

Column #	Transcript	Cluster ID	gene_assignment	Gene Symbol	RefSeq	p-value(Gene)	p-value(VA vs. Control)	Ratio(VA vs. Control)	Fold-Change(VA vs. Control)	Fold-Change(VA vs. Control)	Fold-Change(VA vs. Control)	(Description)	(tGene)	(SSGene)	(SSError)	(tError)
25413	8105049	NM_023566	SPINK7 // serpin peptidase inhibitor, Kazal type 7 (putative) // 5a	SPINK7	NM_023566	0.000481089	0.000481089	1.0	0.0258712	-38.653	Vk down vs Control		31.9293	66.7185	16.7166	1
4806	806032	NM_003245	TGM3 // transglutaminase 3 (p-olypeptide, protein-lysine-aminomethyltransferase)	TGM3	NM_003245	4.24E-05	4.24E-05	0.0457455		-21.8601	Vk down vs Control		64.5243	47.5308	5.98308	1
18071	8081308	NM_196538	SERN // serpin peptidase inhibitor, clade B (ovalbumin), member 1	SERN	NM_196538	3.28E-05	3.28E-05	0.0476884		-20.9494	Vk down vs Control		89.2785	46.2607	5.87577	1
14926	8000412	NM_000967	ITIH4 // inter-alpha-trypsin inhibitor 4 (type 1)	ITIH4	NM_000967	0.0002921	0.0002921	0.0569221		-14.6208	Vk down vs Control		11.2464	44.2565	32.8174	1
5902	7905515	NM_010025231	KPRP // keratinocyte proline-rich protein // 1a2.13 // 4488.84	KPRP	NM_010025231	0.00023404	0.00023404	0.0573658		-17.432	Vk down vs Control		39.8095	40.811	8.2037	1
10746	7961673	NM_021957	GS2 // glycogen synthase 2 (liver) // 12a1.2 // 2998 // ENST000000000000	GS2	NM_021957	0.00166379	0.00166379	0.0595864		-16.7823	Vk down vs Control		21.54	39.7337	14.5774	1
8020	8020130	NM_019492	DGSI // desmoglein 1 // 18a1.1 // 1828 // ENST00000257192 // 0561	DGSI	NM_019492	0.0001642	0.0001642	0.0597411		-14.0663	Vk down vs Control		39.8171	21.54	5.6687	1
2572	7920182	NM_178435	UCE1 // late cornified envelope 3 // 12a1.2 // 353145 // ENST000000000000	UCE1	NM_178435	0.00067774	0.00067774	0.0615129		-15.3464	Vk down vs Control		10.6753	37.2534	10.7372	1
16528	8021594	NM_021663	LCE3D // late cornified envelope 3D // 1a1.1 // 84648 // ENST000000000000	LCE3D	NM_021663	0.00327332	0.00327332	0.0624852		-14.6075	Vk down vs Control		17.1209	35.9192	16.3075	1
6628	8021908	NM_080474	SERPBNB12 // serpin peptidase inhibitor, clade B (ovalbumin), member 12	SERPBNB12	NM_080474	0.00147164	0.00147164	0.0708944		-14.1055	Vk down vs Control		72.2054	34.9885	12.8278	1
7555	8021019	NM_021709	SRFBP3 // serpin peptidase inhibitor, clade B (ovalbumin), member 3	SRFBP3	NM_021709	0.00026299	0.00026299	0.074311		-14.6208	Vk down vs Control		36.585	34.2078	6.48017	1
18069	8036072	NM_207392	KRTAP4 // keratinocyte differentiation-associated protein // 19a1.3	KRTAP4	NM_207392	0.00216392	0.00216392	0.0764524		-13.08	Vk down vs Control		19.726	33.0213	13.3972	1
2149	8069790	NM_011231	CLDN17 // claudin 17 // 21a2.11 // 26285 // ENST00000286808 // CL	CLDN17	NM_011231	0.00198787	0.00198787	0.0776486		-12.8785	Vk down vs Control		20.2986	32.6237	11.825	1
1993	7963491	NM_006211	KRT1 // keratin 1 // 12a1.2-q3 // 3848 // ENST0000025244 // KRT1	KRT1	NM_006211	0.00115579	0.00115579	0.0834338		-11.9855	Vk down vs Control		24.2618	30.8148	10.1608	1
10387	8130807	NM_023737	LCC1 // late cornified envelope 1 // 1a1.1 // 441178 // AK056500 // LCC1	LCC1	NM_023737	0.00466575	0.00466575	0.0918464		-10.8877	Vk down vs Control		15.0776	27.4772	15.1116	1
2768	8130980	NM_0441178	hypothetical LOC441178 // 6a2 // 441178 // AK056500 // LCC1	LOC441178	AK41178	0.00466575	0.00466575	0.0918464		-10.8877	Vk down vs Control		15.0776	27.4772	15.1116	1
5401	8127854	NM_002395	ME1 // metallopeptidase 1, NADPH-dependent, cytosolic // 6a2 // 4199	ME1	NM_002395	0.00132211	0.00132211	0.094627		-10.5678	Vk down vs Control		23.2281	27.7702	9.56433	1
2702	7905486	NM_019060	CRC1 // cysteine-rich C-terminal 1 // 1a1 // 54544 // ENST000000000000	CRC1	NM_019060	0.00385853	0.00385853	0.10203		-10.2586	Vk down vs Control		16.1144	26.0242	12.9037	1
17308	8126905	NM_006061	CRISP3 // cysteine-rich secretory protein 3 // 6a1.2.3 // 10321	CRISP3	NM_006061	0.00875558	0.00875558	0.10272		-7.9426	Vk down vs Control		11.8686	25.036	17.4585	1
2300	7964687	NM_0099676	CL20F56 // chromosome 12 open reading frame 56 // 12a1.2 // 11	CL20F56	NM_0099676	0.00115745	0.00115745	0.107874		-8.19604	Vk down vs Control		22.2506	24.916	8.1249	1
1394	8129261	NM_019663	UVGG6C // lymphocyte antigen 6 complex, locus G6C // 6a2.1.3 // 807	UVGG6C	NM_019663	0.00476655	0.00476655	0.110685		-8.03465	Vk down vs Control		14.9365	24.206	12.9619	1
3216	8175856	NM_021261	UVGG6G // lymphocyte antigen 6 complex, locus G6G // 6a2.1.3 // 807	UVGG6G	NM_021261	0.00469074	0.00469074	0.113355		-8.9802	Vk down vs Control		15.0357	24.0682	12.8054	1
2714	8125042	NM_021261	UVGG6G // lymphocyte antigen 6 complex, locus G6G // 6a2.1.3 // 807	UVGG6G	NM_021261	0.00467873	0.00467873	0.117779		-8.49049	Vk down vs Control		15.0488	22.859	12.1484	1
2066	8059723	NM_01013442	EPGN // epithelial nitric oxide hemoglobin (mouse) // 4a1.3 // 253234	EPGN	NM_01013442	0.00131442	0.00131442	0.117964		-8.47716	Vk down vs Control		17.365	22.8203	10.5133	1
1428	7904780	NM_0094762	AFIL1 // alpha-1-fetoprotein 1 // 3'-phosphoadenosine 5'-phosphoribosyl transferase 2 // 12a2.3	AFIL1	NM_0094762	0.000895102	0.000895102	0.122636		-8.1542	Vk down vs Control		25.5375	21.9985	6.8135	1
24016	8158771	NM_013426	AFIL1 // alpha-1-fetoprotein 1-like // 9a3.13-q3.4.3 // 1	AFIL1	NM_013426	0.000985012	0.000985012	0.122636		-8.1542	Vk down vs Control		25.5375	21.9985	6.8135	1
17754	8033151	NM_133492	AFIL1 // alkaline ceramidase 1 // 19a1.3 // 125981 // ENST000000000000	AFIL1	NM_133492	0.00076524	0.00076524	0.123971		-8.0664	Vk down vs Control		27.6526	21.7721	6.29873	1
80430	804340	NM_145693	UPN1 // hemoglobin // 2a2.3 // 23175 // ENST0000025070 // UPN1 // 1	UPN1	NM_145693	0.000824594	0.000824594	0.125617		-7.96072	Vk down vs Control		27.014	21.4979	6.30643	1
92743	80113756	NM_01317556	FAM25B // family with sequence similarity 25, member B // 10a1.1	FAM25B	NM_01317556	0.000808751	0.000808751	0.126216		-7.92295	Vk down vs Control		26.4611	21.994	6.4697	1
7823	7933327	NM_01137556	FAM25B // family with sequence similarity 25, member B // 10a1.1	FAM25B	NM_01137556	0.000808751	0.000808751	0.126216		-7.92295	Vk down vs Control		26.4611	21.994	6.4697	1
7834	7933423	NM_01137556	FAM25B // family with sequence similarity 25, member B // 10a1.1	FAM25B	NM_01137556	0.000808751	0.000808751	0.126216		-7.92295	Vk down vs Control		26.4611	21.994	6.4697	1
80430	804340	NM_145693	UPN1 // hemoglobin // 2a2.3 // 23175 // ENST0000025070 // UPN1 // 1	UPN1	NM_145693	0.000824594	0.000824594	0.125617		-7.96072	Vk down vs Control		27.014	21.4979	6.30643	1
92743	80113756	NM_01317556	FAM25B // family with sequence similarity 25, member B // 10a1.1	FAM25B	NM_01317556	0.000808751	0.000808751	0.126216		-7.92295	Vk down vs Control		26.4611	21.994	6.4697	1
7823	7933327	NM_01137556	FAM25B // family with sequence similarity 25, member B // 10a1.1	FAM25B	NM_01137556	0.000808751	0.000808751	0.126216		-7.92295	Vk down vs Control		26.4611	21.994	6.4697	1
7834	7933423	NM_01137556	FAM25B // family with sequence similarity 25, member B // 10a1.1	FAM25B	NM_01137556	0.000808751	0.000808751	0.126216		-7.92295	Vk down vs Control		26.4611	21.994	6.4697	1
80430	804340	NM_145693	UPN1 // hemoglobin // 2a2.3 // 23175 // ENST0000025070 // UPN1 // 1	UPN1	NM_145693	0.000824594	0.000824594	0.125617		-7.96072	Vk down vs Control		27.014	21.4979	6.30643	1
92743	80113756	NM_01317556	FAM25B // family with sequence similarity 25, member B // 10a1.1	FAM25B	NM_01317556	0.000808751	0.000808751	0.126216		-7.92295	Vk down vs Control		26.4611	21.994	6.4697	1
7823	7933327	NM_01137556	FAM25B // family with sequence similarity 25, member B // 10a1.1	FAM25B	NM_01137556	0.000808751	0.000808751	0.126216		-7.92295	Vk down vs Control		26.4611	21.994	6.4697	1
7834	7933423	NM_01137556	FAM25B // family with sequence similarity 25, member B // 10a1.1	FAM25B	NM_01137556	0.000808751	0.000808751	0.126216		-7.92295	Vk down vs Control		26.4611	21.994	6.4697	1
80430	804340	NM_145693	UPN1 // hemoglobin // 2a2.3 // 23175 // ENST0000025070 // UPN1 // 1	UPN1	NM_145693	0.000824594	0.000824594	0.125617		-7.96072	Vk down vs Control		27.014	21.4979	6.30643	1
92743	80113756	NM_01317556	FAM25B // family with sequence similarity 25, member B // 10a1.1	FAM25B	NM_01317556	0.000808751	0.000808751	0.126216		-7.92295	Vk down vs Control		26.4611	21.994	6.4697	1
7823	7933327	NM_01137556	FAM25B // family with sequence similarity 25, member B // 10a1.1	FAM25B	NM_01137556	0.000808751	0.000808751	0.126216		-7.92295	Vk down vs Control		26.4611	21.994	6.4697	1
7834	7933423	NM_01137556	FAM25B // family with sequence similarity 25, member B // 10a1.1	FAM25B	NM_01137556	0.000808751	0.000808751	0.126216		-7.92295	Vk down vs Control		26.4611	21.994	6.4697	1
80430	804340	NM_145693	UPN1 // hemoglobin // 2a2.3 // 23175 // ENST0000025070 // UPN1 // 1	UPN1	NM_145693	0.000824594	0.000824594	0.125617		-7.96072	Vk down vs Control		27.014	21.4979	6.30643	1
