

Appendix 2

Tables of up and down regulated genes in microarray investigations (chapter 6)

Appendix for Microarray studies

List of 19 genes 'up-regulated' by 2-fold or more in all three slides

<i>Number</i>	<i>Accession ID</i>	<i>Unigene No.</i>	<i>Symbol</i>	<i>Description</i>
1	Z95114	Hs.241535	APOL3	Apolipoprotein L, 3
2	BG704851	Hs.85539	ATP5I	ATP synthase, H ⁺ transporting, mitochondrial F0 complex, subunit e
3	AV722422	Hs.146409	CDC42	Cell division cycle 42 (GTP binding protein, 25kd)
4	AV652811	Hs.99886	C4BPB	Complement component 4 binding protein, beta
5	NM_001261	Hs.150423	CDK9	Cyclin-dependent kinase 9 (CDC2-related kinase)
6	AF029403	Hs.144877	CYP7B1	Cytochrome P450, subfamily VIIB (oxysterol 7 alpha-hydroxylase), polypeptide 1
7	AW183567	Hs.96513		Homo sapiens, clone MGC:4459 IMAGE:2960564, mrna, complete cds
8	AI249658	Hs.13075	MGC3207	Hypothetical protein MGC3207
9	BE799139	Hs.178728	MBD3	Methyl-cpg binding domain protein 3
10	AI888832	Hs.24719	MAP-1	Modulator of apoptosis 1
11	AI280973	Hs.100724	PPARG	Peroxisome proliferative activated receptor, gamma
12	AI640735	Hs.285306	SCLY	Putative selenocysteine lyase
13	N92548	Hs.263671	RDX	Radixin
14	BE091961	Hs.102336	ARHGAP8	Rho gtpase activating protein 8
15	AW973154	Hs.184014	RPL31	Ribosomal protein L31
16	AV709655	Hs.180450	RPS24	Ribosomal protein S24
17	BG479933	Hs.3297	RPS27A	Ribosomal protein s27a
18	AA927505	Hs.108957	RPS27L	Ribosomal protein S27-like
19	AV763087	Hs.76136	TXN	Thioredoxin

List of 41 genes 'down-regulated' by 2-fold or more in all three slides

<i>Number</i>	<i>Accession</i>	<i>Unigene No.</i>	<i>Symbol</i>	<i>Description</i>
1	AA334424	Hs.155421	AFP	Alpha-fetoprotein
2	NM_004034	Hs.78637	ANXA7	Annexin A7
3	NM_001673	Hs.75692	ASNS	Asparagine synthetase
4	NM_001689	Hs.429	ATP5G3	ATP synthase, H ⁺ transporting, mitochondrial F0 complex, subunit c (subunit 9) isoform 3
5	NM_014670	Hs.155291	BZAP45	Basic leucine-zipper protein BZAP45
6	BC007340	Hs.106880	BYSL	Bystin-like
7	BG389453	Hs.182278	CALM2	Calmodulin 2 (phosphorylase kinase, delta)
8	NM_001746	Hs.155560	CANX	Calnexin
9	BE884067	Hs.296634	CP	Ceruloplasmin (ferroxidase)

10	AA314436	Hs.108809	CCT7	Chaperonin containing TCP1, subunit 7 (eta)
11	BG824258	Hs.15591	MOV34-34KD	COP9 subunit 6 (MOV34 homolog, 34 kd)
12	BG683393	Hs.254105	ENO1	Enolase 1, (alpha)
13	BG503248	Hs.151777	EIF2S1	Eukaryotic translation initiation factor 2, subunit 1 (alpha, 35kd)
14	BG678179	Hs.173912	EIF4A2	Eukaryotic translation initiation factor 4A, isoform 2
15	NM_004958	Hs.338207	FRAP1	FK506 binding protein 12-rapamycin associated protein 1
16	W02972	Hs.296261	GNAQ	Guanine nucleotide binding protein (G protein), q polypeptide
17	BG035543	Hs.3352	HDAC2	Histone deacetylase 2
18	BG743005	Hs.168694		Homo sapiens clone 23763 unknown mrna, partial cds
19	AI911657	Hs.76095	IER3	Immediate early response 3
20	AL550285	Hs.177559	IFNGR2	Interferon gamma receptor 2 (interferon gamma transducer 1)
21	BG560803	Hs.81892	KIAA0101	KIAA0101 gene product
22	BE886912	Hs.75574	MRPL19	Mitochondrial ribosomal protein L19
23	AA345289	Hs.233936	MLCB	Myosin, light polypeptide, regulatory, non-sarcomeric (20kd)
24	BG753137	Hs.80595	NDUFS5	NADH dehydrogenase (ubiquinone) Fe-S protein 5 (15kd) (NADH-coenzyme Q reductase)
25	BG619874	Hs.137476	PEG10	Paternally expressed 10
26	AW949594	Hs.171834	PCTK1	PCTAIRE protein kinase 1
27	AL547497	Hs.173125	PPIF	Peptidylprolyl isomerase F (cyclophilin F)
28	NM_014754	Hs.77329	PTDSS1	Phosphatidylserine synthase 1
29	NM_000928	Hs.992	PLA2G1B	Phospholipase A2, group IB (pancreas)
30	Y11950	Hs.196177	PHKG2	Phosphorylase kinase, gamma 2 (testis)
31	BG829879	Hs.4745	PSMC1	Proteasome (prosome, macropain) 26S subunit, atpase, 1
32	BG397566	Hs.155975	PTPRCAP	Protein tyrosine phosphatase, receptor type, C-associated protein
33	AW327267	Hs.183698		Ribosomal protein L29
34	BF669160	Hs.350108	RPLP0	Ribosomal protein, large, P0
35	J04982	Hs.2043	SLC25A4	Solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 4
36	N41981	Hs.78869	TCEA1	Transcription elongation factor A (SII), 1
37	AJ006412	Hs.158688	IF2	Translation initiation factor IF2
38	BC004354	Hs.211607	TNRC11	Trinucleotide repeat containing 11 (THR-associated protein, 230 kd subunit)
39	AL556551	Hs.75103	YWHAZ	Tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, zeta polypeptide
40	AU118783	Hs.77578	USP9X	Ubiquitin specific protease 9, X chromosome (fat facets-like Drosophila)
41	BG200978	Hs.183596	UGT2B17	UDP glycosyltransferase 2 family, polypeptide B17

List of 267 genes that were classified as 'switch-off'

