

Supplementary Table S1 Clinicopathological characteristics of the metastatic CRC patients analysed by immunohistochemistry dichotomised by VDR protein expression levels in tumour stromal fibroblasts or in carcinoma cells

Characteristics	VDR protein expression in stromal fibroblasts (n=658)			VDR protein expression in carcinoma cells (n=658)		
	Low (n=478)	High (n=180)	p Value	Low (n=490)	High (n=168)	p Value
Age, median (range)	68 (24-88)	68 (35-86)		68 (24-88)	68 (35-86)	
Gender, n (%)						
Female	191 (40.0)	68 (37.8)	0.803	193 (39.4)	66 (39.3)	0.979
Male	287 (60.0)	112 (62.2)		297 (60.6)	102 (60.7)	
ECOG, n (%)						
0	157 (32.8)	58 (32.2)	0.770	164 (33.5)	48 (28.6)	0.465
1	208 (43.6)	77 (42.8)		216 (44.1)	72 (42.9)	
2	76 (15.9)	36 (20.0)		74 (15.1)	38 (22.6)	
3	37 (7.7)	9 (5.0)		36 (7.3)	10 (5.9)	
Number of metastatic sites, n (%)						
1-2	447 (93.5)	164 (91.1)	0.431	450 (91.8)	161 (95.8)	0.196
>2	31 (6.5)	16 (8.9)		40 (8.2)	7 (4.2)	
Liver metastases only, n (%)						
No	321 (67.2)	141 (78.3)	0.810	335 (68.4)	127 (75.6)	0.810
Yes	157 (32.8)	39 (21.7)		155 (31.6)	41 (24.4)	
Prior adjuvant chemotherapy, n (%)						
No	369 (77.2)	122 (67.8)	0.120	385 (78.6)	106 (63.1)	0.091
Yes	109 (22.8)	58 (32.2)		105 (21.4)	62 (36.9)	
Treatment 1st line metastatic, n (%)						
5-Fluorouracil	283 (59.2)	97 (53.9)	0.269	283 (57.8)	97 (57.7)	0.893
Oxaliplatin	88 (18.4)	26 (14.4)		87 (17.8)	27 (16.1)	
Irinotecan	107 (22.4)	57 (31.7)		120 (24.4)	44 (26.2)	

p Values are calculated by χ^2 test (Fisher's exact test).

ECOG, Eastern Cooperative Oncology Group.

Supplementary Table S2 Univariate and multivariate Cox regression analysis of VDR protein expression levels and overall survival of metastatic CRC patients

Variable	Overall survival			
	Univariate analysis		Multivariate analysis	
	HR (95% CI)	p Value	HR (95% CI)	p Value
Gender				
Female	1.00	0.271		
Male	1.11 (0.71 to 1.12)			
ECOG				
0	1.00	0.001	1.00	0.019
1	1.57 (1.15 to 2.12)		1.49 (0.89 to 2.07)	
2	2.82 (1.77 to 4.44)		1.90 (0.93 to 2.48)	
3	2.83 (1.98 to 4.04)		2.51 (1.61 to 5.61)	
Number of metastatic sites				
1-2	1.00	0.087		
>2	1.34 (0.95 to 1.86)			
Prior adjuvant chemotherapy				
No	1.00	0.003	1.00	0.002
Yes	0.54 (0.42 to 0.69)		0.42 (0.38 to 0.62)	
Treatment 1st line metastatic				
5-Fluorouracil	1.00	0.004	1.00	0.076
Oxaliplatin	0.73 (0.54 to 0.96)		0.77 (0.58 to 1.93)	
Irinotecan	0.68 (0.52 to 0.87)		0.70 (0.47 to 1.01)	
VDR protein expression in stromal fibroblasts				
Low	1.00	0.012	1.00	0.043
High	0.70 (0.52 to 0.92)		0.71 (0.46 to 1.14)	
VDR protein expression in carcinoma cells				
Low	1.00	0.003	1.00	0.165
High	0.69 (0.52 to 0.93)		0.81 (0.65 to 1.25)	

ECOG, Eastern Cooperative Oncology Group.