92743	80113756	NM_01317556	FAM25B // family with sequence similarity 25, member B // 10a1.1	FAM25B	NM_01317556	0.000808751	0.000808751	0.126216		-7.92295	Vk down vs Control		26.4611	21.994	6.4697	1
7823	7933327	NM_01137556	FAM25B // family with sequence similarity 25, member B // 10a1.1	FAM25B	NM_01137556	0.000808751	0.000808751	0.126216		-7.92295	Vk down vs Control		26.4611	21.994	6.4697	1
7834	7933423	NM_01137556	FAM25B // family with sequence similarity 25, member B // 10a1.1	FAM25B	NM_01137556	0.000808751	0.000808751	0.126216		-7.92295	Vk down vs Control		26.4611	21.994	6.4697	1
80430	804340	NM_145693	UPN1 // hemoglobin // 2a2.3 // 23175 // ENST0000025070 // UPN1 // 1	UPN1	NM_145693	0.000824594	0.000824594	0.125617		-7.96072	Vk down vs Control		27.014	21.4979	6.30643	1
92743	80113756	NM_01317556	FAM25B // family with sequence similarity 25, member B // 10a1.1	FAM25B	NM_01317556	0.000808751	0.000808751	0.126216		-7.92295	Vk down vs Control		26.4611	21.994	6.4697	1
7823	7933327	NM_01137556	FAM25B // family with sequence similarity 25, member B // 10a1.1	FAM25B	NM_01137556	0.000808751	0.000808751	0.126216		-7.92295	Vk down vs Control		26.4611	21.994	6.4697	1
7834	7933423	NM_01137556	FAM25B // family with sequence similarity 25, member B // 10a1.1	FAM25B	NM_01137556	0.000808751	0.000808751	0.126216		-7.92295	Vk down vs Control		26.4611	21.994	6.4697	1
80430	804340	NM_145693	UPN1 // hemoglobin // 2a2.3 // 23175 // ENST0000025070 // UPN1 // 1	UPN1	NM_145693	0.000824594	0.000824594	0.125617		-7.96072	Vk down vs Control		27.014	21.4979	6.30643	1
92743	80113756	NM_01317556	FAM25B // family with sequence similarity 25, member B // 10a1.1	FAM25B	NM_01317556	0.000808751	0.000808751	0.126216		-7.92295	Vk down vs Control		26.4611	21.99		

Column #	Transcript	Cluster ID	gene_assignment	Gene Symbol	RefSeq	p-value(Gene)	p-value(VA vs Control)	Ratio(VA vs Control)	Fold-Change(VA vs Control)	Fold-Change(VA vs Control)	Description	IGS	SS(Gene)	SS(Gene)	IF(Rer)
19607	8045229	NM 032995	ARHGFE4 // rho guanine nucleotide exchange factor (GEF) 4 // 2a22 /	ARHGFE4	NM 032995	0.00341914	0.00031914	0.312207	-3.203	Vk down vs Control		16.8423	6.7692	3.2153	1
9167	7941761	NM 015478	RHO // ras homology gene family, member D // 11a13.3 // 29984 // 11	RHO	NM 015478	0.00133124	0.00133124	0.313129	-1.19357	Vk down vs Control		17.4621	6.7386	2.3276	1
18843	8122426	NM 014721	PHACTR2 // phosphatase and actin regulator 2 // 6a24.2 // 9749 // 11	PHACTR2	NM 014721	0.00105532	0.00105532	0.313395	-1.19086	Vk down vs Control		24.981	6.7250	2.1534	1
27625	7971515	CNCR3 // CNCR3 family member 3 // 154043 // ENST00000200306	CNCR3	NM 028151	0.00105532	0.00105532	0.313395	-1.19086	Vk down vs Control		16.6274	6.7274	2.8932	1	
13010	7983867	CGNL1 // CGNL1-like family 1 // 15213.3 // 84952 // ENST00000201822 // 11	CGNL1	NM 032866	0.00091963	0.00091963	0.31957	-1.19291	Vk down vs Control		11.4616	6.50076	2.4762	1	
18189	8037179	CMN // CMN // cornifin-like 1 // 19a13.2 // 84518 // ENST00000220231 // CMN	CMN	NM 032488	0.00186805	0.00186805	0.319661	-1.12831	Vk down vs Control		8.6496	6.49749	2.00581	1	
79731	811874	RNASE7 // RNASE7 // ribonuclease, RNase A family 7 // 14a11.2 // 84659 // 11	RNASE7	NM 033472	0.00111557	0.00111557	0.322448	-1.03998	Vk down vs Control		10.57134	6.4211	2.09518	1	
62056	8120756	---	---	---	---	0.00111557	0.00111557	0.322448	-1.03998	Vk down vs Control		10.57134	6.4211	2.09518	1
5762	8052654	NM 020651	PEL1 // eukaryotic homolog 1 (Drosophila) // 2a13.3 // 57162 // ENST	PEL1	NM 020651	0.00039357	0.00039357	0.32286	-0.97371	Vk down vs Control		10.6408	6.38453	1.83971	1
19323	7907847	---	---	---	---	0.00257496	0.00257496	0.323405	-3.0921	Vk down vs Control		74.0647	6.3651	6.82074	1
26901	8122368	SNX9 // sorting nexin 9 // 6a25.1 a26.1 // 51420 // ENST00000391285	SNX9	NM 026234	0.00726627	0.00726627	0.324487	-1.29295	Vk down vs Control		12.7634	6.33212	1.96883	1	
20376	8107632	NM 010405	SNX24 // sorting nexin 24 // 5a23.2 // 28966 // ENST00000261369 // 11	SNX24	NM 010405	0.0118787	0.0118787	0.324684	-1.07821	Vk down vs Control		10.4972	6.13483	4.12729	1
155602	810012421	ANKRD20A2 // ankyrin repeat domain 20 family, member A2 // 9a12	ANKRD20A2	NM 001012421	0.0116225	0.0116225	0.324804	-1.06365	Vk down vs Control		10.5918	6.2617	4.87547	1	
42793	8096544	ENST00000370520 // RP1-93914-6 // hypothetical protein FLJ12154 // 20a13.3 // 11	RP1-93914-6	ENST00000370520	0.00688477	0.00688477	0.326255	-1.06255	Vk down vs Control		10.7029	6.2577	3.84206	1	
1550	7920297	NM 020872	SNOA14 // small nuclear RNA, H/ACA box 14 // 16a13.3 // 57402 // 11	SNOA14	NM 020872	0.00168606	0.00168606	0.326555	-1.04382	Vk down vs Control		21.4432	6.18925	2.3908	1
12139	7997664	NR 002327	SNOA10 // small nuclear RNA, H/ACA box 10 // 16a13.3 // 57404	SNOA10	NR 002327	0.0288233	0.0288233	0.328672	-1.03225	Vk down vs Control		10.7348	6.1863	6.99472	1
18627	8041204	NR 002327	SNOA10 // small nuclear RNA, H/ACA box 10 // 16a13.3 // 57404	SNOA10	NR 002327	0.0288233	0.0288233	0.328672	-1.03225	Vk down vs Control		10.7348	6.1863	6.99472	1
16328	8019732	AKO57217	TRMP2 // TRMP phosphatase-like domain protein 2 // 17a25 // 703	AKO57217	AKO57217	0.01321139	0.01321139	0.329299	-1.04975	Vk down vs Control		10.0426	6.16243	4.90971	1
17470	8030367	NM 004605	SULT3B1 // sulfotransferase family, cytosolic, 2b, member 1 // 19a1	SULT3B1	NM 004605	0.00796634	0.00796634	0.329524	-1.03468	Vk down vs Control		12.1172	6.15587	3.99821	1
974762	8104580	ATB2 // ankyrin repeat and BTB (POZ) domain containing 2 // 11p13	ATB2	NM 145894	0.0491291	0.0491291	0.329962	-1.03065	Vk down vs Control		5.3697	6.1414	1.94933	1	
1293	7972487	NM 015296	DOCK9 // dedicator of cytokinesis 9 // 33a23.3 // 2348 // NM 0011	DOCK9	NM 015296	0.00102537	0.00102537	0.330858	-1.02245	Vk down vs Control		25.2122	6.1116	1.93931	1
11543	7970372	NM 003366	ANKRD20B // ankyrin repeat domain 20B // 1 // 72b1.1 // NM 00	ANKRD20B	NM 003366	0.0109162	0.0109162	0.332284	-1.00052	Vk down vs Control		10.8667	6.0922	4.46443	1
1977	7962274	NM 017441	NF21A // kinesin family member 21A // 12a12 // 55605 // ENST00000	NF21A	NM 017441	0.00455419	0.00455419	0.33289	-1.00392	Vk down vs Control		15.2093	6.04339	1.17878	1
14424	7999709	NM 011116	ADCY9 // adenylyl cyclase 9 // 16a13.3 // 115 // ENST00000294016	ADCY9	NM 011116	0.0094459	0.0094459	0.33328	-1.00391	Vk down vs Control		11.5183	6.04335	4.1974	1
22306	8078227	NM 003884	KAT2B // kinase II/kinase activator 2B // 18a10 // ENST000	KAT2B	NM 003884	0.00621858	0.00621858	0.332905	-1.00386	Vk down vs Control		13.4249	6.04139	3.66981	1
2277	8031277	NR 004779	LOC10212 // LOC10212 // 16a12.1 // 9813 // 11	LOC10212	NR 004779	0.00321179	0.00321179	0.333037	-1.00377	Vk down vs Control		17.6123	6.0392	2.8846	1
4306	7901675	NM 152607	LOC10212 // Chromosome 1 open reading frame 17 // 1a23.3 // 163747	LOC10212	NM 152607	0.033447	0.033447	0.333447	-1.99988	Vk down vs Control		16.9602	6.0251	3.13682	1
5790	7902520	NM 004425	ECM1 // extracellular matrix protein 1 // 1a21 // 1893 // NM 0226	ECM1	NM 004425	0.0024399	0.0024399	0.333722	-2.9995	Vk down vs Control		18.9367	6.01623	5.21487	1
11049	7965040	NM 007450	PLCL1 // pleckstrin homology-like domain, family A, member 1 // 12	PLCL1	NM 007450	0.00155292	0.00155292	0.334008	-2.9941	Vk down vs Control		9.37746	6.00949	1.52863	1
18930	8044046	NM 003854	IKZF1 // interferon lambda 1 // 2a12 // 8089 // ENST00000200306	IKZF1	NM 003854	0.00284192	0.00284192	0.334192	-1.99988	Vk down vs Control		13.7423	5.9973	2.8846	1
20453	8097998	NM 010950	USP53 // ubiquitin specific peptidase 53 // 4a26 // 5453 // ENST0	USP53	NM 010950	0.00175188	0.00175188	0.335427	-1.98128	Vk down vs Control		11.4744	5.96053	2.2598	1
21171	8060187	NM 019854	CZorf54 // chromatin specific open reading frame 4 // 2a37.3 // 79919	CZorf54	NM 019854	0.00524354	0.00524354	0.33579	-2.97805	Vk down vs Control		14.433	5.94873	3.2973	1
12968	7983161	---	---	---	---	0.00245622	0.00245622	0.334487	-1.29295	Vk down vs Control		12.7634	6.33212	1.96883	1
2438	8098470	NM 024949	WWC2 // WW and C2 domain containing 2 // 4a35.1 // 80014 // ENST0	WWC2	NM 024949	0.0115268	0.0115268	0.340044	-2.93993	Vk down vs Control		10.6278	5.89099	4.37276	1
793159	8191859	NM 017422	CALML5 // calmodulin-like 5 // 10p15.1 // 51806 // ENST00000380332	CALML5	NM 017422	0.0115908	0.0115908	0.340244	-2.92803	Vk down vs Control		10.6037	5.76548	3.43979	1
10494	7959131	NM 007141	CDC64 // coiled-coil domain containing 64 // 12a12.3 // 92558 // 11	CDC64	NM 007141	0.00308385	0.00308385	0.342605	-2.91881	Vk down vs Control		16.6644	5.73168	2.86629	1
11960	7973072	NM 005194	NSD1 // nuclear domain 1 // 16a12.1 // 5683 // ENST00000407031 // PA	NSD1	NM 005194	0.0034621	0.0034621	0.343427	-2.91199	Vk down vs Control		10.6278	5.73168	2.86629	1
7099	8192407	NM 001004470	STR5A6 // STR alpha-N-acetylneuraminidase domain-2.8-sialyltran	STR5A6	NM 001004470	0.00740692	0.00740692	0.343473	-2.91144	Vk down vs Control		12.6655	5.70464	3.60212	1
