Number of Different SAGE Tags	P1mon	P2mon	C1mon	A1mon	A2mon	P1nonmon	A1nonmon	Description	Unigene	P-value for P1	P-value for P2	P1mon/C1mon	P2mon/C1mon	Total Tags
1		2	10	8	6	8	8	proteasome (prosome, macropain) subunit, beta type, 2	432607	0.000983082	0.069822313	0.05	0.2	25
1	1	2	14	6	8	6	10	scotin	414579	0.000461656	0.017262997	0.071428571	0.142857143	30
1	1	4	14	3	6	2	2	likely ortholog of mouse D11lgp2	55918	0.000461656	0.047985875	0.071428571	0.285714286	26
11	1	8	14	11	8	8	2	ubiquitin specific protease 22	12064	0.000461656	0.147729792	0.071428571	0.571428571	38
4	1	6	13	6	8	4		interleukin 6 signal transducer (gp130, oncostatin M receptor)	71968	0.000861238	0.119239898	0.076923077	0.461538462	31
3	1	6	12	6	6	2	2	activin A receptor, type IB	371974	0.001598474	0.148470141	0.083333333	0.5	28
3	1	4	11	9	5	2	2	FLJ22794 protein	19525	0.002949244	0.112255916	0.090909091	0.363636364	28
7	1	4	10	10	7		6	chromosome 19 open reading frame 28	347803	0.005403678	0.145563579	0.1	0.4	30
2	2	6	17	1	2			interferon-induced protein 44	82316	0.000329328	0.044011058	0.117647059	0.352941176	25
2	1	4	8	6	8	6		fragile X mental retardation, autosomal homolog 1	408096	0.017663385	0.233082469	0.125	0.5	25
8	2	6	11	4	5	10	8	F-box and leucine-rich repeat protein 11	219614	0.009579245	0.18202174	0.181818182	0.545454545	25
8	1	2	5	13	7	10	10	PRP4 pre-mRNA processing factor 4 homolog B (yeast)	198891	0.094033929	0.321901919	0.2	0.4	27
1	3	2	14	5	9	4	6	nasal embryonic LHRH factor	455336	0.005225776	0.017262997	0.214285714	0.142857143	32
4	2	4	9	4	8		6	CDNA FLJ10131 fis, clone HEMBA1003041	274128	0.026985717	0.185894111	0.222222222	0.444444444	25
11	4	6	17	10	16	6	10	SH3-domain kinase binding protein 1	153260	0.002878136	0.044011058	0.235294118	0.352941176	50
2	4	6	17	25	15	12	26	immune associated nucleotide	124675	0.002878136	0.044011058	0.235294118	0.352941176	64
9	2	4	8	9	10	6	2	FOS-like antigen 2	301612	0.044131744	0.233082469	0.25	0.5	31
6	2	4	8	6	12	4	8	Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain, 2	82071	0.044131744	0.233082469	0.25	0.5	30
5	1	2	4	15	6	92	164	lymphotoxin beta (TNF superfamily, member 3)	376208	0.156628445	0.411089585	0.25	0.5	27
23			2	33	6	324	1180	hemoglobin, alpha 2	398636	0.250454066	0.555709133	0.25	0.5	41
2	19	34	72	26	26	8	4	vanin 2	293130	7.57425E-09	0.000695519	0.263888889	0.472222222	160
3	4	8	15	3	4	6	10	carnitine palmitoyltransferase II	274336	0.007446729	0.122105794	0.266666667	0.533333333	30
10	3	2	11	6	4	12	16	Treacher Collins-Franceschetti syndrome 1	301266	0.022338047	0.049703691	0.272727273	0.181818182	25
4	3	4	11	7	2	4	12	MRNA; cDNA DKFZp686D0374 (from clone DKFZp686D0374)	126133	0.022338047	0.112255916	0.272727273	0.363636364	25
10	3	6	11	8	6	2	4	cytoplasmic FMR1 interacting protein 1	26704	0.022338047	0.18202174	0.272727273	0.545454545	31
2	3	6	11	13	10	8	22	nucleoside phosphorylase	75514	0.022338047	0.18202174	0.272727273	0.545454545	40
6	5	10	17	6	9	8	10	interferon induced transmembrane protein 2 (1-8D)	174195	0.006328068	0.122740608	0.294117647	0.588235294	42
7	3	4	10	7	6		4	ADP-ribosylation factor GTPase activating protein 3	13014	0.035081419	0.145563579	0.3	0.4	28
3	3	6	10	4	5			CDNA FLJ32589 fis, clone SPLEN2000443	400590	0.035081419	0.219170483	0.3	0.6	25
6	30	34	99	22	19	24	16	interferon, alpha-inducible protein (clone IFI-6-16)	287721	3.08035E-10	9.25898E-07	0.303030303	0.343434343	187
7	7	12	23	8	12	8	8	interferon induced transmembrane protein 3 (1-8U)	374650	0.001915578	0.059391686	0.304347826	0.52173913	56
1	4	2	13	10	6			homer homolog 3 (Drosophila)	410683	0.018268098	0.02469148	0.307692308	0.153846154	34
3	4	4	13	6	8	8	8	telomeric repeat binding factor 2, interacting protein	274428	0.018268098	0.064345122	0.307692308	0.307692308	33
