc finger 2	5. 39 02 9	5. 79 53 9	6. 51 78 7	4. 66 73	5. 04 15 5	4. 94 66	-2. 022 350 887	-1. 016 033 333	2.0 22 35 08 87	D o w n	0.0 07 50 59 27	0.9 30 85 92 11
11 59	CKM T1B	Creatine kinase, mitochondrial 1B	9. 12 40 1	8. 82 88 9	9. 40 33 8	8. 26 93 6	8. 96 94 6	8. 24 30 1	-1. 542 014 858	-0. 624 816 667	1.5 42 01 48 58	D o w n	0.0 33 73 71 98	0.9 30 85 92 11
28 75 5	TRA C	T-cell receptor $\alpha$ constant	7. 52 97 9	7. 71 63 8	7. 94 6 3	6. 34 80 6	6. 65 49 6	7. 71 79 6	-1. 769 988 516	-0. 823 74 85	1.7 69 98 85 16	D o w n	0.0 42 37 23 06	0.9 30 85 92 11
63 89	SDH A	Succinate dehydrogenase complex subunit A, flavoprotein (Fp)	9. 64 26 8	9. 91 69 4	10 .0 53 34	9. 48 21 6	9. 02 82 7	9. 14 54 5	-1. 571 737 185	-0. 652 36 71	1.5 71 73 71 85	D o w n	0.0 06 23 94 1	0.9 30 85 92 11
28 93 0	IGK V1-3 9	Immunoglobulin $\kappa$ variable 1-39 (gene/pseudogene)	5. 59 67 6	6. 29 76 1	6. 34 30 7	5. 39 94 4	5. 52 59 6	5. 10 19 3	-1. 666 363 719	-0. 736 703 333	1.6 66 36 37 19	D o w n	0.0 14 84 42 4	0.9 30 85 92 11
92 70	ITG B1B	Integrin $\beta$ 1 binding protein 1	6. 65	6. 47	6. 93	5. 12	6. 02	5. 43	-2. 237	-1. 161	2.2 37	D o	0.0 01	0.9 30

	P1		25 2	44 3	86 1	05 7	08 4	89 1	281 307	746 667	28 13 07	w n	92 23 76	85 92 11
11 73	AP2 M1	Adaptor-related protein complex 2, mu 1 subunit	9. 44 63 1	9. 57 40 6	9. 94 81 5	8. 61 26 2	8. 68 95 3	9. 13 27 6	-1. 795 687 953	-0. 844 536 667	1.7 95 68 79 53	D o w n	0.0 03 08 69 33	0.9 30 85 92 11
34 19	IDH3 A	Isocitrate dehydrogenase 3 (NAD+) $\alpha$	4. 29 39 1	4. 32 98 6	5. 09 09 4	4. 20 00 9	3. 59 90 1	3. 91 46 4	-1. 587 756 856	-0. 666 99	1.5 87 75 68 56	D o w n	0.0 29 63 03 65	0.9 30 85 92 11
10 05 05 38 5	IQCJ -SCH IP1	IQCJ-SCHIP1 readthrough	4. 55 75 6	5. 25 84 1	4. 92 18 8	4. 02 64 1	4. 25 97 1	4. 39 80 1	-1. 607 230 299	-0. 684 576 667	1.6 07 23 02 99	D o w n	0.0 09 85 40 85	0.9 30 85 92 11
57 50 9	MTU S1	Microtubule associated tumor suppressor 1	7. 93 24 7	7. 65 29 5	7. 09 04 6	8. 42 74 6	7. 94 74 2	8. 14 75 7	1.5 321 136 66	0.6 155 233 33	1.5 32 11 36 66	U p	0.0 35 29 56 4	0.9 30 85 92 11
26 18	GAR T	Phosphoribosylgly cinamide formyltransferase, phosphoribosylglyc inamide synthetase, phosphoribosylami	4. 34 62 8	4. 61 66 2	4. 96 04 5	4. 26 60 2	3. 37 06 9	4. 18 10 5	-1. 626 604 301	-0. 701 863 333	1.6 26 60 43 01	D o w n	0.0 31 00 17 4	0.9 30 85 92 11

		noimidazole synthetase												
98 67	PJA2	Praja ring finger 2, E3 ubiquitin protein ligase	6. 00 17 4	6. 52 16 2	7. 10 99 3	6. 19 94 4	4. 99 88 9	5. 60 39 5	-1. 923 414 9	-0. 943 67 9	1.9 23 41 49	D o w n	0.0 33 96 11	0.9 30 85 92 06 11
56 25 6	SER TAD 4	SERTA domain containing 4	5. 34 34 1	5. 92 63 2	5. 96 80 4	4. 75 78 7	5. 21 56 7	5. 20 95 6	-1. 607 605 405	-0. 684 913 333	1.6 07 60 54 05	D o w n	0.0 15 74 52 61	0.9 30 85 92 11
88 76	VNN 1	Vanin 1	8. 54 04 3	8. 56 20 2	7. 50 46 9	9. 59 73 9	8. 47 51 1	9. 40 01 4	1.9 388 439 17	0.9 551 966 67	1.9 38 84 39 17	U p	0.0 36 03 97 74	0.9 30 85 92 11
28 6	ANK 1	Ankyrin 1	4. 13 64 8	3. 43 03 7	4. 00 15 7	5. 54 03 4	5. 50 37 7	3. 78 40 8	2.1 237 490 96	1.0 866 133 33	2.1 23 74 90 96	U p	0.0 47 80 90 22	0.9 30 85 92 11
10 75	CTS C	Cathepsin C	8. 06 29 9	8. 25 58 7	8. 51 27 5	7. 45 94 5	7. 26 14 4	7. 42 77 2	-1. 858 750 762	-0. 894 333 333	1.8 58 75 07 62	D o w n	0.0 00 69 33 91	0.9 30 85 92 11
92 55	AIM P1	Aminoacyl trna synthetase	7. 76	7. 69	8. 13	7. 33	6. 26	7. 15	-1. 926	-0. 945	1.9 26	D o	0.0 12	0.9 30

		complex-interactin g multifunctional protein 1	21 3	92 1	19 3	35 1	39 3	86 3	167 724	733 333	16 77 24	w n	09 77 82	85 92 11
84 68 0	ACC S	l-aminocyclopropa ne-1-carboxylate synthase homolog (inactive)	7. 08 74 4	6. 95 07 9	7. 49 94 3	7. 99 61 4	7. 37 53 8	7. 96 46 2	1.5 151 843 49	0.5 994 933 33	1.5 15 18 43 49	U p	0.0 31 35 06 81	0.9 30 85 92 11
10 72 0	UGT 2B11	UDP glucuronosyltransf erases 2 family, polypeptide B11	7. 23 94	7. 63 80 2	8. 20 27 5	8. 51 62 9	9. 78 62 2	8. 89 26 51	2.5 871 194 51	1.3 713 466 67	2.5 87 11 94 51	U p	0.0 05 77 87 14	0.9 30 85 92 11
38 42	TNP O1	Transportin 1	4. 11 49 2	4. 54 24 4	4. 56 00 3	3. 93 80 4	3. 50 54 4	3. 73 03 7	-1. 603 465 522	-0. 681 193 333	1.6 03 46 55 22	D o w n	0.0 04 65 64 52	0.9 30 85 92 11
28 89 3	IGK VID- 39	Immunoglobulin $\kappa$ variable 1D-39	5. 59 67 6	6. 29 76 1	6. 34 30 7	5. 39 94 4	5. 52 59 6	5. 10 19 3	-1. 666 363 719	-0. 736 703 333	1.6 66 36 37 19	D o w n	0.0 14 84 42 4	0.9 30 85 92 11
28 7	ANK 2	Ankyrin 2, neuronal	4. 90 16 4	3. 99 43 1	3. 55 74 7	5. 97 35 7	5. 89 65 5	4. 40 04 7	2.4 156 531 7	1.2 724 133 33	2.4 15 65 31 7	U p	0.0 31 32 29 72	0.9 30 85 92 11
41	MCF	MCF.2 cell line	7.	7.	6.	6.	5.	4.	-3.	-1.	3.3	D	0.0	0.9

68	2	derived transforming sequence	52 15 1	23 07 3	38 59 3	17 63 2	53 48 5	18 27 5	359 119 997	748 083 333	59 11 99 97	o w n	09 60 46 59	30 85 92 11
62 85	S100 B	S100 calcium binding protein B	6. 86 44 2	7. 37 46 7	6. 83 51 8	5. 89 32 2	6. 28 57 4	6. 33 35 3	-1. 807 413 579	-0. 853 926 667	1.8 07 41 35 79	D o w n	0.0 03 79 51 47	0.9 30 85 92 11
51 64	PDK 2	Pyruvate dehydrogenase kinase, isozyme 2	6. 97 15 6	7. 39 81 8	7. 08 75 6	6. 83 67 9	6. 17 24 6	6. 50 80 2	-1. 565 557 684	-0. 646 676 667	1.5 65 55 76 84	D o w n	0.0 16 52 64 21	0.9 30 85 92 11
30 32	HAD HB	Hydroxyacyl-coa dehydrogenase/3-ketoacyl-coa thiolase/enoyl-coa hydratase (trifunctional protein), $\beta$ subunit	8. 73 96 3	8. 77 87 1	9. 00 88 7	8. 49 67 6	7. 81 72 7	8. 43 85 3	-1. 506 864 821	-0. 591 55 48	1.5 06 86 48 21	D o w n	0.0 22 74 98 06	0.9 30 85 92 11
29 84 2	TFC P2L1	Transcription factor CP2-like 1	6. 59 73 4	6. 82 85 4	7. 45 70 2	8. 42 01 5	7. 43 83 2	7. 42 24 7	1.7 403 128 37	0.7 993 466 67	1.7 40 31 28 37	U p	0.0 42 64 13 92	0.9 30 85 92 11
50 9	ATP5 C1	ATP synthase, H <sup>+</sup> transporting, mitochondrial F1	9. 38 70	9. 32 92	9. 74 08	8. 88 35	8. 49 72	9. 00 14	-1. 615 129	-0. 691 65	1.6 15 12	D o w	0.0 06 42	0.9 30 85



		complex, polypeptide 1	γ	4	5	2			6	675		96	n	65	92
												75		5	11
10	LOC	Uncharacterized		4.	5.	5.	4.	5.	4.	-1.	-0.	1.5	D	0.0	0.9
53	1053	LOC105377283		98	29	69	13	12	69	595	674	95	o	45	30
77	7728			97	40	11	25	87	13	623	12	62	w	31	85
28	3			5	8	8	8		7	194		31	n	76	92
3												94		42	11
54	CKM	Creatine kinase,		9.	8.	9.	8.	8.	8.	-1.	-0.	1.5	D	0.0	0.9
85	T1A	mitochondrial 1A		12	82	40	26	96	24	542	624	42	o	33	30
96				40	88	33	93	94	30	014	816	01	w	73	85
				1	9	8	6	6	1	858	667	48	n	71	92
												58		98	11
10	NPIP	Nuclear pore		5.	5.	6.	4.	4.	5.	-1.	-0.	1.8	D	0.0	0.9
01	B5	complex		15	57	33	89	32	20	841	881	41	o	31	30
32		interacting protein		31	97	36	51	09	72	706	043	70	w	97	85
24		family, member B5			5		7		5	712	333	67	n	36	92
7												12		18	11
91	MAR	MARVEL domain		6.	6.	6.	7.	7.	7.	1.6	0.7	1.6	U	0.0	0.9
86	VEL	containing 3		81	90	50	93	36	08	436	169	43	p	17	30
2	D3			50	58	99	31	42	42	996	466	69		89	85
				3	3	2		3	9	09	67	96		57	92
												09		16	11
53	ATP6	Atpase, H <sup>+</sup>		4.	4.	5.	4.	4.	4.	-1.	-0.	1.5	D	0.0	0.9
4	V1G	transporting,		80	93	67	39	82	42	501	586	01	o	47	30
	2	lysosomal 13kda,		16	04	35	50	06	94	922	81	92	w	98	85
		V1 subunit G2			6	1	5	2	7	114		21	n	88	92
												14		37	11
10	POM	POM121		6.	6.	6.	6.	7.	7.	1.5	0.6	1.5	U	0.0	0.9
01	121C	transmembrane		93	35	04	85	32	06	534	354	53	p	35	30

01		nucleoporin C	23	22	64	11	10	53	473	733	44		44	85
26			9	1	9	3	3	5	36	33	73		52	92
7											36		56	11
81	SGP	Sphingosine-1-phosphate phosphatase 1	5.	6.	6.	6.	4.	5.	-1.	-0.	1.8	D	0.0	0.9
53	P1		99	53	38	10	73	51	806	853	06	o	35	30
7			67	12	32	18	77	19	549	236	54	w	52	85
			6	9	3	4	6	7	351	667	93	n	19	92
											51		91	11
56	PRT	Phosphoribosyl transferase domain containing 1	5.	4.	5.	4.	3.	4.	-1.	-0.	1.5	D	0.0	0.9
95	FDC		06	87	14	72	85	70	513	597	13	o	40	30
2	1		56	21	09	65	92	04	053	463	05	w	96	85
				5	7	7	9	7	849	333	38	n	09	92
											49		29	11
22	FCG	Fc fragment of igg, low affinity iia, receptor (CD32)	6.	6.	6.	5.	6.	6.	-1.	-0.	1.6	D	0.0	0.9
12	R2A		86	75	81	45	71	13	637	711	37	o	44	30
			53	45	51	44	51	16	210	24	21	w	11	85
			4	1	2	8	2	5	699		06	n	55	92
											99		06	11
57	DSC	Down syndrome cell adhesion molecule like 1	4.	4.	5.	6.	6.	6.	2.4	1.3	2.4	U	0.0	0.9
45	AML		88	98	53	94	16	19	712	052	71	p	01	30
3	1		15	04	15	93	72	25	083	166	20		47	85
					5		9	1	77	67	83		02	92
											77		29	11
10	PRD	Peroxiredoxin 3	8.	8.	9.	8.	7.	8.	-1.	-0.	1.6	D	0.0	0.9
93	X3		66	97	45	32	89	78	617	694	17	o	38	30
5			54	01	48	60	23	98	852	08	85	w	74	85
			9	9	4	9	8	1	407		24	n	78	92
											07		88	11
14	CIA	Circadian	5.	5.	5.	7.	5.	7.	2.5	1.3	2.5	U	0.0	0.9

85	RT	associated	16	23	41	51	29	12	922	741	92	p	29	30
23		repressor of	77	16	02	80	40	00	232	9	22		83	85
		transcription	9	4	3	5	9	9	99		32		73	92
											99		55	11
22	TTC	Tetratricopeptide	8.	8.	8.	9.	8.	8.	1.6	0.7	1.6	U	0.0	0.9
99	39A	repeat domain 39A	03	24	49	19	98	77	557	275	55	p	03	30
6			21	13	75	02	91	42	826	133	78		87	85
			2	6	8	2	8		81	33	26		55	92
											81		09	11
46	MY	Myosin, heavy	10	11	11	7.	11	8.	-4.	-2.	4.1	D	0.0	0.9
29	H11	chain 11, smooth	.6	.5	.5	52	.3	62	193	068	93	o	46	30
		muscle	20	85	35	62	88	33	553	173	55	w	29	85
			69	61	85	7	04	2	708	333	37	n	46	92
											08		82	11
53	PLP1	Proteolipid protein	5.	5.	4.	4.	4.	4.	-1.	-0.	1.8	D	0.0	0.9
54		1	62	76	85	63	18	71	875	907	75	o	09	30
			80	98	10	04	61	11	276	103	27	w	98	85
			6	5	8	3	5		505	333	65	n	81	92
											05		13	11
56	MAS	Mannan-binding	6.	6.	5.	7.	7.	7.	2.2	1.1	2.2	U	0.0	0.9
48	P1	lectin serine	43	02	41	04	12	19	370	615	37	p	02	30
		peptidase 1 (C4/C2	48	92	32	08	39	73	435	933	04		05	85
		activating	7	8	3	2	8	6	36	33	35		17	92
		component of									36		91	11
		Ra-reactive factor)												
12	COL	Collagen, type IV,	5.	6.	7.	4.	6.	4.	-2.	-1.	2.4	D	0.0	0.9
87	4A5	$\alpha$ 5	49	38	46	63	13	63	492	317	92	o	48	30
			71	96	06	23	04	23	206	423	20	w	91	85
			4	6	2	6	3	6	018	333	60	n	15	92

											18		45	11
11	AP1	Adaptor-related	6.	5.	5.	6.	6.	6.	1.5	0.5	1.5	U	0.0	0.9
74	S1	protein complex 1	24	67	59	14	69	44	040	888	04	p	34	30
		Σ 1 subunit	88	64	64	33	73	75	508	533	05		52	85
			5	4	5	6	6	8	39	33	08		49	92
											39		04	11
12	COL	Collagen, type IV,	7.	8.	9.	4.	8.	5.	-5.	-2.	5.2	D	0.0	0.9
88	4A6	α 6	70	63	33	23	30	95	261	395	61	o	34	30
			35	78	40	17	28	45	521	48	52	w	18	85
			9	7	3		2	3	314		13	n	42	92
											14		57	11
76	ZNF	Zinc finger protein	4.	5.	4.	4.	4.	4.	-1.	-0.	1.5	D	0.0	0.9
78	124	124	78	02	68	00	18	48	523	607	23	o	07	30
			5	23	83	38	54	43	433	326	43	w	13	85
				3	1	3	9	4	649	667	36	n	23	92
											49		52	11
14	TME	Transmembrane	5.	5.	6.	4.	4.	4.	-1.	-0.	1.8	D	0.0	0.9
85	M56	protein 56	74	17	36	64	99	93	873	905	73	o	14	30
34			26	94	97	46	15	87	345	616	34	w	83	85
			2	9	7	8	6	9	068	667	50	n	74	92
											68		28	11
11	MOR	MORN repeat	5.	5.	5.	5.	3.	4.	-2.	-1.	2.2	D	0.0	0.9
88	N4	containing 4	49	29	97	11	95	14	274	185	74	o	06	30
12			02	76	69	05	26	47	653	646	65	w	66	85
			2	2	6	1	5		298	667	32	n	28	92
											98		91	11
19	EDN	Endothelin receptor	5.	5.	6.	3.	4.	4.	-2.	-1.	2.2	D	0.0	0.9
10	RB	type B	44	49	19	99	92	67	264	179	64	o	04	30
			64	78	07	81	78	20	213	01	21	w	16	85

			2	2	6	3		4	498		34	n	17	92
											98		99	11
63	SCT	Secretin receptor	4.	5.	5.	4.	5.	4.	-1.	-0.	1.7	D	0.0	0.9
44	R		82	50	93	32	00	63	702	767	02	o	34	30
			05	51	48	34	19	16	726	846	72	w	95	85
			2	2	3		2	1	436	667	64	n	89	92
											36		67	11
51	GUL	GULP, engulfment	5.	5.	6.	5.	4.	5.	-1.	-0.	1.5	D	0.0	0.9
45	P1	adaptor PTB	61	94	23	57	75	51	567	648	67	o	40	30
4		domain containing	50	81	54	83	90	65	240	226	24	w	79	85
		1	9	2	2	1	6	8	589	667	05	n	17	92
											89		54	11
11	MO	Monoacylglycerol	10	9.	9.	10	10	10	1.6	0.7	1.6	U	0.0	0.9
62	GAT	O-acyltransferase 1	.1	49	59	.7	.7	.0	862	537	86	p	18	30
55	1		39	00	57	34	40	12	011	766	20		63	85
			99	4	5	1	22	79	72	67	11		26	92
											72		98	11
83	AXI	Axin 2	4.	4.	5.	3.	4.	4.	-1.	-0.	1.5	D	0.0	0.9
13	N2		50	73	28	85	44	38	529	613	29	o	37	30
			52	79	67	45	67	83	856	396	85	w	14	85
				1	8	6	6	8	852	667	68	n	53	92
											52		66	11
23	FOX	Forkhead box L1	6.	5.	6.	7.	6.	6.	1.8	0.8	1.8	U	0.0	0.9
00	L1		70	42	00	00	83	88	124	579	12	p	22	30
			44	96	72	29	12	10	987	8	49		10	85
			6	3		8	3	2	5		87		26	92
											5		11	11
66	SIGL	Sialic acid binding	5.	4.	5.	5.	7.	6.	2.3	1.2	2.3	U	0.0	0.9
14	EC1	Ig-like lectin 1,	47	97	20	50	15	65	299	202	29	p	15	30

		sialoadhesin	80 4	05 2	93 2	95 1	74 5	17 5	139 39	766 67	91 39		06 02 12	85 92 11
55 72 9	ATF7 IP	Activating transcription factor 7 interacting protein	5. 55 40 7	5. 73 44 1	5. 24 88 2	4. 94 84 6	4. 79 76 1	4. 83 85 2	-1. 570 151 027	-0. 650 903 333	1.5 70 15 10 27	D o w n	0.0 04 38 89 93	0.9 30 85 92 11
69 43	TCF 21	Transcription factor 21	5. 47 30 4	6. 60 75 2	6. 83 31	4. 17 13 2	5. 70 90 6	5. 36 38 1	-2. 334 569 708	-1. 223 156 667	2.3 34 56 97 08	D o w n	0.0 33 54 98 76	0.9 30 85 92 11
22 91 3	RAL Y	RALY heterogeneous nuclear ribonucleoprotein	7. 19 76 9	7. 45 52 3	7. 72 91 9	6. 84 56 7	6. 42 68 5	7. 14 79 2	-1. 573 404 92	-0. 653 89	1.5 73 40 49 2	D o w n	0.0 21 89 80 32	0.9 30 85 92 11
94 44	QKI	QKI, KH domain containing, RNA binding	4. 18 23 2	4. 52 42 1	4. 82 96 7	3. 52 79 9	3. 62 56 3	4. 19 17 7	-1. 658 949 535	-0. 730 27	1.6 58 94 95 35	D o w n	0.0 13 15 16 45	0.9 30 85 92 11
65 18	SLC 2A5	Solute carrier family (facilitated glucose/fructose transporter), member 5	5. 96 25 4	5. 98 71 2	6. 39 93 6	5. 44 44 2	5. 28 31 4	5. 63 18 6	-1. 583 591 249	-0. 663 2	1.5 83 59 12 49	D o w n	0.0 06 70 79 59	0.9 30 85 92 11

57	NLG	Neurologin	4,	4.	3.	4.	3.	4.	3.	-1.	-0.	1.7	D	0.0	0.9
50	N4X	X-linked		71	95	67	33	10	59	705	769	05	o	19	30
2				37	98	38	82	08	87	124	876	12	w	52	85
				6	2	8	7	4	2	009	667	40	n	10	92
												09		87	11
84	ST6	ST6		6.	7.	7.	5.	6.	4.	-2.	-1.	2.7	D	0.0	0.9
62	GAL	$\beta$ -galactosamide		28	12	03	07	17	76	784	477	84	o	05	30
0	2	$\alpha$ -2,6-sialyltransferase 2		26	90	50	41	40	66	290	31	29	w	66	85
				3	3	8	3	3	5	996		09	n	66	92
												96		2	11
72	TXK	TXK tyrosine		4.	5.	4.	5.	5.	5.	1.6	0.7	1.6	U	0.0	0.9
94		kinase		44	00	76	46	66	19	301	050	30	p	07	30
				54	13	24	47	57	37	672	2	16		40	85
				2	3	8	4	6	9	64		72		85	92
												64		12	11
39	LGA	Lectin,		10	10	11	8.	10	9.	-2.	-1.	2.2	D	0.0	0.9
56	LS1	galactoside-binding		.0	.7	.0	39	.4	56	243	165	43	o	44	30
		, soluble, 1		97	26	52	11	25	39	005	433	00	w	78	85
				96	87	33	2	78	6	773	333	57	n	49	92
												73		52	11
59	ACT	Actin, $\alpha$ 2, smooth		4.	4.	4.	3.	4.	3.	-1.	-0.	1.6	D	0.0	0.9
	A2	muscle, aorta		28	59	86	47	48	71	617	693	17	o	36	30
				53	60	52	23	27	02	519	783	51	w	17	85
				2	9	9	5	6	4	756	333	97	n	67	92
												56		7	11
57	AKR	Aldo-keto		11	11	11	10	10	11	-1.	-0.	1.6	D	0.0	0.9
01	1B10	reductase family 1,		.6	.2	.8	.5	.8	.1	610	687	10	o	09	30
6		member B10		06	89	29	69	98	94	806	783	80	w	67	85
		(aldose reductase)		77	22	75	48	64	27	65	333	66	n	63	92

											5		43	11
75	ZNF	Zinc finger protein	5.	5.	6.	4.	5.	4.	-1.	-0.	1.9	D	0.0	0.9
52	711	711	16	98	24	60	60	33	929	947	29	o	41	30
			39	36	32	20	95	54	142	96	14	w	56	85
			6	3	8	9			881		28	n	20	92
											81		48	11
23	STX	Syntaxin 12	6.	6.	6.	6.	4.	6.	-1.	-0.	1.8	D	0.0	0.9
67	12		15	40	92	04	76	01	848	886	48	o	45	30
3			16	19	55	53	09	40	425	296	42	w	73	85
			4	9	3		3	4	204	667	52	n	99	92
											04		66	11
93	GTF	General	4.	4.	4.	3.	3.	3.	-1.	-0.	1.5	D	0.0	0.9
30	3C3	transcription factor	52	19	78	84	76	91	581	661	81	o	04	30
		IIIC subunit 3	52	34	67	18	32	70	302	113	30	w	37	85
			9		9	4	7	3	45	333	24	n	33	92
											5		6	11
44	CBW	COBW domain	4.	3.	4.	3.	3.	3.	-1.	-0.	1.6	D	0.0	0.9
55	D3	containing 3	45	86	15	71	32	19	674	744	74	o	05	30
71			21	23	27	57	17	77	812		81	w	34	85
			2	7	1	4	2	4	975		29	n	61	92
											75		82	11



Table SV. DEGs in comparison V.

En try	Gene symb ol	Gene name	A 10	A 10	A 10	A 10	A 10	A 10	Fol d-c han ge	log FC	abs olu teFC	Re gu lat ion	P-v alu e	FD R
30846	EHD2	EH domain containing 2	593408	678377	646231	822781	772344	670535	2.232797	1.158833	2.232797	Up	0.0256421	0.6633274
23743	BHM2	Bine--homocysteine S-methyltransferase 2	352481	401604	415429	554651	449426	459435	1.9724562	0.979933	1.9724562	Up	0.0166501	0.6633274
729230	CCR2	Chemokine (C-C motif) receptor 2	452296	520992	448186	556436	520666	534245	1.5832729	0.66291	1.5832729	Up	0.0287972	0.6633274
221303	FAM162B	Family with sequence similarity 162 member B	456611	569016	518336	657025	728559	620509	2.908428	1.54024	2.908428	Up	0.0041860	0.6633274
2313	FLI1	Fli-1 proto-oncogene, ETS transcription	37486	42752	47669	57217	55562	46667	2.072367	1.051339	2.072367	Up	0.02096	0.6633274

		factor	7	2	6		9	6	25		64		38	74
											25		25	04
40	MAR	Myristoylated	5.	6.	6.	7.	7.	7.	1.7	0.8	1.7	U	0.0	0.6
82	CKS	alanine-rich protein	94	54	74	55	02	12	754	282	75	p	15	63
		kinase C substrate	32	51	06	99	92	43	769	066	47		21	32
			1		7	8	9	3	94	67	69		62	74
											94		86	04
22	NLR	NLR family, pyrin	5.	6.	6.	8.	7.	6.	2.2	1.1	2.2	U	0.0	0.6
86	P1	domain containing	82	95	00	25	53	54	734	848	73	p	42	63
1		1	80	39	84	70	92	87	395	766	43		29	32
			3	5	4	5	2	8	86	67	95		67	74
											86		31	04
69	HNF	HNF1 homeobox B	10	10	10	9.	9.	9.	-1.	-0.	1.5	D	0.0	0.6
28	1B		.5	.2	.2	42	97	73	514	598	14	o	17	63
			21	13	04	86	97	51	575	913	57	w	96	32
			79	73	77	4	2	9	328	333	53	n	84	74
											28		53	04
63	CCL	Chemokine (C-C	5.	6.	5.	6.	6.	7.	1.8	0.8	1.8	U	0.0	0.6
48	3	motif) ligand 3	61	18	73	22	45	51	483	862	48	p	41	63
			87	27	16	15	80	23	013		30		15	32
			8	7	8	1	1	1	56		13		18	74
											56		01	04
21	F11	Coagulation factor	8.	7.	8.	5.	6.	7.	-3.	-1.	3.2	D	0.0	0.6
60		XI	53	83	21	49	42	58	227	690	27	o	11	63
			23	49	16	90	44	47	111	243	111	w	70	32
			2	5	5	1	3	5	294	333	29	n	83	74
											4		9	04
11	PHB	Prohibitin 2	7.	7.	8.	9.	8.	8.	1.6	0.7	1.6	U	0.0	0.6
33	2		86	53	29	18	21	55	839	518	83	p	42	63

1			68	75	62	34	43	85	975	9	99		19	32
			9	5	6	9	7	1	04		75		89	74
											04		44	04
94	CHS	Carbohydrate	3.	3.	3.	4.	5.	3.	1.7	0.8	1.7	U	0.0	0.6
35	T2	(N-acetylglucosami	54	84	79	62	10	94	807	325	80	p	22	63
		ne-6-O)	93	13	45	83	59	85	808	1	78		14	32
		sulfotransferase 2	9	7	7	3	7	6	7		08		98	74
											7		59	04
29	FAM	Family with	3.	4.	3.	5.	4.	4.	1.7	0.8	1.7	U	0.0	0.6
90	216A	sequence similarity	45	25	96	28	63	18	498	071	49	p	39	63
2		216 member A	86	21	98	98	20	02	040	933	80		88	32
				8	5	8	8	5	03	33	40		50	74
											03		45	04
10	FXY	FXYD6-FXYD2	4.	7.	6.	8.	7.	7.	3.1	1.6	3.1	U	0.0	0.6
05	D6-F	readthrough	87	22	08	39	30	40	224	426	22	p	27	63
33	XYD		02	80	07	00	87	82	316	7	43		61	32
18	2		9	4	6	5	6	9	68		16		40	74
1											68		75	04
23	PLX	Plexin D1	5.	6.	6.	7.	7.	6.	2.0	1.0	2.0	U	0.0	0.6
12	ND1		75	58	38	82	57	44	500	356	50	p	34	63
9			99	85	15	27	25	15	323	466	03		93	32
					3	5	3	9	37	67	23		55	74
											37		35	04
55	SOB	Sine oculis binding	3.	4.	3.	4.	4.	4.	1.7	0.7	1.7	U	0.0	0.6
08	P	protein homolog	38	33	86	67	33	94	292	901	29	p	22	63
4			42	01	12	1	28	21	382	366	23		05	32
			3		7		2	9	66	67	82		70	74
											66		47	04
79	PVRI	Poliovirus receptor	5.	6.	6.	5.	5.	5.	-1.	-0.	1.5	D	0.0	0.6

03	G	related	58	09	20	35	32	43	508	592	08	o	20	63
7		immunoglobulin	91	27	45	07	37	31	282	906	28	w	47	32
		domain containing	1	1	3		7	6	497	667	24	n	26	74
											97		17	04
10	SCG	Secretagoin,	4.	4.	4.	6.	6.	5.	2.4	1.3	2.4	U	0.0	0.6
59	N	EF-hand calcium	80	44	94	66	20	27	850	133	85	p	07	63
0		binding protein	43	61	83	51	30	05	932		09		70	32
			8	2	7	7	9	1	7		32		57	74
											7		26	04
54	TME	Transmembrane	4.	4.	5.	6.	6.	5.	1.9	0.9	1.9	U	0.0	0.6
97	M13	protein 132A	85	92	04	57	13	05	671	761	67	p	33	63
2	2A		07	95	90	44	30	00	632	166	16		41	32
			3		2	8	6	6	21	67	32		98	74
											21		55	04
14	MAC	MACRO domain	6.	4.	5.	3.	4.	4.	-1.	-0.	1.9	D	0.0	0.6
07	ROD	containing 2	09	92	22	79	53	93	987	990	87	o	37	63
33	2		06	29	78	91	36	61	350	846	35	w	07	32
			8	8	7	7	9	3	955	667	09	n	34	74
											55		25	04
13	CRIP	Cysteine-rich	7.	6.	7.	8.	8.	7.	1.7	0.7	1.7	U	0.0	0.6
97	2	protein 2	39	74	50	20	43	39	377	972	37	p	45	63
			49	85	13	55	98	09	292	033	72		73	32
			3	4		5	8	5	68	33	92		73	74
											68		41	04
11	PKIG	Protein kinase	6.	6.	6.	7.	6.	6.	1.7	0.7	1.7	U	0.0	0.6
14		(camp-dependent,	19	56	43	93	84	78	244	861	24	p	46	63
2		catalytic) inhibitor	65	68	92	40	59	09	305	2	43		25	32
		$\gamma$	1	9	7	7	7	9	18		05		74	74
											18		57	04

290	ANP EP	Alanyl (membrane) aminopeptidase	12 .9 22 82	12 .5 61 2	12 .6 00 4	11 .1 53 74	11 .5 77 1	12 .5 55 34	-1. 908 906 8	-0. 932 746 667	1.9 08 90 68	D o w n	0.0 31 50 80 04	0.6 63 32 74 04
28299	IGK V1-5	Immunoglobulin $\kappa$ variable 1-5	6. 19 85 1	6. 53 61 1	6. 32 50 1	6. 74 64 1	9. 73 04 1	9. 47 33 2	4.9 137 915 8	2.2 968 366 67	4.9 13 79 15 8	U p	0.0 16 97 44 36	0.6 63 32 74 04
65012	SLC2 6A10	Solute carrier family 26, member 10	4. 51 28 2	5. 06 98 3	4. 28 62 6	6. 56 41 8	5. 28 20 1	5. 19 78 1	2.0 825 627 99	1.0 583 6 99	2.0 82 56 27 99	U p	0.0 32 83 58 07	0.6 63 32 74 04
57677	ZFP1 4	ZFP14 zinc finger protein	5. 47 75 1	4. 72 04 6	5. 39 73 9	4. 43 53 7	4. 25 5 4	4. 73 76 4	-1. 649 981 673	-0. 722 45 16 73	1.6 49 98 16 73	D o w n	0.0 21 21 52 97	0.6 63 32 74 04
348094	ANK DD1 A	Ankyrin repeat and death domain containing 1A	3. 63 37 2	4. 30 65 5	4. 09 33 1	5. 34 00 7	4. 77 32 3	4. 19 90 2	1.6 929 976 84	0.7 595 8 76 84	1.6 92 99 76 84	U p	0.0 45 33 72 44	0.6 63 32 74 04
64377	CHS T8	Carbohydrate (N-acetylgalactosa mine 4-0) sulfotransferase 8	5. 31 40 5	5. 37 1 5	6. 12 38 6	3. 81 69 6	5. 26 38 6	4. 48 41 4	-2. 115 936 99	-1. 081 296 667	2.1 15 93 69	D o w n	0.0 28 65 64	0.6 63 32 74

											9		06	04
51	ARM	Armadillo repeat	6.	7.	7.	7.	7.	7.	1.6	0.7	1.6	U	0.0	0.6
30	CX1	containing,	63	07	41	91	92	42	451	182	45	p	24	63
9		X-linked 1	25	06	37	69	86	60	395	1	13		91	32
			7	9	9	9	6	3	88		95		39	74
											88		3	04
85	SCIN	Scinderin	6.	5.	6.	5.	3.	6.	-2.	-1.	2.4	D	0.0	0.6
47			74	92	27	03	94	09	446	290	46	o	42	63
7			70	38	76	64	50	42	840	92	84	w	03	32
			2	1	3	2	5	3	397		03	n	50	74
											97		24	04
49	NR4	Nuclear receptor	3.	3.	3.	4.	7.	5.	5.0	2.3	5.0	U	0.0	0.6
29	A2	subfamily 4 group	20	70	50	69	52	16	011	222	01	p	11	63
		A member 2	73	23	74	03	46	89	042	466	10		27	32
			1	5	8	2	5	1	08	67	42		44	74
											08		63	04
57	CAM	Calmodulin	7.	7.	7.	5.	6.	6.	-1.	-0.	1.7	D	0.0	0.6
66	SAP3	regulated spectrin	48	04	17	76	55	95	754	810	54	o	36	63
2		associated protein	95	80	27	23	93	57	402	98	40	w	81	32
		family member 3	2	9	1	2	6		776		27	n	07	74
											76		1	04
84	USM	Up-regulated	6.	4.	5.	3.	3.	4.	-2.	-1.	2.5	D	0.0	0.6
83	G5	during skeletal	23	12	93	84	93	39	592	374	92	o	35	63
3		muscle growth 5	63	54	43	92	15	24	456	32	45	w	32	32
		homolog (mouse)	3	5	8	3	7		892		68	n	39	74
											92		83	04
51	MZB	Marginal zone B	3.	3.	3.	3.	5.	4.	2.1	1.0	2.1	U	0.0	0.6
23	1	and B1	32	43	15	22	04	88	206	845	20	p	48	63
7		cell-specific	12	61	19	97	36	95	452	033	64		44	32

		protein	7	5	3	2	4		97	33	52		98	74
											97		19	04
58	RAB	RAB6A, member	3.	2.	3.	3.	4.	4.	1.7	0.7	1.7	U	0.0	0.6
70	6A	RAS oncogene	74	92	45	90	23	29	017	670	01	p	11	63
		family	72	60	54	01	96	00	510	2	75		79	32
			6	1	7	3	4	3	5		10		69	74
											5		62	04
10	SAE	SUMO1 activating	6.	6.	6.	7.	6.	7.	1.6	0.6	1.6	U	0.0	0.6
05	1	enzyme subunit 1	50	35	72	53	89	22	128	896	12	p	13	63
5			19	68	78	08	75	70	810	4	88		99	32
			2	3	4	7	7	7	01		10		79	74
											01		56	04
55	ARH	Rho guanine	7.	6.	6.	5.	6.	6.	-1.	-0.	1.8	D	0.0	0.6
70	GEF	nucleotide	10	64	65	40	09	25	848	886	48	o	12	63
1	40	exchange factor	85	74	67	83	19	24	942	7	94	w	48	32
		(GEF) 40		8	5	3			04		20	n	63	74
											4		86	04
56	PCD	Protocadherin $\alpha$ 2	7.	7.	6.	6.	6.	6.	-1.	-0.	1.5	D	0.0	0.6
14	HA2		44	73	91	53	83	80	557	639	57	o	31	63
6			20	45	29	69	18	31	526	256	52	w	81	32
			9	2	9		2	1	454	667	64	n	64	74
											54		86	04
57	SLC4	Solute carrier	7.	7.	7.	6.	7.	7.	-1.	-0.	1.5	D	0.0	0.6
21	5A4	family 45, member	79	53	55	59	03	32	562	644	62	o	22	63
0		4	95	65	24	49	51	64	688	03	68	w	64	32
			3	7	8	4		5	255		82	n	32	74
											55		14	04
94	QKI	QKI, KH domain	3.	3.	3.	4.	3.	4.	1.8	0.8	1.8	U	0.0	0.6
44		containing, RNA	35	30	73	87	97	15	279	702	27	p	11	63

		binding	24 1	77 8	17 6	61 9	29	36 1	796 38	5	97 96 38		02 58 69	32 74 04
65 9	BMP R2	Bone morphogenetic protein receptor type II	7. 63 08 3	7. 63 12 7	7. 79 27	8. 89 10 4	8. 33 53 9	7. 82 34 9	1.5 856 122 35	0.6 650 4 35	1.5 85 61 22 35	U p	0.0 45 01 05 61	0.6 63 32 74 04
51 56	PDG FRA	Platelet-derived growth factor receptor, polypeptide	6. 29 71 6	6. 94 49 3	7. 57 13 1	8. 81 06 7	8. 21 18 8	7. 89 33 8	2.5 802 484 71	1.3 675 1 84	2.5 80 24 84 71	U p	0.0 07 73 33 17	0.6 63 32 74 04
25 48 27	NAA LAD L2	N-acetylated $\alpha$ -linked acidic dipeptidase-like 2	5. 51 38 4	4. 85 46 9	5. 18 52 4	4. 39 98 1	4. 16 66 8	4. 58 94 7	-1. 740 220 357	-0. 799 27 03	1.7 40 22 03 57	D o w n	0.0 06 79 30 12	0.6 63 32 74 04
57 45 3	DSC AML 1	Down syndrome cell adhesion molecule like 1	6. 87 82 1	6. 03 80 8	6. 15 59 3	4. 22 57 9	4. 18 79 9	5. 23 00 9	-3. 505 159 27	-1. 809 48 92 7	3.5 05 15 92 7	D o w n	0.0 01 32 63 34	0.6 63 32 74 04
72 73	TTN	Titin	9. 30 06 7	8. 80 38 3	8. 75 49 4	5. 70 97 1	5. 90 17	8. 58 55 8	-4. 661 572 376	-2. 220 816 667	4.6 61 57 23 76	D o w n	0.0 18 35 43 32	0.6 63 32 74 04
65	ZDH	Zinc finger,	8.	7.	7.	4.	5.	7.	-3.	-1.	3.6	D	0.0	0.6



30	HC11	DHHC-type	42	32	20	87	43	09	600	848	00	o	17	63
82	B	containing 11B	05	92	32	69	64	46	847	336	84	w	48	32
			4	2	4	1	7	1	913	667	79	n	68	74
											13		04	04
51	NLK	Nemo-like kinase	7.	7.	7.	6.	6.	7.	-1.	-0.	1.9	D	0.0	0.6
70			89	62	82	21	85	36	958	969	58	o	13	63
1			62	12	84	26	8	67	143	486	14	w	18	32
			3		1	6		2	733	667	37	n	81	74
											33		52	04
85	SHA	SH3 and multiple	7.	7.	7.	8.	9.	7.	2.1	1.1	2.1	U	0.0	0.6
35	NK3	ankyrin repeat	11	71	50	67	49	52	769	222	76	p	48	63
8		domains 3	22	07	32	10	25	95	123	833	91		33	32
			7	3	6	2	8	1	69	33	23		08	74
											69		44	04
51	SCL	Selenocysteine	7.	6.	6.	5.	6.	6.	-1.	-0.	1.6	D	0.0	0.6
54	Y	lyase	20	87	83	83	29	66	626	701	26	o	23	63
0			04	82	10	97	98	58	123	436	12	w	83	32
			4	1	7	2	7	2	315	667	33	n	63	74
											15		95	04
22	ALD	Aldehyde	10	10	10	9.	9.	10	-1.	-0.	1.8	D	0.0	0.6
4	H3A	dehydrogenase 3	.5	.3	.7	02	50	.4	893	921	93	o	34	63
	2	family member A2	57	86	84	12	77	35	484	043	48	w	05	32
			44	31	13	2	2	81	135	333	41	n	02	74
											35		08	04
56	PCD	Protocadherin $\alpha$ 11	7.	7.	6.	6.	6.	6.	-1.	-0.	1.5	D	0.0	0.6
13	HA1		44	73	91	53	83	80	557	639	57	o	31	63
8	1		20	45	29	69	18	31	526	256	52	w	81	32
			9	2	9		2	1	454	667	64	n	64	74
											54		86	04

55	PRI	Primase, DNA,	4.	4.	4.	5.	5.	4.	1.5	0.6	1.5	U	0.0	0.6
57	M1	polypeptide (49kda)	35	24	89	49	17	83	935	722	93	p	28	63
			04	36	67	81	56	37	747	666	57		57	32
			2	1	6	9	4	6	21	67	47		79	74
											21		33	04
30	ANX	Annexin A6	5.	7.	6.	9.	7.	7.	2.6	1.4	2.6	U	0.0	0.6
9	A6		79	67	61	09	69	51	556	090	55	p	43	63
			60	43	31	48	93	65	223	5	62		72	32
			5	5	1	3		3	52		23		11	74
											52		34	04
70	THB	Thrombospondin 4	3.	4.	4.	5.	5.	4.	1.6	0.7	1.6	U	0.0	0.6
60	S4		98	72	07	31	10	55	567	283	56	p	31	63
			85	06	81	30	63	31	776	8	77		75	32
			9	1	9	2	4	7	54		76		94	74
											54		6	04
41	MC	Minichromosome	4.	4.	4.	6.	5.	5.	2.2	1.2	2.2	U	0.0	0.6
75	M6	maintenance	12	34	93	07	89	04	988	009	98	p	07	63
		complex	80	51	93	49	06	96	728	266	87		92	32
		component 6	7	1	2	9	8	1	4	67	28		38	74
											4		99	04
10	LHF	Lipoma HMGIC	5.	7.	7.	9.	8.	7.	3.0	1.6	3.0	U	0.0	0.6
18	P	fusion partner	36	19	34	30	11	35	857	256	85	p	42	63
6			28	77	12	27	63	94	118	033	71		71	32
			1	2	1	6	8	1	22	33	18		89	74
											22		83	04
55	BIN3	Bridging integrator	9.	9.	9.	8.	8.	8.	-1.	-0.	1.5	D	0.0	0.6
90		3	54	13	16	76	62	64	516	600	16	o	09	63
9			01	29	29	03	88	48	413	663	41	w	50	32
			8	3	6	5	6	7	634	333	36	n	17	74

												34		26	04
78	CAC	Calcium channel,	3.	4.	3.	6.	4.	5.	3.0	1.5	3.0	U	0.0	0.6	
3	NB2	voltage-dependent,	45	18	87	07	78	42	126	910	12	p	02	63	
		$\beta$ 2 subunit	18	19	83	69	17	66	853	5	68		48	32	
			5	3	8	9		2	43		53		74	74	
											43		28	04	
26	TIM	Translocase of	7.	6.	6.	6.	6.	6.	-1.	-0.	1.6	D	0.0	0.6	
51	M10	inner	07	98	98	04	23	50	681	750	81	o	03	63	
5	B	mitochondrial	11	47	34	23	67	99	878	073	87	w	51	32	
		membrane 10	6	1	8	9	5	9	32	333	83	n	42	74	
		homolog B (yeast)									2		77	04	
23	FOS	FBJ murine	10	7.	10	11	12	11	4.3	2.1	4.3	U	0.0	0.6	
53		osteosarcoma viral	.1	62	.6	.2	.1	.5	980	368	98	p	24	63	
		oncogene homolog	84	65	71	19	13	59	885	766	08		82	32	
			25	5	33	35	66	75	97	67	85		36	74	
											97		89	04	
46	NAP	Nucleosome	3.	3.	3.	5.	4.	3.	2.1	1.0	2.1	U	0.0	0.6	
75	1L3	assembly protein	11	67	29	19	21	96	369	955	36	p	12	63	
		1-like 3	53	01	80	53	43	05	947	833	99		20	32	
			2	5	5	9	2	6	05	33	47		53	74	
											05		55	04	
96	FEZ1	Fasciculation and	4.	4.	3.	5.	5.	4.	1.6	0.7	1.6	U	0.0	0.6	
38		elongation protein	05	81	98	41	16	55	921	588	92	p	40	63	
		zeta 1	34	3	49	04	52	23	647	7	16		84	32	
			5		4	8	2		07		47		29	74	
											07		07	04	
91	ZNF	Zinc finger protein	5.	5.	5.	4.	5.	5.	-1.	-0.	1.6	D	0.0	0.6	
12	682	682	80	69	78	56	25	32	640	714	40	o	16	63	
0			88	16	45	20	74	35	421	066	42	w	83	32	

			9	8	6	1		2	624	667	16	n	54	74	
											24		58	04	
56	ADA	ADAM	5.	6.	6.	7.	8.	6.	2.6	1.4	2.6	U	0.0	0.6	
99	MTS	metallopeptidase	67	60	13	75	52	42	929	292	92	p	29	63	
9	9	with	19	73	77	20	31	95	734		97		28	32	
		thrombospondin	5	6	8	2	4	3	38		34		11	74	
		type 1 motif 9									38		32	04	
11	FAM	Family with	3.	4.	4.	5.	6.	4.	2.3	1.2	2.3	U	0.0	0.6	
17	107A	sequence similarity	88	16	10	01	46	31	216	151	21	p	44	63	
0		107 member A	70	61	07	90	19	83	706	633	67		01	32	
			3		7	3	8	8	6	33	06		43	74	
											6			04	
11	PRD	PR domain	7.	7.	6.	6.	6.	6.	-1.	-0.	1.5	D	0.0	0.6	
10	M4	containing 4	40	27	96	28	73	68	561	643	61	o	15	63	
8			74	35	31	79	74	93	684	103	68	w	30	32	
			1	1	8	6	5	8	837	333	48	n	47	74	
											37		06	04	
15	LOC	Uncharacterized	3.	3.	3.	4.	5.	3.	2.0	1.0	2.0	U	0.0	0.6	
75	1575	LOC157503	31	13	02	03	04	53	666	473	66	p	21	63	
03	03		83	10	10	31	56	36	775	133	67		66	32	
			5	4	9	8	1	3	8	33	75		41	74	
											8		89	04	
36	IDO1	Indoleamine	3.	3.	4.	4.	4.	4.	1.7	0.8	1.7	U	0.0	0.6	
20		2,3-dioxygenase 1	85	66	17	82	81	48	567	129	56	p	02	63	
			96	03	08	65	81	48	675	233	76		79	32	
			2	3	3	8	4	3	77	33	75		27	74	
											77		78	04	
28	DLL	$\Delta$ -like	1	4.	5.	4.	7.	7.	6.	3.8	1.9	3.8	U	0.0	0.6
51	1	( <i>Drosophila</i> )	69	29	85	30	33	03	439	425	43	p	01	63	

4			60 4	33 2	25 5	02 2	42 4	51 9	245	8	92 45		29 46 13	32 74 04
11 60 39	OSR 2	Odd-skipped related transcription factor 2	4. 06 66 8	3. 64 31 4	3. 92 8	5. 02 94 5	4. 54 84 3	4. 15 36 1	1.6 221 306 25	0.6 978 9	1.6 22 13 06 25	U p	0.0 22 93 70 78	0.6 63 32 74 04
10 92 3	SUB 1	SUB1 homolog, transcriptional regulator	4. 27 19 7	4. 09 26	4. 42 71 1	5. 39 00 2	4. 43 80 3	4. 76 43 4	1.5 159 652 32	0.6 002 366 67	1.5 15 96 52 32	U p	0.0 49 40 52 34	0.6 63 32 74 04
28 98 4	RGC C	Regulator of cell cycle	5. 17 54 2	5. 62 70 6	6. 13 27 5	7. 28 23 7	8. 56 19 2	6. 08 31 3	3.1 690 783 61	1.6 640 633 33	3.1 69 07 83 61	U p	0.0 26 76 55 69	0.6 63 32 74 04
25 30	FUT 8	Fucosyltransferase 8 ( $\alpha$ (1,6) fucosyltransferase)	5. 86 04 3	6. 17 29 2	5. 70 42 7	7. 33 93 5	7. 27 14 8	5. 97 21 2	1.9 297 892 93	0.9 484 433 33	1.9 29 78 92 93	U p	0.0 40 47 16 53	0.6 63 32 74 04
70 57	THB S1	Thrombospondin 1	5. 86 54 3	7. 99 09	6. 48 33 9	10 .9 56 07	8. 66 34 7	8. 17 96 6	5.6 041 413 07	2.4 864 933 33	5.6 04 14 13 07	U p	0.0 18 51 98 61	0.6 63 32 74 04
83	TMT	Transmembrane	4.	5.	5.	6.	6.	5.	2.4	1.2	2.4	U	0.0	0.6

85 7	C1	and tetratricopeptide repeat containing 1	67 91 1	54 34 5	04 4	74 03	86 42 1	53 90 5	492 386 14	923 333 33	49 23 86 14	p	13 66 85 4	63 32 74 04
20 12	EMP 1	Epithelial membrane protein 1	3. 90 22 7	3. 32 54 9	3. 91 61 4	5. 48 11 6	5. 49 83 6	4. 59 23 5	2.7 817 446 62	1.4 759 9 46 62	2.7 81 74 46 62	U p	0.0 01 51 46 33	0.6 63 32 74 04
56 14 1	PCD HA7	Protocadherin $\alpha$ 7	7. 44 20 9	7. 73 45 2	6. 91 29 9	6. 53 69 2	6. 83 18 2	6. 80 31 1	-1. 557 526 454	-0. 639 256 667	1.5 57 52 64 54	D o w n	0.0 31 81 64 86	0.6 63 32 74 04
56 14 0	PCD HA8	Protocadherin $\alpha$ 8	7. 44 20 9	7. 73 45 2	6. 91 29 9	6. 53 69 2	6. 83 18 2	6. 80 31 1	-1. 557 526 454	-0. 639 256 667	1.5 57 52 64 54	D o w n	0.0 31 81 64 86	0.6 63 32 74 04
11 33 2	ACO T7	Acyl-coa thioesterase 7	5. 98 21 8	6. 49 33 2	6. 04 63 2	7. 67 57 4	7. 35 07 3	6. 37 33 2	1.9 443 977 01	0.9 593 233 33	1.9 44 39 77 01	U p	0.0 28 34 01 84	0.6 63 32 74 04
10 58 1	IFIT M2	Interferon induced transmembrane protein 2	7. 67 36	8. 56 84 8	8. 88 56 1	10 .2 01 15	9. 99 83 6	8. 51 92 2	2.2 926 455 6	1.1 970 133 33	2.2 92 64 55 6	U p	0.0 49 00 11 28	0.6 63 32 74 04

40 92	SMA D7	SMAD family member 7	3. 80 07 6	4. 63 34 2	4. 50 70 7	6. 94 99 8	5. 30 6	4. 95 89	2.6 842 951 92	1.4 245 433 33	2.6 84 29 51 92	U p	0.0 28 76 73 56	0.6 63 32 74 04
14 45 81	RPL1 4P1	Ribosomal protein L14 pseudogene 1	10 .7 61 29	10 .4 01 69	10 .9 32 75	11 .6 07 78	11 .2 38 4	11 .0 92 42	1.5 308 044 5	0.6 142 9 44 5	1.5 30 80 44	U p	0.0 21 88 94 54	0.6 63 32 74 04
56 34	PRPS 2	Phosphoribosyl pyrophosphate synthetase 2	7. 04 61 1	7. 28 94 7	7. 39 74 6	8. 36 15 4	7. 78 98 9	7. 78 73 6	1.6 646 859 13	0.7 352 5 59 13	1.6 64 68 59	U p	0.0 10 92 84 68	0.6 63 32 74 04
57 0	BAA T	Bile acid-coa:amino acid N-acyltransferase	10 .4 21 83	10 .3 07 16	10 .0 98 21	8. 69 58 9	8. 60 25 4	9. 89 17	-2. 317 158 395	-1. 212 356 667	2.3 17 15 83 95	D o w n	0.0 10 15 56 85	0.6 63 32 74 04
23 46 4	GCA T	Glycine C-acetyltransferase	6. 97 45 9	7. 01 75 7	7. 07 41 2	6. 38 79 3	5. 95 23 6	6. 91 58 8	-1. 519 261 276	-0. 603 37 276	1.5 19 26 12 76	D o w n	0.0 48 53 34 26	0.6 63 32 74 04
64 42 3	INF2	Inverted formin, FH2 and WH2 domain containing	8. 74 29 9	8. 44 91 3	8. 25 53 7	7. 37 59	8. 11 17	7. 88 04 3	-1. 616 813 568	-0. 693 153 333	1.6 16 81 35	D o w n	0.0 22 85 52	0.6 63 32 74

											68		87	04
86	KCN	Potassium channel,	10	10	10	9.	9.	10	-1.	-0.	1.6	D	0.0	0.6
45	K5	two pore domain	.8	.3	.7	40	90	.3	692	758	92	o	21	63
		subfamily K,	17	62	06	11	48	03	270	96	27	w	68	32
		member 5	14	54	55	5	6	34	273		02	n	96	74
											73		7	04
18	JAG1	Jagged 1	3.	3.	4.	6.	5.	4.	2.9	1.5	2.9	U	0.0	0.6
2			91	31	21	49	40	25	720	714	72	p	22	63
			34	21	69	20	50	98	945	8	09		61	32
			3	9	2	8	9	1	24		45		51	74
											24		32	04
66	SPIN	Serine peptidase	9.	9.	9.	8.	8.	9.	-1.	-0.	1.6	D	0.0	0.6
92	T1	inhibitor, Kunitz	83	53	27	37	78	22	685	753	85	o	22	63
		type 1	61	20	17	25	45	25	873	496	87	w	92	32
			9	6	9	1	2	2	943	667	39	n	28	74
											43		31	04
60	RGS	Regulator of	3.	4.	3.	4.	4.	4.	1.9	0.9	1.9	U	0.0	0.6
03	13	G-protein signaling	53	12	34	56	69	60	428	581	42	p	02	63
		13	89	14	01	84	96	69	753	933	87		60	32
			2	4		5	5	4	35	33	53		88	74
											35		53	04
56	ANK	Ankyrin repeat and	5.	5.	4.	4.	4.	4.	-1.	-0.	1.7	D	0.0	0.6
89	S1B	sterile $\alpha$ motif	81	54	80	12	62	91	781	833	81	o	33	63
9		domain containing	93	49	19	53	58	49	879	4	87	w	09	32
		1B	5	6	9	3	4	3	775		97	n	85	74
											75		14	04
2	A2M	A-2-macroglobulin	8.	10	10	11	11	10	2.8	1.5	2.8	U	0.0	0.6
			86	.4	.0	.6	.3	.9	836	279	83	p	08	63
			74	97	69	96	94	27	978	2	69		83	32



			4		7	44	39	07	32		78		28	74
											32		37	04
46	MYH	Myosin, heavy	6.	6.	7.	7.	7.	7.	1.5	0.6	1.5	U	0.0	0.6
27	9	chain 9,	87	53	05	99	19	22	676	486	67	p	45	63
		non-muscle	01	83	71	50	43	21	860	366	68		71	32
			7			5		3	47	67	60		53	74
											47		08	04
12	COL	Collagen, type IV,	7.	7.	7.	6.	6.	6.	-1.	-0.	1.6	D	0.0	0.6
86	4A4	$\alpha$ 4	55	08	08	41	20	82	694	761	94	o	12	63
			29	99	92	00	90	97	739	063	73	w	40	32
			6	1	3	8	4	9	266	333	92	n	70	74
											66		36	04
38	VGL	Vestigial like	3.	4.	4.	6.	4.	4.	2.2	1.1	2.2	U	0.0	0.6
91	L3	family member 3	50	82	21	26	85	97	678	813	67	p	38	63
36			21	95	73	28	50	51	260	1	82		17	32
			1	8	7	2	4	3	74		60		93	74
											74		41	04
12	COL	Collagen, type V, $\alpha$	5.	7.	5.	9.	7.	7.	3.6	1.8	3.6	U	0.0	0.6
89	5A1	1	14	14	88	61	11	09	847	815	84	p	47	63
			93	91	79	96	22	94	583	7	75		33	32
			9	9	9	2	1	5	27		83		83	74
											27		33	04
79	GAL	Polypeptide	5.	5.	5.	3.	5.	4.	-2.	-1.	2.5	D	0.0	0.6
62	NT14	N-acetylgalactosa	92	69	37	31	30	37	516	331	16	o	24	63
3		minyltransferase	63	66	16	83	95	24	490	413	49	w	99	32
		14	4			5	3	2	817	333	08	n	78	74
											17		28	04
48	NGF	Nerve growth	4.	5.	4.	5.	5.	5.	1.6	0.6	1.6	U	0.0	0.6
04	R	factor receptor	56	08	83	70	80	03	156	921	15	p	28	63

			02 4	12 1	32 5	42 7	90 1	77 4	410 04	066 67	64 10 04		36 01 45	32 74 04
84 81	OFD 1	Oral-facial-digital syndrome 1	8. 23 83 3	8. 20 41 7	7. 77 10 7	7. 00 12 6	7. 25 09 6	7. 44 60 8	-1. 788 119 721	-0. 838 443 333	1.7 88 11 97 21	D o w n	0.0 04 40 29 09	0.6 63 32 74 04
56 14 5	PCD HA3	Protocadherin $\alpha$ 3	7. 44 20 9	7. 73 45 2	6. 91 29 9	6. 53 69 2	6. 83 18 2	6. 80 31 1	-1. 557 526 454	-0. 639 256 667	1.5 57 52 64 54	D o w n	0.0 31 81 64 86	0.6 63 32 74 04
70 10	TEK	TEK tyrosine kinase, endothelial	4. 54 22 6	5. 20 05 1	5. 23 90 4	7. 11 55 2	7. 43 46 2	5. 53 31 2	3.2 500 832 36	1.7 004 766 67	3.2 50 08 32 36	U p	0.0 10 89 30 32	0.6 63 32 74 04
39 12	LAM B1	Laminin subunit $\beta$ 1	7. 83 61 5	8. 05 81 4	7. 44 67 4	9. 24 77 1	9. 22 03 6	8. 11 60 6	2.1 155 410 3	1.0 810 266 67	2.1 15 54 10 3	U p	0.0 15 58 09 12	0.6 63 32 74 04
55 92	PRK G1	Protein kinase, cgmp-dependent, type I	4. 25 21	4. 69 27 9	3. 46 62 7	6. 63 50 3	5. 10 50 3	4. 80 92 3	2.6 060 775 22	1.3 818 8 22	2.6 06 07 75 22	U p	0.0 33 04 09 31	0.6 63 32 74 04
12	MBO	Membrane bound	4.	4.	4.	5.	5.	4.	1.7	0.7	1.7	U	0.0	0.6

96	AT2	O-acyltransferase	75	46	67	85	69	70	284	894	28	p	36	63
42		domain containing	05	56	50	56	77	62	353	666	43		97	32
		2	8	4	1	2	6	5	79	67	53		54	74
											79		61	04
55	SCY	SCY1-like,	8.	7.	8.	7.	7.	7.	-1.	-0.	1.5	D	0.0	0.6
68	L2	kinase-like 2	47	84	07	13	59	74	555	637	55	o	32	63
1			32	43	71	33	91	96	667	533	66	w	67	32
			4	8	9	4	9	8	062	333	70	n	88	74
											62		21	04
55	ACS	Acyl-coa	8.	8.	8.	7.	8.	8.	-1.	-0.	1.5	D	0.0	0.6
90	S2	synthetase	76	67	44	71	00	19	573	654	73	o	09	63
2		short-chain family	02	17	94	99	38	52	619	086	61	w	54	32
		member 2			3	5	9	3	42	667	94	n	43	74
											2		91	04
94	AKA	A-kinase anchoring	8.	8.	9.	7.	7.	8.	-2.	-1.	2.2	D	0.0	0.6
65	P7	protein 7	93	77	37	51	90	10	280	189	80	o	01	63
			66	88	42	54	27	35	499	35	49	w	33	32
			2	8	4	8	1		731		97	n	11	74
											31		55	04
88	FCG	Fc fragment of igg	13	13	13	11	13	11	-2.	-1.	2.2	D	0.0	0.6
57	BP	binding protein	.2	.1	.2	.6	.1	.3	230	157	30	o	35	63
			20	26	97	28	72	71	195	17	19	w	01	32
			12	21	94	53	97	26	217		52	n	58	74
											17		6	04
23	ARH	Rho/Rac guanine	9.	9.	9.	8.	8.	9.	-1.	-0.	1.6	D	0.0	0.6
37	GEF	nucleotide	65	41	49	50	73	23	616	692	16	o	15	63
0	18	exchange factor 18	59	04	19	99	75	23	454	833	45	w	02	32
			4	9	8	8	5	8	987	333	49	n	07	74
											87		76	04

35	CXC	Chemokine	4.	4.	4.	5.	7.	4.	2.5	1.3	2.5	U	0.0	0.6
76	L8	(C-X-C motif) ligand 8	26	62	44	67	06	60	210	340	21	p	48	63
			59	09	47	27	04	05	359	166	03		23	32
			7	6	6	6	5	3	07	67	59		23	74
											07		84	04
22	PTG	Prostaglandin	10	9.	10	8.	9.	10	-2.	-1.	2.0	D	0.0	0.6
94	R1	reductase 1	.7	73	.4	65	06	.1	043	031	43	o	42	63
9			03	72	82	17	20	15	912	333	91	w	93	32
			51		9	3	3	85	355	333	23	n	06	74
											55		43	04
87	PAB	Poly(A) binding	6.	6.	6.	7.	6.	6.	1.9	0.9	1.9	U	0.0	0.6
61	PC4	protein,	02	02	63	99	84	81	868	904	86	p	27	63
		cytoplasmic	38	98	00	30	30	9	046	5	80		70	32
		(inducible form)	3	3	4	1	4		11		46		09	74
											11		33	04
40	M6P	Mannose-6-phosph	7.	6.	7.	8.	7.	7.	1.5	0.6	1.5	U	0.0	0.6
74	R	ate receptor (cation	23	83	50	01	64	77	391	221	39	p	24	63
		dependent)	33	69	88	77	84	93	281	133	12		33	32
			5	1	9	4	5		24	33	81		43	74
											24		08	04
57	KIA	KIAA1456	7.	7.	7.	5.	6.	7.	-2.	-1.	2.0	D	0.0	0.6
60	A145		59	01	49	46	43	07	058	041	58	o	36	63
4	6		59	48	86	94	76	75	523	61	52	w	14	32
			8	4	7	1	8	7	616		36	n	18	74
											16		57	04
26	HEY	Hes-related family	3.	4.	3.	5.	5.	4.	2.7	1.4	2.7	U	0.0	0.6
50	L	bhlh transcription	31	33	98	58	98	49	843	773	84	p	10	63
8		factor with YRPW	83	92	32	91	80	57	681	5	36		08	32
		motif-like	5	7	5	1	4	7	94		81		00	74

												94		6	04
22	DZIP	DAZ interacting	4.	5.	4.	6.	5.	5.	2.3	1.2	2.3	U	0.0	0.6	
87	1	zinc finger protein	16	06	45	34	97	02	233	162	23	p	15	63	
3		1	86	84	81	43	89	04	502	066	35		40	32	
			3	6	2	8	9	6	61	67	02		54	74	
											61		6	04	
51	RAS	RAS-like, family	4.	6.	5.	7.	6.	6.	3.1	1.6	3.1	U	0.0	0.6	
28	L12	12	31	26	04	51	66	40	445	528	44	p	15	63	
5			43	03	58	23	07	60	858	7	58		01	32	
			3	5	7	7	1	8			58		01	74	
													04	04	
40	TNF	TNFSF12-TNFSF1	10	10	11	10	9.	10	-1.	-0.	1.5	D	0.0	0.6	
79	SF12	3 readthrough	.7	.3	.0	.0	86	.3	566	647	66	o	25	63	
77	-TNF		36	75	80	39	36	48	067	146	06	w	13	32	
	SF13		66	99	84	84	1	6	793	667	77	n	84	74	
											93		39	04	
40	SAM	Sterile $\alpha$ motif	8.	8.	8.	7.	8.	8.	-1.	-0.	1.5	D	0.0	0.6	
14	D12	domain containing	76	75	66	79	15	41	524	608	24	o	16	63	
74		12	54	40	80	26	63	32	613	443	61	w	29	32	
			1	8	9	4	2	9	265	333	32	n	39	74	
											65		89	04	
10	EDA	Ectodysplasin A	4.	5.	5.	6.	5.	5.	1.6	0.6	1.6	U	0.0	0.6	
91	R	receptor	96	43	20	18	96	53	152	917	15	p	17	63	
3			27	95	40	65	36	14	490	566	24		56	32	
			4	5	7	4	7	2	95	67	90		00	74	
											95		35	04	
39	FAD	Fatty acid	4.	6.	5.	7.	6.	5.	2.0	1.0	2.0	U	0.0	0.6	
92	S1	desaturase 1	85	34	35	02	78	95	971	684	97	p	43	63	
			79	15	68	95	09	11	160	066	11		20	32	



86	EIF3	Eukaryotic	8.	7.	8.	9.	8.	8.	1.8	0.8	1.8	U	0.0	0.6
67	H	translation	22	42	41	33	35	93	101	561	10	p	40	63
		initiation factor 3	77	12	21	86	84	24	843	366	18		99	32
		subunit H	7	8	4	7	6	7	97	67	43		56	74
											97		94	04
18	GPR	G protein-coupled	2.	4.	4.	5.	4.	4.	2.4	1.2	2.4	U	0.0	0.6
80	183	receptor 183	82	43	00	51	88	73	487	920	48	p	17	63
			90	03	06	69	24	68	859	666	78		92	32
			3		5	5	3		4	67	59		77	74
											4		05	04
64	AID	Axin interactor,	4.	4.	5.	5.	5.	5.	1.5	0.6	1.5	U	0.0	0.6
85	A	dorsalization	94	71	56	62	62	84	465	290	46	p	34	63
3		associated	21	11	34	92	97	47	069	133	50		40	32
			8		3	4	9	2	68	33	69		23	74
											68		68	04
55	TTC	Tetratricopeptide	8.	8.	8.	7.	7.	8.	-1.	-0.	1.6	D	0.0	0.6
02	38	repeat domain 38	63	26	42	61	23	36	631	705	31	o	49	63
0			43	47	79	58	06	30	011	766	011	w	10	32
			3	2		9	8	8	175	667	17	n	44	74
											5		12	04
33	ID1	Inhibitor of DNA	8.	6.	7.	8.	10	8.	4.3	2.1	4.3	U	0.0	0.6
97		binding 1,	42	81	01	93	.8	87	673	267	67	p	12	63
		dominant negative	79	58	72	60	31	35	152	466	31		05	32
		helix-loop-helix	4	4	4	6	62	8	27	67	52		08	74
		protein									27		22	04
57	LRC	Leucine-rich	3.	3.	3.	5.	4.	3.	2.2	1.1	2.2	U	0.0	0.6
63	H2	repeats and	32	11	00	03	17	74	544	727	54	p	07	63
1		calponin homology	10	47	15	89	52	15	622	833	46		16	32
		(CH) domain	2	2	7	4	2		19	33	22		65	74

		containing 2									19		95	04
34	IDH2	Isocitrate	6.	6.	5.	5.	5.	5.	-1.	-0.	1.5	D	0.0	0.6
18		dehydrogenase 2	57	58	96	82	67	81	518	602	18	o	24	63
		(NADP+),	83	20	44	77	63	30	390	543	39	w	43	32
		mitochondrial	6	4		5	3	9	986	333	09	n	14	74
											86		9	04
88	ST3	ST3 $\beta$ -galactoside	9.	8.	9.	7.	8.	8.	-1.	-0.	1.8	D	0.0	0.6
69	GAL	$\alpha$ -2,3-sialyltransfer	32	75	18	43	42	80	822	865	22	o	47	63
5		ase 5	08	68	70	73	49	49	450	88	45	w	02	32
			1	8	6			1	968		09	n	96	74
											68		96	04
91	NEX	Nexilin (F actin	3.	6.	4.	8.	5.	6.	4.7	2.2	4.7	U	0.0	0.6
62	N	binding protein)	51	17	35	59	96	28	975	622	97	p	35	63
4			85	66	72	10	81	01	128	866	51		64	32
			7	9	8	7	4	9	37	67	28		86	74
											37		68	04
40	HAC	3-hydroxyacyl-coa	3.	5.	4.	6.	5.	4.	2.5	1.3	2.5	U	0.0	0.6
14	D4	dehydratase 4	66	12	07	31	80	73	166	315	16	p	31	63
94			57	01	74	45	47	85	536	066	65		26	32
			7				4	5	24	67	36		27	74
											24		89	04
51	PEG	Paternally	4.	5.	5.	6.	6.	6.	1.7	0.7	1.7	U	0.0	0.6
78	3	expressed 3	75	83	75	16	22	31	219	840	21	p	33	63
			64	86	56	68	53	05	023	033	90		82	32
			7	6		6	3	5	55	33	23		65	74
											55		98	04
58	JAM	Junctional	4.	5.	5.	7.	6.	5.	2.9	1.5	2.9	U	0.0	0.6
49	2	adhesion molecule	04	05	16	00	82	15	785	746	78	p	21	63
4			12	01	89	20	66	53	289		52		97	32



			8	1	1	2	9	9	88		89		64	74
											88		85	04
55	ADI1	Acireductone	11	11	11	11	10	11	-1.	-0.	1.6	D	0.0	0.6
25		dioxygenase 1	.7	.6	.7	.0	.5	.5	634	708	34	o	28	63
6			88	60	58	02	30	48	485	836	48	w	40	32
			37	87	2		33	6	6	667	56	n	64	74
													49	04
15	FAA	Fatty acid amide	6.	6.	6.	5.	5.	5.	-1.	-0.	1.5	D	0.0	0.6
85	H2	hydrolase 2	21	21	13	40	57	56	597	676	97	o	02	63
84			77	77	36	19	24	66	773	063	77	w	32	32
			8	8	6	4	2	7	973	333	39	n	15	74
											73		71	04
57	ALP	A kinase 3	6.	5.	5.	4.	5.	4.	-1.	-0.	1.8	D	0.0	0.6
53	K3		34	54	63	47	47	95	832	873	32	o	28	63
8			08	34	65	57	27	06	555	856	55	w	62	32
			6	5	1	9	8	8	214	667	52	n	56	74
											14		77	04
23	SYT1	Synaptotagmin 11	4.	5.	4.	6.	6.	4.	2.6	1.4	2.6	U	0.0	0.6
20	1		00	43	17	85	15	83	593	110	59	p	44	63
8			90	57	64	87	85	70	002	466	30		44	32
			4	2	5	1	5	9	35	67	02		12	74
											35		15	04
25	TAB	TGF- $\beta$ activated	7.	7.	7.	6.	6.	7.	-1.	-0.	1.7	D	0.0	0.6
73	3	kinase 1/MAP3K7	89	01	13	20	26	05	789	839	89	o	36	63
97		binding protein 3	62	09	07	63	04	13	934	906	93	w	21	32
			7	1	1	7	5	5	341	667	43	n	00	74
											41		87	04
22	CPN	Copine II	6.	6.	6.	7.	7.	6.	1.5	0.6	1.5	U	0.0	0.6
11	E2		17	64	58	30	28	63	234	073	23	p	41	63

84			31	16	73	26	74	40	125	066	41		54	32
			5	6	3		2	4	3	67	25		18	74
											3		35	04
38	ZNF	Zinc finger protein	9.	8.	9.	6.	6.	8.	-4.	-2.	4.0	D	0.0	0.6
85	761	761	21	12	51	01	63	21	000	000	00	o	12	63
61			89	48	41	26	32	15	406	146	40	w	89	32
			3	6	8	8	6	9	667	667	66	n	52	74
											67		63	04
64	SELP	Selectin P	5.	5.	6.	6.	7.	6.	2.0	1.0	2.0	U	0.0	0.6
03			23	71	26	81	43	12	759	538	75	p	30	63
			41	42	09	03	93	10	955	033	99		511	32
			9		1	1	9	1	24	33	55		14	74
											24		7	04
83	MAD	MAD1 mitotic	6.	6.	7.	6.	6.	6.	-1.	-0.	1.6	D	0.0	0.6
79	1L1	arrest deficient-like	91	97	39	05	05	95	668	738	68	o	37	63
		1 (yeast)	57	39	27	63	69	38	359	43	35	w	50	32
			3	8	5	1	7	9	274		92	n	54	74
											74		83	04
23	ATP1	Atpase, class V,	8.	8.	8.	6.	7.	8.	-2.	-1.	2.4	D	0.0	0.6
12	0B	type 10B	89	84	07	22	39	27	471	305	71	o	37	63
0			02	90	21	63	49	48	025	11	02	w	50	32
			7	6	4	3	3	8	673		56	n	64	74
											73		48	04
13	RNF	Ring finger protein	6.	6.	6.	5.	5.	5.	-1.	-0.	1.6	D	0.0	0.6
80	183	183	35	03	12	87	08	47	613	689	13	o	20	63
65			11	83	00	49	8	68	212	936	21	w	20	32
			7	6	3	1		4	698	667	26	n	82	74
											98		42	04
51	RAB	RAB6B, member	3.	4.	4.	5.	5.	4.	1.6	0.7	1.6	U	0.0	0.6

56	6B	RAS oncogene family	99	66	39	11	50	54	302	051	30	p	42	63
0			17	60	37	66	75	26	614	033	26		87	32
			2	3	6	3	8	1	28	33	14		22	74
											28		38	04
55	ATF7	Activating transcription factor 7 interacting protein	4.	4.	4.	5.	5.	5.	1.5	0.6	1.5	U	0.0	0.6
72	IP		70	69	48	29	30	26	798	597	79	p	02	63
9			40	34	46	10	32	72	343	733	83		02	32
			7	8	7	2	6	6	91	33	43		19	74
											91		55	04
74	WAR	Tryptophanyl-trna synthetase	3.	2.	3.	4.	4.	4.	1.7	0.8	1.7	U	0.0	0.6
53	S		71	96	80	21	47	22	552	117	55	p	10	63
			39	72	39	95	36	71	866	066	28		44	32
			6	7	3	3	1	4	68	67	66		96	74
											68		56	04
38	SAM	Sterile $\alpha$ motif domain containing 5	8.	7.	7.	6.	6.	7.	-1.	-0.	1.7	D	0.0	0.6
94	D5		22	95	27	82	69	50	748	806	48	o	38	63
32			40	49	31	73	83	70	955	493	95	w	46	32
			9	7	2	8	1	1	198	333	51	n	32	74
											98		71	04
20	ENG	Endoglin	4.	6.	5.	7.	7.	6.	3.3	1.7	3.3	U	0.0	0.6
22			49	11	65	33	61	52	310	359	31	p	07	63
			17	80	71	90	14	42	415	733	04		09	32
			2	2	4	8	7	5	12	33	15		79	74
											12		54	04
57	NLG	Neurologin 4,	3.	3.	3.	5.	6.	4.	3.3	1.7	3.3	U	0.0	0.6
50	N4X	X-linked	13	81	24	08	12	17	303	356	30	p	07	63
2			03	19	53	95	56	94	104	566	31		47	32
			7	1	8	5	6	2	4	67	04		96	74
											4		39	04

10	SOR	Sorbin and SH3	7.	8.	8.	10	8.	9.	2.8	1.5	2.8	U	0.0	0.6
58	BS1	domain containing	27	76	14	.7	58	37	730	225	73	p	39	63
0		1	56	24	09	93	16	18	305	733	03		35	32
			6	7	8	34	6	3	49	33	05		19	74
											49		51	04
23	PAL	Palladin,	6.	8.	7.	10	8.	8.	2.8	1.4	2.8	U	0.0	0.6
02	LD	cytoskeletal	84	65	27	.2	52	46	184	949	18	p	47	63
2		associated protein	86	77	54	70	91	73	852	2	48		34	32
			4	6	1	04	9	4	16		52		37	74
											16		79	04
14	CSR	Cysteine and	6.	7.	6.	9.	7.	7.	2.8	1.5	2.8	U	0.0	0.6
65	P1	glycine rich protein	18	17	50	39	18	86	781	251	78	p	29	63
		1	92	74	44	44	45	75	397	366	13		06	32
			6		8	2	7	6	94	67	97		69	74
											94		77	04
84	ZMY	Zinc finger,	6.	7.	6.	5.	6.	6.	-1.	-0.	1.6	D	0.0	0.6
22	ND1	MYND-type	79	21	52	89	24	19	664	735	64	o	13	63
5	5	containing 15	40	96	41	41	50	24	832	376	83	w	00	32
			5		2	6	5	3	076	667	20	n	69	74
											76		36	04
37	KCN	Potassium channel,	9.	9.	9.	8.	8.	9.	-1.	-0.	1.5	D	0.0	0.6
84	Q1	voltage gated	55	32	22	62	51	07	546	628	46	o	16	63
		KQT-like	64	72	06	50	61	72	135	666	13	w	68	32
		subfamily Q,	6	9	7	7	2	3	401	667	54	n	82	74
		member 1									01		79	04
23	TME	Transmembrane	7.	6.	7.	8.	7.	7.	1.5	0.6	1.5	U	0.0	0.6
42	D3	p24 trafficking	35	85	81	25	92	87	973	756	97	p	38	63
3		protein 3	68	42	61	64	00	77	568	866	35		94	32
			2	8		7	7	2	71	67	68		25	74

											71		4	04
65	WAS	WAS protein	8.	8.	7.	7.	7.	7.	-1.	-0.	1.5	D	0.0	0.6
36	H7P	family homolog 7	71	39	93	33	98	74	583	662	83	o	38	63
35		pseudogene	93	44	59	68	36	07	159	806	15	w	99	32
			2	1	2	8	5		561	667	95	n	95	74
											61		13	04
63	ANO	Anoctamin 3	9.	8.	9.	7.	6.	8.	-2.	-1.	2.9	D	0.0	0.6
98	3		40	41	02	08	46	59	972	571	72	o	23	63
2			96	35	57	12	19	11	238	55	23	w	10	32
			1	5	3	3	1		735		87	n	33	74
											35		08	04
58	PVR	Poliovirus	9.	9.	9.	8.	9.	9.	-1.	-0.	1.6	D	0.0	0.6
19	L2	receptor-related 2	94	49	34	30	03	23	668	738	68	o	36	63
		(herpesvirus entry mediator B)	55	94	61	37	70	60	031	146	03	w	69	32
			7	6	8	1	1	5	654	667	16	n	94	74
											54		08	04
34	IGF2	Insulin like growth	6.	6.	7.	8.	8.	7.	2.3	1.2	2.3	U	0.0	0.6
81		factor 2	76	86	33	62	74	23	133	1	13	p	21	63
			55	78	06	01	29	09	763		37		90	32
			2	1	6	2	7		68		63		93	74
											68		35	04
10	GPN	Glycoprotein	2.	3.	3.	4.	3.	4.	1.6	0.7	1.6	U	0.0	0.6
45	MB	(transmembrane)	80	07	66	21	37	17	723	418	72	p	41	63
7		nmb	27	72	44	38	62	99	150	466	31		54	32
			4	2	6	2	1	3	52	67	50		16	74
											52		28	04
94	REC	Recq helicase-like	7.	7.	7.	6.	6.	6.	-1.	-0.	1.5	D	0.0	0.6
00	QL5	5	36	73	17	58	94	78	569	650	69	o	15	63
			04	53	09	22	89	41	672	463	67	w	00	32

			9	9		9	5	5	228	333	22	n	30	74
											28		11	04
25	PAM	Peptidase domain	4.	5.	5.	7.	6.	6.	2.6	1.4	2.6	U	0.0	0.6
89	R1	containing	91	69	53	69	43	29	780	211	78	p	09	63
1		associated with	94	82	82	37	10	46	755	966	07		90	32
		muscle		2	8	6	7	6	62	67	55		79	74
		regeneration 1									62		41	04
12	NIPA	Non imprinted in	8.	7.	7.	6.	7.	7.	-1.	-0.	1.7	D	0.0	0.6
36	1	Prader-Willi/Angel	40	66	80	70	01	72	754	810	54	o	37	63
06		man syndrome 1	92	08	62	92	45	06	017	663	01	w	35	32
			7	5	9	7	4	1	733	333	77	n	47	74
											33		5	04
27	AMY	Amylase, $\alpha$ 1A	8.	8.	8.	7.	7.	8.	-1.	-0.	1.6	D	0.0	0.6
6	1A	(salivary)	63	58	49	49	82	12	695	761	95	o	06	63
			92	12	99	12	35	14	126	393	12	w	00	32
			8	6	3	9	6	4	963	333	69	n	48	74
											63		73	04
96	KDM	Lysine (K)-specific	7.	7.	7.	6.	6.	6.	-1.	-0.	1.6	D	0.0	0.6
82	4A	demethylase 4A	04	71	10	03	67	91	679	747	79	o	36	63
			86	85	26	90	60	08	412	956	41	w	61	32
			7	9	2	4	8	9	542	667	25	n	49	74
											42		6	04
47	NFIL	Nuclear factor,	3.	4.	4.	5.	6.	5.	2.8	1.5	2.8	U	0.0	0.6
83	3	interleukin 3	95	88	07	97	28	14	319	017	31	p	04	63
		regulated	39	38	11	60	84	98	517	966	95		29	32
			1	6	4	5	1	4	13	67	17		44	74
											13		16	04
55	PPP3	Protein	6.	6.	6.	7.	7.	6.	1.5	0.6	1.5	U	0.0	0.6
30	CA	phosphatase 3,	34	29	76	33	34	75	960	744	96	p	22	63

		catalytic subunit, $\alpha$ isozyme	68 4	00 5	90 6	09 7	46 2	37 5	029 67	633 33	00 29 67		81 24 3	32 74 04
23	EPB4	Erythrocyte	2.	2.	3.	3.	3.	3.	1.5	0.6	1.5	U	0.0	0.6
13	1L3	membrane protein	94	74	32	69	46	77	605	420	60	p	07	63
6		band 4.1-like 3	48	55	82	85	67	93	089	166	50		51	32
			4	4	7	7	9	4	88	67	89		57	74
											88		33	04
79	MCT	Multiple C2	3.	5.	3.	6.	6.	4.	3.6	1.8	3.6	U	0.0	0.6
77	P1	domains,	00	07	05	15	06	55	778	788	77	p	24	63
2		transmembrane 1	46	78	22	63	22	29	517	633	85		67	32
			7	8	9		1	2	65	33	17		42	74
											65		86	04
28	IGK	Immunoglobulin $\kappa$	4.	3.	4.	5.	8.	8.	9.2	3.2	9.2	U	0.0	0.6
89	V1D-	variable 1D-33	13	77	06	43	05	11	351	071	35	p	02	63
6	33		79	90	70	04	72	77	154	3	11		29	32
			3	5	6	3	3	7	71		54		32	74
											71		51	04
57	AS3	Arsenite	7.	7.	8.	5.	4.	8.	-3.	-1.	3.8	D	0.0	0.6
41	MT	methyltransferase	93	81	68	47	96	19	818	933	18	o	45	63
2			68	55	91	93	83	47	536	02	53	w	45	32
			7	2	7	5	7	8	992		69	n	65	74
											92		54	04
19	CEL	Cadherin, EGF	7.	6.	6.	6.	6.	6.	-1.	-0.	1.6	D	0.0	0.6
52	SR2	LAG seven-pass	54	67	58	17	29	14	657	728	57	o	31	63
		G-type receptor 2	07	52	31	41	39	43	413	933	41	w	17	32
			6	7	8	2	7	2	218	333	32	n	21	74
											18		41	04
10	ZAS	ZO-2 associated	6.	6.	6.	5.	5.	6.	-1.	-0.	1.6	D	0.0	0.6

19	P	speckle protein	62	38	17	29	59	02	695	761	95	o	13	63
27			65	32	94	29	14	04	166	426	16	w	53	32
65			1	1	6	8	8	4	129	667	61	n	85	74
5											29		69	04
97	PIEZ	Piezo-type	7.	8.	7.	9.	8.	7.	1.9	0.9	1.9	U	0.0	0.6
80	O1	mechanosensitive	38	08	52	15	82	80	063	308	06	p	41	63
		ion channel	35	55	47	53	91	18	724	3	37		52	32
		component 1	6	4	3	5		7	4		24		77	74
											4		23	04
53	PMA	Phorbol-12-myrista	3.	3.	2.	3.	4.	3.	1.8	0.9	1.8	U	0.0	0.6
66	IP1	te-13-acetate-induc	32	07	56	50	41	76	753	071	75	p	14	63
		ed protein 1	10	72	71	14	79	75	328	466	33		51	32
			9	2	2	5		2	33	67	28		40	74
											33		91	04
32	HP	Haptoglobin	3.	3.	3.	4.	4.	3.	1.9	0.9	1.9	U	0.0	0.6
40			30	69	58	57	91	98	504	638	50	p	06	63
			14	55	69	50	79	24	675	2	46		05	32
			8	1	6	3		8	55		75		53	74
											55		13	04
27	GLI2	GLI family zinc	2.	3.	2.	6.	3.	4.	2.7	1.4	2.7	U	0.0	0.6
36		finger 2	69	91	90	01	73	13	441	563	44	p	48	63
			82	79	58	88	32	90	449	566	14		84	32
			7	8		8	2	2	08	67	49		26	74
											08		83	04
12	MIE	Mitochondrial	6.	6.	6.	6.	5.	5.	-1.	-0.	1.5	D	0.0	0.6
51	F2	elongation factor 2	83	55	36	00	82	95	580	660	80	o	07	63
70			72	33	41	10	05	24	360	253	36	w	55	32
			6	4	8	5	7		106	333	01	n	69	74
											06		64	04



12 81	COL 3A1	Collagen, type III, $\alpha$ 1	6. 02 62 6	8. 61 68 3	8. 06 12 9	11 .9 23 81	9. 09 15 7	9. 21 88 9	5.6 960 560 13	2.5 099 633 33	5.6 96 05 60 13	U p	0.0 30 19 13 82	0.6 63 32 74 04
11 36 12	CYP 2U1	Cytochrome P450, family 2, subfamily U, polypeptide 1	3. 74 87	4. 06 11 4	4. 14 07 4	5. 57 39	4. 70 04 1	4. 44 23 2	1.8 947 620 3	0.9 220 166 67 3	1.8 94 76 20 3	U p	0.0 17 35 18 62	0.6 63 32 74 04
10 15 7	AAS S	Amino adipate-semi aldehyde synthase	8. 81 97 5	8. 90 23 3	8. 03 05 1	7. 23 90 9	7. 02 60 1	8. 03 51	-2. 220 364 707	-1. 150 796 667	2.2 20 36 47 07	D o w n	0.0 11 87 43 88	0.6 63 32 74 04
11 06 7	C10o rf10	Chromosome 10 open reading frame 10	6. 13 05 1	5. 79 76 5	6. 43 74 2	8. 24 82 4	7. 23 07 7	6. 73 89 9	2.4 353 683 55	1.2 841 4	2.4 35 36 83 55	U p	0.0 13 08 72 92	0.6 63 32 74 04
80 31 0	PDG FD	Platelet derived growth factor D	5. 41 29 1	5. 20 46 5	6. 41 75 4	6. 98 22 5	6. 60 2 5	6. 29 76 9	1.9 304 626 83	0.9 489 466 67	1.9 30 46 26 83	U p	0.0 29 63 92 28	0.6 63 32 74 04
10 65 9	CEL F2	CUGBP, Elav-like family member 2	5. 92 84 4	6. 45 56 1	6. 03 10 5	7. 04 46 7	6. 85 66 7	6. 40 81 7	1.5 491 426 52	0.6 314 7	1.5 49 14 26	U p	0.0 30 39 50	0.6 63 32 74

											52		07	04
26	PLE	Pleckstrin	7.	7.	7.	6.	7.	7.	-1.	-0.	1.5	D	0.0	0.6
03	KHG	homology and	91	56	50	73	15	31	508	593	08	o	26	63
0	3	rhogef domain	51	72	71	75	95	19	909	506	90	w	70	32
		containing G3	8	1	6	5	8		905	667	99	n	41	74
											05		25	04
57	CAR	Carnosine synthase	8.	8.	8.	5.	7.	7.	-2.	-1.	2.2	D	0.0	0.6
57	NS1	1	26	10	39	97	55	67	277	187	77	o	30	63
1			46	88	83	90	54	46	629	533	62	w	51	32
			6			5	4	7	893	333	98	n	50	74
											93		21	04
57	NYN	NYN domain and	6.	6.	6.	5.	5.	5.	-1.	-0.	1.5	D	0.0	0.6
52	RIN	retroviral integrase	32	34	23	67	96	28	581	661	81	o	14	63
3		containing	07	74	78	19	42	48	894	653	89	w	24	32
			7	1	2	9	1	4	442	333	44	n	92	74
											42		19	04
25	PNK	Paroxysmal	8.	8.	8.	7.	7.	7.	-1.	-0.	1.7	D	0.0	0.6
95	D	nonkinesigenic	61	16	29	52	49	67	734	794	34	o	02	63
3		dyskinesia	18	58	68	19	71	15	616	616	61	w	60	32
			3	4	3	9		6	414	667	64	n	90	74
											14		87	04
10	RAM	Receptor (G	6.	6.	6.	8.	8.	6.	2.6	1.4	2.6	U	0.0	0.6
26	P3	protein-coupled)	23	83	22	29	31	90	572	099	57	p	10	63
8		activity modifying	22	16	16	45	77	29	058	1	20		68	32
		protein 3	2	7	4	3	5	8	58		58		37	74
											58		07	04
55	PAG	Phosphoprotein	7.	7.	7.	6.	6.	6.	-1.	-0.	1.6	D	0.0	0.6
82	1	membrane anchor	62	08	33	59	37	96	626	701	26	o	16	63
4		with	64	32	00	70	25	59	085	403	08	w	67	32

		glycosphingolipid microdomains 1	3	7	4	3	1	9	744	333	57	n	53	74
											44		88	04
23	LY96	Lymphocyte antigen 96	4.	6.	5.	7.	7.	6.	2.5	1.3	2.5	U	0.0	0.6
64			79	16	98	64	08	21	221	346	22	p	25	63
3			94	70	18	54	90	77	603	6	16		36	32
				3	8	1	9	9	5		03		01	74
											5		79	04
14	TME	Transmembrane protein 99	8.	8.	8.	7.	7.	7.	-1.	-0.	1.7	D	0.0	0.6
71	M99		40	00	10	27	54	36	714	778	14	o	03	63
84			92	34	80	52	22	87	946	163	94	w	01	32
			5	6	4	4	3	9	218	333	62	n	07	74
											18		3	04
63	SCN	Sodium channel, voltage gated, type IV $\beta$ subunit	3.	4.	4.	5.	5.	4.	1.9	0.9	1.9	U	0.0	0.6
30	4B		38	53	22	35	35	30	423	578	42	p	42	63
			04	10	30	07	07	65	591	1	35		86	32
			6	3	3			5	69		91		88	74
											69		07	04
30	HAB	Hyaluronan binding protein 2	10	10	10	8.	9.	10	-1.	-0.	1.7	D	0.0	0.6
26	P2		.3	.3	.3	84	65	.1	749	806	49	o	39	63
			98	73	05	19	06	64	339	81	33	w	63	32
			33	76	74	8	4	78	13		91	n	71	74
											3		72	04
15	CYP	Cytochrome P450, family 2, subfamily C, polypeptide 9	9.	9.	9.	7.	8.	9.	-2.	-1.	2.1	D	0.0	0.6
59	2C9		69	83	92	89	61	71	110	077	10	o	39	63
			72	05	98	21	33	90	668	7	66	w	18	32
			4	7	3	1	8	5	488		84	n	04	74
											88		36	04
10	LOC	Uncharacterized	7.	7.	7.	6.	6.	6.	-1.	-0.	1.5	D	0.0	0.6
53	1053	LOC105379278	49	64	07	85	68	88	511	595	11	o	18	63

79	7927		63	48	38	24	84	76	010	513	01	w	43	32
27	8		6	5	5	1	4	7	131	333	01	n	06	74
8											31		8	04
10	CAL	Calcitonin receptor	4.	4.	4.	6.	6.	4.	2.5	1.3	2.5	U	0.0	0.6
20	CRL	like receptor	13	73	61	16	70	65	383	438	38	p	31	63
3			45	97	21	26	34	19	540	933	35		45	32
			5	2	1	6	3	7	9	33	40		73	74
											9		37	04
84	ZNF	Zinc finger protein	5.	4.	4.	3.	4.	4.	-1.	-0.	1.5	D	0.0	0.6
43	528	528	10	87	88	86	38	83	509	593	09	o	49	63
6			98	83	09	52	57	67	181	766	18	w	85	32
				8	1	7	7	5	862	667	18	n	99	74
											62		47	04
14	CRY	Crystallin $\alpha$ B	7.	8.	7.	9.	9.	8.	2.3	1.2	2.3	U	0.0	0.6
10	AB		28	39	56	54	39	03	639	412	63	p	31	63
			86	46	15	03	68	12	617	066	96		21	32
			9	2	9	8	5	9	08	67	17		05	74
											08		61	04
10	LY75	LY75-CD302	6.	7.	7.	8.	8.	8.	1.9	0.9	1.9	U	0.0	0.6
05	-CD3	readthrough	91	27	69	36	28	08	317	498	31	p	04	63
26	02		19	82	17	37	02	75	030	733	70		11	32
66			2	9		2	3	8	49	33	30		47	74
4											49		26	04
84	CAS	Calsequestrin 2	4.	4.	3.	5.	4.	5.	1.9	0.9	1.9	U	0.0	0.6
5	Q2		12	57	82	37	93	16	758	825	75	p	03	63
			57	64	97	63	42	89	955	066	89		32	32
			7	9	2	2	7	1	25	67	55		69	74
											25		7	04
27	AMY	Amylase, $\alpha$ 1C	8.	8.	8.	7.	7.	8.	-1.	-0.	1.6	D	0.0	0.6

8	1C	(salivary)	63 92 8	58 12 6	49 99 3	49 12 9	82 35 6	12 14 4	695 126 963	761 393 333	95 12 69 63	o w n	06 00 48 73	63 32 74 04
19 60	EGR 3	Early growth response 3	5. 67 63 3	5. 37 65 6	5. 26 57 8	6. 62 62	9. 45 73 2	7. 51 62 9	5.3 779 139 32	2.4 270 466 67	5.3 77 91 39 32	U p	0.0 07 46 36 26	0.6 63 32 74 04
28 69	GRK 5	G protein-coupled receptor kinase 5	5. 04 83 1	5. 76 66 8	6. 03 06	7. 46 46 1	6. 79 45 8	6. 13 57 8	2.2 706 415 88	1.1 831	2.2 70 64 15 88	U p	0.0 19 03 73 99	0.6 63 32 74 04
59 99	RGS 4	Regulator of G-protein signaling 4	3. 70 42	4. 88 48 5	4. 37 24 7	7. 29 12 9	5. 04 49 4	5. 19 24 6	2.8 726 654 76	1.5 223 9	2.8 72 66 54 76	U p	0.0 43 51 52 64	0.6 63 32 74 04
25 85 4	FAM 149A	Family with sequence similarity 149 member A	9. 32 81 2	8. 70 64 9	8. 83 56 8	8. 06 44 3	8. 34 10 2	8. 44 05 3	-1. 596 342 257	-0. 674 77	1.5 96 34 22 57	D o w n	0.0 16 21 82 39	0.6 63 32 74 04
64 94 3	NT5 DC2	5'-nucleotidase domain containing 2	3. 99 87 3	5. 18 84 3	4. 14 00 7	7. 44 06 3	6. 34 25	4. 84 54 6	3.4 037 380 21	1.7 671 2	3.4 03 73 80 21	U p	0.0 29 50 66 12	0.6 63 32 74 04

27	GNA	GNAS complex	9.	9.	10	10	10	10	1.5	0.5	1.5	U	0.0	0.6
78	S	locus	85	65	.5	.5	.6	.6	090	935	09	p	44	63
			24	99	55	99	29	19	040	966	00		92	32
			7		42	71	14	73	38	67	40		60	74
											38		44	04
41	MC	Minichromosome	3.	3.	4.	4.	5.	4.	1.7	0.8	1.7	U	0.0	0.6
71	M2	maintenance	70	67	05	28	24	33	545	110	54	p	21	63
		complex	06	51	52	64	02	75	203	766	52		43	32
		component 2	3	8	3	3	6	8	32	67	03		61	74
											32		92	04
39	LAM	Laminin subunit $\alpha$	4.	6.	5.	8.	6.	6.	2.7	1.4	2.7	U	0.0	0.6
10	A4	4	83	61	87	03	75	84	005	332	00	p	27	63
			49	67	92	31	35	39	314	433	53		84	32
			5	4	3		9	6	19	33	14		49	74
											19		22	04
81	FAH	Fumarylacetoacetat	9.	9.	9.	8.	8.	9.	-1.	-0.	1.9	D	0.0	0.6
88	D1	e hydrolase domain	96	40	93	58	62	25	928	947	28	o	07	63
9		containing 1	63	90	21	33	37	86	220	27	22	w	11	32
			2	5	6	7	5		448		04	n	09	74
											48		51	04
41	MAP	Microtubule	3.	5.	4.	6.	5.	4.	2.9	1.5	2.9	U	0.0	0.6
31	1B	associated protein	47	11	27	93	84	74	252	485	25	p	38	63
		1B	97	22	75	14	20	16	163	433	21		52	32
			3		3	4	5		55	33	63		34	74
											55		64	04
55	GPR	G protein-coupled	9.	9.	9.	7.	8.	8.	-2.	-1.	2.0	D	0.0	0.6
89	C5C	receptor, class C,	54	19	04	44	49	77	033	023	33	o	22	63
0		group 5, member C	86	80	15	91	24	54	225	77	22	w	64	32
			9	8	8	8		6	176		51	n	27	74

												76		79	04
34	ZNF	Zinc finger protein	5.	5.	5.	4.	4.	5.	-1.	-0.	1.7	D	0.0	0.6	
54	879	879	76	20	49	46	60	06	711	775	111	o	10	63	
62			38	06	22	06	73	38	190		90	w	75	32	
			9	3	6	3	3	2	051		05	n	84	74	
											1		74	04	
84	TEA	TEA domain	5.	6.	5.	7.	7.	6.	2.3	1.2	2.3	U	0.0	0.6	
63	D2	family member 2	24	46	75	48	60	10	667	428	66	p	33	63	
			10	56	85	51	36	51	161	866	71		80	32	
			1	9	5	4		7	15	67	61		32	74	
											15		01	04	
99	DLE	Deleted in lung and	4.	4.	4.	3.	3.	3.	-1.	-0.	1.5	D	0.0	0.6	
40	C1	esophageal cancer	37	39	28	63	78	78	531	615	31	o	01	63	
		1	24	20	65	86	17	50	749	18	74	w	10	32	
			7	2		8	6	1	096		90	n	84	74	
											96		89	04	
10	N4B	NEDD4 binding	9.	8.	8.	7.	7.	8.	-2.	-1.	2.3	D	0.0	0.6	
44	P2L2	protein 2-like 2	24	92	60	44	39	22	361	239	61	o	03	63	
3			39	97	35	23	29	30	335	603	33	w	13	32	
			5	8		7	9	6	988	333	59	n	25	74	
											88		32	04	
38	KLK	Kallikrein B1	8.	7.	7.	5.	6.	7.	-2.	-1.	2.6	D	0.0	0.6	
18	B1		25	63	76	65	22	49	693	429	93	o	16	63	
			67	27	68	49	08	15	944	72	94	w	43	32	
			6	9	9	2	3	3	259		42	n	67	74	
											59		1	04	
94	HAN	Heart and neural	6.	8.	7.	10	9.	8.	4.6	2.2	4.6	U	0.0	0.6	
64	D2	crest derivatives	10	60	04	.2	72	42	884	291	88	p	15	63	
		expressed 2	12	73	13	87	84	16	899	233	48		88	32	

			1	2	1	12	3	6	28	33	99		53	74
											28		19	04
55	TME	Transmembrane	9.	8.	8.	8.	8.	8.	-1.	-0.	1.5	D	0.0	0.6
09	M51	protein 51	44	86	89	26	31	62	592	671	92	o	16	63
2			39	82	84	08	22	25	919	673	91	w	15	32
			9		4	1	2	8	47	333	94	n	16	74
											7		14	04
79	TMC	Transmembrane	8.	7.	7.	6.	6.	7.	-1.	-0.	1.6	D	0.0	0.6
83	5	channel like 5	09	73	52	80	80	59	641	715	41	o	34	63
8			93	15	75	76	55	95	744	23	74	w	64	32
			5	6	1	6	4	3	93		49	n	21	74
											3		93	04
27	PDLI	PDZ and LIM	3.	4.	3.	8.	4.	5.	5.0	2.3	5.0	U	0.0	0.6
29	M3	domain 3	27	46	56	06	38	84	455	350	45	p	30	63
5			34	53	01	87	95	57	795	2	57		14	32
			9	3	8	8	8		81		95		53	74
											81		72	04
51	EIF3	Eukaryotic	7.	7.	8.	9.	8.	8.	1.9	0.9	1.9	U	0.0	0.6
38	L	translation	99	62	39	45	44	92	174	392	17	p	18	63
6		initiation factor 3	23	30	74	88	74	40	691	033	46		88	32
		subunit L	1	2		3	5	6	06	33	91		56	74
											06		09	04
46	NAIP	NLR family,	5.	6.	5.	6.	6.	6.	1.5	0.6	1.5	U	0.0	0.6
71		apoptosis	32	11	77	64	34	15	649	461	64	p	33	63
		inhibitory protein	23	15	08	21	77	31	356	033	93		96	32
			5	2	8	9	3	4	48	33	56		39	74
											48		74	04
23	NFA	Neurofascin	4.	5.	4.	7.	6.	6.	3.2	1.7	3.2	U	0.0	0.6
11	SC		30	80	87	94	01	17	800	137	80	p	22	63



4			95	88	92	38	80	69	701	266	07		37	32
			9	7	1	5	3	7	43	67	01		64	74
											43		43	04
27	DIM	DIM1	6.	6.	6.	7.	6.	6.	1.5	0.6	1.5	U	0.0	0.6
29	T1	dimethyladenosine	20	15	53	24	98	51	333	166	33	p	32	63
2		transferase 1	29	67	40	44	47	45	177	566	31		03	32
		homolog	8	7	3	3	8	4	16	67	77		12	74
											16		42	04
30	HIP1	Huntingtin	4.	4.	4.	5.	5.	4.	1.8	0.9	1.8	U	0.0	0.6
92		interacting protein	06	47	10	73	23	39	687	020	68	p	30	63
		1	68	41	62	16	04	13	755	933	77		54	32
			4	2	1	8	7		88	33	55		18	74
											88		28	04
71	TNN	Troponin I type 2	10	10	9.	6.	7.	9.	-3.	-1.	3.5	D	0.0	0.6
36	I2	(skeletal, fast)	.2	.1	09	79	64	50	590	844	90	o	29	63
			03	78	87	93	24	61	280	096	28	w	57	32
			52	03	2	3	9	6	759	667	07	n	30	74
											59		83	04
74	TRP	Transient receptor	5.	5.	5.	5.	5.	5.	-1.	-0.	1.5	D	0.0	0.6
42	V1	potential cation	88	89	76	23	11	35	533	617	33	o	04	63
		channel, subfamily	85	68	87	17	95	10	927	23	92	w	10	32
		V, member 1	6		1	7	6	5	185		71	n	38	74
											85		71	04
31	NR4	Nuclear receptor	8.	6.	7.	8.	11	9.	5.9	2.5	5.9	U	0.0	0.6
64	A1	subfamily 4 group	48	95	16	83	.5	95	432	712	43	p	08	63
		A member 1	25	38	75	11	36	05	964	633	29		29	32
			5	7	5	7	07	2	06	33	64		11	74
											06		28	04
70	TFD	Transcription	8.	8.	8.	7.	7.	8.	-1.	-0.	1.8	D	0.0	0.6

29	P2	factor Dp-2 (E2F dimerization partner 2)	61 78 6	80 78 5	64 74 7	63 42 5	31 88 2	35 56 2	894 079 212	921 496 667	94 07 92 12	o w n	11 71 14 46	63 32 74 04
44 00 34	Dkfz p686 k168 4	Uncharacterized LOC440034	4. 19 20 5	4. 23 30 9	4. 54 16 1	5. 92 43 8	5. 09 71 8	4. 64 42 9	1.8 656 435 01	0.8 996 733 33	1.8 65 64 35 01	U p	0.0 25 99 45 88	0.6 63 32 74 04
91 66 3	MYA DM	Myeloid-associated differentiation marker	7. 18 16 2	8. 07 74 1	8. 00 45 4	9. 99 43 4	8. 81 61 4	8. 42 78 6	2.5 051 725 92	1.3 249 1 92	2.5 05 17 25 92	U p	0.0 19 25 54 94	0.6 63 32 74 04
51 38	PDE 2A	Phosphodiesterase 2A	5. 86 45 6	6. 78 25	6. 72 79	7. 63 29 1	8. 16 58 3	6. 82 40 3	2.1 178 542 89	1.0 826 033 33	2.1 17 85 42 89	U p	0.0 28 98 28 76	0.6 63 32 74 04
31 18	HLA -DQ A2	Major histocompatibility complex, class II, DQ $\alpha$ 2	7. 16 46	6. 85 72 4	6. 48 57 4	7. 73 24 1	7. 87 64 6	7. 13 24 2	1.6 754 748 14	0.7 445 7 48 14	1.6 75 47 48 14	U p	0.0 26 47 72 27	0.6 63 32 74 04
63 66	CCL 21	Chemokine (C-C motif) ligand 21	4. 47 66 9	6. 62 76 5	5. 96 48 8	7. 86 15 8	7. 19 60 5	7. 18 96 8	3.3 081 622 64	1.7 260 3 64	3.3 08 16 22 64	U p	0.0 13 61 65 65	0.6 63 32 74 04