Supplementary Table S3 Univariate and multivariate Cox regression analysis of VDR protein expression levels and progression-free survival of metastatic CRC patients

Variable	Progression-free survival			
	Univariate analysis		Multivariate analysis	
	HR (95% CI)	p Value	HR (95% CI)	p Value
Gender				
Female	1.00	0.527		
Male	0.95 (0.81 to 1.11)			
ECOG				
0	1.00	0.011	1.00	0.101
1	1.36 (1.12 to 1.62)		1.32 (0.95 to 1.86)	
2	1.36 (1.05 to 1.73)		1.20 (0.79 to 1.82)	
3	1.77 (1.08 to 1.97)		1.76 (0.96 to 1.95)	
Number of metastatic sites				
1-2	1.00	0.362		
>2	1.13 (0.87 to 1.45)			
Prior adjuvant chemotherapy				
No	1.00	0.001	1.00	0.002
Yes	0.63 (0.52 to 0.75)		0.55 (0.39 to 0.75)	
Treatment 1st line metastatic				
5-Fluorouracil	1.00	0.012	1.00	0.057
Oxaliplatin	0.61 (0.41 to 1.03)		0.83 (0.58 to 1.19)	
Irinotecan	0.61 (0.45 to 1.12)		0.88 (0.61 to 1.27)	
VDR protein expression in stromal fibroblasts				
Low	1.00	0.036	1.00	0.067
High	0.75 (0.56 to 1.01)		0.83 (0.61 to 1.14)	
VDR protein expression in carcinoma cells				
Low	1.00	0.112	1.00	0.815
High	0.95 (0.64 to 1.12)		0.94 (0.75 to 1.43)	

ECOG, Eastern Cooperative Oncology Group.

Supplementary Table S4 Clinicopathological characteristics of the CRC patients from which biopsies NF and CAF primary cultures were established

Patient	Gender	Age (years)	Tumour localization	Tumour differentiation	AJCC stage	Lymph node metastases	Distant metastases
9	Female	84	Right	Moderate	II	Negative	Negative
11	Male	60	Left	Poor	II	Negative	Negative
16	Female	77	Left	Moderate	II	Negative	Negative
17	Female	49	Left	Moderate	II	Negative	Negative
20	Male	80	Left	Moderate	II	Negative	Negative
23	Male	87	Right	Moderate	IV	Negative	Positive
24	Female	58	Left	Moderate	II	Negative	Negative
25	Male	81	Left	Poor	III	Positive	Negative
27	Female	55	Right	Moderate	III	Positive	Negative
28	Male	58	Right	Moderate	IV	Positive	Positive
29	Male	86	Left	Moderate	II	Negative	Negative
30	Male	81	Left	Moderate	III	Positive	Negative
34	Male	76	Right	Moderate	II	Negative	Negative
35	Male	70	Right	Moderate	II	Negative	Negative
36	Male	68	Right	Moderate	II	Negative	Negative
38	Male	58	Right	Moderate	III	Positive	Negative
42	Female	80	Left	Poor	III	Positive	Negative
43	Female	47	Right	Moderate	IV	Positive	Positive
44	Female	68	Left	Moderate	III	Positive	Negative
45	Male	75	Left	Moderate	I	Negative	Negative
46	Female	76	Right	Moderate	II	Negative	Negative
47	Female	77	Right	Poor	II	Negative	Negative
48	Male	83	Left	Moderate	IV	Positive	Positive
49	Male	60	Left	Moderate	II	Negative	Negative
50	Male	72	Left	Poor	IV	Positive	Positive
51	Male	84	Left	Moderate	II	Negative	Negative
52	Female	83	Left	Moderate	II	Negative	Negative
53	Male	81	Left	Moderate	II	Negative	Negative
54	Male	47	Left	Moderate	III	Positive	Negative
55	Male	63	Left	Moderate	III	Positive	Negative
56	Female	82	Left	Moderate	IV	Negative	Positive
58	Female	86	Left	Moderate	I	Negative	Negative

AJCC, American Joint Committee on Cancer.