3	4	6	13	7	10	2	4	nuclear receptor binding protein	272736	0.018268098	0.119239898	0.307692308	0.461538462	37
1	9	10	29	13	18	14	8	HLA-B associated transcript 3	440900	0.000600612	0.007730118	0.310344828	0.344827586	74
2	7	4	22	11	9	14	12	tubulin-specific chaperone a	355627	0.002935444	0.003628173	0.318181818	0.181818182	51
2	9	14	28	20	24		2	nuclear factor (erythroid-derived 2), 45kDa	75643	0.000916169	0.034563007	0.321428571	0.5	88
4	4		12	5	8	4	8	enoyl Coenzyme A hydratase 1, peroxisomal	196176	0.027922549	0.007778682	0.333333333	0.083333333	29
6	3	2	9	11	9	16	10	hypothetical protein MGC10471	24998	0.053938778	0.097273759	0.333333333	0.222222222	33
7	4	4	12	3	5	12	2	hematological and neurological expressed 1	109706	0.027922549	0.0854598	0.333333333	0.333333333	26
3	4	4	12	2	5	4	4	2'-5'-oligoadenylate synthetase 2, 69/71kDa	414332	0.027922549	0.0854598	0.333333333	0.333333333	25
1	3	4	9	8	4			2'-5'-oligoadenylate synthetase 3, 100kDa	528634	0.053938778	0.185894111	0.333333333	0.444444444	26
10	4	8	12	4	5			cytochrome P450, family 1, subfamily B, polypeptide 1	154654	0.027922549	0.206350894	0.333333333	0.666666667	29
3	4	8	12	4	6	18	22	cyclin-dependent kinase (CDC2-like) 10	77313	0.027922549	0.206350894	0.333333333	0.666666667	30
11	4	8	12	5	9	6	12	chromosome 14 open reading frame 92	194035	0.027922549	0.206350894	0.333333333	0.666666667	34
4	3	6	9	7	8	10	6	hypothetical protein MGC4618	89072	0.053938778	0.258364515	0.333333333	0.666666667	30
4	12	12	33	14	10	4	20	ring-box 1	373992	0.000828355	0.00571004	0.363636364	0.363636364	75
7	4	4	11	8	4	4	2	Rab geranylgeranyltransferase, alpha subunit	377992	0.041858496	0.112255916	0.363636364	0.363636364	29
5	4	4	11	5	11	6	4	interferon regulatory factor 7	166120	0.041858496	0.112255916	0.363636364	0.363636364	33
11	8	10	22	16	10	10	8	membrane cofactor protein (CD46, trophoblast-lymphocyte cross-reactive antigen)	83532	0.005500627	0.044517998	0.363636364	0.454545455	61
6	4	6	11	4	3	6	4	hypothetical protein DKFZp547K1113	323053	0.041858496	0.18202174	0.363636364	0.545454545	25
8	4	6	11	11	9	2	2	quiescin Q6	77266	0.041858496	0.18202174	0.363636364	0.545454545	38
3	7	10	19	11	18	8	8	adaptor-related protein complex 2, sigma 1 subunit	119591	0.009879339	0.084355409	0.368421053	0.526315789	60
4	3	4	8	5	8	2		myxovirus (influenza virus) resistance 2 (mouse)	926	0.080859243	0.233082469	0.375	0.5	26
14	8	8	21	12	13	6	16	ubiquitin-activating enzyme E1 (A1S9T and BN75 temperature sensitivity complementing)	406693	0.008062708	0.030766501	0.380952381	0.380952381	58
26	12	14	31	12	13	12	4	superoxide dismutase 2, mitochondrial	384944	0.001765022	0.018023367	0.387096774	0.451612903	75
1	12	20	31	11	21	8	6	hypothetical protein MGC33867	438889	0.001765022	0.067163547	0.387096774	0.64516129	85
11	7	10	18	8	7	8	8	S-phase kinase-associated protein 1A (p19A)	171626	0.014430302	0.102340951	0.388888889	0.555555556	45
9	14	24	36	25	29	14	14	hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), a	75860	0.000844639	0.059616969	0.388888889	0.666666667	116
12	7	12	18	7	11	8	10	RNA binding motif protein, X-linked	380118	0.014430302	0.142238342	0.388888889	0.666666667	49
4	13	14	33	14	17		4	apolipoprotein B mRNA editing enzyme, catalytic polypeptide-like 3A	348983	0.001464665	0.011337265	0.393939394	0.424242424	84
6	4		10	10	9	50	76	hypothetical protein FLJ22635	353181	0.061355338	0.018268139	0.4	0.1	33
4	4	4	10	6	9	16	6	T-cell leukemia translocation altered gene	250894	0.061355338	0.145563579	0.4	0.4	31
4	4	4	10	5	4	4	4	SM-11044 binding protein	8203	0.061355338	0.145563579	0.4	0.4	25
5	4	4	10	9	7	6	8	hypothetical protein LOC149603	356377	0.061355338	0.145563579	0.4	0.4	32
6	4	4	10	8	7	4	6	zinc finger protein 403	149055	0.061355338	0.145563579	0.4	0.4	31
