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
5	29	76	1	1	42	18	20	napsin B pseudogene	322854	2.74868E-08	1.19064E-16	29	76	111
6	6	10		5	10	8	4	diazepam binding inhibitor (GABA receptor modulator, acyl-Coenzyme A binding protein)	78888	0.015577782	0.006609552	12	20	26
7	11	30	2	8	11		4	ras homolog gene family, member B	406064	0.009475483	9.81737E-06	5.5	15	47
4	6	14	1	7	12	6	10	lymphoid-restricted membrane protein	124922	0.054555224	0.004165646	6	14	33
1	26	6		10	15	8	8	flightless I homolog (Drosophila)	531027	1.46774E-08	0.054746652	52	12	54
5	10	12	1	15	10	28	32	NADPH oxidase-related, C2 domain-containing protein	25895	0.005345146	0.010490186	10	12	42
5	8	12	1	10	7	4	12	fibrillarin	99853	0.017514394	0.010490186	8	12	32
2	7	10	1	8	4	2		chromosome 9 open reading frame 83	415534	0.031155552	0.025877907	7	10	25
4	5	10	1	11	9	10	10	male-specific lethal 3-like 1 (Drosophila)	371233	0.093579863	0.025877907	5	10	31
11	3	10	1	7	12	8	4	mitogen-activated protein kinase-activated protein kinase 2	75074	0.249848553	0.025877907	3	10	28
7	9	8	1	5	10	14	14	hypothetical protein FLJ13213	190114	0.009724332	0.062064129	9	8	29
19	111	138	19	27	11	8	4	v-fos FBJ murine osteosarcoma viral oncogene homolog	25647	2.0967E-17	7.33919E-17	5.842105263	7.263157895	237
5	14	14	2	3	3	12	14	chromosome 6 open reading frame 82	107187	0.001818903	0.012232092	7	7	29
5	12	14	2	9	9	4	4	PAP associated domain containing 4	220277	0.005524021	0.012232092	6	7	39
1	8	14	2	3	7	6	4	hypothetical protein FLJ14627	347310	0.043812478	0.012232092	4	7	27
8	7	6	1	8	12	30	10	hypothetical protein FLJ20297	94491	0.031155552	0.142897097	7	6	31
3	12	12	2	5	5	10	8	chromosome 20 open reading frame 6	369284	0.005524021	0.027380982	6	6	30
3	10	12	2	4	6	2	6	suppressor of Ty 4 homolog 1 (S. cerevisiae)	79058	0.016045141	0.027380982	5	6	28
4	7	12	2	8	2	12	14	diacylglycerol kinase, delta 130kDa	115907	0.070142406	0.027380982	3.5	6	25
7	7	18	3	5	3	2	6	chromosome 20 open reading frame 111	75798	0.116974743	0.005888996	2.333333333	6	27
23	19	32	6	13	8	14	18	zinc finger protein 216	406096	0.005239783	0.000339314	3.166666667	5.333333333	62
1	9	16	3	6	3	18	6	hypothetical protein FLJ22814	528682	0.053548565	0.012711455	3	5.333333333	29
7	7	16	3	4	4	4	6	SAR1a gene homolog 1 (S. cerevisiae)	110796	0.116974743	0.012711455	2.333333333	5.333333333	26
2	5	16	3	3	7	2	4	ethylmalonic encephalopathy 1	7486	0.218617324	0.012711455	1.666666667	5.333333333	26
1	12	10	2	4	4	10	8	FLJ45744 protein	528491	0.005524021	0.059102118	6	5	27
1	12	10	2	4	4	10	8	hypothetical protein LOC339834	383008	0.005524021	0.059102118	6	5	27
2	12	10	2	4	4	10	10	zinc finger protein 563	345226	0.005524021	0.059102118	6	5	27
3	7	10	2	8	7	2	2	mitogen-activated protein kinase kinase kinase 1	170610	0.070142406	0.059102118	3.5	5	29
2	45	70	14	11	6	32	20	chemokine (C-X-C motif) receptor 4	421986	2.2654E-05	1.91133E-07	3.214285714	5	111
1	6	10	2	7	6	2	6	ARC/mediator transcriptional coactivator subunit	528688	0.109176466	0.059102118	3	5	26
7	5	10	2	6	8	6		ets variant gene 6 (TEL oncogene)	171262	0.163863846	0.059102118	2.5	5	26
9	5	10	2	9	5			pituitary tumor-transforming 1 interacting protein	369026	0.163863846	0.059102118	2.5	5	26
7	5	10	2	10	7	6	10	ATPase, H+ transporting, lysosomal 31kDa, V1 subunit E isoform 1	77805	0.163863846	0.059102118	2.5	5	29
1	10	30	6	3	4	2		sin3-associated polypeptide, 30kDa	512813	0.121970405	0.000710217	1.666666667	5	38
13	7	14	3	7	8	4		stabilin 1	301989	0.116974743	0.026606351	2.333333333	4.666666667	32
6	5	14	3	8	9	2	2	small membrane protein 1	107979	0.218617324	0.026606351	1.666666667	4.666666667	32
5	13	18	4	9	16	24	26	integrin, alpha L (antigen CD11A (p180), lymphocyte function-associated antigen 1; alpha polypeptide)	174103	0.018070219	0.01248908	3.25	4.5	51
9	14	36	8	8	14	22	32	chromosome 6 open reading frame 32	389488	0.076008493	0.000365233	1.75	4.5	62
9	6	18	4	3	9	10	8	Clone IMAGE:5285814, mRNA	200022	0.204953666	0.01248908	1.5	4.5	31