13	DPC	Diffuse	9.	8.	9.	8.	7.	8.	-2.	-1.	2.0	D	0.0	0.6
56	R1	panbronchiolitis	01	59	54	01	96	11	031	022	31	o	04	63
56		critical region 1	87	89	94	66	56	73	436	5	43	w	64	32
				7	5	1	2	9	122		61	n	45	74
											22		15	04
47	GIM	Gtpase, IMAP	4.	4.	5.	6.	6.	4.	2.2	1.1	2.2	U	0.0	0.6
43	AP6	family member 6	34	25	14	27	08	97	910	960	91	p	19	63
44			13	82	43	12	72	35	887	333	08		21	32
			5	9	6	8	4	8	31	33	87		53	74
											31		47	04
55	STA	Signal transducing	8.	8.	8.	7.	7.	7.	-1.	-0.	1.5	D	0.0	0.6
62	P2	adaptor family	08	16	04	09	45	89	531	614	31	o	28	63
0		member 2	61	72	75	81	91	95	236	696	23	w	70	32
			7	8	6	4	9	9	014	667	60	n	54	74
											14		45	04
11	MAR	Membrane	6.	5.	6.	4.	5.	5.	-1.	-0.	1.9	D	0.0	0.6
51	CH3	associated	83	71	16	97	03	82	945	960	45	o	28	63
23		ring-CH-type	25	60	07	25	00	64	404	07	40	w	55	32
		finger 3	3	1	7	5	6	9	284		42	n	53	74
											84		76	04
26	GCH	GTP	8.	7.	8.	6.	6.	7.	-2.	-1.	2.0	D	0.0	0.6
44	FR	cyclohydrolase I	67	63	02	36	93	91	052	037	52	o	47	63
		feedback regulator	23	87	22	90	90	29	520	396	52	w	36	32
			3	8	1	7	9	7	55	667	05	n	08	74
											5		46	04
28	CYP	Cytochrome P450,	5.	4.	4.	4.	4.	3.	-1.	-0.	1.5	D	0.0	0.6
54	4V2	family 4, subfamily	12	59	23	19	21	59	571	652	71	o	48	63
40		V, polypeptide 2	83	58	50	04	43	68	926	533	92	w	20	32
			2	3	6		2	9	033	333	60	n	81	74

												33		91	04
15	ATP6	Atpase, H+	8.	8.	8.	7.	7.	8.	-1.	-0.	1.7	D	0.0	0.6	
50	V0E2	transporting V0	44	52	13	10	43	04	787	838	87	o	15	63	
66		subunit e2	03	28	05	58	28	05	780	17	78	w	55	32	
			9	6	7	8	4	9	976		09	n	24	74	
											76		91	04	
99	DGC	Digeorge syndrome	8.	7.	8.	7.	7.	7.	-1.	-0.	1.5	D	0.0	0.6	
93	R2	critical region gene	18	86	06	22	39	46	598	676	98	o	04	63	
		2	98	65	14	57	38	87	242	486	24	w	40	32	
			2	2	4	7	2	3	88	667	28	n	64	74	
											8		99	04	
84	PPFI	PTPRF interacting	3.	3.	4.	5.	4.	4.	1.7	0.8	1.7	U	0.0	0.6	
96	BP1	protein, binding	70	87	09	54	47	15	770	294	77	p	48	63	
		protein 1 (liprin $\beta$	96	41	28	07	08	35	447	8	04		02	32	
		1)	8		2			4	35		47		61	74	
											35		78	04	
44	MT1	Metallothionein 1H	9.	8.	9.	7.	5.	8.	-4.	-2.	4.0	D	0.0	0.6	
96	H		64	88	18	80	53	36	012	004	12	o	22	63	
			14	54	44	1	13	56	375	456	37	w	57	32	
			3	8	3		5	2	609	667	56	n	44	74	
											09		88	04	
57	STI	Stromal interaction	7.	6.	7.	6.	6.	6.	-1.	-0.	1.6	D	0.0	0.6	
62	M2	molecule 2	21	69	12	28	02	67	610	687	10	o	21	63	
0			56	88	83	04	20	67	899	866	89	w	51	32	
			6		1	1	3	3	696	667	96	n	72	74	
											96		57	04	
32	HSD	Hydroxysteroid	6.	6.	6.	4.	5.	6.	-2.	-1.	2.1	D	0.0	0.6	
93	17B3	(17- $\beta$ )	70	59	64	72	75	24	101	071	01	o	22	63	
		dehydrogenase 3	36	70	33	36	88	77	287	273	28	w	39	32	

			3	6	7	1	5	8	161	333	71	n	37	74
											61		48	04
84	RGS	Regulator of	4.	5.	5.	8.	8.	6.	7.8	2.9	7.8	U	0.0	0.6
90	5	G-protein signaling	53	28	70	80	97	64	256	682	25	p	02	63
		5	38	54	33	88	19	65	106	033	61		31	32
			8	5	7	2	2	7	51	33	06		52	74
											51		53	04
19	EGR	Early growth	4.	4.	4.	7.	7.	7.	6.9	2.7	6.9	U	1.8	0.1
59	2	response 2	30	99	09	01	56	20	590	988	59	p	30	19
			75	15	67	96	36	93	803	966	08		31	19
			8	3	2	2			58	67	03		E-0	56
											58		5	43
64	POL	Polymerase (RNA)	4.	4.	4.	5.	4.	4.	1.6	0.6	1.6	U	0.0	0.6
42	R1E	I polypeptide E	04	22	53	39	80	64	076	849	07	p	22	63
5			00	33	00	65	71	45	499	533	64		99	32
			9	5	1	5	7	9	78	33	99		36	74
											78		1	04
10	RAB	RAB40B, member	8.	7.	7.	7.	7.	7.	-1.	-0.	1.5	D	0.0	0.6
96	40B	RAS oncogene	31	88	94	58	13	66	502	587	02	o	27	63
6		family	70	22	10	47	20	05	817	67	81	w	60	32
			9		5		8	5	686		76	n	17	74
											86		83	04
28	CES4	Carboxylesterase	3.	3.	4.	2.	3.	3.	-1.	-0.	1.6	D	0.0	0.6
38	A	4A	81	91	10	68	22	87	604	682	04	o	48	63
48			36	56	62	18	78	86	829	42	82	w	45	32
			8	2	1		2	3	466		94	n	40	74
											66		21	04
22	FCG	Fc fragment of igg,	5.	6.	5.	6.	6.	6.	1.8	0.8	1.8	U	0.0	0.6
12	R2A	low affinity iia,	07	37	77	81	79	29	633	979	63	p	33	63

		receptor (CD32)	52 1	17 6	02 4	95 4	57 1	56 8	775 28	2	37 75 28		49 89 37	32 74 04
12 77 03	C1orf 216	Chromosome 1 open reading frame 216	5. 55 46 2	5. 91 89 2	5. 69 44 7	7. 10 56 4	6. 33 34 5	5. 92 88 5	1.6 624 489 05	0.7 333 1	1.6 62 44 89 05	U p	0.0 47 57 98 75	0.6 63 32 74 04
34 25 38	NAC A2	Nascent polypeptide-associ ated complex $\alpha$ subunit 2	9. 71 90 5	9. 29 93 6	10 .1 36 06	10 .7 26 41	10 .1 91 68	10 .2 03 59	1.5 754 201 86	0.6 557 366 67	1.5 75 42 01 86	U p	0.0 40 37 88 97	0.6 63 32 74 04
95 86	CRE B5	Camp responsive element binding protein 5	8. 18 14 3	7. 27 37 5	7. 63 15 5	6. 85 09 6	6. 80 51 7	7. 36 54 9	-1. 611 461 812	-0. 688 37	1.6 11 46 18 12	D o w n	0.0 42 32 68 55	0.6 63 32 74 04
28 4	ANG PT1	Angiopietin 1	4. 88 31 7	6. 66 76 8	5. 35 14 8	7. 64 72 7	6. 91 77 6	6. 64 90 5	2.7 080 417 85	1.4 372 5	2.7 08 04 17 85	U p	0.0 20 50 84 86	0.6 63 32 74 04
83 53 9	CHS T9	Carbohydrate (N-acetylgalactosa mine 4-0) sulfotransferase 9	5. 75 41 3	4. 97 65 6	5. 32 76 6	4. 20 8 7	4. 66 18 4	4. 70 23 4	-1. 776 076 02	-0. 828 693 333	1.7 76 07 60 2	D o w n	0.0 11 32 69 85	0.6 63 32 74 04
51	GINS	GINS complex	3.	3.	3.	4.	4.	3.	1.8	0.9	1.8	U	0.0	0.6

65	2	subunit 2 (Psf2	08	44	34	28	81	48	670	007	67	p	26	63
9		homolog)	32	97	66	66	45	07	061	266	00		03	32
			6	7	2	1	1	1	33	67	61		65	74
											33		28	04
31	HLA	Major	7.	6.	6.	7.	7.	7.	1.6	0.7	1.6	U	0.0	0.6
17	-DQ	histocompatibility	16	85	48	73	87	13	754	445	75	p	26	63
	A1	complex, class II,	46	72	57	24	64	24	748	7	47		47	32
		DQ $\alpha$ 1		4	4	1	6	2	14		48		72	74
											14		27	04
75	ZFP3	ZFP36 ring finger	10	9.	10	10	12	11	2.2	1.1	2.2	U	0.0	0.6
38	6	protein	.6	81	.6	.9	.2	.2	269	551	26	p	19	63
			47	65	01	73	87	69	975		99		94	32
			28	6	18	39	88	05	95		75		61	74
											95		79	04
88	TSC2	TSC22 domain	6.	6.	7.	7.	7.	7.	1.9	0.9	1.9	U	0.0	0.6
48	2D1	family member 1	80	43	03	52	77	79	205	415	20	p	02	63
			83	98	31	91	92	74	550	233	55		24	32
			5	3	1	2	6	8	71	33	50		77	74
											71		97	04
96	CD6	CD69 molecule	4.	3.	4.	5.	6.	4.	2.6	1.4	2.6	U	0.0	0.6
9	9		11	60	46	73	20	50	763	202	76	p	15	63
			51	09	55	16	56	50	250	533	32		14	32
			6		6	8	5	5	24	33	50		56	74
											24		91	04
94	TNF	Tumor necrosis	4.	4.	4.	3.	3.	4.	-1.	-0.	1.5	D	0.0	0.6
3	RSF8	factor receptor	31	47	15	32	65	15	520	604	20	o	30	63
		superfamily	43	96	88	42	64	88	395	446	39	w	24	32
		member 8	4	7	2	5	2	2	507	667	55	n	96	74
											07		1	04

23 17 7	CEP6 8	Centrosomal protein 68kda	6. 94 28 9	7. 22 69 4	7. 43 88 9	8. 38 25 8	7. 96 13 4	7. 67 36 6	1.7 446 689 76	0.8 029 533 33	1.7 44 66 89 76	U p	0.0 10 99 73 81	0.6 63 32 74 04
23 09 0	ZNF 423	Zinc finger protein 423	5. 29 20 5	5. 78 49 8	6. 44 60 2	7. 36 95 2	7. 45 58 1	6. 05 47 1	2.1 719 586 94	1.1 189 966 67	2.1 71 95 86 94	U p	0.0 40 91 76 43	0.6 63 32 74 04
66 7	DST	Dystonin	5. 25 85 7	5. 38 56 2	5. 59 05 3	6. 26 61 9	6. 05 82 8	5. 81 57 1	1.5 531 028 09	0.6 351 533 33	1.5 53 10 28 09	U p	0.0 10 49 20 22	0.6 63 32 74 04
52 56	PHK A2	Phosphorylase kinase, $\alpha$ 2 (liver)	8. 73 98 5	8. 51 78 1	7. 96 28 3	7. 44 01 6	7. 69 66 5	8. 05 42 2	-1. 598 242 88	-0. 676 486 667	1.5 98 24 28 8	D o w n	0.0 34 90 70 41	0.6 63 32 74 04
15 53 82	VPS3 7D	Vacuolar protein sorting 37 homolog D (S. Cerevisiae)	7. 14 54 9	6. 64 80 1	6. 56 96 8	6. 01 16 6	6. 08 31 9	6. 39 94 7	-1. 540 024 533	-0. 622 953 333	1.5 40 02 45 33	D o w n	0.0 22 77 40 13	0.6 63 32 74 04
28 97 0	C11o rf54	Chromosome 11 open reading frame 54	10 .5 10 57	9. 75 72 7	10 .0 04 66	8. 70 20 7	9. 05 92 8	9. 63 91 5	-1. 941 717 52	-0. 957 333 333	1.9 41 71 75	D o w n	0.0 14 54 07	0.6 63 32 74



												2		74	04
69 25	TCF4	Transcription factor 4	4. 51 2	5. 70 88 6	5. 67 89 2	7. 54 84	6. 96 16	6. 17 09 2	3.0 182 521 44	1.5 937 133 33	3.0 18 25 21 44	U p	0.0 08 99 46 54	0.6 63 32 74 04	
23 10 7	MRP S27	Mitochondrial ribosomal protein S27	4. 77 83	4. 04 26 7	4. 75 15 3	5. 66 05 3	5. 00 77 5	4. 98 03 1	1.6 155 551 49	0.6 920 3 49	1.6 15 55 51 49	U p	0.0 41 32 48 47	0.6 63 32 74 04	
66 78	SPA RC	Secreted protein, acidic, cysteine-rich (osteonectin)	3. 73 86 4	5. 74 48 5	5. 77 62 3	9. 80 91 1	7. 38 79 2	6. 69 76 1	7.3 528 658 65	2.8 783 066 67	7.3 52 86 58 65	U p	0.0 14 09 49 62	0.6 63 32 74 04	
79 63 0	Clorf 54	Chromosome 1 open reading frame 54	6. 91 55 1	7. 67 44 3	7. 13 40 3	8. 60 08 9	8. 21 85 9	7. 89 09 3	1.9 937 437 55	0.9 954 8 37 55	1.9 93 74 37 55	U p	0.0 07 50 55 72	0.6 63 32 74 04	
12 11	CLT A	Clathrin, light chain A	3. 82 08 6	4. 06 86 9	4. 17 88 1	4. 69 82 5	4. 53 06 6	4. 61 23 9	1.5 062 695 85	0.5 909 8 95	1.5 06 26 95 85	U p	0.0 04 48 87 02	0.6 63 32 74 04	
10 63 6	RGS 14	Regulator of G-protein signaling 14	7. 43 53	7. 31 91	7. 62 15	6. 43 88	6. 74 43	7. 01 26	-1. 654 864	-0. 726 713	1.6 54 86	D o w	0.0 07 97	0.6 63 32	

			3	5	1	3	7	5	774	333	47	n	40	74
											74		51	04
64	IGK	Immunoglobulin κ	5.	4.	5.	6.	9.	8.	6.6	2.7	6.6	U	0.0	0.6
24	V10	variable 1/OR10-1	42	89	48	01	11	90	900	420	90	p	09	63
24	R10-	(pseudogene)	99	86	02	56	58	33	175	1	01		79	32
	1		9	3	1	4	5	7	71		75		54	74
											71		34	04
31	HLA	Major	4.	4.	7.	9.	9.	8.	8.0	3.0	8.0	U	0.0	0.6
15	-DPB	histocompatibility	96	91	88	07	36	34	388	069	38	p	06	63
	1	complex, class II,	26	58	30	23	69	32	734	933	87		56	32
		DP β 1	9	2	2	4	3	4	16	33	34		01	74
											16		82	04
25	SLC3	Solute carrier	4.	4.	4.	6.	4.	5.	1.7	0.7	1.7	U	0.0	0.6
80	9A6	family 39 (zinc	55	44	99	03	82	50	294	902	29	p	42	63
0		transporter),	47	70	31	53	59	45	260	933	42		77	32
		member 6	9	6	3	8	7	1	59	33	60		52	74
											59		4	04
79	SCD	Stearoyl-coa	6.	6.	5.	7.	7.	6.	2.2	1.1	2.2	U	0.0	0.6
96	5	desaturase 5	97	11	40	63	61	78	581	751	58	p	28	63
6			88	51	65	03	36	20	531	433	15		24	32
			6		8	3		4	48	33	31		24	74
											48		8	04
54	PON	Paraoxonase 1	4.	3.	3.	2.	3.	3.	-1.	-0.	1.8	D	0.0	0.6
44	1		05	83	51	29	17	37	806	853	06	o	22	63
			57	53	69	08	95	75	753	4	75	w	65	32
			7	7	6	1	9		889		38	n	83	74
											89		39	04
11	AP2	Adaptor-related	8.	8.	8.	9.	9.	9.	1.6	0.7	1.6	U	0.0	0.6
73	M1	protein complex 2,	35	47	92	47	15	29	529	250	52	p	08	63

		mu 1 subunit	24 1	37 6	50 6	97 2	55 9	09 9	273 7	233 33	92 73 7		66 66 64	32 74 04
62 28	RPS2 3	Ribosomal protein S23	8. 49 04	8. 99 33 3	9. 09 37 7	9. 99 3	9. 47 29 1	9. 25 79 2	1.6 419 877 15	0.7 154 433 33	1.6 41 98 77 15	U p	0.0 26 20 35 58	0.6 63 32 74 04
57 80 1	HES 4	Hes family bhlh transcription factor 4	6. 00 37 5	7. 00 57 4	6. 07 23 4	7. 80 93 2	7. 18 12 9	7. 08 56 8	1.9 974 600 75	0.9 981 666 67	1.9 97 46 00 75	U p	0.0 18 96 24 35	0.6 63 32 74 04
95 3	ENT PD1	Ectonucleoside triphosphate diphosphohydrolas e 1	3. 79 12 3	5. 47 20 4	4. 48 59 1	6. 60 84 3	6. 09 13 4	5. 48 74 9	2.7 882 501 51	1.4 793 6 51	2.7 88 25 01 51	U p	0.0 14 92 86 91	0.6 63 32 74 04
33 95 62 18	IGK V10 R2-1 18	Immunoglobulin $\kappa$ variable 1/OR2-118 (pseudogene)	5. 42 99 9	4. 89 86 3	5. 48 02 1	6. 01 56 4	9. 11 58 5	8. 90 33 7	6.6 900 175 71	2.7 420 1 75	6.6 90 01 75 71	U p	0.0 09 79 54 34	0.6 63 32 74 04
10 01 31 54 1	LOC 1001 3154 1	Uncharacterized LOC100131541	4. 99 23 4	5. 47 23 9	5. 42 64 3	7. 16 54 6	6. 18 05 5	5. 75 52 8	2.0 994 964 28	1.0 700 433 33	2.0 99 49 64 28	U p	0.0 21 39 89 1	0.6 63 32 74 04
11	CHN	Chimerin 2	7.	7.	7.	6.	6.	7.	-1.	-0.	1.8	D	0.0	0.6

24	2		67	55	75	91	23	23	822	866	22	o	13	63
			79	51	39	09	97	80	754	12	75	w	69	32
			5	5	4	1	6	1	167		41	n	54	74
											67		28	04
23	SEL1	Sel-1 suppressor of	12	11	11	10	10	11	-1.	-0.	1.7	D	0.0	0.6
23	L3	lin-12-like 3 (C.	.0	.7	.8	.8	.9	.3	771	824	71	o	02	63
1		Elegans)	37	72	36	47	70	54	338	84	33	w	66	32
			82	51	35	53	14	49	58		85	n	15	74
											8		62	04
55	TME	Transmembrane	5.	6.	6.	8.	8.	8.	6.2	2.6	6.2	U	4.4	0.0
27	M10	protein 100	59	01	18	48	78	43	002	323	00	p	54	43
3	0		74	86	73	46	32	24	798	333	27		57	85
			5	6		8	7	6	51	33	98		E-0	47
											51		6	1
10	IGLL	Immunoglobulin	4.	4.	4.	5.	6.	5.	2.1	1.1	2.1	U	0.0	0.6
04	5	lambda-like	55	63	74	04	59	63	663	152	66	p	18	63
23		polypeptide 5	85	56	19	92	54	71	104	4	31		80	32
06			3	7		9	3		38		04		78	74
2											38		32	04
14	MYL	Myosin light chain	5.	6.	6.	7.	6.	6.	1.5	0.6	1.5	U	0.0	0.6
04	6B	6B	67	32	05	13	47	37	596	412	59	p	47	63
65			71	46	33	14	14	59	691	4	66		64	32
			5	6	6	1	9	9	23		91		24	74
											23		28	04
48	NID1	Nidogen 1	4.	7.	6.	9.	8.	7.	3.9	1.9	3.9	U	0.0	0.6
11			69	80	34	21	00	62	981	993	98	p	37	63
			83	93	11	38	46	83	427	3	14		51	32
			2	2	8	5	3	3	97		27		53	74
											97		15	04

44	MSH	Muts homolog 5	7.	7.	7.	7.	6.	6.	-1.	-0.	1.5	D	0.0	0.6
39	5		65	26	30	10	82	52	500	585	00	o	26	63
			11	02	47	70	43	80	607	546	60	w	58	32
			2		4	7	1	4	492	667	74	n	68	74
											92		01	04
11	KCT	Potassium channel	5.	6.	7.	8.	8.	7.	3.0	1.6	3.0	U	0.0	0.6
52	D12	tetramerization	97	52	11	89	35	20	655	161	65	p	11	63
07		domain containing	27	10		22	81	19	798	6	57		01	32
		12	8	4			6	4	85		98		20	74
											85		15	04
10	TOM	Target of myb1	8.	7.	7.	6.	6.	7.	-1.	-0.	1.6	D	0.0	0.6
04	1	membrane	18	92	81	81	97	90	675	744	75	o	44	63
3		trafficking protein	80	27	14	12	18	52	536	623	53	w	08	32
			6	4	8	8	6	7	754	333	67	n	42	74
											54		18	04
26	HSP	Heat shock protein	5.	6.	5.	8.	6.	7.	3.2	1.6	3.2	U	0.0	0.6
35	B8	family B (small)	21	88	18	73	51	07	012	786	01	p	41	63
3		member 8	20	98	90	98	49	20	011	133	20		64	32
			1	8	7	5	4	1	52	33	11		13	74
											52		75	04
64	NUC	Nuclear casein	7.	6.	7.	8.	7.	7.	1.8	0.8	1.8	U	0.0	0.6
71	KS1	kinase and	43	29	39	29	49	99	494	870	49	p	43	63
0		cyclin-dependent	18	46	45	97	12	13	333	833	43		40	32
		kinase substrate 1	9	1	8	4	3	6	81	33	33		46	74
											81		97	04
20	TUB	Tubulin, $\beta$ class I	8.	7.	8.	9.	8.	8.	1.5	0.6	1.5	U	0.0	0.6
30	B		21	90	41	02	68	78	740	544	74	p	111	63
68			25	59	06	69	00	54	048	4	00		80	32
			6	2		1	2	7	65		48		71	74

												65		2	04
47 39	NED D9	Neural precursor cell expressed, developmentally down-regulated 9	4. 01 12 7	3. 93 06 4	4. 49 02 1	5. 56 39 2	5. 88 54 6	4. 73 85 1	2.3 815 871 35	1.2 519 233 33	2.3 81 58 71 35	U p	0.0 05 34 03 54	0.6 63 32 74 04	
83 48 3	PLV AP	Plasmalemma vesicle associated protein	4. 99 67 2	5. 94 70 8	5. 69 44 5	7. 09 10 5	7. 56 34 2	6. 01 80 3	2.5 398 618 02	1.3 447 5 18 02	2.5 39 86 18 02	U p	0.0 16 56 82 44	0.6 63 32 74 04	
73 4	OSGI N2	Oxidative stress induced growth inhibitor family member 2	6. 92 88 2	6. 32 61 7	6. 80 91 3	5. 68 62 5	6. 04 35 8	6. 45 07 4	-1. 545 260 427	-0. 627 85 04	1.5 45 26 04 27	D o w n	0.0 45 04 53 33	0.6 63 32 74 04	
56 14 7	PCD HA1	Protocadherin $\alpha$ 1	7. 44 20 9	7. 73 45 2	6. 91 29 9	6. 53 69 2	6. 83 18 2	6. 80 31 1	-1. 557 526 454	-0. 639 256 667	1.5 57 52 64 54	D o w n	0.0 31 81 64 86	0.6 63 32 74 04	
54 51 0	PCD H18	Protocadherin 18	4. 27 42 8	6. 11 49 9	5. 92 27 3	7. 97 37 8	6. 76 33 8	6. 78 98 6	3.3 365 103 98	1.7 383 4 03 98	3.3 36 51 03 98	U p	0.0 16 14 67 81	0.6 63 32 74 04	
10 23 1	RCA N2	Regulator of calcineurin 2	3. 83 86	5. 71 16	6. 03 73	7. 37 47	6. 40 30	6. 29 50	2.8 188 238	1.4 950 933	2.8 18 82	U p	0.0 40 16	0.6 63 32	

			6	7	1	9	8	5	65	33	38		28	74
											65		15	04
23	SIRT	Sirtuin 4	4.	4.	4.	3.	4.	4.	-1.	-0.	1.6	D	0.0	0.6
40	4		55	57	62	28	02	32	632	706	32	o	29	63
9			42	93	65	72	79	43	243	856	24	w	24	32
			3	4	7	9	6	2	919	667	39	n	67	74
											19		06	04
12	DEG	$\Delta$ (4)-desaturase,	8.	9.	8.	6.	7.	8.	-2.	-1.	2.2	D	0.0	0.6
30	S2	sphingolipid 2	99	01	94	83	91	74	225	153	25	o	33	63
99			14	47	87	37	88	08	063	846	06	w	92	32
			1	4	7	1	6	1	743	667	37	n	31	74
											43		8	04
94	PPP1	Protein	5.	8.	6.	10	8.	8.	5.0	2.3	5.0	U	0.0	0.6
27	R14	phosphatase 1	92	84	10	.8	31	66	089	245	08	p	43	63
4	A	regulatory inhibitor	57	20	80	72	19	55	793	166	97		32	32
		subunit 14A	8	4	4		1		59	67	93		97	74
											59		1	04
62	RPS1	Ribosomal protein	7.	6.	7.	8.	8.	7.	1.8	0.8	1.8	U	0.0	0.6
10	5A	s15a	24	63	63	32	06	73	288	709	28	p	19	63
			46	87	22	65	63	56	879	666	88		39	32
			2	7	3	2	2	8	22	67	79		93	74
											22		12	04
10	LRR	Leucine rich repeat	3.	3.	3.	5.	5.	4.	2.6	1.3	2.6	U	0.0	0.6
01	C70	containing 70	29	49	49	08	36	03	376	992	37	p	03	63
30			25	99	52	58	68	28	991	8	69		80	32
73			6	2		7	1	4	07		91		01	74
3											07		24	04
12	CNN	Calponin 3, acidic	7.	7.	8.	8.	8.	8.	2.1	1.0	2.1	U	0.0	0.6
66	3		18	33	11	80	78	28	135	796	13	p	07	63

			07	21	62	04	58	18	330	566	53		21	32
			2	8	6	5	2	6	42	67	30		06	74
											42		77	04
57	RHO	Ras homolog	3.	4.	3.	5.	5.	4.	2.3	1.2	2.3	U	0.0	0.6
38	J	family member J	24	11	75	49	03	19	052	049	05	p	13	63
1			18	95	04	98	25	43	555	266	25		01	32
			6	7	7		7	1	13	67	55		38	74
											13		66	04
80	ESR	Epithelial splicing	8.	8.	8.	7.	8.	7.	-1.	-0.	1.7	D	0.0	0.6
00	P2	regulatory protein	80	79	41	53	19	93	718	781	18	o	09	63
4		2	87	45	12	47	77	83	647	273	64	w	78	32
			6	6	4	2	1	1	094	333	70	n	82	74
											94		44	04
37	JUN	Jun	9.	7.	9.	9.	10	10	2.2	1.1	2.2	U	0.0	0.6
25		proto-oncogene	07	94	06	16	.2	.1	638	787	63	p	24	63
			76	19	17	07	83	73	159	566	81		71	32
			3	4	3	9	55	23	44	67	59		28	74
											44		42	04
56	MAS	Mannan-binding	6.	6.	6.	5.	5.	6.	-1.	-0.	1.8	D	0.0	0.6
48	P1	lectin serine	56	65	78	77	44	19	813	858	13	o	05	63
		peptidase 1 (C4/C2	01	79	25	91	73	71	763	986	76	w	86	32
		activating	1	7	5	8	5	4	895	667	38	n	65	74
		component of									95		93	04
		Ra-reactive factor)												
23	MTC	Microtubule	11	10	10	9.	10	10	-2.	-1.	2.0	D	0.0	0.6
25	L1	crosslinking factor	.1	.6	.8	04	.1	.3	028	020	28	o	23	63
5		1	33	90	11	02	43	89	926	716	92	w	42	32
			56	19	37	5	72		59	667	65	n	59	74
											9		63	04



29	GUC	Guanylate cyclase	7.	6.	7.	8.	8.	7.	1.8	0.8	1.8	U	0.0	0.6
83	Y1B	1, soluble, $\beta$ 3	23	76	17	11	30	41	494	870	49	p	13	63
	3		58	19	32	15	34	72	248	766	42		36	32
			9	6	2	5	8	7	34	67	48		38	74
											34		7	04
11	TSE	Trna splicing	5.	4.	5.	6.	5.	5.	1.5	0.6	1.5	U	0.0	0.6
64	N15	endonuclease	38	80	28	13	47	73	417	245	41	p	35	63
61		subunit 15	49	51	01	92	20	25	547	733	75		35	32
				2	5	6	8	5	95	33	47		63	74
											95		25	04
84	PAR	Par-6 family cell	5.	6.	5.	3.	5.	5.	-1.	-0.	1.9	D	0.0	0.6
61	D6B	polarity regulator $\beta$	64	04	19	83	09	03	962	972	62	o	38	63
2			78	57	53	78	39	83	836	94	83	w	79	32
			4	2	9	7	5	1	494		64	n	82	74
											94		48	04
10	LOC	Cytochrome P450,	6.	5.	5.	5.	4.	4.	-1.	-0.	1.8	D	0.0	0.6
19	1019	family 2, subfamily	31	89	46	44	70	76	896	923	96	o	15	63
29	2982	D, polypeptide 6	07		89	01	02	00	137	063	13	w	23	32
82	9	pseudogene	3		6	5	8	7	168	333	71	n	86	74
9											68		05	04
65	SPAT	Spermatogenesis	7.	7.	7.	6.	6.	6.	-1.	-0.	1.7	D	0.0	0.6
24	S2	associated, serine	72	12	33	14	76	89	728	789	28	o	18	63
4		rich 2	20	31	06	74	57	37	643	64	64	w	58	32
			4	1	6	3	2	4	055		30	n	20	74
											55		6	04
42	MID	Midline 1	5.	5.	4.	6.	6.	5.	1.7	0.8	1.7	U	0.0	0.6
81	1		64	83	91	89	14	83	720	253	72	p	49	63
			75	87	45	85	72	12	221	966	02		55	32
			3	4	7	1	4	8	86	67	21		70	74

											86		87	04
47 72	NFA TC1	Nuclear factor of activated T-cells, cytoplasmic, calcineurin-depend ent 1	4. 31 53 1	4. 75 87 9	4. 49 00 4	5. 35 01 4	5. 46 98 6	4. 78 76 2	1.6 034 284 75	0.6 811 6 84 75	1.6 03 42 84 75	U p	0.0 18 97 94 19	0.6 63 32 74 04
11 32 20	KIF1 2	Kinesin family member 12	9. 09 51 5	8. 94 33 5	9. 02 42 5	8. 47 39 5	8. 01 24 4	8. 76 63 174	-1. 519 226 667	-0. 603 336 61 74	1.5 19 22 61 74	D o w n	0.0 26 94 67 62	0.6 63 32 74 04
51 40 9	HEM K1	Hemk methyltransferase family member 1	5. 38 17 1	5. 32 34 5	4. 94 47 5	4. 46 06 1	4. 59 89 6	4. 78 39 7	-1. 517 949 014	-0. 602 123 333	1.5 17 94 90 14	D o w n	0.0 11 66 35 81	0.6 63 32 74 04
80 02 5	PAN K2	Pantothenate kinase 2	5. 64 80 8	5. 74 51 9	5. 64 43 6	6. 44 93 6	6. 66 56 9	5. 82 47 9	1.5 519 370 07	0.6 340 7 07	1.5 51 93 70 07	U p	0.0 31 45 21 64	0.6 63 32 74 04
81 69 3	AMN	Amnion associated transmembrane protein	9. 98 27 1	9. 66 54 5	9. 62 18 3	7. 33 66 3	8. 65 95 7	9. 52 76 7	-2. 376 304 969	-1. 248 72 49 69	2.3 76 30 49 69	D o w n	0.0 43 15 14 7	0.6 63 32 74 04
50 81 0	HDG FRP3	Hepatoma-derived growth factor, related protein 3	4. 16 88	4. 80 78	4. 60 02	6. 00 80	6. 36 88	5. 16 89	2.5 017 656	1.3 229 466	2.5 01 76	U p	0.0 05 16	0.6 63 32

			6	6	2	7		1	74	67	56		94	74
											74		93	04
19	EGF	Epidermal growth	7.	7.	7.	6.	7.	7.	-1.	-0.	1.5	D	0.0	0.6
56	R	factor receptor	91	92	94	72	41	67	579	659	79	o	36	63
			76	60	13	00	48	22	341	323	34	w	20	32
			5	6	7	1	8	2	692	333	16	n	74	74
											92		17	04
42	CTA	CTAGE family	8.	8.	8.	7.	7.	8.	-1.	-0.	1.7	D	0.0	0.6
53	GE5	member 5	88	52	99	41	93	63	750	808	50	o	38	63
			10	65	88	39	51	29	899	096	89	w	52	32
			7	3	4	7	9	9	973	667	99	n	84	74
											73		68	04
63	CCL	Chemokine (C-C	5.	6.	6.	6.	8.	7.	2.2	1.1	2.2	U	0.0	0.6
51	4	motif) ligand 4	72	37	64	68	05	55	685	817	68	p	19	63
			31	54	34	61	00	12	807	9	58		15	32
			6	2	5		8	2	29		07		84	74
											29		57	04
36	ABC	ATP binding	7.	7.	7.	6.	6.	6.	-1.	-0.	1.8	D	0.0	0.6
8	C6	cassette subfamily	42	06	51	07	38	99	803	850	03	o	15	63
		C member 6	96	80	23	26	87	57	717	973	71	w	50	32
			8	4	4	4	5	5	417	333	74	n	61	74
											17		17	04
57	VPS1	VPS18,	8.	8.	7.	7.	7.	7.	-1.	-0.	1.6	D	0.0	0.6
61	8	CORVET/HOPS	15	50	60	16	39	56	639	712	39	o	26	63
7		core subunit	12	31	96	26	77	46	156	953	15	w	73	32
			1	3	5	9	5	9	193	333	61	n	50	74
											93		54	04
30	ANX	Annexin A5	6.	4.	6.	7.	7.	7.	2.4	1.3	2.4	U	0.0	0.6
8	A5		18	97	92	78	10	13	838	125	83	p	29	63

			30	56	73	64	39	32	246	633	82		52	32
			3	3		6		9	6	33	46		06	74
											6		23	04
95	ADA	ADAM	2.	3.	2.	5.	6.	3.	3.6	1.8	3.6	U	0.0	0.6
07	MTS	metallopeptidase	76	51	93	03	28	46	132	533	13	p	24	63
	4	with	35	7	64	12	47	09	990	166	29		48	32
		thrombospondin	2		2	2	7		6	67	90		38	74
		type 1 motif 4									6		18	04
83	CCD	Coiled-coil domain	4.	4.	4.	6.	5.	4.	2.3	1.2	2.3	U	0.0	0.6
98	C8	containing 8	07	75	07	62	32	70	790	503	79	p	34	63
7			10	48	20	5	17	23	682	966	06		62	32
			3	8	2		8	4	61	67	82		66	74
											61		94	04
22	WDR	WD repeat domain	5.	5.	5.	6.	6.	6.	1.5	0.6	1.5	U	0.0	0.6
91	47	47	52	61	77	48	30	05	607	422	60	p	07	63
1			80	54	62	36	45	82	866	733	78		99	32
			6		3	7	6	8	39	33	66		48	74
											39		25	04
17	DXO	Decapping	5.	6.	5.	7.	7.	6.	2.6	1.3	2.6	U	0.0	0.6
97		exoribonuclease	45	81	52	65	58	72	160	873	16	p	13	63
			80	72	93	81	09	77	497	9	04		85	32
			2	6	5	3		7	91		97		90	74
											91		96	04
22	MM	Multimerin 1	4.	5.	5.	6.	7.	6.	3.2	1.6	3.2	U	0.0	0.6
91	RN1		31	33	26	74	19	03	144	845	14	p	03	63
5			48	18	92	25	04	66	234	6	42		04	32
			8	9	2		9	8	63		34		86	74
											63		74	04
40	LRP5	LDL receptor	8.	8.	7.	7.	7.	7.	-1.	-0.	1.5	D	0.0	0.6

41		related protein 5	35	04	90	12	55	83	510	594	10	o	36	63
			32	29	68	41	93	44	448	976	44	w	41	32
			2	3	1	9	8	6	156	667	81	n	23	74
											56		07	04
27	TNF	Tumor necrosis	6.	5.	5.	6.	6.	5.	1.6	0.7	1.6	U	0.0	0.6
24	RSF2	factor receptor	11	19	60	65	56	94	792	478	79	p	39	63
2	1	superfamily	96	53	79	06	75	83	883	5	28		57	32
		member 21	4	9	8	4	8	4	78		83		16	74
											78		31	04
57	C6orf	Chromosome 6	7.	6.	6.	6.	6.	6.	-1.	-0.	1.5	D	0.0	0.6
82	47	open reading frame	33	83	80	44	33	42	501	585	01	o	18	63
7		47	08	51	45	83	74	68	051	973	05	w	18	32
			6	7	4	4	5	6	352	333	13	n	05	74
											52		57	04
12	ADH	Alcohol	10	9.	11	8.	8.	10	-2.	-1.	2.2	D	0.0	0.6
6	1C	dehydrogenase 1C	.4	97	.0	86	95	.1	209	143	09	o	27	63
		(class I), $\gamma$	32	39	13	58	41	69	214	533	21	w	46	32
		polypeptide	96	2	09	1	4	42	242	333	42	n	24	74
											42		77	04
32	HPN	Hepsin	9.	9.	9.	6.	6.	8.	-4.	-2.	4.2	D	0.0	0.6
49			27	22	10	39	37	57	238	083	38	o	08	63
			47	38	02	64	34	84	420	526	42	w	11	32
			6	9	5	4	1	7	324	667	03	n	01	74
											24		61	04
25	ASP	Aspartate	9.	8.	8.	7.	7.	8.	-1.	-0.	1.8	D	0.0	0.6
39	HD1	$\beta$ -hydroxylase	40	80	95	73	99	79	845	884	45	o	23	63
82		domain containing	86	51	78	32	39	13	928	346	92	w	89	32
		1	2	9		5	4	8	492	667	84	n	43	74
											92		84	04

16 40 91	PAQ R7	Progestin and adipoq receptor family member VII	7. 20 00 7	7. 18 78 4	6. 90 00 9	5. 96 82 4	5. 65 08	6. 76 86 9	-1. 954 441 857	-0. 966 756 667	1.9 54 44 18 57	D o w n	0.0 13 82 01 38	0.6 63 32 74 04
98 06	SPO CK2	Sparc/osteonectin, cwcv and kazal-like domains proteoglycan (testican) 2	7. 58 72 3	7. 23 84 3	8. 27 79	5. 35 07	6. 37 52 2	7. 45 49 9	-2. 475 191 247	-1. 307 54 12 47	2.4 75 19 12 47	D o w n	0.0 43 52 53 76	0.6 63 32 74 04
64 41 0	KLH L25	Kelch like family member 25	6. 01 05 7	6. 14 03 5	5. 77 70 7	5. 06 42 1	5. 5. 93 1	5. 52 42 1	-1. 533 424 002	-0. 616 756 667	1.5 33 42 40 02	D o w n	0.0 15 30 45 35	0.6 63 32 74 04
81 57 8	COL 21A1	Collagen, type XXI, $\alpha$ 1	4. 89 86 3	5. 16 07 1	5. 39 55 4	7. 53 23 1	7. 81 31 2	5. 19 72 6	3.2 398 716 63	1.6 959 366 67	3.2 39 87 16 63	U p	0.0 34 97 26 74	0.6 63 32 74 04
30 21	H3F3 B	H3 histone, family 3B (H3.3B)	7. 94 91	8. 01 08 3	8. 46 86 3	9. 31 72 3	9. 47 70 7	8. 35 00 8	1.8 728 993 01	0.9 052 733 33	1.8 72 89 93 01	U p	0.0 26 39 53 64	0.6 63 32 74 04
91 36 8	CDK N2AI PNL	CDKN2A interacting protein N-terminal like	3. 77 45 2	4. 34 56 3	4. 08 94 4	3. 42 38 5	3. 34 90 2	3. 46 98 9	-1. 575 281 873	-0. 655 61 18	1.5 75 28 18	D o w n	0.0 04 90 15	0.6 63 32 74

												73		18	04
26	PCO	Procollagen	4.	5.	7.	4.	4.	3.	-3.	-1.	3.5	D	0.0	0.6	
57	LCE	C-endopeptidase	44	97	41	62	19	50	569	835	69	o	35	63	
7	2	enhancer 2	39	94	41	89	38	74	569	75	56	w	13	32	
			1	5	8	8	3	8	273		92	n	57	74	
											73		05	04	
80	ASR	Asparaginase like 1	10	10	9.	8.	9.	9.	-1.	-0.	1.7	D	0.0	0.6	
15	GL1		.4	.1	78	74	36	79	783	834	83	o	27	63	
0			34	93	51	77	72	30	692	866	69	w	46	32	
			42	05	5	8	2	2	183	667	21	n	61	74	
											83		17	04	
85	BAG	B melanoma	7.	7.	7.	6.	6.	6.	-1.	-0.	1.5	D	0.0	0.6	
31	E2	antigen family	49	64	07	85	68	88	511	595	11	o	18	63	
9		member 2	63	48	38	24	84	76	010	513	01	w	43	32	
			6	5	5	1	4	7	131	333	01	n	06	74	
											31		8	04	
52	CDK	Cyclin-dependent	9.	9.	8.	8.	8.	8.	-1.	-0.	1.6	D	0.0	0.6	
18	14	kinase 14	36	08	87	28	16	64	675	744	75	o	08	63	
			77	95	90	98	74	55	381	49	38	w	06	32	
				9	4	4	8	4	909		19	n	07	74	
											09		69	04	
19	EDN	Endothelin	3.	4.	4.	5.	6.	5.	3.0	1.6	3.0	U	0.0	0.6	
10	RB	receptor type B	51	52	24	06	67	36	460	069	46	p	09	63	
			95	78	47	59	79	90	507	4	05		52	32	
			8	3		3	6	4	95		07		87	74	
											95		55	04	
25	ACK	Atypical	6.	6.	6.	8.	8.	6.	2.1	1.1	2.1	U	0.0	0.6	
32	R1	chemokine	23	66	82	11	18	73	465	020	46	p	29	63	
		receptor 1 (Duffy	75	62	68	06	79	82	900	466	59		40	32	

		blood group)	7	3	8	1	3	8	07	67	00		21	74
											07		02	04
16	ZNF	Zinc finger protein	4.	4.	4.	3.	3.	3.	-1.	-0.	1.6	D	0.0	0.6
32	540	540	66	67	41	80	70	99	673	743	73	o	01	63
55			09	31	05	84	81	80	985	286	98	w	28	32
			2	4	1	7	7	7	077	667	50	n	73	74
											77		43	04
55	BEX	Brain expressed	6.	6.	6.	6.	7.	7.	1.7	0.8	1.7	U	0.0	0.6
85	1	X-linked 1	24	74	30	67	64	40	507	079	50	p	25	63
9			40	98	71	49	58	40	017	333	70		86	32
			5	7	5	2	7	8	58	33	17		62	74
											58		73	04
38	CEP8	Centrosomal	5.	6.	6.	7.	6.	6.	1.8	0.8	1.8	U	0.0	0.6
71	5L	protein 85kda-like	65	16	07	14	73	58	096	557	09	p	06	63
19			14	93	85	26	42	95	365		63		30	32
			4	6		3	3	4	83		65		67	74
											83		32	04
13	HIN	Histidine triad	7.	6.	6.	5.	5.	6.	-1.	-0.	1.6	D	0.0	0.6
51	T3	nucleotide binding	24	47	28	85	97	07	625	701	25	o	33	63
14		protein 3	97	52	88	94	28	75	969	3	96	w	70	32
			5	3	6	9	7	8	28		92	n	71	74
											8		37	04
80	ACA	Acyl-coa	7.	7.	7.	6.	6.	7.	-1.	-0.	1.5	D	0.0	0.6
72	D10	dehydrogenase	26	27	19	38	38	19	503	588	03	o	48	63
4		family member 10	27	27	89	85	29	67	901	71	90	w	88	32
			3	5	2	6	6	5	418		14	n	66	74
											18		71	04
99	CLE	C-type lectin	6.	6.	7.	8.	7.	7.	2.0	1.0	2.0	U	0.0	0.6
76	C2B	domain family 2,	15	55	34	06	84	15	083	059	08	p	27	63



		member B	66 4	89 4	07 5	72 7	70 6	99 6	165 26	866 67	31 65 26		12 87 45	32 74 04
52 38	PGM 3	Phosphoglucomutase 3	6. 44 11 6	6. 35 41 2	6. 64 99 2	5. 51 33 4	5. 67 31 6	5. 74 72 6	-1. 786 513 315	-0. 837 146 667	1.7 86 51 33 15	D o w n	0.0 01 29 25 1	0.6 63 32 74 04
67 23	SRM	Spermidine synthase	6. 70 41 1	7. 17 90 8	7. 43 02 8	8. 33 59 7	8. 19 68 7	7. 35 35 9	1.8 120 590 88	0.8 576 3 88	1.8 12 05 90 88	U p	0.0 29 21 56 83	0.6 63 32 74 04
66 41	SNT B1	Syntrophin, $\beta$ 1 (dystrophin-associated protein A1, 59kda, basic component 1)	4. 69 47 4	4. 73 66 6	4. 75 48 6	6. 63 58 8	5. 98 74 3	4. 85 18 1	2.1 380 367 73	1.0 962 866 67	2.1 38 03 67 73	U p	0.0 33 45 68 14	0.6 63 32 74 04
59 97	RGS 2	Regulator of G-protein signaling 2	8. 21 32 4	8. 93 12 8	8. 24 07 6	9. 80 09 6	10. 3 19 01	9. 69 06 3	2.7 800 805 16	1.4 751 266 67	2.7 80 08 05 16	U p	0.0 00 86 07 06	0.6 63 32 74 04
13 05	COL 13A1	Collagen, type XIII, $\alpha$ 1	4. 44 01 8	5. 78 49 8	4. 57 51 8	6. 43 82 9	7. 10 27 4	5. 20 94 6	2.4 909 855 74	1.3 167 166 67	2.4 90 98 55 74	U p	0.0 46 59 10 91	0.6 63 32 74 04
46	NAC	Nascent	8.	8.	9.	10	9.	9.	1.9	0.9	1.9	U	0.0	0.6

66	A	polypeptide-associated complex $\alpha$ subunit	77 52 7	63 37 5	42 70 1	.3 54 19	72 28 8	75 16 1	966 064 61	975 5 64	96 60 64 61	p	08 48 83 5	63 32 74 04
10 33 5	MRV I1	Murine retrovirus integration site 1 homolog	3. 29 80 8	4. 42 55 1	3. 53 28 9	5. 84 41 1	3. 95 12 2	5. 05 04 3	2.2 917 134 53	1.1 964 266 67	2.2 91 71 34 53	U p	0.0 48 63 79 71	0.6 63 32 74 04
51 06 2	ATL1	Atlastin gtpase 1	3. 95 28	4. 59 06 2	4. 23 12 4	5. 28 69 1	5. 08 30 8	4. 45 39 6	1.6 055 823 55	0.6 830 966 67	1.6 05 58 23 55	U p	0.0 36 00 86 41	0.6 63 32 74 04
23 32 8	SAS H1	SAM and SH3 domain containing 1	5. 98 68 7	6. 67 24 6	7. 09 24 6	7. 86 89 3	7. 86 74 5	6. 85 55 5	1.9 274 810 37	0.9 467 166 67	1.9 27 48 10 37	U p	0.0 40 93 48 99	0.6 63 32 74 04
34 86	IGFB P3	Insulin like growth factor binding protein 3	3. 90 06 7	5. 95 24 3	5. 01 92 6	7. 80 75 1	6. 77 00 1	5. 66 48 65	3.4 581 169 65	1.7 899 866 67	3.4 58 11 69 65	U p	0.0 30 35 93 44	0.6 63 32 74 04
64 06 5	PER P	PERP, TP53 apoptosis effector	6. 15 66 9	6. 60 06 4	6. 11 13 8	5. 25 43 5	5. 98 54 5	5. 29 47 9	-1. 714 799 617	-0. 778 04 96	1.7 14 79 96 17	D o w n	0.0 18 46 80 07	0.6 63 32 74 04

10 87 5	FGL 2	Fibrinogen-like 2	7. 09 79 4	7. 41 82 1	7. 29 65	8. 44 17 5	8. 02 94	7. 99 58 3	1.8 464 787 59	0.8 847 766 67	1.8 46 47 87 59	U p	0.0 02 22 25 6	0.6 63 32 74 04
10 78 1	ZNF 266	Zinc finger protein 266	8. 28 07 1	8. 28 42 6	8. 21 35 8	7. 63 26 2	7. 48 16	7. 63 81 5	-1. 597 032 125	-0. 675 393 333	1.5 97 03 21 25	D o w n	0.0 02 17 60 02	0.6 63 32 74 04
54 52 1	WDR 44	WD repeat domain 44	7. 17 79 7	6. 81 55 5	6. 74 40 8	5. 61 28 2	6. 29 58 4	6. 65 30 4	-1. 653 244 383	-0. 725 3 43 83	1.6 53 24 43 83	D o w n	0.0 39 67 22 15	0.6 63 32 74 04
14 05 97	TCE AL2	Transcription elongation factor A (SII)-like 2	4. 23 57 1	7. 65 62 5	5. 07 48 7	8. 03 01 1	7. 42 62 7	7. 25 35 9	3.7 695 178 41	1.9 143 8 78 41	3.7 69 51 78 41	U p	0.0 49 90 38 23	0.6 63 32 74 04
13 08 88	FBX O36	F-box protein 36	4. 05 18 8	3. 81 87 7	3. 88 9	3. 39 12 2	3. 39 26 8	3. 18 00 3	-1. 514 218 43	-0. 598 573 333	1.5 14 21 84 3	D o w n	0.0 01 78 58 74	0.6 63 32 74 04
54 97 0	TTC 12	Tetratricopeptide repeat domain 12	6. 89 08 1	7. 12 08 4	6. 77 94 3	5. 73 88 1	6. 51 96 3	6. 39 57 7	-1. 638 402 702	-0. 712 29	1.6 38 40 27	D o w n	0.0 21 58 42	0.6 63 32 74



28	IGK	Immunoglobulin $\kappa$	5.	5.	4.	6.	9.	8.	7.8	2.9	7.8	U	0.0	0.6
93	V1-3	variable 1-39	10	31	80	05	17	94	924	804	92	p	06	63
0	9	(gene/pseudogene)	81	25	69	00	36	53	871	8	48		50	32
			6	7	8	9	8	8	14		71		31	74
											14		33	04
93	TCE	Transcription	7.	7.	7.	9.	7.	7.	1.8	0.8	1.8	U	0.0	0.6
38	AL1	elongation factor A	40	50	45	16	93	87	291	711	29	p	40	63
		(SII)-like 1	33	75	19	90	41	32	710	9	17		64	32
			9	2	2	4	3	3	61		10		09	74
											61		92	04
69	TCF2	Transcription	3.	5.	4.	6.	6.	5.	3.6	1.8	3.6	U	0.0	0.6
43	1	factor 21	63	03	41	34	67	68	725	767	72	p	02	63
			03	17	21	30	43	70	530	833	55		19	32
			4	4	2	8	8	9	57	33	30		13	74
											57		9	04
24	FJX1	Four jointed box 1	3.	4.	4.	6.	5.	5.	2.9	1.5	2.9	U	0.0	0.6
14			75	95	17	62	54	33	054	387	05	p	08	63
7			30	96	62	65	25	62	198	466	41		31	32
			6	5	9	1	2	1	71	67	98		95	74
											71		18	04
18	DPP4	Dipeptidyl-peptida	9.	9.	9.	5.	7.	9.	-3.	-1.	3.9	D	0.0	0.6
03		se 4	75	15	70	95	42	27	964	987	64	o	33	63
			27	55	49	06	92	17	741	226	74	w	26	32
			8	8	4	3	1	8	118	667	111	n	96	74
											8		88	04
10	LOC	Uncharacterized	7.	6.	6.	5.	5.	6.	-1.	-0.	1.9	D	0.0	0.6
53	1053	protein c21orf124	17	70	53	03	71	69	986	990	86	o	48	63
72	7282		23	08	35	14	14	26	676	356	67	w	63	32
82	4			3		7	1	8	081	667	60	n	47	74

4											81		28	04
55	PPP1	Protein	6.	6.	6.	5.	6.	6.	-1.	-0.	1.6	D	0.0	0.6
60	R9A	phosphatase 1,	61	70	46	49	06	07	642	716	42	o	11	63
7		regulatory subunit	37	92	05	06	90	53	833	186	83	w	01	32
		9A	2	7	9	2	1	9	95	667	39	n	47	74
											5		69	04
46	MYO	Myosin VA	4.	4.	4.	5.	5.	4.	1.7	0.8	1.7	U	0.0	0.6
44	5A		06	90	59	91	28	79	531	099	53	p	45	63
			20	76	96	86	16	89	992	9	19		13	32
			5	6	3	4	9	8	9		92		67	74
											9		66	04
91	SLF	Schlafen family	3.	4.	4.	5.	5.	4.	1.9	0.9	1.9	U	0.0	0.6
60	N11	member 11	39	16	43	35	00	58	742	812	74	p	16	63
7			65	61	77	07	93	42	070	733	20		22	32
			5	7	9		7	6	9	33	70		05	74
											9		11	04
94	SH3	SH3-domain	6.	8.	7.	8.	8.	7.	1.7	0.7	1.7	U	0.0	0.6
67	BP5	binding protein 5	73	01	34	01	49	99	407	997	40	p	48	63
		(BTK-associated)	08	66	85	40	08	03	632	2	76		61	32
			9	5	5	8	6	1	44		32		96	74
											44		44	04
90	CH2	Cholesterol	5.	5.	4.	7.	6.	5.	2.7	1.4	2.7	U	0.0	0.6
23	5H	25-hydroxylase	50	08	89	16	80	90	642	669	64	p	03	63
			91	18	21	91	68	77	791	033	27		69	32
				8	3	8	6	8	88	33	91		44	74
											88		07	04
10	PNM	Paraneoplastic Ma	3.	4.	4.	5.	4.	4.	1.9	0.9	1.9	U	0.0	0.6
68	A2	antigen 2	39	26	45	76	94	34	733	806	73	p	49	63
7			12	68	12	22	4	51	998	833	39		54	32

			2	1	7	3		2	9	33	98		33	74
											9		1	04
60	ACT B	Actin, $\beta$	11 .1 29 72	10 .4 02 18	10 .6 87 43	11 .8 97 93	10 .9 61 82	11 .7 68 29	1.7 446 085 11	0.8 029 033 33	1.7 44 60 85 11	U p	0.0 32 22 49 6	0.6 63 32 74 04
51 17 6	LEF1	Lymphoid enhancer-binding factor 1	4. 06 62 6	4. 42 68 3	3. 71 45	6. 48 80 5	6. 58 79 3	4. 41 68 7	3.3 911 000 11	1.7 617 533 33	3.3 91 10 00 11	U p	0.0 17 61 98 53	0.6 63 32 74 04
28 62 62	TPR N	Taperin	7. 49 82 1	7. 25 86 9	6. 66 79	5. 75 37 5	6. 11 14 1	6. 75 18 3	-1. 913 132 329	-0. 935 936 667	1.9 13 13 23 29	D o w n	0.0 22 26 56 64	0.6 63 32 74 04
40 6	ARN TL	Aryl hydrocarbon receptor nuclear translocator like	5. 08 6	5. 89 27 6	4. 64 06	7. 00 76	7. 14 38 9	5. 39 62 6	2.4 784 932 56	1.3 094 633 33	2.4 78 49 32 56	U p	0.0 41 14 97 37	0.6 63 32 74 04
84 34	REC K	Reversion-inducing -cysteine-rich protein with kazal motifs	4. 75 63	5. 43 42 9	5. 98 04	7. 41 56 6	6. 86 43 1	5. 88 06 4	2.5 137 827 98	1.3 298 6 98	2.5 13 78 27 98	U p	0.0 21 89 07 44	0.6 63 32 74 04
55 11	PLE KHJ1	Pleckstrin homology domain	9. 86	9. 74	9. 54	8. 96	8. 87	9. 51	-1. 516	-0. 600	1.5 16	D o	0.0 26	0.6 63

1		containing J1	64 4	77 8	33 1	70 1	18	62 4	585 324	826 667	58 53 24	w n	26 17 01	32 74 04
22 80 8	MRA S	Muscle RAS oncogene homolog	5. 13 36	6. 37 35 6	5. 27 75 3	7. 81 44 1	6. 95 68	5. 86 03 3	2.4 322 361 9	1.2 822 833 33	2.4 32 23 61 9	U p	0.0 48 47 99 06	0.6 63 32 74 04
91 89	ZBE D1	Zinc finger, BED-type containing 1	10 .1 95	9. 66 7	9. 95 16 6	9. 15 81 2	8. 77 83 9	9. 79 11 2	-1. 619 269 742	-0. 695 343 333	1.6 19 26 97 42	D o w n	0.0 44 18 4	0.6 63 32 74 04
54 86 3	TOR 4A	Torsin family 4, member A	8. 37 77 6	7. 58 56 8	7. 83 67 3	6. 49 33 7	7. 28 54 5	7. 32 31 7	-1. 865 281 45	-0. 899 393 333	1.8 65 28 14 5	D o w n	0.0 20 86 17 74	0.6 63 32 74 04
80 16 9	CTC 1	CTS telomere maintenance complex component 1	7. 06 74 5	6. 81 60 6	6. 70 37 9	5. 96 14 7	6. 22 93 3	6. 43 40 2	-1. 573 699 41	-0. 654 16 41	1.5 73 69 94 1	D o w n	0.0 111 23 50 5	0.6 63 32 74 04
57 27	PTC H1	Patched 1	6. 73 63 3	7. 88 03 8	7. 40 34 8	9. 66 09 2	8. 65 18 7	8. 50 65 9	3.0 309 218 77	1.5 997 566 67	3.0 30 92 18 77	U p	0.0 04 89 72 67	0.6 63 32 74 04
98	ZNF	Zinc finger protein	4.	4.	3.	3.	3.	4.	-1.	-0.	1.5	D	0.0	0.6



49	518A	518A	63 89 9	30 91 9	91 57 9	68 53 5	15 32 4	03 40 3	584 198 738	663 753 333	84 19 87 38	o w n	44 06 78 21	63 32 74 04
79 92 5	SPEF 2	Sperm flagellar 2	2. 66 68 2	3. 30 79 5	3. 38 47 5	3. 89 21 1	3. 86 96 3	3. 46 69 41	1.5 401 348 41	0.6 230 566 67	1.5 40 13 48 41	U p	0.0 26 02 21 31	0.6 63 32 74 04
61 42	RPL1 8A	Ribosomal protein 118a	11 .4 76 01	11 .3 86 18	11 .8 54 99	12 .6 58 25	12 .0 31 64	11 .8 20 01	1.5 131 692 18	0.5 975 733 33	1.5 13 16 92 18	U p	0.0 49 63 14 06	0.6 63 32 74 04
85 01 2	TCE AL3	Transcription elongation factor A (SII)-like 3	8. 11 85	8. 72 42 3	8. 32 78	9. 84 90 5	8. 88 98 8	8. 76 18 2	1.7 132 551 22	0.7 767 4 22	1.7 13 25 51 22	U p	0.0 46 30 35 16	0.6 63 32 74 04
74 24	VEG FC	Vascular endothelial growth factor C	4. 00 81 9	6. 00 90 4	5. 28 10 4	7. 76 26 2	6. 78 02 4	6. 22 94 64	3.5 422 433 64	1.8 246 633 33	3.5 42 24 33 64	U p	0.0 15 40 60 99	0.6 63 32 74 04
74 33	VIPR 1	Vasoactive intestinal peptide receptor 1	8. 96 53 3	8. 73 12 2	9. 52 55 2	6. 59 35 1	6. 96 57 9	8. 47 08 8	-3. 318 727 098	-1. 730 63 70 98	3.3 18 72 70 98	D o w n	0.0 09 36 17 42	0.6 63 32 74 04

56 21	PRN P	Prion protein	5. 87 68 2	5. 03 59 9	5. 72 04 3	6. 77 58 1	6. 16 69 7	6. 53 28 19	1.9 284 833 19	0.9 474 666 67	1.9 28 48 33 19	U p	0.0 10 52 09 85	0.6 63 32 74 04
23 70 4	KCN E4	Potassium channel, voltage gated subfamily E regulatory $\beta$ subunit 4	3. 61 32 7	5. 18 08 2	3. 76 86 4	7. 73 32 2	5. 70 14 1	5. 94 31 9	4.8 289 069 59	2.2 716 966 67 59	4.8 28 90 69 59	U p	0.0 08 47 54 35	0.6 63 32 74 04
55 34 0	GIM AP5	Gtpase, IMAP family member 5	5. 00 17 8	5. 73 93 9	5. 83 87 4	7. 57 28 1	6. 65 78 8	6. 05 89 8	2.3 564 036 07	1.2 365 866 67	2.3 56 40 36 07	U p	0.0 19 79 49 8	0.6 63 32 74 04
86 3	CBF A2T3	Core-binding factor, runt domain, $\alpha$ subunit 2; translocated to, 3	4. 02 54 8	4. 52 13 6	4. 24 17 8	4. 91 05 9	5. 26 18 1	4. 64 91 4	1.5 995 210 74	0.6 776 4 10 74	1.5 99 52 10 74	U p	0.0 14 50 05 31	0.6 63 32 74 04
44 16 31	TSPA N11	Tetraspanin 11	5. 27 45 5	5. 54 38 5	5. 32 48 1	6. 99 74 5	6. 91 05 5	6. 20 49 5	2.5 022 859 55	1.3 232 466 67	2.5 02 28 59 55	U p	0.0 00 94 97 2	0.6 63 32 74 04
84 90 9	C9orf 3	Chromosome 9 open reading frame 3	5. 43 69 3	5. 38 56 2	5. 16 89 1	6. 94 42 3	5. 76 89 3	5. 99 82 3	1.8 746 656 79	0.9 066 333 33	1.8 74 66 56	U p	0.0 22 29 65	0.6 63 32 74

											79		48	04
34 92	IGH	Immunoglobulin heavy locus	8. 49 73 6	9. 04 95 4	8. 21 78 7	9. 41 80 9	11 .8 59 83	11 .5 63 57	5.1 298 145 33	2.3 589 066 67	5.1 29 81 45 33	U p	0.0 06 85 66 94	0.6 63 32 74 04
54 65	PPA RA	Peroxisome proliferator-activat ed receptor $\alpha$	8. 54 50 1	8. 67 86 8	8. 33 93 7	7. 86 63 6	7. 50 99 1	8. 29 91 1	-1. 546 735 669	-0. 629 226 667	1.5 46 73 56 69	D o w n	0.0 30 08 97 91	0.6 63 32 74 04
10 01 30 93 3	SMI M6	Small integral membrane protein 6	9. 05 13 4	8. 59 27 5	9. 03 10 9	7. 35 28 9	7. 67 79 9	8. 68 51 9	-1. 981 193 785	-0. 986 37 37	1.9 81 19 37 85	D o w n	0.0 26 00 67 11	0.6 63 32 74 04
84 08 4	RAB 6C	RAB6C, member RAS oncogene family	3. 74 72 6	2. 92 60 1	3. 45 54 7	3. 90 01 3	4. 23 96 4	4. 29 00 3	1.7 017 510 5	0.7 670 2 5	1.7 01 75 10 5	U p	0.0 11 79 69 62	0.6 63 32 74 04
31 78	HNR NPA	Heterogeneous nuclear ribonucleoprotein A1	10 .5 41 79	9. 84 63 8	10 .5 54 8	11 .2 45 93	10 .7 69 17	10 .7 90 45	1.5 378 200 2	0.6 208 866 67	1.5 37 82 00 2	U p	0.0 41 12 90 93	0.6 63 32 74 04
97 83	RIM S3	Regulating synaptic membrane exocytosis 3	4. 52 47	5. 10 6	4. 83 32	6. 13 68	5. 69 57	4. 95 45	1.7 104 429	0.7 743 7	1.7 10 44	U p	0.0 45 02	0.6 63 32

			6		5	1	3	8	67		29		67	74
											67		89	04
10	CEB	CCAAT/enhancer	8.	8.	8.	9.	10	8.	2.0	1.0	2.0	U	0.0	0.6
52	PD	binding protein	45	75	12	60	.3	55	758	536	75	p	46	63
		(C/EBP), Δ	61	25	26	63	33	21	228	833	82		02	32
			4	5	7	7	85	9	55	33	28		28	74
											55		16	04
19	S1PR	Sphingosine-1-pho	3.	5.	4.	7.	6.	6.	4.1	2.0	4.1	U	0.0	0.6
03	3	sphate receptor 3	92	95	17	52	24	49	913	674	91	p	09	63
			66	35	88	07	46	58	451	133	34		21	32
			6	4	1	1	7	7	6	33	51		08	74
											6		02	04
58	PYG	Phosphorylase,	3.	4.	3.	5.	4.	3.	1.8	0.9	1.8	U	0.0	0.6
36	L	glycogen, liver	21	11	80	06	82	97	779	091	77	p	30	63
			60	57	69	23	62	74	040	233	90		79	32
			9	1	3	4	9	7	26	33	40		70	74
											26		63	04
11	EPB4	EPB41L4A	8.	7.	8.	9.	8.	8.	1.7	0.7	1.7	U	0.0	0.6
49	1L4A	antisense RNA 1	09	70	01	30	42	41	135	770	13	p	26	63
15	-AS1		35	58	66	92	71	06	955	266	59		32	32
			1	6	5	2	9	9	83	67	55		07	74
											83			04
58	BCA	Branched chain	4.	4.	4.	6.	5.	5.	2.0	1.0	2.0	U	0.0	0.6
6	T1	amino-acid	08	99	49	14	43	01	099	071	09	p	22	63
		transaminase 1,	97	68	16	98	35	61	133	333	91		01	32
		cytosolic	1	2	2	2	7	6	88	33	33		92	74
											88		25	04
79	CEN	Centromere protein	3.	3.	3.	5.	6.	3.	2.6	1.4	2.6	U	0.0	0.6
68	PU	U	53	57	96	66	03	65	840	244	84	p	43	63

2			55 2	29 7	33 4	01 2	35 5	13 7	347 19	033 33	03 47 19		61 43 01	32 74 04
23	PPP1	Protein	7.	7.	7.	7.	8.	7.	1.6	0.7	1.6	U	0.0	0.6
64	R15	phosphatase 1	26	10	07	49	22	85	327	072	32	p	13	63
5	A	regulatory subunit 15A	21 3	52	92 8	05 4	17	62 3	304 87	866 67	73 04 87		30 25 15	32 74 04
55	ZCW	Zinc finger, CW	5.	5.	4.	4.	4.	4.	-1.	-0.	1.5	D	0.0	0.6
06	PW1	type with PWWP	44	02	78	14	50	59	588	667	88	o	17	63
3		domain 1	53 2	11	35 8	56 4	74 6	32 1	755 001	896 667	75 50 01	w n	96 14 4	32 74 04
62	BDH	3-hydroxybutyrate	7.	7.	7.	6.	6.	7.	-2.	-1.	2.2	D	0.0	0.6
2	1	dehydrogenase, type 1	84 84 5	99 43 3	31 65 2	15 85 9	07 01 6	48 33 5	217 703 765	149 066 667	17 70 37 65	o w n	24 62 78 18	63 32 74 04
30	ANX	Annexin A1	5.	7.	7.	9.	9.	7.	3.8	1.9	3.8	U	0.0	0.6
1	A1		49 85 5	68 22 5	30 17 9	23 26 8	39 40 4	64 63 9	110 098 4	301 733 33	11 00 98 4	p	24 23 29 82	63 32 74 04
28	FAM	Family with	9.	8.	8.	8.	8.	8.	-1.	-0.	1.5	D	0.0	0.6
60	83H	sequence similarity	14	73	67	10	55	11	509	593	09	o	24	63
77		83 member H	06 3	36 4	85 4	76 7	22 7	15	216 732	8	21 67 32	w n	07 62 79	32 74 04
20	EPH	EPH receptor A4	4.	4.	4.	5.	6.	5.	2.5	1.3	2.5	U	0.0	0.6

43	A4		66 03 3	83 17 2	23 72 7	38 98 3	69 76 2	70 44 9	565 649 29	542 066 67	56 56 49 29	p	06 27 41 55	63 32 74 04
53 84 1	CDH R5	Cadherin related family member 5	9. 25 72 7	8. 86 94 4	8. 44 68 2	7. 35 20 1	7. 51 84 7	8. 57 76 1	-2. 058 813 765	-1. 041 813 333	2.0 58 81 37 65	D o w n	0.0 24 70 41 73	0.6 63 32 74 04
74 74	WNT 5A	Wingless-type MMTV integration site family member 5A	4. 39 81	4. 59 91 7	4. 47 01 9	6. 11 44 3	5. 32 50 3	5. 54 90 6	2.2 558 742 77	1.1 736 866 67	2.2 55 87 42 77	U p	0.0 01 18 79 95	0.6 63 32 74 04
20 04	ELK 3	ELK3, ETS-domain protein (SRF accessory protein 2)	6. 83 25	7. 29 14 7	7. 81 05 3	8. 68 76 9	8. 69 45 5	7. 56 68 5	2.0 067 533 88	1.0 048 633 33	2.0 06 75 33 88	U p	0.0 33 18 88 45	0.6 63 32 74 04
10 23 0	NBR 2	Neighbor of BRCA1 gene 2 (non-protein coding)	6. 25 85 3	6. 55 83 8	6. 92 05 1	6. 02 64 5	5. 41 54 4	6. 27 99 2	-1. 593 136 63	-0. 671 87 63	1.5 93 13 66 3	D o w n	0.0 46 70 43 38	0.6 63 32 74 04
51 31 3	FAM 198B	Family with sequence similarity 198 member B	4. 17 22 6	4. 41 07 1	4. 57 91 1	7. 02 57 3	6. 34 05 8	4. 64 26 9	3.0 644 751 37	1.6 156 4 37	3.0 64 47 51 37	U p	0.0 23 07 79 71	0.6 63 32 74 04

54	FBLI	Filamin binding	9.	9.	8.	8.	8.	8.	-1.	-0.	1.6	D	0.0	0.6
75	M1	LIM protein 1	29	00	71	08	29	58	606	683	06	o	15	63
1			09	43	15	28	06	15	536	953	53	w	40	32
			1	7	8	5	5		026	333	60	n	79	74
											26		28	04
10	TGO	Trans-golgi	7.	7.	7.	6.	7.	7.	-1.	-0.	1.5	D	0.0	0.6
61	LN2	network protein 2	54	67	33	50	16	10	502	586	02	o	34	63
8			07	33	00	95	41	98	026	91	02	w	01	32
			5	9	6	4	3		223		62	n	23	74
											23		52	04
57	ARH	Rho gtpase	5.	6.	5.	7.	6.	6.	2.3	1.2	2.3	U	0.0	0.6
63	GAP	activating protein	03	10	52	53	77	10	823	523	82	p	19	63
6	23	23	62	40	13	88	87	11	411	8	34		33	32
			2	8	7	7	9	5	15		111		98	74
											5		91	04
12	NEU	Neuraminidase 4	7.	7.	7.	6.	6.	7.	-1.	-0.	1.5	D	0.0	0.6
98	4	(sialidase)	63	91	98	94	96	68	563	644	63	o	33	63
07			61	22	56	99	16	91	157	463	15	w	30	32
			6	7	8	8		4	701	333	77	n	89	74
											01		8	04
90	USP2	Ubiquitin specific	6.	5.	5.	3.	5.	5.	-2.	-1.	2.5	D	0.0	0.6
99		peptidase 2	73	88	96	81	20	50	550	350	50	o	22	63
			04	22	12	92	15	16	028	513	02	w	10	32
				3	5	2	2		433	333	84	n	11	74
											33		25	04
51	GMN	Geminin, DNA	6.	6.	6.	7.	7.	6.	1.7	0.7	1.7	U	0.0	0.6
05	N	replication	57	68	93	71	99	82	152	784	15	p	40	63
3		inhibitor	94	61	97	34	91	79	672	333	26		65	32
			1		7	9	5	4		33	72		46	74

													31	04
51	PDG	Platelet-derived	5.	7.	6.	9.	8.	7.	3.3	1.7	3.3	U	0.0	0.6
59	FRB	growth factor	74	25	59	04	30	51	809	574	80	p	08	63
		receptor, $\beta$	03	86	68	40	81	60	999	5	99		88	32
		polypeptide	1	9	8	3	4	6	62		99		42	74
											62		07	04
51	CD3	CD320 molecule	6.	6.	6.	7.	7.	6.	1.5	0.6	1.5	U	0.0	0.6
29	20		08	38	31	26	00	49	807	605	80	p	24	63
3			18	32	35	14	74	14	325	933	73		28	32
			7	1	8	7	8	9	94	33	25		21	74
											94		08	04
53	PMP	Peripheral myelin	7.	9.	8.	10	10	9.	2.7	1.4	2.7	U	0.0	0.6
76	22	protein 22	16	06	89	.2	.1	10	644	670	64	p	33	63
			55	56	87	94	30	67	963	166	49		04	32
			4	5	7	17	05	9	5	67	63		12	74
											5		45	04
83	GLT8	Glycosyltransferas	4.	5.	5.	7.	5.	5.	2.1	1.0	2.1	U	0.0	0.6
46	D2	e 8 domain	49	41	32	09	67	73	298	907	29	p	40	63
8		containing 2	69	59	55	89	73	44	571	566	85		93	32
			7	3	3	4	6		42	67	71		61	74
											42		41	04
55	APP	Adaptor protein,	8.	8.	9.	7.	8.	8.	-1.	-0.	1.5	D	0.0	0.6
19	L2	phosphotyrosine	95	73	12	93	19	83	537	620	37	o	47	63
8		interaction, PH	78	88	89	30	22	80	681	756	68	w	40	32
		domain and leucine	7	9		8	7	4	455	667	14	n	08	74
		zipper containing 2									55		55	04
86	SLC4	Solute carrier	9.	9.	8.	7.	8.	8.	-1.	-0.	1.8	D	0.0	0.6
71	A4	family 4 (sodium	20	07	72	41	26	61	873	906	73	o	25	63
		bicarbonate	98	58	57	18	32	82	899	043	89	w	78	32



		cotransporter), member 4		6	8	2	9		178	333	91	n	61	74
											78		04	04
66	SOA	Sterol	8.	7.	8.	7.	7.	7.	-1.	-0.	1.5	D	0.0	0.6
46	T1	O-acyltransferase 1	46	85	29	29	64	76	557	638	57	o	23	63
			68	88	90	84	84	13	047	813	04	w	02	32
			1	4	3	3	5	6	907	333	79	n	98	74
											07		2	04
37	PEA	Platelet endothelial	3.	3.	4.	6.	5.	4.	2.3	1.2	2.3	U	0.0	0.6
50	R1	aggregation	61	90	08	00	33	03	878	556	87	p	30	63
33		receptor 1	61	56	90	31	61	85	022	833	80		07	32
			1	2	9	4	8	5	02	33	22		94	74
											02		02	04
35	IGK	Immunoglobulin $\kappa$	9.	10	10	10	13	12	4.3	2.1	4.3	U	0.0	0.6
14	C	constant	98	.5	.0	.8	.1	.9	213	114	21	p	07	63
			69	22	69	78	14	19	437	8	34		52	32
			2	86	24	67	85	94	57		37		56	74
											57		87	04
64	ABC	ATP binding	8.	7.	8.	5.	3.	7.	-7.	-2.	7.1	D	0.0	0.6
24	G5	cassette subfamily	67	87	56	42	52	64	168	841	68	o	18	63
0		G member 5	81	63	18	15	19	75	940	76	94	w	43	32
			4	4	6	1	6	9	906		09	n	14	74
											06		98	04
56	PCD	Protocadherin $\alpha$ 12	7.	7.	6.	6.	6.	6.	-1.	-0.	1.5	D	0.0	0.6
13	HA1		44	73	91	53	83	80	557	639	57	o	31	63
7	2		20	45	29	69	18	31	526	256	52	w	81	32
			9	2	9		2	1	454	667	64	n	64	74
											54		86	04
18	E2F5	E2F transcription	7.	7.	7.	6.	6.	7.	-1.	-0.	1.6	D	0.0	0.6
75		factor 5,	79	41	99	89	80	38	636	710	36	o	18	63

		p130-binding	74 8	90 7	43 2	15 2	02 4	69 5	620 695	72	62 06 95	w n	51 15 3	32 74 04
50 19	OXC T1	3-oxoacid coa-transferase 1	3. 39 85 6	4. 50 65 7	3. 53 36 3	6. 68 59 9	4. 43 98 8	4. 70 30 7	2.7 575 620 19	1.4 633 933 33	2.7 57 56 20 19	U p	0.0 47 06 01 9	0.6 63 32 74 04
64 29 46	FLV CR1- AS1	FLVCR1 antisense RNA 1 (head to head)	7. 42 37 4	7. 08 02 6	7. 05 86 2	6. 20 56 5	6. 18 59 4	5. 72 75 3	-2. 215 808 701	-1. 147 833 333	2.2 15 80 87 01	D o w n	0.0 00 76 73 12	0.6 63 32 74 04
28 91 2	IGK V3-2 0	Immunoglobulin κ variable 3-20	2. 96 15 1	3. 44 17 2	3. 50 44 4	3. 70 34 7	7. 00 72 6	5. 93 52 2	4.7 439 648 93	2.2 460 933 33	4.7 43 96 48 93	U p	0.0 20 64 83 96	0.6 63 32 74 04
23 41 4	ZFP M2	Zinc finger protein, FOG family member 2	3. 26 45 1	3. 56 81 4	4. 38 59 6	6. 53 78 7	5. 16 30 7	4. 42 68 6	3.1 088 837 4	1.6 363 966 67	3.1 08 88 37 4	U p	0.0 19 74 49 35	0.6 63 32 74 04
79 63 3	FAT4	FAT atypical cadherin 4	4. 43 49 5	5. 15 70 5	4. 51 48 4	6. 99 33 9	6. 04 77 1	5. 75 31 3	2.9 535 772 25	1.5 624 633 33	2.9 53 57 72 25	U p	0.0 03 25 20 33	0.6 63 32 74 04
30	ST6	ST6	4.	4.	5.	6.	5.	5.	1.6	0.7	1.6	U	0.0	0.6

81	GAL	( $\alpha$ -N-acetyl-neuraminyl-2,3- $\beta$ -galactosyl-1,3)-N-acetylglucosaminide	92	42	02	17	31	12	754	445	75	p	47	63
5	NAC		94	53	93	44	49	83	012	066	40		33	32
6			7	4	3	3	1	2	64	67	12		89	74
		alactosaminide									64		38	04
		$\alpha$ -2,6-sialyltransferase 6												
39	ARH	Rho GDP dissociation inhibitor (GDI) $\beta$	6.	7.	7.	8.	8.	7.	1.7	0.8	1.7	U	0.0	0.6
7	GDI		77	57	75	47	35	69	485	061	48	p	41	63
B			55	37	31	68	30	09	188	333	51		17	32
			2	7	4	8	2	3	31	33	88		29	74
											31		56	04
12	KLH	Kelch domain containing 7A	7.	6.	6.	6.	5.	6.	-1.	-0.	1.5	D	0.0	0.6
77	DC7		07	58	58	13	88	36	531	615	31	o	23	63
07	A		53	58	19	94	96	81	851	276	85	w	49	32
			5	5		7	9	1	733	667	17	n	02	74
											33		18	04
34	ID4	Inhibitor of DNA binding 4, dominant negative helix-loop-helix protein	4.	3.	3.	6.	6.	6.	6.9	2.7	6.9	U	4.4	0.0
00			01	46	43	28	72	27	189	905	18	p	89	43
			14	48	63	25	43	73	510	533	95		4E-	85
			4	9	1	9	8	3	46	33	10		06	47
											46			1
87	SER	Serpin peptidase inhibitor, clade H (heat shock protein 47), member 1, (collagen binding protein 1)	6.	6.	6.	8.	7.	7.	1.7	0.7	1.7	U	0.0	0.6
1	PINH		82	71	81	25	20	24	185	811	18	p	33	63
1			74	45	43	36	30	31	359	8	53		15	32
			7		4	7	7	1	12		59		56	74
											12		47	04
11	CLIC	Chloride intracellular	3.	3.	3.	4.	5.	3.	2.3	1.2	2.3	U	0.0	0.6
93	2		13	52	69	98	26	75	228	159	22	p	16	63

		channel 2	31	49	24	63	00	19	993	266	89		35	32
			3	9	5	5	6	4	86	67	93		06	74
											86		45	04
71	TPM	Tropomyosin 4	8.	8.	8.	9.	9.	8.	1.6	0.7	1.6	U	0.0	0.6
71	4		76	62	28	83	23	79	586	300	58	p	37	63
			22	55	34	39	15	58	927	466	69		53	32
			9		1	5	5	4	44	67	27		39	74
											44		12	04
33	HSP	Heat shock protein	9.	8.	10	10	10	11	1.8	0.8	1.8	U	0.0	0.6
12	A8	family A (Hsp70)	92	99	.3	.6	.2	.0	420	813	42	p	48	63
		member 8	68	95	70	64	66	09	939	466	09		39	32
			5	5	01	72	23	5	8	67	39		47	74
											8		04	04
15	CXA	Coxsackie virus	12	12	12	11	11	12	-1.	-0.	1.7	D	0.0	0.6
25	DR	and adenovirus	.9	.7	.4	.6	.9	.1	718	780	18	o	05	63
		receptor	05	07	79	16	55	77	142	85	14	w	55	32
			64	81	23	88	4	85	862		28	n	20	74
											62		84	04
25	CLIC	Chloride	5.	5.	5.	7.	6.	5.	1.8	0.9	1.8	U	0.0	0.6
93	4	intracellular	64	84	70	25	69	95	736	058	73	p	25	63
2		channel 4	87	59	03	78	96	52	827	766	68		34	32
			9	4	3	5		4	09	67	27		21	74
											09		87	04
56	SERT	SERTA domain	4.	4.	4.	6.	5.	5.	1.9	0.9	1.9	U	0.0	0.6
25	AD4	containing 4	42	82	93	56	41	05	309	492	30	p	43	63
6			36	73	36	05	38	80	087	8	90		01	32
			8	6	4	9	9	4	66		87		10	74
											66		57	04
79	NSU	NOP2/Sun RNA	5.	4.	4.	3.	3.	4.	-2.	-1.	2.3	D	0.0	0.6

73 0	N7	methyltransferase family member 7	56 51 6	72 04 1	92 62 8	51 40 8	87 79 7	14 20 8	338 980 769	225 88 69	38 98 07 69	o w n	02 32 60 8	63 32 74 04
37 76 77	CA1 3	Carbonic anhydrase XIII	10 .0 83 86	9. 53 70 7	10 .0 97 13	7. 65 10 5	8. 45 95 5	9. 78 15 7	-2. 420 485 861	-1. 275 296 667	2.4 20 48 58 61	D o w n	0.0 40 07 85 89	0.6 63 32 74 04
20 09 58	MUC 20	Mucin 20, cell surface associated	9. 72 94 7	9. 50 13 9	8. 95 06 7	7. 34 98 5	8. 89 87 1	8. 70 46 6	-2. 108 333 851	-1. 076 103 333	2.1 08 33 38 51	D o w n	0.0 40 43 36 21	0.6 63 32 74 04
25 87 8	MXR A5	Matrix-remodelling associated 5	4. 37 30 1	5. 78 09 8	4. 83 67 8	7. 86 50 1	5. 79 49 1	6. 47 62 18	3.2 832 926 18	1.7 151 433 33	3.2 83 29 26 18	U p	0.0 20 09 79 16	0.6 63 32 74 04
82 91	DYS F	Dysferlin	4. 81 82 5	4. 64 03 8	4. 84 44 6	5. 39 93 8	5. 87 88 4	5. 17 56 8	1.6 436 882 16	0.7 169 366 67	1.6 43 68 82 16	U p	0.0 10 99 24 24	0.6 63 32 74 04
23 25 4	KAZ N	Kazrin, periplakin interacting protein	5. 10 34	5. 48 93 4	4. 79 63 2	5. 85 15 8	6. 55 85 3	5. 66 25 3	1.8 589 998 67	0.8 945 266 67	1.8 58 99 98 67	U p	0.0 17 46 57 33	0.6 63 32 74 04

12 85	COL 4A3	Collagen, type IV, $\alpha$ 3 (Goodpasture antigen)	6. 24 73 9	5. 31 36 9	5. 39 23 6	4. 78 21 6	4. 65 82 9	5. 05 80 4	-1. 763 347 322	-0. 818 316 667	1.7 63 34 73 22	D o w n	0.0 20 96 72 84	0.6 63 32 74 04
28 23	GPM 6A	Glycoprotein M6A	2. 89 51 5	4. 15 28 3	3. 23 80 2	4. 93 59 9	3. 91 67 3	4. 69 09 43	2.1 226 600 43	1.0 858 733 33	2.1 22 66 00 43	U p	0.0 24 70 17 66	0.6 63 32 74 04
35 8	AQP 1	Aquaporin 1 (Colton blood group)	12 .0 11 75	11 .7 22 46	11 .5 84 83	9. 94 09 8	9. 85 61 9	11 .7 29 71	-2. 401 695 639	-1. 264 053 333	2.4 01 69 56 39	D o w n	0.0 35 90 50 19	0.6 63 32 74 04
11 40 88	TRI M9	Tripartite motif containing 9	7. 00 50 2	7. 63 14 3	7. 34 75 3	5. 73 07 3	6. 20 22 4	7. 12 21 4	-1. 967 404 126	-0. 976 293 333	1.9 67 40 41 26	D o w n	0.0 31 71 18 19	0.6 63 32 74 04
51 77 6	ZAK	Sterile $\alpha$ motif and leucine zipper containing kinase AZK	7. 18 60 8	7. 41 76 1	7. 49 04 3	8. 77 94 9	7. 70 20 2	8. 01 10 7	1.7 404 817 26	0.7 994 866 67	1.7 40 48 17 26	U p	0.0 26 90 96 08	0.6 63 32 74 04
88 70	IER3	Immediate early response 3	8. 43 65 9	8. 64 74 7	8. 07 13 6	9. 63 07 6	10 .0 42 64	8. 53 22 1	2.0 233 557 51	1.0 167 5 57	2.0 23 35 57	U p	0.0 34 19 24	0.6 63 32 74

												51		75	04
51 29 9	NRN 1	Neuritin 1	4. 13 55 2	4. 25 42 1	5. 54 16 5	6. 04 69 6	7. 11 63 7	5. 16 51 7	2.7 619 425 93	1.4 656 833 33	2.7 61 94 25 93	U p	0.0 34 77 09 59	0.6 63 32 74 04	
54 14	SEPT 4	Septin 4	3. 72 62 8	4. 55 20 2	3. 80 54 2	6. 37 77 9	5. 78 83 8	4. 24 86 4	2.7 201 697 16	1.4 436 966 67 16	2.7 20 16 97 16	U p	0.0 30 27 63 59	0.6 63 32 74 04	
17 03 94	PW WP2 B	PWWP domain containing 2B	8. 56 76 1	7. 93 8 1	8. 10 94 1	7. 35 76 1	7. 62 08 3	7. 76 42 7	-1. 541 252 605	-0. 624 103 333	1.5 41 25 26 05	D o w n	0.0 23 67 11 61	0.6 63 32 74 04	
40 45	LSA MP	Limbic system-associated membrane protein	4. 09 44 6	4. 78 86 4	4. 37 24 7	4. 96 37 2	5. 22 78 3	4. 91 84 9	1.5 349 127 68	0.6 181 566 67	1.5 34 91 27 68	U p	0.0 21 00 91 57	0.6 63 32 74 04	
57 47 6	GRA MD1 B	GRAM domain containing 1B	10 .2 24 44	9. 77 06 2	9. 81 41 2	8. 19 06 8	9. 25 89 9	9. 39 21 3	-1. 984 983 021	-0. 989 126 667	1.9 84 98 30 21	D o w n	0.0 21 25 33 36	0.6 63 32 74 04	
96 48	GCC 2	GRIP and coiled-coil domain containing 2	7. 66 18	6. 99 29	6. 96 16	6. 47 66	6. 34 25	6. 83 25	-1. 574 474	-0. 654 87	1.5 74 47	D o w	0.0 33 03	0.6 63 32	

			1	5		8	4	3	072		40	n	08	74
											72		84	04
57	PTK	Protein tyrosine	3.	4.	3.	6.	4.	4.	2.6	1.4	2.6	U	0.0	0.6
54	7	kinase 7 (inactive)	99	49	87	68	95	93	432	023	43	p	21	63
			34	01	64	07	32	31	996	4	29		57	32
				9	6	4	1	2	84		96		94	74
											84		24	04
56	PRSS	Protease, serine 8	11	10	10	9.	9.	10	-2.	-1.	2.2	D	0.0	0.6
52	8		.1	.9	.4	02	74	.2	261	177	61	o	09	63
			60	32	14	53	13	09	541	306	54	w	84	32
			83	85	71		1	86	808	667	18	n	79	74
											08		11	04
11	CFA	Cilia and flagella	6.	5.	6.	4.	4.	5.	-2.	-1.	2.6	D	0.0	0.6
84	P70	associated protein	70	80	55	48	70	73	604	380	04	o	08	63
91	70		92	00	15	25	37	23	067	766	06	w	83	32
			7	3	9	4	3	2	178	667	71	n	90	74
											78		36	04
54	NEU	Neuralized E3	5.	6.	6.	8.	8.	7.	3.8	1.9	3.8	U	0.0	0.6
49	RL1	ubiquitin protein	15	80	33	69	31	12	487	443	48	p	08	63
2	B	ligase 1B	55	94	36	33	80	03	056	733	70		26	32
			5	2	5	9	4	1	38	33	56		38	74
											38		79	04
11	RWD	RWD domain	6.	6.	6.	6.	5.	6.	-1.	-0.	1.6	D	0.0	0.6
26	D2A	containing 2A	90	27	87	01	78	11	642	715	42	o	14	63
11			71	70	30	21	19	65	139	576	13	w	20	32
				8	8	1	1	1	474	667	94	n	17	74
											74		55	04
93	SLC9	Solute carrier	11	10	10	9.	10	10	-1.	-0.	1.8	D	0.0	0.6
68	A3R	family 9, subfamily	.2	.9	.9	38	.3	.7	801	848	01	o	43	63



	1	A (NHE3, cation proton antiporter 3), member 3 regulator 1	25 51	05 69	05 69	27 2	29 44	78 32	006 432	803 333	00 64 32	w n	91 69 1	32 74 04
33 99	ID3	Inhibitor of DNA binding 3, dominant negative helix-loop-helix protein	5. 24 54 8	5. 21 87 6	4. 94 00 3	8. 07 54 9	8. 03 25 9	6. 91 18 3	5.8 099 134 28	2.5 385 166 67	5.8 09 91 34 28	U p	0.0 00 111 35 7	0.4 35 11 63 4
28 89 3	IGK V1D- 39	Immunoglobulin $\kappa$ variable 1D-39	5. 10 81 6	5. 31 25 7	4. 80 69 8	6. 05 00 9	9. 17 36 8	8. 94 53 8	7.8 924 871 14	2.9 804 8 14	7.8 92 48 71 14	U p	0.0 06 50 31 33	0.6 63 32 74 04
14 34 58	LDL RAD 3	Low density lipoprotein receptor class A domain containing 3	5. 05 26 9	5. 41 39 4	5. 03 20 9	7. 08 29 2	7. 38 31 1	5. 54 76 6	2.8 382 270 39	1.5 049 9 39	2.8 38 22 70 39	U p	0.0 13 67 28 86	0.6 63 32 74 04
11 27 24	RDH 13	Retinol dehydrogenase 13 (all-trans/9-cis)	9. 32 73 5	9. 26 26 8	8. 59 00 8	8. 11 65 1	8. 56 50 7	8. 60 37 3	-1. 549 282 25	-0. 631 6 25	1.5 49 28 22 5	D o w n	0.0 41 01 63 78	0.6 63 32 74 04
14 39 03	LAY N	Layilin	3. 65 37 3	6. 06 18 8	4. 07 45 6	7. 59 53 7	6. 56 29 5	5. 88 90 4	4.2 448 983 3	2.0 857 3 83 3	4.2 44 89 83 3	U p	0.0 19 03 97 69	0.6 63 32 74 04

32	APB	Amyloid $\beta$ (A4)	5.	5.	5.	6.	5.	5.	1.7	0.8	1.7	U	0.0	0.6
3	B2	precursor	09	18	41	58	91	60	468	047	46	p	19	63
		protein-binding,	50	13	20	37	25	62	027	166	80		39	32
		family B, member	1		4	5		5	01	67	27		98	74
		2									01		75	04
70	TGF	Transforming	3.	3.	3.	4.	4.	4.	2.0	1.0	2.0	U	0.0	0.6
43	B3	growth factor $\beta$ 3	38	88	50	91	43	48	304	218	30	p	01	63
			19	16	50	45	88	06	835	233	48		17	32
				5	7	7	8	4	42	33	35		98	74
											42		61	04
35	IGK	Immunoglobulin $\kappa$	5.	4.	5.	6.	9.	8.	6.6	2.7	6.6	U	0.0	0.6
25	V1O	variable 1/OR1-1	42	89	48	01	11	90	900	420	90	p	09	63
	R1-1	(pseudogene)	99	86	02	56	58	33	175	1	01		79	32
			9	3	1	4	5	7	71		75		54	74
											71		34	04
79	ARH	Rho guanine	7.	7.	6.	6.	6.	6.	-1.	-0.	1.5	D	0.0	0.6
84	GEF	nucleotide	75	05	95	54	44	87	547	629	47	o	42	63
	5	exchange factor 5	23	24	19	29	79	70	089	556	08	w	87	32
			1		3		9	8	507	667	95	n	63	74
											07		89	04
51	TAF9	TATA-box binding	4.	4.	4.	5.	4.	5.	1.6	0.7	1.6	U	0.0	0.6
61	B	protein associated	50	24	75	48	95	16	256	010	25	p	11	63
6		factor 9b	45	06	43	55	16	54	612	266	66		04	32
			4	6	6	9		5	52	67	12		90	74
											52		49	04
37	ITPR	Inositol	4.	7.	6.	8.	7.	7.	3.3	1.7	3.3	U	0.0	0.6
08	1	1,4,5-trisphosphate	93	04	02	64	20	34	221	320	22	p	22	63
		receptor, type 1	59	62	09	32	73	88	026	966	10		05	32
			7	7	4	4	6	7	84	67	26		97	74

												84		96	04
14	SAM	Sterile $\alpha$ motif	6.	6.	6.	7.	7.	6.	1.7	0.8	1.7	U	0.0	0.6	
83	D11	domain containing	12	82	44	88	11	93	964	451	96	p	26	63	
98		11	42	06	51	02	07	44	764	7	47		09	32	
			9		2	8	8	6	21		64		47	74	
											21		07	04	
84	ANT	Anthrax toxin	4.	8.	6.	10	8.	8.	4.7	2.2	4.7	U	0.0	0.6	
16	XR1	receptor 1	76	07	71	.0	07	11	352	434	35	p	40	63	
8			06	88	07	96	39	01	152	3	21		66	32	
				3		35	7		23		52		08	74	
											23		59	04	
65	SLC2	Solute carrier	6.	6.	7.	5.	6.	6.	-1.	-0.	1.6	D	0.0	0.6	
81	2A3	family 22 (organic	99	64	04	51	26	62	691	758	91	o	39	63	
		cation transporter),	62	10	69	06	93	82	848	6	84	w	69	32	
		member 3	2	4		9	8	9	048		80	n	13	74	
											48		86	04	
78	TUB	Tubulin, $\alpha$ 1a	8.	10	9.	11	10	10	2.8	1.5	2.8	U	0.0	0.6	
46	A1A		31	.2	13	.4	.6	.1	965	343	96	p	20	63	
			38	17	98	30	49	94	588	4	55		44	32	
			7	72	9	32	97	21	96		88		35	74	
											96		08	04	
28	IGK	Immunoglobulin $\kappa$	2.	3.	3.	3.	7.	5.	4.7	2.2	4.7	U	0.0	0.6	
87	V3D-	variable 3D-20	96	44	50	70	00	93	439	460	43	p	20	63	
4	20		15	17	44	34	72	52	648	933	96		64	32	
			1	2	4	7	6	2	93	33	48		83	74	
											93		96	04	
44	MSN	Moesin	6.	7.	7.	9.	8.	7.	2.4	1.2	2.4	U	0.0	0.6	
78			61	39	68	10	64	82	495	925	49	p	13	63	
			08	49	92	67	13	45	894	4	58		98	32	

			2	8	8	4	9	7	93		94		59	74
											93		06	04
27	LAM	Lysosomal-associat	4.	4.	4.	5.	5.	4.	1.7	0.7	1.7	U	0.0	0.6
07	P3	ed membrane	02	01	37	45	00	26	047	695	04	p	38	63
4		protein 3	13	37	47	45	35	04	497	6	74		14	32
				9	8	2	5	8	82		97		73	74
											82		84	04
10	LOC	Uncharacterized	9.	9.	8.	8.	8.	8.	-1.	-0.	1.7	D	0.0	0.6
02	1002	LOC100287175	58	31	65	14	00	97	753	810	53	o	47	63
87	8717		04	67	10	05	28	48	235	02	23	w	80	32
17	5		6	6	4	5	4	1	747		57	n	00	74
5											47		75	04
65	SLC2	Solute carrier	6.	6.	6.	4.	5.	6.	-2.	-1.	2.2	D	0.0	0.6
80	2A1	family 22 (organic	74	52	61	66	43	31	228	156	28	o	20	63
		cation transporter),	75	66	04	98	00	58	845	296	84	w	46	32
		member 1	8	3	6	9	4	5	58	667	55	n	14	74
											8		18	04
48	ATP1	Atpase, Na+/K+	4.	4.	4.	5.	5.	4.	1.5	0.6	1.5	U	0.0	0.6
2	B2	transporting, $\beta$ 2	37	22	37	01	09	68	232	071	23	p	06	63
		polypeptide	24	65	24	32	62	33	435	466	24		32	32
			7	4	7	6	7	9	87	67	35		61	74
											87		29	04
34	CLE	C-type lectin	6.	6.	6.	4.	5.	5.	-2.	-1.	2.1	D	0.0	0.6
81	C18	domain family 18,	87	64	15	97	72	75	110	077	10	o	07	63
74	A	member A	89	41	82	01	35	50	439	543	43	w	09	32
			9	8		8	3	3	297	333	92	n	44	74
											97		89	04
96	CD4	CD44 molecule	5.	4.	5.	7.	7.	4.	3.1	1.6	3.1	U	0.0	0.6
0	4	(Indian blood	11	71	00	39	39	95	061	351	06	p	37	63

		group)	94	20	93	98	43	20	266	166	12		16	32
			7	9	9	2	9	9	74	67	66		86	74
											74		41	04
10	ARL	ADP ribosylation	9.	8.	9.	9.	9.	9.	1.5	0.6	1.5	U	0.0	0.6
55	6IP5	factor like gtpase 6	04	83	07	76	50	57	501	324	50	p	04	63
0		interacting protein	44	66	20	83	81	40	988	533	19		90	32
		5	9	9	1	9	1	5	99	33	88		56	74
											99		45	04
64	MT1I	Metallothionein 1I,	6.	6.	6.	5.	5.	6.	-1.	-0.	1.5	D	0.0	0.6
43	P	pseudogene	51	46	62	43	87	27	592	670	92	o	23	63
14			29	20	71	70	64	59	069	903	06	w	43	32
			8	6	4	9	5	3	519	333	95	n	69	74
											19		9	04
35	IGH	Immunoglobulin	6.	7.	6.	7.	10	8.	3.5	1.8	3.5	U	0.0	0.6
02	G3	heavy constant $\gamma$ 3	96	48	70	76	.3	63	999	479	99	p	18	63
		(G3m marker)	97	78	47	40	05	67	910	933	99		41	32
			1	7	9	2	54	9	84	33	10		96	74
											84		03	04
81	MAD	Mucosal vascular	5.	6.	5.	6.	8.	6.	2.9	1.5	2.9	U	0.0	0.6
74	CAM	addressin cell	42	35	22	97	39	24	038	379	03	p	29	63
	1	adhesion molecule	64	69	76	90	93	64	025	433	80		08	32
		1	5	3	6	6	9	2	01	33	25		76	74
											01		89	04
79	MM	Multimerin 2	4.	5.	5.	6.	7.	5.	2.4	1.3	2.4	U	0.0	0.6
81	RN2		52	13	27	60	17	08	782	093	78	p	39	63
2			22	42	34	16	20	42	183	033	21		82	32
			9	6	6	4	3	5	98	33	83		71	74
											98		51	04
48	NOS	Nitric oxide	3.	4.	4.	5.	6.	4.	2.2	1.1	2.2	U	0.0	0.6

46	3	synthase 3	92	16	17	42	11	18	202	507	20	p	36	63
			41	78	83	18	15	91	518	233	25		44	32
			5	3	4	2	6	1	47	33	18		45	74
											47		61	04
14	TTC	Tetratricopeptide	4.	5.	5.	6.	6.	5.	2.0	1.0	2.0	U	0.0	0.6
55	7B	repeat domain 7B	71	69	24	74	28	69	328	235	32	p	20	63
67			01	55	45	50	57	00	634	133	86		52	32
			7	2	7	3	2	5	82	33	34		97	74
											82		82	04
72	INS-I	INS-IGF2	6.	6.	7.	8.	8.	7.	2.3	1.2	2.3	U	0.0	0.6
39	GF2	readthrough	76	86	33	62	74	23	133	1	13	p	21	63
61			55	78	06	01	29	09	763		37		90	32
			2	1	6	2	7		68		63		93	74
											68		35	04
23	COB	Cordon-bleu WH2	7.	6.	7.	5.	5.	6.	-2.	-1.	2.4	D	0.0	0.6
24	L	repeat protein	19	87	04	44	35	45	445	290	45	o	04	63
2			92	33	57	59	07	07	800	306	80	w	08	32
			3	4	7	8		4	392	667	03	n	95	74
											92		19	04
29	GST	Glutathione	6.	6.	5.	5.	5.	5.	-1.	-0.	1.9	D	0.0	0.6
54	Z1	S-transferase zeta 1	54	71	98	26	47	60	956	968	56	o	03	63
			93	37	72	73	30	54	384	19	38	w	81	32
			5		8	1	5		582		45	n	68	74
											82		36	04
39	LIPA	Lipase A,	6.	5.	5.	6.	6.	6.	1.9	0.9	1.9	U	0.0	0.6
88		lysosomal acid,	14	42	78	81	59	94	971	979	97	p	02	63
		cholesterol esterase	44	53	66	94	01	06	693	566	16		89	32
			2	2	7	9	4	5	44	67	93		66	74
											44		18	04

11	ABC	ATP binding	6.	6.	6.	5.	5.	5.	-1.	-0.	1.6	D	0.0	0.6
19	B8	cassette subfamily	06	36	15	29	31	94	601	679	01	o	18	63
4		B member 8	90	25	93	60	01	77	055	023	05	w	51	32
			4		7	1	1	2	516	333	55	n	46	74
											16		88	04
39	LIFR	Leukemia	4.	4.	4.	5.	6.	4.	2.2	1.1	2.2	U	0.0	0.6
77		inhibitory factor	89	41	56	87	75	70	261	545	26	p	46	63
		receptor $\alpha$	32	56	78	73	55	76	744	666	17		59	32
			8	3	6	2	3	2	74	67	44		66	74
											74		43	04
25	SNE	Sushi, nidogen and	3.	4.	4.	4.	5.	4.	2.0	1.0	2.0	U	0.0	0.6
99	D1	EGF-like domains	49	26	06	96	63	28	286	204	28	p	25	63
2		1	93	07	25	66	14	59	031	866	60		09	32
			5	7	7	9	8	8	56	67	31		13	74
											56		76	04
27	AMY	Amylase, $\alpha$ 1B	8.	8.	8.	7.	7.	8.	-1.	-0.	1.6	D	0.0	0.6
7	1B	(salivary)	63	58	49	49	82	12	695	761	95	o	06	63
			92	12	99	12	35	14	126	393	12	w	00	32
			8	6	3	9	6	4	963	333	69	n	48	74
											63		73	04
98	SEPT	Septin 7	6.	5.	6.	7.	6.	6.	1.6	0.7	1.6	U	0.0	0.6
9	7		05	79	09	09	39	57	290	040	29	p	15	63
			66	35	39	15	13	35	904	666	09		78	32
			9	9	4	2	4	6	04	67	04		82	74
											04		56	04
28	PDX	Pyridoxal-depende	5.	5.	5.	6.	5.	6.	1.6	0.7	1.6	U	0.0	0.6
39	DC2	nt decarboxylase	40	29	91	56	68	53	480	207	48	p	44	63
70	P	domain containing	27	94	79	33	66	25	309	433	03		35	32
		2, pseudogene	7	9	9	4	3	1	46	33	09		87	74

											46			04
86 11	PLPP 1	Phospholipid phosphatase 1	7. 40 41 3	7. 71 33 8	7. 60 49 8	9. 09 12 6	8. 62 13 2	8. 46 05 3	2.2 194 978 84	1.1 502 333 33	2.2 19 49 78 84	U p	0.0 00 90 14 67	0.6 63 32 74 04
80 76 0	ITIH 5	Inter- $\alpha$ -trypsin inhibitor heavy chain family member 5	4. 92 59 9	6. 41 78 4	5. 00 68 2	7. 29 43 3	6. 36 02 2	6. 30 22 9	2.3 006 847 83	1.2 020 633 33	2.3 00 68 47 83	U p	0.0 34 79 12 02	0.6 63 32 74 04
22 47	FGF2	Fibroblast growth factor 2 (basic)	2. 81 25 9	3. 52 82 6	3. 12 15 1	4. 75 36 4	4. 05 60 3	3. 60 29 9	1.9 771 650 83	0.9 834 333 33	1.9 77 16 50 83	U p	0.0 16 29 96 29	0.6 63 32 74 04
15 15 56	GPR 155	G protein-coupled receptor 155	5. 34 21 5	5. 71 05 6	5. 11 90 6	7. 40 56 4	6. 20 43 7	5. 68 40 6	2.0 573 491 7	1.0 407 866 67	2.0 57 34 91 7	U p	0.0 45 67 23 99	0.6 63 32 74 04
28 82 4	IGLV 1-41	Immunoglobulin lambda variable 1-41 (pseudogene)	5. 07 23 8	4. 98 42 5	5. 12 46 1	5. 37 98 6	6. 83 04 2	7. 06 93 7	2.5 777 934 44	1.3 661 366 67	2.5 77 79 34 44	U p	0.0 14 36 23 89	0.6 63 32 74 04
10 36	CDO 1	Cysteine dioxygenase type 1	4. 28 11	5. 44 08	4. 99 90	7. 08 09	6. 22 69	5. 74 67	2.7 217 036	1.4 445 1	2.7 21 70	U p	0.0 09 97	0.6 63 32



