

Down-Regulated Transcripts (U133A 133B)

Fold Change	Gene ID	Gene Identifier	Other ID	Gene Title	UG Cluster	LocusLink	Chromosome
-1.5	ATM	U26455	210858_x_at	Ataxia telangiectasia mutated	Hs.367437	472	11
-1.5	CPSF3L	NM_017871	217994_x_at	Cleavage and polyadenylation specific factor 3-like	Hs.6449	54973	1
-1.5	DDX5	NM_004396	200033_at	DEAD (Asp-Glu-Ala-Asp) box polypeptide 5	Hs.279806	1655	17
-1.5	GTF2IRD2	AC004883	215569_at	general transcription factor III	-	2969	-
-1.5	GRAMD1B	BE044440	212906_at	GRAM domain containing 1B	Hs.144725	57476	11
-1.5	RPL15	AF279903	221476_s_at	Ribosomal protein L15	Hs.381219	6138	3
-1.5	FTH1	AA083483	214211_at	Ferritin, heavy polypeptide 1	Hs.524910	2495	11
-1.5	ANXA11	BG177920	214783_s_at	Annexin A11	Hs.530291	311	10
-1.5	PABPC1	AI734929	215157_x_at	Poly(A) binding protein, cytoplasmic 1	Hs.387804	26986	8
-1.5	MAP3K3	BF971923	203514_at	Mitogen-activated protein kinase kinase 3	Hs.29282	4215	17
-1.5	AKAP13	BF222823	209534_x_at	A kinase (PRKA) anchor protein 13	Hs.710656	11214	15
-1.5	BRD2	AA902767	208685_x_at	Bromodomain containing 2	Hs.75243	6046	6
-1.5	LARP7	AK000089	215246_at	La ribonucleoprotein domain family, member 7	Hs.713663	51574	4
-1.5	CYP7B1	NM_004820	207386_at	Cytochrome P450, family 7, subfamily B, polypeptide 1	Hs.667720	9420	8
-1.6	MAML3	NM_005878	207946_at	mastermind-like 3 (Drosophila)	-	-	-
-1.6	PUS3	NM_031307	221277_s_at	Pseudouridylate synthase 3	Hs.660922	83480	11
-1.6	FLI1-AS1	AI860159	239641_at	Homo sapiens, clone IMAGE:5173389, mRNA	-	-	-
-1.6	ZNF350	NM_021632	219266_at	Zinc finger protein 350	Hs.407694	59348	19
-1.6	SLC28A3	NM_022127	220475_at	Solute carrier family 28 (sodium-coupled nucleoside transporter), member 3	Hs.591877	64078	9
-1.6	BIN1	NM_004305	202931_x_at	Bridging integrator 1	Hs.193163	274	2
-1.6	HLA-E	M31183	217456_x_at	Major histocompatibility complex, class I, E	Hs.650174	3133	6
-1.6	ZFAND5	AF062347	210275_s_at	Zinc finger, AN1-type domain 5	Hs.406096	7763	9
-1.6	HSP90AA1	R01140	214328_s_at	heat shock protein 90kDa alpha (cytosolic), class A member 1	-	-	-
-1.6	CYTH4	NM_013385	219183_s_at	Cytohesin 4	Hs.170944	27128	22
-1.6	ADAM22	AW242701	213411_at	Transcribed locus	Hs.592567	-	7
-1.6	BMP2K	AU145366	226853_at	BMP2 inducible kinase	-	-	-
-1.6	TYRO3	D50479	211431_s_at	TYRO3 protein tyrosine kinase	Hs.381282	7301	15
-1.6	RPL23	NM_000978	200888_s_at	Ribosomal protein L23	Hs.406300	9349	17
-1.6	CABIN1	AB002328	37652_at	Calcineurin binding protein 1	Hs.517478	23523	22
-1.6	SP140	NM_007237	207777_s_at	SP140 nuclear body protein	Hs.632549	11262	2
-1.6	RPS17	NM_001021	201665_x_at	Ribosomal protein S17	Hs.433427	6218	15
-1.6	LOC441996	AL021877	217337_at	Human DNA sequence from clone RP1-101G11 on chromosome 22q12 Contains an ACO2 (Mitochondrial Aconitate Hydratase (Aconitase, Citrate Hydro-Lyase, EC 4.2.1.3)) pseudogene, ESTs, STSs, GSSs and a CpG islandn	-	-	-
-1.6	TRPV1	AF196175	219632_s_at	Transient receptor potential cation channel, subfamily V, member 1	Hs.655380	7442	17
-1.6	SSR3	AW087870	222411_s_at	Signal sequence receptor, gamma (translocon-associated protein gamma)	-	-	-
-1.6	TAZ	X92762	37278_at	Tafazzin	Hs.409911	6901	X
-1.6	ZNF335	AA845577	78330_at	Zinc finger protein 335	Hs.174193	63925	20
-1.6	EEF1B2	NM_001959	200705_s_at	Eukaryotic translation elongation factor 1 beta 2	Hs.421608	1933	2
-1.6	HIVEP1	NM_002114	204512_at	Human immunodeficiency virus type I enhancer binding protein 1	Hs.567284	3096	6
-1.6	GPR35	AF089087	210264_at	G protein-coupled receptor 35	Hs.239891	2859	2
-1.6	RPL22	NM_000983	220960_x_at	Ribosomal protein L22	Hs.515329	6146	1
-1.6	LOC647979	AV729406	224597_at	Transcribed locus, moderately similar to XP_001367988.1 PREDICTED: similar to keratin 19 [Monodelphis domestica]	-	-	-
-1.6	RPS14	AF116710	208645_s_at	ribosomal protein S14	-	-	-
-1.6	RNF130	AW194818	222058_at	Ring finger protein 130	Hs.484363	55819	5
-1.6	CD99	NM_002414	201029_s_at	CD99 molecule	Hs.654354	4267	X Y
-1.6	RPL4	BC005817	211710_x_at	Ribosomal protein L4	Hs.644628	6124	15
-1.7	EIF4A2	NM_001967	200912_s_at	Eukaryotic translation initiation factor 4A, isoform 2	Hs.518475	1974	3
-1.7	TRAK1	AK000754	214924_s_at	Trafficking protein, kinesin binding 1	Hs.535711	22906	3
-1.7	MAP4	AL523310	212566_at	Microtubule-associated protein 4	Hs.517949	4134	3
-1.7	BBS1	NM_024649	218471_s_at	Bardet-Biedl syndrome 1	Hs.502915	582	11
-1.7	H3F3B	Z48950	211999_at	H3 histone, family 3B (H3.3B)	-	3021	-
-1.7	RPAP1	NM_015540	218441_s_at	RNA polymerase II associated protein 1	Hs.371045	26015	15
-1.7	SLC16A2	NM_006517	204462_s_at	Solute carrier family 16, member 2 (monocarboxylic acid transporter 8)	Hs.75317	6567	X
-1.7	C1orf151	BF244614	224867_at	Chromosome 1 open reading frame 151	-	-	-
-1.7	EEF1D	AI613383	214394_x_at	Eukaryotic translation elongation factor 1 delta (guanine nucleotide exchange protein)	Hs.333388	1936	8
-1.7	TSPYL1	AL136629	221493_at	TSPY-like 1	Hs.458358	7259	6
-1.7	NDE1	NM_017668	218414_s_at	NudE nuclear distribution gene E homolog 1 (A. nidulans)	Hs.655378	54820	16
-1.7	NACA	BF976260	208635_x_at	Nascent polypeptide-associated complex alpha subunit	Hs.505735	4666	12
-1.7	RPL14	U16738	200074_s_at	Ribosomal protein L14	Hs.719095	9045	3
-1.7	RPL5	NM_000969	200937_s_at	Ribosomal protein L5	Hs.532359	6125	1

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-1.7	ZNF573	BE515346	217627_at	Zinc finger protein 573	Hs.531262	126231	19
-1.7	FBXL7	AU145127	213249_at	F-box and leucine-rich repeat protein 7	Hs.433057	23194	5
-1.7	POFUT2	BC000626	209578_s_at	Protein O-fucosyltransferase 2	Hs.592164	23275	21
-1.7	CNST	AV700816	225550_at	Chromosome 1 open reading frame 71			
-1.7	RPL17	BE733979	212537_x_at	Ribosomal protein L17	Hs.485090	6139	18
-1.7	PTCD2	NM_024754	219658_at	Pentatricopeptide repeat domain 2	Hs.126906	79810	5
-1.7	CCNL2	NM_030937	221427_s_at	Cyclin L2	Hs.515704	81669	1
-1.7	HIP1R	AB014555	38340_at	Huntingtin interacting protein 1 related	Hs.524815	9026	12
-1.7	STAT5A	NM_003152	203010_at	Signal transducer and activator of transcription 5A	Hs.437058	6776	17
-1.7	CLK4	AF212224	210346_s_at	CDC-like kinase 4	-	-	-
-1.7	DPH5	NM_015958	219590_x_at	DPH5 homolog (S. cerevisiae)	Hs.440776	51611	1
-1.7	LOC100130938	AW139393	230574_at	Hypothetical protein LOC100130938			
-1.7	-	AI633618	243115_at	CDNA FLJ36110 fis, clone TESTI201939			
-1.7	PL-5283	BE738276	224751_at	PL-5283 protein			
-1.7	RPL29	NM_000992	200823_x_at	Ribosomal protein L29	Hs.425125	6159	3
-1.7	CNIH4	AL136930	223993_s_at	Cornichon homolog 4 (Drosophila)			
-1.7	SPPL2A	AI674647	226353_at	Signal peptide peptidase-like 2A			
-1.7	CIRBP	NM_001280	200811_at	Cold inducible RNA binding protein	Hs.634522	1153	19
-1.7	GNB4	H99792	225710_at	Guanine nucleotide binding protein (G protein), beta polypeptide 4			
-1.7	SCMH1	NM_012236	221216_s_at	Sex comb on midleg homolog 1 (Drosophila)	Hs.571874	22955	1
-1.7	ZSCAN18	NM_023926	218312_s_at	Zinc finger and SCAN domain containing 18	Hs.235390	65982	19
-1.7	UBE2T	AB032931	223229_at	Ubiquitin-conjugating enzyme E2T (putative)			
-1.7	GTF2A1	AU144104	225433_at	General transcription factor IIA, 1, 19/37kDa			
-1.7	EDA2R	NM_021783	221399_at	Ectodysplasin A2 receptor	Hs.302017	60401	X
-1.7	SH2B2	NM_020979	205367_at	SH2B adaptor protein 2	Hs.489448	10603	7
-1.7	SFRS17A	NM_005088	203624_at	Splicing factor, arginine/serine-rich 17A	Hs.522572	8227	X Y
-1.8	EIF5	AK026933	208706_s_at	Eukaryotic translation initiation factor 5	Hs.433702	1983	14
-1.8	RPL36AP52	Z98950	217256_x_at	ribosomal protein L36a pseudogene 52	-	207032	-
-1.8	DDX3X	NM_001356	201210_at	DEAD (Asp-Glu-Ala-Asp) box polypeptide 3, X-linked	Hs.719127	1654	X
-1.8	LOC729082	BF791544	225225_at	Hypothetical protein LOC729082			
-1.8	TMEM40	AI087937	222892_s_at	Transmembrane protein 40			
-1.8	SFRS5	NM_006925	203380_x_at	Splicing factor, arginine/serine-rich 5	Hs.632326	6430	14
-1.8	TMEM60	AF260336	223396_at	Transmembrane protein 60			
-1.8	FBXO41	AA524093	44040_at	F-box protein 41	Hs.23158	150726	2
-1.8	NFKBIZ	AB037925	223218_s_at	Nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, zeta			
-1.8	TRPC4	NM_016179	220818_s_at	Transient receptor potential cation channel, subfamily C, member 4	Hs.262960	7223	13
-1.8	PCIF1	AI743331	89948_at	PDX1 C-terminal inhibiting factor 1	Hs.716563	63935	20
-1.8	TTY15	AL080135	214983_at	Transcribed locus	Hs.433656	64595	Y
-1.8	SCOC	AL133580	224786_at	Short coiled-coil protein			
-1.8	PNKD	AB033010	233177_s_at	Paroxysmal nonkinesigenic dyskinesia			
-1.8	LOC441454	AF257099	216384_x_at	similar to prothymosin alpha	-	-	-
-1.8	TPD52	AA524023	201690_s_at	Tumor protein D52	Hs.368433	7163	8
-1.8	TRIM29	AF230389	211001_at	tripartite motif-containing 29	-	23650	-
-1.8	HCST	AF285447	223640_at	Hematopoietic cell signal transducer			
-1.8	OGT	BF001665	212307_s_at	O-linked N-acetylglucosamine (GlcNAc) transferase (UDP-N-acetylglucosamine:polypeptide-N-acetylglucosaminyl transferase)	Hs.405410	8473	X
-1.8	AMPD2	AI916249	212360_at	Adenosine monophosphate deaminase 2 (isoform L)	Hs.82927	271	1
-1.8	-	AI357639	225716_at	Transcribed locus			
-1.8	CLSTN1	NM_014944	201561_s_at	Calsyntenin 1	Hs.29665	22883	1
-1.8	DNNTIP2	NM_014597	202776_at	Deoxynucleotidyltransferase, terminal, interacting protein 2	Hs.85769	30836	1
-1.8	IGF2BP2	NM_006548	218847_at	Insulin-like growth factor 2 mRNA binding protein 2	Hs.35354	10644	3
-1.8	EIF3E	BC000734	208697_s_at	Eukaryotic translation initiation factor 3, subunit E	Hs.405590	3646	8
-1.8	BTG3	AI765445	213134_x_at	BTG family, member 3	Hs.473420	10950	21
-1.8	SH2B1	AL049924	40149_at	SH2B adaptor protein 1	Hs.15744	25970	16
-1.8	UBASH3B	AI927919	238587_at	Ubiquitin associated and SH3 domain containing, B			
-1.8	IRGQ	AW003091	64488_at	Immunity-related GTPase family, Q	Hs.6217	126298	19
-1.8	PNN	AW152664	212036_s_at	Pinin, desmosome associated protein	Hs.409965	5411	14
-1.8	TOMM5	BF969806	225036_at	Translocase of outer mitochondrial membrane 5 homolog (yeast)			
-1.8	PLDN	BF680495	224892_at	pallidin homolog (mouse)			
-1.8	GPR56	AL554008	212070_at	G protein-coupled receptor 56	Hs.513633	9289	16
-1.8	SP110	AF280094	209762_x_at	SP110 nuclear body protein	Hs.145150	3431	2
-1.8	SUSD1	AL137432	226264_at	Sushi domain containing 1			
-1.8	SLC6A8	U17986	210854_x_at	Solute carrier family 6 (neurotransmitter transporter, creatine), member 8	Hs.540696	6535	X
-1.8	RALGDS	AI421559	209050_s_at	Ral guanine nucleotide dissociation stimulator	Hs.106185	5900	9
-1.9	RRP7A	NM_015703	202938_x_at	Ribosomal RNA processing 7 homolog A (S. cerevisiae)	Hs.534041	27341	22

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-1.9	EEF2	AI004246	200094_s_at	Eukaryotic translation elongation factor 2	Hs.515070	1938	19
-1.9	TNK2	NM_005781	203839_s_at	Tyrosine kinase, non-receptor, 2	Hs.518513	10188	3
-1.9	CD22	X59350	38521_at	CD22 molecule	Hs.579691	933	19
-1.9	USP19	AW451502	214674_at	Ubiquitin specific peptidase 19	Hs.255596	10869	3
-1.9	MZT	AI885466	225578_at	Chromosome 13 open reading frame 37			
-1.9	KCTD20	AV707142	228299_at	Potassium channel tetramerisation domain containing 20			
-1.9	ACSS2	AK000162	234312_s_at	Acyl-CoA synthetase short-chain family member 2			
-1.9	LYSMD2	AI674731	226748_at	LysM, putative peptidoglycan-binding, domain containing 2			
-1.9	PHLDA1	AA576961	217996_at	Pleckstrin homology-like domain, family A, member 1	Hs.602085	22822	12
-1.9	ACACB	AI057637	49452_at	Acetyl-Coenzyme A carboxylase beta	Hs.234898	32	12
-1.9	RPL26	AL121871	222229_x_at	ribosomal protein L26 pseudogene 37	-	-	-
-1.9	IPO9	AW269792	213785_at	Importin 9	Hs.596014	55705	1
-1.9	-	AK022254	215876_at	CDNA FLJ12192 fis, clone MAMMA1000851	Hs.600188	-	9
-1.9	SNAPC4	AK023513	215926_x_at	Small nuclear RNA activating complex, polypeptide 4, 190kDa	Hs.113265	6621	9
-1.9	ZNF644	AK023596	222580_at	Zinc finger protein 644			
-1.9	SPATA6	NM_019073	220299_at	Spermatogenesis associated 6	Hs.538103	54558	1
-1.9	CDC42SE1	BG150636	229120_s_at	CDC42 small effector 1			
-1.9	TUFT1	NM_020127	205807_s_at	Tuftelin 1	Hs.489922	7286	1
-1.9	HNF4A	X87870	214851_at	Hepatocyte nuclear factor 4, alpha	Hs.116462	3172	20
-1.9	EIF4B	BF247371	211938_at	CDNA clone IMAGE:4181418	Hs.702041	-	12
-1.9	CASP1	U13700	211368_s_at	Caspase 1, apoptosis-related cysteine peptidase (interleukin 1, beta, convertase)	Hs.2490	834	11
-1.9	PDE4D	AF012074	210837_s_at	Phosphodiesterase 4D, cAMP-specific (phosphodiesterase E3 dunce homolog, Drosophila)	Hs.117545	5144	5
-1.9	RPS10	AL118510	217336_at	ribosomal protein S10 pseudogene 2	-	140758	-
-1.9	PIAS2	AF077953	214442_s_at	Protein inhibitor of activated STAT, 2	Hs.658013	9063	18
-1.9	RGS14	AF037195	38290_at	Regulator of G-protein signaling 14	Hs.9347	10636	5
-1.9	VPS37B	BC005882	221704_s_at	Vacuolar protein sorting 37 homolog B (S. cerevisiae)	Hs.507162	79720	12
-1.9	AKR1C1	S68290	216594_x_at	Aldo-keto reductase family 1, member C1 (dihydrodiol dehydrogenase 1; 20-alpha (3-alpha)-hydroxysteroid dehydrogenase)	Hs.460260	1645	10
-1.9	TSPYL4	AL050331	212928_at	TSPY-like 4	-	-	-
-1.9	NIPSNAP3A	BC005935	224436_s_at	Nipsnap homolog 3A (C. elegans)			
-1.9	FAM65C	AI056877	227654_at	Family with sequence similarity 65, member C			
-1.9	PBXIP1	AI935162	214177_s_at	Pre-B-cell leukemia homeobox interacting protein 1	Hs.505806	57326	1
-1.9	STAC	NM_003149	205743_at	SH3 and cysteine rich domain	Hs.56045	6769	3
-1.9	RBM39	NM_004902	207941_s_at	RNA binding motif protein 39	Hs.282901	9584	20
-1.9	HSPA5	AF216292	211936_at	Heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa)	Hs.716396	3309	9
-2.0	1	AV702487	225826_at	Methylmalonic aciduria (cobalamin deficiency) cblB type			
-2.0	1	AW149498	225389_at	BTB (POZ) domain containing 6			
-2.0	SRRT	AI523895	222046_at	Serrate RNA effector molecule homolog (Arabidopsis)	Hs.111801	51593	7
-2.0	VPRBP	NM_014703	204376_at	Vpr (HIV-1) binding protein	Hs.716623	9730	3
-2.0	1	BG170743	225084_at	Exocyst complex component 5			
-2.0	MAPK11	U92268	211499_s_at	mitogen-activated protein kinase 11	-	5600	-
-2.0	NEUROG2	AF303002	215632_at	neurogenin 2	-	63973	-
-2.0	GOLGA8A	AW006438	213650_at	Golgi autoantigen, golgin subfamily a, 8A	Hs.182982	23015	15
-2.0	-	AF053356	37796_at	leucine-rich repeats and calponin homology (CH) domain containing 4	-	-	-
-2.0	-	M30448	211623_s_at	fibrillarin	-	-	-
-2.0	-	AL121916	216342_x_at	ribosomal protein S4X pseudogene 13 /// ribosomal protein S4X pseudogene 17 /// ribosomal protein S4X pseudogene 7 /// ribosomal protein S4, X-linked	-	-	-
-2.0	AES	NM_001130	217729_s_at	Amino-terminal enhancer of split	Hs.515053	166	19
-2.0	CDCA3	BC002551	223307_at	Cell division cycle associated 3			
-2.0	AMT	NM_000481	204294_at	Aminomethyltransferase	Hs.102	275	3
-2.0	TRIM14	NM_014788	203148_s_at	Tripartite motif-containing 14	Hs.575631	9830	9
-2.0	CAMLG	NM_001745	203538_at	Calcium modulating ligand	Hs.529846	819	5
-2.0	ZNF337	AL049942	214760_at	Zinc finger protein 337	Hs.661684	26152	20
-2.0	LILRB3	NM_024318	208594_x_at	Leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 3	Hs.688335	11025	19
-2.0	-	BE671038	230793_at	Transcribed locus			
-2.0	ME3	NM_006680	204663_at	Malic enzyme 3, NADP(+)-dependent, mitochondrial	Hs.199743	10873	11
-2.0	SEP6	D50918	212413_at	Septin 6	Hs.496666	23157	X
-2.0	-	AW500340	242714_at	Transcribed locus			
-2.0	RASA4	AI738591	212707_s_at	RAS p21 protein activator 4	Hs.530089	10156	7
-2.0	ZDHHC5	AK023130	224858_at	Zinc finger, DHHC-type containing 5			
-2.0	SLC17A9	NM_022082	219559_at	Solute carrier family 17, member 9	Hs.512686	63910	20
-2.0	MYO5C	NM_018728	218966_at	Myosin VC	Hs.487036	55930	15
-2.0	TIAF1	NM_004740	202039_at	TGFBI-induced anti-apoptotic factor 1	Hs.462590	9220	17