2	8	22	5	6	6	4	4	formin binding protein 1	440808	0.156914091	0.006010732	1.6	4.4	36
8	15	30	7	26	6	26	10	chromobox homolog 3 (HP1 gamma homolog, Drosophila)	381189	0.040488837	0.001456538	2.142857143	4.285714286	69
12	26	2		45	37	54	52	ribosomal protein S4, Y-linked	180911	1.46774E-08	0.453464282	52	4	109
5	23	16	4	8	10	46	56	glutamyl-prolyl-tRNA synthetase	171292	0.000129341	0.024884124	5.75	4	53
7	16	16	4	6	11	2	4	CDNA FLJ44273 fis, clone TOVAR2001281	142074	0.004589884	0.024884124	4	4	45
8	8	8	2	9	8	2		CD33 antigen (gp67)	83731	0.043812478	0.121497618	4	4	31
7	11	12	3	8	8	2	2	RAB2, member RAS oncogene family	78305	0.022122838	0.053601399	3.666666667	4	36
2	12	16	4	5	3			Transcribed sequence with weak similarity to protein ref:NP_071385.1 (H.sapiens) hypothetical protein FLJ20958	77542	0.027653538	0.024884124	3	4	32
5	9	12	3	10	3	10	16	a disintegrin and metalloproteinase domain 8	86947	0.053548565	0.053601399	3	4	31
3	6	8	2	8	6	18	8	radical fringe homolog (Drosophila)	12862	0.109176466	0.121497618	3	4	26
1	14	20	5	11	11	18	14	small nuclear ribonucleoprotein D2 polypeptide 16.5kDa	424327	0.022071474	0.011893039	2.8	4	51
1	8	12	3	7	8	10	4	HSPC038 protein	449945	0.080371477	0.053601399	2.666666667	4	32
1	15	24	6	8	11	14	28	tripartite motif-containing 52	458412	0.025750044	0.005792011	2.5	4	52
8	10	16	4	14	11	6	6	solute carrier family 20 (phosphate transporter), member 1	110855	0.060911471	0.024884124	2.5	4	47
3	7	12	3	7	6	4	2	transmembrane protein 14C	30376	0.116974743	0.053601399	2.333333333	4	29
5	7	12	3	9	3	10	22	CDNA FLJ13267 fis, clone OVARC1000964	57079	0.116974743	0.053601399	2.333333333	4	28
6	11	20	5	7	6	12	12	Similar to RIKEN cDNA 1810037I17 (LOC401152), mRNA	173705	0.066448853	0.011893039	2.2	4	39
1	6	12	3	8	9	12	12	ATP synthase, H+ transporting, mitochondrial F1 complex, O subunit (oligomycin sensitivity conferring protein)	409140	0.163863786	0.053601399	2	4	32
7	5	12	3	7	12	8	14	periphilin 1	371140	0.218617324	0.053601399	1.666666667	4	33
5	6	16	4	4	7	14	8	STARD3 N-terminal like	13467	0.204953666	0.024884124	1.5	4	29
13	71	92	24	17	14	12	2	dual specificity phosphatase 1	171695	4.80602E-07	1.23891E-07	2.958333333	3.833333333	172
6	17	30	8	8	12	16	28	MRS2-like, magnesium homeostasis factor (S. cerevisiae)	146030	0.032077647	0.002732534	2.125	3.75	60
2	14	30	8	13	8	14	6	proteasome (prosome, macropain) 26S subunit, non-ATPase, 4	505059	0.076008493	0.002732534	1.75	3.75	58
6	14	22	6	7	10			Fc fragment of IgG, high affinity Ia, receptor for (CD64)	77424	0.036808048	0.011112989	2.333333333	3.666666667	48
8	11	22	6	12	9	4	4	MBC3205	8036	0.094192832	0.011112989	1.833333333	3.666666667	49
12	10	22	6	12	6	34	16	tumor rejection antigen (gp96) 1	192374	0.121970405	0.011112989	1.666666667	3.666666667	45
2	30	60	17	1	1		2	period homolog 1 (Drosophila)	445534	0.019336242	4.25688E-05	1.764705882	3.529411765	79
1	10	14	4	5	7	18	20	superoxide dismutase 1, soluble (amyotrophic lateral sclerosis 1 (adult))	443914	0.060911471	0.047744557	2.5	3.5	33
6	10	14	4	4	8		22	ATP-binding cassette, sub-family A (ABC1), member 7	134514	0.060911471	0.047744557	2.5	3.5	33
2	9	14	4	2	8	6		cut-like 1, CCAAT displacement protein (Drosophila)	438974	0.087069068	0.047744557	2.25	3.5	30
8	7	14	4	16	12	10	12	proteasome (prosome, macropain) subunit, beta type, 1	352768	0.160937588	0.047744557	1.75	3.5	46
6	6	14	4	5	6	8		methionine-tRNA synthetase	355867	0.204953666	0.047744557	1.5	3.5	28
2	16	24	7	13	12	6	14	NACHT, leucine rich repeat and PYD containing 1	511937	0.029083744	0.010258664	2.285714286	3.428571429	60
1	11	24	7	12	12	2	10	chromosome 6 open reading frame 49	525899	0.121178345	0.010258664	1.571428571	3.428571429	54
8	13	10	3	3	9	2		zinc finger protein 333	343604	0.008498491	0.102843683	4.333333333	3.333333333	33
3	8	10	3	6	6	2		chromosome 14 open reading frame 147	353161	0.080371477	0.102843683	2.666666667	3.333333333	28