Supplementary Table S5 *VDR* RNA expression in human cultured cells and tissues measured by RT-qPCR, normalized against three reference housekeeping genes (*GAPDH*, *B2M* and *RPLP0*) and calculated in relation to that of CCD18Co fibroblasts

Cell/Tissue	Normalized <i>VDR</i> RNA expression
Cultured cells	
CCD18Co colon fibroblasts	1.00
Colon NF primary cultures	0.74-3.18
Colon CAF primary cultures	0.39-3.53
IMR90 lung fibroblasts	0.48
BJ-hTERT foreskin fibroblasts	2.34
THP1 monocytic leukemia cells	0.82
CACO2 colon carcinoma cells	3.17
HCT116 colon carcinoma cells	3.57
SW480-ADH colon carcinoma cells	6.28
MCF7 breast carcinoma cells	6.67
Tissues	
Skeletal muscle	0.05
Heart	0.13
Liver	0.13
Kidney	1.31
Colon	2.69
Small intestine	4.93

Supplementary Table S6 List of genes differentially-expressed in 1,25(OH)₂D₃- vs vehicle-treated human colon NFs

Agilent ID	Log ₂ fold-change	p Value	Adjusted p Value	Gene symbol	Gene name
A_23_P28815	4.046	0.000	0.003	<i>CYP24A1</i>	cytochrome P450, family 24, subfamily A, polypeptide 1
A_23_P86470	3.104	0.000	0.001	<i>CH25H</i>	cholesterol 25-hydroxylase
A_23_P151895	3.079	0.000	0.003	<i>CILP</i>	cartilage intermediate layer protein, nucleotide pyrophosphohydrolase
A_23_P142424	2.353	0.000	0.001	<i>IGFLR1</i>	IGF-like family receptor 1
A_24_P168925	1.660	0.000	0.001	<i>CHRD1</i>	chordin-like 1
A_23_P25706	1.586	0.000	0.007	<i>CLMN</i>	calmin (calponin-like, transmembrane)
A_33_P3289296	1.566	0.000	0.005	<i>TMEM37</i>	transmembrane protein 37
A_23_P152055	1.563	0.000	0.005	<i>EFTUD1</i>	elongation factor Tu GTP binding domain containing 1
A_24_P55496	1.562	0.000	0.004	<i>OSR2</i>	odd-skipped related 2 (Drosophila)
A_23_P58676	1.533	0.000	0.002	<i>NPR3</i>	natriuretic peptide receptor C/guanylate cyclase C (atriuretic peptide receptor C)
A_33_P3511265	1.531	0.000	0.002	<i>POSTN</i>	periostin, osteoblast specific factor
A_23_P74609	1.529	0.005	0.030	<i>G0S2</i>	G0/G1switch 2
A_23_P148879	1.492	0.000	0.004	<i>ATP1A2</i>	ATPase, Na ⁺ /K ⁺ transporting, alpha 2 polypeptide
A_23_P105002	1.460	0.000	0.002	<i>ROM1</i>	retinal outer segment membrane protein 1
A_23_P163087	1.440	0.000	0.003	<i>NID2</i>	nidogen 2 (osteonidogen)
A_23_P62932	1.434	0.000	0.002	<i>ATP1B1</i>	ATPase, Na ⁺ /K ⁺ transporting, beta 1 polypeptide
A_23_P1782	1.424	0.000	0.002	<i>CD82</i>	CD82 molecule
A_23_P26024	1.419	0.000	0.006	<i>C15orf48</i>	chromosome 15 open reading frame 48
A_23_P215634	1.404	0.000	0.001	<i>IGFBP3</i>	insulin-like growth factor binding protein 3
A_23_P148990	1.367	0.000	0.001	<i>HMCN1</i>	hemicentin 1
A_23_P45185	1.366	0.003	0.022	<i>FIGF</i>	c-fos induced growth factor (vascular endothelial growth factor D)
