

Supplemental table 3. List of differentially expressed genes identified by SAM analysis (5% FDR) for each separate CRS syndrome compared with NSS controls.

AS

Probe Set ID	Gene Symbol	Gene Title	Fold ch	Entrez Gene	Chromosomal Location
227510_x_at	PRO1073	PRO1073 protein	-7.69	29005	11cen-q12.3
224568_x_at	MALAT1	metastasis associated lung adenocarcinoma transcript 1 (non-protein coding)	-7.69	378938	11q13.1
209277_at	TFPI2	tissue factor pathway inhibitor 2	-7.14	7980	7q22
238320_at	TncRNA	trophoblast-derived noncoding RNA	-6.67	283131	11q13.1
228964_at	PRDM1	PR domain containing 1, with ZNF domain	-6.67	639	6q21-q22.1
223940_x_at	MALAT1	metastasis associated lung adenocarcinoma transcript 1 (non-protein coding)	-6.67	378938	11q13.1
229070_at	C6orf105	chromosome 6 open reading frame 105	-6.67	84830	6p24.1
219789_at	NPR3	natriuretic peptide receptor C/guanylate cyclase C (atrionatriuretic peptide receptor C)	-6.25	4883	5p14-p13
209278_s_at	TFPI2	tissue factor pathway inhibitor 2	-5.88	7980	7q22
208719_s_at	DDX17	DEAD (Asp-Glu-Ala-Asp) box polypeptide 17	-5.88	10521	22q13.1
227461_at	STON2	stonin 2	-5.56	85439	14q31.1
206172_at	IL13RA2	interleukin 13 receptor, alpha 2	-5.56	3598	Xq13.1-q28
230425_at	EPHB1	EPH receptor B1	-5.56	2047	3q21-q23
208798_x_at	GOLGA8A	golgi autoantigen, golgin subfamily a, 8A	-5.26	23015	15q11.2
214657_s_at	TncRNA	Trophoblast-derived noncoding RNA	-4.76	283131	11q13.1
223578_x_at	PRO1073	PRO1073 protein	-4.76	29005	11cen-q12.3
203888_at	THBD	thrombomodulin	-4.55	7056	20p11.2
205798_at	IL7R	interleukin 7 receptor	-4.55	3575	5p13
239331_at	FLJ43663	Transcribed locus	-4.55	---	---
227082_at	DKFZp586K1922	DKFZp586K1922	-4.55	---	---
227062_at	TncRNA	trophoblast-derived noncoding RNA	-4.35	283131	11q13.1
219054_at	C5orf23	chromosome 5 open reading frame 23	-4.35	79614	5p13.3
203887_s_at	THBD	thrombomodulin	-4.17	7056	20p11.2
238185_at	RBMS1	Transcribed locus	-4.17	---	---
226218_at	IL7R	interleukin 7 receptor	-4.17	3575	5p13
213107_at	TNIK	TRAF2 and NCK interacting kinase	-4	23043	3q26.2-q26.31
224566_at	TncRNA	trophoblast-derived noncoding RNA	-4	283131	11q13.1
209875_s_at	SPP1	secreted phosphoprotein 1 (osteopontin, bone sialoprotein I, early T-lymphocyte activation 1)	-4	6696	4q21-q25
238619_at	FLJ43663	FLJ26188	-4	---	---
232541_at	EGFR	FLJ20099	-4	---	---
208151_x_at	DDX17	DEAD (Asp-Glu-Ala-Asp) box polypeptide 17	-4	10521	22q13.1
1555938_x_at	VIM	vimentin	-3.85	7431	10p13
1556641_at	FLJ37228	hypothetical protein FLJ37228	-3.85	285264	3q26.2
222895_s_at	BCL11B	B-cell CLL/lymphoma 11B (zinc finger protein)	-3.85	64919	14q32.2
242110_at	ARHGAP5	Transcribed locus	-3.85	---	---
218340_s_at	UBA6	ubiquitin-like modifier activating enzyme 6	-3.7	55236	4q13.2
203908_at	SLC4A4	solute carrier family 4, sodium bicarbonate cotransporter, member 4	-3.7	8671	4q21
215206_at	EXT1	FLJ21490	-3.7	---	---
219528_s_at	BCL11B	B-cell CLL/lymphoma 11B (zinc finger protein)	-3.7	64919	14q32.2
223395_at	ABI3BP	ABI gene family, member 3 (NESH) binding protein	-3.7	25890	3q12
228582_x_at	---	Transcribed locus, moderately similar to XP_001103824.1 PREDICTED: similar to 60S ribosomal protein L39 [Macaca mulatta]	-3.7	---	---
232138_at	MBNL2	Muscleblind-like 2 (Drosophila)	-3.57	10150	13q32.1

228030_at	---	Transcribed locus, strongly similar to NP_005768.1 RNA binding motif protein 6	-3.57	---	---
235046_at	---	Transcribed locus	-3.57	---	---
234989_at	TncRNA	trophoblast-derived noncoding RNA	-3.45	283131	11q13.1
232748_at	PAPPA	pregnancy-associated plasma protein A, pappalysin 1	-3.45	5069	9q33.2
229437_at	MIRN155, BIC	microRNA 155	-3.45	114614	21q21.3
1558678_s_at	MALAT1	metastasis associated lung adenocarcinoma transcript 1 (non-protein coding)	-3.45	378938	11q13.1
224567_x_at	MALAT1	metastasis associated lung adenocarcinoma transcript 1 (non-protein coding)	-3.45	378938	11q13.1
226675_s_at	MALAT1	metastasis associated lung adenocarcinoma transcript 1 (non-protein coding)	-3.45	378938	11q13.1
228250_at	FNIP1	folliculin interacting protein 1	-3.45	96459	5q23.3
235009_at	FAM44A	family with sequence similarity 44, member A	-3.45	259282	4p16.1
204363_at	F3	coagulation factor III (thromboplastin, tissue factor)	-3.45	2152	1p22-p21
211478_s_at	DPP4	dipeptidyl-peptidase 4 (CD26, adenosine deaminase complexing protein 2)	-3.45	1803	2q24.3
242476_at	---	Transcribed locus	-3.45	---	---
240395_at	---	FLJ42406	-3.45	---	---
230130_at	SLIT2	Transcribed locus	-3.33	---	---
238317_x_at	RBMS1	---	-3.33	---	---
231735_s_at	PRO1073	PRO1073 protein	-3.33	29005	11cen-q12.3
243683_at	MORF4L2	Mortality factor 4 like 2	-3.33	9643	Xq22
235567_at	LOC283666	Hypothetical protein LOC283666	-3.33	283666	15q21.3
211958_at	IGFBP5	insulin-like growth factor binding protein 5	-3.33	3488	2q33-q36
213359_at	HNRPD	Heterogeneous nuclear ribonucleoprotein D (AU-rich element RNA binding protein 1, 37kDa)	-3.33	3184	4q21.1-q21.2
244026_at	ELL2	Transcribed locus	-3.33	---	---
1561123_at	PRRX1	Full length insert cDNA clone ZD75H02	-3.23	---	---
233286_at	PDZRN3	FLJ12196	-3.23	---	---
205828_at	MMP3	matrix metalloproteinase 3 (stromelysin 1, progelatinase)	-3.23	4314	11q22.3
227314_at	ITGA2	integrin, alpha 2 (CD49B, alpha 2 subunit of VLA-2 receptor)	-3.23	3673	5q23-q31
204863_s_at	IL6ST	interleukin 6 signal transducer (gp130, oncostatin M receptor)	-3.23	3572	5q11
213865_at	DCBLD2	discoidin, CUB and LCCL domain containing 2	-3.23	131566	3q12.1 3
242693_at	CDC2L5	Transcribed locus	-3.23	---	---
237252_at	THBD	thrombomodulin	-3.12	7056	20p11.2
212240_s_at	PIK3R1	phosphoinositide-3-kinase, regulatory subunit 1 (p85 alpha)	-3.12	5295	5q13.1
203434_s_at	MME	membrane metallo-endopeptidase	-3.12	4311	3q25.1-q25.2
203435_s_at	MME	membrane metallo-endopeptidase	-3.12	4311	3q25.1-q25.2
224559_at	MALAT1	metastasis associated lung adenocarcinoma transcript 1 (non-protein coding)	-3.12	378938	11q13.1
211000_s_at	IL6ST	interleukin 6 signal transducer (gp130, oncostatin M receptor)	-3.12	3572	5q11
225107_at	HNRNPA2B1	heterogeneous nuclear ribonucleoprotein A2/B1	-3.12	3181	7p15
220085_at	HELLS	helicase, lymphoid-specific	-3.12	3070	10q24.2
223730_at	GPC6	glypican 6	-3.12	10082	13q32
229800_at	DCLK1	Doublecortin-like kinase 1	-3.12	9201	13q13
226810_at	C6orf155	MRNA full length insert cDNA clone EUROIMAGE 1509279	-3.12	---	---
226663_at	ANKRD10	ankyrin repeat domain 10	-3.12	55608	13q34
225750_at	---	FLJ14162	-3.12	---	---
244433_at	---	---	-3.12	---	---
228157_at	ZNF207	zinc finger protein 207	-3.03	7756	17q11.2
230560_at	STXBP6	syntaxin binding protein 6 (amisyn)	-3.03	29091	14q12
243768_at	SENP6	Transcribed locus	-3.03	---	---
202600_s_at	NRIP1	nuclear receptor interacting protein 1	-3.03	8204	21q11.2
242059_at	ETNK1	Transcribed locus	-3.03	---	---
230180_at	DDX17	DEAD (Asp-Glu-Ala-Asp) box polypeptide 17	-3.03	10521	22q13.1
205830_at	CLGN	calmegin	-3.03	1047	4q28.3-q31.1
230319_at	C4orf31	Chromosome 4 open reading frame 31	-3.03	79625	4q27
231205_at	---	---	-3.03	---	---