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-2.0	RPS8	NM_001012	200858_s_at	Ribosomal protein S8	Hs.512675	6202	1
-2.1	PDLIM2	NM_021630	219165_at	PDZ and LIM domain 2 (mystique)	Hs.632034	64236	8
-2.1	BSPRY	NM_017688	218792_s_at	B-box and SPRY domain containing	Hs.614517	54836	9
-2.1	GABARAPL3	AF180519	211458_s_at	GABA(A) receptors associated protein like 3 (pseudogene)	Hs.592014	23766	15
-2.1	HAU55	AW189966	213053_at	HAUS augmin-like complex, subunit 5	Hs.7426	23354	19
-2.1	-	BE616825	223158_s_at	NIMA (never in mitosis gene a)-related kinase 6			
-2.1	RCC1	AJ006835	215011_at	Regulator of chromosome condensation 1	Hs.469723	1104	1
-2.1	ALDH1A1	NM_000689	212224_at	Aldehyde dehydrogenase 1 family, member A1	Hs.76392	216	9
-2.1	-	NM_023941	218641_at	hypothetical protein LOC65998	-	-	-
-2.1	HINT2	AF356515	224415_s_at	Histidine triad nucleotide binding protein 2			
-2.1	-	AA601208	60815_at	Williams Beuren syndrome chromosome region 19 pseudogene, mRNA (cDNA clone IMAGE:4826159)	Hs.645327	-	7
-2.1	ZNF395	NM_018660	221123_x_at	Zinc finger protein 395	Hs.699209	55893	8
-2.1	CEP164	NM_014956	204251_s_at	Centrosomal protein 164kDa	Hs.504009	22897	11
-2.1	EIF1	W67644	212227_x_at	Eukaryotic translation initiation factor 1	Hs.150580	10209	17
-2.1	-	BG291685	225413_at	up-regulated during skeletal muscle growth 5 homolog (mouse)			
-2.1	MYH11	NM_022844	201497_x_at	Myosin, heavy chain 11, smooth muscle	Hs.460109	4629	16
-2.1	ATXN7	AF032105	209964_s_at	Ataxin 7	Hs.476595	6314	3
-2.1	ARHGAP26	BE671084	205068_s_at	Rho GTPase activating protein 26	Hs.654668	23092	5
-2.1	BBS9	U87408	37549_g_at	Bardet-Biedl syndrome 9	Hs.372360	27241	7
-2.1	MXI1	NM_005962	202364_at	MAX interactor 1	Hs.719185	4601	10
-2.1	STK17B	AA203487	217503_at	Serine/threonine kinase 17b	Hs.88297	9262	2
-2.1	NR112	AF061056	207203_s_at	Nuclear receptor subfamily 1, group I, member 2	Hs.7303	8856	3
-2.2	F11R	AF172398	223000_s_at	F11 receptor			
-2.2	EMR2	NM_013447	207610_s_at	Egf-like module containing, mucin-like, hormone receptor-like 2	Hs.531619	30817	19
-2.2	-	AW290940	226773_at	Transcribed locus			
-2.2	-	AF077053	221617_at	TAF9B RNA polymerase II, TATA box binding protein (TBP)-associated factor, 31kDa	-	51616	-
-2.2	-	AI807023	226633_at	RAB8B, member RAS oncogene family			
-2.2	-	NM_022448	219610_at	Rho-guanine nucleotide exchange factor	-	-	-
-2.2	SLC39A9	AK025831	222445_at	Solute carrier family 39 (zinc transporter), member 9			
-2.2	XPA	NM_000380	205672_at	Xeroderma pigmentosum, complementation group A	Hs.654364	7507	9
-2.2	NIN	AL359571	225921_at	Ninein (GSK3B interacting protein)			
-2.2	UGGT1	AK025416	231968_at	CDNA: FLJ121763 fis, clone COLF6967			
-2.2	LRR1	AA742244	235113_at	Peptidylprolyl isomerase (cyclophilin)-like 5			
-2.2	ZCCHC17	AF151077	223107_s_at	Zinc finger, CCHC domain containing 17			
-2.2	-	AL137067	216821_at	keratin 8 /// keratin 8 pseudogene 9 /// similar to keratin 8 /// similar to keratin 8	-	-	-
-2.2	PPP3CC	NM_005605	207000_s_at	Protein phosphatase 3 (formerly 2B), catalytic subunit, gamma isoform	Hs.655661	5533	8
-2.2	-	N32051	229307_at	Ankyrin repeat domain 28			
-2.2	C20orf111	AF217514	209020_at	Chromosome 20 open reading frame 111	Hs.75798	51526	20
-2.2	COL7A1	NM_000094	204136_at	Collagen, type VII, alpha 1	Hs.476218	1294	3
-2.2	SDC2	AL577322	212158_at	Syndecan 2	Hs.1501	6383	8
-2.2	TTC17	NM_018259	218972_at	Tetrapeptide repeat domain 17	Hs.696109	55761	11
-2.2	-	BF589251	227776_at	Alkaline ceramidase 3			
-2.2	ARMCX2	NM_014782	203404_at	Armadillo repeat containing, X-linked 2	Hs.48924	9823	X
-2.2	NOTCH4	AI743713	205247_at	Notch homolog 4 (Drosophila)	Hs.436100	4855	6
-2.2	C13orf15	NM_014059	218723_s_at	Chromosome 13 open reading frame 15	Hs.507866	28984	13
-2.2	CNTN1	U07820	211203_s_at	Contactin 1	Hs.143434	1272	12
-2.2	LZTS1	BE312985	222107_x_at	Leucine zipper, putative tumor suppressor 1	Hs.521432	11178	8
-2.2	GRB2	AF246238	223049_at	Growth factor receptor-bound protein 2			
-2.2	JKAMP	AF151047	223215_s_at	Chromosome 14 open reading frame 100			
-2.3	-	BF675979	239355_at	Transcribed locus			
-2.3	CAPRIN2	NM_023925	218456_at	Caprin family member 2	Hs.234355	65981	12
-2.3	AIM1	U83115	212543_at	Absent in melanoma 1	Hs.643590	202	6
-2.3	RIPK2	AF064824	209545_s_at	Receptor-interacting serine-threonine kinase 2	Hs.103755	8767	8
-2.3	-	AI683552	217679_x_at	Consensus includes gb:A1683552 /FEA=EST /DB_XREF=gi:4893734 /DB_XREF=est:tx67h02.x1 /CLONE=IMAGE:2274675 /UG=Hs.201605 ESTs, Moderately similar to ALU8_HUMAN ALU SUBFAMILY SX SEQUENCE CONTAMINATION WARNING ENTRY H.sapiens	-	-	-
-2.3	TXNDC17	BC006405	224511_s_at	Thioredoxin domain containing 17			
-2.3	LOC129851	AF131743	224628_at	Chromosome 2 open reading frame 30			
-2.3	-	AA001203	224765_at	Male-specific lethal 1 homolog (Drosophila)			
-2.3	LETMD1	NM_015416	207170_s_at	LETM1 domain containing 1	Hs.655272	25875	12
-2.3	RARA	AI806984	203749_s_at	Retinoic acid receptor, alpha	Hs.654583	5914	17
-2.3	ESRP1	NM_017697	219121_s_at	Epithelial splicing regulatory protein 1	Hs.487471	54845	8

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-2.3	-	AV761453	222282_at	Consensus includes gb:AV761453 /FEA=EST /DB_XREF=gi:10919301 /DB_XREF=est:AV761453 /CLONE=MDSBZA03 /UG=Hs.294014 ESTs	-	-	-
-2.3	RPL31	BC001663	221593_s_at	Ribosomal protein L31	Hs.469473	6160	2
-2.3	BEX2	AF251053	224367_at	Brain expressed X-linked 2			
-2.3	SELK	AF085359	223070_at	Selenoprotein K			
-2.3	SSBP1	BE220360	214060_at	Single-stranded DNA binding protein 1	Hs.490394	6742	7
-2.3	BRD2	D42040	208686_s_at	Bromodomain containing 2	Hs.75243	6046	6
-2.3	-	AV715993	226007_at	Iron-sulfur cluster assembly 2 homolog (<i>S. cerevisiae</i>)			
-2.3	IER3IP1	AL136667	223071_at	Immediate early response 3 interacting protein 1			
-2.3	RPL13P12	AW574664	212191_x_at	Ribosomal protein L13 pseudogene 12	Hs.448879	388344	17
-2.3	ZNF136	NM_003437	206240_s_at	Zinc finger protein 136	Hs.479874	7695	19
-2.3	-	BG167841	227066_at	MOB1, Mps One Binder kinase activator-like 2C (yeast)			
-2.3	SEPT2	NM_004404	200015_s_at	Septin 2			
-2.3	ACAP1	NM_014716	205213_at	ArfGAP with coiled-coil, ankyrin repeat and PH domains 1	Hs.337242	9744	17
-2.3	SNX26	AL137579	213827_at	Sorting nexin 26	Hs.515364	115703	19
-2.4	-	AI307808	226106_at	Ring finger protein 141			
-2.4	LOC112488	AK000490	222958_s_at	DEP domain containing 1			
-2.4	MSH5	AF034759	210410_s_at	MutS homolog 5 (<i>E. coli</i>)	Hs.647011	4439	6
-2.4	MKNK2	NM_017572	218205_s_at	MAP kinase interacting serine/threonine kinase 2	Hs.515032	2872	19
-2.4	HIST1H2AL	NM_003511	214554_at	Histone cluster 1, H2al	Hs.233568	8332	6
-2.4	LZTFL1	NM_020347	218437_s_at	Leucine zipper transcription factor-like 1	Hs.30824	54585	3
-2.4	-	BE644830	225171_at	Rho GTPase activating protein 18			
-2.4	ANKRD36	AB046861	214723_x_at	ankyrin repeat domain 36B		57730	
-2.4	KDM2A	AK024505	208987_s_at	Lysine (K)-specific demethylase 2A	Hs.124147	22992	11
-2.4	SFRS15	AA648521	222310_at	Splicing factor, arginine/serine-rich 15	Hs.17255	57466	21
-2.4	-	N37023	225407_at	Myelin basic protein			
-2.4	IER3	NM_003897	201631_s_at	Immediate early response 3	Hs.591785	8870	6
-2.4	CSNK1E	NM_001894	202332_at	Casein kinase 1, epsilon	Hs.474833	1454	22
-2.4	-	NM_021730	218380_at	NLR family, pyrin domain containing 1		22861	
-2.4	CTH	NM_001902	206085_s_at	Cystathionase (cystathionine gamma-lyase)	Hs.19904	1491	1
-2.4	CTPTM1L	AB045223	223020_at	CLPTM1-like			
-2.4	PLEKHA1	NM_021622	219024_at	Pleckstrin homology domain containing, family A (phosphoinositide binding specific) member 1	Hs.643512	59338	10
-2.4	-	AI640157	229801_at	Chromosome 10 open reading frame 47			
-2.4	FMNL1	NM_005892	204789_at	Formin-like 1	Hs.100217	752	17
-2.4	C14orf119	AF061731	223060_at	Chromosome 14 open reading frame 119			
-2.4	CYP1A1	NM_000499	205749_at	Cytochrome P450, family 1, subfamily A, polypeptide 1	Hs.72912	1543	15
-2.4	RUNX3	NM_004350	204197_s_at	Runt-related transcription factor 3	Hs.170019	864	1
-2.4	SERTAD2	BG107456	220656_s_at	SERTA domain containing 2	Hs.591569	9792	2
-2.4	-	BG250585	235740_at	Transcribed locus			
-2.4	-	AI963476	225585_at	RAP2A, member of RAS oncogene family			
-2.4	TCF7L2	AA664011	216037_x_at	Transcription factor 7-like 2 (T-cell specific, HMG-box)	Hs.593995	6934	10
-2.4	C16orf45	BE299456	212736_at	Chromosome 16 open reading frame 45	Hs.401798	89927	16
-2.4	GCH1	NM_000161	204224_s_at	GTP cyclohydrolase 1	Hs.86724	2643	14
-2.4	-	AA632295	227461_at	Stonin 2			
-2.4	-	AI676103	222533_at	Cereblon			
-2.4	TOB2	AB051450	222243_s_at	Transducer of ERBB2, 2	Hs.719120	10766	22
-2.5	FLT1	AA058828	222033_s_at	Fms-related tyrosine kinase 1 (vascular endothelial growth factor/vascular permeability factor receptor)	Hs.654360	2321	13
-2.5	EPDR1	BC000686	223253_at	Ependymin related protein 1 (zebrafish)			
-2.5	CYTH1	NM_004762	202880_s_at	Cytohesin 1	Hs.191215	9267	17
-2.5	C6orf62	AW972292	222309_at	Chromosome 6 open reading frame 62	Hs.519930	81688	6
-2.5	IL23A	M15564	210915_x_at	Interleukin 23, alpha subunit p19	Hs.621281	51561	12
-2.5	-	BF211019	224637_at	Dolichyl-diphosphooligosaccharide-protein glycosyltransferase subunit 4			
-2.5	-	AW088063	229610_at	Cytoskeleton associated protein 2-like			
-2.5	UNC84A	BE615699	214169_at	Unc-84 homolog A (<i>C. elegans</i>)	Hs.438072	23353	7
-2.5	ENGASE	NM_022759	220349_s_at	endo-beta-N-acetylglucosaminidase		64772	
-2.5	LPAR2	NM_004720	206722_s_at	Lysophosphatidic acid receptor 2	Hs.122575	9170	19
-2.5	FOXN3	NM_005197	205022_s_at	Forkhead box N3	Hs.434286	1112	14
-2.5	RPL10	AW057781	221989_at	Ribosomal protein L10	Hs.534404	6134	X
-2.5	-	BG432489	225460_at	SEC22 vesicle trafficking protein homolog C (<i>S. cerevisiae</i>)			
-2.5	-	AK026659	231925_at	CDNA: FLI23006 fis, clone LNG00414			
-2.5	-	BF003112	228725_x_at	Protein arginine methyltransferase 2			
-2.5	LOC92334	AK025925	224748_at	WD repeat domain 68			
-2.5	IL18R1	NM_003855	206618_at	Interleukin 18 receptor 1	Hs.469521	8809	2

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-2.5	PFN2	NM_002628	204992_s_at	Profilin 2	Hs.91747	5217	3
-2.6	LOC728844	AW450929	221919_at	Hypothetical LOC728844	Hs.656277	728844	12
-2.6	MXD4	BC002713	210778_s_at	MAX dimerization protein 4	Hs.655020	10608	4
-2.6	FGFR1	M60485	211535_s_at	Fibroblast growth factor receptor 1	Hs.264887	2260	8
-2.6	-	BF975327	225849_s_at	SFT2 domain containing 1			
-2.6	SFRS11	AW241752	213742_at	Splicing factor, arginine/serine-rich 11	Hs.479693	9295	1
-2.6	JMJD1C	AI694023	221763_at	Jumonji domain containing 1C	Hs.413416	221037	10
-2.6	-	BG496998	225684_at	Family with sequence similarity 33, member A			
-2.6	SIAH1	AV700132	221834_at	Seven in absentia homolog 1 (Drosophila)	Hs.295923	6477	16
-2.6	MOB1B	AL162039	225997_at	MOB1, Mps One Binder kinase activator-like 1A (yeast)			
-2.6	-	AA613031	225447_at	Glycerol-3-phosphate dehydrogenase 2 (mitochondrial)			
-2.6	-	AV715391	225297_at	HAUS augmin-like complex, subunit 1			
-2.6	C7orf23	NM_024315	204215_at	Chromosome 7 open reading frame 23	Hs.719226	79161	7
-2.6	GAB2	NM_012296	203853_s_at	GRB2-associated binding protein 2	Hs.429434	9846	11
-2.6	PLCL2	AL117515	213309_at	Phospholipase C-like 2	Hs.202010	23228	3
-2.6	DUSP10	N36770	221563_at	Dual specificity phosphatase 10	Hs.497822	11221	1
-2.6	FLJ10357	R42449	58780_s_at	Hypothetical protein FLJ10357	Hs.35125	55701	14
-2.6	RRAGB	NM_016656	205540_s_at	Ras-related GTP binding B	Hs.50282	10325	X
-2.6	-	Y09908	217371_s_at	interleukin 15	-	-	-
-2.6	RARRES2	BC000069	209496_at	Retinoic acid receptor responder (tazarotene induced) 2	Hs.647064	5919	7
-2.6	-	BF244081	224602_at	Chromosome 4 open reading frame 3			
-2.6	LOX	L16895	215446_s_at	lysyl oxidase	-	-	-
-2.6	NINJ1	NM_004148	203045_at	Ninjurin 1	Hs.494457	4814	9
-2.7	SMAD7	NM_005904	204790_at	SMAD family member 7	Hs.465087	4092	18
-2.7	CD53	NM_000560	203416_at	CD53 molecule	Hs.443057	963	1
-2.7	-	BF512139	225367_at	Phosphoglucomutase 2			
-2.7	-	W47179	213275_x_at	cathepsin B	-	-	-
-2.7	-	AI917716	228253_at	Lysyl oxidase-like 3			
-2.7	NBL1	D28124	37005_at	Neuroblastoma, suppression of tumorigenicity 1	Hs.654502	4681	1
-2.7	ZNF146	NM_007145	200050_at	Zinc finger protein 146			
-2.7	DNAH3	AL096732	215266_at	Dynein, axonemal, heavy chain 3	Hs.526500	55567	16
-2.7	GNA15	NM_002068	205349_at	Guanine nucleotide binding protein (G protein), alpha 15 (Gq class)	Hs.73797	2769	19
-2.7	ICAM1	NM_000201	202638_s_at	Intercellular adhesion molecule 1	Hs.643447	3383	19
-2.7	-	AI889717	242282_at	Zinc finger protein, multitype 1			
-2.7	-	AL573637	225583_at	UDP-glucuronate decarboxylase 1			
-2.7	CCRK	NM_012119	205271_s_at	Cell cycle related kinase	Hs.522274	23552	9
-2.7	-	BE348597	226464_at	Chromosome 3 open reading frame 58			
-2.7	SNED1	N73970	213488_at	Sushi, nidogen and EGF-like domains 1	Hs.471834	25992	2
-2.7	RPS19	BC000023	202648_at	Ribosomal protein S19	Hs.438429	6223	19
-2.8	-	BE875567	225059_at	Angiotensin II receptor-associated protein			
-2.8	TAF1D	BC001972	221580_s_at	TATA box binding protein (TBP)-associated factor, RNA polymerase I, D, 41kDa	-	79101	-
-2.8	NEDD1	AA236927	234984_at	Neural precursor cell expressed, developmentally down-regulated 1			
-2.8	-	NM_024679	219145_at	latrophilin 1	-	22859	-
-2.8	EZR	J05021	208623_s_at	Ezrin	Hs.487027	7430	6
-2.8	ARAP2	AB011152	213618_at	ArfGAP with RhoGAP domain, ankyrin repeat and PH domain 2	Hs.479451	116984	4
-2.8	ATP2B4	AW517686	212135_s_at	ATPase, Ca++ transporting, plasma membrane 4	Hs.343522	493	1
-2.8	CDH7	NM_004361	220679_s_at	Cadherin 7, type 2	Hs.657522	1005	18
-2.9	C9orf91	BF969986	221865_at	Chromosome 9 open reading frame 91	Hs.522357	203197	9
-2.9	SNAPIN	BC000761	223066_at	SNAP-associated protein			
-2.9	-	BE551691	224844_at	SLAIN motif family, member 2			
-2.9	SVIL	NM_003174	202565_s_at	Supervillin	Hs.499209	6840	10
-2.9	-	AU151357	228456_s_at	Hypothetical protein LOC149832			
-2.9	TEKT2	AB033823	210323_at	Tektin 2 (testicular)	Hs.127111	27285	1
-2.9	SGK2	NM_016276	220357_s_at	Serum/glucocorticoid regulated kinase 2	Hs.300863	10110	20
-2.9	TCF4	BF592782	212386_at	Transcription factor 4	Hs.605153	6925	18
-2.9	WDR33	NM_018383	218851_s_at	WD repeat domain 33	Hs.620490	55339	2
-2.9	C16orf80	NM_013242	217957_at	Chromosome 16 open reading frame 80	Hs.532755	29105	16
-2.9	-	AA608749	228095_at	PHD finger protein 14			
-2.9	-	BF248364	228323_at	Cancer susceptibility candidate 5			
-2.9	ARG2	NM_001172	203945_at	Arginase, type II	Hs.708024	384	14
-2.9	-	BE466926	217671_at	Transcribed locus	Hs.673795	-	9
-2.9	KLHL3	NM_017415	221221_s_at	Kelch-like 3 (Drosophila)	Hs.655084	26249	5
-2.9	NLGN3	NM_018977	219726_at	Neurologin 3	Hs.438877	54413	X
-2.9	-	BE220026	225240_s_at	Transcribed locus			
-3.0	-	AW500180	225793_at	Transcribed locus			