8	4	4	10	6	7	2	6	H326	120904	0.061355338	0.145563579	0.4	0.4	29
3	4	4	10	4	5		4	interferon-stimulated transcription factor 3, gamma 48kDa	1706	0.061355338	0.145563579	0.4	0.4	25
6	2	2	5	11	7	2	2	solute carrier family 12 (potassium/chloride transporters), member 7	172613	0.164459808	0.321901919	0.4	0.4	26
4	2	2	5	5	12	10	14	hypothetical protein FLJ13111	288382	0.164459808	0.321901919	0.4	0.4	25
2	6	8	15	10	9	10	12	DNA fragmentation factor, 45kDa, alpha polypeptide	484782	0.02603202	0.122105794	0.4	0.533333333	44
13	8	12	20	8	13	22	10	copine I	166887	0.011669965	0.103599613	0.4	0.6	55
5	6	10	15	16	19	10	10	calpain 1, (mu/I) large subunit	356181	0.02603202	0.169708466	0.4	0.666666667	61
3	23	16	57	13	15	8	4	cystinosis, nephropathic	187667	5.77139E-05	3.78873E-05	0.403508772	0.280701754	116
5	7	8	17	13	9	4	4	hypothetical protein DKFZp762N1910	406377	0.02076707	0.08028388	0.411764706	0.470588235	50
7	7	10	17	10	8	2	4	solute carrier organic anion transporter family, member 3A1	113657	0.02076707	0.122740608	0.411764706	0.588235294	47
11	5	8	12	7	5	4	12	ankyrin repeat and KH domain containing 1	406840	0.047439612	0.206350894	0.416666667	0.666666667	33
1	99	100	237	113	151	10	14	endothelial cell growth factor 1 (platelet-derived)	435067	#NUM!	#NUM!	0.417721519	0.421940928	650
6	8	6	19	2	3	2		immediate early response 3	76095	0.016661297	0.025315667	0.421052632	0.315789474	35
2	3	2	7	17	5	6	24	CDC-like kinase 1	433732	0.117542325	0.182756989	0.428571429	0.285714286	33
8	9	10	21	11	11	10	16	SP110 nuclear body protein	38125	0.013429716	0.055588979	0.428571429	0.476190476	57
9	3	4	7	7	8	10	6	pre-mRNA cleavage complex II protein Pcf11	123654	0.117542325	0.285754943	0.428571429	0.571428571	27
6	10	2	23	10	16	2	2	glucosidase, alpha; acid (Pompe disease, glycogen storage disease type II)	1437	0.01086712	0.000592501	0.434782609	0.086956522	60
2	7	6	16	7	8	14	14	xeroderma pigmentosum, complementation group C	320	0.029402226	0.057329069	0.4375	0.375	41
4	7	6	16	9	8	8	10	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit c (subunit 9), isoform 1	80986	0.029402226	0.057329069	0.4375	0.375	43

7	7	8	16	5	5	6	10	hypothetical protein FLJ20580	146861	0.029402226	0.099598347	0.4375	0.5	37
2	4	4	9	12	6			phospholipase A2, group VII (platelet-activating factor acetylhydrolase, plasma)	93304	0.087597481	0.185894111	0.444444444	0.444444444	33
3	8	12	18	11	15	54	40	epidermodysplasia verruciformis 2	511843	0.023435053	0.142238342	0.444444444	0.666666667	58
5	4	6	9	4	7	4	2	KIAA1076 protein	154525	0.087597481	0.258364515	0.444444444	0.666666667	27
1	4	6	9	4	14	4	2	Clone IMAGE:5200861, mRNA	446474	0.087597481	0.258364515	0.444444444	0.666666667	34
11	5	2	11	9	14	4	2	activating transcription factor 5	9754	0.066933071	0.049703691	0.454545455	0.181818182	40
1	5	2	11	10	10	8	14	SEC24 related gene family, member C (S. cerevisiae)	512852	0.066933071	0.049703691	0.454545455	0.181818182	37
3	5	4	11	6	6	10	2	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 7, 14.5kDa	19561	0.066933071	0.112255916	0.454545455	0.363636364	30
8	5	4	11	8	6	2	4	DnaJ (Hsp40) homolog, subfamily C, member 5	165563	0.066933071	0.112255916	0.454545455	0.363636364	32
6	5	6	11	7	2	2	10	ring finger and WD repeat domain 1	334479	0.066933071	0.18202174	0.454545455	0.545454545	28
6	11	16	24	6	5	8	14	chemokine (C-X-C motif) ligand 16	82407	0.012246088	0.103604745	0.458333333	0.666666667	54
3	6	2	13	7	6	8		elongation of very long chain fatty acids (FEN1/Elo2, SUR4/Elo3, yeast)-like 1	25597	0.052001094	0.02469148	0.461538462	0.153846154	33
5	6	6	13	5	14	8	6	follicular lymphoma variant translocation 1	74050	0.052001094	0.119239898	0.461538462	0.461538462	41
6	6	6	13	9	7	4	4	chromosome 6 open reading frame 166	201864	0.052001094	0.119239898	0.461538462	0.461538462	38
