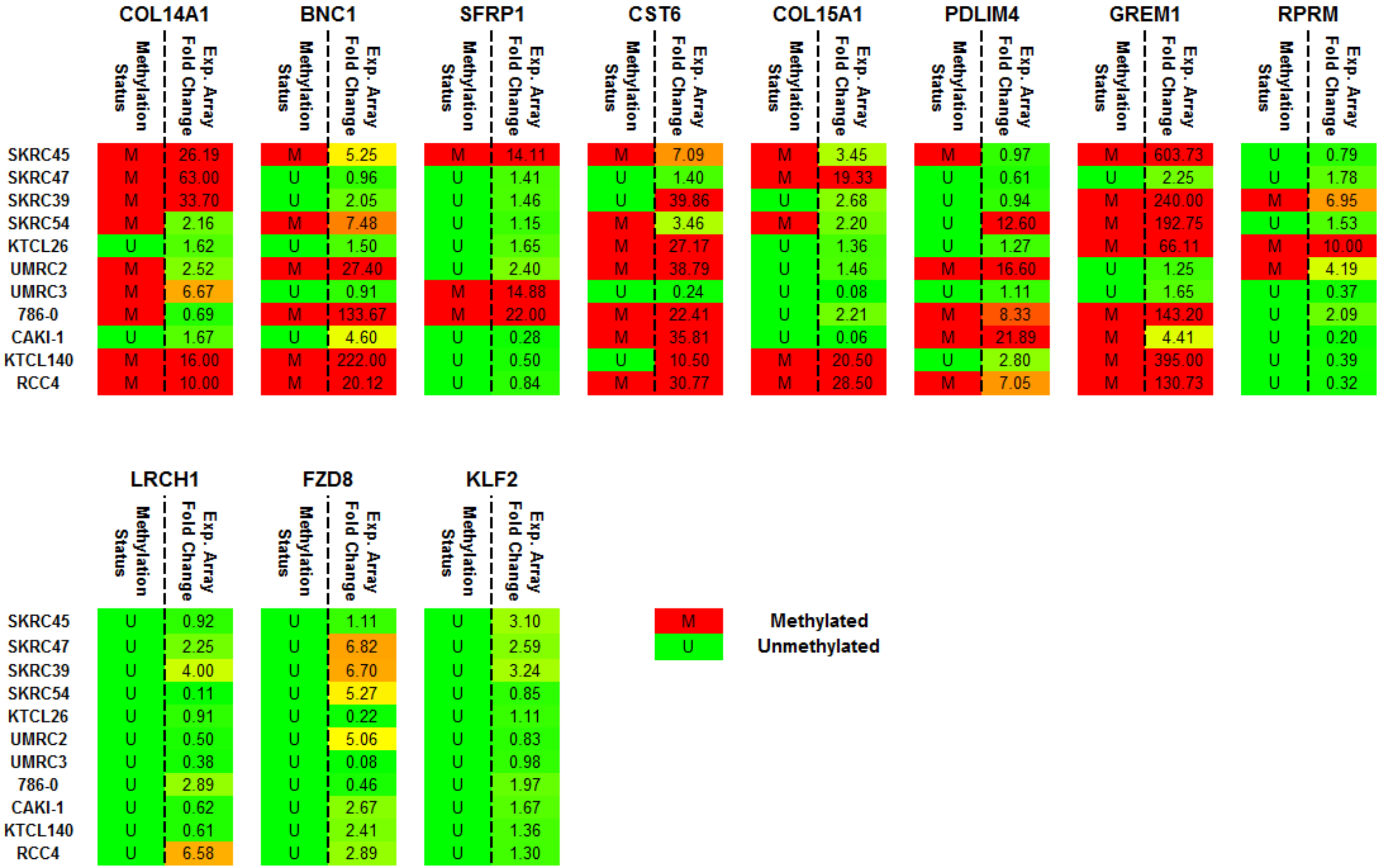
SUPPLEMENTARY FIGURE AND TABLE LEGENDS

Supplementary Figure 1. A comparison of promoter methylation status, as determined by bisulphite sequencing and MSP, and expression fold-increase as determined by Affymetrix U133 plus 2 array analysis in RCC-derived cell lines following global demethylation. Upper panel: genes that were frequently methylated in sporadic RCC. Lower panel: Control genes that had relatively low expression increases and no promoter methylation in cell lines.

Supplementary Figure 2. Representative traces of direct bisulphite sequencing of tumour DNA. **H**: Hemi-methylation, **M**: Complete methylation

Supplementary table 1. Primers used for methylation analysis.

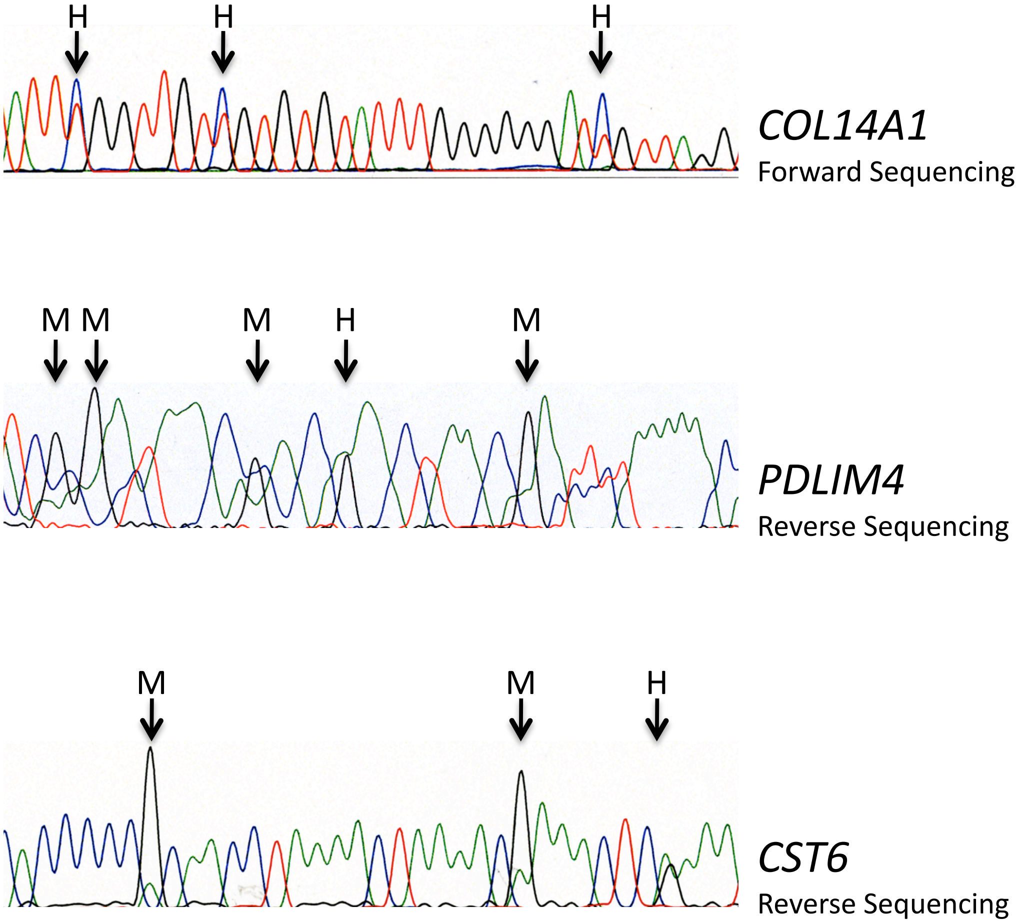
Supplementary table 2. Shortlist of genes (406) identified (see results for details of filtering procedure) following global demethylation of 11 RCC-derived cell lines and analysis of Affymetrix U133 plus 2 arrays. The numbers in the heat-map cells represent fold changes of expression after demethylation. The genes have been ordered into the following groups: Yellow: genes analysed in this study. Blue: genes previously known to be frequently methylated in RCC. Green: genes that we have previously analysed for promoter methylation and found low frequencies of methylation in RCC. Grey: genes with no promoter region CpG island present. Pink: genes that are not expressed in kidney tissue. Aqua: Genes not analysed thus far.



	COL14A1		BNC1		SFRP1		CST6		COL15A1		PDLIM4		GREM1		RPRM	
	Methylation Status	Exp. Array Fold Change	Methylation Status	Exp. Array Fold Change	Methylation Status	Exp. Array Fold Change	Methylation Status	Exp. Array Fold Change	Methylation Status	Exp. Array Fold Change	Methylation Status	Exp. Array Fold Change	Methylation Status	Exp. Array Fold Change	Methylation Status	Exp. Array Fold Change
SKRC45	M	26.19	M	5.25	M	14.11	M	7.09	M	3.45	M	0.97	M	603.73	U	0.79
SKRC47	M	63.00	U	0.96	U	1.41	U	1.40	M	19.33	U	0.61	U	2.25	U	1.78
SKRC39	M	33.70	U	2.05	U	1.46	U	39.86	U	2.68	U	0.94	M	240.00	M	6.95
SKRC54	M	2.16	M	7.48	U	1.15	M	3.46	M	2.20	U	12.60	M	192.75	U	1.53
KTCL26	U	1.62	U	1.50	U	1.65	M	27.17	U	1.36	U	1.27	M	66.11	M	10.00
UMRC2	M	2.52	M	27.40	U	2.40	M	38.79	U	1.46	M	16.60	U	1.25	M	4.19
UMRC3	M	6.67	U	0.91	M	14.88	U	0.24	U	0.08	U	1.11	U	1.65	U	0.37
786-0	M	0.69	M	133.67	M	22.00	M	22.41	U	2.21	M	8.33	M	143.20	U	2.09
CAKI-1	U	1.67	U	4.60	U	0.28	M	35.81	U	0.06	M	21.89	M	4.41	U	0.20
KTCL140	M	16.00	M	222.00	U	0.50	U	10.50	M	20.50	U	2.80	M	395.00	U	0.39
RCC4	M	10.00	M	20.12	U	0.84	M	30.77	M	28.50	M	7.05	M	130.73	U	0.32

	LRCH1		FZD8		KLF2	
	Methylation Status	Exp. Array Fold Change	Methylation Status	Exp. Array Fold Change	Methylation Status	Exp. Array Fold Change
SKRC45	U	0.92	U	1.11	U	3.10
SKRC47	U	2.25	U	6.82	U	2.59
SKRC39	U	4.00	U	6.70	U	3.24
SKRC54	U	0.11	U	5.27	U	0.85
KTCL26	U	0.91	U	0.22	U	1.11
UMRC2	U	0.50	U	5.06	U	0.83
UMRC3	U	0.38	U	0.08	U	0.98
786-0	U	2.89	U	0.46	U	1.97
CAKI-1	U	0.62	U	2.67	U	1.67
KTCL140	U	0.61	U	2.41	U	1.36
RCC4	U	6.58	U	2.89	U	1.30

M	**Methylated**
U	**Unmethylated**



Supplementary Figure 2. Representative traces of direct bisulphite sequencing of tumour DNA. **H**: Hemi-methylation, **M**: Complete methylation.