<i>No.</i>	<i>Accession</i>	<i>Symbol</i>	<i>Unigene</i>	<i>Description</i>
1	BF515855	ADAM12	Hs.8850	A disintegrin and metalloproteinase domain 12 (meltrin alpha)
2	NM_003816	ADAM9	Hs.2442	A disintegrin and metalloproteinase domain 9 (meltrin gamma)
3	NM_005759	AIP-1	Hs.343575	Abl-interactor 12 (SH3-containing protein)
4	NM_000019	ACAT1	Hs.37	Acetyl-Coenzyme A acetyltransferase 1 (acetoacetyl Coenzyme A thiolase)
5	AK027723	OA48-18	Hs.278670	Acid-inducible phosphoprotein
6	AL560125	ARPC5	Hs.82425	Actin related protein 2/3 complex, subunit 5 (16 kd)
7	BG481840	ACTB	Hs.288061	Actin, beta
8	BG422944	ACTG1	Hs.14376	Actin, gamma 1
9	NM_001615	ACTG2	Hs.78045	Actin, gamma 2, smooth muscle, enteric
10	AU138067	ADPRT	Hs.177766	ADP-ribosyltransferase (NAD ⁺ ; poly (ADP-ribose) polymerase)
11	AL558086	ALB	Hs.184411	Albumin
12	BG481883	ALDOA	Hs.273415	Aldolase A, fructose-bisphosphate
13	NM_003905	APPBP1	Hs.61828	Amyloid beta precursor protein binding protein 1, 59kd
14	NM_020987	ANK3	Hs.75893	Ankyrin 3, node of Ranvier (ankyrin G)
15	AA974308	ARMET	Hs.75412	Arginine-rich, mutated in early stage tumors
16	BF316073	ASL	Hs.61258	Argininosuccinate lyase
17	AL040940	ACTR3	Hs.5321	ARP3 actin-related protein 3 homolog (yeast)
18	AW409774	ASTN2	Hs.30898	Astrotactin 2
19	AV763549	ATP5C1	Hs.155433	ATP synthase, H ⁺ transporting, mitochondrial F1 complex, gamma polypeptide 1
20	NM_000052	ATP7A	Hs.606	Atpase, Cu ⁺⁺ transporting, alpha polypeptide (Menkes syndrome)
21	BE780536	BCL2L1	Hs.305890	BCL2-like 1
22	NM_004328	BCS1L	Hs.150922	BCS1-like (yeast)
23	BF237719	BCRP1	Hs.268763	Breakpoint cluster region protein, uterine leiomyoma, 1; barrier to autointegration factor
24	BG197310	CDH2	Hs.161	Cadherin 2, type 1, N-cadherin (neuronal)
25	BE302598	CAPN3	Hs.40300	Calpain 3, (p94)
26	BG681089	CAST	Hs.279607	Calpastatin
27	AI869526	CALU	Hs.7753	Calumenin
28	AU117908	CFLAR	Hs.195175	CASP8 and FADD-like apoptosis regulator
29	AL546380	CTSB	Hs.297939	Cathepsin B
30	AK025306	CLK1	Hs.2083	CDC-like kinase 1
31	NM_004749	CPR2	Hs.347349	Cell cycle progression 2 protein

32	NM_016343	CENPF	Hs.77204	Centromere protein F (350/400kd, mitotin)
33	NM_001762	CCT6A	Hs.82916	Chaperonin containing TCP1, subunit 6A (zeta 1)
34	NM_003965	CCRL2	Hs.302043	Chemokine (C-C motif) receptor-like 2
35	NM_004067	CHN2	Hs.286055	Chimerin (chimaerin) 2
36	NM_001270	CHD1	Hs.22670	Chromodomain helicase DNA binding protein 1
37	BG619551	C14orf2	Hs.109052	Chromosome 14 open reading frame 2
38	NM_001326	CSTF3	Hs.180034	Cleavage stimulation factor, 3' pre-RNA, subunit 3, 77kd
39	NM_000082	CKN1	Hs.32967	Cockayne syndrome 1 (classical)
40	M65134	C5	Hs.1281	Complement component 5
41	AI557255	CXADR	Hs.79187	Coxsackie virus and adenovirus receptor
42	BG531987	CCNH	Hs.514	Cyclin H
43	BG165160	CCNI	Hs.79933	Cyclin I
44	NM_006094	DLC1	Hs.8700	Deleted in liver cancer 1
45	AL552970	DKK1	Hs.40499	Dickkopf homolog 1 (Xenopus laevis)
46	Y00978	DLAT	Hs.115285	Dihydrolipoamide S-acetyltransferase (E2 component of pyruvate dehydrogenase complex)
47	BG680858	DKFZP434J1813	Hs.1098	Dkfzp434j1813 protein
48	BF309422	DFFA	Hs.105658	DNA fragmentation factor, 45 kd, alpha polypeptide
49	NM_006260	DNAJC3	Hs.9683	Dnaj (Hsp40) homolog, subfamily C, member 3
50	NM_014890	DOC1	Hs.15432	Downregulated in ovarian cancer 1
51	NM_001952	E2F6	Hs.42287	E2F transcription factor 6
52	AL559590	ELF1	Hs.154365	E74-like factor 1 (ets domain transcription factor)
53	AL523212	EHD1	Hs.155119	EH-domain containing 1
54	NM_012081	ELL2	Hs.173334	Ell-related rna polymerase ii, elongation factor
55	NM_014693	ECE2	Hs.129801	Endothelin converting enzyme 2
56	NM_001980	EPIM	Hs.99865	Epimorphin
57	NM_000120	EPHX1	Hs.89649	Epoxide hydrolase 1, microsomal (xenobiotic)
58	BG167914		Hs.31388	Ests
59	AA824285		Hs.144622	Ests
60	BG110974		Hs.351110	Ests
61	BG032173		Hs.351990	Ests, Highly similar to CH60_HUMAN 60 KDA HEAT SHOCK PROTEIN, MITOCHONDRIAL PRECURSOR [H.sapiens]
62	AW950447		Hs.9521	Ests, Moderately similar to G02075 transcription repressor zinc finger protein 85 [H.sapiens]
63	BE243545		Hs.57637	Ests, Weakly similar to A49364 59 protein, brain [H.sapiens]
64	AA417878		Hs.48401	Ests, Weakly similar to ALU8 HUMAN ALU SUBFAMILY SX SEQUENCE CONTAMINATION WARNING