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-3.0	TRA2B	U87836	210180_s_at	Transformer 2 beta homolog (Drosophila)	Hs.533122	6434	3
-3.0	SLC5A5	D87920	211123_at	Solute carrier family 5 (sodium iodide symporter), member 5	Hs.584804	6528	19
-3.0	GDPD5	AL041124	32502_at	Glycerophosphodiester phosphodiesterase domain containing 5	Hs.503297	81544	11
-3.0	TICAM1	AF070530	213191_at	Toll-like receptor adaptor molecule 1	Hs.29344	148022	19
-3.0	-	BG250721	224606_at	Kruppel-like factor 6			
-3.0	KIAA0644	NM_014817	205151_s_at	KIAA0644 gene product	Hs.719240	9865	7
-3.0	-	BF185904	226881_at	GrpE-like 2, mitochondrial (E. coli)			
-3.0	CCNDBP1	AF246144	223084_s_at	Cyclin D-type binding-protein 1			
-3.1	ADM	NM_001124	202912_at	Adrenomedullin	Hs.441047	133	11
-3.1	DPT	AI146848	213068_at	Dermatopontin	Hs.80552	1805	1
-3.1	BLNK	NM_013314	207655_s_at	B-cell linker	Hs.665244	29760	10
-3.1	RAPSN	BC004196	211570_s_at	Receptor-associated protein of the synapse	Hs.81218	5913	11
-3.1	SLMAP	AB046821	225243_s_at	Sarcolemma associated protein			
-3.1	HLA-DQB1	AI583173	212998_x_at	Major histocompatibility complex, class II, DQ beta 1	Hs.409934	3119	6
-3.1	KLHL12	AK024412	225068_at	Kelch-like 12 (Drosophila)			
-3.1	REPS2	NM_004726	205645_at	RALBP1 associated Eps domain containing 2	Hs.186810	9185	X
-3.1	C19orf33	AF213678	223631_s_at	Chromosome 19 open reading frame 33			
-3.1	PIGA	NM_002641	205281_s_at	Phosphatidylinositol glycan anchor biosynthesis, class A	Hs.137154	5277	X
-3.1	PRKRIP1	NM_024653	218378_s_at	PRKR interacting protein 1 (IL11 inducible)	Hs.406395	79706	7
-3.1	-	AL520657	225052_at	Transmembrane protein 203			
-3.1	ZNF10	X52332	216350_s_at	Zinc finger protein 10	Hs.507355	7556	12
-3.1	ZBTB20	NM_015642	205383_s_at	Zinc finger and BTB domain containing 20	Hs.655108	26137	3
-3.1	-	AI869704	225419_at	Chromosome 7 open reading frame 11			
-3.1	DLK1	U15979	209560_s_at	Delta-like 1 homolog (Drosophila)	Hs.533717	8788	14
-3.1	SKAP1	NM_003726	205790_at	Src kinase associated phosphoprotein 1	Hs.316931	8631	17
-3.1	-	BG054744	226678_at	Unc-13 homolog D (C. elegans)			
-3.1	EGR3	NM_004430	206115_at	Early growth response 3	Hs.534313	1960	8
-3.2	SPCS3	AL136660	222753_s_at	Signal peptidase complex subunit 3 homolog (S. cerevisiae)			
-3.2	HECA	NM_016217	218603_at	Headcase homolog (Drosophila)	Hs.197644	51696	6
-3.2	RAB18	AL136734	223336_s_at	RAB18, member RAS oncogene family			
-3.2	-	N64686	225904_at	Chromosome 1 open reading frame 96			
-3.2	IER5	NM_016545	218611_at	Immediate early response 5	Hs.716489	51278	1
-3.2	C14orf138	NM_024558	218940_at	Chromosome 14 open reading frame 138	Hs.558541	79609	14
-3.2	-	AV734582	226544_x_at	muted homolog (mouse)			
-3.2	GNB2L1	AA443762	222034_at	Guanine nucleotide binding protein (G protein), beta polypeptide 2-like 1	Hs.5662	10399	5
-3.2	SH3BP4	AF015043	222258_s_at	SH3-domain binding protein 4	Hs.516777	23677	2
-3.2	FBX05	AK026197	234863_x_at	F-box protein 5			
-3.2	PITPNM2	AB040890	232950_s_at	Phosphatidylinositol transfer protein, membrane-associated 2			
-3.2	-	AV756867	225693_s_at	Calmodulin binding transcription activator 1			
-3.2	-	AI418253	242201_at	Postmeiotic segregation increased 2-like 5			
-3.2	MAP3K14	NM_003954	205192_at	Mitogen-activated protein kinase kinase kinase 14	Hs.404183	9020	17
-3.2	CXXC5	AK001782	233955_x_at	CXXC finger 5			
-3.2	ADAM8	NM_001109	205180_s_at	ADAM metallopeptidase domain 8	Hs.501574	101	10
-3.2	LTBP4	NM_003573	204442_x_at	Latent transforming growth factor beta binding protein 4	Hs.466766	8425	19
-3.3	CD79B	NM_000626	205297_s_at	CD79b molecule, immunoglobulin-associated beta	Hs.89575	974	17
-3.3	-	L34409	215746_at	(clone B3B3E13) chromosome 4p16.3 DNA fragment	Hs.660165	-	4
-3.3	CDC42	M35543	210232_at	Cell division cycle 42 (GTP binding protein, 25kDa)	Hs.690198	998	1
-3.3	-	BE967331	225621_at	Asparagine-linked glycosylation 2, alpha-1,3-mannosyltransferase homolog (S. cerevisiae)			
-3.3	KIAA0368	AB002366	212427_at	KIAA0368	Hs.368255	23392	9
-3.3	-	NM_024530	218881_s_at	FOS-like antigen 2		2355	-
-3.3	KHDRBS3	AF069681	209781_s_at	KH domain containing, RNA binding, signal transduction associated 3	Hs.444558	10656	8
-3.3	CP5F2	AK023583	225994_at	Cleavage and polyadenylation specific factor 2, 100kDa			
-3.3	-	BF693302	238451_at	membrane protein, palmitoylated 7 (MAGUK p55 subfamily member 7)			
-3.3	SLC38A3	NM_006841	205972_at	Solute carrier family 38, member 3	Hs.76460	10991	3
-3.3	TBC1D23	AK001750	225121_at	TBC1 domain family, member 23			
-3.3	-	AA628423	224861_at	Transcribed locus			
-3.3	-	AA524669	227074_at	Hypothetical protein LOC100131564			
-3.3	-	BF055271	222472_at	Aftiphilin			
-3.3	KLF10	NM_005655	202393_s_at	Kruppel-like factor 10	Hs.435001	7071	8
-3.4	-	BE964043	200719_at	S-phase kinase-associated protein 1	-	-	-
-3.4	ZBTB10	NM_023929	219312_s_at	Zinc finger and BTB domain containing 10	Hs.591868	65986	8
-3.4	-	BE222668	227791_at	Solute carrier family 9 (sodium/hydrogen exchanger), member 9			
-3.4	-	AA628398	226390_at	STAR-related lipid transfer (START) domain containing 4			
-3.4	-	AW270158	226345_at	CDNA FLJ12853 fis, clone NT2RP2003456			

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-3.4	-	AA029155	235103_at	Mannosidase, alpha, class 2A, member 1			
-3.4	FOXL2	NM_023067	220102_at	Forkhead box L2	Hs.289292	668	3
-3.4	EMP1	BF445047	213895_at	Epithelial membrane protein 1	Hs.707901	2012	12
-3.4	SELL	NM_000655	204563_at	Selectin L	Hs.82848	6402	1
-3.4	VTA1	BC005937	224437_s_at	Vps20-associated 1 homolog (S. cerevisiae)			
-3.4	PPP1R15A	NM_014330	202014_at	Protein phosphatase 1, regulatory (inhibitor) subunit 15A	Hs.631593	23645	19
-3.4	-	AU147889	222180_at	CDNA FLJ14122 fis, clone MAMMA1002033	Hs.658859	-	18
-3.4	ZNF394	AK022360	214714_at	Zinc finger protein 394	Hs.386324	84124	7
-3.4	-	AW469790	227708_at	Eukaryotic translation elongation factor 1 alpha 1			
-3.4	C12orf23	AK001731	224759_s_at	Chromosome 12 open reading frame 23			
-3.5	ZNF331	NM_018555	219228_at	Zinc finger protein 331	Hs.185674	55422	19
-3.5	-	AW450293	226823_at	Phosphatase and actin regulator 4			
-3.5	-	AL578668	225101_s_at	Sorting nexin 14			
-3.5	DNITP1	AL050348	224825_at	deoxynucleotidyltransferase, terminal, interacting protein 1			
-3.5	-	AA761169	225412_at	Transmembrane protein 87B			
-3.5	TOB1	AA675892	202704_at	Transducer of ERBB2, 1	Hs.719207	10140	17
-3.5	-	BG150485	228754_at	Solute carrier family 6 (neurotransmitter transporter, taurine), member 6			
-3.5	-	AW503390	217682_at	CDNA FLJ37032 fis, clone BRACE2011265	Hs.654689	-	16
-3.5	APOL3	NM_014349	221087_s_at	Apolipoprotein L, 3	Hs.474737	80833	22
-3.5	IDS	NM_000202	202439_s_at	Iduronate 2-sulfatase	Hs.460960	3423	X
-3.5	IWS1	AK001717	224768_at	IWS1 homolog (S. cerevisiae)			
-3.5	PHF23	BC002509	223081_at	PHD finger protein 23			
-3.5	HSPA1A	NM_005345	200799_at	Heat shock 70kDa protein 1A	Hs.274402	3303	6
-3.5	-	AI743979	224819_at	Transcription elongation factor A (SII)-like 8			
-3.5	-	AL520900	224981_at	Transmembrane protein 219			
-3.5	CRYGD	NM_006891	207532_at	Crystallin, gamma D	Hs.546247	1421	2
-3.6	ITGA9	NM_002207	206009_at	Integrin, alpha 9	Hs.113157	3680	3
-3.6	HIST1H2AM	NM_003514	214481_at	Histone cluster 1, H2am	Hs.134999	8336	6
-3.6	-	AI681917	229638_at	Iroquois homeobox 3			
-3.6	-	BE907429	225148_at	Ribosomal protein S19 binding protein 1			
-3.6	UBXN1	BC001372	210623_at	UBX domain protein 1	Hs.351296	51035	11
-3.6	ZNF609	AW165979	212620_at	Zinc finger protein 609	Hs.719276	23060	15
-3.6	DICER1	AK001827	216260_at	Dicer 1, ribonuclease type III	Hs.87889	23405	14
-3.7	GNAS	AA401492	214157_at	GNAS complex locus	Hs.125898	2778	20
-3.7	MRPL27	AB049647	224330_s_at	Mitochondrial ribosomal protein L27			
-3.7	-	AL162044	216456_at	MRNA; cDNA DKFpZ761L0812 (from clone DKFpZ761L0812); partial cds	Hs.675517	-	13
-3.7	SOX4	BG528420	201416_at	SRY (sex determining region Y)-box 4	Hs.643910	6659	6
-3.7	MCL1	BF981280	214056_at	Myeloid cell leukemia sequence 1 (BCL2-related)	Hs.719112	4170	1
-3.7	COL3A1	AU144167	215076_s_at	Collagen, type III, alpha 1	Hs.443625	1281	2
-3.7	-	BF675985	225783_at	Ubiquitin-conjugating enzyme E2F (putative)			
-3.7	OSR2	AI811298	213568_at	Odd-skipped related 2 (Drosophila)	Hs.253247	116039	8
-3.7	BTBD10	BC005071	223174_at	BTB (POZ) domain containing 10			
-3.7	-	AV715153	226921_at	Ubiquitin protein ligase E3 component n-recognin 1			
-3.7	-	N25727	227305_s_at	Smith-Magenis syndrome chromosome region, candidate 8			
-3.7	ADAM28	NM_021777	208268_at	ADAM metalloproteinase domain 28	Hs.174030	10863	8
-3.7	-	AI160540	225755_at	Kelch domain containing 8B			
-3.7	-	AA521267	213146_at	lysine (K)-specific demethylase 6B	-	-	-
-3.8	-	AW574798	228167_at	Transcribed locus			
-3.8	-	AL524045	224643_at	Proline-rich coiled-coil 1			
-3.8	AASS	AF229180	210852_s_at	Amino adipate-semialdehyde synthase	Hs.156738	10157	7
-3.8	-	AF070581	214078_at	Primary neuroblastoma cDNA, clone:Nbla04246, full insert sequence	Hs.655757	-	X
-3.8	FOS	BC004490	209189_at	V-fos FBJ murine osteosarcoma viral oncogene homolog	Hs.707896	2353	14
-3.8	-	BE855799	227230_s_at	KIAA1211			
-3.8	-	AL135396	225834_at	Transcribed locus, strongly similar to NP_001094380.1 hypothetical protein LOC653820 [Homo sapiens]			
-3.8	SDHAF2	BC002331	223048_at	Chromosome 11 open reading frame 79			
-3.8	-	BF246131	225000_at	Protein kinase, cAMP-dependent, regulatory, type II, alpha			
-3.8	-	AI208342	243318_at	WD repeat domain 42A			
-3.8	PTGER2	NM_000956	206631_at	Prostaglandin E receptor 2 (subtype EP2), 53kDa	Hs.2090	5732	14
-3.8	HEMGN	AF130060	223669_at	hemogen			
-3.9	-	AI982535	227309_at	YOD1 OTU deubiquinating enzyme 1 homolog (S. cerevisiae)			
-3.9	KCNK6	AF134149	223658_at	Potassium channel, subfamily K, member 6			
-3.9	FAM124B	NM_024785	220637_at	Family with sequence similarity 124B	Hs.147585	79843	2
-3.9	YPEL5	NM_016061	217783_s_at	Yippee-like 5 (Drosophila)	Hs.515890	51646	2
-3.9	-	AV662196	235509_at	Chromosome 8 open reading frame 38			

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-3.9	BMP2	NM_001200	205290_s_at	Bone morphogenetic protein 2	Hs.73853	650	20
-3.9	ZFP36	NM_003407	201531_at	Zinc finger protein 36, C3H type, homolog (mouse)	Hs.534052	7538	19
-3.9	FAM134B	NM_019000	218532_s_at	Family with sequence similarity 134, member B	Hs.481704	54463	5
-3.9	SYNGR1	BC000731	210613_s_at	Synaptogyrin 1	Hs.216226	9145	22
-3.9	FAIM3	AI084226	221601_s_at	Fas apoptotic inhibitory molecule 3	Hs.58831	9214	1
-4.0	-	AI017106	224635_s_at	Baculoviral IAP repeat-containing 6			
-4.0	-	AI016855	241133_at	T cell receptor beta variable 27			
-4.0	-	AI916948	235670_at	Syntaxin 11			
-4.0	COMMD10	BC005179	222637_at	COMM domain containing 10			
-4.0	HLF	AI810712	204753_s_at	Hepatic leukemia factor	Hs.196952	3131	17
-4.0	ACOX2	NM_003500	205364_at	Acyl-Coenzyme A oxidase 2, branched chain	Hs.444959	8309	3
-4.0	-	BG168471	225102_at	Monoglyceride lipase			
-4.0	-	BG251521	213156_at	Homo sapiens, clone IMAGE:4214654, mRNA	Hs.592414	-	3
-4.0	-	AV734839	227239_at	Family with sequence similarity 126, member A			
-4.0	-	BE858995	242648_at	Transcribed locus			
-4.0	-	AL528911	224608_s_at	Vacuolar protein sorting 25 homolog (S. cerevisiae)			
-4.0	OClAD1	AF323665	223011_s_at	OClA domain containing 1			
-4.0	-	AA532655	229872_s_at	Transcribed locus, moderately similar to XP_001722851.1 PREDICTED: hypothetical protein [Homo sapiens]			
-4.1	-	AI798098	226326_at	Polycomb group ring finger 5			
-4.1	BTG2	NM_006763	201236_s_at	BTG family, member 2	Hs.519162	7832	1
-4.1	CD34	M81104	209543_s_at	CD34 molecule	Hs.374990	947	1
-4.1	-	AI341541	227407_at	Transmembrane anterior posterior transformation 1			
-4.1	NR4A3	NM_006981	207978_s_at	Nuclear receptor subfamily 4, group A, member 3	Hs.279522	8013	9
-4.1	-	AV700721	224788_at	ADP-ribosylation factor 6			
-4.1	-	AI559701	225386_s_at	Heterogeneous nuclear ribonucleoprotein L-like			
-4.2	-	AW513835	224791_at	ArfGAP with SH3 domain, ankyrin repeat and PH domain 1			
-4.2	-	AA973551	226993_at	Transcribed locus			
-4.2	-	BG541668	226027_at	Chromosome 9 open reading frame 119			
-4.2	-	AI188653	226275_at	MAX dimerization protein 1			
-4.2	-	AI742043	228507_at	CDNA FLJ37884 fis, clone BRSTN2012451			
-4.2	TFPI	AF021834	210665_at	Tissue factor pathway inhibitor (lipoprotein-associated coagulation inhibitor)	Hs.516578	7035	2
-4.2	-	BF969428	224862_at	Guanine nucleotide binding protein (G protein), q polypeptide			
-4.2	USP36	NM_025090	220370_s_at	Ubiquitin specific peptidase 36	Hs.464243	57602	17
-4.2	RNF125	NM_017831	207735_at	Ring finger protein 125	Hs.633703	54941	18
-4.2	ICAM3	NM_002162	204949_at	Intercellular adhesion molecule 3	Hs.654563	3385	19
-4.2	FLJ14107	NM_025026	207287_at	hypothetical LOC80094	-	80094	-
-4.2	SOD2	AL050388	215078_at	Superoxide dismutase 2, mitochondrial	Hs.487046	6648	6
-4.2	RGS3	NM_017790	220300_at	Regulator of G-protein signaling 3	Hs.494875	5998	9
-4.2	FAM117A	NM_030802	221249_s_at	Family with sequence similarity 117, member A	Hs.514308	81558	17
-4.2	HIST1H1D	NM_005320	214537_at	Histone cluster 1, H1d	Hs.136857	3007	6
-4.3	ZMYM2	AL136621	210281_s_at	Zinc finger, MYM-type 2	Hs.644041	7750	13
-4.3	-	BF439522	226276_at	Transmembrane protein 167A			
-4.3	ARMC1	AK024053	222550_at	Armadillo repeat containing 1			
-4.3	MRPS36	AF271777	224302_s_at	mitochondrial ribosomal protein S36			
-4.3	-	AI244908	227697_at	Suppressor of cytokine signaling 3			
-4.3	-	AI808746	227418_at	KIAA1826			
-4.3	MAGEL2	NM_019066	219894_at	MAGE-like 2	Hs.141496	54551	15
-4.3	-	AI890604	226175_at	Tetratricopeptide repeat domain 9C			
-4.3	-	W93523	238633_at	Enhancer of polycomb homolog 1 (Drosophila)			
-4.3	-	AI627538	225313_at	Chromosome 20 open reading frame 177			
-4.3	-	AL530596	226531_at	ORAI calcium release-activated calcium modulator 1			
-4.4	-	W74622	229871_at	Sterile alpha motif domain containing 4B			
-4.4	SFPQ	AL558875	214016_s_at	Splicing factor proline/glutamine-rich (polypyrimidine tract binding protein associated)	Hs.355934	6421	1
-4.4	TGM2	AL031651	201042_at	transglutaminase 2 (C polypeptide, protein-glutamine-gamma-glutamyltransferase)	-	-	-
-4.4	-	AI042017	223405_at	N-acetylneuraminase pyruvate lyase (dihydrodipicolinate synthase)			
-4.4	-	AI340270	227932_at	Ariadne homolog 2 (Drosophila)			
-4.5	-	BF438417	225892_at	Iron-responsive element binding protein 2			
-4.5	-	AA495984	228410_at	GRB2-associated binding protein 3			
-4.5	LOC100129652	AA670344	208622_s_at	Hypothetical protein LOC100129652	Hs.714371	100129652	6
-4.5	PP1L1	BC003048	222500_at	Peptidylprolyl isomerase (cyclophilin)-like 1			
-4.5	BTG1	NM_001731	200921_s_at	B-cell translocation gene 1, anti-proliferative	Hs.255935	694	12
-4.5	HIST1H1E	AL353759	222067_x_at	histone cluster 1, H2bd	-	-	-

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-4.5	PSTPIP1	AF038602	211178_s_at	Proline-serine-threonine phosphatase interacting protein 1	Hs.129758	9051	15
-4.5	-	AW022607	226806_s_at	Nuclear factor I/A			
-4.5	-	BE503286	225302_at	Thioredoxin-related transmembrane protein 3			
-4.6	LGALS12	AF222694	223828_s_at	Lectin, galactoside-binding, soluble, 12			
-4.6	IAM2	NM_021219	219213_at	Junctional adhesion molecule 2	Hs.517227	58494	21
-4.6	RHOH	NM_004310	204951_at	Ras homolog gene family, member H	Hs.654594	399	4
-4.6	COQ5	BC004916	223114_at	Coenzyme Q5 homolog, methyltransferase (<i>S. cerevisiae</i>)			
-4.6	-	AA747303	227916_x_at	Exosome component 3			
-4.6	-	AV703462	224880_at	Transcribed locus			
-4.6	-	AV698647	215379_x_at	Immunoglobulin lambda locus	Hs.449585	3535	22
-4.6	-	AI081246	228869_at	Transcribed locus			
-4.7	-	T90295	226661_at	Cell division cycle associated 2			
-4.7	-	AV699857	225039_at	Ribulose-5-phosphate-3-epimerase			
-4.7	-	AL390857	216820_at	Human DNA sequence from clone RP11-51N22 on chromosome 13 Contains ESTs, STSs and GSSs. Contains an HNRPA1 (heterogeneous nuclear ribonucleoprotein A1) pseudogene			
-4.7	CD97	NM_001784	202910_s_at	Leucocyte antigen CD97	Hs.466039	100130656	19
-4.7	DCUN1D5	BC004169	223151_at	DCN1, defective in cullin neddylation 1, domain containing 5 (<i>S. cerevisiae</i>)			
-4.7	-	N73682	226128_at	Consensus includes gb:N73682 /FEA=EST /DB_XREF=gi:1230967 /DB_XREF=est:yz79b06.s1 /CLONE=IMAGE:289235 /UG=Hs.6236 Homo sapiens cDNA: FLJ21487 fis, clone COL05419			
-4.8	-	AI520949	225418_at	Poliovirus receptor-related 2 (herpesvirus entry mediator B)			
-4.8	IL8	NM_000584	202859_x_at	Interleukin 8	Hs.624	3576	4
-4.8	ARL4A	NM_005738	205020_s_at	ADP-ribosylation factor-like 4A	Hs.245540	10124	7
-4.8	PER1	AF022991	36829_at	Period homolog 1 (<i>Drosophila</i>)	Hs.445534	5187	17
-4.8	EPHB4	NM_004444	202894_at	EPH receptor B4	Hs.437008	2050	7
-4.8	-	AI469788	235572_at	SPC24, NDC80 kinetochore complex component, homolog (<i>S. cerevisiae</i>)			
-4.8	CKLF	AF096895	223451_s_at	Chemokine-like factor			
-4.8	-	BG259856	226628_at	THO complex 2			
-4.8	-	BG339450	225402_at	TP53 regulating kinase			
-4.9	RARS2	AK023550	225264_at	Arginyl-tRNA synthetase 2, mitochondrial			
-4.9	-	AI633734	228334_x_at	KIAA1712			
-4.9	-	NM_014120	206962_x_at	Homo sapiens PRO0214 protein (PRO0214), mRNA.			
-5.0	-	AW043782	234985_at	Transcribed locus			
-5.0	TRIM59	N90779	227801_at	Tripartite motif-containing 59			
-5.0	NFKBIA	AI078167	201502_s_at	Nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, alpha	Hs.81328	4792	14
-5.0	KLF9	AI690205	203542_s_at	Kruppel-like factor 9	Hs.150557	687	9
-5.0	-	AW612657	226851_at	Lysophospholipase-like 1			
-5.0	FTSJD1	AK023183	222811_at	FtsJ methyltransferase domain containing 1			
-5.0	-	BF970340	238010_at	Chromosome 1 open reading frame 174			
-5.0	-	AA722799	224911_s_at	Discoidin, CUB and LCCL domain containing 2			
-5.0	ADAM33	AL117415	233868_x_at	ADAM metalloproteinase domain 33			
-5.0	-	AI678096	225890_at	Chromosome 20 open reading frame 72			
-5.1	-	AI458208	238389_s_at	Transcribed locus			
-5.1	-	AI679555	243395_at	Transcribed locus			
-5.1	TSPAN32	AF176071	233467_s_at	Tetraspanin 32			
-5.1	LTBP3	NM_021070	219922_s_at	Latent transforming growth factor beta binding protein 3	Hs.289019	4054	11
-5.1	RASSF5	BC004270	223322_at	Ras association (RalGDS/AF-6) domain family member 5			
-5.1	-	AW504569	237753_at	Transcribed locus			
-5.1	-	NM_025120	220728_at	Homo sapiens hypothetical protein FLJ13480 (FLJ13480), mRNA.			
-5.1	-	BG168139	235389_at	PHD finger protein 20			
-5.1	-	AL589591	225497_at	Transcribed locus			
-5.1	-	BE552215	222754_at	tRNA nucleotidyl transferase, CCA-adding, 1			
-5.2	-	AI638155	239122_at	Transcribed locus			
-5.2	ELP6	BC000623	223277_at	Chromosome 3 open reading frame 75			
-5.2	-	AI479923	231056_at	Transcribed locus, moderately similar to NP_660275.2 ATP binding domain 3 [Homo sapiens]			
-5.2	PCDH9	AI524125	219737_s_at	Protocadherin 9	Hs.654709	5101	13
-5.2	SPNS1	AF212371	223173_at	Spinster homolog 1 (<i>Drosophila</i>)			
-5.2	-	AL577977	225837_at	chromosome 12 open reading frame 32			
-5.2	SMAD3	NM_005902	205398_s_at	SMAD family member 3	Hs.714621	4088	15
-5.2	OTUD5	AK026260	224745_x_at	OTU domain containing 5			
-5.2	-	AW473802	224934_at	Yip1 domain family, member 5			
-5.2	-	N31982	226159_at	Chromosome 5 open reading frame 51			
-5.2	FGFR1OP2	AL117545	233898_s_at	FGFR1 oncogene partner 2			