Supplementary table 1
Nestesd primers for amplification and sequencing of bisulphite modified DNA
(F: Forward, R: Reverse, I: Internal)

Col14a COBRA F: 5' g tat ata gta ttt gag aat agg agg gtt yga gat 3'
Col14a COBRA IF: 5' ggg ttt ggt ttg gga gtt tgt agt agt 3'
Col14a COBRA R: 5' c taa aac tac ctc crc ctc tcc aac taa 3'

CST6 COBRA F : 5' ttt tgt gaa tyg ttt ttg tat tgg tat ttg ttg t 3'
CST6 COBRA IR: 5' ata ccr tcr aaa ccc tca aaa ccr taa ata 3'
CST6 COBRA R: 5' ata cta tta cta ccc ata tta taa cta acc acr a 3'

COL15A1 COBRA F: 5' gta ttt agg agt tta gtg tag ttt ggg at 3'
COL15A1 COBRA IF: 5' gat ttt agt ttt ttt ggg ttg tgg aga gga ttt 3'
COL15A1 COBRA R: 5' cta crc act cac rcc cra aaa ata ccr a 3'

LOXL-1 COBRA F: 5' ggg tgg tgt tga tat ttt agt tty gtt ttg ttt gt 3'
LOXL-1 COBRA IF: 5' ttg tgg ttt ggt tgg gaa ttt tag gga t 3'
LOXL-1 COBRA R: 5' cra acr aac aaa acc rcc tat aaa cct tac ata a 3'

EMX2 COBRA F: 5' g aay gta tyg att ttg gga ttt yga ggt taa gyg 3'
EMX2 COBRA IF: 5' ggt tga tgg ggt ggg agg att tyg tat 3'
EMX2 COBRA R: 5' taa atc ccr aac cta cct crc cca aac taa 3'

PDLM4 COBRA F: 5' gy ggt ttg tag att taa ggt tyg agt agg att 3'
PDLM4 COBRA IF: 5' ggt ygt tyg aat gyg ggg att ttt gag agt 3'
PDLM4 COBRA R: 5' acr aaa acc cca aaa cra aaa ccc rcr caa 3'

GREM1 COBRA F: 5' gga gyg gaa aat gtg att tgt tgt gta ttt t 3'
GREM1 COBRA IF: 5' gtt tgg tta atg gag agg ygy ggt tt 3'
GREM COBRA IR: 5' ctc acc tat caa tac rac raa tcc tcr aaa 3'
GREM COBRA R: 5' cta crt ttc cct aca aac cca aaa caa cra aa 3'

Claudin 6 COBRA F: 5' tt tgt tag tty gag gyg ggt tta gyg att 3'
Claudin 6 COBRA IF: 5' gtt gty gtt agg gat agg gtt ttt gtt 3'
Claudin 6 COBRA R: 5' acr ttt aac cct taa aaa ccc cra aaa acc 3'

FZD8 COBRA F: 5' gty gag tgg tgg tyg tta ggg ttg att 3'
FZD8 COBRA IF: 5' g tat ygy ggt ttt aga gga aat ttg ygg ygt t 3'
FZD8 COBRA R: 5' ata atc taa aat ctc cct tat act tcr ccc raa 3'

MKK6 COBRA F: 5' ggg agt ttt ttt tay gga gat ygg ggt 3'
MKK6 COBRA IF: 5' ggg ttg gag gga att ggg aag tat tgt 3'
MKK6 COBRA R: 5' ac tac rtt crc rac cca acr ttc tcc caa 3’

Noggin COB F: 5' gt tag tgg ttt tta tgg tga tgg agt 3'
Noggin COB IF: 5' att taa agg ttt gga ttt tgy gag ata gat 3'
Noggin COB R: 5' caa ctc ctc tcc cra atc tac taa 3'

ITGBL1 COBRA F: 5' g cag ygt ttg gat ttt aga gag atg tgg gtt 3'

ITGBL1 COBRA IF: 5' ggg ttg tay gtt tgt att tgg agg gga tat 3'
ITGBL1 COBRA R: 5' ccr tcr taa atc tcr cac acc cac tca taa 3'
'

ZFP42/REX-1 COBRA F: 5’ ata gat att tat tga gyg ttt att ayg tgt t 3’
ZFP42/REX-1 COBRA IR: 5’ caa taa aaa crt aaa cta ccc tac rcc 3’
ZFP42/REX-1 COBRA R: 5’ cac tct act att tcc aat acc ac 3’

DMRTB1 COBRA IF: 5’ gat gta gga att atg gtt ttt tgg tgt t 3’
DMRTB1 COBRA R: 5’ ac crc cca aaa ccr act aaa aaa ctc 3’
DMRTB1 COBRA F: 5’ t ggt tgt gtt ayg aag gtt gat ttt gtt 3’

KLF4 COBRA F: 5' g tgt ttt agt tgt tty ggg ttg tyg agg att 3'
KLF4 COBRA IR: 5' cct crt tca ata act ctt aat aac ccc aaa ac 3'
KLF4 COBRA R: 5' c ata cac aac taa acc aaa aac acr aaa act atc 3'

KLF2 COBRA F: 5' ggt ttt gta gtt ttt ttt gag gtt gga gtt 3'
KLF2 COBRA IF: 5' gg tgt ttt ttt gag agt ttt tga gag gtt 3'
KLF2 COBRA R: 5' c cra taa ata act acc cra aac cra act aa 3'
KLF2 COBRA IR: 5' c cra taa ata act acc cra aac cra act aa 3'

HERC5 COBRA F: 5' atg ttt ygt ttt tta ttg gag ttg tag gtt 3'
HERC5 COBRA R: 5' aca aca aaa tta acr crt cac ctc cac 3'
HERC5 COBRA IR: 5' ccr cra crc taa aaa aaa acc aaa act ata 3'

LRCH4 COBRA F: 5' gtg tyg gtg ttt ttt ttt ttt ggt tgg att 3'
LRCH4 COBRA IR: 5' aac cta aaa acc cra aca cra aaa tcr taa 3'
LRCH4 COBRA R: 5' cac tca cca acc taa ata ata tct aac aaa 3'

PTGIS COBRA F: 5' gta ggg ttt tta ata gag ygt tty ggt ttg att 3'
PTGIS COBRA IR: 5' ccr aaa atc tcr cct tac ccr aaa tac taa 3'
PTGIS COBRA R: 5' ct tcc cac ctt aca cct tct taa caa 3'

RANBP2L1 COBRA F: 5' ttg aat tta ttt att att att gat agt tta ggt t 3'
RANBP2L1 COBRA IF: 5' aag gtt ttt tat aga taa gat tat gtt aag ata tt 3'
RANBP2L1 COBRA R: 5' aca atc rcc act tcc aaa aaa aaa ata 3'

FBXO2 COBRA F: 5' at tyg gaa ttt agg agt ttt tty ggt agt t 3'
FBXO2 COBRA IF: 5' ta tga tty gtt ggg tyg ttt aag ttg tat 3'
FBXO2 COBRA R: 5' cta aaa aaa aat ccr att taa aac atc tcr caa 3'

TLL1 COBRA F: 5' g gtt tta gyg ttt ttt gtt gtt gta att tgt aat 3'
TLL1 COBRA IF: 5' gt agt ttt gag gat ttt agt ttt tag taa aat 3'
TLL COBRA R: 5' cat aca atc aaa atc aaa atc cra acc aca a 3'

DiCKKOPF-1 COBRA F: 5' ggg tat tta agt ttt tag agt ttt tgt tgt 3'
DiCKKOPF-1 COBRA IF: 5' gta gtt ttt att tyg aag atg agt ygg gtt 3'
DiCKKOPF-1 COBRA R: 5' caa aat aac rct cac tcc caa caa aaa ata a 3'

SYCP3 COBRA F: 5' ttg gaa ggt att agg ttt taa gtg tat 3'

SYCP3 COBRA R: 5' ta aac cct atc cta ctc aaa acc cta 3'
SYCP3 COBRA IR: 5' c aaa aac aac ctc taa cct aaa cac cta 3'

Methylation Specific primers to amplify Col15A promoter region:

Col15a MSPF: 5' gg ttg tgg aga gga ttt ttt tag cg 3'
Col15a USPF: 5' ggg ttg tgg aga gga ttt ttt tag tg 3'
Col15a MSPR: 5' tc tac tac ctc cac ccg cg 3'
Col15a USPR: 5' ctc tac tac ctc cac cca ca 3'