ENTRY [H.sapiens]			
65	BF243409	EEF1E1	Hs.298581 Eukaryotic translation elongation factor 1 epsilon 1
66	BG484643	EIF3S2	Hs.192023 Eukaryotic translation initiation factor 3, subunit 2 (beta, 36kd)
67	AL520387	EIF4EBP1	Hs.71819 Eukaryotic translation initiation factor 4E binding protein 1
68	BG697239	XPO1	Hs.79090 Exportin 1 (CRM1 homolog, yeast)
69	NM_001441	FAAH	Hs.326190 Fatty acid amide hydrolase
70	BG698967	FADS1	Hs.132898 Fatty acid desaturase 1
71	AL552895	FACVL1	Hs.11729 Fatty-acid-Coenzyme A ligase, very long-chain 1
72	NM_004459	FALZ	Hs.99872 Fetal Alzheimer antigen
73	BG566030	FGA	Hs.351593 Fibrinogen, A alpha polypeptide
74	BG618299	FGL1	Hs.107 Fibrinogen-like 1
75	BC001257	FAP48	Hs.49105 FKBP-associated protein
76	X69962	FMR1	Hs.89764 Fragile X mental retardation 1
77	BG747743	SIAHBP1	Hs.74562 Fuse-binding protein-interacting repressor
78	AL522814	KIAA0110	Hs.124 Gene predicted from cDNA with a complete coding sequence
79	BG500905	GLE1L	Hs.169363 GLE1 RNA export mediator-like (yeast)
80	NM_000848	GSTM2	Hs.279837 Glutathione S-transferase M2 (muscle)
81	D45286	GPM6A	Hs.75819 Glycoprotein M6A
82	NM_005113	GOLGA5	Hs.241572 Golgi autoantigen, golgin subfamily a, 5
83	BG545676	GCA	Hs.79381 Grancalcin, EF-hand calcium binding protein
84	BG928406	HMGE	Hs.151903 Grpe-like protein cochaperone
85	BG395645	GNB3	Hs.71642 Guanine nucleotide binding protein (G protein), beta polypeptide 3
86	BG424817	HSPA9B	Hs.3069 Heat shock 70kd protein 9B (mortalin-2)
87	AI741735	HSF4	Hs.75486 Heat shock transcription factor 4
88	BE870129	HS6ST	Hs.6363 Heparan sulfate 6-O-sulfotransferase
89	AL132772	HNF4A	Hs.54424 Hepatocyte nuclear factor 4, alpha
90	AU126203	HNRPA1	Hs.249495 Heterogeneous nuclear ribonucleoprotein A1
91	AL134884	HNRPH2	Hs.278857 Heterogeneous nuclear ribonucleoprotein H2 (H')
92	BE618313	HMG1	Hs.337757 High-mobility group (nonhistone chromosomal) protein 1
93	BG250825	HMGIC	Hs.2726 High-mobility group (nonhistone chromosomal) protein isoform I-C
94	BF792457	H2AV	Hs.301005 Histone H2A.F/Z variant
95	AI004324	BAT4	Hs.247478 HLA-B associated transcript 4
96	AK022433		Hs.324179 Homo sapiens cDNA FLJ12371 fis, clone MAMMA1002434 Homo sapiens cDNA: FLJ21897 fis, clone HEP03447, highly similar to AF052178 Homo sapiens clone 24523 mRNA sequence
97	AW296083		Hs.173108

98	AK026295		Hs.288232	Homo sapiens cdna: FLJ22642 fis, clone HSI06970
99	AF070590		Hs.90869	Homo sapiens clones 24622 and 24623 mrna sequence
100	AF064606		Hs.306242	Homo sapiens KB07 protein mrna, partial cds
101	AA169411		Hs.9414	Homo sapiens mrna for KIAA1488 protein, partial cds
102	AF092132		Hs.284275	Homo sapiens PAK2 mrna, complete cds
103	AI492167		Hs.292057	Homo sapiens PNAS-13 mrna, complete cds
104	BC009518		Hs.135265	Homo sapiens, clone MGC:10965 IMAGE:3633884, mrna, complete cds
105	L19183	MAC30	Hs.199695	Hypothetical protein
106	AL122095	FLJ00002	Hs.55879	Hypothetical protein FLJ00002
107	BG260450	FLJ14393	Hs.23294	Hypothetical protein FLJ14393
108	AL519357	FLJ20343	Hs.252692	Hypothetical protein FLJ20343
109	BG036183	MGC11061	Hs.66309	Hypothetical protein MGC11061
110	AU134078	HIF1A	Hs.197540	Hypoxia-inducible factor 1, alpha subunit (basic helix-loop-helix transcription factor)
111	M87790	IGL@	Hs.181125	Immunoglobulin lambda locus
112	NM_001555	IGSF1	Hs.22111	Immunoglobulin superfamily, member 1
113				Incyte EST
114	AV660068	ID2	Hs.180919	Inhibitor of DNA binding 2, dominant negative helix-loop-helix protein
115	BI054765	IGF1R	Hs.239176	Insulin-like growth factor 1 receptor
116	NM_002219	ITM1	Hs.287850	Integral membrane protein 1
117	NM_002216	ITIH2	Hs.75285	Inter-alpha (globulin) inhibitor, H2 polypeptide
118	J03143	IFNGR1	Hs.180866	Interferon gamma receptor 1
119	BG506643	IFITM1	Hs.146360	Interferon induced transmembrane protein 1 (9-27)
120	BC001770	ILF3	Hs.256583	Interleukin enhancer binding factor 3, 90kd
121	U90304	IRX5	Hs.25351	Iroquois homeobox protein 5
122	AI279534	JM4	Hs.29595	JM4 protein
123	NM_002267	KPNA3	Hs.3886	Karyopherin alpha 3 (importin alpha 4)
124	NM_005886	KATNB1	Hs.275675	Katanin p80 (WD40-containing) subunit B 1
125	BE544428	KDEL2	Hs.118778	KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 2
126	NM_016657	KDEL3	Hs.250696	KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 3
127	BI087140	KIAA0008	Hs.77695	KIAA0008 gene product
128	BE784260	KIAA0077	Hs.112396	KIAA0077 protein
129	BG495280	KIAA0102	Hs.77665	KIAA0102 gene product
130	BF107279	KIAA0164	Hs.80338	KIAA0164 gene product
131	NM_014666	KIAA0171	Hs.132853	KIAA0171 gene product

132	D83776	KIAA0191	Hs.12413	KIAA0191 protein
133	BC006474	KIAA0332	Hs.7976	KIAA0332 protein
134	AB011125	KIAA0553	Hs.105749	KIAA0553 protein
135	AL031428	KIAA0601	Hs.174174	KIAA0601 protein
136	AB014514	KIAA0614	Hs.7314	KIAA0614 protein
137	AW302200	KIAA0672	Hs.6336	KIAA0672 gene product
138	AK023032	KIAA0863	Hs.131915	KIAA0863 protein
139	AU142698	LDHA	Hs.2795	Lactate dehydrogenase A
140	BG261015	LRRFIP1	Hs.326159	Leucine rich repeat (in FLII) interacting protein 1
141	NM_005901	MADH2	Hs.82483	MAD, mothers against decapentaplegic homolog 2 (Drosophila)
142	BG527529	MAD2L1	Hs.79078	MAD2 mitotic arrest deficient-like 1 (yeast)
143	NM_013446	MKRN1	Hs.7838	Makorin, ring finger protein, 1
144	AU119410	MAN1A1	Hs.25253	Mannosidase, alpha, class 1A, member 1
145	AK026606	MESDC2	Hs.78871	Mesoderm development candidate 2
146	BG178390	MCCC2	Hs.167531	Methylcrotonoyl-Coenzyme A carboxylase 2 (beta)
147	BE737147	MICA	Hs.90598	MHC class I polypeptide-related sequence A
148	BF222194	MFN1	Hs.197877	Mitofusin 1
149	BF508841	MRS2L	Hs.30057	MRS2-like, magnesium homeostasis factor (S. Cerevisiae)
150	NM_003970	MYOM2	Hs.79227	Myomesin (M-protein) 2 (165kd)
151	NM_002477	MYL5	Hs.170482	Myosin, light polypeptide 5, regulatory
152	AV716792	MYL6	Hs.77385	Myosin, light polypeptide 6, alkali, smooth muscle and non-muscle
153	AF013160	NDUFS2	Hs.173611	NADH dehydrogenase (ubiquinone) Fe-S protein 2 (49kd) (NADH-coenzyme Q reductase)
154	U88573	NBR2	Hs.321170	Nbr2
155	AW960243	NEDD8	Hs.75512	Neural precursor cell expressed, developmentally down-regulated 8
156	AW161393	NNAT	Hs.117546	Neuronatin
157	BF968938	NIPSNAP1	Hs.173878	Nipsnap homolog 1 (C. Elegans)
158	BE408656	NSAP1	Hs.155489	NS1-associated protein 1
159	NM_002486	NCBP1	Hs.89563	Nuclear cap binding protein subunit 1, 80kd
160	NM_006163	NFE2	Hs.75643	Nuclear factor (erythroid-derived 2), 45kd
161	X64318	NFIL3	Hs.79334	Nuclear factor, interleukin 3 regulated
162	AV713026	P84	Hs.1540	Nuclear matrix protein p84
163	M64497	NR2F2	Hs.347991	Nuclear receptor subfamily 2, group F, member 2
164	NM_004741	NOLC1	Hs.75337	Nucleolar and coiled-body phosphprotein 1
165	AV724878	NCL	Hs.79110	Nucleolin