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-5.2	OXT	NM_000915	207576_x_at	Oxytocin, prepropeptide	Hs.113216	5020	20
-5.2	VIM	AI922599	201426_s_at	Vimentin	Hs.628678	7431	10
-5.2	GATAD2A	AK024670	222526_at	GATA zinc finger domain containing 2A			
-5.2	RHOB	AI263909	212099_at	Ras homolog gene family, member B	Hs.502876	388	2
-5.2	C16orf67	NM_024048	219442_at	chromosome 16 open reading frame 67	-	79014	
-5.3	AHNAK	BG287862	211986_at	AHNAK nucleoprotein	Hs.502756	79026	11
-5.3	ZC3H12A	NM_025079	218810_at	Zinc finger CCHC-type containing 12A	Hs.656294	80149	1
-5.3	-	BG292405	224899_s_at	Magnesium transporter 1			
-5.3	-	BE672260	225612_s_at	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 5			
-5.3	-	BF446961	226178_at	Transcribed locus			
-5.3	HIST1H2BM	NM_003521	208515_at	Histone cluster 1, H2bm	Hs.182432	8342	6
-5.3	POLR3GL	BC004355	223269_at	Polymerase (RNA) III (DNA directed) polypeptide G (32kD)-like			
-5.3	-	BE218028	222488_s_at	Dynactin 4 (p62)			
-5.4	-	AI889373	227414_at	Rhomboid domain containing 1			
-5.4	-	AA630626	234986_at	Transcribed locus			
-5.4	-	AI025829	235227_at	Consensus includes gb:AI025829 /FEA=EST /DB_XREF=gi:3241442 /DB_XREF=est:ow12a02.s1 /CLONE=IMAGE:1646570 /UG=Hs.86320 ESTs			
-5.4	-	AW118175	227622_at	PCF11, cleavage and polyadenylation factor subunit, homolog (S. cerevisiae)			
-5.4	-	AI762915	225214_at	Hypothetical protein LOC100129034			
-5.4	-	BF508705	225124_at	Protein phosphatase 1, regulatory (inhibitor) subunit 9B			
-5.4	-	AI091372	225557_at	Cysteine-serine-rich nuclear protein 1			
-5.4	SLC17A5	AK026921	223441_at	Solute carrier family 17 (anion/sugar transporter), member 5			
-5.4	PNRC1	AF279899	209034_at	Proline-rich nuclear receptor coactivator 1	Hs.75969	10957	6
-5.4	-	BF732480	225974_at	Transmembrane protein 64			
-5.5	-	AF161371	225788_at	Chromosome 6 open reading frame 153			
-5.5	FAM120C	NM_017848	220685_at	Family with sequence similarity 120C	Hs.86045	54954	X
-5.5	AHRR	AB033060	229354_at	Programmed cell death 6			
-5.5	CLEC2B	BC005254	209732_at	C-type lectin domain family 2, member B	Hs.85201	9976	12
-5.6	-	BF033615	235346_at	FUN14 domain containing 1			
-5.6	SLC22A23	AL512737	223194_s_at	Solute carrier family 22, member 23			
-5.6	-	BE962679	222415_at	Myeloid/lymphoid or mixed-lineage leukemia 3			
-5.6	-	AA626884	224708_at	KIAA2013			
-5.6	-	AA524700	225232_at	Myotubularin related protein 12			
-5.6	-	AA604382	226338_at	Transmembrane protein 55A			
-5.6	STK32B	NM_018401	219686_at	Serine/threonine kinase 32B	Hs.133062	55351	4
-5.6	HOXA5	NM_019102	213844_at	Homeobox A5	Hs.655218	3202	7
-5.6	-	BF591556	228487_s_at	Transcribed locus			
-5.6	-	AI079540	226437_at	Yip1 interacting factor homolog B (S. cerevisiae)			
-5.6	-	AI934828	227116_at	Transcribed locus			
-5.7	-	AI769745	226648_at	Hypoxia inducible factor 1, alpha subunit inhibitor			
-5.7	-	BF569593	225201_s_at	Mitochondrial ribosomal protein L14			
-5.7	-	W60810	223282_at	Teashirt zinc finger homeobox 1			
-5.7	-	AW138815	227959_at	Transcribed locus			
-5.7	GUK1	BC006249	200075_s_at	Guanylate kinase 1			
-5.7	-	AW576871	217577_at	Transcribed locus	Hs.670136	-	2
-5.7	-	AA416756	244677_at	Transcribed locus			
-5.7	-	AA554833	226084_at	Microtubule-associated protein 1B			
-5.7	-	AW966474	227182_at	Sushi domain containing 3			
-5.8	-	AA954994	238021_s_at	HCG1815491			
-5.8	-	AL559283	224684_at	Sorting nexin 12			
-5.8	TSPYL2	NM_022117	218012_at	TSPY-like 2	Hs.136164	64061	X
-5.8	-	AK027035	224750_at	Ring finger protein 185			
-5.9	-	AW006067	235142_at	Zinc finger and BTB domain containing 8A			
-5.9	-	AU157541	222872_x_at	Transcribed locus			
-5.9	-	AA936745	225537_at	Trafficking protein particle complex 6B			
-5.9	CCM2	BC004903	223164_at	Cerebral cavernous malformation 2			
-5.9	-	AW572609	226860_at	Transmembrane protein 19			
-5.9	-	AA526970	225199_at	Consensus includes gb:AA526970 /FEA=EST /DB_XREF=gi:2269039 /DB_XREF=est:ni06c09.s1 /CLONE=IMAGE:967216 /UG=Hs.12396 ESTs, Weakly similar to 2004399A chromosomal protein H.sapiens			
-5.9	-	BE504653	226503_at	RAP1 interacting factor homolog (yeast)			
-5.9	PLK3	NM_004073	204958_at	Polo-like kinase 3 (Drosophila)	Hs.632415	1263	1
-5.9	-	BF515132	227002_at	Family with sequence similarity 78, member A			
-5.9	TNFAIP8L2	AF271774	223583_at	Tumor necrosis factor, alpha-induced protein 8-like 2			
-5.9	-	BF247054	225274_at	Prenylcysteine oxidase 1			

Down-Regulated Transcripts (U133A 133B)

-5.9	-	AI763287	225352_at	SEC62 homolog (<i>S. cerevisiae</i>)				
-5.9	-	AL562950	223024_at	Adaptor-related protein complex 1, mu 1 subunit				
-6.0	-	AA994178	225947_at	Myosin XIX				
-6.0	-	BF507862	227385_at	Phosphatidic acid phosphatase type 2 domain containing 2				
-6.0	-	BE503186	226146_at	CDNA clone IMAGE:5294560				
-6.0	-	AI683621	231181_at	Transcribed locus				
-6.0	-	AW511595	228336_at	PWWP domain containing 2A				
-6.0	-	AI635756	232370_at	hypothetical protein LOC254057				
-6.0	ANKFY1	AK025960	224900_at	Ankyrin repeat and FYVE domain containing 1				
-6.1	COG6	AF116827	225769_at	Component of oligomeric golgi complex 6				
-6.1	FOSL1	BG251266	204420_at	FOS-like antigen 1	Hs.283565	8061		11
-6.1	-	AL138875	233647_s_at	cytidine and dCMP deaminase domain containing 1				
-6.1	-	AI208857	239238_at	Transcribed locus				
-6.1	ARRDC2	AK000689	226055_at	Arrestin domain containing 2				
-6.1	-	AU146532	226452_at	Pyruvate dehydrogenase kinase, isozyme 1				
-6.1	CISH	D83532	223961_s_at	Cytokine inducible SH2-containing protein				
-6.2	LAG3	NM_002286	206486_at	Lymphocyte-activation gene 3	Hs.409523	3902		12
-6.2	FOXO1	AW117498	202723_s_at	Forkhead box O1	Hs.370666	2308		13
-6.2	-	AW138757	226160_at	Hexose-6-phosphate dehydrogenase (glucose 1-dehydrogenase)				
-6.2	-	AW135012	229344_x_at	Ribosomal modification protein rimK-like family member B				
-6.2	BCR	AA845710	214623_at	Breakpoint cluster region	Hs.517461	613		22
-6.2	-	AL565381	227307_at	Transcribed locus				
-6.3	-	AI638714	225371_at	GLE1 RNA export mediator homolog (yeast)				
-6.3	-	AV706522	235061_at	protein phosphatase 1K (PP2C domain containing)				
-6.4	-	N95414	227314_at	Integrin, alpha 2 (CD49B, alpha 2 subunit of VLA-2 receptor)				
-6.4	-	AU152162	227979_at	Full length insert cDNA clone YX44E03				
-6.4	-	AF095723	216943_at	Homo sapiens GABA-B receptor splice variant 1 mRNA, partial cds.	-	-	-	-
-6.4	-	AA954994	238022_at	HCG1815491				
-6.4	-	BF753047	244726_at	Transcribed locus				
-6.4	-	AL138431	239035_at	5,10-methylenetetrahydrofolate reductase (NADPH)				
-6.5	TMEM164	BC002716	223202_s_at	Transmembrane protein 164				
-6.5	-	AA151838	226170_at	Eyes absent homolog 3 (<i>Drosophila</i>)				
-6.5	NAMPT	NM_005746	217739_s_at	Nicotinamide phosphoribosyltransferase	Hs.489615	10135		7
-6.5	-	AA526907	225356_at	Transcribed locus				
-6.5	TM2D2	AF353991	224413_s_at	TM2 domain containing 2				
-6.5	SIAE	AF303378	224391_s_at	Sialic acid acetyltransferase				
-6.6	-	BF115203	226092_at	Membrane protein, palmitoylated 5 (MAGUK p55 subfamily member 5)				
-6.6	-	BC001294	223401_at	chromosome 17 open reading frame 48				
-6.6	RAB11FIP1	NM_025151	219681_s_at	RAB11 family interacting protein 1 (class I)	Hs.696035	80223		8
-6.6	-	AI366784	235020_at	TAF4b RNA polymerase II, TATA box binding protein (TBP)-associated factor, 105kDa				
-6.6	TET2	AB046766	227624_at	Tet oncogene family member 2				
-6.6	-	W63776	229862_x_at	Zinc finger and BTB domain containing 45				
-6.7	-	AI684591	231106_at	Transcribed locus				
-6.7	-	AW977401	223288_at	Ubiquitin specific peptidase 38				
-6.7	ECHDC1	BC003549	223088_x_at	Enoyl Coenzyme A hydratase domain containing 1				
-6.7	-	AU151331	227569_at	Ligand of numb-protein X 2				
-6.7	-	N92500	229905_at	Transcribed locus				
-6.7	-	AL572206	224957_at	Chromosome 18 open reading frame 32				
-6.7	-	AI655611	226869_at	multiple EGF-like-domains 6				
-6.7	-	BF939473	229295_at	Hypothetical protein LOC150166				
-6.8	-	AW665656	242281_at	Transcribed locus				
-6.8	-	AV717041	226996_at	Lysocardiolipin acyltransferase 1				
-6.8	-	AA886888	227728_at	Protein phosphatase 1A (formerly 2C), magnesium-dependent, alpha isoform				
-6.8	-	BF724558	241722_x_at	Transcribed locus				
-6.8	LACTB2	BC000878	222714_s_at	Lactamase, beta 2				
-6.9	ANLN	AK023208	222608_s_at	Anillin, actin binding protein				
-6.9	KLF13	AL390127	225390_s_at	Kruppel-like factor 13				
-6.9	-	AW203959	230944_at	Transcribed locus				
-6.9	-	BE327172	213281_at	Jun oncogene	-	-	-	-
-6.9	-	AI935657	224945_at	BTB (POZ) domain containing 7				
-7.0	JUND	AI762296	203751_x_at	Jun D proto-oncogene	Hs.2780	3727		19
-7.0	-	AW575350	225208_s_at	Family with sequence similarity 103, member A1				
-7.0	COL6A2	AY029208	209156_s_at	Collagen, type VI, alpha 2	Hs.420269	1292		21
-7.0	PELI1	NM_020651	218319_at	Pellino homolog 1 (<i>Drosophila</i>)	Hs.7886	57162		2

Down-Regulated Transcripts (U133A 133B)

-7.0	-	AU153746	222569_at	UDP-glucose ceramide glucosyltransferase-like 1				
-7.0	-	BF219240	225945_at	Zinc finger protein 655				
-7.1	B3GNT2	AF288208	222870_s_at	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 2				
-7.1	-	BF439595	226180_at	WD repeat domain 36				
-7.1	-	BE856541	227133_at	Chromosome X open reading frame 39				
-7.1	-	BF680438	226038_at	Transcribed locus				
-7.1	LOC87420	AK026764	226348_at	Homo sapiens cDNA: FLJ23111 fis, clone LNG07835.				
-7.1	TMEM33	BC000948	222642_s_at	Transmembrane protein 33				
-7.1	-	AI742810	222323_at	Transcribed locus, moderately similar to XP_582033.1 PREDICTED: crystallin, gamma E [Bos taurus]	Hs.131057	-		2
-7.1	-	BF476076	227121_at	MRNA; cDNA DKFp586K1922 (from clone DKFp586K1922)				
-7.1	MTRFR1L	ALS12766	224280_s_at	Family with sequence similarity 54, member B				
-7.2	-	AK023950	222467_s_at	SAPS domain family, member 3				
-7.2	-	AW471145	226279_at	Protease, serine, 23				
-7.2	IGHG1	AI858004	213674_x_at	Immunoglobulin heavy constant gamma 1 (G1m marker)	Hs.510635	3500		14
-7.2	-	ALS75306	224997_x_at	H19, imprinted maternally expressed transcript (non-protein coding)				
-7.2	DUSP2	NM_004418	204794_at	Dual specificity phosphatase 2	Hs.1183	1844		2
-7.2	ZC3HC1	BC000190	223163_s_at	Zinc finger, C3HC-type containing 1				
-7.2	-	T90642	230291_s_at	Transcribed locus				
-7.2	COX4I1	AW337510	213758_at	Cytochrome c oxidase subunit IV isoform 1	Hs.433419	1327		16
-7.2	-	AI741469	234970_at	Tandem C2 domains, nuclear				
-7.2	-	AA621580	222489_s_at	Werner helicase interacting protein 1				
-7.3	-	AU154401	225741_at	THUMP domain containing 3				
-7.4	-	AV712694	227637_at	Transcription factor CP2				
-7.4	-	AW270138	226909_at	Zinc finger protein 518B				
-7.4	-	AW575754	226459_at	Phosphoinositide-3-kinase adaptor protein 1				
-7.5	-	AI268231	229574_at	Transcribed locus				
-7.5	FAM220A	BC006110	224452_s_at	Hypothetical protein LOC84792				
-7.5	-	BF111780	225400_at	TRNA splicing endonuclease 15 homolog (S. cerevisiae)				
-7.5	CYLD	AK024212	222142_at	Cylindromatosis (turban tumor syndrome)	Hs.578973	1540		16
-7.6	-	AI279536	230734_x_at	ELISC-1				
-7.6	-	AW664953	227335_at	Death inducer-oblierator 1				
-7.6	-	AA579630	225320_at	Coiled-coil domain containing 109A				
-7.6	-	N62126	235721_at	Deltex homolog 3 (Drosophila)				
-7.6	-	AW183080	230252_at	lysophosphatidic acid receptor 5				
-7.7	-	AK021962	233214_at	CDNA FLJ11900 fis, clone HEMBA1007341				
-7.7	-	AV726956	229963_at	Brain expressed, X-linked 5				
-7.7	-	BE326710	229778_at	Chromosome 12 open reading frame 39				
-7.7	-	AW294894	226265_at	Glutamine and serine rich 1				
-7.7	-	R38084	225558_at	G protein-coupled receptor kinase interacting ArfGAP 2				
-7.7	-	AW025216	225210_s_at	Transcribed locus, moderately similar to XP_001714790.1 PREDICTED: hypothetical protein [Homo sapiens]				
-7.7	-	AW205632	238156_at	Transcribed locus				
-7.7	-	AI457965	225256_at	Transcribed locus				
-7.8	DUSP1	NM_004417	201041_s_at	Dual specificity phosphatase 1	Hs.171695	1843		5
-7.8	-	AW183154	236641_at	Kinesin family member 14				
-7.8	TIPARP	ALS56438	212665_at	TCDD-inducible poly(ADP-ribose) polymerase	Hs.719169	25976		3
-7.8	-	AV706396	226969_at	5-methyltetrahydrofolate-homocysteine methyltransferase				
-7.8	-	AF090887	215642_at	Clone HQ0085	Hs.612030	-		10
-7.8	NAV2-AS4	AK023501	233077_at	Hypothetical gene supported by AK023501				
-7.9	MED28	AF358829	224416_s_at	Mediator complex subunit 28				
-7.9	-	AA633196	222476_at	CCR4-NOT transcription complex, subunit 6				
-7.9	-	N31731	230165_at	Shugoshin-like 2 (S. pombe)				
-7.9	-	AI972599	230761_at	Transcribed locus				
-8.0	-	AI190755	228263_at	GRP1 (general receptor for phosphoinositides 1)-associated scaffold protein				
-8.0	-	AL529634	225470_at	Nucleoporin 35kDa				
-8.0	-	AL039384	225005_at	Transcribed locus				
-8.0	-	AV728521	224958_at	Nuclear fragile X mental retardation protein interacting protein 2				
-8.0	-	ALS46529	235593_at	Zinc finger E-box binding homeobox 2				
-8.0	GPRC5B	NM_016235	203632_s_at	G protein-coupled receptor, family C, group 5, member B	Hs.148685	51704		16
-8.1	-	AI992290	226896_at	Coiled-coil-helix-coiled-coil-helix domain containing 1				
-8.1	-	AA588400	229396_at	Ovo-like 1(Drosophila)				
-8.1	-	AK025220	234942_s_at	Thyroid hormone receptor associated protein 3				
-8.1	VPS18	AF308802	223346_at	Vacuolar protein sorting 18 homolog (S. cerevisiae)				
-8.1	-	AI866426	225378_at	vacuolar protein sorting 37 homolog A (S. cerevisiae)				

Down-Regulated Transcripts (U133A 133B)