			6	9	4	7	2	3	71		36		69	74
											71		41	04
17	SYN	Synaptopodin 2	4.	6.	4.	8.	7.	6.	5.1	2.3	5.1	U	0.0	0.6
10	PO2		05	72	79	65	04	96	451	632	45	p	15	63
24			87	22	73	69	38	72	031		10		43	32
			8	3	9	4		6	47		31		39	74
											47		09	04
10	TSPA	Tetraspanin 5	3.	4.	3.	5.	5.	3.	2.6	1.3	2.6	U	0.0	0.6
09	N5		13	41	61	79	54	96	024	798	02	p	34	63
8			70	07	35	65	23	21	672	8	46		96	32
			6	8	5	5	1	7	35		72		56	74
											35		26	04
54	FNB	Formin binding	5.	4.	4.	3.	4.	4.	-1.	-0.	1.5	D	0.0	0.6
87	P1L	protein 1-like	32	94	82	87	53	77	558	639	58	o	44	63
4			68	93	62	63	34	29	231	91	23	w	83	32
			5	8			8	2	949		19	n	38	74
											49		66	04
62	RRA	Related RAS viral	7.	8.	8.	9.	8.	8.	1.6	0.6	1.6	U	0.0	0.6
37	S	(r-ras) oncogene	69	03	29	19	49	42	203	963	20	p	34	63
		homolog	04	51	8	18	87	19	925	433	39		09	32
			2			3	7	5	23	33	25		33	74
											23		91	04
40	CYP	Cytochrome P450,	9.	9.	9.	7.	8.	9.	-2.	-1.	2.3	D	0.0	0.6
51	4F3	family 4, subfamily	82	95	63	67	73	39	306	205	06	o	21	63
		F, polypeptide 3	64	68	39	32	66	04	416	653	41	w	02	32
			5	8	5	3	2	7	932	333	69	n	86	74
											32		49	04
23	RGL	Ral guanine	3.	4.	4.	5.	4.	4.	1.8	0.8	1.8	U	0.0	0.6
17	1	nucleotide	32	17	38	11	88	53	422	814	42	p	21	63

9		dissociation stimulator-like 1	42 7	10 7	89 5	56 5	24 3	05 7	301 81	533 33	23 01 81		73 25 98	32 74 04
36 25	INH BB	Inhibin $\beta$ B	5. 26 01 9	5. 19 53 9	4. 74 96 8	6. 44 79 9	6. 13 55 5	5. 52 02 3	1.9 536 472 52	0.9 661 7 72 52	1.9 53 64 72 52	U p	0.0 09 69 40 38	0.6 63 32 74 04
47 7	ATP1 A2	Atpase, Na <sup>+</sup> /K <sup>+</sup> transporting, $\alpha$ 2 polypeptide	4. 41 42 1	6. 17 90 8	5. 01 26 7	6. 31 97 8	7. 55 74 9	6. 08 23 5	2.7 343 918 46	1.4 512 2 46	2.7 34 39 18 46	U p	0.0 311 16 05 6	0.6 63 32 74 04
38 22	KLR C2	Killer cell lectin-like receptor subfamily C, member 2	4. 71 45 9	5. 20 65 8	5. 70 24 8	4. 62 74 6	3. 76 04 8	4. 40 00 8	-1. 925 469 139	-0. 945 21 139	1.9 25 46 91 39	D o w n	0.0 20 16 58 71	0.6 63 32 74 04
84 36	SDP R	Serum deprivation response	4. 81 80 6	6. 82 06 5	5. 17 57 2	7. 97 09 5	7. 38 34 6	7. 48 44 2	4.0 226 140 73	2.0 081 333 33	4.0 22 61 40 73	U p	0.0 05 32 60 82	0.6 63 32 74 04
16 66 14	DCL K2	Doublecortin like kinase 2	4. 49 42	5. 59 06 5	5. 01 64 3	6. 90 59 5	5. 79 37 7	5. 63 38 3	2.1 102 637 63	1.0 774 233 33	2.1 10 26 37 63	U p	0.0 33 46 19 95	0.6 63 32 74 04
26	LRR	Leucine rich repeat	5.	6.	5.	8.	7.	6.	3.2	1.6	3.2	U	0.0	0.6

15	C32	containing 32	18 46 3	34 27 4	72 18	71 48	05 7	55 35 7	311 924 2	920 666 67	31 19 24 2	p	21 00 29 34	63 32 74 04
29 76 3	PAC SIN3	Protein kinase C and casein kinase substrate in neurons 3	4. 43 97 8	4. 61 27 9	4. 44 27	6. 49 19 5	4. 87 70 4	5. 08 55 5	1.9 825 033 91	0.9 873 233 33 91	1.9 82 50 33	U p	0.0 45 22 13 48	0.6 63 32 74 04
59 34 5	GNB 4	Guanine nucleotide binding protein (G protein), $\beta$ polypeptide 4	5. 87 04 4	6. 87 00 5	6. 80 49 2	8. 59 05 2	8. 00 63 2	7. 06 51 6	2.5 886 322 04	1.3 721 9 04	2.5 88 63 22 04	U p	0.0 16 38 89 68	0.6 63 32 74 04
80 31 8	GKA P1	G kinase anchoring protein 1	6. 41 32 1	6. 34 84 6	6. 20 58 4	5. 12 83 2	5. 72 06 3	5. 89 70 3	-1. 670 766 359	-0. 740 51 63 59	1.6 70 76 63 59	D o w n	0.0 14 06 63 13	0.6 63 32 74 04
12 72	CNT N1	Contactin 1	2. 26 38 4	4. 71 03 6	2. 91 31 1	5. 80 00 6	6. 36 30 3	4. 81 62 4	5.1 479 807 78	2.3 640 066 67	5.1 47 98 07 78	U p	0.0 08 93 19 41	0.6 63 32 74 04
29 96 5	CDIP 1	Cell death-inducing p53 target 1	7. 99 75 7	8. 09 96 6	7. 39 68	6. 76 56	7. 16 70 8	7. 37 66 6	-1. 656 605 404	-0. 728 23	1.6 56 60 54 04	D o w n	0.0 24 24 05 23	0.6 63 32 74 04

93 08	CD8 3	CD83 molecule	4. 18 59 7	4. 82 62 3	4. 82 62 3	5. 33 86 5	5. 07 78 4	5. 75 46 3	1.7 142 331 4	0.7 775 633 33	1.7 14 23 31 4	U p	0.0 18 22 70 45	0.6 63 32 74 04
38 83 72	CCL 4L1	Chemokine (C-C motif) ligand 4-like 1	5. 72 31 6	6. 37 54 2	6. 64 34 5	6. 68 61 8	8. 05 00 2	7. 55 12 2	2.2 685 807 29	1.1 817 9 29	2.2 68 58 07 29	U p	0.0 19 15 84 57	0.6 63 32 74 04
35 01	IGH G2	Immunoglobulin heavy constant $\gamma$ 2 (G2m marker)	6. 96 97 1	7. 48 78 7	6. 70 47 9	7. 76 40 2	10 .3 05 54	8. 63 67 9	3.5 999 910 84	1.8 479 933 33	3.5 99 99 10 84	U p	0.0 18 41 96 03	0.6 63 32 74 04
51 24 1	COX 16	COX16 cytochrome c oxidase assembly homolog	7. 77 00 8	7. 45 92 3	7. 68 22 4	6. 65 13 4	7. 02 37 3	7. 46 87 3	-1. 504 460 957	-0. 589 246 667	1.5 04 46 09 57	D o w n	0.0 41 26 49 22	0.6 63 32 74 04
85 36 0	SYD E1	Synapse defective 1, Rho gtpase, homolog 1 (C. Elegans)	5. 21 42 2	6. 79 17 2	5. 60 96 5	7. 58 28 2	7. 00 48 5	6. 38 72 8	2.1 731 483 55	1.1 197 866 67	2.1 73 14 83 55	U p	0.0 46 52 14 95	0.6 63 32 74 04
10 81 0	WAS F3	WAS protein family member 3	5. 12 83 2	5. 97 46 7	6. 11 87 7	6. 59 05 5	6. 53 87 2	6. 33 08 6	1.6 772 797 5	0.7 461 233 33	1.6 77 27 97	U p	0.0 31 25 98	0.6 63 32 74

											5		38	04
22	FOX	Forkhead box F2	4.	4.	4.	5.	5.	5.	1.9	0.9	1.9	U	0.0	0.6
95	F2		16	96	37	60	46	28	331	509	33	p	04	63
			54	73	52	56	57	95	407	466	14		57	32
			8	2	3		6	1	29	67	07		55	74
											29		52	04
99	WDR	WD repeat domain	5.	4.	5.	6.	5.	6.	1.6	0.7	1.6	U	0.0	0.6
48	1	1	52	68	21	05	50	03	526	247	52	p	29	63
			49	29	98	28	99	91	142	5	61		64	32
			5	5	8	8	7	8	35		42		95	74
											35		94	04
71	TSPA	Tetraspanin 4	5.	6.	6.	7.	7.	7.	2.1	1.0	2.1	U	0.0	0.6
06	N4		46	82	82	96	21	14	008	709	00	p	37	63
			82	02	23	63	10	63	793	933	87		41	32
			1	4	8	9	5	7	8	33	93		39	74
											8		18	04
64	AEN	Apoptosis	8.	7.	7.	6.	7.	6.	-1.	-0.	1.6	D	0.0	0.6
78		enhancing nuclease	35	89	39	86	56	92	694	760	94	o	40	63
2			81	43	25	59	83	79	610	953	61	w	48	32
			6	2	6		7	1	054	333	00	n	87	74
											54		49	04
11	GLIP	GLI	4.	5.	4.	6.	5.	5.	2.3	1.2	2.3	U	0.0	0.6
01	R1	pathogenesis-relate	30	33	61	90	28	70	124	093	12	p	31	63
0		d 1	65	66	67	19	2	42	091	966	40		91	32
			5	9	6	2		7	19	67	91		79	74
											19		84	04
14	CCM	Cerebral cavernous	4.	5.	4.	5.	5.	5.	1.5	0.6	1.5	U	0.0	0.6
07	2L	malformation	50	14	83	53	72	04	226	065	22	p	42	63
06		2-like	31	07	89	63	60	01	172	533	61		48	32

			8	2	6	3	7	2	56	33	72		93	74
											56		46	04
84	C19o	Chromosome 19	5.	5.	5.	4.	4.	4.	-1.	-0.	1.8	D	0.0	0.6
16	rf44	open reading frame	43	37	27	92	30	29	810	856	10	o	04	63
7		44	15	92	91	36	65	12	222	166	22	w	11	32
			7		6	4	5	4	039	667	20	n	54	74
											39		78	04
28	AMY	Amylase, $\alpha$ 2B	8.	7.	7.	6.	6.	7.	-1.	-0.	1.6	D	0.0	0.6
0	2B	(pancreatic)	01	38	61	45	91	48	650	722	50	o	46	63
			81	33	35	25	05	41	107	56	10	w	37	32
			1	3		5	5	6	483		74	n	38	74
											83		05	04
55	GOL	Golgin A2	5.	5.	5.	4.	4.	4.	-1.	-0.	1.5	D	0.0	0.6
59	GA2	pseudogene 5	49	52	22	50	84	90	581	661	81	o	06	63
2	P5		02	17	04	49	31	06	408	21	40	w	86	32
			5	2	1	4	4	7	408		84	n	44	74
											08		65	04
13	CMB	Carboxymethylene	10	10	10	9.	9.	10	-1.	-0.	1.7	D	0.0	0.6
41	L	butenolidase	.7	.2	.9	69	54	.4	711	774	111	o	30	63
47		homolog	48	88	49	16	23	28	103	926	03	w	11	32
		(Pseudomonas)	7	83	77	9	3	5	072	667	07	n	30	74
											2		76	04
43	MMP	Matrix	8.	8.	8.	6.	8.	8.	-2.	-1.	2.0	D	0.0	0.6
24	15	metallopeptidase	94	81	30	73	08	11	060	043	60	o	34	63
		15	86	03	35	80	01	50	688	126	68	w	04	32
			5		7	2		2	825	667	88	n	44	74
											25		12	04
87	TNF	Tumor necrosis	10	10	11	10	9.	10	-1.	-0.	1.5	D	0.0	0.6
41	SF13	factor superfamily	.7	.3	.0	.0	86	.3	566	647	66	o	25	63

		member 13	36 66	75 99	80 84	39 84	36 1	48 6	067 793	146 667	06 77 93	w n	13 84 39	32 74 04
40 60	LUM	Lumican	7. 53 06 1	9. 14 27 9	8. 99 52 9	11 .2 50 11	10 .4 95 3	10 .0 93 85	4.1 608 741 89	2.0 568 866 67	4.1 60 87 41 89	U p	0.0 03 77 64 94	0.6 63 32 74 04
98 02	DAZ AP2	DAZ associated protein 2	7. 41 27 2	7. 07 71 2	7. 24 59 2	6. 12 85 7	6. 57 03 7	6. 94 25 8	-1. 622 370 51	-0. 698 103 333	1.6 22 37 05 1	D o w n	0.0 21 51 92 46	0.6 63 32 74 04
25 78 0	RAS GRP 3	RAS guanyl releasing protein 3 (calcium and DAG-regulated)	4. 38 51 4	5. 13 39 4	4. 96 77 4	6. 08 32 5	6. 08 32 5	4. 97 46 8	1.8 465 256 89	0.8 848 133 33	1.8 46 52 56 89	U p	0.0 40 59 87 97	0.6 63 32 74 04
28 53 43	TCAI M	T cell activation inhibitor, mitochondrial	8. 38 32	8. 36 53	8. 80 33 1	6. 72 01 4	7. 23 2 4	7. 93 80 8	-2. 330 323 102	-1. 220 53 102	2.3 30 32 31 02	D o w n	0.0 06 43 87 08	0.6 63 32 74 04
92 67 5	DTD 1	D-tyrosyl-trna deacylase 1	4. 70 71 2	4. 98 3 6	5. 12 04 6	6. 40 78 4	5. 44 68 7	5. 64 16 64	1.8 599 235 64	0.8 952 433 33	1.8 59 92 35 64	U p	0.0 13 77 91 34	0.6 63 32 74 04
66	HNR	Heterogeneous	10	9.	10	11	10	10	1.5	0.6	1.5	U	0.0	0.6

47	NPA	nuclear	.5	84	.5	.2	.7	.7	378	208	37	p	41	63
09	IP10	ribonucleoprotein	41	63	54	45	69	90	200	866	82		12	32
		A1 pseudogene 10	79		8	93	17	45	2	67	00		90	74
											2		93	04
67	SRE	Sterol regulatory	7.	7.	7.	6.	6.	6.	-1.	-0.	1.7	D	0.0	0.6
20	BF1	element binding	55	47	49	61	41	95	797	846	97	o	02	63
		transcription factor	30	30	16	72	02	10	987	383	98	w	43	32
		1	9	6		4	8	8	927	333	79	n	80	74
											27		05	04
44	PAL	PALM2-AKAP2	8.	8.	8.	9.	8.	8.	1.5	0.6	1.5	U	0.0	0.6
58	M2-	readthrough	27	20	22	33	52	74	544	363	54	p	27	63
15	AKA		71	76	09	92	59	97	382	933	43		04	32
	P2		8	4	3	2	4	7	79	33	82		00	74
											79		58	04
16	TRP	Transient receptor	6.	6.	6.	5.	5.	5.	-1.	-0.	1.7	D	0.0	0.6
25	V3	potential cation	97	26	33	23	97	85	786	837	86	o	20	63
14		channel, subfamily	87	62	07	50	57	38	414	066	41	w	35	32
		V, member 3	1	6	8	1	1	3	253	667	42	n	70	74
											53		62	04
57	TRIB	Tribbles	6.	7.	6.	6.	6.	5.	-1.	-0.	1.5	D	0.0	0.6
76	3	pseudokinase 3	94	09	64	49	54	70	570	651	70	o	44	63
1			55	27	96	20	06	21	267	01	26	w	66	32
			2	1	1	2	9		122		71	n	54	74
											22		87	04
48	NPM	Nucleophosmin	10	9.	10	11	10	10	1.7	0.7	1.7	U	0.0	0.6
69	1	(nucleolar	.1	85	.3	.3	.7	.5	395	986	39	p	12	63
		phosphoprotein	37	45	37	42	86	95	007	733	50		18	32
		B23, numatrin)	14	6	39	99	74	38	89	33	07		47	74
											89		46	04



19 01	S1PR 1	Sphingosine-1-phosphate receptor 1	3. 93 77 5	3. 90 78 7	4. 22 13 4	5. 74 95 4	6. 64 06 2	4. 44 64 2	3.0 102 291 89	1.5 898 733 33	3.0 10 22 91 89	U p	0.0 15 83 34 55	0.6 63 32 74 04
92 20	TIAF 1	TGFB1-induced anti-apoptotic factor 1	8. 99 75 7	9. 08 04 9	8. 52 07 8	7. 13 58 5	8. 12 67 8	8. 34 74 9	-1. 994 794 32	-0. 996 24 32	1.9 94 79 43 2	D o w n	0.0 21 75 32 49	0.6 63 32 74 04
74 12	VCA M1	Vascular cell adhesion molecule 1	3. 25 37 8	3. 67 32 9	4. 12 47 7	6. 02 93 4	5. 80 43 4	5. 90 61 3	4.6 890 965 99	2.2 293 1 99	4.6 89 09 65 99	U p	2.7 59 16 E-0 5	0.1 34 76 40 92
63 63	CCL 19	Chemokine (C-C motif) ligand 19	4. 77 18 6	6. 41 17 4	5. 26 75 2	7. 63 72 4	6. 54 61 1	6. 22 50 6	2.4 950 983 2	1.3 190 966 67	2.4 95 09 83 2	U p	0.0 35 49 85 91	0.6 63 32 74 04
85 01	SLC4 3A1	Solute carrier family 43 (amino acid system L transporter), member 1	10 .4 74 18	10 .2 87 79	10 .2 33 7	8. 79 62 6	8. 42 32 2	10 .3 82 22	-2. 190 595 838	-1. 131 323 333	2.1 90 59 58 38	D o w n	0.0 48 93 62 99	0.6 63 32 74 04
26 47 0	SEZ6 L2	Seizure related 6 homolog (mouse)-like 2	8. 38 56 3	8. 08 49 9	8. 56 71 1	7. 14 28 7	7. 43 61 3	8. 09 97 2	-1. 724 689 516	-0. 786 336 667	1.7 24 68 95	D o w n	0.0 24 37 56	0.6 63 32 74

											16		57	04
40	LOX	Lysyl oxidase	3.	3.	3.	4.	4.	4.	1.6	0.7	1.6	U	0.0	0.6
15			25	83	67	92	03	02	721	416	72	p	32	63
			78	58	11	14	89	94	218	8	12		50	32
			2	9	4	9	4	6	7		18		30	74
											7		06	04
38	KIT	V-kit	6.	7.	6.	7.	7.	7.	2.0	1.0	2.0	U	0.0	0.6
15		Hardy-Zuckerman	17	14	04	90	08	40	121	087	12	p	22	63
		4 feline sarcoma	10	92	97	38	98	25	297	233	12		70	32
		viral oncogene	9	1	9	5	6	5	42	33	97		36	74
		homolog									42		06	04
51	PLC	Phospholipase C	2.	3.	3.	4.	4.	3.	1.8	0.8	1.8	U	0.0	0.6
19	E1	epsilon 1	92	37	62	36	82	39	486	864	48	p	46	63
6			57	59	72	58	48	78	515	733	65		53	32
			6	8	9	3		2	69	33	15		54	74
											69		1	04
56	TCE	Transcription	3.	4.	4.	6.	5.	4.	3.1	1.6	3.1	U	0.0	0.6
84	AL7	elongation factor A	05	71	22	08	93	97	774	678	77	p	09	63
9		(SII)-like 7	87	51	25	36	99	65	806	833	48		44	32
			5	7	2	8		1	36	33	06		65	74
											36		17	04
92	TIFA	TRAF-interacting	5.	5.	5.	6.	5.	5.	1.5	0.6	1.5	U	0.0	0.6
61		protein with	28	07	37	36	59	68	528	348	52	p	31	63
0		forkhead-associate	46	24	74	07	03	82	193	9	81		77	32
		d domain	9	8	6		1	9	49		93		00	74
											49		58	04
15	SCF	Sec1 family	5.	5.	5.	5.	6.	5.	1.5	0.6	1.5	U	0.0	0.6
25	D2	domain containing	34	05	29	88	17	57	723	529	72	p	13	63
79		2	52	08	09	85	84	86	292	033	32		78	32

			7		3	8	7	6	28	33	92		47	74
											28		99	04
83	CRIS	Cysteine-rich	2.	4.	3.	5.	4.	3.	2.2	1.1	2.2	U	0.0	0.6
69	PLD	secretory protein	90	09	37	55	70	67	727	844	72	p	49	63
0	1	LCCL domain	96	91	59	93	23	64	725	533	77		21	32
		containing 1	6	2	8	2	4	6	83	33	25		86	74
											83		63	04
51	RSL2	Ribosomal L24	6.	6.	6.	7.	6.	7.	1.6	0.7	1.6	U	0.0	0.6
18	4D1	domain containing	25	00	42	22	56	11	699	398	69	p	13	63
7		1	88	58	49	64	77	48	481	033	94		79	32
			4				2	3	78	33	81		15	74
											78		66	04
37	JUN	Jun B	7.	6.	7.	8.	8.	7.	2.4	1.3	2.4	U	0.0	0.6
26	B	proto-oncogene	19	79	17	18	95	95	778	090	77	p	02	63
			22	62	65	28	86	08	634	966	86		50	32
			5	1	5	1	8	1	17	67	34		89	74
											17		79	04
28	IGLV	Immunoglobulin	3.	4.	3.	3.	5.	4.	1.9	0.9	1.9	U	0.0	0.6
77	8-61	lambda variable	51	09	25	78	15	91	932	951	93	p	36	63
4		8-61	05	99	86	28	54	61	463	2	24		78	32
			6		7	8	3	8	12		63		28	74
											12		54	04
24	LAC	Lactation elevated	5.	5.	5.	4.	5.	4.	-1.	-0.	1.5	D	0.0	0.6
62	E1	1	34	39	25	40	12	62	529	612	29	o	21	63
69			17	12	99	54	83	11	090	673	09	w	71	32
			2	5		3	2		01	333	00	n	06	74
											1		59	04
10	CDH	Cadherin 13	3.	4.	4.	8.	6.	5.	7.7	2.9	7.7	U	0.0	0.6
12	13		24	11	13	22	50	61	095	466	09	p	02	63

			94	18	80	83	08	00	322	433	53		35	32
			7	1	3	9	3	2	57	33	22		58	74
											57		5	04
39	MYO	Myosin XVIII	8.	9.	8.	7.	8.	8.	-1.	-0.	1.9	D	0.0	0.6
96	18A		99	08	52	13	12	34	994	996	94	o	21	63
87			75	04	07	58	67	74	794	24	79	w	75	32
			7	9	8	5	8	9	32		43	n	32	74
											2		49	04
57	KIA	KIAA1161	6.	5.	6.	4.	5.	5.	-1.	-0.	1.7	D	0.0	0.6
46	A116		12	90	02	76	00	93	718	780	18	o	37	63
2	1		31	37	22	62	95	04	234	926	23	w	02	32
			1			7	4	2	168	667	41	n	78	74
											68		94	04
95	ADA	ADAM	4.	4.	4.	5.	7.	5.	2.6	1.3	2.6	U	0.0	0.6
10	MTS	metallopeptidase	30	70	44	07	17	39	254	925	25	p	31	63
	1	with	94	78	99	31	36	81	535	666	45		01	32
		thrombospondin	7	9	8	9	7	8	41	67	35		73	74
		type 1 motif 1									41		2	04
10	ADC	Adenylate cyclase	6.	7.	7.	7.	8.	7.	1.7	0.7	1.7	U	0.0	0.6
9	Y3	3	46	18	21	81	22	22	388	981	38	p	40	63
			92	86	02	44	36	44	658	466	86		14	32
			4		2	1	4	5	87	67	58		73	74
											87		04	04
59	RAP	RAP1 gtpase	9.	10	10	8.	8.	9.	-1.	-0.	1.9	D	0.0	0.6
09	1GA	activating protein	44	.0	.0	16	85	72	915	937	15	o	49	63
	P		94	66	43	97	01	60	596	793	59	w	67	32
			1	53	44	5	9	6	007	333	60	n	04	74
											07		83	04
20	EPH	EPH receptor A3	3.	5.	5.	8.	6.	6.	6.4	2.6	6.4	U	0.0	0.6

42	A3		64	50	02	89	95	42	967	997	96	p	07	63
			50	69	75	60	53	73	581	2	75		14	32
			1	9	3	3	2	4	5		81		12	74
											5		04	04
91	SLC2	Solute carrier	9.	9.	9.	6.	6.	8.	-3.	-1.	3.5	D	0.0	0.6
53	8A2	family 28	48	07	17	87	98	36	576	838	76	o	02	63
		(concentrative	84	47	63	29	41	70	355	49	35	w	44	32
		nucleoside	3	8	2	1	4	1	124		51	n	58	74
		transporter),									24		73	04
		member 2												
10	CYS	Cysteinyln	3.	3.	3.	4.	4.	3.	1.5	0.6	1.5	U	0.0	0.6
80	LTR1	leukotriene	57	47	75	15	86	78	879	671	87	p	41	63
0		receptor 1	84	71	20	31	63	95	659	8	96		44	32
			2	2	4	8	8	6	74		59		50	74
											74		61	04
25	SUN	Sad1 and UNC84	4.	3.	4.	5.	4.	4.	1.6	0.7	1.6	U	0.0	0.6
77	2	domain containing	43	80	21	43	47	72	543	262	54	p	37	63
7		2	58	55	82	64	34	85	486	633	34		75	32
			2	8	7	7	7	2	76	33	86		43	74
											76		92	04
11	GBP	Guanylate binding	4.	4.	5.	6.	5.	5.	1.8	0.8	1.8	U	0.0	0.6
53	4	protein 4	55	58	06	17	56	00	012	490	01	p	29	63
61			16	13	71	26	67	76	727	166	27		74	32
			3			9	6	3	69	67	27		34	74
											69		03	04
10	ADI	Adipogenesis	7.	8.	8.	9.	10	8.	2.4	1.2	2.4	U	0.0	0.6
97	RF	regulatory factor	70	02	63	66	.3	22	540	951	54	p	45	63
4			23	23	39	69	52	41	080	4	00		72	32
			3	3	6	7	93	4	81		80		09	74

												81		61	04
32	HOX	Homeobox B5	3.	3.	3.	6.	5.	3.	2.3	1.2	2.3	U	0.0	0.6	
15	B5		78	74	83	04	22	83	721	461	72	p	42	63	
			96	43	09	47	78	09	523	966	15		01	32	
			2	4	1	2	3	1	46	67	23		80	74	
											46		99	04	
51	MLX	MLX interacting	10	9.	9.	7.	8.	9.	-2.	-1.	2.1	D	0.0	0.6	
08	IPL	protein-like	.0	43	15	84	08	30	177	122	77	o	30	63	
5			18	18	64	19	85	91	053	376	05	w	41	32	
			43	3	7	1	7	2	206	667	32	n	47	74	
											06		04	04	
46	NAP	Nucleosome	8.	7.	8.	9.	8.	8.	1.5	0.6	1.5	U	0.0	0.6	
73	IL1	assembly protein	04	72	17	19	42	29	847	642	84	p	44	63	
		1-like 1	13	29	01	95	83	93	954	966	79		21	32	
			3	3	3	8	8	2	76	67	54		67	74	
											76		27	04	
27	GJA5	Gap junction	3.	3.	3.	4.	4.	3.	1.6	0.7	1.6	U	0.0	0.6	
02		protein $\alpha$ 5	45	61	37	61	29	68	459	189	45	p	18	63	
			53	41	83	86	89	7	456	166	94		77	32	
			5	9	1	6	4		14	67	56		30	74	
											14		4	04	
27	PGA	Post-GPI	5.	4.	5.	6.	5.	5.	1.6	0.7	1.6	U	0.0	0.6	
31	P2	attachment to	28	59	44	09	56	87	669	372	66	p	27	63	
5		proteins 2	57	79	40	86	51	54	567	166	95		14	32	
				4	1	6	5	9	42	67	67		44	74	
											42		42	04	
84	CILP	Cartilage	6.	6.	9.	5.	4.	5.	-5.	-2.	5.9	D	0.0	0.6	
83		intermediate layer	77	99	14	09	46	61	982	580	82	o	05	63	
		protein	24	08	82	13	02	74	934	853	93	w	00	32	

			7	8	9	1	9	8	768	333	47	n	50	74
											68		53	04
53	PKH	Polycystic kidney	6.	5.	5.	4.	5.	5.	-1.	-0.	1.8	D	0.0	0.6
14	D1	and hepatic disease	51	69	42	64	21	11	847	885	47	o	25	63
		1 (autosomal	94	62	45	85	61	83	652	693	65	w	00	32
		recessive)	3	5	1	7	7	7	357	333	23	n	05	74
											57		69	04
51	WBP	WW domain	7.	7.	7.	8.	7.	7.	1.7	0.8	1.7	U	0.0	0.6
18	5	binding protein 5	01	26	00	42	81	58	966	452	96	p	10	63
6			47	99	34	13	36	90	300	933	63		06	32
			2	4	9	9	1	3	05	33	00		01	74
											05		29	04
11	XKR	X-linked Kx blood	3.	3.	3.	4.	5.	3.	2.0	1.0	2.0	U	0.0	0.6
47	4	group related 4	31	13	02	03	04	53	666	473	66	p	21	63
86			83	10	10	31	56	36	775	133	67		66	32
			5	4	9	8	1	3	8	33	75		41	74
											8		89	04
28	LUR	Leucine rich	6.	7.	7.	7.	8.	7.	1.5	0.6	1.5	U	0.0	0.6
63	AP1	adaptor protein	96	04	04	85	10	07	798	597	79	p	45	63
43	L	1-like	39	28	92	75	05	74	599	966	85		47	32
			6	4	8	5	1	1	43	67	99		32	74
											43		32	04
64	MRO	Maestro heat-like	7.	6.	6.	5.	6.	6.	-2.	-1.	2.0	D	0.0	0.6
24	H6	repeat family	22	83	94	45	05	36	063	045	63	o	05	63
75		member 6	73	42	17	52	16	06	752	27	75	w	01	32
			4	3	6	3	7	2	553		25	n	30	74
											53		57	04
96	ABC	ATP binding	8.	7.	8.	7.	6.	7.	-2.	-1.	2.0	D	0.0	0.6
19	G1	cassette subfamily	25	55	19	33	01	58	034	024	34	o	48	63

		G member 1	97 4	94 6	02 3	89 6	03 3	53 2	874 754	94	87 47 54	w n	04 51 91	32 74 04
28 39 6	IGH V4-3 1	Immunoglobulin heavy variable 4-31	6. 96 97 1	7. 48 78 7	6. 70 47 9	7. 76 40 2	10 .3 05 54	8. 63 67 9	3.5 999 910 84	1.8 479 933 33	3.5 99 99 10 84	U p	0.0 18 41 96 03	0.6 63 32 74 04
18 27	RCA N1	Regulator of calcineurin 1	6. 26 62 6	5. 48 03 1	6. 36 15 3	6. 95 12 6	7. 72 43 8	7. 04 06 9	2.3 017 694 44	1.2 027 433 33	2.3 01 76 94 44	U p	0.0 06 30 57 97	0.6 63 32 74 04
65 13	SLC2 A1	Solute carrier family 2 (facilitated glucose transporter), member 1	10 .0 12 51	9. 29 38 5	8. 94 11 8	7. 41 47 8	8. 50 69 7	8. 89 98 4	-2. 206 841 985	-1. 141 983 333	2.2 06 84 19 85	D o w n	0.0 33 48 31 76	0.6 63 32 74 04
34 91	CYR 61	Cysteine-rich, angiogenic inducer, 61	5. 77 17 7	6. 55 45 2	5. 52 71 5	9. 76 61 5	9. 54 01 5	8. 81 19 4	10. 715 297 5	3.4 216 52 97 5	10. 71 52 97 5	U p	2.3 53 74 E-0 5	0.1 31 38 59 88
52 74	SER PINI 1	Serpin peptidase inhibitor, clade I (neuroserpin), member 1	3. 86 53 5	3. 85 78 3	3. 76 04 8	4. 71 46 1	5. 33 29 5	4. 18 06 1	1.8 853 556 11	0.9 148 366 67	1.8 85 35 56 11	U p	0.0 13 00 59 69	0.6 63 32 74 04
14	CTG	Connective tissue	3.	6.	5.	10	9.	7.	12.	3.6	12.	U	0.0	0.6



90	F	growth factor	87	77	30	.2	30	40	721	691	72	p	04	63
			47	84	39	57	43	28	115	533	111		86	32
			5	1	6	35	8	5	98	33	59		41	74
											8		22	04
46	CEA	Carcinoembryonic	7.	6.	7.	8.	9.	7.	2.1	1.1	2.1	U	0.0	0.6
80	CAM	antigen-related cell	20	99	51	36	31	44	956	346	95	p	38	63
	6	adhesion molecule	65	63	35	54	23	26	731	633	67		00	32
		6 (non-specific	1	4	6		5	5	86	33	31		53	74
		cross reacting									86		53	04
		antigen)												
25	ANK	Ankyrin repeat and	7.	7.	7.	6.	6.	7.	-1.	-0.	1.6	D	0.0	0.6
76	S4B	sterile $\alpha$ motif	61	04	25	51	13	12	635	709	35	o	42	63
29		domain containing	11	16	13	81	33	43	142	416	14	w	76	32
		4B	4		7		9	7	837	667	28	n	04	74
											37		3	04
11	ELF	Extracellular	7.	7.	8.	6.	6.	7.	-1.	-0.	1.9	D	0.0	0.6
47	N2	leucine-rich repeat	44	62	51	55	48	56	989	992	89	o	38	63
94		and fibronectin	20	60	83	58	75	60	404	336	40	w	04	32
		type III domain	2	8	9	8	3	7	53	667	45	n	27	74
		containing 2									3		78	04
55	BRI	BRX1, biogenesis	4.	3.	3.	4.	4.	4.	1.6	0.6	1.6	U	0.0	0.6
29	X1	of ribosomes	02	22	92	55	47	22	146	911	14	p	20	63
9			94	38	40	35	47	26	147	9	61		47	32
			6		4	4	2	1	76		47		14	74
											76		21	04
26	CYFI	Cytoplasmic	7.	7.	7.	6.	6.	7.	-1.	-0.	1.6	D	0.0	0.6
99	P2	FMR1 interacting	92	09	14	30	70	02	641	714	41	o	44	63
9		protein 2	96	88	29	05	12	46	430	953	43	w	61	32
				2	2	7	9	2	122	333	01	n	62	74

											22		36	04
98	EPM	EPM2A (laforin)	6.	7.	6.	6.	6.	6.	-1.	-0.	1.5	D	0.0	0.6
52	2AIP	interacting protein	98	03	86	32	25	51	515	599	15	o	06	63
	1	1	21	69	84	28	17	29	702	986	70	w	21	32
			3	5	6	2	9	7	558	667	25	n	60	74
											58		84	04
70	TFD	Transcription	5.	5.	6.	6.	6.	6.	1.5	0.6	1.5	U	0.0	0.6
27	P1	factor Dp-1	65	23	07	47	17	19	460	285	46	p	34	63
			05	21	37	06	30	84	568	933	05		71	32
			7		2	2	9	6	11	33	68		49	74
											11		97	04
14	CRY	Crystallin mu	8.	8.	8.	7.	7.	8.	-1.	-0.	1.9	D	0.0	0.6
28	M		67	87	57	14	70	42	933	951	33	o	20	63
			16	97	52	52	81	02	243	023	24	w	03	32
				8	2		2	1	461	333	34	n	81	74
											61		18	04
37	WAS	WAS protein	8.	8.	7.	7.	7.	7.	-1.	-0.	1.5	D	0.0	0.6
46	H3P	family homolog 3	71	39	93	33	98	74	583	662	83	o	38	63
66		pseudogene	93	44	59	68	36	07	159	806	15	w	99	32
			2	1	2	8	5		561	667	95	n	95	74
											61		13	04
44	MT1	Metallothionein 1E	8.	7.	8.	7.	7.	7.	-1.	-0.	1.6	D	0.0	0.6
93	E		32	80	30	45	86	06	605	682	05	o	32	63
			28	21	66	24	74	33	259	806	25	w	75	32
			1	7	9	4	4	7	645	667	96	n	10	74
											45		15	04
80	RAS	Ras association	10	9.	9.	8.	9.	9.	-1.	-0.	1.8	D	0.0	0.6
45	SF7	(ralgds/AF-6)	.3	53	46	46	01	18	847	885	47	o	19	63
		domain family	13	83	60	38	65	15	165	313	16	w	69	32

		(N-terminal) member 7	45	1	6	3		5	757	333	57	n	64	74
											57		9	04
77	SLC3	Solute carrier	10	10	10	7.	7.	9.	-4.	-2.	4.5	D	0.0	0.6
80	0A2	family 30 (zinc transporter), member 2	.3	.2	.4	13	78	63	503	170	03	o	07	63
			84	22	53	59	18	00	167	94	16	w	35	32
			38	99	28	3	8	2	059		70	n	49	74
											59		35	04
28	IGLV	Immunoglobulin	5.	4.	5.	5.	6.	7.	2.5	1.3	2.5	U	0.0	0.6
82	1-51	lambda variable	07	98	12	37	83	06	777	661	77	p	14	63
0		1-51	23	42	46	98	04	93	934	366	79		36	32
			8	5	1	6	2	7	44	67	34		23	74
											44		89	04
18	DUS	Dual specificity	4.	4.	4.	4.	5.	5.	1.5	0.6	1.5	U	0.0	0.6
44	P2	phosphatase 2	51	41	77	93	61	19	983	766	98	p	15	63
			96	36	91	29	38	53	942	233	39		30	32
			2	1	3	6	8	9	89	33	42		19	74
											89		55	04
55	RFK	Riboflavin kinase	9.	9.	9.	8.	8.	9.	-1.	-0.	1.5	D	0.0	0.6
31			39	12	29	14	69	11	537	621	37	o	47	63
2			96	82	75	90	33	99	958	016	95	w	08	32
			2	1	2	8	1	1	598	667	85	n	36	74
											98		93	04
22	LRR	Leucine rich repeat	4.	4.	4.	3.	3.	4.	-1.	-0.	1.6	D	0.0	0.6
14	C73	containing 73	64	26	83	70	73	24	610	687	10	o	15	63
24			72	10	32	01	38	49	601	6	60	w	21	32
			9	8	5			2	967		19	n	35	74
											67		39	04
22	C6orf	Chromosome 6	6.	6.	6.	4.	4.	6.	-2.	-1.	2.1	D	0.0	0.6
14	223	open reading frame	65	73	03	85	88	31	180	124	80	o	32	63

16		223	54 2	94 9	12 8	36 3	76	09 9	496 488	656 667	49 64 88	w n	48 80 58	32 74 04
55 04 0	EPN 3	Epsin 3	9. 00 53 3	8. 25 08 1	7. 99 30 7	7. 06 60 9	7. 43 63	8. 00 76 1	-1. 883 048 293	-0. 913 07	1.8 83 04 82 93	D o w n	0.0 30 47 42 16	0.6 63 32 74 04
56 14 3	PCD HA5	Protocadherin $\alpha$ 5	7. 44 20 9	7. 73 45 2	6. 91 29 9	6. 53 69 2	6. 83 18 2	6. 80 31 1	-1. 557 526 454	-0. 639 256 667	1.5 57 52 64 54	D o w n	0.0 31 81 64 86	0.6 63 32 74 04
83 85 6	FSD1 L	Fibronectin type III and SPRY domain containing 1-like	5. 91 03 8	4. 49 14 2	5. 11 87 4	3. 76 98 9	2. 99 11 4	4. 85 51 1	-2. 464 793 301	-1. 301 466 667	2.4 64 79 33 01	D o w n	0.0 42 53 34 33	0.6 63 32 74 04
83 45 0	DRC 3	Dynein regulatory complex subunit 3	6. 25 63 8	6. 53 04 3	5. 62 52 3	5. 21 92 3	5. 03 25 7	5. 26 46 5	-1. 952 316 11	-0. 965 186 667	1.9 52 31 61 1	D o w n	0.0 06 14 91 58	0.6 63 32 74 04
10 29 9	MAR CH6	Membrane associated ring-CH-type finger 6	9. 75 32	9. 74 45 1	9. 49 85 9	8. 86 82 2	9. 28 69 4	8. 87 19 2	-1. 576 151 995	-0. 656 406 667	1.5 76 15 19 95	D o w n	0.0 08 44 82 27	0.6 63 32 74 04
55	PNM	Paraneoplastic Ma	3.	5.	3.	6.	6.	5.	3.8	1.9	3.8	U	0.0	0.6

22	AL1	antigen family-like	13	28	56	57	15	08	560	471	56	p	15	63
8		1	61	38	17	97	93	40	666	3	06		47	32
			1		3			3	82		66		99	74
											82		83	04
57	PTG	Prostaglandin D2	9.	10	9.	11	10	11	2.1	1.0	2.1	U	0.0	0.6
30	DS	synthase	42	.4	48	.1	.1	.2	272	890	27	p	24	63
			99	28	78	94	74	44	751	066	27		68	32
			4	84	7	3	78	59	76	67	51		30	74
											76		72	04
11	BOR	BLOC-1 related	7.	7.	7.	6.	6.	7.	-1.	-0.	1.6	D	0.0	0.6
90	CS7	complex subunit 7	55	12	77	33	94	09	609	687	09	o	36	63
32			00	15	02	76	43	87	947	013	94	w	15	32
			9		3	8	3	7	154	333	71	n	20	74
											54		5	04
23	CBL	Cbl	7.	7.	7.	6.	6.	6.	-1.	-0.	1.9	D	0.0	0.6
62	C	proto-oncogene C,	88	25	08	25	31	79	935	952	35	o	08	63
4		E3 ubiquitin	65	65	51	63	72	6	715	866	71	w	61	32
		protein ligase	4	1	7	4	8		147	667	51	n	20	74
											47		28	04
80	BAI	BAI1-associated	9.	9.	9.	7.	8.	9.	-2.	-1.	2.0	D	0.0	0.6
11	AP2	protein 2-like 2	74	58	34	64	58	24	097	068	97	o	27	63
5	L2		21	79	77	81	04	23	930	966	93	w	12	32
			6	5	2	9	3	1	182	667	01	n	77	74
											82		13	04
55	AP5	Adaptor-related	4.	4.	3.	3.	3.	3.	-1.	-0.	1.5	D	0.0	0.6
74	M1	protein complex 5,	33	07	53	27	12	52	595	674	95	o	18	63
5		mu 1 subunit	41	62	36	13	76	30	490		49	w	64	32
			7		3	4	2	4	48		04	n	07	74
											8		89	04

79	TME	Transmembrane protein 204	6.	6.	6.	7.	7.	6.	2.2	1.1	2.2	U	0.0	0.6
65	M20		16	67	00	91	78	73	909	959	90	p	111	63
2	4		76	77	11	35	54	54	299	333	92		16	32
				1	9				3	33	99		19	74
										3			8	04
18	APL	Apelin receptor	3.	4.	4.	7.	6.	4.	3.6	1.8	3.6	U	0.0	0.6
7	NR		58	89	48	58	01	99	843	814	84	p	23	63
			27	16	41	70	80	77	837	233	38		53	32
			6	7	1	6	3	2	47	33	37		57	74
										47			48	04
79	TFPI	Tissue factor pathway inhibitor 2	3.	3.	2.	4.	4.	4.	1.9	0.9	1.9	U	0.0	0.6
80	2		53	64	96	00	49	46	195	407	19	p	03	63
			32	31	72	64	25	69	436	633	54		94	32
			7	4	7	8	8	1	05	33	36		19	74
										05			98	04
74	VIM	Vimentin	9.	9.	10	12	11	10	3.0	1.6	3.0	U	0.0	0.6
31			18	88	.7	.3	.7	.6	752	207	75	p	17	63
			32	89	68	33	37	32	563	066	25		97	32
			5	6	45	22	5	06	28	67	63		18	74
										28			01	04
28	CLE	C-type lectin domain family 18, member C	6.	6.	6.	4.	5.	5.	-2.	-1.	2.1	D	0.0	0.6
39	C18C		87	64	15	97	72	75	110	077	10	o	07	63
71			89	41	82	01	35	50	439	543	43	w	09	32
			9	8		8	3	3	297	333	92	n	44	74
										97			89	04
55	STR	Spermatid perinuclear RNA binding protein	8.	7.	7.	6.	7.	7.	-1.	-0.	1.5	D	0.0	0.6
34	BP		39	62	91	92	54	54	555	637	55	o	48	63
2			09	23	23	83	41	14	375	263	37	w	57	32
			4	6	8	6		3	947	333	59	n	02	74

											47		68	04
90	OTU	OTU	6.	5.	5.	5.	5.	5.	-1.	-0.	1.5	D	0.0	0.6
26	LIN	deubiquitinase with	26	89	76	27	36	45	533	616	33	o	11	63
8		linear linkage	94	57	93	32	11	08	101	453	10	w	43	32
		specificity	8	4	8	2	7	5	626	333	16	n	34	74
											26		04	04
65	RAS	RAS-like, family	3.	3.	2.	5.	3.	3.	2.2	1.1	2.2	U	0.0	0.6
99	L11B	11, member B	13	42	99	51	94	52	037	399	03	p	48	63
7			61	21	69	21	01	28	796	8	77		39	32
			1	2	5	8	1	3	81		96		40	74
											81		47	04
29	PDZ	PDZ domain	2.	3.	2.	4.	3.	4.	2.0	1.0	2.0	U	0.0	0.6
95	RN4	containing ring	54	95	82	68	69	09	668	474	66	p	34	63
1		finger 4	98	32	77	44	86	01	590	4	85		99	32
			5	3	9	7	2		4		90		65	74
											4		78	04
29	CXC	Chemokine	4.	4.	4.	7.	7.	4.	4.2	2.0	4.2	U	0.0	0.6
19	L1	(C-X-C motif)	31	57	68	63	78	37	191	769	19	p	45	63
		ligand 1	25	18	50	29	86	86	137	4	11		30	32
		(melanoma growth	7	1	6	4	5	7	97		37		94	74
		stimulating									97		39	04
		activity, $\alpha$ )												
54	POU	POU class 2	8.	9.	8.	6.	7.	7.	-3.	-1.	3.8	D	0.0	0.6
50	2AF1	associating factor 1	51	54	97	32	37	48	861	949	61	o	01	63
			88	58	05	26	61	90	362	11	36	w	43	32
			4	1		9	2	1	502		25	n	83	74
											02		26	04
30	GZM	Granzyme K	3.	4.	4.	5.	5.	5.	2.2	1.1	2.2	U	0.0	0.6
03	K		74	98	04	58	16	60	870	935	87	p	08	63

			60	42	11	37	57	24	903	133	09		12	32
			6	5	8	9	5	9	08	33	03		68	74
											08		18	04
57	TWS	Twisted	6.	6.	6.	7.	7.	7.	1.5	0.6	1.5	U	0.0	0.6
04	G1	gastrulation BMP	89	49	67	95	03	08	915	704	91	p	47	63
5		signaling	89	30	12	31	55	58	399	233	53		03	32
		modulator 1	9	9	1	7	4	5	08	33	99		33	74
											08		67	04
22	POM	POM121 and ZP3	5.	6.	7.	5.	5.	4.	-2.	-1.	2.2	D	0.0	0.6
93	ZP3	fusion	40	60	05	39	34	79	265	179	65	o	26	63
2			74	32	95	11	05	99	024	526	02	w	50	32
			9	5	6	7	6	9	518	667	45	n	29	74
											18		38	04
10	COR	Corin, serine	4.	5.	5.	6.	5.	6.	2.2	1.1	2.2	U	0.0	0.6
69	IN	peptidase	71	37	53	37	84	88	327	588	32	p	09	63
9			78	07	63	39	54	20	318	1	73		09	32
			2	6	7		1	7	58		18		23	74
											58		57	04
37	KCN	Potassium channel,	5.	5.	5.	3.	4.	5.	-1.	-0.	1.8	D	0.0	0.6
51	D2	voltage gated Shal	44	48	44	83	69	28	805	852	05	o	42	63
		related subfamily	57	50	57	20	72	92	852	68	85	w	46	32
		D, member 2	5	1	5	2	5		425		24	n	03	74
											25		85	04
76	ZNF	Zinc finger protein	8.	7.	7.	6.	7.	7.	-1.	-0.	1.7	D	0.0	0.6
20	69	69	55	53	86	53	39	49	794	843	94	o	47	63
			97	92	61	76	91	84	132	286	13	w	55	32
			5	1	2	4	4	4	782	667	27	n	74	74
											82		24	04
74	MYR	Myelin regulatory	10	10	10	9.	9.	9.	-1.	-0.	1.5	D	0.0	0.6



5	F	factor	.4 63 4	.0 92 71	.2 72 36	41 42 7	80 37 6	81 55	513 945 565	598 313 333	13 94 55 65	o w n	13 92 44 6	63 32 74 04
11 07 5	STM N2	Stathmin 2	2. 81 17 8	3. 41 03 8	3. 60 17 1	5. 66 10 8	6. 88 42	4. 11 81 9	4.8 563 306 97	2.2 798 666 67	4.8 56 33 06 97	U p	0.0 09 23 97 04	0.6 63 32 74 04
22 12 23	CES5 A	Carboxylesterase 5A	4. 99 09 5	4. 49 13 7	5. 55 35 1	2. 80 94 2	3. 09 62 8	4. 36 14 9	-3. 009 547 666	-1. 589 546 667	3.0 09 54 76 66	D o w n	0.0 08 80 00 89	0.6 63 32 74 04
60 67 7	CEL F6	CUGBP, Elav-like family member 6	5. 53 83 8	5. 06 95 5	5. 32 74 4	4. 61 98 9	4. 56 68	4. 95 14 8	-1. 514 736 31	-0. 599 066 667	1.5 14 73 63 1	D o w n	0.0 15 11 42 15	0.6 63 32 74 04
14 66	CSR P2	Cysteine and glycine rich protein 2	4. 21 27 1	5. 94 20 5	4. 57 11 3	7. 54 26 1	7. 21 24 2	5. 57 04 5	3.6 465 445	1.8 665 3	3.6 46 54 45	U p	0.0 20 15 16 71	0.6 63 32 74 04
90 99 0	KIFC 2	Kinesin family member C2	7. 41 71 4	7. 27 59 6	6. 81 59 9	6. 18 98 9	6. 54 7 5	6. 78 40 5	-1. 583 027 883	-0. 662 686 667	1.5 83 02 78 83	D o w n	0.0 25 59 71 68	0.6 63 32 74 04

25	FAM	Family with	3.	3.	3.	5.	5.	3.	2.6	1.4	2.6	U	0.0	0.6
81	19A5	sequence similarity	26	87	40	68	22	87	616	123	61	p	15	63
7		19 (chemokine	75	14	54	13	78	23	975	466	69		91	32
		(C-C motif)-like),	9		6		3	6	87	67	75		45	74
		member A5									87		96	04
63	CEA	Carcinoembryonic	5.	5.	5.	6.	5.	5.	1.6	0.6	1.6	U	0.0	0.6
4	CAM	antigen-related cell	26	21	52	35	99	69	000	781	00	p	14	63
	1	adhesion molecule	2	46	83	19	49	24	755	4	07		87	32
		1 (biliary		2	1	4	3	8	21		55		92	74
		glycoprotein)									21		53	04
28	IGK	Immunoglobulin κ	9.	10	10	10	13	12	4.3	2.1	4.3	U	0.0	0.6
92	V2-2	variable 2-24	98	.5	.0	.8	.1	.9	213	114	21	p	07	63
3	4		69	22	69	78	14	19	437	8	34		52	32
			2	86	24	67	85	94	57		37		56	74
											57		87	04
19	VST	V-set and	2.	3.	3.	5.	3.	3.	2.2	1.1	2.2	U	0.0	0.6
67	M4	transmembrane	99	68	38	61	97	96	369	615	36	p	37	63
40		domain containing	75	39	50	38	04	68	298	2	92		21	32
		4	9	9	2	8	3	5	28		98		97	74
											28		57	04
28	IGLJ	Immunoglobulin	4.	4.	4.	5.	6.	5.	2.1	1.1	2.1	U	0.0	0.6
83	3	lambda joining 3	55	63	74	04	59	63	663	152	66	p	18	63
1			85	56	19	92	54	71	104	4	31		80	32
			3	7		9	3		38		04		78	74
											38		32	04
51	EMC	Endomucin	4.	4.	5.	7.	7.	5.	4.0	2.0	4.0	U	0.0	0.6
70	N		33	60	47	43	70	33	588	210	58	p	15	63
5			46	27	08	81	31	00	189	6	81		74	32
			6	5	2	9	5	7	84		89		85	74

											84		37	04
53 37	PLD 1	Phospholipase D1	10 .9 78 8	10 .2 67 72	10 .8 69 83	9. 13 39 7	9. 83 91 4	10 .3 56 9	-1. 903 665 5	-0. 928 78	1.9 03 66 55	D o w n	0.0 29 74 58 95	0.6 63 32 74 04
57 55 6	SEM A6A	Sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6A	10 .3 35 36	10 .0 69 41	9. 82 64 7	8. 16 72 8	9. 00 46 1	9. 96 88 7	-2. 042 250 732	-1. 030 16 732	2.0 42 25 07 32	D o w n	0.0 47 53 06 67	0.6 63 32 74 04
12 54 88	TTC 39C	Tetratricopeptide repeat domain 39C	8. 28 21 3	8. 01 73 6	8. 02 53 9	6. 02 47 2	7. 16 64 1	7. 91 37 2	-2. 104 304 282	-1. 073 343 333	2.1 04 30 42 82	D o w n	0.0 45 46 37 34	0.6 63 32 74 04
11 15 6	PTP4 A3	Protein tyrosine phosphatase type IVA, member 3	5. 98 05 4	6. 39 82 4	6. 14 53	7. 21 72 8	7. 35 19 8	6. 23 46 7	1.6 934 319 34	0.7 599 5 34	1.6 93 43 19 34	U p	0.0 45 92 77 99	0.6 63 32 74 04
13 24 30	PAB PC4L	Poly(A) binding protein, cytoplasmic 4-like	3. 39 95 2	4. 06 64 1	3. 79 05 4	4. 62 44 6	4. 58 39 7	4. 09 72 7	1.6 055 600 97	0.6 830 766 67	1.6 05 56 00 97	U p	0.0 18 01 10 07	0.6 63 32 74 04
50 69	PAPP A	Pregnancy-associat ed plasma protein	3. 99	4. 61	4. 17	5. 91	5. 23	4. 52	1.9 514	0.9 645	1.9 51	U p	0.0 30	0.6 63

		A, pappalysin 1	70 5	03 8	16 5	40 3	83 3	04 7	998 25	833 33	49 98 25		03 21 94	32 74 04
16 11 98	CLE C14 A	C-type lectin domain family 14, member A	5. 25 36	4. 81 34	5. 55 29	6. 95 53	7. 12 02	5. 67 44	2.5 966 411	1.3 766 466	2.5 96 64	U p	0.0 11 47 69 5	0.6 63 32 74 04
10 10 0	TSPA N2	Tetraspanin 2	3. 32 12 9	4. 32 77 6	3. 14 63 6	6. 12 23 9	4. 69 27 8	4. 15 36 1	2.6 228 282 4	1.3 911 233 33	2.6 22 82 82 4	U p	0.0 35 51 92	0.6 63 32 74 04
15 20 07	GLIP R2	GLI pathogenesis-relate d 2	4. 57 52 5	5. 06 05 6	4. 94 51 4	7. 06 60 9	5. 52 36 5	5. 33 43 1	2.1 649 994 62	1.1 143 666 67	2.1 64 99 94 62	U p	0.0 42 06 60 12	0.6 63 32 74 04
30 2	ANX A2	Annexin A2	9. 57 07 1	9. 10 10 2	9. 85 70 3	10 .6 73 15	10 .9 87 5	9. 69 46 4	1.9 214 250 04	0.9 421 766 67	1.9 21 42 50 04	U p	0.0 35 45 28 06	0.6 63 32 74 04
56 90 7	SPIR E1	Spire-type actin nucleation factor 1	4. 71 86 9	5. 05 08	4. 79 13 7	5. 55 96 9	5. 42 90 3	5. 42 52 9	1.5 344 447 14	0.6 177 166 67	1.5 34 44 47 14	U p	0.0 05 21 27 78	0.6 63 32 74 04
37	MAL	Metastasis	7.	7.	7.	8.	8.	8.	1.8	0.8	1.8	U	0.0	0.6

89	AT1	associated lung	58	57	48	40	57	19	010	488	01	p	01	63	
38		adenocarcinoma	17	15	15	54	94	65	605	466	06		20	32	
		transcript	1	5	9	2	8		2	28	67	05	16	74	
		(non-protein coding)										28	76	04	
57	PTP	Protein tyrosine	11	11	11	10	10	10	-1.	-0.	1.6	D	0.0	0.6	
92	RF	phosphatase,	.2	.1	.1	.0	.5	.9	608	685	08	o	25	63	
		receptor type, F	99	72	71	48	63	74	430	653	43	w	19	32	
			79	11	16	73	27	1	204	333	02	n	71	74	
											04		88	04	
42	MAP	Mitogen-activated	7.	6.	6.	7.	7.	7.	1.5	0.6	1.5	U	0.0	0.6	
17	3K5	protein kinase	20	92	87	58	99	27	337	170	33	p	27	63	
		kinase kinase 5	59	45	02	01	41	74	251	4	72		92	32	
			2			9	1	4	83		51		61	74	
											83		19	04	
80	SLC1	Solute carrier	9.	8.	7.	6.	5.	8.	-2.	-1.	2.7	D	0.0	0.6	
70	9A3	family	19	04	38	80	89	84	06	778	474	78	o	36	63
4		(thiamine		34	23	05	09	79	51	160	13	16	w	40	32
		transporter),		8	7	5		3	8	598		05	n	39	74
		member 3										98		07	04
10	LOC	Uncharacterized	7.	7.	7.	6.	6.	7.	-1.	-0.	1.8	D	0.0	0.6	
19	1019	LOC101928168	67	55	75	91	23	23	822	866	22	o	13	63	
28	2816		79	51	39	09	97	80	754	12	75	w	69	32	
16	8		5	5	4	1	6	1	167		41	n	54	74	
8											67		28	04	
76	CA3	Carbonic	6.	5.	5.	4.	4.	5.	-1.	-0.	1.8	D	0.0	0.6	
1		anhydrase III	26	61	84	69	88	47	849	886	49	o	12	63	
			94	78	01	97	95	73	245	936	24	w	24	32	
			7	9	4	7	3	9	374	667	53	n	04	74	

											74		18	04
37 82	KCN N3	Potassium channel, calcium activated intermediate/small conductance subfamily N $\alpha$ , member 3	4. 19 24 1	4. 90 44 7	4. 59 38 6	5. 02 89 9	5. 62 26 6	5. 32 84 57	1.6 971 373 33	0.7 631 033 73	1.6 97 13 73	U p	0.0 15 15 50	0.6 63 32 74
11 72 45	HRA SLS5	HRAS like suppressor family member 5	4. 40 68 3	4. 68 35 6	5. 10 62 9	3. 66 39 2	4. 30 56 2	4. 38 55 2	-1. 530 369 472	-0. 613 88 88	1.5 30 36 94 72	D o w n	0.0 49 21 40 88	0.6 63 32 74 04
98 39	ZEB 2	Zinc finger E-box binding homeobox 2	5. 42 70 5	6. 91 85 2	6. 13 34 8	7. 99 13 6	7. 76 57 6	6. 92 05 1	2.6 381 501 3	1.3 995 266 67	2.6 38 15 01 3	U p	0.0 14 06 78 74	0.6 63 32 74 04
55 47	PRC P	Prolylcarboxypepti dase	7. 52 16	7. 40 99 8	7. 93 60 9	8. 32 57 5	8. 28 85 3	8. 14 53 6	1.5 482 695 54	0.6 306 566 67	1.5 48 26 95 54	U p	0.0 11 94 95 26	0.6 63 32 74 04
61 96	RPS6 KA2	Ribosomal protein S6 kinase, 90kda, polypeptide 2	6. 85 48 9	7. 73 28 6	7. 50 09 5	8. 25 35 3	8. 17 64 5	7. 76 55 4	1.6 270 666 31	0.7 022 733 33	1.6 27 06 66 31	U p	0.0 33 88 45 03	0.6 63 32 74 04
34 82	CCL 15-C	CCL15-CCL14 readthrough (NMD	7. 03	7. 60	7. 46	8. 16	8. 29	7. 51	1.5 378	0.6 209	1.5 37	U p	0.0 49	0.6 63

49	CL14	candidate)	81	72	46	17	75	35	377	033	83		95	32
			1	9	5		5	1	86	33	77		22	74
											86		04	04
10	LOC	Multidrug	7.	7.	7.	6.	6.	6.	-1.	-0.	1.8	D	0.0	0.6
53	1053	resistance-associate	42	06	51	07	38	99	803	850	03	o	15	63
69	6923	d protein 6	96	80	23	26	87	57	717	973	71	w	50	32
23	9		8	4	4	4	5	5	417	333	74	n	61	74
9											17		17	04
10	BAS	Brain abundant,	5.	7.	6.	9.	7.	7.	2.7	1.4	2.7	U	0.0	0.6
40	P1	membrane attached	49	38	49	01	21	52	512	600	51	p	46	63
9		signal protein 1	18	60	40	62	24	35	552	9	25		62	32
			2	3	7	2	2	5	63		52		68	74
											63		02	04
20	CC2	Coiled-coil and C2	5.	5.	5.	4.	5.	4.	-1.	-0.	1.5	D	0.0	0.6
00	D1B	domain containing	76	72	59	95	30	89	553	635	53	o	07	63
14		1B	07	11	01	86	76	93	425	453	42	w	02	32
				6	4	6		8	801	333	58	n	89	74
											01		02	04
64	RAB	RAB17, member	10	10	10	8.	8.	10	-2.	-1.	2.0	D	0.0	0.6
28	17	RAS oncogene	.5	.2	.0	70	84	.0	099	070	99	o	23	63
4		family	59	21	39	32	6	62	443	006	44	w	18	32
			87	96	88	9		4	069	667	30	n	41	74
											69		65	04
10	CITE	Cbp/p300-interacti	4.	4.	5.	5.	5.	5.	1.7	0.8	1.7	U	0.0	0.6
37	D2	ng transactivator,	51	54	59	81	67	60	540	107	54	p	31	63
0		with Glu/Asp rich	54	54	91	53	26	40	623		06		90	32
		carboxy-terminal	2		7	5	7	7	13		23		91	74
		domain, 2									13			04
17	DST	Destrin (actin	4.	4.	4.	4.	3.	3.	-1.	-0.	1.5	D	0.0	0.6

12	NP2	depolymerizing	95	54	47	09	90	99	575	655	75	o	05	63
20		factor) pseudogene	35	33	12	77	64	71	252	583	25	w	53	32
		2	7	3	2	7	8	2	756	333	27	n	73	74
											56		89	04
33	ICA	Intercellular	4.	5.	5.	6.	7.	5.	2.0	1.0	2.0	U	0.0	0.6
84	M2	adhesion molecule	95	57	75	30	15	87	235	168	23	p	26	63
		2	33	59	05	41	36	26	567	933	55		98	32
				3	4	3	6	6	83	33	67		73	74
											83		99	04
57	PTP	Protein tyrosine	8.	7.	7.	6.	6.	6.	-1.	-0.	1.8	D	0.0	0.6
74	N3	phosphatase,	26	25	29	54	90	58	898	924	98	o	16	63
		non-receptor type 3	08	94	37	87	31	74	570	913	57	w	77	32
			6	6	9	8	3	6	186	333	01	n	13	74
											86		39	04
57	TSH	Teashirt zinc finger	3.	4.	3.	6.	4.	5.	2.9	1.5	2.9	U	0.0	0.6
61	Z3	homeobox 3	56	88	96	86	96	31	814	760	81	p	23	63
6			36	90	47	94	52	08	621	2	46		61	32
			2	6	3		5	2	05		21		41	74
											05		64	04
46	ATF3	Activating	6.	4.	5.	6.	10	8.	6.0	2.5	6.0	U	0.0	0.6
7		transcription factor	56	94	25	31	.0	14	622	998	62	p	25	63
		3	29	03	55	73	95	53	919	633	29		04	32
			4	1	8	7	72	3	57	33	19		61	74
											57		76	04
11	RNF	Ring finger protein	5.	5.	5.	6.	6.	5.	1.9	0.9	1.9	U	0.0	0.6
23	24	24	17	46	04	63	18	71	308	492	30	p	08	63
7			91	47	76	78	37	76	195	133	81		12	32
			4	9	4	5	4	2	42	33	95		00	74
											42		13	04



94	FAD	Fatty acid	5.	6.	5.	7.	6.	5.	1.9	0.9	1.9	U	0.0	0.6
15	S2	desaturase 2	04	11	22	11	14	94	236	438	23	p	47	63
			94	02	12	63	93	67	415	4	64		54	32
			9	7	1	7	4	8	59		15		38	74
											59		77	04
54	FAM	Family with	7.	7.	7.	6.	7.	7.	-1.	-0.	1.5	D	0.0	0.6
85	83E	sequence similarity	88	18	48	42	08	08	573	653	73	o	42	63
4		83 member E	25	77	23	20	71	15	510	986	51	w	73	32
			4	3	6	1	6		348	667	03	n	58	74
											48		81	04
79	EPS8	EPS8-like 3	10	10	10	9.	9.	10	-1.	-0.	1.7	D	0.0	0.6
57	L3		.8	.8	.3	51	72	.3	747	805	47	o	18	63
4			26	29	99	49	98	94	206	05	20	w	03	32
			13	64	07		5	94	344		63	n	06	74
											44		34	04
84	RAB	RAB11 family	7.	7.	7.	6.	6.	6.	-1.	-0.	1.7	D	0.0	0.6
44	11FI	interacting protein	55	47	25	10	90	95	716	779	16	o	19	63
0	P4	4 (class II)	95	72	86	04	01	74	147	173	14	w	89	32
			7	8	9	5	2	5	236	333	72	n	32	74
											36		22	04
93	SDR	Short chain	5.	5.	5.	4.	4.	5.	-1.	-0.	1.5	D	0.0	0.6
51	42E1	dehydrogenase/red	81	44	58	75	80	27	589	668	89	o	12	63
7		uctase family 42E,	40	03	86	51	59	68	280	373	28	w	29	32
		member 1	2	7	8	7	8		013	333	00	n	15	74
											13		05	04
10	MSH	MSH5-SAPCD1	7.	7.	7.	7.	6.	6.	-1.	-0.	1.5	D	0.0	0.6
05	5-SA	readthrough (NMD	65	26	30	10	82	52	500	585	00	o	26	63
32	PCD	candidate)	11	02	47	70	43	80	607	546	60	w	58	32
73	1		2		4	7	1	4	492	667	74	n	68	74

2												92		01	04
11	TM4	Transmembrane 4	3.	4.	4.	5.	6.	4.	2.5	1.3	2.5	U	0.0	0.6	
64	SF18	L six family	42	45	94	93	12	75	184	325	18	p	28	63	
41		member 18	05	62	03	27	69	50	335	266	43		61	32	
			1	9	3	1	5	5	52	67	35		56	74	
											52		96	04	
13	COL	Collagen, type XV,	5.	7.	6.	9.	9.	7.	5.0	2.3	5.0	U	0.0	0.6	
06	15A1	$\alpha$ 1	61	23	91	83	11	79	116	252	11	p	06	63	
			92	85	72	57	95	56	303	8	63		16	32	
			7	6		6	1		23		03		55	74	
											23		38	04	
16	FAM	Family with	5.	5.	5.	6.	7.	6.	1.9	0.9	1.9	U	0.0	0.6	
52	171B	sequence similarity	96	76	57	94	22	08	757	824	75	p	15	63	
15		171 member B	51	56	02	16	53	13	859	266	78		00	32	
			3	7	7	9	4	2	61	67	59		07	74	
											61		76	04	
54	C1orf	Chromosome 1	7.	7.	7.	6.	6.	6.	-1.	-0.	1.5	D	0.0	0.6	
96	56	open reading frame	16	12	11	60	11	88	514	599	14	o	29	63	
4		56	81	15	11	61	14	61	732	063	73	w	96	32	
			1	7	5	3	1		81	333	28	n	82	74	
											1		56	04	
95	TP53	Tumor protein p53	7.	7.	7.	6.	7.	7.	-1.	-0.	1.9	D	0.0	0.6	
37	I11	inducible protein	95	53	99	28	27	05	944	959	44	o	12	63	
		11	33	51	92	45	07	32	927	716	92	w	38	32	
			3	5	2	4	5	6	89	667	78	n	19	74	
											9		73	04	
22	NID2	Nidogen 2	5.	5.	5.	7.	6.	6.	2.3	1.2	2.3	U	0.0	0.6	
79			00	81	82	64	69	03	761	486	76	p	23	63	
5			11	21	37	83	99	47	896	5	18		23	32	

			8	6	1		6	4	73		96		63	74
											73		96	04
10	CFL2	Cofilin 2 (muscle)	3.	4.	3.	5.	4.	4.	1.9	0.9	1.9	U	0.0	0.6
73			91	05	86	76	24	65	190	404	19	p	36	63
			41	34	80	31	36	01	957	266	09		41	32
			8	2	9	8	9		13	67	57		96	74
											13		05	04
35	JCH	Joining chain of	6.	6.	6.	7.	9.	9.	4.4	2.1	4.4	U	0.0	0.6
12	AIN	multimeric iga and	68	68	64	28	46	69	198	439	19	p	08	63
		igm	68	63	62	96	32	85	170	866	81		69	32
			4	8	3	4	2	5	91	67	70		26	74
											91		49	04
81	TXN	Thioredoxin	9.	8.	9.	10	9.	9.	1.6	0.7	1.6	U	0.0	0.6
56	DC5	domain containing	30	98	05	.2	94	28	266	018	26	p	29	63
7		5 (endoplasmic	08	73	77	23	18	65	268	833	62		88	32
		reticulum)	1	3	3	05	8	9	5	33	68		68	74
											5		44	04
12	COL	Collagen, type IV,	4.	5.	4.	7.	6.	6.	3.0	1.6	3.0	U	0.0	0.6
87	4A5	$\alpha$ 5	47	96	38	18	33	12	475	076	47	p	12	63
			53	73	86	91	99	51	079	3	50		01	32
			6	1	8	8	1	5	83		79		78	74
											83		55	04
54	GNG	Guanine nucleotide	6.	7.	7.	7.	8.	7.	1.8	0.9	1.8	U	0.0	0.6
33	2	binding protein (G	23	00	26	68	38	16	789	099	78	p	48	63
1		protein), $\gamma$ 2	01	98	68	45	66	54	456	233	94		67	32
			8	2	7	1	4	9	46	33	56		66	74
											46		59	04
25	QPC	Glutaminyl-peptide	3.	3.	3.	5.	5.	4.	3.5	1.8	3.5	U	0.0	0.6
79	T	cyclotransferase	40	47	56	89	79	25	653	340	65	p	03	63

7			21	53	64	39	38	83	984	633	39		17	32
			8	5	1	5	5	3	99	33	84		72	74
											99		08	04
80	SEM	Sema domain,	4.	5.	4.	5.	6.	5.	2.2	1.1	2.2	U	0.0	0.6
03	A6D	transmembrane	42	26	84	94	17	83	022	389	02	p	02	63
1		domain (TM), and	06	57	94	18	59	50	323	666	23		08	32
		cytoplasmic	3	8	9	5	4	1	13	67	23		62	74
		domain,									13		26	04
		(semaphorin) 6D												
64	EPS8	EPS8-like 2	10	9.	9.	8.	8.	9.	-1.	-0.	1.8	D	0.0	0.6
78	L2		.1	64	41	41	94	20	830	872	30	o	14	63
7			21	69	07	27	40	58	633	343	63	w	82	32
			89	9	1		6		94	333	39	n	70	74
											4		66	04
70	TLL1	Tolloid like 1	3.	3.	3.	5.	6.	3.	2.9	1.5	2.9	U	0.0	0.6
92			08	85	53	41	05	73	739	723	73	p	26	63
			51	59	73	22	08	23	010	566	90		24	32
				2	5	9	2	3	93	67	10		02	74
											93		7	04
85	NKD	Naked cuticle	3.	4.	3.	4.	4.	4.	1.7	0.8	1.7	U	0.0	0.6
40	2	homolog 2	60	84	55	77	88	89	991	473	99	p	41	63
9		(Drosophila)	96	86	65	77	76	13	473	133	14		63	32
				1	3	3	1	4	32	33	73		37	74
											32		46	04
53	PLA	Plasminogen	4.	5.	6.	7.	7.	6.	3.2	1.7	3.2	U	0.0	0.6
27	T	activator, tissue	98	20	18	50	36	64	880	172	88	p	02	63
			32	28		54	36	86	373	266	03		34	32
			5	4		5	5	7	03	67	73		00	74
											03		12	04

24	ALO	Arachidonate	4.	4.	4.	5.	6.	5.	1.7	0.8	1.7	U	0.0	0.6
0	X5	5-lipoxygenase	99	50	68	39	12	13	727	259	72	p	21	63
			01	34	18	20	32	8	101	566	71		25	32
			3	5	3	1	7		52	67	01		20	74
											52		67	04
83	DYN	Dynein, light	4.	5.	4.	4.	3.	3.	-1.	-0.	1.9	D	0.0	0.6
65	LRB	chain,	80	02	88	23	68	83	987	991	87	o	00	63
7	2	roadblock-type 2	85	92	89	61	57	11	828	193	82	w	80	32
			2	2		8	3	5	555	333	85	n	65	74
											55		53	04
34	IGFB	Insulin like growth	5.	5.	4.	9.	7.	6.	4.8	2.2	4.8	U	0.0	0.6
85	P2	factor binding	04	93	89	27	33	05	121	666	12	p	20	63
		protein 2	44	85	04	68	84	82	668	866	16		54	32
			5	3	7		3	8	55	67	68		12	74
											55		15	04
11	HAU	HAUS augmin like	5.	5.	6.	6.	6.	6.	1.7	0.7	1.7	U	0.0	0.6
51	S1	complex subunit 1	59	40	36	75	78	18	248	864	24	p	34	63
06			75	28	74	50	45	78	728	9	87		42	32
			5	9	8	1		8	3		28		38	74
											3		43	04
25	GAB	$\Gamma$ -aminobutyric	8.	8.	8.	6.	7.	8.	-2.	-1.	2.5	D	0.0	0.6
62	RB3	acid (GABA) A	99	69	52	47	41	19	595	375	95	o	12	63
		receptor, $\beta$ 3	27	31	31	17	26	70	279	89	27	w	66	32
			7	7	2	3	1	5	646		96	n	19	74
											46		39	04
84	AFA	Actin filament	3.	3.	3.	6.	6.	3.	3.5	1.8	3.5	U	0.0	0.6
63	P1L2	associated protein	24	85	82	38	12	93	747	378	74	p	20	63
2		1 like 2	79	67	81	88	46	28	937	6	79		68	32
			4	9	4	8	8	9	32		37		66	74

											32		31	04
72	MAG	Melanoma antigen	6.	6.	6.	6.	5.	6.	-1.	-0.	1.5	D	0.0	0.6
82	ED4	family D4	44	68	56	14	62	01	554	636	54	o	11	63
39			49	92	18	30	80	45	858	783	85	w	94	32
			2	1	2	1	2	7	543	333	85	n	28	74
											43		04	04
23	SSBP	Single stranded	10	10	10	9.	9.	10	-1.	-0.	1.8	D	0.0	0.6
64	3	DNA binding	.8	.6	.5	45	87	.2	821	864	21	o	06	63
8		protein 3	63	97	93	01	60	33	104	813	10	w	08	32
			3	13	43	2	8	22	024	333	40	n	02	74
											24		4	04
23	ZNF	Zinc finger protein	9.	8.	8.	7.	8.	8.	-1.	-0.	1.6	D	0.0	0.6
03	292	292	40	54	54	77	13	37	667	737	67	o	37	63
6			83	44	64	16	62	77	700	86	70	w	72	32
			8	4	5	6	4	9	245		02	n	12	74
											45		28	04
69	BTG	B-cell translocation	9.	9.	9.	10	10	10	1.5	0.6	1.5	U	0.0	0.6
4	1	gene 1,	92	42	48	.1	.1	.4	255	093	25	p	17	63
		anti-proliferative	17	76	46	06	02	52	505	3	55		60	32
			1	9	7	69	59	78	66		05		01	74
											66		83	04
12	COL	Collagen, type IV,	3.	6.	4.	9.	7.	6.	5.3	2.4	5.3	U	0.0	0.6
82	4A1	$\alpha$ 1	89	69	87	43	06	23	600	222	60	p	39	63
			77	45	41	22	16	92	507	466	05		83	32
			5	5	7	8	6	7	73	67	07		99	74
											73		3	04
31	HMG	High mobility	6.	7.	7.	8.	8.	7.	2.1	1.0	2.1	U	0.0	0.6
48	B2	group box 2	64	23	15	73	17	33	042	732	04	p	21	63
			74	32	13	47	94	77	216	866	22		29	32

			1	5	4	3		3	3	67	16		78	74
											3		15	04
23	PDZ	PDZ domain	4.	4.	4.	7.	5.	5.	2.6	1.3	2.6	U	0.0	0.6
02	RN3	containing ring	12	89	88	07	43	57	329	966	32	p	19	63
4		finger 3	45	86	24	96	64	95	558	833	95		05	32
			8	3	3	9	7	3	56	33	58		05	74
											56		39	04
61	RPL1	Ribosomal protein	8.	8.	8.	9.	9.	9.	1.6	0.7	1.6	U	0.0	0.6
38	5	L15	81	25	84	90	03	24	871	545	87	p	30	63
			50	7	80	13	97	27	325	733	13		21	32
			7		3	7	5		61	33	25		69	74
											61		55	04
86	RUN	Runt-related	4.	6.	5.	7.	6.	5.	2.5	1.3	2.5	U	0.0	0.6
2	X1T1	transcription factor	39	14	05	24	45	90	258	367	25	p	32	63
		1; translocated to, 1	62	12	54	40	89	00	284	566	82		57	32
		(cyclin D-related)	1		8	8	9	9	67	67	84		40	74
											67		05	04
83	CTT	Cortactin binding	8.	7.	8.	6.	6.	7.	-1.	-0.	1.9	D	0.0	0.6
99	NBP	protein 2	27	38	14	77	70	39	972	979	72	o	13	63
2	2		75	75	23	02	73	08	046	693	04	w	68	32
			3	8	9	3	7	2	176	333	61	n	35	74
											76		27	04
25	FUT	Fucosyltransferase	7.	7.	7.	6.	7.	7.	-1.	-0.	1.5	D	0.0	0.6
28	6	6	87	83	67	80	10	50	579	659	79	o	17	63
			89	49	86	22	32	79	761	706	76	w	01	32
			5	8		1	8	2	389	667	13	n	58	74
											89		7	04
24	AKR	Aldo-keto	8.	8.	8.	7.	7.	8.	-2.	-1.	2.0	D	0.0	0.6
61	7L	reductase family	71	15	39	01	11	12	000	000	00	o	17	63

81		7-like (gene/pseudogene)	23 4	05 7	38 9	44 8	50 8	71 5	041 589	03	04 15 89	w n	94 25 5	32 74 04
16 26 81	C18o rf54	Chromosome 18 open reading frame 54	3. 07 62 5	3. 78 49 5	3. 20 20 4	4. 34 68 5	4. 14 22 4	3. 53 18 4	1.5 719 587 21	0.6 525 633 33	1.5 71 95 87 21	U p	0.0 44 24 93 64	0.6 63 32 74 04
11 48 01	TME M20 0A	Transmembrane protein 200A	3. 33 09 2	4. 26 60 7	4. 17 46 3	5. 71 68	5. 08 76	4. 82 48	2.4 382 735 65	1.2 858 6	2.4 38 27 35 65	U p	0.0 05 34 72 51	0.6 63 32 74 04
20 13	EMP 2	Epithelial membrane protein 2	4. 40 52 5	4. 87 92 5	5. 39 90 9	6. 78 62 2	7. 18 59 1	4. 99 10 3	2.6 879 817 32	1.4 265 233 33	2.6 87 98 17 32	U p	0.0 40 85 13 86	0.6 63 32 74 04
11 12 6	CD1 60	CD160 molecule	4. 21 36 6	4. 28 12 8	4. 51 81 4	3. 04 38	3. 46 52 2	4. 23 26 5	-1. 690 132 868	-0. 757 136 667	1.6 90 13 28 68	D o w n	0.0 35 55 17 22	0.6 63 32 74 04
89 82 2	KCN K17	Potassium channel, two pore domain subfamily K, member 17	4. 51 68	5. 50 97 4	4. 82 42 5	5. 65 30 4	6. 53 65 5	5. 53 69 6	1.9 434 051 09	0.9 585 866 67	1.9 43 40 51 09	U p	0.0 29 56 71 86	0.6 63 32 74 04
64	SH3	SH3 domain	8.	8.	8.	9.	9.	9.	1.6	0.7	1.6	U	0.0	0.6



51	BGR	binding	55	10	92	66	06	09	768	457	76	p	27	63
	L	glutamate-rich	54	84	63	91	55	29	845	833	88		37	32
		protein like	5		5	3	1	1	12	33	45		54	74
											12		75	04
70	THB	Thrombomodulin	4.	5.	5.	6.	7.	5.	2.6	1.4	2.6	U	0.0	0.6
56	D		60	52	21	87	05	71	982	320	98	p	09	63
			32	95	79	38	53	77	923	466	29		10	32
				8	8	3	4	3	49	67	23		82	74
											49		91	04
97	LZT	Leucine zipper,	9.	9.	9.	8.	8.	9.	-1.	-0.	1.5	D	0.0	0.6
62	S3	putative tumor	33	63	11	28	97	00	524	608	24	o	45	63
		suppressor family	58	52	65	14	53	65	285	133	28	w	68	32
		member 3	5	7	5	1		6	698	333	56	n	51	74
											98		95	04
27	GNA	Guanine nucleotide	9.	9.	9.	8.	8.	9.	-1.	-0.	1.7	D	0.0	0.6
81	Z	binding protein (G	59	33	63	21	65	22	765	820	65	o	18	63
		protein), $\alpha$ z	56	03	12	58	56	53	569	133	56	w	29	32
		polypeptide	9	8	4	8	7	6	158	333	91	n	08	74
											58		11	04
34	FRE	FRAS1 related	4.	4.	4.	3.	3.	4.	-1.	-0.	1.5	D	0.0	0.6
16	M2	extracellular matrix	60	25	47	80	55	01	568	649	68	o	06	63
40		protein 2	12	1	02	18	46	80	425	316	42	w	06	32
			4		2	6	4	1	134	667	51	n	11	74
											34		54	04
30	CDR	Cerebellar	9.	9.	9.	8.	8.	8.	-1.	-0.	1.5	D	0.0	0.6
85	2L	degeneration-relate	71	11	12	44	81	78	555	637	55	o	23	63
0		d protein 2-like	79	75	06	17	45	82	296	19	29	w	69	32
				4	8	2	9	4	888		68	n	25	74
											88		14	04

13	CPA3	Carboxypeptidase	6.	8.	7.	8.	8.	8.	2.1	1.1	2.1	U	0.0	0.6
59		A3 (mast cell)	92	08	19	94	14	44	622	125	62	p	14	63
			09	31	18	48	11	76	200	133	22		88	32
			9	6	8	1	1	5	19	33	00		17	74
											19		76	04
86	PLPP	Phospholipid	7.	7.	8.	8.	8.	8.	1.6	0.7	1.6	U	0.0	0.6
13	3	phosphatase 3	44	52	20	46	33	48	300	048	30	p	18	63
			08	46	44	68	74	02	053	766	00		39	32
			1	5	9		9	9	13	67	53		75	74
											13		54	04
84	DNA	Dnaj heat shock	8.	8.	8.	7.	7.	8.	-1.	-0.	1.5	D	0.0	0.6
27	JC30	protein family	74	43	27	73	83	02	534	617	34	o	11	63
7		(Hsp40) member	51	03	40	50	94	12	678	936	67	w	83	32
		C30	2	5	5	6	1	4	723	667	87	n	69	74
											23		53	04
63	PRD	PR domain	4.	5.	5.	6.	7.	5.	2.7	1.4	2.7	U	0.0	0.6
9	M1	containing 1, with	83	32	22	69	12	95	461	574	46	p	02	63
		ZNF domain	93	74	76	52	07	07	809	266	18		33	32
			1	6	8	5	8		06	67	09		03	74
											06		27	04
88	SAP3	Sin3A associated	4.	4.	4.	6.	5.	4.	2.0	1.0	2.0	U	0.0	0.6
19	0	protein 30kda	72	53	64	42	81	85	895	632	89	p	24	63
			93	34	72	70	49	76	708	066	57		16	32
			2	3	9	8		8	36	67	08		21	74
											36		98	04
92	RCS	RCSD domain	5.	5.	5.	6.	6.	6.	1.5	0.6	1.5	U	0.0	0.6
24	D1	containing 1	25	90	99	70	39	02	762	564	76	p	44	63
1			26	62	09	09	36	45	102	6	21		24	32
			4	1	3	9	3	4	63		02		24	74

											63		39	04
63 93 3	MCU R1	Mitochondrial calcium uniporter regulator 1	6. 23 15 1	6. 64 10 4	6. 38 69 3	7. 10 36 9	7. 06 94 7	7. 23 11 2	1.6 414 073 67	0.7 149 333 33	1.6 41 40 73 67	U p	0.0 03 95 92 33	0.6 63 32 74 04
33 06	HSP A2	Heat shock protein family A (Hsp70) member 2	4. 26 90 4	3. 69 11 1	4. 13 31 4	6. 19 67 1	5. 22 68 2	4. 51 50 9	2.4 313 821 52	1.2 817 766 67	2.4 31 38 21 52	U p	0.0 16 54 97 6	0.6 63 32 74 04
31 76	HNM T	Histamine N-methyltransferase	8. 66 76 4	8. 25 65 5	8. 19 87 4	7. 38 53 1	7. 13 57 7	7. 72 28 9	-1. 944 842 51	-0. 959 653 333	1.9 44 84 25 1	D o w n	0.0 03 17 09 11	0.6 63 32 74 04
18 09	DPY SL3	Dihydropyrimidina se like 3	2. 77 77 8	4. 02 01 2	2. 84 14 7	7. 35 70 7	4. 11 68 3	4. 49 01 1	4.3 115 700 91	2.1 082 133 33	4.3 11 57 00 91	U p	0.0 40 11 25 27	0.6 63 32 74 04
16 12 53	REM 2	RAS (RAD and GEM)-like GTP binding 2	4. 48 13 4	4. 55 94 2	4. 54 47 3	3. 57 65 4	3. 78 19 9	4. 33 57 6	-1. 547 994 129	-0. 630 4 41 29	1.5 47 99 41 29	D o w n	0.0 17 90 64 81	0.6 63 32 74 04
14 79 68	CAP N12	Calpain 12	10 .3 61	10 .9 22	10 .4 79	8. 92 72	9. 91 14	8. 87 97	-2. 546 183	-1. 348 336	2.5 46 18	D o w	0.0 03 56	0.6 63 32

			93	16	35	7	1	5	978	667	39	n	64	74
											78		75	04
51	TRM	Trna	7.	7.	8.	8.	8.	8.	1.7	0.7	1.7	U	0.0	0.6
50	T112	methyltransferase	72	64	17	89	55	44	198	822	19	p	07	63
4		11-2 homolog (S. Cerevisiae)	69	84	94	81	87	46	030	433	80		66	32
			6	2	1	3	8	1	2	33	30		54	74
											2		8	04
54	ZSC	Zinc finger and	5.	5.	4.	4.	4.	4.	-1.	-0.	1.6	D	0.0	0.6
99	AN2	SCAN domain	13	11	98	06	48	60	617	693	17	o	05	63
3		containing 2	07	94	83	37	77	52	672	92	67	w	89	32
			3	6		8	1	4	991		29	n	06	74
											91		93	04
88	SOC	Suppressor of	3.	4.	5.	6.	6.	5.	3.5	1.8	3.5	U	0.0	0.6
35	S2	cytokine signaling	66	58	17	61	96	38	947	458	94	p	08	63
		2	36	67	54	62	16	56	297	833	72		38	32
			1	5	9	8		2	99	33	97		46	74
											99		07	04
55	CCD	Coiled-coil domain	6.	6.	5.	5.	5.	5.	-1.	-0.	1.6	D	0.0	0.6
08	C186	containing 186	61	53	78	30	89	53	659	730	59	o	33	63
8			29	87	03	54	60	86	363	63	36	w	03	32
			3	2	6	7	1	4	549		35	n	85	74
											49		33	04
57	PLE	Pleckstrin	6.	5.	5.	6.	6.	6.	1.5	0.6	1.5	U	0.0	0.6
48	KHG	homology and	07	86	63	65	78	16	962	746	96	p	18	63
0	1	rhogef domain	96	67	06	06	09	93	205	6	22		25	32
		containing G1	1	8	2	4	9	6	47		05		05	74
											47		84	04
91	FCG	Fc fragment of igg,	5.	6.	5.	6.	6.	6.	1.8	0.8	1.8	U	0.0	0.6
03	R2C	low affinity iic,	07	37	77	81	79	29	633	979	63	p	33	63

		receptor for (CD32) (gene/pseudogene)	52 1	17 6	02 4	95 1	57 1	56 8	775 28	2	37 75 28		49 89 37	32 74 04
46 00	MX2	MX dynamin-like gtpase 2	7. 96 27 2	8. 26 40 1	8. 40 13 1	7. 21 57 1	7. 08 47 7	7. 88 81 3	-1. 757 035 491	-0. 813 143 333	1.7 57 03 54 91	D o w n	0.0 14 59 78 93	0.6 63 32 74 04
16 30 50	ZNF 564	Zinc finger protein 564	5. 46 30 6	5. 72 11 4	5. 51 10 7	4. 98 07 5	4. 39 23 5	5. 16 55 205	-1. 645 934 667	-0. 718 906 667	1.6 45 93 42 05	D o w n	0.0 15 89 03 44	0.6 63 32 74 04
40 34	LRC H4	Leucine-rich repeats and calponin homology (CH) domain containing 4	6. 62 65 1	6. 38 32 1	6. 17 94 6	5. 29 29 8	5. 59 14 8	6. 02 04 4	-1. 695 166 129	-0. 761 426 667	1.6 95 16 61 29	D o w n	0.0 13 53 85 69	0.6 63 32 74 04
15 07 86	WTH 3DI	RAB6C-like	3. 74 72 6	2. 92 60 1	3. 45 54 7	3. 90 01 3	4. 23 96 4	4. 29 00 3	1.7 017 510 5	0.7 670 2 5	1.7 01 75 10 5	U p	0.0 11 79 69 62	0.6 63 32 74 04
22 91 8	CD9 3	CD93 molecule	4. 49 22 1	5. 77 40 4	5. 28 25 9	7. 66 98 7	7. 70 57 4	5. 43 46 3	3.3 724 568 87	1.7 538 45 68 87	3.3 72 45 68 87	U p	0.0 30 38 24 01	0.6 63 32 74 04
87	MPD	Multiple PDZ	3.	5.	4.	7.	6.	5.	3.4	1.7	3.4	U	0.0	0.6

77	Z	domain protein	78	46	69	17	37	72	238	756	23	p	09	63
			96	04	43	46	41	25	986	4	89		46	32
			9	6	8	7	9	9	56		86		02	74
											56		14	04
52	PFN2	Profilin 2	3.	3.	4.	5.	4.	4.	1.5	0.6	1.5	U	0.0	0.6
17			66	79	22	07	11	45	693	501	69	p	47	63
			98	17	76	29	20	46	059	266	30		97	32
			4	9	7	9	5	4	73	67	59		39	74
											73		85	04
59	RBM	RNA binding	7.	7.	7.	8.	8.	7.	1.5	0.6	1.5	U	0.0	0.6
37	S1	motif, single	54	72	60	85	09	87	710	517	71	p	43	63
		stranded	07	17	49	18	64	43	509	3	05		50	32
		interacting protein	7	6	7	2	9	8	84		09		42	74
		1									84		9	04
56	PCD	Protocadherin $\alpha$	7.	7.	6.	6.	6.	6.	-1.	-0.	1.5	D	0.0	0.6
13	HAC	subfamily C, 1	44	73	91	53	83	80	557	639	57	o	31	63
5	1		20	45	29	69	18	31	526	256	52	w	81	32
			9	2	9		2	1	454	667	64	n	64	74
											54		86	04
84	GPT	Glutamic pyruvate	9.	8.	9.	7.	8.	8.	-1.	-0.	1.7	D	0.0	0.6
70	2	transaminase	03	66	28	61	50	44	756	812	56	o	26	63
6		(alanine	66	82	83	14	2	15	515	716	51	w	27	32
		aminotransferase)		8	3	9		7	937	667	59	n	51	74
		2									37		54	04
65	REE	Receptor accessory	7.	6.	6.	6.	6.	6.	-1.	-0.	1.5	D	0.0	0.6
05	P1	protein 1	08	92	95	43	12	49	557	639	57	o	06	63
5			96	87	25	10	60	63	414	153	41	w	63	32
			8	2		4	8	2	899	333	48	n	30	74
											99		25	04

90	MAP	Mitogen-activated	6.	7.	6.	6.	6.	6.	-1.	-0.	1.5	D	0.0	0.6
20	3K14	protein kinase	95	15	92	34	13	65	552	634	52	o	11	63
		kinase kinase 14	38	27	54	48	17	30	015	143	01	w	80	32
			7	3	4	6	1	4	895	333	58	n	52	74
											95		76	04
49	CLE	C-type lectin	6.	6.	6.	4.	5.	5.	-2.	-1.	2.1	D	0.0	0.6
71	C18B	domain family 18,	87	64	15	97	72	75	110	077	10	o	07	63
90		member B	89	41	82	01	35	50	439	543	43	w	09	32
			9	8		8	3	3	297	333	92	n	44	74
											97		89	04
10	EFS	Embryonal	3.	5.	4.	6.	5.	5.	2.6	1.3	2.6	U	0.0	0.6
27		Fyn-associated	54	16	70	68	75	12	064	820	06	p	31	63
8		substrate	90	25	23	08	10	83	689	966	46		13	32
			1	2	4		4	2	37	67	89		80	74
											37		58	04
97	KIA	KIAA0101	4.	4.	4.	6.	6.	4.	2.4	1.2	2.4	U	0.0	0.6
68	A010		40	74	70	60	41	70	402	870	40	p	31	63
	1		68	83	83	45	17	83	517	3	25		61	32
			6	5	5	6	4	5	64		17		00	74
											64		36	04
54	PRR	Proline rich 13	11	11	11	10	11	11	-1.	-0.	1.5	D	0.0	0.6
45	13		.8	.8	.6	.6	.1	.5	553	635	53	o	34	63
8			40	26	59	59	70	88	928	92	92	w	64	32
			37	28	35	46	46	32	367		83	n	76	74
											67		25	04
21	F3	Coagulation factor	5.	4.	4.	5.	5.	5.	1.7	0.8	1.7	U	0.0	0.6
52		III (thromboplastin,	05	09	84	47	84	12	672	215	67	p	28	63
		tissue factor)	30	18	11	74	82	48	751	266	27		94	32
			7	9		6	9	9	42	67	51		52	74

												42		49	04
28	TSE	Trna splicing	9.	9.	9.	7.	8.	9.	-1.	-0.	1.7	D	0.0	0.6	
39	N54	endonuclease	79	24	14	91	84	05	729	790	29	o	49	63	
89		subunit 54	17	15	88	27	67	17	454	316	45	w	49	32	
			6	2	6	2	4	3	03	667	40	n	17	74	
											3		58	04	
83	PLA	Phospholipase A2	7.	7.	7.	7.	6.	7.	-1.	-0.	1.5	D	0.0	0.6	
98	2G6	group VI	76	84	93	02	92	57	597	676	97	o	14	63	
			57	80	58	26	24	62	799	086	79	w	50	32	
			2	7	2	5	9	1	814	667	98	n	87	74	
											14		99	04	
56	PCD	Protocadherin $\alpha$	7.	7.	6.	6.	6.	6.	-1.	-0.	1.5	D	0.0	0.6	
13	HAC	subfamily C, 2	44	73	91	53	83	80	557	639	57	o	31	63	
4	2		20	45	29	69	18	31	526	256	52	w	81	32	
			9	2	9		2	1	454	667	64	n	64	74	
											54		86	04	
99	ARN	Aryl hydrocarbon	3.	4.	3.	5.	4.	4.	2.0	1.0	2.0	U	0.0	0.6	
15	T2	receptor nuclear	39	62	64	57	70	38	025	018	02	p	43	63	
		translocator 2	06	59	43	61	79	23	847	633	58		77	32	
				4	1	6	3	5	97	33	47		37	74	
											97		49	04	
54	ERR	ERBB receptor	8.	8.	8.	9.	10	8.	2.4	1.2	2.4	U	0.0	0.6	
20	FI1	feedback inhibitor	26	16	39	71	.1	87	434	889	43	p	04	63	
6		1	92	15	15	07	05	27	281	066	42		22	32	
						3	47	2	24	67	81		60	74	
											24		25	04	
19	EDN	Endothelin 3	2.	3.	3.	4.	5.	3.	2.0	1.0	2.0	U	0.0	0.6	
08	3		95	33	92	65	11	61	791	559	79	p	36	63	
			71	09	48	69	23	17	300	8	13		93	32	



			9	4	6	1	2		47		00		49	74
											47		09	04
10	CDH	Cadherin 5, type 2	5.	5.	5.	7.	8.	5.	3.0	1.6	3.0	U	0.0	0.6
03	5	(vascular endothelium)	19	92	89	90	00	94	619	144	61	p	22	63
			97	18	23	79	00	93	484	5	94		37	32
			8	8	1	2	7	3	62		84		12	74
											62		05	04
44	MT1	Metallothionein 1F	11	10	11	8.	7.	10	-5.	-2.	5.0	D	0.0	0.6
94	F		.2	.8	.1	58	63	.1	051	336	51	o	04	63
			95	74	71	87	67	06	691	766	69	w	42	32
			8	7	53	7	4	22	949	667	19	n	51	74
											49		9	04
47	NF1C	Nuclear factor I/C	10	10	10	9.	10	9.	-1.	-0.	1.5	D	0.0	0.6
82		(CCAAT-binding transcription factor)	.2	.8	.4	68	.2	58	572	653	72	o	33	63
			35	32	40	45	78	61	721	263	72	w	46	32
			32	49	72	5	03	6	625	333	16	n	05	74
											25		85	04
13	CPE	Carboxypeptidase	4.	5.	6.	7.	7.	6.	2.8	1.5	2.8	U	0.0	0.6
63	E		62	52	60	76	54	00	672	196	67	p	43	63
			03	63	71	68	41	19	876	866	28		70	32
			6	1	6	9			93	67	76		67	74
											93		61	04
25	Cxorf	Chromosome X	6.	5.	6.	4.	5.	5.	-1.	-0.	1.8	D	0.0	0.6
66	23	open reading frame	26	69	08	90	29	25	814	859	14	o	04	63
43	23		19	09	24	39	41	95	078	236	07	w	42	32
			4	1	7	3	1	7	224	667	82	n	41	74
											24		86	04
54	CLIC	Chloride	8.	8.	8.	6.	7.	7.	-2.	-1.	2.3	D	0.0	0.6
10	6	intracellular	31	00	67	24	76	25	363	240	63	o	15	63

2		channel 6	44 1	02 3	28 9	92 8	51 8	05 2	322 751	816 667	32 27 51	w n	71 44 84	32 74 04
33 98	ID2	Inhibitor of DNA binding 2, dominant negative helix-loop-helix protein	11 .2 96 48	10 .8 48 71	11 .2 22 95	10 .1 45 31	10 .2 70 13	10 .9 66 91	-1. 582 197 832	-0. 661 93	1.5 82 19 78 32	D o w n	0.0 35 45 87 99	0.6 63 32 74 04
68 19	SUL T1C2	Sulfotransferase family 1C member 2	10 .3 20 71	9. 38 49 3	9. 79 66 2	8. 98 01 3	7. 91 59 3	9. 33 63 5	-2. 128 681 345	-1. 089 96	2.1 28 68 13 45	D o w n	0.0 30 79 82 14	0.6 63 32 74 04
10 75	CTS C	Cathepsin C	7. 31 26 3	7. 11 42 8	7. 29 17 7	9. 02 71 3	8. 23 08 4	8. 33 96 1	2.4 503 140 49	1.2 929 666 67	2.4 50 31 40 49	U p	0.0 00 96 09 18	0.6 63 32 74 04
65 75	SLC2 0A2	Solute carrier family 20 (phosphate transporter), member 2	8. 44 08 4	8. 24 07 5	8. 29 80 5	7. 19 76 6	7. 55 18 1	8. 05 95 8	-1. 651 198 235	-0. 723 513 333	1.6 51 19 82 35	D o w n	0.0 18 67 23 74	0.6 63 32 74 04
25 90 7	TME M15 8	Transmembrane protein 158 (gene/pseudogene)	4. 92 30 9	6. 67 08 3	5. 00 37 3	10 .4 09 29	7. 28 73 5	6. 48 33 6	5.7 655 170 73	2.5 274 5	5.7 65 51 70 73	U p	0.0 40 93 79 49	0.6 63 32 74 04
34	CAT	Cation channel,	5.	4.	4.	3.	4.	4.	-1.	-0.	1.5	D	0.0	0.6

77	SPE	sperm associated 3	15	37	51	68	03	30	592	671	92	o	32	63
32	R3		37	52	65	60	94	60	573	36	57	w	87	32
			7	5	7	4	5	2	548		35	n	96	74
											48		25	04
14	CDC	CDC42 effector	4.	5.	5.	6.	6.	5.	1.9	0.9	1.9	U	0.0	0.6
81	42EP	protein (Rho gtpase	85	50	01	53	32	51	952	965	95	p	14	63
70	5	binding) 5	79	89	63	39	40	48	506	7	25		49	32
			1	7	3	6	9	7	58		06		36	74
											58		31	04
11	AKA	A-kinase anchoring	8.	8.	8.	9.	8.	8.	1.5	0.6	1.5	U	0.0	0.6
21	P2	protein 2	27	20	22	33	52	74	544	363	54	p	27	63
7			71	76	09	92	59	97	382	933	43		04	32
			8	4	3	2	4	7	79	33	82		00	74
											79		58	04
15	GIM	Gtpase, IMAP	4.	4.	5.	6.	6.	5.	2.2	1.1	2.2	U	0.0	0.6
50	AP8	family member 8	51	70	43	75	10	24	101	441	10	p	28	63
38			86	54	84	15	03	31	893	7	18		02	32
			6	1	3	2	1	8	92		93		02	74
											92		1	04
23	VPS1	Vacuolar protein	9.	9.	9.	8.	8.	9.	-1.	-0.	1.5	D	0.0	0.6
23	3A	sorting 13 homolog	79	24	38	93	42	17	545	628	45	o	38	63
0		A (S. Cerevisiae)	05	50	45	61	48	36	988	53	98	w	42	32
			7	8	5		4	7	942		89	n	39	74
											42		19	04
27	NDO	NADPH dependent	7.	7.	6.	5.	6.	6.	-1.	-0.	1.6	D	0.0	0.6
15	R1	diflavin	18	03	96	89	44	56	693	760	93	o	09	63
8		oxidoreductase 1	08	44	57	21	01	82	686	166	68	w	45	32
			3	2	3	3	2	3	276	667	62	n	72	74
											76		31	04

63 3	BGN	Biglycan	3. 56 38 7	3. 64 31 4	3. 43 23	5. 70 42 7	4. 30 65 5	4. 01 56	2.1 871 265 01	1.1 290 366 67	2.1 87 12 65 01	U p	0.0 28 59 19 43	0.6 63 32 74 04
74 21	VDR	Vitamin D (1,25- dihydroxyvitamin D3) receptor	8. 28 95 7	8. 00 23 8	8. 04 89 8	6. 72 43 2	7. 10 69 3	8. 01 93 6	-1. 777 816 802	-0. 830 106 667	1.7 77 81 68 02	D o w n	0.0 39 12 62 9	0.6 63 32 74 04
44 85	MST 1	Macrophage stimulating 1	9. 83 82 9	8. 77 68 1	8. 69 80 2	8. 23 50 1	7. 66 34 8	8. 62 64 7	-1. 904 466 178	-0. 929 386 667	1.9 04 46 61 78	D o w n	0.0 41 92 63 07	0.6 63 32 74 04
27 34 7	STK 39	Serine/threonine kinase 39	9. 06 15 1	8. 45 24 7	8. 78 31 7	7. 61 00 8	8. 43 51 5	8. 18 87 6	-1. 610 735 938	-0. 687 72 735	1.6 10 73 59 38	D o w n	0.0 35 64 73 08	0.6 63 32 74 04
26 11 8	WSB 1	WD repeat and SOCS box containing 1	4. 77 15 7	4. 83 51 4	4. 78 77 9	5. 89 67 2	5. 36 66 7	5. 07 78 5	1.5 679 867 12	0.6 489 133 33	1.5 67 98 67 12	U p	0.0 22 74 10 63	0.6 63 32 74 04
10 19 29 81	LOC 1019 2981 5	D(1B) dopamine receptor-like	7. 49 63 6	7. 64 48 5	7. 07 38 5	6. 85 24 1	6. 68 84 4	6. 88 76 7	-1. 511 010 131	-0. 595 513 333	1.5 11 01 01	D o w n	0.0 18 43 06	0.6 63 32 74

5											31		8	04
50	IGK	Immunoglobulin $\kappa$	9.	10	10	10	13	12	4.3	2.1	4.3	U	0.0	0.6
80		locus	98	.5	.0	.8	.1	.9	213	114	21	p	07	63
2			69	22	69	78	14	19	437	8	34		52	32
			2	86	24	67	85	94	57		37		56	74
											57		87	04
10	KLF	Kruppel-like factor	7.	7.	8.	8.	9.	8.	2.3	1.2	2.3	U	0.0	0.6
36	2	2	92	14	12	85	62	42	629	405	62	p	12	63
5			55	27	31	74	79	78	460	866	94		79	32
			6	5	4	5	2	4	11	67	60		42	74
											11		81	04
10	CDC	CDC42 effector	4.	4.	4.	7.	6.	5.	3.2	1.6	3.2	U	0.0	0.6
60	42EP	protein (Rho gtpase	30	64	85	06	76	05	392	956	39	p	12	63
2	3	binding) 3	76	44	3	33	97	91	803	733	28		10	32
			6	9			2	5	47	33	03		01	74
											47		95	04
28	IGK	Immunoglobulin $\kappa$	4.	3.	4.	5.	8.	8.	9.2	3.2	9.2	U	0.0	0.6
93	V1-3	variable 1-33	13	77	06	43	05	11	351	071	35	p	02	63
3	3		79	90	70	04	72	77	154	3	11		29	32
			3	5	6	3	3	7	71		54		32	74
											71		51	04
10	GAD	Growth arrest and	8.	7.	8.	6.	7.	7.	-1.	-0.	1.7	D	0.0	0.6
91	D45	DNA damage	14	94	00	70	43	55	742	801	42	o	13	63
2	G	inducible $\gamma$	26	98	93	97	81	06	400	076	40	w	84	32
			3		8	2	8	8	975	667	09	n	43	74
											75		88	04
34	IGFB	Insulin like growth	4.	5.	5.	6.	6.	6.	1.8	0.8	1.8	U	0.0	0.6
87	P4	factor binding	66	34	80	30	09	00	180	623	18	p	21	63
		protein 4	53	37	96	04	84	7	266	733	02		57	32