166	BG776422	NPM1	Hs.9614	Nucleophosmin (nucleolar phosphoprotein B23, numatrin)
167	AW673911	NUP155	Hs.23255	Nucleoporin 155kd
168	BG577287	OAT	Hs.75485	Ornithine aminotransferase (gyrate atrophy)
169	NM_015878	OAZIN	Hs.223014	Ornithine decarboxylase antizyme inhibitor
170	NM_002570	PACE4	Hs.170414	Paired basic amino acid cleaving system 4
171	AL522004	PKNOX1	Hs.158225	PBX/knotted 1 homeobox 1
172	BG831846	PAM	Hs.83920	Peptidylglycine alpha-amidating monooxygenase
173	BG481674	PPIB	Hs.699	Peptidylprolyl isomerase B (cyclophilin B)
174	NM_014303	PES1	Hs.13501	Pescadillo homolog 1, containing BRCT domain (zebrafish)
175	NM_000277	PAH	Hs.1870	Phenylalanine hydroxylase
176	NM_000314	PTEN	Hs.10712	Phosphatase and tensin homolog (mutated in multiple advanced cancers 1)
177	NM_002647	PIK3C3	Hs.32971	Phosphoinositide-3-kinase, class 3
178	BF337301	PCBP1	Hs.2853	Poly(rc) binding protein 1
179	AL558755	RPC62	Hs.250745	Polymerase (RNA) III (DNA directed) (62kd)
180	AL121893	POLR3F	Hs.128207	Polymerase (RNA) III (DNA directed) polypeptide F (39 kd)
181	NM_002702	POU6F1	Hs.2815	POU domain, class 6, transcription factor 1
182	NM_000935	PLOD2	Hs.41270	Procollagen-lysine, 2-oxoglutarate 5-dioxygenase (lysine hydroxylase) 2
183	AL540876	PRCP	Hs.75693	Prolylcarboxypeptidase (angiotensinase C)
184	AW236221	PFC	Hs.53155	Properdin P factor, complement
185	AL577683	PRSS25	Hs.115721	Protease, serine, 25
186	D31889	PSMD5	Hs.193725	Proteasome (prosome, macropain) 26S subunit, non-atpase, 5
187	BG386309	PSMB3	Hs.82793	Proteasome (prosome, macropain) subunit, beta type, 3
188	BG480549	PRKAR1B	Hs.1519	Protein kinase, camp-dependent, regulatory, type I, beta
189	U34994	PRKDC	Hs.155637	Protein kinase, DNA-activated, catalytic polypeptide
190	AI992326	PPM1G	Hs.17883	Protein phosphatase 1G (formerly 2C), magnesium-dependent, gamma isoform
191	BF063245	PPP2CB	Hs.80350	Protein phosphatase 2 (formerly 2A), catalytic subunit, beta isoform
192	BC001970	PPP5C	Hs.75180	Protein phosphatase 5, catalytic subunit
193	BI088031	PME-1	Hs.63304	Protein phosphatase methylesterase-1
194	NM_002822	PTK9	Hs.82643	Protein tyrosine kinase 9
195	AL121905	PTPRA	Hs.26045	Protein tyrosine phosphatase, receptor type, A
196	BG178374	HSA9761	Hs.125819	Putative dimethyladenosine transferase
197	AF119836	RAB6A	Hs.5636	RAB6A, member RAS oncogene family
198	BE890059	RAB6A	Hs.5636	RAB6A, member RAS oncogene family
199	AL543484	RASSF1	Hs.26931	Ras association (ralgds/AF-6) domain family 1

200	BF309129	ARHC	Hs.179735	Ras homolog gene family, member C
201	AL532485	RFC5	Hs.171075	Replication factor C (activator 1) 5 (36.5kd)
202	BG333934	RPA2	Hs.79411	Replication protein A2 (32kd)
203	NM_002901	RCN1	Hs.167791	Reticulocalbin 1, EF-hand calcium binding domain
204	BG437683	RPL3	Hs.119598	Ribosomal protein L3
205	NM_004586	RPS6KA3	Hs.173965	Ribosomal protein S6 kinase, 90kd, polypeptide 3
206	BI092279	RNF10	Hs.5094	Ring finger protein 10
207	BG167309	RBMX	Hs.146381	RNA binding motif protein, X chromosome
208	NM_006867	RBPMS	Hs.80248	RNA-binding protein gene with multiple splicing
209	NM_003012	SFRP1	Hs.7306	Secreted frizzled-related protein 1
210	AA962810	SERPINA1	Hs.297681	Serine (or cysteine) proteinase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 1
211	BF339409	SERPINA3	Hs.234726	Serine (or cysteine) proteinase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 3
212	NM_005412	SHMT2	Hs.75069	Serine hydroxymethyltransferase 2 (mitochondrial)
213	BC001149	SDCCAG16	Hs.271926	Serologically defined colon cancer antigen 16
214	NM_003135	SRP19	Hs.2943	Signal recognition particle 19kd
215	BG613238	SRP9	Hs.75975	Signal recognition particle 9kd
216	BF793092	SSR4	Hs.102135	Signal sequence receptor, delta (translocon-associated protein delta)
217	NM_003086	SNAPC4	Hs.113265	Small nuclear RNA activating complex, polypeptide 4, 190kd
218	AL527028	SLC25A6	Hs.164280	Solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 6
219	BG491863	SLC25A3	Hs.78713	Solute carrier family 25 (mitochondrial carrier; phosphate carrier), member 3
220	AL549188	SLC31A1	Hs.73614	Solute carrier family 31 (copper transporters), member 1
221	NM_000342	SLC4A1	Hs.185923	Solute carrier family 4, anion exchanger, member 1 (erythrocyte membrane protein band 3, Diego blood group)
222	BG291471	SLC7A11	Hs.6682	Solute carrier family 7, (cationic amino acid transporter, y+ system) member 11
223	NM_003563	SPOP	Hs.129951	Speckle-type POZ protein
224	BG419824	SPF30	Hs.79968	Splicing factor 30, survival of motor neuron-related
225	BG251495	SFPQ	Hs.180610	Splicing factor proline/glutamine rich (polypyrimidine tract binding protein associated)
226	NM_004719	SFRS2IP	Hs.51957	Splicing factor, arginine/serine-rich 2, interacting protein
227	BG287081	SFRS3	Hs.167460	Splicing factor, arginine/serine-rich 3
228	NM_014720	SLK	Hs.105751	Ste20-related serine/threonine kinase
229	BG431313	SDF2	Hs.118684	Stromal cell-derived factor 2
230	L25275	SULT1A3	Hs.274614	Sulfotransferase family, cytosolic, 1A, phenol-preferring, member 3
231	AA029190	SMN1	Hs.288986	Survival of motor neuron 1, telomeric
232	NM_005816	TACTILE	Hs.142023	T cell activation, increased late expression
233	NM_015686	TED	Hs.87619	TED protein