1556035_s_at	ZNF207	zinc finger protein 207	-2.94	7756	17q11.2
229765_at	ZNF207	zinc finger protein 207	-2.94	7756	17q11.2
224565_at	TncRNA	trophoblast-derived noncoding RNA	-2.94	283131	11q13.1
207334_s_at	TGFB2	transforming growth factor, beta receptor II (70/80kDa)	-2.94	7048	3p22
203096_s_at	RAPGEF2	Rap guanine nucleotide exchange factor (GEF) 2	-2.94	9693	4q32.1
240450_at	PAPPA	Transcribed locus	-2.94	---	---
223533_at	LRRC8C	leucine rich repeat containing 8 family, member C	-2.94	84230	1p22.2
203716_s_at	DPP4	dipeptidyl-peptidase 4 (CD26, adenosine deaminase complexing protein 2)	-2.94	1803	2q24.3
243514_at	---	Transcribed locus	-2.94	---	---
235138_at	VPS35	Transcribed locus	-2.86	---	---
226864_at	PKIA	Protein kinase (cAMP-dependent, catalytic) inhibitor alpha	-2.86	5569	8q21.12
243993_at	PCTK2	---	-2.86	---	---
243296_at	PBEF1	Pre-B-cell colony enhancing factor 1	-2.86	10135	7q22.2
228399_at	OSR1	odd-skipped related 1 (Drosophila)	-2.86	130497	2p24.1
1558111_at	MBNL1	muscleblind-like (Drosophila)	-2.86	4154	3q25
244341_at	MAK3	Transcribed locus	-2.86	---	---
202156_s_at	CUGBP2	CUG triplet repeat, RNA binding protein 2	-2.86	10659	10p13
235333_at	B4GALT6	UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, polypeptide 6	-2.86	9331	18q11
203788_s_at	SEMA3C	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3C	-2.78	10512	7q21-q31
1555878_at	RPS24	Ribosomal protein S24	-2.78	6229	10q22-q23
223577_x_at	PRO1073	PRO1073 protein	-2.78	29005	11cen-q12.3
214375_at	PPFIBP1	PTPRF interacting protein, binding protein 1 (liprin beta 1)	-2.78	729222	12p11.23
220940_at	KIAA1641	KIAA1641	-2.78	57730	2q11.2
239835_at	KBTBD8	kelch repeat and BTB (POZ) domain containing 8	-2.78	84541	3p14
242126_at	EXT1	Transcribed locus	-2.78	---	---
218498_s_at	ERO1L	ERO1-like (<i>S. cerevisiae</i>)	-2.78	30001	14q22.1
240038_at	ELL2	Transcribed locus	-2.78	---	---
1570351_at	ADAMTS6	ADAM metalloproteinase with thrombospondin type 1 motif, 6	-2.78	11174	5q12
213805_at	ABHD5	abhydrolase domain containing 5	-2.78	51099	3p21
202566_s_at	SVIL	supervillin	-2.7	6840	10p11.2
230494_at	SLC20A1	Solute carrier family 20 (phosphate transporter), member 1	-2.7	6574	2q11-q14
221768_at	SFPQ	Splicing factor proline/glutamine-rich (polypyrimidine tract binding protein associated)	-2.7	6421	1p34.3
213459_at	RPL37A	ribosomal protein L37a	-2.7	6168	2q35
232431_at	NR3C1	Glucocorticoid receptor alpha mRNA, variant 3' UTR	-2.7	---	---
1558028_x_at	LOC647979	hypothetical protein LOC647979	-2.7	647979	---
204864_s_at	IL6ST	interleukin 6 signal transducer (gp130, oncostatin M receptor)	-2.7	3572	5q11
242320_at	FOXO3A	IMAGE:4769230, mRNA	-2.7	---	---
203717_at	DPP4	dipeptidyl-peptidase 4 (CD26, adenosine deaminase complexing protein 2)	-2.7	1803	2q24.3
202158_s_at	CUGBP2	CUG triplet repeat, RNA binding protein 2	-2.7	10659	10p13
242467_at	CSNK1A1	Transcribed locus	-2.7	---	---
1552717_s_at	CEP170	centrosomal protein 170kDa	-2.7	645455	1q44
204508_s_at	CA12	carbonic anhydrase XII	-2.7	771	15q22
227260_at	ANKRD10	Ankyrin repeat domain 10	-2.7	55608	13q34
222816_s_at	ZCCHC2	zinc finger, CCHC domain containing 2	-2.63	54877	18q21.33
210807_s_at	SLC16A7	solute carrier family 16, member 7 (monocarboxylic acid transporter 2)	-2.63	9194	12q13
243963_at	SDCCAG8	Serologically defined colon cancer antigen 8	-2.63	10806	1q43-q44
241897_at	RBPMS	---	-2.63	---	---
222846_at	RAB8B	RAB8B, member RAS oncogene family	-2.63	51762	15q22.2
1552670_a_at	PPP1R3B	protein phosphatase 1, regulatory (inhibitor) subunit 3B	-2.63	79660	8p23.1
204612_at	PKIA	protein kinase (cAMP-dependent, catalytic) inhibitor alpha	-2.63	5569	8q21.12
239227_at	EXT1	---	-2.63	---	---
230229_at	DLG1	Discs, large homolog 1 (Drosophila)	-2.63	1739	3q29