			8	1	9	8	2		32	33	66		45	74
											32		09	04
77	ZP3	Zona pellucida	5.	6.	7.	5.	5.	4.	-2.	-1.	2.2	D	0.0	0.6
84		glycoprotein 3	40	60	05	39	34	79	265	179	65	o	26	63
		(sperm receptor)	74	32	95	11	05	99	024	526	02	w	50	32
			9	5	6	7	6	9	518	667	45	n	29	74
											18		38	04
53	PLA	Phospholipase A2	3.	3.	4.	6.	5.	4.	3.0	1.6	3.0	U	0.0	0.6
21	2G4	group IVA	83	78	57	14	90	95	362	023	36	p	02	63
	A		92	17	81	53	29	76	838	066	28		86	32
			1	6	1	6	9	5	45	67	38		52	74
											45		8	04
52	PGC	Progastricsin	5.	5.	5.	6.	7.	5.	2.4	1.2	2.4	U	0.0	0.6
25		(pepsinogen C)	23	19	10	30	65	40	275	795	27	p	41	63
			76	53	29	98	92	54	819	2	58		61	32
			2	9	1	5		3	52		19		06	74
											52		58	04
51	IPO1	Importin 11	3.	3.	3.	5.	5.	4.	2.6	1.3	2.6	U	0.0	0.6
19	1		29	49	49	08	36	03	376	992	37	p	03	63
4			25	99	52	58	68	28	991	8	69		80	32
			6	2		7	1	4	07		91		01	74
											07		24	04
87	SNX	Sorting nexin 3	7.	6.	7.	7.	7.	8.	1.7	0.7	1.7	U	0.0	0.6
24	3		07	70	46	67	74	16	182	809	18	p	15	63
			20	13	76	80	23	33	500	4	25		36	32
			1	5	1	2	8	9	48		00		08	74
											48		83	04
72	TUB	Tubby bipartite	3.	5.	4.	6.	6.	5.	3.6	1.8	3.6	U	0.0	0.6
75		transcription factor	40	05	11	77	15	19	088	515	08	p	08	63

			44	19	35	00	92	53	937	566	89		87	32
			2	3	8	1		9	44	67	37		11	74
											44		08	04
21	ETV	Ets variant 4	9.	8.	8.	8.	7.	8.	-2.	-1.	2.0	D	0.0	0.6
18	4		13	91	75	16	28	22	057	040	57	o	07	63
			17	04	53	72	19	65	068	59	06	w	49	32
			8	6	5	8	7	7	734		87	n	21	74
											34		76	04
51	ZC2	Zinc finger,	5.	5.	5.	6.	6.	5.	1.6	0.7	1.6	U	0.0	0.6
10	HC1	C2HC-type	73	57	85	92	35	99	271	023	27	p	27	63
1	A	containing 1A	55	68	23	01	73	42	042	066	10		54	32
			8	1	7	1	5	2	25	67	42		61	74
											25		39	04
10	ZBT	Zinc finger and	7.	6.	6.	5.	6.	6.	-1.	-0.	1.7	D	0.0	0.6
01	B42	BTB domain	20	57	91	94	01	34	738	798	38	o	07	63
28		containing 42	23	80	81	11	80	46	970	233	97	w	67	32
92			5	6	2	5	3	5	349	333	03	n	09	74
7											49		43	04
10	GJC1	Gap junction	3.	3.	3.	4.	4.	3.	1.6	0.6	1.6	U	0.0	0.6
05		protein $\gamma$ 1	47	81	34	48	43	79	187	948	18	p	17	63
2			46	71	56	46	80	93	198	533	71		05	32
			3	9	6	5	3	6	63	33	98		37	74
											63		63	04
26	STE	STEAP2	8.	8.	8.	7.	7.	8.	-1.	-0.	1.5	D	0.0	0.6
17	AP2	metalloreductase	54	06	61	53	53	18	581	661	81	o	33	63
29			92	77	44	37	09	30	404	206	40	w	10	32
			1	3	5	6	3	8	754	667	47	n	87	74
											54		07	04
72	TRO	Trophinin	4.	4.	4.	6.	5.	4.	2.1	1.0	2.1	U	0.0	0.6

16			05	90	14	35	45	56	254	877	25	p	49	63
			91	94	09	56	60	11	622	766	46		61	32
			5	8	1	1	8	8	96	67	22		97	74
											96		73	04
84	FAR	Fatty acyl coa	5.	4.	4.	6.	5.	5.	1.9	0.9	1.9	U	0.0	0.6
18	1	reductase 1	09	98	97	50	74	65	362	532	36	p	06	63
8			51	42	15	99	39	67	474	633	24		16	32
			6	5	1	9	9	3	42	33	74		76	74
											42		53	04
10	AKT	V-akt murine	4.	5.	4.	5.	5.	5.	1.5	0.6	1.5	U	0.0	0.6
00	3	thymoma viral	47	15	75	88	41	09	913	702	91	p	38	63
0		oncogene homolog	17	74	33	60	35	35	266	3	32		67	32
		3		2	4	2	8	5	43		66		23	74
											43		79	04
78	BTG	BTG family	5.	5.	5.	7.	8.	6.	3.2	1.6	3.2	U	0.0	0.6
32	2	member 2	86	38	98	34	13	80	165	854	16	p	01	63
			01	84	86	78	69	89	110	966	51		95	32
			5	4	5	6	7		98	67	10		02	74
											98		83	04
85	CAV	Caveolin 1	6.	8.	7.	10	9.	9.	3.8	1.9	3.8	U	0.0	0.6
7	1		38	15	79	.0	09	01	632	498	63	p	05	63
			29	66	88	72	82	73	722	233	27		95	32
			1	4	6	35	2	1	06	33	22		87	74
											06		53	04
28	P2R	Purinergic receptor	3.	3.	3.	5.	4.	4.	1.8	0.8	1.8	U	0.0	0.6
65	Y8	P2Y, G-protein	42	89	92	23	19	40	212	649	21	p	20	63
30		coupled, 8	38	21	11	16	08	94	470	266	24		49	32
			8			5		1	89	67	70		26	74
											89		98	04



90	DIR	DIRAS family,	3.	5.	3.	6.	5.	5.	3.6	1.8	3.6	U	0.0	0.6
77	AS3	GTP-binding	45	12	67	61	93	26	063	505	06	p	08	63
		RAS-like 3	78	82	32	15	03	91	847	533	38		30	32
			6	7		4	2	3	83	33	47		58	74
											83		19	04
29	CXC	Chemokine	6.	6.	6.	7.	9.	6.	2.6	1.4	2.6	U	0.0	0.6
20	L2	(C-X-C motif)	18	48	82	75	16	82	678	157	67	p	36	63
		ligand 2	92	96	32	77	82	32	915		89		90	32
			6	3	6	8	1	6	09		15		22	74
											09		47	04
26	AMD	Adenosylmethionin	10	10	9.	8.	9.	10	-1.	-0.	1.9	D	0.0	0.6
2	1	e decarboxylase 1	.7	.6	97	69	75	.0	903	928	03	o	48	63
			47	05	91	16	72	97	260	473	26	w	35	32
			45		6	6	3	3	89	333	08	n	14	74
											9		93	04
46	PPP1	Protein	5.	4.	5.	6.	5.	6.	1.7	0.7	1.7	U	0.0	0.6
59	R12	phosphatase 1	49	64	53	51	53	00	355	953	35	p	49	63
	A	regulatory subunit	35	33	91	71	58	92	384	833	53		54	32
		12A	6	1	2	3	1		57	33	84		84	74
											57			04
56	CLD	Claudin domain	6.	5.	6.	7.	6.	6.	1.6	0.7	1.6	U	0.0	0.6
65	ND1	containing 1	42	64	10	06	66	64	640	347	64	p	19	63
0			24	62	23	74	11	65	552	033	05		29	32
			1	2	9	7	2	4	48	33	52		89	74
											48		86	04
85	FHD	FH2 domain	8.	8.	8.	6.	7.	7.	-1.	-0.	1.9	D	0.0	0.6
46	C1	containing 1	43	33	09	50	67	88	904	929	04	o	36	63
2			01	15	10	64		83	391	33	39	w	31	32
			4	4	8	2		5	375		13	n	02	74

											75			04
11 64	CKS 2	CDC28 protein kinase regulatory subunit 2	5. 17 77 5	5. 44 58 3	5. 45 84 6	6. 60 81 6	6. 26 93 7	5. 99 14 3	1.9 039 206 25	0.9 289 733 33	1.9 03 92 06 25	U p	0.0 02 63 56 23	0.6 63 32 74 04
25 70 19	FRM D3	FERM domain containing 3	3. 85 92 4	3. 91 56 2	3. 80 84 7	4. 52 22 9	4. 46 76 6 7	4. 85 15 7	1.6 849 782 86	0.7 527 3 86	1.6 84 97 82 86	U p	0.0 01 29 83 58	0.6 63 32 74 04
41 70	MCL 1	Myeloid cell leukemia 1	9. 69 08 2	8. 74 71 3	9. 46 12 1	10 .2 74 54	10 .2 26 04	9. 80 66 4	1.7 443 465 23	0.8 026 866 67	1.7 44 34 65 23	U p	0.0 22 68 16 81	0.6 63 32 74 04
91 3	CD1 E	CD1e molecule	3. 89 43 8	4. 55 78 5	4. 33 35	5. 66 96 1	5. 28 71 9	4. 90 75 2	2.0 366 480 14	1.0 261 966 67	2.0 36 64 80 14	U p	0.0 04 91 86 19	0.6 63 32 74 04
24 87	FRZ B	Frizzled-related protein	3. 50 41 9	6. 78 58 3	5. 00 68 2	8. 39 35 8	7. 07 68	6. 85 53 2	5.0 734 014 86	2.3 429 533 33	5.0 73 40 14 86	U p	0.0 23 75 69 01	0.6 63 32 74 04
92 29 1	CAP N13	Calpain 13	7. 54 86	7. 14 94	7. 61 57	6. 44 79	6. 39 24	7. 15 87	-1. 707 083	-0. 771 533	1.7 07 08	D o w	0.0 19 81	0.6 63 32

			1	6	3	9	2	9	152	333	31	n	21	74
											52		97	04
12	CNN	Calponin 2	3.	3.	3.	6.	4.	4.	2.5	1.3	2.5	U	0.0	0.6
65	2		39	84	48	01	13	59	319	402	31	p	21	63
			61	83	05	95	20	42	694	6	96		62	32
			2	3	4	5	2		54		94		04	74
											54		23	04
51	DTL	Denticleless E3	2.	3.	3.	5.	5.	3.	2.9	1.5	2.9	U	0.0	0.6
51		ubiquitin protein	76	72	15	37	34	66	891	797	89	p	14	63
4		ligase homolog	02	81	07	29	35	18	459	333	14		36	32
		(Drosophila)		7	7	3	8	3	35	33	59		69	74
											35		87	04
29	LMC	LIM and	4.	5.	5.	7.	7.	5.	3.5	1.8	3.5	U	0.0	0.6
99	D1	cysteine-rich	34	49	22	96	02	53	222	165	22	p	20	63
5		domains 1	70	62	48	31	14	31	565		25		64	32
			8	8	3	1	8		64		65		05	74
											64		45	04
28	GPX	Glutathione	4.	5.	4.	6.	5.	5.	1.7	0.7	1.7	U	0.0	0.6
82	7	peroxidase 7	76	31	73	33	40	45	348	947	34	p	33	63
			30	84	26	59	71	54	288	933	82		12	32
			8	3	1		6	4	42	33	88		48	74
											42		82	04
14	SLC2	Solute carrier	3.	3.	3.	4.	4.	4.	1.6	0.7	1.6	U	0.0	0.6
41	A14	family 2	68	95	68	76	75	01	696	395	69	p	14	63
95		(facilitated glucose	23	90	23	85	57	80	472	433	64		14	32
		transporter),	5	4	5	4	6	7	5	33	72		36	74
		member 14									5		69	04
54	RASI	Ras interacting	5.	5.	5.	6.	7.	5.	1.9	0.9	1.9	U	0.0	0.6
92	P1	protein 1	29	81	59	67	25	63	298	484	29	p	49	63

2			87 2	39 8	90 7	03 3	35 3	33 8	517 17	9	85 17 17		39 56 21	32 74 04
22 85 6	CHS Y1	Chondroitin sulfate synthase 1	6. 57 26 7	7. 07 06 4	6. 70 67 1	8. 15 18 8	8. 01 29 4	7. 13 34 4	1.9 762 242 53	0.9 827 466 67	1.9 76 22 42 53	U p	0.0 13 43 63 74 62	0.6 63 32 74 04
10 27 24 56 2	LOC 1027 2456 2	Hepatocyte growth factor-like protein	7. 83 79 7	5. 90 32 9	6. 13 64	4. 57 05 6	4. 20 38 3	6. 19 99 5	-3. 104 670 15	-1. 634 44	3.1 04 67 01 5	D o w n	0.0 44 13 69 92	0.6 63 32 74 04
37 91	KDR	Kinase insert domain receptor	5. 27 99 3	6. 44 71 2	6. 32 64 5	7. 47 06 1	7. 91 89	6. 78 67 5	2.5 923 370 98	1.3 742 533 33 70 98	2.5 92 33 70 98	U p	0.0 10 78 69	0.6 63 32 74 04
27 06 7	STA U2	Staufen double-stranded RNA binding protein 2	7. 75 16 8	7. 13 66 7	6. 87 58 5	6. 82 45 8	6. 64 01 1	6. 53 68 3	-1. 502 703 107	-0. 587 56	1.5 02 70 31 07	D o w n	0.0 49 91 85 72	0.6 63 32 74 04
50 85 4	C6orf 48	Chromosome 6 open reading frame 48	9. 32 34 3	9. 12 21 5	9. 37 73	10 .5 30 19	9. 45 72 2	9. 90 65 1	1.6 136 712 23	0.6 903 466 67	1.6 13 67 12 23	U p	0.0 40 94 56 61	0.6 63 32 74 04
58	IL22	Interleukin 22	7.	7.	8.	5.	6.	7.	-2.	-1.	2.8	D	0.0	0.6

98	RA1	receptor, $\alpha$ 1	58	92	37	32	31	75	818	495	18	o	35	63
5			35	14	45	86	53	02	778	07	77	w	43	32
				8	3	9	9	2	275		82	n	91	74
											75		21	04
28	NTM	N-terminal	7.	7.	7.	6.	6.	6.	-1.	-0.	1.5	D	0.0	0.6
98	T1	Xaa-Pro-Lys	37	26	29	28	86	88	550	633	50	o	17	63
9		N-methyltransferase 1	42	63	63	83	27	64	933	136	93	w	19	32
			3	6	5	9	2	2	326	667	33	n	77	74
											26		76	04
23	KCN	Potassium channel,	7.	7.	6.	5.	6.	6.	-1.	-0.	1.9	D	0.0	0.6
41	H3	voltage gated eag	27	00	80	59	07	53	948	962	48	o	08	63
6		related subfamily	34	53	77	25	18	50	544	396	54	w	85	32
		H, member 3	4	2	6	2		1	213	667	42	n	73	74
											13		17	04
59	RGS	Regulator of	4.	5.	4.	6.	7.	4.	2.9	1.5	2.9	U	0.0	0.6
96	1	G-protein signaling	20	40	48	64	33	79	451	583	45	p	47	63
		1	43	41	86	82	24	15	953	633	19		37	32
			2	7	4	5		7	59	33	53		56	74
											59		74	04
47	RPL1	Ribosomal protein	10	10	10	11	11	10	1.6	0.7	1.6	U	0.0	0.6
36	0A	110a	.5	.3	.9	.7	.2	.9	633	341	63	p	26	63
			41	10	81	78	59	97	863	233	38		42	32
			72	32	58	96	09	94	91	33	63		18	74
											91		35	04
51	KLH	Kelch like family	3.	3.	4.	5.	4.	4.	1.8	0.8	1.8	U	0.0	0.6
08	L5	member 5	52	81	20	18	58	32	007	485	00	p	15	63
8			26	55	86	58	10	56	442	933	74		99	32
			8	3	4	7	8	8	95	33	42		48	74
											95		69	04

34	IDH3	Isocitrate	3.	3.	3.	4.	4.	4.	1.6	0.6	1.6	U	0.0	0.6
19	A	dehydrogenase 3 (NAD+) $\alpha$	84	33	61	24	30	34	240	995	24	p	02	63
			14	90	59	84	65	01	394	866	03		57	32
			1	2	7	7	5	4	37	67	94		80	74
											37		45	04
93	SLIT	Slit guidance	5.	6.	7.	7.	8.	6.	2.2	1.1	2.2	U	0.0	0.6
53	2	ligand 2	88	94	04	94	42	92	031	395	03	p	41	63
			05	35	34	36	21	05	585	733	15		73	32
			7	9	1	2	6	1	67	33	85		65	74
											67		78	04
29	MSH	Muts homolog 6	3.	2.	3.	4.	3.	3.	1.7	0.8	1.7	U	0.0	0.6
56	6		15	66	64	55	65	66	449	032	44	p	43	63
			35	21	77	43	52	35	713	033	97		06	32
			4	8	5	5	2	1	3	33	13		24	74
											3		24	04
10	SYN	SYNJ2BP-COX16	7.	7.	7.	6.	7.	7.	-1.	-0.	1.5	D	0.0	0.6
05	J2BP	readthrough	77	45	68	65	02	46	504	589	04	o	41	63
29	-CO		00	92	22	13	37	87	460	246	46	w	26	32
25	X16		8		3	4		3	957	667	09	n	49	74
7											57		22	04
22	FOX	Forkhead box F1	5.	7.	5.	8.	7.	7.	3.4	1.7	3.4	U	0.0	0.6
94	F1		29	01	81	54	25	64	168	726	16	p	09	63
			80	09	74	94	25	24	257	566	82		38	32
			9	1	6	5	3	5	29	67	57		31	74
											29		53	04
10	BLO	BLOC1S5-TXND	9.	8.	9.	10	9.	9.	1.6	0.7	1.6	U	0.0	0.6
05	C1S5	C5 readthrough	30	98	05	.2	94	28	266	018	26	p	29	63
26	-TX	(NMD candidate)	08	73	77	23	18	65	268	833	62		88	32
83	NDC		1	3	3	05	8	9	5	33	68		68	74

6	5										5		44	04
90	RPL1	Ribosomal protein	10	10	10	11	11	11	1.5	0.6	1.5	U	0.0	0.6
45	4	L14	.7	.4	.9	.6	.2	.0	308	142	30	p	21	63
			61	01	32	07	38	92	044	9	80		88	32
			29	69	75	78	4	42	5		44		94	74
											5		54	04
91	LRP5	LDL receptor	6.	5.	6.	5.	5.	5.	-1.	-0.	1.5	D	0.0	0.6
35	L	related protein 5	27	97	21	39	80	47	513	597	13	o	12	63
5		like	22	72	62	21	48	52	431	823	43	w	89	32
			2	6	4	4	7	4	453	333	14	n	92	74
											53		27	04
63	CCL	Chemokine (C-C	7.	7.	7.	8.	8.	7.	1.5	0.6	1.5	U	0.0	0.6
58	14	motif) ligand 14	03	60	46	16	29	51	378	209	37	p	49	63
			81	72	46	17	75	35	377	033	83		95	32
			1	9	5		5	1	86	33	77		22	74
											86		04	04
79	FA2	Fatty acid	9.	8.	8.	6.	7.	8.	-2.	-1.	2.5	D	0.0	0.6
15	H	2-hydroxylase	22	24	26	26	19	16	590	373	90	o	28	63
2			86	46	68	24	73	07	421	186	42	w	62	32
			5	2	1	2	8	2	144	667	11	n	79	74
											44		96	04
13	SOW	Sosondowah	8.	6.	7.	5.	5.	7.	-2.	-1.	2.3	D	0.0	0.6
45	AHA	ankyrin repeat	13	94	65	67	96	34	378	250	78	o	37	63
48		domain family	05	47	90	17	79	42	700	173	70	w	48	32
		member A	8	8	8	4	6	2	003	333	00	n	71	74
											03		75	04
11	CYY	Cysteine/tyrosine-r	4.	5.	5.	7.	7.	5.	3.8	1.9	3.8	U	0.0	0.6
61	R1	ich 1	50	26	34	67	91	32	133	310	13	p	23	63
59			72	64	64	11	33	88	880	733	38		35	32

			7	3	2	5	5	4	14	33	80		41	74
											14		45	04
12	USP4	Ubiquitin specific	6.	6.	6.	4.	5.	5.	-1.	-0.	1.9	D	0.0	0.6
47	3	peptidase 43	48	20	27	75	79	59	914	936	14	o	12	63
39			17	09	46	89	69	06	503	97	50	w	97	32
			2	9	6	6			105		31	n	37	74
											05		35	04
51	UPB	Ureidopropionase,	5.	4.	5.	3.	3.	5.	-2.	-1.	2.1	D	0.0	0.6
73	1	$\beta$	38	97	62	66	73	28	145	101	45	o	41	63
3			07	60	19	15	31	07	172	093	17	w	19	32
			7	3	4	6	8	2	008	333	20	n	91	74
											08		37	04
12	ZNF	Zinc finger protein	5.	4.	5.	4.	4.	4.	-1.	-0.	1.7	D	0.0	0.6
58	816	816	87	84	61	39	70	87	724	785	24	o	28	63
93			04	62	00	64	05	25	004	763	00	w	34	32
			7	6	7	1	3	7	253	333	42	n	33	74
											53		83	04
92	LRR	Leucine rich repeat	5.	5.	5.	6.	6.	5.	1.6	0.7	1.6	U	0.0	0.6
08	FIP1	(in FLII)	59	75	82	90	60	79	383	122	38	p	44	63
		interacting protein	09	73	37	64	98	23	156	133	31		68	32
		1	8	4	1	4	9	4	38	33	56		91	74
											38		56	04
12	GGT	$\Gamma$ -glutamyltransfer	7.	7.	7.	6.	6.	6.	-1.	-0.	1.8	D	0.0	0.6
49	6	ase 6	39	73	32	41	64	63	893	921	93	o	01	63
75			05	64	99	73	19	36	807	29	80	w	25	32
			1	1	8	7	8	8	904		79	n	16	74
											04		2	04
19	EEF1	Eukaryotic	10	10	10	11	11	10	1.5	0.6	1.5	U	0.0	0.6
33	B2	translation	.7	.2	.8	.6	.2	.8	351	183	35	p	49	63



		elongation factor 1 β 2	67 95	81 51	14 62	56 66	59 99	02 58	539 42	833 33	15 39 42		25 97 02	32 74 04
26 18	GAR T	Phosphoribosylgly cinamide formyltransferase, phosphoribosylglyc inamide synthetase, phosphoribosylami noimidazole synthetase	3. 98 50 3	3. 34 30 9	4. 04 26 7	4. 68 73 6	4. 35 85 2	4. 50 32 7	1.6 541 843 22	0.7 261 2 43	1.6 54 18 43 22	U p	0.0 11 58 77 13	0.6 63 32 74 04
85 19	IFIT M1	Interferon induced transmembrane protein 1	8. 37 15 5	8. 93 58 1	9. 89 57 8	11 .0 42 33	10 .9 00 55	9. 49 31 3	2.6 591 343 44	1.4 109 566 67	2.6 59 13 43 44	U p	0.0 29 88 69 61	0.6 63 32 74 04
55 38	PPT1	Palmitoyl-protein thioesterase 1	5. 06 21	4. 70 46 7	5. 60 86 7	6. 30 2 4	5. 86 87 4	5. 98 48 9	1.9 009 624 05	0.9 267 3 24 05	1.9 00 96 24 05	U p	0.0 09 05 27 54	0.6 63 32 74 04
50 86 1	STM N3	Stathmin 3	4. 29 83 7	5. 05 08	5. 59 37	6. 93 82 7	6. 56 06 3	5. 16 61 3	2.3 631 480 23	1.2 407 1 80 23	2.3 63 14 80 23	U p	0.0 46 54 51 38	0.6 63 32 74 04
46 38	MYL K	Myosin light chain kinase	4. 89 87	8. 35 27	6. 39 61	10 .7 93	7. 94 37	9. 05 11	6.5 598 523	2.7 136 633	6.5 59 85	U p	0.0 28 91	0.6 63 32

			6	8	3	77	1	8	07	33	23		70	74
											07		3	04
10	FAM	Family with	8.	8.	8.	6.	6.	8.	-1.	-0.	1.8	D	0.0	0.6
01	47E	sequence similarity	41	11	00	87	92	15	814	859	14	o	46	63
29		47 member E	14	05	54	12	50	33	115	266	11	w	82	32
58				9	6	9	6		947	667	59	n	13	74
3											47		21	04
57	PTP	Protein tyrosine	4.	4.	4.	5.	4.	5.	1.5	0.6	1.5	U	0.0	0.6
88	RC	phosphatase,	33	78	78	65	82	24	247	085	24	p	44	63
		receptor type, C	11	29	29	25	12	90	753	966	77		22	32
			6	7	7	9	6	4	13	67	53		96	74
											13		35	04
19	ACS	Acyl-coa	7.	7.	7.	6.	7.	6.	-1.	-0.	1.6	D	0.0	0.6
73	F3	synthetase family	87	95	63	98	45	81	667	737	67	o	10	63
22		member 3	30	76	52	88	37	12	133	37	13	w	43	32
			9	1	1		2	8	92		39	n	35	74
											2		1	04
72	LOC	Uncharacterized	5.	6.	6.	8.	7.	6.	2.2	1.1	2.2	U	0.0	0.6
83	7283	LOC728392	82	95	00	25	53	54	734	848	73	p	42	63
92	92		80	39	84	70	92	87	395	766	43		29	32
			3	5	4	5	2	8	86	67	95		67	74
											86		31	04
84	SPIR	Spire-type actin	7.	7.	7.	6.	6.	6.	-1.	-0.	1.5	D	0.0	0.6
50	E2	nucleation factor 2	79	41	16	62	91	86	578	658	78	o	15	63
1			39	42	52	08	44	19	736	77	73	w	43	32
			7	6	6		6	2	065		60	n	50	74
											65		15	04
89	AP1S	Adaptor-related	6.	7.	7.	8.	8.	7.	2.4	1.2	2.4	U	0.0	0.6
05	2	protein complex 1	11	01	06	23	49	34	482	917	48	p	111	63

		Σ 2 subunit	70 8	96 6	18 5	10 8	91 6	35 3	089 03	266 67	20 89 03		26 39	32 74 04
88 28	NRP 2	Neuropilin 2	5. 76 15	6. 68 20 5	5. 97 77 7	7. 70 72 8	6. 90 69 3	6. 78 34 4	1.9 890 919 92	0.9 921 1	1.9 89 09 19 92	U p	0.0 20 62 00 03	0.6 63 32 74 04
39 56	LGA LS1	Lectin, galactoside-binding , soluble, 1	8. 19 40 5	10 .2 34 36	9. 35 64 6	11 .7 09 43	10 .6 67 54	10 .3 37 99	3.1 239 326 13	1.6 433 633 33	3.1 23 93 26 13	U p	0.0 21 87 45 62	0.6 63 32 74 04
36 88	ITGB 1	Integrin β 1	8. 40 28 6	8. 04 33 3	8. 83 69 6	9. 81 46 4	9. 33 68 1	9. 20 85 5	2.0 358 293 95	1.0 256 166 67	2.0 35 82 93 95	U p	0.0 05 53 88 6	0.6 63 32 74 04
12 68	CNR 1	Cannabinoid receptor 1 (brain)	5. 07 94 2	4. 04 26 7	4. 64 48 9	5. 44 99 4	5. 91 47 3	5. 09 8 3	1.8 642 086 39	0.8 985 633 33	1.8 64 20 86 39	U p	0.0 24 91 77 59	0.6 63 32 74 04
28 46 54	RSP O1	R-spondin 1	3. 90 32	4. 63 51 7	3. 92 28 5	5. 53 47 2	4. 73 30 5	4. 49 17 3	1.7 006 583 39	0.7 660 933 33	1.7 00 65 83 39	U p	0.0 48 99 59 64	0.6 63 32 74 04
23	ACO	Acyl-coa	4.	5.	4.	5.	5.	5.	1.6	0.6	1.6	U	0.0	0.6

59	T9	thioesterase 9	46	10	84	81	09	60	210	968	21	p	26	63
7			79	10	99	26	49	19	141	966	01		68	32
			1	2	3	7	3	5	3	67	41		24	74
											3		55	04
35	IGH	Immunoglobulin	6.	7.	6.	7.	10	8.	3.5	1.8	3.5	U	0.0	0.6
00	G1	heavy constant $\gamma$ 1	96	48	70	76	.3	63	999	479	99	p	18	63
		(G1m marker)	97	78	47	40	05	67	910	933	99		41	32
			1	7	9	2	54	9	84	33	10		96	74
											84		03	04
26	GAT	GATA binding	5.	6.	5.	7.	6.	6.	1.9	0.9	1.9	U	0.0	0.6
24	A2	protein 2	70	84	40	45	64	80	700	782	70	p	45	63
			98	17	91	01	26	27	879	6	08		63	32
			3	9	3	6	6	1			79		13	74
													3	04
84	CMA	Cytidine	3.	3.	3.	6.	5.	3.	3.6	1.8	3.6	U	0.0	0.6
18	HP	monophospho-N-a	32	41	63	48	55	94	515	685	51	p	14	63
		cetylneuraminic	04	57	84	64	07	30	610	133	56		26	32
		acid hydroxylase,	6	7	1	1	6	1	05	33	10		05	74
		pseudogene									05		89	04
34	TUB	Tubulin, $\beta$ 2B class	5.	6.	5.	7.	7.	6.	2.6	1.3	2.6	U	0.0	0.6
77	B2B	iib	45	81	52	65	58	72	160	873	16	p	13	63
33			80	72	93	81	09	77	497	9	04		85	32
			2	6	5	3		7	91		97		90	74
											91		96	04
96	CD5	CD59 molecule,	4.	5.	5.	6.	5.	5.	1.8	0.8	1.8	U	0.0	0.6
6	9	complement	73	41	09	28	93	68	504	878	50	p	07	63
		regulatory protein	60	08	62	10	93	65	763	966	47		37	32
			9	4	6	4	4		11	67	63		82	74
											11		36	04

14	S100	S100 calcium binding protein	7.	7.	8.	9.	9.	8.	1.7	0.8	1.7	U	0.0	0.6
05	A16	A16	97	69	36	20	12	15	598	154	59	p	39	63
76			48	97	25	54	12	67	713	7	87		33	32
				1	7	7	8	4	88		13		42	74
											88		25	04
11	CAC	Calcium channel	8.	8.	8.	7.	7.	8.	-1.	-0.	1.7	D	0.0	0.6
09	FD1	flower domain	76	61	48	36	78	39	712	776	12	o	24	63
4		containing 1	83	72	72	02	94	44	653	233	65	w	30	32
			8	3	4	3	7	5	542	333	35	n	44	74
											42		49	04
28	CDH	Cadherin 19, type 2	3.	4.	3.	5.	8.	4.	5.0	2.3	5.0	U	0.0	0.6
51	19		63	08	82	95	14	44	400	334	40	p	25	63
3			45	37	77	83	43	37	684	433	06		68	32
			8	3	3	1	4	2	71	33	84		44	74
											71		09	04
54	PPIA	Peptidylprolyl isomerase A (cyclophilin A)	4.	4.	4.	5.	5.	5.	1.7	0.7	1.7	U	0.0	0.6
78			30	53	83	54	03	39	041	690	04	p	07	63
			40	05	87	54	62	88	511	533	15		47	32
			3	7	9	7	2	6	88	33	11		57	74
											88		6	04
23	DAA	Dishevelled associated activator of morphogenesis 2	4.	5.	5.	6.	7.	5.	2.3	1.2	2.3	U	0.0	0.6
50	M2		87	71	28	77	11	58	025	032	02	p	23	63
0			57	06	41	59	58	85	992	633	59		54	32
			9	7		5	7	3	35	33	92		54	74
											35		33	04
14	FAM	Family with sequence similarity 109 member A	6.	6.	6.	5.	5.	6.	-1.	-0.	1.5	D	0.0	0.6
47	109A		76	64	58	66	83	58	552	634	52	o	42	63
17			35	27	32	64	56	32	665	746	66	w	93	32
			7	5	6	2	6	6	082	667	50	n	40	74

												82		74	04
41	MAO	Monoamine	5.	5.	5.	5.	6.	6.	1.6	0.6	1.6	U	0.0	0.6	
29	B	oxidase B	42	63	91	95	50	58	146	912	14	p	19	63	
			92	01	09	12	31	95	520	233	65		83	32	
			3	3	3	6	6	4	82	33	20		60	74	
											82		4	04	
54	SYT	Synaptotagmin like	6.	7.	6.	9.	7.	7.	2.4	1.3	2.4	U	0.0	0.6	
84	L2	2	83	07	55	24	69	48	983	209	98	p	23	63	
3			77	54	36	88	51	56	864	966	38		14	32	
			1		1	6	8	7	79	67	64		46	74	
											79		14	04	
90	SOC	Suppressor of	3.	3.	3.	7.	7.	4.	6.7	2.7	6.7	U	0.0	0.6	
21	S3	cytokine signaling	80	80	37	01	61	62	529	555	52	p	05	63	
		3	75	73	76	37	69	84	755	233	97		99	32	
			6	3	9	2	5	8	47	33	55		29	74	
											47		86	04	
14	CSF2	Colony stimulating	4.	5.	4.	6.	5.	5.	1.9	0.9	1.9	U	0.0	0.6	
39	RB	factor 2 receptor, $\beta$ ,	73	50	96	55	67	79	176	393	17	p	17	63	
		low-affinity	34	67	26	41	63	01	241	2	62		17	32	
		(granulocyte-macro	1	1	3	9	3	9	72		41		74	74	
		phage)									72		15	04	
24	NR5	Nuclear receptor	8.	7.	8.	7.	7.	8.	-1.	-0.	1.7	D	0.0	0.6	
94	A2	subfamily 5 group	22	99	66	09	03	21	795	844	95	o	47	63	
		A member 2	22	80	22	94	96	08	322	243	32	w	05	32	
			6	7	7	3	4		885	333	28	n	81	74	
											85		75	04	
23	LRR	Leucine-rich repeat	7.	6.	7.	5.	6.	6.	-1.	-0.	1.8	D	0.0	0.6	
50	C8B	containing 8 family	61	63	23	77	47	46	892	920	92	o	21	63	
7		member B	32	15	21	22	54	71	985	663	98	w	12	32	

			9			7	9	4	465	333	54	n	34	74
											65		44	04
11	AP1S	Adaptor-related	6.	6.	6.	6.	5.	6.	-1.	-0.	1.6	D	0.0	0.6
74	1	protein complex 1	66	88	92	18	83	38	612	689	12	o	09	63
		$\Sigma$ 1 subunit	56	28	05	07	66	43	277	1	27	w	21	32
			8	3	1	3	8	1	414		74	n	37	74
											14		05	04
50	NTM	Neurotrimin	4.	6.	5.	7.	7.	6.	3.1	1.6	3.1	U	0.0	0.6
86			93	40	64	90	49	51	332	476	33	p	09	63
3			26	12	04	67	68	37	502	6	25		72	32
			7	2	5	5	2	5	48		02		42	74
											48		11	04
64	ST6	ST6	5.	5.	6.	6.	6.	6.	1.8	0.8	1.8	U	0.0	0.6
80	GAL	$\beta$ -galactosamide	46	14	14	91	48	03	552	916	55	p	28	63
	1	$\alpha$ -2,6-sialyltransferase 1	31	93	58	85	27	19	496	133	24		83	32
			9	2	1	2		4	48	33	96		62	74
											48		8	04
14	GLT1	Glycosyltransferase 1 domain	5.	6.	5.	4.	4.	5.	-2.	-1.	2.1	D	0.0	0.6
44	D1	containing 1	58	87	70	38	77	70	148	103	48	o	43	63
23			39	82	49	22	32	15	530	35	53	w	97	32
			1	1		2	3	2	117		01	n	45	74
											17		63	04
95	CCL	Chemokine (C-C motif) ligand 4-like	5.	6.	6.	6.	8.	7.	2.2	1.1	2.2	U	0.0	0.6
60	4L2	2	72	37	64	68	05	55	685	817	68	p	19	63
			31	54	34	61	00	12	807	9	58		15	32
			6	2	5		8	2	29		07		84	74
											29		57	04
79	ZNF	Zinc finger protein	7.	7.	7.	6.	7.	6.	-1.	-0.	1.7	D	0.0	0.6
89	671	671	62	56	68	47	09	96	719	782	19	o	05	63

1			79	82	88	82	83	16	842	276	84	w	78	32
				6	7	7	3		756	667	27	n	98	74
											56		08	04
14	C1orf	Chromosome 1	7.	6.	7.	5.	5.	6.	-2.	-1.	2.0	D	0.0	0.6
94	210	open reading frame	17	36	33	37	62	79	042	030	42	o	45	63
66		210	84	20	62	11	42	00	609	413	60	w	54	32
			9	7		9	8	5	377	333	93	n	02	74
											77		21	04
25	WW	WW domain	7.	7.	7.	9.	8.	7.	1.7	0.8	1.7	U	0.0	0.6
93	TR1	containing	93	67	74	34	50	99	746	275	74	p	42	63
7		transcription	88	86	48	97	39	13	485	333	64		29	32
		regulator 1	5	7	9	5		6	38	33	85		64	74
											38		25	04
93	ASIC	Acid sensing ion	6.	6.	6.	5.	5.	5.	-1.	-0.	1.6	D	0.0	0.6
11	3	channel 3	06	36	15	29	31	94	601	679	01	o	18	63
			90	25	93	60	01	77	055	023	05	w	51	32
			4		7	1	1	2	516	333	55	n	46	74
											16		88	04
79	AGB	ATP/GTP binding	4.	4.	4.	3.	3.	3.	-1.	-0.	1.8	D	0.0	0.6
84	L2	protein-like 2	50	14	70	38	74	52	870	903	70	o	01	63
1			96	20	69	06	20	59	425	366	42	w	63	32
			8	9	4	4	1	6	711	667	57	n	48	74
											11		88	04
20	TME	Transmembrane	6.	6.	6.	5.	6.	6.	-1.	-0.	1.5	D	0.0	0.6
29	M18	protein 184A	84	88	98	86	40	44	587	667	87	o	12	63
15	4A		11	82	21	8	02	19	874	096	87	w	31	32
			8	3			5	7	253	667	42	n	56	74
											53		99	04
25	REX	RNA exonuclease	6.	5.	6.	8.	6.	7.	2.2	1.1	2.2	U	0.0	0.6



99 6	O2	2	05 07 7	58 70 4	84 93 1	00 12 9	89 78 1	12 08 6	620 225 84	776 133 33	62 02 25 84	p	21 98 39 33	63 32 74 04
28 79 7	IGLV 3-19	Immunoglobulin lambda variable 3-19	4. 55 85 3	4. 63 56 7	4. 74 19	5. 04 92 9	6. 59 54 3	5. 63 71	2.1 663 104 38	1.1 152 4	2.1 66 31 04 38	U p	0.0 18 80 78 32	0.6 63 32 74 04
95 81	PRE PL	Prolyl endopeptidase-like	7. 76 01 8	7. 60 34 6	7. 29 54	6. 38 88 3	6. 75 44 9	7. 34 09 5	-1. 652 812 801	-0. 724 923 333	1.6 52 81 28 01	D o w n	0.0 31 88 07 15	0.6 63 32 74 04
41 73	MC M4	Minichromosome maintenance complex component 4	3. 44 50 5	3. 72 74 8	3. 81 37	4. 82 68 7	5. 00 81 3	4. 02 67 6	1.9 433 018 37	0.9 585 1 37	1.9 43 30 18 37	U p	0.0 08 72 52 61	0.6 63 32 74 04
29 09 4	LGA LSL	Lectin, galactoside-binding -like	8. 53 77 6	7. 60 37 1	8. 49 27	7. 17 28 2	7. 42 97 1	7. 84 29 6	-1. 658 163 958	-0. 729 586 667	1.6 58 16 39 58	D o w n	0.0 48 21 70 26	0.6 63 32 74 04
32 68	AGF G2	Arfgap with FG repeats 2	7. 45 13	7. 22 62 2	6. 99 76 9	5. 29 05 7	6. 13 01 8	6. 87 33 9	-2. 184 076 415	-1. 127 023 333	2.1 84 07 64 15	D o w n	0.0 22 10 08 76	0.6 63 32 74 04

10 02 88 77 8	LOC 1002 8877 8	WAS protein family homolog 1 pseudogene	8. 71 93 2	8. 39 44 1	7. 93 59 2	7. 33 68 8	7. 98 36 5	7. 74 07	-1. 583 159 561	-0. 662 806 667	1.5 83 15 95 61	D o w n	0.0 38 99 95 13	0.6 63 32 74 04
29 08 9	UBE 2T	Ubiquitin conjugating enzyme E2T	3. 99 91 2	4. 96 07 1	4. 70 23 4	6. 05 56 3	5. 64 01 5	4. 75 93 6	1.9 065 838 75	0.9 309 9 75	1.9 06 58 38 75	U p	0.0 45 37 53 97	0.6 63 32 74 04
33 09	HSP A5	Heat shock protein family A (Hsp70) member 5	8. 58 60 2	7. 36 77 9	8. 54 10 1	8. 98 42 4	8. 78 89 4	9. 44 92	1.8 779 691 11	0.9 091 733 33 911 1	1.8 77 96 911 1	U p	0.0 40 18 43 86	0.6 63 32 74 04
27 35	GLI1	GLI family zinc finger 1	4. 58 37 8	4. 97 02 7	5. 19 95 6	5. 89 53 3	5. 58 27 2	5. 24 79 2	1.5 772 958 99	0.6 574 533 33	1.5 77 29 58 99	U p	0.0 27 00 38 97	0.6 63 32 74 04
28 89 8	IGK V1D- 27	Immunoglobulin $\kappa$ variable 1D-27 (pseudogene)	5. 42 99 9	4. 89 86 3	5. 48 02 1	6. 01 56 4	9. 11 58 5	8. 90 33 7	6.6 900 175 71	2.7 420 1 71	6.6 90 01 75 71	U p	0.0 09 79 54 34	0.6 63 32 74 04
27 13 4	TJP3	Tight junction protein 3	7. 07	6. 31 32 6	6. 36 61 1	5. 41 67 7	6. 03 59 9	6. 19 59 3	-1. 624 760 044	-0. 700 226 667	1.6 24 76 00	D o w n	0.0 47 67 81	0.6 63 32 74

												44		25	04
29 92	GYG 1	Glycogenin 1	4. 95 25 1	4. 57 98 2	5. 27 40 5	6. 30 69 5	5. 25 21 1	5. 85 52 4	1.8 268 058 73	0.8 693 233 33	1.8 26 80 58 73	U p	0.0 25 13 67 75	0.6 63 32 74 04	
20 78	ERG	V-ets avian erythroblastosis virus E26 oncogene homolog	3. 25 88 7	3. 55 83 3	3. 55 48 5	4. 93 58 3	5. 21 10 7	3. 90 60 8	2.3 407 594 25	1.2 269 766 67	2.3 40 75 94 25	U p	0.0 07 17 52 75	0.6 63 32 74 04	
84 04	SPA RCL 1	SPARC like 1	5. 86 12 3	8. 44 72 7	7. 72 48 4	10. .6 38 74	9. 93 54 4	8. 89 96 4	5.5 795 418 62	2.4 801 466 67	5.5 79 54 18 62	U p	0.0 09 97 69 79	0.6 63 32 74 04	
84 66 8	FAM 126A	Family with sequence similarity 126 member A	6. 55 15 6	7. 42 43 2	6. 50 16 5	8. 47 58 6	8. 10 21 3	7. 31 96 3	2.2 038 407 83	1.1 400 2 83	2.2 03 84 07 83	U p	0.0 17 61 71 54	0.6 63 32 74 04	
11 32 0	MGA T4A	Mannosyl ( $\alpha$ -1,3-)-glycoprote in $\beta$ -1,4-N-acetylgluc osaminyltransferas e, isozyme A	4. 10 95 6	4. 47 76 2	3. 95 92 2	3. 51 54 1	3. 58 42 9	3. 68 89 9	-1. 500 971 586	-0. 585 896 667	1.5 00 97 15 86	D o w n	0.0 08 11 89 14	0.6 63 32 74 04	
51 75	PEC AM1	Platelet/endothelial cell adhesion	4. 65	5. 05	5. 67	7. 32	7. 41	5. 65	3.1 812	1.6 696	3.1 81	U p	0.0 13	0.6 63	

		molecule 1	68 3	06 1	26 8	01 7	61 3	26 3	711 29	033 33	27 11 29		07 47 22	32 74 04
38 7	RHO A	Ras homolog family member A	8. 08 55 4	7. 25 41 7	8. 01 01 4	8. 74 92 1	8. 13 27 6	8. 46 09 2	1.5 848 504 01	0.6 643 466 67	1.5 84 85 04 01	U p	0.0 47 75 10 86	0.6 63 32 74 04
21 96 54	ZCC HC2 4	Zinc finger, CCHC domain containing 24	5. 26 94 5	7. 14 92 1	6. 46 51	8. 77 74 8	7. 64 77 2	7. 05 88 9	2.8 947 591 81	1.5 334 433 33	2.8 94 75 91 81	U p	0.0 33 17 01 53	0.6 63 32 74 04
28 32 19	KCT D21	Potassium channel tetramerization domain containing 21	6. 17 68 2	5. 91 38 6	6. 47 93	5. 34 00 4	5. 27 03 2	5. 80 38 1	-1. 645 588 177	-0. 718 603 333	1.6 45 58 81 77	D o w n	0.0 14 78 24 45	0.6 63 32 74 04
72 99 74	RFP L4A L1	Ret finger protein-like 4A-like 1	4. 49 86 4	4. 13 04 2	5. 02 82 1	3. 46 77 1	3. 92 05 5	4. 18 26 1	-1. 619 408 176	-0. 695 466 667	1.6 19 40 81 76	D o w n	0.0 39 53 41 22	0.6 63 32 74 04
18 07	DPY S	Dihydropyrimidina se	8. 15 29 9	8. 52 93 2	8. 53 75 3	5. 73 42 8	7. 51 19 4	7. 94 93 7	-2. 534 000 25	-1. 341 416 667	2.5 34 00 02 5	D o w n	0.0 41 41 28 07	0.6 63 32 74 04
12	OSC	Organic solute	5.	4.	5.	4.	3.	4.	-1.	-0.	1.8	D	0.0	0.6

77 00	P1	carrier partner 1	05 05 1	72 79 1	19 36 7	07 13 2	94 32 1	19 16 3	894 709 497	921 976 667	94 70 94 97	o w n	00 87 24 36	63 32 74 04
19 38	EEF2	Eukaryotic translation elongation factor 2	8. 08 61 3	7. 82 34 8	8. 26 31 9	9. 78 79 5	8. 11 95 3	9. 11 84 8	1.9 332 836 62	0.9 510 533 33	1.9 33 28 36 62	U p	0.0 49 92 43 3	0.6 63 32 74 04
26 05 1	PPP1 R16B	Protein phosphatase 1 regulatory subunit 16B	4. 68 78 7	4. 87 98 1	5. 30 38 1	6. 24 73 5	6. 13 37 6	5. 15 21 6	1.8 496 385 01	0.8 872 433 33	1.8 49 63 85 01	U p	0.0 29 31 93 13	0.6 63 32 74 04
11 62 55	MOG AT1	Monoacylglycerol O-acyltransferase 1	10 .5 37 48	10 .5 37 32	9. 79 54 4	8. 47 51 1	9. 41 55 2	9. 73 27 8	-2. 117 374 801	-1. 082 276 667	2.1 17 37 48 01	D o w n	0.0 21 08 15 31	0.6 63 32 74 04
54 47 2	TOL LIP	Toll interacting protein	8. 79 48 2	8. 68 51 8	8. 31 06 5	7. 54 83 4	8. 15 17 5	8. 16 86 9	-1. 559 002 599	-0. 640 623 333	1.5 59 00 25 99	D o w n	0.0 28 75 79 11	0.6 63 32 74 04
84 61 7	TUB B6	Tubulin, $\beta$ 6 class V	6. 43 15 1	7. 91 76 3	6. 84 60 9	9. 95 68 8	9. 08 36 5	8. 17 31 09	4.0 170 414 09	2.0 061 333 33	4.0 17 04 14 09	U p	0.0 06 87 60 5	0.6 63 32 74 04

11	CLC	Chloride channel,	7.	7.	6.	5.	5.	6.	-1.	-0.	1.8	D	0.0	0.6
84	N5	voltage-sensitive 5	18	06	66	53	94	88	805	852	05	o	46	63
			78	63	01	32	24	15	418	333	41	w	47	32
			2		8	7	6	7	547	333	85	n	52	74
											47		92	04
22	CFA	Cilia and flagella	4.	4.	4.	3.	4.	4.	-1.	-0.	1.6	D	0.0	0.6
01	P53	associated protein	81	45	68	83	01	04	608	685	08	o	02	63
36		53	88	36	13	45	90	43	036	3	03	w	36	32
			3	9	5	5	8	4	328		63	n	69	74
											28		4	04
79	ARH	Rho gtpase	4.	5.	4.	5.	5.	5.	2.1	1.0	2.1	U	0.0	0.6
82	GAP	activating protein	32	23	40	89	66	68	313	917	31	p	04	63
2	28	28	35	22	94	28	27	48	339	566	33		09	32
			1	6	5	6	4	9	59	67	39		99	74
											59		41	04
31	HLA	Major	6.	7.	7.	9.	8.	8.	2.1	1.1	2.1	U	0.0	0.6
22	-DR	histocompatibility	93	81	96	00	47	63	901	31	90	p	07	63
	A	complex, class II,	9	23	84	26	93	08	049		10		14	32
		DR $\alpha$		7	5	2	6	4	42		49		36	74
											42		92	04
55	SRG	Serglycin	6.	6.	6.	8.	8.	7.	3.1	1.6	3.1	U	0.0	0.6
52	N		38	77	85	41	79	73	225	427	22	p	00	63
			69	52	82	37	72	75	831	4	58		80	32
			2	6	2	8	7	7	73		31		31	74
											73		85	04
10	EDIL	EGF-like repeats	6.	8.	5.	10	8.	8.	4.3	2.1	4.3	U	0.0	0.6
08	3	and discoidin I-like	53	19	90	.2	42	36	326	152	32	p	19	63
5		domains 3	87	79	87	01	00	96	709	566	67		43	32
			2		1	38	8	4	29	67	09		03	74

											29		25	04
87	CTN	Catenin $\alpha$ -like 1	5.	5.	6.	8.	7.	6.	3.4	1.8	3.4	U	0.0	0.6
27	NAL		73	50	17	01	88	91	860	016	86	p	00	63
	1		75	03	72	93	53	53	662		06		98	32
			5	7	7	6	1	2	81		62		83	74
											81		27	04
67	STC1	Stanniocalcin 1	3.	4.	3.	5.	6.	3.	2.5	1.3	2.5	U	0.0	0.6
81			39	00	67	04	31	82	924	743	92	p	46	63
			12	27	11	22	86	72	748	3	47		95	32
			2		4	5			62		48		53	74
											62		6	04
10	STA	Star related lipid	11	10	11	9.	10	10	-1.	-0.	1.7	D	0.0	0.6
80	RD1	transfer domain	.0	.7	.3	83	.1	.7	766	821	66	o	19	63
9	0	containing 10	98	70	51	78	56	61	797	136	79	w	81	32
			01	26	02	4	39	65	464	667	74	n	44	74
											64		03	04
54	EPS8	EPS8 like 1	8.	7.	7.	6.	7.	6.	-1.	-0.	1.5	D	0.0	0.6
86	L1		08	62	48	73	52	93	582	662	82	o	40	63
9			47	39	10	89	69	77	314	036	31	w	70	32
			8	2	8	4	9	4	817	667	48	n	02	74
											17		24	04
55	RAB	RAB20, member	9.	8.	9.	8.	8.	8.	-1.	-0.	1.5	D	0.0	0.6
64	20	RAS oncogene	42	88	15	38	75	51	521	605	21	o	17	63
7		family	55	22	75	30	13	46	404	403	40	w	98	32
			1		2	1	7	4	032	333	40	n	01	74
											32		44	04
28	ANK	Ankyrin 1	6.	5.	4.	4.	4.	4.	-1.	-0.	1.9	D	0.0	0.6
6	1		10	33	85	45	77	20	941	957	41	o	22	63
			89	22	88	23	32	32	385	086	38	w	27	32

			4	6	9	1	3	9	56	667	55	n	71	74
											6		85	04
80	MFA	Microfibrillar	5.	6.	8.	5.	4.	3.	-5.	-2.	5.7	D	0.0	0.6
76	P5	associated protein	93	83	52	79	48	41	769	528	69	o	14	63
		5	72	16	02	88	83	66	408	423	40	w	62	32
			5	4	6	9	8	1	168	333	81	n	16	74
											68		62	04
91	DEP	DEP domain	6.	6.	6.	5.	5.	6.	-1.	-0.	1.7	D	0.0	0.6
61	DC7	containing 7	47	38	65	18	48	44	741	800	41	o	42	63
4			36	53	79	59	94	06	459	296	45	w	29	32
			7	2	1	3	6	2	192	667	91	n	56	74
											92		81	04
94	ARH	Rac/Cdc42 guanine	6.	7.	6.	8.	7.	7.	1.7	0.8	1.7	U	0.0	0.6
59	GEF	nucleotide	33	07	87	13	50	05	453	035	45	p	41	63
	6	exchange factor 6	00	41	85	30	96	05	422	1	34		13	32
			8	6	6	9	6	8	9		22		25	74
											9		95	04
64	ADG	Adhesion G	5.	5.	6.	7.	8.	6.	2.8	1.4	2.8	U	0.0	0.6
12	RL4	protein-coupled	50	72	11	69	10	00	064	887	06	p	24	63
3		receptor L4	21	43	12	33	64	41	765	6	47		71	32
			1	5	8	5	8	9	41		65		88	74
											41		75	04
10	CAP	CAP, adenylate	5.	6.	5.	7.	6.	6.	2.2	1.1	2.2	U	0.0	0.6
48	2	cyclase-associated	30	41	39	79	44	32	278	556	27	p	42	63
6		protein, 2 (yeast)	19	07	28	81	48	94	261	366	82		51	32
			8	2	1	9	3		67	67	61		47	74
											67		71	04
15	CYP	Cytochrome P450,	6.	5.	5.	5.	4.	4.	-1.	-0.	1.8	D	0.0	0.6
64	2D7	family 2, subfamily	31	89	46	44	70	76	896	923	96	o	15	63



		D, polypeptide 7 (gene/pseudogene)	07 3		89 6	01 5	02 8	00 7	137 168	063 333	13 71 68	w n	23 86 05	32 74 04
84 94 1	HSB 2D	Hematopoietic SH2 domain containing	5. 04 87 7	5. 06 93 6	5. 07 80 4	4. 18 51 2	4. 30 65 5	4. 86 37 1	-1. 530 068 95	-0. 613 596 667	1.5 30 06 89 5	D o w n	0.0 18 21 43 91	0.6 63 32 74 04
10 35 2	WAR S2	Tryptophanyl trna synthetase 2, mitochondrial	6. 15 37 2	6. 00 35 4	5. 84 74 4	6. 87 82 1	6. 68 84 4	6. 63 27 5	1.6 604 412 37	0.7 315 666 67	1.6 60 44 12 37	U p	0.0 02 93 02 71	0.6 63 32 74 04
23 08 6	EXP H5	Exophilin 5	4. 06 47 7	4. 00 58 9	4. 15 45 7	3. 25 91 2	3. 64 46 1	3. 48 03 7	-1. 530 189 151	-0. 613 71	1.5 30 18 91 51	D o w n	0.0 02 68 41 8	0.6 63 32 74 04
10 13 0	PDIA 6	Protein disulfide isomerase family A member 6	8. 29 3	8. 02 49 8	8. 57 19	8. 77 20 5	9. 09 59 1	9. 01 01 9	1.5 831 046 94	0.6 627 566 67	1.5 83 10 46 94	U p	0.0 11 35 09 5	0.6 63 32 74 04
63 82	SDC 1	Syndecan 1	13 .1 57 75	13 .0 76 11	13 .0 02 65	11 .8 07 37	12 .5 27 39	12 .8 74 07	-1. 597 585 71	-0. 675 893 333	1.5 97 58 57 1	D o w n	0.0 40 24 89 28	0.6 63 32 74 04
34	IGH	Immunoglobulin	8.	9.	8.	9.	11	11	5.1	2.3	5.1	U	0.0	0.6

93	A1	heavy constant $\alpha$ 1	49 73 6	04 95 4	21 78 7	41 80 9	.8 59 83	.5 63 57	298 145 33	589 066 67	29 81 45 33	p	06 85 66 94	63 32 74 04
60 91	ROB O1	Roundabout guidance receptor 1	5. 60 21 8	6. 54 32 5	6. 09 78 1	7. 78 44 5	7. 71 99 7	6. 48 41 7	2.3 758 602 86	1.2 484 5 86	2.3 75 86 02 86	U p	0.0 17 60 29 36	0.6 63 32 74 04
23 70 5	CAD M1	Cell adhesion molecule 1	4. 92 32 7	5. 86 66 2	5. 54 84 3	6. 33 49 1	6. 75 86 2	5. 84 54 3	1.8 237 146 32	0.8 668 8 32	1.8 23 71 46 32	U p	0.0 30 20 31 36	0.6 63 32 74 04
54 85 8	PGP EP1	Pyroglutamyl-pepti dase I	7. 68 94 7	7. 66 16 7	7. 29 73 8	6. 42 24 5	6. 92 24 9	7. 10 63 3	-1. 661 419 816	-0. 732 416 667	1.6 61 41 98 16	D o w n	0.0 14 82 36 16	0.6 63 32 74 04
23 21	FLT1	Fms-related tyrosine kinase 1	3. 60 41 9	3. 78 17 5	4. 51 07 6	6. 44 79 9	7. 10 85 5	4. 78 02 2	4.4 280 965 12	2.1 466 866 67	4.4 28 09 65 12	U p	0.0 07 49 48 43	0.6 63 32 74 04
92 8	CD9	CD9 molecule	6. 96 65 1	8. 31 55 6	8. 07 87 7	10 .5 30 18	10 .5 03 38	8. 90 82 6	4.5 746 456 59	2.1 936 6 56 59	4.5 74 64 56 59	U p	0.0 04 33 49 93	0.6 63 32 74 04

22 01 08	FAM 124A	Family with sequence similarity 124 member A	2. 91 96 5	3. 78 17 6	3. 29 24 1	4. 47 17 8	3. 83 62 2	3. 84 73 6	1.6 477 682 32	0.7 205 133 33	1.6 47 76 82 32	U p n	0.0 29 99 93 4	0.6 63 32 74 04
89 12	CAC NA1 H	Calcium channel, voltage-dependent, T type, $\alpha$ 1H subunit	8. 78 2	8. 77 87 9	8. 98 90 1	8. 00 48 4	7. 80 68 8	8. 62 16 7	-1. 630 675 819	-0. 705 47 58	1.6 30 67 58 19	D o w n	0.0 20 06 77 29	0.6 63 32 74 04
81 60 6	LBH	Limb bud and heart development	3. 89 79 3	4. 88 89 4	4. 23 29 4	7. 64 34 1	5. 19 97 2	5. 78 66 2	3.6 552 751 28	1.8 699 8 28	3.6 55 27 51 28	U p n	0.0 18 46 31 96	0.6 63 32 74 04
43 11	MM E	Membrane metallo-endopeptid ase	10 .4 07 24	9. 47 82 5	10 .0 27 18	8. 62 31 7	8. 41 97 6	9. 60 73 5	-2. 125 000 725	-1. 087 463 333	2.1 25 00 07 25	D o w n	0.0 21 38 00 55	0.6 63 32 74 04
64 77 1	C6orf 106	Chromosome 6 open reading frame 106	8. 85 45 8	8. 68 18 7	8. 39 79 1	8. 01 34 5	7. 80 28 7	8. 24 86 8	-1. 540 202 454	-0. 623 12 24 54	1.5 40 20 24 54	D o w n	0.0 15 18 42 31	0.6 63 32 74 04
23 65 4	PLX NB2	Plexin B2	11 .8 46 77	11 .8 17 03	11 .4 83 77	10 .2 52 27	11 .3 59 18	11 .0 30 6	-1. 784 071 374	-0. 835 173 333	1.7 84 07 13	D o w n	0.0 24 36 68	0.6 63 32 74

											74			04
69 35	ZEB 1	Zinc finger E-box binding homeobox 1	6. 22 02 9	7. 82 71 9	7. 04 17 1	9. 34 31 3	8. 59 37 1	7. 69 09 6	2.8 537 718 49	1.5 128 7 18 49	2.8 53 77 18 49	U p	0.0 22 86 76 97	0.6 63 32 74 04
43 45	CD2 00	CD200 molecule	4. 92 42 3	5. 44 20 5	4. 43 25 4	7. 08 70 8	6. 13 64 4	5. 61 93 4	2.5 455 898 71	1.3 48 58 98 71	2.5 45 58 98 71	U p	0.0 14 05 91 71	0.6 63 32 74 04
26 13 6	TES	Testin LIM domain protein	9. 16 25 8	9. 13 95 6	8. 40 77 9	7. 65 40 1	8. 49 45 1	8. 33 15 4	-1. 673 988 945	-0. 743 29 89 45	1.6 73 98 89 45	D o w n	0.0 43 33 63 79	0.6 63 32 74 04
26 90	GHR	Growth hormone receptor	3. 34 56 4	5. 19 53 9	4. 97 94 2	5. 81 40 9	6. 23 19 9	5. 36 24 3	2.4 554 770 41	1.2 960 033 33 41	2.4 55 47 70 41	U p	0.0 35 09 21 43	0.6 63 32 74 04
70 74	TIA M1	T-cell lymphoma invasion and metastasis 1	5. 55 75 8	6. 79 62 1	6. 38 30 4	7. 62 71 5	7. 89 59 2	6. 65 88 9	2.2 166 433 53	1.1 483 766 67 53	2.2 16 64 33 53	U p	0.0 28 78 39 66	0.6 63 32 74 04
79 81 9	WDR 78	WD repeat domain 78	5. 42 74	5. 02 30	5. 56 12	4. 34 12	4. 32 85	4. 64 00	-1. 866 893	-0. 900 64	1.8 66 89	D o w	0.0 02 18	0.6 63 32

			7	5	5	4	3	8	98		39	n	79	74
											8		06	04
79	BEN	BEN domain	7.	7.	6.	6.	5.	6.	-1.	-0.	1.9	D	0.0	0.6
65	D5	containing 5	73	21	98	09	90	98	979	985	79	o	21	63
6			97	27	78	14	62	65	802	356	80	w	16	32
			8	3	5	9	1	9	704	667	27	n	60	74
											04		56	04
13	GAL	Galactose	8.	8.	8.	7.	7.	8.	-1.	-0.	1.6	D	0.0	0.6
05	M	mutarotase (aldose	63	47	25	46	78	05	612	689	12	o	11	63
89		1-epimerase)	27	31	69	27	00	18	649	433	64	w	95	32
			5	7	8		6	4	972	333	99	n	71	74
											72		98	04
29	ABR	Active	10	10	10	10	10	10	-1.	-0.	1.5	D	0.0	0.6
		BCR-related	.9	.7	.7	.2	.0	.2	563	644	63	o	03	63
			85	81	88	81	70	69	732	993	73	w	39	32
			44	65	83	63	12	19	06	333	20	n	08	74
											6		61	04
56	PCD	Protocadherin $\alpha$ 10	7.	7.	6.	6.	6.	6.	-1.	-0.	1.5	D	0.0	0.6
13	HA1		44	73	91	53	83	80	557	639	57	o	31	63
9	0		20	45	29	69	18	31	526	256	52	w	81	32
			9	2	9		2	1	454	667	64	n	64	74
											54		86	04
86	RUN	Runt-related	4.	5.	5.	6.	6.	5.	2.0	1.0	2.0	U	0.0	0.6
0	X2	transcription factor	69	17	00	11	32	50	272	194	27	p	04	63
		2	86	14	68	03	38	11	022	9	20		90	32
			9	6	2	9	9	6	07		22		89	74
											07		48	04
79	HAN	HAND2 antisense	3.	5.	4.	7.	5.	5.	3.3	1.7	3.3	U	0.0	0.6
80	D2-A	RNA 1 (head to	90	59	37	51	88	66	102	269	10	p	23	63

4	S1	head)	32 7	90 7	77	54 8	19 5	34 6	725 37	5	27 25 37		44 94 48	32 74 04
11 49 71	PTP MT1	Protein tyrosine phosphatase, mitochondrial 1	6. 40 84 7	6. 49 62 7	6. 06 28 1	5. 52 24 5	5. 77 17	5. 83 33 9	-1. 529 793 228	-0. 613 336 667	1.5 29 79 32 28	D o w n	0.0 12 81 83 57	0.6 63 32 74 04
13 16	KLF 6	Kruppel-like factor 6	5. 15 95 1	4. 80 28 5	5. 68 98 9	6. 96 70 9	6. 95 26 4	5. 89 85 5	2.6 183 839 55	1.3 886 766 67	2.6 18 38 39 55	U p	0.0 06 04 92 84	0.6 63 32 74 04
88 87	TAX 1BP1	Tax1 (human T-cell leukemia virus type I) binding protein 1	7. 63 62 7	6. 96 58 1	7. 18 53 7	5. 92 75 3	5. 79 01 2	7. 21 00 3	-1. 936 238 495	-0. 953 256 667	1.9 36 23 84 95	D o w n	0.0 47 59 85 16	0.6 63 32 74 04
39 0	RND 3	Rho family gtpase 3	6. 58 15 9	6. 99 54 8	6. 29 54 7	9. 03 55 7	9. 28 83	7. 72 75 8	4.1 688 130 23	2.0 596 366 67	4.1 68 81 30 23	U p	0.0 01 72 26 7	0.6 63 32 74 04
79 84 4	ZDH HC11	Zinc finger, DHHC-type containing 11	8. 42 05 4	7. 32 92 2	7. 20 32 4	4. 87 69 1	5. 43 64 7	7. 09 46 1	-3. 600 847 913	-1. 848 336 667	3.6 00 84 79 13	D o w n	0.0 17 48 68 04	0.6 63 32 74 04
26	CHI	Cysteine rich	5.	5.	5.	6.	6.	6.	1.5	0.6	1.5	U	0.0	0.6

51 1	C2	hydrophobic domain 2	67 40 9	92 85 4	99 94	90 03 1	37 64 5	29 17 1	751 399 32	554 8	75 13 99 32	p	17 92 81 97	63 32 74 04
53 32	PLC B4	Phospholipase C $\beta$ 4	2. 78 43	3. 50 42 3	3. 31 22 7	7. 14 51	5. 04 45 9	3. 85 6	4.4 330 408 8	2.1 482 966 67	4.4 33 04 08 8	U p	0.0 24 49 44 5	0.6 63 32 74 04
20 74	ERC C6	Excision repair cross-complementa tion group 6	4. 84 01	4. 86 96 4	4. 97 31 3	4. 21 94 8	4. 45 01 4	4. 22 07 8	-1. 513 081 816	-0. 597 49	1.5 13 08 18 16	D o w n	0.0 03 24 27 08	0.6 63 32 74 04
11 47 57	CYG B	Cytoglobin	7. 00 28 1	7. 60 91 2	7. 44 69 2	7. 99 21 6	8. 20 17 1	7. 78 85 6	1.5 596 186 73	0.6 411 933 33	1.5 59 61 86 73	U p	0.0 19 96 94 63	0.6 63 32 74 04
10 09	CDH 11	Cadherin 11, type 2, OB-cadherin (osteoblast)	3. 71 82 7	6. 01 97 8	4. 83 30 4	8. 97 74 7	6. 40 29 3	7. 14 81	6.2 874 281 13	2.6 524 7	6.2 87 42 81 13	U p	0.0 11 24 59 42	0.6 63 32 74 04
80 72 3	SLC3 5G2	Solute carrier family 35 member G2	3. 64 69 4	3. 64 31 4	3. 94 73 7	4. 85 66	4. 71 45 2	4. 14 84 1	1.7 744 353 35	0.8 273 6	1.7 74 43 53 35	U p	0.0 05 74 25 43	0.6 63 32 74 04

10	MTH	Methylenetetrahydr	5.	5.	6.	7.	7.	5.	2.7	1.4	2.7	U	0.0	0.6
79	FD2	ofolate	18	48	16	88	51	82	644	670	64	p	30	63
7		dehydrogenase	08	03	12	02	40	92	963	166	49		50	32
		(NADP+	5		9	3	4	2	5	67	63		67	74
		dependent) 2,									5		88	04
		methenyltetrahydro												
		folate												
		cyclohydrolase												
63	CXC	Chemokine	5.	7.	6.	7.	7.	7.	1.9	0.9	1.9	U	0.0	0.6
87	L12	(C-X-C motif)	87	00	98	78	92	14	953	966	95	p	28	63
		ligand 12	78	79	59	88	57	71	981	766	39		47	32
			7	1	5	5	2	9	84	67	81		86	74
											84		6	04
10	CRT	Cartilage	7.	7.	7.	8.	8.	7.	1.7	0.7	1.7	U	0.0	0.6
49	AP	associated protein	50	13	80	81	08	95	396	987	39	p	26	63
1			98	67	98	50	59	17	454	933	64		51	32
			1	8	1	8	1	9	83	33	54		42	74
											83		64	04
72	TWI	Twist family bhlh	4.	4.	4.	5.	4.	4.	1.7	0.8	1.7	U	0.0	0.6
91	ST1	transcription factor	35	32	47	89	96	75	691	230	69	p	26	63
		1	50	19	21	84	57	40	258	366	12		87	32
			3	3	1	2	1	5	33	67	58		47	74
											33		67	04
89	CCN	Cyclin D2	7.	8.	8.	9.	9.	8.	2.1	1.0	2.1	U	0.0	0.6
4	D2		61	73	22	96	27	60	316	919	31	p	31	63
			36	70	08	34	99	40	639	8	66		56	32
			2	2	8	5	2	9	21		39		07	74
											21		36	04
41	ARS	Arylsulfatase D	10	9.	10	9.	9.	9.	-1.	-0.	1.6	D	0.0	0.6



4	D		.3	56	.3	11	13	80	681	750	81	o	39	63
			51	82	83	19	16	90	796	003	79	w	26	32
			18	5	12	3		1	716	333	67	n	62	74
											16		34	04
25	TNF	TNF $\alpha$ induced	4.	4.	4.	5.	4.	5.	1.7	0.7	1.7	U	0.0	0.6
81	AIP8	protein 8	20	71	64	90	88	10	113	750	11	p	32	63
6			7	94	35	27	36	88	047	966	30		45	32
				1	8	9	6	3	12	67	47		94	74
											12		55	04
57	PTG	Prostaglandin E	3.	3.	4.	5.	5.	4.	2.1	1.0	2.1	U	0.0	0.6
32	ER2	receptor 2	80	79	11	15	20	61	193	836	19	p	00	63
			84	63	41	24	29	45	423	166	34		98	32
			7	6	5	2	1		69	67	23		31	74
											69		95	04
83	AXI	Axin 2	3.	4.	4.	6.	5.	4.	2.5	1.3	2.5	U	0.0	0.6
13	N2		63	36	23	04	60	66	639	583	63	p	08	63
			58	56	57	34	49	40	474	666	94		14	32
			9	1	7	1	1	5	03	67	74		51	74
											03		35	04
23	SYN	Spectrin repeat	4.	5.	5.	7.	6.	5.	2.2	1.1	2.2	U	0.0	0.6
34	E1	containing, nuclear	87	59	75	31	39	94	110	447	11	p	22	63
5		envelope 1	77	26	78	88	65	70	423	266	04		28	32
			7	8		7	5	1	62	67	23		60	74
											62		52	04
15	WBS	Williams Beuren	5.	6.	5.	5.	5.	5.	-1.	-0.	1.7	D	0.0	0.6
53	CR27	syndrome	95	36	79	05	31	30	757	813	57	o	04	63
68		chromosome	95	25	14	53	49	27	473	503	47	w	42	32
		region 27	6	8	1	5	1	8	984	333	39	n	20	74
											84		57	04

88 05	TRI M24	Tripartite motif containing 24	7. 46 77 7	7. 06 09 9	6. 89 88 9	6. 92 73 3	6. 30 79 5	6. 30 84 5	-1. 545 410 387	-0. 627 99 87	1.5 45 41 03	D o w n	0.0 37 18 67 03	0.6 63 32 74 04
70 78	TIM P3	TIMP metallopeptidase inhibitor 3	4. 56 27 3	6. 12 34 7	6. 65 62 7	8. 03 41 9	8. 04 28 7	6. 68 14 4	3.4 951 797 85	1.8 053 666 67	3.4 95 17 97 85	U p	0.0 19 78 07 05	0.6 63 32 74 04
20 09 16	RPL2 2L1	Ribosomal protein L22-like 1	8. 04 14 1	7. 81 73 8	8. 00 95 1	9. 29 32 1	9. 38 39 5	8. 25 16 8	2.0 281 766 78	1.0 201 833 33	2.0 28 17 66 78	U p	0.0 13 37 76 78	0.6 63 32 74 04
38 8	RHO B	Ras homolog family member B	6. 33 98 4	5. 84 53 9	5. 70 12 2	6. 88 53 9	7. 59 22 9	7. 04 22 6	2.3 152 425 37	1.2 111 633 33	2.3 15 24 25 37	U p	0.0 02 24 06 72	0.6 63 32 74 04
69 20	TCE A3	Transcription elongation factor A (SII), 3	8. 68 46 2	8. 40 81 1	8. 71 39 2	8. 20 82 2	7. 32 45 2	7. 93 55 1	-1. 716 504 136	-0. 779 473 333	1.7 16 50 41 36	D o w n	0.0 17 11 91 67	0.6 63 32 74 04
15 40 91	SLC2 A12	Solute carrier family 2 (facilitated glucose transporter),	6. 24 55 5	5. 99 24 8	6. 46 90 8	4. 61 76 1	5. 31 41 6	6. 12 87 3	-1. 843 188 133	-0. 882 203 333	1.8 43 18 81	D o w n	0.0 49 41 67	0.6 63 32 74

		member 12									33		1	04
81	CAB	Calcium binding	4.	5.	5.	6.	6.	5.	2.0	1.0	2.0	U	0.0	0.6
61	39L	protein 39 like	89	46	20	50	49	62	232	167	23	p	09	63
7			21	89	92	33	25	44	903	033	29		53	32
			2	8	4	8	9	8	03	33	03		74	74
											03		91	04
21	FAA	Fatty acid amide	8.	8.	7.	6.	7.	7.	-1.	-0.	1.7	D	0.0	0.6
66	H	hydrolase	20	13	72	70	33	58	759	815	59	o	18	63
			85	13	77	29	84	02	631	273	63	w	10	32
				3	3	8	8	8	5	333	15	n	05	74
													34	04
13	C4orf	Chromosome 4	4.	4.	4.	5.	5.	4.	1.6	0.7	1.6	U	0.0	0.6
27	32	open reading frame	74	77	91	82	84	92	470	198	47	p	31	63
20		32	96	46	45	74	79	31	450	8	04		00	32
			8	5	7	6	4	4	31		50		90	74
											31		77	04
62	RSU	Ras suppressor	6.	7.	7.	8.	8.	7.	1.7	0.8	1.7	U	0.0	0.6
51	1	protein 1	89	08	43	27	18	40	620	172	62	p	21	63
			19	29	85	10	89	51	359	433	03		54	32
			3		3	6	2	1	18	33	59		09	74
											18		46	04
56	SH3	SH3-domain	5.	5.	4.	4.	4.	4.	-1.	-0.	1.5	D	0.0	0.6
90	GLB	GRB2-like	27	11	96	25	77	44	543	626	43	o	10	63
4	2	endophilin B2	11	64	59	59	34	49	700	393	70	w	60	32
			7	5		2	6	6	989	333	09	n	83	74
											89		33	04
63	ABH	Abhydrolase	8.	8.	9.	7.	8.	8.	-1.	-0.	1.5	D	0.0	0.6
87	D4	domain containing	54	97	04	79	25	60	554	636	54	o	39	63
4		4	37	85	70	57	69	64	804	733	80	w	93	32

			7		1	1	1	6	656	333	46	n	37	74
											56		7	04
55	CCD	Coiled-coil domain	3.	4.	4.	5.	4.	4.	2.0	1.0	2.0	U	0.0	0.6
70	C88	containing 88A	26	29	30	82	50	58	256	183	25	p	49	63
4	A		95	16	38	96	97	06	056	533	60		95	32
			1	2	3	2	8	2	49	33	56		26	74
											49		44	04
54	LY6	Lymphocyte	5.	4.	5.	4.	4.	4.	-1.	-0.	1.8	D	0.0	0.6
74	K	antigen 6 complex,	63	92	83	55	77	51	802	850	02	o	11	63
2		locus K	03	75	18	39	32	16	884	306	88	w	64	32
			7	6		8	3		115	667	41	n	73	74
											15		58	04
85	RER	RAS-like,	3.	4.	4.	6.	6.	5.	4.1	2.0	4.1	U	0.0	0.6
00	G	estrogen-regulated,	62	33	75	80	83	27	923	677	92	p	03	63
4		growth inhibitor	40	47	06	06	74	46	136	466	31		51	32
			5	1	8	4	2	2	79	67	36		63	74
											79		44	04
71	TPD	Tumor protein D52	10	9.	10	9.	9.	9.	-1.	-0.	1.9	D	0.0	0.6
63	52		.4	83	.7	55	61	07	909	933	09	o	11	63
			90	38	25	55	93	53	299	043	29	w	23	32
			32	9	2	6	8	4	376	333	93	n	62	74
											76		25	04
57	PTP	Protein tyrosine	5.	5.	5.	7.	6.	6.	2.2	1.1	2.2	U	0.0	0.6
93	RG	phosphatase,	31	70	56	18	89	01	547	729	54	p	07	63
		receptor type, G	51	51	9	97	99	84	591	733	75		06	32
			7	2		4	9	8	47	33	91		48	74
											47		18	04
10	MAP	Mitogen-activated	6.	6.	6.	5.	5.	6.	-1.	-0.	1.5	D	0.0	0.6
74	3K2	protein kinase	78	65	32	97	95	06	504	589	04	o	11	63

6		kinase kinase 2	53 7	51 9	42 2	91	33 4	31 7	958 113	723 333	95 81 13	w n	93 18 98	32 74 04
34 29 31	RFP L4A	Ret finger protein-like 4A	4. 49 86 4	4. 13 04 2	5. 02 82 1	3. 46 77 1	3. 92 05 5	4. 18 26 1	-1. 619 408 176	-0. 695 466 667	1.6 19 40 81 76	D o w n	0.0 39 53 41 22	0.6 63 32 74 04
85 66	PDX K	Pyridoxal (pyridoxine, vitamin B6) kinase	7. 17 23	6. 70 08 3	6. 53 35	5. 03 14 7	5. 71 14 1	6. 69 26 8	-1. 986 676 081	-0. 990 356 667	1.9 86 67 60 81	D o w n	0.0 48 63 47 28	0.6 63 32 74 04
37 05	ITPK 1	Inositol-tetrakispho sphate 1-kinase	9. 30 38 9	9. 32 09 4	9. 32 44 7	8. 05 33 2	8. 54 35 5	9. 08 90 2	-1. 687 011 724	-0. 754 47 724	1.6 87 01 17 24	D o w n	0.0 23 99 97 24	0.6 63 32 74 04
55 71 5	DOK 4	Docking protein 4	9. 92 10 5	9. 43 73 2	9. 61 70 2	8. 41 74 1	9. 09 90 5	9. 43 59	-1. 595 862 846	-0. 674 336 667	1.5 95 86 28 46	D o w n	0.0 48 95 53 04	0.6 63 32 74 04
61 93	RPS5	Ribosomal protein S5	11 .0 19 29	11 .0 37 41	11 .5 59 2	12 .2 85 56	11 .9 45 26	11 .4 60 26	1.6 152 155 07	0.6 917 266 67	1.6 15 21 55 07	U p	0.0 31 47 02 05	0.6 63 32 74 04
59	RCN	Reticulocalbin 1	4.	4.	4.	5.	5.	4.	1.8	0.8	1.8	U	0.0	0.6

54	1		19	23	54	92	09	64	656	996	65	p	25	63
			20	30	16	43	71	42	435	733	64		99	32
			5	9	1		8	9	01	33	35		45	74
											01		88	04
46	MYC	V-myc avian	4.	4.	4.	8.	8.	5.	5.7	2.5	5.7	U	0.0	0.6
09		myelocytomatosis	40	94	81	03	23	45	390	208	39	p	08	63
		viral oncogene	16	32	40	02	36	76	687	166	06		67	32
		homolog	7	4	7	3			89	67	87		89	74
											89		66	04
65	RPL1	Ribosomal protein	10	10	11	11	11	11	1.7	0.8	1.7	U	0.0	0.6
32	5P3	L15 pseudogene 3	.8	.5	.1	.9	.6	.5	990	472	99	p	04	63
32			11	62	48	25	28	10	184	1	01		20	32
			67	48	35	35	17	61	72		84		22	74
											72		42	04
81	MAG	Melanoma antigen	6.	6.	6.	6.	5.	6.	-1.	-0.	1.5	D	0.0	0.6
55	ED4	family D4B	44	68	56	14	62	01	554	636	54	o	11	63
7	B		49	92	18	30	80	45	858	783	85	w	94	32
			2	1	2	1	2	7	543	333	85	n	28	74
											43		04	04
25	ABI3	ABI family	9.	8.	8.	9.	9.	9.	1.7	0.7	1.7	U	0.0	0.6
89	BP	member 3 binding	28	94	82	97	52	87	130	765	13	p	05	63
0		protein	60	21	16	18	93	84	611	766	06		69	32
			5	4	9	4	7		68	67	11		91	74
											68		47	04
10	STIP	Stress induced	4.	3.	5.	5.	5.	5.	1.6	0.7	1.6	U	0.0	0.6
96	1	phosphoprotein 1	89	99	01	24	12	79	848	526	84	p	48	63
3			86	89	30	16	89	80	809	466	88		33	32
			3	7	8	6	5	1	61	67	09		94	74
											61		65	04

27	PCD	Protocadherin 17	4.	5.	4.	6.	6.	5.	3.5	1.8	3.5	U	0.0	0.6
25	H17		06	31	47	95	52	90	955	462	95	p	01	63
3			51	07	01	64	31	50	355	066	53		96	32
			2	2	2	5	2	1	32	67	55		18	74
											32		16	04
10	UBE	UBE2F-SCLY	7.	6.	6.	5.	6.	6.	-1.	-0.	1.6	D	0.0	0.6
05	2F-S	readthrough (NMD	20	87	83	83	29	66	626	701	26	o	23	63
33	CLY	candidate)	04	82	10	97	98	58	123	436	12	w	83	32
17			4	1	7	2	7	2	315	667	33	n	63	74
9											15		95	04
28	FAM	Family with	10	9.	10	7.	8.	10	-2.	-1.	2.5	D	0.0	0.6
50	150B	sequence similarity	.4	83	.3	68	80	.0	576	365	76	o	43	63
16		150 member B	79	05	38	62	57	60	382	346	38	w	39	32
			36	5	35	7	4	21	266	667	22	n	30	74
											66		56	04
19	EDN	Endothelin	4.	5.	4.	7.	6.	5.	3.9	1.9	3.9	U	0.0	0.6
09	RA	receptor type A	36	45	72	83	71	95	691	888	69	p	05	63
			80	21	33	16	92	91	864	433	18		08	32
			7	3	1	5	4	5	49	33	64		32	74
											49		42	04
46	MYH	Myosin, heavy	5.	4.	4.	3.	3.	4.	-1.	-0.	1.9	D	0.0	0.6
21	3	chain 3, skeletal	06	47	41	36	63	00	975	982	75	o	04	63
		muscle, embryonic	06	53	54	32	21	87	822	453	82	w	32	32
			4	9	3		2	8	482	333	24	n	14	74
											82		69	04
16	GRA	GRP1 (general	6.	6.	6.	7.	8.	6.	1.8	0.8	1.8	U	0.0	0.6
06	SP	receptor for	33	74	54	29	08	86	322	735	32	p	27	63
22		phosphoinositides	67	65	62	89	55	58	249	966	22		89	32
		1)-associated	9	3		5	4	2	84	67	49		24	74





				2	9	6	3		81		01		56	74
											81		89	04
57	PTG	Prostaglandin-endo	3.	4.	2.	5.	6.	6.	6.1	2.6	6.1	U	0.0	0.6
43	S2	peroxide synthase	06	64	86	70	00	74	831	283	83	p	01	63
		2 (prostaglandin	11	44	29	51	01	82	842	5	18		19	32
		G/H synthase and	3	4	3	3	7	5	65		42		54	74
		cyclooxygenase)									65		79	04
10	BOR	BORCS7-ASMT	7.	7.	8.	5.	4.	8.	-3.	-1.	3.8	D	0.0	0.6
05	CS7-	readthrough (NMD	93	81	68	47	96	19	818	933	18	o	45	63
28	ASM	candidate)	68	55	91	93	83	47	536	02	53	w	45	32
00	T		7	2	7	5	7	8	992		69	n	65	74
7											92		54	04
10	SPR	Sprouty RTK	7.	7.	8.	9.	9.	8.	2.1	1.1	2.1	U	0.0	0.6
25	Y1	signaling	97	70	10	10	62	38	567	088	56	p	09	63
2		antagonist 1	59	39	75	05	73	60	017	266	70		94	32
			6	9	1	9		5	3	67	17		34	74
											3		52	04
55	PRK	Protein kinase,	3.	3.	3.	4.	5.	4.	2.3	1.2	2.3	U	0.0	0.6
77	AR2	camp-dependent,	59	80	54	74	39	41	006	020	00	p	02	63
	B	regulatory subunit	41	79	00	20	53	08	954	7	69		07	32
		type II $\beta$	2	1	1	5	2	8	14		54		78	74
											14		47	04
27	GNG	Guanine nucleotide	6.	7.	7.	8.	9.	8.	2.6	1.4	2.6	U	0.0	0.6
91	11	binding protein (G	68	65	33	77	00	13	604	116	60	p	03	63
		protein), $\gamma$ 11	47	46	82	13	66	46	924	933	49		22	32
			1		3	8		4	94	33	24		87	74
											94		36	04
38	AFF3	AF4/FMR2 family	3.	4.	4.	5.	4.	4.	2.0	1.0	2.0	U	0.0	0.6
99		member 3	16	24	01	53	72	17	060	043	06	p	41	63

			55	87	58	58	97	77	580	633	05		86	32
			9	7	4	1	4	4	21	33	80		52	74
											21		43	04
92	LMB	LMBR1 domain	4.	4.	4.	3.	3.	3.	-1.	-0.	1.5	D	0.0	0.6
25	RD2	containing 2	51	28	14	48	72	93	517	601	17	o	08	63
5			63	08	65	26	11	44	626	816	62	w	55	32
			2		6	5	2	6	385	667	63	n	83	74
											85		15	04
10	STA	Stromal antigen 3	5.	6.	6.	5.	5.	5.	-1.	-0.	1.5	D	0.0	0.6
73	G3		58	09	20	35	32	43	508	592	08	o	20	63
4			91	27	45	07	37	31	282	906	28	w	47	32
			1	1	3		7	6	497	667	24	n	26	74
											97		17	04
90	TM4	Transmembrane 4	8.	8.	9.	7.	6.	8.	-2.	-1.	2.0	D	0.0	0.6
32	SF5	L six family	99	60	04	96	92	66	041	029	41	o	43	63
		member 5	40	96	15	56	24	92	057	316	05	w	83	32
			6	9	8	2	9	7	274	667	72	n	38	74
											74		17	04
56	SEM	Sema domain,	3.	4.	4.	5.	6.	5.	2.4	1.2	2.4	U	0.0	0.6
92	A3G	immunoglobulin	98	91	73	79	72	00	511	934	51	p	24	63
0		domain (Ig), short	80	63	82	13	47	70	690	7	16		13	32
		basic domain,	4	4	7	4		2	74		90		11	74
		secreted,									74		3	04
		(semaphorin) 3G												
88	VNN	Vanin 1	5.	5.	5.	4.	4.	5.	-1.	-0.	1.5	D	0.0	0.6
76	1		45	65	39	56	77	29	545	628	45	o	23	63
			98	97	06	13	32	01	928	473	92	w	53	32
			1	1	9	8	3	8	219	333	82	n	56	74
											19		67	04

23 03 4	SAM D4A 4A	Sterile $\alpha$ motif domain containing 4A	6. 17 34 8	6. 91 99 3	6. 36 79 5	8. 49 95 4	7. 18 80 8	7. 47 41 5	2.3 513 185 43	1.2 334 7 85 43	2.3 51 31 85 43	U p	0.0 12 74 73 85	0.6 63 32 74 04
55 19 5	C14o rf105 105	Chromosome 14 open reading frame 105	8. 79 60 3	7. 91 99 5	8. 24 52 2	7. 29 85 1	7. 35 27 4	8. 09 27 4	-1. 666 710 265	-0. 737 003 333	1.6 66 71 02 65	D o w n	0.0 46 44 09 69	0.6 63 32 74 04
10 76 6	TOB 2 6	Transducer of ERBB2, 2	8. 59 42 2	8. 76 57 3	7. 82 33 3	6. 90 31 3	7. 67 43 1	7. 71 52 1	-1. 950 084 537	-0. 963 536 667	1.9 50 08 45 37	D o w n	0.0 21 28 07 76	0.6 63 32 74 04
31 75 1	ONE CUT 1	One cut homeobox 1	7. 42 79 9	7. 75 84 7	7. 34 02 8	6. 89 12 2	6. 64 61 8	7. 06 94 9	-1. 558 275 153	-0. 639 95 153	1.5 58 27 51 53	D o w n	0.0 12 59 41 77	0.6 63 32 74 04
11 27 8	KLF 12 8	Kruppel-like factor 12	4. 16 03 2	4. 22 18 7	4. 71 13 9	5. 05 66 2	5. 07 54 6	4. 81 78 5	1.5 355 796 36	0.6 187 833 33	1.5 35 57 96 36	U p	0.0 13 83 40 33	0.6 63 32 74 04
97 2	CD7 4	CD74 molecule, major histocompatibility complex, class II	5. 58 87 1	7. 05 01 6	6. 57 84 5	7. 63 64 9	7. 33 92 3	7. 37 51 7	2.0 626 847 35	1.0 445 233 33	2.0 62 68 47	U p	0.0 23 05 16	0.6 63 32 74

		invariant chain									35		51	04
80	MYC	Myc target 1	3.	4.	4.	4.	4.	4.	1.5	0.6	1.5	U	0.0	0.6
17	T1		95	20	20	84	98	33	165	008	16	p	19	63
7			39	01	48	17	37	59	783	2	57		18	32
			1	5	8		3	7	15		83		12	74
											15		36	04
74	VWF	Von Willebrand	4.	5.	6.	7.	7.	5.	3.3	1.7	3.3	U	0.0	0.6
50		factor	25	04	39	50	71	64	009	228	00	p	43	63
			70	42	43	92	32	17	165	666	91		18	32
			8	8	2	5	7	6	5	67	65		81	74
											5		12	04
99	HNR	Heterogeneous	7.	6.	7.	7.	8.	7.	1.9	0.9	1.9	U	0.0	0.6
87	NPD	nuclear	13	25	26	95	05	48	278	469	27	p	17	63
	L	ribonucleoprotein	18	15	23	06	35	24	239	733	82		62	32
		D like	3	7	8	4	7	9	81	33	39		31	74
											81		52	04
93	KLF	Kruppel-like factor	5.	5.	6.	8.	9.	6.	4.2	2.0	4.2	U	0.0	0.6
14	4	4 (gut)	43	34	78	22	02	58	468	864	46	p	15	63
			64	85	85	35	38	54	995	1	89		96	32
			7	5	1		2	4	92		95		69	74
											92		15	04
80	TSG	Testis specific 10	5.	4.	5.	3.	3.	3.	-2.	-1.	2.5	D	0.0	0.6
70	A10		25	12	21	21	48	84	553	352	53	o	04	63
5			75	76	82	23	82	49	719	6	71	w	63	32
			3	1		2	3	9	379		93	n	85	74
											79		84	04
88	WIS	WNT1 inducible	6.	6.	8.	5.	5.	4.	-3.	-1.	3.9	D	0.0	0.6
39	P2	signaling pathway	43	55	10	08	57	51	929	974	29	o	04	63
		protein 2	27	67	46	02	54	55	284	266	28	w	85	32

			5	3	3	6	8	7	6	667	46	n	04	74
													83	04
80	NR4	Nuclear receptor	3.	3.	3.	4.	5.	5.	2.1	1.0	2.1	U	0.0	0.6
13	A3	subfamily 4 group	74	82	87	23	41	09	430	996	43	p	07	63
		A member 3	68	55	56	18	92	58	269	5	02		07	32
			3		1	6		3	6		69		02	74
											6		58	04
11	RPL3	Ribosomal protein	4.	5.	5.	7.	6.	5.	2.1	1.1	2.1	U	0.0	0.6
68	9L	L39 like	76	40	11	02	23	33	478	028	47	p	33	63
32			46	57	34	50	26	48	501	933	85		19	32
			5	6	3	3		9	35	33	01		09	74
											35		79	04
25	MSR	Methionine	5.	5.	4.	6.	5.	5.	1.8	0.8	1.8	U	0.0	0.6
38	B3	sulfoxide reductase	13	49	96	91	59	70	348	756	34	p	48	63
27		B3	36	62	31	84	74	42	727	8	87		54	32
			9	8	4	3	5	7	32		27		37	74
											32		33	04
14	PPP1	Protein	7.	7.	7.	6.	6.	6.	-1.	-0.	1.6	D	0.0	0.6
53	R36	phosphatase 1	54	03	28	40	44	88	633	708	33	o	12	63
76		regulatory subunit	53	89	10	38	79	84	968	38	96	w	46	32
		36	8	1	5	1	9		306		83	n	13	74
											06		46	04
79	CPE	Cadherin-like and	5.	7.	6.	8.	7.	7.	3.6	1.8	3.6	U	0.0	0.6
97	D1	PC-esterase	31	35	19	91	91	60	284	593	28	p	12	63
4		domain containing	49	20	01	94	00	57	833	666	48		17	32
		1	9	1	5	1	8	6	92	67	33		41	74
											92		42	04
38	SER	Stress-associated	5.	5.	5.	6.	6.	5.	1.8	0.8	1.8	U	0.0	0.6
79	P2	endoplasmic	26	96	00	27	75	75	010	488	01	p	39	63

23		reticulum protein family member 2	46 7	27 3	57 1	23 7	13 6	59 3	646 9	5	06 46 9		17 21 94	32 74 04
18 38	DTN B	Dystrobrevin $\beta$	6. 60 18 7	6. 80 85 2	6. 27 05 4	5. 23 27 5	5. 98 60 9	5. 90 13	-1. 807 000 201	-0. 853 596 667	1.8 07 00 02 01	D o w n	0.0 12 50 29 81	0.6 63 32 74 04
80 77 7	CYB 5B	Cytochrome b5 type B (outer mitochondrial membrane)	4. 68 32 1	4. 54 98 9	4. 84 34 3	5. 54 34 4	5. 14 69 9	5. 18 51 5	1.5 153 839 08	0.5 996 833 33	1.5 15 38 39 08	U p	0.0 10 08 13 77	0.6 63 32 74 04
79 76 7	ELM O3	Engulfment and cell motility 3	8. 72 04 3	8. 52 69 9	8. 14 69 9	7. 37 43 8	7. 55 86 2	8. 14 22 8	-1. 708 870 809	-0. 773 043 333	1.7 08 87 08 09	D o w n	0.0 19 28 08 58	0.6 63 32 74 04
67 78 13	SNO RA3 0	Small nucleolar RNA, H/ACA box 30	5. 66 10 2	5. 65 93 2	5. 78 21 9	4. 92 54 3	5. 10 04 8	5. 27 65 5	-1. 515 741 081	-0. 600 023 333	1.5 15 74 10 81	D o w n	0.0 06 50 51 95	0.6 63 32 74 04
11 20 9	MST 1P2	Macrophage stimulating (hepatocyte growth factor-like) pseudogene 2	9. 83 82 9	8. 77 68 1	8. 69 80 2	8. 23 50 1	7. 66 34 8	8. 62 64 7	-1. 904 466 178	-0. 929 386 667	1.9 04 46 61 78	D o w n	0.0 41 92 63 07	0.6 63 32 74 04
23	AFF2	AF4/FMR2 family	4.	4.	4.	3.	4.	4.	-1.	-0.	1.6	D	0.0	0.6

34		member 2	43	75	79	42	29	19	614	691	14	o	28	63
			39	69	54	65	00	53	887	433	88	w	31	32
			3	2	6	8	7	6	13	333	71	n	18	74
											3		81	04
25	CNR	Cannabinoid	5.	6.	6.	7.	7.	6.	2.2	1.1	2.2	U	0.0	0.6
92	IP1	receptor interacting	49	92	51	96	83	64	478	685	47	p	42	63
7		protein 1	46	79	97	10	70	98	150	233	81		34	32
			1	5	1	3	1		46	33	50		94	74
											46		72	04
83	FZD	Frizzled class	5.	6.	5.	7.	7.	6.	2.2	1.1	2.2	U	0.0	0.6
24	7	receptor 7	10	23	65	04	32	13	535	721	53	p	19	63
			08	14	60	22	37	88	039	7	50		97	32
			1	8	4	6	8		83		39		2	74
											83			04
14	WIP	WAS/WASL	7.	6.	6.	6.	5.	6.	-1.	-0.	1.6	D	0.0	0.6
71	F2	interacting protein	21	88	98	32	95	69	628	703	28	o	16	63
79		family member 2	54	87	25	86	50	29	251	323	25	w	64	32
			1		1	4	5	6	249	333	12	n	27	74
											49		94	04
65	GRA	GRAM domain	4.	5.	5.	5.	5.	5.	1.5	0.5	1.5	U	0.0	0.6
98	MD3	containing 3	96	03	55	96	58	78	106	951	10	p	25	63
3			29	54	32	16	69	86	785	966	67		63	32
			2	4	7		7	5	06	67	85		87	74
											06		43	04
65	SLC2	Solute carrier	3.	3.	3.	4.	4.	4.	1.6	0.7	1.6	U	0.0	0.6
15	A3	family 2	68	95	68	76	75	01	696	395	69	p	14	63
		(facilitated glucose	23	90	23	85	57	80	472	433	64		14	32
		transporter),	5	4	5	4	6	7	5	33	72		36	74
		member 3									5		69	04

91	MYO	Myozenin 3	3.	4.	3.	5.	5.	4.	2.2	1.1	2.2	U	0.0	0.6
97	Z3		81	98	85	70	79	62	291	564	29	p	29	63
7			83	42	52	42	80	50	236	766	12		36	32
			6	5	9	7	1	5	83	67	36		28	74
											83		13	04
27	TIN	Tubulointerstitial	5.	4.	3.	2.	2.	3.	-2.	-1.	2.3	D	0.0	0.6
28	AG	nephritis antigen	06	98	30	96	92	68	390	257	90	o	35	63
3			33	42	19	72	37	7	319	203	31	w	29	32
			8	5	8	7	3		277	333	92	n	54	74
											77		9	04
22	PHL	Pleckstrin	5.	5.	5.	6.	7.	6.	2.9	1.5	2.9	U	0.0	0.6
82	DA1	homology-like	50	66	04	94	63	29	310	514	31	p	03	63
2		domain, family A,	58	26	86	09	27	75	346	1	03		07	32
		member 1	7		2	5	9	8	03		46		90	74
											03		35	04
10	GPC	Glypican 6	7.	7.	7.	9.	8.	8.	2.1	1.0	2.1	U	0.0	0.6
08	6		54	59	29	01	20	48	287	899	28	p	02	63
2			85	84	15	78	24	82	256	9	72		50	32
			1	6	8	2	2	8	1		56		48	74
											1		36	04
48	NPH	Nephronophthisis 1	5.	5.	5.	4.	4.	4.	-1.	-0.	1.7	D	0.0	0.6
67	P1	(juvenile)	43	92	12	90	64	63	701	766	01	o	12	63
			58	35	30	40	82	01	385	71	38	w	13	32
			8	7	2	2		2	425		54	n	10	74
											25		44	04
38	KLR	Killer cell	4.	5.	5.	4.	3.	4.	-1.	-0.	1.9	D	0.0	0.6
21	C1	lectin-like receptor	71	20	70	62	76	40	925	945	25	o	20	63
		subfamily C,	45	65	24	74	04	00	469	21	46	w	16	32
		member 1	9		8		6	8	139		91	n	58	74



											39		71	04
94	ORM	ORMDL	6.	6.	6.	5.	5.	6.	-1.	-0.	1.7	D	0.0	0.6
10	DL1	sphingolipid	46	28	36	40	26	05	735	795	35	o	11	63
1		biosynthesis	09	43	24	21	00	82	987	756	98	w	52	32
		regulator 1	6	7		4	4	8	629	667	76	n	16	74
											29		28	04
10	FST	Follistatin	4.	4.	4.	5.	5.	5.	1.8	0.8	1.8	U	0.0	0.6
46			85	62	96	88	47	73	414	808	41	p	01	63
8			79	98	89	93	83	16	854	7	48		58	32
			1	8	8	4	6	8	52		54		48	74
											52		84	04
10	GIM	GIMAP1-GIMAP5	5.	5.	5.	7.	6.	6.	2.3	1.2	2.3	U	0.0	0.6
05	AP1-	readthrough	00	73	83	57	65	05	564	365	56	p	19	63
27	GIM		17	93	87	28	78	89	036	866	40		79	32
94	AP5		8		9	4	1	8	07	67	36		49	74
9											07		8	04
10	LOC	Hepatocyte growth	7.	5.	6.	4.	4.	6.	-3.	-1.	3.1	D	0.0	0.6
53	1053	factor-like protein	83	90	13	57	20	19	104	634	04	o	44	63
69	6925		79	32	64	05	38	99	670	44	67	w	13	32
25	2		7	9		6	3	5	15		01	n	69	74
2											5		92	04
57	ATP8	Atpase,	5.	6.	6.	7.	6.	6.	2.3	1.2	2.3	U	0.0	0.6
19	B2	aminophospholipid	17	20	28	99	85	42	071	061	07	p	35	63
8		transporter, class I,	29	08	16	36	55	46	790	3	17		90	32
		type 8B, member 2	7	3	3	6	5	1	99		90		82	74
											99		4	04
11	FMN	Formin like 2	6.	7.	6.	8.	7.	7.	2.2	1.2	2.2	U	0.0	0.6
47	L2		37	16	52	89	59	18	985	007	98	p	32	63
93			40	79	31	22	04	45	169	033	51		57	32

			8	7	2	8	1	9	95	33	69		91	74
											95		45	04
10	RAM	Receptor (G	5.	5.	5.	6.	7.	5.	2.0	1.0	2.0	U	0.0	0.6
26	P2	protein-coupled)	04	04	38	36	06	19	747	529	74	p	48	63
6		activity modifying	84	25	10	62	91	53	344	266	73		97	32
		protein 2	2	1	9	5	6	9	1	67	44		30	74
											1		69	04
26	GEM	GTP binding	3.	5.	4.	7.	6.	5.	4.6	2.2	4.6	U	0.0	0.6
69		protein	48	05	34	81	11	59	391	138	39	p	09	63
		overexpressed in	17	58	96	14	99	74	912	733	19		41	32
		skeletal muscle	8	4	3	2	7	8	85	33	12		72	74
											85		92	04
27	AMP	Amphiphysin	3.	4.	3.	5.	4.	3.	1.9	0.9	1.9	U	0.0	0.6
3	H		19	31	56	22	71	97	288	477	28	p	43	63
			47	53	34	78	30	58	219	2	82		94	32
			7	2	4	3	4	2	85		19		58	74
											85		87	04
57	SCU	Signal peptide,	5.	6.	5.	7.	6.	7.	2.3	1.2	2.3	U	0.0	0.6
75	BE2	CUB domain,	26	66	56	56	40	25	707	453	70	p	24	63
8		EGF-like 2	58	11	63	89	30	73	003	133	70		70	32
			6	9	2	8	1	2	69	33	03		56	74
											69		57	04
15	CYP	Cytochrome P450,	6.	5.	5.	5.	4.	4.	-1.	-0.	1.8	D	0.0	0.6
65	2D6	family 2, subfamily	31	89	46	44	70	76	896	923	96	o	15	63
		D, polypeptide 6	07		89	01	02	00	137	063	13	w	23	32
			3		6	5	8	7	168	333	71	n	86	74
											68		05	04
81	MAP	Microtubule	5.	4.	5.	6.	5.	5.	1.6	0.7	1.6	U	0.0	0.6
63	1LC3	associated protein	17	66	48	08	57	93	896	567	89	p	19	63

1	B	1 light chain 3 $\beta$	98 4	63 4	06 3	72 7	40 5	57	643 28	366 67	66 43 28		84 92 47	32 74 04
21 14	ETS2	V-ets avian erythroblastosis virus E26 oncogene homolog 2	7. 38 77 7	6. 59 45 7	7. 00 59 1	7. 85 71 6	8. 18 42 1	7. 33 50 9	1.7 363 647 02	0.7 960 7	1.7 36 36 47 02	U p	0.0 28 48 44 93	0.6 63 32 74 04
79 40	LST1	Leukocyte specific transcript 1	6. 61 01 7	7. 53 54 7	7. 17 01 9	8. 24 64 5	7. 68 38 5	7. 53 63 5	1.6 436 730 25	0.7 169 233 33	1.6 43 67 30 25	U p	0.0 45 33 26 44	0.6 63 32 74 04
51 75 1	HIG D1B	HIG1 hypoxia inducible domain family member 1B	5. 03 00 9	5. 66 51 2	5. 18 13	6. 58 05 8	7. 06 10 2	5. 78 80 8	2.2 726 728 12	1.1 843 9	2.2 72 67 28 12	U p	0.0 10 77 97 04	0.6 63 32 74 04
53 5	ATP6 V0A 1	Atpase, H <sup>+</sup> transporting, lysosomal subunit a1	9. 52 13 2	9. 27 29 1	8. 82 74	8. 40 22 7	8. 37 34 9	8. 66 00 9	-1. 657 087 748	-0. 728 65	1.6 57 08 77 48	D o w n	0.0 11 69 92 73	0.6 63 32 74 04
94	ACV RL1	Activin A receptor type II	5. 04 85 5	5. 08 45 2	5. 11 73 7	6. 13 06 2	6. 35 52 3	5. 19 80 1	1.7 545 973 56	0.8 111 4	1.7 54 59 73 56	U p	0.0 30 36 94 97	0.6 63 32 74 04
25	ADG	Adhesion G	6.	7.	6.	9.	8.	8.	3.1	1.6	3.1	U	0.0	0.6

960	RA2	protein-coupled receptor A2	32 63 2	95 47 5	85 51 4	42 43 7	70 23 7	03 02	900 447 6	735 766 67	90 04 47 6	p	11 42 77 2	63 32 74 04
7512	XPN PEP2	X-prolyl aminopeptidase (aminopeptidase P) 2, membrane-bound	4. 08 45 9	4. 38 41 9	4. 56 57 1	3. 59 77 3	3. 80 92 8	3. 63 10 1	-1. 586 106 89	-0. 665 49	1.5 86 10 68 9	D o w n	0.0 03 99 17 82	0.6 63 32 74 04
6591	SNAI 2	Snail family zinc finger 2	4. 35 20 4	4. 93 01 4	4. 47 39	6. 70 92 7	7. 45 37 2	5. 74 16 5	4.1 396 821 5	2.0 495 2	4.1 39 68 21 5	U p	0.0 01 77 88 8	0.6 63 32 74 04
81575	APO LD1	Apolipoprotein L domain containing 1	4. 66 5	4. 32 52 4	4. 64 12 4	7. 99 58 5	9. 99 79 3	5. 88 61 8	10. 674 969 18	3.4 161 6	10. 67 49 69 18	U p	0.0 07 14 59 05	0.6 63 32 74 04
5796	PTP RK	Protein tyrosine phosphatase, receptor type, K	11 .8 18 51	11 .4 46 6	11 .8 15 1	10 .5 18 86	11 .1 46 38	11 .2 72 61	-1. 640 482 268	-0. 714 12	1.6 40 48 22 68	D o w n	0.0 19 31 67 68	0.6 63 32 74 04
2701	GJA4	Gap junction protein $\alpha$ 4	3. 70 33	3. 78 62 7	4. 07 60 1	5. 52 59 9	5. 88 41 2	4. 20 33 7	2.5 478 847 13	1.3 493	2.5 47 88 47 13	U p	0.0 13 65 28 77	0.6 63 32 74 04