86715	7942118	NM 138768	MYEOV // myeloma overexpressed (in a subset of t(11;14) positive m	MYEOV	NM 138768	0.00206261	0.00206261	0.343521	-2.91103	Vk down vs Control		18.5221	5.70317	2.4633	1
16107	8021470	NM 021127	MAP1P // phospho-12-methyl-13-acetate-inducible protein 1 // 18a2	MAP1P	NM 021127	0.0121888	0.0121888	0.343994	-2.90703	Vk down vs Control		8.13062	5.68847	5.61573	1
9886	809861	NM 010428	ADP1 // ankyrin domain protein 1 // 16a13.3 // 57402	ADP1	NM 010428	0.0041007	0.0041007	0.344007	-2.90703	Vk down vs Control		10.6278	5.68847	5.61573	1
15586	8110678	NM 004623	CDC127 // coiled-coil domain containing 127 // 5p15.3 // 133957	CDC127	NM 004623	0.0132253	0.0132253	0.344672	-2.90131	Vk down vs Control		10.0383	5.66752	4.2503	1
25793	8013384	NM 145691	ALDH3A1 // aldehyde dehydrogenase 3 family, member A1 // 17a12.1 //	ALDH3A1	NM 145691	0.0034253	0.0034253	0.345257	-2.89639	Vk down vs Control		9.74187	5.6496	4.69392	1
17626	8176369	NM 018398	ERCC1 // ERCC1 // 16a12.1 // 5683 // ENST00000407031 // PA	ERCC1	NM 018398	0.00444881	0.00444881	0.345485	-1.4689	Vk down vs Control		15.4689	5.64238	2.96346	1
13528	7929567	NM 138440	WASN // wason // 15a13.3 // 114900 // ENST00000340735 // WASN //	WASN	NM 138440	0.00935301	0.00935301	0.346482	-2.88615	Vk down vs Control		13.4659	5.61189	3.89764	1
15874	7907830	NM 002826	GSXL // quiescin Q6 sulfhydryl oxidase 1 // 1a24 // 5768 // 11	GSXL	NM 002826	0.00627487	0.00627487	0.347464	-2.8769	Vk down vs Control		13.9669	5.57797	3.20621	1
12219	7976988	NM 00108707	EML1 // echinoderm microtubule associated protein like 1 // 14a3	EML1	NM 00108707	0.0134241	0.0134241	0.348975	-2.86553	Vk down vs Control		9.97649	5.56221	4.03924	1
12478	7979179	NM 015484	ERCC1 // ERCC1 // 16a12.1 // 5683 // ENST00000407031 // PA	ERCC1	NM 015484	0.00444881	0.00444881	0.349249	-2.86553	Vk down vs Control		15.4689	5.64238	2.96346	1
18995	8057341	NR 003366	ANKRD20B // ankyrin repeat domain 20B // 1 // 72b1.1 // NM 00	ANKRD20B	NR 003366	0.0289253	0.0289253	0.350001	-2.8564	Vk down vs Control		7.30322	5.50271	6.22762	1
1943	8049726	NM 002374	MAP2 // microtubule-associated protein 2 // 2a14-4a5 // 4133 // NM 0	MAP2	NM 002374	0.0145216	0.0145216	0.350587	-2.85236	Vk down vs Control		9.60501	5.48788	4.54993	1
2973	8150076	NM 001394	ADP1 // dual specificity phosphatase 1 // 8a21-01 // 1846 // NM 0226	ADP1	NM 001394	0.0179221	0.0179221	0.351187	-2.84804	Vk down vs Control		11.6262	5.47203	7.0993	1
16081	816021	NM 190282	ANKRD20B // ankyrin repeat domain 20B // 1 // 72b1.1 // NM 00	ANKRD20B	NM 190282	0.00291217	0.00291217	0.352919	-2.71799	Vk down vs Control		14.6654	5.49929	3.68832	1
1411	8165808	NM 001141919	XG // Xg blood group system // Xp22.3 // 7499 // NM 175569 // XG // X	XG	NM 001141919	0.00780416	0.00780416	0.353736	-2.79692	Vk down vs Control		12.4161	5.28428	3.4048	1
28990	8143127	AF358803 // FAM180A // family with sequence similarity 180, member A // 7a3	FAM180A	AF358803	0.0314496	0.0314496	0.354969	-2.77561	Vk down vs Control		6.77786	5.20598	6.14469	1	
8146955	8146955	---	---	---	---	0.000267107	0.000267107	0.361402	-2.767	Vk down vs Control		38.0993	5.17344	1.08621	1
1804	7904466	NM 005555	KRT6B // keratin 6b // 12a12-03 // 3854 // ENST0000025252 // KRT												

Column #	Transcript	Cluster ID	gene_assignment	Gene Symbol	RefSeq	p-value(Gene)	p-value(VA vs. Control)	Ratio(VA vs. Control)	Fold-Change(VA vs. Control)	Fold-Change(VA vs. Control)	Fold-Change(VA vs. Control)	(Description)	(fGene)	(SSGene)	(SSError)	(fError)	
19595	890519	NM_006277	ITSN2 // ITSN2 // intersectin 2 // 2pter-q25.1 // 90616 // NM_019595 // IT13	ITSN2	NM_006277	0.0100184	0.0100194	0.430604	-2.3222	VN down vs Control	11.2499	5.4624	2.5218				
23809	8093974	---	---	---	---	0.0011782	0.0011782	0.43123	-2.3194	VN down vs Control	21.4125	3.5343	1.17262				
803893	NM_00713	BURB // biliverdin reductase B (flavin reductase (NADPH)) // IT13	BURB	NM_00713	0.0262854	0.0262854	0.431487	-2.3177	VN down vs Control	7.8955	3.52902	3.01851					
22395	8079140	NM_01719	SNF1-related kinase 2 // 15q21.1 // 5486 // NM_0103959 // S	SNF1	NM_01719	0.0015249	0.0015249	0.43162	-2.317	VN down vs Control	18.5747	3.5266	1.17262				
17670	8130803	AK12120 // L0C01286 // hypothetical LOC401286 // 6q21 // 401286 // ENST000003	LOC401286	AK12120	0.0162537	0.0162537	0.433391	-2.3079	VN down vs Control	9.19453	3.49215	3.03846					
133076	8130976	AK12120 // L0C01286 // hypothetical LOC401286 // 6q21 // 401286 // ENST000003	LOC401286	AK12120	0.0162537	0.0162537	0.433391	-2.3079	VN down vs Control	9.19453	3.49215	3.03846					
4758	8020016	LOC100136 // hypothetical LOC100136 // 11p15.5 // 5187 // EN	LOC100136	8020016	0.0084064	0.0084064	0.433641	-2.3079	VN down vs Control	6.85613	3.47772	3.01851					
12667	7966839	NM_019086 // LOC100136 // hypothetical LOC100136 // 11p15.5 // 5187 // EN	LOC100136	NM_019086	0.0083203	0.0083203	0.434361	-2.3075	VN down vs Control	12.1101	3.46813	3.02046					
13369	7988812	NM_015347 // TMEM86A // transmembrane protein 86A // 11p15.1 // 144110 // ENST0	TMEM86A	NM_015347	0.00714495	0.00714495	0.434986	-2.2989	VN down vs Control	12.8642	3.46153	3.15568					
83466	7987180	NM_024713 // C15orf29 // chromosome 15 open reading frame 29 // 15q14 // 79768 //	C15orf29	NM_024713	0.00714495	0.00714495	0.437024	-2.2882	VN down vs Control	16.1122	3.42277	3.07862					
1568	8012349	NM_02516 // PRL1 // period homolog 1 (Drosophila) // 17q11.1 // 42 // 5187 // EN	PRL1	NM_02516	0.0126263	0.0126263	0.437024	-2.2979	VN down vs Control	6.29232	3.42178	3.07945					
17768	8032804	NM_030025 // SH3GL1 // SH3 domain GRB2-like 1 // 19p13.3 // 6455 // ENST0000026	SH3GL1	NM_030025	0.0120461	0.0120461	0.437171	-2.2873	VN down vs Control	10.4168	3.41997	2.62147					
4059854	NM_05737	ARLAC // ADP-ribosylation factor-like 4C // 2q37.1 // 10123 // ENS	ARLAC	NM_05737	0.0119385	0.0119385	0.437488	-2.2857	VN down vs Control	10.4755	3.41398	2.62147					
4199	898725	---	---	---	---	0.0213948	0.0213948	0.437955	-2.2834	VN down vs Control	8.17078	3.40557	3.3482				
8196	7937443	NM_027772 // PPS2B // PPS2-like 2 // 11p15.5 // 64787 // ENST00000318562 // EP	PPS2B	NM_027772	0.0004676	0.0004676	0.437978	-2.2832	VN down vs Control	15.0415	3.40475	3.18085					
15058	8005638	NM_010330 // ALDH3A2 // aldehyde dehydrogenase 3 family, member A2 // 17q11.1	ALDH3A2	NM_010330	0.0024486	0.0024486	0.438	-2.2814	VN down vs Control	14.8317	3.3987	3.14756					
13447	7985851	NM_014701 // SEC5BP2 // SEC5 binding protein 2-like // 15q21.1 // 9728 // EN	SEC5BP2	NM_014701	0.0149586	0.0149586	0.438408	-2.2808	VN down vs Control	9.52923	3.39667	2.85158					
8044031	NM_023016 // ANKRD57 // ankyrin repeat domain 57 // 2q13 // 65124 // ENST000003	ANKRD57	NM_023016	0.0009388	0.0009388	0.438577	-2.2798	VN down vs Control	11.6984	3.3916	3.13936						
789479	---	---	---	---	---	0.0009388	0.0009388	0.438577	-2.2798	VN down vs Control	11.6984	3.3916	3.13936				
8103	7936463	NM_020313 // ABLM1 // actin binding LIM protein 1 // 10q25 // 3983 // NM_00100	ABLM1	NM_020313	0.0008659	0.0008659	0.439463	-2.2751	VN down vs Control	7.26117	3.3769	3.10164					
8354	7938687	NM_05113 // NUCB2 // nucleobindin 2 // 11q15.1 // 4925 // ENST0000032888	NUCB2	NM_05113	0.0277991	0.0277991	0.439664	-2.2747	VN down vs Control	26.019	3.37314	3.74694					
7528	7930276	NM_014720 // SKL1 // STK20-like kinase (yeast) // 10q24.3 // 9748 // ENST000003	SKL	NM_014720	0.0013564	0.0013564	0.440003	-2.2729	VN down vs Control	13.249	3.36682	3.16765					
12740	8027604	NM_014686 // KIAA0355 // KIAA0355 // 19q13.11 // 9710 // ENST00000299505 // KIA	KIAA0355	NM_014686	0.00914832	0.00914832	0.440609	-2.2699	VN down vs Control	11.6657	3.3554	3.20112					
2896	8114120	NM_05221 // DUX5 // distal-less homolog 5 // 7q22 // 1749 // ENST0000022598	DUX5	NM_05221	0.042318	0.042318	0.442354	-2.2603	VN down vs Control	5.81366	3.32025	4.5703					
1920	7952249	NM_04025 // USP2 // ubiquitin specific peptidase 2 // 11q23 // 9099 // NM_17	USP2	NM_04025	0.048928	0.048928	0.442487	-2.2595	VN down vs Control	5.41462	3.3208	4.90245					
8036812	NM_02307	GCAL57 // lectin, galactose-binding, soluble 7 // 19q13.2 // 398	GCAL57	NM_02307	0.0042307	0.0042307	0.442732	-2.2574	VN down vs Control	10.4714	3.3157	3.27242					
81627	8163149	NM_02829 // PTPN3 // protein tyrosine phosphatase, non-receptor type 3 // 9q31	PTPN3	NM_02829	0.0114674	0.0114674	0.443006	-2.2575	VN down vs Control	10.6503	3.31126	4.90245					
19340	8047854	NM_01142300 // CENPL // cyclin Y-like 1 // 2q33.3 // 151195 // NM_152523 // C	CENPL	NM_01142300	0.0013624	0.0013624	0.443539	-2.2549	VN down vs Control	19.9517	3.30148	4.66373					
8018579	NM_01988	EVL // evoviolanin // 7q25 // 2125 // ENST00000301007 // EVL //	EVL	NM_01988	0.0027902	0.0027902	0.444393	-2.2506	VN down vs Control	18.0624	3.28588	3.5573					