213998_s_at	DDX17	DEAD (Asp-Glu-Ala-Asp) box polypeptide 17	-2.63	10521	22q13.1
224829_at	CPEB4	cytoplasmic polyadenylation element binding protein 4	-2.63	80315	5q21
229831_at	CNTN3	contactin 3 (plasmacytoma associated)	-2.63	5067	3p26
217523_at	CD44	CD44 molecule (Indian blood group)	-2.63	960	11p13
238563_at	ABI1	Transcribed locus	-2.63	---	---
235927_at	---	---	-2.63	---	---
206108_s_at	SFRS6	splicing factor, arginine/serine-rich 6	-2.56	6431	20q12-q13.1
204326_x_at	MT1X	metallothionein 1X	-2.56	4501	16q13
212859_x_at	MT1E	metallothionein 1E	-2.56	4493	16q13
233219_at	MKLN1	FLJ13365	-2.56	---	---
226210_s_at	MEG3	maternally expressed 3	-2.56	55384	14q32
212196_at	IL6ST	Interleukin 6 signal transducer (gp130, oncostatin M receptor)	-2.56	3572	5q11
235060_at	DKFZp547E087	hypothetical gene LOC283846	-2.56	283846	18p11.21
227259_at	CD47	CD47 molecule	-2.56	961	3q13.1-q13.2
213158_at	---	IMAGE:4214654, mRNA	-2.56	---	---
212758_s_at	ZEB1	zinc finger E-box binding homeobox 1	-2.5	6935	10p11.2
232528_at	UBE2E3	FLJ11226	-2.5	---	---
238883_at	THRAP2	Transcribed locus	-2.5	---	---
228483_s_at	TAF9B	TAF9B RNA polymerase II, TATA box binding protein (TBP)-associated factor, 31kDa	-2.5	51616	Xq13.1-q21.1
1556416_s_at	SEC31L1	Full length insert cDNA clone ZD37D10	-2.5	---	---
207177_at	PTGFR	prostaglandin F receptor (FP)	-2.5	5737	1p31.1
236752_at	PKP4	Transcribed locus	-2.5	---	---
239597_at	PAN3	---	-2.5	---	---
212214_at	OPA1	optic atrophy 1 (autosomal dominant)	-2.5	4976	3q28-q29 3q28-q29
208368_s_at	BRC A2	breast cancer 2, early onset	-2.5	675	13q12.3
212286_at	ANKRD12	ankyrin repeat domain 12	-2.5	23253	18p11.22
214895_s_at	ADAM10	ADAM metalloproteinase domain 10	-2.5	102	15q2 15q22
242853_at	---	Transcribed locus	-2.5	---	---
234036_x_at	---	FLJ21384	-2.5	---	---
229858_at	---	FLJ12024	-2.5	---	---
222600_s_at	UBA6	ubiquitin-like modifier activating enzyme 6	-2.44	55236	4q13.2
226625_at	TGFBR3	Transforming growth factor, beta receptor III	-2.44	7049	1p33-p32
203789_s_at	SEMA3C	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3C	-2.44	10512	7q21-q31
1556049_at	RTN4	reticulon 4	-2.44	57142	2p16.3
1560271_at	PTBP2	CDNA clone IMAGE:4797534	-2.44	---	---
213517_at	PCBP2	poly(rC) binding protein 2	-2.44	5094	12q13.12-q13.13
235067_at	MKLN1	muskelin 1, intracellular mediator containing kelch motifs	-2.44	4289	7q32
226211_at	MEG3	maternally expressed 3	-2.44	55384	14q32
1556425_a_at	LOC284219	hypothetical protein LOC284219	-2.44	284219	18p11.22
214453_s_at	IFI44	interferon-induced protein 44	-2.44	10561	1p31.1
1552921_a_at	FIGNL1	figetin-like 1	-2.44	63979	7p12.2
210839_s_at	ENPP2	ectonucleotide pyrophosphatase/phosphodiesterase 2 (autotaxin)	-2.44	5168	8q24.1
235592_at	ELL2	FLJ36210	-2.44	---	---
225656_at	EFHC1	EF-hand domain (C-terminal) containing 1	-2.44	114327	6p12.3
205046_at	CENPE	centromere protein E, 312kDa	-2.44	1062	4q24-q25
211814_s_at	CCNE2	cyclin E2	-2.44	9134	8q22.1
230127_at	---	Transcribed locus	-2.44	---	---
215287_at	---	ELISC-1	-2.44	---	---
218149_s_at	ZNF395	zinc finger protein 395	-2.38	55893	8p21.1
201295_s_at	WSB1	---	-2.38	---	---
209897_s_at	SLIT2	slit homolog 2 (Drosophila)	-2.38	9353	4p15.2
218000_s_at	PHLDA1	pleckstrin homology-like domain, family A, member 1	-2.38	22822	12q15

236907_at	PABPC1	FLJ25706	-2.38	---	---
225752_at	NIPA1	non imprinted in Prader-Willi/Angelman syndrome 1	-2.38	123606	15q11.2
223494_at	MGEA5	meningioma expressed antigen 5 (hyaluronidase)	-2.38	10724	10q24.1-q24.3
241681_at	MBNL1	Transcribed locus	-2.38	---	---
232356_at	KIAA0143	FLJ13539	-2.38	---	---
208814_at	HSPA4	Heat shock 70kDa protein 4	-2.38	3308	5q31.1-q31.2
207387_s_at	GK	glycerol kinase	-2.38	2710	Xp21.3
242665_at	FMNL2	formin-like 2	-2.38	114793	2q23.3
224999_at	EGFR	Placenta mRNA, clone PL45, partial sequence	-2.38	---	---
237290_at	DDAH1	Transcribed locus	-2.38	---	---
201487_at	CTSC	cathepsin C	-2.38	1075	11q14.1-q14.3
212746_s_at	CEP170	centrosomal protein 170kDa	-2.38	9859	1q44
239413_at	CEP152	centrosomal protein 152kDa	-2.38	22995	15q21.1
235244_at	CCDC58	coiled-coil domain containing 58	-2.38	131076	3q21.1
215867_x_at	CA12	carbonic anhydrase XII	-2.38	771	15q22
1558105_a_at	---	Homo sapiens, Similar to LOC169932, clone IMAGE:4499203, mRNA	-2.38	---	---
229824_at	---	FLJ45325	-2.38	---	---
210875_s_at	ZEB1	zinc finger E-box binding homeobox 1	-2.33	6935	10p11.2
231899_at	ZC3H12C	zinc finger CCCH-type containing 12C	-2.33	85463	11q22.3
233595_at	USP34	ubiquitin specific peptidase 34	-2.33	9736	2p15
235652_at	SCML1	CDNA FLJ37623 fis, clone BRCOC2014013	-2.33	---	---
226310_at	RICTOR	rapamycin-insensitive companion of mTOR	-2.33	253260	5p13.1
225946_at	RASSF8	Ras association (RalGDS/AF-6) domain family 8	-2.33	11228	12p12.3
241970_at	PVRL3	Transcribed locus	-2.33	---	---
212629_s_at	PKN2	protein kinase N2	-2.33	5586	1p22.2
212582_at	OSBPL8	oxysterol binding protein-like 8	-2.33	114882	12q14
1567224_at	HMGA2	high mobility group AT-hook 2	-2.33	8091	12q15
226568_at	FAM102B	family with sequence similarity 102, member B	-2.33	284611	1p13.3
237310_at	EXT1	Transcribed locus	-2.33	---	---
240593_x_at	CAMK2D	Transcribed locus	-2.33	---	---
233112_at	C9orf150	CDNA FLJ10263 fis, clone HEMBB1000991	-2.33	---	---
209006_s_at	C1orf63	chromosome 1 open reading frame 63	-2.33	57035	1p36.13-p35.1
244033_at	C14orf145	chromosome 14 open reading frame 145	-2.33	145508	14q31.1
1555326_a_at	ADAM9	ADAM metallopeptidase domain 9 (meltrin gamma)	-2.33	8754	8p11.23
202604_x_at	ADAM10	ADAM metallopeptidase domain 10	-2.33	102	15q21 15q22
202342_s_at	TRIM2	tripartite motif-containing 2	-2.27	23321	4q31.3
236545_at	PPP3CA	Transcribed locus	-2.27	---	---
204887_s_at	PLK4	polo-like kinase 4 (Drosophila)	-2.27	10733	4q28
241425_at	NUPL1	Nucleoporin like 1	-2.27	9818	13q12.13
213328_at	NEK1	NIMA (never in mitosis gene a)-related kinase 1	-2.27	4750	4q33
226520_at	MLR2	Primary neuroblastoma cDNA, clone:Nbla11485	-2.27	---	---
212188_at	KCTD12	potassium channel tetramerisation domain containing 12	-2.27	115207	13q22.3
206864_s_at	HRK	harakiri, BCL2 interacting protein (contains only BH3 domain)	-2.27	8739	12q24.22
208025_s_at	HMGA2	high mobility group AT-hook 2	-2.27	8091	12q15
213895_at	EMP1	epithelial membrane protein 1	-2.27	2012	12p12.3
219469_at	DYNC2H1	dynein, cytoplasmic 2, heavy chain 1	-2.27	79659	11q21-q22.1
212253_x_at	DST	dystonin	-2.27	667	6p12.1
210735_s_at	CA12	carbonic anhydrase XII	-2.27	771	15q22
210896_s_at	ASPH	aspartate beta-hydroxylase	-2.27	444	8q12.1
230099_at	---	Transcribed locus	-2.27	---	---
235716_at	---	Transcribed locus	-2.27	---	---
228850_s_at	---	---	-2.27	---	---