234	X98248	PEAS	Hs.281706	Testis intracellular mediator protein
235	AU139227	TXNIP	Hs.179526	Thioredoxin interacting protein
236	BG678099	TARS	Hs.84131	Threonyl-trna synthetase
237	N94350	THY1	Hs.125359	Thy-1 cell surface antigen
238	AI174883	TYMS	Hs.82962	Thymidylate synthetase
239	U09088	TMPO	Hs.11355	Thymopoietin
240	BE740238	TRIP4	Hs.116784	Thyroid hormone receptor interactor 4
241	BF795918	TOP2A	Hs.156346	Topoisomerase (DNA) II alpha (170kd)
242	NM_003205	TCF12	Hs.21704	Transcription factor 12 (HTF4, helix-loop-helix transcription factors 4)
243	AL365456	TIF1	Hs.183858	Transcriptional intermediary factor 1
244	NM_014755	TRIP-Br2	Hs.77293	Transcriptional regulator interacting with the PHS-bromodomain 2
245	NM_005077	TLE1	Hs.28935	Transducin-like enhancer of split 1 (E(sp1) homolog, Drosophila)
246	NM_001063	TF	Hs.284176	Transferrin
247	AL533554	TSN	Hs.75066	Translin
248	AU131018	KIAA0016	Hs.75187	Translocase of outer mitochondrial membrane 20 (yeast) homolog
249	AL523342	TRAM	Hs.4147	Translocating chain-associating membrane protein
250	NM_003275	TMOD	Hs.170453	Tropomodulin
251	NM_002546	TNFRSF11B	Hs.81791	Tumor necrosis factor receptor superfamily, member 11b (osteoprotegerin)
252	AU142852	YWHAH	Hs.349530	Tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, eta polypeptide
253	NM_003680	YARS	Hs.239307	Tyrosyl-trna synthetase
254	BG740524	USP15	Hs.23168	Ubiquitin specific protease 15
255	BE019497	USP5	Hs.3759	Ubiquitin specific protease 5 (isopeptidase T)
256	NM_005154	USP8	Hs.152818	Ubiquitin specific protease 8
257	AF135416	UGT2B4	Hs.89691	UDP glycosyltransferase 2 family, polypeptide B4
258	AV715367	P115	Hs.325948	Vesicle docking protein p115
259	W78201	KIAA0105	Hs.119	Wilms' tumour 1-associating protein
260	NM_003436	ZNF135	Hs.159582	Zinc finger protein 135 (clone phz-17)
261	AA195154	ZNF161	Hs.6557	Zinc finger protein 161
262	BG254958	ZNF184	Hs.158174	Zinc finger protein 184 (Kruppel-like)
263	AU128446	ZNF267	Hs.145498	Zinc finger protein 267
264	AL535717	ZNF354A	Hs.100932	Zinc finger protein 354A
265	X07290	ZNF38	Hs.155470	Zinc finger protein 38 (KOX 25)
266	NM_003425	ZNF45	Hs.41728	Zinc finger protein 45 (a Kruppel-associated box (KRAB) domain polypeptide)
267	NM_003416	ZNF7	Hs.2076	Zinc finger protein 7 (KOX 4, clone HF.16)

The following functionalities were compiled from information held in data bases that can be accessed via:

Lotus like at ncib: <http://www.ncbi.nlm.nih.gov/LocusLink//>

Weizmann Institute of science: <http://bioinfo.weizmann.ac.il/cards/index.html>

Biocarter: <http://www.biocarta.com/genes/index.asp>

Up-regulated genes

Name	Functions
1. Apolipoprotein 1, 3	This gene is a member of the apolipoprotein L gene family. The encoded protein is found in the cytoplasm, where it may affect the movement of lipids or allow the binding of lipids to organelles. In addition, expression of this gene is upregulated by tumor necrosis factor-alpha in endothelial cells lining the normal and atherosclerotic iliac artery and aorta. Six transcript variants encoding three different isoforms have been found for this gene. Proteome Summary: Protein that is induced by tumor necrosis factor alpha; has similarity to apolipoprotein-L. Involved with gene synthesis of triglycerides and cholesterol. It has been associated with schizophrenia and atherosclerosis.
2. Atp synthase, h+ transporting, mitochondrial f0 complex, subunit e	Strongly similar to murine Atp5l; may act in catalyzing ATP synthesis during oxidative phosphorylation
3. Cell division cycle 42 (gtp binding protein, 25kd)	CID42 is a Rho GTPase and it is proposed that it can alter regulation of normal cell growth and initiate tumourigenic signals. It is a gene with a protein product, function unknown but causes the formation of thin, actin-rich surface projections called filopodia cell division cycle 42 (GTP binding protein).
4. Complement component 4 binding protein, beta	C4bp controls the classical pathway of complement activation. It binds as a cofactor to c3b/c4b inactivator (c3bina), which then hydrolyzes the complement fragment c4b. It also accelerates the degradation of the c4bc2a complex (c3 convertase) by dissociating the complement fragment c2a. It also interacts with anticoagulant protein s and with serum amyloid p component. The beta chain binds protein s.
5. Cyclin-dependent kinase 9 (cdc2-related kinase)	Member of the cyclin-dependent kinase pair (cdk9/cyclin t) complex, also called positive transcription elongation factor b (p-tefb), which is proposed to facilitate the transition from abortive to production elongation by phosphorylating the ctd (carboxy-terminal domain) of the large subunit of rna polymerase ii (rnap ii). The cdk9/cyclin k complex has also a kinase activity toward ctd of rnap ii and can substitute for p-tefb in vitro. In vitro, phosphorylates retinoblastoma and myelin basic protein. Subunit: associates with cyclin t to form p-tefb. Also associates with cyclin k. It is targeted by the HIV virus to activate elongation of the integrated pro-viral genome.
6. Cytochrome p450, subfamily viib (oxysterol 7 alpha-	Pathway: first and rate-limiting step in the conversion of cholesterol to bile acids. Pathway: synthesis of primary bile acids from cholesterol via the acidic pathway.