12092	807541	LOC100136 // hypothetical LOC100136 // 11p15.5 // 5187 // EN	LOC100136	807541	0.0027902	0.0027902	0.444393	-2.2506	VN down vs Control	18.0624	3.28588	3.5573					
18233	8034909	NM_02518 // NPAS2 // neuronal PAS domain protein 2 // 2q12.1 // 4822 // ENST0	NPAS2	NM_02518	0.019037	0.019037	0.445683	-2.2475	VN down vs Control	8.57708	3.26243	3.04764					
28920	8038390	NM_00882 // IL12A // interleukin 12 (natural killer cell stimulatory factor 1,	IL12A	NM_00882	0.0259094	0.0259094	0.447021	-2.2370	VN down vs Control	7.55803	3.23828	3.42724					
20114	805568	NM_02159 // C22orf41 // chromosome 22 open reading frame 41 // 19q13.1 // 5885 //	C22orf41	NM_02159	0.047021	0.047021	0.447021	-2.2368	VN down vs Control	10.4745	3.23772	4.06292					
24730	8102518	NM_00101701 // C6orf3 // chromosome 4 open reading frame 3 // 4q26 // 401512 //	C6orf3	NM_00101701	0.0113787	0.0113787	0.447125	-2.2365	VN down vs Control	10.6842	3.2364	2.42331					
9009	7944931	NM_198277 // SLC37A2 // solute carrier family 37 (dyeroid-3-phosphate transport	SLC37A2	NM_198277	0.0253207	0.0253207	0.4476	-2.2344	VN down vs Control	7.52556	3.22788	3.43138					
1910	7936439	NM_00101936 // ARAF1 // aryl hydrocarbon receptor associated protein 1-like 2 // 10q25.3	ARAF1	NM_00101936	0.0079925	0.0079925	0.447771	-2.2329	VN down vs Control	12.3015	3.22481	2.97818					
5103	8195485	NM_03125 // SPRB1 // small proline-rich protein 18 (cornifin) // 1q21-q21.1 // 6	SPRB1	NM_03125	0.0478343	0.0478343	0.448143	-2.2329	VN down vs Control	6.19335	3.22292	3.19345					
28884	8122856	---	---	---	---	0.0124517	0.0124517	0.448072	-2.2317	VN down vs Control	10.4722	3.2194	2.5018				
8035	8155048	NM_01806 // RUSC2 // RUN and SH3 domain containing 2 // 9q13.3 // 9853 // NM_0	RUSC2	NM_01806	0.012259	0.012259	0.44932	-2.2254	VN down vs Control	7.9079	3.19648	3.22193					
792020	NM_05891	PCVPR9 // phosphatidylinositol recognition protein 9 // 1q21 // 14774 //	PCVPR9	NM_05891	0.0113322	0.0113322	0.44957	-2.2259	VN down vs Control	10.7833	3.19537	3.27127					
929747	NM_024951	DFEF6 // zinc finger protein 365 // 10q21.1 // 2398 // NM_190453	DFEF6	NM_024951	0.004965	0.004965	0.450243	-2.2243	VN down vs Control	10.243	3.19322	3.22322					
44691	7901497	NM_01004339 // ZYG11A // zyg-11 homolog (C. elegans) // 1q23.3 // 40590 // S	ZYG11A	NM_01004339	0.0054851	0.0054851	0.449642	-2.2240	VN down vs Control	14.1947	3.19159	3.79873					
24885	8100231	NM_03215 // TCC1 // test protein tyrosine kinase // 4p12 // 7006 // ENST00000381	TCC1	NM_03215	0.016102	0.016102	0.449899	-2.2228	VN down vs Control	9.25334	3.1826	2.75383					
5881	8013258	NM_022841 // IZ2F41 // interdigitin 22 receptor, alpha 1 // 19q13.1 // 5885 //	IZ2F41	NM_022841	0.0121289	0.0121289	0.45077	-2.2228	VN down vs Control	6.85095	3.17144	2.8212					
31061	8164217	NM_028283 // FAM129B // family with sequence similarity 129, member B // 9q33.3	FAM129B	NM_028283	0.0147105	0.0147105	0.451558	-2.2146	VN down vs Control	9.95754	3.15858	2.63318					
8152453	NM_014112 // TRPS1 // trichorhinalphalangecty syndrome 1 // 8q24.12 // 7227 // EN	TRPS1	NM_014112	0.0072574	0.0072574	0.451656	-2.2147	VN down vs Control	12.7693	3.15583	3.9713						
8005469	NM_01004272 // ABHD12 // abhydrolase domain containing 12 // 20p12.1 // 26900	ABHD12	NM_01004272	0.00335833	0.00335833	0.451989	-2.2124	VN down vs Control	16.6495	3.14998	3.48678						
277	8131475	NM_02516 // C12orf41 // chromosome 12 open reading frame 41 // 12q13.1 // 200	C12orf41	NM_02516	0.0026461	0.0026461	0.452086	-2.2123	VN down vs Control	10.123	3.14806	3.14806					
1005	7954527	NM_001813 // ARNTL2 // aryl hydrocarbon receptor nuclear translocator-like 2 //	ARNTL2	NM_001813	0.011428	0.011428	0.452068	-2.2106	VN down vs Control	16.9643	3.1466	3.16714					
31061	8165334	NM_004669 // CLIC3 // chloride intracellular channel 3 // 9q34.3 // 9022 // ENS	CLIC3	NM_004669	0.0207266	0.0207266	0.452193	-2.2115	VN down vs Control	8.25532	3.14641	3.90491					
27999	8133176	NM_015404 // RABGF1 // RAB guanine nucleotide exchange factor (GEP) 1 // 7q11.2	RABGF1	NM_015404	0.00540897	0.00540897	0.452474	-2.2107	VN down vs Control	14.268	3.1447	3.74161					
26912	8014200	NM_024040 // RAB11B // Rab11 protein, cytosolic (ribonucleoside triphosphate-de	RAB11B	NM_024040	0.0029676	0.0029676	0.452676	-2.2107	VN down vs Control	10.4734	3.1318	3.90028					
15317	8007976	NM_006310 // NPEPP3 // aminopeptidase puromycin sensitive // 17q21 // 9520 // I	NPEPP3	NM_006310	0.00533691	0.00533691	0.453252	-2.2028	VN down vs Control	14.3391	3.12788	3.74161					
21231	8076233	NM_06139 // SNORD43 // small nuclear RNA, C/D box 43 // 21q13 // 28807 // I	SNORD43	NM_06139	0.00800263	0.00800263	0.453454	-2.2053	VN down vs Control	12.9255	3.12437	2.02286					
21759	8072539	NR_024914 // TOM1 // target of mitl (chicken) // 22q13.1 // 10044 // NM_05488	TOM1	NR_024914	0.0066943	0.0066943	0.453549	-2.2043	VN down vs Control	11.17	3.1227	3.86869					
7990	8005834	NM_02889 // SHROOM3 // shroom family protein 3 // 4q21.1 // 5769 // ENST000002	SHROOM														

Column #	Transcript	Cluster ID	gene_assignment	Gene Symbol	RefSeq	p-value(Gene)	p-value(VA vs Control)	Ratio(VA vs Control)	Fold-Change(VA vs Control)	Fold-Change(VA vs Control)	Description	(fGene)	(SSGene)	(SEError)	(fError)
1144	7966035	NM_006825	CKAP4 // cytoskeleton-associated protein 4 [12a32.3] / 10970 [10]	CKAP4	NM_006825	0.00425317	0.00425317	0.490825	-2.03739	VM down vs Control	15.2362	2.52997	1.92844	1	
21658	8071649	BC043345	BMS1 // BMS1 homolog, ribosome assembly protein (yeast) // 10q11.21	BMS1	BC043345	0.00176906	0.00176906	0.491267	-2.03555	VM down vs Control	21.1057	2.52357	3.05644	1	
26144	8115918	nm_007067	CLTB // clathrin, light chain (Lc3) // 4q24-q31S6p3 // 12q11 [NM 007067]	CLTB	nm_007067	0.00871037	0.00871037	0.482573	-2.03515	VM down vs Control	11.6544	2.50475	1.71957	1	
29849	8150575	U04781	RLC1 // RLC1-inducible coiled-coil 1 // 8q21.31-q11.4 // 12q10.2	RLC1	U04781	0.00427171	0.00427171	0.482877	-2.03515	VM down vs Control	7.60529	2.48271	1.61338	1	
24546	8100655	nm_000496	GNRH1R // gonadotropin-releasing hormone receptor // 4q21.12 // 2798	GNRH1R	nm_000496	0.0124669	0.0124669	0.483606	-2.02991	VM down vs Control	10.2895	2.48996	1.93593	1	
22396	8079149	---	---	---	---	0.0184549	0.0184549	0.483983	-2.02497	VM down vs Control	8.86639	2.48671	2.28758	1	
22112	8078273	NM_005106	NR1D2 // nuclear receptor subfamily 1, group D, member 2 // 3q24.2	NR1D2	NM_005106	0.00176544	0.00176544	0.484078	-2.02739	VM down vs Control	7.60529	2.48271	1.61338	1	
1728	7927280	NM_005972	PPYR1 // pancreatic polypeptide receptor 1 // 10q11.2 // 5540 [1]	PPYR1	NM_005972	0.0205353	0.0205353	0.484501	-2.02224	VM down vs Control	8.29006	2.47719	2.30052	1	
9228	8046726	NM_00130445	SFS2 // sperm specific antigen 2 // 2a3.3 / 6744 [1] / NM 00675	SFS2	NM_00130445	0.0010882	0.0010882	0.484564	-2.02198	VM down vs Control	24.7766	2.47629	8.80852	1	
18347	808774	1A4055	NR1H3 // nuclear receptor subfamily 1, group D, member 3 // 12q10.2	NR1H3	1A4055	0.00502168	0.00502168	0.485028	-2.02019	VM down vs Control	5.9206	2.47004	3.3505	1	
10485	7959070	NM_002567	PEBP1 // phosphatidylethanolamine binding protein 1 // 12q24.23 [1]	PEBP1	NM_002567	0.020314	0.020314	0.486796	-2.01929	VM down vs Control	8.30375	2.44473	2.34767	1	
9068	7945503	U01088	DEAF1 // deformed epidermal autoregulatory factor 1 (Drosophila) [1]	DEAF1	U01088	0.0291426	0.0291426	0.496872	-2.01259	VM down vs Control	7.5828	2.44366	2.77856	1	
1271	7893774	---	---	---	---	0.00636051	0.00636051	0.497108	-2.01163	VM down vs Control	13.6952	2.44034	1.42551	1	
26857	8122343	NM_016217	HECA // heparanase (lysosomal) [1] 6q23-q24 // 5196 // ENST	HECA	NM_016217	0.00134627	0.00134627	0.497966	-2.00817	VM down vs Control	9.95759	2.42881	1.9474	1	
15223	7979698	NM_015994	ATP5V1 // ATPase, H+ transporting, lysosomal 340Da, V1 subunit D [1]	ATP5V1	NM_015994	0.0181552	0.0181552	0.498611	-2.00557	VM down vs Control	8.75967	2.4193	2.20949	1	
16473	8020183	NM_014214	IMPA2 // inositol(1-myo)-1-or-4-monomethylphosphate 2 // 18p11.2 // 3613	IMPA2	NM_014214	0.00902053	0.00902053	0.498838	-2.00466	VM down vs Control	11.7309	2.41614	1.6477	1	
8071651	004327	BCR // BCR // immunoglobulin constant region // 22q11.22q11.23 // 11q23 [1] / NM 021	BCR	NM_004327	0.01247498	0.01247498	0.499298	-2.00288	VM down vs Control	10.0251	2.40974	1.97436	1		
30301	8154872	NM_016825	UBAP1 // ubiquitin associated protein 1 // 9q13.3 // 52173 [ENST]	UBAP1	NM_016825	0.01305243	0.01305243	0.499524	-2.00003	VM down vs Control	10.0684	2.40105	1.90276	1	
20255	8057744	NM_007115	STAT1 // signal transducer and activator of transcription 1, 91kDa	STAT1	NM_007115	0.01823	0.01823	0.50179	-2.0019	VM up vs Control	8.74377	2.40658	2.20187	1	
30881	8160146	NM_00101915	PTRFAD2 // protein tyrosine phosphatase-like A domain containing	PTRFAD2	NM_00101915	0.0431518	0.0431518	0.502028	-2.00008	VM up vs Control	2.76178	2.40721	1.34421	1	