242343_x_at	ZNF518	---	-2.22	---	---
216228_s_at	WDHD1	WD repeat and HMG-box DNA binding protein 1	-2.22	11169	14q22.3
234994_at	TMEM200A	transmembrane protein 200A	-2.22	114801	6q23.1
227891_s_at	TAF15	TAF15 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 68kDa	-2.22	8148	17q11.1-q11.2
204240_s_at	SMC2	structural maintenance of chromosomes 2	-2.22	10592	9q31.1
213649_at	SFRS7	splicing factor, arginine/serine-rich 7, 35kDa	-2.22	6432	2p22.1
227533_at	RALGPS2	Transcribed locus	-2.22	---	---
238706_at	PAPD4	PAP associated domain containing 4	-2.22	167153	5q14.1
236472_at	OSBPL9	Transcribed locus	-2.22	---	---
212585_at	OSBPL8	oxysterol binding protein-like 8	-2.22	114882	12q14
202599_s_at	NRIP1	nuclear receptor interacting protein 1	-2.22	8204	21q11.2
210756_s_at	NOTCH2	Notch homolog 2 (Drosophila)	-2.22	4853	1p13-p11
243857_at	MORF4L2	Mortality factor 4 like 2	-2.22	9643	Xq22
215177_s_at	ITGA6	integrin, alpha 6	-2.22	3655	2q31.1
224840_at	FKBP5	FK506 binding protein 5	-2.22	2289	6p21.3-p21.2
241457_at	FBXL7	Transcribed locus	-2.22	---	---
232264_at	EDD1	CDNA FLJ12142 fis, clone MAMMA1000356	-2.22	---	---
235236_at	DOCK2	FLJ31436	-2.22	---	---
235341_at	DNAJC3	DnaJ (Hsp40) homolog, subfamily C, member 3	-2.22	5611	13q32
214164_x_at	CA12	carbonic anhydrase XII	-2.22	771	15q22
226630_at	C14orf106	chromosome 14 open reading frame 106	-2.22	55320	14q21.3
229694_at	BRWD2	bromodomain and WD repeat domain containing 2	-2.22	55717	10q26
235028_at	---	FLJ42313	-2.22	---	---
231862_at	---	CDNA clone IMAGE:4842353	-2.22	---	---
227501_at	WSB1	Transcribed locus	-2.17	---	---
202316_x_at	UBE4B	ubiquitination factor E4B (UFD2 homolog, yeast)	-2.17	10277	1p36.3
208944_at	TGFR2	transforming growth factor, beta receptor II (70/80kDa)	-2.17	7048	3p22
228370_at	SNRPN	Small nuclear ribonucleoprotein polypeptide N	-2.17	6638	15q11.2
206376_at	SLC6A15	solute carrier family 6, member 15	-2.17	55117	12q21.3
241786_at	PPP3R1	Transcribed locus	-2.17	---	---
214753_at	PFAAP5	Phosphonoformate immuno-associated protein 5	-2.17	10443	13q13.1
242865_at	NPTN	---	-2.17	---	---
208003_s_at	NFAT5	nuclear factor of activated T-cells 5, tonicity-responsive	-2.17	10725	16q22.1
205018_s_at	MBNL2	muscleblind-like 2 (Drosophila)	-2.17	10150	13q32.1
1557987_at	LOC653786	otoancorin pseudogene	-2.17	653786	16p12.1
211930_at	HNRPA3	heterogeneous nuclear ribonucleoprotein A3	-2.17	220988	2q31.2
226184_at	FMNL2	formin-like 2	-2.17	114793	2q23.3
226432_at	ETNK1	ethanolamine kinase 1	-2.17	55500	12p12.1
220386_s_at	EML4	echinoderm microtubule associated protein like 4	-2.17	27436	2p22-p21
220342_x_at	EDEM3	ER degradation enhancer, mannosidase alpha-like 3	-2.17	80267	1q24-q25
228033_at	E2F7	E2F transcription factor 7	-2.17	144455	12q21.2
232898_at	DAB2	disabled homolog 2, mitogen-responsive phosphoprotein (Drosophila)	-2.17	1601	5p13
206488_s_at	CD36	CD36 molecule (thrombospondin receptor)	-2.17	948	7q11.2
203963_at	CA12	carbonic anhydrase XII	-2.17	771	15q22
205808_at	ASPH	aspartate beta-hydroxylase	-2.17	444	8q12.1
216266_s_at	ARFGEF1	ADP-ribosylation factor guanine nucleotide-exchange factor 1(brefeldin A-inhibited)	-2.17	10565	8q13
228314_at	---	FLJ37485	-2.17	---	---
224549_x_at	---	---	-2.17	---	---
212368_at	ZNF292	zinc finger protein 292	-2.13	23036	6q15
1558733_at	ZBTB38	zinc finger and BTB domain containing 38	-2.13	253461	3q23
240383_at	UBE2D3	ubiquitin-conjugating enzyme E2D 3 (UBC4/5 homolog, yeast)	-2.13	7323	4q24
201645_at	TNC	tenascin C (hexabrachion)	-2.13	3371	9q33

212994_at	THOC2	THO complex 2	-2.13	57187	Xq25-q26.3
204731_at	TGFBR3	transforming growth factor, beta receptor III	-2.13	7049	1p33-p32
233300_at	TAS2R14	CDNA FLJ11548 fis, clone HEMBA1002944	-2.13	---	---
222088_s_at	SLC2A3	solute carrier family 2 (facilitated glucose transporter), member 3	-2.13	6515	12p13.3
207057_at	SLC16A7	solute carrier family 16, member 7 (monocarboxylic acid transporter 2)	-2.13	9194	12q13
202127_at	PRPF4B	PRP4 pre-mRNA processing factor 4 homolog B (yeast)	-2.13	8899	6p25.2
208995_s_at	PPIG	peptidylprolyl isomerase G (cyclophilin G)	-2.13	9360	2q31.1
205729_at	OSMR	oncostatin M receptor	-2.13	9180	5p13.1
207108_s_at	NIPBL	Nipped-B homolog (Drosophila)	-2.13	25836	5p13.2
235879_at	MBNL1	Muscleblind-like (Drosophila)	-2.13	4154	3q25
242471_at	LOC647135	Clone HLS_IMAGE_238756 mRNA sequence	-2.13	---	---
226561_at	LOC285086	hypothetical protein LOC285086	-2.13	285086	2q36.3
231866_at	LNPEP	leucyl/cystinyl aminopeptidase	-2.13	4012	5q15
232935_at	LHFP	Primary neuroblastoma cDNA, clone:Nbla03614, full insert sequence	-2.13	---	---
203285_s_at	HS2ST1	heparan sulfate 2-O-sulfotransferase 1	-2.13	9653	1p31.1-p22.1
214093_s_at	FUBP1	far upstream element (FUSE) binding protein 1	-2.13	8880	1p31.1
231576_at	ETNK1	Transcribed locus	-2.13	---	---
206710_s_at	EPB41L3	erythrocyte membrane protein band 4.1-like 3	-2.13	23136	18p11.32
224911_s_at	DCBLD2	discoidin, CUB and LCCL domain containing 2	-2.13	131566	3q12.1 3
202157_s_at	CUGBP2	CUG triplet repeat, RNA binding protein 2	-2.13	10659	10p13
239629_at	FLAR	CASP8 and FADD-like apoptosis regulator	-2.13	8837	2q33-q34
208859_s_at	ATRX	alpha thalassemia/mental retardation syndrome X-linked (RAD54 homolog, S. cerevisiae)	-2.13	546	Xq13.1-q21.1
224797_at	ARRDC3	arrestin domain containing 3	-2.13	57561	5q14.3
203526_s_at	APC	adenomatous polyposis coli	-2.13	324	5q21-q22
212289_at	ANKRD12	ankyrin repeat domain 12	-2.13	23253	18p11.22
229334_at	---	Transcribed locus	-2.13	---	---
230003_at	---	Transcribed locus	-2.13	---	---
233506_at	---	Full length insert cDNA clone ZB81B12	-2.13	---	---
218396_at	VPS13C	vacuolar protein sorting 13 homolog C (S. cerevisiae)	-2.08	54832	15q22.2
226035_at	USP31	ubiquitin specific peptidase 31	-2.08	57478	16p12.1
227256_at	USP31	ubiquitin specific peptidase 31	-2.08	57478	16p12.1
242673_at	UBE3C	Transcribed locus	-2.08	---	---
201730_s_at	TPR	translocated promoter region (to activated MET oncogene)	-2.08	7175	1q25
214600_at	TEAD1	TEA domain family member 1 (SV40 transcriptional enhancer factor)	-2.08	7003	11p15.2
227454_at	TAOK1	TAO kinase 1	-2.08	57551	17q11.2
230165_at	SGOL2	shugoshin-like 2 (S. pombe)	-2.08	151246	2q33.1
227224_at	RALGPS2	Ral GEF with PH domain and SH3 binding motif 2	-2.08	55103	1q25.2
235484_at	PTAR1	protein prenyltransferase alpha subunit repeat containing 1	-2.08	375743	9q21.11
230270_at	PRPF38B	PRP38 pre-mRNA processing factor 38 (yeast) domain containing B	-2.08	55119	1p13.3
222719_s_at	PDGFC	platelet derived growth factor C	-2.08	56034	4q32
212298_at	NRP1	neuropilin 1	-2.08	8829	10p12
204475_at	MMP1	matrix metalloproteinase 1 (interstitial collagenase)	-2.08	4312	11q22.3
244414_at	MAML2	mastermind-like 2	-2.08	84441	11q21
233518_at	LSP1	CDNA FLJ11493 fis, clone HEMBA1001940	-2.08	---	---
225176_at	LNPEP	CDNA FLJ42149 fis, clone THYMU1000692	-2.08	---	---
242366_at	KIAA0701	Homo sapiens, clone IMAGE:3858719, mRNA	-2.08	---	---
210261_at	KCNK2	potassium channel, subfamily K, member 2	-2.08	3776	1q41
225115_at	HIPK2	homeodomain interacting protein kinase 2	-2.08	28996	7q32-q34
225116_at	HIPK2	homeodomain interacting protein kinase 2	-2.08	28996	7q32-q34
227350_at	HELLS	CDNA FLJ11381 fis, clone HEMBA1000501	-2.08	---	---
242890_at	HELLS	CDNA FLJ34225 fis, clone FCBBF3023372	-2.08	---	---
227059_at	GPC6	Glypican 6	-2.08	10082	13q32