Probe	SK45	SK47	SK39	SK54	KT26	UM2	UM3	786O	CAKI	KT140	RCC4	Gene Symbol	Chromosomal Location	RefSeq Transcript ID
1552487_a_at	5.25	0.96	2.05	7.48	1.50	27.40	0.91	133.67	4.60	222.00	20.12	BNC1	chr15q25.2	NM_001717
205627_at	17.30	1.80	114.67	29.29	23.44	18.75	1.11	12.91	2.55	95.50	16.54	SCYA20	chr1p36.2	NM_001785
237810_at	0.48	1.29	36.82	0.21	2.12	16.64	0.12	1.50	20.29	25.22	77.94	CLDN6	chr16p13.3	NM_021195
212865_s_at	26.19	63.00	33.70	2.16	1.62	2.52	6.67	0.69	1.67	1.09	10.00	COL14A1	chr8q23	NM_021110
203477_at	3.45	19.33	2.68	2.20	1.36	1.46	0.08	2.21	0.06	20.50	28.50	COL15A1	chr9q21-q22	NM_001855
206595_at	7.09	1.40	39.86	3.46	27.17	38.79	0.24	22.41	35.81	10.50	30.77	CST6	chr11q13	NM_001323
204602_at	3.73	1.30	2.64	28.10	2.16	2.68	1.24	38.84	4.07	14.38	1.97	DKK1	chr10q11.2	NM_012242
240313_at	6.74	17.38	55.16	5.17	12.56	10.25	0.85	8.25	23.94	3.81	7.85	DMRTB1	chr1p32.3	NM_033067
221950_at	0.46	2.14	0.25	1.50	0.50	3.25	14.25	27.50	32.67	0.22	0.48	EMX2	chr10q26.1	NM_004098
206018_at	1.39	89.67	12.91	14.67	2.05	26.57	0.31	0.67	1.79	13.48	0.45	FOXG1B	chr14q12-q13	NM_005249
218468_s_at	322.25	25.00	24.65	38.08	9.93	1.60	9.17	464.33	8.67	230.33	30.29	GREM1	chr15q13-q15	NM_013372
205422_s_at	11.77	1.44	1.70	1.09	5.65	2.00	0.47	50.67	1.74	2.09	32.09	ITGBL1	chr13q33	NM_004791
220266_s_at	2.68	0.68	12.44	1.14	10.68	1.44	0.84	2.72	2.35	2.15	10.20	KLF4	chr9q31	NM_004235
203570_at	0.46	0.42	36.00	1.11	3.02	2.25	1.39	0.61	23.60	13.60	2.33	LOXL1	chr15q24	NM_005576
231798_at	2.88	1.03	5.09	26.57	1.36	1.79	1.36	3.32	1.69	12.40	11.17	NOG	chr17q21-q22	NM_005450
211564_s_at	0.97	0.61	0.94	12.60	1.27	16.60	1.11	8.33	21.89	2.80	7.05	PDLIM4	chr5q31.1	NM_003687
208131_s_at	0.36	57.33	7.37	10.66	3.27	20.38	0.74	9.11	2.20	1.59	27.52	PTGIS	chr20q13.13	NM_000961
206392_s_at	1.38	25.50	42.00	1.67	1.44	71.50	3.33	1.05	7.51	0.43	0.59	RARRES1	chr3q25.32	NM_206963
211324_s_at	1.17	0.33	10.00	1.13	19.00	5.00	1.27	2.52	0.10	1.68	22.75	RGPD5	chr2q13	NM_005054
202037_s_at	14.11	1.41	1.46	1.15	1.65	2.40	14.88	22.00	0.28	0.50	0.84	SFRP1	chr8p12-p11.1	NM_003012
206415_at	3.83	18.00	7.00	0.02	0.42	0.04	13.00	0.50	1.00	10.25	1.17	TLL1	chr4q32-q33	NM_012464
204083_s_at	6.58	1.04	4.48	7.29	3.91	107.55	0.99	42.14	0.57	28.25	45.44	TPM2	chr9p13.2	NM_213674
202233_s_at	13.27	1.21	0.71	74.45	1.13	80.82	1.05	1.12	1.02	0.90	0.99	UQCRH	chr1p33	NM_006004
1554776_at	0.45	20.00	2.63	0.56	29.33	0.52	0.78	1.95	66.47	21.40	1.10	ZFP42	chr4q35.2	NM_174900
214936_at	0.92	2.25	4.00	0.11	0.91	0.50	0.38	2.89	0.62	0.61	6.58	LRCH1	chr13q14.13	NM_015116
216587_s_at	1.11	6.82	6.70	5.27	0.22	5.06	0.08	0.46	2.67	2.41	2.89	FZD8	chr10p11.21	NM_031866
219371_s_at	3.10	2.59	3.24	0.85	1.11	0.83	0.98	1.97	1.67	1.36	1.30	KLH2	chr19p13.13	NM_016270
219370_at	0.79	1.78	6.95	1.53	10.00	4.19	0.37	2.09	0.20	0.39	0.32	REPRIMO	chr2q23.3	NM_019845
1556499_s_at	9.48	2.79	10.84	20.22	18.01	19.77	1.04	19.07	8.36	69.61	32.56	COL1A1	chr17q21.33	NM_000088
205302_at	11.79	32.76	3.36	0.56	2.73	2.72	1.86	1.18	1.85	0.89	13.77	IGFBP1	chr7p13-p12	NM_000596
201650_at	33.75	8.33	216.00	0.83	74.13	99.00	1.05	1.75	1.18	317.00	1.87	KRT19	chr17q21.2	NM_002276
208352_x_at	1.00	1.62	0.18	6.17	0.72	0.28	1.09	31.50	13.13	15.45	22.38	ANK1	chr8p11.1	NM_020481
205780_at	5.00	3.73	17.85	2.96	2.21	5.66	1.11	9.25	2.69	35.29	10.40	BIK	chr22q13.31	NM_001197
202790_at	6.06	6.00	88.45	58.67	39.63	4.08	0.53	28.08	10.33	7.86	4.02	CLDN7	chr17p13	NM_001307
206806_at	18.06	17.00	1.51	1.45	1.17	1.67	2.07	4.49	0.54	7.88	47.00	DGKI	chr7q32.3	NM_004717
204273_at	35.00	26.00	18.50	0.20	27.00	3.00	1.50	0.50	1.65	1.56	1.00	EDNRB	chr13q22	NM_003991
201809_s_at	6.97	1.53	1.60	1.37	1.47	16.39	1.03	101.14	1.26	46.08	1.10	ENG	chr9q33-q34.1	NM_000118
201508_at	1.50	1.00	39.32	2.04	0.88	5.36	0.22	12.44	3.12	45.18	15.11	IGFBP4	chr17q12-q21.1	NM_001552
1554252_a_at	36.00	0.11	0.62	1.50	0.56	11.17	1.79	1.86	0.19	20.75	1.39	LASS3	chr15q26.3	NM_178842
202086_at	5.43	2.94	5.20	1.37	2.47	10.91	0.23	20.85	4.33	78.89	1.88	MX1	chr21q22.3	NM_002462
229494_s_at	12.50	0.26	13.75	7.00	12.50	1.56	1.10	0.06	0.08	11.20	0.22	PHLDA2	chr11p15.5	NM_003311
206772_at	37.00	29.20	1.03	47.20	1.46	4.41	50.50	4.69	10.15	35.00	19.60	PTHR2	chr2q33	NM_005048
219395_at	1.52	2.86	1.87	12.73	8.94	3.36	0.97	2.59	19.40	32.76	1.16	RBM35B	chr16q22.1	NM_024939
213921_at	0.88	2.50	12.86	69.54	6.94	0.68	8.00	8.05	43.00	15.12	32.81	SST	chr3q28	NM_001048
1553599_a_at	13.04	15.31	45.58	12.49	2.89	11.04	0.87	12.54	12.93	32.38	11.98	SYCP3	chr12q	NM_153694
213869_x_at	15.75	3.01	11.34	0.90	24.39	15.26	0.94	16.90	6.42	39.88	10.32	THY1	chr11q22.3	NM_006288
230193_at	11.18	11.81	14.28	2.90	2.39	3.83	1.16	220.50	47.67	83.65	28.52	WDR66	chr12q24.31	NM_144668
1564307_a_at	0.38	8.20	3.09	7.83	7.07	4.78	0.10	32.60	1.45	12.50	12.30	A2ML1	chr12p13.31	NM_144670
207583_at	0.56	0.52	0.07	1.40	3.00	1.20	27.67	1.65	0.17	28.50	41.50	ABCD2	chr12q11-q12	NM_005164
237974_at	2.00	2.00	24.50	10.10	0.82	8.25	2.09	1.73	8.71	10.63	26.00	ABHD12B	chr14q22.1	NM_181533
1568970_at	13.00	0.05	1.33	1.63	0.26	10.00	14.00	1.26	12.83	1.36	2.89	ADAM18	chr8p11.22	NM_014237
201792_at	32.08	0.36	10.73	10.33	1.49	0.79	3.82	0.52	43.14	3.32	1.91	AEBP1	chr7p13	NM_001129
210081_at	0.22	0.51	1.57	0.05	0.91	12.33	21.83	0.50	1.52	14.60	0.32	AGER	chr6p21.3	NM_172197
209173_at	12.71	3.50	39.00	2.69	0.50	1.75	0.43	44.29	0.38	2.00	0.62	AGR2	chr7p21.3	NM_006408
1560098_at	0.03	31.00	0.33	1.24	21.50	0.34	0.33	3.50	54.00	0.65	10.00	AKR1C2	chr10p15-p14	NM_001354
1562261_at	1.18	4.22	6.58	1.70	10.25	0.56	2.86	3.61	1.03	10.74	23.87	AMZ1	chr7p22.2	NM_133463
239183_at	20.50	2.43	1.18	1.94	22.00	2.75	0.67	0.60	0.16	40.00	0.06	ANGPTL1	chr1q25.2	NM_004673
1564000_at	1.43	0.43	10.50	12.67	1.33	1.00	0.50	20.40	1.36	7.00	0.33	ANKRD31	chr5q13.3	XM_927671
203074_at	2.99	1.58	5.79	2.19	5.49	18.33	0.74	9.40	6.62	17.11	84.49	ANXA8	chr10q11.2	NM_001630
1552691_at	48.00	23.67	26.33	5.00	3.00	182.00	2.83	1.96	27.00	175.00	1.00	ARL11	chr13q14.3	NM_138450
229062_at	11.27	10.13	19.57	2.38	1.43	12.09	1.50	3.53	2.66	3.63	1.00	ARL9	chr4q12	NM_206919
235503_at	72.00	3.33	19.61	1.25	20.86	50.50	2.35	26.18	14.14	5.78	8.77	ASB5	chr4q34.2	NM_080874
214498_at	11.80	8.50	0.34	3.94	1.08	11.25	0.61	2.00	27.20	11.57	0.15	ASIP	chr20q11.2-q12	NM_001672
237338_at	0.19	0.11	12.18	4.67	0.71	9.50	0.56	2.43	4.32	20.13	12.40	B3GNT8	chr19q13.2	NM_198540
1560683_at	3.03	0.43	13.50	16.50	0.40	14.50	0.53	0.38	0.07	17.00	2.00	BCL8	chr15q11-q13	XM_001125807
1561263_at	1.47	9.38	0.08	0.82	0.35	19.25	12.50	14.00	8.18	0.38	1.24	C1QTNF3	chr5p13.3	NM_181435
204865_at	1.62	1.27	69.40	2.10	1.99	11.43	0.29	2.11	3.09	28.65	20.75	CA3	chr8q13-q22	NM_005181