-8.1	CARD6	AF356193	224414_s_at	Caspase recruitment domain family, member 6			
-8.1	CCNL1	NM_020307	220046_s_at	Cyclin L1	Hs.4859	57018	3
-8.1	CD38	NM_001775	205692_s_at	CD38 molecule	Hs.479214	952	4
-8.2	-	AI818048	225048_at	PHD finger protein 10			
-8.2	MTRF1L	AL049992	217204_at	Mitochondrial translational release factor 1-like	Hs.225836	54516	6
-8.2	-	BG179317	227111_at	Zinc finger and BTB domain containing 34			
-8.2	-	R11899	238879_at	CDNA FLJ38454 fis, clone FEBRA2019690			
-8.2	-	BC004528	224298_s_at	UBA domain containing 2			
-8.3	-	AW269340	226985_at	FYVE, RhoGEF and PH domain containing 5			
-8.3	-	BE392119	243707_at	Transcribed locus, strongly similar to XP_001140852.1 PREDICTED: hypothetical protein [Pan troglodytes]			
-8.4	-	AW952781	235174_s_at	Transcribed locus			
-8.4	-	AV734843	233085_s_at	Transcribed locus			
-8.4	PPP1R16B	AB020630	41577_at	Protein phosphatase 1, regulatory (inhibitor) subunit 16B	Hs.45719	26051	20
-8.4	-	AI339426	228990_at	Small nucleolar RNA host gene 12 (non-protein coding)			
-8.4	-	AW274503	228396_at	Transcribed locus			
-8.4	-	AA044835	225872_at	Solute carrier family 35, member F5			
-8.4	RPS27L	BC003667	222487_s_at	Ribosomal protein S27-like			
-8.5	-	AW439242	229640_x_at	CDNA FLJ26856 fis, clone PRS08123			
-8.5	-	AF172327	223964_x_at	Homo sapiens clone 709724 unknown mRNA, complete cds.			
-8.6	MS4A6A	AB013104	223922_x_at	Membrane-spanning 4-domains, subfamily A, member 6A			
-8.6	-	AI889093	226232_at	Growth differentiation factor 11			
-8.6	CCDC88C	AB040942	227228_s_at	Coiled-coil domain containing 88C			
-8.6	-	AL563795	226199_at	Uracil phosphoribosyltransferase (FUR1) homolog (S. cerevisiae)			
-8.7	ASB4	NM_016116	208481_at	Ankyrin repeat and SOCS box-containing 4	Hs.666357	51666	7
-8.7	-	AA889952	226277_at	Collagen, type IV, alpha 3 (Goodpasture antigen) binding protein			
-8.7	-	BF977231	226868_at	Glycosyltransferase 8 domain containing 3			
-8.7	-	AA639752	225284_at	DnaJ (Hsp40) homolog, subfamily C, member 3			
-8.7	-	AL569506	228702_at	Hypothetical LOC378805			
-8.7	DEPCD1B	AK001166	226980_at	DEP domain containing 1B			
-8.8	-	AL161622	234689_at	chromosome 6 open reading frame 138			
-8.8	-	BF025955	223314_at	Tetraspanin 14			
-8.8	-	AW880875	242277_at	Transcribed locus			
-8.8	-	AI800998	230411_at	CDNA FLJ41934 fis, clone PERIC2005111			
-8.8	SPATA2	U28164	204433_s_at	Spermatogenesis associated 2	Hs.48513	9825	20
-8.9	-	AI130705	226448_at	Family with sequence similarity 89, member A			
-8.9	-	AI017750	227166_at	DnaJ (Hsp40) homolog, subfamily C, member 18			
-8.9	TMEM189	AB044550	223186_at	Ubiquitin-conjugating enzyme E2 variant 1			
-8.9	-	AW572279	244428_at	DNA (cytosine-5-)methyltransferase 3 alpha			
-8.9	-	AW629014	227988_s_at	Vacuolar protein sorting 13 homolog A (S. cerevisiae)			
-8.9	EMCN	AF205940	222885_at	Endomucin			
-8.9	-	AI927208	239273_s_at	Matrix metalloproteinase 28			
-9.0	-	BE748802	235526_at	Chromosome 11 open reading frame 58			
-9.0	-	BE670797	230958_s_at	Transcribed locus			
-9.0	-	BG029566	225154_at	Synapse associated protein 1, SAP47 homolog (Drosophila)			
-9.0	-	BE858787	226384_at	Phosphatidic acid phosphatase type 2 domain containing 1B			
-9.0	-	AW170591	228424_at	N-acetylated alpha-linked acidic dipeptidase-like 1			
-9.0	RXRA	BE675800	202426_s_at	Retinoid X receptor, alpha	Hs.590886	6256	9
-9.0	-	AI825998	226794_at	Syntaxin binding protein 5 (tomosyn)			
-9.1	-	AA541716	226230_at	Transcribed locus			
-9.2	-	AA235663	244842_x_at	Transcribed locus			
-9.2	-	T30183	226602_s_at	Breakpoint cluster region			
-9.2	-	AA074729	235096_at	Leo1, Paf1/RNA polymerase II complex component, homolog (S. cerevisiae)			
-9.2	-	AL520984	225347_at	ADP-ribosylation factor-like 8A			
-9.3	-	AI927692	228528_at	CDNA FLJ41270 fis, clone BRAMY2036387			
-9.3	-	BG289314	232306_at	Cadherin-like 26			
-9.3	-	BF131248	225851_at	Farnesyltransferase, CAAX box, beta			
-9.3	CCDC82	AF245436	223301_s_at	Coiled-coil domain containing 82			
-9.3	-	AL161979	232384_s_at	Clone IMAGE:111705 mRNA sequence			
-9.4	-	H87708	229100_s_at	Transcribed locus			
-9.4	NUDT22	BC006129	224464_s_at	Nudix (nucleoside diphosphate linked moiety X)-type motif 22			
-9.4	-	BF671187	232349_x_at	IQ motif and WD repeats 1			
-9.4	TBC1D14	AB037743	224622_at	TBC1 domain family, member 14			
-9.5	-	AW292751	225318_at	CDNA: FLJ22049 fis, clone HEP09444			
-9.5	-	AI939336	240592_at	Ligand dependent nuclear receptor corepressor-like			

Down-Regulated Transcripts (U133A 133B)

-9.5	-	BF001267	225384_at	Dedicator of cytokinesis 7			
-9.5	-	AV707506	224876_at	Transcribed locus			
-9.5	-	BG433539	235164_at	Zinc finger protein 25			
-9.5	-	BE349614	226409_at	TBC1 domain family, member 20			
-9.6	-	BF338045	227420_at	Tumor necrosis factor, alpha-induced protein 8-like 1			
-9.6	-	AA127686	225319_s_at	Component of oligomeric golgi complex 1			
-9.6	CDH1	NM_004360	201131_s_at	Cadherin 1, type 1, E-cadherin (epithelial)	Hs.461086	999	16
-9.7	-	AI139993	230099_at	Transcribed locus			
-9.7	-	AW073741	226518_at	Potassium channel tetramerisation domain containing 10			
-9.7	-	AI939422	241294_at	Consensus includes gb:A1939422 /FEA=EST /DB_XREF=gi:5678385 /DB_XREF=est:qy97b05.x5 /CLONE=IMAGE:2019921 /UG=Hs.170332 ESTs			
-9.7	-	BF514509	239050_s_at	Consensus includes gb:BF514509 /FEA=EST /DB_XREF=gi:11599688 /DB_XREF=est:UI-H-BW1-anf-g-03-0-UI.s1 /CLONE=IMAGE:3082180 /UG=Hs.262571 ESTs			
-9.8	-	BG284709	222622_at	Phosphoglycolate phosphatase			
-9.8	-	BF793454	226563_at	SMAD family member 2			
-9.8	-	AI188518	226686_at	CDGSH iron sulfur domain 2			
-9.9	TSC22D3	AL110191	208763_s_at	TSC22 domain family, member 3	Hs.716410	1831	X
-9.9	-	W68737	239098_at	Potassium channel regulator			
-9.9	-	BG024886	224784_at	Transcribed locus			
-9.9	-	AI828221	226366_at	SNF2 histone linker PHD RING helicase			
-9.9	FAR1	N63551	224865_at	Fatty acyl CoA reductase 1			
-10.0	-	BE622486	226562_at	Zinc finger and SCAN domain containing 29			
-10.0	ATL1	AF131801	223340_at	Atlastin GTPase 1			
-10.0	-	AI857629	229507_at	Chromosome 3 open reading frame 54			
-10.0	C2orf29	AK024221	224695_at	Chromosome 2 open reading frame 29			
-10.0	-	AA722069	227657_at	Ring finger protein 150			
-10.1	-	AU146850	225732_at	Transcribed locus			
-10.1	-	AA056099	222566_at	Transcribed locus			
-10.1	-	AI056692	227278_at	Transcribed locus			
-10.2	-	AI870583	222780_s_at	Brain and acute leukemia, cytoplasmic			
-10.2	-	AI434790	239070_at	Transcribed locus			
-10.3	-	AI214996	226901_at	Chromosome 17 open reading frame 58			
-10.3	EREG	NM_001432	205767_at	Epiregulin	Hs.115263	2069	4
-10.3	-	AI738556	227345_at	Tumor necrosis factor receptor superfamily, member 10d, decoy with truncated death domain			
-10.3	-	BF514723	225910_at	Helicase with zinc finger			
-10.3	-	BF791801	226871_s_at	ATG4 autophagy related 4 homolog D (S. cerevisiae)			
-10.4	-	R24779	235396_at	Chromosome 22 open reading frame 25			
-10.4	-	AW294765	225734_at	F-box protein 22			
-10.5	-	AW340595	227383_at	Hypothetical LOC728875			
-10.5	-	AI674915	232130_at	Transcribed locus			
-10.5	ATG16L2	AK024423	225883_at	ATG16 autophagy related 16-like 2 (S. cerevisiae)			
-10.5	-	AW003459	226743_at	Schlafen family member 11			
-10.5	-	AA156022	226028_at	Roundabout homolog 4, magic roundabout (Drosophila)			
-10.5	-	BF577193	234982_at	Transcribed locus			
-10.5	-	AI991103	227877_at	Chromosome 5 open reading frame 39			
-10.5	-	BF515755	236850_at	Cell cycle associated protein 1			
-10.5	-	AI656807	228401_at	ATPase family, AAA domain containing 2			
-10.5	-	AI708776	225456_at	Mediator complex subunit 1			
-10.5	-	N39230	229934_at	Mir-223 transcript variant 1 mRNA, complete sequence			
-10.6	-	AA191741	226756_at	CDNA FLJ25556 fis, clone JTH02629			
-10.6	-	BE788266	238424_at	Adenosine deaminase-like			
-10.6	-	AW139915	233749_at	Hypothetical protein LOC100129014			
-10.6	-	AA058578	226252_at	CDNA FLJ34585 fis, clone KIDNE2008758			
-10.7	NUF2	AF326731	223381_at	NUF2, NDC80 kinetochore complex component, homolog (S. cerevisiae)			
-10.7	-	AI638593	230021_at	Chromosome 15 open reading frame 42			
-10.7	GPR160	BC000181	223423_at	G protein-coupled receptor 160			
-10.8	-	AI393309	227008_at	HD domain containing 3			
-10.8	-	AI697160	230936_at	DnaJ (Hsp40) related, subfamily B, member 13			
-10.8	-	AI928513	227985_at	Transcribed locus			
-10.8	KRTAP1-5	AJ406928	233533_at	Keratin associated protein 1-5			
-10.8	-	AI825302	238700_at	Transcribed locus			
-10.8	COL5A1	AI130969	203325_s_at	Collagen, type V, alpha 1	Hs.210283	1289	9
-10.8	-	AL563613	226532_at	Transcribed locus			
-10.8	AVIL	AK022448	233333_x_at	Advillin			

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-10.8	SETBP1	NM_015559	205933_at	SET binding protein 1	Hs.435458	26040	18
-10.8	-	AW006952	228730_s_at	Secernin 2			
-10.8	-	BG401568	227506_at	Solute carrier family 16, member 9 (monocarboxylic acid transporter 9)			
-10.8	-	AI807204	223197_s_at	SWI/SNF-related, matrix-associated actin-dependent regulator of chromatin, subfamily a, containing DEAD/H box 1			
-10.9	-	AI475680	243509_at	Transcribed locus			
-10.9	-	AA608834	242068_at	Transcribed locus			
-10.9	-	BE394201	226298_at	RUN domain containing 1			
-11.0	-	BF060783	242138_at	Distal-less homeobox 1			
-11.0	-	AW298438	225141_at	Transcribed locus			
-11.0	-	AW195360	225426_at	Protein phosphatase 6, catalytic subunit			
-11.0	-	AI934347	226140_s_at	OTU domain containing 1			
-11.0	-	AU145807	233196_at	CDNA FLJ11777 fis, clone HEMBA1005909			
-11.0	SLC35B3	AL355815	222691_at	solute carrier family 35, member B3			
-11.0	-	T90760	244357_at	Transcribed locus			
-11.1	-	BF108666	230435_at	Hypothetical protein LOC375190			
-11.1	-	AW140122	239859_x_at	Transcribed locus			
-11.1	-	AW152589	225677_at	B-cell receptor-associated protein 29			
-11.1	-	AI129941	229167_at	Transcribed locus			
-11.2	-	BG492359	226936_at	Chromosome 6 open reading frame 173			
-11.2	-	BE962119	225603_s_at	chromosome 8 open reading frame 83			
-11.2	SLX4	AL442083	232147_at	BTB (POZ) domain containing 12			
-11.2	-	AV691296	232012_at	Transcribed locus			
-11.2	-	AA527531	225704_at	Fibrosin-like 1			
-11.2	-	AU157155	225459_at	Angiotensin like 1			
-11.2	-	AI859280	242234_at	XIAP associated factor 1			
-11.3	-	AI692645	230206_at	Dedicator of cytokinesis 5			
-11.3	FUCA2	BC003060	223120_at	Fucosidase, alpha-L- 2, plasma			
-11.3	-	W44578	228775_at	Transcribed locus			
-11.3	-	AL036662	235984_at	Transcribed locus			
-11.3	-	L21961	234877_x_at	Human Ig rearranged lambda-chain mRNA, subgroup VL3, V-J region, partial cds.			
-11.3	TRIM35	AA115933	227102_at	Tripartite motif-containing 35			
-11.3	STRIP2	AB032996	231880_at	Family with sequence similarity 40, member B			
-11.3	-	AA193515	228162_at	Esterase D/formylglutathione hydrolase			
-11.3	-	AA805653	228180_at	Transcribed locus			
-11.3	-	AI760366	236907_at	CDNA FLJ25706 fis, clone TST04817			
-11.4	-	AA876371	239081_at	Transcribed locus			
-11.4	-	AI022632	239405_at	Transcribed locus			
-11.4	-	AV725947	228760_at	Splicing factor, arginine/serine-rich 2B			
-11.4	-	H10318	225476_at	HLA-B associated transcript 4			
-11.4	-	AW051345	225690_at	Cdc2-related kinase, arginine/serine-rich			
-11.5	-	AA225165	228721_at	Chemokine binding protein 2			
-11.5	B3GALNT1	AF154848	223374_s_at	beta-1,3-N-acetylgalactosaminyltransferase 1 (globoside blood group)			
-11.5	SKIL	BF725121	217591_at	SKI-like oncogene	Hs.581632	6498	3
-11.5	-	AI871620	222803_at	Phosphoribosyl transferase domain containing 1			
-11.6	-	BF342223	235035_at	Solute carrier family 35, member E1			
-11.6	POMP	BC003390	222402_at	Proteasome maturation protein			
-11.6	-	BE893995	234983_at	Transcribed locus			
-11.6	-	AW182575	227295_at	IKK interacting protein			
-11.6	-	AI306487	222849_s_at	Secernin 3			
-11.6	-	AL577758	226515_at	Coiled-coil domain containing 127			
-11.7	-	AW576195	227476_at	Lysophosphatidylglycerol acyltransferase 1			
-11.7	-	AI279532	228652_at	zinc finger protein 776			
-11.7	-	BG106919	231810_at	BRI3 binding protein			
-11.8	-	AW051899	242602_x_at	Zinc finger protein 254			
-11.8	-	AA994026	237886_at	Transcribed locus			
-11.8	-	BE464843	236696_at	U2-associated SR140 protein			
-11.8	-	W93048	224717_s_at	Chromosome 19 open reading frame 42			
-11.9	-	AU147698	215401_at	CDNA FLJ12248 fis, clone MAMMA1001408	Hs.661985	-	13
-11.9	-	BE856242	223512_at	SAR1 homolog B (S. cerevisiae)			
-11.9	-	N21600	224704_at	Trinucleotide repeat containing 6A			
-12.0	-	BE895304	243452_at	Hypothetical LOC646778			
-12.0	TRAPPC11	AK023390	233558_s_at	Chromosome 4 open reading frame 41			
-12.1	-	BF970431	228151_at	Transcribed locus			
-12.1	-	BG540188	241396_at	Neural precursor cell expressed, developmentally down-regulated 4-like			

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-12.1	COMMD5	BC002672	223198_x_at	COMM domain containing 5			
-12.2	-	BF434224	225543_at	MRNA full length insert cDNA clone EUROIMAGE 1674211			
-12.2	-	AW275658	242349_at	HECT domain containing 1			
-12.2	-	BG340967	225294_s_at	Trafficking protein particle complex 1			
-12.2	-	AI659020	225161_at	G elongation factor, mitochondrial 1			
-12.2	NCOA5	AB046857	225145_at	Nuclear receptor coactivator 5			
-12.2	-	AW269686	238622_at	RAP2B, member of RAS oncogene family			
-12.2	KCNK17	AF339912	224049_at	Potassium channel, subfamily K, member 17			
-12.2	-	BE300882	244627_at	Dihydroxyacetone kinase 2 homolog (S. cerevisiae)			
-12.3	-	AA961515	229882_at	Ribosomal protein S15a			
-12.3	-	AI224977	227928_at	Chromosome 12 open reading frame 48			
-12.3	-	AW072102	230698_at	Calneuron 1			
-12.3	-	AA738440	227840_at	Chromosome 2 open reading frame 76			
-12.4	-	AA532718	236545_at	Transcribed locus			
-12.5	RIPK3	NM_006871	228139_at	Receptor-interacting serine-threonine kinase 3			
-12.5	FLJ10213	NM_018029	219906_at	Hypothetical protein FLJ10213	Hs.658858	55096	3
-12.5	-	AI672432	229211_at	Dual specificity phosphatase 28			
-12.6	AUNIP	BC000209	222946_s_at	Chromosome 1 open reading frame 135			
-12.6	AVP	NM_000490	207848_at	Arginine vasopressin	Hs.89648	551	20
-12.6	-	AI554705	226378_s_at	Chromosome 19 open reading frame 25			
-12.6	-	BF109310	236593_at	Similar to hCG1775037			
-12.6	-	AJ001863	234264_at	MRNA partial cDNA sequence from cDNA selection, DCR1-8.0			
-12.7	-	AU146891	227798_at	SMAD family member 1			
-12.7	-	AI146450	228073_at	N-acetylneuraminic acid phosphatase			
-12.7	-	AA287457	226943_at	Chromosome 12 open reading frame 73			
-12.8	-	NM_024826	220145_at	microtubule-associated protein 9	-	79884	-
-12.8	-	AW293012	236989_at	Transcribed locus			
-12.9	-	AI972094	232175_at	Transcribed locus, weakly similar to NP_001006352.1 ADP-ribosylation factor 1 [Gallus gallus]			
-12.9	-	BF032717	232129_s_at	Leucine zipper, putative tumor suppressor 2			
-12.9	-	AI274095	232224_at	Mannan-binding lectin serine peptidase 1 (C4/2 activating component of Ra-reactive factor)			
-12.9	-	BF433103	230868_at	Transcribed locus			
-12.9	RERE	H71242	242407_at	Consensus includes gb:H71242 /FEA=EST /DB_XREF=gi:1043058 /DB_XREF=est:ys12g09.s1 /CLONE=IMAGE:214624 /UG=Hs.117864 ESTs			
-13.0	-	AI458003	228665_at	Cysteine/tyrosine-rich 1			
-13.0	SCYL1	AF297709	223033_s_at	SCY1-like 1 (S. cerevisiae)			
-13.0	-	T86344	238657_at	UBX domain protein 10			
-13.0	-	AV758821	235052_at	Zinc finger protein 792			
-13.0	-	AA088857	235871_at	Lipase, member H			
-13.0	-	AA778095	243966_at	Consensus includes gb:AA778095 /FEA=EST /DB_XREF=gi:2837496 /DB_XREF=est:zf43f09.s1 /CLONE=IMAGE:379721 /UG=Hs.191593 ESTs			
-13.1	-	AK026630	234947_s_at	Chromosome 10 open reading frame 84			
-13.1	-	AA632758	232615_at	Transcribed locus			
-13.1	-	AW972855	222315_at	Consensus includes gb:AW972855 /FEA=EST /DB_XREF=gi:8162701 /DB_XREF=est:EST384950 /UG=Hs.292853 ESTs	-	-	-
-13.1	-	AA156998	227006_at	Protein phosphatase 1, regulatory (inhibitor) subunit 14A			
-13.1	-	AW362945	242558_at	CDNA FLJ45490 fis, clone BRTHA2005831			
-13.2	-	BE514414	226473_at	Chromobox homolog 2 (Pc class homolog, Drosophila)			
-13.2	-	BF433759	230295_at	Small optic lobes homolog (Drosophila)			
-13.2	-	AI925574	226707_at	Nicotinate phosphoribosyltransferase domain containing 1			
-13.2	MLF1	NM_022443	204784_s_at	Myeloid leukemia factor 1	Hs.85195	4291	3
-13.3	-	AI701170	231370_at	Transcribed locus			
-13.3	-	AW057545	223083_s_at	Egl nine homolog 2 (C. elegans)			
-13.3	-	R61857	243992_at	Transcribed locus			
-13.4	NR4A2	AI935096	204621_s_at	Nuclear receptor subfamily 4, group A, member 2	Hs.563344	4929	2
-13.4	RNF135	BC005084	223591_at	Ring finger protein 135			
-13.4	-	AA778938	244700_at	Sec61 beta subunit			
-13.4	MAFF	NM_012323	205193_at	V-maf musculoaponeurotic fibrosarcoma oncogene homolog F (avian)	Hs.517617	23764	22
-13.5	-	N49841	228144_at	Zinc finger protein 300			
-13.5	-	AA894611	228595_at	hydroxysteroid (17-beta) dehydrogenase 1			
-13.5	-	BF446688	227573_s_at	Obscurin-like 1			
-13.5	-	AI675152	229264_at	Hypothetical protein LOC100132999			
-13.5	-	AW514783	225323_at	coiled-coil and C2 domain containing 1B			
-13.5	FUBP1	N54783	240307_at	Transcribed locus			