1555996_s_at	EIF4A2	eukaryotic translation initiation factor 4A, isoform 2	-2.08	1974	3q28
213295_at	CYLD	cyldromatosis (turban tumor syndrome)	-2.08	1540	16q12.1
1556007_s_at	CSNK1A1	Casein kinase 1, alpha 1	-2.08	1452	5q32
201732_s_at	CLCN3	chloride channel 3	-2.08	1182	4q33
207719_x_at	CEP170	centrosomal protein 170kDa	-2.08	9859	1q44
225919_s_at	C9orf72	chromosome 9 open reading frame 72	-2.08	203228	9p21.2
217936_at	ARHGAP5	Rho GTPase activating protein 5	-2.08	394	14q12
210962_s_at	AKAP9	A kinase (PRKA) anchor protein (yotiao) 9	-2.08	10142	7q21-q22
243249_at	ACIN1	Transcribed locus	-2.08	---	---
226550_at	---	Homo sapiens, Similar to LOC169932, clone IMAGE:4499203, mRNA	-2.08	---	---
241906_at	ZNF708	---	-2.04	---	---
219062_s_at	ZCCHC2	zinc finger, CCHC domain containing 2	-2.04	54877	18q21.33
219221_at	ZBTB38	zinc finger and BTB domain containing 38	-2.04	253461	3q23
205383_s_at	ZBTB20	zinc finger and BTB domain containing 20	-2.04	26137	3q13.2
223324_s_at	TRPM7	transient receptor potential cation channel, subfamily M, member 7	-2.04	54822	15q21
209257_s_at	SMC3	structural maintenance of chromosomes 3	-2.04	9126	10q25
202498_s_at	SLC2A3	solute carrier family 2 (facilitated glucose transporter), member 3	-2.04	6515	12p13.3
227176_at	SLC2A13	solute carrier family 2 (facilitated glucose transporter), member 13	-2.04	114134	12q12
209681_at	SLC19A2	solute carrier family 19 (thiamine transporter), member 2	-2.04	10560	1q23.3
218273_s_at	PPM2C	protein phosphatase 2C, magnesium-dependent, catalytic subunit	-2.04	54704	8q22.1
232615_at	PDE4DIP	CDNA: FLJ22765 fis, clone KAIA1180	-2.04	---	---
209750_at	NR1D2	nuclear receptor subfamily 1, group D, member 2	-2.04	9975	3p24.2
225997_at	MOBK1A	MOB1, Mps One Binder kinase activator-like 1A (yeast)	-2.04	92597	4q13.3
224558_s_at	MALAT1	metastasis associated lung adenocarcinoma transcript 1 (non-protein coding)	-2.04	378938	11q13.1
225575_at	LIFR	leukemia inhibitory factor receptor alpha	-2.04	3977	5p13-p12
212779_at	KIAA1109	KIAA1109	-2.04	84162	4q27
211959_at	IGFBP5	insulin-like growth factor binding protein 5	-2.04	3488	2q33-q36
220794_at	GREM2	gremlin 2, cysteine knot superfamily, homolog (Xenopus laevis)	-2.04	64388	1q43
215203_at	GOLGA4	golgi autoantigen, golgin subfamily a, 4	-2.04	2803	3p22-p21.3
213212_x_at	FLJ40113	hypothetical protein LOC161527	-2.04	161527	15q25.2
225290_at	ETNK1	ethanolamine kinase 1	-2.04	55500	12p12.1
239719_at	CD109	CD109 molecule	-2.04	135228	6q13
226713_at	CCDC50	coiled-coil domain containing 50	-2.04	152137	3q28
228323_at	CASC5	cancer susceptibility candidate 5	-2.04	57082	15q14
231793_s_at	CAMK2D	calcium/calmodulin-dependent protein kinase (CaM kinase) II delta	-2.04	817	4q26
228728_at	C7orf58	chromosome 7 open reading frame 58	-2.04	79974	7q31.31
239151_at	BMS1P5	BMS1 pseudogene 5	-2.04	399761	10q11.22
241986_at	BMPER	BMP binding endothelial regulator	-2.04	168667	7p14.3
208703_s_at	APLP2	amyloid beta (A4) precursor-like protein 2	-2.04	334	11q23-q25 11q24
229307_at	ANKRD28	ankyrin repeat domain 28	-2.04	23243	3p24.3
234997_x_at	---	CDNA clone IMAGE:4794941	-2.04	---	---
206874_s_at	---	---	-2.04	---	---
221727_at	---	---	-2.04	---	---
227620_at	---	---	-2.04	---	---
201294_s_at	WSB1	WD repeat and SOCS box-containing 1	-2	26118	17q11.1
212577_at	SMCHD1	structural maintenance of chromosomes flexible hinge domain containing 1	-2	23347	18p11.32
222837_s_at	NARG1	NMDA receptor regulated 1	-2	80155	4q31.1
225160_x_at	MGC5370	hypothetical protein MGC5370	-2	84825	12q14.3
1554154_at	GDAP2	ganglioside induced differentiation associated protein 2	-2	54834	1p12
235791_x_at	CHD1	chromodomain helicase DNA binding protein 1	-2	1105	5q15-q21
226545_at	CD109	CD109 molecule	-2	135228	6q13
215198_s_at	CALD1	caldesmon 1	-2	800	7q33