228083_at	4.46	4.45	34.00	32.67	0.69	3.58	1.05	11.15	1.14	11.94	0.74	CACNA2D4	chr12p13.33	NM_172364
1555544_a_at	0.17	0.26	0.13	10.60	2.29	1.50	0.10	1.00	11.80	0.40	19.33	CADM2	chr3p12.1	NM_153184
243804_at	0.96	2.36	0.22	1.09	0.08	1.87	16.57	18.00	10.08	1.11	0.19	CCBE1	chr18q21.32	NM_133459
223710_at	1.78	0.90	1.24	2.14	3.30	5.88	1.74	41.00	3.00	15.00	10.71	CCL26	chr7q11.23	NM_006072
205114_s_at	22.14	5.65	7.38	2.26	1.95	15.33	0.58	18.42	9.00	23.46	1.07	CCL3	chr17q11-q21	NM_002983
1405_i_at	38.07	33.75	2.71	6.82	2.89	62.20	0.63	3.87	14.27	42.09	5.29	CCL5	chr17q11.2-q12	NM_002985
214551_s_at	0.95	0.54	13.50	0.05	0.29	15.86	14.75	0.33	1.67	7.64	0.79	CD7	chr17q25.2	NM_006137
211188_at	14.57	1.00	1.26	10.33	0.19	0.08	1.12	18.80	0.57	0.52	1.04	CD84	chr1q24	NM_003874
227850_x_at	0.47	17.00	4.07	30.50	3.25	18.00	1.33	9.14	0.85	2.72	0.56	CDC42EP5	chr19q13.42	NM_145057
209498_at	6.30	3.00	3.48	3.61	2.93	22.13	1.10	15.63	3.00	14.07	0.54	CEACAM1	chr19q13.2	NM_001712
206198_s_at	0.44	1.00	0.13	2.00	8.50	1.00	0.12	20.00	26.67	16.00	2.00	CEACAM7	chr19q13.2	NM_006890
1553970_s_at	0.39	2.00	4.73	2.61	1.06	15.30	0.56	2.17	13.64	10.41	12.22	CEL	chr9q34.3	NM_001807
206210_s_at	20.25	1.00	12.37	22.67	16.83	32.33	1.00	0.19	12.19	1.40	0.86	CETP	chr16q21	NM_000078
234702_x_at	16.00	0.05	0.50	0.38	1.55	29.00	12.33	145.00	0.16	0.33	0.43	CFTR	chr7q31.2	NM_000492
207047_s_at	12.71	5.25	12.57	0.93	10.75	4.12	0.79	0.26	0.70	0.82	3.82	CLCNKA	chr1p36	NM_000085
207342_at	1.18	10.67	31.14	10.17	1.90	15.08	1.00	2.36	10.45	3.03	1.73	CNGB1	chr16q13	NM_001297
237177_at	2.50	0.51	1.00	8.60	1.20	0.20	19.00	14.25	2.90	36.33	0.86	CNTN4	chr3p26-p25	NM_175613
1553441_at	1.00	0.20	5.25	1.12	15.00	21.00	15.00	0.14	0.08	17.00	5.33	CNTNAP4	chr16q23.1	NM_033401
37892_at	1.37	11.33	39.17	7.22	0.62	7.89	1.07	0.35	114.43	5.04	7.12	COL11A1	chr1p21	NM_001854
202404_s_at	2.56	4.75	273.00	1.05	4.51	1.44	0.43	16.33	209.50	45.40	15.34	COL1A2	chr7q22.1	NM_000089
201438_at	174.90	54.20	110.88	1.67	33.97	2.00	1.03	23.03	1.66	133.24	47.46	COL6A3	chr2q37	NM_004369
231265_at	6.00	9.86	12.00	17.47	14.92	21.80	1.29	6.17	64.96	11.56	2.74	COX7B2	chr4p12	NM_130902
210229_s_at	3.12	0.67	5.35	4.09	3.77	0.50	1.85	10.25	0.77	37.82	10.47	CSF2	chr5q31.1	NM_000758
207442_at	259.50	25.95	2.82	2.13	1.10	1.71	0.76	15.00	10.08	54.07	0.31	CSF3	chr17q11.2-q12	NM_172220
204533_at	7.99	5.17	3.92	3.69	8.44	102.55	0.29	2.03	27.20	105.55	0.13	CXCL10	chr4q21	NM_001565
211122_s_at	8.63	1.17	3.96	11.50	19.17	3.85	0.20	3.23	21.00	105.25	1.21	CXCL11	chr4q21.2	NM_005409
214974_x_at	1.35	119.40	405.00	1.57	1.81	5.30	1.35	5.44	1.15	31.02	4.06	CXCL5	chr4q12-q13	NM_002994
226632_at	0.94	3.63	1.39	5.92	55.25	2.11	1.28	14.03	166.00	6.85	12.26	CYGB	chr17q25.3	NM_134268
206754_s_at	37.40	2.56	1.43	6.33	1.00	11.36	0.29	17.60	3.33	0.47	1.97	CYP2B7P1	chr19q13.2	NR_001278
208126_s_at	14.45	13.00	2.16	0.88	4.50	91.50	0.36	0.29	0.90	1.50	1.08	CYP2C18	chr10q24	NM_000772
208147_s_at	16.85	0.69	56.85	3.84	1.26	42.00	6.75	0.17	2.26	2.63	3.40	CYP2C8	chr10q23.33	NM_000770
216307_at	10.63	21.00	1.79	1.55	5.67	45.00	2.00	6.86	15.27	8.43	4.62	DGKB	chr7p21.2	NM_145695
240301_at	3.68	1.87	1.48	6.62	2.56	15.27	8.55	2.77	79.50	13.25	42.00	DPPA2	chr3q13.13	NM_138815
228339_at	9.13	0.29	4.78	1.36	2.67	0.23	20.00	7.03	11.41	7.34	40.67	ECSM2	chr5q31.2	NM_001077693
201324_at	22.91	0.98	5.75	1.51	1.86	1.00	1.05	16.24	2.08	36.93	0.76	EMP1	chr12p12.3	NM_001423
232164_s_at	0.39	1.30	36.25	12.11	2.31	8.37	0.35	1.79	15.47	26.10	34.67	EPPK1	chr8q24.3	NM_031308
205738_s_at	2.81	0.30	24.31	6.13	4.00	31.82	3.33	13.00	8.13	0.17	1.87	FABP3	chr1p33-p32	NM_004102
227711_at	54.08	27.67	318.42	1.32	21.24	28.38	3.00	24.72	54.62	130.68	16.63	FAM112B	chr12q13.2	NM_144594
241829_at	2.07	1.84	3.00	14.67	3.25	12.40	11.50	0.61	0.61	0.30	2.61	FAM124A	chr13q14.3	NM_145019
220759_at	0.23	6.00	4.40	0.42	20.00	1.50	1.00	11.17	0.25	15.33	0.85	FAM12B	chr14q11.2	NM_022360
236029_at	1.69	0.17	0.35	0.81	1.45	1.98	20.50	12.00	19.00	9.00	2.20	FAT3	chr11q14.3	XM_926199
1555412_at	0.89	14.00	29.00	2.00	0.68	14.00	0.50	0.43	3.41	2.18	0.66	FBXL21	chr5q31	NM_012159
1556325_at	275.00	1.80	132.25	3.96	46.33	2.29	0.73	156.00	2.34	8.53	9.96	FILIP1	chr6q14.1	NM_015687
232010_at	14.86	1.50	9.00	10.25	1.41	1.83	1.12	0.75	166.33	6.78	2.33	FSTL5	chr4q32.3	NM_020116
1566272_at	1.46	9.00	0.55	0.13	21.00	0.79	12.00	13.86	1.32	1.83	1.33	GARNL1	chr14q13.2	NM_014990
238581_at	10.84	0.41	2.51	11.36	4.52	1.17	0.63	47.00	1.39	11.80	10.13	GBP5	chr1p22.2	NM_052942
219777_at	0.25	4.83	15.50	0.88	0.33	1.07	0.33	0.08	0.06	14.00	25.00	GIMAP6	---	NM_024711
220191_at	0.46	1.33	5.31	13.00	1.30	2.86	11.33	0.18	1.27	29.33	1.00	GKN1	chr2p14	NM_019617
205349_at	29.57	1.32	1.42	1.85	1.56	4.10	0.59	13.69	2.79	24.77	1.07	GNA15	chr19p13.3	NM_002068
235139_at	5.87	1.80	1.92	2.77	11.46	3.78	14.62	10.50	1.18	10.80	19.69	GNGT2	chr17q21	NM_031498
205220_at	68.00	1.83	48.00	6.43	17.50	73.00	0.49	3.18	1.93	75.33	0.64	GPR109B	chr12q24.31	NM_006018
212951_at	7.33	10.56	4.67	8.25	1.44	12.00	1.33	2.20	15.30	22.38	15.20	GPR116	chr6p12.3	NM_015234
244493_at	0.07	5.00	10.00	22.00	0.00	2.00	3.00	30.50	0.05	0.75	50.00	GPR22	chr7q22-q31.1	NM_005295
219936_s_at	6.20	13.00	24.50	17.64	2.00	1.30	0.61	10.18	37.22	69.00	2.41	GPR87	chr3q24	NM_023915
230252_at	21.08	2.62	1.16	6.67	1.17	14.67	0.29	25.36	8.00	12.00	4.93	GPR92	chr12p13.31	NM_020400
206643_at	1.98	8.14	0.65	0.04	17.80	2.39	0.55	12.40	1.00	0.10	10.86	HAL	chr12q22-q24.1	NM_002108
216063_at	11.33	0.71	10.75	0.15	0.48	1.32	0.50	4.33	12.00	1.92	2.91	HBBP1	chr11p15.5	NR_001589
202957_at	30.88	6.51	39.53	21.22	6.37	10.24	2.26	139.77	15.14	8.61	9.65	HCLS1	chr3q13	NM_005335
1552758_at	0.82	0.23	9.15	0.97	0.75	21.30	1.88	12.38	0.98	7.44	11.31	HDAC9	chr7p21.1	NM_014707
1564285_at	0.05	40.00	1.29	15.67	0.61	2.13	1.29	0.09	0.65	0.40	11.33	HFM1	chr1p22.2	NM_198550
219863_at	5.51	1.39	5.65	1.35	1.30	55.17	1.07	15.58	1.85	14.85	2.96	HERC5	chr4q22.1	NM_016323
1553568_a_at	1.45	2.38	15.13	1.35	0.59	10.21	2.80	0.88	0.76	32.33	0.65	HIST1H1T	chr6p21.3	NM_005323
221169_s_at	2.10	0.68	21.67	0.11	2.46	0.52	19.60	7.00	18.25	0.85	1.38	HRH4	chr18q11.2	NM_021624
220249_at	2.81	1.25	1.95	7.46	0.68	16.43	0.94	2.00	14.42	13.57	0.80	HYAL4	chr7q31.3	NM_012269
202411_at	5.13	3.43	6.36	2.01	1.98	35.20	0.82	3.57	4.33	91.16	170.86	IFI27	chr14q32	NM_005532
201601_x_at	13.43	3.78	1.70	1.39	1.86	18.30	0.90	4.70	3.15	30.80	0.90	IFITM1	chr11p15.5	NM_003641
211338_at	0.23	31.00	2.00	0.12	10.60	2.26	0.31	16.67	0.36	0.73	0.38	IFNA2	chr9p22	NM_000605
211959_at	17.41	1.26	9.39	1.01	10.33	0.88	3.30	1.11	1.68	7.32	33.24	IGFBP5	chr2q33-q36	NM_000599
220273_at	3.53	0.86	19.29	1.17	2.67	1.31	1.17	18.00	4.13	17.50	0.38	IL17B	chr5q32-q34	NM_014443