92164	7947378	NM_002725	FANCF // Fanconi anemia, complementation group F // 11p15.1 // 2188 [1]	FANCF	NM_002725	0.0425027	0.0425027	0.503	-2.002	VM up vs Control	5.8085	2.40939	3.35051	1	
559	7893061	---	---	---	---	0.0383688	0.0383688	0.50328	-2.00328	VM up vs Control	6.12902	2.4115	1.34745	1	
10266	7956613	NM_005981	TSPAN31 // tetraspanin 31 // 12q13.3 // 6302 [1] / ENST00000257910 [1]	TSPAN31	NM_005981	0.00654914	0.00654914	0.500428	-2.00405	VM up vs Control	13.2901	2.41402	1.45421	1	
30326	8155192	NM_021343	GLP2R // Glu2-pituitary-related 2 // 9p13-p12 // 152007 [1] / NM 021343	GLP2R	NM_021343	0.0287269	0.0287269	0.500462	-2.00462	VM up vs Control	7.08497	2.41401	2.72804	1	
1111	7966049	NM_011423	MLML1 // chromatin-like factor 1 // 12q24.1 // 1240 [1] / NM 02183	MLML1	NM_011423	0.005607	0.005607	0.500507	-2.00507	VM up vs Control	7.42822	2.41755	1.67387	1	
30304	8180078	NM_002118	HMB-DMB // major histocompatibility complex, class II, DM beta [1] / 6	HMB-DMB	NM_002118	0.0268575	0.0268575	0.500511	-2.00531	VM up vs Control	7.31803	2.41839	2.64375	1	
3867	8178188	NR_001329	RNF5P1 // ring finger protein 5 pseudogene 1 // 10p11.2 // 286140 [1]	RNF5P1	NR_001329	0.00011231	0.00011231	0.500554	-2.00554	VM up vs Control	44.1888	2.4192	4.037975	1	
384	7892884	---	---	---	---	0.0250106	0.0250106	0.50056	-2.00556	VM up vs Control	7.58937	2.41925	2.55689	1	
8071652	001834	RNF130 // ring finger protein 130 // 5a3.5 // 55815 [1] / ENST000002	RNF130	NM_01834	0.001424	0.001424	0.50072	-2.00726	VM up vs Control	2.0079	2.42094	2.79642	1		
13400	7969081	NM_201524	GRP56 // G-protein-coupled receptor 56 // 16q12.2-q21 // 9289 [1] / NM 201524	GRP56	NM_201524	0.0269424	0.0269424	0.50059	-2.00959	VM up vs Control	7.30701	2.42326	2.66402	1	
24304	8088848	NM_015009	P2X domain containing ring finger 3 // 3q13 // 23024 [1]	P2XDN3	NM_015009	0.0348187	0.0348187	0.501199	-2.01199	VM up vs Control	6.50183	2.44156	3.00415	1	
8125239	002118	HMB-DMB // major histocompatibility complex, class II, DM beta [1] / 6	HMB-DMB	NM_002118	0.0268575	0.0268575	0.500511	-2.00531	VM up vs Control	7.31803	2.41839	2.64375	1		
6664	7921637	NM_003874	CDB4 // CDB4 molecule // 1q24 // 882 [1] / ENST00000380524 // CDB4	CDB4	NM_003874	0.024248	0.024248	0.501506	-2.01506	VM up vs Control	8.39112	2.45224	2.14263	1	
11073	7956335	NM_001946	DUSP6 // dual specificity phosphatase 6 // 12q22-q23 // 1848 [1] / NM 1946	DUSP6	NM_001946	0.0157361	0.0157361	0.50155	-2.0155	VM up vs Control	9.32414	2.45375	2.1029	1	
1756	7894264	---	---	---	---	0.00219407	0.00219407	0.501972	-2.01782	VM up vs Control	19.6338	2.46181	1.90309	1	
10814	7962174	15320	ZNF41 // zinc finger protein 41 // 12q13.31 // 121274 [1] / ENST000	ZNF41	15320	0.0012947	0.0012947	0.501913	-2.01913	VM up vs Control	2.00923	2.46388	1.90309	1	
14922	800184	NM_017523	XAF1 // XAP associated factor 1 // 17p13.1 // 54739 [1] / NM 17523	XAF1	NM_017523	0.0206948	0.0206948	0.501975	-2.01975	VM up vs Control	8.21066	2.46853	2.30052	1	
20617	8061564	NM_181353	HD1 // inhibitor of DNA binding 1, dominant negative helix-loop-hel	HD1	NM_181353	0.0118244	0.0118244	0.50218	-2.02238	VM up vs Control	10.157	2.47769	1.88471	1	
1814010	002198	HMB-DMB // major histocompatibility complex, class II, DM beta [1] / 6	HMB-DMB	NM_002198	0.0268575	0.0268575	0.500511	-2.00531	VM up vs Control	7.31803	2.41839	2.64375	1		
7969189	001870	ORAM1 // ORN domain related autophagy modulator 1 // 12q24.1 // 59	ORAM1	1870	0.001423	0.001423	0.502474	-2.02474	VM up vs Control	1.8784	2.47964	1.97169	1		
29769	8150014	NM_018250	INTS9 // integrator complex subunit 9 // 8q21.1 // 55756 // NM 001	INTS9	NM_018250	0.0215555	0.0215555	0.502509	-2.02509	VM up vs Control	8.57933	2.48709	2.45556	1	
8040365	001643	TRIB2 // tribbles homolog 2 (Drosophila) // 2a3.3 // 28951 [1] / NR	TRIB2	NM_01643	0.043297	0.043297	0.502521	-2.02511	VM up vs Control	10.1934	2.48719	3.45364	1		
8142459	012522	TRAF1 // TNF receptor associated factor 1 // 7q31.3 // 2279 [1] / NM 00101805	TRAF1	12522	0.002625	0.002625	0.502525	-2.02525	VM up vs Control	8.3912	2.48705	2.37158	1		
5177	8159104	NM_001417	FUCAL // fucosylase, alpha-L, tissue 4 // 10q24.1 // 2517 [1] / ENST000	FUCAL	NM_001417	0.00730134	0.00730134	0.502565	-2.02565	VM up vs Control	12.7397	2.48907	1.56302	1	
4865	789691	---	---	---	---	0.0265919	0.0265919	0.502595	-2.02595	VM up vs Control	7.3528	2.49012	2.7093	1	
20087	8078886	NM_000878	IL2RB // interleukin 2 receptor, beta // 22q13.22q13.1 // 3560 [1]	IL2RB	NM_000878	0.0265919	0.0265919	0.502595	-2.02595	VM up vs Control	7.3528	2.49012	2.7093	1	
14512	8002036	NM_015044	ARL1 // Arp2/3 complex, Arp1 binding domain containing 1 // 12q24.1 // 1240 [1] / NM 02183	ARL1	NM_015044	0.005607	0.005607	0.500507	-2.00507	VM up vs Control	7.42822	2.41755	1.67387	1	
905	7945666	NM_003978	CTSD // cathepsin D // 11p15.5 // 5059 [1] / ENST0000236671 [1] / CTSD	CTSD	NM_003978	0.00375307	0.00375307	0.502697	-2.02697	VM up vs Control	16.2947	2.49367	1.22428	1	
15185	8006239	NM_0104492	NF1 // neurofibromin 1 // 17q12.1 // 4763 [1] / NM 000267 [NF1]	NF1	NM_0104492	0.042514	0.042514	0.502731	-2.02731	VM up vs Control	5.80768	2.49482	3.43659	1	
22787	8083872	NM_004293	GLP2R // Glu2-pituitary-related 2 // 9p13-p12 // 152007 [1] / NM 021343	GLP2R	NM_004293	0.0054903	0.0054903	0.502781	-2.02781	VM up vs Control	10.86216	2.49657	1.2016	1	
2891	8143869	NM_01528	AP3B1 // adaptor protein 3B1 // 12q24.1 // 1240 [1] / NM 02183	AP3B1	NM_01528	0.001628	0.001628	0.502782	-2.02782	VM up vs Control	7.42822	2.41755	1.67387	1	
11063	8073081	NM_145298	APOR3C // apolipoprotein B mRNA editing enzyme, catalytic polypep	APOR3C	NM_145298	1.82E-05	1.82E-05	0.503186	-2.03186	VM up vs Control	81.3682	2.5107	2.64848	1	
21869	7961059	NM_002258	KLHL1 // killer cell lectin-like receptor subfamily B, member 1 // 1	KLHL1	NM_002258	0.0414694	0.0414694	0.503234	-2.03234	VM up vs Control	5.88478	2.51237	3.41541	1	
26055	8115076	NM_005211	CSF1R // colony stimulating factor 1 receptor // 5q33-q35 // 1436 [1]	CSF1R	NM_005211	0.00977723	0.00977723	0.503	-2.03	VM up vs Control	11.8608	2.51465	1.97978	1	
26078	8082100	NM_017954	POU4F1 // POU domain, class 4, transcription factor 1 // 3q21.3 // 2433.1	POU4F1	NM_017954	0.0036446	0.0036446	0.503236	-2.03236	VM up vs Control	7.23664	2.52255	1.93398	1	
7892454	---	---	---	---	---	0.0166736	0.0166736	0.503669	-2.03669	VM up vs Control	21.5247	2.52753	2.93938	1	
24672	8082035	NM_17862	CDB6 // CDB6 molecule // 3q21 // 942 [1] / NM 006889 // CDB6 // CDB6	CDB6	NM_17862	0.0127732	0.0127732	0.503688	-2.03688	VM up vs Control	10.1861	2.52821	1.98561	1	
6486	7918298	NM_018716	USL2 // USL2 // UAG1 homolog, ceramide synthase 2 // 1q21.3 // 29956 [1] / NM 18716	USL2	NM_018716	0.005451	0.005451	0.503764	-2.03764	VM up vs Control	14.744	2.52488	1.97978	1</	

Column #	Transcript	Cluster ID	gene_assignment	Gene Symbol	RefSeq	p-value(Gene)	p-value(VA vs. Control)	Ratio(VA vs. Control)	Fold Change(VA vs. Control)	Fold Change(VA vs. Control)	Fold Change(VA vs. Control)	Description	(fGene)	(SSGene)	(SSError)	(fError)
8573	7904979	NM 0164905	TMEM116 // transmembrane protein 216 // 11a13.1 // 51259 // ENST00	TMEM116	NM 0164905	0.0044832	0.0043462	2.15378	2.15378	2.15378	2.15378	2.15378	15.4556	2.94041	1.52198	1.80
22828	8083673	NM 01042706	ICI // ICI motif containing 1 // 3a25.32 // 654502 // NM 01042706	ICI	NM 01042706	0.0039316	0.0039316	2.1546	2.1546	2.1546	2.1546	2.1546	16.8904	2.94332	1.39408	1.80
4174	7896700	---	---	---	---	0.0171367	0.0171367	2.15547	2.15547	2.15547	2.15547	2.15547	8.96505	2.9464	2.62338	1.80
23702	8092176	NM 021101	CLDN4 // claudin 11 // 3a28-a29 // 9076 // ENST000029552 // CLDN1	CLDN1	NM 021101	0.0045695	0.0045695	2.15591	2.15591	2.15591	2.15591	2.15591	15.0582	2.94798	1.56362	1.80
16100	8016387	NM 021300	ATAD4 // ATPase family AAA domain containing 4 // 17a21.32 // 7917	ATAD4	NM 021300	0.0024217	0.0024217	2.15629	2.15629	2.15629	2.15629	2.15629	18.9851	2.94933	1.2428	1.80
2182	8125556	NM 033554	HLA-DPA1 // major histocompatibility complex, class II, DP alpha 1	HLA-DPA1	NM 033554	0.020777	0.020777	2.15692	2.15692	2.15692	2.15692	2.15692	8.24623	2.95156	2.86343	1.80
8178844	NM 033554	HLA-DPA1 // major histocompatibility complex, class II, DP alpha 1	HLA-DPA1	NM 033554	0.020777	0.020777	2.15692	2.15692	2.15692	2.15692	2.15692	2.15692	8.24623	2.95156	2.86343	1.80
4172	7896718	---	---	---	---	0.0015894	0.0015894	2.15705	2.15705	2.15705	2.15705	2.15705	15.0582	2.95195	2.92195	1.80
29713	8149448	NM 020445	MSR1 // macrophage scavenger receptor 1 // 8a22 // 4481 // NM 1387	MSR1	NM 020445	0.00031686	0.00031686	2.15924	2.15924	2.15924	2.15924	2.15924	34.8117	2.95983	0.68191	1.80
1552	7894057	---	---	---	---	0.0082893	0.0082893	2.16423	2.16423	2.16423	2.16423	2.16423	12.1278	2.97716	1.96415	1.80
4162	7896688	---	---	---	---	0.0028982	0.0028982	2.20383	2.20383	2.20383	2.20383	2.20383	8.66368	2.97796	2.76815	1.80