210858_x_at	ATM	ataxia telangiectasia mutated	-2	472	11q22-q23
218659_at	ASXL2	additional sex combs like 2 (Drosophila)	-2	55252	2p24.1
202955_s_at	ARFGEF1	ADP-ribosylation factor guanine nucleotide-exchange factor 1(brefeldin A-inhibited)	-2	10565	8q13
202760_s_at	AKAP2	A kinase (PRKA) anchor protein 2	-2	11217	9q31-q33
242629_at	---	Transcribed locus	-2	---	---
230175_s_at	---	---	-2	---	---
226074_at	PPM1M	protein phosphatase 1M (PP2C domain containing)	2.01	132160	3p21.1
202150_s_at	NEDD9	neural precursor cell expressed, developmentally down-regulated 9	2.01	4739	6p25-p24
204112_s_at	HNMT	histamine N-methyltransferase	2.01	3176	2q22.1
213170_at	GPX7	glutathione peroxidase 7	2.01	2882	1p32
212154_at	SDC2	syndecan 2	2.02	6383	8q22-q23
227219_x_at	MAP1LC3A	microtubule-associated protein 1 light chain 3 alpha	2.02	84557	20cen-q13
205462_s_at	HPCAL1	hippocalcin-like 1	2.02	3241	2p25.1
224719_s_at	C12orf57	chromosome 12 open reading frame 57	2.02	113246	12p13.31
225314_at	OCIAD2	OCIA domain containing 2	2.03	132299	4p12
210319_x_at	MSX2	msh homeobox 2	2.03	4488	5q34-q35
227655_at	FLJ38512	FLJ38512	2.03	---	---
219785_s_at	FBXO31	F-box protein 31	2.03	79791	16q24.2
203417_at	MFAP2	microfibrillar-associated protein 2	2.04	4237	1p36.1-p35
229874_x_at	LOC729604	hypothetical protein LOC729604	2.04	729604	1p36.13
209759_s_at	DCI	dodecenoyl-Coenzyme A delta isomerase (3,2 trans-enoyl-Coenzyme A isomerase)	2.04	1632	16p13.3
225894_at	SYNPO2	synaptopodin 2	2.06	171024	4q26
226674_at	TMEM58	transmembrane protein 58	2.07	149345	1q32.1
209651_at	TGFB11	transforming growth factor beta 1 induced transcript 1	2.07	7041	16p11.2
230963_at	EMX2OS	empty spiracles homeobox 2 opposite strand	2.07	196047	10q26.1
202720_at	TES	testis derived transcript (3 LIM domains)	2.08	26136	7q31.2
201397_at	PHGDH	phosphoglycerate dehydrogenase	2.08	26227	1p12
201137_s_at	HLA-DPB1	major histocompatibility complex, class II, DP beta 1	2.08	3115	6p21.3
204400_at	EFS	embryonal Fyn-associated substrate	2.08	10278	14q11.2-q12
219729_at	PRRX2	paired related homeobox 2	2.09	51450	9q34.1
222379_at	KCNE4	potassium voltage-gated channel, Isk-related family, member 4	2.09	23704	2q36.3
235173_at	hCG_1806964	hCG1806964	2.09	401093	3q25.1
206039_at	RAB33A	RAB33A, member RAS oncogene family	2.1	9363	Xq25
219806_s_at	C11orf75	chromosome 11 open reading frame 75	2.1	56935	11q13.3-q23.3
225895_at	SYNPO2	synaptopodin 2	2.11	171024	4q26
231559_at	NNMT	Nicotinamide N-methyltransferase	2.11	4837	11q23.1
227850_x_at	CDC42EP5	CDC42 effector protein (Rho GTPase binding) 5	2.11	148170	19q13.42
226434_at	C7orf47	chromosome 7 open reading frame 47	2.12	221908	7q22.1
220230_s_at	CYB5R2	cytochrome b5 reductase 2	2.13	51700	11p15.4
214293_at	Septin 11	Septin 11	2.14	55752	4q21.1
206969_at	KRT34	keratin 34	2.14	3885	17q12-q21
204929_s_at	VAMP5	vesicle-associated membrane protein 5 (myobrevin)	2.15	10791	2p11.2
219215_s_at	SLC39A4	solute carrier family 39 (zinc transporter), member 4	2.15	55630	8q24.3
1555851_s_at	SEPW1	selenoprotein W, 1	2.15	6415	19q13.3
216268_s_at	JAG1	jagged 1 (Alagille syndrome)	2.15	182	20p12.1-p11.23
213260_at	FOXC1	forkhead box C1	2.16	2296	6p25
235666_at	---	Transcribed locus	2.16	---	---
210880_s_at	EFS	embryonal Fyn-associated substrate	2.18	10278	14q11.2-q12
202196_s_at	DKK3	dickkopf homolog 3 (Xenopus laevis)	2.18	27122	11p15.2
230508_at	DKK3	dickkopf homolog 3 (Xenopus laevis)	2.18	27122	11p15.2
203395_s_at	HES1	hairy and enhancer of split 1, (Drosophila)	2.2	3280	3q28-q29
209917_s_at	TP53AP1	TP53 activated protein 1	2.21	11257	7q21.1

1598_g_at	GAS6	growth arrest-specific 6	2.21	2621	13q34
200706_s_at	LITAF	lipopolysaccharide-induced TNF factor	2.22	9516	16p13.13
209293_x_at	ID4	inhibitor of DNA binding 4, dominant negative helix-loop-helix protein	2.22	3400	6p22-p21
224378_x_at	MAP1LC3A	microtubule-associated protein 1 light chain 3 alpha	2.24	84557	20cen-q13
214265_at	ITGA8	integrin, alpha 8	2.24	8516	10p13
205824_at	HSPB2	heat shock 27kDa protein 2	2.24	3316	11q22-q23
205555_s_at	MSX2	msh homeobox 2	2.25	4488	5q34-q35
202177_at	GAS6	growth arrest-specific 6	2.25	2621	13q34
208690_s_at	PDLIM1	PDZ and LIM domain 1 (elfin)	2.26	9124	10q22-q26.3
242888_at	PRRT3	Transcribed locus, strongly similar to NP_997234.2 hypothetical protein LOC285368	2.29	---	---
241440_at	FLJ30375	---	2.3	---	---
204015_s_at	DUSP4	dual specificity phosphatase 4	2.33	1846	8p12-p11
227372_s_at	BAIAP2L1	BAI1-associated protein 2-like 1	2.33	55971	7q21.3
225767_at	---	---	2.36	---	---
221127_s_at	RIG	regulated in glioma	2.37	10530	11p15.1
223292_s_at	MRPS15	mitochondrial ribosomal protein S15	2.37	64960	1p35-p34.1
226504_at	FAM109B	family with sequence similarity 109, member B	2.37	150368	22q13.2
1554819_a_at	ITGA11	integrin, alpha 11	2.38	22801	15q23
213747_at	---	---	2.38	---	---
1555480_a_at	FBLIM1	filamin binding LIM protein 1	2.39	54751	1p36.21
212848_s_at	C9orf3	chromosome 9 open reading frame 3	2.4	84909	9q22.32
204079_at	TPST2	tyrosylprotein sulfotransferase 2	2.41	8459	22q12.1
201194_at	SEPW1	selenoprotein W, 1	2.42	6415	19q13.3
212807_s_at	SORT1	sortilin 1	2.43	6272	1p21.3-p13.1
222450_at	TMEPAI	transmembrane, prostate androgen induced RNA	2.44	56937	20q13.31-q13.33
207076_s_at	ASS1	argininosuccinate synthetase 1	2.45	445	9q34.1
206117_at	TPM1	tropomyosin 1 (alpha)	2.47	7168	15q22.1
227262_at	HAPLN3	hyaluronan and proteoglycan link protein 3	2.49	145864	15q26.1
219310_at	C20orf39	chromosome 20 open reading frame 39	2.49	79953	20p11.21
225016_at	APCDD1	adenomatosis polyposis coli down-regulated 1	2.52	147495	18p11.22
223734_at	OSAP	ovary-specific acidic protein	2.53	84709	4q31.1
229872_s_at	LOC642441	hypothetical LOC642441	2.54	642441	1q21.1
228737_at	TOX2	TOX high mobility group box family member 2	2.55	84969	20q13.12
227959_at	---	Transcribed locus, weakly similar to XP_001113311.1 PREDICTED: hypothetical protein [Macaca mulatta]	2.55	---	---
223499_at	C1QTNF5	C1q and tumor necrosis factor related protein 5	2.58	114902	11q23.3
202149_at	NEDD9	neural precursor cell expressed, developmentally down-regulated 9	2.6	4739	6p25-p24
204044_at	QPRT	quinolinate phosphoribosyltransferase (nicotinate-nucleotide pyrophosphorylase (carboxylating))	2.64	23475	16p11.2
209292_at	ID4	Inhibitor of DNA binding 4, dominant negative helix-loop-helix protein	2.65	3400	6p22-p21
204255_s_at	VDR	vitamin D (1,25-dihydroxyvitamin D3) receptor	2.66	7421	12q13.11
229693_at	LOC388335	similar to RIKEN cDNA A730055C05 gene	2.68	388335	17p13.1
203394_s_at	HES1	hairy and enhancer of split 1, (Drosophila)	2.74	3280	3q28-q29
207030_s_at	CSRP2	cysteine and glycine-rich protein 2	2.75	1466	12q21.1
221900_at	COL8A2	collagen, type VIII, alpha 2	2.78	1296	1p34.2
231183_s_at	JAG1	Jagged 1 (Alagille syndrome)	2.81	182	20p12.1-p11.23
211126_s_at	CSRP2	cysteine and glycine-rich protein 2	2.85	1466	12q21.1
219270_at	CHAC1	ChaC, cation transport regulator homolog 1 (E. coli)	2.89	79094	15q15.1
209291_at	ID4	inhibitor of DNA binding 4, dominant negative helix-loop-helix protein	2.92	3400	6p22-p21
236640_at	LOC399959	Hypothetical gene supported by BX647608	2.98	399959	11q24.1
213942_at	MEGF6	multiple EGF-like-domains 6	2.99	1953	1p36.3
205992_s_at	IL15	interleukin 15	2.99	3600	4q31
202718_at	IGFBP2	insulin-like growth factor binding protein 2, 36kDa	3.02	3485	2q33-q34
211538_s_at	HSPA2	heat shock 70kDa protein 2	3.05	3306	14q24.1