2	8	10	3	10	12	4	4	mitochondrial ribosomal protein L33	14454	0.080371477	0.102843683	2.666666667	3.333333333	38
10	14	20	6	11	11	14	10	serine/threonine kinase 10	16134	0.036808048	0.020695094	2.333333333	3.333333333	52
4	6	10	3	8	10	8	4	Transcribed sequence with strong similarity to protein ref:NP_060755.1 (H.sapiens) mitochondrial ribosomal prote	6118	0.163863786	0.102843683	2	3.333333333	32
1	5	10	3	4	9	6		integrin, beta 3 (platelet glycoprotein IIIa, antigen CD61)	87149	0.218617324	0.102843683	1.666666667	3.333333333	26
3	5	10	3	4	9	6		epithelial membrane protein 2	356835	0.218617324	0.102843683	1.666666667	3.333333333	26
1	5	10	3	7	10	8	2	chromosome 15 open reading frame 12	513041	0.218617324	0.102843683	1.666666667	3.333333333	30
7	17	36	11	4	7	2	2	insulin receptor substrate 2	143648	0.079755482	0.00224736	1.545454545	3.272727273	57
8	12	16	5	9	5	14	10	RNA binding motif protein 8A	10283	0.047039459	0.04221838	2.4	3.2	39
8	12	16	5	7	5	10	8	tumor necrosis factor, alpha-induced protein 3	211600	0.047039459	0.04221838	2.4	3.2	37
9	48	100	32	63	55	30	30	lymphocyte-specific protein 1	56729	0.017959718	1.005E-06	1.5	3.125	248

1	14	28	9	19	12	14	30	chemokine (C-X3-C motif) receptor 1	78913	0.097180728	0.00855289	1.555555556	3.111111111	68
4	26	6	2	8	18	4		signal-regulatory protein beta 1	194784	1.38869E-06	0.233114486	13	3	57
10	10	6	2	9	7	8	4	F-box only protein 9	388387	0.016045141	0.233114486	5	3	31
3	8	6	2	10	9	2		Kruppel-like factor 4 (gut)	376206	0.043812478	0.233114486	4	3	32
4	8	6	2	5	11	4	2	golgi phosphoprotein 2	352662	0.043812478	0.233114486	4	3	29
6	7	6	2	5	8	6	4	hypothetical protein FLJ20533	106650	0.070142406	0.233114486	3.5	3	25
6	6	6	2	10	4	6	4	ATP-binding cassette, sub-family E (OABP), member 1	12013	0.109176466	0.233114486	3	3	25
3	17	18	6	7	8	12	4	MRNA; cDNA DKFZp686M14190 (from clone DKFZp686M14190)	380801	0.011961176	0.037225469	2.833333333	3	47
3	11	12	4	4	7	6	12	chromosome 19 open reading frame 22	388956	0.04150542	0.087442381	2.75	3	32
9	10	12	4	2	4	6	10	DKFZP434C171 protein	132994	0.060911471	0.087442381	2.5	3	26
4	9	12	4	7	8	12	4	HSPC038 protein	374485	0.087069068	0.087442381	2.25	3	34
4	8	12	4	7	4	10	4	high-mobility group 20B	406534	0.120630159	0.087442381	2	3	29
2	8	12	4	9	6	8	16	v-rel reticuloendotheliosis viral oncogene homolog A, nuclear factor of kappa light polypeptide gene enhancer in B	132594	0.120630159	0.087442381	2	3	33
4	8	12	4	9	5	6	14	zinc finger RNA binding protein	173518	0.120630159	0.087442381	2	3	32
7	4	6	2	12	5		4	C2f protein	135643	0.234232933	0.233114486	2	3	26
7	17	30	10	3	13	26	18	hypothetical protein FLJ31031	107101	0.062627129	0.00775686	1.7	3	58
3	10	18	6	6	16	2	2	transcription factor EB	23391	0.121970405	0.037225469	1.666666667	3	47
8	6	12	4	9	5	4	4	Rac/Cdc42 guanine nucleotide exchange factor (GEF) 6	372800	0.204953666	0.087442381	1.5	3	30
6	6	12	4	6	10	4	6	peptidylprolyl isomerase F (cyclophilin F)	381072	0.204953666	0.087442381	1.5	3	32
7	15	26	9	15	14	14	28	mitochondrial ribosomal protein L20	182698	0.077697542	0.014983244	1.666666667	2.888888889	66
1	11	14	5	7	4	10	6	surfeit 1	423854	0.066448853	0.074772337	2.2	2.8	34
6	11	14	5	7	5	4	4	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 1, 7kDa	183435	0.066448853	0.074772337	2.2	2.8	35
12	40	56	20	10	15	16	16	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, alpha	81328	0.003594247	0.000598135	2	2.8	113
3	9	14	5	9	5	8	8	chromosome 14 open reading frame 39	335754	0.12197045	0.074772337	1.8	2.8	35
6	8	14	5	6	8	4	2	calmodulin binding transcription activator 1	253254	0.156914091	0.074772337	1.6	2.8	34
5	20	22	8	9	11	6	10	spinster-like	379091	0.011501726	0.028898856	2.5	2.75	59
2	27	30	11	24	24	16	20	ADP-ribosylation factor-like 10A	424552	0.004338079	0.011963892	2.454545455	2.727272727	101
5	11	8	3	3	6	14	6	component of oligomeric golgi complex 1	283109	0.022122838	0.184990913	3.666666667	2.666666667	27