10467	7958884	NM 016816	OAS1 // 2',5'-oligoadenylate synthetase 1, 40kDa // 12a24.1 // 4	OAS1	NM 016816	0.0072137	0.0072137	2.16553	2.16553	2.16553	2.16553	2.16553	12.7972	2.98225	1.86431	1.80
7942824	NM 010013	RP528 // ribosomal protein S28 // 19s13.2 // 6234 // ENST000004170	RP528	NM 010013	0.0031795	0.0031795	2.16574	2.16574	2.16574	2.16574	2.16574	2.16574	17.2823	2.98299	1.38115	1.80
20880	8064388	NM 039409	CCZorf54 // chromosome 20 open reading frame 54 // 20a13 // 133278	CCZorf54	NM 039409	0.0120532	0.0120532	2.16657	2.16657	2.16657	2.16657	2.16657	10.2443	2.98597	2.28396	1.80
4875	7903507	NM 00110883	FAM102B // sequence similarity 102, member B // 9 // 1a13	FAM102B	NM 00110883	0.0045315	0.0045315	2.17015	2.17015	2.17015	2.17015	2.17015	15.0266	2.99871	1.75552	1.80
20314	8078286	NM 009695	RARB // retinoic acid receptor, beta // 3a24 // 5915 // NM 016152	RARB	NM 009695	0.0130231	0.0130231	2.17038	2.17038	2.17038	2.17038	2.17038	10.1041	2.99954	2.37491	1.80
8053484	NM 003896	STG3A15 // ST beta-galactosidase alpha-2, sialyltransferase 5 // 2a	STG3A15	NM 003896	0.0189996	0.0189996	2.1705	2.1705	2.1705	2.1705	2.1705	2.1705	8.5846	2.99955	2.75666	1.80
7904287	NM 017607	CD2 // CD2 molecule // 1a13.1 // 914 // ENST0000369478 // CD2 //	CD2	NM 017607	0.0177323	0.0177323	2.17173	2.17173	2.17173	2.17173	2.17173	2.17173	5.50091	3.024	4.39391	1.80
128610	8081431	NM 004527	ALCAM // activated leukocyte cell adhesion molecule // 3a13.1 // 21	ALCAM	NM 004527	0.0145844	0.0145844	2.18036	2.18036	2.18036	2.18036	2.18036	9.63281	3.03517	2.52069	1.80
21122	7965812	NM 024312	GNPATB // N-acetylglucosamine 1-phosphate transferase, alpha and beta	GNPATB	NM 024312	0.0305858	0.0305858	2.18147	2.18147	2.18147	2.18147	2.18147	15.3913	3.03912	3.53822	1.80
8057079	NM 030643	APOLA // apolipoprotein L // 22a11.1-a13.2 // 80832 // NM 14566	APOLA	NM 030643	0.0072819	0.0072819	2.18154	2.18154	2.18154	2.18154	2.18154	2.18154	12.7526	3.03936	1.90665	1.80
1549	7904954	---	---	---	---	0.0071262	0.0071262	2.18282	2.18282	2.18282	2.18282	2.18282	12.6534	3.04595	1.92299	1.80
21465	8067040	NM 012340	NFATC2 // nuclear factor of activated T-cells, cytoplasmic, calcine	NFATC2	NM 012340	0.00194501	0.00194501	2.18293	2.18293	2.18293	2.18293	2.18293	20.4476	3.04443	1.91047	1.80
8048717	NM 152386	SGP2 // sphingosine 1-phosphate phosphatase 2 // 2a36.1 // 130367	SGP2	NM 152386	0.0368815	0.0368815	2.18303	2.18303	2.18303	2.18303	2.18303	2.18303	6.24658	3.05184	3.90849	1.80
8203	7937508	NM 004357	CD151 // CD151 molecule (Raph blood group) // 11a15.5 // 977 // NM 1	CD151	NM 004357	0.0097278	0.0097278	2.18374	2.18374	2.18374	2.18374	2.18374	6.9628	3.05438	3.50937	1.80
8045148	NM 172111	STON1 // STON1, CTF2A1L, readthrough transcript // 2a13.3 // 21	STON1	NM 172111	0.0014278	0.0014278	2.18379	2.18379	2.18379	2.18379	2.18379	2.18379	15.0582	3.05438	2.82762	1.80
7942569	NM 00114521	SLOC2B1 // solute carrier organic anion transporter family, mem	SLOC2B1	NM 00114521	0.0097039	0.0097039	2.18638	2.18638	2.18638	2.18638	2.18638	2.18638	11.3951	3.05666	1.51495	1.80
11072	7964701	NM 002076	GNS // glucosamine (N-acetyl)-6-sulfatase // 12a14 // 2799 // ENST	GNS	NM 002076	0.0050486	0.0050486	2.18721	2.18721	2.18721	2.18721	2.18721	14.6362	3.05965	1.67238	1.80
8025295	NM 010013	RP528 // ribosomal protein S28 // 19s13.2 // 6234 // ENST000004170	RP528	NM 010013	0.0028983	0.0028983	2.18826	2.18826	2.18826	2.18826	2.18826	2.18826	17.85	3.06338	1.37295	1.80
7904954	---	---	---	---	---	0.0089717	0.0089717	2.18857	2.18857	2.18857	2.18857	2.18857	10.6452	3.0645	6.90752	1.80
7924029	NM 00107402	LAMB3 // laminin, beta 3 // 1a32 // 3914 // NM 00112764 // LAM	LAMB3	NM 00107402	0.0084207	0.0084207	2.18909	2.18909	2.18909	2.18909	2.18909	2.18909	11.3067	3.06634	2.16477	1.80
9619	7950391	NM 173582	PGCMB1 // phosphoglucomutase 2-like 1 // 11a13.4 // 28209 // ENST	PGCMB1	NM 173582	0.0092729	0.0092729	2.19259	2.19259	2.19259	2.19259	2.19259	11.6033	3.07886	2.12274	1.80
8102133	NM 000538	TGFB // transforming growth factor, beta // 10a10.6 // 5a33 // 1	TGFB	NM 000538	0.0059154	0.0059154	2.19287	2.19287	2.19287	2.19287	2.19287	2.19287	30.6161	3.17324	0.82767	1.80
6095	7915955	NM 19073	SPN7A // spermatogenesis associated 6 // 1a33 // 5455 // ENST00000	SPN7A	NM 19073	0.0205531	0.0205531	2.20084	2.20084	2.20084	2.20084	2.20084	8.2868	3.1084	3.0003	1.80
7919800	NM 040979	CTSS // cathepsin S // 1a24 // 1520 // ENST000036888 // CTSS //	CTSS	NM 040979	0.010365	0.010365	2.20215	2.20215	2.20215	2.20215	2.20215	2.20215	11.0973	3.1131	2.24423	1.80
28301	8136849	NM 01143769	GSTK1 // glutathione S-transferase kappa 1 // 7a35 // 371356 // EN	GSTK1	NM 01143769	0.0270425	0.0270425	2.20338	2.20338	2.20338	2.20338	2.20338	7.29407	3.11751	3.14324	1.80
8078388	NM 01822	APOLC1 // apolipoprotein L1 mRNA editing enzyme, catalytic subp	APOLC1	NM 01822	0.0028983	0.0028983	2.20395	2.20395	2.20395	2.20395	2.20395	2.20395	12.6534	3.11953	2.72366	1.80
7959267	NM 020560	PRRX4 // purinergic receptor P2X, ligand-gated ion channel, 4 // 12	PRRX4	NM 020560	0.0024625	0.0024625	2.20625	2.20625	2.20625	2.20625	2.20625	2.20625	18.8924	3.12777	1.24466	1.80
80718	793251	NM 015631	TCTN3 // tectonic family member 3 // 10a21.1 // 26123 // NM 001143	TCTN3	NM 015631	0.0488102	0.0488102	2.21249	2.21249	2.21249	2.21249	2.21249	5.38905	3.15015	4.67637	1.80
8112803	NM 055779	HPH2 // HPH2, P100a NIMIC fusion partner-like 2 // 5a14.1 // 10184 //	HPH2	NM 055779	0.0123207	0.0123207	2.21312	2.21312	2.21312	2.21312	2.21312	2.21312	6.6885	3.15239	3.77052	1.80
24786	8102049	NM 003866	WPP4 // inositol polyphosphate 4-phosphatase, type II, 105kDa //	WPP4	NM 003866	0.0001402	0.0001402	2.21423	2.21423	2.21423	2.21423	2.21423	16.8448	3.15589	2.74261	1.80
6236	7917514	---	---	---	---	0.010925	0.010925	2.21453	2.21453	2.21453	2.21453	2.21453	10.8631	3.15746	3.20023	1.80
9948	7953428	NM 000616	CD4 // CD4 molecule // 12pter-1 // 920 // ENST0000011653 // CD4	CD4	NM 000616	0.0199272	0.0199272	2.21555	2.21555	2.21555	2.21555	2.21555	8.40236	3.16113	3.03547	1.80
8114528	NM 198282	TMEM173 // transmembrane protein 173 // 5a13.2 // 340061 // ENST00	TMEM173	NM 198282	0.0002551	0.0002551	2.21671	2.21671	2.21671	2.21671	2.21671	2.21671	13.6123	3.16527	1.26161	1.80
1085	7949698	---	---	---	---	0.0029819	0.0029819	2.21733	2.21733	2.21733	2.21733	2.21733	20.7612	3.1675	1.43478	1.80
7957966	NM 024655	MYBPC1 // myosin binding protein C, slow type // 12a23.2 // 4604 //	MYBPC1	NM 024655	0.0098969	0.0098969	2.21808	2.21808	2.21808	2.21808	2.21808	2.21808	14.7213	3.1702	1.72278	1.80
8255	7937802	NM 004363	CD81 // CD81 molecule // 11a15.5 // 975 // ENST000026345 // CD81	CD81	NM 004363	0.00496495	0.00496495	2.21808	2.21808	2.21808	2.21808	2.21808	30.6161	3.17324	0.82767	1.80
8044291	NM 003643	TRAF1 // TNF receptor-associated factor 1 // 11a12.1 // 1046 //	TRAF1	NM 003643	0.0049331	0.0049331	2.21927	2.21927	2.21927	2.21927	2.21927	2.21927	5.36432	3.17445	4.73497	1.80
8479	7939839	NM 028843	PTPRJ // protein tyrosine phosphatase, receptor type, j // 11a12.1 //	PTPRJ	NM 028843	0.0092331	0.0092331	2.22014	2.22014	2.22014	2.22014	2.22014	16.7478	3.17761	1.2231	1.80
24211	8097657	NM 05900	SMAD5 // SMAD family member 5 // 4a31 // 4086 // NM 001003688 // 5	SMAD5	NM 05900	0.00494518	0.00494518	2.22014	2.22014	2.22014	2.22014	2.22014	14.7478	3.17761	1.2231	1.80
15004	8005471	NM 010013	RP528 // ribosomal protein S28 // 19s13.2 // 6234 // ENST000004170	RP528	NM 010013	0.0028983	0.0028983	2.22437	2.22437	2.22437	2.22437	2.22437	16.7478	3.17761	1.2231	1.80
9619	7950391	NM 173582	PGCMB1 // phosphoglucomutase 2-like 1 // 11a13.4 // 28209 // ENST	PGCMB1	NM 173582	0.0092729	0.0092729	2.22437	2.22437	2.22437	2.22437	2.22437	16.7478	3.17761	1.2231	1.80
7942569	NM 00114521	SLOC2B1 // solute carrier organic anion transporter family, mem	SLOC2B1	NM 00114521	0.0097039	0.0097039	2.23121	2.23121	2.23121	2.23121	2.23121	2.23121	12.7526	3.18254	2.54123	1.80
6507	7919800	NM 040979	CTSS // cathepsin S // 1a24 // 1520 // ENST000036888 // CTSS //	CTSS	NM 040979	0.010365	0.010365	2.2321	2.2321	2.2321	2.2321	2.2321	8.1002	3.22454	3.15744	1.80
8129458	NM 03155	ARHGAP18 // Rho GTPase activating protein 18 // 6a22.33 // 93663 //	ARHGAP18	NM 03155	0.00775714	0.00775714	2.23538	2.23538	2.23538	2.23538	2.23					

Column #	Transcript	Cluster ID	gene_assignment	Gene Symbol	RefSeq	p-value(Gene)	p-value(VA vs Control)	Ratio(VA vs Control)	Fold-Change(VA vs Control)	Fold-Change(VA vs Control)	Description	(tGene)	(SSGene)	(SSError)	(tError)
21516	807485	NM_003355	UBA7 // ubiquitin-like modifier activating enzyme 7 // 3621 // 7318	UBA7	NM_003355	0.00237894	0.00237894	2.503	2.503	VMA vs Control	15.0101	4.20499	1.76115		
12187	7979663	NM_198886	RAB15 // RAB15, member RAS oncogene family // 14q23.3 // 376267 //	RAB15	NM_198886	0.00474392	0.00474392	2.51085	2.51085	VMA vs Control	14.9739	4.23733	2.03212		