225056_at	SIPA1L2	signal-induced proliferation-associated 1 like 2	3.07	57568	1q42.2
228400_at	SHROOM3	shroom family member 3	3.07	57619	4q21.1
57588_at	SLC24A3	solute carrier family 24 (sodium/potassium/calcium exchanger), member 3	3.08	57419	20p13
210372_s_at	TPD52L1	tumor protein D52-like 1	3.29	7164	6q22-q23
222899_at	ITGA11	integrin, alpha 11	3.37	22801	15q23
1558048_x_at	---	---	3.56	---	---
224550_s_at	MRV11	murine retrovirus integration site 1 homolog	3.63	10335	11p15
226933_s_at	ID4	Inhibitor of DNA binding 4, dominant negative helix-loop-helix protein	3.66	3400	6p22-p21
209343_at	EFHD1	EF-hand domain family, member D1	3.66	80303	2q37.1
209167_at	GPM6B	glycoprotein M6B	3.71	2824	Xp22.2
207302_at	SGCG	sarcoglycan, gamma (35kDa dystrophin-associated glycoprotein)	3.78	6445	13q12
240382_at	DSP	Clone IMAGE:110436 mRNA sequence	3.88	---	---
225548_at	SHROOM3	shroom family member 3	3.93	57619	4q21.1
205048_s_at	PSPH	phosphoserine phosphatase	3.93	5723	7p15.2-p15.1
229566_at	LOC645638	similar to WDNM1-like protein	3.94	645638	17q23.1
203126_at	IMPA2	inositol(myo)-1(or 4)-monophosphatase 2	3.96	3613	18p11.2
205132_at	ACTC1	actin, alpha, cardiac muscle 1	3.98	70	15q11-q14
203786_s_at	TPD52L1	tumor protein D52-like 1	3.99	7164	6q22-q23
227099_s_at	LOC387763	hypothetical LOC387763	4.23	387763	11p11.2
219090_at	SLC24A3	solute carrier family 24 (sodium/potassium/calcium exchanger), member 3	4.25	57419	20p13
214027_x_at	DES	desmin	4.42	1674	2q35
203766_s_at	LMOD1	leiomodoin 1 (smooth muscle)	4.52	25802	1q32
211990_at	HLA-DPA1	major histocompatibility complex, class II, DP alpha 1	4.52	3113	6p21.3
227347_x_at	HES4	hairy and enhancer of split 4 (Drosophila)	4.56	57801	1p36.33
229296_at	FLJ34873	FLJ34873	4.6	---	---
219478_at	WFDC1	WAP four-disulfide core domain 1	5.02	58189	16q24.3
209170_s_at	GPM6B	glycoprotein M6B	5.06	2824	Xp22.2
237206_at	MYOCD	myocardin	5.29	93649	17p11.2
229479_at	LOC646324	Transcribed locus	5.49	---	---
203868_s_at	VCAM1	vascular cell adhesion molecule 1	5.68	7412	1p32-p31
229339_at	---	Transcribed locus	5.79	---	---
230784_at	PRAC	small nuclear protein PRAC	6.02	84366	17q21
202222_s_at	DES	desmin	6.57	1674	2q35
227006_at	PPP1R14A	protein phosphatase 1, regulatory (inhibitor) subunit 14A	6.9	94274	19q13.1
203951_at	CNN1	calponin 1, basic, smooth muscle	11.45	1264	19p13.2-p13.1
203924_at	GSTA1	glutathione S-transferase A1	13.55	2938	6p12.1
209948_at	KCNMB1	potassium large conductance calcium-activated channel, subfamily M, beta member 1	21.52	3779	5q34

Probe Set ID	Gene Symbol	Gene Title	Fold ch	Entrez Gene	Chromosomal Location
1554997_a_at	PTGS2	prostaglandin-endoperoxide synthase 2 (prostaglandin G/H synthase and cyclooxygenase)	-7.69	5743	1q25.2-q25.3
204748_at	PTGS2	prostaglandin-endoperoxide synthase 2 (prostaglandin G/H synthase and cyclooxygenase)	-7.14	5743	1q25.2-q25.3
208719_s_at	DDX17	DEAD (Asp-Glu-Ala-Asp) box polypeptide 17	-3.57	10521	22q13.1
209875_s_at	SPP1	secreted phosphoprotein 1 (osteopontin, bone sialoprotein I, early T-lymphocyte activation 1)	-3.12	6696	4q21-q25
203887_s_at	THBD	thrombomodulin	-2.86	7056	20p11.2
201578_at	PODXL	podocalyxin-like	-2.86	5420	7q32-q33
203888_at	THBD	thrombomodulin	-2.63	7056	20p11.2
232174_at	FLJ21635	FLJ21635	-2.56	---	---
219759_at	ERAP2	endoplasmic reticulum aminopeptidase 2	-2.5	64167	5q15
208581_x_at	MT1X	metallothionein 1X	-2.5	4501	16q13
238320_at	TncRNA	trophoblast-derived noncoding RNA	-2.44	283131	11q13.1