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-13.6	-	AI708334	230029_x_at	Ubiquitin protein ligase E3 component n-recognin 3 (putative)			
-13.6	C6orf223	BF515759	239137_x_at	Chromosome 6 open reading frame 223			
-13.6	-	AW451683	231023_at	CysteinyI-tRNA synthetase 2, mitochondrial (putative)			
-13.6	-	AU152456	226217_at	Solute carrier family 30 (zinc transporter), member 7			
-13.7	-	AA872471	242146_at	Small nuclear ribonucleoprotein polypeptide A'			
-13.7	-	AV713913	235198_at	Osteopetrosis associated transmembrane protein 1			
-13.8	-	BF740245	227579_at	CDNA FLJ35001 fis, clone OCBBF2011887			
-13.8	-	BF676081	225880_at	Consensus includes gb:BF676081 /FEA=EST /DB_XREF=gi:11949976 /DB_XREF=est:602084056F1 /CLONE=IMAGE:4248445 /UG=Hs.24359 Homo sapiens cDNA FLJ11174 fis, clone PLACE1007367			
-13.8	-	AI807103	222473_s_at	ErbB2 interacting protein			
-13.9	-	BF592842	243913_at	Transcribed locus			
-13.9	C12orf65	AF061733	223477_s_at	Chromosome 12 open reading frame 65			
-13.9	YAE1D1	AF226046	223433_at	Chromosome 7 open reading frame 36			
-14.0	RBM33	AL137724	231833_at	RNA binding motif protein 33			
-14.0	-	AA618420	225792_at	Hook homolog 1 (Drosophila)			
-14.1	-	BG028213	225581_s_at	Mitochondrial ribosomal protein L50			
-14.1	-	AI969773	227430_at	Zinc finger CCCH-type containing 10			
-14.1	IFFO2	AK024480	225615_at	Intermediate filament family orphan 2			
-14.1	-	AW793677	243527_at	Consensus includes gb:AW793677 /FEA=EST /DB_XREF=gi:7845547 /DB_XREF=est:MR1-UM0008-200300-004-c02 /UG=Hs.190334 ESTs			
-14.2	-	AK026487	234192_s_at	G kinase anchoring protein 1			
-14.2	-	AI950069	242939_at	Transcription factor Dp-1			
-14.3	-	AW139300	230659_at	Transcribed locus			
-14.3	-	AI803568	239313_at	Hypothetical LOC401320			
-14.3	-	AW269397	225564_at	Spermatogenesis associated 13			
-14.3	-	AI524068	242066_at	CDNA FLJ36420 fis, clone THYMU2011257			
-14.3	-	BE738988	238790_at	CLR pseudogene			
-14.4	-	BF508977	243213_at	Transcribed locus			
-14.5	-	AI640434	241627_x_at	Full length insert cDNA clone YI72E07			
-14.5	-	AI742582	229920_at	Transcribed locus			
-14.5	-	AI745624	226982_at	Elongation factor, RNA polymerase II, 2			
-14.5	-	AI733360	240126_x_at	Bromodomain PHD finger transcription factor			
-14.5	-	BF062287	236609_at	Hypothetical protein LOC100129592			
-14.5	-	AW105337	225969_at	AlkB, alkylation repair homolog 6 (E. coli)			
-14.6	-	BF336159	239494_at	Transcribed locus			
-14.6	-	AF339815	233434_at	Clone IMAGE:32553, mRNA sequence			
-14.6	-	AI439157	226387_at	Round spermatid basic protein 1-like			
-14.6	-	AW009630	227368_at	Transcribed locus, moderately similar to XP_001091208.1 PREDICTED: hypothetical protein [Macaca mulatta]			
-14.7	-	BF194875	239709_at	Transcribed locus			
-14.7	-	AW006941	230677_at	Chromosome 14 open reading frame 73			
-14.7	-	AI817145	227751_at	Programmed cell death 5			
-14.7	-	BG231494	225955_at	Similar to meteorin, glial cell differentiation regulator-like			
-14.7	-	BE896490	239084_at	Synaptosomal-associated protein, 29kDa			
-14.8	-	AA760738	229483_at	CDNA FLJ42331 fis, clone TSTOM2000588			
-14.8	-	AA705029	239474_at	Transcribed locus			
-14.9	-	AU150386	229355_at	Transcribed locus			
-14.9	NLRP3	NM_004895	207075_at	NLR family, pyrin domain containing 3	Hs.159483	114548	1
-15.0	-	AW291023	235508_at	Promyelocytic leukemia			
-15.0	-	AI972367	238547_at	Hexamethylene bis-acetamide inducible 2			
-15.2	-	AL540867	225605_at	Tumor protein p53 inducible protein 13			
-15.2	-	BE856657	226135_at	Transcribed locus			
-15.3	-	AV700298	217523_at	CD44 molecule (Indian blood group)	-	-	-
-15.3	-	AI085534	242765_at	Myelin-associated oligodendrocyte basic protein			
-15.3	PTX3	NM_002852	206157_at	Pentraxin-related gene, rapidly induced by IL-1 beta	Hs.591286	5806	3
-15.4	-	AI016894	228326_at	WD repeat domain 27			
-15.4	-	AI927382	228330_at	Zinc finger with UFM1-specific peptidase domain			
-15.4	-	AI791138	242968_at	Transcribed locus			
-15.4	NAV1	AB033039	233870_at	Neuron navigator 1			
-15.5	-	AL542359	225593_at	LSM10, U7 small nuclear RNA associated			
-15.5	-	AW081685	236553_at	Transcribed locus			
-15.5	-	AI820875	230634_x_at	Secretory carrier membrane protein 4			
-15.5	-	AA480858	230413_s_at	Transcribed locus			
-15.5	UBXN6	AF272894	223012_at	UBX domain protein 6			

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-15.6	GAB1	AK022142	226002_at	GRB2-associated binding protein 1			
-15.6	ALG1	BC004402	223355_at	Asparagine-linked glycosylation 1, beta-1,4-mannosyltransferase homolog (S. cerevisiae)			
-15.6	-	AW449624	239379_at	Leucine rich repeat (in FLII) interacting protein 1			
-15.7	-	AW205664	231406_at	ORAI calcium release-activated calcium modulator 2			
-15.7	-	AI758223	228268_at	Flavin containing monooxygenase 2 (non-functional)			
-15.7	61E3.4	AC003007	231989_s_at	SMG1 homolog, phosphatidylinositol 3-kinase-related kinase pseudogene			
-15.7	NRBF2	AF267866	223650_s_at	Nuclear receptor binding factor 2			
-15.8	-	BF515959	230526_at	Hypothetical LOC100131096			
-15.9	-	AU144266	231057_at	Consensus includes gb:AU144266 /FEA=EST /DB_XREF=gi:11005787 /DB_XREF=est:AU144266 /CLONE=HEMBA1001395 /UG=Hs.269908 Homo sapiens cDNA FLJ11991 fis, clone HEMBB1001424			
-15.9	-	N29918	228562_at	Transcribed locus			
-15.9	-	AA045042	227317_at	LIM and cysteine-rich domains 1			
-15.9	-	AI024610	233340_at	Serine PI Kazal type 5-like 3			
-15.9	-	BF195340	238000_at	Transcribed locus			
-16.0	-	BE326857	235719_at	Kallikrein B, plasma (Fletcher factor) 1			
-16.0	-	AA169554	244334_at	Translocation associated membrane protein 1-like 1			
-16.0	C6orf203	AF151064	223576_at	Chromosome 6 open reading frame 203			
-16.0	-	AW590090	241096_at	Transcribed locus			
-16.1	-	R05895	239512_at	splicing factor, arginine/serine-rich 4			
-16.2	SERAC1	AA128978	232183_at	Serine active site containing 1			
-16.2	-	H22448	242530_at	CDNA FLJ37676 fis, clone BRHIP2012627			
-16.2	-	BF109303	227415_at	Diacylglycerol kinase, eta			
-16.2	-	AA830144	243037_at	Consensus includes gb:AA830144 /FEA=EST /DB_XREF=gi:2903243 /DB_XREF=est:oc44e12.s1 /CLONE=IMAGE:1352590 /UG=Hs.135613 ESTS, Moderately similar to ALU6_HUMAN ALU SUBFAMILY SP SEQUENCE CONTAMINATION WARNING ENTRY H.sapiens			
-16.3	-	AI433468	238804_at	Transcribed locus			
-16.3	-	N32860	230854_at	Transcribed locus			
-16.3	-	BF431867	239619_at	Consensus includes gb:BF431867 /FEA=EST /DB_XREF=gi:11443981 /DB_XREF=est:nab76b05.x1 /CLONE=IMAGE:3273560 /UG=Hs.253177 ESTS			
-16.4	-	AA827728	244341_at	Transcribed locus			
-16.4	-	AI695695	242051_at	Transcribed locus			
-16.4	-	AW292746	228098_s_at	Myosin regulatory light chain interacting protein			
-16.5	-	AW983691	235940_at	Chromosome 9 open reading frame 64			
-16.5	RAD18	AB035274	224200_s_at	RAD18 homolog (S. cerevisiae)			
-16.5	-	AI087792	231136_at	Transcribed locus			
-16.5	-	AA099118	226308_at	HAUS augmin-like complex, subunit 8			
-16.5	-	AW057518	240038_at	Transcribed locus			
-16.6	-	AI264121	227276_at	Plexin domain containing 2			
-16.7	-	BE645242	229219_s_at	N-terminal asparagine amidase			
-16.7	-	AV706971	230673_at	Polycystic kidney and hepatic disease 1 (autosomal recessive)-like 1			
-16.8	-	AI669235	222869_s_at	ElaC homolog 1 (E. coli)			
-16.8	-	AA938184	236312_at	Transcribed locus			
-16.8	-	AW130077	230032_at	Transcribed locus			
-16.8	-	BE790884	224982_at	AKT1 substrate 1 (proline-rich)			
-16.9	-	AW300612	243947_s_at	Transcribed locus			
-16.9	-	AW444778	228031_at	Tocopherol (alpha) transfer protein-like			
-16.9	-	BF575466	232082_x_at	small proline-rich protein 3			
-16.9	-	BF510801	222505_at	Limb region 1 homolog (mouse)			
-16.9	-	BF508609	230934_at	Serine/threonine kinase 32C			
-16.9	-	BF725804	243209_at	Potassium voltage-gated channel, KQT-like subfamily, member 4			
-17.0	SPAG5AS1	AL157421	231542_at	CDNA FLJ25772 fis, clone TST06461			
-17.0	OR2H4P	AJ302634	234760_at	Homo sapiens 6M1-7P*01 pseudogene, cell line LG2			
-17.0	-	AW512339	239328_at	CDNA FLJ35362 fis, clone SKMUS2000330			
-17.1	-	AW450206	243856_at	Transcribed locus			
-17.1	-	AF116659	210717_at	Transcribed locus	Hs.621370	-	5
-17.2	-	BF513404	239469_at	Transcribed locus			
-17.2	-	AA401429	229106_at	Dynein, light chain, LC8-type 2			
-17.2	-	AI640483	235536_at	Ring finger protein 149			
-17.3	-	AI354636	235171_at	Transcribed locus			
-17.4	-	AW002876	237034_at	Transcribed locus, strongly similar to XP_001164900.1 PREDICTED: hypothetical protein [Pan troglodytes]			
-17.4	-	AI708256	229342_at	CDNA FLJ32162 fis, clone PLACE6000325			

Down-Regulated Transcripts (U133A 133B)

-17.4	-	AL044007	229828_at	Transcribed locus			
-17.5	-	AA228366	236251_at	Transcribed locus			
-17.5	-	BE671123	235798_at	Transmembrane protein 170B			
-17.5	ZHX1	AF195766	223214_s_at	Zinc fingers and homeoboxes 1			
-17.6	-	AI332536	242780_at	VAMP (vesicle-associated membrane protein)-associated protein A, 33kDa			
-17.6	-	AA504356	229467_at	Poly(rC) binding protein 2			
-17.7	DNAJC27	AL117490	223504_at	Dnaj (Hsp40) homolog, subfamily C, member 27			
-17.7	-	BE467566	236982_at	CDNA clone IMAGE:5270500			
-17.7	-	AW003508	226688_at	Chromosome 3 open reading frame 23			
-17.7	SLC7A6OS	AK023353	232057_at	Solute carrier family 7, member 6 opposite strand			
-17.9	-	AV724827	224881_at	Vitamin K epoxide reductase complex, subunit 1-like 1			
-17.9	MND1	AY028916	223700_at	Meiotic nuclear divisions 1 homolog (S. cerevisiae)			
-17.9	-	AA702946	242646_at	Transcribed locus			
-18.0	-	AV753357	242975_s_at	Transcribed locus			
-18.0	-	AA204752	243904_at	CDNA clone IMAGE:5287121			
-18.0	MRPL35	AK026220	222775_s_at	Mitochondrial ribosomal protein L35			
-18.1	-	AA824624	239531_at	Transcribed locus			
-18.1	ZNF577	BC004992	223581_at	Zinc finger protein 577			
-18.1	-	BF594228	237696_at	Transcribed locus			
-18.2	-	AA490685	227792_at	Transcribed locus			
-18.2	-	AA629944	243664_at	Thioredoxin-like 1			
-18.4	-	AU144093	222716_s_at	Sorting nexin 24			
-18.4	-	AI912566	239518_at	Transcribed locus			
-18.5	-	AI939472	237510_at	Myoneurin			
-18.5	-	AI733222	237728_at	Transcribed locus			
-18.5	-	BE467907	230346_x_at	Transcribed locus			
-18.5	-	AA062971	225774_at	Ring finger and SPRY domain containing 1			
-18.5	-	BE550957	231036_at	Transcribed locus			
-18.6	-	BF793552	226161_at	Solute carrier family 30 (zinc transporter), member 6			
-18.6	-	AI799695	230685_at	Hypothetical LOC644873			
-18.7	-	BE736287	241606_s_at	TruB pseudouridine (psi) synthase homolog 1 (E. coli)			
-18.8	-	AI769569	235457_at	Mastermind-like 2 (Drosophila)			
-18.9	TBCD	AL096745	229192_s_at	Tubulin folding cofactor D			
-19.0	-	AU157441	226511_at	WD repeat domain 32			
-19.0	-	BF059124	229879_at	Transcribed locus			
-19.1	-	AI471969	239278_at	CDNA clone IMAGE:5301129			
-19.1	-	AI821399	242877_at	Transcribed locus			
-19.1	-	BG028209	230521_at	Chromosome 9 open reading frame 100			
-19.2	ATG7	BC000091	224025_s_at	ATG7 autophagy related 7 homolog (S. cerevisiae)			
-19.2	-	AL039862	225864_at	Family with sequence similarity 84, member B			
-19.3	-	AA534210	225679_at	N-acetyltransferase 12 (GCN5-related, putative)			
-19.3	-	AA725644	228982_s_at	Ubiquitin specific peptidase 42			
-19.4	EIF4E3	AL161983	225939_at	Eukaryotic translation initiation factor 4E family member 3			
-19.4	-	W90446	243314_at	Transcribed locus			
-19.4	-	AI741739	230484_at	Choline dehydrogenase			
-19.6	-	N57510	234998_at	CDNA clone IMAGE:5313062			
-19.7	-	AL534848	225620_at	Similar to hCG1778032			
-19.7	-	AW138883	236821_at	Transcribed locus			
-19.7	LOC438848	AL117475	233618_at	MRNA; cDNA DKFpZ727C211 (from clone DKFpZ727C211)			
-19.8	-	AI765886	230758_at	Gem (nuclear organelle) associated protein 8			
-20.0	-	BE219849	240180_at	MRNA full length insert cDNA clone EUROIMAGE 1090207			
-20.0	-	AK023264	233068_at	CDNA FLJ13202 fis, clone NT2RP3004503			
-20.0	-	AU147777	232145_at	Transcribed locus			
-20.2	-	AL531790	226958_s_at	Mediator complex subunit 11			
-20.2	OR4A1P	AF065869	234395_at	olfactory receptor, family 4, subfamily A, member 1 pseudogene			
-20.2	NRIP3	AJ400877	222900_at	nuclear receptor interacting protein 3			
-20.3	-	W90764	230077_at	Succinate dehydrogenase complex, subunit A, flavoprotein pseudogene 1			
-20.3	-	AW151660	239744_at	Transcribed locus			
-20.4	-	AI473843	239436_at	Cysteine and histidine-rich domain (CHORD)-containing 1			
-20.4	-	BF541967	238551_at	fucosyltransferase 11 (alpha (1,3) fucosyltransferase)			
-20.5	-	AA769986	241425_at	Nucleoporin like 1			
-20.6	ETNK1	BC006111	224454_at	Ethanolamine kinase 1			
-20.6	-	AA025858	227138_at	Cartilage associated protein			
-20.6	HSPA12B	AL109804	234610_at	heat shock 70kD protein 12B			
-20.6	MEX3B	AL136778	223627_at	Mex-3 homolog B (C. elegans)			

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-20.7	-	BG413366	236704_at	MRNA; cDNA DKFZp686N0886 (from clone DKFZp686N0886)			
-20.7	-	AK026189	229280_s_at	Hypothetical locus LOC401237			
-20.7	-	BE882538	227945_at	TBC1 (tre-2)/USP6, BUB2, cdc16 domain family, member 1			
-20.8	LONRF1	AA007596	242379_at	Transcribed locus			
-20.9	-	BF801735	238712_at	Transcribed locus			
-20.9	-	AI669749	229285_at	Ribonuclease L (2',5'-oligoadenylate synthetase-dependent)			
-21.0	-	BF432941	231055_at	Consensus includes gb:BF432941 /FEA=EST /DB_XREF=gi:11445104 /DB_XREF=est:7n28g07.x1 /CLONE=IMAGE:3566028 /UG=Hs.263462 ESTs			
-21.0	-	W46994	229417_at	Transcribed locus			
-21.0	-	AW206286	239823_at	Transcribed locus			
-21.1	MED17	AK022156	232483_at	mediator complex subunit 17			
-21.1	-	AI807950	229849_at	Transcribed locus			
-21.1	GPATCH2L	AB032978	229514_at	chromosome 14 open reading frame 118			
-21.1	-	AW665440	226619_at	SUMO1/sentrin specific peptidase 1			
-21.1	-	AI357143	239826_at	Transcribed locus			
-21.2	LINC00467	BC005997	224443_at	chromosome 1 open reading frame 97			
-21.2	-	AL566294	236699_at	CDNA FLJ90129 fis, clone HEMBB1000309			
-21.2	-	AW089574	229966_at	Ewing sarcoma breakpoint region 1			
-21.3	-	AW025411	242040_at	Glucosaminyl (N-acetyl) transferase family member 7			
-21.4	-	AI076335	236019_at	RAB12, member RAS oncogene family			
-21.4	-	BE675229	243350_at	Transcribed locus			
-21.4	USP31	AB033029	226033_at	Ubiquitin specific peptidase 31			
-21.5	-	BG330541	231763_at	polymerase (RNA) III (DNA directed) polypeptide A, 155kDa			
-21.5	-	N66622	227036_at	Full length insert cDNA YH97B03			
-21.5	-	AA778694	228566_at	Regulation of nuclear pre-mRNA domain containing 1A			
-21.5	-	AI809760	236213_at	Transcribed locus, strongly similar to XP_001716704.1 PREDICTED: hypothetical protein [Homo sapiens]			
-21.5	-	AI769954	229398_at	Transcribed locus			
-21.5	-	AW674195	243372_at	Heat shock 60kDa protein 1 (chaperonin)			
-21.5	FAM135B	AF131744	224001_at	Family with sequence similarity 135, member B			
-21.5	-	AI475574	236625_at	Transcribed locus			
-21.6	-	AI261321	235349_at	Family with sequence similarity 82, member A1			
-21.6	-	AI474448	227294_at	Zinc finger protein 689			
-21.6	-	BF196963	243054_at	Transcribed locus			
-21.9	-	AI092930	227693_at	WD repeat domain 20			
-21.9	-	AA887211	243951_at	ATP-binding cassette, sub-family B (MDR/TAP), member 1			
-21.9	-	AL563297	227757_at	Cullin 4A			
-22.0	-	AI954700	225348_at	FUS interacting protein (serine/arginine-rich) 1			
-22.0	-	AW470714	229739_s_at	Family with sequence similarity 116, member B			
-22.1	-	AV652437	243487_at	AF4/FMR2 family, member 4			
-22.1	-	AW969030	239616_at	REX2, RNA exonuclease 2 homolog (S. cerevisiae)			
-22.1	PNPLA3	AK025665	233030_at	Patatin-like phospholipase domain containing 3			
-22.2	-	AI768826	229202_at	Transcribed locus			
-22.2	-	AI653013	237150_at	Transcribed locus			
-22.3	-	AA973041	225702_at	Chromosome 8 open reading frame 76			
-22.3	CLDN12	AL136770	223249_at	Claudin 12			
-22.3	-	BE856748	227401_at	Interleukin 17D			
-22.4	-	BF062383	228244_at	Biogenesis of lysosomal organelles complex-1, subunit 3			
-22.5	-	AI129346	226209_at	NADH dehydrogenase (ubiquinone) flavoprotein 3, 10kDa			
-22.5	-	AA701890	240206_at	Threonyl-tRNA synthetase			
-22.6	-	BC006236	224480_s_at	1-acylglycerol-3-phosphate O-acyltransferase 9			
-22.6	-	AI824976	235285_at	Transcribed locus			
-22.6	-	AA875908	241917_at	Transcribed locus			
-22.6	-	AI744591	227188_at	Chromosome 21 open reading frame 63			
-22.6	-	AL038191	240271_at	Transcribed locus			
-22.6	-	AW838569	235558_at	RNA binding motif, single stranded interacting protein 2			
-22.7	-	AI375101	242507_at	CDNA FLJ35645 fis, clone SPLEN2012611			
-22.7	-	BF109387	230535_s_at	Transcribed locus			
-23.0	-	AI285730	230633_at	Transmembrane protein 102			
-23.0	-	AW293422	237125_at	Consensus includes gb:AW293422 /FEA=EST /DB_XREF=gi:6700058 /DB_XREF=est:UI-H-B12-ahm-a-10-0-UI.s1 /CLONE=IMAGE:2727090 /UG=Hs.255199 ESTs			
-23.1	-	AI538546	244207_at	Transcribed locus			
-23.1	-	BF513474	226918_at	Junctophilin 4			
-23.1	-	AW613053	243829_at	V-raf murine sarcoma viral oncogene homolog B1			
-23.4	-	AI335191	244803_at	Transcribed locus			

Down-Regulated Transcripts (U133A 133B)