210118_s_at	20.58	14.49	57.08	3.84	25.29	5.38	0.95	30.03	0.92	249.57	0.18	IL1A	chr2q14	NM_000575
231755_at	17.57	18.00	0.53	2.43	6.00	0.25	1.56	15.71	2.80	23.13	0.71	IL1F8	chr2q12-q14.1	NM_014438
220322_at	11.66	0.94	0.30	15.23	2.43	0.28	0.31	0.62	0.76	30.25	1.13	IL1F9	chr2q12-q21	NM_019618
209821_at	8.33	11.75	1.00	0.33	11.50	1.50	26.00	15.80	26.33	0.26	0.29	IL33	chr9p24.1	NM_033439
207054_at	26.00	11.00	1.50	0.75	2.50	21.00	5.00	0.38	0.17	0.75	0.29	IMPG1	chr6q14.2	NM_001563
1563335_at	0.12	1.33	28.50	0.17	0.60	0.23	0.50	2.50	2.00	24.17	17.80	IRGM	chr5q33.1	XM_293893
204698_at	11.38	2.11	7.57	0.94	2.04	58.76	0.55	10.67	4.94	245.13	13.36	ISG20	chr15q26	NM_002201
217522_at	5.57	1.03	8.02	1.08	2.51	4.06	0.19	21.71	12.26	21.75	9.22	KCNV2	chr9p24.2	NM_133497
1555275_a_at	3.20	17.50	1.37	1.09	0.05	1.47	33.50	14.57	0.57	1.43	1.35	KLHL6	---	NM_130446
207811_at	6.07	25.00	6.13	170.50	10.71	31.60	0.63	36.50	29.20	28.80	5.15	KRT12	chr17q12	NM_000223
207935_s_at	0.40	61.00	0.71	27.83	4.07	0.42	7.89	2.11	0.19	0.63	22.83	KRT13	chr17q12-q21.2	NM_153490
205157_s_at	21.56	6.75	8.24	15.55	30.89	15.77	0.93	18.44	5.39	34.28	61.75	KRT17	chr17q12-q21	NM_000422
206969_at	7.92	50.29	20.53	5.99	13.69	3.00	0.74	3.56	23.10	10.63	29.04	KRT34	chr17q12-q21	NM_021013
201720_s_at	11.93	1.75	8.13	5.13	26.11	12.88	1.10	41.96	14.48	6.02	12.57	LAPTM5	chr1p34	NM_006762
204428_s_at	0.55	1.85	15.40	1.05	1.43	16.28	0.29	2.31	2.84	19.64	3.10	LCAT	chr16q22.1	NM_000229
212531_at	1.53	17.74	9.80	9.17	5.44	14.89	1.00	3.72	3.29	14.02	1.09	LCN2	chr9q34	NM_005564
205269_at	3.33	21.00	0.20	0.44	1.44	1.31	1.00	16.00	0.31	11.00	0.03	LCP2	chr5q33.1	NM_005565
1563899_at	0.28	0.10	0.19	11.50	11.50	0.37	0.52	14.17	2.18	2.91	1.16	LCTL	chr15q22.31	NM_207338
213371_at	11.25	0.26	4.00	7.80	0.33	0.03	0.50	12.00	14.50	1.03	0.17	LDB3	chr10q22.3	NM_007078
230865_at	31.00	23.00	0.03	0.62	0.59	0.08	7.00	12.33	0.01	0.08	0.15	LIX1	chr5q15	NM_153234
1553729_s_at	6.22	5.00	6.33	38.63	2.13	13.80	0.95	3.54	0.74	15.84	33.05	LRRC43	chr12q24.31	NM_152759
201744_s_at	1.34	0.00	1.22	0.94	1.37	12.33	4.00	1.35	5.56	22.67	36.52	LUM	chr12q21.3-q22	NM_002345
206276_at	17.00	2.05	1.50	9.75	3.13	4.00	1.36	64.36	2.14	12.12	2.36	LY6D	chr8q24-qter	NM_003695
202888_s_at	1.66	3.46	14.26	1.58	3.41	10.27	0.99	7.41	0.69	1.69	14.96	MAP7	chr6q23.3	NM_003980
1552456_a_at	1.74	1.11	6.81	14.30	7.80	0.38	1.00	1.44	11.89	166.50	3.55	MBD3L2	chr19p13.2	NM_144614
230498_at	0.39	0.21	2.80	14.91	0.79	0.14	11.20	0.61	0.98	3.08	11.18	MCHR1	chr22q13.2	NM_005297
213764_s_at	2.31	0.00	2.54	15.50	0.33	12.67	3.00	22.20	1.32	157.50	366.67	MFAP5	chr12p13.1	NM_003480
204475_at	88.98	11.37	7.63	2.86	188.27	2.32	1.45	20.80	46.01	70.70	6.44	MMP1	chr11q22.3	NM_002421
1554892_a_at	11.75	10.40	0.70	10.22	1.07	0.41	0.97	0.09	1.52	2.11	2.61	MS4A3	chr11q12.1	NM_006138
220790_s_at	16.00	0.57	5.13	1.89	0.19	0.63	2.29	15.20	14.43	0.58	0.77	MS4A5	chr11q12	NM_023945
217110_s_at	0.02	15.00	13.00	0.26	1.52	1.30	1.50	2.10	0.91	22.50	7.41	MUC4	chr3q29	NM_004532
204994_at	7.63	2.15	1.43	2.44	1.95	91.75	0.88	3.47	69.00	66.01	12.61	MX2	chr21q22.3	NM_002463
227799_at	20.61	2.74	5.08	1.92	24.93	7.50	1.07	22.63	0.51	8.74	11.38	MYO1G	chr7p13-p11.2	NM_033054
1552578_a_at	37.00	22.00	0.41	0.86	12.25	7.89	29.00	6.60	0.13	0.35	1.15	MYO3B	chr2q31.1	NM_138995
1562790_at	1.53	1.32	1.08	2.30	12.33	10.50	0.91	0.64	6.83	1.25	11.71	NCALD	chr8q22.2	NM_032041
209949_at	20.58	0.15	20.88	2.49	6.67	2.32	2.04	2.74	1.91	33.57	4.40	NCF2	chr1q25	NM_000433
210113_s_at	17.95	1.14	2.82	3.40	6.88	5.88	1.27	2.17	0.33	65.00	20.45	NLRP1	chr17p13.2	NM_033007
221690_s_at	30.38	35.67	0.53	3.31	0.64	2.83	1.00	7.81	12.86	25.36	5.19	NLRP2	chr19q13.42	NM_017852
1556029_s_at	20.91	1.15	1.43	1.85	0.34	30.00	1.23	11.75	2.75	7.92	1.55	NMNAT2	chr1q25	NM_170706
206801_at	65.64	11.67	5.74	1.39	2.94	3.29	1.59	1.55	26.00	2.60	1.52	NPPB	chr1p36.2	NM_002521
207089_at	0.81	12.83	13.75	0.81	0.06	1.09	15.67	0.05	3.80	2.00	0.11	NRAP	chr10q24-q26	NM_198060
232598_at	13.67	1.18	0.09	0.87	1.49	0.85	0.75	0.15	1.35	11.20	15.00	NUP210L	chr1q21.3	NM_207308
205660_at	20.80	2.07	2.82	0.91	1.92	11.88	0.39	3.87	5.55	77.89	1.61	OASL	chr12q24.2	NM_198213
218162_at	1.04	2.25	2.37	11.33	2.27	12.83	0.87	20.67	1.78	5.28	2.18	OLFML3	chr1p13.2	NM_020190
1567298_at	1.03	15.62	4.42	0.62	2.22	1.42	0.16	11.25	11.33	0.79	2.45	OR13C4	chr9q31.1	NM_001001919
1567246_at	0.60	0.33	2.33	25.00	1.80	1.06	36.00	52.00	0.63	0.53	2.92	OR5H1	chr3q11.2	NM_001005338
205040_at	0.85	0.43	14.20	2.78	1.33	1.41	1.96	1.75	29.86	28.33	0.09	ORM1	chr9q31-q32	NM_000607
231725_at	0.82	1.20	1.59	1.06	38.25	2.65	0.57	0.63	33.78	13.23	36.33	PCDHB2	chr5q31	NM_018936
244183_x_at	1.09	32.00	0.08	2.63	1.00	13.00	13.00	3.00	0.84	0.02	1.53	PCDHB3	chr5q31	NM_018937
239443_at	19.00	4.00	0.76	2.32	1.04	0.75	9.40	1.47	16.31	29.00	4.81	PCDHB6	chr5q31	NM_018939
204869_at	0.43	0.17	0.93	2.71	11.33	6.36	12.71	5.67	8.67	18.00	0.53	PCSK2	chr20p11.2	NM_002594
224224_s_at	0.34	2.48	11.25	0.92	66.00	1.21	0.64	22.00	0.64	0.78	0.84	PDE11A	chr2q31.2	NM_016953
220595_at	0.61	0.70	0.55	13.60	0.38	12.80	12.67	0.20	0.73	1.52	10.67	PDZRN4	chr12q12	NM_013377
207815_at	37.00	0.40	0.64	32.00	0.12	0.13	0.15	12.00	0.78	1.00	0.13	PF4V1	chr4q12-q21	NM_002620
203691_at	10.49	11.94	1.11	23.94	0.29	1.59	1.81	2.00	3.45	0.50	1.07	PI3	chr20q12-q13	NM_002638
1557085_at	1.17	12.00	1.59	0.57	1.50	4.33	2.18	0.67	18.25	11.43	1.20	PLAC1L	chr11q12.1	NM_173801
1553364_at	4.86	0.56	2.78	10.25	0.11	0.67	0.30	0.67	22.86	13.80	2.21	PNPLA1	chr6p21.31	NM_173676
210809_s_at	5.16	4.36	90.47	3.61	58.00	9.94	3.81	50.56	39.15	30.45	24.55	POSTN	chr13q13.3	NM_006475
207846_at	0.11	0.91	0.18	0.84	0.05	14.40	19.00	5.58	0.15	12.00	7.40	POU1F1	chr3p11	NM_000306
227006_at	1.17	30.67	69.00	2.25	10.63	17.00	1.67	72.33	3.96	40.25	3.33	PPP1R14A	chr19q13.1	NM_033256
212187_x_at	2.97	0.24	14.38	13.05	3.56	7.26	0.72	11.07	23.41	0.59	0.30	PTGDS	chr9q34.2	NM_000954
217267_s_at	1.52	1.09	0.18	0.41	4.80	0.08	0.59	42.00	11.20	14.00	0.14	RAB7A	chr3q21.3	NM_004637
1554745_at	24.00	10.50	0.15	0.22	5.42	1.80	0.32	3.33	0.92	11.11	4.25	RALGPS1	chr9q33.3	NM_014636
230563_at	4.86	62.67	3.69	66.29	1.52	2.31	1.13	15.62	0.94	11.54	23.32	RASGEF1A	chr10q11.21	NM_145313
236563_at	11.17	0.33	0.78	11.40	0.83	1.09	1.75	13.18	0.38	4.13	0.56	RD3	chr1q32.3	NM_183059
211021_s_at	1.04	17.80	1.00	0.13	5.63	18.22	0.33	0.52	15.57	2.45	0.71	RGS14	chr5q35.3	NM_006480
204338_s_at	0.46	0.16	26.75	0.65	0.67	0.30	1.56	4.28	1.74	10.94	11.75	RGS4	chr1q23.3	NM_005613
206145_at	0.92	34.50	3.08	0.88	0.15	0.28	0.68	14.50	1.24	0.83	35.50	RHAG	chr6p21.1	NM_000324
234699_at	1.25	18.75	7.50	20.67	0.71	0.35	0.21	35.00	0.07	1.30	25.33	RNASE7	chr14q11.2	NM_032572