8395	7993120	NM_002061	RNC1 // reticulocalbin-1, EF-hand calcium binding domain // 11p13.3	RNC1	NM_002061	0.0243025	0.0243025	2.51249	2.51249	VMA vs Control	7.0173	4.23975	4.03094		
16773	8023845	NM_002402	RNP2 // protein-serine/threonine phosphatase 2 // 12q24.31	RNP2	NM_002402	0.00021166	0.00021166	2.52116	2.52116	VMA vs Control	13.2641	4.27144	2.4471		
769047	NM_000161	ADM // alpha-2-macroglobulin // 12p13.3-p12.3 // 2 // ENST0000000318	ADM	NM_000161	0.00534065	0.00534065	2.52123	2.52123	VMA vs Control	14.3354	4.27175	2.3839			
26835	8122334	NM_00849 // CRLR // chemokine (C-C motif) receptor-like 1 // 3q22 // 51554 //	CRLR1	NM_00849	0.0191501	0.0191501	2.52187	2.52187	VMA vs Control	8.55444	4.27711	3.99709			
870	7893127	NM_179954	RBM3 // ribonucleoprotein family class B member 3 // 10q24.3 // 10184	RBM3	NM_179954	0.0280175	0.0280175	2.52815	2.52815	VMA vs Control	5.28254	4.28156	2.38675		
25330	NM_001176	BTN3A3 // butyrophilin, subfamily 3, member A3 // 6q21.3 // 10184	BTN3A3	NM_001176	0.0186808	0.0186808	2.54531	2.54531	VMA vs Control	14.6277	4.30002	2.02777			
3282	8180400	---	---	---	---	0.00517595	0.00517595	2.55632	2.55632	VMA vs Control	14.5623	4.30097	2.4167		
990	7893124	---	---	---	---	0.00747592	0.00747592	2.55632	2.55632	VMA vs Control	14.5623	4.30097	2.4167		
33003	8179481	NM_019111	HLA-DRA // major histocompatibility complex, class II, DR alpha //	HLA-DRA	NM_019111	0.00410436	0.00410436	2.56275	2.56275	VMA vs Control	15.781	4.24	2.427		
18748	802468	NM_01153	ANXA4 // annexin A4 // 2p13 // 307 // ENST00000394295 // ANXA4 //	ANXA4	NM_01153	0.029511	0.029511	2.57076	2.57076	VMA vs Control	6.99286	4.4534	5.09479		
15445	8009553	NM_181671	PITPN1C1 // phosphatidylinositol transfer protein, cytoplasmic 1 // 3	PITPN1C1	NM_181671	0.000839213	0.000839213	2.57947	2.57947	VMA vs Control	26.8681	4.48535	1.33522		
5330	7907893	NM_001531	NR1 // major histocompatibility complex, class II-related // 10q25.3	NR1	NM_001531	0.00175722	0.00175722	2.58029	2.58029	VMA vs Control	12.8525	4.4884	2.78957		
6740	7922404	NR_003940	SNORD80 // small nuclear RNA, C/D box 80 // 2p77.1 // 8	SNORD80	NR_003940	0.04003754	0.04003754	2.58885	2.58885	VMA vs Control	15.4874	4.50878	2.27223		
28995	8143188	NM_194071	CREB3L2 // cAMP response element binding protein 3-like 2 // 7q34	CREB3L2	NM_194071	0.00625568	0.00625568	2.58612	2.58612	VMA vs Control	13.2982	4.50973	2.713		
5189	7986400	NM_005531	NR1 // major histocompatibility complex, class II-related // 10q25.3	NR1	NM_005531	0.0114048	0.0114048	2.58916	2.58916	VMA vs Control	15.2142	4.52992	3.30828		
25677	8111772	NM_001343	DAB2 // disabled homolog 2, mitogen-activated protein kinase phosphatase 2 // 11q23.3	DAB2	NM_001343	0.0141914	0.0141914	2.58919	2.58919	VMA vs Control	10.4612	4.51023	3.98889		
7596	790498	NM_016234	ACSL5 // acyl-CoA synthetase long-chain family member 5 // 10q25.1-5	ACSL5	NM_016234	0.005082	0.005082	2.59338	2.59338	VMA vs Control	14.8006	4.5364	4.2856		
1746	803128	NM_006847	IL18RA // interleukin-18 receptor, subfamily B with sialomucin domain	IL18RA	NM_006847	0.0178734	0.0178734	2.59699	2.59699	VMA vs Control	8.62041	4.54965	4.12647		
30554	815765	NM_004099	STOM // stomatin // 9q34.1 // 2040 // NM_198194 // STOM // stomatin	STOM	NM_004099	0.00426392	0.00426392	2.6055	2.6055	VMA vs Control	15.4528	4.55092	2.35772		
23078	8086125	NM_014811	IL8 // lipopolysaccharide-induced cytokine // 3q22.2 // 981 // ENST00000301807	IL8	NM_014811	0.00251992	0.00251992	2.6055	2.6055	VMA vs Control	18.7286	4.58092	1.95676		
26454	8118594	NM_001211	HLA-DPB1 // major histocompatibility complex, class II, DP beta 1 //	HLA-DPB1	NM_001211	0.00961787	0.00961787	2.60725	2.60725	VMA vs Control	11.4357	4.58732	3.20913		
31318	8180256	---	---	---	---	0.0129098	0.0129098	2.60897	2.60897	VMA vs Control	6.6671	4.59364	5.4566		
7963124	NM_001629	ALOKSAP // arachidonate 5-lipoxygenase-activating protein // 13q12	ALOKSAP	NM_001629	0.0061957	0.0061957	2.61415	2.61415	VMA vs Control	14.5914	4.61285	2.45052			
11354	8165843	NM_004042	ARF // arylsulfinyltransferase // 12q13.3 // 416 // ENST00000393615 // ARF	ARF	NM_004042	0.00365959	0.00365959	2.61447	2.61447	VMA vs Control	16.2411	4.61385	2.24502		
21763	8072710	NM_030641	APOL6 // apolipoprotein L6 // 22q12.3 // 80830 // ENST0000040965	APOL6	NM_030641	0.000349197	0.000349197	2.61662	2.61662	VMA vs Control	35.1813	4.62175	1.0106		
28808	8089378	NM_20705	NAALADL // N-acetylated alpha-linked acidic dipeptidase-like 2 //	NAALADL	NM_20705	0.00838828	0.00838828	2.63052	2.63052	VMA vs Control	11.826	4.62729	3.03604		
4849	791782	NM_019111	HLA-DRA // major histocompatibility complex, class II, DR alpha //	HLA-DRA	NM_019111	0.00410436	0.00410436	2.63029	2.63029	VMA vs Control	15.781	4.24	2.427		
2684	7903753	NM_00848	GSTM2 // glutathione S-transferase mu (2) // 1p13.3 // 2946	GSTM2	NM_00848	0.0146312	0.0146312	2.64183	2.64183	VMA vs Control	9.16367	4.71434	3.92058		
4849	8118548	NM_019111	HLA-DRA // major histocompatibility complex, class II, DR alpha //	HLA-DRA	NM_019111	0.00410436	0.00410436	2.64419	2.64419	VMA vs Control	15.781	4.24	2.427		
7419	7926742	NM_001031	IFIT3 // interferon-induced protein with tetratricopeptide repeats 3 // 12q24.31	IFIT3	NM_001031	0.00431982	0.00431982	2.64548	2.64548	VMA vs Control	15.2107	4.73489	2.5774		
28808	8085544	NM_195111	CDC80 // coiled-coil domain containing 80 // 3q13.2 // 151887 //	CDC80	NM_195111	0.0432198	0.0432198	2.65061	2.65061	VMA vs Control	5.75693	4.74659	6.95959		
21801	8073068	NM_014508	AP0BEC3 // apolipoprotein B mRNA editing enzyme, catalytic polypeptide 3 //	AP0BEC3	NM_014508	0.00174897	0.00174897	2.65152	2.65152	VMA vs Control	21.1861	4.74994	1.79361		
20700	8121212	---	---	---	---	0.0399387	0.0399387	2.65184	2.65184	VMA vs Control	6.00235	4.75111	3.33224		
17623	7961320	NM_15321	ERP2 // endoplasmic reticulum protein 27 // 12q13.3 // 121506 //	ERP2	NM_15321	0.0040485	0.0040485	2.65496	2.65496	VMA vs Control	12.1598	4.76256	2.58123		
21570	8016670	NM_000397	CVB // cytochrome B-24, beta polypeptide // 9p21.1 // 1536 // EN	CVB	NM_000397	0.0262181	0.0262181	2.65619	2.65619	VMA vs Control	7.14022	4.7711	6.82324		
12326	7977615	NM_198232	RNASE1 // ribonuclease, RNase A family, 1 (concentric) // 14q11.2 //	RNASE1	NM_198232	0.0062598	0.0062598	2.65748	2.65748	VMA vs Control	13.5992	4.77183	2.82583		
24333	8089611	NM_001265	TR1 // toll-like receptor 3 // 9q33 // 7098 // ENST00000296795 //	TR1	NM_001265	0.0242938	0.0242938	2.65859	2.65859	VMA vs Control	7.92421	4.77592	8.4045		
7407	792867	NM_004897	MRP1 // multidrug resistance protein 1 // 12q13.3 // 121506 //	MRP1	NM_004897	0.0094292	0.0094292	2.65985	2.65985	VMA vs Control	14.9254	4.7849	6.06544		
28808	8179519	NM_019111	HLA-DRA // major histocompatibility complex, class II, DR alpha //	HLA-DRA	NM_019111	0.0147171	0.0147171	2.6663	2.6663	VMA vs Control	10.4612	4.80243	3.93096		
33003	8141872	NM_0112388	NAPRED1 // major histocompatibility complex, class II, DR alpha //	NAPRED1	NM_0112388	0.0493817	0.0493817	2.66906	2.66906	VMA vs Control	5.33448	4.7203	7.16736		
813789	807052	NM_0112388	NAPRED1 // major histocompatibility complex, class II, DR alpha //	NAPRED1	NM_0112388	0.0493817	0.0493817	2.67475	2.67475	VMA vs Control	5.33448	4.7203	7.16736		
31024	8163618	NM_005118	TNFSF15 // tumor necrosis factor (ligand) superfamily, member 15 // 1	TNFSF15	NM_005118	0.0355721	0.0355721	2.677	2.677	VMA vs Control	6.37187	4.84358	3.0112		
9048	7945663	ENST00000340134	CTSD // cathepsin D // 11p15.5 // 1509 // ENST00000382123 //	CTSD	ENST00000340134	0.00355095	0.00355095	2.67786	2.67786	VMA vs Control	16.6184	4.84673	6.38318		
9245	7946977	NM_005122	SAA4 // serum amyloid A4, constitutive // 11p15.1-p14 // 6291 // E	SAA4	NM_005122	0.0277076	0.0277076	2.68474	2.68474	VMA vs Control	7.20958	4.872	5.40614		
6318	8191495	---	---	---	---	0.0049912	0.0049912	2.68499	2.68499	VMA vs Control	5.43409	4.87312	3.1222		
13608	7996020	NM_05724	TSPN3 // tetraspanin 3 // 15q24.3 // 10099 // NM_198902 // TSPN3	TSPN3	NM_05724	0.0068222	0.0068222	2.68652	2.68652	VMA vs Control	13.0724	4.87878	2.98569		
6018	810486	NM_003044	STCTM1 // secreted and transmembrane 1 // 17q25 // 6398 // ENST000	STCTM1	NM_003044	0.0230878	0.0230878	2.69803	2.69803	VMA vs Control	7.92538	4.92084	5.01482		
14734	7929047	NM_015172	IFIT2 // interferon-induced protein with tetratricopeptide repeats 2 //	IFIT2	NM_015172	0.0238782	0.0238782	2.69953	2.69953	VMA vs Control	7.7538	4.9236	5.09888		
9411	7948133	NM_00811	UPK // urokinase-type 1 // 9q34 // 1 // 9404 // NM_00143995 // UPK // uro	UPK	NM_00811	0.0035085	0.0035085	2.7058	2.7058	VMA vs Control	19.2504	4.94941	1.97913		
2554	7985909	---	---	---	---	0.000370451	0.000370451	2.71058	2.71058	VMA vs Control	34.5618	4.96697	1.1497		
1566	8167185	NM_001254	TMP1 // TIMP metalloproteinase inhibitor 1 // 8p11.2-p11.23 // 7076	TMP1	NM_001254	0.00656473	0.00656473	2.71857	2.71857	VMA vs Control	13.2881	4.99633	3.02123		