8	10	8	3	4	4	4	4	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit f, isoform 2	235557	0.034785507	0.184990913	3.333333333	2.666666667	25
3	7	8	3	1	11	4	8	general transcription factor IIB	258561	0.116974743	0.184990913	2.333333333	2.666666667	26
5	20	24	9	28	16	12	10	chromosome 20 open reading frame 24	184062	0.01854177	0.025481165	2.222222222	2.666666667	85
6	6	8	3	7	7	14	8	hypothetical protein from EUROIMAGE 1977056	8694	0.163863786	0.184990913	2	2.666666667	27
3	6	8	3	7	8			hypothetical protein MGC15619	334637	0.163863786	0.184990913	2	2.666666667	28
2	6	8	3	2	18		10	1-aminocyclopropane-1-carboxylate synthase	126706	0.163863786	0.184990913	2	2.666666667	33
4	11	16	6	6	7	6	8	hypothetical protein FLJ20647	234149	0.094192832	0.064281232	1.833333333	2.666666667	38
11	16	24	9	11	18	6	4	MRNA; cDNA DKFZp762M127 (from clone DKFZp762M127)	12853	0.060664477	0.025481165	1.777777778	2.666666667	66
1	10	16	6	10	15	12	20	KIAA0754 protein	159183	0.121970405	0.064281232	1.666666667	2.666666667	49
18	9	16	6	4	4	4	2	Clone IMAGE:5302006, mRNA	351680	0.152555311	0.064281232	1.5	2.666666667	31
8	9	16	6	17	9	12	12	heterogeneous nuclear ribonucleoprotein M	385766	0.152555311	0.064281232	1.5	2.666666667	49
3	20	26	10	18	20	2	2	frequently rearranged in advanced T-cell lymphomas 2	140720	0.027829483	0.022487415	2	2.6	81
2	15	26	10	7	7	12	12	cytochrome c-1	289271	0.097180692	0.022487415	1.5	2.6	52
2	27	28	11	20	17	12	22	tubulin, alpha, ubiquitous	446608	0.004338079	0.019864752	2.454545455	2.545454545	89
2	10	10	4	7	3	14	4	LOC388789 (LOC388789), mRNA	349092	0.060911471	0.150996188	2.5	2.5	29
2	8	10	4	5	7	12	2	UBX domain containing 1	435255	0.120630159	0.150996188	2	2.5	29
5	8	10	4	7	3	8	6	putative membrane protein	93832	0.120630159	0.150996188	2	2.5	27
3	7	10	4	6	7	12		translocase of inner mitochondrial membrane 17 homolog B (yeast)	19105	0.160937588	0.150996188	1.75	2.5	29
6	7	10	4	7	5	6	2	polymerase (RNA) III (DNA directed) polypeptide H (22.9kD)	202505	0.160937588	0.150996188	1.75	2.5	28
7	7	10	4	7	7	8	4	chromosome 10 open reading frame 45	103378	0.160937588	0.150996188	1.75	2.5	30
8	7	10	4	5	5	16	22	retinoblastoma binding protein 6	188553	0.160937588	0.150996188	1.75	2.5	26
10	6	10	4	10	9	8	6	casein kinase 1, delta	378918	0.204953666	0.150996188	1.5	2.5	34
2	6	10	4	11	7			PDZ and LIM domain 7 (enigma)	436339	0.204953666	0.150996188	1.5	2.5	33
7	6	10	4	8	10	4	16	splicing factor YT521-B	86405	0.204953666	0.150996188	1.5	2.5	33
18	54	88	36	22	41	20	12	potassium channel tetramerisation domain containing 12	109438	0.013832754	0.000126171	1.5	2.444444444	197
7	11	12	5	8	11			ubiquitin-conjugating enzyme E2D 1 (UBC4/5 homolog, yeast)	129683	0.066448853	0.12553086	2.2	2.4	41
1	21	24	10	16	13	22	26	CDNA FLJ46261 fis, clone TESTI4025062	447456	0.020528381	0.036580346	2.1	2.4	72
1	21	24	10	16	13	22	26	Similar to eukaryotic initiation factor 5A isoform I variant A (LOC143244), mRNA	511828	0.020528381	0.036580346	2.1	2.4	72
4	9	12	5	6	4	8	4	protein tyrosine phosphatase, non-receptor type 12	62	0.12197045	0.12553086	1.8	2.4	30
2	9	12	5	4	5	6	4	tetratricopeptide repeat domain 15	5008	0.12197045	0.12553086	1.8	2.4	29
1	9	12	5	8	5			hypothetical protein FLJ20701	424598	0.12197045	0.12553086	1.8	2.4	33
3	9	12	5	8	9	4	4	nucleoporin 93kDa	295014	0.12197045	0.12553086	1.8	2.4	37
5	8	12	5	10	10	6	26	splicing factor 3a, subunit 3, 60kDa	77897	0.156914091	0.12553086	1.6	2.4	39
8	25	26	11	24	12		4	hypothetical protein DKFZp434L142	323583	0.00867431	0.032015769	2.272727273	2.363636364	85
3	40	28	12	15	18	4	12	CCAAT/enhancer binding protein (C/EBP), beta	99029	4.50825E-05	0.028085432	3.333333333	2.333333333	99
1	18	14	6	19	9	10		arrestin, beta 2	435811	0.007969293	0.105715556	3	2.333333333	59
10	9	14	6	18	8	12	6	signal peptidase 12kDa	11125	0.152555311	0.105715556	1.5	2.333333333	48
5	9	14	6	6	6	8	6	DEAD (Asp-Glu-Ala-Asp) box polypeptide 54	203581	0.152555311	0.105715556	1.5	2.333333333	34