hydroxylase), polypeptide 1	Subcellular location: membrane-bound. Endoplasmic reticulum. tissue specificity: brain, testis, ovary, prostate, liver, colon, kidney, and small intestine. Similarity: belongs to the cytochrome p450 family.
7. Homo sapiens, clone mgc:4459 image:2960564, mrna, complete cds	Hypothetical protein FLJ10785
8. Hypothetical protein mgc3207	Gene with protein product, function unknown hypothetical protein
9. Methyl-cpg binding domain protein 3	DNA methylation is the major modification of eukaryotic genomes and plays an essential role in mammalian development. Human proteins MECP2, MBD1, MBD2, MBD3, and MBD4 comprise a family of nuclear proteins related by the presence in each of a methyl-cpg binding domain (MBD). However, unlike the other family members, MBD3 is not capable of binding to methylated DNA. The predicted MBD3 protein shares 71% and 94% identity with MBD2 (isoform 1) and mouse Mbd3. MBD3 is a subunit of the nurd, a multisubunit complex containing nucleosome remodeling and histone deacetylase activities. MBD3 mediates the association of metastasis-associated protein 2 (MTA2) with the core histone. Proteome Summary: Similar to methyl-cpg binding proteins; does not bind methylated DNA
10. Modulator of apoptosis 1	The protein encoded by this gene was identified by its interaction with apoptosis regulator BAX protein. This protein contains a Bcl-2 homology 3 (BH3)-like motif, which is required for the association with BAX. When overexpressed, this gene has been shown to mediate caspase-dependent apoptosis.
11. Peroxisome proliferative activated receptor, gamma	Function: receptor that bind peroxisome proliferators such as hypolipidemic drugs and fatty acids. Once activated by a ligand, the receptor binds to a promoter element in the gene for acyl-coa oxidase and activates its transcription. It therefore controls the peroxisomal beta-oxidation pathway of fatty acids. Key regulator of adipocyte differentiation and glucose homeostasis.
12. Putative selenocysteine lyase	Putative selenocysteine lyase; may decompose L-selenocysteine to L-alanine and elemental selenium, may function with selenophosphate synthetase in selenoprotein synthesis. This gene is known to be induced in selenium toxicity.
13. Radixin	Probably plays a crucial role in the binding of the barbed end of actin filaments to the plasma membrane. It is thought to be involved in cell growth, transformatin, morphogenesis and apoptosis. Subcellular location: highly concentrated in the undercoat of the cell-to-cell adherens junction and the cleavage furrow in the interphase and mitotic phase, respectively. Radixin is a cytoskeletal protein that may be important in linking actin to the plasma membrane. It is highly similar in sequence to both ezrin and moesin. The rdx gene has been localized by fluorescence in situ hybridization to 11q23. A truncated version representing a pseudogene (rdxp2) was assigned to xp21.3. Another pseudogene that seemed to lack introns (rdxp1) was mapped to 11p by southern and pcr analyses. Proteome summary: radixin; may regulate cell adhesion and cortical morphogenesis; member of a

	protein family that links cytoskeleton to plasma membrane.
14. Rho gtpase activating protein 8	Protein of unknown function
15. Ribosomal protein l31	Ribosomes, the organelles that catalyze protein synthesis, consist of a small 40S subunit and a large 60S subunit. Together these subunits are composed of 4 RNA species and approximately 80 structurally distinct proteins. This gene encodes a ribosomal protein that is a component of the 60S subunit. The protein belongs to the L31E family of ribosomal proteins. It is located in the cytoplasm. Higher levels of expression of this gene in familial adenomatous polyps compared to matched normal tissues have been observed. As is typical for genes encoding ribosomal proteins, there are multiple processed pseudogenes of this gene dispersed through the genome.
16. Ribosomal protein s24	Ribosomes, the organelles that catalyze protein synthesis, consist of a small 40S subunit and a large 60S subunit. Together these subunits are composed of 4 RNA species and approximately 80 structurally distinct proteins. This gene encodes a ribosomal protein that is a component of the 40S subunit. The protein belongs to the S24E family of ribosomal proteins. It is located in the cytoplasm. Alternative splice variants that encode different protein isoforms exist. As is typical for genes encoding ribosomal proteins, there are multiple processed pseudogenes of this gene dispersed through the genome.
17. Ribosomal protein s27a	Ubiquitin, a highly conserved protein that has a major role in targeting cellular proteins for degradation by the 26S proteasome, is synthesized as a precursor protein consisting of either polyubiquitin chains or a single ubiquitin fused to an unrelated protein. This gene encodes a fusion protein consisting of ubiquitin at the N terminus and ribosomal protein S27a at the C terminus. When expressed in yeast, the protein is post-translationally processed, generating free ubiquitin monomer and ribosomal protein s27a. Ribosomal protein S27a is a component of the 40S subunit of the ribosome and belongs to the S27AE family of ribosomal proteins. It contains C4-type zinc finger domains and is located in the cytoplasm. Pseudogenes derived from this gene are present in the genome. As with ribosomal protein s27a, ribosomal protein L40 is also synthesized as a fusion protein with ubiquitin; similarly, ribosomal protein S30 is synthesized as a fusion protein with the ubiquitin-like protein fubi.
18. Ribosomal protein s27-like	This gene encodes a protein sharing sequence similarity with ribosomal protein S27. It is not currently known whether the encoded protein is a functional ribosomal protein or whether it has evolved a function that is independent of the ribosome.
19. Thioredoxin	Thioredoxin; has dithiol-disulfide oxidoreductase activity. Its expression was found in response to oxidative agents. It is also known to be involved in the regeneration of proteins inactivated by oxidative stress. Function: thioredoxin participates in various redox reactions through the reversible oxidation of its active center dithiol, to a disulfide, & catalyzes dithiol-disulfide exchange reactions. function: adf augments the expression of the interleukin-2 receptor tac (il2r/p55). Similarity: belongs to the thioredoxin family.