1	6	6	13	10	9	10	12	KIAA0563 gene product	433113	0.052001094	0.119239898	0.461538462	0.461538462	41
1	6	6	13	10	9	10	12	aryl-hydrocarbon receptor nuclear translocator 2	6111	0.052001094	0.119239898	0.461538462	0.461538462	41
1	6	8	13	10	10	8	2	hypothetical protein FLJ10420	437385	0.052001094	0.176083138	0.461538462	0.615384615	43
7	6	8	13	4	13	2		leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 4	67846	0.052001094	0.176083138	0.461538462	0.615384615	40
6	13	12	28	18	26	24	20	RNA binding motif protein 10	348276	0.008090567	0.019894557	0.464285714	0.428571429	91
1	7	4	15	8	14	10	18	ARD1 homolog, N-acetyltransferase (S. cerevisiae)	433291	0.040882709	0.035487624	0.466666667	0.266666667	46
2	7	8	15	17	10	10	22	HS1 binding protein	199625	0.040882709	0.122105794	0.466666667	0.533333333	53
9	8	8	17	3	5	4	2	chromosome 20 open reading frame 104	301055	0.032428914	0.08028388	0.470588235	0.470588235	37
5	18	12	38	14	15	2	2	hypothetical protein MGC34680	321635	0.002984291	0.001461665	0.473684211	0.315789474	91
11	9	8	19	8	7	12	18	chaperonin containing TCP1, subunit 4 (delta)	374334	0.025901891	0.050578326	0.473684211	0.421052632	47
11	9	10	19	10	20	10	16	protein phosphatase 1, catalytic subunit, gamma isoform	79081	0.025901891	0.084355409	0.473684211	0.526315789	63
10	10	10	21	6	9	2	12	yippee protein	184542	0.020803465	0.055588979	0.476190476	0.476190476	51
13	12	8	25	20	13	10	6	phosphonoformate immuno-associated protein 5	131727	0.013593152	0.010473525	0.48	0.32	74
7	5		10	4	8	8	6	KIAA0195 gene product	301132	0.091977321	0.018268139	0.5	0.1	27
14	5		10	8	12	4	10	splicing factor, arginine/serine-rich 1 (splicing factor 2, alternate splicing factor)	68714	0.091977321	0.018268139	0.5	0.1	35
9	4		8	10	9	10	14	glyoxylate reductase/hydroxypyruvate reductase	155742	0.121215478	0.042902501	0.5	0.125	31
5	6	2	12	6	6	4	6	zinc finger, FYVE domain containing 26	8663	0.071116362	0.035136346	0.5	0.166666667	31
2	5	2	10	7	5	2	2	Similar to SMT3 suppressor of mif two 3 homolog 2 (LOC222019), mRNA	356279	0.091977321	0.069822313	0.5	0.2	28
10	8	4	16	3	4	2	2	phospholipid scramblase 1	348478	0.044076654	0.026051654	0.5	0.25	33
8	4	2	8	11	2	4	2	chromosome 6 open reading frame 37	10784	0.121215478	0.134162877	0.5	0.25	26
13	10	6	20	17	12	2	2	cathepsin Z	252549	0.028168297	0.018997351	0.5	0.3	62
2	6	4	12	8	15	14	12	hypothetical protein BC002942	150540	0.071116362	0.0854598	0.5	0.333333333	43
6	6	4	12	8	10	16	26	retinoblastoma-like 2 (p130)	283604	0.071116362	0.0854598	0.5	0.333333333	38
1	5	4	10	7	6	4	2	Transcribed sequence with strong similarity to protein ref:NP_002992.1 (H.sapiens) succinate dehydrogenase complex, subunit	355964	0.091977321	0.145563579	0.5	0.4	30
1	5	4	10	7	6	4	2	succinate dehydrogenase complex, subunit C, integral membrane protein, 15kDa	433982	0.091977321	0.145563579	0.5	0.4	30
1	5	4	10	15	4			cisplatin resistance associated	425144	0.091977321	0.145563579	0.5	0.4	36
8	5	4	10	3	8		2	nicastrin	4788	0.091977321	0.145563579	0.5	0.4	28
5	7	6	14	10	10	6	6	synaptosomal-associated protein, 23kDa	202308	0.055715437	0.094481837	0.5	0.428571429	44
6	7	6	14	7	11	6	8	RAN binding protein 3	176657	0.055715437	0.094481837	0.5	0.428571429	42
5	9	8	18	7	10	16	18	misshapen/NIK-related kinase	112028	0.03513131	0.064030129	0.5	0.444444444	48
9	14	14	28	22	7	32	44	chromosome 20 open reading frame 149	79625	0.012128508	0.034563007	0.5	0.5	78
7	6	6	12	3	4	4	4	guanine nucleotide binding protein (G protein), alpha activating activity polypeptide, olfactory type	136295	0.071116362	0.148470141	0.5	0.5	28
2	6	6	12	6	11	6	8	hypothetical protein MGC11275	6949	0.071116362	0.148470141	0.5	0.5	38
2	6	6	12	3	9	4	6	F-box and leucine-rich repeat protein 6	12271	0.071116362	0.148470141	0.5	0.5	33