30073	8152522	NM_006209	ENPP2 // ectonucleotide pyrophosphatase/phosphodiesterase 2 // 8q24	ENPP2	NM_006209	0.0478082	0.0478082	2.72262	2.72262	VMA vs Control	5.45092	5.01123	3.847		
10397	7979782	NM_15321	ERP2 // endoplasmic reticulum protein 27 // 12q13.3 // 121506 //	ERP2	NM_15321	0.0040485	0.0040485	2.72727	2.72727	VMA vs Control	12.1598	4.76256	2.58123		
21801	8073062	NM_004900	AP0BEC3 // apolipoprotein B mRNA editing enzyme, catalytic polypeptide 3 //	AP0BEC3	NM_004900	0.00283296	0.00283296	2.72772	2.72772	VMA vs Control	21.1861	4.75992	2.37009		
2003	7915286	NM_001030	PPT1 // palmitoyl transferase 1 // 10p12 // 5538 // NM_001	PPT1	NM_001030	0.00569498	0.00569498	2.72828	2.72828	VMA vs Control	14.7063	5.03204	2.85987		
4803	8073044	NM_008501	GSTM2 // glutathione S-transferase mu (2) // 1p13.3 // 2946	GSTM2	NM_008501	0.0146312	0.0146312	2.72879	2.72879	VMA vs Control	9.16367	4.71434	3.92058		
6055	8113250	NM_01040458	ERAP1 // endoplasmic reticulum aminopeptidase 1 // 5q15 // 5152	ERAP1	NM_01040458	0.0236863	0.0236863	2.72884	2.72884	VMA vs Control	10.4612	4.80243	3.93096		
31754	8168424	NM_005137	SLC16A2 // solute carrier family 16, member 2 (monocarboxylate) //	SLC16A2	NM_005137	0.00085347									

Column #	Transcript	Cluster ID	gene_assignment	Gene Symbol	RefSeq	p-value(Group)	p-value(VA vs. Control)	Ratio(VA vs. Control)	Fold-Change(VA vs. Control)	Fold-Change(VA vs. Control)	(Description)	f(Group)	SS(Group)	SS(Error)	f(Error)
7232	7927215	NM_006988	ALOX5 // arachidonate 5-lipoxygenase 1 // 10q11.2 // 240 // ENST0000	ALOX5	NM_006988	0.00215357	0.00215357	4.0618	4.0618	VMA up vs Control	19.758	9.8135	3.97347	1	
24013	8095697	NM_001511	CXCL1 // chemokine (C-X-C motif) ligand 1 (melanoma growth stimulat	CXCL1	NM_001511	0.0208458	0.0208458	4.1128	4.1128	VMA up vs Control	8.23387	9.98093	9.97531	1	
25823	8112980	NM_005711	EDL3 // EGF-like repeats and discoidin-like domains 3 // 5q14 //	EDL3	NM_005711	0.0104406	0.0104406	4.1419	4.1419	VMA up vs Control	11.0647	10.0889	7.29444	1	
2778	7895294	—	—	—	—	0.0247558	0.0247558	4.17242	4.17242	VMA up vs Control	7.60589	10.1934	10.7215	1	
31924	8170179	NM_016267	VGLL1 // vestigial like 1 (Drosophila) // 4z6.3 // 51442 // ENST0	VGLL1	NM_016267	0.00314646	0.00314646	4.17335	4.17335	VMA up vs Control	17.3417	10.1966	4.70386	1	
6937	7924450	NM_007207	DUSP10 // dual specificity phosphatase 10 // 1q41 // 11221 // NM_1	DUSP10	NM_007207	0.0120063	0.0120063	4.20147	4.20147	VMA up vs Control	10.4511	10.2927	7.87874	1	
6379	7918936	NM_024626	VFCN1 // V-set domain containing 1 cell activation inhibitor 3 // 1	VFCN1	NM_024626	0.000781297	0.000781297	4.26249	4.26249	VMA up vs Control	27.4796	10.5004	3.05694	1	
24711	8102328	NM_000204	CFI // complement factor 1 // 4q25 // 3426 // ENST00000394634 // C	CFI	NM_000204	0.000981277	0.000981277	4.34863	4.34863	VMA up vs Control	25.5684	10.7923	3.19726	1	
15946	8014903	NM_001042471	GSDMB // gasdermin B // 17q12 // 5587 // NM_018530 // GSDMB //	GSDMB	NM_001042471	0.00420067	0.00420067	4.36206	4.36206	VMA up vs Control	15.6497	10.8376	5.54007	1	
27560	8129637	NM_004665	VNN2 // vanin 2 // 6p23-q24 // 8875 // NM_078488 // VNN2 // vanin	VNN2	NM_004665	0.01322713	0.01322713	4.36472	4.36472	VMA up vs Control	6.69173	10.8466	12.9671	1	
6240	7917528	—	—	—	—	0.00151142	0.00151142	4.39448	4.39448	VMA up vs Control	22.2335	10.9468	3.93886	1	
28607	8139488	NM_00103398	IGFBP3 // insulin-like growth factor binding protein 3 // 7p13-p	IGFBP3	NM_00103398	0.0126214	0.0126214	4.52008	4.52008	VMA up vs Control	10.237	11.3676	8.88357	1	
21769	8072735	NM_145343	APOLL // apolipoprotein L 1 // 22q13.1 // 8542 // NM_003661 // AP	APOLL	NM_145343	0.00630136	0.00630136	4.63164	4.63164	VMA up vs Control	13.4755	11.738	9.68652	1	
16739	8022656	NM_013422	CHST9 // carbohydrate (N-acetylglucosamine 4-0) sulfotransferase	CHST9	NM_013422	0.00331626	0.00331626	4.63306	4.63306	VMA up vs Control	17.4246	11.7427	5.51798	1	
7316	7928046	NM_012139	TSNALS // tetraspanin 15 // 10q22.1 // 2355 // ENST00000373290 /	TSNALS	NM_012139	0.000827128	0.000827128	4.74166	4.74166	VMA up vs Control	29.4296	12.1003	3.28929	1	
9665	7950810	NM_206927	SYTL2 // synaptotagmin-like 2 // 11q14 // 54843 // NM_206928 // SY	SYTL2	NM_206927	0.019227	0.019227	4.79767	4.79767	VMA up vs Control	5.83912	12.2836	11.508	1	
8605	7940775	NM_004585	RARRES3 // retinoic acid receptor responder (isoxanthone induced) 3	RARRES3	NM_004585	0.00369514	0.00369514	4.82656	4.82656	VMA up vs Control	16.3852	12.3778	6.04339	1	
26119	8135015	AB030783	MUC3B // mucin 3B, cell surface associated // 7q22 // 57876 // AF00	MUC3B	AB030783	0.0164248	0.0164248	4.9025	4.9025	VMA up vs Control	9.15284	12.6245	11.0344	1	
23594	8091723	NM_206963	RARRES1 // retinoic acid receptor responder (isoxanthone induced) 1	RARRES1	NM_206963	0.0166452	0.0166452	5.00433	5.00433	VMA up vs Control	9.09993	12.9532	11.3875	1	
24035	8095886	NM_006419	CXCL13 // chemokine (C-X-C motif) ligand 13 // 4q21 // 10563 // EN	CXCL13	NM_006419	0.0209222	0.0209222	5.17779	5.17779	VMA up vs Control	8.2202	13.5072	13.1453	1	
30080	8152617	NM_005328	HAS2 // hyaluronan synthase 2 // 8q24.12 // 3037 // ENST0000030392	HAS2	NM_005328	0.00690095	0.00690095	5.30686	5.30686	VMA up vs Control	13.0182	13.9147	8.55092	1	
25851	8112124	NM_022064	GLRX // glutaredoxin (thioltransferase) // 5q14 // 2745 // NM_0011	GLRX	NM_022064	0.00357609	0.00357609	5.3636	5.3636	VMA up vs Control	16.5769	14.0926	6.80104	1	
24628	8101429	NM_016619	PLAC8 // placenta-specific 8 // 4q21.22 // 51316 // NM_001130716 /	PLAC8	NM_016619	0.0202948	0.0202948	5.51333	5.51333	VMA up vs Control	8.34331	14.5584	19.9744	1	
30689	8158671	NM_000050	ASS1 // argininosuccinate synthetase 1 // 9q34.1 // 445 // NM_0540	ASS1	NM_000050	0.00305059	0.00305059	5.70001	5.70001	VMA up vs Control	17.5303	15.1319	6.90547	1	
33020	8179617	NM_007028	TRIM31 // tripartite motif-containing 31 // 6p21.3 // 11074 // ENS	TRIM31	NM_007028	0.0476641	0.0476641	5.84906	5.84906	VMA up vs Control	5.45995	15.584	2.8314	1	
28469	8138381	NM_006408	AGR2 // anterior gradient homolog 2 (Xenopus laevis) // 7q21.3 // 1	AGR2	NM_006408	0.0150326	0.0150326	6.17577	6.17577	VMA up vs Control	9.50915	16.5579	13.9301	1	
4639	7901175	NM_005727	TSNPN1 // tetraspanin 1 // 1q34.1 // 10103 // ENST00000372003 // T	TSNPN1	NM_005727	0.0246151	0.0246151	6.29974	6.29974	VMA up vs Control	7.62656	16.9214	17.7507	1	
24011	8095688	NM_002993	CXCL6 // chemokine (C-X-C motif) ligand 6 (granulocyte chemotactic	CXCL6	NM_002993	0.0180624	0.0180624	6.50333	6.50333	VMA up vs Control	8.77954	15.5113	15.9565	1	
20745	8063000	NM_006103	WFDLC2 // WAP four-disulfide core domain 2 // 20q12-q13.2 // 10406 /	WFDLC2	NM_006103	0.00832392	0.00832392	6.61473	6.61473	VMA up vs Control	12.108	17.8304	11.761	1	
26440	8118345	NM_001710	CFB // complement factor B // 6p21.3 // 629 // BC004143 // CFB //	CFB	NM_001710	0.0477693	0.0477693	6.93188	6.93188	VMA up vs Control	5.45335	18.7523	27.4669	1	
28482	8138487	—	—	—	—	0.00208	0.00208	7.09501	7.09501	VMA up vs Control	19.9914	19.178	7.6745	1	
29824	8150509	NM_000930	PLAT // plasminogen activator, tissue // 8p12 // 5327 // NM_033011	PLAT	NM_000930	0.0222861	0.0222861	7.19491	7.19491	VMA up vs Control	17.98642	19.4527	19.4857	1	
32663	8178115	NM_001710	CFB // complement factor B // 6p21.3 // 629 // BC004143 // CFB //	CFB	NM_001710	0.0469248	0.0469248	7.32622	7.32622	VMA up vs Control	5.50684	19.8109	28.78	1	
3185	8180303	—	—	—	—	0.0225969	0.0225969	7.72813	7.72813	VMA up vs Control	7.93568	20.8877	21.057	1	
30690	8158684	—	—	—	—	0.00949802	0.00949802	8.28307	8.28307	VMA up vs Control	11.493	22.2884	15.5422	1	
5442	7909250	NM_153758	IL19 // interleukin 19 // 1q32.2 // 29949 // NM_013371 // IL19 //	IL19	NM_153758	0.0324829	0.0324829	8.3067	8.3067	VMA up vs Control	6.67001	22.2886	26.8529	1	
6887	7923029	NM_022644	PIGR // polymeric immunoglobulin receptor // 1q21-q41 // 5284 // E	PIGR	NM_022644	0.0200583	0.0200583	8.63577	8.63577	VMA up vs Control	8.37849	23.2179	22.149	1	
5710	7908459	NM_000186	CFH // complement factor H // 1q32 // 3075 // NM_001014975 // CFH	CFH	NM_000186	0.00479345	0.00479345	8.71593	8.71593	VMA up vs Control	14.9172	23.4173	12.5586	1	
27150	8125149	NM_025257	SLC44A4 // solute carrier family 44, member 4 // 6p21.3 // 80736 //	SLC44A4	NM_025257	0.0222679	0.0222679	9.19378	9.19378	VMA up vs Control	7.98943	24.5861	24.6186	1	
32922	8178653	NM_025257	SLC44A4 // solute carrier family 44, member 4 // 6p21.3 // 80736 //	SLC44A4	NM_025257	0.0222679	0.0222679	9.19378	9.19378	VMA up vs Control	7.98943	24.5861	24.6186	1	
33947	8179861	NM_025257	SLC44A4 // solute carrier family 44, member 4 // 6p21.3 // 80736 //	SLC44A4	NM_025257	0.0222679	0.0222679	9.19378	9.19378	VMA up vs Control	7.98943	24.5861	24.6186	1	
9714	7951217	NM_002423	MMP7 // matrix metalloproteinase 7 (matrilysin, uterine) // 11q21-q2	MMP7	NM_002423	0.0077285	0.0077285	13.7483	13.7483	VMA up vs Control	12.4629	34.3135	22.0261	1	