13	9	14	6	10	8	6	6	ROD1 regulator of differentiation 1 (S. pombe)	374634	0.152555311	0.105715556	1.5	2.333333333	40
6	30	30	13	13	8	8	6	major histocompatibility complex, class II, DQ beta 2	375115	0.004118211	0.024687742	2.307692308	2.307692308	79
1	80	106	46	74	67	146	104	Transcribed sequence with weak similarity to protein pdb:2RMA (H.sapiens) S Chain S, Cyclophilin A	404768	0.000694046	7.14658E-05	1.739130435	2.304347826	320
2	80	106	46	74	67	146	104	Similar to peptidyl-Pro cis trans isomerase (LOC391532), mRNA	177285	0.000694046	7.14658E-05	1.739130435	2.304347826	320
11	27	34	15	18	27	8	4	N-acylsphingosine amidohydrolase (acid ceramidase)-like	264330	0.022286511	0.019175658	1.8	2.266666667	104
9	47	70	31	20	34	44	36	Fc fragment of IgG, low affinity IIIa, receptor for (CD16)	372679	0.01745958	0.001278764	1.516129032	2.258064516	167
2	14	18	8	7	6	18	8	chromosome 19 open reading frame 20	370411	0.076008493	0.076989722	1.75	2.25	44
6	68	80	36	50	42	46	60	attractin	373838	0.000540168	0.000742987	1.888888889	2.222222222	236
3	28	40	18	28	27	14	20	MARCKS-like protein	75061	0.039841838	0.013266023	1.555555556	2.222222222	121
12	14	20	9	12	7	16	18	ATP synthase, H+ transporting, mitochondrial F1 complex, alpha subunit, isoform 1, cardiac muscle	298280	0.097180728	0.066332969	1.555555556	2.222222222	52
10	32	42	19	7	5	16	12	inhibitor of DNA binding 2, dominant negative helix-loop-helix protein	180919	0.021364439	0.011759952	1.684210526	2.210526316	84
12	110	152	69	69	92	52	26	integrin, beta 2 (antigen CD18 (p95), lymphocyte function-associated antigen 1; macrophage antigen 1 (mac-1) be	375957	#NUM!	6.75058E-06	1.594202899	2.202898551	416
3	31	30	14	21	21	26	28	Transcribed sequence with strong similarity to protein pir:S02061 (H.sapiens) S02061 heterogeneous ribonuclear	374637	0.004697036	0.033370075	2.214285714	2.142857143	102
1	76	100	47	63	47	86	76	ribosomal protein L12	408054	0.002303002	0.000342667	1.617021277	2.127659574	283
32	105	126	60	94	86	162	122	peptidylprolyl isomerase A (cyclophilin A)	356331	0.000125496	8.63327E-05	1.75	2.1	408
8	51	56	27	29	52	78	46	FLJ20758 protein	323489	0.002187727	0.006885787	1.888888889	2.074074074	187
2	13	8	4	16	11	4	8	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit e	85539	0.018070219	0.241427222	3.25	2	48
7	16	10	5	10	12	8	8	v-raf-1 murine leukemia viral oncogene homolog 1	257266	0.009644588	0.197061519	3.2	2	48
6	15	10	5	4	5	10	8	ceroid-lipofuscinosis, neuronal 8 (epilepsy, progressive with mental retardation)	127675	0.014705413	0.197061519	3	2	34
1	9	6	3	15	7	6	2	protein phosphatase 1, regulatory (inhibitor) subunit 12C	437055	0.053548565	0.304232148	3	2	37

	4	9	6	3	6	4		2	interferon gamma receptor 1	180866	0.053548565	0.304232148	3	2	25
	3	6	4	2	5	10		2	chromosome 2 open reading frame 24	4973	0.109176466	0.402543918	3	2	25
	2	11	8	4	3	5		6	KIAA1244	194408	0.04150542	0.241427222	2.75	2	27
	4	13	10	5	17	7	14	4	Transcribed sequence with strong similarity to protein pir:S12566 (H.sapiens) S12566 translation initiation factor e	381018	0.032546075	0.197061519	2.6	2	47
	3	23	18	9	7	9	22	16	hypothetical protein LOC148206	135553	0.006479414	0.100477448	2.555555556	2	57
	3	10	8	4	7	17	4	2	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 5, 16kDa	19236	0.060911471	0.241427222	2.5	2	42
	6	10	8	4	6	8			hepatocellular carcinoma-associated antigen 112	12126	0.060911471	0.241427222	2.5	2	32
	12	5	4	2	6	10	2	4	peroxiredoxin 3	397062	0.163863846	0.402543918	2.5	2	25
	5	12	10	5	10	9	2	16	histone deacetylase 1	88556	0.047039459	0.197061519	2.4	2	41
	4	30	26	13	19	14	6	8	ribosomal protein S6 kinase, 90kDa, polypeptide 4	105584	0.004118211	0.0568021	2.307692308	2	89
	10	11	10	5	5	11	6	4	thyroid hormone receptor interactor 6	380230	0.066448853	0.197061519	2.2	2	37
	10	11	10	5	12	11	6	6	nuclear receptor coactivator 3	382168	0.066448853	0.197061519	2.2	2	44
	6	13	12	6	6	7	4	8	jun D proto-oncogene	2780	0.051562465	0.163827327	2.166666667	2	38