3	4	4	8	5	7	2		2',5'-oligoadenylate synthetase 1, 40/46kDa	442936	0.121215478	0.233082469	0.5	0.5	26
1	4	4	8	12	3	6	8	ring finger protein 44	511936	0.121215478	0.233082469	0.5	0.5	29
5	4	4	8	7	11	4	12	DNA (cytosine-5-)-methyltransferase 1	202672	0.121215478	0.233082469	0.5	0.5	32
3	4	4	8	5	8	4	12	hydroxyacylglutathione hydrolase	155482	0.121215478	0.233082469	0.5	0.5	27
8	9	10	18	14	6	12	12	mitogen-activated protein kinase kinase 2	366546	0.03513131	0.102340951	0.5	0.555555556	52
3	7	8	14	8	5	14	6	NADH dehydrogenase (ubiquinone) flavoprotein 2, 24kDa	51299	0.055715437	0.147729792	0.5	0.571428571	38
1	5	6	10	7	3			ribonuclease, RNase A family, k6	23262	0.091977321	0.219170483	0.5	0.6	28
9	8	10	16	7	16	4	2	homeodomain interacting protein kinase 3	30148	0.044076654	0.145347868	0.5	0.625	52
6	9	12	18	5	13	2	4	KIAA1033 protein	12144	0.03513131	0.142238342	0.5	0.666666667	51
3	9	12	18	21	23	2	4	paired immunoglobin-like type 2 receptor alpha	122591	0.03513131	0.142238342	0.5	0.666666667	77
8	6	8	12	10	8	4	6	cell cycle progression 8 protein	259326	0.071116362	0.206350894	0.5	0.666666667	40
1	3	4	6	5	10	4	2	Parkinson disease (autosomal recessive, early onset) 7	419640	0.164459747	0.340599052	0.5	0.666666667	26
4	3	4	6	10	4	6	8	retinoblastoma-associated factor 600	287616	0.164459747	0.340599052	0.5	0.666666667	25
5	3	4	6	11	5	6	8	ubiquitination factor E4A (UFD2 homolog, yeast)	75275	0.164459747	0.340599052	0.5	0.666666667	27
6	20	26	39	20	23	12	18	glycolipid transfer protein	381256	0.00490676	0.052461535	0.512820513	0.666666667	115
9	35	38	68	36	48	6	4	adaptor-related protein complex 1, sigma 2 subunit	40368	0.000388963	0.004269127	0.514705882	0.558823529	206
1	30	30	58	22	33	48	50	hematopoietic cell signal transducer	117339	0.00097824	0.004355431	0.517241379	0.517241379	158
2	25	30	48	29	30	12	4	trinucleotide repeat containing 5	414099	0.002493878	0.026130855	0.520833333	0.625	147
12	9	8	17	13	12	10	22	calmodulin 3 (phosphorylase kinase, delta)	334330	0.046813423	0.08028388	0.529411765	0.470588235	55
11	9	10	17	10	6	20	26	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, theta polypeptide	74405	0.046813423	0.122740608	0.529411765	0.588235294	47
4	8	2	15	4	11	2		immune receptor expressed on myeloid cells 2	158954	0.058733335	0.012015747	0.533333333	0.133333333	39
1	8	6	15	2	7	2	2	Transcribed sequence with weak similarity to protein sp:P02794 (H.sapiens) FRIH_HUMAN Ferritin heavy chain	381015	0.058733335	0.073983593	0.533333333	0.4	35
7	8	6	15	4	5	10	10	chromosome 15 open reading frame 15	274772	0.058733335	0.073983593	0.533333333	0.4	35
6	8	8	15	8	5	8	2	integrin, alpha 5 (fibronectin receptor, alpha polypeptide)	149609	0.058733335	0.122105794	0.533333333	0.533333333	40
5	8	10	15	12	6	6	8	chaperonin containing TCP1, subunit 6A (zeta 1)	82916	0.058733335	0.169708466	0.533333333	0.666666667	46
20	23	20	43	23	20	24	34	KIAA1049 protein	227835	0.004783726	0.006962644	0.534883721	0.465116279	119
4	7	8	13	10	11	12	12	transcription termination factor, RNA polymerase II	201774	0.074242329	0.176083138	0.538461538	0.615384615	45
8	20	20	37	21	29	12	18	signal sequence receptor, beta (translocon-associated protein beta)	74564	0.008489804	0.023949267	0.540540541	0.540540541	117
7	13	10	24	16	18	4	12	protein tyrosine phosphatase, non-receptor type 6	63489	0.026109063	0.02788459	0.541666667	0.416666667	76
1	6	2	11	11	15			hypothetical protein FLJ10521	436849	0.094764478	0.049703691	0.545454545	0.181818182	44
3	6	4	11	10	8	10	10	activator of basal transcription 1	254406	0.094764478	0.112255916	0.545454545	0.363636364	37
7	6	6	11	5	10	10	8	dipeptidylpeptidase 7	37916	0.094764478	0.18202174	0.545454545	0.545454545	35
1	6	6	11	7	12			sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4A	408846	0.094764478	0.18202174	0.545454545	0.545454545	39