207569_at	16.00	0.85	0.71	3.89	2.37	1.67	0.52	6.23	1.24	13.00	56.25	ROS1	chr6q22	NM_002944
213797_at	19.75	1.09	5.19	0.15	2.07	32.28	2.02	5.64	40.00	81.47	0.93	RSAD2	chr2p25.2	NM_080657
1552568_at	0.10	17.60	0.99	0.63	2.35	7.83	10.43	27.33	0.71	4.20	1.57	RTP3	chr3p21.3	NM_031440
205529_s_at	2.78	14.75	0.55	0.94	0.52	17.00	1.32	28.40	0.71	0.55	26.43	RUNX1T1	chr8q22	NM_175636
230287_at	0.19	0.59	20.25	1.17	0.26	0.95	5.33	0.77	0.64	15.33	18.50	RUTBC2	chr22q11.23	NM_133454
203186_s_at	4.53	5.97	2.31	8.37	5.41	13.81	0.90	15.85	13.66	6.24	7.64	S100A4	chr1q21	NM_019554
204351_at	38.50	110.89	44.14	1.48	35.20	28.69	0.55	4.35	18.56	5.78	4.75	S100P	chr4p16	NM_005980
229839_at	1.67	1.17	0.51	11.00	10.25	21.00	6.44	1.00	9.70	0.16	1.90	SCARA5	chr8p21.1	NM_173833
1552365_at	0.87	0.30	3.00	0.75	1.04	11.61	21.50	27.13	0.89	35.00	2.41	SCIN	chr7p21.3	NM_033128
209720_s_at	1.00	0.80	15.00	10.00	6.00	6.00	2.25	106.00	16.86	0.50	2.25	SERPINB3	chr18q21.3	NM_006919
204855_at	188.75	3.97	13.00	1.07	12.43	5.00	0.56	26.67	47.45	432.67	0.50	SERPINB5	chr18q21.3	NM_002639
206421_s_at	5.52	3.22	8.65	11.13	11.78	0.83	1.42	2.81	26.31	90.31	4.30	SERPINB7	chr18q21.33	NM_003784
205576_at	3.02	69.83	13.36	4.06	1.07	2.25	0.50	43.50	5.85	83.00	9.36	SERPIND1	chr22q11.2	NM_000185
202283_at	196.13	0.97	2.52	104.83	1.58	3.71	3.15	12.23	9.40	12.03	32.24	SERPINF1	chr17p13.1	NM_002615
33323_r_at	5.21	1.22	1.46	10.73	2.24	2.26	1.02	19.01	8.07	40.48	27.72	SFN	chr1p36.11	NM_006142
222838_at	17.09	1.08	0.82	1.46	0.80	12.33	1.18	22.25	1.76	34.33	16.22	SLAMF7	chr1q23.1	NM_021181
208354_s_at	4.28	3.33	20.42	2.90	10.76	87.80	1.67	1.61	2.43	2.73	4.25	SLC12A3	chr16q13	NM_000339
1565925_at	10.75	0.07	0.20	31.00	16.00	7.00	3.17	0.51	0.69	0.11	0.04	SLC17A4	chr6p22-p21.3	NM_005495
207201_s_at	14.44	20.90	13.77	2.59	5.45	2.80	1.00	2.55	11.52	6.48	91.00	SLC22A1	chr6q26	NM_153187
1561951_at	11.50	0.16	0.17	2.25	0.10	2.13	21.00	1.00	0.25	0.86	22.33	SLC5A12	chr11p14.2	NM_178498
1567682_x_at	1.05	2.00	0.59	0.03	17.33	1.23	0.18	10.67	1.50	19.50	0.23	SNORA74A	chr5q31.2	NR_002915
223869_at	0.99	34.00	24.49	25.83	0.24	36.50	0.40	1.25	31.40	12.20	37.67	SOST	chr17q11.2	NM_025237
241961_at	0.14	15.00	1.55	0.03	11.00	3.50	0.06	6.13	0.58	14.25	2.50	SRD5A2L2	chr4q13.1	NM_001010874
1563595_at	0.88	0.13	15.57	10.40	0.14	4.50	0.04	0.61	0.44	0.39	10.20	SRGAP3	chr3p25.3	NM_014850
201858_s_at	1.63	1.10	8.18	1.17	5.66	45.00	1.12	584.14	0.84	111.91	63.39	SRGN	chr10q22.1	NM_002727
1570306_at	0.10	2.00	1.20	0.26	0.67	11.50	2.75	14.00	4.50	15.60	0.39	ST18	chr8q11.23	NM_014682
223883_s_at	33.88	21.00	14.92	6.00	3.57	54.17	1.59	44.75	23.81	8.18	9.70	STK31	chr7p15.3	NM_032944
203998_s_at	28.00	6.86	1.38	0.61	1.14	32.33	0.08	19.63	0.90	1.18	0.56	SYT1	chr12cen-q21	NM_005639
205513_at	0.90	0.32	23.75	2.89	0.50	54.00	12.17	2.12	2.17	1.95	0.53	TCN1	chr11q11-q12	NM_001062
209937_at	2.27	1.27	2.33	16.75	3.04	372.33	0.53	0.55	25.32	3.06	1.54	TM4SF4	chr3q25	NM_004617
209904_at	1.00	0.86	62.29	1.57	27.55	107.63	2.17	8.58	60.64	0.75	0.48	TNNC1	chr3p21.3	NM_003280
214601_at	8.67	0.07	19.67	1.20	12.00	1.29	2.00	0.29	10.88	1.82	1.80	TPH1	chr11p15.3	NM_004179
231339_at	3.81	32.00	32.90	4.71	21.50	1.82	16.50	12.60	5.06	13.90	2.76	TSPYL6	chr2p16.2	NM_001003937
1556666_a_at	0.50	63.00	1.00	1.97	0.24	0.22	43.00	4.50	1.00	12.50	3.26	TTC6	chr14q21.1	NM_001007795
228352_at	10.50	3.57	33.89	1.79	8.00	29.15	1.06	13.21	3.89	13.75	3.87	UNC13D	chr17q25.1	NM_199242
214382_at	11.00	10.11	0.78	7.46	0.73	0.18	1.50	12.00	0.14	8.67	7.00	UNC93A	chr6q27	NM_018974
210064_s_at	2.09	0.61	7.06	2.52	2.41	195.00	5.65	7.64	7.09	32.50	63.12	UPK1B	chr3q13.3	NM_006952
205844_at	2.17	1.70	4.36	5.45	3.86	402.67	1.63	2.66	4.42	10.77	16.92	VNN1	chr6q23-q24	NM_004666
1562209_at	4.16	44.00	7.89	3.57	3.37	14.09	3.20	30.82	8.43	14.13	206.50	WDR21B	chr4p13	NM_001029955
213725_x_at	0.44	19.25	1.33	4.29	2.38	1.67	2.00	1.11	0.53	11.87	14.00	XYLT1	chr16p12.3	NM_022166
1552946_at	9.68	28.00	4.78	5.24	1.12	1.41	0.93	37.43	14.48	3.65	0.55	ZNF114	chr19q13.32	NM_153608
1568646_x_at	6.33	3.42	2.50	1.18	0.51	84.00	0.11	12.75	1.20	23.50	0.86	ZNF208	chr19p12	NM_007153
231470_at	35.00	8.00	3.00	0.49	0.88	35.67	0.86	0.95	11.00	2.92	2.33	ZNF493	chr19p12	NM_175910
219995_s_at	10.50	1.64	23.00	0.59	1.50	1.63	0.67	2.50	10.50	21.00	6.87	ZNF750	chr17q25.3	NM_024702
234212_at	2.53	6.50	25.00	0.31	0.48	15.67	0.11	0.57	0.71	13.50	0.65	ACTR2	chr2p14	NM_005722
1560369_at	2.06	13.60	1.92	4.10	0.32	5.90	0.38	0.35	11.00	10.10	0.45	ANKH	chr5p15.1	NM_054027
1554816_at	0.57	22.00	0.25	0.05	12.00	0.18	0.80	4.00	5.50	15.00	6.57	ASTN2	chr9q33.1	NM_198188
206787_at	5.69	3.20	1.50	20.50	4.60	9.00	1.60	20.00	13.73	6.42	0.70	BRDT	chr1p22.1	NM_001726
205476_at	1.52	8.04	124.42	22.14	139.69	157.08	0.75	659.12	11.17	295.18	362.78	CCL20	chr2q33-q37	NM_004591
219529_at	6.43	3.25	12.69	55.75	10.79	218.45	1.15	10.68	3.53	26.08	155.60	CLIC3	chr9q34.3	NM_004669
209083_at	20.21	8.77	20.86	1.14	5.89	9.21	0.37	19.62	1.73	2.59	11.38	CORO1A	chr16p11.2	NM_007074
204570_at	4.42	38.14	10.80	22.31	2.80	98.67	4.29	12.16	24.68	20.21	30.90	COX7A1	chr19q13.1	NM_001864
205081_at	4.26	26.09	34.05	2.22	20.80	21.83	1.31	2.13	26.24	15.36	0.46	CRIP1	chr14q32.33	NM_001311
1552368_at	5.81	87.00	14.75	1.65	4.02	1.04	11.75	1.21	3.08	6.79	2.91	CTCFL	chr20q13.31	NM_080618
225681_at	0.71	20.33	230.45	21.34	0.87	6.37	1.09	1.47	43.90	340.14	0.74	CTHRC1	chr8q22.3	NM_138455
216351_x_at	6.00	0.80	2.19	56.42	13.50	20.00	0.46	19.88	14.50	1.57	12.33	DAZ1	chrYq11.223	NM_004081
206588_at	599.36	40.45	200.60	47.40	13.25	24.16	1.69	26.85	93.05	41.69	20.30	DAZL	chr3p24.3	NM_001351
227081_at	30.25	1.14	4.44	10.00	1.67	21.44	0.12	0.67	11.64	0.18	0.36	DNALI1	chr1p35.1	NM_003462
205493_s_at	2.85	0.20	0.59	0.98	0.66	25.50	2.20	0.77	5.84	25.33	10.85	DPYSL4	chr10q26	NM_006426
241224_x_at	4.63	14.19	117.82	23.03	48.55	11.06	0.38	120.40	23.50	58.40	4.51	DSCR8	chr21q22.2	NM_032589
215356_at	25.50	44.90	18.38	9.65	10.57	75.50	3.56	31.07	68.93	62.11	18.55	ECAT8	chr19q13.11	NM_001015890
224225_s_at	4.97	14.00	7.68	7.85	1.54	40.50	0.83	3.59	2.95	18.67	11.50	ETV7	chr6p21	NM_016135
226847_at	7.13	2.32	5.17	4.80	51.33	29.50	1.57	0.90	4.47	3.64	29.50	FST	chr5q11.2	NM_013409
211264_at	0.47	14.00	0.15	1.00	23.50	4.83	17.00	5.00	0.75	0.97	1.38	GAD2	chr10p11.23	NM_000818
232195_at	44.25	8.88	126.71	24.14	4.69	61.33	1.02	6.15	171.33	41.62	27.17	GPR158	chr10p12.1	NM_020752
236538_at	16.50	4.00	11.00	16.00	0.33	0.10	0.22	5.50	0.21	1.50	0.47	GRIA2	chr4q32-q33	NM_000826
223861_at	64.76	11.65	22.44	3.58	114.75	23.05	5.88	9.82	289.67	141.00	33.56	HORMAD1	chr1q21.2	NM_032132
203332_s_at	1.22	18.17	1.32	3.12	1.38	8.63	1.47	22.13	4.12	14.00	1.68	INPP5D	chr2q37.1	NM_005541