	9	23	22	11	22	24	8	16	zinc finger protein 106 homolog (mouse)	188199	0.016542507	0.074943673	2.090909091	2	91
	11	38	38	19	25	26	26	38	glutathione S-transferase subunit 13 homolog	390667	0.004372041	0.026225016	2	2	127
	7	18	18	9	22	11	24	14	APEX nuclease (multifunctional DNA repair enzyme) 1	73722	0.034750772	0.100477448	2	2	69
	2	12	12	6	10	24	18	14	annexin A6	412117	0.07060188	0.163827327	2	2	58
	9	8	8	4	12	6	2		KIAA0513 gene product	301658	0.120630159	0.241427222	2	2	34
	1	8	8	4	2	12	6	4	KIAA0415 gene product	505758	0.120630159	0.241427222	2	2	30
	8	6	6	3	10	7	6		protein phosphatase 1, regulatory (inhibitor) subunit 15B	355489	0.163863786	0.304232148	2	2	29
	5	6	6	3	5	10	8	4	metaxin 1	247551	0.163863786	0.304232148	2	2	27
	3	6	6	3	7	6	2	10	immunoglobulin (CD79A) binding protein 1	3631	0.163863786	0.304232148	2	2	25
	3	11	12	6	7	9	4	2	arrestin, beta 1	112278	0.094192832	0.163827327	1.833333333	2	39
	1	11	12	6	4	14	14	14	Similar to MGC9515 protein (LOC388240), mRNA	454681	0.094192832	0.163827327	1.833333333	2	41
	1	11	12	6	4	14	14	14	Similar to MGC9515 protein (LOC400520), mRNA	528462	0.094192832	0.163827327	1.833333333	2	41
	1	11	12	6	4	14	14	14	Similar to nuclear pore complex interacting protein (LOC388237), mRNA	512290	0.094192832	0.163827327	1.833333333	2	41
	1	11	12	6	4	14	14	14	hypothetical protein MGC9515	460311	0.094192832	0.163827327	1.833333333	2	41
	1	11	12	6	4	14	14	14	Similar to nuclear pore complex interacting protein (LOC400515), mRNA	528464	0.094192832	0.163827327	1.833333333	2	41
	5	16	18	9	5	4	6	2	furin (paired basic amino acid cleaving enzyme)	59242	0.060664477	0.100477448	1.777777778	2	43
	1	21	24	12	14	14	18	18	zinc finger protein 514	512794	0.04110646	0.065136534	1.75	2	73
	3	7	8	4	4	9	6	2	similar to RIKEN cDNA B230118G17 gene	337228	0.160937588	0.241427222	1.75	2	28
	5	19	22	11	13	15	6	12	oxoglutarate (alpha-ketoglutarate) dehydrogenase (lipoamide)	168669	0.050660328	0.074943673	1.727272727	2	69
	7	36	42	21	24	23	4	2	leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 2	306230	0.014671393	0.020530574	1.714285714	2	125
	4	12	14	7	7	7	12	14	purinergic receptor P2Y, G-protein coupled, 5	123464	0.095874812	0.137966848	1.714285714	2	40
	9	10	12	6	5	10			egf-like module containing, mucin-like, hormone receptor-like 2	137354	0.121970405	0.163827327	1.666666667	2	37
	2	10	12	6	2	8	2	4	hypothetical protein FLJ20607	345908	0.121970405	0.163827327	1.666666667	2	32
	6	5	6	3	6	8	8		HMBA-inducible	15299	0.218617324	0.304232148	1.666666667	2	25
	8	5	6	3	9	5	4	4	secretory carrier membrane protein 4	144980	0.218617324	0.304232148	1.666666667	2	25
	11	8	10	5	7	10	6	4	chromosome 14 open reading frame 170	303775	0.156914091	0.197061519	1.6	2	35
	3	8	10	5	9	6	10	8	ubiquitin-conjugating enzyme E2D 2 (UBC4/5 homolog, yeast)	108332	0.156914091	0.197061519	1.6	2	33
	5	8	10	5	13	4	4	6	phosphatidylinositol transfer protein, membrane-associated 1	93837	0.156914091	0.197061519	1.6	2	35
	9	8	10	5	11	9	2	8	serologically defined breast cancer antigen 84	169992	0.156914091	0.197061519	1.6	2	38
	3	22	28	14	16	5	2	8	ninjurin 1	11342	0.05500954	0.049675609	1.571428571	2	71
	5	11	14	7	7	11	2	4	centromere protein B, 80kDa	85004	0.121178345	0.137966848	1.571428571	2	43
	6	25	32	16	20	20	16	6	methyl-CpG binding domain protein 2	25674	0.046647494	0.038262894	1.5625	2	97
	15	12	16	8	8	13	12	16	cancer susceptibility candidate 3	350229	0.119916027	0.117305695	1.5	2	49
	6	6	8	4	8	6	8	2	aconitase 2, mitochondrial	300463	0.204953666	0.241427222	1.5	2	28
	11	57	62	32	34	55	86	62	translocase of outer mitochondrial membrane 7 homolog (yeast)	112318	0.002464874	0.008188245	1.78125	1.9375	209
	5	52	52	27	23	49	72	44	hypothetical protein LOC201725	380920	0.001660825	0.014517921	1.925925926	1.925925926	177
	18	85	90	47	69	56	82	90	eukaryotic translation elongation factor 2	75309	0.000275661	0.002224447	1.808510638	1.914893617	302