2	6	6	11	5	5	14	14	ARF GTPase-activating protein	448618	0.094764478	0.18202174	0.545454545	0.545454545	30
5	6	6	11	4	3	2	4	signal peptidase complex (18kD)	9534	0.094764478	0.18202174	0.545454545	0.545454545	27
3	5		9	6	5			potassium large conductance calcium-activated channel, subfamily M, beta member 1	93841	0.122562272	0.027995515	0.555555556	0.111111111	25
5	5	2	9	7	7	6	6	SNARE protein Ykt6	296244	0.122562272	0.097273759	0.555555556	0.222222222	29
2	5	2	9	5	5		2	similar to RIKEN cDNA 2610524G09	380851	0.122562272	0.097273759	0.555555556	0.222222222	25

9	5	4	9	9	10	6	8	LUC7-like 2 (S. cerevisiae)	308777	0.122562272	0.185894111	0.555555556	0.444444444	35
8	5	4	9	6	9	4	8	nuclear receptor coactivator 1	386092	0.122562272	0.185894111	0.555555556	0.444444444	31
8	5	4	9	4	6	4	10	RNA binding motif protein 23	4997	0.122562272	0.185894111	0.555555556	0.444444444	26
8	10	12	18	21	17	16	12	proteasome (prosome, macropain) subunit, alpha type, 1	82159	0.049154076	0.142238342	0.555555556	0.666666667	72
1	5	6	9	6	4	8	8	CDNA FLJ26687 fis, clone MPG06534	405966	0.122562272	0.258364515	0.555555556	0.666666667	27
1	5	6	9	6	4	8	8	KIAA0408	335157	0.122562272	0.258364515	0.555555556	0.666666667	27
5	5	6	9	4	5	2	2	NEDD9 interacting protein with calponin homology and LIM domains	33476	0.122562272	0.258364515	0.555555556	0.666666667	26
10	5	6	9	7	7	8	10	hypothetical protein PRO2730	194110	0.122562272	0.258364515	0.555555556	0.666666667	31
3	5	6	9	8	7	2	10	hypothetical protein MGC3207	439370	0.122562272	0.258364515	0.555555556	0.666666667	32
1	19	14	34	28	23	2	14	synaptogyrin 2	433753	0.013343671	0.008921114	0.558823529	0.411764706	111
7	37	44	66	35	34	14	16	ornithine decarboxylase antizyme 2	74563	0.001327201	0.018249187	0.560060061	0.666666667	194
21	9	6	16	13	11	32	30	meningioma expressed antigen 5 (hyaluronidase)	5734	0.061180535	0.057329069	0.5625	0.375	52
6	9	6	16	8	8	2	2	major histocompatibility complex, class II, DM beta	1162	0.061180535	0.057329069	0.5625	0.375	44
4	9	8	16	4	6	2		rhysin 2	334875	0.061180535	0.099598347	0.5625	0.5	39
2	8	2	14	8	10	2	4	XIAP associated factor-1	441975	0.076562374	0.017262997	0.571428571	0.142857143	41
2	4	2	7	5	8	10	10	immune associated nucleotide 4 like 1 (mouse)	412331	0.161522907	0.182756989	0.571428571	0.285714286	25
9	4	2	7	11	11	8	12	hypothetical protein FLJ10154	406114	0.161522907	0.182756989	0.571428571	0.285714286	34
9	4	2	7	12	7	2	4	RAB11A, member RAS oncogene family	75618	0.161522907	0.182756989	0.571428571	0.285714286	31
6	8	8	14	10	7	10	10	coatomer protein complex, subunit beta 2 (beta prime)	75724	0.076562374	0.147729792	0.571428571	0.571428571	43
1	4	4	7	9	3	10	6	CDNA FLJ32756 fis, clone TESTI2001758	350692	0.161522907	0.285754943	0.571428571	0.571428571	25
11	15	12	26	12	14		12	membrane-spanning 4-domains, subfamily A, member 7	188011	0.029055636	0.031481218	0.576923077	0.461538462	73
1	11	6	19	9	3	4		brain abundant, membrane attached signal protein 1	511745	0.051153146	0.025315667	0.578947368	0.315789474	45
2	11	8	19	7	12	12	12	mitogen-activated protein kinase kinase 1	132311	0.051153146	0.050578326	0.578947368	0.421052632	53
12	22	18	38	53	47	2	10	dual specificity phosphatase 6	298654	0.012403673	0.011836062	0.578947368	0.473684211	169
5	7		12	6	5	6	8	DNA methyltransferase 1 associated protein 1	8008	0.096456666	0.007778682	0.583333333	0.083333333	30
6	7	2	12	4	9	8	2	5'-3' exoribonuclease 2	268555	0.096456666	0.035136346	0.583333333	0.166666667	33
14	7	4	12	5	5	8	10	3-phosphoinositide dependent protein kinase-1	154729	0.096456666	0.0854598	0.583333333	0.333333333	31
3	14	12	24	22	22	4	2	elongation factor-2 kinase	259855	0.035412289	0.048444169	0.583333333	0.5	88