10060	ABC C9	ATP binding cassette subfamily C member 9	4. 41 54 9	5. 45 82 2	5. 06 91 4	6. 56 49 2	6. 56 46 7	5. 39 02 9	2.2 852 362 71	1.1 923 433 33	2.2 85 23 62 71	U p	0.0 20 05 69 25	0.6 63 32 74 04
196743	PAO X	Polyamine oxidase (exo-N4-amino)	7. 42 06 9	7. 47 00 8	6. 91 47 9	6. 21 16 9	5. 91 00 3	6. 59 13 2	-2. 043 213 553	-1. 030 84 35 53	2.0 43 21 35 53	D o w n	0.0 03 87 91 67	0.6 63 32 74 04
3790	KCN S3	Potassium voltage-gated channel, modifier subfamily S, member 3	3. 13 61 1	3. 88 77 2	3. 60 37 4	6. 34 71 8	5. 80 81 6	4. 11 91 6	3.6 865 977 23	1.8 822 9 77 23	3.6 86 59 77 23	U p	0.0 10 69 86 33	0.6 63 32 74 04
11130	ZWI NT	ZW10 interacting kinetochore protein	5. 74 10 5	5. 99 01 5	6. 24 00 1	7. 08 74 1	7. 71 52 1	6. 07 62 1	1.9 577 592 08	0.9 692 033 33	1.9 57 75 92 08	U p	0.0 46 43 67 79	0.6 63 32 74 04
4172	MC M3	Minichromosome maintenance complex component 3	6. 09 18 5	6. 03 02 2	6. 38 77 4	7. 00 90 4	7. 18 06 3	6. 46 53 9	1.6 415 932 08	0.7 150 966 67	1.6 41 59 32 08	U p	0.0 16 99 02 01	0.6 63 32 74 04
10272511	LOC 1027 2511 7	Rho guanine nucleotide exchange factor 5-like	7. 75 23 1	7. 05 24 3	6. 95 19 3	6. 54 29 9	6. 44 79 8	6. 87 70 8	-1. 547 089 507	-0. 629 556 667	1.5 47 08 95	D o w n	0.0 42 87 63	0.6 63 32 74

7												07		89	04
18 43	DUS P1	Dual specificity phosphatase 1	6. 52 14 3	6. 06 26 7	7. 02 79 7	8. 81 12 1	9. 92 79 4	8. 40 72 3	5.7 018 760 07	2.5 114 366 67	5.7 01 87 60 07	U p	0.0 00 59 50 47	0.6 63 32 74 04	
65 26 7	WN K3	WNK lysine deficient protein kinase 3	5. 26 57 8	5. 34 67 1	5. 49 29	4. 12 70 3	4. 54 14	5. 10 35 5	-1. 714 518 336	-0. 777 803 333	1.7 14 51 83 36	D o w n	0.0 18 17 85 95	0.6 63 32 74 04	
28 33 77	SPR YD4	SPRY domain containing 4	6. 66 73	6. 95 28	6. 66 01	5. 67 11 9	5. 88 19 6	6. 61 68 3	-1. 628 394 214	-0. 703 45	1.6 28 39 42 14	D o w n	0.0 33 81 20 98	0.6 63 32 74 04	
12 66 69	SHE	Src homology 2 domain containing E	3. 90 46 6	4. 47 65	4. 60 34	5. 05 80 4	5. 57 25 2	4. 60 78 8	1.6 833 011 84	0.7 512 933 33	1.6 83 30 11 84	U p	0.0 37 04 07 76	0.6 63 32 74 04	
54 92 8	IMP AD1	Inositol monophosphatase domain containing 1	5. 05 62 5	4. 46 19 4	5. 05 34 8	5. 54 71 5	5. 75 18	5. 21 00 2	1.5 645 704 98	0.6 457 666 67	1.5 64 57 04 98	U p	0.0 26 88 22 3	0.6 63 32 74 04	
11 31 89	CHS T14	Carbohydrate (N-acetylgalactosa mine 4-0)	6. 79 05	7. 03 36	7. 34 52	8. 19 35	7. 58 71	7. 31 30	1.5 598 961	0.6 414 5	1.5 59 89	U p	0.0 48 49	0.6 63 32	

		sulfotransferase 14		4	6	3	8	4	66		61		13	74
											66		53	04
26	MOX	Monooxygenase,	4.	4.	4.	7.	5.	4.	2.4	1.3	2.4	U	0.0	0.6
00	D1	DBH-like 1	47	54	28	07	31	82	688	038	68	p	44	63
2			78	33	03	32	49	48	570	433	85		84	32
			1		6	9	1		98	33	70		63	74
											98		36	04
12	SGS	Small G protein	5.	4.	4.	4.	4.	4.	-1.	-0.	1.6	D	0.0	0.6
90	M1	signaling	32	89	48	13	02	30	679	748	79	o	12	63
49		modulator 1	76	26	82	36	74	21	936	406	93	w	94	32
			9		2	8	5	6	459	667	64	n	70	74
											59		13	04
63	TNN	Tenascin N	3.	4.	3.	5.	4.	4.	2.2	1.1	2.2	U	0.0	0.6
92			78	06	64	93	35	68	328	588	32	p	21	63
3			78	91	64	73	91	35	247	7	82		36	32
				3	7	9		2	17		47		52	74
											17		9	04
16	ZFP	Zinc finger protein,	9.	8.	8.	7.	7.	8.	-2.	-1.	2.0	D	0.0	0.6
18	M1	FOG family	10	84	91	84	61	34	025	018	25	o	02	63
82		member 1	96	17	71	56	93	83	671	4	67	w	40	32
			3	8	6	9	5	3	172		11	n	95	74
											72		8	04
19	EEF1	Eukaryotic	10	9.	10	11	11	11	1.7	0.8	1.7	U	0.0	0.6
37	G	translation	.7	98	.9	.7	.0	.2	644	191	64	p	30	63
		elongation factor 1	30	15	36	88	56	60	150	9	41		311	32
		$\gamma$	06	3	37	37	84	32	85		50		15	74
											85		3	04
98	LRB	LPS-responsive	8.	7.	8.	7.	7.	7.	-1.	-0.	1.5	D	0.0	0.6
7	A	vesicle trafficking,	35	97	38	29	58	95	543	626	43	o	26	63

		beach and anchor containing	37 6	23 4	91 1	59 4	54 4	5	576 159	276 667	57 61 59	w n	09 81 7	32 74 04
15 32 01	SLC3 6A2	Solute carrier family (proton/amino acid symporter), member 2	3. 95 39 1	3. 91 86 6	3. 76 49 6	2. 68 18 6	2. 92 81 6	3. 48 66 5	-1. 798 698 441	-0. 846 953 333	1.7 98 69 84 41	D o w n	0.0 04 65 16 63	0.6 63 32 74 04
28 85 0	IGK V10 R22- 5	Immunoglobulin $\kappa$ variable 1/OR22-5 (pseudogene)	5. 42 99 9	4. 89 86 3	5. 48 02 1	6. 01 56 4	9. 11 58 5	8. 90 33 7	6.6 900 175 71	2.7 420 1 71	6.6 90 01 75 71	U p	0.0 09 79 54 34	0.6 63 32 74 04
27 33 3	GOL IM4	Golgi integral membrane protein 4	7. 46 90 6	7. 76 32 4	7. 29 06 5	6. 57 99 4	6. 66 72 8	7. 32 05 4	-1. 571 050 984	-0. 651 73 09	1.5 71 05 09 84	D o w n	0.0 33 55 65 55	0.6 63 32 74 04
54 46 3	FAM 134B	Family with sequence similarity 134 member B	8. 70 74 2	9. 18 65 3	8. 89 37 1	8. 07 55 3	8. 63 37 7	8. 13 95 6	-1. 565 112 831	-0. 646 266 667	1.5 65 11 28 31	D o w n	0.0 20 61 50 28	0.6 63 32 74 04
19 73	EIF4 A1	Eukaryotic translation initiation factor 4A1	6. 08 82	5. 82 79 5	5. 92 62 3	6. 54 60 6	7. 17 33 7	6. 22 13 2	1.6 238 931 03	0.6 994 566 67	1.6 23 89 31 03	U p	0.0 30 59 21 41	0.6 63 32 74 04
20	FBX	F-box protein 15	5.	4.	5.	4.	4.	4.	-1.	-0.	1.6	D	0.0	0.6



14	O15		59	68	08	30	31	64	625	700	25	o	26	63
56			44	40	79	31	39	72	255	666	25	w	03	32
			2	3	5	8	3	9	647	667	56	n	90	74
											47		36	04
65	SLC7	Solute carrier	4.	5.	5.	4.	4.	4.	-1.	-0.	1.7	D	0.0	0.6
41	A1	family 7 (cationic	94	17	10	00	33	45	748	806	48	o	01	63
		amino acid	21	21	04	00	92	60	926	47	92	w	92	32
		transporter, y+	7	8	9	9	5	9	912		69	n	19	74
		system), member 1									12		47	04
14	TME	Transmembrane	4.	4.	4.	6.	4.	5.	1.8	0.9	1.8	U	0.0	0.6
85	M56	protein 56	56	80	64	18	92	66	937	212	93	p	20	63
34			47	78	72	92	62	81	772	666	77		85	32
			1	6	9	6	5	5	74	67	72		02	74
											74		47	04
38	L1C	L1 cell adhesion	5.	4.	5.	6.	7.	5.	2.2	1.1	2.2	U	0.0	0.6
97	AM	molecule	44	99	64	25	42	87	310	577	31	p	24	63
			3	17	47	86	01	38	198	033	01		17	32
				4	2	3	1	3	25	33	98		25	74
											25		77	04
11	C12o	Chromosome 12	9.	9.	10	10	10	10	1.5	0.6	1.5	U	0.0	0.6
32	rf57	open reading frame	45	67	.1	.5	.4	.2	912	702	91	p	16	63
46		57	47	06	18	82	59	13	935		29		49	32
			7	2	36	11	07	17	52		35		15	74
											52		61	04
54	POD	Podocalyxin-like	5.	6.	6.	8.	8.	6.	3.4	1.7	3.4	U	0.0	0.6
20	XL		70	09	50	50	86	31	715	955	71	p	26	63
			01	44	33	10	93	42	100	633	51		65	32
			6	9	1	5	3	7	15	33	00		38	74
											15		7	04

85 02 7	SMI M3 3	Small integral membrane protein	5. 54 79 5	5. 34 38 9	5. 67 65	6. 48 8	7. 61 56 3	5. 85 46 4	2.1 885 520 06	1.1 299 766 67	2.1 88 55 20 06	U p	0.0 30 80 56 96	0.6 63 32 74 04
86 04	SLC2 5A12	Solute carrier family 25 (aspartate/glutamate carrier), member 12	3. 51 25 8	4. 20 35 8	3. 83 73 5	5. 57 04 4	4. 38 75 4	4. 32 16 1	1.8 773 270 44	0.9 086 8 44	1.8 77 32 70 44	U p	0.0 39 44 87 73	0.6 63 32 74 04
46 48	MYO 7B	Myosin VIIB	8. 60 75 3	8. 62 37 8	8. 22 16 1	7. 43 76 1	7. 94 60 7	8. 24 36 8	-1. 524 694 287	-0. 608 52 42 87	1.5 24 69 42 87	D o w n	0.0 41 96 94 96	0.6 63 32 74 04
11 03 1	RAB 31	RAB31, member RAS oncogene family	5. 12 63 7	6. 53 87 2	5. 11 53	7. 91 77 7	6. 75 93 5	6. 07 77 2	2.5 050 105 28	1.3 248 166 67	2.5 05 01 05 28	U p	0.0 49 20 26 94	0.6 63 32 74 04
34 29 79	PAL M3	Paralemmin 3	8. 43 37 8	8. 60 50 6	7. 63 29	6. 82 57 2	6. 43 76 7	7. 97 89 6	-2. 208 596 7	-1. 143 13 7	2.2 08 59 67	D o w n	0.0 35 02 94 12	0.6 63 32 74 04
59 18	RAR RES1	Retinoic acid receptor responder (tazarotene induced) 1	4. 73 39 9	5. 21 68 9	5. 81 04 9	7. 55 22 1	8. 10 82 2	5. 70 59 3	3.6 510 970 05	1.8 683 3 70	3.6 51 09 70	U p	0.0 18 54 00	0.6 63 32 74

											05		45	04
70	KLF	Kruppel-like factor	7.	6.	6.	7.	7.	6.	1.6	0.6	1.6	U	0.0	0.6
71	10	10	09	33	84	51	81	98	018	797	01	p	48	63
			09	76	36	52	49	13	843	7	88		34	32
			5	7	6	8	9	2	56		43		18	74
											56		7	04
19	EME	Essential meiotic	5.	6.	5.	4.	5.	4.	-1.	-0.	1.8	D	0.0	0.6
73	2	structure-specific	53	35	52	67	26	82	847	885	47	o	16	63
42		endonuclease	54	63	67	11	54	48	703	733	70	w	07	32
		subunit 2	6	1	5		2		585	333	35	n	80	74
											85		67	04
51	PDE	Phosphodiesterase	3.	4.	3.	4.	5.	4.	1.5	0.6	1.5	U	0.0	0.6
40	3B	3B	81	15	82	44	06	10	223	063	22	p	47	63
			86	45	38	33	34	92	956	433	39		79	32
				1	3		7		38	33	56		26	74
											38		47	04
26	GBP	Guanylate binding	5.	5.	6.	6.	6.	6.	1.8	0.8	1.8	U	0.0	0.6
34	2	protein 2,	19	93	42	50	97	75	535	902	53	p	27	63
		interferon-inducibl	77	62	27	16	55	03	229	7	52		12	32
		e	3	9	2	2	8	5	78		29		50	74
											78		02	04
29	SNX	Sorting nexin 10	3.	4.	4.	5.	5.	4.	1.7	0.7	1.7	U	0.0	0.6
88	10		98	83	83	43	70	87	251	867	25	p	38	63
7			97	83	32	90	42	82	956	6	19		11	32
			3	4	5	9	7	4	7		56		61	74
											7		47	04
97	PCD	Protocadherin $\alpha$ 9	7.	7.	6.	6.	6.	6.	-1.	-0.	1.5	D	0.0	0.6
52	HA9		44	73	91	53	83	80	557	639	57	o	31	63
			20	45	29	69	18	31	526	256	52	w	81	32

			9	2	9		2	1	454	667	64	n	64	74
											54		86	04
29	MDF	Myod family	3.	3.	3.	5.	4.	3.	2.0	1.0	2.0	U	0.0	0.6
96	IC	inhibitor domain	24	28	70	03	67	70	804	568	80	p	16	63
9		containing	56	68	48	16	14	48	034	633	40		18	32
			2	2	1	3		1	47	33	34		07	74
											47		55	04
13	IL17	Interleukin 17	8.	8.	8.	6.	7.	8.	-1.	-0.	1.8	D	0.0	0.6
20	RE	receptor E	32	16	13	74	17	03	851	888	51	o	27	63
14			16	47	55	17	66	75	412	626	41	w	93	32
				3	2	4	6	7	884	667	28	n	61	74
											84		39	04
84	SRP	Sushi-repeat	5.	7.	6.	8.	8.	7.	3.1	1.6	3.1	U	0.0	0.6
06	X	containing protein,	58	10	77	16	48	74	173	403	17	p	05	63
		X-linked	60	29	70	11	12	46	064		30		02	32
			5	8	5	6	1	1	77		64		32	74
											77		48	04
27	PPA2	Pyrophosphatase	7.	7.	7.	6.	7.	7.	-1.	-0.	1.5	D	0.0	0.6
06		(inorganic) 2	75	27	67	49	08	27	533	617	33	o	43	63
8			90	20	52	82	02	66	742	056	74	w	70	32
			1	9	1	3	7	4	901	667	29	n	02	74
											01		77	04
58	KMT	Lysine (K)-specific	7.	7.	7.	6.	6.	6.	-1.	-0.	1.5	D	0.0	0.6
50	2C	methyltransferase	49	64	07	85	68	88	511	595	11	o	18	63
8		2C	63	48	38	24	84	76	010	513	01	w	43	32
			6	5	5	1	4	7	131	333	01	n	06	74
											31		8	04
47	NED	Neural precursor	4.	3.	4.	4.	4.	4.	1.5	0.6	1.5	U	0.0	0.6
34	D4	cell expressed,	50	68	42	90	80	73	274	111	27	p	33	63

		developmentally down-regulated 4, E3 ubiquitin protein ligase	25 5 46 3	65 2 82 1	71 1 82 3	57 6 09 91	52 9 41 61	85 5 72 3	657 17 878 71	4 17 6 71	46 57 48 78 71		79 97 43 2	32 74 04 04
81 67 1	VMP 1	Vacuole membrane protein 1	9. 81 46 3	8. 77 82 1	9. 39 82 3	10 .2 09 91	10 .8 41 61	9. 97 72 3	2.0 174 878 71	1.0 125 6 78 71	2.0 17 48 78 71	U p	0.0 17 46 53 2	0.6 63 32 74 04
84 91 3	ATO H8	Atonal bhlh transcription factor 8	6. 52 48 6	6. 82 84 7	6. 67 23 8	7. 74 32 1	7. 50 50 9	6. 81 03 6	1.5 995 321 61	0.6 776 5 21 61	1.5 99 53 21 61	U p	0.0 35 70 33 73	0.6 63 32 74 04
20 34	EPAS 1	Endothelial PAS domain protein 1	8. 36 18 2	9. 01 53 8	9. 00 67 8	10 .0 62 01	9. 93 67 8	9. 49 30 4	2.0 504 634 11	1.0 359 5 34 11	2.0 50 46 34 11	U p	0.0 04 14 64 35	0.6 63 32 74 04
10 39 5	DLC 1	DLC1 Rho gtpase activating protein	6. 33 17 9	6. 82 31 2	6. 66 89 4	7. 85 59 5	8. 19 69 2	7. 49 79 7	2.3 658 030 89	1.2 423 3 30 89	2.3 65 80 30 89	U p	0.0 01 08 28 64	0.6 63 32 74 04
10 40	CDS 1	CDP-diacylglycero l synthase 1	9. 35 77 6	8. 67 23 3	8. 71 00 4	7. 25 71 1	7. 80 93 2	8. 79 47 1	-1. 944 855 991	-0. 959 663 333	1.9 44 85 59 91	D o w n	0.0 48 53 49 87	0.6 63 32 74 04

74	VAV	Vav guanine	8.	8.	8.	7.	7.	7.	-1.	-0.	1.7	D	0.0	0.6
10	2	nucleotide	86	42	35	50	84	95	720	782	20	o	07	63
		exchange factor 2	68	61	82	09	77	38	578	893	57	w	23	32
			6	5		5	7	1	044	333	80	n	20	74
											44		44	04
54	SOX	SRY-box 18	5.	5.	5.	7.	6.	5.	2.2	1.2	2.2	U	0.0	0.6
34	18		03	74	86	29	99	96	984	006	98	p	17	63
5			50	68	95	47	30	55	373	533	43		31	32
			5	2	3	9	1	6	36	33	73		69	74
											36		74	04
34	IGFB	Insulin like growth	8.	11	9.	12	11	10	4.1	2.0	4.1	U	0.0	0.6
90	P7	factor binding	01	.1	88	.6	.5	.9	039	370	03	p	36	63
		protein 7	39	17	56	54	53	20	410	1	94		89	32
			2	89	5	96	3	23	28		10		58	74
											28		11	04
16	TME	Transmembrane	7.	7.	7.	6.	7.	7.	-1.	-0.	1.5	D	0.0	0.6
11	M22	protein 229B	77	65	31	66	02	02	599	677	99	o	10	63
45	9B		90	19	69	52	39	70	088	25	08	w	43	32
			7	4	4	1	1	8	738		87	n	39	74
											38		93	04
51	FKB	FK506 binding	4.	5.	4.	6.	5.	5.	1.7	0.8	1.7	U	0.0	0.6
66	P7	protein 7	39	30	84	17	65	12	473	051	47	p	44	63
1			67	27	54	91	73	40	839	966	38		98	32
			6	8	6	7	8	4	77	67	39		48	74
											77		82	04
10	POS	Periostin,	3.	3.	4.	6.	6.	4.	3.7	1.9	3.7	U	0.0	0.6
63	TN	osteoblast specific	86	40	02	59	39	01	339	006	33	p	22	63
1		factor	89	50	95	21	41	94	259	933	92		40	32
			9	6	7	1	3	6	93	33	59		17	74

												93		24	04
90	LDB	LIM domain	3.	3.	4.	5.	6.	4.	3.3	1.7	3.3	U	0.0	0.6	
79	2	binding 2	72	38	35	71	33	59	104	270	10	p	06	63	
			2	85	45	77	43	41	943	466	49		85	32	
				7		8		3	47	67	43		86	74	
											47		45	04	
51	PDE	Phosphodiesterase	5.	7.	6.	7.	7.	7.	2.2	1.1	2.2	U	0.0	0.6	
36	1A	1A	48	49	34	95	61	30	650	795	65	p	43	63	
			93	35	75	15	40	34	192	233	01		92	32	
			8	7	2	2	8	4	84	33	92		71	74	
											84		99	04	
84	PPFI	PTPRF interacting	8.	8.	8.	7.	7.	8.	-1.	-0.	1.5	D	0.0	0.6	
95	BP2	protein, binding	54	38	56	37	94	31	535	618	35	o	43	63	
		protein 2 (liprin $\beta$	68	00	14	49	13	65	270	493	27	w	47	32	
		2)	5	8	1	6	7	3	996	333	09	n	49	74	
											96		79	04	
30	HIST	Histone cluster 1,	6.	5.	6.	5.	5.	6.	-1.	-0.	1.6	D	0.0	0.6	
12	1H2	h2ae	36	95	16	09	08	07	669	739	69	o	41	63	
	AE		30	35	00	35	66	74	801	676	80	w	79	32	
			5	4	7	5		8	565	667	15	n	15	74	
											65		43	04	
67	ZFP3	ZFP36 ring finger	7.	6.	6.	8.	8.	7.	2.5	1.3	2.5	U	0.0	0.6	
8	6L2	protein-like 2	23	98	67	53	62	84	882	719	88	p	01	63	
			85	23	39	38	93	76	853	966	28		19	32	
			2	6	6	7	4	2	29	67	53		92	74	
											29		81	04	
71	TPD	Tumor protein	4.	4.	4.	5.	4.	4.	1.5	0.5	1.5	U	0.0	0.6	
65	52L2	D52-like 2	21	14	53	26	58	80	044	892	04	p	27	63	
			64	65	05	57	94	60	644	5	46		33	32	

			4	2	7	8	1	9	33		44		35	74
											33		09	04
15	CTS	Cathepsin W	5.	6.	6.	5.	5.	5.	-1.	-0.	1.6	D	0.0	0.6
21	W		22	09	03	06	01	01	684	752	84	o	20	63
			11	74	34	77	39	39	254	11	25	w	28	32
			4	3	1	3	6	6	32		43	n	44	74
											2			04
53	GPR	G protein-coupled	3.	4.	4.	3.	3.	3.	-1.	-0.	1.6	D	0.0	0.6
83	84	receptor 84	54	59	13	24	37	61	604	682	04	o	35	63
1			88	03	82	17	18	75	451	08	45	w	41	32
			6	8		8	9	3	3		13	n	63	74
													81	04
31	HLA	Major	4.	4.	5.	5.	5.	6.	2.0	1.0	2.0	U	0.0	0.6
09	-DM	histocompatibility	00	98	28	99	04	25	085	061	08	p	49	63
	B	complex, class II,	57	10	5	11	22	68	114	266	51		35	32
		DM $\beta$	7	4		1	4	4	23	67	14		30	74
											23		86	04
17	DIO2	Deiodinase,	2.	3.	3.	6.	4.	3.	3.2	1.6	3.2	U	0.0	0.6
34		iodothyronine, type	73	72	01	14	57	79	064	809	06	p	22	63
		II	09	50	13	14	27	61	272	666	42		46	32
			7	8	3	4		4	33	67	72		74	74
											33		93	04
25	AMB	A-1-microglobulin/	5.	5.	6.	4.	4.	5.	-2.	-1.	2.0	D	0.0	0.6
9	P	bikunin precursor	56	70	15	50	33	43	069	049	69	o	13	63
			67	01	59	55	57	40	295	14	29	w	38	32
			6	4	3	4	9	8	959		59	n	06	74
											59		75	04
54	AFT	Aftiphilin	8.	8.	8.	7.	7.	7.	-1.	-0.	1.5	D	0.0	0.6
81	PH		55	05	25	52	63	81	547	629	47	o	12	63



2			88	29	13	28	50	57	379	826	37	w	14	32
			8		4	4	7	3	072	667	90	n	44	74
											72		59	04
78	CXC	Chemokine	5.	5.	5.	7.	7.	6.	3.6	1.8	3.6	U	0.0	0.6
52	R4	(C-X-C motif) receptor 4	39	12	79	65	72	57	731	770	73	p	00	63
			63	83	26	01	01	81	810	3	18		94	32
			1	2	8		6	4	3		10		67	74
											3		28	04
38	KLC	Kinesin light chain	5.	6.	5.	8.	6.	6.	2.1	1.1	2.1	U	0.0	0.6
31	1	1	59	47	83	03	95	25	623	126	62	p	45	63
			01	14	68	06	23	33	798	2	37		91	32
			6	3	4	2	5	2	9		98		15	74
											9		76	04
32	HOX	Homeobox D8	3.	3.	3.	5.	5.	4.	2.0	1.0	2.0	U	0.0	0.6
34	D8		83	66	95	03	49	02	499	355	49	p	21	63
			12	96	94	91	94	85	423	833	94		89	32
			9		3		2	5	44	33	23		14	74
											44		78	04
39	STM	Stathmin 1	4.	5.	5.	6.	5.	5.	1.7	0.8	1.7	U	0.0	0.6
25	N1		95	54	52	79	96	69	482	059	48	p	40	63
			29	77	86	18	51	00	400	033	24		24	32
				8	9	8	8	2	97	33	00		34	74
											97		72	04
10	BAI	BAI1-associated	8.	7.	7.	7.	7.	7.	-1.	-0.	1.5	D	0.0	0.6
45	AP2	protein 2	23	85	43	18	17	16	584	663	84	o	20	63
8			33	26	16	35	64	56	411	946	41	w	42	32
			4			8	9	3	048	667	10	n	75	74
											48		86	04
56	EMS	EMSY,	6.	5.	5.	5.	5.	5.	-1.	-0.	1.5	D	0.0	0.6

94	Y	BRCA2-interacting	12	98	84	04	03	89	580	659	80	o	39	63
6		transcriptional	18	54	51	35	74	17	005	93	00	w	21	32
		repressor	1	5	9		3	3	959		59	n	46	74
											59		3	04
71	TSPA	Tetraspanin 7	6.	7.	6.	7.	7.	6.	1.8	0.9	1.8	U	0.0	0.6
02	N7		34	01	58	85	95	88	843	140	84	p	26	63
			34	45	68	09	05	55	800	9	38		64	32
			6	3	3	8	7	4	98		00		75	74
											98		51	04
36	ISG2	Interferon	11	10	11	8.	10	10	-2.	-1.	2.6	D	0.0	0.6
69	0	stimulated	.2	.9	.1	34	.0	.7	697	431	97	o	34	63
		exonuclease gene	42	75	36	84	05	05	238	483	23	w	48	32
		20kda	32	51	12	3	12	95	944	333	89	n	01	74
											44		44	04
57	PLX	Plexin domain	3.	4.	4.	5.	4.	5.	1.6	0.7	1.6	U	0.0	0.6
12	DC1	containing 1	96	85	28	36	87	14	996	652	99	p	19	63
5			04	00	45	47	68	92	762	6	67		88	32
			9	2	2	4	2	5	83		62		61	74
											83		76	04
11	EFH	EF-hand domain	5.	5.	5.	4.	4.	5.	-1.	-0.	1.5	D	0.0	0.6
43	C1	(C-terminal)	39	51	61	53	99	11	549	632	49	o	13	63
27		containing 1	86	29	87	05	17	15	876	153	87	w	60	32
			7	1	8	7	9	4	578	333	65	n	65	74
											78		75	04
50	COP	COP9 signalosome	5.	5.	5.	6.	5.	6.	1.7	0.8	1.7	U	0.0	0.6
81	S7A	subunit 7A	58	01	56	65	65	30	592	149	59	p	28	63
3			43	22	9	06	43	54	493	6	24		34	32
			4	1		4	9		74		93		24	74
											74		75	04

85	TSLP	Thymic stromal lymphopoietin	2.45716	3.6942	2.8897	5.9095	4.1664	5.3027	4.3248	2.1125	4.3248	U	0.0032	0.6632
33	TME	Transmembrane protein 119	6.06708	6.66256	6.62751	7.7374	6.8519	6.6964	1.6938	0.7603	1.693	U	0.04432	0.6632
57	PLE	Pleckstrin	7.30656	7.2662	6.9391	5.9862	6.6515	6.658	-1.631	-0.706	1.638	D	0.02363	0.632
47	KHH	homology, myth4 and FERM domain containing H1	30656	2662	9391	9862	6515	7558	631384	706096	3138	o	2363	32
80	BHL	Basic	4.26271	4.5424	4.6597	4.0179	3.7156	3.9734	-1.501	-0.585	1.501	D	0.007737	0.6632
82	HB9	helix-loop-helix domain containing, class B, 9	271	249	974	799	569	349	030543	953333	0305	w	7737	32
84	FAM	Family with	9.58046	9.31676	8.65104	8.8055	8.8054	8.801	-1.753	-0.810	1.753	D	0.047800	0.6632
33	195A	sequence similarity 195 member A	58046	31676	65104	14055	00284	97481	753235	81002	5323	o	478000	63
44	FAM	Family with	5.02322	5.88928	5.5375	6.8610	6.649	5.8418	1.7933	0.8426	1.793	U	0.03520	0.6632
11	26F	sequence similarity 26 member F	02322	88928	5375	8610	2749	8418	933163	4263	9331	p	352047	63



19	RILP	Rab interacting	4.	4.	4.	5.	5.	4.	1.5	0.6	1.5	U	0.0	0.6
63	L2	lysosomal	18	29	49	20	05	65	700	507	70	p	10	63
83		protein-like 2	05	31	26	88	91	07	313	933	03		43	32
			2		9	4	5		14	33	13		71	74
											14		64	04
69	TBX	T-box 3	3.	4.	4.	5.	5.	4.	2.6	1.3	2.6	U	0.0	0.6
26	3		51	20	09	74	48	76	341	973	34	p	02	63
			76	11	16	9	79	56	667	466	16		27	32
			8	8	8		3	5	35	67	67		72	74
											35		54	04
25	ZNF	Zinc finger protein	6.	6.	6.	5.	5.	5.	-1.	-0.	1.5	D	0.0	0.6
60	549	549	32	07	18	59	48	72	510	594	10	o	06	63
51			53	44	92	46	16	89	036	583	03	w	95	32
			6	1	6	9	7	2	407	333	64	n	09	74
											07		51	04
55	PLC	Phosphatidylinosit	8.	8.	7.	6.	6.	7.	-2.	-1.	2.2	D	0.0	0.6
34	XD1	ol-specific	52	15	37	52	59	45	235	160	35	o	15	63
4		phospholipase C, X	23	80	95	11	91	69	979	906	97	w	92	32
		domain containing	6	5	4	1	3	9	043	667	90	n	49	74
		1									43		14	04
22	FAM	Family with	3.	3.	4.	6.	6.	4.	4.1	2.0	4.1	U	0.0	0.6
09	13C	sequence similarity	51	99	74	64	94	77	143	406	14	p	10	63
65		13 member C	15	35	19	73	17	99	656	7	36		75	32
			9			2	1	7	1		56		52	74
											1		75	04
56	PCD	Protocadherin $\alpha$ 6	7.	7.	6.	6.	6.	6.	-1.	-0.	1.5	D	0.0	0.6
14	HA6		44	73	91	53	83	80	557	639	57	o	31	63
2			20	45	29	69	18	31	526	256	52	w	81	32
			9	2	9		2	1	454	667	64	n	64	74

												54		86	04
12 90	COL 5A2	Collagen, type V, $\alpha$ 2	3. 57 45 4	4. 48 23 2	4. 41 90 2	7. 71 59 5	5. 53 73 4	5. 13 95 2	3.9 239 590 89	1.9 723 1 90	3.9 23 95 90 89	U p	0.0 19 83 52 31	0.6 63 32 74 04	
74 32	VIP	Vasoactive intestinal peptide	3. 35 04 4	3. 88 80 2	3. 52 23 6	4. 33 64 2	5. 95 54 3	5. 47 83 1	3.1 816 607 19	1.6 697 8 66 07 19	3.1 81 66 07 19	U p	0.0 04 10 92 7	0.6 63 32 74 04	
64 77 8	FND C3B	Fibronectin type III domain containing 3B	4. 58 36 1	4. 24 92 4	4. 51 22 9	5. 78 39 2	4. 74 55 1	4. 92 08 5	1.6 264 351 88	0.7 017 133 33	1.6 26 43 51 88	U p	0.0 42 13 65 61	0.6 63 32 74 04	
20 06	ELN	Elastin	6. 60 12 1	8. 50 17 3	7. 42 38 4	11 .4 27 04	9. 05 82 3	8. 16 15 8	4.1 125 218 2	2.0 400 233 33	4.1 12 52 18 2	U p	0.0 48 54 25 76	0.6 63 32 74 04	
69 09	TBX 2	T-box 2	5. 20 30 2	5. 76 45 4	4. 68 12 7	7. 31 22 1	6. 65 71 4	5. 96 31 2	2.6 905 106 17	1.4 278 8 06 17	2.6 90 51 06 17	U p	0.0 09 25 47 95	0.6 63 32 74 04	
84 28 1	C2orf 88	Chromosome 2 open reading frame 88	5. 19 06	3. 92 98	3. 62 93	5. 93 70	6. 34 49	5. 33 31	3.0 776 233	1.6 218 166	3.0 77 62	U p	0.0 08 04	0.6 63 32	

				4	5	9	8	7	2	67	33		42	74
											2		84	04
51	EGF	EGF-like-domain,	5.	5.	5.	6.	6.	5.	2.0	1.0	2.0	U	0.0	0.6
16	L7	multiple 7	55	31	60	88	80	89	496	353	49	p	08	63
2			89	45	70	13	84	69	629	866	66		27	32
			8	9	1	2	6	6	17	67	29		51	74
											17		77	04
38	C11o	Chromosome 11	7.	9.	7.	10	10	9.	4.7	2.2	4.7	U	0.0	0.6
77	r96	open reading frame	20	33	01	.4	.3	48	505	480	50	p	08	63
63		96	78	28	23	42	71	37	569	966	55		57	32
			5	7	5	24	41	1	61	67	69		06	74
											61		29	04
40	MIR	Microrna 21	9.	8.	9.	10	10	9.	2.0	1.0	2.0	U	0.0	0.6
69	21		81	77	39	.2	.8	97	174	125	17	p	17	63
91			46	82	82	09	41	72	878	6	48		46	32
			3	1	3	91	61	3	71		78		53	74
											71		2	04
19	EGR	Early growth	8.	6.	7.	9.	10	10	6.3	2.6	6.3	U	0.0	0.6
58	1	response 1	31	26	86	50	.8	.0	213	602	21	p	02	63
			38	16	60	84	46	67	089	233	30		29	32
			7	2	7	1	37	45	76	33	89		55	74
											76		08	04
20	TME	TMEM51	7.	6.	5.	5.	5.	6.	-1.	-0.	1.8	D	0.0	0.6
01	M51-	antisense RNA 1	11	31	98	12	69	03	806	853	06	o	45	63
97	AS1		57	62	90	78	59	75	545	233	54	w	26	32
			1	4	5	1	4	5	177	333	51	n	87	74
											77		12	04
34	IGH	Immunoglobulin	8.	9.	8.	9.	11	11	5.1	2.3	5.1	U	0.0	0.6
94	A2	heavy constant $\alpha$ 2	49	04	21	41	.8	.5	298	589	29	p	06	63

		(A2m marker)	73 6	95 4	78 7	80 9	59 83	63 57	145 33	066 67	81 45 33		85 66 94	32 74 04
55 31 4	TME M14 4	Transmembrane protein 144	7. 96 17 8	7. 65 44 1	7. 56 00 5	6. 70 88 1	7. 05 13 5	7. 56 89 6	-1. 532 308 375	-0. 615 706 667	1.5 32 30 83 75	D o w n	0.0 43 95 40 49	0.6 63 32 74 04
43 27	MMP 19	Matrix metallopeptidase 19	3. 04 94 2	3. 45 92 1	3. 29 34 3	4. 57 05 6	4. 05 60 3	3. 43 55 2	1.6 857 025 63	0.7 533 5 63	1.6 85 70 25 63	U p	0.0 31 53 91 23	0.6 63 32 74 04
28 40 76	TTL L6	Tubulin tyrosine ligase like 6	6. 34 33 5	6. 39 33 9	6. 76 38 7	5. 25 62 5	5. 41 99 6	5. 99 71 1	-1. 921 762 43	-0. 942 43 43	1.9 21 76 24 3	D o w n	0.0 05 76 32 45	0.6 63 32 74 04
15 45	CYP 1B1	Cytochrome P450, family 1, subfamily B, polypeptide 1	11 .2 25 1	9. 28 62 2	9. 76 76 5	7. 38 69 5	7. 87 65 4	9. 36 03 2	-3. 693 623 117	-1. 885 036 667	3.6 93 62 31 17	D o w n	0.0 21 82 70 58	0.6 63 32 74 04
96 49	RAL GPS1	Ral GEF with PH domain and SH3 binding motif 1	8. 24 49 6	7. 69 04 5	8. 09 08 9	7. 21 72 8	7. 19 05 7	7. 84 21 7	-1. 507 432 428	-0. 592 093 333	1.5 07 43 24 28	D o w n	0.0 46 65 39 49	0.6 63 32 74 04
53	PLC	Phospholipase C, $\gamma$	9.	9.	8.	7.	7.	8.	-2.	-1.	2.1	D	0.0	0.6



36	G2	2 (phosphatidylinosit ol-specific)	21 99 2	03 10 2	90 06 6	33 67 6	51 48 4	96 68 933	160 052 667	111 066 667	60 05 29 33	o w n	32 72 48 53	63 32 74 04
23 55	FOS L2	FOS-like antigen 2	6. 92 65	6. 44 52 3	6. 97 75 9	7. 56 70 1	8. 20 48 8	7. 32 24 5	1.8 855 777 85	0.9 150 066 67	1.8 85 57 77 85	U p	0.0 12 36 35 86	0.6 63 32 74 04
28 65 27	TMS B15B	Thymosin $\beta$ 15B	3. 39 12 2	4. 44 22 7	3. 88 27	5. 83 00 5	4. 77 53 4	4. 26 12 6	2.0 707 499 21	1.0 501 533 33	2.0 70 74 99 21	U p	0.0 45 77 42 45	0.6 63 32 74 04
14 76 85	C19o rf18	Chromosome 19 open reading frame 18	4. 75 41 2	5. 57 31 2	4. 57 31 9	3. 84 75 6	4. 07 24 6	4. 58 99 1	-1. 737 307 744	-0. 796 853 333	1.7 37 30 77 44	D o w n	0.0 36 68 61 63	0.6 63 32 74 04
25 96	GAP 43	Growth associated protein 43	4. 10 62 1	4. 69 17 6	4. 57 84	8. 57 73 2	7. 55 33 2	4. 58 69 3	5.4 530 624 08	2.4 470 666 67	5.4 53 06 24 08	U p	0.0 32 95 28 59	0.6 63 32 74 04
51 47 7	ISYN A1	Inositol-3-phosphat e synthase 1	5. 74 15 3	5. 99 80 7	6. 04 12 8	6. 84 35 6	6. 95 17 6	6. 21 89 62	1.6 753 083 62	0.7 444 266 67	1.6 75 30 83 62	U p	0.0 14 98 39 03	0.6 63 32 74 04

28	C3orf	Chromosome 3	4.	6.	4.	8.	6.	6.	3.3	1.7	3.3	U	0.0	0.6
53	70	open reading frame	07	16	92	08	21	08	380	390	38	p	38	63
82		70	47	31	43	69	02	20	679	133	06		52	32
				6	9	9	9	1	75	33	79		72	74
											75		04	04
19	MYR	Myelin regulatory	6.	6.	6.	4.	4.	4.	-3.	-1.	3.5	D	5.2	0.2
64	FL	factor-like	20	43	44	13	76	69	556	830	56	o	66	28
46			02	94	49	51	35	48	323	386	32	w	86	66
			7	5	4	3		7	752	667	37	n	E-0	37
											52		5	82
42	MEO	Mesenchyme	2.	3.	3.	5.	5.	3.	2.9	1.5	2.9	U	0.0	0.6
22	X1	homeobox 1	84	10	99	47	64	47	167	443	16	p	36	63
			77	93	94	41	38	17	936	833	79		46	32
			6	8	5	5	7	2	65	33	36		18	74
											65		69	04
57	EPB4	Erythrocyte	7.	6.	6.	4.	5.	6.	-2.	-1.	2.7	D	0.0	0.6
66	1L5	membrane protein	38	68	73	55	49	36	763	466	63	o	14	63
9		band 4.1 like 5	40	97	17	14	05	41	449	47	44	w	13	32
			7		5	5		6	024		90	n	52	74
											24		34	04
76	ZNF	Zinc finger protein	6.	6.	6.	5.	5.	6.	-1.	-0.	1.6	D	0.0	0.6
96	137P	137, pseudogene	90	55	23	58	69	25	642	716	42	o	26	63
			51	56	01	50	80	98	659	033	65	w	76	32
			9	9	3	2	8	1	355	333	93	n	96	74
											55		07	04
70	TIE1	Tyrosine kinase	4.	4.	4.	6.	7.	4.	3.1	1.6	3.1	U	0.0	0.6
75		with	08	87	61	68	08	78	636	615	63	p	23	63
		immunoglobulin-li	40	73	38	20	91	87	353	833	63		96	32
		ke and EGF-like	5	7	6	8	9	6	79	33	53		15	74

		domains 1									79		57	04
17	NQO	NAD(P)H	11	12	11	10	11	11	-1.	-0.	1.9	D	0.0	0.6
28	1	dehydrogenase,	.8	.0	.8	.0	.3	.5	918	940	18	o	38	63
		quinone 1	66	74	13	72	55	05	967	33	96	w	92	32
			23	78	93	76	29	9	13		71	n	25	74
											3		64	04
39	COL	Colorectal cancer	7.	7.	7.	6.	6.	7.	-1.	-0.	1.5	D	0.0	0.6
99	CA1	associated 1	71	30	38	40	80	26	563	644	63	o	36	63
48			55	62	77	90	28	31	576	85	57	w	82	32
			9		7	1	3	7	709		67	n	09	74
											09		11	04
97	PTD	Phosphatidylserine	5.	5.	5.	6.	5.	6.	1.6	0.7	1.6	U	0.0	0.6
91	SS1	synthase 1	10	08	73	46	55	05	455	185	45	p	42	63
			38	47	52	91	63	38	197	433	51		47	32
			3	4	1	3	9	9	4	33	97		06	74
											4		12	04
85	DIX	DIX domain	5.	6.	6.	8.	7.	6.	2.6	1.4	2.6	U	0.0	0.6
45	DC1	containing 1	81	70	44	58	67	91	485	051	48	p	14	63
8			87	09	25	78	90	08	021	766	50		94	32
			1	3	7	7	6	1	26	67	21		38	74
											26		33	04
53	BCL	B-cell	6.	6.	6.	5.	5.	6.	-1.	-0.	1.5	D	0.0	0.6
33	11A	CLL/lymphoma	39	40	72	40	84	28	585	665	85	o	33	63
5		11A (zinc finger	73	44	35	03	18	79	648	073	64	w	18	32
		protein)	5	6		2	1	6	871	333	88	n	64	74
											71		98	04
91	NMI	N-myc and STAT	5.	4.	5.	6.	5.	5.	1.6	0.6	1.6	U	0.0	0.6
11		interactor	07	43	18	01	15	60	193	954	19	p	47	63
			36	33	51	67	56	59	595	233	35		33	32

				2	6	4	9	2	36	33	95		43	74
											36		02	04
84 25	LTBP 4	Latent transforming growth factor $\beta$ binding protein 4	6. 73 31 7	7. 50 89 6	7. 50 66 2	8. 87 36 6	8. 60 44 2	8. 02 92 5	2.3 831 338 77	1.2 528 6	2.3 83 13 38 77	U p	0.0 04 40 91 32	0.6 63 32 74 04
64 17 00	ECS CR	Endothelial cell surface expressed chemotaxis and apoptosis regulator	4. 61 15 7	4. 89 91 7	5. 00 50 7	6. 19 59 9	6. 96 86 5	5. 23 18 8	2.4 513 786 28	1.2 935 933 33	2.4 51 37 86 28	U p	0.0 16 38 62 86	0.6 63 32 74 04
84 07	TAG LN2	Transgelin 2	7. 98 11 6	7. 87 09 7	8. 68 28	9. 48 3 24	9. 12 24	8. 72 21 4	1.9 064 252 97	0.9 308 7	1.9 06 42 52 97	U p	0.0 14 29 30 84	0.6 63 32 74 04
37 64	KCN J8	Potassium channel, inwardly rectifying subfamily J, member 8	3. 25 74 9	4. 29 34 4	3. 40 87 8	4. 84 77 5	4. 81 82 6	4. 42 63	2.0 622 225 03	1.0 442	2.0 62 22 25 03	U p	0.0 08 25 05 36	0.6 63 32 74 04
90 95 2	ESA M	Endothelial cell adhesion molecule	5. 85 25 4	6. 59 79 7	6. 56 52 6	7. 65 70 8	8. 10 47 2	6. 60 02 5	2.1 665 907 5	1.1 154 266 67	2.1 66 59 07 5	U p	0.0 29 12 66 61	0.6 63 32 74 04
10 20	INA DL	Inad-like (Drosophila)	7. 26	7. 06	7. 39	6. 01	6. 47	7. 08	-1. 641	-0. 715	1.6 41	D o	0.0 38	0.6 63

7			80	27	63	80	87	54	490	006	49	w	51	32
			8	8	6	3	5	2	803	667	08	n	91	74
											03		66	04
56	NXF	Nuclear RNA	8.	8.	8.	6.	7.	7.	-2.	-1.	2.2	D	0.0	0.6
00	3	export factor 3	25	49	24	06	98	35	293	197	93	o	33	63
0			20	84	83	17	63	73	869	783	86	w	38	32
			1		9	7	8		525	333	95	n	24	74
											25		09	04
35	IL3R	Interleukin 3	4.	5.	4.	5.	6.	4.	1.8	0.9	1.8	U	0.0	0.6
63	A	receptor, $\alpha$ (low affinity)	52	15	39	88	09	81	814	118	81	p	43	63
			45	03	02	61	56	88	391	366	43		39	32
			5	8		1	4	9	98	67	91		76	74
											98		54	04
92	MSC	Musculin	4.	4.	4.	5.	4.	4.	1.7	0.8	1.7	U	0.0	0.6
42			21	67	00	56	94	87	761	287	76	p	13	63
			79	01	47	59	19	12	827	8	18		86	32
				2	5	4	7		17		27		68	74
											17		58	04
22	RHO	Rho-related BTB	4.	5.	5.	7.	7.	5.	3.0	1.6	3.0	U	0.0	0.6
83	BTB	domain containing	95	46	44	68	12	86	346	015	34	p	09	63
6	3	3	36	45	99	16	87	23	777	433	67		00	32
			8	4	3	5	7	6	65	33	77		41	74
											65		56	04
35	IGH	Immunoglobulin	6.	6.	7.	7.	9.	10	4.7	2.2	4.7	U	0.0	0.6
07	M	heavy constant mu	67	66	50	34	84	.3	094	355	09	p	20	63
			26	09	02	03	44	55	328	533	43		09	32
			4	2		6	3	63	65	33	28		19	74
											65		67	04
97	FAM	Family with	3.	3.	3.	4.	4.	4.	1.9	0.9	1.9	U	0.0	0.6

50	65B	sequence similarity 65 member B	52 06 6	35 94 7	89 87 2	87 45 2	70 23 4	15 3	774 894 53	836 7	77 48 94 53	p	03 72 62 41	63 32 74 04
10 35 1	ABC A8	ATP binding cassette subfamily A member 8	6. 59 44 6	6. 97 30 2	7. 82 84 4	8. 78 69 2	8. 31 05 2	7. 81 51	2.2 535 508 44	1.1 722	2.2 53 55 08 44	U p	0.0 16 44 49 48	0.6 63 32 74 04
31 2	ANX A13	Annexin A13	12 .2 40 38	12 .0 54 6	12 .1 94 28	10 .5 27 11	11 .6 13 55	11 .8 09 49	-1. 797 971 31	-0. 846 37	1.7 97 97 13 1	D o w n	0.0 36 89 47 54	0.6 63 32 74 04
63 83	SDC 2	Syndecan 2	3. 69 49 6	4. 00 16 5	4. 30 38 5	6. 63 07 3	4. 71 46 6	5. 47 77 6	3.0 474 023 66	1.6 075 8	3.0 47 40 23 66	U p	0.0 09 85 32 52	0.6 63 32 74 04
62 36	RRA D	Ras-related associated with diabetes	5. 77 70 7	5. 49 40 4	5. 23 41 9	6. 90 33 9	6. 44 79 9	5. 83 52 33	1.8 580 122 33	0.8 937 6	1.8 58 01 22 33	U p	0.0 19 38 09 07	0.6 63 32 74 04
86 54	PDE 5A	Phosphodiesterase 5A	7. 80 42 1	7. 57 65 2	8. 16 2	8. 99 75 6	8. 84 61 5	8. 05 30 1	1.7 226 902 66	0.7 846 633 33	1.7 22 69 02 66	U p	0.0 30 32 04 96	0.6 63 32 74 04

25	KAN	KN motif and	4.	5.	4.	5.	5.	5.	1.5	0.6	1.5	U	0.0	0.6
69	K3	ankyrin repeat	47	14	79	43	65	23	561	380	56	p	21	63
49		domains 3	25	75	06	19	78	50	811	1	18		62	32
			3	3	9		3	5	4		11		45	74
											4		22	04
54	ROB	Roundabout	6.	7.	7.	8.	8.	7.	2.3	1.2	2.3	U	0.0	0.6
53	O4	guidance receptor 4	31	85	50	71	85	84	762	487	76	p	26	63
8			43	21	85	92	38	81	830	066	28		60	32
			3	5	7	4		3	08	67	30		32	74
											08		16	04
21	ETS1	V-ets avian	6.	7.	7.	9.	9.	7.	2.5	1.3	2.5	U	0.0	0.6
13		erythroblastosis	71	59	71	16	09	86	795	671	79	p	14	63
		virus E26	98	18	51	59	98	25	629	266	56		05	32
		oncogene homolog	8	5	9		3	7	73	67	29		97	74
		1									73		99	04
10	FER	Fermitin family	4.	4.	4.	6.	5.	5.	1.8	0.8	1.8	U	0.0	0.6
97	MT2	member 2	44	53	87	12	04	35	573	932	57	p	18	63
9			49	44	06	98	27	70	169	2	31		50	32
			1	7	2	5	7	4	1		69		80	74
											1		95	04
48	NPR	Natriuretic peptide	5.	5.	5.	6.	8.	7.	3.2	1.7	3.2	U	0.0	0.6
83	3	receptor 3	69	92	41	62	27	28	792	133	79	p	03	63
			33	92	26	32	09	10	820	8	28		79	32
			6			9	3	8	66		20		72	74
											66		39	04
58	MS4	Membrane-spanning	5.	6.	6.	8.	7.	7.	2.2	1.1	2.2	U	0.0	0.6
47	A7	g 4-domains,	96	74	46	06	47	14	391	629	39	p	06	63
5		subfamily A,	71	91	71	00	01	20	223	333	12		09	32
		member 7	9	2	4	5	5	5	05	33	23		22	74

											05		76	04
56 63	PSE N1	Presenilin 1	9. 91 89 5	9. 76 75 9	9. 43 88 5	8. 83 6	9. 10 56 2	9. 20 46 6	-1. 579 757 739	-0. 659 703 333	1.5 79 75 77 39	D o w n	0.0 10 40 03 18	0.6 63 32 74 04
31 13	HLA -DPA 1	Major histocompatibility complex, class II, DP $\alpha$ 1	8. 49 90 1	9. 09 00 6	9. 17 42	10. .1 80 08	9. 60 6 2	9. 76 02 86	1.9 022 101 86	0.9 276 766 67	1.9 02 21 01 86	U p	0.0 06 89 59 31	0.6 63 32 74 04
23 27	FMO 2	Flavin containing monooxygenase 2	4. 05 29 2	4. 53 01 7	4. 85 33	5. 72 96 1	5. 28 46 1	4. 98 81 2	1.8 091 558 15	0.8 553 166 67	1.8 09 15 58 15	U p	0.0 15 87 13 07	0.6 63 32 74 04
36 80	ITG A9	Integrin $\alpha$ 9	2. 67 88 9	5. 16 34 1	3. 72 85 9	7. 16 16 8	4. 98 07 5	5. 10 36 2	3.7 107 736 45	1.8 917 2 45	3.7 10 77 36 45	U p	0.0 44 10 40 72	0.6 63 32 74 04
46 64	NAB 1	NGFI-A binding protein 1	6. 33 15 5	5. 78 54 9	6. 16 49 8	7. 78 50 9	7. 01 45 5	6. 36 86 6	1.9 481 345 65	0.9 620 933 33	1.9 48 13 45 65	U p	0.0 31 94 84 38	0.6 63 32 74 04
57 47 4	ZNF 490	Zinc finger protein 490	5. 46 30	5. 72 11	5. 51 10	4. 98 07	4. 39 23	5. 16 55	-1. 645 934	-0. 718 906	1.6 45 93	D o w	0.0 15 89	0.6 63 32



			6	4	7		5		205	667	42	n	03	74
											05		44	04
22	ADG	Adhesion G	4.	5.	6.	7.	8.	6.	4.8	2.2	4.8	U	0.0	0.6
13	RF5	protein-coupled	46	30	14	87	42	47	747	853	74	p	06	63
95		receptor F5	53	97	61	53	79	40	784	366	77		01	32
			5	5	2	2		1	98	67	84		35	74
											98		84	04
57	THO	THO complex 2	7.	7.	6.	6.	6.	6.	-1.	-0.	1.5	D	0.0	0.6
18	C2		36	29	98	42	85	53	524	607	24	o	15	63
7			16	18	96	53	53	87	007	87	00	w	07	32
			9		1	4	6	9	497		74	n	84	74
											97		68	04
11	MST	Macrophage	7.	5.	6.	4.	4.	6.	-3.	-1.	3.1	D	0.0	0.6
22	IL	stimulating 1-like	83	90	13	57	20	19	104	634	04	o	44	63
3			79	32	64	05	38	99	670	44	67	w	13	32
			7	9		6	3	5	15		01	n	69	74
											5		92	04
64	SMI	Small integral	3.	4.	4.	6.	6.	5.	4.4	2.1	4.4	U	0.0	0.6
45	M10	membrane protein	76	53	30	87	83	31	154	425	15	p	01	63
38		10	9	05	57	57	83	88	077	466	40		88	32
				7	7	8	2	8	32	67	77		41	74
											32		46	04
71	CLD	Claudin 5	5.	6.	6.	8.	8.	6.	2.6	1.4	2.6	U	0.0	0.6
22	N5		82	36	41	13	14	52	402	006	40	p	17	63
			49	09	73	40	97	15	599	8	25		62	32
			2	7	7	4	2	4	89		99		51	74
											89		86	04
22	FHL	Four and a half	4.	6.	5.	8.	6.	6.	4.1	2.0	4.1	U	0.0	0.6
73	1	LIM domains 1	16	00	74	36	70	98	365	484	36	p	11	63

			66	21	94	88	83	62	556	3	55		04	32
			5	6	2	6	9	7	75		56		23	74
											75		68	04
11	C1Q	C1q and tumor	3.	4.	3.	7.	4.	4.	3.8	1.9	3.8	U	0.0	0.6
49	TNF	necrosis factor	07	56	76	52	84	82	096	296	09	p	39	63
05	7	related protein 7	39	93	09	57	26	48	188	466	61		09	32
			5	5	9	8	5		57	67	88		74	74
											57		71	04
57	HEG	Heart development	5.	7.	6.	9.	8.	7.	3.5	1.8	3.5	U	0.0	0.6
49	1	protein with	91	36	78	88	33	37	950	459	95	p	25	63
3		EGF-like domains	11	62	33	51	57	78	038	933	00		33	32
		1	3	8	2	5	1	5	94	33	38		43	74
											94		46	04
13	PAC	PARK2	5.	5.	5.	4.	4.	5.	-1.	-0.	1.8	D	0.0	0.6
51	RG	co-regulated	87	70	77	53	93	14	887	916	87	o	02	63
38			31	71	82	05	38	51	268	3	26	w	11	32
			1		7	7	9	2	908		89	n	30	74
											08		64	04
49	OGN	Osteoglycin	3.	5.	5.	7.	5.	6.	2.9	1.5	2.9	U	0.0	0.6
69			97	74	57	87	98	13	605	658	60	p	44	63
			95	51	00	40	80	02	050	433	50		06	32
			6	9	7	5	4	6	88	33	50		54	74
											88		83	04
37	PNP	Patatin like	7.	8.	7.	7.	7.	7.	-1.	-0.	1.5	D	0.0	0.6
57	LA7	phospholipase	95	30	68	22	39	32	588	667	88	o	11	63
75		domain containing	67	51	77	69	52	55	105	306	10	w	39	32
		7	7	5	4	4	5	5	402	667	54	n	75	74
											02		44	04
27	DKK	Dickkopf WNT	5.	7.	6.	10	8.	7.	4.9	2.3	4.9	U	0.0	0.6

12	3	signaling pathway	59	48	33	.2	13	94	623	110	62	p	14	63
2		inhibitor 3	99	47	92	78	69	16	838	333	38		29	32
			7	4	5	53		3	45	33	38		58	74
											45		97	04
23	FOS	FBJ murine	5.	5.	6.	7.	10	8.	8.6	3.1	8.6	U	0.0	0.6
54	B	osteosarcoma viral	99	46	04	94	.1	72	902	194	90	p	00	63
		oncogene homolog	76	22	61	62	93	49	639		26		64	32
		B	8	2	6	5	02	9	69		39		06	74
											69		89	04
81	CAL	Calumenin	5.	4.	5.	7.	5.	5.	2.2	1.1	2.2	U	0.0	0.6
3	U		43	57	57	19	94	86	066	418	06	p	30	63
			42	40	05	51	31	61	686	7	66		99	32
			4	9	8	9	4	9	3		86		21	74
											3		47	04
96	GNA	Guanine nucleotide	2.	3.	3.	5.	3.	3.	2.1	1.1	2.1	U	0.0	0.6
30	14	binding protein (G	69	56	32	04	89	96	561	084	56	p	17	63
		protein), $\alpha$ 14	52	24	34	51	65	49	586	633	15		07	32
			2	8	8		2	5	47	33	86		56	74
											47		69	04
28	IGK	Immunoglobulin $\kappa$	5.	4.	5.	6.	9.	8.	6.6	2.7	6.6	U	0.0	0.6
93	V1-2	variable 1-27	42	89	48	01	11	90	900	420	90	p	09	63
5	7		99	86	02	56	58	33	175	1	01		79	32
			9	3	1	4	5	7	71		75		54	74
											71		34	04
12	FRM	FERM domain	4.	5.	4.	7.	6.	6.	3.4	1.8	3.4	U	0.0	0.6
27	D6	containing 6	26	69	77	47	30	37	940	049	94	p	04	63
86			86	12	52	37	37	24	978	2	09		91	32
			1	5	7	1	5	3	24		78		68	74
											24		68	04

78	COL	Collectin	6.	8.	6.	9.	9.	9.	3.7	1.9	3.7	U	0.0	0.6
98	EC11	subfamily member	64	44	83	44	01	19	667	133	66	p	04	63
9		11	16	16	24	23	81	53	840	333	78		30	32
			6	6	8	7	1	2	7	33	40		59	74
											7		79	04
34	IFI16	Interferon,	6.	6.	7.	7.	8.	7.	1.7	0.8	1.7	U	0.0	0.6
28		$\gamma$ -inducible protein	64	74	40	85	16	26	790	311	79	p	28	63
		16	06	51	78	48	67	54	577	133	05		75	32
			8	7	6	7	7	1	38	33	77		47	74
											38		32	04
52	SER	Serpin peptidase	6.	7.	6.	5.	5.	6.	-1.	-0.	1.6	D	0.0	0.6
70	PINE	inhibitor, clade E	41	11	47	66	70	46	648	721	48	o	44	63
	2	(nexin,	04	51	40	69	42	40	872	48	87	w	00	32
		plasminogen	6	8	6		7	9	676		26	n	25	74
		activator inhibitor									76		42	04
		type 1), member 2												
79	ERM	Endoplasmic	10	10	10	8.	9.	9.	-1.	-0.	1.6	D	0.0	0.6
95	P1	reticulum	.4	.2	.0	82	99	76	686	753	86	o	45	63
6		metallopeptidase 1	60	93	92	83	54	07	353	906	35	w	38	32
			09	57	72	9	8	9	12	667	31	n	85	74
											2		86	04
56	PCD	Protocadherin $\alpha$ 13	7.	7.	6.	6.	6.	6.	-1.	-0.	1.5	D	0.0	0.6
13	HA1		44	73	91	53	83	80	557	639	57	o	31	63
6	3		20	45	29	69	18	31	526	256	52	w	81	32
			9	2	9		2	1	454	667	64	n	64	74
											54		86	04
56	PCD	Protocadherin $\alpha$ 4	7.	7.	6.	6.	6.	6.	-1.	-0.	1.5	D	0.0	0.6
14	HA4		44	73	91	53	83	80	557	639	57	o	31	63
4			20	45	29	69	18	31	526	256	52	w	81	32

			9	2	9		2	1	454	667	64	n	64	74
											54		86	04
55	BTB	BTB (POZ)	6.	5.	5.	4.	5.	5.	-2.	-1.	2.0	D	0.0	0.6
72	D7	domain containing	50	39	95	47	17	08	055	039	55	o	14	63
7		7	74	02	98	98	45	41	757	67	75	w	66	32
			8		8	5	9	1	369		73	n	80	74
											69		11	04

Table SVI. DEGs in comparison VI.

En try	Gene symbol	Gene name	A 11 13 2	A 11 13 5	A 11 13 8	A 11 13 9	A 11 14 2	A 11 14 3	Fol d-c han ge	log FC	abs olu teF C	Re gu lat ion	P-v alu e	FD R
38 85 66	ZNF470	Zinc finger protein 470	4. 73 01	5. 22 61 6	5. 55 58 2	3. 62 37 5	3. 93 89	4. 82 12	-2. 060 141 359	-1. 042 743 333	2.0 60 14 13 59	D o w n	0.0 24 71 93 24	0.3 83 13 18 63
50 50 6	DUOX2	Dual oxidase 2	11. 0 39 7	7. 17 74 1	9. 99 73 9	4. 21 46 1	8. 20 12 9	5. 34 11 8	-11 .20 294 918	-3. 485 806 667	11. 20 29 49 18	D o w n	0.0 29 08 09 23	0.3 94 49 63 82
69 47	TCN1	Transcobalamin I	8. 66 44 3	9. 48 78 2	10. .1 54 6	3. 86 63 9	6. 30 29 9	7. 11 77 1	-12 .75 731 958	-3. 673 253 333	12. 75 73 19 58	D o w n	0.0 03 17 57 3	0.2 34 23 93 82
58 47 6	TP53I NP2	Tumor protein p53 inducible nuclear protein 2	8. 57 57	7. 74 26 3	7. 85 12 7	6. 70 56 2	7. 67 35	6. 58 79 2	-2. 095 827 531	-1. 067 52	2.0 95 82 75 31	D o w n	0.0 25 64 58 11	0.3 84 82 70 3
55 08 4	SOBP	Sine oculis binding protein homolog	5. 93 99 3	6. 19 87 1	6. 41 61 9	3. 52 77 9	4. 81 48 3	3. 79 60 2	-4. 403 742 156	-2. 138 73	4.4 03 74 21 56	D o w n	0.0 00 58 30 43	0.1 65 32 01 52
65 98 7	KCTD14	Potassium channel tetramerization domain containing 14	6. 56 54 9	8. 62 03 7	8. 64 64 5	3. 64 40 5	3. 83 58 3	5. 48 01 8	-12 .32 984 991	-3. 624 083 333	12. 32 98 49 91	D o w n	0.0 01 42 99 44	0.1 87 10 78 18
10 34 6	TRIM2	Tripartite motif containing 22	9. 64 4	9. 08 84	9. 44 96 3	5. 39 48 5	8. 78 09	7. 49 45 6	-4. 502 022 707	-2. 170 573 333	4.5 02 02 27 07	D o w n	0.0 27 77 76 45	0.3 91 45 80 68
10 05	HNRN PUL2-	HNRNPUL2-BSC L2 readthrough	7. 44	7. 92	7. 69	6. 65	6. 34	6. 86	-2. 094	-1. 066	2.0 94	D o	0.0 03	0.2 34

34 59 5	BSCL2	(NMD candidate)	39 1	17 2	99 7	62 6	63 1	25	844 756	843 333	84 47 56	w n	16 71 19	23 93 82
20 34 27	SLC25 A43	Solute carrier family 25, member 43	4. 53 71 1	4. 96 85	4. 82 80 6	5. 51 25 2	6. 08 77 1	7. 01 52 9	2.6 893 981 12	1.4 272 833 33	2.6 89 39 81 12	U p	0.0 08 06 25 1	0.2 99 13 95 54
53 60	PLTP	Phospholipid transfer protein	8. 95 80 9	8. 80 82 5	7. 57 00 9	5. 81 92 9	7. 77 55	6. 76 38 8	-3. 158 530 127	-1. 659 253 333	3.1 58 53 01 27	D o w n	0.0 23 66 53 56	0.3 81 10 09 72
10 48	CEAC AM5	Carcinoembryonic antigen-related cell adhesion molecule 5	2. 90 91 5	4. 78 49 5	5. 38 01 8	10 .6 77 56	11 .4 89 78	12 .3 99 11	143 .41 545 24	7.1 640 566 67	14 3.4 15 45 24	U p	2.0 60 62 E- 05	0.0 89 45 15 48
33 71	TNC	Tenascin C	5. 27 00 9	5. 15 77 3	5. 40 08 93	5. 87 19 4	8. 06 19 14	6. 37 14	2.8 180 033 63	1.4 946 733 33 63	2.8 18 00 33 63	U p	0.0 27 36 23 41	0.3 89 83 37 07
29 92 0	PYCR 2	Pyrroline-5-carbox ylate reductase family member 2	5. 16 62 9	5. 79 03	5. 54 06 3	7. 39 80 7	6. 81 91 6	5. 99 73	2.3 605 177 53	1.2 391 033 33	2.3 60 51 77 53	U p	0.0 14 72 39 13	0.3 47 51 10 24
13 05 74	LYPD6	LY6/PLAUR domain containing 6	8. 25 35 2	6. 85 38 8	7. 86 96 2	6. 90 19	6. 54 54 4	6. 34 05	-2. 089 358 418	-1. 063 06 84	2.0 89 35 84 18	D o w n	0.0 29 17 83 77	0.3 94 49 63 82
51 11 0	LACT B2	Lactamase $\beta$ 2	6. 10 00 3	5. 06 01	5. 34 22 5	6. 92 29 8	6. 82 72 5	6. 04 35 3	2.1 392 819 94	1.0 971 266 67	2.1 39 28 19 94	U p	0.0 20 09 07 93	0.3 70 24 86 67
28 32 19	KCTD 21	Potassium channel tetramerization domain containing 21	7. 29 81 2	6. 64 21 6	6. 59 63 1	5. 46 81 4	6. 10 45 8	5. 37 88 9	-2. 289 437 742	-1. 194 993 333	2.2 89 43 77 42	D o w n	0.0 05 91 47 33	0.2 79 42 28 73
10	GTF2I	General	7.	8.	8.	7.	6.	7.	-2.	-1.	2.1	D	0.0	0.2

0093631	P4	transcription factor iii, pseudogene 4	83213	52857	56697	3868	9157	25453	178819474	123546667	78819474	o w n	05285487	6846247
1373	CPS1	Carbamoyl-phosphate synthase 1	4.33046	4.58116	4.55213	4.66769	10.46137	9.80141	14.14519343	3.82224	14.14519343	U p	0.02998467	0.397944578
55799	CACNA2D3	Calcium channel, voltage-dependent, $\alpha$ 2/ $\Delta$ subunit 3	7.08439	5.68674	4.17955	3.04571	3.24361	4.39213	-4.256723358	-2.089743333	4.256723358	D o w n	0.02453909	0.383089258
275	AMT	Aminomethyltransferase	6.09108	6.67132	6.63612	5.98253	4.4771	5.67572	-2.146059387	-1.10169	2.146059387	D o w n	0.034629935	0.408423981
9235	IL32	Interleukin 32	8.05169	5.92376	6.08448	8.54678	8.60601	7.89194	3.163671927	1.661671927	3.163671927	U p	0.024190892	0.38258708
59084	ENPP5	Ectonucleotide pyrophosphatase/phosphodiesterase 5 (putative)	7.17305	6.67075	6.2358	5.16498	5.16886	6.32537	-2.20400824	-1.14013	2.20400824	D o w n	0.025445383	0.384426011
6286	S100P	S100 calcium binding protein P	5.84806	6.12302	6.91097	9.84056	7.98171	9.02831	6.3036055	2.656176667	6.3036055	U p	0.001281333	0.187107818
216	ALDH1A1	Aldehyde dehydrogenase 1 family member A1	10.2939	9.04638	8.71905	5.4857	7.74199	8.09062	-4.67674035	-2.22550333	4.67674035	D o w n	0.019440091	0.367664157
5284	PIGR	Polymeric immunoglobulin receptor	10.44617	11.85376	12.16181	5.66903	9.83153	10.25119	-7.48140892	-2.90331	7.48140892	D o w n	0.045856621	0.439135361



30 84 5	EHD3	EH domain containing 3	5. 15 09 8	6. 73 64 3	6. 54 02	4. 90 72 5	5. 15 78 8	5. 08 25 3	-2. 133 639 837	-1. 093 316 667	2.1 33 63 98 37	D o w n	0.0 36 32 71 18	0.4 13 67 97 96
39 98	LMAN 1	Lectin, mannose-binding, 1	5. 03 72 8	6. 24 19 6	5. 97 04 1	4. 84 17 2	5. 03 01 6	4. 11 47	-2. 125 334 617	-1. 087 69	2.1 25 33 46 17	D o w n	0.0 26 91 49 29	0.3 88 45 19 23
87 75	NAPA	N-ethylmaleimide- sensitive factor attachment protein, $\alpha$	9. 09 87	9. 64 88	9. 53 02 6	9. 03 33 8	8. 24 31 4	7. 02 22	-2. 507 656 951	-1. 326 34	2.5 07 65 69 51	D o w n	0.0 32 64 73 43	0.4 04 71 37 9
27 28 4	SULT1 B1	Sulfotransferase family 1B member 1	3. 26 11 6	4. 83 99 7	4. 26 10 2	9. 31 73 2	5. 35 88 7	5. 44 91 4	6.0 115 068 63	2.5 877 266 67	6.0 11 50 68 63	U p	0.0 45 87 97 52	0.4 39 13 53 61
70 25	NR2F1	Nuclear receptor subfamily 2 group F member 1	9. 32 64	9. 53 67 1	9. 60 35 7	6. 75 42	7. 52 65	7. 00 39 1	-5. 256 211 519	-2. 394 023 333	5.2 56 21 15 19	D o w n	4.0 82 3E -05	0.0 96 05 29 42
55 22 5	RAVE R2	Ribonucleoprotein , PTB-binding 2	6. 92 10 5	7. 76 59 6	8. 62 21 9	5. 96 25 2	7. 13 79 3	6. 09 5	-2. 586 946 109	-1. 371 25	2.5 86 94 61 09	D o w n	0.0 29 83 43 56	0.3 97 50 17 86
28 44 06	ZFP82	ZFP82 zinc finger protein	6. 87 23 7	6. 52 17	6. 51 10 1	4. 30 38 2	6. 12 59 1	5. 38 83 5	-2. 571 006 635	-1. 362 333 333	2.5 71 00 66 35	D o w n	0.0 19 42 01 26	0.3 67 66 41 57
57 13 9	RGL3	Ral guanine nucleotide dissociation stimulator-like 3	6. 78 34 6	7. 71 2	7. 41 74 7	6. 26 83 4	5. 06 84 9	6. 44 09 1	-2. 599 792 835	-1. 378 396 667	2.5 99 79 28 35	D o w n	0.0 15 13 13 3	0.3 48 67 95 47
58 49 9	ZNF46 2	Zinc finger protein 462	5. 16 37 2	5. 54 03 9	5. 86 51 9	3. 62 84 4	4. 04 67 5	4. 73 89 4	-2. 611 767 849	-1. 385 026 667	2.6 11 76 78	D o w n	0.0 04 38 39	0.2 50 46 95

												49		3	
55 57 8	SUPT2 0H	SPT20 homolog, SAGA complex component	5. 44 54 6	5. 38 84	5. 31 40 1	5. 46 76 8	6. 87 70 7	7. 94 06 2	2.6 011 807 76	1.3 791 666 67	2.6 01 18 07 76	U p	0.0 47 74 37 69	0.4 43 31 90 56	
35 7	SHRO OM2	Shroom family member 2	4. 76 62 2	5. 33 37 9	5. 61 25 8	2. 50 38 7	2. 98 54 7	4. 91 59 6	-3. 408 404 75	-1. 769 096 667	3.4 08 40 47 5	D o w n	0.0 23 36 69 25	0.3 80 85 39 85	
59 50	RBP4	Retinol binding protein 4	3. 71 94 3	4. 34 72 5	4. 10 46 1	4. 59 21 8	6. 35 17 5	5. 10 28 2	2.4 483 672 92	1.2 918 2	2.4 48 36 72 92	U p	0.0 24 39 22 78	0.3 82 66 40 12	
63 93 5	PCIF1	PDX1 C-terminal inhibiting factor 1	4. 68 84 7	3. 35 19 8	4. 31 60 8	5. 77 34 5	6. 42 83 1	5. 29 56 5	3.2 798 427 94	1.7 136 266 67	3.2 79 84 27 94	U p	0.0 05 16 88 14	0.2 66 23 90 84	
84 45	DYRK 2	Dual specificity tyrosine-(Y)-phos phorylation regulated kinase 2	4. 67 69 6	3. 82 94 6	3. 90 39 9	7. 94 56 6	5. 72 53 2	4. 70 54 2	3.9 686 912 59	1.9 886 633 33	3.9 68 69 12 59	U p	0.0 37 39 65 07	0.4 16 53 88 03	
86 35	RNAS ET2	Ribonuclease T2	9. 55 24 5	10 .4 29 61	10 .6 48 92	7. 26 96	9. 09 71 2	9. 58 82 3	-2. 945 835 084	-1. 558 676 667	2.9 45 83 50 84	D o w n	0.0 40 83 82 72	0.4 26 34 37 07	
71 0	SERPI NG1	Serpin peptidase inhibitor, clade G (C1 inhibitor), member 1	10 .4 73 36	8. 52 86 5	9. 29 72 3	6. 31 65	8. 73 95 7	7. 27 50 1	-3. 970 681 566	-1. 989 386 667	3.9 70 68 15 66	D o w n	0.0 26 88 04 07	0.3 88 38 41 04	
10 33	CDKN 3	Cyclin-dependent kinase inhibitor 3	5. 21 87 6	4. 09 23 1	4. 80 74 9	6. 67 18 7	7. 96 28 4	6. 52 92 5	5.0 928 268 45	2.3 484 666 67	5.0 92 82 68 45	U p	0.0 01 50 04 14	0.1 87 10 78 18	
21 98 54	TMEM 218	Transmembrane protein 218	5. 54 52	5. 22 41	5. 40 12	3. 89 59	4. 19 62	4. 73 96	-2. 162 869	-1. 112 946	2.1 62 86	D o w	0.0 03 69	0.2 38 59	

			6	2	8	5	5	2	569	667	95	n	28	85
33	ID2	Inhibitor of DNA binding 2, dominant negative helix-loop-helix protein	8.23711	8.84918	8.86974	7.35655	7.06276	7.0772	-2.80209655	-1.486506667	2.80209655	D	0.00658715	0.172631847
79	THSD4	Thrombospondin type 1 domain containing 4	8.52752	7.18644	7.33974	4.53711	6.78696	6.76309	-3.150352651	-1.655513333	3.150352651	D	0.04485911	0.435527714
26	BSCL2	Berardinelli-Seip congenital lipodystrophy 2 (seipin)	7.44391	7.92172	7.69997	6.65626	6.34631	6.8625	-2.094844756	-1.066843333	2.094844756	D	0.03167119	0.2349382
55	ZNF415	Zinc finger protein 415	5.25114	5.45495	5.28652	3.20697	4.18467	4.39236	-2.644270927	-1.40287	2.644270927	D	0.03533123	0.23766
10	LOC102723872	Putative protein FAM157B	8.27782	8.11345	7.66239	5.84476	5.87111	6.62628	-3.742070312	-1.903836667	3.742070312	D	0.0426253	0.163378734
34	IGF1R	Insulin like growth factor 1 receptor	5.65891	6.49335	6.25641	5.4463	5.01632	4.80537	-2.066076013	-1.046893333	2.066076013	D	0.066680498	0.313660293
23	FRMD4B	FERM domain containing 4B	8.1092	7.78426	8.08516	7.75006	5.81557	7.01529	-2.192484535	-1.132566667	2.192484535	D	0.048384549	0.44483505
80	ULBP2	UL16 binding protein 2	5.41502	5.18697	4.64681	6.32896	5.96492	7.31171	2.7363728	1.4522633	2.7363728	U	0.07987247	0.29913954
48	NOTCH2	Notch 2	7.77	7.35	7.50	9.02	8.39	8.23	2.0108	1.0078	2.0108	U	0.08	0.304

			63	32	59	15	94	79	702	2	87		35	72
					9	2	5	8	56		02		33	02
											56		07	15
65	FAM1	Family with	6.	6.	6.	3.	3.	5.	-4.	-2.	4.6	D	0.0	0.2
33	53C	sequence	87	80	70	93	95	88	613	205	13	o	04	44
16		similarity 153,	68	65	38	42	25	33	089	733	08	w	08	25
		member C	9	5	9	4	1	8	661	333	96	n	31	17
											61		77	2
22	ALDO	Aldolase,	7.	5.	7.	7.	9.	9.	4.3	2.1	4.3	U	0.0	0.4
9	B	fructose-bisphosph	33	39	47	37	89	30	619	249	61	p	31	01
		ate B	28	73	34	83	33	69	906	866	99		62	56
			7	5	1		5	4	17	67	06		53	52
											17		32	84
68	SULT1	Sulfotransferase	3.	3.	6.	10	7.	7.	15.	3.9	15.	U	0.0	0.2
19	C2	family 1C member	46	71	03	.0	41	63	554	592	55	p	03	37
		2	17	58	72	44	15	64	642	733	46		46	14
			5			52	6	9	51	33	42		24	66
											51		02	6
29	CNIH4	Cornichon family	7.	6.	6.	8.	8.	7.	2.1	1.1	2.1	U	0.0	0.2
09		AMPA receptor	20	72	78	29	23	50	559	083	55	p	06	88
7		auxiliary protein 4	2	15	16	39	29	31	593	3	95		80	45
				1	1	9	7	5	85		93		95	97
											85		99	19
10	CENP	Centromere	5.	5.	5.	8.	7.	6.	4.1	2.0	4.1	U	0.0	0.2
63	F	protein F	79	04	47	14	69	58	076	383	07	p	02	07
			04	34	20	08	42	58	312	066	63		14	75
			5	8	8	1	8	4	29	67	12		00	59
											29		71	05
90	PRC1	Protein regulator	5.	5.	4.	6.	6.	6.	2.5	1.3	2.5	U	0.0	0.2
55		of cytokinesis 1	48	05	65	54	71	04	816	683	81	p	02	21
			77	14	57	32	23	42	856	133	68		56	48
			8	8	1	7	7	7	26	33	56		23	56
											26		4	65
10	CDX2	Caudal type	5.	5.	5.	5.	6.	6.	2.0	1.0	2.0	U	0.0	0.3
45		homeobox 2	36	31	34	97	99	11	320	229	32	p	11	29
			33	46	09	64	50	62	557	4	05		83	73
			7	9	3	9	9	3	73		57		27	79
											73		22	49
24	KIF4A	Kinesin family	4.	4.	4.	5.	6.	5.	2.0	1.0	2.0	U	0.0	0.3
13		member 4A	58	68	79	61	31	20	332	238	33	p	11	30
7			75	40	65	71	34	89	674		26		87	28
			6	5	5	8	3	5	56		74		55	63
											56		09	88
88	VNN1	Vanin 1	6.	3.	3.	9.	7.	6.	11.	3.5	11.	U	0.0	0.3

76			43 18 9	27 64 8	02 71 2	34 89	40 48 8	66 57 2	805 086 16	613 366 67	80 50 86 16	p	11 57 26 47	27 65 98 66
46 81	NBL1	Neuroblastoma 1, DAN family BMP antagonist	8. 82 00 7	7. 40 03	8. 58 86 1	9. 66 77 5	10 .3 22 91	9. 08 30 1	2.6 787 562 92	1.4 215 633 33	2.6 78 75 62 92	U p	0.0 19 34 57 08	0.3 67 66 41 57
53 18	PKP2	Plakophilin 2	8. 56 47 5	8. 91 63	8. 41 44	10 .6 97 59	11 .2 79 34	9. 89 59 5	3.9 791 951 84	1.9 924 766 67	3.9 79 19 51 84	U p	0.0 01 12 34 33	0.1 86 14 79 2
80 01 2	PHC3	Polyhomeotic homolog 3 (Drosophila)	3. 63 61 9	4. 75 89 6	3. 72 13 4	4. 47 53 5	4. 99 32 9	5. 98 51 5	2.1 621 001 23	1.1 124 333 33	2.1 62 10 01 23	U p	0.0 47 45 42 3	0.4 42 16 29 65
23 47 4	ETHE1	Ethylmalonic encephalopathy 1	6. 89 61 3	6. 67 75 2	7. 68 36 2	8. 66 99 2	8. 20 09 4	8. 27 78 2	2.4 574 067 4	1.2 971 366 67	2.4 57 40 67 4	U p	0.0 04 73 18 19	0.2 58 19 47 48
10 66	CES1	Carboxylesterase 1	12 .5 86 02	7. 96 52 6	9. 64 43	5. 60 04 1	7. 40 13 3	5. 87 52 7	-13 .66 919 774	-3. 772 856 667	13. 66 91 97 74	D o w n	0.0 12 42 41 69	0.3 34 46 67 31
71 53	TOP2 A	Topoisomerase (DNA) II $\alpha$	6. 82 27 3	5. 26 12 6	6. 18 07 6	8. 53 57	8. 69 82 2	7. 69 67 8	4.6 653 435 83	2.2 219 833 33	4.6 65 34 35 83	U p	0.0 01 87 20 44	0.1 95 55 85 68
81 03 4	SLC25 A32	Solute carrier family 25 (mitochondrial folate carrier), member 32	4. 31 96 5	4. 25 86 8	4. 13 42 8	5. 46 85	5. 62 77 4	4. 91 56 1	2.1 431 705 57	1.0 997 466 67	2.1 43 17 05 57	U p	0.0 02 34 43 02	0.2 13 49 53 85
95 7	ENTP D5	Ectonucleoside triphosphate diphosphohydrolas e 5	9. 75 16 1	8. 67 54 8	9. 70 32 6	9. 02 59	7. 98 70 3	7. 56 65 3	-2. 271 475 902	-1. 183 63	2.2 71 47 59 02	D o w n	0.0 37 99 71 13	0.4 17 70 09 62

28 98 2	FLVC R1	Feline leukemia virus subgroup C cellular receptor 1	5. 79 04 7	5. 37 60 9	5. 53 81 2	7. 27 83 4	6. 81 10 6	6. 07 89	2.2 261 333 26	1.1 545 4	2.2 26 13 33 26	U p	0.0 10 85 49 19	0.3 23 87 84 16
71 64	TPD52 L1	Tumor protein D52-like 1	7. 52 88 9	6. 76 75 4	7. 01 68 5	5. 13 74 2	3. 67 85 5	4. 53 24	-6. 298 332 841	-2. 654 97	6.2 98 33 28 41	D o w n	0.0 00 33 41 15	0.1 60 90 15 41
55 82 5	PECR	Peroxisomal trans-2-enoyl-coa reductase	6. 08 04 9	5. 59 74 8	6. 18 71 3	5. 62 76 3	4. 66 69 1	4. 38 57	-2. 087 274 003	-1. 061 62	2.0 87 27 40 03	D o w n	0.0 22 26 05 19	0.3 78 45 78 86
64 27	SRSF2	Serine/arginine-rich splicing factor 2	7. 63 76 2	7. 72 75 7	7. 63 85 3	8. 36 55 3	8. 71 82 2	9. 17 88 7	2.1 232 878 97	1.0 863	2.1 23 28 78 97	U p	0.0 04 16 31 34	0.2 45 18 04 58
17 19	DHFR	Dihydrofolate reductase	5. 88 26	5. 25 53 9	5. 39 77	7. 84 15 5	7. 49 69	6. 98 36 1	3.8 073 573 91	1.9 287 9	3.8 07 35 73 91	U p	0.0 00 37 82 4	0.1 60 90 15 41
13 97	CRIP2	Cysteine-rich protein 2	6. 46 20 9	8. 01 19 1	8. 24 60 7	5. 57 06 5	6. 36 50 8	6. 66 83	-2. 588 315 23	-1. 372 013 333	2.5 88 31 52 3	D o w n	0.0 35 33 27 86	0.4 09 98 41 4
21 52	F3	Coagulation factor III (thromboplastin, tissue factor)	5. 96 80 2	6. 45 65 6	5. 86 93 7	7. 23 34 3	8. 42 96	8. 45 29 4	3.8 388 477 23	1.9 406 733 33	3.8 38 84 77 23	U p	0.0 01 50 15 36	0.1 87 10 78 18
86 71	SLC4A 4	Solute carrier family 4 (sodium bicarbonate cotransporter), member 4	9. 09 86 8	7. 83 98 4	9. 27 77 4	8. 00 03 8	6. 47 25	5. 99 49 7	-3. 774 110 509	-1. 916 136 667	3.7 74 11 05 09	D o w n	0.0 15 76 42 38	0.3 50 93 61 89
28 96 9	BZW2	Basic leucine zipper and W2 domains 2	5. 06 74	4. 70 22 3	4. 89 37 5	6. 24 50 4	6. 72 15 1	5. 52 40 5	2.4 212 297 79	1.2 757 4	2.4 21 22 97	U p	0.0 06 08 67	0.2 79 48 17

												79		16	42
65 38 20	FAM7 2B	Family with sequence similarity 72 member B	4. 81 14 4	3. 76 74 3	4. 33 53 2	7. 00 88 8	6. 35 93 6	5. 57 41 2	4.0 261 195 17	2.0 093 9	4.0 26 11 95 17	U p	0.0 02 23 84 85	0.2 11 69 45 53	
68 67	TACC 1	Transforming, acidic coiled-coil containing protein 1	6. 34 63 1	7. 13 09 6	7. 15 34 4	3. 87 11	6. 27 16 8	5. 46 05 3	-3. 194 964 719	-1. 675 8	3.1 94 96 47 19	D o w n	0.0 27 14 23 45	0.3 89 57 54 13	
51 52 3	CXXC 5	CXXC finger protein 5	7. 91 1	8. 11 92 9	7. 95 05 7	6. 51 56 9	7. 00 08 9	7. 18 12 6	-2. 135 153 809	-1. 094 34	2.1 35 15 38 09	D o w n	0.0 02 93 17 53	0.2 31 33 53 69	
73 66	UGT2 B15	UDP glucuronosyltransf erases 2 family, polypeptide B15	10. 9 10 11	8. 01 51 7	8. 28 27 8	8. 06 83 1	6. 67 74 6	6. 25 52 4	-4. 196 005 784	-2. 069 016 667	4.1 96 00 57 84	D o w n	0.0 42 98 40 93	0.4 32 07 88 1	
89 92 7	C16orf 45	Chromosome 16 open reading frame 45	7. 15 51 4	7. 20 44 4	8. 18 35 2	5. 54 77 8	6. 51 20 1	5. 37 92 6	-3. 252 051 265	-1. 701 35	3.2 52 05 12 65	D o w n	0.0 04 56 06 74	0.2 54 41 63 12	
11 13 0	ZWIN T	ZW10 interacting kinetochore protein	5. 66 66 4	5. 26 78 2	5. 72 02 7	6. 88 52 7	6. 87 28 7	6. 26 27 9	2.1 765 854 61	1.1 220 666 67	2.1 76 58 54 61	U p	0.0 03 82 37 31	0.2 38 90 72 74	
55 42 82	FAM7 2C	Family with sequence similarity 72 member C	4. 81 14 4	3. 76 74 3	4. 33 53 2	7. 00 88 8	6. 35 93 6	5. 57 41 2	4.0 261 195 17	2.0 093 9	4.0 26 11 95 17	U p	0.0 02 23 84 85	0.2 11 69 45 53	
83 93 8	C10orf 11	Chromosome 10 open reading frame 11	7. 17 64 1	8. 43 51 3	8. 03 22 2	5. 76 64 1	5. 66 67 3	6. 74 73 2	-3. 533 505 121	-1. 821 1	3.5 33 50 51 21	D o w n	0.0 03 80 95 74	0.2 38 90 72 74	
97 62	LZTS3	Leucine zipper, putative tumor suppressor family	7. 57 70	8. 33 33	8. 09 42	6. 83 05	6. 79 36	7. 10 01	-2. 133 787	-1. 093 416	2.1 33 78	D o w	0.0 04 25	0.2 46 47	

		member 3	4			6	2	1	735	667	77 35	n	83 49	32 18
10 96 1	ERP29	Endoplasmic reticulum protein 29	7. 39 11 5	6. 99 82 9	7. 05 5	5. 82 59 5	6. 07 31 9	5. 89 82 1	-2. 322 529 09	-1. 215 696 667	2.3 22 52 90 9	D o w n	0.0 00 77 12 53	0.1 77 73 29 45
55 43 13	HIST2 H4B	Histone cluster 2, h4b	8. 73 56 8	8. 01 41 9	8. 24 88 9	9. 86 20 7	9. 68 07 1	8. 55 79	2.0 476 559 52	1.0 339 733 33	2.0 47 65 59 52	U p	0.0 35 06 84 07	0.4 08 55 78 26
37 09	ITPR2	Inositol 1,4,5-trisphosphat e receptor, type 2	5. 63 11 5	7. 18 69 8	7. 17 77 4	4. 51 31 2	5. 85 81 8	4. 73 41 5	-3. 095 430 355	-1. 630 14 355	3.0 95 43 03 55	D o w n	0.0 18 97 82 62	0.3 67 34 80 71
21 4	ALCA M	Activated leukocyte cell adhesion molecule	8. 62 22 1	8. 95 81 1	8. 35 47 1	6. 97 25 4	7. 99 18 9	6. 35 10 9	-2. 907 676 296	-1. 539 866 667	2.9 07 67 62 96	D o w n	0.0 09 02 80 51	0.3 09 79 61 38
26 25 5	PTTG3 P	Pituitary tumor-transformin g 3, pseudogene	4. 44 43 1	4. 07 68 1	4. 48 38 5	6. 19 54 4	6. 81 31	5. 63 29 9	3.6 778 262 72	1.8 788 533 33	3.6 77 82 62 72	U p	0.0 00 72 00 42	0.1 72 63 18 47
52 25	PGC	Progastricsin (pepsinogen C)	4. 45 76 9	14 .1 75 86	13 .9 16 86	4. 84 13 1	4. 21 68	4. 87 89 2	-73 .74 431 857	-6. 204 46	73. 74 43 18 57	D o w n	0.0 38 90 03 93	0.4 20 99 70 79
74 14	VCL	Vinculin	6. 79 58 4	6. 31 03	5. 97 90 8	7. 32 69 9	8. 53 85 1	7. 30 86 8	2.5 721 711 95	1.3 629 866 67	2.5 72 17 11 95	U p	0.0 11 88 49	0.3 30 28 63 88
25 75 9	SHC2	SHC (Src homology 2 domain containing) transforming protein 2	6. 79 34 3	7. 28 65 7	6. 86 54 8	6. 37 28	5. 23 02 8	6. 05 61 6	-2. 136 742 907	-1. 095 413 333	2.1 36 74 29 07	D o w n	0.0 14 46 33 41	0.3 46 82 70 31
64	SRSF1	Serine/arginine-ric	6.	6.	6.	7.	7.	7.	2.1	1.0	2.1	U	0.0	0.3



26		h splicing factor 1	05 43 2	97 21	68 23 3	93 54 2	32 61 4	71 55 3	279 240 61	894 466 67	27 92 40 61	p	09 69 02 4	13 66 02 93
22 84 1	RAB11 FIP2	RAB11 family interacting protein 2 (class I)	7. 85 45 2	7. 68 14 9	7. 91 6 2	6. 46 62 9	6. 91 73 9	6. 61 42 7	-2. 221 257 53	-1. 151 376 667	2.2 21 25 75 3	D o w n	0.0 01 17 49 03	0.1 86 14 79 2
10 54	CEBP G	CCAAT/enhancer binding protein (C/EBP), $\gamma$	5. 60 17 3	5. 05 3 3	5. 62 33 3	6. 30 11 4	6. 83 74 6	7. 05 88 4	2.4 733 390 15	1.3 064 6 90 15	2.4 73 33 90 15	U p	0.0 02 70 11 7	0.2 26 76 71 12
18 71	E2F3	E2F transcription factor 3	4. 21 22 4	3. 91 08 9	3. 77 59 8	5. 13 73 8	4. 68 96 6	5. 15 09 8	2.0 368 362 49	1.0 263 3 49	2.0 36 83 62 49	U p	0.0 02 25 81 33	0.2 11 69 45 53
55 65 2	SLC48 A1	Solute carrier family 48 (heme transporter), member 1	7. 22 80 7	6. 95 99 7	6. 94 07 7	5. 03 35 9	5. 47 80 1	5. 52 62 3	-3. 242 245 497	-1. 696 993 333	3.2 42 24 54 97	D o w n	0.0 00 15 63	0.1 28 62 18 94
37 42 86	CDRT 1	CMT1A duplicated region transcript 1	4. 16 91 4	5. 45 48 3	5. 29 83 3	4. 14 97 6	3. 24 73 8	3. 82 49 6	-2. 351 188 162	-1. 233 39 162	2.3 51 18 81 62	D o w n	0.0 17 65 37 54	0.3 61 12 33 37
32 16	HOXB 6	Homeobox B6	5. 21 4	3. 84 47 4	4. 47 72 3	7. 35 89 9	6. 47 64 7	8. 33 70 6	7.3 556 355 49	2.8 788 5 49	7.3 55 63 55 49	U p	0.0 01 10 11 94	0.1 86 14 79 2
25 48 96	LOC25 4896	Uncharacterized LOC254896	7. 34 89	7. 40 31 1	7. 61 38 5	7. 17 95 3	5. 24 00 7	5. 70 63 2	-2. 663 481 635	-1. 413 313 333	2.6 63 48 16 35	D o w n	0.0 22 73 81 22	0.3 79 55 65 1
40 08	LMO7	LIM domain 7	4. 95 74 8	5. 12 42 1	5. 41 74 2	5. 87 34 1	7. 28 84 3	6. 14 35	2.4 095 159 2	1.2 687 433 33	2.4 09 51 59 2	U p	0.0 14 02 43 92	0.3 45 57 11 86

64 75 6	ATPAF 1	ATP synthase mitochondrial F1 complex assembly factor 1	7. 51 16 6	7. 19 41 8	7. 19 17 9	5. 80 50 6	6. 82 54	5. 87 00 5	-2. 192 190 744	-1. 132 373 333	2.1 92 19 07 44	D o w n	0.0 09 85 85 47	0.3 15 70 78 58
25 94 5	PVRL3	Poliovirus receptor-related 3	7. 65 81	8. 07 38 8	7. 86 16 3	6. 19 89 9	7. 58 30 7	6. 39 50 5	-2. 202 028 793	-1. 138 833 333	2.2 02 02 87 93	D o w n	0.0 22 13 76 16	0.3 78 35 72 21
11 62 55	MOGA T1	Monoacylglycerol O-acyltransferase 1	9. 72 81	9. 17 82 5	9. 66 55	8. 99 75	5. 75 48	2. 89 75 8	-12 .47 230 896	-3. 640 656 667	12. 47 23 08 96	D o w n	0.0 31 77 90 4	0.4 02 73 83 8
10 61 0	ST6G ALNA C2	ST6 ( $\alpha$ -N-acetyl-neura minyl-2,3- $\beta$ -galact osyl-1,3)-N-acetyl galactosaminide $\alpha$ -2,6-sialyltransfer ase 2	4. 09 84 9	3. 77 27 4	3. 39 78 6	5. 45 30 7	4. 54 44 2	5. 64 19	2.7 449 248 78	1.4 567 666 67	2.7 44 92 48 78	U p	0.0 03 64 04 06	0.2 38 59 85 3
15 09	CTSD	Cathepsin D	10 .8 07 11	9. 99 21 7	9. 90 14 8	8. 18 5	9. 37 03	8. 52 46 1	-2. 908 516 187	-1. 540 283 333	2.9 08 51 61 87	D o w n	0.0 05 80 72 64	0.2 76 07 88 98
26 04 7	CNTN AP2	Contactin associated protein-like 2	4. 23 59 2	4. 52 35 2	4. 42 70 5	7. 32 03 6	5. 89 15 7	4. 59 87 7	2.9 107 750 17	1.5 414 033 33	2.9 10 77 50 17	U p	0.0 43 25 20 23	0.4 32 33 09 01
15 76 95	TDRP	Testis development related protein	5. 52 44	5. 48 57 9	5. 27 67 9	4. 08 95 2	4. 61 33 5	4. 23 06 1	-2. 170 208 017	-1. 117 833 333	2.1 70 20 80 17	D o w n	0.0 01 19 26 05	0.1 86 14 79 2
10 01 28 25 2	ZNF66 7-AS1	ZNF667 antisense RNA 1 (head to head)	6. 74 06 1	6. 61 25 3	7. 61 35 6	3. 73 47 3	5. 78 63 1	4. 56 71	-4. 900 243 136	-2. 292 853 333	4.9 00 24 31 36	D o w n	0.0 03 99 48 97	0.2 42 71 06 82
40 57	LTF	Lactotransferrin	5. 21	12 .5	12 .2	4. 99	5. 74	5. 91	-21 .51	-4. 427	21. 51	D o	0.0 46	0.4 41

			43 7	19 32	05 24	38 7	67 7	62 8	598 028	336 667	59 80 28	w n	79 79 98	19 21 25
80 78 1	COL18 A1	Collagen, type XVIII, $\alpha$ 1	8. 94 47 1	9. 27 90 6	9. 08 64 2	8. 44 83 1	7. 54 59 1	7. 34 50 7	-2. 502 956 7	-1. 323 633 333	2.5 02 95 67	D o w n	0.0 04 92 94 66	0.2 62 38 32 57
11 71 53	MIA2	Melanoma inhibitory activity 2	4. 49 85	4. 45 24 6	4. 60 62 8	2. 64 04 8	3. 04 38 6	4. 31 69 6	-2. 274 127 802	-1. 185 313 333	2.2 74 12 78 02	D o w n	0.0 23 95 93 49	0.3 81 89 69 49
20 30 68	TUBB	Tubulin, $\beta$ class I	8. 77 14 9	8. 39 9	8. 31 69 8	9. 49 14 9	10. .2 14 69	8. 85 20 9	2.0 329 856 05	1.0 236 56	2.0 32 98 56 05	U p	0.0 27 40 97 84	0.3 89 83 37 07
20 32 28	C9orf7 2	Chromosome 9 open reading frame 72	6. 47 45 5	6. 15 06 2	6. 39 92 9	7. 07 55 6	8. 16 77	6. 90 24 7	2.0 568 311 05	1.0 404 233 33	2.0 56 83 11 05	U p	0.0 23 80 36 74	0.3 81 26 89 97
87 41	TNFSF 13	Tumor necrosis factor superfamily member 13	8. 30 84 8	8. 37 08 2	9. 27 54 4	7. 44 21 4	7. 87 41 9	6. 30 38 9	-2. 722 326 301	-1. 444 84	2.7 22 32 63 01	D o w n	0.0 17 59 14 11	0.3 61 12 33 37
11 49 07	FBXO 32	F-box protein 32	6. 35 39 7	6. 49 91 6	6. 46 61 5	6. 91 63 3	8. 76 32 5	7. 90 57 1	2.6 795 733 96	1.4 220 033 33	2.6 79 57 33 96	U p	0.0 15 66 60 91	0.3 50 84 39 38
50 51 5	CHST1 1	Carbohydrate (chondroitin 4) sulfotransferase 11	7. 88 18 2	7. 15 34 3	6. 95 65 1	5. 41 08 4	7. 11 32 1	5. 59 73 1	-2. 445 506 558	-1. 290 133 333	2.4 45 50 65 58	D o w n	0.0 36 06 96 75	0.4 12 47 33 32
18 38	DTNB	Dystrobrevin $\beta$	7. 70 58 7	8. 08 23 1	8. 03 35 9	5. 83 69 8	6. 05 74 2	6. 30 12 9	-3. 668 931 578	-1. 875 36	3.6 68 93 15 78	D o w n	8.4 19 04 E- 05	0.1 26 50 89 75
26	GJA1	Gap junction	11	9.	10	9.	9.	8.	-3.	-1.	3.1	D	0.0	0.3

97		protein $\alpha$ 1	.5 93 41	84 50 7	.9 77 4	70 87 7	25 39 5	46 39 7	166 882 484	663 063 333	66 88 24 84	o w n	14 21 92 81	46 79 70 53
64 48 44	PHGR 1	Proline/histidine/g lycine-rich 1	4. 21 45 7	4. 88 42 7	5. 02 97 7	6. 79 19 6	9. 11 85 9	5. 24 20 5	5.0 677 780 23	2.3 413 533 33	5.0 67 77 80 23	U p	0.0 34 93 59 97	0.4 08 42 81 41
15 30 90	DAB2I P	DAB2 interacting protein	8. 22 47	8. 29 75 9	8. 24 63 1	7. 40 64 1	7. 04 11	7. 15 73	-2. 077 137 421	-1. 054 596 667	2.0 77 13 74 21	D o w n	0.0 01 32 83 93	0.1 87 10 78 18
83 43	HIST1 H2BF	Histone cluster 1, h2bf	7. 34 51 3	6. 40 79 9	6. 40 99 4	8. 42 02 7	9. 50 46 8	8. 17 31 6	3.9 404 216 08	1.9 783 5 16	3.9 40 42 16 08	U p	0.0 02 63 46 82	0.2 24 74 75 95
26 03 1	OSBP L3	Oxysterol binding protein like 3	6. 34 27 9	5. 78 5 7	6. 39 64 7	7. 93 16 8	7. 53 25 3	7. 28 68 3	2.6 553 953 37	1.4 089 266 67	2.6 55 39 53 37	U p	0.0 01 45 80 2	0.1 87 10 78 18
12 91	COL6 A1	Collagen, type VI, $\alpha$ 1	8. 72 34 7	7. 78 59 2	7. 59 68 7	8. 43 79 9	9. 24 99 8	9. 84 65 9	2.2 080 405 49	1.1 427 666 67	2.2 08 04 05 49	U p	0.0 38 39 73 6	0.4 19 34 43 95
79 69 4	MANE A	Mannosidase, endo- $\alpha$	7. 99 40 3	9. 29 43 9	8. 53 10 4	6. 79 99 8	7. 77 65 6	6. 60 86 3	-2. 917 562 038	-1. 544 763 333	2.9 17 56 20 38	D o w n	0.0 09 83 90 49	0.3 15 60 08 4
23 67 0	TMEM 2	Transmembrane protein 2	7. 13 97 6	8. 39 29 2	8. 40 21 9	6. 42 98 2	7. 17 08 4	7. 04 12	-2. 140 087 82	-1. 097 67	2.1 40 08 78 2	D o w n	0.0 31 20 82 88	0.4 00 46 67 53
14 79 47	ZNF54 2P	Zinc finger protein 542, pseudogene	5. 04 49 8	4. 94 68 3	5. 09 35 9	3. 22 84 8	4. 23 89 2	3. 61 82 8	-2. 519 679 087	-1. 333 24	2.5 19 67 90 87	D o w n	0.0 01 86 83 71	0.1 95 55 85 68

74 74	WNT5 A	Wingless-type MMTV integration site family member 5A	7. 79 37 3	7. 41 50 8	6. 68 61 4	5. 42 35 3	6. 68 85 6	6. 14 33 8	-2. 318 449 014	-1. 213 16	2.3 18 44 90 14	D o w n	0.0 22 54 84 08	0.3 78 90 05 37
67 17	SRI	Sorcin	5. 61 15 9	6. 19 10 2	5. 83 71 8	6. 93 23 2	7. 79 69 2	8. 36 71	3.5 279 986 28	1.8 188 5	3.5 27 99 86 28	U p	0.0 02 31 61 4	0.2 12 91 59 14
13 78 72	ADHF E1	Alcohol dehydrogenase, iron containing 1	6. 15 33 4	7. 08 03 4	6. 62 79 8	4. 66 52 2	5. 54 19 5	5. 62 16 4	-2. 539 040 37	-1. 344 283 333	2.5 39 04 03 7	D o w n	0.0 07 26 92 55	0.2 92 18 66 83
28 47 16	RIMK LA	Ribosomal modification protein rimk-like family member A	5. 55 81 7	6. 78 52 2	6. 85 00 4	4. 73 64 5	5. 16 00 9	5. 71 49 7	-2. 287 819 658	-1. 193 973 333	2.2 87 81 96 58	D o w n	0.0 26 41 74 81	0.3 87 35 84 1
51 65 9	GINS2	GINS complex subunit 2 (Psf2 homolog)	4. 97 71 2	5. 05 67 4	4. 96 10 4	6. 69 21 5	7. 14 49 7	6. 04 27 8	3.0 915 564 17	1.6 283 333 33	3.0 91 55 64 17	U p	0.0 01 07 41 31	0.1 86 14 79 2
25 92 4	MYRI P	Myosin VIIA and Rab interacting protein	5. 78 29 9	7. 12 40 3	6. 14 28 8	4. 85 72 1	5. 45 41	5. 69 20 1	-2. 021 640 773	-1. 015 526 667	2.0 21 64 07 73	D o w n	0.0 39 36 88 71	0.4 22 57 97 15
51 74 7	LUC7 L3	LUC7-like 3 pre-mrna splicing factor	5. 98 80 4	6. 39 68 4	6. 28 19 6	7. 06 42 2	7. 04 77 4	8. 15 81	2.2 991 065 59	1.2 010 733 33	2.2 99 10 65 59	U p	0.0 10 73 36 35	0.3 23 87 84 16
23 12 9	PLXN D1	Plexin D1	7. 18 16 4	7. 34 01 2	7. 32 87 1	5. 60 49 8	6. 55 96	5. 61 89 8	-2. 559 100 254	-1. 355 636 667	2.5 59 10 02 54	D o w n	0.0 03 06 72 17	0.2 34 04 90 49
57 1	BACH 1	BTB and CNC homology 1, basic leucine zipper transcription factor	4. 81 47 2	3. 57 04 6	3. 81 18 5	4. 65 38 8	6. 10 95 6	5. 64 22	2.6 442 709 27	1.4 028 7	2.6 44 27 09	U p	0.0 19 79 55	0.3 68 10 68