Down regulated

Name	Functions
1. Alpha-fetoprotein	This gene encodes alpha-fetoprotein, a major plasma protein produced by the yolk sac and the liver during fetal life. Alpha-fetoprotein expression in adults is often associated with hepatoma or teratoma. However, hereditary persistence of alpha-fetoprotein may also be found in individuals with no obvious pathology. The protein is thought to be the fetal counterpart of serum albumin, and the alpha-fetoprotein and albumin genes are present in tandem in the same transcriptional orientation on chromosome 4. Alpha-fetoprotein is found in monomeric as well as dimeric and trimeric forms, and binds copper, nickel, fatty acids and bilirubin. The level of alpha-fetoprotein in amniotic fluid is used to measure renal loss of protein to screen for spina bifida and anencephaly. Proteome Summary: Alpha-fetoprotein; may play a role in the maintenance of osmotic pressure; member of the albumin protein family. Binds copper, nickel, and fatty acids as well as, and bilirubin less well than, serum albumin. Only a small percentage (less than 2%) of the human AFP shows estrogen-binding properties.
2. Annexin a7	Calcium/phospholipid-binding protein which promotes membrane fusion and is involved in exocytosis. Annexin vii is a member of the annexin family of calcium-dependent phospholipid binding proteins. Structural analysis of the protein suggests that annexin vii is a membrane binding protein with diverse properties including voltage-sensitive calcium channel activity, ion selectivity and membrane fusion. Proteome summary: annexin vii (synexin); calcium-dependent membrane-binding protein, fuses membranes and acts as a voltage-dependent calcium channel
3. Asparagine synthetase	The protein encoded by this gene is involved in the synthesis of asparagine. This gene complements a mutation in the temperature-sensitive hamster mutant ts11, which blocks progression through the G1 phase of the cell cycle at nonpermissive temperature. There are two alternatively spliced transcript variants encoding the same protein described for this gene.
4. Atp synthase, h+ transporting, mitochondrial f0 complex, subunit c (subunit 9) isoform 3	function: this protein is one of the chains of the nonenzymatic membrane component (f0) of mitochondrial atpase. subunit: f-type atpases have 2 components, cf(1) - the catalytic core - and cf(0) - the membrane proton channel. Cf(1) has five subunits: alpha(3), beta(3), gamma(1), delta(1), epsilon(1). Cf(0) has three main subunits: a, b and c. subcellular location: mitochondrial membrane. Isoform 3 (P3) of subunit c, H ⁺ -translocating subunit of F0 ATP synthase; catalyzes the synthesis of ATP during oxidative phosphorylation
5. Basic leucine-zipper protein bzap45	Stimulates cell cycle regulation of histone H4 gene transcription.
6. Bystin-like	Bystin is expressed as a 2-kb major transcript and a 3.6-kb minor transcript in SNG-M cells and in human trophoblastic teratocarcinoma HT-H cells. Protein binding assays determined that bystin binds directly to trophinin and tastin, and that binding is enhanced when cytokeratins 8 and 18 are present. Immunocytochemistry of HT-H cells showed that bystin colocalizes with trophinin, tastin, and the cytokeratins, suggesting that these molecules form a complex in trophectoderm cells at the time of implantation. Using immunohistochemistry it was determined that trophinin and bystin are found in the placenta from the sixth

	<p>week of pregnancy. Both proteins were localized in the cytoplasm of the syncytiotrophoblast in the chorionic villi and in endometrial decidual cells at the uteroplacental interface. After week 10, the levels of trophinin, tastin, and bystin decreased and then disappeared from placental villi.</p> <p>Proteome Summary: Bystin; forms cell adhesion molecule complex with trophinin (TRO) and TASTIN, may be important for embryo implantation</p>
7. Calmodulin 2 (phosphorylase kinase, delta)	Calmodulin 2; may modulate calcium signalling; member of a family of calcium-binding proteins
8. Calnexin	Calnexin; calcium binding protein, may function as a chaperone in the endoplasmic reticulum, involved in the secretion of proteins from the ER to the outer cellular membrane
9. Ceruloplasmin (ferroxidase)	Ceruloplasmin is a plasma metalloprotein that binds most of the copper in plasma. Human ceruloplasmin is composed of a single polypeptide chain. Ceruloplasmin deficiency leads to iron accumulation and causes damage to a variety of tissues and organs. Proteome Summary: Ceruloplasmin; ferrous oxidase, binds copper in plasma and maintains iron homeostasis
10. Chaperonin containing tcp1, subunit 7 (eta)	Eta subunit of the cytosolic chaperonin containing TCP-1 (CCT); assists in the proper folding of tubulin, actin and contractin
11. Cop9 subunit 6 (mov34 homolog, 34 kd)	Very strongly similar to murine Cops6 and is involved in signal transduction.
12. Enolase 1, (alpha)	<p>This gene encodes one of three enolase isoenzymes found in mammals; it encodes alpha-enolase, a homodimeric soluble enzyme, and also encodes a shorter monomeric structural lens protein, tau-crystallin. The two proteins are made from the same message. The full length protein, the isoenzyme, is found in the cytoplasm. The shorter protein is produced from an alternative translation start, is localized to the nucleus, and has been found to bind to an element in the c-myc promoter. A pseudogene has been identified that is located on the other arm of the same chromosome.</p> <p>Proteome Summary: DNA-binding protein that negatively regulates MYC gene expression and is a transcription repressor.</p> <p>Proteome Summary: Alpha enolase (non-neuronal enolase); converts 2-phospho-D-glycerate to phosphoenolpyruvate in glycolysis, may bind c-myc</p>
13. Eukaryotic translation initiation factor 2, subunit 1 (alpha, 35kd)	<p>Alpha subunit of translation initiation factor 2; binds GTP and assists with Met-trnai binding to the 40S ribosomal subunit.</p> <p>Increased expression of both eif-4E and eif-2alpha in aggressive thyroid carcinoma compared to conventional papillary carcinoma suggesting a role in the progression of thyroid cancer</p>
14. Eukaryotic translation initiation factor 4a, isoform 2	Translation initiation factor 4A2 isoform 2; involved in the binding of mrna to the ribosome; contains a conserved DEAD-box motif
15. Fk506 binding protein 12-rapamycin associated protein 1	<p>The protein encoded by this gene belongs to a family of phosphatidylinositol kinase-related kinases. These kinases mediate cellular responses to stresses such as DNA damage and nutrient deprivation. This protein acts as the target for the cell-cycle arrest and immunosuppressive effects of the FKBP12-rapamycin complex. The CDT6 gene is located in an intron of this gene.</p> <p>Proteome Summary: FKBP-rapamycin associated protein; phosphatidylinositol kinase that may mediate rapamycin inhibition of the</p>

	cell cycle progression through G1
16. Guanine nucleotide binding protein (g protein), q polypeptide	Guanine nucleotide-binding proteins are a family of heterotrimeric proteins that couple cell surface, 7-transmembrane domain receptors to intracellular signaling pathways. Receptor activation catalyzes the exchange of GTP for GDP bound to the inactive G protein alpha subunit resulting in a conformational change and dissociation of the complex. The G protein alpha and beta-gamma subunits are capable of regulating various cellular effectors. Activation is terminated by a gtpase intrinsic to the G-alpha subunit. G-alpha-q is the alpha subunit of one of the heterotrimeric GTP-binding proteins that mediates stimulation of phospholipase C-beta Proteome Summary: G-protein alpha subunit q, a component of heterotrimeric G-protein complexes; heterotrimer transduces signals from G protein-coupled receptors and mediates activation of phospholipase C beta
17. Histone deacetylase 2	Histone deacetylase 2 (HDAC2), or transcriptional regulator homolog RPD3 L1, is highly homologous to the yeast transcription factor RPD3 (reduced potassium dependency 3) gene. As in yeast, human HDA2 is likely to be involved in regulating chromatin structure during transcription. It has been implicated to associate with YY1, a mammalian zinc-finger transcription factor, which negatively regulates transcription by tethering RPD3 to DNA as a cofactor. This process is highly conserved from yeast to human. Proteome Summary: Histone deacetylase 2; regulates transcription through its effect on chromatin structure
18. Homo sapiens clone 23763 unknown mrna, partial cds	Gene with protein product, function known or inferred
19. Immediate early response 3	This gene functions in the protection of cells from Fas- or tumor necrosis factor type alpha-induced apoptosis. Alternative splicing of this gene results in two transcript variants. It inhibits apoptosis due to Fas or tumor necrosis factor type alpha and is known to be involved in cell growth and maintenance and an inhibitor of apoptosis.
20. Interferon gamma receptor 2 (interferon gamma transducer 1)	Required for activation of interferon (IFN)-gamma receptor (IFNGR1)
21. Kiaa0101 gene product	Gene with protein product, function unknown
22. Mitochondrial ribosomal protein 119	Mammalian mitochondrial ribosomal proteins are encoded by nuclear genes and catalyze protein synthesis within the mitochondrion. The mitochondrial ribosome (mitoribosome) consists of a small 28S subunit and a large 39S subunit. They have an estimated 75% protein to rna composition compared to prokaryotic ribosomes, where this ratio is reversed. Another difference between mammalian mitoribosomes and prokaryotic ribosomes is that the latter contain a 5S rna.
23. Myosin, light polypeptide, regulatory, non-sarcomeric (20kd)	Very strongly similar to rat RLC-A, myosin regulatory light chain; may regulate myosin head atpase activity in smooth muscle at rest
24. Nadh dehydrogenase (ubiquinone) fe-s protein 5 (15kd) (nadh-coenzyme q	Subunit of mitochondrial NADH-ubiquinone oxidoreductase (complex I); transports electrons from NADH to ubiquinone