235236_at	DOCK2	FLJ31436	-2.44	---	---
212859_x_at	MT1E	metallothionein 1E	-2.38	4493	16q13
212185_x_at	MT2A	metallothionein 2A	-2.27	4502	16q13
206461_x_at	MT1H	metallothionein 1H	-2.27	4496	16q13
237290_at	DDAH1	Transcribed locus	-2.22	---	---
227487_s_at	SERPINE2	Serpin peptidase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 2	-2.22	5270	2q33-q35
216336_x_at	MT1E/MT1M	metallothionein 1E/metallothionein 1M	-2.17	4493	16q13
203096_s_at	RAPGEF2	Rap guanine nucleotide exchange factor (GEF) 2	-2.17	9693	4q32.1
211456_x_at	MT1P2	metallothionein 1 pseudogene 2	-2.13	645745	1q43
210735_s_at	CA12	carbonic anhydrase XII	-2.13	771	15q22
204326_x_at	MT1X	metallothionein 1X	-2.13	4501	16q13
241435_at	AA702930	AA702930	-2.04		
204011_at	SPRY2	sprouty homolog 2 (Drosophila)	-2.04	10253	13q31.1
202434_s_at	CYP1B1	cytochrome P450, family 1, subfamily B, polypeptide 1	-2.04	1545	2p21
1566482_at	DKFZp313L2229	DKFZp313L2229	-2.04	---	---
227404_s_at	EGR1	Early growth response 1	-2	1958	5q31.1
203180_at	ALDH1A3	aldehyde dehydrogenase 1 family, member A3	-2	220	15q26.3
208690_s_at	PDLIM1	PDZ and LIM domain 1 (elfin)	2	9124	10q22-q26.3
227674_at	ZNF585A	zinc finger protein 585A	2.05	199704	19q13.12
226196_s_at	C14orf179	chromosome 14 open reading frame 179	2.07	112752	14q24.3
229874_x_at	LOC729604	LOC729604	2.08	---	---
204929_s_at	VAMP5	vesicle-associated membrane protein 5 (myobrevin)	2.11	10791	2p11.2
226195_at	C14orf179	chromosome 14 open reading frame 179	2.13	112752	14q24.3
220230_s_at	CYB5R2	cytochrome b5 reductase 2	2.14	51700	11p15.4
214293_at	SEPT11	Septin 11	2.16	55752	4q21.1
222001_x_at	FAM91A2	family with sequence similarity 91, member A2	2.19	57234	1q21.1
205872_x_at	PDE4DIP	phosphodiesterase 4D interacting protein (myomegalin)	2.28	9659	1q12
223305_at	MGC13379	HSPC244	2.29	51259	11q13.1
228235_at	MGC16121	hypothetical protein MGC16121	2.49	84848	Xq26.3
207076_s_at	ASS1	argininosuccinate synthetase 1	2.74	445	9q34.1
206932_at	CH25H	cholesterol 25-hydroxylase	2.81	9023	10q23
204112_s_at	HNMT	histamine N-methyltransferase	2.81	3176	2q22.1
205992_s_at	IL15	interleukin 15	2.9	3600	4q31
211732_x_at	HNMT	histamine N-methyltransferase	3.11	3176	2q22.1
236640_at	LOC399959	Hypothetical gene supported by BX647608	3.25	399959	11q24.1
228400_at	SHROOM3	shroom family member 3	3.48	57619	4q21.1
225548_at	SHROOM3	shroom family member 3	4.03	57619	4q21.1
218332_at	BEX1	brain expressed, X-linked 1	4.23	55859	Xq21-q23
203126_at	IMPA2	inositol(myo)-1(or 4)-monophosphatase 2	4.28	3613	18p11.2
205439_at	GSTT2	glutathione S-transferase theta 2	6.88	2953	22q11.2
203001_s_at	STMN2	stathmin-like 2	8.7	11075	8q21.13

SCS

Probe Set ID	Gene Symbol	Gene Title	Fold ch	Entrez Gene	Chromosomal Location
227314_at	ITGA2	integrin, alpha 2 (CD49B, alpha 2 subunit of VLA-2 receptor)	-5.56	3673	5q23-q31
219789_at	NPR3	natriuretic peptide receptor C/guanylate cyclase C (atrionatriuretic peptide receptor C)	-5	4883	5p14-p13
205032_at	ITGA2	integrin, alpha 2 (CD49B, alpha 2 subunit of VLA-2 receptor)	-4.76	3673	5q23-q31
201578_at	PODXL	podocalyxin-like	-4.55	5420	7q32-q33
219054_at	C5orf23	chromosome 5 open reading frame 23	-3.33	79614	5p13.3
228399_at	OSR1	odd-skipped related 1 (Drosophila)	-3.33	130497	2p24.1

212859_x_at	MT1E	metallothionein 1E	-3.23	4493	16q13
203887_s_at	THBD	thrombomodulin	-3.03	7056	20p11.2
204011_at	SPRY2	sprouty homolog 2 (Drosophila)	-2.94	10253	13q31.1
210310_s_at	FGF5	fibroblast growth factor 5	-2.94	2250	4q21
215177_s_at	ITGA6	integrin, alpha 6	-2.94	3655	2q31.1
203888_at	THBD	thrombomodulin	-2.86	7056	20p11.2
210311_at	FGF5	fibroblast growth factor 5	-2.86	2250	4q21
204475_at	MMP1	matrix metalloproteinase 1 (interstitial collagenase)	-2.78	4312	11q22.3
217999_s_at	PHLDA1	pleckstrin homology-like domain, family A, member 1	-2.7	22822	12q15
208378_x_at	FGF5	fibroblast growth factor 5	-2.63	2250	4q21
217998_at	LOC652993	pleckstrin homology-like domain, family A, member 1	-2.63	22822	12q15
218000_s_at	PHLDA1	pleckstrin homology-like domain, family A, member 1	-2.63	22822	12q15
238178_at	---	Transcribed locus	-2.63	---	---
206298_at	ARHGAP22	Rho GTPase activating protein 22	-2.56	58504	10q11.22
217997_at	PHLDA1	pleckstrin homology-like domain, family A, member 1	-2.5	22822	12q15
209189_at	FOS	v-fos FBJ murine osteosarcoma viral oncogene homolog	-2.44	2353	14q24.3
216336_x_at	MT1E/MT1M	metallothionein 1E/metallothionein 1M	-2.44	4499	16q13
229824_at	BC042431	FLJ45325 fis, clone BRHIP3006717	-2.44	---	---
236834_at	SCFD2	sec1 family domain containing 2	-2.44	152579	4q12
229011_at	---	Transcribed locus	-2.33	---	---
201976_s_at	MYO10	myosin X	-2.17	4651	5p15.1-p14.3
203186_s_at	S100A4	S100 calcium binding protein A4	-2.17	6275	1q21
213865_at	DCBLD2	discoidin, CUB and LCCL domain containing 2	-2.17	131566	3q12.1 3
217996_at	PHLDA1	pleckstrin homology-like domain, family A, member 1	-2.17	22822	12q15
222889_at	DCLRE1B	DNA cross-link repair 1B (PSO2 homolog, S. cerevisiae)	-2.17	64858	1p13.2
230973_at	SH2D5	SH2 domain containing 5	-2.13	400745	1p36.12
1552921_a_at	FIGNL1	figetin-like 1	-2.08	63979	7p12.2
207334_s_at	TGFBR2	transforming growth factor, beta receptor II (70/80kDa)	-2.08	7048	3p22
209457_at	DUSP5	dual specificity phosphatase 5	-2.04	1847	10q25
225173_at	ARHGAP18	Rho GTPase activating protein 18	-2.04	93663	6q22.33
225842_at	PHLDA1	pleckstrin homology-like domain, family A, member 1	-2.04	22822	12q15
241986_at	BMPER	BMP binding endothelial regulator	-2.04	168667	7p14.3
208025_s_at	HMG2	high mobility group AT-hook 2	-2	8091	12q15
232183_at	SERAC1	serine active site containing 1	2.05	84947	6q25.3
229872_s_at	LOC642441	hypothetical LOC642441	2.1	642441	1q21.1
202238_s_at	NNMT	nicotinamide N-methyltransferase	2.19	4837	11q23.1
219806_s_at	C11orf75	chromosome 11 open reading frame 75	2.24	56935	11q13.3-q23.3
227550_at	LOC143381	hypothetical protein LOC143381	2.29	143381	10q26.11
231987_at	LOC728264	hypothetical protein LOC728264	2.46	728264	5q33.1
213942_at	MEGF6	multiple EGF-like-domains 6	2.56	1953	1p36.3
241769_at	---	Transcribed locus	2.6	---	---
228772_at	HNMT	histamine N-methyltransferase	3.09	3176	2q22.1
211732_x_at	HNMT	histamine N-methyltransferase	3.37	3176	2q22.1
222899_at	ITGA11	integrin, alpha 11	3.78	22801	15q23
203786_s_at	TPD52L1	tumor protein D52-like 1	3.95	7164	6q22-q23
204984_at	GPC4	glypican 4	4.05	2239	Xq26.1
206101_at	ECM2	extracellular matrix protein 2, female organ and adipocyte specific	4.17	1842	9q22.3
228235_at	MGC16121	hypothetical protein MGC16121	4.79	84848	Xq26.3
229296_at	---	FLJ34873	5.92	---	---
203001_s_at	STMN2	stathmin-like 2	12.04	11075	8q21.13