		1										27		56	92
15 82 19	TTC39 B	Tetratricopeptide repeat domain 39B	6. 97 05 7	7. 30 86 2	8. 44 59 7	5. 16 19	7. 13 15 2	5. 99 69 2	-2. 786 150 776	-1. 478 273 333	2.7 86 15 07 76	D o w n	0.0 38 63 69 58	0.4 19 56 12 9	
26 17 26	TIPRL	TOR signaling pathway regulator	6. 15 55 3	6. 69 20 8	6. 57 50 3	8. 13 92 8	7. 44 39 6	7. 20 47 6	2.1 761 630 67	1.1 217 866 67	2.1 76 16 30 67	U p	0.0 08 42 01 82	0.3 05 83 03 66	
53 3	ATP6V 0B	Atpase, H+ transporting, lysosomal 21kda, V0 subunit b	7. 55 60 7	7. 28 67 7	7. 36 23 4	5. 94 94 2	6. 36 68 4	5. 18 97 1	-2. 961 654 468	-1. 566 403 333	2.9 61 65 44 68	D o w n	0.0 02 00 59 75	0.2 02 25 09 29	
23 12 7	COLG ALT2	Collagen $\beta$ (1-O)galactosyltransferase 2	4. 28 74 5	9. 90 76 9	9. 50 45 5	3. 90 41 5	4. 35 13 7	5. 24 78 9	-10 .54 699 422	-3. 398 76	10. 54 69 94 22	D o w n	0.0 48 16 85 89	0.4 44 29 99 39	
10 74 2	RAI2	Retinoic acid induced 2	8. 42 07	8. 54 27 1	8. 61 07 6	6. 48 55 6	7. 53 50 2	7. 94 94 8	-2. 299 579 381	-1. 201 37	2.2 99 57 93 81	D o w n	0.0 16 47 38 86	0.3 55 13 62 17	
72 78 97	MUC5 B	Mucin 5B, oligomeric mucus/gel-formin g	10 .0 86 52	10 .8 17 83	10 .9 97 71	9. 78 95 5	7. 50 96 9	8. 06 89 6	-4. 525 111 476	-2. 177 953 333	4.5 25 11 14 76	D o w n	0.0 08 01 83 31	0.2 99 13 95 54	
69 26	TBX3	T-box 3	5. 76 93 1	7. 37 92 7	7. 70 59 3	4. 92 14 4	6. 19 24 2	5. 41 44 2	-2. 717 116 956	-1. 442 076 667	2.7 17 11 69 56	D o w n	0.0 38 28 49 78	0.4 19 01 93 74	
69 41	TCF19	Transcription factor 19	5. 90 36 1	4. 94 78 8	4. 96 62 9	6. 07 74 6	6. 77 82 5	6. 04 18 5	2.0 371 845 3	1.0 265 766 67	2.0 37 18 45 3	U p	0.0 22 32 45 08	0.3 78 66 05 33	
50 04	ORM1	Orosomuroid 1	3. 80 83	4. 63 54	5. 54 52	6. 97 44	8. 07 24	5. 47 83	4.5 276 946	2.1 787 766	4.5 27 69	U p	0.0 18 27	0.3 64 08	

			1	1	6	8	4	9	54	67	46		69	78
28 56 71	RNF180	Ring finger protein 180	5.6419	6.5101	6.03617	3.14281	5.44105	5.15065	-2.798305	-1.484553	2.798305	D o w n	0.044575	0.4352941
11 64	CKS2	CDC28 protein kinase regulatory subunit 2	5.35426	4.33286	5.19969	7.73001	6.95544	5.80284	3.648137	1.86716	3.648137	U p	0.00911485	0.31047429
40 05 81	GRAPL	GRB2-related adaptor protein-like	5.31815	7.64792	6.615	4.71043	4.87504	5.41042	-2.884644	-1.528393	2.884644	D o w n	0.030863593	0.3993030908
11 06 5	UBE2C	Ubiquitin conjugating enzyme E2C	6.1793	5.17869	5.40581	7.77279	8.76221	7.19619	5.0018553	2.3224633	5.0018553	U p	0.00144852	0.187107818
46 80	CEACAM6	Carcinoembryonic antigen-related cell adhesion molecule 6 (non-specific cross reacting antigen)	6.96745	7.10356	7.66467	10.070656	10.036336	11.0236	10.606276	3.4068466	10.606276	U p	3.111E-05	0.0960542
39 98 44	LINC01002	Long intergenic non-protein coding RNA 1002	8.03359	8.30848	7.49201	5.71049	6.09297	7.81824	-2.646575	-1.404126	2.646575	D o w n	0.040058298	0.424359444
40 57 53	DUOX2	Dual oxidase maturation factor 2	9.43212	6.93978	8.33202	6.51114	7.12037	6.51971	-2.863077	-1.517566	2.863077	D o w n	0.039203222	0.4226
55 33 2	DRAM1	DNA damage regulated autophagy modulator 1	6.51589	6.56418	5.46836	3.76189	5.67287	4.91325	-2.639271	-1.40014	2.639271	D o w n	0.034075273	0.40827355
11	PRAP1	Proline-rich acidic	7.	6.	6.	8.	9.	6.	3.3	1.7	3.3	U	0.0	0.4

84 71		protein 1	06 45 2	77 75 7	21 07 6	90 88 1	57 53 8	77 72 7	315 726 02	362 033 33	31 57 26 02	p	41 23 31 47	26 96 10 48
22 4	ALDH 3A2	Aldehyde dehydrogenase 3 family member A2	10 .0 98 78	8. 99 95 8	9. 37 99 1	7. 77 59 1	8. 47 12 1	6. 67 78 1	-3. 607 793 254	-1. 851 116 667	3.6 07 79 32 54	D o w n	0.0 07 90 51 05	0.2 99 13 95 54
92 08 6	GGTL C1	Γ-glutamyltransfer ase light chain 1	9. 16 15 7	9. 31 31 4	8. 59 69 8	7. 48 88 1	7. 56 93 1	5. 95 58 1	-4. 053 739 364	-2. 019 253 333	4.0 53 73 93 64	D o w n	0.0 03 67 15 27	0.2 38 59 85 3
89 70	HIST1 H2BJ	Histone cluster 1, h2bj	5. 29 89 9	4. 46 46 2	4. 76 98 1	5. 23 29 1	6. 95 67 4	5. 79 47 6	2.2 196 466 05	1.1 503 3 66 05	2.2 19 64 66 05	U p	0.0 41 99 51 27	0.4 30 07 43 46
91 41	PDCD 5	Programmed cell death 5	5. 46 34 7	5. 03 57 9	5. 27 08 7	6. 20 47 5	6. 58 47 1	6. 04 47 1	2.0 298 080 9	1.0 213 433 33	2.0 29 80 80 9	U p	0.0 03 54 83 7	0.2 37 14 66 6
14 71 11	NOTU M	Notum pectinacylesteras e homolog (Drosophila)	5. 32 59	11 .6 50 8	10 .5 10 7	5. 42 99 5	4. 94 97 6	5. 35 47 3	-15 .11 232 086	-3. 917 653 333	15. 11 23 20 86	D o w n	0.0 34 63 79 56	0.4 08 42 39 81
71 63	TPD52	Tumor protein D52	6. 39 73 8	6. 57 03 2	7. 37 05 1	9. 25 86 3	9. 52 07 4	7. 81 22 6	4.2 412 024 33	2.0 844 733 33	4.2 41 20 24	U p	0.0 04 25 54 85	0.2 46 47 32 18
50 65 0	ARHG EF3	Rho guanine nucleotide exchange factor 3	6. 51 87 9	7. 49 64 4	7. 67 40 8	4. 78 94 5	5. 11 33 1	5. 58 39 2	-4. 191 722 856	-2. 067 543 333	4.1 91 72 28 56	D o w n	0.0 00 88 48 69	0.1 81 04 09 24
23 71 0	GABA RAPL1	GABA(A) receptor-associate d protein like 1	10 .1 18 69	9. 03 81 7	8. 66 99 5	7. 84 58 5	8. 03 14 9	7. 53 35 6	-2. 773 972 207	-1. 471 953 333	2.7 73 97 22 07	D o w n	0.0 07 50 57 38	0.2 94 41 93 61



38 87 53	COA6	Cytochrome c oxidase assembly factor 6	5.98 91	5.04 46 3	5.51 40 3	7.50 75 2	7.00 24 7	5.93 93 1	2.4631 651 03	1.3005 133 33	2.463 16 51 03	U p	0.022 85 29 1	0.379 93 20 65
57 52 3	NYNR IN	NYN domain and retroviral integrase containing	7.13 84 7	7.14 67 9	8.35 78 4	5.82 82 1	7.01 83	6.09 46 2	-2.352 166 197	-1.233 99	2.352 16 61 97	D o w n	0.029 51 96 56	0.396 72 89 24
89 82 2	KCNK 17	Potassium channel, two pore domain subfamily K, member 17	5.40 83 6	7.17 69 6	7.68 19 9	4.83 45 5	4.30 16 1	4.90 51 7	-4.214 398 294	-2.075 326 667	4.214 39 82 94	D o w n	0.008 56 04 64	0.307 29 63 95
11 62 38	TLCD 1	TLC domain containing 1	5.31 09 6	5.06 58 4	5.51 10 7	6.67 51 4	6.46 81	6.07 38 2	2.1580 525 56	1.1097 3	2.158 05 25 56	U p	0.002 76 62 59	0.228 79 54 43
51 71 6	CES1P 1	Carboxylesterase 1 pseudogene 1	12.5 86 02	7.96 52 6	9.64 43	5.60 04 1	7.40 13 3	5.87 52 7	-13.66 919 774	-3.772 856 667	13.66 91 97 74	D o w n	0.012 42 41 69	0.334 46 67 31
40 13	VWA5 A	Von Willebrand factor A domain containing 5A	7.49 18 1	6.81 63 1	7.37 13 2	4.57 11 3	6.23 58	6.78 61 2	-2.570 644 303	-1.362 13	2.570 64 43 03	D o w n	0.045 89 32 12	0.439 13 53 61
64 41 8	TMEM 168	Transmembrane protein 168	4.18 69 6	4.90 98 6	4.79 18 7	5.09 99 1	5.60 57 6	6.34 63 8	2.0769 310 66	1.0544 533 33	2.076 93 10 66	U p	0.023 78 69 79	0.381 26 89 97
64 51	SH3B GRL	SH3 domain binding glutamate-rich protein like	7.14 65 2	6.87 04 8	6.59 62 5	7.07 79 7	8.51 28 5	8.04 76 8	2.0117 020 79	1.0084 166 67	2.011 70 20 79	U p	0.036 48 56 1	0.414 09 00 13
65 65	SLC15 A2	Solute carrier family 15 (oligopeptide transporter),	7.39 51 3	7.20 26 5	7.01 71 5	4.88 82 8	5.03 04 3	6.12 99 1	-3.618 612 605	-1.855 436 667	3.618 61 26	D o w n	0.001 34 81	0.187 10 78

		member 2										05		67	18
84 52 7	ZNF55 9	Zinc finger protein 559	5. 41 43 1	5. 60 37	5. 57 95 6	2. 78 44 5	3. 78 11 1	4. 36 03 7	-3. 707 756 926	-1. 890 546 667	3.7 07 75 69 26	D o w n	0.0 01 83 36 41	0.1 93 61 76 74	
19 33	EEF1B 2	Eukaryotic translation elongation factor 1 β 2	8. 52 74 4	8. 65 52 5	8. 96 32 8	10 .7 19 7	10 .2 70 42	8. 78 65 8	2.3 137 665 88	1.2 102 433 33	2.3 13 76 65 88	U p	0.0 43 42 63 13	0.4 32 33 09 01	
54 43 2	YIPF1	Yip1 domain family member 1	7. 22 91 1	7. 97 26 8	7. 65 82 3	5. 94 94	6. 62 00 5	6. 30 00 5	-2. 514 328 816	-1. 330 173 333	2.5 14 32 88 16	D o w n	0.0 02 47 21 06	0.2 17 69 67 67	
66 7	DST	Dystonin	4. 42 26 2	3. 31 77 7	3. 43 92 2	6. 83 01 1	6. 19 30 3	5. 64 21 8	5.6 382 078 64	2.4 952 366 67	5.6 38 20 78 64	U p	0.0 00 50 42 25	0.1 64 24 82 94	
22 73	FHL1	Four and a half LIM domains 1	5. 85 85 8	5. 25 90 1	5. 03 28 1	5. 42 99 1	8. 27 25 6	7. 36 69	3.1 159 167 03	1.6 396 566 67	3.1 15 91 67 03	U p	0.0 49 13 25 69	0.4 46 17 48	
25 39 82	ASPH D1	Aspartate β-hydroxylase domain containing 1	7. 93 88 7	7. 61 14 3	7. 61 69 7	7. 19 74 1	5. 24 26 6	6. 86 23	-2. 442 400 856	-1. 288 3	2.4 42 40 08 56	D o w n	0.0 37 31 95 16	0.4 16 34 38 48	
52 13	PFKM	Phosphofructokina se, muscle	5. 73 86 9	7. 88 31	7. 28 90 4	4. 56 13 9	4. 86 09 4	5. 16 57 8	-4. 309 657 841	-2. 107 573 333	4.3 09 65 78 41	D o w n	0.0 05 71 14 38	0.2 74 12 79 94	
39 14	LAMB 3	Laminin subunit β 3	5. 10 28 2	5. 71 96 5	5. 68 24 3	7. 33 99 4	6. 89 68	7. 82 73 3	3.6 126 479 37	1.8 530 566 67	3.6 12 64 79 37	U p	0.0 00 61 83 6	0.1 68 94 20 05	
90 71	CLDN 10	Claudin 10	7. 87 28	7. 86 82	7. 79 79	5. 40 9	5. 58 08	6. 35 63	-4. 182 252	-2. 064 28	4.1 82 25	D o w	0.0 00 19	0.1 35 27	

				7	7		6	4	019		20	n	51	95
											19		61	77
64 79 8	DEPT OR	DEP domain containing MTOR-interacting protein	2. 72 28 3	4. 34 88 5	4. 58 43 7	5. 86 24 9	5. 57 83 9	4. 45 70 3	2.6 646 634 55	1.4 139 533 33	2.6 64 66 34 55	U p	0.0 43 56 89 68	0.4 32 33 09 01
32 48	HPGD	Hydroxyprostagla ndin dehydrogenase 15-(NAD)	4. 68 73	3. 35 37 2	4. 25 97 9	7. 36 08 5	7. 45 47 9	5. 03 22 1	5.7 186 713 63	2.5 156 8	5.7 18 67 13 63	U p	0.0 08 60 80 65	0.3 07 29 63 95
33 39 32	HIST2 H3A	Histone cluster 2, h3a	6. 19 18 1	5. 50 18 7	5. 70 53 8	7. 08 31 2	7. 49 99 7	6. 87 60 8	2.5 550 827 22	1.3 533 7	2.5 55 08 27 22	U p	0.0 01 87 90 27	0.1 95 76 45 58
54 84 7	SIDT1	SID1 transmembrane family member 1	6. 44 81 6	6. 41 30 8	7. 41 39 4	6. 14 15 8	5. 38 62 5	5. 36 75 7	-2. 183 425 541	-1. 126 593 333	2.1 83 42 55 41	D o w n	0.0 17 79 31 14	0.3 61 50 23 21
10 15	CDH1 7	Cadherin 17, LI cadherin (liver-intestine)	4. 75 86 4	6. 01 14 8	7. 41 61 8	10 .3 35 51	11 .0 02 37	8. 88 83 2	16. 148 183 71	4.0 133	16. 14 81 83 71	U p	0.0 01 31 49 2	0.1 87 10 78 18
57 44 7	NDRG 2	NDRG family member 2	8. 53 64 1	9. 49 66 2	10 .1 28 39	8. 65 48 6	7. 67 07 2	7. 70 18 1	-2. 599 096 14	-1. 378	2.5 99 09 61 4	D o w n	0.0 21 68 76 04	0.3 76 41 62 63
72 73	TTN	Titin	7. 85 24 4	4. 83 60 4	5. 83 12 6	4. 62 21 4	4. 06 43 9	3. 64 99 3	-4. 173 024 334	-2. 061 093 333	4.1 73 02 43 34	D o w n	0.0 25 56 43 37	0.3 84 73 53 87
55 30 4	SPTLC 3	Serine palmitoyltransfera se, long chain base subunit 3	7. 98 13 4	6. 43 73 7	7. 51 96 7	5. 98 55 8	6. 43 57 8	5. 97 98 3	-2. 264 297 203	-1. 179 063 333	2.2 64 29 72 03	D o w n	0.0 24 03 91 04	0.3 81 89 69 49
80 70	SLC19 A3	Solute carrier family 19	4. 47	7. 26	7. 36	2. 87	3. 35	4. 31	-7. 214	-2. 850	7.2 14	D o	0.0 09	0.3 13

4		(thiamine transporter), member 3	41 5	28	17 7	54	09 8	96 9	419 594	883 333	41 95 94	w n	64 12 71	66 02 93
72 98	TYMS	Thymidylate synthetase	6. 18 65 4	5. 67 18 4	6. 12 52 6	7. 03 88 6	7. 81 32 3	7. 90 10 3	3.0 101 318 19	1.5 898 266 67	3.0 10 13 18 19	U p	0.0 01 25 96 19	0.1 87 10 78 18
26 24 9	KLHL 3	Kelch like family member 3	7. 40 66 2	5. 76 58 4	6. 42 89 9	5. 48 98 3	4. 39 84 3	5. 64 79 7	-2. 558 101 19	-1. 355 073 333	2.5 58 10 11 9	D o w n	0.0 31 10 03 84	0.3 99 91 77 84
56 70 4	JPH1	Junctophilin 1	3. 72 87 7	4. 54 74 3	4. 67 08 1	6. 31 86 8	5. 27 17 2	5. 06 45 5	2.3 554 129 26	1.2 359 8	2.3 55 41 29 26	U p	0.0 19 04 19 6	0.3 67 48 02 31
57 22 4	NHSL 1	NHS like 1	4. 99 35	5. 45 58 3	5. 83 43 1	7. 10 11 6	7. 10 03 2	5. 81 80 2	2.3 706 565 5	1.2 452 866 67	2.3 70 65 65 5	U p	0.0 20 26 80 92	0.3 71 13 26 99
10 01 33 94 1	CD24	CD24 molecule	12. 0 76 91	10. 3 63 66	11. 2 61 96	10. 0 63 08	7. 93 43 2	8. 64 15 2	-5. 114 299 562	-2. 354 536 667	5.1 14 29 95 62	D o w n	0.0 07 62 21 39	0.2 96 60 29 56
10 05 08 22 6	LOC10 050822 6	HHSL751	6. 01 29 9	6. 15 19 1	6. 19 75 4	5. 44 39 4	4. 42 10 8	4. 56 23 8	-2. 482 304 329	-1. 311 68	2.4 82 30 43 29	D o w n	0.0 03 51 83 93	0.2 37 14 66 6
79 86 6	BORA	Bora, aurora kinase A activator	5. 18 87 4	4. 69 67 3	4. 68 79 6	5. 85 04 2	6. 95 53 1	6. 25 89 1	2.8 226 821 19	1.4 970 666 67	2.8 22 68 21 19	U p	0.0 02 64 53	0.2 25 16 16 96
99 6	CDC27	Cell division cycle 27	6. 48 45 1	6. 09 74 9	6. 37 60 1	7. 13 64 5	7. 80 02 7	7. 24 93 7	2.1 082 218 14	1.0 760 266 67	2.1 08 22 18 14	U p	0.0 04 20 23 93	0.2 45 36 29 85
30	HELL	Helicase,	3.	3.	3.	6.	7.	5.	5.7	2.5	5.7	U	0.0	0.1

70	S	lymphoid-specific	92 46 9	58 10 2	96 73 9	21 51	02 32 7	77 95	156 728 13	149 233 33	15 67 28 13	p	00 15 05 14	28 62 18 94
77 84	ZP3	Zona pellucida glycoprotein 3 (sperm receptor)	4. 14 45	3. 65 73 9	4. 18 01 7	5. 97 10 7	5. 17 65 3	4. 76 18 7	2.4 779 321 19	1.3 091 366 67	2.4 77 93 21 19	U p	0.0 06 31 95 57	0.2 83 73 24 96
42 33	MET	MET proto-oncogene, receptor tyrosine kinase	7. 90 99 2	6. 64 85 3	7. 33 12 7	8. 43 91 9	8. 77 02	9. 03 83 1	2.7 371 224 92	1.4 526 6	2.7 37 12 24 92	U p	0.0 04 97 02 3	0.2 63 83 41 07
55 35 1	STK32 B	Serine/threonine kinase 32B	6. 19 90 6	8. 98 87 7	7. 89 40 7	3. 97 97	4. 77 51 9	4. 69 20 5	-9. 264 116 098	-3. 211 653 333	9.2 64 11 60 98	D o w n	0.0 02 04 93 22	0.2 04 15 41 68
84 41 8	CYST M1	Cysteine-rich transmembrane module containing 1	9. 32 08 9	10 .2 25 23	10 .3 14 98	8. 76 66 3	8. 41 36 5	9. 02 51 2	-2. 327 153 971	-1. 218 566 667	2.3 27 15 39 71	D o w n	0.0 08 17 19 13	0.3 01 19 66 52
49 3	ATP2B 4	Atpase, Ca <sup>++</sup> transporting, plasma membrane 4	5. 72 02 3	4. 91 19 2	5. 22 75 4	5. 80 92 9	6. 66 64 7	6. 60 09 8	2.1 028 559 12	1.0 723 5	2.1 02 85 59 12	U p	0.0 14 02 84 09	0.3 45 57 11 86
15 38 30	RNF14 5	Ring finger protein 145	5. 97 71	5. 77 10 1	6. 42 73 7	6. 82 31 2	7. 13 58	7. 89 80 3	2.3 410 514 91	1.2 271 566 67	2.3 41 05 14 91	U p	0.0 08 58 26 88	0.3 07 29 63 95
15 84 71	PRUN E2	Prune homolog 2 (Drosophila)	5. 66 35 7	3. 18 29 7	3. 20 17	4. 73 55	7. 15 47 4	7. 79 24 4	5.8 353 263 1	2.5 448 133 33	5.8 35 32 63 1	U p	0.0 33 21 64 97	0.4 06 85 22 16
14 68 80	LOC14 6880	Rho gtpase activating protein 27 pseudogene	6. 28 76 3	5. 64 95 5	6. 57 03 2	7. 70 07 1	6. 81 67 2	8. 66 05 8	2.9 420 803 88	1.5 568 366 67	2.9 42 08 03 88	U p	0.0 15 83 26 02	0.3 51 16 74 61

38 83 36	SHISA 6	Shisa family member 6	5. 24 62 5	8. 98 87 7	7. 73 35 8	4. 73 89 4	4. 13 47 7	5. 07 39 1	-6. 380 458 058	-2. 673 66	6.3 80 45 80 58	D o w n	0.0 19 12 18 81	0.3 67 65 39 22
16 70	DEFA5	Defensin $\alpha$ 5	5. 19 19	11. .4 39 67	11. .5 66 41	4. 89 23 2	3. 97 91 8	4. 52 25	-30. .58 304 181	-4. 934 66	30. 58 30 41 81	D o w n	0.0 18 99 32 28	0.3 67 34 80 71
22 82 2	PHLD A1	Pleckstrin homology-like domain, family A, member 1	6. 67 02	8. 38 20 9	8. 32 90 1	5. 33 85	7. 22 72 7	5. 73 90 2	-3. 231 423 863	-1. 692 17	3.2 31 42 38 63	D o w n	0.0 33 12 74 62	0.4 06 36 00 72
94 55	HOME R2	Homer scaffolding protein 2	9. 37 21 6	9. 30 08 2	9. 00 02 6	7. 30 47	6. 15 62 2	8. 80 03 8	-3. 491 821 957	-1. 803 98	3.4 91 82 19 57	D o w n	0.0 22 41 77 26	0.3 78 66 05 33
44 19 51	ZFAS1	ZNFX1 antisense RNA 1	8. 82 86 2	8. 16 49	8. 59 28	10. .1 72 64	9. 32 98 2	9. 15 03 1	2.0 309 433 52	1.0 221 5	2.0 30 94 33 52	U p	0.0 19 25 85 78	0.3 67 66 41 57
55 21 5	FANCI	Fanconi anemia complementation group I	4. 59 16 7	4. 36 90 9	4. 42 91 7	5. 97 78 8	6. 14 35 8	6. 10 66 1	3.0 582 648 11	1.6 127 133 33	3.0 58 26 48 11	U p	5.3 66 62 E- 05	0.1 04 83 42 9
13 65	CLDN 3	Claudin 3	8. 66 37 5	7. 46 37 7	7. 87 07 2	8. 72 87 9	9. 72 96 6	10. .0 81 5	2.8 558 166 01	1.5 139 033 33	2.8 55 81 66 01	U p	0.0 11 97 96 4	0.3 31 43 90 01
72	ACTG 2	Actin, $\gamma$ 2, smooth muscle, enteric	5. 45 34 6	4. 78 78 4	4. 92 65	5. 40 73	8. 25 86 5	7. 33 55 1	3.8 491 858 58	1.9 445 533 33	3.8 49 18 58 58	U p	0.0 24 77 36 82	0.3 83 13 18 63
30 84	NRG1	Neuregulin 1	7. 05 38 1	7. 16 15 1	6. 84 54 6	4. 98 19 4	5. 74 22 5	6. 18 48 3	-2. 609 765 175	-1. 383 92	2.6 09 76 51	D o w n	0.0 04 24 59	0.2 46 47 32

												75		89	18
51 19 6	PLCE1	Phospholipase C epsilon 1	5. 05 07 3	6. 07 44 7	4. 38 57	7. 59 64 5	7. 51 48 9	7. 48 40 6	5.1 390 439 84	2.3 615	5.1 39 04 39 84	U p	0.0 00 78 62 02	0.1 77 73 29 45	
67 90	AURK A	Aurora kinase A	4. 22 84 3	4. 39 75 6	4. 30 84 3	5. 26 47 5	5. 97 38 3	5. 00 88 8	2.1 500 149 13	1.1 043 466 67	2.1 50 01 49 13	U p	0.0 05 39 52 36	0.2 69 32 15 26	
30 13	HIST1 H2AD	Histone cluster 1, h2ad	9. 22 00 5	8. 79 40 3	8. 36 35 4	9. 99 62 8	10 .5 65 51	9. 57 93 7	2.3 858 665 22	1.2 545 133 33	2.3 85 86 65 22	U p	0.0 08 08 39 68	0.2 99 13 95 54	
31 74	HNF4 G	Hepatocyte nuclear factor 4, $\gamma$	3. 91 70 3	2. 64 12 6	3. 36 86 7	4. 97 69 9	4. 76 23 6	4. 25 61	2.5 600 346 43	1.3 561 633 33	2.5 60 03 46 43	U p	0.0 06 74 04 64	0.2 88 45 97 19	
10 03 79 66 1	GRIK1 -AS2	GRIK1 antisense RNA 2	4. 81 47 2	3. 57 04 6	3. 81 18 5	4. 65 38 8	6. 10 95 6	5. 64 22	2.6 442 709 27	1.4 028 7	2.6 44 27 09 27	U p	0.0 19 79 55 56	0.3 68 10 68 92	
29 69	GTF2I	General transcription factor iii	7. 83 21 3	8. 52 85 7	8. 56 69 7	7. 38 68	6. 91 57	7. 25 45 3	-2. 178 819 474	-1. 123 546 667	2.1 78 81 94 74	D o w n	0.0 05 28 54 87	0.2 68 46 24 7	
65 50	SLC9A 3	Solute carrier family 9, subfamily A (NHE3, cation proton antiporter 3), member 3	10 .0 07 39	9. 90 14 4	11 .0 10 3	6. 06 48 2	7. 41 51	6. 55 3	-12 .36 968 337	-3. 628 736 667	12. 36 96 83 37	D o w n	8.3 14 47 E- 05	0.1 26 50 89 75	
90 58 9	ZNF62 5	Zinc finger protein 625	7. 08 67 1	7. 47 19 2	7. 41 44 2	4. 66 41 3	6. 17 38 7	5. 85 55 3	-3. 386 605 642	-1. 759 84	3.3 86 60 56 42	D o w n	0.0 03 44 84 71	0.2 37 14 66 6	
10 37	IRF9	Interferon regulatory factor 9	8. 59	7. 51	8. 16	6. 14	7. 58	7. 06	-2. 227	-1. 155	2.2 27	D o	0.0 34	0.4 08	

9			49 5	35 5	23 7	88 1	62 2	94 2	573 961	473 333	57 39 61	w n	36 50 9	33 62 87
34 86	IGFBP 3	Insulin like growth factor binding protein 3	5. 66 98 1	6. 30 73 7	6. 38 42 9	7. 27 14 4	10 .1 80 59	8. 02 62 4	5.1 775 395 42	2.3 722 666 67	5.1 77 53 95 42	U p	0.0 12 48 51 87	0.3 34 46 67 31
15 16 48	SGOL 1	Shugoshin-like 1 (S. Pombe)	4. 10 59 2	3. 96 51 7	3. 83 01 8	4. 76 99 2	5. 26 21 1	4. 94 38 3	2.0 347 666 21	1.0 248 633 33	2.0 34 76 66 21	U p	0.0 01 44 34 72	0.1 87 10 78 18
56 00 0	NXF3	Nuclear RNA export factor 3	6. 89 72	8. 63 07 6	8. 91 59 7	3. 80 12 4	4. 19 94 2	4. 55 98 5	-15 .57 478 13	-3. 961 14	15. 57 47 81 3	D o w n	0.0 00 16 39 86	0.1 28 62 18 94
51 28 0	GOLM 1	Golgi membrane protein 1	10 .2 20 66	10 .8 91 67	11 .8 78 06	7. 20 31 3	9. 29 35 7	9. 13 87 8	-5. 470 363 367	-2. 451 636 667	5.4 70 36 33 67	D o w n	0.0 07 35 72 09	0.2 92 40 97 69
11 16 3	NUDT 4	Nudix hydrolase 4	5. 90 68 7	4. 50 84 1	5. 12 77	3. 52 15 6	4. 35 53 6	3. 47 68 2	-2. 632 463 145	-1. 396 413 333	2.6 32 46 31 45	D o w n	0.0 11 24 71 44	0.3 24 85 44 65
80 15 0	ASRG L1	Asparaginase like 1	6. 49 12 7	7. 81 52 5	7. 93 19	6. 47 73 2	5. 97 37 6	6. 41 77 4	-2. 178 295 986	-1. 123 2	2.1 78 29 59 86	D o w n	0.0 30 53 02 86	0.3 99 30 90 08
51 02 8	VPS36	Vacuolar protein sorting 36 homolog (S. Cerevisiae)	4. 42 2	5. 30 28 1	4. 84 81 3	5. 72 02 5	6. 02 71 7	5. 89 97 3	2.0 345 879 79	1.0 247 366 67	2.0 34 58 79 79	U p	0.0 06 74 18 53	0.2 88 45 97 19
10 05 26 83 1	SLX1B -SULT 1A4	SLX1B-SULT1A4 readthrough (NMD candidate)	6. 47 72 2	6. 93 54 7	6. 66 10 6	7. 80 23 3	8. 02 89 9	7. 66 66 2	2.2 059 447 64	1.1 413 966 67	2.2 05 94 47 64	U p	0.0 01 52 38 01	0.1 87 10 78 18
76	RELL1	RELT-like 1	7.	8.	8.	6.	7.	6.	-2.	-1.	2.6	D	0.0	0.3



82 11			91 07 6	80 59 6	24 44 3	24 38 6	53 01 1	92 69 3	676 009 677	420 083 333	76 00 96 77	o w n	08 61 26 99	07 29 63 95
37 03	STT3A	STT3A, subunit of the oligosaccharyltransferase complex (catalytic)	8. 78 9	9. 53 67 7	8. 95 06 7	8. 08 46 1	7. 99 30 8	7. 96 40 4	-2. 111 453 78	-1. 078 236 667	2.1 11 45 37 8	D o w n	0.0 04 00 07 6	0.2 42 71 06 82
55 28 89	ATXN 7L3B	Ataxin 7-like 3B	8. 01 91 6	8. 77 15 6	8. 51 25 3	7. 14 87 7	7. 35 94 8	7. 63 36 8	-2. 075 952 356	-1. 053 773 333	2.0 75 95 23 56	D o w n	0.0 06 23 54 34	0.2 81 63 25 5
14 38 72	ARHG AP42	Rho gtpase activating protein 42	5. 36 26 8	4. 58 82	4. 98 35 2	5. 65 27 3	6. 82 85 6	5. 69 20 1	2.1 134 988 59	1.0 796 333 33	2.1 13 49 88 59	U p	0.0 25 75 93 94	0.3 85 33 44 54
65 98 2	ZSCA N18	Zinc finger and SCAN domain containing 18	7. 10 39 3	7. 06 83 8	7. 59 12 6	3. 59 99 2	6. 12 45 5	4. 73 89 4	-5. 401 599 466	-2. 433 386 667	5.4 01 59 94 66	D o w n	0.0 04 83 14 31	0.2 60 37 51 7
84 74 7	UNC1 19B	Unc-119 lipid binding chaperone B	5. 90 02 1	6. 39 29 9	7. 10 06 1	5. 02 22 1	5. 34 09 3	5. 21 15 6	-2. 416 697 107	-1. 273 036 667	2.4 16 69 71 07	D o w n	0.0 06 13 27 53	0.2 79 59 97 64
51 20 3	NUSA P1	Nucleolar and spindle associated protein 1	4. 16 22 2	3. 26 89 2	3. 49 95 7	5. 90 60 3	6. 66 57 7	5. 47 05	5.1 713 107 48	2.3 705 3	5.1 71 31 07 48	U p	0.0 00 39 68 69	0.1 60 90 15 41
10 32 4	KLHL 41	Kelch like family member 41	6. 88 80 7	4. 96 23 1	5. 02 33 9	4. 41 69 8	4. 31 60 8	3. 46 17 8	-2. 947 809 58	-1. 559 643 333	2.9 47 80 95 8	D o w n	0.0 26 86 75 27	0.3 88 38 41 04
83 53 9	CHST9	Carbohydrate (N-acetylgalactosamine 4-0) sulfotransferase 9	4. 91 65 3	4. 94 78 8	4. 70 22 7	3. 98 22 4	3. 53 15	3. 86 36 7	-2. 089 401 865	-1. 063 09	2.0 89 40 18 65	D o w n	0.0 00 95 76 9	0.1 86 14 79 2

21 97 90	RTKN 2	Rhotekin 2	3. 07 51 2	4. 11 54 6	4. 03 55 7	5. 04 35	4. 94 30 9	5. 59 10 8	2.7 330 401 74	1.4 505 066 67	2.7 33 04 01 74	U p	0.0 03 54 59 31	0.2 37 14 66 6
51 01 2	PRELI D3B	PRELI domain containing 3B	5. 29 92 6	5. 42 88 8	5. 40 48 4	7. 04 23 5	7. 02 03 7	5. 76 05 9	2.3 458 487 54	1.2 301 1 84 87 54	2.3 45 84 87 54	U p	0.0 12 97 31 33	0.3 36 17 41 55
81 55 7	MAGE D4B	Melanoma antigen family D4B	6. 73 66 1	7. 78 26 7	7. 88 61 3	5. 55 04	5. 72 10 3	6. 69 70 9	-2. 787 483 631	-1. 478 963 333	2.7 87 48 36 31	D o w n	0.0 11 09 69 59	0.3 24 51 13 09
93 66 4	CADP S2	Ca <sup>++</sup> -dependent secretion activator 2	6. 23 92	7. 03 66 4	7. 05 97 1	5. 29 26 7	4. 73 58 5	4. 61 46 3	-3. 725 584 194	-1. 897 466 667	3.7 25 58 41 94	D o w n	0.0 00 55 54 31	0.1 64 81 87 25
89 35	SKAP2	Src kinase associated phosphoprotein 2	5. 64 61 9	4. 28 29 6	4. 86 03 8	5. 33 18 1	7. 29 69 7	6. 69 56 5	2.8 513 266 67	1.5 116 333 33	2.8 51 32 66 67	U p	0.0 31 60 98 85	0.4 01 56 52 84
97 35	KNTC 1	Kinetocho associated 1	5. 07 48 4	5. 17 49 7	5. 35 88 9	5. 81 66 6	7. 05 65 6	6. 63 38 5	2.4 613 616 79	1.2 994 566 67	2.4 61 36 16 79	U p	0.0 06 27 24 22	0.2 82 64 96 74
65 35 13	LOC65 3513	Phosphodiesterase 4D interacting protein-like	4. 99 21 9	4. 38 48 7	4. 28 01 9	5. 74 22 8	5. 56 32	5. 69 20 1	2.1 635 693 03	1.1 134 133 33	2.1 63 56 93 03	U p	0.0 02 59 35 02	0.2 22 69 34 33
79 60 7	FAM11 8B	Family with sequence similarity 118 member B	6. 96 96 5	7. 28 93 7	7. 53 53 9	5. 66 93	6. 15 48 2	6. 74 18 3	-2. 108 406 922	-1. 076 153 333	2.1 08 40 69 22	D o w n	0.0 12 94 23 67	0.3 36 17 41 55
54 73 3	SLC35 F2	Solute carrier family 35 member F2	7. 40 09 7	7. 63 89 5	7. 44 68 5	5. 90 29 1	7. 31 98 8	6. 24 28	-2. 009 811 225	-1. 007 06	2.0 09 81 12	D o w n	0.0 32 44 00	0.4 04 71 37

												25		79	9
54 47 2	TOLLI P	Toll interacting protein	6. 61 29 5	6. 45 69 4	6. 87 28 7	5. 56 05 1	5. 67 55 5	5. 02 98 2	-2. 338 570 086	-1. 225 626 667	2.3 38 57 00 86	D o w n	0.0 01 94 76 5	0.1 98 67 55 98	
25 43	GAGE 1	G antigen 1	4. 52 15 8	4. 21 77 2	4. 33 54 7	4. 46 90 8	6. 30 03 5	5. 69 14 3	2.1 866 111 21	1.1 286 966 67	2.1 86 61 11 21	U p	0.0 39 74 28 51	0.4 23 82 07 35	
58 27	PXMP 2	Peroxisomal membrane protein 2	6. 75 13 3	5. 71 99 9	6. 10 63 5	5. 39 77 5	5. 36 60 6	4. 75 00 2	-2. 029 718 985	-1. 021 28 89 85	2.0 29 71 89 85	D o w n	0.0 17 96 45 32	0.3 62 48 76 38	
49 39	OAS2	2'-5'-oligoadenyla te synthetase 2	7. 42 31 3	7. 12 18 5	7. 33 59 7	5. 12 39 2	6. 79 44 4	6. 64 23 5	-2. 153 594 554	-1. 106 746 667	2.1 53 59 45 54	D o w n	0.0 43 96 87 69	0.4 33 73 23 05	
52 22	PGA5	Pepsinogen 5, group I (pepsinogen A)	7. 40 62 9	7. 50 49 7	7. 27 61 2	6. 42 32 5	5. 58 08 6	6. 58 08 9	-2. 298 660 388	-1. 200 793 333	2.2 98 66 03 88	D o w n	0.0 05 62 13 45	0.2 72 48 17 95	
72 88 33	FAM7 2D	Family with sequence similarity member D	4. 81 14 4	3. 76 74 3	4. 33 53 2	7. 00 88 8	6. 35 93 6	5. 57 41 2	4.0 261 195 17	2.0 093 9 17	4.0 26 11 95 17	U p	0.0 02 23 84 85	0.2 11 69 45 53	
55 60 3	FAM4 6A	Family with sequence similarity member A	8. 82 21 3	8. 10 99 9	8. 16 29 3	7. 69 48 6	7. 13 42 1	7. 04 45 1	-2. 105 009 387	-1. 073 826 667	2.1 05 00 93 87	D o w n	0.0 08 83 67 56	0.3 08 52 19 75	
13 98 86	SPIN4	Spindlin family member 4	4. 58 68 6	4. 67 77 4	4. 81 39 4	5. 61 22 1	6. 55 18 1	6. 04 83 5	2.5 989 700 35	1.3 779 4 35	2.5 98 97 00 35	U p	0.0 01 58 52 13	0.1 87 10 78 18	
11 86 63	BTBD 16	BTB (POZ) domain containing 16	3. 80 03	4. 13 50	4. 48 49	5. 01 08	4. 50 49	5. 91 16	2.0 032 697	1.0 023 566	2.0 03 26	U p	0.0 34 57	0.4 08 42	

			6	1	2		4	2	04	67	97		27	39
27	GNG7	Guanine nucleotide binding protein (G protein), $\gamma$ 7	4.41284	4.90527	5.25769	3.98864	3.69186	3.55994	-2.161131	-1.111786	2.161113	D	0.003	0.23853
28	CES4A	Carboxylesterase 4A	5.78111	6.94668	5.59121	3.68093	4.40493	5.81129	-2.77813	-1.47395	2.77781	D	0.043	0.43373
28	TRDC	T cell receptor $\Delta$ constant	4.4263	6.75331	6.17855	3.08817	4.14957	3.82033	-4.287182	-2.10003	4.28718	D	0.010	0.32243
72	LOC729737	Uncharacterized LOC729737	8.03359	8.30848	7.49201	5.71049	6.09297	7.81824	-2.646575	-1.404126	2.64652	D	0.040	0.42435
52	PGM1	Phosphoglucomutase 1	7.0429	7.33283	7.18712	5.18152	6.94968	5.67531	-2.381900	-1.252113	2.38108	D	0.026	0.3841
13	ADH6	Alcohol dehydrogenase 6 (class V)	5.78562	7.70429	7.66583	6.00123	4.82238	5.45192	-2.650516	-1.406273	2.65061	D	0.032	0.40382
78	CACNA2D1	Calcium channel, voltage-dependent, $\alpha$ 2/ $\Delta$ subunit 1	5.46459	4.53931	4.35603	5.95447	6.25203	5.50581	2.169646	1.1746	2.16964	U	0.016	0.35380
79	AGMAT	Agmatinase	4.86416	4.88425	5.34797	7.53826	7.54528	5.36752	3.445952	1.784893	3.44598	U	0.019	0.36776
80	WNT10A	Wingless-type MMTV	3.43	4.10	3.60	4.03	5.49	6.06	2.7986	1.4847	2.798	U	0.022	0.379

6		integration site family member 10A	40 5	78 7	49 8	45 9	83 2	81 9	543 82	333 33	65 43 82		83 51 91	92 11 68
59	ACTA 2	Actin, $\alpha$ 2, smooth muscle, aorta	8. 42 96 2	7. 81 67 3	7. 87 39 3	8. 24 65 3	11 .1 63 5	9. 77 58 4	3.2 232 810 77	1.6 885 3	3.2 23 28 10 77	U p	0.0 42 95 78 79	0.4 32 07 88 1
39 25	STMN 1	Stathmin 1	5. 88 37 1	4. 97 20 2	5. 13 69 8	6. 68 94 5	6. 84 61 9	6. 46 84 5	2.5 264 763 35	1.3 371 266 67	2.5 26 47 63 35	U p	0.0 02 61 05 24	0.2 23 66 35 21
27 12 1	DKK4	Dickkopf WNT signaling pathway inhibitor 4	5. 21 34	12 .7 60 59	12 .7 22 89	5. 34 09 3	4. 70 01 1	5. 18 09 7	-35 .71 083 592	-5. 158 29	35. 71 08 35 92	D o w n	0.0 31 59 29 24	0.4 01 56 52 84
10 53 76 33 3	LOC10 537633 3	Formin-like protein 6	8. 03 35 9	8. 30 84 8	7. 49 20 1	5. 71 04 9	6. 09 29 7	7. 81 82 4	-2. 646 575 235	-1. 404 126 667	2.6 46 57 52 35	D o w n	0.0 40 05 82 98	0.4 24 35 94 44
71 03	TSPA N8	Tetraspanin 8	9. 83 56 8	9. 23 66 5	8. 97 73 7	12 .4 13 15	11 .7 09 58	11 .3 37 28	5.5 408 347 22	2.4 701 033 33	5.5 40 83 47 22	U p	0.0 00 24 23 06	0.1 47 96 12 36
85 36 3	TRIM5	Tripartite motif containing 5	5. 88 03 3	6. 14 83	5. 99 27 3	4. 75 92 2	5. 08 09 1	5. 13 91 1	-2. 019 563 255	-1. 014 043 333	2.0 19 56 32 55	D o w n	0.0 01 77 64 14	0.1 92 29 25 84
28 44 22	SMIM 24	Small integral membrane protein 24	9. 90 47	8. 39 14 2	10 .6 36 65	7. 65 75 8	8. 57 33 5	7. 60 47 8	-3. 246 803 334	-1. 699 02	3.2 46 80 33 34	D o w n	0.0 23 31 82 95	0.3 80 85 39 85
22 82 1	RASA 3	RAS p21 protein activator 3	6. 01 18 2	4. 40 62 2	4. 59 12 1	5. 87 20 2	6. 65 31 5	6. 30 98 8	2.4 204 355 29	1.2 752 666 67	2.4 20 43 55 29	U p	0.0 27 36 50 7	0.3 89 83 37 07
37	KCNS	Potassium	8.	5.	6.	4.	4.	4.	-5.	-2.	5.0	D	0.0	0.3

87	1	voltage-gated channel, modifier subfamily S, member 1	4699	2831	3740	3005	2737	5744	014166837	32601	14166837	o w n	16090218	52385371
134285	TMEM171	Transmembrane protein 171	46313	4918	5384	64014	86034	7185	5.35209355	2.42010333	5.3520935	U p	0.0180448	0.234239382
2305	FOXM1	Forkhead box M1	549011	481952	536481	709182	78029	61426	3.4431843	1.7837433	3.44318413	U p	0.00479551	0.260263927
10517	FBXW10	F-box and WD repeat domain containing 10	416914	54548	529833	414976	324738	382496	-235188162	-123339	2.351188162	D o w n	0.017653754	0.361123337
643752	RAP1BL	RAP1B, member of RAS oncogene family pseudogene	687926	645431	64404	9294	72915	719915	2.896364821	1.5342433	2.8964821	U p	0.0127739	0.372540654
55966	AJAP1	Adherens junctions associated protein 1	466522	653278	630433	42629	417423	41737	-285585	-1513936667	2.855882585	D o w n	0.016935456	0.358424346
4782	NFIC	Nuclear factor I/C (CCAAT-binding transcription factor)	762041	70614	710072	633194	616048	50687	-2652126	-1407146667	2.6521126	D o w n	0.007575616	0.295829027
29899	GPSM2	G-protein signaling modulator 2	391558	469379	452522	605471	671237	512498	3.001790585	1.5858233	3.001790585	U p	0.007809961	0.299139554
728441	GGT2	Γ-glutamyltransferase 2	916157	931314	859698	748881	756931	595581	-4053739364	-2019253333	4.053739364	D o w n	0.003671527	0.2385983

219902	TMEM136	Transmembrane protein 136	6.41197	5.76339	5.35414	4.08074	5.15736	5.10282	-2.089068	-1.06286	2.089068	D	0.031161	0.4003398
57464	STRIP2	Striatin interacting protein 2	6.8528	6.38219	5.25826	5.23615	5.23615	4.76132	-2.123646	-1.086543	2.123646	D	0.0359435	0.4124733
57604	KIAA1456	KIAA1456	7.92697	6.48541	6.16856	6.14762	5.38256	5.58893	-2.225212	-1.153943	2.225212	D	0.0252841	0.444553
678	ZFP36L2	ZFP36 ring finger protein-like 2	8.21199	7.62164	7.79481	8.91886	9.41289	9.38952	2.574456	1.364267	2.574456	U	0.0012096	0.1861479
6734	SRPRA	SRP receptor $\alpha$ subunit	9.54969	10.59367	9.87539	7.97419	8.38233	8.48141	-3.310249	-1.72694	3.310249	D	0.0012497	0.1861479
285440	CYP4V2	Cytochrome P450, family 4, subfamily V, polypeptide 2	9.22768	9.03516	9.15246	8.87377	7.4972	7.9009	-2.067389	-1.04781	2.067389	D	0.0240366	0.3816949
407977	TNFSF12-TNFSF13	TNFSF12-TNFSF13 readthrough	8.30848	8.37082	9.27544	7.44214	7.87419	6.30389	-2.722326	-1.44484	2.722326	D	0.0223263	0.3611337
51704	GPRC5B	G protein-coupled receptor, class C, group 5, member B	8.24991	8.11348	6.91822	5.96946	6.93405	6.83896	-2.265317	-1.179713	2.265317	D	0.0312642	0.4007422
38	ACAT1	Acetyl-coa acetyltransferase 1	7.2016	7.78037	7.3237	6.18713	6.91257	5.68653	-2.265474	-1.179813	2.265474	D	0.0654746	0.3361741

												28		82	55
93 19	TRIP1 3	Thyroid hormone receptor interactor 13	4. 16 16 3	3. 79 93 2	3. 86 29 7	4. 72 38 9	5. 80 11 8	5. 27 14 8	2.5 039 573 69	1.3 242 1	2.5 03 95 73 69	U p	0.0 03 05 02 02	0.2 34 00 38 89	
62 81	S100A 10	S100 calcium binding protein A10	9. 86 81 4	9. 53 82 5	9. 97 41 9	10 .8 75	11 .2 84 2	12 .0 48 67	3.0 506 077 03	1.6 090 966 67	3.0 50 60 77 03	U p	0.0 01 98 81 48	0.2 01 23 04 31	
52 08	PFKFB 2	6-phosphofructo-2 -kinase/fructose-2, 6-biphosphatase 2	4. 21 07 8	5. 00 34 5	4. 98 88 4	7. 37 27 7	6. 39 97 6	5. 35 82 9	3.1 222 441 01	1.6 425 833 33	3.1 22 24 41 01	U p	0.0 15 60 72 24	0.3 50 84 39 38	
98 3	CDK1	Cyclin-dependent kinase 1	5. 27 41 5	4. 16 41 6	4. 85 05 2	6. 76 35 1	7. 37 47	5. 95 50 2	3.8 232 512 18	1.9 348	3.8 23 25 12 18	U p	0.0 03 08 45 28	0.2 34 23 93 82	
29 08 9	UBE2 T	Ubiquitin conjugating enzyme E2T	6. 34 94 6	6. 37 94 2	6. 72 83 3	8. 82 22 4	8. 72 43 8	7. 58 76 9	3.7 124 373 17	1.8 923 666 67	3.7 12 43 73 17	U p	0.0 01 32 48 19	0.1 87 10 78 18	
10 19 29 53 0	FANCD2P2	Fanconi anemia complementation group D2 pseudogene 2	4. 59 27 4	3. 96 19 3	4. 03 95 2	5. 16 71	5. 71 96	5. 33 09 1	2.3 098 620 07	1.2 078 066 67	2.3 09 86 20 07	U p	0.0 02 18 84 52	0.2 10 07 53 08	
25 92 17	HSPA1 2A	Heat shock protein family A (Hsp70) member 12A	7. 45 02 3	5. 90 20 5	5. 32 82 5	4. 57 22 3	4. 45 74 5	3. 64 62 9	-4. 004 216 556	-2. 001 52	4.0 04 21 65 56	D o w n	0.0 08 97 37 05	0.3 09 26 17 51	
21 22	MECOM	MDS1 and EVI1 complex locus	6. 35 63 9	7. 24 01 6	5. 80 35 8	8. 67 72 5	8. 18 61 5	8. 79 13 9	4.2 424 176 82	2.0 848 866 67	4.2 42 41 76 82	U p	0.0 01 17 36 61	0.1 86 14 79 2	
70 42	TGFB2	Transforming growth factor $\beta$ 2	5. 82 01	7. 51 22	7. 42 66	5. 70 94	5. 51 33	5. 87 18	-2. 331 858	-1. 221 48	2.3 31 85	D o w	0.0 33 87	0.4 08 23	



			5	8	8	7	6	4	101		81	n	18	98
26	HSPB8	Heat shock protein family B (small) member 8	6.92993	7.44949	5.29762	4.18345	5.25748	5.05475	-3.310662	-1.72712	3.310662	D	0.0	0.3
35											10	o	20	71
3											66	w	90	99
											26	n	90	34
											26		99	38
41	MAN1	Mannosidase, $\alpha$ , class 1A, member 1	9.14218	8.45795	8.76062	6.46788	8.45134	7.1627	-2.687522	-1.426276	2.687522	D	0.0	0.3
21	A1										87	o	25	83
											52	w	28	71
											21	n	00	27
											9		19	62
88	ST3G	ST3 $\beta$ -galactoside $\alpha$ -2,3-sialyltransferase 5	5.87519	5.524	5.54874	3.75544	4.46329	4.70694	-2.338629	-1.225663	2.338629	D	0.0	0.2
69	AL5										38	o	05	69
											62	w	37	32
											95	n	26	15
											23		82	26
15	CDCA	Cell division cycle associated 2	5.08689	5.09782	5.09782	6.76416	6.34826	6.25228	2.568177	1.360733	2.568177	U	0.0	0.1
73	2										68	p	00	63
13											13		41	37
											90		57	87
											77		65	34
10	PLK4	Polo-like kinase 4	4.36849	4.400581	3.82253	5.522162	5.681233	4.884833	2.292517	1.19695	2.292517	U	0.0	0.2
73											92	p	02	32
3											54		96	32
											49		14	78
											17		08	35
55	CNDP	CNDP dipeptidase 2 (metallopeptidase M20 family)	8.78507	8.78247	9.17903	8.47809	7.63875	6.53131	-2.577799	-1.36614	2.577799	D	0.0	0.3
74	2										77	o	24	83
8											79	w	57	08
											94	n	14	92
													15	58
23	FN1	Fibronectin 1	8.38712	6.15369	6.42419	9.90123	11.37627	8.48352	6.198892	2.632066	6.198892	U	0.0	0.3
35											98	p	20	71
											87		64	59
											60		57	28
											92			73
53	PLD1	Phospholipase D1	10.92043	9.20562	10.81853	9.22306	8.16638	8.26539	-3.394619	-1.76325	3.394619	D	0.0	0.3
37											94	o	12	34
											61	w	51	46
											97	n	28	67
											99		77	31
44	NR2F1	NR2F1 antisense RNA 1	7.66	8.62	8.821	6.620	7.09	6.64	-2.874	-1.523	2.874	D	0.0	0.2
10	-AS1										74	o	03	34

94			79 1	88 6	57 8	26 9	48 4	44 8	903 106	513 333	90 31 06	w n	06 06 36	00 38 89
55 07	PPP1R 3C	Protein phosphatase 1 regulatory subunit 3C	6. 17 37 9	5. 97 35 6	5. 36 7	3. 51 03	4. 10 79 3	4. 98 85	-3. 107 756 206	-1. 635 873 333	3.1 07 75 62 06	D o w n	0.0 05 40 93 32	0.2 69 32 15 26
10 53 79 25 2	LOC10 537925 2	Coiled-coil domain-containing protein 29-like	7. 46 14 8	7. 42 23 2	7. 32 89 1	7. 15 84 3	5. 30 81 1	5. 41 93 7	-2. 717 474 819	-1. 442 266 667	2.7 17 47 48 19	D o w n	0.0 22 22 55 45	0.3 78 35 72 21
64 35 9	NXN	Nucleoredoxin	6. 70 78 4	7. 57 80 2	7. 51 87 4	5. 52 96	6. 39 78 6	6. 17 67 8	-2. 351 291 379	-1. 233 453 333	2.3 51 29 13 79	D o w n	0.0 09 11 57 39	0.3 10 47 42 9
68 11	STX5	Syntaxin 5	7. 88 63 7	8. 79 86 6	8. 56 33 4	6. 86 49 8	7. 59 93 2	7. 50 84 5	-2. 131 506 321	-1. 091 873 333	2.1 31 50 63 21	D o w n	0.0 13 06 11 85	0.3 36 17 41 55
58 01	PTPRR	Protein tyrosine phosphatase, receptor type, R	6. 32 24 8	3. 43 2	3. 56 29 7	6. 79 83 5	5. 87 06 5	6. 29 56 5	3.6 868 788 23	1.8 824	3.6 86 87 88 23	U p	0.0 43 65 92 09	0.4 32 55 70 49
91 86 0	CALM L4	Calmodulin like 4	8. 33 47 8	7. 80 79 4	9. 07 81 9	9. 68 32 9	9. 75 63 3	9. 17 47 6	2.1 903 427 85	1.1 311 566 67	2.1 90 34 27 85	U p	0.0 17 25 76 58	0.3 60 36 31 48
55 77 1	PRR11	Proline rich 11	5. 70 60 2	5. 14 96 5	5. 19 69	6. 08 09 7	6. 77 11 2	6. 33 05 9	2.0 610 364 22	1.0 433 7	2.0 61 03 64 22	U p	0.0 06 60 98 93	0.2 86 61 99 1
50 05	ORM2	Orosomuroid 2	3. 80 83 1	4. 63 54 1	5. 54 52 6	6. 97 44 8	8. 07 24 4	5. 47 83 9	4.5 276 946 54	2.1 787 766 67	4.5 27 69 46 54	U p	0.0 18 27 69 55	0.3 64 08 78 05
79	MLPH	Melanophilin	9.	10	10	8.	7.	8.	-2.	-1.	2.7	D	0.0	0.3

08 3			18 86 3	.1 17 43	.6 62 13	83 15 7	80 86 2	91 44 8	772 472 851	471 173 333	72 47 28 51	o w n	15 71 49 8	50 84 39 38
55 19 5	C14orf 105	Chromosome 14 open reading frame 105	10 .5 17 34	10 .2 10 82	10 .1 22 71	9. 24 84 6	6. 50 30 7	9. 04 27 2	-4. 052 671 766	-2. 018 873 333	4.0 52 67 17 66	D o w n	0.0 24 00 99 7	0.3 81 89 69 49
84 18 7	TMEM 164	Transmembrane protein 164	6. 55 50 5	6. 58 58 3	6. 89 36	8. 17 88	7. 75 02 8	7. 50 27 4	2.1 923 021 77	1.1 324 466 67	2.1 92 30 21 77	U p	0.0 02 90 61 87	0.2 31 33 53 69
64 38 34	PGA3	Pepsinogen 3, group I (pepsinogen A)	7. 40 62 9	7. 50 49 7	7. 27 61 2	6. 42 32 5	5. 58 08 6	6. 58 08 9	-2. 298 660 388	-1. 200 793 333	2.2 98 66 03 88	D o w n	0.0 05 62 13 45	0.2 72 48 17 95
11 91	CLU	Clusterin	12 .8 46 59	12 .0 71 13	12 .2 51 49	11 .9 51 3	9. 69 93	8. 13 46 3	-5. 507 229 257	-2. 461 326 667	5.5 07 22 92 57	D o w n	0.0 26 79 91 35	0.3 88 38 41 04
44 14 25	ANKR D20A3	Ankyrin repeat domain 20 family member A3	7. 46 14 8	7. 42 23 2	7. 32 89 1	7. 15 84 3	5. 30 81 1	5. 41 93 7	-2. 717 474 819	-1. 442 266 667	2.7 17 47 48 19	D o w n	0.0 22 22 55 45	0.3 78 35 72 21
21 19	ETV5	Ets variant 5	5. 49 82 7	7. 88 40 2	7. 53 79 4	5. 68 50 8	4. 68 40 6	3. 95 55 4	-4. 590 071 627	-2. 198 516 667	4.5 90 07 16 27	D o w n	0.0 17 11 68 35	0.3 59 72 97 69
54 71 6	SLC6A 20	Solute carrier family 6 (proline IMINO transporter), member 20	7. 28 66 5	5. 37 60 9	5. 26 13 8	8. 25 40 2	7. 38 97 8	6. 76 60 7	2.8 191 299 86	1.4 952 5	2.8 19 12 99 86	U p	0.0 48 30 35 58	0.4 44 42 78 55
40 84	MXD1	MAX dimerization protein 1	6. 02 06 5	5. 63 52 6	5. 95 33 5	7. 09 80 4	7. 93 11 4	6. 18 92 6	2.3 022 747 3	1.2 030 6	2.3 02 27 47 3	U p	0.0 27 77 85 05	0.3 91 45 80 68

79 71 8	TBL1 XR1	Transducin ( $\beta$ )-like 1 X-linked receptor 1	6. 11 48 8	5. 85 04 2	5. 95 10 2	7. 45 99 3	7. 66 81 3	7. 47 72 4	2.9 546 624 74	1.5 629 933 33	2.9 54 66 24 74	U p	0.0 00 11 22 38	0.1 27 84 98 29
10 27 25 10 4	LOC10 272510 4	Coiled-coil domain-containing protein 29-like	7. 46 14 8	7. 42 23 2	7. 32 89 1	7. 15 84 3	5. 30 81 1	5. 41 93 7	-2. 717 474 819	-1. 442 266 667	2.7 17 47 48 19	D o w n	0.0 22 22 55 45	0.3 78 35 72 21
73 51	UCP2	Uncoupling protein 2 (mitochondrial, proton carrier)	7. 59 61 2	7. 29 76 8	8. 34 35 7	5. 65 93 8	6. 65 32 9	6. 13 28 2	-3. 025 751 137	-1. 597 293 333	3.0 25 75 11 37	D o w n	0.0 03 62 35 77	0.2 38 59 85 3
54 90 8	SPDL1	Spindle apparatus coiled-coil protein 1	4. 51 58 3	4. 03 37 8	4. 10 41 1	5. 21 10 5	5. 47 86 9	5. 59 87 8	2.3 159 434 08	1.2 116 94 34 08	2.3 15 94 34 08	U p	0.0 00 89 15 61	0.1 81 04 09 24
89 8	CCNE 1	Cyclin E1	4. 13 99 7	3. 83 85 2	4. 04 45 3	5. 47 40 2	4. 80 77 7	5. 11 49 6	2.1 803 755 79	1.1 245 766 67	2.1 80 37 55 79	U p	0.0 01 67 80 26	0.1 89 76 50 67
84 91	MAP4 K3	Mitogen-activated protein kinase kinase kinase kinase 3	5. 78 67 9	5. 54 28 6	5. 68 01 5	7. 18 58 4	7. 14 48 1	5. 72 99 3	2.0 236 035 38	1.0 169 266 67	2.0 23 60 35 38	U p	0.0 42 66 59 11	0.4 32 07 88 1
63 97 6	PRDM 16	PR domain containing 16	4. 56 72 2	6. 04 98 2	6. 13 39 5	3. 62 40 4	4. 12 29 5	4. 30 58 2	-2. 960 949 736	-1. 566 06 333	2.9 60 94 97 36	D o w n	0.0 10 16 11 28	0.3 18 26 13 04
98 44	ELMO 1	Engulfment and cell motility 1	7. 47 43 3	6. 30 73 7	7. 14 49 7	5. 11 80 4	6. 45 57 8	6. 12 84 8	-2. 106 493 309	-1. 074 843 333	2.1 06 49 33 09	D o w n	0.0 46 29 63 23	0.4 39 77 72 08
91 88	DDX2 1	DEAD (Asp-Glu-Ala-Asp ) box helicase 21	4. 59 75 1	4. 83 31 6	5. 06 05 4	6. 21 28 9	6. 44 06 8	5. 02 00 5	2.0 860 927 94	1.0 608 033 33	2.0 86 09 27	U p	0.0 30 26 16	0.3 97 94 45

												94		74	78
55 36 6	LGR4	Leucine-rich repeat containing G protein-coupled receptor 4	4.23019	4.431635	4.428579	4.487359	5.5011	5.56392	2.11439	1.08019	2.11439	U p	0.003410873	0.2371466	
30 06 1	SLC40A1	Solute carrier family 40 (iron-regulated transporter), member 1	8.15468	8.827012	8.860115	7.725583	7.78423	5.596803	-2.530279	-1.339296	2.53027	D o w n	0.023119952	0.380484164	
84 76 6	CRACR2A	Calcium release activated channel regulator 2A	6.33537	7.72809	7.737129	5.51101	5.547538	5.588402	-3.149406	-1.65508	3.1494	D o w n	0.004682063	0.256554706	
64 38 47	PGA4	Pepsinogen 4, group I (pepsinogen A)	7.40629	7.750497	7.727612	6.642325	5.58086	6.58089	-2.298660	-1.200793	2.29866	D o w n	0.005621345	0.272481795	
79 96 2	DNAJC22	Dnaj heat shock protein family (Hsp40) member C22	7.90406	8.83311	8.821574	6.643078	6.607182	6.671319	-3.293382	-1.71957	3.29338	D o w n	0.00192399	0.135279577	
71 69	TPM2	Tropomyosin 2 ( $\beta$ )	7.0639	7.722424	7.711994	8.846266	8.896431	8.855642	2.741217	1.454866	2.74121	U p	0.00504078	0.164248294	
62 9	CFB	Complement factor B	6.80709	6.665957	7.71744	5.503398	4.48899	5.5695	-3.417307	-1.77286	3.4173	D o w n	0.00287057	0.152732	
83 64 1	FAM107B	Family with sequence similarity 107 member B	7.78708	8.898854	8.890984	7.738522	6.653237	7.70944	-2.942705	-1.557143	2.9427	D o w n	0.005850672	0.27740275	
94 79	MAPK8IP1	Mitogen-activated protein kinase 8 interacting protein	6.9884	7.72120	6.69195	5.55782	5.58753	6.64515	-2.101733	-1.07158	2.10173	D o w	0.00617	0.28038	

		1	6	1	2	8	9	8	869		38	n	19	54
											69		39	68
93 69	NRXN 3	Neurexin 3	6. 57 87	5. 05 3	5. 80 55 7	3. 94 31 6	4. 31 60 8	4. 38 68 7	-3. 025 247 829	-1. 597 053 333	3.0 25 24 78 29	D o w n	0.0 04 62 82 22	0.2 55 03 52 42
64 1	BLM	Bloom syndrome, recq helicase-like	4. 67 44 4	4. 35 08 5	4. 46 42 8	5. 27 20 3	5. 91 68 2	5. 42 52 7	2.0 583 904 47	1.0 415 166 67	2.0 58 39 04 47	U p	0.0 03 12 83 11	0.2 34 23 93 82
80 70 5	TSGA 10	Testis specific 10	5. 95 99	4. 94 82 7	5. 48 52 5	4. 93 38 4	3. 61 67 7	4. 37 58 7	-2. 227 841 61	-1. 155 646 667	2.2 27 84 16 1	D o w n	0.0 23 85 37 83	0.3 81 50 64 9
23 50 8	TTC9	Tetratricopeptide repeat domain 9	8. 20 77 2	8. 66 99 6	8. 74 87 2	5. 55 04	6. 27 82 8	6. 72 94 5	-5. 119 809 036	-2. 356 09	5.1 19 80 90 36	D o w n	0.0 00 25 73 21	0.1 50 04 90 39
22 72	FHIT	Fragile histidine triad	7. 63 38 8	6. 24 26 2	7. 71 33 8	6. 12 45 6	5. 42 96 7	5. 34 02 6	-2. 959 041 643	-1. 565 13	2.9 59 04 16 43	D o w n	0.0 10 25 41 72	0.3 18 71 14 25
79 95 6	ERMP 1	Endoplasmic reticulum metallopeptidase 1	9. 11 18 3	8. 90 90 6	9. 29 52	8. 12 89 9	7. 94 42 5	7. 18 00 4	-2. 556 677 163	-1. 354 27	2.5 56 67 71 63	D o w n	0.0 02 86 00 74	0.2 31 19 75 39
10 10 60 22 6	NBPF1 9	Neuroblastoma breakpoint family member 19	7. 77 63	7. 35 32	7. 50 59 9	9. 02 15 2	8. 39 94 5	8. 23 79 8	2.0 108 702 56	1.0 078 2	2.0 10 87 02 56	U p	0.0 08 35 33 07	0.3 04 72 02 15
76 78 46	PFN1P 2	Profilin 1 pseudogene 2	4. 56 47 2	4. 54 17 8	4. 56 26 5	5. 50 50 2	5. 60 16 8	5. 75 35 5	2.0 902 854 93	1.0 637	2.0 90 28 54 93	U p	0.0 00 58 39 46	0.1 65 32 01 52
53	ACP2	Acid phosphatase 2, lysosomal	9. 37	9. 50	9. 13	7. 34	8. 89	7. 90	-2. 448	-1. 292	2.4 48	D o	0.0 14	0.3 46

			73 4	20 8	86 2	60 7	06 8	51 8	735 02	036 667	73 50 2	w n	40 03 28	82 70 31
55 88 8	ZKSC AN7	Zinc finger with KRAB and SCAN domains 7	5. 34 60 4	5. 59 97 6	5. 10 36 1	3. 95 55	4. 39 29 7	4. 69 92	-2. 000 804 212	-1. 000 58	2.0 00 80 42 12	D o w n	0.0 06 04 63 88	0.2 79 48 17 42
55 78 5	FGD6	FYVE, rhogef and PH domain containing 6	5. 63 02 4	5. 34 09 3	5. 15 44	6. 64 61 4	6. 02 13 6	6. 58 20 3	2.0 581 098 69	1.0 413 2	2.0 58 10 98 69	U p	0.0 05 03 02 56	0.2 64 76 00 1
32 49	HPN	Hepsin	8. 17 25 8	7. 46 26 8	7. 06 43 4	4. 45 78 1	4. 26 88 5	4. 38 57	-9. 162 534 126	-3. 195 746 667	9.1 62 53 41 26	D o w n	1.8 16 94 E- 05	0.0 88 73 23 2
68 79	TAF7	TATA-box binding protein associated factor 7	5. 20 80 4	5. 08 67 2	5. 61 42 2	6. 09 32 5	6. 38 55 4	6. 61 36 3	2.0 865 893 02	1.0 611 466 67	2.0 86 58 93 02	U p	0.0 03 53 96 89	0.2 37 14 66 6
57 27	PTCH1	Patched 1	4. 68 53 7	4. 22 43 4	4. 42 82 7	4. 93 64 4	6. 90 96 4	5. 29 17 6	2.4 059 722 45	1.2 666 2	2.4 05 97 22 45	U p	0.0 39 88 42 53	0.4 24 07 99 26
72 95 33	FAM7 2A	Family with sequence similarity member A	4. 81 14 4	3. 76 74 3	4. 33 53 2	7. 00 88 8	6. 35 93 6	5. 57 41 2	4.0 261 195 17	2.0 093 9	4.0 26 11 95 17	U p	0.0 02 23 84 85	0.2 11 69 45 53
38 86 77	NOTC H2NL	Notch 2 N-terminal like	7. 77 63	7. 35 32	7. 50 59 9	9. 02 15 2	8. 39 94 5	8. 23 79 8	2.0 108 702 56	1.0 078 2	2.0 10 87 02 56	U p	0.0 08 35 33 07	0.3 04 72 02 15
84 06 4	HDHD 2	Haloacid dehalogenase like hydrolase domain containing 2	6. 15 50 3	6. 38 51 6	6. 39 82 4	6. 06 38 7	5. 41 58 3	4. 20 10 4	-2. 122 694 374	-1. 085 896 667	2.1 22 69 43 74	D o w n	0.0 49 09 14 38	0.4 46 17 48
34	DPY19	DPY19L2	4.	3.	3.	4.	5.	5.	2.8	1.5	2.8	U	0.0	0.2

91 52	L2P2	pseudogene 2	65 20 6	31 09 2	19 81 9	85 36 3	39 53 4	51 77 1	982 258 01	351 7	98 22 58 01	p	08 07 09 57	99 13 95 54
10 05 1	SMC4	Structural maintenance of chromosomes 4	6. 62 07 9	6. 61 98 7	6. 79 17 5	7. 60 20 6	8. 24 57	8. 15 66 6	2.5 035 987 02	1.3 240 033 33	2.5 03 59 87 02	U p	0.0 01 02 21 74	0.1 86 14 79 2
83 35	HIST1 H2AB	Histone cluster 1, h2ab	5. 31 81 5	4. 50 41 1	4. 83 05 6	6. 00 35 5	6. 56 12 3	5. 25 29 6	2.0 776 798 03	1.0 549 733 33	2.0 77 67 98 03	U p	0.0 28 26 04	0.3 93 02 56 24
57 40 2	S100A 14	S100 calcium binding protein A14	5. 23 20 6	6. 35 64 7	7. 30 98 3	10 .2 09 7	8. 22 49 5	7. 00 83 6	4.5 364 067 4	2.1 815 5	4.5 36 40 67 4	U p	0.0 39 68 65 9	0.4 23 75 38 65
84 91 9	PPP1R 15B	Protein phosphatase 1 regulatory subunit 15B	5. 92 44 2	5. 95 54 2	5. 60 80 5	7. 37 14 5	6. 97 01 4	6. 34 66 4	2.0 947 527 96	1.0 667 8	2.0 94 75 27 96	U p	0.0 09 94 39 08	0.3 16 36 68 89
79 82 8	METT L8	Methyltransferase like 8	4. 91 07 2	4. 69 89 9	4. 60 58 9	6. 47 90 4	5. 77 63 5	5. 10 80 2	2.0 694 824 3	1.0 492 7	2.0 69 48 24 3	U p	0.0 21 08 46 77	0.3 72 54 06 54
26 38	GC	Group-specific component (vitamin D binding protein)	10 .5 28 45	11 .3 07 36	12 .1 04 23	3. 65 82 5	8. 17 42 5	3. 33 64 6	-76 .48 085 076	-6. 257 026 667	76. 48 08 50 76	D o w n	0.0 01 59 87 97	0.1 87 19 40 74
20 13	EMP2	Epithelial membrane protein 2	6. 24 70 1	6. 32 74 9	7. 09 79 1	8. 06 44 9	8. 18 05 4	8. 03 62 5	2.9 004 766 4	1.5 362 9	2.9 00 47 66 4	U p	0.0 00 93 67 66	0.1 84 70 58 65
26 79	GGT3 P	Γ-glutamyltransferase 3 pseudogene	9. 16 15 7	9. 31 31 4	8. 59 69 8	7. 48 88 1	7. 56 93 1	5. 95 58 1	-4. 053 739 364	-2. 019 253 333	4.0 53 73 93 64	D o w n	0.0 03 67 15 27	0.2 38 59 85 3



80 85 6	KIAA1 715	KIAA1715	4. 95 59 8	4. 77 92	4. 94 24 6	5. 51 39 6	6. 64 21 4	5. 54 68 7	2.0 117 392 64	1.0 084 433 33	2.0 11 73 92 64	U p	0.0 19 69 24 96	0.3 67 76 00 84
74 77	WNT7 B	Wingless-type MMTV integration site family member 7B	5. 41 51 6	5. 73 45 9	6. 02 77 5	4. 85 88 2	4. 03 82 7	5. 23 57 6	-2. 020 739 475	-1. 014 883 333	2.0 20 73 94 75	D o w n	0.0 22 17 42 93	0.3 78 35 72 21
57 08 2	CASC 5	Cancer susceptibility candidate 5	4. 70 56 4	3. 56 58	4. 80 19 8	6. 23 26	6. 54 47 9	5. 66 16 3	3.4 546 351 03	1.7 885 333 33	3.4 54 63 51 03	U p	0.0 02 93 21 09	0.2 31 33 53 69
84 70	SORB S2	Sorbin and SH3 domain containing 2	6. 08 78 2	6. 24 10 5	5. 64 47 3	5. 45 49 5	3. 35 33 5	5. 19 40 7	-2. 503 147 548	-1. 323 743 333	2.5 03 14 75 48	D o w n	0.0 46 93 61 12	0.4 41 20 29 14
12 45 65	SLC38 A10	Solute carrier family 38, member 10	6. 56 07 6	6. 79 05 4	6. 51 01 6	5. 70 62	5. 01 62 4	5. 99 32	-2. 068 531 126	-1. 048 606 667	2.0 68 53 11 26	D o w n	0.0 09 16 93 56	0.3 10 47 42 9
83 46 1	CDCA 3	Cell division cycle associated 3	5. 38 52	4. 96 02 7	5. 18 44 3	6. 83 95 9	7. 10 14 7	6. 04 69 2	2.8 011 644 18	1.4 860 266 67	2.8 01 16 44 18	U p	0.0 02 23 20 66	0.2 11 69 45 53
93 59 4	TBC1 D31	TBC1 domain family member 31	4. 34 41 3	4. 09 35 1	4. 18 48 6	5. 76 21 3	5. 81 47 1	4. 30 99 3	2.1 259 239 67	1.0 880 9	2.1 25 92 39 67	U p	0.0 33 76 73 4	0.4 07 80 71 68
16 28	DBP	D site of albumin promoter (albumin D-box) binding protein	7. 95 61 2	8. 40 73 3	9. 35 45 8	7. 31 76 8	7. 59 52 9	7. 13 88 1	-2. 332 833 485	-1. 222 083 333	2.3 32 83 34 85	D o w n	0.0 14 56 44 66	0.3 46 82 70 31
83 31	HIST1 H2AJ	Histone cluster 1, h2aj	6. 58 63 2	5. 47 89 7	5. 92 98 3	7. 17 94 1	8. 36 02 9	6. 75 66 3	2.7 014 550 31	1.4 337 366 67	2.7 01 45 50	U p	0.0 19 84 42	0.3 68 20 43

												31		04	05
48 54	NOTC H3	Notch 3	4. 52 82 7	4. 53 14 1	4. 64 51 4	5. 16 28 2	6. 02 72 4	5. 70 43 6	2.0 895 611 8	1.0 632	2.0 89 56 11 8	U p	0.0 04 52 06 31	0.2 53 69 15 42	
31 75	ONEC UT1	One cut homeobox 1	10. 4 65 52	9. 57 93 7	10. .1 63 65	10. .2 22 92	6. 29 98 8	5. 30 68 9	-6. 930 454 656	-2. 792 95	6.9 30 45 46 56	D o w n	0.0 49 00 38 65	0.4 46 17 48	
67 78 00	SNOR A12	Small nucleolar RNA, H/ACA box 12	7. 63 53 6	8. 66 00 1	7. 86 33 6	8. 45 77 6	9. 06 74	9. 82 36 8	2.0 898 074 18	1.0 633 7	2.0 89 80 74 18	U p	0.0 41 07 40 02	0.4 26 78 72 82	
94 93	KIF23	Kinesin family member 23	5. 28 94 2	4. 57 84 6	4. 92 32 6	6. 17 62 7	6. 52 92 5	5. 82 86 7	2.3 745 980 59	1.2 476 833 33	2.3 74 59 80 59	U p	0.0 03 10 92 69	0.2 34 23 93 82	
57 57 3	ZNF47 1	Zinc finger protein 471	5. 36 43 6	5. 81 05 2	6. 00 82 8	2. 11 88 8	4. 24 33	2. 50 38 7	-6. 832 293 731	-2. 772 37	6.8 32 29 37 31	D o w n	0.0 01 38 37 08	0.1 87 10 78 18	
11 63	CKS1 B	CDC28 protein kinase regulatory subunit 1B	6. 51 89 5	6. 06 74 8	6. 00 63 6	7. 84 52 9	7. 14 8	6. 81 41 2	2.1 016 755 97	1.0 715 4	2.1 01 67 55 97	U p	0.0 12 45 94 41	0.3 34 46 67 31	
23 64 1	LDOC 1	Leucine zipper, down-regulated in cancer 1	8. 21 36 1	7. 80 29 3	8. 20 20 8	3. 92 02 2	6. 02 96 7	4. 82 18 8	-8. 870 097 729	-3. 148 95	8.8 70 09 77 29	D o w n	0.0 00 47 34 48	0.1 64 24 82 94	
65 26 6	WNK4	WNK lysine deficient protein kinase 4	3. 98 64	4. 08 98 8	4. 60 04 2	4. 53 71 1	6. 27 04 7	6. 51 09 1	2.9 226 221 71	1.5 472 633 33	2.9 22 62 21 71	U p	0.0 21 15 91 73	0.3 72 54 06 54	
24 59 73	ATP6V 1C2	Atpase, H+ transporting, lysosomal 42kda,	4. 05 14	4. 78 88	4. 91 29	6. 70 73	7. 21 41	5. 13 98	3.4 091 057	1.7 693 933	3.4 09 10	U p	0.0 14 37	0.3 46 79	

		V1 subunit C2		6		6	3	5	05	33	57 05		99 75	70 53
55 63	PRKA A2	Protein kinase, AMP-activated, $\alpha$ 2 catalytic subunit	5. 26 97 2	5. 61 61	5. 21 60 2	3. 70 68 9	3. 59 24 2	4. 84 70 7	-2. 494 043 566	-1. 318 486 667	2.4 94 04 35 66	D o w n	0.0 07 93 40 98	0.2 99 13 95 54
96 59	PDE4 DIP	Phosphodiesterase 4D interacting protein	4. 99 21 9	4. 38 48 7	4. 28 01 9	5. 74 22 8	5. 56 32	5. 69 20 1	2.1 635 693 03	1.1 134 133 33	2.1 63 56 93 03	U p	0.0 02 59 35 02	0.2 22 69 34 33
88 54	ALDH 1A2	Aldehyde dehydrogenase 1 family member A2	9. 75 28 7	5. 26 81 3	7. 74 77 1	4. 84 01 6	5. 75 99 5	4. 16 97 8	-6. 347 873 301	-2. 666 273 333	6.3 47 87 33 01	D o w n	0.0 40 62 71 01	0.4 26 25 43 06
65 98 5	AACS	Acetoacetyl-coa synthetase	5. 94 07 3	7. 35 71 6	6. 43 39 3	5. 08 01 3	4. 94 78 8	5. 58 96 7	-2. 587 179 227	-1. 371 38	2.5 87 17 92 27	D o w n	0.0 10 25 04 12	0.3 18 71 14 25
10 05 32 72 6	NDUF C2-KC TD14	NDUFC2-KCTD1 4 readthrough	6. 56 54 9	8. 62 03 7	8. 64 64 5	3. 64 40 5	3. 83 58 3	5. 48 01 8	-12 .32 984 991	-3. 624 083 333	12. 32 98 49 91	D o w n	0.0 01 42 99 44	0.1 87 10 78 18
38 65 93	CHKB -CPT1 B	CHKB-CPT1B readthrough (NMD candidate)	7. 38 68 5	7. 57 94 4	7. 26 70 7	6. 21 08	5. 82 94 3	7. 15 15 6	-2. 019 301 965	-1. 013 856 667	2.0 19 30 19 65	D o w n	0.0 25 55 73 56	0.3 84 73 53 87
37 50 56	MIA3	Melanoma inhibitory activity family member 3	9. 41 56 2	10 .7 18 65	10 .4 23 68	9. 31 81 9	8. 99 91 8	8. 99 51 4	-2. 116 694 898	-1. 081 813 333	2.1 16 69 48 98	D o w n	0.0 20 36 33 18	0.3 71 13 26 99
22 25 84	FAM8 3B	Family with sequence similarity member B	6. 16 95 8	5. 50 11	5. 63 23	8. 72 54 5	7. 97 96 4	7. 35 13 9	4.7 606 767 28	2.2 511 666 67	4.7 60 67 67 28	U p	0.0 00 67 05 95	0.1 72 63 18 47
55 72	ASF1B	Anti-silencing function 1B	4. 83	3. 98	4. 74	6. 56	6. 47	5. 27	2.9 929	1.5 815	2.9 92	U p	0.0 06	0.2 88

3		histone chaperone	82 3	41 4	77 8	47 5	91 4	09	053 75	466 67	90 53 75		83 34 48	45 97 19
65 36 04	HIST2 H3D	Histone cluster 2, h3d	6. 19 18 1	5. 50 18 7	5. 70 53 8	7. 08 31 2	7. 49 99 7	6. 87 60 8	2.5 550 827 22	1.3 533 7	2.5 55 08 27 22	U p	0.0 01 87 90 27	0.1 95 76 45 58
36 58	IREB2	Iron responsive element binding protein 2	3. 99 40 5	3. 92 82 5	4. 06 24 6	5. 08 51 5	5. 11 35 6	5. 15 39 3	2.1 774 304 93	1.1 226 266 67	2.1 77 43 04 93	U p	0.0 00 23 91 58	0.1 47 96 12 36
22 99 8	LIMC H1	LIM and calponin homology domains 1	8. 23 21 4	7. 44 35	8. 07 23 6	6. 55 14 2	5. 65 82 4	5. 47 45 3	-4. 059 409 833	-2. 021 27	4.0 59 40 98 33	D o w n	0.0 00 86 72 78	0.1 81 04 09 24
15 35 79	BTNL 9	Butyrophilin-like 9	3. 35 09 9	4. 53 68 7	3. 76 82 5	5. 93 38 8	4. 64 60 7	4. 85 27 8	2.3 930 878 07	1.2 588 733 33	2.3 93 08 78 07	U p	0.0 22 77 86 94	0.3 79 66 75 7
70 53	TGM3	Transglutaminase 3	6. 79 97 7	6. 36 54 7	5. 46 04 8	4. 90 38 3	4. 28 74 8	5. 08 10 9	-2. 734 177 05	-1. 451 106 667	2.7 34 17 70 5	D o w n	0.0 07 83 48 18	0.2 99 13 95 54
55 23 3	MOB1 A	MOB kinase activator 1A	7. 83 48 9	6. 84 00 6	6. 97 99 6	8. 06 65 9	8. 69 27	8. 35 80 9	2.2 255 419 06	1.1 541 566 67	2.2 25 54 19 06	U p	0.0 10 26 48 7	0.3 18 79 03 09
51 39	PDE3 A	Phosphodiesterase 3A	4. 37 25 6	4. 63 45 4	4. 31 60 8	4. 59 04 7	6. 31 31 1	5. 50 68 1	2.0 407 083 32	1.0 290 7	2.0 40 70 83 32	U p	0.0 44 42 84 89	0.4 35 14 07 99
80 23 7	ELL3	Elongation factor RNA polymerase II-like 3	3. 80 56 1	4. 50 55 4	4. 87 25 4	6. 10 40 1	6. 24 71 7	4. 70 20 8	2.4 450 376 26	1.2 898 566 67	2.4 45 03 76 26	U p	0.0 30 13 41 99	0.3 97 94 45 78
46	MYB	V-myb avian	4.	5.	6.	6.	8.	7.	4.7	2.2	4.7	U	0.0	0.3

02		myeloblastosis viral oncogene homolog	00 62 3	88 13 1	13 52 7	29 41	55 96 7	87 45 1	081 381 92	351 566 67	08 13 81 92	p	20 06 33 66	70 15 38 07
64 05	SEMA 3F	Sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3F	5. 75 55 1	7. 22 22 8	6. 92 35	5. 72 60 1	5. 69 47 3	5. 35 82 4	-2. 057 325 403	-1. 040 77	2.0 57 32 54 03	D o w n	0.0 34 28 80 4	0.4 08 27 35 55
91	ACVR 1B	Activin A receptor type IB	8. 28 16 9	8. 30 93 9	8. 46 81 1	6. 55 76 5	7. 23 50 4	7. 83 24 6	-2. 210 970 843	-1. 144 68	2.2 10 97 08 43	D o w n	0.0 11 95 53 39	0.3 31 43 90 01
20	ABCA 2	ATP binding cassette subfamily A member 2	8. 19 45 3	7. 72 64 2	7. 79 06 9	7. 17 71 9	6. 45 50 7	6. 97 53 3	-2. 048 663 922	-1. 034 683 333	2.0 48 66 39 22	D o w n	0.0 06 70 60 53	0.2 87 91 07 42
56 08	MAP2 K6	Mitogen-activated protein kinase kinase 6	5. 61 75 2	7. 08 42 4	7. 49 07 2	5. 68 26 8	5. 18 63 8	5. 29 36 7	-2. 537 222 428	-1. 343 25	2.5 37 22 24 28	D o w n	0.0 27 45 40 47	0.3 89 83 37 07
59 51 01	SMG1 P5	SMG1 pseudogene 5	5. 95 62 4	6. 50 92 3	6. 39 43 8	8. 01 35 7	7. 61 26 5	7. 36 25 8	2.5 960 472 95	1.3 763 166 67	2.5 96 04 72 95	U p	0.0 01 36 24 71	0.1 87 10 78 18
56 46	PRSS3	Protease, serine 3	6. 85 99 7	6. 47 43 2	8. 36 68 7	8. 79 26 3	8. 63 16 9	7. 96 38 4	2.3 440 445 67	1.2 29	2.3 44 04 45 67	U p	0.0 48 42 41 2	0.4 44 62 56 03
20 03 16	APOB EC3F	Apolipoprotein B mrna editing enzyme, catalytic polypeptide-like 3F	5. 19 62	5. 08 68 8	5. 66 22 7	3. 33 27 8	4. 29 89 6	4. 78 31 6	-2. 260 773 824	-1. 176 816 667	2.2 60 77 38 24	D o w n	0.0 18 91 93 52	0.3 67 34 80 71
78 02	DNAL I1	Dynein, axonemal, light intermediate chain 1	6. 80 46 6	6. 94 62 8	7. 31 63 5	3. 67 72 4	4. 71 16 7	6. 10 39 7	-4. 567 706 65	-2. 191 47	4.5 67 70 66	D o w n	0.0 06 78 09	0.2 88 45 97

											5		62	19
70 27	TFDP1	Transcription factor Dp-1	4. 60 51 7	4. 60 74 8	4. 88 42	6. 04 60 5	6. 30 78 3	5. 68 5	2.4 863 165 72	1.3 140 1	2.4 86 31 65 72	U p	0.0 00 80 17 39	0.1 78 59 49 75
72 63	TST	Thiosulfate sulfurtransferase (rhodanese)	8. 28 63 6	9. 07 33 1	9. 30 48	7. 92 41	7. 55 38 5	7. 50 55 2	-2. 340 829 734	-1. 227 02	2.3 40 82 97 34	D o w n	0.0 06 09 79 7	0.2 79 48 17 42
40 04 51	FAM1 74B	Family with sequence similarity 174 member B	5. 43 44 3	8. 05 65 6	7. 26 08 1	5. 34 44 1	4. 84 78 4	5. 85 39 9	-2. 966 002 883	-1. 568 52	2.9 66 00 28 83	D o w n	0.0 48 30 08 4	0.4 44 42 78 55
79 05 8	ASPSC R1	Alveolar soft part sarcoma chromosome region, candidate 1	7. 40 80 7	9. 73 15 5	9. 01 96 7	7. 39 73 7	6. 81 19 8	7. 38 48 1	-2. 871 311 793	-1. 521 71	2.8 71 31 17 93	D o w n	0.0 33 04 25 23	0.4 06 21 09 32
66 38	SNRP N	Small nuclear ribonucleoprotein polypeptide N	9. 90 52 3	8. 46 53 6	9. 54 75 4	7. 89 77 3	8. 28 39 7	7. 41 10 2	-2. 716 602 22	-1. 441 803 333	2.7 16 60 22 2	D o w n	0.0 11 56 95 93	0.3 27 65 98 66
20 01	ELF5	E74-like factor 5 (ets domain transcription factor)	4. 31 00 4	8. 63 93 2	7. 60 04 2	4. 01 62 3	4. 02 41 8	4. 71 12 8	-6. 060 191 291	-2. 599 363 333	6.0 60 19 12 91	D o w n	0.0 38 79 46 88	0.4 20 31 88 17
51 51 4	DTL	Denticleless E3 ubiquitin protein ligase homolog (Drosophila)	3. 96 56	3. 69 64 9	3. 61 44 7	5. 31 65 6	5. 15 13 9	4. 38 56 7	2.2 852 521 11	1.1 923 533 33	2.2 85 25 21 11	U p	0.0 03 77 04 42	0.2 38 59 85 3
84 89 7	TBRG 1	Transforming growth factor $\beta$ regulator 1	7. 64 65 2	7. 75 77 4	8. 16 35 9	6. 15 17 4	6. 55 50 5	6. 83 71	-2. 533 830 467	-1. 341 32	2.5 33 83 04 67	D o w n	0.0 01 57 88 04	0.1 87 10 78 18
27 44	GLS	Glutaminase	5. 69 23	4. 51 71	4. 35 58	5. 37 93	7. 91 98	6. 24 07	3.1 561 373	1.6 581 6	3.1 56 13	U p	0.0 43 97	0.4 33 73

			2	8	6	2		2	71		73		38	23
											71		09	05
53 65	PLXN B3	Plexin B3	6. 07 25	6. 96 18	6. 77 51 9	5. 98 50 7	5. 25 26 6	5. 44 68 9	-2. 058 542 641	-1. 041 623 333	2.0 58 54 26 41	D o w n	0.0 14 37 94 49	0.3 46 79 70 53
84 95	PPFIB P2	PTPRF interacting protein, binding protein 2 (liprin $\beta$ 2)	10 .0 19 24	9. 69 79	9. 71 04 1	7. 98 12	8. 69 56 4	8. 47 92 4	-2. 682 955 886	-1. 423 823 333	2.6 82 95 58 86	D o w n	0.0 00 92 21 79	0.1 82 88 63 95
92 60	PDLI M7	PDZ and LIM domain 7	7. 22 59 9	6. 27 31	6. 61 72	7. 15 38 1	8. 04 95 7	9. 46 88 8	2.8 652 413 48	1.5 186 566 67	2.8 65 24 13 48	U p	0.0 35 78 15 07	0.4 12 27 05 35
37 60	KCNJ3	Potassium channel, inwardly rectifying subfamily J, member 3	4. 92 74 6	4. 83 67 4	4. 79 56 1	6. 01 69 3	7. 41 71 9	5. 83 86 1	2.9 710 509 24	1.5 709 733 33	2.9 71 05 09 24	U p	0.0 07 38 44 17	0.2 92 72 51 41
23 28 6	WWC1	WW and C2 domain containing 1	7. 90 61 5	7. 90 93 3	7. 99 82	5. 75 59 1	6. 69 33 8	7. 46 79 3	-2. 460 275 71	-1. 298 82	2.4 60 27 57 1	D o w n	0.0 17 71 00 08	0.3 61 12 33 37
10 01 32 40 3	FAM1 57B	Family with sequence similarity 157 member B	8. 27 78 2	8. 11 34 5	7. 66 23 9	5. 84 47 6	5. 87 11 1	6. 62 62 8	-3. 742 070 312	-1. 903 836 667	3.7 42 07 03 12	D o w n	0.0 00 42 62 53	0.1 63 37 87 34
73 36	UBE2 V2	Ubiquitin conjugating enzyme E2 variant 2	5. 90 65 9	5. 80 49 3	5. 62 52 7	7. 14 00 2	7. 51 02 6	5. 97 02 6	2.1 363 726 7	1.0 951 633 33	2.1 36 37 26 7	U p	0.0 30 02 14 55	0.3 97 94 45 78
10 28 3	CWC2 7	CWC27 spliceosome-associated protein homolog	5. 70 80 8	7. 65 85 2	9. 22 24 6	5. 67 27 8	5. 28 84	5. 58 86	-4. 036 467 661	-2. 013 093 333	4.0 36 46 76 61	D o w n	0.0 40 12 69 4	0.4 24 74 11 08
11 23	SEC63	SEC63 homolog, protein	6. 01	6. 28	5. 88	4. 81	5. 63	4. 74	-2. 004	-1. 003	2.0 04	D o	0.0 11	0.3 27

1		translocation regulator	47 9	90 3	82 7	04 2	02 4	23 2	214 147	036 667	21 41 47	w n	42 30 56	65 98 66
66 46	SOAT1	Sterol O-acyltransferase 1	7. 46 27 2	7. 17 02 3	7. 30 98 9	6. 13 90 4	6. 37 65 4	6. 17 77 2	-2. 118 700 996	-1. 083 18 70 09 96	2.1 18 70 09 96	D o w n	0.0 01 12 69 49	0.1 86 14 79 2
57 16 2	PELI1	Pellino E3 ubiquitin protein ligase 1	6. 38 52 6	6. 57 16 9	6. 57 79 7	7. 56 46 4	8. 25 86 2	7. 29 33 7	2.2 877 086 55	1.1 939 033 33	2.2 87 70 86 55	U p	0.0 04 60 17 05	0.2 54 41 63 12
84 45 6	L3MB TL3	L(3)mbt-like 3 (Drosophila)	4. 36 51 6	3. 67 54 3	3. 95 68 6	5. 11 05	5. 34 09 3	4. 71 98 8	2.0 819 758 49	1.0 579 533 33	2.0 81 97 58 49	U p	0.0 04 77 89 53	0.2 60 26 39 27
88 63	PER3	Period circadian clock 3	7. 11 57 9	8. 05 90 6	9. 30 43 9	4. 81 46 7	7. 62 00 6	5. 44 57 9	-4. 593 434 744	-2. 199 573 333	4.5 93 43 47 44	D o w n	0.0 32 67 22 31	0.4 04 71 37 9
71 71	TPM4	Tropomyosin 4	8. 12 47 7	8. 27 37 6	8. 21 57 1	9. 35 46 6	9. 61 41	9. 63 35 8	2.5 129 233 51	1.3 293 666 67	2.5 12 92 33 51	U p	0.0 00 31 04 71	0.1 57 71 83 51
30 17	HIST1 H2BD	Histone cluster 1, h2bd	7. 73 83	7. 93 24 7	7. 74 25 4	9. 91 24 4	8. 75 06 3	8. 55 74 1	2.4 100 392 9	1.2 690 566 67	2.4 10 03 92 9	U p	0.0 11 80 74	0.3 29 50 23 79
96 58	ZNF51 6	Zinc finger protein 516	9. 02 18 7	7. 85 45 7	8. 16 40 5	7. 65 16 2	7. 04 83 8	6. 74 13 4	-2. 296 945 565	-1. 199 716 667	2.2 96 94 55 65	D o w n	0.0 16 63 82 23	0.3 56 68 17 47
26 28	GATM	Glycine amidinotransferase (L-arginine:glycin e amidinotransferase )	8. 39 33 7	9. 88 98 9	9. 66 98 1	4. 19 95 1	6. 98 87 4	8. 72 15 2	-6. 413 432 348	-2. 681 096 667	6.4 13 43 23 48	D o w n	0.0 42 06 31 54	0.4 30 12 48 54



64 82	ST3G AL1	ST3 $\beta$ -galactoside $\alpha$ -2,3-sialyltransfer ase 1	9. 04 54 7	6. 21 98 4	7. 83 12 8	4. 77 61	6. 08 99 7	4. 97 05 8	-5. 351 636 029	-2. 419 98	5.3 51 63 60 29	D o w n	0.0 12 17 39 41	0.3 33 39 53 91
11 04 1	B4GA T1	B-1,4-glucuronyltr ansferase 1	5. 73 03 5	6. 48 38 5	6. 58 66 8	4. 72 28 7	5. 27 78 8	4. 99 28 2	-2. 410 117 249	-1. 269 103 333	2.4 10 11 72 49	D o w n	0.0 03 80 74 08	0.2 38 90 72 74
25 38 27	MSRB 3	Methionine sulfoxide reductase B3	4. 34 28 6	4. 14 37	3. 63 73 4	5. 01 77	6. 99 15 4	5. 82 52	3.7 412 317 43	1.9 035 133 33	3.7 41 23 17 43	U p	0.0 06 32 24 13	0.2 83 73 24 96
14 8	ADRA 1A	Adrenoceptor $\alpha$ 1A	7. 77 71 8	8. 27 51 7	7. 29 98 6	5. 97 78 9	6. 42 55 4	7. 13 91 8	-2. 411 392 785	-1. 269 866 667	2.4 11 39 27 85	D o w n	0.0 12 90 79 16	0.3 36 17 41 55
59 23	RASG RF1	Ras protein specific guanine nucleotide releasing factor 1	4. 37 97 3	8. 87 27 7	8. 67 84 5	4. 60 23 8	4. 06 56 7	4. 62 49	-7. 358 100 255	-2. 879 333 333	7.3 58 10 02 55	D o w n	0.0 39 41 33 54	0.4 22 68 46 91
11 22 8	RASSF 8	Ras association (ralgds/AF-6) domain family (N-terminal) member 8	8. 63 31 1	7. 78 59 2	8. 60 61 1	6. 90 51 7	7. 79 32 5	6. 57 26 6	-2. 380 646 37	-1. 251 353 333	2.3 80 64 63 7	D o w n	0.0 15 89 99 19	0.3 51 31 08 12
41 51 17	STX19	Syntaxin 19	5. 25 29	5. 36 12 6	4. 67 56 6	6. 70 97 7	5. 97 39 4	6. 14 54 2	2.2 654 065 82	1.1 797 7	2.2 65 40 65 82	U p	0.0 05 22 50 35	0.2 66 84 56 14
10 61 2	TRIM3	Tripartite motif containing 3	5. 65 48 6	7. 23 41 6	7. 05 61	4. 01 99 3	5. 45 06 1	4. 88 33 9	-3. 639 474 106	-1. 863 73	3.6 39 47 41 06	D o w n	0.0 09 51 06 19	0.3 13 03 31 69
85 47 7	SCIN	Scinderin	4. 98 64 9	4. 58 10 6	4. 88 42	5. 32 82 8	7. 48 71	6. 40 99 1	3.0 129 568 26	1.5 911 8	3.0 12 95 68	U p	0.0 17 65 60	0.3 61 12 33

												26		1	37
84 07	TAGL N2	Transgelin 2	7. 19 62 8	6. 72 16 8	7. 60 38 5	8. 97 21 3	8. 04 17 9	7. 65 97	2.0 713 959 22	1.0 506 033 33	2.0 71 39 59 22	U p	0.0 34 26 87 6	0.4 08 27 35 55	
79 77 2	MCTP 1	Multiple C2 domains, transmembrane 1	5. 63 52 6	6. 39 28 4	6. 49 29 5	3. 55 16 1	5. 62 79 8	4. 78 13 8	-2. 867 963 507	-1. 520 026 667	2.8 67 96 35 07	D o w n	0.0 24 62 49 06	0.3 83 13 18 63	
79 93 2	KIAA0 319L	KIAA0319-like	8. 28 17	9. 05 91 8	8. 81 00 5	7. 91 39 1	7. 13 64 5	7. 82 14 3	-2. 133 240 564	-1. 093 046 667	2.1 33 24 05 64	D o w n	0.0 10 67 15 19	0.3 23 69 99 74	
81 88 8	HYI	Hydroxypyruvate isomerase (putative)	7. 47 97 4	8. 25 03 3	6. 80 77 4	5. 43 82 9	6. 56 22	6. 45 86 2	-2. 566 080 922	-1. 359 566 667	2.5 66 08 09 22	D o w n	0.0 20 85 14 86	0.3 71 99 34 38	
78 51	MALL	Mal, T-cell differentiation protein-like	7. 63 57 2	7. 33 66 1	7. 26 30 4	8. 49 80 4	9. 69 81 5	8. 63 86 2	2.8 941 639 82	1.5 331 466 67	2.8 94 16 39 82	U p	0.0 03 48 49 67	0.2 37 14 66 6	
84 13 3	ZNRF3	Zinc and ring finger 3	4. 72 30 8	7. 40 18 4	7. 03 18	4. 65 60 6	5. 11 24 9	4. 01 75 8	-3. 458 620 369	-1. 790 196 667	3.4 58 62 03 69	D o w n	0.0 38 66 38 21	0.4 19 70 54 36	
31 92	HNRN PU	Heterogeneous nuclear ribonucleoprotein U (scaffold attachment factor A)	6. 65 39 9	7. 69 93 5	7. 51 70 9	9. 05 40 7	8. 41 20 3	8. 60 65 3	2.6 403 575 95	1.4 007 333 33	2.6 40 35 75 95	U p	0.0 04 54 07 03	0.2 53 79 21 57	
49 25	NUCB 2	Nucleobindin 2	4. 56 50 4	7. 37 47 1	6. 14 17 8	3. 40 91	4. 32 73 3	3. 62 24	-4. 726 918 531	-2. 240 9	4.7 26 91 85 31	D o w n	0.0 12 82 10 7	0.3 36 17 41 55	
23 78	APOL 2	Apolipoprotein L, 2	7. 01	7. 34	7. 78	6. 30	6. 45	6. 03	-2. 168	-1. 116	2.1 68	D o	0.0 04	0.2 48	

0			47 3	05 7	99 1	96 9	18 3	43 8	108 065	436 667	10 80 65	w n	32 43 24	58 48 05
11 48 97	C1QT NF1	C1q and tumor necrosis factor related protein 1	6. 27 20 8	6. 94 91 7	7. 75 53	5. 46 09 9	6. 38 64 2	5. 97 61 1	-2. 071 979 889	-1. 051 01	2.0 71 97 98 89	D o w n	0.0 43 24 37 06	0.4 32 33 09 01
55 76 1	TTC17	Tetratricopeptide repeat domain 17	4. 96 24	5. 50 06 8	5. 53 37 4	3. 84 79 4	4. 80 00 5	4. 28 30 2	-2. 030 643 056	-1. 021 936 667	2.0 30 64 30 56	D o w n	0.0 11 67 76 91	0.3 28 47 02 47
89 1	CCNB 1	Cyclin B1	4. 60 32 5	3. 97 06 7	4. 07 72 8	5. 96 88 4	6. 64 54 7	5. 29 32 3	3.3 685 164 24	1.7 521 133 33	3.3 68 51 64 24	U p	0.0 02 26 00 76	0.2 11 69 45 53
10 44	CDX1	Caudal type homeobox 1	5. 10 28 2	5. 38 07 5	5. 76 32 7	5. 53 19 2	8. 24 57	7. 28 60 9	3.0 432 721 04	1.6 056 233 33	3.0 43 27 21 04	U p	0.0 42 48 66 52	0.4 31 73 19 52
29 52	GSTT1	Glutathione S-transferase theta 1	6. 42 06 6	6. 86 61 8	6. 89 34 9	3. 84 26 4	5. 56 36 3	5. 91 78 5	-3. 071 059 931	-1. 618 736 667	3.0 71 05 99 31	D o w n	0.0 19 04 14 98	0.3 67 48 02 31
10 01 32 06 2	LOC10 013206 2	Uncharacterized LOC100132062	8. 03 35 9	8. 30 84 8	7. 49 20 1	5. 71 04 9	6. 09 29 7	7. 81 82 4	-2. 646 575 235	-1. 404 126 667	2.6 46 57 52 35	D o w n	0.0 40 05 82 98	0.4 24 35 94 44
23 34	AFF2	AF4/FMR2 family member 2	7. 18 61 4	5. 53 66 1	7. 12 26 9	5. 24 52 4	4. 32 63 2	4. 72 61 5	-3. 603 111 59	-1. 849 243 333	3.6 03 11 15 9	D o w n	0.0 07 12 25 31	0.2 89 31 65 01
89 0	CCNA 2	Cyclin A2	6. 11 44 7	5. 72 92 6	6. 21 28 3	8. 34 77 6	8. 41 06 2	6. 88 91 4	3.6 392 807 05	1.8 636 533 33	3.6 39 28 07 05	U p	0.0 03 72 67 98	0.2 38 59 85 3
23	CADM	Cell adhesion	8.	9.	8.	6.	7.	6.	-3.	-1.	3.9	D	0.0	0.1

70 5	1	molecule 1	45 34	13 85 4	68 47 2	37 07	05 01 8	92 27 5	938 582 967	977 676 667	38 58 29 67	o w n	00 25 00 13	47 99 60 59
37 43 54	NHLR C2	NHL repeat containing 2	4. 24 10 9	5. 14 11 7	4. 13 58 1	5. 75 35	5. 62 35 8	5. 45 08	2.1 484 109 8	1.1 032 7	2.1 48 41 09 8	U p	0.0 08 40 42 19	0.3 05 72 10 78
10 52 5	HYOU 1	Hypoxia up-regulated 1	8. 59 97 5	9. 28 00 2	8. 30 73 1	7. 43 68 1	7. 82 67 4	7. 17 55 9	-2. 377 282 467	-1. 249 313 333	2.3 77 28 24 67	D o w n	0.0 06 09 77 75	0.2 79 48 17 42
17 06 88	NUDT 4P2	Nudix hydrolase 4 pseudogene 2	5. 90 68 7	4. 50 84 1	5. 12 77	3. 52 15 6	4. 35 53 6	3. 47 68 2	-2. 632 463 145	-1. 396 413 333	2.6 32 46 31 45	D o w n	0.0 11 24 71 44	0.3 24 85 44 65
12 69 61	HIST2 H3C	Histone cluster 2, h3c	6. 19 18 1	5. 50 18 7	5. 70 53 8	7. 08 31 2	7. 49 99 7	6. 87 60 8	2.5 550 827 22	1.3 533 7	2.5 55 08 27 22	U p	0.0 01 87 90 27	0.1 95 76 45 58
10 48 4	SEC23 A	Sec23 homolog A, COPII coat complex component	5. 12 73 6	4. 54 74 3	4. 73 79 5	5. 39 27 3	6. 49 22	5. 73 12	2.0 962 294 88	1.0 677 966 67	2.0 96 22 94 88	U p	0.0 14 27 65 78	0.3 46 79 70 53
57 67 4	RNF21 3	Ring finger protein 213	7. 78 22 2	5. 94 97 4	6. 87 27 9	5. 62 19 6	5. 76 09 1	5. 84 66	-2. 181 156 568	-1. 125 093 333	2.1 81 15 65 68	D o w n	0.0 39 47 55 39	0.4 22 88 72 64
55 58	PRIM2	Primase, DNA, polypeptide 2 (58kda)	4. 41 41 5	4. 31 94 7	4. 47 67 9	5. 37 27 9	5. 91 26 7	5. 29 05 7	2.1 762 586 01	1.1 218 5	2.1 76 25 86 01	U p	0.0 01 68 56 63	0.1 89 79 01 16
33 2	BIRC5	Baculoviral IAP repeat containing 5	4. 10 13 1	3. 69 62 2	3. 72 51 2	4. 91 08 1	5. 13 26 4	4. 72 60 1	2.1 173 650 17	1.0 822 7	2.1 17 36 50 17	U p	0.0 01 17 49 54	0.1 86 14 79 2