3	7	6	12	6	9	6	18	death-associated protein kinase 2	129208	0.096456666	0.148470141	0.583333333	0.5	37
21	80	80	137	85	90	60	54	GABA(A) receptor-associated protein	84359	#NUM!	#NUM!	0.583941606	0.583941606	432
7	10	4	17	24	15		2	LR8 protein	190161	0.063159882	0.01899966	0.588235294	0.235294118	68
6	10	8	17	13	8	16	14	ubiquitin-conjugating enzyme E2G 2 (UBC7 homolog, yeast)	250387	0.063159882	0.08028388	0.588235294	0.470588235	52
2	13	14	22	14	19	8	10	proteasome (prosome, macropain) subunit, beta type, 10	9661	0.043227563	0.103909881	0.590909091	0.636363636	75
7	16	16	27	13	24	14	12	aldehyde dehydrogenase 3 family, member B1	274235	0.030367164	0.064414103	0.592592593	0.592592593	88
6	9	6	15	11	9	12	12	peroxiredoxin 6	120	0.078263731	0.073983593	0.6	0.4	47
3	6	4	10	5	12	6	8	RAB4B, member RAS oncogene family	25367	0.122562227	0.145563579	0.6	0.4	35
1	6	4	10	3	7		2	excision repair cross-complementing rodent repair deficiency, complementation group 1 (includes overlapping antisense sequen	435981	0.122562227	0.145563579	0.6	0.4	28
4	6	6	10	3	3	6	6	N-myristoyltransferase 2	60339	0.122562227	0.219170483	0.6	0.6	25
14	6	6	10	14	11	2	10	transforming, acidic coiled-coil containing protein 1	279245	0.122562227	0.219170483	0.6	0.6	44
1	20	16	33	17	32	18	20	mannosyl (alpha-1,3-)-glycoprotein beta-1,4-N-acetylglucosaminyltransferase, isoenzyme B	437277	0.022656807	0.02018875	0.606060606	0.484848485	110
8	11	6	18	14	21	8	2	a disintegrin and metalloproteinase domain 15 (metargidin)	312098	0.064754805	0.033505372	0.611111111	0.333333333	67
7	11	6	18	8	18	10	16	calponin 2	169718	0.064754805	0.033505372	0.611111111	0.333333333	58
4	11	8	18	6	11	18	16	cholinergic receptor, nicotinic, epsilon polypeptide	313227	0.064754805	0.064030129	0.611111111	0.444444444	50
3	11	10	18	18	15	6	10	growth factor receptor-bound protein 2	411366	0.064754805	0.102340951	0.611111111	0.555555556	67
6	8	6	13	12	7	6	12	lin-10 protein homolog	55923	0.097384098	0.119239898	0.615384615	0.461538462	43
4	8	8	13	3	12	12	4	cytochrome b-561 domain containing 2	149443	0.097384098	0.176083138	0.615384615	0.615384615	40
5	26	24	42	27	16	2	2	likely ortholog of mouse zinc finger protein EZI	112158	0.014982442	0.022660586	0.619047619	0.571428571	123
3	5	2	8	7	5	12	8	enthoprotin	132853	0.157484777	0.134162877	0.625	0.25	26
6	10	6	16	7	6	2	2	hypothetical protein ET	296924	0.079486573	0.057329069	0.625	0.375	42
6	10	8	16	19	16	8	14	stannin	76691	0.079486573	0.099598347	0.625	0.5	65
6	5	4	8	6	6	8	6	procollagen (type III) N-endopeptidase	183138	0.157484777	0.233082469	0.625	0.5	27
9	5	4	8	6	4	16	14	hypothetical protein FLJ22028	192570	0.157484777	0.233082469	0.625	0.5	25
8	25	24	40	39	22	14	32	glutaminyl-tRNA synthetase	79322	0.017835648	0.03202012	0.625	0.6	138
11	10	10	16	13	9	18	18	hypothetical protein FLJ20657	353191	0.079486573	0.145347868	0.625	0.625	53
21	10	10	16	16	14	24	24	KIAA1554 protein	195642	0.079486573	0.145347868	0.625	0.625	61
10	17	8	27	12	22	18	32	AT-hook transcription factor AKNA	159578	0.039274905	0.005908135	0.62962963	0.296296296	82
6	12	12	19	13	13	10	24	SCAN domain containing 2	283825	0.066032836	0.122126226	0.631578947	0.631578947	63
10	52	54	82	45	39	8	20	actin related protein 2/3 complex, subunit 5, 16kDa	126222	0.002431843	0.009190229	0.634146341	0.658536585	245
1	14	6	22	32	14	20	32	Similar to Elongation factor 1-delta (EF-1-delta) (Antigen NY-CO-4) (LOC126037), mRNA	446919	0.055544667	0.010505435	0.636363636	0.272727273	85
4	14	6	22	12	13		4	chemokine (C-C motif) receptor 1	301921	0.055544667	0.010505435	0.636363636	0.272727273	64
3	14	8	22	10	22	18	26	orosomucoid 2	278388	0.055544667	0.023726552	0.636363636	0.363636364	72
7	7	4	11	2	4	8	8	cyclic AMP phosphoprotein, 19 kD	7351	0.121766324	0.112255916	0.636363636	0.363636364	26