-23.4	CWC15	AF110775	223067_at	CWC15 spliceosome-associated protein homolog (<i>S. cerevisiae</i>)			
-23.4	-	AW105010	235898_at	Transcribed locus			
-23.5	-	AW071804	242329_at	CAMP responsive element binding protein 5			
-23.6	-	AU158474	233350_s_at	Testis expressed 264			
-23.6	-	AI912315	236269_at	Zinc finger protein 628			
-23.7	-	AI351653	242904_x_at	Transcribed locus			
-23.7	-	AI689935	236645_at	HMG-box transcription factor 1			
-23.8	-	AA829836	241754_at	Chromosome 9 open reading frame 126			
-23.8	-	AV713062	235421_at	CDNA clone IMAGE:4689481			
-23.8	-	AW629515	234988_at	Valosin containing protein (p97)/p47 complex interacting protein 1			
-23.8	-	AA132172	236742_at	Transcribed locus			
-23.9	-	AW450033	243098_at	Transcribed locus			
-23.9	-	BE467023	229221_at	CD44 molecule (Indian blood group)			
-23.9	RRP12	AK021460	216913_s_at	Ribosomal RNA processing 12 homolog (<i>S. cerevisiae</i>)	Hs.434251	23223	10
-23.9	-	AL390159	233474_at	Transcribed locus, strongly similar to XP_001721774.1 PREDICTED: similar to HCG1645807 [Homo sapiens]			
-24.1	WEN_t30492	T03492	238115_at	Transcribed locus			
-24.3	-	BF115231	225933_at	Coiled-coil domain containing 137			
-24.3	NUDT12	AL136592	223535_at	Nudix (nucleoside diphosphate linked moiety X)-type motif 12			
-24.3	-	AK024593	225165_at	Protein phosphatase 1, regulatory (inhibitor) subunit 1B			
-24.4	-	AK022197	233154_at	CDNA FLJ12135 fis, clone MAMMA1000307			
-24.4	-	AI797462	229035_s_at	Kelch domain containing 4			
-24.7	SYTL4	AL391688	227703_s_at	synaptotagmin-like 4			
-24.9	-	AK022838	232511_at	CDNA FLJ12776 fis, clone NT2RP2001678			
-24.9	-	AI813331	229097_at	Diaphanous homolog 3 (<i>Drosophila</i>)			
-24.9	VP54	AL359939	233656_s_at	Vacuolar protein sorting 54 homolog (<i>S. cerevisiae</i>)			
-24.9	-	N94835	232549_at	RNA binding motif protein 11			
-25.0	-	BF108964	228468_at	Microtubule associated serine/threonine kinase-like			
-25.0	LOC643529	AL137595	232239_at	HCG2024094			
-25.0	XRN1	AL117516	233632_s_at	5'-3' exoribonuclease 1			
-25.1	-	BE735175	236766_at	Transcribed locus			
-25.2	-	AI863675	238988_at	Transcribed locus			
-25.2	RAB23	AF161486	223463_at	RAB23, member RAS oncogene family			
-25.2	-	AW445213	241019_at	Transcribed locus			
-25.3	-	AI890591	237051_at	Transcribed locus			
-25.4	-	AW975772	236918_s_at	Leucine rich repeat containing 34			
-25.4	-	AI810497	225984_at	Protein kinase, AMP-activated, alpha 1 catalytic subunit			
-25.4	-	AW193600	232001_at	Hypothetical gene supported by AY007155			
-25.5	XYLB	AA777793	214776_x_at	Xylulokinase homolog (<i>H. influenzae</i>)	Hs.659985	9942	3
-25.5	G2E3	BC000973	223258_s_at	G2/M-phase specific E3 ubiquitin ligase			
-25.6	-	AI928507	225388_at	Tetraspanin 5			
-25.7	-	AI761584	229654_at	Transcribed locus			
-25.7	-	AW467480	236202_at	Transcribed locus			
-25.8	-	AA923524	240862_at	RAS guanyl releasing protein 4			
-25.9	-	AI003777	227552_at	Septin 1			
-26.0	KIAA1377	AL045516	232166_at	KIAA1377			
-26.1	-	AA524740	225249_at	Signal peptide peptidase-like 2B			
-26.1	-	AK024380	232789_at	CDNA FLJ14318 fis, clone PLACE3000402			
-26.2	-	AI732206	238228_at	Component of oligomeric golgi complex 3			
-26.3	SAV1	AJ292969	234491_s_at	Salvador homolog 1 (<i>Drosophila</i>)			
-26.4	-	AL034403	234372_at	Human DNA sequence from clone 31B8 on chromosome Xq22.2-23. Contains a GAPD (glyceraldehyde-3-phosphate dehydrogenase pseudogene) pseudogene, ESTs, STSs and GSSs			
-26.4	-	BF512183	229885_at	Transcribed locus			
-26.4	-	AI401105	240118_at	Transcribed locus			
-26.5	-	BE348466	228802_at	RNA binding protein with multiple splicing 2			
-26.5	-	BF514975	242669_at	Ubiquitin-fold modifier 1			
-26.6	-	AA868356	242480_at	Transcribed locus			
-26.7	-	AA026388	243768_at	Transcribed locus			
-26.7	-	AU144437	232887_at	Phosphoinositide-interacting regulator of transient receptor potential channels			
-26.9	-	H12084	242292_at	Chromosome X open reading frame 50B			
-27.0	-	AW003313	231435_at	Chromosome 7 open reading frame 34			
-27.0	-	BF057084	227726_at	Ring finger protein 166			
-27.1	-	AI239832	240383_at	Ubiquitin-conjugating enzyme E2D 3 (UBC4/5 homolog, yeast)			
-27.4	-	AA279462	237107_at	Protein kinase, interferon-inducible double stranded RNA dependent activator			

Down-Regulated Transcripts (U133A 133B)

-27.5	-	AI307251	235704_at	DAZ associated protein 2			
-27.6	-	AI344332	227227_at	Transcribed locus, strongly similar to XP_001719754.1 PREDICTED: similar to LRRC37A3 protein, partial [Homo sapiens]			
-27.6	-	BE669782	244110_at	Myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila)			
-27.6	-	BF593625	226068_at	Spleen tyrosine kinase			
-27.7	-	AI341321	227822_at	Zinc finger protein 605			
-28.0	-	AI373299	226649_at	Pantothenate kinase 1			
-28.2	ACTRT3	AB049117	223665_at	Actin related protein M1			
-28.3	-	AA281853	239505_at	Transcribed locus			
-28.3	DEPDC7	AJ245600	228293_at	DEP domain containing 7			
-28.3	-	BG034114	239627_at	Transmembrane emp24 protein transport domain containing 9			
-28.5	-	AI018235	240314_at	Full length insert cDNA clone ZE12G01			
-28.5	-	BE965311	232269_x_at	Meteorin, glial cell differentiation regulator			
-28.5	-	AW207642	239788_at	Transcribed locus			
-28.6	-	AA233885	244647_at	Transcribed locus			
-28.8	-	AI703465	236023_at	Cyclin-dependent kinase 9			
-28.8	TNFAIP3	AI738896	202643_s_at	Tumor necrosis factor, alpha-induced protein 3	Hs.211600	7128	6
-29.0	-	BG231554	243179_at	Hypothetical protein LOC100130360			
-29.0	-	BE740761	232035_at	Transcribed locus, strongly similar to XP_981474.1 PREDICTED: similar to histone H4 [Mus musculus]			
-29.2	-	AW292872	236198_at	Consensus includes gb:AW292872 /FEA=EST /DB_XREF=gi:6699508 /DB_XREF=est:UI-H-BW0-aif-f-02-0-UI.s1 /CLONE=IMAGE:2729211 /UG=Hs.124554 ESTs			
-29.3	-	BF063382	225069_at	Phosphate cytidyltransferase 1, choline, alpha			
-29.4	-	BE302305	228284_at	Transducin-like enhancer of split 1 (E(sp1) homolog, Drosophila)			
-29.4	-	AI038577	242109_at	Synaptotagmin-like 3			
-29.5	-	BF938956	237096_at	Transcribed locus			
-29.5	-	AL133091	233984_at	Transcribed locus, strongly similar to NP_766187.1 hypothetical protein LOC218978 [Mus musculus]			
-29.6	-	AA744843	239655_at	Transcribed locus			
-29.7	-	BE897518	241924_at	Transcribed locus			
-29.7	-	AI023707	243435_at	KCNQ1 overlapping transcript 1 (non-protein coding)			
-29.8	-	BE886165	238502_at	Transcribed locus			
-29.9	-	AW409794	225978_at	Transcribed locus			
-30.1	-	BE302085	239161_at	Ferredoxin 1			
-30.1	-	BF913667	235055_x_at	Mucin 4, cell surface associated			
-30.2	-	AL133564	234010_at	Transcribed locus			
-30.3	-	AA629020	233504_at	Chromosome 9 open reading frame 84			
-30.4	-	N25952	228926_s_at	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 2			
-30.6	ZNF461	AB021641	232391_at	Zinc finger protein 461			
-30.6	ZNF226	AK023091	233461_x_at	Zinc finger protein 226			
-30.8	-	AW003138	238207_at	Similar to CG32736-PA			
-31.0	FOSL2	AA019641	241824_at	Transcribed locus			
-31.1	-	W72315	229425_at	Transcribed locus			
-31.2	-	AI939493	241982_at	Transcribed locus			
-31.2	NOXA1	AI860821	232373_at	NADPH oxidase activator 1			
-31.3	OBSCN	AB046859	233029_at	Obscurin, cytoskeletal calmodulin and titin-interacting RhoGEF			
-31.3	-	BF591611	227978_s_at	Zinc binding alcohol dehydrogenase domain containing 2			
-31.4	-	BE148503	241626_at	Wilms tumor 1 associated protein			
-31.4	-	BC006204	224471_s_at	Beta-transducin repeat containing			
-31.6	-	AW978811	242080_at	Consensus includes gb:AW978811 /FEA=EST /DB_XREF=gi:8170087 /DB_XREF=est:EST390920 /UG=Hs.314451 ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAMILY J SEQUENCE			
-31.7	-	AI821584	241080_at	CONTAMINATION WARNING ENTRY H.sapiens			
-31.7	-	AI821584	241080_at	Transcribed locus			
-31.8	-	AA975422	242829_x_at	F-box and leucine-rich repeat protein 3			
-32.0	-	AW080618	226321_at	LysM, putative peptidoglycan-binding, domain containing 3			
-32.2	-	BF195118	229127_at	CDNA FLJ31517 fis, clone NT2RI2000007			
-32.3	-	AW003222	226513_at	Ankyrin repeat and SOCS box-containing 7			
-32.4	ANKRD32	AL136560	223542_at	Ankyrin repeat domain 32			
-32.7	PRRT3-AS1	AI861893	242888_at	Transcribed locus			
-32.8	-	AI630830	243150_at	Transcribed locus			
-33.1	GMCL1P1	AF198534	234488_s_at	Germ cell-less homolog 1 (Drosophila)-like			
-33.2	-	AI279879	230681_at	Transcribed locus, strongly similar to XP_859029.1 PREDICTED: similar to transforming growth factor beta regulated gene 1 (pr			
-33.3	-	AW292830	244447_at	Transcribed locus			

Down-Regulated Transcripts (U133A 133B)

-33.7	-	BF000155	242473_at	TNF receptor-associated factor 4			
-33.8	FANCM	AK001672	234733_s_at	Fanconi anemia, complementation group M			
-33.9	ANAPC7	AL137586	225521_at	Anaphase promoting complex subunit 7			
-33.9	FBXO4	AF176703	233366_at	F-box protein 4			
-34.0	-	AW510927	239393_at	Transcribed locus			
-34.1	DUSP6	BC005047	208893_s_at	Dual specificity phosphatase 6	Hs.298654	1848	12
-34.1	-	AL544576	229452_at	Transmembrane protein 88			
-34.4	-	AA417099	240156_at	Consensus includes gb:AA417099 /FEA=EST /DB_XREF=gi:2077180 /DB_XREF=est:zu13e02.s1 /CLONE=IMAGE:731738 /UG=Hs.192148 ESTs			
-34.6	-	AI970972	235800_at	CDNA FLJ34029 fis, clone FCBBF2003636			
-34.9	-	AA657818	232097_at	TOX high mobility group box family member 4			
-35.0	-	AU119437	227289_at	Protocadherin 17			
-35.1	-	AA490928	238631_at	Zinc finger protein 140			
-35.3	-	AK024901	234322_at	CDNA: FLJ21248 fis, clone COL01235			
-35.4	-	AI191591	237075_at	Transcribed locus			
-35.4	-	BF965447	241716_at	Transcribed locus			
-35.4	-	AI743151	230369_at	G protein-coupled receptor 161			
-35.5	-	AL117506	234434_at	MRNA; cDNA DKFZp434F0535 (from clone DKFZp434F0535)			
-35.5	FCRL4	AF343659	224401_s_at	Fc receptor-like 4			
-35.5	C10orf54	AK024449	225372_at	Chromosome 10 open reading frame 54			
-35.7	PRKCZ	NM_002744	202178_at	Protein kinase C, zeta	Hs.496255	5590	1
-35.8	-	BE620832	224831_at	Cytoplasmic polyadenylation element binding protein 4			
-35.8	-	AI743332	242188_at	Transcribed locus			
-35.9	-	AA581439	244650_at	family with sequence similarity 105, member A			
-36.0	-	AF130085	223679_at	catenin (cadherin-associated protein), beta 1, 88kDa			
-36.1	-	AA740875	235387_at	Glutathione S-transferase, C-terminal domain containing			
-36.3	-	BE082914	243206_at	Transcribed locus			
-36.3	-	AU156755	226107_at	CDNA FLJ13495 fis, clone PLACE1004425			
-36.4	LOC85648	AK021551	232589_at	CDNA FLJ11489 fis, clone HEMBA1001915			
-36.5	-	BE349115	228873_at	Collagen, type XXII, alpha 1			
-36.6	EGR4	NM_001965	207768_at	Early growth response 4	Hs.3052	1961	2
-36.6	-	AI004137	242720_at	Inter-alpha (globulin) inhibitor H4 (plasma Kallikrein-sensitive glycoprotein)			
-36.7	-	AI681419	229071_at	Chromosome 17 open reading frame 100			
-36.7	-	BE674964	242143_at	Transcribed locus			
-36.9	-	BF197089	228670_at	Telomerase-associated protein 1			
-36.9	-	BF196250	244051_at	Transcribed locus			
-37.1	-	AI740796	240277_at	Transcribed locus			
-37.1	GADD45B	NM_015675	207574_s_at	Growth arrest and DNA-damage-inducible, beta	Hs.110571	4616	19
-37.1	-	BF591040	229723_at	Transcribed locus			
-37.1	-	AI815001	228047_at	Ribosomal protein L30			
-37.4	IFRD1	BF061555	230048_at	Transcribed locus			
-37.5	-	AV733347	242905_at	Partner of NOB1 homolog (S. cerevisiae)			
-37.5	-	BE544070	238448_at	mitochondrial ribosomal protein L19			
-37.7	-	H79861	222706_at	Coiled-coil domain containing 49			
-37.8	-	BF185264	237040_at	CWF19-like 2, cell cycle control (S. pombe)			
-37.8	-	N36160	241792_x_at	Consensus includes gb:N36160 /FEA=EST /DB_XREF=gi:1157302 /DB_XREF=est:yy29e02.s1 /CLONE=IMAGE:272666 /UG=Hs.32112 ESTs			
-37.9	-	AI824719	242086_at	CDNA clone IMAGE:4798227			
-38.0	-	R55286	237132_at	Tight junction protein 2 (zona occludens 2)			
-38.6	-	AW269818	222908_at	Family with sequence similarity 38, member B			
-38.7	-	BF477980	242775_at	Prostaglandin reductase 1			
-38.7	KIAA1109	AB037792	233096_at	KIAA1109			
-39.0	-	AA775731	228857_at	Hypothetical protein LOC285831			
-39.1	FOSB	NM_006732	202768_at	FBJ murine osteosarcoma viral oncogene homolog B	Hs.590958	2354	19
-39.5	-	BF592779	229197_at	Inhibitor of growth family, member 5			
-39.9	-	S69873	234907_x_at	Mutant DNA polymerase beta			
-40.1	-	AA001414	225648_at	Serine/threonine kinase 35			
-40.6	-	AA150501	229011_at	Transcribed locus			
-40.6	-	AI308101	237400_at	Transcribed locus			
-40.7	-	BE564430	235093_at	peroxisomal biogenesis factor 13			
-40.7	-	AI767447	225338_at	Zyg-11 homolog B (C. elegans)			
-40.7	-	AI935789	238248_at	Uromodulin			
-40.8	-	AI220157	232610_at	Poly (ADP-ribose) polymerase family, member 14			
-40.8	CNTNAP4	AB051550	232388_at	Contactin associated protein-like 4			
-41.2	NAA50	H16725	239138_at	CDNA clone IMAGE:4797099			

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-41.3	-	W87626	239555_at	CDNA clone IMAGE:40114646			
-41.3	RPTOR	AB037724	225715_at	Raptor			
-41.5	-	AI479082	238127_at	Hypothetical LOC650669			
-41.6	-	R34396	231902_at	Zinc finger protein 827			
-41.7	-	AW169333	229804_x_at	COBW domain containing 1			
-41.8	-	T51136	241756_at	Consensus includes gb:T51136 /FEA=EST /DB_XREF=gi:652996 /DB_XREF=est:yb94b11.s1 /CLONE=IMAGE:78813 /UG=Hs.90489 ESTs			
-42.0	-	BF110792	228818_at	CDNA FLJ12727 fis, clone NT2RP2000027			
-42.0	-	AW573027	244425_at	Consensus includes gb:AW573027 /FEA=EST /DB_XREF=gi:7237760 /DB_XREF=est:hf30b05.x1 /CLONE=IMAGE:2933361 /UG=Hs.258397 ESTs			
-42.1	-	N32557	226907_at	Protein phosphatase 1, regulatory (inhibitor) subunit 14C			
-42.1	-	AI807379	231010_at	Chromosome 4 open reading frame 16			
-42.6	-	AA890362	237616_at	Consensus includes gb:AA890362 /FEA=EST /DB_XREF=gi:3017241 /DB_XREF=est:aj94d06.s1 /CLONE=IMAGE:1404107 /UG=Hs.124170 ESTs			
-42.8	-	AL135700	235904_at	UDP glycosyltransferase 3 family, polypeptide A1			
-43.0	-	AI760978	243957_at	Hypothetical protein LOC100128108			
-43.4	-	AW611777	240554_at	A kinase (PRKA) anchor protein 8-like			
-43.6	-	AW963951	235334_at	ST6 (alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1,3)-N-acetylgalactosaminide alpha-2,6-sialyltransferase 3			
-43.7	-	D55880	226976_at	Karyopherin alpha 6 (importin alpha 7)			
-43.8	BUB3	AA218973	237245_at	Transcribed locus			
-43.9	-	AW085505	227198_at	AF4/FMR2 family, member 3			
-44.0	-	AI972469	242433_at	Transcribed locus, strongly similar to NP_001100567.1 zinc finger and BTB domain containing 11 [Rattus norvegicus]			
-44.1	-	AI738675	240064_at	Transcribed locus			
-44.2	-	BF725250	227996_at	FERM, RhoGEF (ARHGEF) and pleckstrin domain protein 1 (chondrocyte-derived)			
-44.4	-	AW303359	222493_s_at	Zinc finger, AN1-type domain 3			
-44.8	PRO1925	AF116673	224214_at	Transcribed locus			
-45.2	-	BF109197	242577_at	Transcribed locus			
-45.2	-	AA810452	235885_at	Transcribed locus, strongly similar to XP_001917763.1 PREDICTED: mediator complex subunit 12-like [Equus caballus]			
-45.3	-	AI740541	231029_at	Coagulation factor V (proaccelerin, labile factor)			
-45.3	-	AI417007	243279_at	Transcribed locus			
-45.4	-	AI202664	233536_at	Additional sex combs like 3 (Drosophila)			
-45.6	-	N51717	235146_at	Transmembrane and coiled-coil domain family 3			
-45.8	-	AI953022	236460_at	Transcribed locus			
-45.9	-	N67108	230837_at	Transcribed locus			
-46.1	-	AA262228	243923_at	Transcribed locus			
-46.3	-	AW005640	229781_at	Transcribed locus			
-46.5	-	AW204095	236090_at	Transcribed locus			
-47.0	-	AL561281	222547_at	Transcribed locus			
-47.6	MBNL1-AS1	AK026494	232298_at	Hypothetical LOC401093			
-47.8	-	BE880820	225584_at	Tripartite motif-containing 26			
-48.3	-	AA765786	243293_at	Transcribed locus			
-48.3	-	BF690134	238331_at	Shadow of prion protein homolog (zebrafish)			
-48.4	ARMC2	AL136754	223866_at	Armadillo repeat containing 2			
-48.4	-	AW205659	229604_at	Cytidine monophosphate-N-acetylneuraminic acid hydroxylase (CMP-N-acetylneuraminase pseudogene)			
-48.9	-	AW117206	239402_at	Transcribed locus			
-49.1	MICAL3	AB037785	231985_at	Microtubule associated monooxygenase, calponin and LIM domain containing 3			
-49.2	EMILIN2	AL552384	242288_s_at	Elastin microfibril interfacer 2			
-49.8	-	AW195407	227341_at	BEN domain containing 7			
-50.3	-	AA429262	235920_at	CDNA clone IMAGE:4779711			
-50.8	-	BE380045	243026_x_at	X-linked inhibitor of apoptosis			
-51.0	SMG9	AL136606	223188_at	Chromosome 19 open reading frame 61			
-51.5	-	BF878343	235204_at	COX15 homolog, cytochrome c oxidase assembly protein (yeast)			
-51.6	-	BF063821	230598_at	Transcribed locus			
-51.7	-	AW172914	243661_at	Zinc finger protein 273			
-51.8	-	BE964704	228164_at	adaptor-related protein complex 4, epsilon 1 subunit			
-51.9	-	AU156202	233473_x_at	CDNA FLJ13434 fis, clone PLACE1002578			
-52.2	-	BF840360	239404_at	Transcribed locus			
-52.4	-	AV729072	226301_at	Chromosome 6 open reading frame 192			
-52.4	KIF13A	AY014403	223520_s_at	Kinesin family member 13A			