232352_at	16.78	29.13	1.26	1.00	0.77	0.88	2.68	0.78	1.00	10.88	1.15	ISL2	chr15q23	NM_145805
229475_at	40.46	12.73	397.00	5.90	94.47	8.96	0.91	29.33	55.79	24.25	21.43	MAEL	chr1q24.1	NM_032858
220850_at	7.50	0.47	14.00	17.17	32.00	0.24	2.00	1.00	1.84	0.23	0.05	MORC1	chr3q13	NM_014429
33767_at	6.82	9.50	195.50	0.38	2.56	15.95	0.87	56.80	35.50	10.48	2.12	NEFH	chr22q12.2	NM_021076
1560527_at	169.08	19.54	23.86	8.98	174.33	73.00	0.58	55.00	150.53	231.50	12.05	NF-E4	chr7q22.1	NM_001085386
209652_s_at	72.07	0.99	3.54	2.06	2.30	16.73	0.74	61.06	23.35	6.12	16.10	PGF	chr14q24-q31	NM_002632
219014_at	15.92	3.70	8.50	22.71	4.54	18.43	1.03	1.49	1.28	2.73	23.86	PLAC8	chr4q21.22	NM_016619
231544_s_at	2.08	0.41	11.00	3.50	1.20	0.25	3.58	25.00	0.63	13.33	17.75	POLR3G	chr5q14.3	NM_006467
210550_s_at	8.22	2.25	18.43	42.22	11.57	6.71	3.69	2.08	2.15	6.04	2.42	RASGRF1	chr15q24	NM_153815
238357_at	13.00	1.29	0.41	1.65	12.90	0.14	0.22	0.26	0.90	11.25	1.67	RBM39	chr20q11.22	NM_184244
1559882_at	2.42	6.71	0.78	0.05	0.81	17.00	43.00	28.50	0.87	5.76	5.50	SAMHD1	chr20pter-q12	NM_015474
1558338_at	6.40	1.33	19.00	1.27	1.80	4.00	3.50	0.37	10.13	22.50	0.14	SEMA6A	chr5q23.1	NM_020796
221037_s_at	52.00	1.45	55.00	2.77	1.46	5.75	16.00	2.50	7.92	2.38	0.80	SLC25A31	chr4q28.1	NM_031291
1558668_s_at	0.15	7.38	11.00	8.14	27.33	6.15	7.00	1.80	2.59	22.50	4.22	SPATA22	chr17p13.3	NM_032598
229352_at	13.80	1.73	0.80	0.92	1.11	19.20	10.80	21.00	69.23	3.65	5.58	SPESP1	chr15q23	NM_145658
209437_s_at	16.80	0.73	1.02	4.25	12.11	15.71	0.44	3.28	1.95	0.03	26.00	SPON1	chr11p15.2	NM_006108
205691_at	32.75	1.06	2.27	1.99	1.62	0.50	0.19	29.60	26.00	6.80	2.65	SYNGR3	chr16p13	NM_004209
232692_at	0.48	2.43	19.50	0.93	5.40	0.53	1.00	26.67	33.00	2.68	16.71	TDRD6	chr6p12.3	NM_001010870
228285_at	4.58	5.84	12.64	1.53	8.00	30.25	0.12	12.64	1.31	4.33	1.24	TDRD9	chr14q32.33	NM_153046
1566606_a_at	18.00	1.52	0.28	1.29	0.05	0.30	1.41	1.14	16.50	29.00	10.17	TEX9	chr15q21.3	NM_198524
223829_at	11.60	1.33	0.87	1.77	0.42	16.67	0.19	2.65	32.20	2.58	13.00	TKTL2	chr4q32.3	NM_032136
1553276_at	0.44	0.50	27.00	10.00	1.67	1.40	0.17	1.45	27.33	60.33	2.54	ZNF560	chr19p13.2	NM_152476
227952_at	49.00	1.54	1.79	16.99	1.61	2.51	1.20	24.33	8.92	22.59	4.83	ZNF718	chr4p16.3	NM_001039127
1553604_at	0.14	0.00	0.03	2.82	6.63	30.50	10.00	5.11	4.00	29.00	22.00	ABCA13	chr7p12.3	NM_152701
239579_at	19.25	0.95	0.82	0.89	0.33	1.13	3.70	10.25	2.04	16.60	0.67	ABHD7	chr1p22.1	NM_173567
229534_at	25.00	1.59	5.57	1.53	13.80	1.57	21.00	0.55	3.56	2.71	20.25	ACOT4	chr14q24.3	NM_152331
223918_at	1.15	4.17	19.00	0.13	31.50	1.04	1.02	1.17	2.20	17.20	0.04	ACSL6	chr5q31	NM_015256
203862_s_at	53.00	2.00	17.83	1.68	0.73	1.96	0.05	0.30	20.19	10.09	10.10	ACTN2	chr1q42-q43	NM_001103
207206_s_at	2.26	10.60	2.09	1.89	0.87	6.50	0.26	11.88	9.44	41.67	0.16	ALOX12	chr17p13.1	NM_000697
1553261_x_at	8.17	17.50	0.50	10.75	0.28	30.50	2.00	0.58	0.40	1.13	0.66	ALS2CR11	chr2q33.1	NM_152525
229596_at	0.34	0.64	7.85	0.21	0.57	13.00	1.60	2.02	13.61	38.00	2.31	AMDHD1	chr12q23.1	NM_152435
223333_s_at	6.09	0.79	13.72	0.89	1.18	1.49	1.19	34.57	1.52	3.77	11.43	ANGPTL4	chr19p13.3	NM_139314
230275_at	0.29	2.04	21.17	0.89	44.20	70.83	3.48	0.59	4.16	14.70	11.86	ARSI	chr5q33.1	NM_001012301
239457_at	1.57	0.56	45.00	0.28	1.12	13.59	2.75	0.15	1.53	14.43	1.25	ATP8B3	chr19p13.3	NM_138813
211107_s_at	35.13	4.39	16.20	1.92	1.19	18.92	3.40	52.33	1.46	10.00	2.11	AURKC	chr19q13.43	NM_003160
1555963_x_at	80.57	5.57	2.08	34.13	1.47	40.80	1.00	7.54	3.34	13.39	10.94	B3GNT7	chr2q37.1	NM_145236
1563620_at	0.35	0.50	2.33	0.85	0.64	0.73	11.00	47.00	39.00	1.06	0.41	BTRC	chr10q24.32	NM_033637
1559420_x_at	29.00	2.30	3.32	7.79	1.03	16.00	10.22	0.44	7.26	14.00	0.39	CACNB2	chr10p12	NM_201597
209616_s_at	30.08	1.14	11.08	14.80	0.69	0.28	15.14	1.10	3.36	10.33	0.28	CES1	chr16q13-q22.1	NM_001025194
228335_at	1.70	1.87	8.08	3.21	5.93	15.63	0.11	286.50	1.67	17.52	22.80	CLDN11	chr3q26.2-q26.3	NM_005602
203953_s_at	16.00	3.79	0.46	0.50	1.02	11.00	0.33	0.50	0.42	11.45	0.17	CLDN3	chr7q11.23	NM_001306
234329_at	0.22	2.43	0.14	0.10	2.83	10.10	0.81	16.00	2.69	25.60	0.42	CLIC5	chr6p21.1-p12.1	NM_016929
233109_at	0.27	33.50	0.77	10.22	1.30	2.29	0.34	4.67	3.56	13.22	0.20	COL12A1	chr6q12-q13	NM_080645
231487_at	73.33	70.00	4.93	5.60	38.00	2.00	3.33	5.51	8.02	129.00	17.44	COX8C	chr14q32.13	NM_182971
216314_at	22.00	1.67	0.60	0.12	1.63	2.50	13.75	3.00	1.36	0.25	35.00	CRISP1	chr6p21.3	NM_001131
227702_at	0.54	3.33	4.50	0.12	16.00	0.37	0.14	0.18	17.20	3.00	25.33	CYP4X1	chr1p33	NM_178033
235044_at	1.15	1.46	6.43	0.42	0.60	7.69	4.44	13.25	32.00	22.40	6.29	CYYR1	chr21q21.2	NM_052954
220004_at	80.00	291.00	79.88	5.57	20.30	6.73	0.12	116.00	10.58	11.35	6.58	DDX43	chr6q12-q13	NM_018665
53991_at	3.06	4.06	1.26	7.25	2.69	5.40	0.81	39.73	6.29	51.33	23.58	DENND2A	chr7q34	NM_015689
219908_at	12.00	0.23	0.11	22.50	1.00	1.67	0.10	0.75	0.90	2.50	11.75	DKK2	chr4q25	NM_014421
231778_at	0.34	1.83	27.78	1.55	10.14	13.29	3.67	1.18	3.93	0.73	2.02	DLX3	chr17q21	NM_005220
1553159_at	12.93	1.43	6.23	8.80	0.98	1.70	0.19	16.47	10.36	1.35	1.29	DNAH11	chr7p21	NM_003777
207768_at	3.50	1.63	2.00	0.19	18.00	1.17	6.40	25.00	0.10	13.50	0.67	EGR4	chr2p13	NM_001965
219134_at	106.00	2.73	15.08	0.85	3.00	0.64	1.00	3.25	62.33	45.75	2.89	ELTD1	chr1p33-p32	XM_371262
1552394_a_at	0.67	1.67	12.20	0.28	0.29	11.00	0.64	1.25	1.62	0.12	12.80	ENTHD1	chr22q13.1	NM_152512
225369_at	13.00	1.41	50.56	2.75	2.40	17.22	1.13	4.89	24.10	2.67	27.75	ESAM	chr11q24.2	NM_138961
227194_at	15.33	0.33	1.50	0.18	2.43	0.54	0.56	0.93	10.87	15.00	0.95	FAM3B	chr21q22.3	NM_058186
1555480_a_at	17.00	1.21	24.70	0.10	1.55	3.53	0.82	2.75	2.37	32.13	1.00	FBLIM1	chr1p36.21	NM_017556
203886_s_at	16.40	10.20	11.70	1.06	3.57	1.43	2.13	1.52	2.15	1.63	2.88	FBLN2	chr3p25.1	NM_001998
206987_x_at	0.77	2.26	4.11	31.70	2.11	0.07	6.22	22.64	14.10	14.80	1.74	FGF18	chr5q34	NM_003862
223985_at	1.05	1.98	3.86	17.25	13.60	5.06	17.00	12.00	7.25	1.40	10.14	FSD1L	chr9q31	NM_207647
205498_at	1.37	17.50	1.12	0.86	2.64	0.56	0.16	24.50	1.78	48.00	1.21	GHR	chr5p13-p12	NM_000163
1569886_a_at	13.00	5.60	6.92	1.43	0.50	2.19	0.71	1.40	10.29	18.00	13.60	GLB1L3	chr11q25	NM_001080407
210600_s_at	0.30	15.50	7.20	10.50	0.10	1.56	0.40	32.00	4.00	4.00	1.00	GRK4	chr4p16.3	NM_182982
217151_at	23.50	0.93	10.33	0.54	0.20	0.50	0.14	1.23	5.67	0.67	13.57	HLA-C	chr6p21.3	NM_002117
212873_at	1.98	1.25	26.34	1.92	5.11	32.00	1.24	10.59	16.29	2.55	0.54	HMHA1	chr19p13.3	NM_012292
206024_at	8.43	1.22	2.84	3.16	11.88	18.47	0.70	45.67	2.17	2.67	41.00	HPD	chr12q24-qter	NM_002150
1554121_at	1.67	17.00	0.06	20.67	12.00	1.29	0.09	0.99	0.24	2.46	0.43	HSD17B12	chr11p11.2	NM_016142