5	7	6	11	9	13	16	12	diacylglycerol kinase, zeta 104kDa	277445	0.121766324	0.18202174	0.636363636	0.545454545	43
6	7	6	11	6	12	10	14	metastasis associated 1	101448	0.121766324	0.18202174	0.636363636	0.545454545	39
2	25	26	39	24	25	14	22	basigin (OK blood group)	501293	0.021938293	0.052461535	0.641025641	0.666666667	126
4	9	2	14	13	8	8	6	caspase 8, apoptosis-related cysteine protease	243491	0.097770507	0.017262997	0.642857143	0.142857143	45
1	9	2	14	5	7	2	2	leukotriene B4 receptor	445013	0.097770507	0.017262997	0.642857143	0.142857143	36
4	9	6	14	9	17	16	8	DR1-associated protein 1 (negative cofactor 2 alpha)	356742	0.097770507	0.094481837	0.642857143	0.428571429	52
2	9	6	14	15	10	16	16	Transcribed sequences	304130	0.097770507	0.094481837	0.642857143	0.428571429	51
2	9	6	14	15	10	12	14	egl nine homolog 2 (C. elegans)	324277	0.097770507	0.094481837	0.642857143	0.428571429	51
3	9	6	14	13	8	2	16	SECIS binding protein 2	288141	0.097770507	0.094481837	0.642857143	0.428571429	47
8	15	14	23	26	20	2	2	Notch homolog 2 (Drosophila)	8121	0.05659114	0.088441503	0.652173913	0.608695652	91
10	71	48	107	62	66	66	34	guanine nucleotide binding protein (G protein), beta polypeptide 2	185172	#NUM!	2.02684E-05	0.663551402	0.448598131	330
7	6	2	9	7	7	8	6	hypothetical protein FLJ20308	356770	0.153110143	0.097273759	0.666666667	0.222222222	30
1	12	6	18	4	14	10	8	metallothionein 2A	418241	0.080894531	0.033505372	0.666666667	0.333333333	51
3	12	6	18	16	20	4	10	BH3 interacting domain death agonist	300825	0.080894531	0.033505372	0.666666667	0.333333333	69
4	8	4	12	9	7	8	6	phospholipase A2, group IVB (cytosolic)	198161	0.12049788	0.0854598	0.666666667	0.333333333	38
5	4	2	6	7	8	4	2	PQ loop repeat containing 1	288284	0.2054503	0.245062129	0.666666667	0.333333333	26
2	4	2	6	9	5	4	2	NS5ATP7 (NS5ATP7) mRNA, complete cds	355622	0.2054503	0.245062129	0.666666667	0.333333333	25
2	4	2	6	7	8	4	14	chromosome 10 open reading frame 95	225084	0.2054503	0.245062129	0.666666667	0.333333333	26
11	4	2	6	8	11		6	nudix (nucleoside diphosphate linked moiety X)-type motif 4	355399	0.2054503	0.245062129	0.666666667	0.333333333	30
2	10	6	15	17	16	14	18	karyopherin (importin) beta 1	439683	0.097770471	0.073983593	0.666666667	0.4	61
3	6	4	9	8	10	6	2	N-acetylglucosaminidase, alpha- (Sanfilippo disease IIIB)	50727	0.153110143	0.185894111	0.666666667	0.444444444	35
3	6	4	9	6	5	12	10	cyclin-dependent kinase 4	95577	0.153110143	0.185894111	0.666666667	0.444444444	28
5	6	4	9	9	15			solute carrier family 43, member 3	99962	0.153110143	0.185894111	0.666666667	0.444444444	41
3	8	6	12	8	7	6		tripartite motif-containing 38	511746	0.12049788	0.148470141	0.666666667	0.5	38

12	18	14	27	21	21	8	10	protective protein for beta-galactosidase (galactosialidosis)	118126	0.049063927	0.042373629	0.666666667	0.518518519	94
6	20	20	30	23	25	8	16	NPD014 protein	259412	0.042138283	0.077822578	0.666666667	0.666666667	108
8	16	16	24	25	37	10	28	ubiquitin-activating enzyme E1-like	16695	0.057475356	0.103604745	0.666666667	0.666666667	110
7	8	8	12	8	11	4	2	glucosidase, alpha; neutral AB	76847	0.12049788	0.206350894	0.666666667	0.666666667	43
5	8	8	12	7	6	10	8	hypothetical protein DKFZp434N1923	295866	0.12049788	0.206350894	0.666666667	0.666666667	37
6	6	6	9	3	10	6	2	utrophin (homologous to dystrophin)	250607	0.153110143	0.258364515	0.666666667	0.666666667	31
1	6	6	9	7	8	8	4	mitochondrial ribosomal protein S34	157160	0.153110143	0.258364515	0.666666667	0.666666667	33
6	6	6	9	6	5		4	DKFZP564O123 protein	11449	0.153110143	0.258364515	0.666666667	0.666666667	29
1	4	4	6	8	8		2	hematopoietically expressed homeobox	118651	0.2054503	0.340599052	0.666666667	0.666666667	28
3	4	4	6	7	8	2	4	retinol dehydrogenase 11 (all-trans and 9-cis)	226007	0.2054503	0.340599052	0.666666667	0.666666667	27