	4	27	34	18	18	15	20	22	putative NFkB activating protein	269592	0.048532472	0.042735354	1.5	1.888888889	95
	9	29	24	13	8	8	22	18	talin 1	375001	0.00574982	0.081738592	2.230769231	1.846153846	70
	7	37	22	12	37	20	12	16	RAVER1	205736	0.000161529	0.093731898	3.083333333	1.833333333	117
	4	18	22	12	20	15	24	32	splicing factor, arginine/serine-rich 11	443458	0.08030931	0.093731898	1.5	1.833333333	76
	20	53	42	23	33	24	140	144	ribosomal protein S27a	311640	0.000221871	0.032687628	2.304347826	1.826086957	154
	12	40	40	22	32	28	52	50	splicing factor, arginine/serine-rich 5	166975	0.007364662	0.036804109	1.818181818	1.818181818	142
	10	26	18	10	18	9	10	18	H1 histone family, member X	75307	0.003665462	0.124574181	2.6	1.8	72
	5	18	18	10	21	16	16	16	Src-like-adaptor 2	334489	0.048680517	0.124574181	1.8	1.8	74
	7	33	34	19	25	23	16	18	solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 5	79172	0.016822404	0.052837475	1.736842105	1.789473684	117
	12	19	16	9	12	5	8	2	c-Maf-inducing protein	19597	0.025590339	0.144587702	2.111111111	1.777777778	53
	8	16	16	9	13	14	10	8	transmembrane 9 superfamily member 2	298272	0.060664477	0.144587702	1.777777778	1.777777778	60
	1	293	238	136	185	98	328	240	protein tyrosine phosphatase, non-receptor type 14	512667	#NUM!	#NUM!	2.154411765	1.75	831
	1	293	238	136	185	98	328	240	xylulokinase homolog (H. influenzae)	137580	#NUM!	#NUM!	2.154411765	1.75	831
	2	15	14	8	14	14	8	8	GLI pathogenesis-related 1 (glioma)	511765	0.05823792	0.168803661	1.875	1.75	58
	1	14	14	8	8	15	12	8	citrate synthase	430606	0.076008493	0.168803661	1.75	1.75	52
	3	14	14	8	9	6	22	28	pan-hematopoietic expression	271954	0.076008493	0.168803661	1.75	1.75	44
	2	19	12	7	17	13	8	12	caspase recruitment domain family, member 6	200242	0.009736914	0.198535194	2.714285714	1.714285714	62
	10	11	12	7	7	8	8	4	beta 5-tubulin	356729	0.121178345	0.198535194	1.571428571	1.714285714	39
	10	11	12	7	6	7	2	2	phosphatidylinositol binding clathrin assembly protein	39252	0.121178345	0.198535194	1.571428571	1.714285714	37
	7	27	22	13	35	26	26	18	ubiquinol-cytochrome c reductase binding protein	131255	0.010858325	0.112917472	2.076923077	1.692307692	112
	2	22	22	13	11	8	36	44	sparc/osteonectin, cwcv and kazal-like domains proteoglycan (testican) 3	159425	0.042759326	0.112917472	1.692307692	1.692307692	65
	1	22	22	13	11	7	36	44	Similar to ribosomal protein S15; rat insulinoma gene (LOC401019), mRNA	426104	0.042759326	0.112917472	1.692307692	1.692307692	64
	3	15	10	6	3	12	6	12	hypothetical protein FLJ14154	312841	0.025750044	0.235748592	2.5	1.666666667	41
	4	12	10	6	2	8	12	16	chromosome 10 open reading frame 86	258798	0.07060188	0.235748592	2	1.666666667	33
	3	31	30	18	34	23	22	36	KIAA0101 gene product	81892	0.020375818	0.080908615	1.722222222	1.666666667	121
	1	31	30	18	32	23	20	36	RAB3B, member RAS oncogene family	123072	0.020375818	0.080908615	1.722222222	1.666666667	119
	5	10	10	6	9	5	4		hypothetical protein FLJ31121	350194	0.121970405	0.235748592	1.666666667	1.666666667	35
	12	10	10	6	11	16	4	10	ankyrin repeat domain 11	402727	0.121970405	0.235748592	1.666666667	1.666666667	48
	11	18	20	12	14	10	30	30	small nuclear ribonucleoprotein 70kDa polypeptide (RNP antigen)	174051	0.08030931	0.129016429	1.5	1.666666667	64
	2	9	10	6	8	2	14	12	small nuclear ribonucleoprotein polypeptide G	436656	0.152555311	0.235748592	1.5	1.666666667	30
	5	9	10	6	7	9	2	6	interleukin 17 receptor	129751	0.152555311	0.235748592	1.5	1.666666667	36
	60	330	228	138	292	260	502	602	ribosomal protein L10	401929	#NUM!	#NUM!	2.391304348	1.652173913	1134
	6	13	8	5	5	4	10	4	prohibitin	75323	0.032546075	0.283572811	2.6	1.6	31
	8	13	8	5	12	12	12	14	chromosome 19 open reading frame 13	8258	0.032546075	0.283572811	2.6	1.6	46
	2	13	8	5	18	11	4	8	zinc finger and BTB domain containing 5	3682	0.032546075	0.283572811	2.6	1.6	51
	4	12	8	5	9	6	20	4	BCL2-associated X protein	159428	0.047039459	0.283572811	2.4	1.6	36

2	12	8	5	5	10		2	COMM domain containing 9	279836	0.047039459	0.283572811	2.4	1.6	36