39 64	LGAL S8	Lectin, galactoside-binding, soluble, 8	7. 98 93 7	7. 25 59 3	7. 43 25 6	8. 90 59 7	8. 43 86 9	8. 88 18 1	2.2 702 796 22	1.1 828 7	2.2 70 27 96 22	U p	0.0 03 70 58 62	0.2 38 59 85 3
11 00 4	KIF2C	Kinesin family member 2C	5. 61 13 6	5. 34 19 8	5. 21 71 1	6. 62 02 2	7. 49 07 6	6. 00 83 5	2.4 902 547 46	1.3 162 933 33	2.4 90 25 47 46	U p	0.0 11 21 49 73	0.3 24 75 12 86
91 76 8	CABL ES1	Cdk5 and Abl enzyme substrate 1	6. 20 59 5	7. 56 37 4	7. 60 85 1	5. 54 87 2	6. 12 29 3	4. 88 73 05	-3. 044 946 05	-1. 606 416 667	3.0 44 94 60 5	D o w n	0.0 12 36 27 71	0.3 34 46 67 31
23 64 7	ARFIP 2	ADP ribosylation factor interacting protein 2	7. 37 99 8	9. 03 09 3	8. 65 21 7	6. 63 41 5	7. 07 53 6	7. 17 96 9	-2. 623 137 319	-1. 391 293 333	2.6 23 13 73 19	D o w n	0.0 16 26 57 89	0.3 53 90 90 69
10 00 08 58 6	GAGE 12F	G antigen 12F	4. 52 15 8	4. 21 77 2	4. 33 54 7	4. 46 90 8	6. 30 03 5	5. 69 14 3	2.1 866 111 21	1.1 286 966 67	2.1 86 61 11 21	U p	0.0 39 74 28 51	0.4 23 82 07 35
39 09 27	ZNF79 3	Zinc finger protein 793	5. 71 37 5	6. 03 88 7	6. 14 50 6	3. 19 67 6	4. 08 85 4	4. 83 45 5	-3. 799 852 277	-1. 925 943 333	3.7 99 85 22 77	D o w n	0.0 02 24 47 57	0.2 11 69 45 53
29 10 3	DNAJ C15	Dnaj heat shock protein family (Hsp40) member C15	6. 50 56 6	6. 92 54 7	7. 22 43 9	8. 33 57 8	8. 09 31 9	7. 28 98 6	2.0 294 704 49	1.0 211 033 33	2.0 29 47 04 49	U p	0.0 20 67 03 44	0.3 71 59 28 73
83 98	PLA2 G6	Phospholipase A2 group VI	7. 69 86 6	8. 00 67 3	7. 88 23 7	6. 78 61 2	6. 12 87 3	6. 95 07 9	-2. 363 142 563	-1. 240 706 667	2.3 63 14 25 63	D o w n	0.0 02 80 68 24	0.2 29 42 21 97
40 69 91	MIR21	Microrna 21	10 .3 57 36	8. 72 93 9	8. 29 67 3	9. 88 90 4	11 .2 73 32	11 .7 47 19	3.5 851 247 82	1.8 420 233 33	3.5 85 12 47	U p	0.0 27 73 97	0.3 91 44 86

												82		72	74
59 47	RBP1	Retinol binding protein 1	5. 78 79 3	5. 71 53 9	6. 10 58 5	4. 72 33 7	4. 29 62 9	4. 30 40 7	-2. 691 629 802	-1. 428 48	2.6 91 62 98 02	D o w n	0.0 00 36 30 43	0.1 60 90 15 41	
10 27 25 07 0	LOC10 272507 0	Coiled-coil domain-containing protein 29-like	7. 46 14 8	7. 42 23 2	7. 32 89 1	7. 15 84 3	5. 30 81 1	5. 41 93 7	-2. 717 474 819	-1. 442 266 667	2.7 17 47 48 19	D o w n	0.0 22 22 55 45	0.3 78 35 72 21	
91 39 2	ZNF50 2	Zinc finger protein 502	4. 38 98 4	4. 70 66 6	4. 91 55 9	2. 65 19	4. 33 49 4	3. 85 34 6	-2. 080 980 337	-1. 057 263 333	2.0 80 98 03 37	D o w n	0.0 42 01 31 98	0.4 30 07 43 46	
14 52 26	RDH1 2	Retinol dehydrogenase 12 (all-trans/9-cis/11-cis)	9. 62 38 2	6. 82 06 9	7. 36 95	5. 06 80 6	3. 43 82 2	3. 12 92 4	-16 .67 363 399	-4. 059 496 667	16. 67 36 33 99	D o w n	0.0 01 65 79 17	0.1 88 84 30 44	
38 95 49	FEZF1	FEZ family zinc finger 1	4. 28 47	5. 04 37 1	4. 51 59 5	4. 91 13 5	6. 48 55 1	5. 54 17 6	2.0 440 351 42	1.0 314 2	2.0 44 03 51 42	U p	0.0 45 18 53 48	0.4 36 31 89 27	
51 31 6	PLAC8	Placenta specific 8	6. 65 62 6	6. 81 46 2	6. 73 31 8	10 .7 52 82	8. 87 16 8	8. 41 42 8	6.1 115 853 58	2.6 115 466 67	6.1 11 58 53 58	U p	0.0 02 74 49 48	0.2 28 17 52 85	
55 22	PPP2R 2C	Protein phosphatase 2 regulatory subunit B, $\gamma$	7. 20 97 5	7. 13 16 1	7. 38 80 5	5. 16 33 3	4. 71 16 7	5. 47 47	-4. 366 780 456	-2. 126 57	4.3 66 78 04 56	D o w n	7.3 67 56 E- 05	0.1 26 50 89 75	
81 61 1	ANP32 E	Acidic nuclear phosphoprotein 32 family member E	3. 99 43 2	3. 76 96	3. 72 19 2	5. 79 80 3	5. 80 18 2	4. 96 05 6	3.2 299 757 5	1.6 915 233 33	3.2 29 97 57 5	U p	0.0 00 47 98 28	0.1 64 24 82 94	
10 20 7	INAD L	Inad-like (Drosophila)	9. 10 30	9. 27 04	9. 21 02	7. 56 99	8. 43 61	8. 31 45	-2. 125 354	-1. 087 703	2.1 25 35	D o w	0.0 06 10	0.2 79 48	

			1	9	1	3	4	3	259	333	42	n	73	17
											59		28	42
8000	GREB1L	Growth regulation by estrogen in breast cancer-like	3.88982	4.35786	3.74856	5.29267	5.37609	4.39307	2.0305398	1.0218633	2.0305398	U p	0.0151703	0.3486795
5641	LGMN	Legumain	9.56945	8.36808	8.45817	7.64993	8.02681	7.54063	-2.084127202	-1.059443333	2.084127202	D o w n	0.0231654	0.3807539
23258	DENN D5A	DENN/MADD domain containing 5A	7.64196	7.85285	7.68905	6.15586	7.12656	6.67614	-2.106868104	-1.075186	2.106868104	D o w n	0.0072825	0.2921866
9414	TJP2	Tight junction protein 2	5.86359	6.32315	6.67934	7.69486	7.16826	7.47177	2.228804383	1.15627	2.228804383	U p	0.0047098	0.257322
57713	SFMB T2	Scm-like with four mbt domains 2	5.371	5.93145	6.32842	4.41827	5.06401	4.25361	-2.459434557	-1.298326667	2.44557	D o w n	0.0058241	0.2764811
25840	METT L7A	Methyltransferase like 7A	8.45009	6.64329	7.38071	5.88887	6.79481	5.77059	-2.531407907	-1.33994	2.531407907	D o w n	0.0326532	0.4047137
301	ANXA1	Annexin A1	6.61871	4.46937	3.0406	7.70733	6.74465	6.66218	5.022805233	2.3284933	5.022805233	U p	0.0291484	0.3946382
83481	EPPK1	Epiplakin 1	5.68675	4.54679	5.1423	7.06081	6.58291	5.55289	2.417624189	1.27359	2.417624189	U p	0.0273296	0.3898307
8836	GGH	Γ-glutamyl hydrolase	3.56	5.09	4.456	5.23	6.01	5.37	2.1898	1.1308	2.1898	U p	0.031	0.401

		(conjugase, folylpolyyglutamyl hydrolase)	76 5	44 8	47 2	19 6	67 2	07 2	772 44	5	87 72 44		61 03 18	56 52 84
22 84 9	CPEB3	Cytoplasmic polyadenylation element binding protein 3	5. 88 18 9	6. 46 85 3	6. 11 09 5	5. 60 42 3	4. 28 61 9	5. 15 09 8	-2. 203 794 956	-1. 139 99	2.2 03 79 49 56	D o w n	0.0 17 34 33 55	0.3 60 38 98 23
13 75	CPT1B	Carnitine palmitoyltransferase 1B	7. 38 68 5	7. 57 94 4	7. 26 70 7	6. 21 08	5. 82 94 3	7. 15 15 6	-2. 019 301 965	-1. 013 856 667	2.0 19 30 19 65	D o w n	0.0 25 55 73 56	0.3 84 73 53 87
10 05 06 96 5	PWAR6	Prader Willi/Angelman region RNA 6	6. 75 90 6	5. 45 54	5. 96 89 9	5. 67 82 5	4. 57 90 1	4. 49 24 5	-2. 210 817 596	-1. 144 58	2.2 10 81 75 96	D o w n	0.0 37 20 82 31	0.4 15 71 63 29
38 38	KPNA2	Karyopherin $\alpha$ 2 (RAG cohort 1, importin $\alpha$ 1)	6. 28 76 3	5. 64 95 5	6. 57 03 2	7. 70 07 1	6. 81 67 2	8. 66 05 8	2.9 420 803 88	1.5 568 366 67	2.9 42 08 03 88	U p	0.0 15 83 26 02	0.3 51 16 74 61
26 58 6	CKAP2	Cytoskeleton associated protein 2	5. 71 83 5	5. 25 08 9	5. 51 43 8	6. 90 23 5	7. 67 21 6	6. 47 90 7	2.8 745 178 71	1.5 233 2	2.8 74 51 78 71	U p	0.0 02 85 82 48	0.2 31 19 75 39
26 57 6	SRPK3	SRSF protein kinase 3	6. 07 25	6. 96 18	6. 77 51 9	5. 98 50 7	5. 25 26 6	5. 44 68 9	-2. 058 542 641	-1. 041 623 333	2.0 58 54 26 41	D o w n	0.0 14 37 94 49	0.3 46 79 70 53
80 03 6	TRPM3	Transient receptor potential cation channel, subfamily M, member 3	8. 73 67 5	6. 88 99 4	6. 71 80 3	4. 74 51 8	4. 78 31 6	5. 06 99 5	-5. 988 286 86	-2. 582 143 333	5.9 88 28 68 6	D o w n	0.0 01 85 09 42	0.1 94 39 36 87
17 42	DLG4	Discs, large homolog 4 (Drosophila)	5. 53 13 6	6. 43 92 4	6. 53 29 4	4. 61 91 3	5. 14 13 7	5. 03 11 4	-2. 357 569 007	-1. 237 3	2.3 57 56 90 07	D o w n	0.0 06 63 85 02	0.2 86 90 22 62
32	HOXB	Homeobox B5	4.	4.	3.	6.	5.	7.	4.9	2.3	4.9	U	0.0	0.2



15	5		11 50 7	43 20 7	73 59 9	65 62 6	11 67 4	43 18 8	493 875 04	072 5	49 38 75 04	p	04 80 47 92	60 26 39 27
39 99 48	COLC A1	Colorectal cancer associated 1	7. 35 66 1	8. 51 73 6	8. 06 85 8	6. 57 92 9	6. 35 47 7	7. 38 86 1	-2. 307 973 512	-1. 206 626 667	2.3 07 97 35 12	D o w n	0.0 18 99 77 34 71	0.3 67 34 80 71
16 63 36	PRICK LE2	Prickle homolog 2	5. 79 76 9	5. 83 65 5	5. 64 17 4	4. 08 26 4	5. 46 48 8	4. 44 20 9	-2. 136 787 34	-1. 095 443 333	2.1 36 78 73 4	D o w n	0.0 19 27 61 24	0.3 67 66 41 57
63 95 1	DMRT A1	DMRT-like family A1	6. 36 78	6. 07 76 3	5. 92 03 1	4. 21 01 9	3. 13 54 2	3. 94 13 8	-5. 132 221 133	-2. 359 583 333	5.1 32 22 11 33	D o w n	0.0 00 13 95 48	0.1 27 84 98 29
55 65	PRKA B2	Protein kinase, AMP-activated, $\beta$ 2 non-catalytic subunit	5. 18 94 8	5. 58 69 6	5. 66 51 8	7. 19 94 7	6. 96 37 6	5. 56 57 1	2.1 372 761 61	1.0 957 733 33	2.1 37 27 61 61	U p	0.0 42 66 30 42	0.4 32 07 88 1
28 46 11	FAM1 02B	Family with sequence similarity 102 member B	4. 00 20 1	3. 86 63 2	4. 28 83 2	5. 07 92 8	5. 62 69 4	4. 45 67 4	2.0 029 179 66	1.0 021 033 33	2.0 02 91 79 66	U p	0.0 15 98 37 64	0.3 51 41 79 34
10 02 88 63 7	LOC10 028863 7	OTU deubiquitinase 7A pseudogene	5. 86 99 6	5. 53 95 7	6. 22 91 2	7. 63 44 8	7. 95 97 7	7. 54 28 6	3.5 623 271 16	1.8 328 2	3.5 62 32 71 16	U p	0.0 00 19 91 65	0.1 35 27 95 77
57 57 1	CARN S1	Carnosine synthase 1	6. 13 55 6	5. 29 59 8	5. 43 76 4	4. 42 16 4	4. 05 10 8	5. 12 71 5	-2. 128 401 02	-1. 089 77	2.1 28 40 10 2	D o w n	0.0 17 99 40 69	0.3 62 48 76 38
34 72 52	IGFBP L1	Insulin like growth factor binding protein-like 1	5. 99 26 6	6. 38 12 2	6. 54 93 1	3. 45 06 4	3. 98 86 4	4. 02 87 5	-5. 598 550 425	-2. 485 053 333	5.5 98 55 04 25	D o w n	2.6 14 53 E- 05	0.0 96 05 29 42

55 75 2	SEPT1 1	Septin 11	6. 52 04 9	5. 85 04 2	6. 48 17 5	7. 72 14 7	8. 33 10 4	6. 48 30 7	2.3 418 359 24	1.2 276 4	2.3 41 83 59 24	U p	0.0 38 48 83 7	0.4 19 34 43 95
67 64	ST5	Suppression of tumorigenicity 5	8. 94 69 4	9. 34 06 5	9. 20 51 4	7. 64 76 8	8. 39 35 8	7. 83 72 7	-2. 304 946 61	-1. 204 733 333	2.3 04 94 66 1	D o w n	0.0 02 81 76 87	0.2 29 82 09 33
40 33 13	PLPP6	Phospholipid phosphatase 6	5. 98 74 5	7. 05 8	6. 38 99 5	5. 52 72 8	5. 59 16 9	4. 95 56 7	-2. 173 851 414	-1. 120 253 333	2.1 73 85 14 14	D o w n	0.0 12 60 69 63	0.3 35 59 55 01
52 68	SERPI NB5	Serpin peptidase inhibitor, clade B (ovalbumin), member 5	4. 29 79 3	5. 56 66	6. 41 11 7	10 .8 55 53	9. 09 36 9	6. 73 34 2	11. 073 044 22	3.4 689 8	11. 07 30 44 22	U p	0.0 12 50 02 12	0.3 34 46 67 31
66 35	SNRP E	Small nuclear ribonucleoprotein polypeptide E	7. 92 02 4	7. 74 22 4	7. 57 65 6	9. 70 37 6	8. 67 87 9	7. 96 67 5	2.0 516 054 85	1.0 367 533 33	2.0 51 60 54 85	U p	0.0 47 97 43 21	0.4 43 39 63 77
70 31	TFF1	Trefoil factor 1	5. 78 32	7. 39 74 3	9. 40 70 1	11 .8 89 4	9. 89 77 3	9. 77 88 9	7.9 601 374	2.9 927 933 33	7.9 60 13 74	U p	0.0 17 82 32 77	0.3 61 62 71 34
17 05 06	DHX3 6	DEAH (Asp-Glu-Ala-His) box polypeptide 36	5. 87 07 5	5. 86 44 6	5. 53 05 7	6. 47 97 7	6. 70 95 8	7. 70 77 6	2.3 140 873 67	1.2 104 433 33	2.3 14 08 73 67	U p	0.0 10 82 52 46	0.3 23 87 84 16
83 85 6	FSD1L	Fibronectin type III and SPRY domain containing 1-like	5. 41 04 2	4. 80 79 1	3. 91 68 5	6. 14 35 8	5. 88 00 1	6. 05 67 5	2.4 881 152 85	1.3 150 533 33	2.4 88 11 52 85	U p	0.0 10 37 41 54	0.3 19 58 54 28
77 10	ZNF15 4	Zinc finger protein 154	5. 59 83 8	6. 99 41 2	6. 54 88 3	3. 89 70 3	4. 77 48 1	4. 19 12 9	-4. 265 554 609	-2. 092 733 333	4.2 65 55 46	D o w n	0.0 01 39 42	0.1 87 10 78

												09		74	18
38 88 86	LRRC 75B	Leucine rich repeat containing 75B	6. 44 23 9	6. 92 81 8	6. 52 05 5	5. 34 31 7	5. 64 96 4	5. 47 46 3	-2. 205 684 841	-1. 141 226 667	2.2 05 68 48 41	D o w n	0.0 01 49 46 78	0.1 87 10 78 18	
65 24 4	SPATS 2	Spermatogenesis associated, serine rich 2	9. 07 31	9. 01 92 1	8. 61 73 9	7. 22 05 4	8. 26 88 6	7. 61 61 6	-2. 299 595 32	-1. 201 38	2.2 99 59 53 2	D o w n	0.0 06 92 48 5	0.2 88 73 74 24	
16 04	CD55	CD55 molecule, decay accelerating factor for complement (Cromer blood group)	4. 82 2	4. 93 54 5	4. 93 88 9	9. 25 45 4	8. 22 13 2	8. 71 99 4	14. 252 601 13	3.8 331 533 33	14. 25 26 01 13	U p	3.9 38 45 E- 06	0.0 51 29 04 57	
55 83 5	CENPJ	Centromere protein J	4. 68 76	4. 39 93	4. 38 57	5. 15 24 3	6. 27 64 7	6. 31 34 7	2.6 819 022 72	1.4 232 566 67	2.6 81 90 22 72	U p	0.0 04 50 52 14	0.2 53 49 44 23	
44 10 27	TMEM 150C	Transmembrane protein 150C	5. 90 83 9	6. 22 33 3	6. 26 11 7	4. 75 78 6	5. 29 59 4	4. 46 43 7	-2. 447 948 715	-1. 291 573 333	2.4 47 94 87 15	D o w n	0.0 02 02 19 47	0.2 02 55 23 93	
14 07 38	TMEM 37	Transmembrane protein 37	9. 17 50 6	8. 24 15 1	8. 12 14	6. 46 83 8	7. 26 17 1	7. 35 00 7	-2. 800 989 678	-1. 485 936 667	2.8 00 98 96 78	D o w n	0.0 05 88 62 56	0.2 78 75 16 66	
81 65	AKAP 1	A-kinase anchoring protein 1	4. 66 52 2	5. 01 65 1	5. 69 26 4	6. 63 35	6. 73 11	7. 01 18	3.1 762 915 29	1.6 673 433 33	3.1 76 29 15 29	U p	0.0 00 96 06 51	0.1 86 14 79 2	
10 61 1	PDLI M5	PDZ and LIM domain 5	8. 75 53 1	8. 06 12 8	8. 32 65 5	10 .0 27 29	9. 74 21 3	9. 99 08 5	2.9 060 173 84	1.5 390 433 33	2.9 06 01 73 84	U p	0.0 00 48 67 15	0.1 64 24 82 94	
26 46	PTPN1 8	Protein tyrosine phosphatase,	9. 45	9. 50	10 .0	8. 17	8. 29	8. 52	-2. 517	-1. 331	2.5 17	D o	0.0 00	0.1 86	

9		non-receptor type 18 (brain-derived)	813	711	2055	086	067	829	496897	99	496897	w n	978005	14792
3115	HLA-DPB1	Major histocompatibility complex, class II, DP $\beta$ 1	10109	7.69562	9.11387	5.68136	8.25704	7.25735	-3.753439	-1.908213	3.753439	D o w n	0.0491679	0.4461748
388743	CAPN8	Calpain 8	5.0674	5.6107	7.5592	9.6542	7.5989	8.7433	6.0059674	2.5863966	6.0059674	U p	0.0111617	0.3246119
283450	HECTD4	HECT domain containing E3 ubiquitin protein ligase 4	7.92658	9.6907	9.18617	6.8193	7.98304	8.07092	-2.479558621	-1.310083333	2.479558621	D o w n	0.0448291	0.435527714
388125	C2CD4B	C2 calcium-dependent domain containing 4B	7.40704	8.68745	8.17997	4.3195	5.53337	4.4185	-10.086334	-3.33433	10.086334	D o w n	0.00152342	0.128621894
213	ALB	Albumin	3.36922	4.03672	3.68137	10.2319	6.87745	4.33043	10.91257	3.44792	10.91257	U p	0.0347300	0.4084239
100526830	SLX1A-SULT1A3	SLX1A-SULT1A3 readthrough (NMD candidate)	6.47722	6.93547	6.66106	7.80233	8.02899	7.66662	2.205944764	1.14139667	2.205944764	U p	0.001523801	0.187107818
56892	C8orf4	Chromosome 8 open reading frame 4	5.13931	5.31691	5.58203	8.26158	5.89229	7.34723	3.34380598	1.7415233	3.34380598	U p	0.01957746	0.367760084
25833	POU2F3	POU class 2 homeobox 3	5.47128	6.16327	6.42732	4.22622	4.79247	5.64671	-2.191861541	-1.132156667	2.191861541	D o w n	0.0310196	0.399785461
97	ATG13	Autophagy related	7.	7.	7.	5.	6.	6.	-2.	-1.	2.2	D	0.0	0.2

76		13	20 14 7	73 64 7	74 12	97 78 3	60 53 1	66 16 9	211 108 775	144 77	11 10 87 75	o w n	05 06 75 65	65 39 50 28
84 24 5	MR11	Methylthioribose- 1-phosphate isomerase 1	7. 79 77 5	7. 67 33 4	7. 69 53 8	6. 49 93 7	6. 44 96 1	6. 21 46	-2. 521 525 24	-1. 334 296 667	2.5 21 52 4	D o w n	0.0 00 28 82 19	0.1 52 16 77 32
11 81	CLCN 2	Chloride channel, voltage-sensitive 2	6. 61 13 2	6. 34 92 6	6. 81 61 3	5. 55 77 9	5. 49 51 7	5. 56 57 1	-2. 074 379 71	-1. 052 68	2.0 74 37 97 1	D o w n	0.0 01 57 01 67	0.1 87 10 78 18
64 85 6	VWA1	Von Willebrand factor A domain containing 1	7. 80 43 8	9. 74 07	9. 33 43 9	7. 29 46	7. 51 18 4	7. 77 86 1	-2. 697 220 248	-1. 431 473 333	2.6 97 22 02 48	D o w n	0.0 23 79 43 95	0.3 81 26 89 97
37 12	IVD	Isovaleryl-coa dehydrogenase	7. 28 01 6	7. 57 57 4	7. 57 90 2	4. 85 12 7	4. 94 34 8	6. 39 96	-4. 228 629 027	-2. 080 19	4.2 28 62 90 27	D o w n	0.0 01 92 57 36	0.1 98 67 50 21
83 70	HIST2 H4A	Histone cluster 2, h4a	8. 73 56 8	8. 01 41 9	8. 24 88 9	9. 86 20 7	9. 68 07 1	8. 55 79	2.0 476 559 52	1.0 339 733 33	2.0 47 65 59 52	U p	0.0 35 06 84 07	0.4 08 55 78 26
56 85 2	RAD1 8	RAD18, E3 ubiquitin protein ligase	3. 92 57 9	4. 02 94 6	4. 64 51 6	5. 27 70 8	5. 43 02 8	5. 62 36 6	2.3 677 826 69	1.2 435 366 67	2.3 67 78 26 69	U p	0.0 01 61 86 66	0.1 87 65 47 34
14 06 12	ZFP28	ZFP28 zinc finger protein	6. 45 85 9	6. 59 47	6. 79 15	3. 29 28 4	5. 26 38 3	4. 48 88 2	-4. 811 321 925	-2. 266 433 333	4.8 11 32 19 25	D o w n	0.0 02 09 83 59	0.2 06 94 32 89
29 70	GTF2I P1	General transcription factor iii pseudogene 1	7. 83 21 3	8. 52 85 7	8. 56 69 7	7. 38 68	6. 91 57	7. 25 45 3	-2. 178 819 474	-1. 123 546 667	2.1 78 81 94 74	D o w n	0.0 05 28 54 87	0.2 68 46 24 7

5909	RAP1 GAP	RAP1 gtpase activating protein	8.41827	8.12033	8.5429	6.8337	5.6578	6.0847	-4.495183	-2.16838	4.49518	D	0.003517	0.160901541
10923	SUB1	SUB1 homolog, transcriptional regulator	5.20958	5.30463	5.4644	6.44314	6.12227	6.43966	2.12268	1.0882	2.01226	U	0.00773726	0.192292584
51435	SCAR A3	Scavenger receptor class A, member 3	7.05334	8.61304	8.90748	6.21004	6.51688	6.29302	-3.608268	-1.851306	3.60826	D	0.00634558	0.283732496
3635	INPP5 D	Inositol polyphosphate-5-phosphatase D	9.04125	8.68604	9.52402	7.20585	8.16247	7.04275	-3.059749	-1.613413	3.05974	D	0.00531664	0.2371466
154091	SLC2A12	Solute carrier family 2 (facilitated glucose transporter), member 12	5.60692	5.96824	5.79852	4.443	4.27936	5.06711	-2.289030	-1.194736	2.28903	D	0.0070166	0.22676712
8431	NR0B2	Nuclear receptor subfamily 0 group B member 2	8.01791	4.89776	5.67328	4.28561	4.91401	3.95522	-3.509754	-1.81137	3.50975	D	0.009754291	0.446565527
155066	ATP6V0E2	Atpase, H <sup>+</sup> transporting V0 subunit e2	6.40035	6.78612	6.44279	5.57732	5.28652	5.5081	-2.077530	-1.05487	2.07753	D	0.00927016	0.198675021
51029	DESI2	Desumoylating isopeptidase 2	5.33901	5.9055	5.60081	7.00865	6.73386	6.22306	2.563179	1.400633	2.05631	U	0.007922	0.2079554
3399	ID3	Inhibitor of DNA binding 3, dominant negative helix-loop-helix	6.92755	8.81204	7.81298	6.05594	7.17855	6.36685	-2.491607	-1.317076	2.49160	D	0.00392810	0.4225797

		protein										35		31	15
13 64	CLDN 4	Claudin 4	9. 09 68	6. 97 92 7	8. 62 16 1	9. 16 47 4	10 .5 75 36	10 .5 58 79	3.6 479 096 55	1.8 670 7	3.6 47 90 96 55	U p	0.0 21 36 31 65	0.3 73 02 61 78	
40 01	LMNB 1	Lamin B1	4. 68 84 7	3. 35 19 8	4. 31 60 8	5. 77 34 5	6. 42 83 1	5. 29 56 5	3.2 798 427 94	1.7 136 266 67	3.2 79 84 27 94	U p	0.0 05 16 88 14	0.2 66 23 90 84	
90 63 9	COX1 9	COX19 cytochrome c oxidase assembly factor	6. 80 01 5	6. 56 22 5	6. 52 05 9	8. 33 89	7. 67 92 1	7. 88 18 1	2.5 297 181 7	1.3 389 766 67	2.5 29 71 81 7	U p	0.0 01 00 70 66	0.1 86 14 79 2	
56 65 4	NPDC 1	Neural proliferation, differentiation and control, 1	9. 13 45 5	10 .8 41 97	10 .6 00 4	8. 97 64 9	7. 27 12 7	8. 22 49 4	-4. 097 488 783	-2. 034 74	4.0 97 48 87 83	D o w n	0.0 10 23 55 12	0.3 18 63 84 27	
38 74 96	RASL1 1A	RAS-like, family 11, member A	5. 57 58 3	5. 33 30 7	5. 57 64 7	5. 48 08 6	7. 50 82 4	7. 93 19	2.7 866 722 52	1.4 785 433 33	2.7 86 67 22 52	U p	0.0 45 13 99 14	0.4 36 20 36 37	
47 39	NEDD 9	Neural precursor cell expressed, developmentally down-regulated 9	4. 99 45	6. 48 02	6. 51 83 1	7. 48 90 8	7. 50 74 6	8. 08 53 2	3.2 406 502 69	1.6 962 833 33	3.2 40 65 02 69	U p	0.0 07 03 36 38	0.2 88 96 44 72	
41 33	MAP2	Microtubule associated protein 2	6. 30 73 7	5. 20 01 5	4. 56 55	3. 96 57 5	4. 56 91 3	4. 02 66 8	-2. 250 876 133	-1. 170 486 667	2.2 50 87 61 33	D o w n	0.0 34 01 17 88	0.4 08 27 35 55	
41 89	DNAJ B9	Dnaj heat shock protein family (Hsp40) member B9	6. 05 10 4	7. 84 36 6	6. 77 14 5	5. 12 63 5	5. 73 49 1	3. 84 38 7	-3. 964 136 571	-1. 987 006 667	3.9 64 13 65 71	D o w n	0.0 13 79 65 93	0.3 44 49 38 94	
10 10 60	LOC10 106002 6	Coiled-coil domain-containing protein 29-like	7. 46 14	7. 42 23	7. 32 89	7. 15 84	5. 30 81	5. 41 93	-2. 717 474	-1. 442 266	2.7 17 47	D o w	0.0 22 22	0.3 78 35	

026			8	2	1	3	1	7	819	667	4819	n	5545	7221
10808	HSPH1	Heat shock protein family H (Hsp110) member 1	6.134	5.8012	5.8342	7.8652	6.4928	6.5381	2.05937009	1.04225	2.059437009	U p	0.034267626	0.408273555
151230	KLHL23	Kelch like family member 23	5.0674	4.81491	4.4111	6.2807	6.6503	5.2846	2.47491093	1.3074233	2.474991093	U p	0.011589372	0.327659866
398	ARHG DIG	Rho GDP dissociation inhibitor (GDI) $\gamma$	5.32485	6.87893	7.31877	5.05021	5.17297	5.54782	-2.379266155	-1.250516667	2.379266155	D o w n	0.043252279	0.432330901
3181	HNRN PA2B1	Heterogeneous nuclear ribonucleoprotein A2/B1	8.09576	7.91295	7.77169	8.72309	9.38455	8.68115	2.00380763	1.0027966	2.00380763	U p	0.006838252	0.288459719
63928	CHP2	Calcineurin-like EF-hand protein 2	3.82701	3.53221	4.06835	4.42903	8.39709	7.59482	7.98775439	2.99779	7.987794539	U p	0.015774911	0.350947357
9394	HS6ST1	Heparan sulfate 6-O-sulfotransferase 1	7.13065	6.88597	7.5306	4.71045	5.07127	4.43075	-5.444945	-2.44491667	5.4449451945	D o w n	4.3768E-05	0.096052942
1796	DOK1	Docking protein 1	6.25481	6.69652	6.05326	4.3164	5.48486	5.89172	-2.14943784	-1.10343667	2.14943784	D o w n	0.036285569	0.413668192
284040	CDRT4	CMT1A duplicated region transcript 4	6.2623	7.6214	7.6244	5.80814	5.56614	6.2424	-2.457452163	-1.297163333	2.457452163	D o w n	0.017558715	0.361123337
1005	MINO S1-NB	MINOS1-NBL1 readthrough	8.82	7.40	8.58	9.66	10.3	9.08	2.6787	1.4215	2.6787	U p	0.019	0.367



32 73 6	L1		00 7	03	86 1	77 5	22 91	30 1	562 92	633 33	75 62 92		34 57 08	66 41 57
72 76	TTR	Transthyretin	11 .1 66 29	7. 20 88 8	7. 87 96 3	6. 55 20 6	6. 49 45 5	4. 89 99 7	-6. 818 274 424	-2. 769 406 667	6.8 18 27 44 24	D o w n	0.0 31 75 19 88	0.4 02 73 83 8
55 73 2	C1orf1 12	Chromosome 1 open reading frame 112	3. 88 66 1	3. 96 37 2	3. 81 90 3	4. 82 03 4	4. 68 05 7	5. 21 98 4	2.0 238 887 65	1.0 171 3	2.0 23 88 87 65	U p	0.0 01 49 40 07	0.1 87 10 78 18
22 82 3	MTF2	Metal response element binding transcription factor 2	6. 36 90 8	7. 29 47 5	7. 25 29 5	5. 76 89 9	5. 98 49 7	6. 16 25 9	-2. 000 106 285	-1. 000 076 667	2.0 00 10 62 85	D o w n	0.0 13 97 81 87	0.3 45 20 46 8
51 73 8	GHRL	Ghrelin/obestatin prepropeptide	5. 11 56 7	5. 95 44 7	7. 49 21	4. 73 74 6	4. 54 66 1	4. 80 91 6	-2. 808 247 324	-1. 489 67	2.8 08 24 73 24	D o w n	0.0 32 78 54 67	0.4 05 09 02 6
49 29	NR4A 2	Nuclear receptor subfamily 4 group A member 2	4. 34 51 3	3. 68 76 3	3. 19 93 1	4. 74 39	4. 23 40 1	5. 48 74 8	2.1 107 757 78	1.0 777 733 33	2.1 10 77 57 78	U p	0.0 32 49 11 68	0.4 04 71 37 9
90 26	HIP1R	Huntingtin interacting protein 1 related	5. 91 13 9	5. 78 21 6	5. 71 93 1	4. 38 51 6	4. 24 33 1	5. 38 42 8	-2. 193 705 713	-1. 133 37	2.1 93 70 57 13	D o w n	0.0 10 38 86 33	0.3 19 58 54 28
11 07 4	TRIM3 1	Tripartite motif containing 31	5. 08 67 5	4. 79 7	5. 28 27 5	6. 61 21 3	8. 68 24 9	8. 64 39 6	7.5 896 148 06	2.9 240 266 67	7.5 89 61 48 06	U p	0.0 01 28 07 21	0.1 87 10 78 18
10 53 73 32 6	LOC10 537332 6	Uncharacterized LOC105373326	9. 08 62 8	9. 13 30 1	8. 68 97 9	7. 67 03 6	7. 67 41 3	6. 85 00 7	-2. 972 149 461	-1. 571 506 667	2.9 72 14 94 61	D o w n	0.0 01 21 49 71	0.1 86 14 79 2
12	IQGAP	IQ motif	4.	3.	3.	4.	5.	4.	2.0	1.0	2.0	U	0.0	0.2

82 39	3	containing gtpase activating protein 3	15 06 3	79 01 9	52 99 4	98 81 3	22 56 5	45 64 9	943 511 22	665 033 33	94 35 11 22	p	05 55 53	71 43 14 26
53 47	PLK1	Polo-like kinase 1	6. 43 64 2	6. 03 16 7	6. 09 99 6	7. 55 48 8	7. 52 35 7	6. 92 46 7	2.2 114 970 74	1.1 450 233 33	2.2 11 49 70 74	U p	0.0 03 19 25 37	0.2 34 23 93 82
10 56 2	OLFM 4	Olfactomedin 4	3. 63 80 6	4. 46 29	4. 68 11 7	9. 61 51 9	12 .3 87 43	10 .2 65 78	90. 222 998 79	6.4 954 233 33	90. 22 29 98 79	U p	3.8 92 71 E- 05	0.0 96 05 29 42
52 09	PFKFB 3	6-phosphofructo-2 -kinase/fructose-2, 6-biphosphatase 3	10 .3 34 49	9. 53 66 6	10 .0 64 24	7. 40 55 8	9. 14 61 7	8. 54 63 7	-3. 057 650 123	-1. 612 423 333	3.0 57 65 01 23	D o w n	0.0 10 63 40 79	0.3 23 31 73 76
51 04	SERPI NA5	Serpin peptidase inhibitor, clade A ( $\alpha$ -1 antiproteinase, antitrypsin), member 5	9. 01 19	7. 26 03 6	7. 23 18 7	2. 63 77 8	4. 41 35 4	3. 84 68 9	-18 .40 433 011	-4. 201 973 333	18. 40 43 30 11	D o w n	0.0 00 28 29 56	0.1 52 16 77 32
10 25 7	ABCC 4	ATP binding cassette subfamily C member 4	8. 03 79 9	7. 58 88 4	7. 54 89 1	5. 36 85 5	6. 35 18 3	6. 25 54	-3. 324 920 856	-1. 733 32	3.3 24 92 08 56	D o w n	0.0 01 09 61 95	0.1 86 14 79 2
40 93	SMAD 9	SMAD family member 9	8. 03 76 3	8. 11 53 8	7. 72 41 5	6. 13 51 6	6. 36 84	6. 24 88	-3. 267 679 904	-1. 708 266 667	3.2 67 67 99 04	D o w n	9.3 43 53 E- 05	0.1 27 84 98 29
55 27 7	FGGY	FGGY carbohydrate kinase domain containing	5. 43 25	7. 12 87 2	6. 78 83 3	5. 14 91 5	5. 07 71 8	5. 39 02 3	-2. 369 085 063	-1. 244 33	2.3 69 08 50 63	D o w n	0.0 25 44 18 83	0.3 84 42 60 11
10 19 29 09	LOC10 192909 7	Uncharacterized LOC101929097	4. 41 28 4	4. 90 52 7	5. 25 76 9	3. 98 86 4	3. 69 18 6	3. 55 99 4	-2. 161 131 211	-1. 111 786 667	2.1 61 13 12	D o w n	0.0 03 73 86	0.2 38 59 85

7												11		39	3
87 94	TNFR SF10C	Tumor necrosis factor receptor superfamily member 10c, decoy without an intracellular domain	7. 07 90 7	7. 62 83 6	7. 56 73 7	7. 18 18 7	5. 76 07 1	5. 60 29 3	-2. 367 022 358	-1. 243 073 333	2.3 67 02 23 58	D o w n	0.0 26 78 28 65	0.3 88 38 41 04	
56 64 9	TMPR SS4	Transmembrane protease, serine 4	5. 25 72	5. 37 44 4	5. 55 74 4	6. 40 72	6. 77 54 3	7. 05 92 2	2.5 507 532 29	1.3 509 233 33	2.5 50 75 32 29	U p	0.0 00 83 92 08	0.1 81 04 09 24	
37 30	ANOS 1	Anosmin 1	7. 58 25 3	7. 52 02 1	7. 36 87 9	4. 74 23 8	6. 77 20 1	5. 33 66 2	-3. 664 221 374	-1. 873 506 667	3.6 64 22 13 74	D o w n	0.0 07 02 22 55	0.2 88 96 44 72	
79 37 0	BCL2L 14	BCL2-like 14 (apoptosis facilitator)	4. 80 85 5	4. 52 24 5	5. 34 20 8	6. 47 78 4	6. 56 66 8	5. 54 84 4	2.4 736 247 62	1.3 066 266 67	2.4 73 62 47 62	U p	0.0 07 94 88 3	0.2 99 13 95 54	
10 04 99 48 4	LOC10 049948 4	SUGT1-1300002 K09Rik pseudogene	5. 20 56	5. 44 10 4	5. 73 66 4	4. 11 49 1	4. 38 10 3	4. 78 42 5	-2. 048 209 564	-1. 034 363 333	2.0 48 20 95 64	D o w n	0.0 04 61 04 78	0.2 54 41 63 12	
80 77 7	CYB5 B	Cytochrome b5 type B (outer mitochondrial membrane)	4. 48 19 3	5. 17 98 2	5. 03 77 3	6. 07 12 7	6. 25 79 7	5. 72 85 2	2.1 726 061 5	1.1 194 266 67	2.1 72 60 61 5	U p	0.0 04 10 43 81	0.2 44 25 17 2	
39 20	LAMP 2	Lysosomal-associa ted membrane protein 2	9. 08 62 8	9. 13 30 1	8. 68 97 9	7. 67 03 6	7. 67 41 3	6. 85 00 7	-2. 972 149 461	-1. 571 506 667	2.9 72 14 94 61	D o w n	0.0 01 21 49 71	0.1 86 14 79 2	
56 91 2	IFT46	Intraflagellar transport 46	6. 07 70 8	5. 99 06 3	6. 19 06 5	5. 04 36 5	4. 37 32 3	5. 17 01 7	-2. 335 562 415	-1. 223 77 415	2.3 35 56 24 15	D o w n	0.0 02 30 06 02	0.2 12 16 29 49	
48	ATP2A	Atpase, Ca <sup>++</sup>	8.	9.	10	8.	7.	8.	-2.	-1.	2.1	D	0.0	0.4	

9	3	transporting, ubiquitous	64 32 5	27 55 2	.2 53 22	63 76 3	69 74 4	52 62	148 862 741	103 573 333	48 86 27 41	o w n	47 97 75 53	43 39 63 77
81 53 9	SLC38 A1	Solute carrier family 38, member 1	6. 10 90 7	4. 24 49 3	5. 12 48 7	6. 71 52 1	7. 29 62 8	6. 81 47 4	3.4 401 067 49	1.7 824 533 33	3.4 40 10 67 49	U p	0.0 06 75 66 21	0.2 88 45 97 19
99 65	FGF19	Fibroblast growth factor 19	11 .8 28 82	8. 68 11 9	9. 32 96 5	4. 06 76 1	5. 93 23 5	3. 97 93 6	-39 .03 726 299	-5. 286 78	39. 03 72 62 99	D o w n	0.0 00 61 48 57	0.1 68 94 20 05
27 4	BIN1	Bridging integrator 1	8. 31 46 2	7. 41 99 9	7. 18 59	5. 55 94 5	6. 78 90 9	6. 34 53 3	-2. 655 309 445	-1. 408 88	2.6 55 30 94 45	D o w n	0.0 12 46 43 72	0.3 34 46 67 31
38 32	KIF11	Kinesin family member 11	4. 06 13 9	3. 21 15 9	4. 16 16 2	5. 54 54 1	5. 71 43 2	4. 80 93	2.9 176 564 14	1.5 448 1	2.9 17 65 64 14	U p	0.0 03 17 46 49	0.2 34 23 93 82
84 51 5	MCM8	Minichromosome maintenance 8 homologous recombination repair factor	4. 69 27	4. 32 05 9	4. 49 53 8	4. 83 45 5	6. 28 28 8	5. 67 28 1	2.1 344 386 07	1.0 938 566 67	2.1 34 43 86 07	U p	0.0 21 46 04 69	0.3 73 80 25 25
44 06 86	HIST2 H3PS2	Histone cluster 2, H3, pseudogene 2	6. 19 18 1	5. 50 18 7	5. 70 53 8	7. 08 31 2	7. 49 99 7	6. 87 60 8	2.5 550 827 22	1.3 533 7	2.5 55 08 27 22	U p	0.0 01 87 90 27	0.1 95 76 45 58
11 15 3	FICD	FIC domain containing	5. 10 69 2	6. 94 44 8	5. 82 60 3	4. 28 28 2	4. 20 27 8	4. 82 47 5	-2. 872 605 742	-1. 522 36	2.8 72 60 57 42	D o w n	0.0 13 81 71 33	0.3 44 49 38 94
65 14	SLC2A 2	Solute carrier family 2 (facilitated glucose transporter), member 2	3. 98 76 2	4. 61 70 5	5. 05 15 3	4. 10 19 9	3. 06 68 8	2. 46 16 3	-2. 534 849 336	-1. 341 9	2.5 34 84 93 36	D o w n	0.0 21 93 06 57	0.3 77 76 08 81

79 18 8	TMEM 43	Transmembrane protein 43	6. 20 95 4	5. 54 06 8	5. 94 30 8	6. 85 89 2	7. 37 73 6	6. 54 27 3	2.0 400 011 99	1.0 285 7	2.0 40 00 11 99	U p	0.0 11 09 30 66	0.3 24 51 13 09
14 76 86	ZNF41 8	Zinc finger protein 418	4. 44 19	5. 39 89 6	5. 27 57 2	2. 73 74 3	3. 92 19	3. 84 2	-2. 904 755 365	-1. 538 416 667	2.9 04 75 53 65	D o w n	0.0 06 42 36 58	0.2 84 77 87 82
10 48 6	CAP2	CAP, adenylate cyclase-associated protein, 2 (yeast)	5. 56 10 5	5. 30 39 2	4. 46 32 9	6. 49 62 7	5. 68 27	6. 64 18 9	2.2 410 890 88	1.1 642	2.2 41 08 90 88	U p	0.0 19 09 08 94	0.3 67 52 43 59
51 30 3	FKBP1 1	FK506 binding protein 11	5. 49 62 1	6. 83 61 2	6. 51 61 8	5. 61 56 2	4. 91 00 4	4. 73 32	-2. 291 909 376	-1. 196 55	2.2 91 90 93 76	D o w n	0.0 22 61 27 24	0.3 79 32 86 95
59 83	RFC3	Replication factor C subunit 3	5. 82 65 7	5. 93 25 6	5. 60 17 1	6. 78 03 9	7. 68 79 4	6. 91 93	2.5 354 878 01	1.3 422 633 33	2.5 35 48 78 01	U p	0.0 02 55 80 18	0.2 21 48 56 65
10 16 4	CHST4	Carbohydrate (N-acetylglucosam ine 6-O) sulfotransferase 4	10 .6 81 23	6. 95 28 8	7. 78 74 7	4. 58 93 4	7. 33 18 1	5. 51 65 4	-6. 326 013 64	-2. 661 296 667	6.3 26 01 36 4	D o w n	0.0 42 11 40 28	0.4 30 36 23 78
10 87 3	ME3	Malic enzyme 3, NADP(+)-depende nt, mitochondrial	7. 45 55 8	7. 87 51 4	7. 38 14 9	6. 53 49 1	6. 43 05	6. 45 30 5	-2. 140 453 756	-1. 097 916 667	2.1 40 45 37 56	D o w n	0.0 01 63 71 07	0.1 88 11 80 17
73 21	UBE2 D1	Ubiquitin conjugating enzyme E2D 1	5. 14 41	4. 80 51 2	4. 40 79 6	5. 62 28 3	6. 82 65 1	5. 82 23 3	2.4 705 461 4	1.3 048 3	2.4 70 54 61 4	U p	0.0 09 80 30 2	0.3 14 70 35 37
13 62	CPD	Carboxypeptidase D	7. 66 64	8. 84 35 8	8. 99 33 8	7. 98 30 8	7. 31 74 6	6. 42 24 4	-2. 395 167 692	-1. 260 126 667	2.3 95 16 76	D o w n	0.0 41 34 85	0.4 27 14 11

											92		84	54
64 42 49	LOC64 4249	Coiled-coil domain-containing protein 29-like	7. 46 14 8	7. 42 23 2	7. 32 89 1	7. 15 84 3	5. 30 81 1	5. 41 93 7	-2. 717 474 819	-1. 442 266 667	2.7 17 47 48 19	D o w n	0.0 22 22 55 45	0.3 78 35 72 21
15 83 99	ZNF48 3	Zinc finger protein 483	4. 96 25 3	4. 79 25 7	5. 46 77 2	2. 46 48 7	4. 54 73 1	4. 25 38	-2. 494 838 913	-1. 318 946 667	2.4 94 83 89 13	D o w n	0.0 45 16 28 15	0.4 36 31 70 19
57 47 6	GRAM D1B	GRAM domain containing 1B	8. 30 76 1	8. 47 26 8	8. 95 95 1	6. 98 64 1	5. 16 36 4	5. 71 37	-6. 170 325 797	-2. 625 346 667	6.1 70 32 57 97	D o w n	0.0 00 89 98 58	0.1 81 04 09 24
67 88	STK3	Serine/threonine kinase 3	6. 34 18 7	6. 46 83 6	6. 30 40 9	7. 76 66 7	7. 67 06 3	6. 68 66	2.0 044 318 03	1.0 031 933 33	2.0 04 43 18 03	U p	0.0 17 40 53 29	0.3 60 38 98 23
51 18 1	DCXR	Dicarbonyl/L-xylu lose reductase	7. 14 50 8	8. 74 32 1	8. 00 70 5	7. 13 15 4	6. 84 30 3	5. 90 48 9	-2. 529 104 531	-1. 338 626 667	2.5 29 10 45 31	D o w n	0.0 28 70 62 22	0.3 93 40 55 85
24 91	CENPI	Centromere protein I	4. 16 69 3	3. 64 40 1	4. 04 21 8	4. 73 88 9	5. 55 43 2	4. 76 66 6	2.0 978 574 75	1.0 689 166 67	2.0 97 85 74 75	U p	0.0 07 10 87 82	0.2 89 31 65 01
51 30 1	GCNT 4	Glucosaminyl (N-acetyl) transferase 4, core 2	8. 85 51 3	8. 38 15 6	8. 31 68 7	3. 96 62 1	5. 03 62 4	3. 78 70 5	-19 .08 922 552	-4. 254 686 667	19. 08 92 25 52	D o w n	9.3 82 72 E- 06	0.0 69 64 55 19
36 69	ISG20	Interferon stimulated exonuclease gene 20kda	9. 12 11 8	7. 70 52 7	7. 37 24 2	6. 67 63 8	6. 31 51 8	6. 97 71 5	-2. 657 469 867	-1. 410 053 333	2.6 57 46 98 67	D o w n	0.0 20 28 08 55	0.3 71 13 26 99
50 28	P2RY1	Purinergic receptor P2Y, G-protein coupled,	6. 62 73	6. 07 03	6. 52 92	4. 05 63	5. 63 02	5. 69 20	-2. 433 079	-1. 282 783	2.4 33 07	D o w	0.0 27 98	0.3 92 00

		1	7	2	5	4	4	1	285	333	92	n	63	23
84	FAM2	Family with	6.	5.	6.	5.	5.	5.	-2.	-1.	2.1	D	0.0	0.3
91	22A	sequence	69	91	83	66	02	50	126	088	26	o	11	27
5		similarity 222	96	24	82	01	18	20	911	76	91	w	46	65
		member A	6	3	6	5	3	9	493		14	n	96	98
											93		42	66
83	CAST	Calpastatin	6.	5.	6.	7.	7.	6.	2.2	1.1	2.2	U	0.0	0.2
1			44	95	06	13	84	99	454	670	45	p	05	69
			55	73	56	00	14	80	999	366	49		48	83
			2	2	4	7	7	5	14	67	99		65	57
											14		54	64
10	ZSCA	Zinc finger and	4.	4.	4.	4.	3.	2.	-2.	-1.	2.0	D	0.0	0.4
01	N30	SCAN domain	31	62	83	32	73	59	052	037	52	o	46	39
01		containing 30	26	85	11	44	78	83	254	21	25	w	27	77
46			4	6	2	3	8	8	997		49	n	00	72
7											97		36	08
23	SULF1	Sulfatase 1	5.	5.	5.	5.	10	8.	7.5	2.9	7.5	U	0.0	0.3
21			38	79	06	97	.6	33	052	079	05	p	28	92
3			24	21	07	91	44	50	840	066	28		21	90
			4	8	6	5	93	2	11	67	40		93	93
											11		98	52
38	ARHG	Rho guanine	6.	7.	6.	6.	5.	6.	-2.	-1.	2.3	D	0.0	0.3
93	EF37	nucleotide	61	92	96	18	31	37	310	207	10	o	25	85
37		exchange factor 37	60	23	09	94	58	00	160	993	16	w	96	81
			9	5		5	4	7	894	333	08	n	29	07
											94		73	78
57	NUFIP	Nuclear fragile X	5.	5.	5.	6.	6.	6.	2.1	1.0	2.1	U	0.0	0.2
53	2	mental retardation	28	86	85	47	98	81	295	905	29	p	04	45
2		protein interacting	50	84	04	35	57	63	619	566	56		16	18
		protein 2	3		2	2			02	67	19		69	04
											02		82	58
12	NIPA1	Non imprinted in	7.	7.	7.	6.	6.	6.	-2.	-1.	2.2	D	0.0	0.1
36		Prader-Willi/Angel	64	33	34	37	32	08	262	178	62	o	00	81
06		man syndrome 1	35	35	05	37	84	11	811	116	81	w	88	04
			5		7		7		905	667	19	n	42	09
											05		24	24
58	BBS1	Bardet-Biedl	8.	7.	8.	6.	6.	7.	-2.	-1.	2.3	D	0.0	0.1
2		syndrome 1	03	94	12	78	52	03	383	252	83	o	00	75
			35	51	72	62	92	15	343	986	34	w	75	76
			2	6	8	7	2	1	122	667	31	n	58	93
											22		23	57
53	PLP2	Proteolipid protein	7.	7.	7.	8.	9.	8.	2.0	1.0	2.0	U	0.0	0.3
55		2 (colonic	57	32	17	04	14	07	870	614	87	p	17	62

		epithelium-enriched)	766	313	722	045	693	499	32886	53333	032886		990067	487638
10891	PPARGC1A	Peroxisome proliferator-activated receptor $\gamma$ , coactivator 1 $\alpha$	6.56868	6.37334	6.5076	5.7104	5.42839	3.64886	-2.93623343	-1.553966	2.93623343	Dow n	0.02123888	0.372540654
6035	RNAS E1	Ribonuclease, rnasase A family, 1 (pancreatic)	11.86701	12.0681	11.58814	7.33756	9.45881	9.0283	-9.401254832	-3.232853333	9.401254832	Dow n	0.00543257	0.164531093
3146	HMGB1	High mobility group box 1	6.46867	6.11683	6.36068	7.24126	8.27316	7.48406	2.55047625	1.35076667	2.55047625	U p	0.003441408	0.2371466
3172	HNF4A	Hepatocyte nuclear factor 4, $\alpha$	6.38044	6.80427	7.85574	8.51785	8.7933	7.55607	2.42097852	1.27559	2.42097852	U p	0.031873362	0.403012098
728226	GGTL C3	$\Gamma$ -glutamyltransferase light chain 3	9.16157	9.31314	8.59698	7.48881	7.56931	5.95581	-4.053739364	-2.019253333	4.053739364	Dow n	0.003671527	0.23859853
23654	PLXNB2	Plexin B2	10.92635	10.05873	9.85906	8.99293	8.92649	9.47106	-2.22101633	-1.15122	2.22101633	Dow n	0.011250047	0.324854465
8329	HIST1H2AI	Histone cluster 1, h2ai	4.40129	3.07578	4.0012	7.16327	6.98146	5.71565	6.935644729	2.79403	6.935644729	U p	0.00741761	0.173732248
285513	GPRIN3	GPRIN family member 3	4.18034	3.59416	3.31549	5.80145	5.02294	4.23061	2.49952796	1.32167	2.49952796	U p	0.01719054	0.360012938
42	CIITA	Class II, major	5.	4.	5.	3.	4.	4.	-2.	-1.	2.3	D	0.0	0.3



61		histocompatibility complex, transactivator	84291	92401	72211	51534	84774	36567	384070116	253426667	84070116	o w n	17402627	60389823
84818	IL17RC	Interleukin 17 receptor C	8.16985	8.46092	8.53021	6.99092	7.05018	7.91126	-2.098764074	-1.06954	2.098764074	D o w n	0.00970699	0.316695318
283375	SLC39A5	Solute carrier family 39 (zinc transporter), member 5	6.73982	6.25316	6.32724	8.27773	7.60155	6.70109	2.123901215	1.086716667	2.123901215	U p	0.033113393	0.406315059
23428	SLC7A8	Solute carrier family 7 (amino acid transporter light chain, L system), member 8	6.73749	9.30585	8.54974	6.46171	7.08793	5.15437	-3.89878158	-1.963023333	3.89878158	D o w n	0.034170554	0.408273555
4312	MMP1	Matrix metalloproteinase 1	5.54526	6.62785	8.97191	2.78101	5.92158	3.22258	-8.417022652	-3.07331	8.417022652	D o w n	0.025582037	0.38482703
29760	BLNK	B-cell linker	6.36268	5.17316	5.71313	7.42832	7.20657	6.45637	2.429652521	1.28075	2.429652521	U p	0.013556609	0.342678485
13512	NCOA7	Nuclear receptor coactivator 7	5.31096	4.48489	5.25519	5.26539	7.64925	7.72546	3.6376836	1.86302	3.6376836	U p	0.027710834	0.391408015
728841	NBPF8	Neuroblastoma breakpoint family member 8	6.53963	6.63459	6.41746	7.40056	7.69658	7.70662	2.100471678	1.0707133	2.100471678	U p	0.001292319	0.187107818
353091	RAET1G	Retinoic acid early transcript 1G	5.41502	5.18697	4.64681	6.32896	5.96492	7.31171	2.736370028	1.4522633	2.736370028	U p	0.007987247	0.299139554

1282	COL4A1	Collagen, type IV, $\alpha$ 1	7.83442	7.71517	7.43233	8.95892	10.09358	8.16044	3.05323789	1.61034	3.05323789	U p	0.013690736	0.343500698
171177	RHOV	Ras homolog family member V	3.87304	4.06875	4.13732	5.23802	4.22597	5.69224	2.03592	1.0257	2.03592	U p	0.027987458	0.392002337
11098	PRSS23	Protease, serine 23	8.47042	9.42572	8.20948	6.33418	8.24251	6.77771	-2.997458	-1.58374	2.997458	D o w n	0.02438126	0.382664012
664	BNIP3	BCL2/adenovirus E1B 19kda interacting protein 3	7.3651	7.47063	7.07189	3.84333	5.61933	5.37383	-5.12328837	-2.35705333	5.12328837	D o w n	0.001558672	0.187107818
3872	KRT17	Keratin 17, type I	5.27672	5.76972	5.5041	10.08662	5.67799	10.74934	11.21846461	3.4878033	11.21846461	U p	0.025881794	0.385401082
23281	MTUS2	Microtubule associated tumor suppressor candidate 2	5.33393	4.65271	4.51909	3.20961	3.27082	4.25753	-2.388199459	-1.25592333	2.388199459	D o w n	0.068387	0.313660293
81671	VMP1	Vacuole membrane protein 1	10.35736	8.72939	8.29673	9.88904	11.117332	11.74719	3.58512482	1.8420233	3.58512482	U p	0.027739772	0.391448674
445329	SULT1A4	Sulfotransferase family 1A member 4	6.47722	6.93547	6.66106	7.80233	8.02899	7.66662	2.20594464	1.14139667	2.20594464	U p	0.0523801	0.187107818
387103	CENPW	Centromere protein W	5.84319	5.52329	5.65403	6.3871	7.08305	6.90926	2.3342627	1.22296667	2.3342627	U p	0.0033937	0.23766

											7		44	6
64 77	SIAH1	Siah E3 ubiquitin protein ligase 1	4. 58 41 8	4. 73 88	4. 56 13	6. 24 70	6. 04 65 1	5. 10 08 5	2.2 501 169 69	1.1 7	2.2 50 11 69 69	U p	0.0 08 44 42 01	0.3 06 03 57 14
54 49 2	NEUR L1B	Neuralized E3 ubiquitin protein ligase 1B	4. 08 59 1	4. 12 41 9	4. 25 58 9	4. 75 39 7	6. 61 57 6	5. 26 50 3	2.6 200 421 11	1.3 895 9	2.6 20 04 21 11	U p	0.0 18 65 58 57	0.3 65 23 18 69
56 34	PRPS2	Phosphoribosyl pyrophosphate synthetase 2	6. 97 49 8	7. 36 95 4	7. 20 95 2	8. 14 98 9	8. 86 57 3	7. 79 04 8	2.1 199 349 55	1.0 840 2	2.1 19 93 49 55	U p	0.0 11 12 72 43	0.3 24 61 19 79
57 18 7	THOC 2	THO complex 2	3. 36 86 7	4. 04 50 4	4. 04 45 3	5. 06 20 2	5. 73 65 7	4. 28 40 3	2.3 103 744 08	1.2 081 266 67	2.3 10 37 44 08	U p	0.0 18 40 80 28	0.3 64 58 60 01
10 05 4	UBA2	Ubiquitin-like modifier activating enzyme 2	3. 82 36 5	4. 03 12 4	3. 76 62 3	4. 41 66 1	5. 41 38 3	5. 20 23 7	2.1 995 829 37	1.1 372 3	2.1 99 58 29 37	U p	0.0 05 38 29 93	0.2 69 32 15 26
64 22 5	ATL2	Atlantin gtpase 2	4. 20 70 6	5. 35 59 1	4. 78 69 3	5. 64 73	5. 87 69 8	5. 99 05 6	2.0 776 894 04	1.0 549 8	2.0 77 68 94 04	U p	0.0 12 50 50 06	0.3 34 46 67 31
42 58	MGST 2	Microsomal glutathione S-transferase 2	10 .5 47 46	9. 37 47 4	10 .0 13 92	9. 50 78 2	8. 31 77	8. 49 26 5	-2. 306 944 559	-1. 205 983 333	2.3 06 94 45 59	D o w n	0.0 25 23 96 7	0.3 83 71 27 62
57 16 7	SALL4	Spalt-like transcription factor 4	4. 92 40 8	4. 80 79	4. 93 75 6	5. 87 17 3	5. 31 66 3	7. 64 01 8	2.6 141 344 31	1.3 863 333 33	2.6 14 13 44 31	U p	0.0 43 32 33 15	0.4 32 33 09 01
25 49 58	REXO 1L1P	REX1, RNA exonuclease 1, homolog-like 1,	5. 55 70	5. 00 13	5. 11 74	5. 51 53	7. 13 76	6. 27 46	2.1 197 929	1.0 839 233	2.1 19 79	U p	0.0 36 37	0.4 13 81

		pseudogene	2	9	2		5	5	15	33	29		98	69
64 15 1	NCAP G	Non-SMC condensin I complex subunit G	6. 51 03 2	5. 92 15 9	6. 32 71 1	7. 96 76 5	8. 37 55 5	7. 20 81 3	3.0 260 517 64	1.5 974 366 67	3.0 26 05 17 64	U p	0.0 02 47 40 17	0.2 17 69 67 67
79 90 5	TMC7	Transmembrane channel like 7	5. 55 38 1	5. 00 45 3	5. 82 99 2	8. 97 45	7. 19 11 7	8. 06 74 8	6.1 260 762 9	2.6 149 633 33	6.1 26 07 62 9	U p	0.0 00 87 83 44	0.1 81 04 09 24
23 31	FMOD	Fibromodulin	8. 35 25 3	11 .3 64 62	9. 74 53 4	4. 93 62 4	7. 86 04	8. 06 87 1	-7. 288 961 769	-2. 865 713 333	7.2 88 96 17 69	D o w n	0.0 27 53 46 39	0.3 90 33 04 89
22 99 6	TTC39 A	Tetratricopeptide repeat domain 39A	6. 74 09 1	6. 56 01 8	6. 97 9	5. 65 85 6	5. 95 68 6	4. 94 76 6	-2. 360 386 862	-1. 239 023 333	2.3 60 38 68 62	D o w n	0.0 04 95 43 64	0.2 63 34 97 33
21 46	EZH2	Enhancer of zeste 2 polycomb repressive complex 2 subunit	5. 29 68 8	4. 59 28 7	5. 22 27	6. 67 30 5	7. 05 61 9	5. 61 79 5	2.6 602 835 03	1.4 115 8	2.6 60 28 35 03	U p	0.0 10 88 81 09	0.3 23 87 84 16
62 52	RTN1	Reticulon 1	8. 12 12 6	6. 68 12 7	7. 51 86	3. 92 70 9	5. 19 63 3	5. 37 02	-6. 101 525 544	-2. 609	6.1 01 52 55 44	D o w n	0.0 01 31 39 1	0.1 87 10 78 18
98 37	GINS1	GINS complex subunit 1 (Psf1 homolog)	5. 08 3	4. 63 82 5	4. 86 21 5	6. 47 35 2	7. 24 34 6	6. 12 99 1	3.3 740 858 14	1.7 544 966 67	3.3 74 08 58 14	U p	0.0 01 00 21 14	0.1 86 14 79 2
25 44 28	SLC41 A1	Solute carrier family 41 (magnesium transporter), member 1	6. 33 12 9	7. 57 04 8	7. 13 81 7	5. 76 95 3	5. 29 71 3	5. 85 04 2	-2. 592 396 995	-1. 374 286 667	2.5 92 39 69 95	D o w n	0.0 06 34 72 88	0.2 83 73 24 96
15 77	FAM9 1A1	Family with sequence	4. 23	4. 21	4. 29	5. 33	6. 13	4. 76	2.2 338	1.1 595	2.2 33	U p	0.0 12	0.3 34

69		similarity 91 member A1	83 5	77 4	61 3	01 8	94 1	12 4	567 4	366 67	85 67 4		40 70 29	46 67 31
11 05 1	NUDT 21	Nudix hydrolase 21	4. 40 78 9	4. 00 98 1	4. 54 89 9	5. 52 77 6	6. 02 01 9	4. 77 42 6	2.1 712 211 31	1.1 185 066 67	2.1 71 22 11 31	U p	0.0 14 19 75 69	0.3 46 79 70 53
90 70 1	SEC11 C	SEC11 homolog C, signal peptidase complex subunit	8. 48 90 8	10 .1 43 91	9. 24 75 9	8. 63 44 1	7. 83 44 9	6. 66 25 6	-2. 996 004 935	-1. 583 04	2.9 96 00 49 35	D o w n	0.0 33 05 33 3	0.4 06 21 59 67
66 03 5	SLC2A 11	Solute carrier family 2 (facilitated glucose transporter), member 11	5. 25 09 3	5. 71 96 5	5. 31 92 8	5. 14 19 8	4. 19 57 7	3. 78 54 5	-2. 078 515 25	-1. 055 553 333	2.0 78 51 52 5	D o w n	0.0 23 43 23 09	0.3 80 86 14 11
43 54	MPP1	Membrane protein, palmitoylated 1	5. 58 62 9	4. 71 04	4. 99 77 7	2. 49 54 1	5. 06 59 3	2. 94 56 4	-3. 022 676 674	-1. 595 826 667	3.0 22 67 66 74	D o w n	0.0 44 46 15 86	0.4 35 28 98 64
90 61	PAPSS 1	3'-phosphoadenosi ne 5'-phosphosulfate synthase 1	8. 40 64 9	10 .0 75 97	9. 12 87 4	7. 76 65 2	8. 30 76 2	8. 17 53	-2. 174 353 738	-1. 120 586 667	2.1 74 35 37 38	D o w n	0.0 35 36 21 65	0.4 10 04 57 87
54 80	PPIC	Peptidylprolyl isomerase C (cyclophilin C)	5. 55 73	5. 34 46 7	5. 16 57 9	6. 01 50 3	6. 66 32	6. 91 77	2.2 595 831 8	1.1 760 566 67	2.2 59 58 31 8	U p	0.0 04 60 55 51	0.2 54 41 63 12
15 54 65	AGR3	Anterior gradient 3, protein disulphide isomerase family member	5. 64 48 7	5. 34 29 4	5. 33 84 5	8. 80 79 7	8. 65 03 8	6. 51 93 4	5.8 582 780 4	2.5 504 766 67	5.8 58 27 80 4	U p	0.0 03 71 82 17	0.2 38 59 85 3
85 42	APOL 1	Apolipoprotein L1	8. 41 36 7	8. 66 27 9	8. 83 77 2	7. 99 89 6	7. 65 75	6. 78 61 2	-2. 230 241 593	-1. 157 2	2.2 30 24 15 93	D o w n	0.0 12 25 77 29	0.3 33 39 53 91
79	BEND	BEN domain	6.	5.	6.	5.	5.	5.	-2.	-1.	2.0	D	0.0	0.2

65 6	5	containing 5	59 78 8	82 75 5	10 21 7	04 87 6	01 30 1	42 64 4	018 285 125	013 13	18 28 51 25	o w n	06 87 53 19	88 45 97 19
11 46 09	TIRAP	Toll-interleukin 1 receptor (TIR) domain containing adaptor protein	6. 17 59 2	6. 39 85 2	6. 58 14 2	5. 48 84 8	4. 88 31 2	5. 36 79 2	-2. 201 947 39	-1. 138 78	2.2 01 94 73 9	D o w n	0.0 02 41 16 44	0.2 15 53 16 8
10 27 23 46 2	LOC10 272346 2	Uncharacterized LOC102723462	7. 46 14 8	7. 42 23 2	7. 32 89 1	7. 15 84 3	5. 30 81 1	5. 41 93 7	-2. 717 474 819	-1. 442 266 667	2.7 17 47 48 19	D o w n	0.0 22 22 55 45	0.3 78 35 72 21
48 97	NRCA M	Neuronal cell adhesion molecule	7. 03 54	6. 86 81 8	7. 59 53 6	4. 31 60 8	4. 94 78 8	4. 04 44 9	-6. 635 307 534	-2. 730 163 333	6.6 35 30 75 34	D o w n	6.2 12 98 E- 05	0.1 15 58 79 66
55 42 36	DPY19 L2P1	DPY19L2 pseudogene 1	4. 65 20 6	3. 31 09 2	3. 19 81 9	4. 85 36 3	5. 39 53 4	5. 51 77 1	2.8 982 258 01	1.5 351 7	2.8 98 22 58 01	U p	0.0 08 07 09 57	0.2 99 13 95 54
84 41 9	C15orf 48	Chromosome 15 open reading frame 48	4. 74 54 6	4. 74 79 2	5. 03 68 5	5. 64 55	10 .3 09 4	7. 15 93 9	7.2 669 668 91	2.8 613 533 33	7.2 66 96 68 91	U p	0.0 31 18 68 16	0.4 00 46 67 53
11 13 2	CAPN 10	Calpain 10	3. 60 01 2	3. 97 12	4. 20 73 1	5. 34 20 1	5. 22 35 7	4. 66 52 2	2.2 202 518 47	1.1 507 233 33	2.2 20 25 18 47	U p	0.0 03 19 05 6	0.2 34 23 93 82
54 66 5	RSBN 1	Round spermatid basic protein 1	4. 88 62 9	5. 24 61 2	5. 18 44 3	6. 49 86 1	6. 27 47 9	5. 61 29 6	2.0 323 844 53	1.0 231 733 33	2.0 32 38 44 53	U p	0.0 08 55 96 07	0.3 07 29 63 95
59 62	RDX	Radixin	7. 02 06 6	6. 52 12	6. 12 28 1	4. 90 58 7	6. 29 77 8	5. 13 58 5	-2. 156 049 05	-1. 108 39	2.1 56 04 90 5	D o w n	0.0 34 70 71 3	0.4 08 42 39 81

10013393	SNOR D12B	Small nucleolar RNA, C/D box 12B	4.14084	3.6744	3.91184	4.76666	4.38766	6.61438	2.5441904	1.3472066	2.5441904	U p	0.046178699	0.439638311
11001	SLC27 A2	Solute carrier family 27 (fatty acid transporter), member 2	5.90361	4.54743	4.60748	6.70221	7.45584	5.33622	2.786716	1.4785833	2.786716	U p	0.045090639	0.436078937
56667	MUC13	Mucin 13, cell surface associated	7.8298	7.27881	7.05255	7.89636	8.38773	8.98213	2.049142053	1.03502	2.049142053	U p	0.02132345	0.373026178
6715	SRD5 A1	Steroid-5- $\alpha$ -reductase, $\alpha$ polypeptide 1 (3-oxo-5 $\alpha$ -steroid $\Delta$ 4-dehydrogenase $\alpha$ 1)	3.89286	3.72647	3.74285	5.024	5.57044	4.02861	2.124254567	1.086956667	2.124254567	U p	0.02407193	0.381896949
2286	FKBP2	FK506 binding protein 2	8.22249	8.9038	8.20027	7.2882	7.32087	7.50877	-2.098511933	-1.0693667	2.098511933	D o w n	0.004679701	0.256554706
10468	FST	Follistatin	6.41395	6.94683	7.38565	5.74398	5.37272	5.92861	-2.351704296	-1.233706667	2.351704296	D o w n	0.005213631	0.266845614
7448	VTN	Vitronectin	11.85274	8.86273	9.45855	5.41674	7.65989	5.92183	-13.22491612	-3.725186667	13.22491612	D o w n	0.004072456	0.24425172
10497	UNC13B	Unc-13 homolog B (C. Elegans)	6.83918	7.56269	7.62566	5.58896	5.70128	5.02091	-3.746283293	-1.9054628	3.746283293	D o w n	0.00486797	0.164248294
5034	P4HB	Prolyl 4-hydroxylase, $\beta$ polypeptide	10.756	11.831	11.4480	10.742	10.405	9.7037	-2.102996	-1.072446	2.102996	D o w	0.02623	0.38731

			39	49	94	61	09	8	817	667	68	n	12	24
											17		5	42
24	CLDN	Claudin 15	5.	5.	5.	7.	7.	5.	2.5	1.3	2.5	U	0.0	0.4
14	15		23	56	68	27	85	48	992	780	99	p	49	46
6			32	03	16	33	42	18	042	7	20		89	67
			1	5			2	5	36		42		32	29
											36		89	81
72	HIST2	Histone cluster 2,	10	9.	9.	11	11	10	2.3	1.2	2.3	U	0.0	0.3
37	H2AA	h2aa4	.4	12	52	.0	.2	.4	006	020	00	p	20	71
90	4		75	07	91	78	34	18	900	666	69		74	73
			23	4	4	25	59	47	99	67	00		91	76
											99		62	6
14	CST3	Cystatin C	11	11	11	10	10	10	-2.	-1.	2.1	D	0.0	0.2
71			.7	.3	.7	.9	.1	.4	132	092	32	o	04	53
			14	36	59	14	84	34	205	346	20	w	50	49
			56	27	7	7	3	49	76	667	57	n	50	44
											6		76	23
29	RACG	Rac gtpase	6.	5.	5.	6.	7.	6.	2.1	1.1	2.1	U	0.0	0.3
12	API	activating protein	09	56	95	48	87	55	468	022	46	p	31	99
7	1		86	04	76	78	87	69	925	5	89		02	78
			7	9	7	9	5	4	69		25		52	54
											69		81	61
25	AMBP	A-1-microglobulin	11	6.	7.	6.	5.	5.	-6.	-2.	6.7	D	0.0	0.4
9		/bikunin precursor	.4	97	30	59	66	24	700	744	00	o	49	46
			61	83	05	22	65	90	753	323	75	w	14	17
			92	2	9	3	5	8	489	333	34	n	79	48
											89		14	
41	CD46	CD46 molecule,	6.	6.	7.	8.	8.	8.	2.9	1.5	2.9	U	0.0	0.1
79		complement	88	84	03	48	84	04	006	363	00	p	00	67
		regulatory protein	70	82	41	44	66	75	776	9	67		60	78
			8	5	3	4	3	6	92		76		55	26
											92		28	85
10	TVP23	TVP23C-CDRT4	6.	7.	7.	5.	5.	6.	-2.	-1.	2.4	D	0.0	0.3
05	C-CDR	readthrough	26	62	62	80	56	24	457	297	57	o	17	61
33	T4		23	14	44	81	61	24	452	163	45	w	55	12
49					4	1	4		163	333	21	n	87	33
6											63		15	37
16	TMTC	Transmembrane	6.	6.	6.	5.	5.	5.	-2.	-1.	2.0	D	0.0	0.2
03	2	and	27	73	24	26	34	58	029	021	29	o	03	34
35		tetratricopeptide	96	30	07	09	14	75	568	173	56	w	04	00
		repeat containing 2		9	6	3	9	1	922	333	89	n	16	38
											22		71	89
65	SLC5A	Solute carrier	3.	3.	3.	6.	5.	4.	2.5	1.3	2.5	U	0.0	0.3
26	3	family 5	90	81	81	14	11	30	296	389	29	p	18	63



		(sodium/myo-inositol cotransporter), member 3	805	96	161	2	189	223	77256	53333	6772		0626	0582
79853	TM4S F20	Transmembrane 4 L six family member 20	3.95205	3.73725	3.65284	5.9351	7.81276	5.29199	5.9212564	2.5659033	5.9212564	U p	0.0038436	0.2389072
55701	ARHG EF40	Rho guanine nucleotide exchange factor (GEF) 40	6.8562	6.95002	7.53392	6.84006	5.5889	5.69664	-2.10163675	-1.071513333	2.10163675	D o w n	0.0289846	0.3940729
3157	HMGC S1	3-hydroxy-3-methylglutaryl-coa synthase 1	5.16111	3.90118	4.12982	4.79237	5.68318	5.90358	2.08831595	1.06234	2.08831595	U p	0.0415039	0.4279166
3918	LAMC 2	Laminin subunit $\gamma$ 2	5.9852	5.13681	5.57942	6.74871	7.25207	9.14518	4.4326721	2.1481766	4.4326721	U p	0.0100956	0.3180092
57678	GPAM	Glycerol-3-phosphate acyltransferase, mitochondrial	6.67115	7.33119	5.99032	5.18538	5.37361	5.29063	-2.60451245	-1.381013333	2.60451245	D o w n	0.0055045	0.2698357
353497	POLN	Polymerase (DNA directed) nu	5.05352	5.88572	5.27035	3.81935	4.41728	4.11241	-2.49696848	-1.320176667	2.49696848	D o w n	0.0019332	0.1986750
1968	EIF2S3	Eukaryotic translation initiation factor 2 subunit $\gamma$	7.79363	7.48226	7.72689	8.91889	9.27964	8.10425	2.143591499	1.10003	2.143591499	U p	0.0128820	0.3361741
100133161	LINC0 1001	Long intergenic non-protein coding RNA 1001	8.03359	8.30848	7.49201	5.71049	6.09297	7.81824	-2.64657235	-1.404126667	2.64657235	D o w n	0.0400582	0.4243594
11	MID2	Midline 2	7.	5.	6.	4.	5.	5.	-2.	-1.	2.9	D	0.0	0.3

04 3			46 26 6	42 16 8	94 36	57 69 6	33 96 5	28 65 2	911 178 564	541 603 333	11 17 85 64	o w n	23 44 00 79	80 86 14 11
52 65	SERPI NA1	Serpin peptidase inhibitor, clade A ( $\alpha$ -1 antiproteinase, antitrypsin), member 1	9. 41 07 1	12 .3 48 36	12 .5 79 29	7. 21 68 1	8. 82 58 6	10 .2 00 57	-6. 490 696 657	-2. 698 373 333	6.4 90 69 66 57	D o w n	0.0 34 86 72 97	0.4 08 42 81 41
10 17	CDK2	Cyclin-dependent kinase 2	6. 87 66	6. 86 56 6	7. 20 00 7	9. 10 69 6	8. 15 32 8	7. 44 40 3	2.3 849 846 82	1.2 539 8	2.3 84 98 46 82	U p	0.0 20 34 90 21	0.3 71 13 26 99
30 73	HEXA	Hexosaminidase A ( $\alpha$ polypeptide)	9. 12 54 4	8. 85 06 4	8. 71 03 6	7. 20 11 9	7. 62 36 7	8. 79 70 8	-2. 030 028 526	-1. 021 5	2.0 30 02 85 26	D o w n	0.0 44 84 09 23	0.4 35 52 77 14
72 91 71	ANKR D20A8 P	Ankyrin repeat domain 20 family member A8, pseudogene	7. 46 14 8	7. 42 23 2	7. 32 89 1	7. 15 84 3	5. 30 81 1	5. 41 93 7	-2. 717 474 819	-1. 442 266 667	2.7 17 47 48 19	D o w n	0.0 22 22 55 45	0.3 78 35 72 21
53 90 5	DUOX 1	Dual oxidase 1	5. 52 09 1	5. 93 14 5	7. 72 87 5	4. 52 11 4	4. 42 02 9	5. 54 3	-2. 959 923 727	-1. 565 56	2.9 59 92 37 27	D o w n	0.0 37 31 24 76	0.4 16 34 38 48
10 58	CENP A	Centromere protein A	4. 39 71 5	4. 29 43 3	4. 46 27 6	5. 76 89 9	5. 90 67 6	4. 73 89 4	2.1 240 484 38	1.0 868 166 67	2.1 24 04 84 38	U p	0.0 13 04 07 28	0.3 36 17 41 55
16 55 45	DQX1	DEAQ box RNA-dependent atpase 1	4. 61 22 6	5. 09 57 5	5. 79 31 5	8. 05 27 4	6. 69 73 2	5. 43 89 2	2.9 538 911 55	1.5 626 166 67	2.9 53 89 11 55	U p	0.0 48 87 67 04	0.4 46 17 48
10 16 1	LPAR6	Lysophosphatidic acid receptor 6	7. 61 87 7	7. 84 50 8	6. 97 16 6	6. 91 23 8	6. 05 10 1	6. 01 72	-2. 221 663 01	-1. 151 64	2.2 21 66 30	D o w n	0.0 13 66 94	0.3 43 50 06

											1		47	98
84 30 4	NUDT 22	Nudix hydrolase 22	6. 36 05 3	6. 12 30 2	6. 19 42 4	4. 37 77 6	5. 23 26 2	5. 05 66 1	-2. 526 137 789	-1. 336 933 333	2.5 26 13 77 89	D o w n	0.0 01 73 30 74	0.1 91 04 98 66
16 1	AP2A2	Adaptor-related protein complex 2, $\alpha$ 2 subunit	8. 27 25 3	7. 94 29 2	8. 10 31 8	6. 60 29 7	6. 94 95 8	6. 59 36 8	-2. 622 288 953	-1. 390 826 667	2.6 22 28 89 53	D o w n	0.0 00 39 18 88	0.1 60 90 15 41
81 61 8	ITM2C	Integral membrane protein 2C	6. 58 73 1	8. 18 08 4	7. 53 75 2	9. 69 11 2	9. 65 81 2	9. 63 49 1	4.6 788 695 31	2.2 261 6	4.6 78 86 95 31	U p	0.0 00 84 98 04	0.1 81 04 09 24
23 50 0	DAAM 2	Dishevelled associated activator of morphogenesis 2	4. 52 81 5	7. 56 55 3	7. 35 20 5	4. 10 06 5	5. 15 41 5	4. 08 05 3	-4. 103 343 698	-2. 036 8	4.1 03 34 36 98	D o w n	0.0 40 47 91 83	0.4 25 93 08 38
10 50 7	SEMA 4D	Sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4D	6. 62 73 7	6. 45 35 7	6. 37 25 6	5. 91 49 2	5. 01 46 2	5. 41 04 2	-2. 053 170 352	-1. 037 853 333	2.0 53 17 03 52	D o w n	0.0 06 99 08 23	0.2 88 96 44 72
71 72	TPMT	Thiopurine S-methyltransferase	5. 09 75 8	5. 34 07 5	5. 29 12 5	6. 34 48 3	7. 41 79 1	5. 64 86	2.3 412 083 57	1.2 272 533 33	2.3 41 20 83 57	U p	0.0 25 79 34 94	0.3 85 33 44 54
10 10 59 93 5	LOC10 105993 5	Coiled-coil domain-containing protein 29-like	7. 46 14 8	7. 42 23 2	7. 32 89 1	7. 15 84 3	5. 30 81 1	5. 41 93 7	-2. 717 474 819	-1. 442 266 667	2.7 17 47 48 19	D o w n	0.0 22 22 55 45	0.3 78 35 72 21
50 67	CNTN 3	Contactin 3 (plasmacytoma associated)	6. 75 50 9	6. 98 58 4	7. 19 01 2	5. 59 10 1	4. 12 20 4	5. 41 04 2	-3. 826 061 331	-1. 935 86	3.8 26 06 13 31	D o w n	0.0 02 11 97 03	0.2 07 03 67

58 51 6	FAM6 0A	Family with sequence similarity member A	6. 06 86 6	5. 61 90 7	5. 91 70 4	7. 74 06 9	7. 44 74 4	6. 11 09 2	2.3 479 906 55	1.2 314 266 67	2.3 47 99 06 55	U p	0.0 25 60 16 37	0.3 84 82 70 3
10 02 88 11 4	LOC10 028811 4	Uncharacterized LOC100288114	7. 52 50 3	7. 83 96 7	8. 09 46 8	4. 39 71 5	6. 59 93 6	5. 51 95 2	-4. 974 149 952	-2. 314 45	4.9 74 14 99 52	D o w n	0.0 03 42 97 35	0.2 37 14 66 6
87 63	CD164	CD164 molecule, sialomucin	9. 90 49 3	9. 50 12 3	9. 63 28 6	8. 17 17 4	8. 80 69	8. 44 16 4	-2. 307 365 681	-1. 206 246 667	2.3 07 36 56 81	D o w n	0.0 01 93 42 61	0.1 98 67 50 21
54 79 8	DCHS 2	Dachsous cadherin-related 2	5. 62 71 5	6. 32 23 2	6. 95 12 7	4. 06 25 8	4. 50 29 8	4. 07 57	-4. 247 144 91	-2. 086 493 333	4.2 47 14 49 1	D o w n	0.0 00 63 93 36	0.1 72 63 18 47
12 96 42	MBOA T2	Membrane bound O-acyltransferase domain containing 2	4. 60 31 6	4. 21 94 5	5. 05 23 8	5. 77 65 4	6. 77 84 2	6. 98 33 8	3.7 006 618 98	1.8 877 833 33	3.7 00 66 18 98	U p	0.0 01 69 12 95	0.1 89 87 70 31
10 05 28 01 9	HSPB2 -c11orf 52	HSPB2-c11orf52 readthrough (NMD candidate)	6. 60 85 9	6. 14 75 6	6. 22 97 8	4. 51 20 8	4. 94 78 8	5. 35 58 2	-2. 620 877 639	-1. 390 05	2.6 20 87 76 39	D o w n	0.0 01 62 65 58	0.1 88 01 18 53
27 64	GMFB	Glia maturation factor, $\beta$	4. 60 85 8	4. 33 57 4	4. 74 42 1	5. 08 49 7	6. 30 65 4	6. 15 21 4	2.4 368 880 91	1.2 850 4	2.4 36 88 80 91	U p	0.0 08 15 40 39	0.3 01 10 59 84
56 93 8	ARNT L2	Aryl hydrocarbon receptor nuclear translocator like 2	4. 42 31	4. 10 66 8	4. 48 49 2	5. 57 39 3	6. 27 04 7	5. 15 09 8	2.5 086 189 26	1.3 268 933 33	2.5 08 61 89 26	U p	0.0 03 89 41 46	0.2 39 96 90 73
37 52 98	CERK L	Ceramide kinase like	5. 16 52 9	3. 88 90 1	4. 48 31 9	6. 51 70 1	5. 53 89 9	4. 97 29 3	2.2 404 885 18	1.1 638 133 33	2.2 40 48 85	U p	0.0 44 08 93	0.4 34 02 31

											18		42	21
21 60	F11	Coagulation factor XI	5. 81 69 3	5. 37 11 4	6. 38 65 8	4. 15 44 6	4. 05 98 5	2. 74 34 9	-4. 612 716 629	-2. 205 616 667	4.6 12 71 66 29	D o w n	0.0 01 64 72 4	0.1 88 17 54 66
97 88	MTSS 1	Metastasis suppressor 1	7. 14 67 8	8. 28 18 9	8. 59 48 4	7. 16 19	6. 45 40 5	6. 69 87 8	-2. 355 870 112	-1. 236 26	2.3 55 87 01 12	D o w n	0.0 20 47 39 02	0.3 71 13 26 99
94 9	SCAR B1	Scavenger receptor class B, member 1	8. 05 31 2	7. 35 41	7. 50 57 5	6. 29 11 4	6. 57 03 2	6. 43 60 3	-2. 305 628 382	-1. 205 16	2.3 05 62 83 82	D o w n	0.0 02 11 04 87	0.2 06 94 32 89
10 29 9	MARC H6	Membrane associated ring-CH-type finger 6	5. 13 25 7	5. 31 30 9	5. 27 27 7	6. 25 65 4	6. 55 42 2	5. 98 02 4	2.0 338 171 79	1.0 241 9	2.0 33 81 71 79	U p	0.0 02 56 80 98	0.2 21 48 56 65
84 51	CUL4 A	Cullin 4A	4. 19 89 2	4. 60 74 8	4. 38 57	5. 24 72 5	6. 20 89 1	5. 16 59 5	2.2 089 131 05	1.1 433 366 67	2.2 08 91 31 05	U p	0.0 08 87 43 51	0.3 08 52 19 75
15 06 96	PROM 2	Prominin 2	9. 21 65 8	8. 84 41 2	9. 33 83 9	9. 16 36	7. 11 17 2	6. 94 72	-2. 624 768 163	-1. 392 19	2.6 24 76 81 63	D o w n	0.0 48 86 46 54	0.4 46 17 48
13 26 71	SPATA 18	Spermatogenesis associated 18	7. 30 08	8. 01 21 3	8. 26 80 3	7. 48 21 9	5. 93 22 2	5. 49 04 4	-2. 945 889 535	-1. 558 703 333	2.9 45 88 95 35	D o w n	0.0 23 93 78 34	0.3 81 89 69 49
19 6	AHR	Aryl hydrocarbon receptor	4. 90 87 2	3. 91 85 1	4. 81 9 6	6. 64 94 6	6. 26 40 7	5. 46 29 5	2.9 829 710 99	1.5 767 5	2.9 82 97 10 99	U p	0.0 05 55 79 91	0.2 71 43 14 26
10 48 2	NXF1	Nuclear RNA export factor 1	9. 22 74	9. 37 22	9. 09 93	8. 11 84	8. 31 60	8. 09 69	-2. 079 014	-1. 055 9	2.0 79 01	D o w	0.0 01 26	0.1 87 10

			2	9	8	3	3	3	759		47	n	78	78	
14	CTGF	Connective tissue growth factor	4.7067	5.0712	3.6629	6.2912	8.2912	7.437	7.203	8.1998	3.0356	8.199	U	0.003	0.237
42	MKI67	Marker of proliferation Ki-67	4.4268	3.4021	3.5957	6.1434	7.0301	4.8574	4.6081	2.2014	4.6020	U	0.005	0.276	
57	ADGR G6	Adhesion protein-coupled receptor G6	4.8963	4.458	4.7000	4.8598	6.9871	6.7701	2.7781	1.4741	2.778	U	0.031	0.399	
76	CA3	Carbonic anhydrase III	3.9607	4.3087	4.4057	2.2614	4.677	2.159	-2.131	-1.091	2.131	D	0.043	0.432	
64	CREB 3L2	Camp responsive element binding protein 3-like 2	8.1077	8.1511	8.0356	6.7150	7.6106	6.2704	-2.350	-1.232	2.350	D	0.010	0.318	
50	PAH	Phenylalanine hydroxylase	10.9149	9.2344	10.0959	3.2501	6.0703	4.425	-45.96	-5.522	45.96	D	0.0014	0.127	
11	RMI2	Recq mediated genome instability 2	4.4893	4.6476	4.7754	5.9335	5.9096	5.6611	2.2931	1.1973	2.293	U	0.0048	0.124	
79	NDNF	Neuron-derived neurotrophic factor	7.1897	7.6520	7.4447	4.1199	7.1174	5.0903	-3.962	-1.986	3.962	D	0.025	0.385	
22	KIAA0907	KIAA0907	6.01	6.674	6.640	8.831	6.89	7.72	2.3862	1.2547	2.386	U	0.016	0.353	

9			75 1	82 8	27 9	56 3	22 3	50 3	910 24	7	29 10 24		29 12 94	90 90 69
55 15 1	TMEM 38B	Transmembrane protein 38B	4. 64 19 2	3. 50 26 3	3. 45 32 5	4. 80 27 7	5. 39 60 3	4. 66 83 7	2.1 284 305 26	1.0 897 9	2.1 28 43 05 26	U p	0.0 22 86 79 88	0.3 80 02 10 22
58 85	RAD2 1	RAD21 cohesin complex component	5. 24 45 6	4. 49 86 9	4. 91 34 2	5. 93 19 2	6. 87 38 7	5. 16 29 5	2.1 495 331 11	1.1 040 233 33	2.1 49 53 31 11	U p	0.0 42 80 94 11	0.4 32 07 88 1
40 05	LMO2	LIM domain only 2	6. 88 76	6. 00 65 9	7. 04 71 5	5. 06 91 8	6. 10 59 9	5. 41 36 7	-2. 169 706 65	-1. 117 5	2.1 69 70 66 5	D o w n	0.0 22 82 41 26	0.3 79 92 11 68
81 50 2	HM13	Histocompatibility (minor) 13	5. 17 73 5	6. 49 88 1	5. 91 37 7	4. 65 59 2	4. 84 01 7	4. 48 38 7	-2. 302 694 999	-1. 203 323 333	2.3 02 69 49 99	D o w n	0.0 10 56 93 73	0.3 22 73 69 69
20 00 30	NBPF1 1	Neuroblastoma breakpoint family member 11	6. 53 96 3	6. 63 45 9	6. 41 74	7. 40 05 6	7. 69 65 8	7. 70 66 2	2.1 004 716 78	1.0 707 133 33	2.1 00 47 16 78	U p	0.0 01 29 23 19	0.1 87 10 78 18
34 00	ID4	Inhibitor of DNA binding 4, dominant negative helix-loop-helix protein	5. 42 18 2	7. 08 99 7	5. 58 99 8	3. 14 33 6	4. 93 60 6	2. 50 63 8	-5. 677 765 769	-2. 505 323 333	5.6 77 76 57 69	D o w n	0.0 09 33 22 72	0.3 11 85 21 38
41 75	MCM6	Minichromosome maintenance complex component 6	5. 55 49 9	5. 09 64 2	5. 19 41 6	6. 69 83 9	7. 51 59 4	5. 89 86	2.6 804 093 29	1.4 224 533 33	2.6 80 40 93 29	U p	0.0 10 84 84 52	0.3 23 87 84 16
60 95	RORA	RAR-related orphan receptor A	6. 87 61 2	6. 83 11 6	6. 77 51 9	4. 78 31 6	6. 43 08	5. 74 56 1	-2. 256 833 521	-1. 174 3	2.2 56 83 35 21	D o w n	0.0 23 75 79 8	0.3 81 26 89 97
11	OSBP	Oxysterol binding	5.	8.	7.	4.	5.	4.	-4.	-2.	4.3	D	0.0	0.2

48 80	L6	protein like 6	84 05 4	04 77 2	37 12 7	98 50 1	05 56 5	89 83 5	307 378 194	106 81	07 37 81 94	o w n	05 43 07 18	69 32 15 26
37 75	KCNK 1	Potassium channel, two pore domain subfamily K, member 1	4. 36 70 8	4. 00 35 4	4. 61 40 1	5. 92 03	5. 46 19 5	5. 34 51	2.3 744 170 12	1.2 475 733 33	2.3 74 41 70 12	U p	0.0 01 72 76 23	0.1 91 04 98 66
10 63 1	POST N	Periostin, osteoblast specific factor	5. 28 48	4. 46 67 8	3. 84 98 8	5. 45 41 3	11 .1 80 64	6. 85 90 1	9.8 316 939 03	3.2 974 4	9.8 31 69 39 03	U p	0.0 45 98 43 81	0.4 39 25 30 47
53 14	PKHD 1	Polycystic kidney and hepatic disease 1 (autosomal recessive)	6. 73 91 8	6. 47 69 3	6. 06 52 4	4. 67 31 4	4. 72 62 3	5. 32 66 2	-2. 864 837 549	-1. 518 453 333	2.8 64 83 75 49	D o w n	0.0 01 05 24 27	0.1 86 14 79 2
36 96	ITGB8	Integrin $\beta$ 8	5. 11 79 8	3. 68 90 3	3. 59 93 7	6. 75 50 5	5. 13 74 9	5. 15 05 1	2.9 191 668 37	1.5 455 566 67	2.9 19 16 68 37	U p	0.0 32 04 30 87	0.4 03 67 11 92
57 95	PTPRJ	Protein tyrosine phosphatase, receptor type, J	6. 26 72 5	5. 88 77 5	5. 92 66 8	4. 37 83	5. 32 95 4	5. 22 13 3	-2. 071 730 965	-1. 050 836 667	2.0 71 73 09 65	D o w n	0.0 10 54 72 15	0.3 22 43 28 32
56 60 5	ERO1 B	Endoplasmic reticulum oxidoreductase $\beta$	5. 89 71 8	5. 80 53 2	5. 49 89 5	3. 79 41 8	4. 47 30 7	4. 76 37 3	-2. 621 071 422	-1. 390 156 667	2.6 21 07 14 22	D o w n	0.0 02 05 88 38	0.2 04 15 41 68
87 3	CBR1	Carbonyl reductase 1	4. 54 72 9	5. 29 07 6	6. 03 45 7	4. 08 37	4. 01 94 9	3. 53 41 5	-2. 660 615 438	-1. 411 76	2.6 60 61 54 38	D o w n	0.0 08 26 84 11	0.3 03 32 25 99
10 03 03 45 3	TSNA X-DIS C1	TSNAX-DISC1 readthrough (NMD candidate)	6. 23 02 8	6. 25 33 7	6. 36 51 7	4. 51 18 1	5. 37 2 7	5. 70 05 7	-2. 126 007 471	-1. 088 146 667	2.1 26 00 74 71	D o w n	0.0 12 45 04 84	0.3 34 46 67 31



23600	AMACR	A-methylacyl-coa racemase	6.6288	7.9019	8.1596	7.0571	6.2886	5.0031	-2.726688	-1.44715	2.72668	Dow n	0.049423973	0.4461748
10059	DNM1L	Dynamin 1-like	6.10446	6.05543	5.95484	7.42232	7.16608	6.62493	2.046032	1.03284967	2.046085832	U p	0.00534405	0.269321526
8968	HIST1H3F	Histone cluster 1, h3f	7.51267	6.70604	7.00589	7.80547	8.82491	7.94361	2.168144	1.1164633	2.16814	U p	0.016284617	0.353909069
3672	ITGA1	Integrin $\alpha$ 1	4.60435	5.03875	4.4053	5.39165	6.74465	5.15242	2.114199	1.0801067	2.11419	U p	0.043304662	0.432330901
54602	NDFIP2	Nedd4 family interacting protein 2	4.80342	4.90819	4.74532	5.66132	6.92723	5.52985	2.3302584	1.22049	2.33025	U p	0.015521094	0.350533052
360	AQP3	Aquaporin 3 (Gill blood group)	9.04403	10.9564	10.3903	9.00108	7.28715	8.33491	-3.791082	-1.92261	3.79108	Dow n	0.015523492	0.350533052
7068	THRB	Thyroid hormone receptor, $\beta$	6.07488	6.0933	6.0933	7.85574	7.17674	6.94151	2.357901306	1.2375033	2.35790	U p	0.003055096	0.234003889
100288413	ERVMER34-1	Endogenous retrovirus group MER34, member 1	4.03881	7.53479	7.19506	3.28364	3.30005	4.452	-5.788742569	-2.53325	5.78874	Dow n	0.024138669	0.382496957
9603	NFE2L3	Nuclear factor, erythroid 2 like 3	4.94817	5.1098	5.07456	6.84563	7.47539	6.75083	3.944311065	1.9797733	3.94431	U p	0.001117	0.1278498

												65		56	29
72 04	TRIO	Trio Rho guanine nucleotide exchange factor	3. 98 57 4	3. 80 58 9	3. 52 12 7	4. 47 38 9	5. 56 43 1	5. 03 00 9	2.3 813 780 44	1.2 517 966 67	2.3 81 37 80 44	U p	0.0 04 50 75 2	0.2 53 49 44 23	
10 05 07 38 7	LOC10 050738 7	Uncharacterized LOC100507387	6. 87 68 9	6. 80 65 5	6. 70 38 9	3. 93 42 4	3. 95 25 1	5. 88 33 8	-4. 613 089 661	-2. 205 733 333	4.6 13 08 96 61	D o w n	0.0 04 08 31 77	0.2 44 25 17 2	
10 53 69 24 3	LOC10 536924 3	Sulfotransferase 1A3-like	6. 47 72 2	6. 93 54 7	6. 66 10 6	7. 80 23 3	8. 02 89 9	7. 66 66 2	2.2 059 447 64	1.1 413 966 67	2.2 05 94 47 64	U p	0.0 01 52 38 01	0.1 87 10 78 18	
12 66 61	CCDC 163P	Coiled-coil domain containing 163, pseudogene	4. 46 28 6	5. 29 60 3	4. 97 17 1	4. 00 72 6	3. 91 35 7	3. 75 18 3	-2. 026 953 979	-1. 019 313 333	2.0 26 95 39 79	D o w n	0.0 04 58 44 42	0.2 54 41 63 12	
33 97	ID1	Inhibitor of DNA binding 1, dominant negative helix-loop-helix protein	9. 99 66 2	11 .1 43 64	10 .8 22 25	8. 36 13 5	7. 32 27 2	9. 49 75 6	-4. 790 888 818	-2. 260 293 333	4.7 90 88 88 18	D o w n	0.0 05 72 02 08	0.2 74 20 55 09	
79 64 6	PANK 3	Pantothenate kinase 3	5. 88 68 6	5. 50 90 5	5. 70 96 7	7. 40 72	6. 36 63	6. 59 72	2.1 263 415 21	1.0 883 733 33	2.1 26 34 15 21	U p	0.0 10 43 36 06	0.3 20 71 63 98	
34 05 42	BEX5	Brain expressed X-linked 5	5. 29 11 4	5. 26 87 9	5. 66 04 1	4. 73 90 8	3. 79 36 5	3. 90 47 3	-2. 396 551 595	-1. 260 96 15 95	2.3 96 55 15 95	D o w n	0.0 03 81 15 57	0.2 38 90 72 74	
23 02 2	PALL D	Palladin, cytoskeletal associated protein	7. 53 70 3	7. 34 20 2	6. 72 83 6	8. 17 36 1	10 .5 89 19	8. 44 52 3	3.6 474 124 1	1.8 668 733 33	3.6 47 41 24 1	U p	0.0 22 23 94	0.3 78 42 81 9	
10 82 6	FAXD C2	Fatty acid hydroxylase domain containing	7. 36 44	7. 90 15	8. 01 61	5. 72 55	6. 80 43	7. 42 01	-2. 159 469	-1. 110 676	2.1 59 46	D o w	0.0 42 01	0.4 30 07	

		2	2	2	5	4	4	8	09	667	90	n	78	43
72	TSPYL	TSPY-like 1	9.	9.	9.	8.	8.	9.	-2.	-1.	2.2	D	0.0	0.2
59	1		77	99	83	36	53	11	297	199	97	o	02	15
			98	34	18	06	12	36	157	85	15	w	42	53
			1	7	9	8	9	5	857		78	n	02	16
											57		69	8
21	FBLN1	Fibulin 1	5.	5.	4.	5.	9.	7.	4.8	2.2	4.8	U	0.0	0.4
92			37	68	54	58	26	62	830	877	83	p	33	08
			95	26	36	67	06	18	977	966	09		82	23
			1	8	2	7		3	79	67	77		85	98
											79		26	28
10	ZNF51	ZNF511-PRAP1	7.	6.	6.	8.	9.	6.	3.3	1.7	3.3	U	0.0	0.4
43	1-PRA	readthrough	06	77	21	90	57	77	315	362	31	p	41	26
26	P1		45	75	07	88	53	72	726	033	57		23	96
05			2	7	6	1	8	7	02	33	26		31	10
6											02		47	48
33	APLP1	Amyloid $\beta$ (A4)	6.	6.	5.	3.	3.	5.	-4.	-2.	4.5	D	0.0	0.2
3		precursor-like	67	62	55	94	28	02	579	195	79	o	03	37
		protein 1	21	68	26	93	87	80	330	136	33	w	44	14
			2	8	3	7	8	7	422	667	04	n	27	66
											22		53	6
54	XRN1	5'-3'	4.	3.	4.	4.	5.	5.	2.1	1.1	2.1	U	0.0	0.2
46		exoribonuclease 1	61	88	12	98	80	17	622	125	62	p	07	92
4			68	98	12	51	04	98	300	2	23		31	18
			5	3	6	9	5	6	1		00		56	66
											1		02	83
80	EFHD	EF-hand domain	4.	5.	4.	2.	4.	3.	-2.	-1.	2.4	D	0.0	0.3
30	1	family member D1	26	00	53	79	15	02	424	277	24	o	13	42
3			72	52	63	60	88	14	174	493	17	w	49	22
			6	7	1	5	7	4	132	333	41	n	82	02
											32		08	92
11	KLK11	Kallikrein related	9.	8.	8.	8.	5.	4.	-7.	-2.	7.2	D	0.0	0.3
01		peptidase 11	46	57	78	52	02	67	297	867	97	o	21	77
2			67	41	60	41	23	82	370	376	37	w	78	15
			1	8	3	9	6	4	313	667	03	n	19	66
											13		14	14
25	RAB3	RAB3 gtpase	4.	4.	4.	5.	5.	5.	2.1	1.1	2.1	U	0.0	0.2
78	GAP2	activating	22	39	30	26	97	00	500	043	50	p	05	69
2		non-catalytic	84	75	84	47	38	88	149	466	01		39	32
		protein subunit 2	3	6	3	5	3	8	13	67	49		52	15
											13		36	26
91	EXO1	Exonuclease 1	4.	4.	4.	6.	5.	5.	2.1	1.0	2.1	U	0.0	0.1
56			49	60	83	04	68	49	333	931	33	p	01	92

			85 6	76 6	45 7	05 7	41 2	54 3	342 14	1	33 42 14		80 64 69	63 39 39
55 92	PRKG 1	Protein kinase, cgmp-dependent, type I	6. 10 99 1	5. 77 59 6	6. 14 33 6	8. 01 99 5	8. 63 97 5	8. 35 30 9	5.0 205 775 39	2.3 278 533 33	5.0 20 57 75 39	U p	3.3 25 83 E- 05	0.0 96 05 29 42
64 07 8	SLC28 A3	Solute carrier family 28 (concentrative nucleoside transporter), member 3	4. 70 48 5	8. 03 55 9	9. 54 16 7	4. 03 45 7	5. 29 51 9	4. 40 71	-7. 202 095 185	-2. 848 416 667	7.2 02 09 51 85	D o w n	0.0 40 96 70 51	0.4 26 76 78 27
47 74	NFIA	Nuclear factor I/A	9. 06 01 8	9. 28 94 2	9. 50 79 6	8. 11 85	8. 30 84 8	7. 92 09 7	-2. 249 914 222	-1. 169 87	2.2 49 91 42 22	D o w n	0.0 01 35 22 3	0.1 87 10 78 18
30 81	HGD	Homogentisate 1,2-dioxygenase	8. 62 34 8	7. 05 74 2	7. 68 33 7	6. 03 22	5. 61 97 9	6. 05 94 3	-3. 691 694 918	-1. 884 283 333	3.6 91 69 49 18	D o w n	0.0 02 45 00 76	0.2 17 25 53 34
54 44 3	ANLN	Anillin actin binding protein	4. 59 2	3. 92 53 5	4. 44 04 2	5. 56 73 3	7. 23 30 4	5. 54 89	3.4 753 702 08	1.7 971 666 67	3.4 75 37 02 08	U p	0.0 07 55 41 03	0.2 95 71 33 58
10 02 88 15 2	LOC10 028815 2	Uncharacterized LOC100288152	6. 77 83	8. 04 18 2	6. 50 75	6. 37 45 7	5. 33 81 1	5. 21 66 3	-2. 762 746 772	-1. 466 103 333	2.7 62 74 67 72	D o w n	0.0 20 49 49 79	0.3 71 13 26 99
54 27	POLE2	Polymerase (DNA directed), epsilon 2, accessory subunit	4. 32 81	4. 46 32 9	4. 74 79 2	5. 44 66 5	6. 90 41 2	5. 17 78 3	2.5 136 143 7	1.3 297 633 33	2.5 13 61 43 7	U p	0.0 21 85 51 62	0.3 77 60 64 46
14 79 68	CAPN 12	Calpain 12	6. 98 67 1	8. 82 28 8	9. 64 78 9	4. 98 19 1	5. 36 92 4	6. 65 23	-7. 051 890 143	-2. 818 01	7.0 51 89 01 43	D o w n	0.0 06 48 92 99	0.2 85 18 60 95