reductase)	
25. Paternally expressed 10	Gene with protein product, function known or inferred
26. Pctaire protein kinase 1	The protein encoded by this gene belongs to the cdc2/cdkx subfamily of the ser/thr family of protein kinases. It may play a role in signal transduction cascades in terminally differentiated cells. This gene is thought to escape X inactivation. There are three alternatively spliced transcript variants described for this gene. Proteome Summary: Serine/threonine protein kinase; related to cyclin-dependent protein kinases
27. Peptidylprolyl isomerase f (cyclophilin f)	Cyclophilin F (peptidylprolyl isomerase F); binds the immunosuppressant drug cyclosporin A gene with protein product, function known or inferred
28. Phosphatidylserine synthase 1	Gene with protein product, function known or inferred
29. Phospholipase a2, group ib (pancreas)	Group IB pancreatic phospholipase a2; hydrolyzes the phospholipid sn-2 ester bond; member of the phospholipase family
30. Phosphorylase kinase, gamma 2 (testis)	Gamma 2 catalytic subunit of phosphorylase kinase; phosphorylates and activates glycogen phosphorylase
31. Proteasome (prosome, macropain) 26s subunit, atpase, 1	The 26S proteasome is a multicatalytic proteinase complex with a highly ordered structure composed of 2 complexes, a 20S core and a 19S regulator. Proteasomes are distributed throughout eukaryotic cells at a high concentration and cleave peptides in an ATP/ubiquitin-dependent process in a non-lysosomal pathway. An essential function of a modified proteasome, the immunoproteasome, is the processing of class I MHC peptides. This gene encodes one of the atpase subunits, a member of the triple-A family of atpases which have a chaperone-like activity. This subunit and a 20S core alpha subunit interact specifically with the hepatitis B virus X protein, a protein critical to viral replication. This subunit also interacts with the adenovirus E1A protein and this interaction alters the activity of the proteasome. Finally, this subunit interacts with ataxin-7, suggesting a role for the proteasome in the development of spinocerebellar ataxia type 7, a progressive neurodegenerative disorder.
32. Protein tyrosine phosphatase, receptor type, c-associated protein	The protein encoded by this gene was identified as a transmembrane phosphoprotein specifically associated with tyrosine phosphatase PTPRC/CD45, a key regulator of T- and B-lymphocyte activation. The interaction with PTPRC may be required for the stable expression of this protein. Proteome Summary: Lymphocyte-specific phosphoprotein; stable only when bound to CD45 (PTPRC), a receptor protein tyrosine phosphatase
33. Ribosomal protein l29	Gene with protein product, function known or inferred
34. Ribosomal protein, large, p0	This gene encodes a ribosomal protein that is a component of the 60S subunit. The protein, which is the functional equivalent of the E. Coli L10 ribosomal protein, belongs to the L10P family of ribosomal proteins. It is a neutral phosphoprotein with a C-terminal end that is nearly identical to the C-terminal ends of the acidic ribosomal phosphoproteins P1 and P2. The P0 protein can interact with P1 and P2 to form a pentameric complex consisting of P1 and P2 dimers, and a P0 monomer. The protein is located in the

	cytoplasm. Transcript variants derived from alternative splicing exist; they encode the same protein. As is typical for genes encoding ribosomal proteins, there are multiple processed pseudogenes of this gene dispersed through the genome.
35. Solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 4	Heart-skeletal muscle adenine nucleotide translocator; strongly similar to murine Ant1
36. Transcription elongation factor a (sii), 1	Transcription elongation factor A (SII); stimulates the activity of the RNA polymerase II elongation complex
37. Translation initiation factor if2	This gene encodes a protein that functions as a translation initiation factor and is universally conserved. It encodes one of the two proteins identified as translation initiation factors, the other factor being a complex composed of three subunits. These translation factors act independently of each other, however, their function is the same: to position the initiator methionine trna on the start codon of the mrna in association with the 40S ribosomal subunit and GTP so that translation initiates accurately.
38. Trinucleotide repeat containing 11 (thr-associated protein, 230 kd subunit)	Subunit of TRAP thyroid hormone receptor-associated protein complex; coactivator for nuclear receptors
39. Tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, zeta polypeptide	This gene product belongs to the 14-3-3 family of proteins which mediate signal transduction by binding to phosphoserine-containing proteins. This highly conserved protein family is found in both plants and mammals, and this protein is 99% identical to the mouse, rat and sheep orthologs. The encoded protein has phospholipase A2 activity, and interacts with IRS1 protein, suggesting its role in diverse biochemical activities. Two transcript variants differing in the 5' UTR, but encoding the same protein, have been identified for this gene. Proteome Summary: Member of the dimeric 14-3-3 family; mediates signal transduction by binding to phosphorylated serine residues on a variety of signaling molecules
40. Ubiquitin specific protease 9, x chromosome (fat facets-like drosophila)	This X-linked gene escapes X-inactivation and has a homolog on the Y chromosome. Homology to a Drosophila gene suggests that this gene encodes a ubiquitin-specific protease, which may regulate protein levels by removing ubiquitin from proteins marked for digestion by proteasomes. The protein may also be involved in oocyte proliferation. Two transcript variants for this gene exist. Proteome Summary: Member of the ubiquitin-specific cysteine (thiol) protease family; removes ubiquitin from ubiquitin-conjugated proteins
41. Udp glycosyltransferase 2 family, polypeptide b17	Member 17 of udp-glucuronosyltransferase er glycoprotein subfamily 2b; conjugates lipophilic aglycon substrates to glucuronic acid. udpgt is of major importance in the conjugation and subsequent elimination of potentially toxic xenobiotics and endogenous compounds. The major substrates of this isozyme are eugenol > 4-methylumbelliferone > dihydrotestosterone > androstane-3alpha,17beta-diol (3alpha-diol) > testosterone > androsterone.