5	11	8	5	7	10	16	2	U2 (RNU2) small nuclear RNA auxiliary factor 2	297629	0.066448853	0.283572811	2.2	1.6	37
6	10	8	5	5	8	8	2	olfactomedin-like 2A	357004	0.091422488	0.283572811	2	1.6	32
9	10	8	5	9	8	8	6	axotrophin	5306	0.091422488	0.283572811	2	1.6	36
6	10	8	5	7	5			erythrocyte membrane protein band 4.1-like 3	103839	0.091422488	0.283572811	2	1.6	31
2	9	8	5	7	6	4		asparaginyl-tRNA synthetase	427212	0.12197045	0.283572811	1.8	1.6	31
2	9	8	5	7	4	4	4	Transcribed sequence with weak similarity to protein pir:A46010 (H.sapiens) A46010 X-linked retinopathy protein	106015	0.12197045	0.283572811	1.8	1.6	29
3	9	8	5	6	8	8	8	component of oligomeric golgi complex 4	208680	0.12197045	0.283572811	1.8	1.6	32
1	9	8	5	10	22	6	10	NADH dehydrogenase (ubiquinone) Fe-S protein 6, 13kDa (NADH-coenzyme Q reductase)	408257	0.12197045	0.283572811	1.8	1.6	50
2	8	8	5	8	8	18	14	hypothetical protein FLJ21438	136979	0.156914091	0.283572811	1.6	1.6	33
7	8	8	5	8	3		6	ubiquilin 1	9589	0.156914091	0.283572811	1.6	1.6	28
10	15	16	10	14	7	20	10	LIM and SH3 protein 1	334851	0.097180692	0.169828161	1.5	1.6	54
3	15	14	9	7	3	14	2	general transcription factor II, i	408507	0.077697542	0.195823667	1.666666667	1.555555556	41
3	15	14	9	13	6	12	8	SCY1-like 1 (S. cerevisiae)	238839	0.077697542	0.195823667	1.666666667	1.555555556	50
7	24	20	13	26	19	20	20	DiGeorge syndrome critical region gene 8	350243	0.025763823	0.14894823	1.846153846	1.538461538	92
9	20	20	13	21	10	4	10	low density lipoprotein receptor-related protein associated protein 1	75140	0.066483146	0.14894823	1.538461538	1.538461538	74
10	13	6	4	12	14	16	4	HSPC182 protein	30026	0.018070219	0.347415346	3.25	1.5	46
4	13	6	4	11	9	8	8	makorin, ring finger protein, 2	279474	0.018070219	0.347415346	3.25	1.5	40
6	10	6	4	10	2	4	2	carnitine palmitoyltransferase 1A (liver)	259785	0.060911471	0.347415346	2.5	1.5	29
6	10	6	4	3	5	24	18	DKFZP586N0721 protein	99843	0.060911471	0.347415346	2.5	1.5	25
5	10	6	4	13	9	10	12	microtubule associated serine/threonine kinase 3	173864	0.060911471	0.347415346	2.5	1.5	39
1	10	6	4	11	6	4	8	hypothetical protein LOC283932	421392	0.060911471	0.347415346	2.5	1.5	34
2	10	6	4	6	9	2	4	TPA regulated locus	429961	0.060911471	0.347415346	2.5	1.5	32
4	9	6	4	8	5	2	2	selenoprotein X, 1	279623	0.087069068	0.347415346	2.25	1.5	29
6	9	6	4	5	4	4	6	zinc finger CCCH type domain containing 1	12646	0.087069068	0.347415346	2.25	1.5	25
2	9	6	4	9	2		4	eukaryotic translation initiation factor 2B, subunit 4 delta, 67kDa	169474	0.087069068	0.347415346	2.25	1.5	27
1	8	6	4	6	5	4		KIAA0953	227850	0.120630159	0.347415346	2	1.5	26
6	8	6	4	6	7	2		LATS, large tumor suppressor, homolog 2 (Drosophila)	78960	0.120630159	0.347415346	2	1.5	28
4	8	6	4	5	6	2	2	breast cancer 1, early onset	194143	0.120630159	0.347415346	2	1.5	26
5	8	6	4	5	9	4	4	dishevelled, dsh homolog 3 (Drosophila)	381928	0.120630159	0.347415346	2	1.5	29
8	8	6	4	9	4	4	10	Rab geranylgeranyltransferase, beta subunit	78948	0.120630159	0.347415346	2	1.5	28
5	14	12	8	11	10	8	10	serine/threonine kinase receptor associated protein	3727	0.076008493	0.226715597	1.75	1.5	49
5	14	12	8	11	6	4	10	proteolipid protein 2 (colonic epithelium-enriched)	77422	0.076008493	0.226715597	1.75	1.5	45
2	7	6	4	6	7	14	6	CDNA FLJ30403 fis, clone BRACE2008480	224719	0.160937588	0.347415346	1.75	1.5	27
5	7	6	4	3	8	4	2	COMM domain containing 5	378713	0.160937588	0.347415346	1.75	1.5	25
6	7	6	4	6	11	6	8	beclin 1 (coiled-coil, myosin-like BCL2 interacting protein)	12272	0.160937588	0.347415346	1.75	1.5	31
4	13	12	8	5	10	6	16	mitochondrial ribosomal protein L49	75859	0.09679665	0.226715597	1.625	1.5	42
12	82	78	52	52	63	108	108	ribosomal protein L35a	289093	0.002345143	0.030567929	1.576923077	1.5	288
6	12	12	8	16	15	8	14	APG4 autophagy 4 homolog B (S. cerevisiae)	283610	0.119916027	0.226715597	1.5	1.5	57
10	6	6	4	5	7	8	10	helicase with zinc finger domain	99437	0.204953666	0.347415346	1.5	1.5	25