61 96	RPS6K A2	Ribosomal protein S6 kinase, 90kda, polypeptide 2	7. 51 57 6	7. 04 29	7. 25 29 5	5. 51 72 4	6. 53 13 8	6. 42 95 7	-2. 160 162 733	-1. 111 14	2.1 60 16 27 33	D o w n	0.0 11 13 37 84	0.3 24 61 19 79
89 83 9	ARHG AP11B 11B	Rho gtpase activating protein 11B	5. 86 99 6	5. 53 95 7	6. 22 91 2	7. 63 44 8	7. 95 97 7	7. 54 28 6	3.5 623 271 16	1.8 328 2	3.5 62 32 71 16	U p	0.0 00 19 91 65	0.1 35 27 95 77
28 23 1	SLCO4 A1	Solute carrier organic anion transporter family member 4A1	4. 54 65 5	4. 73 43 8	5. 29 57 3	5. 63 18 8	7. 32 69 8	6. 56 3 8	3.1 348 577 94	1.6 484	3.1 34 85 77 94	U p	0.0 07 91 04 22	0.2 99 13 95 54
97 61	MLEC	Malectin	9. 69 49 9	10 .2 15 76	10 .1 50 19	8. 25 65	9. 83 63 5	8. 63 26 6	-2. 161 166 164	-1. 111 81	2.1 61 16 61 64	D o w n	0.0 34 96 73 74	0.4 08 43 73 33
10 53 76 57 5	LOC10 537657 5	Uncharacterized LOC105376575	4. 56 50 4	7. 37 47 1	6. 14 17 8	3. 40 91	4. 32 73 3	3. 62 24	-4. 726 918 531	-2. 240	4.7 26 91 85 31	D o w n	0.0 12 82 10 7	0.3 36 17 41 55
86 04	SLC25 A12	Solute carrier family 25 (aspartate/glutamat e carrier), member 12	4. 74 15 7	6. 09 01 2	4. 70 62	6. 49 50 2	6. 27 76 8	5. 95 07	2.0 875 874 97	1.0 618 366 67	2.0 87 58 74 97	U p	0.0 35 48 29 31	0.4 111 15 84 6
41 92	MDK	Midkine (neurite growth-promoting factor 2)	9. 24 63 4	8. 62 24 4	8. 74 86 1	10 .3 94 14	10 .2 43 88	9. 98 27 2	2.5 217 932 49	1.3 344 5	2.5 21 79 32 49	U p	0.0 01 16 59 45	0.1 86 14 79 2
18 94	ECT2	Epithelial cell transforming 2	4. 96 55 1	6. 19 47 3	5. 67 32 8	6. 53 32 6	6. 61 17 7	7. 92 65 2	2.6 623 064 9	1.4 126 766 67	2.6 62 30 64 9	U p	0.0 20 74 36 95	0.3 71 73 76 6
92 32	PTTG1	Pituitary tumor-transformin g 1	4. 44 43 1	4. 07 68 1	4. 48 38 5	6. 19 54 4	6. 81 31	5. 63 29 9	3.6 778 262 72	1.8 788 533 33	3.6 77 82 62	U p	0.0 00 72 00	0.1 72 63 18

												72		42	47
10 27 24 19 7	LOC10 272419 7	Inactive $\gamma$ -glutamyltranspe ptidase 2-like	9. 16 15 7	9. 31 31 4	8. 59 69 8	7. 48 88 1	7. 56 93 1	5. 95 58 1	-4. 053 739 364	-2. 019 253 333	4.0 53 73 93 64	D o w n	0.0 03 67 15 27	0.2 38 59 85 3	
64 71 4	PDIA2	Protein disulfide isomerase family A member 2	5. 01 63 2	8. 88 41 3	9. 40 83 9	4. 68 50 7	4. 62 07 8	5. 27 75 1	-7. 508 336 628	-2. 908 493 333	7.5 08 33 66 28	D o w n	0.0 31 20 37 36	0.4 00 46 67 53	
23 10 5	FSTL4	Follistatin-like 4	4. 74 05 7	5. 63 35 6	5. 65 52 4	4. 35 52	3. 70 77	4. 01 49 9	-2. 491 751 16	-1. 317 16	2.4 91 75 11 6	D o w n	0.0 04 16 66 45	0.2 45 18 04 58	
10 20 4	NUTF 2	Nuclear transport factor 2	4. 44 74 5	4. 47 23 9	4. 31 48 9	6. 07 84 5	4. 85 68 5	5. 43 88 6	2.0 654 793 93	1.0 464 766 67	2.0 65 47 93 93	U p	0.0 13 43 89 95	0.3 41 83 96 28	
36 8	ABCC 6	ATP binding cassette subfamily C member 6	5. 34 15	6. 23 23	6. 47 21 2	5. 36 39 3	4. 50 68 1	4. 96 88 4	-2. 097 658 754	-1. 068 78	2.0 97 65 87 54	D o w n	0.0 22 82 16 48	0.3 79 92 11 68	
23 65 0	TRIM2 9	Tripartite motif containing 29	7. 01 34 3	7. 46 87 7	7. 42 48 5	9. 62 08 9	8. 08 10 8	8. 70 86 4	2.8 307 545 61	1.5 011 866 67	2.8 30 75 45 61	U p	0.0 07 50 24 02	0.2 94 41 93 61	
20 08 79	LIPH	Lipase, member H	7. 21 84 6	7. 04 70 4	7. 68 83 9	8. 50 53 5	8. 17 01 1	8. 47 37 9	2.0 923 439 09	1.0 651 2	2.0 92 34 39 09	U p	0.0 03 81 20 53	0.2 38 90 72 74	
20 52	EPHX 1	Epoxide hydrolase 1, microsomal (xenobiotic)	9. 63 02 7	9. 15 54 2	9. 24 10 4	8. 38 76 6	7. 77 33 3	7. 11 85 6	-2. 994 662 321	-1. 582 393 333	2.9 94 66 23 21	D o w n	0.0 02 91 46 7	0.2 31 33 53 69	
72 82 62	FAM1 57A	Family with sequence similarity 157	8. 27 78	8. 11 34	7. 66 23	5. 84 47	5. 87 11	6. 62 62	-3. 742 070	-1. 903 836	3.7 42 07	D o w	0.0 00 42	0.1 63 37	

		member A	2	5	9	6	1	8	312	667	03	n	62	87
											12		53	34
27	APOB	Apolipoprotein B	8.	8.	8.	6.	6.	7.	-2.	-1.	2.2	D	0.0	0.3
35	EC3C	mRNA editing	03	24	36	48	96	65	267	180	67	o	08	06
0		enzyme, catalytic	81	08	50	98	04	11	103	85	10	w	46	05
		polypeptide-like	7	1	3	3	4	9	098		30	n	31	14
		3C									98		5	94
29	GUCY	Guanylate cyclase	4.	2.	3.	6.	6.	4.	4.8	2.2	4.8	U	0.0	0.3
83	1B3	1, soluble, $\beta$ 3	42	62	13	75	02	24	576	802	57	p	15	50
			59	36	32	52	25	57	100	466	61		51	53
			2	4	9	9	6	4	03	67	00		83	30
											03		02	52
37	KCNJ1	Potassium	7.	7.	7.	7.	6.	5.	-2.	-1.	2.4	D	0.0	0.3
72	5	channel, inwardly	75	13	98	18	40	42	443	289	43	o	28	93
		rectifying	69	55	70	20	35	67	761	103	76	w	94	97
		subfamily J,	9	6	7	4	2	5	232	333	12	n	89	60
		member 15									32		69	15
73	UBC	Ubiquitin C	10	9.	9.	8.	9.	9.	-2.	-1.	2.0	D	0.0	0.4
16			.7	71	72	42	50	24	017	012	17	o	43	32
			85	06	28	85	86	32	706	716	70	w	27	33
			08	8	9	9	2	9	968	667	69	n	96	09
											68		76	01
12	ZG16B	Zymogen granule	7.	8.	9.	7.	6.	5.	-4.	-2.	4.0	D	0.0	0.3
42		protein 16B	91	62	76	83	48	90	074	026	74	o	14	46
20			31	93	05	94	22	12	773	72	77	w	48	82
			9	3	3	3	3	3	873		38	n	91	70
											73		91	31
97	PHAC	Phosphatase and	7.	8.	8.	6.	7.	7.	-2.	-1.	2.0	D	0.0	0.3
49	TR2	actin regulator 2	73	52	08	50	57	14	058	041	58	o	19	68
			73	01	89	61	51	02	509	6	50	w	87	20
			2	3	1	4	4	8	348		93	n	61	43
											48		9	05
79	ROGD	Rogdi homolog	7.	7.	8.	6.	6.	6.	-2.	-1.	2.1	D	0.0	0.3
64	I		45	58	22	93	09	97	121	084	21	o	14	48
1			73	65	38	46	99	83	297	946	29	w	96	11
			9	1	8	5	2	7	061	667	70	n	54	05
											61		28	43
39	LBR	Lamin B receptor	7.	6.	6.	8.	9.	7.	2.7	1.4	2.7	U	0.0	0.3
30			59	59	92	62	13	74	620	657	62	p	10	23
			35	17	59	66	90	27	510	4	05		87	87
			4	3	2	7	2	2	79		10		13	84
											79		6	16
33	APLP2	Amyloid $\beta$ (A4)	11	10	10	9.	9.	9.	-2.	-1.	2.0	D	0.0	0.3
4		precursor-like	.0	.0	.3	64	57	19	005	003	05	o	13	45

		protein 2	36 38	45 12	52 44	90 1	35 8	96 9	395 328	886 667	39 53 28	w n	99 79 23	25 55 8
53 61 6	ADAM 22	ADAM metallopeptidase domain 22	3. 99 26 5	4. 53 65 9	4. 47 29 1	6. 30 10 8	7. 71 78 8	6. 42 37 5	5.5 796 965 62	2.4 801 866 67	5.5 79 69 65 62	U p	0.0 00 52 55 35	0.1 64 53 10 93
27 06	GJB2	Gap junction protein $\beta$ 2	3. 54 67 4	3. 49 46 1	3. 99 47 1	4. 77 26 3	5. 63 57 9	4. 64 51 8	2.5 300 747 34	1.3 391 8	2.5 30 07 47 34	U p	0.0 03 38 63 37	0.2 37 14 66 6
23 54 4	SEZ6L	Seizure related 6 homolog (mouse)-like	5. 85 55 8	8. 24 40 7	8. 18 99 9	6. 07 59 7	5. 55 96	5. 92 79 6	-2. 980 119 123	-1. 575 37	2.9 80 11 91 23	D o w n	0.0 42 88 37 72	0.4 32 07 88 1
85 23 6	HIST1 H2BK	Histone cluster 1, h2bk	7. 11 94 5	7. 94 88 2	7. 73 63	10 .6 64 86	9. 33 91 8	9. 04 15 6	4.2 290 784 81	2.0 803 433 33	4.2 29 07 84 81	U p	0.0 02 87 64 49	0.2 31 33 53 69
34 82 49	CCL15 -CCL1 4	CCL15-CCL14 readthrough (NMD candidate)	6. 91 41 9	4. 95 20 6	5. 09 48 1	6. 65 26 4	7. 33 96 8	7. 94 89 6	3.1 603 258 85	1.6 600 733 33	3.1 60 32 58 85	U p	0.0 25 80 14 01	0.3 85 33 44 54
30 12	HIST1 H2AE	Histone cluster 1, h2ae	7. 10 37 1	6. 93 50 3	6. 46 35 1	7. 31 52 1	8. 92 16 8	7. 92 76 7	2.3 307 107 96	1.2 207 7	2.3 30 71 07 96	U p	0.0 24 57 24 66	0.3 83 08 92 58
83 82	NME5	NME/NM23 family member 5	6. 35 42 3	6. 28 18 7	6. 49 28 1	5. 29 11 1	3. 68 70 9	4. 78 89 5	-3. 451 571 412	-1. 787 253 333	3.4 51 57 14 12	D o w n	0.0 03 11 42 53	0.2 34 23 93 82
96 5	CD58	CD58 molecule	6. 95 92 2	5. 97 07 8	6. 08 22 7	8. 00 61 4	7. 89 56 2	7. 03 55 3	2.4 765 641 65	1.3 083 4	2.4 76 56 41 65	U p	0.0 11 05 78 95	0.3 24 27 76 54
62	RRM2	Ribonucleotide	6.	5.	6.	8.	10	7.	5.5	2.4	5.5	U	0.0	0.2



41		reductase M2	31 92 1	97 91 3	23 09 8	30 06 2	.1 06 24	53 40 6	424 864 32	705 333 33	42 48 64 32	p	05 10 39 55	65 67 28 16
10 45 1	VAV3	Vav guanine nucleotide exchange factor 3	5. 72 68 6	3. 58 66 7	3. 65 29 9	9. 71 36 2	9. 35 94 3	5. 91 70 1	16. 087 259 4	4.0 078 466 67	16. 08 72 59 4	U p	0.0 07 65 12 81	0.2 97 44 06 81
11 22 6	GALN T6	Polypeptide N-acetylgalactosa minyltransferase 6	5. 59 06 6	7. 05 62 4	6. 40 77 7	4. 80 41 6	4. 37 21 4	6. 04 06	-2. 427 138 889	-1. 279 256 667	2.4 27 13 88 89	D o w n	0.0 46 59 43 39	0.4 40 05 65 62
28 44 17	TMEM 150B	Transmembrane protein 150B	4. 74 75 2	4. 76 56 3	4. 63 65 6	5. 57 29	6. 67 38 6	5. 12 99 6	2.1 077 006 79	1.0 756 7	2.1 07 70 06 79	U p	0.0 28 51 26 6	0.3 93 40 55 85
21 93 33	USP12	Ubiquitin specific peptidase 12	5. 48 21 1	5. 24 64 8	5. 59 92 2	5. 98 52 1	6. 69 37 4	6. 91 85 5	2.1 285 878 99	1.0 898 966 67	2.1 28 58 78 99	U p	0.0 07 35 66 81	0.2 92 40 97 69
56 99 7	ADCK 3	Aarf domain containing kinase 3	9. 17 81 9	9. 66 47 3	9. 82 68 7	9. 10 02 4	8. 64 22 9	7. 76 28 6	-2. 077 430 194	-1. 054 8	2.0 77 43 01 94	D o w n	0.0 28 06 76 95	0.3 92 00 23 37
58 79	RAC1	Ras-related C3 botulinum toxin substrate 1 (rho family, small GTP binding protein Rac1)	6. 96 94 6	7. 03 38 5	7. 46 15 8	8. 45 16	8. 03 67 1	8. 13 18 8	2.0 730 668 89	1.0 517 666 67	2.0 73 06 68 89	U p	0.0 03 27 22 62	0.2 36 31 05 13
28 34 17	DPY19 L2	Dpy-19-like 2 (C. Elegans)	4. 65 20 6	3. 31 09 2	3. 19 81 9	4. 85 36 3	5. 39 53 4	5. 51 77 1	2.8 982 258 01	1.5 351 7	2.8 98 22 58 01	U p	0.0 08 07 09 57	0.2 99 13 95 54
23 44 6	SLC44 A1	Solute carrier family 44 (choline transporter), member 1	6. 63 85 7	5. 88 66 7	6. 72 55 3	8. 57 80 8	7. 62 91 2	7. 22 73	2.6 291 139 4	1.3 945 766 67	2.6 29 11 39	U p	0.0 11 54 70	0.3 27 65 98

											4		08	66
10 05 26 83 2	PHOS PHO2- KLHL 23	PHOSPHO2-KLH L23 readthrough	5. 06 74	4. 81 49 1	4. 41 11 1	6. 28 07 1	6. 65 03 5	5. 28 46 3	2.4 749 910 93	1.3 074 233 33	2.4 74 99 10 93	U p	0.0 11 58 93 72	0.3 27 65 98 66
67 2	BRCA 1	Breast cancer 1	4. 57 17	4. 37 39 6	4. 43 21 5	6. 05 03 3	5. 71 96 5	5. 52 45 1	2.4 717 965 47	1.3 055 6	2.4 71 79 65 47	U p	0.0 00 46 77 92	0.1 64 24 82 94
30 00 1	ERO1 A	Endoplasmic reticulum oxidoreductase $\alpha$	5. 40 63 6	5. 60 06	5. 49 14	5. 93 14 5	7. 09 48 4	6. 51 11 2	2.0 181 265 82	1.0 130 166 67	2.0 18 12 65 82	U p	0.0 15 14 75 92	0.3 48 67 95 47
10 63 5	RAD5 1AP1	RAD51 associated protein 1	4. 62 32 5	4. 46 32 9	3. 99 97 9	5. 76 89 9	5. 88 11 4	4. 98 98 4	2.2 729 196 22	1.1 845 466 67	2.2 72 91 96 22	U p	0.0 06 20 77 68	0.2 81 25 22 73
23 58 4	VSIG2	V-set and immunoglobulin domain containing 2	7. 85 41 5	10 .5 29 1	9. 95 81 3	6. 45 09 6	5. 75 32 9	8. 09 21 4	-6. 415 951 932	-2. 681 663 333	6.4 15 95 19 32	D o w n	0.0 14 86 06 73	0.3 47 51 10 24
65 05 5	REEP1	Receptor accessory protein 1	6. 79 74 2	7. 21 93 5	7. 72 61 6	5. 58 68 9	4. 71 41 4	4. 79 09 4	-4. 649 213 462	-2. 216 986 667	4.6 49 21 34 62	D o w n	0.0 00 38 05 46	0.1 60 90 15 41
22 96	FOXC 1	Forkhead box C1	7. 93 22 6	5. 87 52 1	7. 50 16 8	5. 64 75 7	5. 53 49 2	4. 96 33 4	-3. 296 892 089	-1. 721 106 667	3.2 96 89 20 89	D o w n	0.0 14 86 32 14	0.3 47 51 10 24
21 50	F2RL1	Coagulation factor II (thrombin) receptor-like 1	5. 40 43 1	4. 10 66 5	4. 39 19 7	5. 18 21 1	5. 84 34 2	5. 92 68 3	2.0 229 724 42	1.0 164 766 67	2.0 22 97 24 42	U p	0.0 34 73 95 41	0.4 08 42 39 81
72 5	C4BPB	Complement component 4 binding protein, $\beta$	4. 13 31	5. 58 71	5. 31 09	7. 28 90	6. 31 92	6. 62 98	3.3 302 488	1.7 356 3	3.3 30 24	U p	0.0 05 74	0.2 74 75

			1	7	6	7		6	84		88		55	30
											84		58	11
83 18	CDC45	Cell division cycle 45	5. 04 62 9	4. 40 28	4. 73 71 4	5. 77 22 6	6. 35 81 8	5. 44 27 2	2.1 870 355 43	1.1 289 766 67	2.1 87 03 55 43	U p	0.0 07 42 12 79	0.2 93 16 68 02
90 36 2	FAM11 0B	Family with sequence similarity member B	5. 58 30 8	5. 74 67 7	5. 63 87 6	4. 53 71 1	4. 22 81 7	3. 71 77 1	-2. 819 045 311	-1. 495 206 667	2.8 19 04 53 11	D o w n	0.0 00 55 77 17	0.1 64 81 87 25
27 07 7	B9D1	B9 protein domain 1	6. 87 76 1	7. 56 52	7. 14 73 4	6. 36 43 5	5. 78 53	6. 15 17 6	-2. 137 977 495	-1. 096 246 667	2.1 37 97 74 95	D o w n	0.0 05 03 10 01	0.2 64 76 00 1
22 16 92	PHAC TR1	Phosphatase and actin regulator 1	5. 81 11 4	6. 87 13 4	6. 13 58 8	4. 57 64 6	5. 45 17 8	5. 63 60 8	-2. 072 463 462	-1. 051 346 667	2.0 72 46 34 62	D o w n	0.0 30 49 57 7	0.3 99 27 58 89
88 29	NRP1	Neuropilin 1	6. 66 98 3	5. 54 97 8	6. 30 97 5	4. 77 86 5	5. 16 17 6	4. 47 57 8	-2. 586 599 459	-1. 371 056 667	2.5 86 59 94 59	D o w n	0.0 05 20 04 58	0.2 66 63 60 57
23 15 7	SEPT6	Septin 6	6. 79 91 3	7. 23 57 4	7. 38 16 7	5. 03 54 3	6. 24 22 5	6. 71 35 5	-2. 206 515 681	-1. 141 77	2.2 06 51 56 81	D o w n	0.0 36 73 46 01	0.4 14 09 55 77
50 25	P2RX4	Purinergic receptor P2X, ligand gated ion channel, 4	7. 61 19 4	7. 08 38 3	7. 00 78 3	5. 06 64 7	6. 87 90 7	6. 12 71 5	-2. 313 862 817	-1. 210 303 333	2.3 13 86 28 17	D o w n	0.0 35 00 86 79	0.4 08 48 58 2
25 37	IFI6	Interferon, $\alpha$ -inducible protein 6	9. 67 04 8	8. 80 32 2	8. 77 06 7	7. 23 77	7. 87 49 9	7. 86 65 9	-2. 679 003 873	-1. 421 696 667	2.6 79 00 38 73	D o w n	0.0 03 74 69 21	0.2 38 59 85 3
25 39	G6PD	Glucose-6-phosph ate dehydrogenase	9. 07	7. 06	7. 24	6. 60	6. 57	6. 44	-2. 388	-1. 255	2.3 88	D o	0.0 47	0.4 42

			54 6	97 2	56 6	30 9	57 9	44 2	072 55	846 667	07 25 5	w n	58 09 72	91 47 71
51 58 2	AZIN1	Antizyme inhibitor 1	5. 82 52 8	5. 91 81	5. 83 94 7	7. 38 78 8	7. 95 35 4	5. 87 33 5	2.3 144 028 42	1.2 106 4	2.3 14 40 28 42	U p	0.0 48 59 53 62	0.4 45 56 96 31
37	ACAD VL	Acyl-coa dehydrogenase, very long chain	9. 63 76 3	9. 64 11	9. 34 27 8	9. 00 66 7	8. 25 04 6	8. 12 73 9	-2. 112 566 37	-1. 078 996 667	2.1 12 56 63 7	D o w n	0.0 07 50 24 87	0.2 94 41 93 61
83 40	HIST1 H2BL	Histone cluster 1, h2bl	6. 54 89 3	5. 51 12 3	6. 19 17 3	6. 88 60 5	8. 14 72 1	6. 63 54 8	2.2 022 068 72	1.1 389 5	2.2 02 20 68 72	U p	0.0 43 57 72 37	0.4 32 33 09 01
67 91	AURK APS1	Aurora kinase A pseudogene 1	4. 22 84 3	4. 39 75 6	4. 30 84 3	5. 26 47 5	5. 97 38 3	5. 00 88 8	2.1 500 149 13	1.1 043 466 67	2.1 50 01 49 13	U p	0.0 05 39 52 36	0.2 69 32 15 26
31 27	HLA- DRB5	Major histocompatibility complex, class II, DR $\beta$ 5	10 .7 30 83	8. 51 18 7	10 .2 04 46	4. 14 84 5	4. 99 48	8. 45 97 2	-15 .43 424 849	-3. 948 063 333	15. 43 42 48 49	D o w n	0.0 10 61 67 79	0.3 23 12 55 57
31 48	HMGB 2	High mobility group box 2	5. 19 58 5	3. 83 44	3. 96 44	6. 45 48 4	8. 35 04 7	5. 92 07 5	5.9 675 413 86	2.5 771 366 67	5.9 67 54 13 86	U p	0.0 06 61 81 06	0.2 86 65 49 71
96 6	CD59	CD59 molecule, complement regulatory protein	9. 36 96	8. 76 23 5	8. 71 30 9	7. 88 09 3	7. 79 69 6	7. 50 27 4	-2. 331 841 938	-1. 221 47	2.3 31 84 19 38	D o w n	0.0 02 30 25 18	0.2 12 16 29 49
84 59	TPST2	Tyrosylprotein sulfotransferase 2	6. 22 29 1	7. 63 96 8	7. 09 25 5	5. 37 36 6	5. 73 14 2	4. 11 90 2	-3. 758 994 141	-1. 910 346 667	3.7 58 99 41 41	D o w n	0.0 07 97 27 17	0.2 99 13 95 54
90	N4BP2	NEDD4 binding	4.	4.	4.	4.	6.	5.	2.3	1.2	2.3	U	0.0	0.3

63 4	L1	protein 2-like 1	59 83 8	35 42 8	07 36 3	60 42 5	29 38 8	83 36 6	540 854 13	351 666 67	54 08 54 13	p	24 99 66 45	83 71 27 62
65 05 9	RAPH 1	Ras association (ralgds/AF-6) and pleckstrin homology domains 1	4. 71 38 8	4. 74 09 5	4. 71 16 7	6. 64 90 6	6. 22 59 2	5. 87 40 4	2.8 828 717 69	1.5 275 066 67	2.8 82 87 17 69	U p	0.0 00 44 74 97	0.1 64 24 82 94
31 77 72	HIST2 H2AB	Histone cluster 2, h2ab	7. 23 94 1	6. 65 26 9	6. 69 37 8	8. 57 45 9	8. 86 54 5	7. 47 83 5	2.7 210 623 22	1.4 441 7 22	2.7 21 06 23 22	U p	0.0 08 51 74 24	0.3 07 29 63 95
86 12	PLPP2	Phospholipid phosphatase 2	9. 52 88 4	9. 37 93 9	9. 69 94 3	8. 40 96 2	7. 55 79 1	8. 04 54 1	-2. 891 009 467	-1. 531 573 333	2.8 91 00 94 67	D o w n	0.0 00 83 82 39	0.1 81 04 09 24
10 62 7	MYL1 2A	Myosin light chain 12A	10 .0 13 83	9. 35 56 4	9. 78 43	10 .9 18 36	10 .6 04 27	11 .0 36 65	2.1 964 444 3	1.1 351 7 44 3	2.1 96 44 44 3	U p	0.0 03 01 45 91	0.2 34 00 38 89
32 13	HOXB 3	Homeobox B3	5. 14 78 7	3. 90 79 4	4. 11 99 1	7. 10 24 5	6. 17 44 7	7. 84 02 1	6.2 642 277 53	2.6 471 366 67	6.2 64 22 77 53	U p	0.0 01 17 51 28	0.1 86 14 79 2
26 78	GGT1	Γ-glutamyltransfer ase 1	9. 16 15 7	9. 31 31 4	8. 59 69 8	7. 48 88 1	7. 56 93 1	5. 95 58 1	-4. 053 739 364	-2. 019 253 333	4.0 53 73 93 64	D o w n	0.0 03 67 15 27	0.2 38 59 85 3
44 03 54	SMG1 P2	SMG1 pseudogene 2	5. 95 62 4	6. 50 92 3	6. 39 43 8	8. 01 35 7	7. 61 26 5	7. 36 25 8	2.5 960 472 95	1.3 763 166 67	2.5 96 04 72 95	U p	0.0 01 36 24 71	0.1 87 10 78 18
22 89 4	DIS3	DIS3 homolog, exosome endoribonuclease and 3'-5' exoribonuclease	3. 99 73	4. 50 92 9	4. 41 70 8	5. 45 98 4	5. 89 72 5	5. 29 12 9	2.3 645 571 31	1.2 415 7 31	2.3 64 55 71 31	U p	0.0 01 55 68 15	0.1 87 10 78 18

26 50 8	HEYL	Hes-related family bhlh transcription factor with YRPW motif-like	5. 86 12	5. 80 12 3	5. 63 37	5. 87 36 9	7. 91 67 2	6. 98 96 8	2.2 366 197 45	1.1 613 2	2.2 36 61 97 45	U p	0.0 49 06 12 03	0.4 46 17 48
19 64 41	ZFC3H 1	Zinc finger, C3H1-type containing	4. 74 58 3	5. 01 9	4. 56 71 4	7. 00 22 2	5. 59 47 7	5. 63 56 1	2.4 626 472 66	1.3 002 1	2.4 62 64 72 66	U p	0.0 15 06 64 08	0.3 48 31 59 84
50 69	PAPPA	Pregnancy-associat ed plasma protein A, pappalysin 1	6. 47 72 6	6. 18 15	5. 60 64 7	4. 53 37 1	5. 75 06 6	4. 61 61 9	-2. 175 816 163	-1. 121 556 667	2.1 75 81 61 63	D o w n	0.0 25 93 86 12	0.3 85 76 15 64
34 90	IGFBP 7	Insulin like growth factor binding protein 7	6. 08 08 5	6. 32 19 5	6. 00 44 3	6. 72 94 9	10 .5 02 31	8. 04 53 5	4.8 904 707 15	2.2 899 733 33	4.8 90 47 07 15	U p	0.0 33 10 13 16	0.4 06 31 50 59
33 78 73	HIST2 H2BC	Histone cluster 2, h2bc (pseudogene)	5. 96 64 8	6. 55 48	6. 16 66 2	9. 62 84 1	7. 40 08 8	7. 74 48 1	4.0 804 643 37	2.0 287 333 33	4.0 80 46 43 37	U p	0.0 09 61 12 85	0.3 13 66 02 93
97 68	KIAA0 101	KIAA0101	4. 22 31 8	3. 68 41 7	3. 76 06 3	6. 22 54 6	5. 05 3 2	5. 10 28 2	2.9 713 117 9	1.5 711	2.9 71 31 17 9	U p	0.0 03 19 96 37	0.2 34 23 93 82
68 09	STX3	Syntaxin 3	7. 67 59 7	6. 48 76	6. 95 84 2	5. 39 48 7	6. 74 64 9	5. 12 72 1	-2. 435 931 11	-1. 284 473 333	2.4 35 93 11 1	D o w n	0.0 36 69 69 01	0.4 14 09 00 13
40 90	SMAD 5	SMAD family member 5	3. 36 86 7	4. 06 74 4	4. 28 74 2	5. 52 38 3	4. 96 45 4	5. 01 44 4	2.3 945 368 98	1.2 597 466 67	2.3 94 53 68 98	U p	0.0 03 87 81 25	0.2 39 96 90 73
31 61	HMM R	Hyaluronan-media ted motility receptor (RHAMM)	4. 30 32 4	3. 73 56 5	4. 12 65 5	5. 35 42	5. 28 14 1	4. 93 64 8	2.1 970 230 41	1.1 355 5	2.1 97 02 30	U p	0.0 01 60 76	0.1 87 19 40

												41		96	74
38 33	KIFC1	Kinesin family member C1	6.20335	5.75907	5.87767	7.14478	7.06133	6.80356	2.0799180	1.0565266	2.0799180	U p	0.002142	0.2116945	
55 63 5	DEPD C1	DEP domain containing 1	3.92367	3.60802	3.84908	4.68052	5.79284	4.66817	2.3843345	1.2535866	2.3843345	U p	0.0069935	0.2889644	
54 68	PPAR G	Peroxisome proliferator-activated receptor $\gamma$	6.05594	4.93721	5.91009	7.98514	7.19123	6.33525	2.9001482	1.5361266	2.9001482	U p	0.0160695	0.3523137	
31 31	HLF	Hepatic leukemia factor	6.08722	6.3909	6.82765	5.93001	5.46467	4.60748	-2.145335	-1.101203	2.145335	D o w n	0.0237793	0.3812689	
10 05 07 42 0	LINC0 1605	Long intergenic non-protein coding RNA 1605	4.19352	4.1728	4.3857	6.67968	5.43076	4.47511	2.4247623	1.2778433	2.4247623	U p	0.0424747	0.4317319	
63 87 4	ABHD 4	Abhydrolase domain containing 4	7.67186	7.12492	7.24072	6.659	6.22574	5.95844	-2.091860	-1.064786	2.091860	D o w n	0.0059363	0.2794817	
10 21 7	CTDS PL	CTD small phosphatase like	7.80733	7.70209	8.30779	6.82378	6.68742	6.64577	-2.567705	-1.36048	2.567705	D o w n	0.0015805	0.1871078	
15 47 96	AMOT	Angiomotin	4.86277	5.19885	5.60081	4.37187	4.428	3.66991	-2.24399	-1.166056	2.24399	D o w n	0.0040389	0.2435152	
90 99	USP2	Ubiquitin specific peptidase 2	5.7871	5.6322	5.4527	4.0581	4.43670	4.4274	-2.416898	-1.273156	2.416898	D o w	0.0072	0.17263	

			8	4	5	5	8	7	131	667	81	n	90	18
											31		76	47
90 76	CLDN 1	Claudin 1	7. 21 42	5. 52 71 9	5. 46 18 7	9. 61 06 2	6. 74 45	8. 20 16	4.3 403 759 2	2.1 178 2	4.3 40 37 59 2	U p	0.0 31 32 03 56	0.4 01 10 39 72
57 21 2	TP73- AS1	TP73 antisense RNA 1	6. 94 16 1	7. 14 03 2	6. 86 24 6	5. 49 04 9	5. 84 17 1	6. 33 11 3	-2. 134 187 11	-1. 093 686 667	2.1 34 18 71 1	D o w n	0.0 04 81 46 83	0.2 60 26 39 27
84 58	TTF2	Transcription termination factor, RNA polymerase II	5. 31 36 5	4. 83 45 5	5. 56 86 1	7. 03 04 2	6. 68 70 7	6. 51 09 1	2.8 360 114 03	1.5 038 633 33	2.8 36 01 14 03	U p	0.0 00 87 63 87	0.1 81 04 09 24
71 66	TPH1	Tryptophan hydroxylase 1	5. 25 01 9	7. 47 19 2	7. 00 66	4. 88 36 4	4. 70 98 2	5. 37 32 1	-3. 004 961 832	-1. 587 346 667	3.0 04 96 18 32	D o w n	0.0 26 41 67 64	0.3 87 35 84 1
15 12 58	SLC38 A11	Solute carrier family 38, member 11	6. 06 85 4	9. 22 41 7	8. 66 99 2	3. 77 14 1	6. 13 54 7	3. 79 78 6	-10 .69 820 365	-3. 419 296 667	10. 69 82 03 65	D o w n	0.0 09 65 02 91	0.3 13 66 02 93
84 66 8	FAM1 26A	Family with sequence similarity member A	5. 34 18 9	4. 39 06 5	4. 13 86 7	5. 81 63 5	6. 06 93 1	5. 44 85	2.2 257 887 41	1.1 543 166 67	2.2 25 78 87 41	U p	0.0 14 12 78 99	0.3 46 27 53 47
30 26	HABP 2	Hyaluronan binding protein 2	10 .7 40 64	9. 92 83 2	10 .2 24 09	8. 55 85 4	7. 48 27 2	6. 32 54 8	-7. 170 647 177	-2. 842 103 333	7.1 70 64 71 77	D o w n	0.0 01 39 54 64	0.1 87 10 78 18
10 27 2	FSTL3	Follistatin-like 3 (secreted glycoprotein)	5. 89 82 6	5. 97 11 5	5. 91 04 9	6. 82 93 7	7. 05 38 7	6. 96 14 6	2.0 301 692 41	1.0 216	2.0 30 16 92 41	U p	0.0 01 10 37 78	0.1 86 14 79 2
11 68	LRG1	Leucine-rich $\alpha$ -2-glycoprotein 1	6. 51	6. 70	6. 75	5. 76	5. 45	5. 67	-2. 038	-1. 027	2.0 38	D o	0.0 01	0.1 87



44			20 5	77 8	99 4	41	49 5	85 9	314 498	376 667	31 44 98	w n	53 21 52	10 78 18
10 09 96 76 3	LOC10 099676 3	Notch homolog 2 N-terminal-like protein	7. 77 63	7. 35 32	7. 50 59 9	9. 02 15	8. 39 94 5	8. 23 79 8	2.0 108 702 56	1.0 078 2	2.0 10 87 02 56	U p	0.0 08 35 33 07	0.3 04 72 02 15
72 94 38	GATS L2	GATS protein-like 2	7. 97 02 4	9. 17 10 3	8. 95 57 7	6. 38 30 4	6. 40 33 9	7. 40 57 7	-3. 913 013 262	-1. 968 28	3.9 13 01 32 62	D o w n	0.0 02 40 38 09	0.2 15 53 16 8
79 96 6	SCD5	Stearoyl-coa desaturase 5	5. 58 98 1	4. 63 45 8	4. 78 14 2	4. 03 94 5	3. 62 74 2	3. 78 07	-2. 275 336 624	-1. 186 08	2.2 75 33 66 24	D o w n	0.0 04 64 62 52	0.2 55 30 86 17
79 77 0	TXND C15	Thioredoxin domain containing 15	5. 27 41 5	5. 68 26 8	5. 57 24 5	4. 14 02 5	4. 92 85 2	4. 42 42 1	-2. 016 844 702	-1. 012 1	2.0 16 84 47 02	D o w n	0.0 06 04 71 85	0.2 79 48 17 42
16 33	DCK	Deoxycytidine kinase	6. 37 2	5. 80 81 4	5. 69 77 7	7. 05 71 9	7. 87 94 3	6. 15 47	2.1 010 881 15	1.0 711 366 67	2.1 01 08 81 15	U p	0.0 49 06 80 58	0.4 46 17 48
84 92	PRSS1 2	Protease, serine 12	6. 73 73 8	5. 33 66 1	5. 71 59 3	8. 09 06	7. 01 66	7. 06 25 8	2.7 509 946 49	1.4 599 533 33	2.7 50 99 46 49	U p	0.0 14 90 95 23	0.3 48 11 05 43
85 40 7	NKD1	Naked cuticle homolog 1 (Drosophila)	4. 89 12 6	11 .4 66 59	10 .5 18 27	3. 79 95 3	5. 05 58 1	4. 66 50 8	-21 .88 544 783	-4. 451 9	21. 88 54 47 83	D o w n	0.0 27 12 96 35	0.3 89 53 60 92
12 77 00	OSCP1	Organic solute carrier partner 1	7. 02 22 3	7. 64 06 3	7. 06 68 9	6. 95 84 3	5. 33 26 7	6. 02 00 7	-2. 203 087 303	-1. 139 526 667	2.2 03 08 73 03	D o w n	0.0 33 28 19 77	0.4 06 85 22 16
63	ZNF66	Zinc finger protein	5.	5.	5.	3.	4.	3.	-3.	-1.	3.0	D	0.0	0.1

934	7	667	33531	54991	89724	99058	41537	55571	046036719	606933333	46036719	o w n	00717261	72631847
23235	SIK2	Salt inducible kinase 2	6.50828	7.33998	7.48124	5.54541	5.96244	5.65908	-2.616291577	-1.387523333	2.616291577	D o w n	0.002931973	0.23133569
10750	GRAP	GRB2-related adaptor protein	5.31815	7.64792	6.6155	4.71043	4.87504	5.41042	-2.884644099	-1.528393333	2.884644099	D o w n	0.030863593	0.39930908
57178	ZMIZ1	Zinc finger, MIZ-type containing 1	9.72634	9.958267	9.22641	7.89069	8.92614	8.0338	-2.342847961	-1.228263333	2.342847961	D o w n	0.007388522	0.292725141
8351	HIST1H3D	Histone cluster 1, h3d	9.22005	8.79403	8.36354	9.99628	10.56551	9.57937	2.385866522	1.2545133	2.385866522	U p	0.0083968	0.29913954
6713	SQLE	Squalene epoxidase	4.416	3.8798	3.97748	4.46678	6.83518	6.26083	2.983673	1.5770933	2.983673	U p	0.040341982	0.42539913
100861540	CYP3A7-CYP3A51P	CYP3A7-CYP3A51P readthrough	7.71903	5.12613	6.91826	4.31608	5.09119	4.2622	-4.08777486	-2.031316667	4.08777486	D o w n	0.016021561	0.351799596
105369239	LOC105369239	Multidrug resistance-associated protein 6	5.3415	6.2323	6.4721	5.36392	4.50681	4.96884	-2.097658754	-1.06878	2.097658754	D o w n	0.022821648	0.37991168
27101	CACYBP	Calcyclin binding protein	4.79634	4.56144	4.55199	6.28904	5.55717	5.14704	2.038950381	1.027826667	2.038950381	U p	0.013371081	0.340991946

46 64	NAB1	NGFI-A binding protein 1	4.87248	5.06991	4.66897	6.85309	6.24502	6.69592	3.311649527	1.72755	3.311649527	U p	0.0020352	0.135279577
14 05 76	S100A16	S100 calcium binding protein A16	6.96775	7.73201	8.22864	10.31010	8.34795	8.81696	2.85941496	1.51572	2.85941496	U p	0.030767835	0.3993030908
83 60	HIST1H4D	Histone cluster 1, h4d	7.65378	7.98614	7.65173	5.99022	6.61451	7.46241	-2.106483575	-1.074836667	2.106483575	D o w n	0.02649972	0.38770253
14 74 95	APCD D1	Adenomatosis coli down-regulated 1	8.85567	11.63766	11.49824	9.53851	6.6787	6.6634	-8.207749307	-3.036986667	8.207749307	D o w n	0.020573706	0.371592873
98 24	ARHGAP11A	Rho gtpase activating protein 11A	5.86996	5.53957	6.22912	7.63448	7.95977	7.54286	3.562327116	1.83282	3.562327116	U p	0.001919565	0.135279577
84 25	LTBP4	Latent transforming growth factor $\beta$ binding protein 4	7.66525	8.67901	7.86268	8.85586	9.35212	11.076752	3.225493702	1.68952	3.225493702	U p	0.024620516	0.383131863
26 69	GEM	GTP binding protein overexpressed in skeletal muscle	4.95819	3.96836	4.20874	5.63005	8.21783	6.41597	5.191626756	2.3761867	5.191626756	U p	0.008198793	0.301902594
97 71	RAPG EF5	Rap guanine nucleotide exchange factor 5	4.96094	3.80846	5.05812	6.25004	6.41009	5.01314	2.431618707	1.2819667	2.431618707	U p	0.033544312	0.407707499
54 43 4	SSH1	Slingshot protein phosphatase 1	8.766	7.50142	7.58159	6.03648	7.50936	6.482	-2.417847635	-1.273723333	2.417847635	D o w n	0.0359116	0.4124733

												35		34	32
84 70 6	GPT2	Glutamic pyruvate transaminase (alanine aminotransferase) 2	6. 51 05 2	9. 87 22 1	9. 02 47 6	6. 11 57 3	4. 83 45 5	5. 19 75 9	-8. 494 564 588	-3. 086 54	8.4 94 56 45 88	D o w n	0.0 08 07 07	0.2 99 13 95 54	
50 61 9	DEF6	DEF6, guanine nucleotide exchange factor	6. 27 09 6	6. 50 70 7	6. 15 07 3	4. 40 53 1	4. 93 58 6	5. 84 71 7	-2. 373 155 551	-1. 246 806 667	2.3 73 15 55 51	D o w n	0.0 12 84 09 59	0.3 36 17 41 55	
60 5	BCL7 A	B-cell CLL/lymphoma 7A	5. 97 66 7	6. 01 11	6. 53 41 1	4. 97 09 9	5. 08 95 5	5. 29 21 2	-2. 079 745 026	-1. 056 406 667	2.0 79 74 50 26	D o w n	0.0 02 93 13 58	0.2 31 33 53 69	
22 09 88	HNRN PA3	Heterogeneous nuclear ribonucleoprotein A3	4. 83 45 5	5. 94 42 2	5. 36 27 9	6. 76 65 7	6. 84 22 7	6. 02 83 7	2.2 426 326 68	1.1 651 933 33	2.2 42 63 26 68	U p	0.0 14 86 12 33	0.3 47 51 10 24	
17 18	DHCR 24	24-dehydrocholesterol reductase	9. 81 52 2	9. 26 90 6	8. 23 1	6. 06 17 7	7. 65 65 2	7. 89 38 8	-3. 734 814 7	-1. 901 036 667	3.7 34 81 47	D o w n	0.0 15 00 46 88	0.3 48 11 05 43	
63 97	SEC14 L1	SEC14-like lipid binding 1	8. 03 08	8. 27 44 8	8. 52 92 5	6. 81 47 5	7. 32 86 5	7. 54 71 3	-2. 067 661 472	-1. 048	2.0 67 66 14 72	D o w n	0.0 06 33 07 06	0.2 83 73 24 96	
27 18 5	DISC1	Disrupted in schizophrenia 1	6. 23 02 8	6. 25 33 7	6. 36 51 7	4. 51 18 1	5. 37 2 7	5. 70 05 7	-2. 126 007 471	-1. 088 146 667	2.1 26 00 74 71	D o w n	0.0 12 45 04 84	0.3 34 46 67 31	
16 74	DES	Desmin	5. 44 54 6	5. 38 84	5. 31 40 1	5. 46 76 8	6. 87 70 7	7. 94 06 2	2.6 011 807 76	1.3 791 666 67	2.6 01 18 07 76	U p	0.0 47 74 37 69	0.4 43 31 90 56	
83 57	HIST1 H3H	Histone cluster 1, h3h	4. 25 32	4. 04 44	3. 99 06	5. 69 79	4. 62 95	5. 20 44	2.1 158 196	1.0 812 166	2.1 15 81	U p	0.0 07 60	0.2 96 36	

			3	3	2	8	5		61	67	96		09	89
29 84 2	TFCP2 L1	Transcription factor CP2-like 1	4. 42 86 4	5. 01 91 6	5. 76 84 5	7. 50 12 7	5. 94 81 1	6. 57 35 7	3.0 361 295 13	1.6 022 333 33	3.0 36 12 95 13	U p	0.0 13 43 94 45	0.3 41 83 96 28
37 76 77	CA13	Carbonic anhydrase XIII	5. 57 77	6. 02 46 7	5. 73 38	3. 55 16 1	5. 31 09 6	3. 72 25 2	-2. 997 362 001	-1. 583 693 333	2.9 97 36 20 01	D o w n	0.0 11 88 06 86	0.3 30 28 63 88
40 72	EPCA M	Epithelial cell adhesion molecule	8. 43 97 4	8. 74 80 2	9. 25 05 4	9. 14 14 5	10 .9 84 56	9. 76 71 6	2.2 216 373 44	1.1 516 233 33 44	2.2 21 63 73 44	U p	0.0 49 73 96 3	0.4 46 17 48
10 14 9	ADGR G2	Adhesion G protein-coupled receptor G2	4. 11 28 7	7. 69 34 7	7. 75 23 1	4. 09 03 5	4. 07 12 1	4. 34 55 6	-5. 100 045 082	-2. 350 51	5.1 00 04 50 82	D o w n	0.0 40 18 24 97	0.4 25 03 95 42
27 73	GNAI3	Guanine nucleotide binding protein (G protein), $\alpha$ inhibiting activity polypeptide 3	4. 13 84 1	4. 55 37 1	3. 95 43 5	6. 14 07 2	5. 27 97 3	4. 88 15 6	2.3 270 679 43	1.2 185 133 33	2.3 27 06 79 43	U p	0.0 10 88 84 5	0.3 23 87 84 16
83 58	HIST1 H3B	Histone cluster 1, h3b	8. 86 40 8	6. 97 94 4	7. 71 11 7	9. 55 91 5	10 .5 31 74	9. 20 25 9	3.7 657 311 39	1.9 129 3 11 39	3.7 65 73 11 39	U p	0.0 10 19 49 03	0.3 18 26 13 04
55 26 8	ECHD C2	Enoyl-coa hydratase domain containing 2	8. 04 90 6	8. 01 14 4	7. 95 93	6. 34 47 6	6. 86 28 4	7. 27 99 3	-2. 261 724 7	-1. 177 423 333	2.2 61 72 47	D o w n	0.0 03 92 28 09	0.2 40 20 47 61
47 73	NFAT C2	Nuclear factor of activated T-cells, cytoplasmic, calcineurin-depend ent 2	6. 86 48 9	6. 23 22 3	7. 11 96 7	3. 62 03 3	5. 87 14 8	5. 67 45 8	-3. 211 988 364	-1. 683 466 667	3.2 11 98 83 64	D o w n	0.0 28 33 83 84	0.3 93 27 26 69
41	MCM4	Minichromosome	6.	6.	6.	9.	9.	7.	3.6	1.8	3.6	U	0.0	0.3

73		maintenance complex component 4	86 21 9	40 18 7	95 20 9	29 34 8	41 68 3	12 20 9	606 081 11	720 833 33	60 60 81 11	p	18 28 40 69	64 08 78 05
98 43	HEPH	Hephaestin	8. 03 81 7	4. 40 59 6	4. 46 66 9	8. 76 92 7	9. 77 40 1	8. 77 34 1	11. 070 307 06	3.4 686 233 33	11. 07 03 07 06	U p	0.0 08 94 74 95	0.3 09 08 01 85
57 64 4	MYH7 B	Myosin, heavy chain 7B, cardiac muscle, $\beta$	5. 56 16 7	8. 75 73 2	8. 48 93 5	5. 31 56 5	5. 27 71 6	6. 10 05 9	-4. 107 602 757	-2. 038 296 667	4.1 07 60 27 57	D o w n	0.0 43 05 16 58	0.4 32 07 88 1
51 51 2	GTSE1	G-2 and S-phase expressed 1	5. 14 10 7	4. 32 67 7	4. 89 51 1	6. 82 90 5	7. 42 01 1	5. 67 67 6	3.6 157 710 6	1.8 543 033 33	3.6 15 77 10 6	U p	0.0 05 41 34 57	0.2 69 32 15 26
46 40	MYO1 A	Myosin IA	5. 13 63 7	5. 34 16	6. 48 04 9	7. 35 50 3	8. 16 94 7	7. 10 54 1	3.7 075 941 62	1.8 904 833 33	3.7 07 59 41 62	U p	0.0 03 70 37 63	0.2 38 59 85 3
31 58	HMGC S2	3-hydroxy-3-methylglutaryl-coa synthase 2 (mitochondrial)	4. 38 25 4	5. 13 27 5	7. 18 02 1	10 .4 25 89	8. 91 72 7	7. 62 71 5	10. 740 108 53	3.4 249 366 67	10. 74 01 08 53	U p	0.0 06 90 08 44	0.2 88 45 97 19
11 32 35	SLC46 A1	Solute carrier family 46 (folate transporter), member 1	8. 47 51 9	8. 01 13 1	7. 42 24 8	6. 38 53 4	6. 69 89 9	6. 71 01 5	-2. 587 394 431	-1. 371 5 44	2.5 87 39 44 31	D o w n	0.0 03 00 28 9	0.2 33 70 50 09
10 05 29 85 5	ZNF62 5-ZNF 20	ZNF625-ZNF20 readthrough (NMD candidate)	7. 08 67 1	7. 47 19 2	7. 41 44 2	4. 66 41 3	6. 17 38 7	5. 85 55 3	-3. 386 605 642	-1. 759 84 60	3.3 86 60 56 42	D o w n	0.0 03 44 84 71	0.2 37 14 66 6
44 06 72	NUDT 4P1	Nudix hydrolase 4 pseudogene 1	5. 90 68 7	4. 50 84 1	5. 12 77	3. 52 15 6	4. 35 53 6	3. 47 68 2	-2. 632 463 145	-1. 396 413 333	2.6 32 46 31 45	D o w n	0.0 11 24 71 44	0.3 24 85 44 65

51 04 6	ST8SI A3	ST8 $\alpha$ -N-acetyl-neuraminidase 3	7. 23 55 1	5. 33 88 6	7. 21 91 1	5. 17 11 4	5. 43 40 9	5. 22 93 3	-2. 496 038 176	-1. 319 64	2.4 96 03 81 76	D o w n	0.0 37 70 38 01	0.4 17 31 42 37
27 19	GPC3	Glypican 3	3. 99 90 2	3. 67 91 7	3. 78 37 2	4. 41 98	5. 84 26 8	5. 53 42 3	2.7 225 024 24	1.4 449 333 33	2.7 22 50 24 24	U p	0.0 06 10 37 88	0.2 79 48 17 42
84 28 8	EFCA B2	EF-hand calcium binding domain 2	4. 42 15 4	5. 00 31 5	4. 79 08 1	4. 23 52 1	2. 98 80 3	3. 83 50 6	-2. 073 977 151	-1. 052 4	2.0 73 97 71 51	D o w n	0.0 18 32 58 56	0.3 64 36 27 9
29 82	GUCY 1A3	Guanylate cyclase 1, soluble, $\alpha$ 3	6. 76 76 4	3. 42 44 6	3. 83 26 9	8. 43 63 5	7. 61 80 8	6. 41 79 2	7.0 413 562 37	2.8 158 533 33	7.0 41 35 62 37	U p	0.0 19 70 82 61	0.3 67 76 00 84
64 28 3	ARHG EF28	Rho guanine nucleotide exchange factor 28	5. 94 80 5	7. 19 21 3	7. 31 71 8	3. 86 08 8	4. 87 52	6. 49 05 4	-3. 348 650 943	-1. 743 58	3.3 48 65 09 43	D o w n	0.0 40 53 74 25	0.4 26 13 61 58
28 96 0	DCPS	Decapping enzyme, scavenger	7. 62 67 3	7. 28 49 1	7. 53 92 4	6. 29 98 1	6. 56 75 5	6. 39 40 8	-2. 089 483 935	-1. 063 146 667	2.0 89 48 39 35	D o w n	0.0 01 47 89 75	0.1 87 10 78 18
62 77	S100A 6	S100 calcium binding protein A6	9. 88 45 8	8. 66 15 1	9. 52 00 2	11 .2 36 62	9. 99 54 8	10 .6 53 51	2.4 169 148 84	1.2 731 666 67	2.4 16 91 48 84	U p	0.0 21 10 33 33	0.3 72 54 06 54
65 35 90	GGTL C5P	$\Gamma$ -glutamyltransferase light chain 5 pseudogene	9. 16 15 7	9. 31 31 4	8. 59 69 8	7. 48 88 1	7. 56 93 1	5. 95 58 1	-4. 053 739 364	-2. 019 253 333	4.0 53 73 93 64	D o w n	0.0 03 67 15 27	0.2 38 59 85 3
72 82 39	MAGE D4	Melanoma antigen family D4	6. 73 66 1	7. 78 26 7	7. 88 61 3	5. 55 04	5. 72 10 3	6. 69 70 9	-2. 787 483 631	-1. 478 963 333	2.7 87 48 36	D o w n	0.0 11 09 69	0.3 24 51 13

												31		59	09
57 65 0	KIAA1 524	KIAA1524	4. 46 56 2	4. 21 07 4	4. 24 61	5. 08 84 7	5. 14 64 2	5. 70 72	2.0 090 915 88	1.0 065 433 33	2.0 09 15 88	U p	0.0 03 36 32 83	0.2 37 14 66 6	
27 35 2	SGSM 3	Small G protein signaling modulator 3	7. 06 51 4	7. 78 10 1	7. 73 43 2	6. 56 21 2	6. 16 91 6	6. 78 35 9	-2. 030 544 531	-1. 021 866 667	2.0 30 54 45 31	D o w n	0.0 09 74 27 19	0.3 14 09 02 13	
57 42	PTGS1	Prostaglandin-end operoxide synthase 1 (prostaglandin G/H synthase and cyclooxygenase)	6. 85 58 3	5. 51 65 5	5. 07 61 5	3. 34 62 7	5. 28 65 2	4. 20 43 5	-2. 902 165 916	-1. 537 13	2.9 02 16 59 16	D o w n	0.0 40 84 01 81	0.4 26 34 37 07	
59 08	RAP1 B	RAP1B, member of RAS oncogene family	4. 52 26 7	4. 56 51 4	4. 54 13 6	7. 70 07 9	5. 53 31 7	5. 26 49 3	3.0 806 611 39	1.6 232 4	3.0 80 66 11 39	U p	0.0 32 96 41 74	0.4 05 79 90 71	
10 94 8	STAR D3	Star related lipid transfer domain containing 3	7. 55 98 9	9. 30 24 3	9. 21 66 1	7. 03 88 8	6. 58 62 2	7. 49 60 5	-3. 143 982 818	-1. 652 593 333	3.1 43 98 28 18	D o w n	0.0 14 42 79 05	0.3 46 82 70 31	
92 23	MAGI 1	Membrane associated guanylate kinase, WW and PDZ domain containing 1	4. 98 32 4	4. 63 75 4	5. 14 65 4	4. 43 56 7	3. 11 88 1	3. 61 42 6	-2. 296 643 082	-1. 199 526 667	2.2 96 64 30 82	D o w n	0.0 11 04 55 9	0.3 24 27 76 54	
10 01	CDH3	Cadherin 3, type 1, P-cadherin (placental)	3. 86 91 9	5. 95 87 7	5. 82 14 1	6. 74 95 2	7. 15 34 4	7. 68 20 4	3.9 409 496 93	1.9 785 433 33	3.9 40 94 96 93	U p	0.0 11 58 57 63	0.3 27 65 98 66	
10 61 3	ERLIN 1	ER lipid raft associated 1	4. 21 44 7	4. 06 18 5	4. 45 56 3	5. 61 75 8	5. 86 32 9	4. 61 54 9	2.1 756 854 59	1.1 214 7	2.1 75 68 54 59	U p	0.0 14 12 11 9	0.3 46 27 53 47	
10	LOC10	Inactive	9.	9.	8.	7.	7.	5.	-4.	-2.	4.0	D	0.0	0.2	



27 24 82 3	272482 3	$\gamma$ -glutamyltranspeptidase 2	16 15 7	31 31 4	59 69 8	48 88 1	56 93 1	95 58 1	053 739 364	019 253 333	53 73 93 64	o w n	03 67 15 27	38 59 85 3
11 02	RCBT B2	Regulator of chromosome condensation (RCC1) and BTB (POZ) domain containing protein 2	7. 96 84 6	8. 48 04 1	7. 75 52 4	6. 81 09 2	7. 10 87 9	6. 63 19 4	-2. 325 412 518	-1. 217 486 667	2.3 25 41 25 18	D o w n	0.0 02 78 16 9	0.2 28 79 54 43
23 55	FOSL2	FOS-like antigen 2	7. 62 45 2	6. 64 05 5	7. 01 25 6	8. 68 40 3	8. 76 94 9	8. 55 55 5	2.9 837 913 75	1.5 771 466 67	2.9 83 79 13 75	U p	0.0 01 00 73 51	0.1 86 14 79 2
29 12 8	UHRF 1	Ubiquitin-like with PHD and ring finger domains 1	4. 00 70 2	3. 76 15 7	3. 95 70 5	5. 69 81 2	6. 28 96 5	3. 94 24 8	2.6 418 282 3	1.4 015 366 67	2.6 41 82 82 3	U p	0.0 41 61 87 14	0.4 28 45 89 05
23 64 8	SSBP3	Single stranded DNA binding protein 3	9. 69 82 3	9. 73 00 4	10. .6 25 04	8. 59 63 6	9. 71 31 4	8. 67 38 7	-2. 032 581 687	-1. 023 313 333	2.0 32 58 16 87	D o w n	0.0 38 98 90 01	0.4 21 22 82 87
15 9	ADSS	Adenylosuccinate synthase	4. 95 50 3	4. 25 38 7	4. 92 61 3	6. 52 65 7	5. 78 61 4	5. 49 48 8	2.3 362 370 49	1.2 241 866 67	2.3 36 23 70 49	U p	0.0 08 74 35 47	0.3 08 52 19 75
55 26 6	TMEM 19	Transmembrane protein 19	5. 79 59 8	4. 93 41 1	5. 26 71 6	7. 49 14 3	6. 43 14 6	5. 72 04 3	2.3 219 818 04	1.2 153 566 67	2.3 21 98 18 04	U p	0.0 36 77 67 72	0.4 14 09 55 77
11 03 3	ADAP 1	Arfgap with dual PH domains 1	7. 49 28 2	7. 00 76 7	7. 13 73 6	8. 88 42 8	8. 01 53 6	8. 15 68 5	2.2 031 178 44	1.1 395 466 67	2.2 03 11 78 44	U p	0.0 06 58 00 13	0.2 86 61 99 1
27 52	GLUL	Glutamate-ammonia ligase	11 .1 46	12 .6 29	12 .2 70	8. 58 72	10 .9 25	10 .4 65	-4. 063 998	-2. 022 9	4.0 63 99	D o w	0.0 19 13	0.3 67 66

			54	74	65	2	26	75	867		88	n	84	41
											67		51	57
76	CA6	Carbonic anhydrase VI	4.37888	6.77691	6.64757	4.26079	3.98548	4.65397	-3.104526	-1.634373	3.104526	D	0.036613	0.4140900
											87		92	13
88	LIN7A	Lin-7 homolog A (C. Elegans)	7.30101	6.25213	5.76903	5.12114	5.28461	4.23386	-2.950282	-1.560853	2.950282	D	0.0116824	0.3284702
											68		94	47
10	N4BP2	NEDD4 binding protein 2-like 2	7.289	7.14744	6.797	6.52615	5.25673	6.06137	-2.188177	-1.12973	2.188177	D	0.0155184	0.3505330
	L2										47		66	52
26	AUTS	Autism susceptibility candidate 2	6.22324	6.96843	6.29985	4.63263	5.66184	5.88338	-2.150327	-1.104556	2.150327	D	0.0251454	0.3837127
	2										94		01	62
31	HMGA	High mobility group AT-hook 1	8.37932	8.85922	8.47145	9.4543	10.2331	8.92852	2.10149	1.07139	2.10149	U	0.0172455	0.3603035
	1										93		83	68
87	MYO	Myomesin 1	9.12786	8.02416	8.85932	8.11391	6.2316	5.92964	-3.763469	-1.912063	3.763469	D	0.0162963	0.3539090
	M1										4		58	69
89	SNUR	SNRPN upstream reading frame	9.90523	8.46536	9.54754	7.89773	8.28397	7.41102	-2.716602	-1.441803	2.716602	D	0.0165959	0.3276598
	F										2		93	66
65	BMP7	Bone morphogenetic protein 7	5.44982	6.78327	6.76044	4.86827	5.11995	5.52412	-2.235188	-1.160396	2.235188	D	0.0180749	0.3831318
											53		49	63
62	S100B	S100 calcium binding protein B	5.93	4.459	4.413	3.360	3.398	3.389	-2.086	-1.060	2.086	D	0.049	0.446

			38 8	63 6	88 1	61 4	17	89 3	030 136	76	03 01 36	w n	29 93 82	17 48
11 21 5	AKAP 11	A-kinase anchoring protein 11	3. 95 17 4	3. 34 76 8	3. 30 37 7	4. 29 16 7	5. 33 13 3	4. 54 95	2.2 811 637 31	1.1 897 7	2.2 81 16 37 31	U p	0.0 07 90 12 62	0.2 99 13 95 54
23 35 3	SUN1	Sad1 and UNC84 domain containing 1	5. 55 62 7	5. 99 51 5	6. 19 20 5	6. 88 26 2	7. 33 43	7. 02 63	2.2 447 944 28	1.1 665 833 33	2.2 44 79 44 28	U p	0.0 02 56 56 49	0.2 21 48 56 65
10 11 2	KIF20 A	Kinesin family member 20A	4. 78 43 8	4. 33 11	4. 42 19 7	6. 87 49 8	5. 79 33 9	5. 84 86 7	3.1 598 658 99	1.6 598 633 33	3.1 59 86 58 99	U p	0.0 01 71 46 41	0.1 90 75 21 3
13 07	COL16 A1	Collagen, type XVI, $\alpha$ 1	5. 89 15 2	5. 41 51	6. 25 32 7	7. 13 43 2	7. 42 96 7	7. 72 44 9	2.9 818 272 25	1.5 761 966 67	2.9 81 82 72 25	U p	0.0 01 02 61 89	0.1 86 14 79 2
39 95 12	SLC25 A35	Solute carrier family 25, member 35	6. 45 24 3	6. 85 01 5	7. 00 71 3	6. 27 44 4	5. 43 28 3	5. 26 73 1	-2. 161 016 369	-1. 111 71	2.1 61 01 63 69	D o w n	0.0 11 20 37 71	0.3 24 71 81 92
69 16	TBXA S1	Thromboxane A synthase 1	6. 03 85 2	4. 84 55 9	5. 34 15 6	3. 57 72 8	4. 60 74 8	4. 08 81 6	-2. 492 482 427	-1. 317 583 333	2.4 92 48 24 27	D o w n	0.0 11 00 61 78	0.3 24 27 76 54
21 77	FANC D2	Fanconi anemia complementation group D2	4. 59 27 4	3. 96 19 3	4. 03 95 2	5. 16 71	5. 71 96	5. 33 09 1	2.3 098 620 07	1.2 078 066 67	2.3 09 86 20 07	U p	0.0 02 18 84 52	0.2 10 07 53 08
68 40	SVIL	Supervillin	5. 94 93 5	5. 61 05 5	6. 19 17 3	6. 81 46 4	7. 26 61 9	6. 91 89 5	2.1 180 206 67	1.0 827 166 67	2.1 18 02 06 67	U p	0.0 03 28 94 24	0.2 36 57 62 18
11	OSBP	Oxysterol binding	5.	4.	5.	6.	6.	7.	2.9	1.5	2.9	U	0.0	0.2

48 84	L10	protein like 10	38 00 6	80 47 8	31 75 1	87 62 7	02 51 1	24 07 9	212 921 94	466 066 67	21 29 21 94	p	03 46 17 23	37 14 66 6
65 84	SLC22 A5	Solute carrier family 22 (organic cation/carnitine transporter), member 5	8. 52 77 8	7. 65 92 4	7. 69 31 1	7. 11 87 6	6. 64 73 6	7. 05 32 9	-2. 028 256 343	-1. 020 24	2.0 28 25 63 43	D o w n	0.0 12 68 65 79	0.3 36 17 41 55
15 51	CYP3 A7	Cytochrome P450, family 3, subfamily A, polypeptide 7	7. 71 90 3	5. 12 61 3	6. 91 82 6	4. 31 60 8	5. 09 11 9	4. 26 22	-4. 087 777 486	-2. 031 316 667	4.0 87 77 74 86	D o w n	0.0 16 02 15 61	0.3 51 79 95 96
86	ACTL 6A	Actin like 6A	4. 84 80 1	4. 87 30 4	4. 88 81	5. 82 40 4	6. 10 26 4	6. 53 75 6	2.4 368 712	1.2 850 3	2.4 36 87 12	U p	0.0 01 01 27 06	0.1 86 14 79 2
64 85 9	NABP 1	Nucleic acid binding protein 1	5. 57 85 8	5. 41 65 9	4. 83 19 5	6. 71 34 4	7. 71 06 3	5. 78 65 6	2.7 533 156 21	1.4 611 7	2.7 53 31 56 21	U p	0.0 20 80 99 12	0.3 71 75 23 82
41 71	MCM2	Minichromosome maintenance complex component 2	4. 92 43 2	4. 36 94 7	4. 62 21 9	5. 85 04 2	6. 54 04 3	5. 00 88 8	2.2 365 112 26	1.1 612 5	2.2 36 51 12 26	U p	0.0 22 41 68 21	0.3 78 66 05 33
55 14 3	CDCA 8	Cell division cycle associated 8	4. 96 34 9	4. 87 68 3	5. 25 67 1	6. 75 52 9	7. 16 82 3	6. 23 12	3.2 174 030 28	1.6 858 966 67	3.2 17 40 30 28	U p	0.0 00 64 37 16	0.1 72 63 18 47
51 05 3	GMNN	Geminin, DNA replication inhibitor	6. 46 02 6	5. 17 28 4	5. 21 67	8. 05 89 8	7. 47 05 7	7. 30 88 3	3.9 894 595 91	1.9 961 933 33	3.9 89 45 95 91	U p	0.0 01 82 68 18	0.1 93 41 99 68
70 06	TEC	Tec protein tyrosine kinase	6. 44 01 6	6. 87 35 1	6. 67 12 5	6. 15 22 9	5. 27 17 4	5. 43 48 5	-2. 059 099 197	-1. 042 013 333	2.0 59 09 91 97	D o w n	0.0 09 07 66 06	0.3 10 47 42 9

68 18	SULT1 A3	Sulfotransferase family 1A member 3	6. 47 72 2	6. 93 54 7	6. 66 10 6	7. 80 23 3	8. 02 89 9	7. 66 66 2	2.2 059 447 64	1.1 413 966 67	2.2 05 94 47 64	U p	0.0 01 52 38 01	0.1 87 10 78 18
10 05 34 61 2	C1QT NF3-A MACR	C1QTNF3-AMAC R readthrough (NMD candidate)	6. 62 88 8	7. 90 19 2	8. 15 96 1	7. 05 71 4	6. 28 86 9	5. 00 31 3	-2. 726 688 699	-1. 447 15	2.7 26 68 86 99	D o w n	0.0 49 42 39 73	0.4 46 17 48
80 34 4	DCAF 11	DDB1 and CUL4 associated factor 11	9. 07 58 6	9. 18 30 2	9. 33 39 7	8. 23 39 5	8. 15 63 9	7. 87 53 3	-2. 157 050 571	-1. 109 06	2.1 57 05 05 71	D o w n	0.0 01 22 64 88	0.1 86 57 68 41
40 92	SMAD 7	SMAD family member 7	6. 14 17 2	7. 57 05 6	6. 87 42 8	4. 86 76 6	6. 47 47 8	4. 85 49 6	-2. 756 912 221	-1. 463 053 333	2.7 56 91 22 21	D o w n	0.0 31 90 61 5	0.4 03 02 01 62
10 01 30 93 3	SMIM 6	Small integral membrane protein 6	7. 53 43	6. 50 36 6	6. 85 33 9	5. 08 24 4	4. 84 13 3	6. 58 78 5	-2. 750 912 02	-1. 459 91	2.7 50 91 20 2	D o w n	0.0 24 22 31 72	0.3 82 58 70 8
13 33 08	SLC9B 2	Solute carrier family 9, subfamily B (NHA2, cation proton antiporter 2), member 2	6. 76 92 1	5. 85 73	7. 36 34 5	5. 66 99 2	5. 84 93 1	4. 48 74 1	-2. 510 149 574	-1. 327 773 333	2.5 10 14 95 74	D o w n	0.0 32 71 35 62	0.4 04 71 37 9
29 20	CXCL 2	Chemokine (C-X-C motif) ligand 2	6. 12 23 4	6. 75 55 5	6. 52 92 5	8. 62 19 4	7. 13 11 4	7. 73 94 2	2.5 700 326 13	1.3 617 866 67	2.5 70 03 26 13	U p	0.0 11 92 07 91	0.3 30 77 65 6
12 84	COL4 A2	Collagen, type IV, $\alpha$ 2	8. 56 94 4	7. 73 15 8	7. 88 74 3	8. 94 56 7	10 .3 26 01	8. 75 88 4	2.4 295 514 76	1.2 806 9	2.4 29 55 14 76	U p	0.0 27 95 72 17	0.3 92 00 23 37
80 01 7	C14orf 159	Chromosome 14 open reading frame 159	8. 62 36	8. 58 50	8. 69 54	6. 41 28	7. 14 68	8. 21 48	-2. 596 407	-1. 376 516	2.5 96 40	D o w	0.0 16 77	0.3 57 44

			5	8	7	8	9	8	208	667	72	n	56	25
											08		46	46
51 36 3	CHST1 5	Carbohydrate (N-acetylgalactosa mine 4-sulfate 6-O) sulfotransferase 15	6. 43 63 7	6. 80 34 5	7. 38 17 6	3. 23 79 6	6. 18 24 2	5. 78 31 2	-3. 496 779 115	-1. 806 026 667	3.4 96 77 91 15	D o w n	0.0 47 96 36 88	0.4 43 39 63 77
29 19	CXCL 1	Chemokine (C-X-C motif) ligand 1 (melanoma growth stimulating activity, $\alpha$ )	6. 01 56 3	6. 83 1	6. 62 25	9. 22 28 4	7. 32 50 5	7. 90 47 1	3.1 626 998 95	1.6 611 566 67	3.1 62 69 98 95	U p	0.0 13 01 36 62	0.3 36 17 41 55
90 52	GPRC 5A	G protein-coupled receptor, class C, group 5, member A	4. 53 71 1	7. 68 27 1	7. 50 82 4	8. 95 45 2	9. 01 76 1	9. 69 49 9	6.2 608 274 18	2.6 463 533 33	6.2 60 82 74 18	U p	0.0 14 50 39 28	0.3 46 82 70 31
80 11 5	BAIAP 2L2	BAI1-associated protein 2-like 2	9. 01 03 5	9. 09 34 1	9. 24 17 5	8. 52 55 9	7. 95 99 7	7. 48 41 7	-2. 181 408 56	-1. 125 26	2.1 81 40 85 6	D o w n	0.0 07 19 64 02	0.2 91 19 36 41
28 55 96	FAM1 53A	Family with sequence similarity 153 member A	6. 87 68 9	6. 80 65 5	6. 70 38 9	3. 93 42 4	3. 95 25 1	5. 88 33 8	-4. 613 089 661	-2. 205 733 333	4.6 13 08 96 61	D o w n	0.0 04 08 31 77	0.2 44 25 17 2
44 14 30	ANKR D20A2	Ankyrin repeat domain 20 family member A2	7. 46 14 8	7. 42 23 2	7. 32 89 1	7. 15 84 3	5. 30 81 1	5. 41 93 7	-2. 717 474 819	-1. 442 266 667	2.7 17 47 48 19	D o w n	0.0 22 22 55 45	0.3 78 35 72 21
79 13	DEK	DEK proto-oncogene	6. 60 95 2	6. 09 51 6	6. 46 63 5	6. 63 41 6	8. 41 62	7. 39 01 5	2.1 284 846 22	1.0 898 266 67	2.1 28 48 46 22	U p	0.0 45 97 40 33	0.4 39 25 30 47
92 30 4	SCGB 3A1	Secretoglobin, family 3A, member 1	6. 11 84 9	11 .9 37 23	11 .5 72 22	6. 30 99 9	5. 93 14 5	6. 36 90 8	-12 .75 042 414	-3. 672 473 333	12. 75 04 24 14	D o w n	0.0 38 92 57 37	0.4 21 03 81 05
57	PDSS2	Prenyl	6.	6.	6.	4.	5.	5.	-2.	-1.	2.0	D	0.0	0.1

107		(decaprenyl) diphosphate synthase, subunit 2	00495	25285	0158	9651	02898	1051	082197138	058106667	82197138	o w n	00870132	81040924
552900	BOLA2	Bola family member 2	5.95624	6.50923	6.39438	8.01357	7.61265	7.36258	2.596047295	1.376316667	2.596047295	U p	0.001362471	0.187107818
81563	C1orf21	Chromosome 1 open reading frame 21	5.25422	4.61825	6.27454	8.57683	7.2181	6.30278	3.95469564	1.983566667	3.95469564	U p	0.018514388	0.364586001
64710	NUCKS1	Nuclear casein kinase and cyclin-dependent kinase substrate 1	7.75286	7.7977	7.71216	9.75686	8.52031	8.83208	2.432053	1.282167	2.432053	U p	0.006939076	0.288892706
4869	NPM1	Nucleophosmin (nucleolar phosphoprotein B23, numatrin)	9.36755	9.59531	10.21948	10.73509	10.67459	11.24587	2.2310713	1.15773667	2.2310713	U p	0.00357066	0.28384482
285220	EPHA6	EPH receptor A6	6.10287	6.54138	7.63206	3.1894	3.53826	4.51907	-8.054862714	-3.00986	8.054862714	D o w n	0.00491776	0.164248294
112495	GTF3C6	General transcription factor IIIC subunit 6	7.74902	6.31843	6.68562	6.10562	5.79173	5.30593	-2.323411	-1.21659667	2.323411	D o w n	0.020902203	0.371993438
51195	RAPGEFL1	Rap guanine nucleotide exchange factor like 1	8.95569	7.27804	8.59529	10.276721	8.91463	9.40047	2.38022872	1.251067	2.38022872	U p	0.048772146	0.446143522
8399	PLA2G10	Phospholipase A2 group X	5.90862	5.88874	6.28563	8.01339	6.56253	8.50266	3.171562	1.66519667	3.171562	U p	0.011590415	0.327659866

22 97 4	TPX2	TPX2, microtubule-associated	5. 30 84 9	4. 40 73 6	4. 95 36 2	7. 30 59 3	8. 17 03 1	6. 66 31 4	5.6 176 626 86	2.4 899 7 66	5.6 17 66 26 86	U p	0.0 00 67 27 99	0.1 72 63 18 47
35 29 54	GATS	GATS, stromal antigen 3 opposite strand	6. 35 48 1	7. 73 48	7. 66 73 5	5. 17 99 7	4. 94 78 8	6. 20 35 3	-3. 502 843 825	-1. 808 526 667	3.5 02 84 38 25	D o w n	0.0 07 55 85 29	0.2 95 71 33 58
63 59	CCL15	Chemokine (C-C motif) ligand 15	6. 91 41 9	4. 95 20 6	5. 09 48 1	6. 65 26 4	7. 33 96 8	7. 94 89 6	3.1 603 258 85	1.6 600 733 33	3.1 60 32 58 85	U p	0.0 25 80 14 01	0.3 85 33 44 54
26 78 3	SNOR A65	Small nucleolar RNA, H/ACA box 65	7. 82 56 8	8. 57 45 8	8. 49 76 8	9. 69 12 1	8. 57 82 4	9. 73 37 9	2.0 492 556 85	1.0 351 25 56 85	2.0 49 25 56 85	U p	0.0 32 07 72 4	0.4 03 67 11 92
77 0	CA11	Carbonic anhydrase XI	7. 70 42	7. 42 66 1	7. 41 73 9	6. 17 37 1	5. 53 15 9	5. 01 11 5	-3. 847 487 573	-1. 943 916 667	3.8 47 48 75 73	D o w n	0.0 00 55 17 31	0.1 64 81 87 25
29 02 8	ATAD 2	Atpase family, AAA domain containing 2	4. 47 41 5	4. 22 60 9	4. 25 67 4	6. 61 93 9	7. 29 39	5. 55 98	4.5 065 914 49	2.1 720 366 67	4.5 06 59 14 49	U p	0.0 01 43 56 43	0.1 87 10 78 18
50 74	PAWR	PRKC, apoptosis, WT1, regulator	4. 47 10 3	4. 68 38 1	4. 02 00 2	4. 90 29 6	6. 41 55 4	5. 47 19 5	2.3 056 869 81	1.2 051 966 67	2.3 05 68 69 81	U p	0.0 20 48 63 58	0.3 71 13 26 99
43 30	MN1	Meningioma (disrupted in balanced translocation) 1	4. 29 58 8	4. 24 13 2	4. 07 85 7	5. 50 98 9	5. 74 22 7	4. 41 51 8	2.0 239 729 38	1.0 171 9 38	2.0 23 97 29 38	U p	0.0 24 17 22 33	0.3 82 49 69 57
13 08	COL17 A1	Collagen, type XVII, $\alpha$ 1	3. 84 20 5	4. 34 57 5	3. 96 49 6	7. 77 44 6	7. 34 74 1	5. 33 48 5	6.8 115 667 09	2.7 679 866 67	6.8 11 56 67	U p	0.0 02 71 18	0.2 26 76 71



												09		72	12
64 38 66	CBLN 3	Cerebellin precursor	3	5. 82 85 7	4. 91 23 6	6. 22 33 2	4. 80 43 8	4. 49 85 6	4. 62 84 3	-2. 015 251 645	-1. 010 96	2.0 15 25 16 45	D o w n	0.0 22 90 66 68	0.3 80 34 02 59
10 01 24 69 6	TEC	Transient erythroblastopenia of childhood		6. 44 01 6	6. 87 35 1	6. 67 12 5	6. 15 22 9	5. 27 17 4	5. 43 48 5	-2. 059 099 197	-1. 042 013 333	2.0 59 09 91 97	D o w n	0.0 09 07 66 06	0.3 10 47 42 9
34 63 89	MACC 1	Metastasis associated in colon cancer 1		5. 94 53 2	6. 76 55 7	6. 82 31 6	6. 93 11	8. 12 51 4	8. 03 35 5	2.2 740 227 17	1.1 852 466 67	2.2 74 02 27 17	U p	0.0 22 84 25 31	0.3 79 92 11 68
23 09 5	KIF1B	Kinesin family member 1B		6. 15 78 3	6. 71 25 2	6. 75 30 6	5. 36 43 9	5. 75 19 2	4. 67 10 1	-2. 426 196 948	-1. 278 696 667	2.4 26 19 69 48	D o w n	0.0 06 60 10 1	0.2 86 61 99 1
15 40 64	RAET 1L	Retinoic acid early transcript 1L		5. 41 50 2	5. 18 69 7	4. 64 68 1	6. 32 89 6	5. 96 49 2	7. 31 17 1	2.7 363 700 28	1.4 522 633 33	2.7 36 37 00 28	U p	0.0 07 98 72 47	0.2 99 13 95 54
91 22 7	GGTL C2	$\Gamma$ -glutamyltransfer ase light chain 2		9. 16 15 7	9. 31 31 4	8. 59 69 8	7. 48 88 1	7. 56 93 1	5. 95 58 1	-4. 053 739 364	-2. 019 253 333	4.0 53 73 93 64	D o w n	0.0 03 67 15 27	0.2 38 59 85 3
11 33 2	ACOT 7	Acyl-coa thioesterase 7		5. 41 99 2	5. 31 84 1	5. 62 66 6	6. 51 06 8	7. 97 26 8	6. 07 74 6	2.6 364 744 21	1.3 986 1 44 21	2.6 36 47 44 21	U p	0.0 22 24 96 07	0.3 78 43 70 47
10 77 8	ZNF27 1P	Zinc finger protein 271, pseudogene		4. 17 26 5	4. 32 98 6	4. 09 63 4	3. 98 06 3	3. 32 46 9	2. 12 20 4	-2. 080 836 1	-1. 057 163 333	2.0 80 83 61	D o w n	0.0 47 42 64 24	0.4 42 16 29 65
71 68	TPM1	Tropomyosin 1 ( $\alpha$ )		9. 95 52	8. 27 08	8. 94 65	10 .8 08	10 .1 93	9. 73 85	2.2 804 206	1.1 893	2.2 80 42	U p	0.0 41 85	0.4 30 06

			8	3		86	09	6	96		06		57	10
											96		63	29
10794	ZNF460	Zinc finger protein 460	4.4974	5.17904	4.80468	6.26405	6.02304	6.47506	2.68886	1.42701	2.68886	U p	0.0791562	0.177732945
80310	PDGFD	Platelet derived growth factor D	7.95359	7.64184	7.3505	5.88122	7.40075	6.15358	-2.250314	-1.170126	2.250314	D o w n	0.027854543	0.391486937
113146	AHNAK2	AHNAK nucleoprotein 2	5.39644	4.86092	4.81214	7.06393	6.70075	7.65228	4.33435	2.11582	4.33435	U p	0.0272108	0.15027275849
378925	RNF148	Ring finger protein 148	4.48208	5.6526	5.37564	4.48261	3.30998	3.63734	-2.567083	-1.36013	2.567083	D o w n	0.012845893	0.336174155
25890	ABI3BP	ABI family member 3 binding protein	4.2126	3.64696	3.75433	6.9172	6.51875	5.56809	5.51508	2.46333	5.51508	U p	0.0312895	0.157718351
22977	AKR7A3	Aldo-keto reductase family 7, member A3 (aflatoxin aldehyde reductase)	8.72992	7.84341	9.01318	8.20103	6.99162	5.83152	-2.869474	-1.520786	2.869474	D o w n	0.042586057	0.431964595
286077	FAM83H	Family with sequence similarity 83 member H	4.81924	4.59483	4.93723	7.20663	6.07069	5.19227	2.58961	1.36333	2.58961	U p	0.025152386	0.383712762
5327	PLAT	Plasminogen activator, tissue	5.06872	5.56338	4.58168	6.03882	7.94888	5.95605	2.982781	1.5766566	2.982781	U p	0.0866727	0.391486937
31	HLA-	Major	9.	8.	9.	5.	8.	7.	-3.	-1.	3.3	D	0.0	0.4

08	DMA	histocompatibility complex, class II, DM $\alpha$	31 76 5	03 15 1	00 99 5	62 25 2	05 27 1	50 77 9	306 633 922	725 363 333	06 63 39 22	o w n	34 79 06 27	08 42 39 81
12 49 89	EFCA B13	EF-hand calcium binding domain 13	4. 97 44 2	4. 62 97 9	4. 51 47 8	6. 78 18 8	4. 81 54 8	6. 34 31	2.4 180 152 33	1.2 738 233 33	2.4 18 01 52 33	U p	0.0 37 47 69 38	0.4 16 79 09 16
26 26	GATA 4	GATA binding protein 4	5. 56 24 3	4. 61 35 4	4. 37 89 1	5. 89 77	7. 19 7	6. 66 34 4	3.3 274 569 48	1.7 344 2 48	3.3 27 45 69 48	U p	0.0 05 41 00 75	0.2 69 32 15 26
67 11	SPTB N1	Spectrin, $\beta$ , non-erythrocytic 1	6. 75 85 3	5. 81 16	6. 27 04 9	7. 92 4	7. 96 01 9	8. 15 66 7	3.3 251 359 64	1.7 334 133 33	3.3 25 13 59 64	U p	0.0 00 50 55 74	0.1 64 24 82 94
12 59 31	CEAC AM20	Carcinoembryonic antigen-related cell adhesion molecule 20	5. 76 23 6	7. 62 83 6	6. 67 85 8	5. 09 33 7	4. 97 56 2	5. 13 82 6	-3. 075 206 591	-1. 620 683 333	3.0 75 20 65 91	D o w n	0.0 08 75 53 4	0.3 08 52 19 75
57 99	PTPR N2	Protein tyrosine phosphatase, receptor type, N polypeptide 2	6. 42 61 1	8. 87 14	9. 21 76 8	5. 35 09 7	6. 28 34 5	6. 09 69 7	-4. 794 122 145	-2. 261 266 667	4.7 94 12 21 45	D o w n	0.0 17 14 62 85	0.3 60 01 29 38
66 09	SMPD 1	Sphingomyelin phosphodiesterase 1, acid lysosomal	6. 23 40 2	6. 17 56 3	5. 93 12 3	4. 91 22 1	4. 93 47 2	4. 70 06 3	-2. 402 339 42	-1. 264 44	2.4 02 33 94 2	D o w n	0.0 00 38 57 83	0.1 60 90 15 41
46 84	NCAM 1	Neural cell adhesion molecule 1	5. 80 38 4	7. 44 18 1	5. 18 44 3	4. 52 40 8	4. 90 74 8	4. 90 35 3	-2. 575 757 308	-1. 364 996 667	2.5 75 75 73 08	D o w n	0.0 42 27 32 55	0.4 31 20 62 22
32 51	HPRT1	Hypoxanthine phosphoribosyltransferase 1	5. 33 47 9	5. 07 25 2	4. 82 88 1	6. 38 5	7. 13 45 4	5. 63 69	2.4 738 762 48	1.3 067 733 33	2.4 73 87 62 48	U p	0.0 12 44 64 19	0.3 34 46 67 31

41 24	MAN2 A1	Mannosidase, $\alpha$ , class 2A, member 1	6. 99 52 3	6. 05 27 1	6. 28 59 6	5. 19 72 1	6. 00 54 6	5. 07 92	-2. 024 188 062	-1. 017 343 333	2.0 24 18 80 62	D o w n	0.0 25 17 87 97	0.3 83 71 27 62
11 28	CHRM 1	Cholinergic receptor, muscarinic 1	4. 09 49 4	7. 10 62 4	6. 35 30 4	4. 29 52	3. 74 19 8	4. 23 62 9	-3. 387 568 219	-1. 760 25	3.3 87 56 82 19	D o w n	0.0 44 74 89 6	0.4 35 52 77 14
22 26 43	UNC5 CL	Unc-5 family C-terminal like	7. 31 77 1	7. 13 23 5	7. 43 07 1	5. 75 30 3	6. 45 59	5. 56 57 1	-2. 582 395 554	-1. 368 71	2.5 82 39 55 54	D o w n	0.0 01 97 99 63	0.2 01 23 04 31
68 8	KLF5	Kruppel-like factor 5 (intestinal)	8. 23 12 9	7. 36 60 2	8. 27 64 6	9. 30 32 1	8. 87 61 7	8. 93 49 9	2.1 143 291 69	1.0 802	2.1 14 32 91 69	U p	0.0 10 22 73 79	0.3 18 63 84 27
10 92 6	DBF4	DBF4 zinc finger	4. 62 98 1	5. 08 94	4. 94 85 4	5. 43 02 4	6. 77 32 5	5. 83 40 8	2.1 784 067 13	1.1 232 733 33	2.1 78 40 67 13	U p	0.0 17 98 22 52	0.3 62 48 76 38
42 53	CTAG E5	CTAGE family member 5	9. 81 78 5	9. 66 57 3	10 .1 47 95	8. 52 84 7	8. 28 96 2	9. 11 92 5	-2. 347 941 831	-1. 231 396 667	2.3 47 94 18 31	D o w n	0.0 03 55 09 18	0.2 37 14 66 6
83 45	HIST1 H2BH	Histone cluster 1, h2bh	10 .0 92 21	8. 93 74 5	9. 01 67 9	10 .5 50 16	11 .6 91 54	10 .4 29 5	2.9 111 382 07	1.5 415 833 33	2.9 11 13 82 07	U p	0.0 11 82 93 48	0.3 29 73 79 49
83 59 3	RASSF 5	Ras association (ralgds/AF-6) domain family member 5	8. 66 90 5	8. 74 65 4	8. 95 40 1	6. 21 66 5	7. 24 46 5	7. 33 37 1	-3. 625 541 949	-1. 858 196 667	3.6 25 54 19 49	D o w n	0.0 00 90 82 4	0.1 81 04 09 24
57 65 3	LOC10 049948 4-C9O RF174	LOC100499484-c 9orf174 readthrough	5. 20 56	5. 44 10 4	5. 73 66 4	4. 11 49 1	4. 38 10 3	4. 78 42 5	-2. 048 209 564	-1. 034 363 333	2.0 48 20 95	D o w n	0.0 04 61 04	0.2 54 41 63

											64		78	12
20 12	EMP1	Epithelial membrane protein 1	4. 56 87 1	3. 41 38 1	3. 51 10 2	4. 89 85	7. 44 82 5	6. 13 80 4	5.0 295 058 67	2.3 304 166 67	5.0 29 50 58 67	U p	0.0 08 92 87 53	0.3 09 00 88 78
47 51	NEK2	NIMA-related kinase 2	4. 72 61 7	4. 28 42 5	4. 69 94 8	7. 53 78 2	7. 72 47	5. 94 39 4	5.6 523 599 18	2.4 988 533 33	5.6 52 35 99 18	U p	0.0 01 25 29 59	0.1 87 10 78 18
10 53 77 75 1	LOC10 537775 1	Uncharacterized LOC105377751	6. 87 68 9	6. 80 65 5	6. 70 38 9	3. 93 42 4	3. 95 25 1	5. 88 33 8	-4. 613 089 661	-2. 205 733 333	4.6 13 08 96 61	D o w n	0.0 04 08 31 77	0.2 44 25 17 2
90 75	CLDN 2	Claudin 2	6. 65 58 1	12 .0 53 15	11 .9 72 38	5. 06 98 6	7. 38 10 2	4. 28 52 7	-25 .07 880 441	-4. 648 396 667	25. 07 88 04 41	D o w n	0.0 19 69 04 8	0.3 67 76 00 84
83 37	HIST2 H2AA 3	Histone cluster 2, h2aa3	10 .4 75 23	9. 12 07 4	9. 52 91 4	11 .0 78 25	11 .2 34 59	10 .4 18 47	2.3 006 900 99	1.2 020 666 67	2.3 00 69 00 99	U p	0.0 20 74 91 62	0.3 71 73 76 6
20 21 34	FAM1 53B	Family with sequence similarity member B	6. 87 68 9	6. 80 65 5	6. 70 38 9	3. 93 42 4	3. 95 25 1	5. 88 33 8	-4. 613 089 661	-2. 205 733 333	4.6 13 08 96 61	D o w n	0.0 04 08 31 77	0.2 44 25 17 2
52 67	SERPI NA4	Serpin peptidase inhibitor, clade A ( $\alpha$ -1 antiproteinase, antitrypsin), member 4	9. 52 23 2	9. 92 65 9	9. 84 96 2	7. 52 51	6. 23 58 8	9. 33 40 8	-4. 192 613 965	-2. 067 85	4.1 92 61 39 65	D o w n	0.0 23 32 83 64	0.3 80 85 39 85
10 09 2	ARPC 5	Actin related protein 2/3 complex subunit 5	7. 97 38 6	7. 16 96 1	7. 47 45 7	8. 48 56 7	8. 87 24 1	8. 35 40 9	2.0 439 737 48	1.0 313 766 67	2.0 43 97 37 48	U p	0.0 08 43 07 07	0.3 05 83 03 66
69 48	TCN2	Transcobalamin II	9. 05	8. 68	9. 01	6. 83	7. 30	6. 44	-4. 149	-2. 052	4.1 49	D o	0.0 00	0.1 28

			174	541	156	959	49	576	162038	82	162038	w	163191	621894
246734	NPCDR1	Nasopharyngeal carcinoma, down-regulated 1	5.72723	4.13972	5.78095	4.4946	3.80259	3.83583	-2.252655	-1.171626	2.252655	D	0.042247	0.4311549
2246	FGF1	Fibroblast growth factor 1 (acidic)	5.0621	5.76176	5.75274	4.16593	4.93309	4.32878	-2.069955	-1.0496	2.069955	D	0.0103409	0.319375494
745	MYRF	Myelin regulatory factor	8.17492	8.801056	8.15524	6.70384	5.78122	6.76081	-3.245145	-1.698283	3.245145	D	0.009027	0.181040924
57175	CORO1B	Coronin, actin binding protein, 1B	6.9408	7.49776	7.06541	6.03008	6.18748	6.10959	-2.083400	-1.05894	2.083400	D	0.0023745	0.2144943
390	RND3	Rho family gtpase 3	6.84746	5.64488	5.31932	7.51629	8.05559	7.30535	3.22326	1.688523	3.22326	U	0.006024	0.279481742
2260	FGFR1	Fibroblast growth factor receptor 1	6.06597	5.67623	6.34101	4.84059	5.18485	4.77562	-2.134724	-1.09405	2.134724	D	0.03220148	0.234716379
972	CD74	CD74 molecule, major histocompatibility complex, class II invariant chain	13.45187	12.41313	13.0121	9.67689	12.25017	11.9246	-3.145290	-1.653193	3.145290	D	0.0470734	0.441457431
8346	HIST1H2BI	Histone cluster 1, h2bi	7.37247	6.42515	6.32847	7.46377	8.92266	7.3238	2.2889934	1.1947133	2.2889934	U	0.0483057	0.44427855
52	PI3	Peptidase inhibitor	5.	6.	6.	9.	8.	8.	5.3	2.4	5.3	U	0.0	0.1

66		3, skin-derived	80 38 4	19 16 2	50 42 6	15 38 4	23 06 4	33 35 8	004 444 37	061 133 33	00 44 44 37	p	00 16 46 09	28 62 18 94
28 43 91	ZNF84 4	Zinc finger protein 844	6. 04 53 2	6. 07 72 6	5. 97 55 5	2. 91 06 4	5. 58 85 9	4. 61 07 2	-3. 166 143 548	-1. 662 726 667	3.1 66 14 35 48	D o w n	0.0 31 55 97 03	0.4 01 56 52 84
21 21	EVC	Ellis van Creveld protein	7. 29 41 8	6. 71 56 5	7. 27 48 5	4. 76 00 7	6. 00 43 1	5. 65 90 8	-3. 074 616 913	-1. 620 406 667	3.0 74 61 69 13	D o w n	0.0 03 11 14 39	0.2 34 23 93 82
19 97 77	ZNF62 6	Zinc finger protein 626	6. 69 05 7	6. 61 70 5	6. 36 73 8	4. 29 18 9	5. 34 54 1	4. 88 86 5	-3. 286 039 905	-1. 716 35	3.2 86 03 99 05	D o w n	0.0 00 77 34 95	0.1 77 73 29 45
10 01 33 33 1	LOC10 013333 1	Uncharacterized LOC100133331	8. 03 35 9	8. 30 84 8	7. 49 20 1	5. 71 04 9	6. 09 29 7	7. 81 82 4	-2. 646 575 235	-1. 404 126 667	2.6 46 57 52 35	D o w n	0.0 40 05 82 98	0.4 24 35 94 44
70 20	TFAP2 A	Transcription factor AP-2 $\alpha$ (activating enhancer binding protein 2 $\alpha$ )	4. 36 61	2. 72 98 5	3. 45 48 9	9. 06 77 6	6. 84 67 7	7. 20 57 7	18. 249 942 33	4.1 898 2	18. 24 99 42 33	U p	0.0 00 39 82 9	0.1 60 90 15 41
37 62	KCNJ5	Potassium channel, inwardly rectifying subfamily J, member 5	5. 19 04 7	7. 07 43 9	6. 07 39 9	4. 97 66	4. 85 28 9	5. 07 70 9	-2. 210 066 836	-1. 144 09	2.2 10 06 68 36	D o w n	0.0 39 58 53 78	0.4 23 36 74 07
83 99 8	REG4	Regenerating family member 4	4. 21 38 7	4. 45 00 3	4. 93 56 3	6. 95 84 2	5. 75 09 9	5. 16 14 3	2.6 828 567 04	1.4 237 7	2.6 82 85 67 04	U p	0.0 18 67 32 57	0.3 65 32 07 18
58 02	PTPRS	Protein tyrosine phosphatase, receptor type, S	8. 06 11 7	7. 81 31 4	8. 34 05 8	6. 83 00 5	6. 17 80 9	5. 50 60 7	-3. 732 718 38	-1. 900 226 667	3.7 32 71 83 8	D o w n	0.0 01 25 14 01	0.1 87 10 78 18

63 34	SCN8 A	Sodium channel, voltage gated, type VIII $\alpha$ subunit	7. 57 53 7	5. 69 51 4	6. 58 48 6	4. 92 38 1	5. 53 81	5. 64 57 6	-2. 377 150 646	-1. 249 233 333	2.3 77 15 06 46	D o w n	0.0 36 14 49 69	0.4 12 66 73 89
25 28	FUT6	Fucosyltransferase 6	7. 77	8. 41 89	8. 38 97	7. 63 81 6	6. 60 04 4	5. 36 77 1	-3. 154 540 777	-1. 657 43	3.1 54 54 07 77	D o w n	0.0 20 67 79 85	0.3 71 59 28 73
98 82	TBC1 D4	TBC1 domain family member 4	6. 48 99	6. 84 36 9	6. 98 17 8	6. 19 19 7	5. 99 88 1	4. 74 36 6	-2. 184 005 768	-1. 126 976 667	2.1 84 00 57 68	D o w n	0.0 27 70 73 71	0.3 91 40 80 15
19 48	EFNB2	Ephrin-B2	2. 68 31 4	5. 63 23 6	5. 64 36 7	7. 30 56 3	7. 48 70 7	6. 42 89 5	5.3 547 776 37	2.4 208 266 67	5.3 54 77 76 37	U p	0.0 20 36 28 63	0.3 71 13 26 99
88 47	DLEU 2	Deleted in lymphocytic leukemia 2 (non-protein coding)	4. 00 35 4	4. 05 01 4	4. 50 13 8	6. 06 23 2	5. 54 75	4. 74 21 8	2.4 043 495 72	1.2 656 466 67	2.4 04 34 95 72	U p	0.0 09 43 35 77	0.3 12 07 48 68
79 98 3	POF1B	Premature ovarian failure, 1B	8. 57 89 5	7. 66 74	8. 38 13 1	8. 80 95 8	10 .2 82 72	9. 54 49 4	2.5 254 258 22	1.3 365 266 67	2.5 25 42 58 22	U p	0.0 16 98 12 9	0.3 58 57 98 86
65 3	BMP5	Bone morphogenetic protein 5	6. 90 93 4	5. 81 06 6	5. 35 89 7	4. 51 76	4. 19 99 6	3. 93 25 7	-3. 505 483 231	-1. 809 613 333	3.5 05 48 32 31	D o w n	0.0 03 16 39 63	0.2 34 23 93 82
91 33	CCNB 2	Cyclin B2	4. 72 79	4. 17 00 7	4. 78 80 8	5. 69 34 3	6. 60 63 3	5. 03 33 5	2.3 225 129 91	1.2 156 866 67	2.3 22 51 29 91	U p	0.0 22 12 85 07	0.3 78 35 72 21
91 89 4	C11orf 52	Chromosome 11 open reading frame 52	6. 60 85 9	6. 14 75 6	6. 22 97 8	4. 51 20 8	4. 94 78 8	5. 35 58 2	-2. 620 877 639	-1. 390 05	2.6 20 87 76	D o w n	0.0 01 62 65	0.1 88 01 18



												39		58	53
89 2	CCNC	Cyclin C	8. 00 18 5	7. 85 57	7. 79 50 9	6. 36 73 2	6. 94 96 4	6. 61 38 6	-2. 362 978 768	-1. 240 606 667	2.3 62 97 87 68	D o w n	0.0 01 05 49 64	0.1 86 14 79 2	
25 80 5	BAMB I	BMP and activin membrane-bound inhibitor	6. 52 32 4	7. 93 97 6	8. 42 26 7	5. 34 23 5	4. 95 38 3	6. 94 95 6	-3. 680 691 073	-1. 879 976 667	3.6 80 69 10 73	D o w n	0.0 25 15 40 84	0.3 83 71 27 62	
54 74 9	EPDR1	Ependymin related 1	5. 36 76 2	5. 07 83 1	3. 72 19 2	6. 37 36 1	6. 94 30 5	5. 42 75 1	2.8 787 45	1.5 254 4	2.8 78 74 5	U p	0.0 25 97 04 47	0.3 85 81 07 78	
20 57	EPOR	Erythropoietin receptor	6. 69 06 6	7. 26 75 2	7. 21 14 6	5. 91 25 6	4. 57 44 5	6. 27 06 1	-2. 771 512 152	-1. 470 673 333	2.7 71 51 21 52	D o w n	0.0 14 57 34 17	0.3 46 82 70 31	
32 95	HSD17 B4	Hydroxysteroid (17- $\beta$ ) dehydrogenase 4	9. 34 34 6	9. 26 38 4	9. 31 32	8. 67 30 8	8. 20 10 8	8. 02 58 4	-2. 009 495 481	-1. 006 833 333	2.0 09 49 54 81	D o w n	0.0 03 93 12 18	0.2 40 20 47 61	
61 93	RPS5	Ribosomal protein S5	7. 82 35 2	8. 97 41 1	8. 75 43 1	9. 87 58 6	9. 75 97 4	9. 64 99 4	2.3 694 189 85	1.2 445 333 33	2.3 69 41 89 85	U p	0.0 07 06 06 38	0.2 89 31 65 01	
10 53 79 55 6	LOC10 537955 6	Nascent polypeptide-associ ated complex subunit $\alpha$ , muscle-specific form-like	8. 03 35 9	8. 30 84 8	7. 49 20 1	5. 71 04 9	6. 09 29 7	7. 81 82 4	-2. 646 575 235	-1. 404 126 667	2.6 46 57 52 35	D o w n	0.0 40 05 82 98	0.4 24 35 94 44	
55 02 2	PID1	Phosphotyrosine interaction domain containing 1	6. 46 53 6	6. 19 37 1	6. 03 30 6	7. 07 35 7	7. 68 57 1	7. 12 04 6	2.0 886 006 47	1.0 625 366 67	2.0 88 60 06 47	U p	0.0 04 40 00 38	0.2 50 69 80 14	
92 1	CD5	CD5 molecule	5. 14	7. 62	7. 28	4. 56	5. 25	5. 23	-3. 180	-1. 669	3.1 80	D o	0.0 35	0.4 09	

			87 3	58 4	30 7	27 1	53 9	21 5	227 558	13	22 75 58	w n	18 99 48	00 19 13
51 37 7	UCHL 5	Ubiquitin C-terminal hydrolase L5	6. 01 56 3	6. 59 47 7	6. 36 86	7. 98 32 3	7. 77 42 3	6. 56 99 2	2.1 676 422 41	1.1 161 266 67	2.1 67 64 22 41	U p	0.0 28 02 61 35	0.3 92 00 23 37
79 89 9	PRR5L	Proline rich 5 like	6. 12 15 7	6. 06 83 7	5. 78 52 2	4. 23 96 7	5. 58 60 1	4. 95 56 5	-2. 091 604 385	-1. 064 61	2.0 91 60 43 85	D o w n	0.0 19 67 40 01	0.3 67 76 00 84
23 30 6	NEMP 1	Nuclear envelope integral membrane protein 1	4. 87 40 9	4. 95 77 7	4. 55 90 1	6. 18 51 6	5. 95 04 7	6. 12 64 5	2.4 459 642 76	1.2 904 033 33	2.4 45 96 42 76	U p	0.0 00 42 65 44	0.1 63 37 87 34
76 94	ZNF13 5	Zinc finger protein 135	6. 95 55 2	6. 96 95	7. 04 65 5	4. 14 38 6	5. 22 35 6	4. 47 9	-5. 187 538 002	-2. 375 05	5.1 87 53 80 02	D o w n	0.0 00 10 82 93	0.1 27 84 98 29
18 24	DSC2	Desmocollin 2	6. 11 59 2	5. 12 07 6	4. 87 42 8	6. 99 77 3	7. 63 20 5	5. 78 85 2	2.7 052 838 95	1.4 357 8	2.7 05 28 38 95	U p	0.0 31 40 41 75	0.4 01 56 52 84
79 89 1	ZNF67 1	Zinc finger protein 671	5. 43 98	5. 90 83 5	5. 70 98 5	3. 93 66 5	4. 17 05 5	4. 94 73 9	-2. 521 828 208	-1. 334 47	2.5 21 82 82 08	D o w n	0.0 03 31 22 79	0.2 36 57 66 81
64 11 6	SLC39 A8	Solute carrier family 39 (zinc transporter), member 8	6. 00 62 1	6. 92 09 1	6. 65 33 8	5. 05 78 4	4. 89 69 4	4. 00 74 8	-3. 662 291 601	-1. 872 746 667	3.6 62 29 16 01	D o w n	0.0 01 46 48 8	0.1 87 10 78 18
54 99 7	TESC	Tescalcin	8. 44 06 1	8. 79 17 5	8. 89 57	7. 90 53 3	6. 16 59 9	7. 88 59	-2. 621 295 503	-1. 390 28	2.6 21 29 55 03	D o w n	0.0 24 82 81 99	0.3 83 25 28 34
57	SYT13	Synaptotagmin 13	8.	7.	8.	5.	4.	3.	-11	-3.	11.	D	0.0	0.1

58 6			55 72 6	63 08	99 27	83 49 4	68 76 9	93 98	.89 906 795	572 776 667	89 90 67 95	o w n	00 34 90 26	60 90 15 41
10 01 32 28 7	LOC10 013228 7	Uncharacterized LOC100132287	8. 03 35 9	8. 30 84 8	7. 49 20 1	5. 71 04 9	6. 09 29 7	7. 81 82 4	-2. 646 575 235	-1. 404 126 667	2.6 46 57 52 35	D o w n	0.0 40 05 82 98	0.4 24 35 94 44
26 11 8	WSB1	WD repeat and SOCS box containing 1	4. 47 41 5	4. 14 01 8	3. 95 29 9	5. 17 11 4	5. 85 91 1	4. 83 38	2.1 419 280 22	1.0 989 1	2.1 41 92 80 22	U p	0.0 08 72 05 93	0.3 08 52 19 75
10 30 8	ZNF26 7	Zinc finger protein 267	4. 22 24 6	3. 26 57 3	3. 92 71 3	4. 83 45 5	5. 02 54 8	5. 84 49 8	2.6 942 741 69	1.4 298 966 67	2.6 94 27 41 69	U p	0.0 05 17 57 57	0.2 66 23 90 84
95 47	CXCL 14	Chemokine (C-X-C motif) ligand 14	7. 26 20 5	9. 54 28 9	8. 36 47 5	5. 64 19 6	7. 07 72 8	6. 76 80 3	-3. 717 003 38	-1. 894 14	3.7 17 00 33 8	D o w n	0.0 19 73 92 54	0.3 67 76 00 84
84 7	CAT	Catalase	9. 77 11 6	9. 34 46 2	9. 33 80 8	9. 12 55 1	8. 69 44 7	7. 57 28 7	-2. 028 392 249	-1. 020 336 667	2.0 28 39 22 49	D o w n	0.0 42 83 33 86	0.4 32 07 88 1
84 76 5	ZNF57 7	Zinc finger protein 577	5. 39 52 8	6. 17 72	6. 31 80 9	3. 64 46 7	4. 90 58 7	4. 11 26 2	-3. 346 075 504	-1. 742 47	3.3 46 07 55 04	D o w n	0.0 03 10 85 13	0.2 34 23 93 82
64 78 3	RBM1 5	RNA binding motif protein 15	4. 90 39 2	5. 57 51 6	5. 44 56 7	7. 22 39 7	6. 59 37 2	5. 82 52	2.3 609 704 75	1.2 393 8	2.3 60 97 04 75	U p	0.0 15 60 91 85	0.3 50 84 39 38
18 2	JAG1	Jagged 1	4. 78 31 6	5. 22 44 1	4. 60 74 8	7. 15 60 5	6. 90 92 6	6. 18 91 7	3.6 802 658 87	1.8 798 1 26 58 87	3.6 80 26 58 87	U p	0.0 00 60 08 3	0.1 67 78 26 85