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-52.5	-	AA677700	241688_at	Consensus includes gb:AA677700 /FEA=EST /DB_XREF=gi:2658222 /DB_XREF=est:zj72h05.s1 /CLONE=IMAGE:460473 /UG=Hs.269600 ESTs, Weakly similar to S72482 hypothetical protein H.sapiens			
-52.8	-	AA491949	241897_at	Consensus includes gb:AA491949 /FEA=EST /DB_XREF=gi:2221511 /DB_XREF=est:ng16g01.s1 /CLONE=IMAGE:929616 /UG=Hs.269392 ESTs			
-52.9	-	AA913885	239795_at	Transcribed locus			
-53.4	-	AA968473	243458_at	Consensus includes gb:AA968473 /FEA=EST /DB_XREF=gi:3143653 /DB_XREF=est:op49f05.s1 /CLONE=IMAGE:1580193 /UG=Hs.212644 ESTs			
-53.7	-	AI377875	236700_at	eukaryotic translation initiation factor 3, subunit C			
-54.0	LINC00626	BC001841	224020_at	Hypothetical LOC79100			
-54.3	-	BF690215	240428_at	Hypothetical protein LOC285000			
-54.5	-	AU144005	232797_at	CDNA FLJ11397 fis, clone HEMBA1000622			
-55.0	-	BF939224	239092_at	Integrin, alpha 8			
-55.3	-	AW450288	237671_at	Transcribed locus			
-55.4	-	AW104936	240708_at	Transcribed locus			
-55.5	-	BE552208	229359_at	Transcribed locus			
-55.6	-	AI906424	238610_s_at	Transcribed locus			
-55.7	-	AW008270	242549_at	Protein kinase D3			
-55.8	-	AI355848	227400_at	nuclear factor I/X (CCAAT-binding transcription factor)			
-55.8	-	AI652926	237546_at	Transcribed locus			
-55.9	-	AI057455	244010_at	MRNA; cDNA DKFZp686J08131 (from clone DKFZp686J08131)			
-55.9	-	AI458949	242903_at	Interferon gamma receptor 1			
-56.1	-	BF514271	242591_at	Dynein, axonemal, heavy chain 1			
-56.2	AI61	AK001347	232810_at	Androgen-induced 1			
-56.7	-	AI950023	244433_at	Consensus includes gb:AI950023 /FEA=EST /DB_XREF=gi:5742333 /DB_XREF=est:wq15g03.x1 /CLONE=IMAGE:2471380 /UG=Hs.270751 ESTs			
-56.8	-	AK024979	232852_at	CDNA: FLJ21326 fis, clone COL02445			
-57.0	-	AI672386	236936_at	Consensus includes gb:AI672386 /FEA=EST /DB_XREF=gi:4852117 /DB_XREF=est:ty64e11.x1 /CLONE=IMAGE:2283884 /UG=Hs.263780 ESTs			
-58.2	-	AI160083	240388_at	Keratin 27			
-58.5	-	AI935766	229054_at	Chromosome 14 open reading frame 181			
-58.8	-	W80594	237747_at	CDNA FLJ26998 fis, clone SLV04689			
-59.0	-	AU154942	232929_at	CDNA FLJ13240 fis, clone OVARC1000496			
-59.9	-	AI733356	239688_at	Structural maintenance of chromosomes 1A			
-60.4	-	T98846	239654_at	Chromodomain helicase DNA binding protein 9			
-60.5	-	AA417971	230572_at	Chromosome 4 open reading frame 38			
-60.6	-	AI139639	236662_at	Transcribed locus			
-60.7	-	BE501712	229659_s_at	Polymeric immunoglobulin receptor			
-60.8	-	AW339783	240631_at	G protein-coupled receptor 98			
-60.9	-	AI823453	243589_at	KIAA1267			
-60.9	-	AU151788	232230_at	Chromosome 10 open reading frame 75			
-61.1	-	AA609053	227803_at	Ectonucleotide pyrophosphatase/phosphodiesterase 5 (putative function)			
-61.4	FLJ21394	AK025047	234785_at	Homo sapiens cDNA: FLJ21394 fis, clone COL03536.			
-62.0	-	BG236289	228759_at	CAMP responsive element binding protein 3-like 2			
-62.2	-	N54957	228042_at	ADP-ribosylarginine hydrolase			
-63.1	-	AF116638	224098_at	Homo sapiens PRO1546 mRNA, complete cds.			
-63.5	-	AI281371	243792_x_at	Protein tyrosine phosphatase, non-receptor type 13 (APO-1/CD95 (Fas)-associated phosphatase)			
-63.6	-	AW972669	242106_at	Transcribed locus			
-64.9	-	AI203405	240409_at	SGT1, suppressor of G2 allele of SKP1 like 1 (S. cerevisiae)			
-65.1	-	AV705309	236278_at	Transcribed locus, strongly similar to NP_724345.1 histone H3 [Drosophila melanogaster]			
-65.2	FOXP1	BC005055	223937_at	Forkhead box P1			
-65.3	-	BF059479	239552_at	Transcribed locus, strongly similar to XP_374405.6 PREDICTED: hypothetical protein LOC221806 [Homo sapiens]			
-65.5	-	AI056238	240468_at	Transcribed locus			
-65.5	-	AW242668	230889_at	Transcribed locus, strongly similar to XP_001714597.1 PREDICTED: hypothetical protein [Homo sapiens]			
-65.5	-	AA609250	240330_at	Transcribed locus			
-66.1	-	BF691634	243840_at	Consensus includes gb:BF691634 /FEA=EST /DB_XREF=gi:11977135 /DB_XREF=est:602248362F1 /CLONE=IMAGE:4333599 /UG=Hs.226414 ESTs, Weakly similar to ALU8_HUMAN ALU SUBFAMILY SX SEQUENCE CONTAMINATION WARNING ENTRY H.sapiens			
-66.2	-	AI681868	236495_at	Transcribed locus			
-66.7	-	AI139114	239918_at	Poliovirus receptor			

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-67.2	-	AI273692	243510_at	Transcribed locus			
				Consensus includes gb:A1821404 /FEA=EST /DB_XREF=gi:5440483 /DB_XREF=est:ye17h09.x5 /CLONE=IMAGE:118049 /UG=Hs.227505 ESTs, Weakly similar to ALU7_HUMAN ALU SUBFAMILY SQ SEQUENCE CONTAMINATION WARNING ENTRY H.sapiens			
-67.3	-	AI821404	237496_at				
-67.9	-	BG290819	226010_at	Solute carrier family 25 (mitochondrial carrier; phosphate carrier), member 23			
-67.9	-	AK026079	234644_x_at	Tumor necrosis factor receptor superfamily, member 10c, decoy without an intracellular domain			
-68.2	-	AA992936	238501_at	Transcribed locus			
-69.0	-	BE858032	228201_at	ADP-ribosylation factor-like 13B			
-69.1	-	AW009638	228596_at	Rho guanine nucleotide exchange factor (GEF) 5			
-69.9	-	AW449589	237525_at	Consensus includes gb:AW449589 /FEA=EST /DB_XREF=gi:6990295 /DB_XREF=est:UI-H-B13-aku-f-01-0-UI.s1 /CLONE=IMAGE:2735736 /UG=Hs.279724 ESTs			
-69.9	-	AI017875	240867_at	Transcribed locus			
-70.7	-	AI268315	227027_at	Glutamine-fructose-6-phosphate transaminase 1			
-71.1	-	BG236366	227645_at	Phosphoinositide-3-kinase, regulatory subunit 5			
-71.2	-	AW665665	237187_at	Transcribed locus			
-71.5	-	BE672379	237583_at	Consensus includes gb:BE672379 /FEA=EST /DB_XREF=gi:10032920 /DB_XREF=est:7a56h12.x1 /CLONE=IMAGE:3222791 /UG=Hs.156825 ESTs			
-71.9	-	AA601031	228919_at	Transcribed locus			
-72.2	-	AI733824	243304_at	Hypothetical protein LOC286109			
-72.6	-	AI377007	241398_at	Metallophosphoesterase domain containing 1			
-73.2	-	AI806500	222667_s_at	Ash1 (absent, small, or homeotic)-like (Drosophila)			
-74.2	-	AU149021	233005_at	CDNA FLJ12602 fis, clone NT2RM4001437			
-74.3	-	N90377	243031_at	Transcribed locus			
-74.6	-	T86874	230607_at	Transcribed locus			
-74.9	ZNF607	BC005085	223680_at	Zinc finger protein 607			
-75.1	ZNF451	AB051489	231885_at	Zinc finger protein 451			
-75.5	-	AA677952	237318_at	Transcribed locus			
-75.7	-	BF063657	244026_at	Transcribed locus			
-76.4	-	AV648669	241812_at	viral DNA polymerase-transactivated protein 6			
-76.6	-	AI884906	230720_at	Ring finger protein 182			
-76.6	-	AA459699	240456_at	Transcribed locus			
-76.9	-	N51107	242632_at	FYVE, RhoGEF and PH domain containing 2			
-77.0	-	AA131302	236032_at	Transcribed locus			
-77.1	-	BE676062	231249_at	Transcribed locus, strongly similar to NP_036437.1 adaptor-related protein complex 2, alpha 2 subunit [Homo sapiens]			
-77.2	-	AA731746	236582_at	Transcribed locus			
-77.7	ELP2	AK022709	232503_at	Elongation protein 2 homolog (S. cerevisiae)			
-78.2	FNBP1	AA262084	239453_at	Transcribed locus			
-78.4	-	AI765006	235775_at	Transmembrane and tetratricopeptide repeat containing 2			
-79.0	-	AA678985	238966_at	bruno-like 4, RNA binding protein (Drosophila)			
-79.8	RUFY2	AB040970	233192_s_at	RUN and FYVE domain containing 2			
-80.2	-	AK022100	233406_at	CDNA FLJ12038 fis, clone HEMBB1001922			
-80.2	-	R53820	227519_at	Placenta-specific 4			
-80.7	-	BE551407	239258_at	Transcribed locus			
-80.7	-	BF514509	239049_at	Consensus includes gb:BF514509 /FEA=EST /DB_XREF=gi:11599688 /DB_XREF=est:UI-H-BW1-anf-g-03-0-UI.s1 /CLONE=IMAGE:3082180 /UG=Hs.262571 ESTs			
-81.0	-	AI694413	235229_at	Consensus includes gb:AI694413 /FEA=EST /DB_XREF=gi:4971753 /DB_XREF=est:wd83d12.x1 /CLONE=IMAGE:2338199 /UG=Hs.332649 olfactory receptor, family 2, subfamily I, member 6			
-81.2	-	AA917932	244179_x_at	Gamma-glutamyltransferase 3 pseudogene			
-81.3	-	N66727	235424_at	Transcribed locus			
-81.3	-	AI867408	235816_s_at	Ral guanine nucleotide dissociation stimulator-like 4			
-82.4	-	AA131694	227222_at	F-box protein 10			
-82.4	-	C18965	242853_at	Transcribed locus			
-82.6	-	BF111088	240797_at	PERP, TP53 apoptosis effector			
-83.0	-	AA521136	239504_at	Consensus includes gb:AA521136 /FEA=EST /DB_XREF=gi:2261679 /DB_XREF=est:aa73a03.s1 /CLONE=IMAGE:826540 /UG=Hs.190176 ESTs			
-83.3	-	AW971123	236446_at	Transcribed locus			
-83.6	-	AA813336	240371_at	Similar to hCG2021878			
-85.5	-	AK024153	233515_at	CDNA FLJ36506 fis, clone TRACH2001060			
-85.5	ZNRF3	AL021393	234843_s_at	zinc and ring finger 3			
-86.0	-	AI700446	229738_at	Dynein, axonemal, heavy chain 10			
-86.4	-	AW089307	235057_at	Itchy E3 ubiquitin protein ligase homolog (mouse)			

Down-Regulated Transcripts (U133A 133B)

-87.1	-	R47946	241536_at	Full length insert cDNA YO61A08			
-87.2	-	AU148054	233106_at	Chromosome 14 open reading frame 82			
-87.2	-	AI654208	244702_at	Transcribed locus			
-89.2	-	AA708470	239988_at	Transcribed locus			
-89.7	-	BF433010	229165_at	Mitochondrial ribosomal protein L12			
-89.8	TCP11L1	AK021448	233472_at	t-complex 11 (mouse)-like 1			
-90.9	TMEFF2	AB017269	223557_s_at	Transmembrane protein with EGF-like and two follistatin-like domains 2			
-91.0	-	AI678013	240165_at	Transcribed locus			
-91.2	-	AI631210	226873_at	CDNA clone IMAGE:4794011			
-91.2	-	AF148949	232827_at	Clone L50 polyadenylated HERV LTR sequence and flanking cellular sequence, mRNA			
-93.8	-	AA176289	227496_at	Hypothetical protein LOC253842			
-93.9	-	AW593060	243657_at	Transcribed locus			
-93.9	-	T53175	238609_at	chromosome 7 open reading frame 38			
-94.2	-	AW206099	240171_at	Transcribed locus			
-94.6	-	AI274308	242773_at	Solute carrier family 5 (sodium/glucose cotransporter), member 1			
-95.3	-	H15073	236685_at	Transcribed locus			
-95.7	-	AW450381	237305_at	Transcribed locus			
-96.1	SEMA4B	AK026133	234725_s_at	Sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4B			
-97.8	-	AI349737	241675_s_at	Consensus includes gb:AI349737 /FEA=EST /DB_XREF=gi:4086943 /DB_XREF=est:ta96a12.x1 /CLONE=IMAGE:2051902 /UG=Hs.217834 ESTs			
-99.4	-	AW167424	236930_at	Numb homolog (Drosophila)			
-101.4	-	AU146893	229858_at	CDNA FLJ12024 fis, clone HEMBB1001797			
-103.9	-	BE463997	229062_at	ADP-ribosylation factor-like 9			
-107.0	-	H28597	227578_at	Hypothetical protein LOC100128191			
-108.7	-	AI283051	244383_at	CDNA clone IMAGE:5175565			
-109.8	-	AI417756	243364_at	Transcribed locus, strongly similar to NP_796021.2 autism susceptibility candidate 2 [Mus musculus]			
-110.4	-	AW663570	243389_at	Proline rich 4 (lacrima)			
-113.9	-	AW136975	240545_at	Transcribed locus			
-114.1	-	AA765470	236160_at	Transcribed locus			
-117.4	-	AI911084	236889_at	Transcribed locus			
-118.3	-	AA002211	239357_at	ATPase, Ca++ transporting, plasma membrane 2			
-119.1	-	BE673651	241890_at	Transcribed locus			
-120.3	-	AI280328	239721_at	Consensus includes gb:AI280328 /FEA=EST /DB_XREF=gi:3918561 /DB_XREF=est:qm68f10.x1 /CLONE=IMAGE:1893931 /UG=Hs.119275 ESTs			
-124.7	-	AA873729	243658_at	Consensus includes gb:AA873729 /FEA=EST /DB_XREF=gi:2969851 /DB_XREF=est:oh55h01.s1 /CLONE=IMAGE:1470577 /UG=Hs.269365 ESTs, Weakly similar to ALU8_HUMAN ALU SUBFAMILY SX SEQUENCE CONTAMINATION WARNING ENTRY H.sapiens			
-124.7	-	AW953794	230968_at	Transcribed locus			
-125.7	-	H72752	234117_at	Asthma-associated alternatively spliced gene 1			
-126.3	C20orf57	AK000652	234829_at	Chromosome 20 open reading frame 57			
-127.1	-	AI066520	231385_at	Developmental pluripotency associated 3			
-132.6	-	BE500990	237710_at	Transcribed locus			
-135.0	-	AI184197	237391_at	Transcribed locus			
-137.5	-	AI082692	242009_at	Solute carrier family 6 (neurotransmitter transporter, serotonin), member 4			
-143.8	-	AI745254	230348_at	Transcribed locus			
-144.2	-	AU144570	232576_at	CDNA FLJ11519 fis, clone HEMBA1002348			
-145.3	-	AL117627	233074_at	MRNA; cDNA DKFZp434B115 (from clone DKFZp434B115)			
-146.5	-	AW340891	242854_x_at	Deleted in lymphocytic leukemia 2 (non-protein coding)			
-149.2	-	BE139246	229979_x_at	Transcribed locus			
-149.9	-	AI954654	241748_x_at	DiGeorge syndrome critical region gene 14			
-160.0	-	AI872645	243938_x_at	Dynein, axonemal, heavy chain 5			
-162.0	TTC26	AL137393	233999_s_at	Tetratricopeptide repeat domain 26			
-164.5	-	AU146329	243819_at	Consensus includes gb:AU146329 /FEA=EST /DB_XREF=gi:11007850 /DB_XREF=est:AU146329 /CLONE=HEMBA1000166 /UG=Hs.187772 ESTs			
-167.1	-	AA522888	225085_at	Ubiquitin specific peptidase 40			
-167.6	-	AW612663	236568_at	Transcribed locus			
-170.2	-	AW298102	236014_at	Mohawk homeobox			
-171.6	-	AI820961	240331_at	Transcribed locus			
-173.4	-	BF064231	240670_at	Transcribed locus			
-175.9	-	BE274992	239704_at	Ring finger protein 144B			
-178.3	-	AW593244	226342_at	Spectrin, beta, non-erythrocytic 1			

Down-Regulated Transcripts (U133A 133B)

-178.7	PPHLN1	AK000186	234459_at	periphilin 1			
-184.9	-	AA461080	244689_at	peroxisome proliferator-activated receptor alpha			
-185.2	-	AI028267	231356_at	Similar to hCG2045213			
-187.7	HIF3A	AK021421	233517_s_at	Hypoxia inducible factor 3, alpha subunit			
-187.8	-	N78412	242899_at	CDNA FLJ33813 fis, clone CTONG2002744			
-188.0	-	AK000839	232979_at	CDNA FLJ20832 fis, clone ADKA03033			
-188.4	-	AL133399	234784_at	Human DNA sequence from clone RP1-305G21 on chromosome 11p13 Contains a pseudogene similar to S100C, STSs and GSSs			
-192.2	-	AI640307	228635_at	Protocadherin 10			
-193.1	-	AW340093	243921_at	Transcribed locus			
-196.9	-	BG252802	229641_at	Consensus includes gb:BG252802 /FEA=EST /DB_XREF=gi:12762618 /DB_XREF=est:602365370F1 /CLONE=IMAGE:4473737 /UG=Hs.49943 ESTs			
-202.0	MYEOV	AK026148	227343_at	Myeloma overexpressed (in a subset of t(11;14) positive multiple myelomas)			
-205.9	-	BE048571	228235_at	Non-steroidal anti-inflammatory drug activated gene 3 mRNA, partial sequence			
-208.0	-	AI379514	230828_at	Transcribed locus			
-209.0	-	AW084511	226622_at	Mucin 20, cell surface associated			
-217.3	-	BF511694	237471_at	Hypothetical LOC154822			
-218.8	-	AA809487	231042_s_at	Transcribed locus			
-221.4	-	BE825318	244347_at	Transcribed locus			
-223.9	-	BF513468	241505_at	Transcribed locus			
-234.8	IFI27L2	AF208232	223626_x_at	Interferon, alpha-inducible protein 27-like 2			
-241.1	-	AK026713	234663_at	CDNA: FLJ23060 fis, clone LNG04601			
-241.2	-	R36546	242198_at	Consensus includes gb:R36546 /FEA=EST /DB_XREF=gi:793447 /DB_XREF=est:yh89f11.s1 /CLONE=IMAGE:136941 /UG=Hs.25151 ESTs			
-243.0	-	BE674736	230702_at	Chromosome 8 open reading frame 16			
-243.1	-	AA833870	230808_at	Transcribed locus			
-257.6	-	AI807728	231315_at	NK2 homeobox 1			
-267.5	-	AW451103	237048_at	CDNA clone IMAGE:4797878			
-268.5	-	T90348	243348_at	Consensus includes gb:T90348 /FEA=EST /DB_XREF=gi:718861 /DB_XREF=est:yd43a05.s1 /CLONE=IMAGE:110960 /UG=Hs.183404 ESTs			
-300.7	-	AI922323	228969_at	Anterior gradient homolog 2 (Xenopus laevis)			
-316.1	-	AK000451	232897_at	hypothetical protein FLJ20444			
-325.0	-	AW268162	238384_x_at	Transcribed locus			
-332.8	-	AI141692	237501_at	CDNA FLJ37024 fis, clone BRACE2010837			
-337.5	KCNIP2	AB044584	224528_s_at	Kv channel interacting protein 2			
-347.3	ZCCHC2	BC006340	224503_s_at	Zinc finger, CCHC domain containing 2			
-349.7	-	AI475902	243514_at	Transcribed locus			
-352.0	-	AL137733	234664_at	Hypothetical protein LOC284701			
-358.8	-	BF060678	229520_s_at	Chromosome 14 open reading frame 118			
-366.7	-	AW615259	231143_at	Hypothetical protein LOC100129514			
-391.7	-	AI831653	227323_at	COX4 neighbor			
-440.5	-	AA700218	244456_at	Consensus includes gb:AA700218 /FEA=EST /DB_XREF=gi:2703181 /DB_XREF=est:zj44h04.s1 /CLONE=IMAGE:453175 /UG=Hs.189047 ESTs			
-446.6	-	AI694242	240045_at	Transcribed locus			
-473.3	ROR1	AK000776	232060_at	CDNA FLJ20769 fis, clone COL06674			
-476.6	-	AW904533	244584_at	Chromosome 11 open reading frame 41			
-481.2	IIFT57	AF139576	222520_s_at	Intraflagellar transport 57 homolog (Chlamydomonas)			
-497.5	-	AA765841	242156_at	Transcribed locus			
-498.3	-	AA778783	240248_at	Transcribed locus			
-510.7	LINC00589	BC003524	232718_at	chromosome 8 open reading frame 75			
-524.4	-	AW452079	231450_at	Transcribed locus			
-547.0	MTBP	AK022122	233211_at	Mdm2, transformed 3T3 cell double minute 2, p53 binding protein (mouse) binding protein, 104kDa			
-548.5	-	BE550855	244635_s_at	Hypothetical protein LOC100129436			
-559.9	-	AFFX-DapX-3	AFFX-DapX-3_at	Bacillus subtilis dihydropicolinate reductase (jojE) gene, complete cds; poly(A) polymerase (jojI) gene, complete cds; biotin acetyl-CoA-carboxylase ligase (birA) gene, complete cds; jojC, jojD, jojF, jojG, jojH genes, complete cds's.			
-570.5	-	AI073396	230856_at	Transcribed locus			
-573.1	-	AI914418	241206_at	Transcribed locus			
-594.2	-	T90358	229328_at	Zinc finger protein 540			
-620.7	ZNF462	AL359561	232393_at	Zinc finger protein 462			
-674.3	-	AW469569	236189_at	Ankyrin repeat domain 50			
-741.3	-	AI191905	242354_at	Transcribed locus			
-971.8	-	AA873726	237422_at	Transcribed locus			
-1424.5	-	AL139327	234473_at	hCG1646718			

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-1592.4	-	AW591969	240703_s_at	Transcribed locus			
-1692.0	-	BE855603	229320_at	Chromosome 2 open reading frame 55			
-1795.3	-	AI769817	240350_at	Transcribed locus			
-1923.1	-	AW736788	233822_x_at	Transcribed locus			
-2754.8	-	BF058422	226311_at	CDNA clone IMAGE:30924414			
-2754.8	-	AA278233	241370_at	hypothetical protein LOC286052			