202597_at	1.82	11.83	0.37	0.84	0.11	0.29	10.78	1.13	13.77	4.10	0.63	IRF6	chr1q32.3-q41	NM_006147
216502_at	17.00	2.75	1.15	0.48	2.57	0.70	11.67	24.67	2.11	24.67	0.93	ISG20L2	chr1q23.1	NM_030980
207110_at	0.97	0.93	14.71	10.29	0.58	0.09	5.67	16.29	0.32	8.11	2.76	KCNJ12	chr17p11.1	NM_021012
224459_at	10.00	2.30	3.00	9.63	18.00	0.14	13.20	16.67	23.75	22.00	3.40	L2HGDH	chr14q22.1	NM_024884
228080_at	1.57	18.40	2.04	1.39	3.10	41.50	1.15	1.21	2.23	14.27	1.81	LAYN	chr11q23.1	NM_178834
207240_s_at	5.88	0.13	16.00	1.46	1.20	0.20	0.10	29.33	18.00	0.45	0.29	LHCGR	chr2p21	NM_000233
229349_at	63.60	7.56	70.75	1.89	1.96	0.56	0.20	23.00	4.75	5.83	2.43	LIN28B	chr6q21	NM_001004317
236156_at	27.40	0.75	20.80	0.58	0.23	8.44	0.85	18.75	7.00	55.13	0.20	LIPA	chr10q23.2-q23.	NM_000235
1555454_at	1.09	0.17	0.09	0.09	0.49	1.21	26.50	1.76	22.75	16.25	0.16	LITAF	chr16p13.13	NM_004862
223687_s_at	12.93	1.39	9.83	3.66	17.85	16.20	1.01	7.67	29.46	24.94	21.56	LY6K	chr8q24.3	NM_017527
205668_at	0.73	2.62	39.50	27.50	0.99	92.00	27.00	4.67	0.94	0.93	1.52	LY75	chr2q24	NM_002349
218559_s_at	1.69	5.60	17.57	1.36	13.14	10.83	0.22	0.17	8.92	11.94	8.67	MAFB	chr20q11.2-q13.	NM_005461
209373_at	3.31	0.80	16.97	1.05	6.48	63.58	0.40	2.68	1.97	4.22	26.91	MALL	chr2q13	NM_005434
209035_at	2.13	1.62	1.47	19.08	1.12	22.77	5.07	7.20	2.16	11.95	16.64	MDK	chr11p11.2	NM_002391
203417_at	12.31	1.47	4.40	0.89	0.81	0.85	0.46	87.71	1.24	2.08	17.19	MFAP2	chr1p36.1-p35	NM_017459
1569751_at	11.75	0.80	4.28	2.00	1.38	1.50	0.55	10.60	0.45	10.14	0.07	ZNF286A	chr17p11.2	NM_178571
224277_at	8.40	4.00	1.50	0.09	0.80	2.17	49.00	12.50	1.75	20.50	1.22	MOP-1	chr4q21.22	XM_926921
1553132_a_at	14.33	3.35	0.50	0.20	1.89	0.54	1.50	22.00	0.22	21.00	0.07	MTAC2D1	chr14q32.12	NM_152332
1563614_at	2.39	0.41	3.11	1.73	4.33	1.71	1.39	14.44	0.36	14.75	10.17	MTBP	chr8q24.12	NM_022045
214156_at	15.00	0.37	20.00	3.00	0.77	0.18	1.25	0.68	23.25	1.24	4.77	MYRIP	chr3p22.1	NM_015460
239548_at	8.00	0.60	0.87	21.00	1.17	23.50	11.80	2.63	0.14	1.18	0.18	NEGR1	chr1p31.1	NM_173808
224169_at	2.63	1.20	2.47	0.98	1.72	1.41	1.57	82.00	2.75	15.00	23.75	NPFFR2	chr4q21	NM_004885
1559732_at	0.57	1.13	0.55	0.09	0.92	17.75	1.42	13.00	1.14	11.80	1.24	NUB1	chr7q36	NM_016118
228863_at	0.10	6.25	0.89	19.33	1.27	2.47	0.80	0.48	16.55	5.02	18.20	PCDH17	chr13q21.1	NM_001040429
211877_s_at	10.33	0.63	3.45	18.14	17.20	0.75	0.81	3.45	1.86	2.31	0.27	PCDHGA11	chr5q31	NM_032092
206691_s_at	1.09	11.89	26.95	4.39	1.23	9.63	1.50	0.26	2.62	11.40	0.35	PDIA2	chr16p13.3	NM_006849
208233_at	21.50	6.29	12.50	0.48	0.86	0.06	32.00	18.40	0.62	2.75	36.33	PDPN	chr1p36.21	NM_198389
209243_s_at	1.25	0.18	1.00	0.04	0.27	21.00	22.00	0.57	12.43	0.75	5.50	PEG3	chr19q13.4	NM_006210
1556990_at	29.00	5.43	3.63	2.00	0.31	10.11	0.67	10.75	2.27	0.85	1.29	PERP	chr6q24	NM_022121
244315_at	1.30	0.31	8.50	1.02	5.00	13.33	11.33	29.00	0.28	16.57	0.07	PLSCR1	chr3q23	NM_021105
1564414_a_at	3.07	12.57	6.71	2.21	1.23	15.20	4.00	1.42	6.48	24.87	1.50	PNLDC1	chr6q25.3	NM_173516
1563690_at	1.50	0.12	1.00	11.50	0.83	0.73	33.00	38.00	0.07	0.87	3.50	PPP4R1	chr18p11.22	NM_005134
206482_at	0.23	1.02	37.80	17.33	0.36	28.71	0.08	6.71	1.33	21.00	2.56	PTK6	chr20q13.3	NM_005975
223149_s_at	1.24	6.64	1.59	0.40	1.31	12.80	19.00	1.00	0.14	0.30	15.20	PTPN23	chr3p21.3	NM_015466
242493_at	0.38	0.12	16.50	1.51	2.43	12.33	2.50	0.13	11.00	16.75	1.00	PTPRD	chr9p23-p24.3	NM_130393
234102_at	0.97	3.33	1.80	9.33	10.50	5.75	0.88	18.14	10.27	1.78	6.30	RASL11B	chr4q12	NM_023940
61734_at	25.84	3.65	1.94	3.03	11.47	1.76	1.55	22.61	3.06	23.41	10.22	RCN3	chr19q13.33	NM_020650
237719_x_at	5.13	16.00	0.80	9.38	11.50	0.08	17.50	0.10	0.06	14.50	0.48	RGS7BP	chr5q12.3	NM_001029875
213716_s_at	2.41	1.35	5.59	11.00	16.00	21.20	1.76	9.05	1.31	45.20	0.80	SECTM1	chr17q25	NM_003004
239913_at	0.75	0.18	1.43	22.00	12.67	2.48	2.00	20.00	5.33	3.39	0.60	SLC10A4	chr4p12	NM_152679
224126_at	1.03	0.80	16.33	0.12	0.50	2.00	2.50	14.00	5.33	16.67	3.00	SLC10A7	chr4q31.22	NM_032128
230687_at	16.50	1.55	7.38	11.53	2.27	0.91	1.55	1.85	14.76	19.14	1.45	SLC13A3	chr20q12-q13.1	NM_022829
227362_at	2.75	0.42	16.00	4.32	0.56	4.89	0.67	14.14	16.60	0.91	1.51	SLC2A4RG	chr20q13.33	NM_020062
1565702_at	24.50	16.33	0.83	20.00	1.02	7.00	1.57	5.00	11.00	9.42	0.50	SMAD4	chr18q21.1	NM_005359
219993_at	2.95	15.80	2.62	0.92	11.17	30.83	1.79	7.94	2.12	1.88	0.68	SOX17	chr8q11.23	NM_022454
210073_at	0.72	22.00	1.20	2.36	29.00	17.00	1.22	0.89	0.65	2.50	1.63	ST8SIA1	chr12p12.1-p11.	NM_003034
230746_s_at	3.48	22.96	12.76	1.22	1.18	1.77	1.03	1.01	1.18	24.36	0.78	STC1	chr8p21-p11.2	NM_003155
201062_at	0.44	15.60	10.33	7.20	1.00	0.90	0.75	22.25	2.25	1.71	0.61	STOM	chr9q34.1	NM_198194
202286_s_at	97.00	0.99	4.65	6.62	15.42	23.83	6.50	8.96	6.56	8.33	7.47	TACSTD2	chr1p32-p31	NM_002353
216373_at	0.31	23.00	0.30	29.50	14.50	2.00	0.57	0.48	1.64	0.24	0.49	TAPT1	chr4p15.32	NM_153365
240304_s_at	3.73	0.49	0.18	27.56	3.50	7.91	0.36	25.00	11.85	10.00	1.67	TMC5	chr16p12.3	NM_024780
238426_at	0.22	0.75	1.50	3.67	0.70	13.29	1.57	1.51	2.31	12.11	12.79	TMEM130	chr7q22.1	NM_152913
1553601_a_at	1.64	6.43	0.67	22.00	0.90	0.23	2.71	22.75	1.13	1.43	31.33	TMIE	chr3p21	NM_147196
206222_at	6.16	1.33	0.58	11.10	7.20	2.58	1.05	4.73	10.37	24.63	1.46	TNFRSF10C	chr8p22-p21	NM_003841
210643_at	13.33	1.25	0.05	0.43	7.13	0.38	2.58	0.59	11.20	18.50	0.15	TNFSF11	chr13q14	NM_003701
215108_x_at	15.00	0.40	1.36	3.05	0.90	0.45	1.84	27.50	19.67	1.73	0.13	TOX3	chr16q12.1	NM_001080430
215047_at	1.67	0.00	20.67	17.00	1.00	1.33	2.50	17.60	3.82	2.68	8.54	TRIM58	chr1q44	NM_015431
234407_s_at	21.00	0.67	0.75	0.83	10.50	3.22	0.50	27.67	1.78	0.50	0.07	TRPC7	chr5q31.2	NM_020389
234336_s_at	16.33	2.00	4.75	14.75	1.25	0.63	14.83	1.30	1.53	0.49	1.57	TTLL9	chr20q11.21	NM_001008409
1555405_at	1.29	0.42	0.89	2.08	1.50	9.33	12.60	0.34	16.13	13.00	6.77	UBE3C	chr7q36.3	NM_014671
224043_s_at	2.00	0.73	2.33	13.00	0.25	0.28	0.80	2.50	23.25	13.00	0.10	UPB1	chr22q11.2	NM_016327
219740_at	10.73	0.79	0.10	0.69	0.78	0.56	1.44	9.09	11.40	10.96	0.16	VASH2	chr1q32.3	NM_024749
1553197_at	2.37	3.05	5.57	74.50	4.40	1.03	2.73	13.71	5.34	49.25	6.88	WDR21C	chr8q21.3	NM_152418
1560562_a_at	5.91	0.77	11.75	24.00	2.50	16.50	0.11	0.46	4.47	6.75	7.26	ZNF677	chr19q13.41	NM_182609
244552_at	47.00	1.52	1.98	0.65	2.38	1.91	0.96	1.70	14.33	10.25	2.37	ZNF788	chr19p13.2	XR_015208

Key:

🟩	< 4-fold expression increase	🟨	Genes analysed in this study
🟨	4-10-fold expression increase	🟦	Genes previously known to be frequently methylated in RCC
🟥	>10-fold expression increase	🟩	Genes previously shown to be infrequently methylated in RCC
		⬛	No promoter CpG island present
		🟪	Not expressed in kidney tissue
		🟦	Genes not analysed thus far