A_23_P132718	1.366	0.000	0.004	<i>SEMA3B</i>	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3B
A_23_P14174	1.336	0.000	0.007	<i>TNFSF13B</i>	tumor necrosis factor (ligand) superfamily, member 13b
A_21_P0005727	1.324	0.000	0.006	<i>XLOC_006850</i>	BROAD Institute lincRNA (XLOC_006850), lincRNA [TCONS_00014769]
A_23_P119943	1.303	0.001	0.009	<i>IGFBP2</i>	insulin-like growth factor binding protein 2, 36kDa
A_23_P129209	1.301	0.000	0.007	<i>IDH2</i>	isocitrate dehydrogenase 2 (NADP ⁺), mitochondrial
A_33_P3251703	1.283	0.000	0.006	<i>CRIP1</i>	cysteine-rich protein 1 (intestinal)
A_32_P452655	1.281	0.002	0.018	<i>LGALS9C</i>	lectin, galactoside-binding, soluble, 9C
A_21_P0014829	1.257	0.000	0.003	<i>LOC100652760</i>	uncharacterized LOC100652760
A_23_P13907	1.249	0.000	0.003	<i>IGF1</i>	insulin-like growth factor 1 (somatomedin C)
A_24_P391586	1.230	0.001	0.013	<i>OAF</i>	OAF homolog (Drosophila)
A_23_P399078	1.221	0.000	0.006	<i>TIMP3</i>	TIMP metalloproteinase inhibitor 3
A_23_P39237	1.188	0.000	0.002	<i>ZFP36</i>	zinc finger protein 36, C3H type, homolog (mouse)
A_23_P63209	1.159	0.000	0.007	<i>HSD11B1</i>	hydroxysteroid (11-beta) dehydrogenase 1
A_33_P3337485	1.119	0.000	0.003	<i>CD248</i>	CD248 molecule, endosialin
A_23_P18078	1.091	0.000	0.001	<i>RARRES1</i>	retinoic acid receptor responder (tazarotene induced) 1
A_23_P91390	1.086	0.003	0.024	<i>THBD</i>	thrombomodulin
A_23_P139912	1.051	0.000	0.001	<i>IGFBP6</i>	insulin-like growth factor binding protein 6
A_33_P3331491	1.050	0.000	0.006	<i>LOC728392</i>	uncharacterized LOC728392
A_23_P143981	1.035	0.000	0.002	<i>FBLN2</i>	fibulin 2
A_33_P3269636	1.022	0.000	0.002	<i>SBSN</i>	suprabasin
A_23_P404494	1.005	0.010	0.046	<i>IL7R</i>	interleukin 7 receptor

A_32_P34444	1.003	0.000	0.003	FHOD3	formin homology 2 domain containing 3
A_21_P0000129	0.990	0.000	0.002	DCLK1	doublecortin-like kinase 1
A_23_P386320	0.989	0.000	0.004	MF12	antigen p97 (melanoma associated) identified by monoclonal antibodies 133.2 and 96.5
A_32_P108254	0.981	0.002	0.016	FAM20A	family with sequence similarity 20, member A
A_23_P256473	0.961	0.000	0.004	SEMA3C	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3C
A_23_P13753	0.960	0.001	0.011	NFE2	nuclear factor (erythroid-derived 2), 45kDa
A_24_P406132	0.941	0.001	0.014	MAPK13	mitogen-activated protein kinase 13
A_33_P3277110	0.940	0.000	0.002	SLC5A3	solute carrier family 5 (sodium/myo-inositol cotransporter), member 3
A_23_P50919	0.937	0.000	0.001	SERPINE2	serpin peptidase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 2
A_23_P216468	0.926	0.001	0.009	SLC1A1	solute carrier family 1 (neuronal/epithelial high affinity glutamate transporter, system Xag), member 1
A_23_P18684	0.912	0.000	0.004	CLGN	calmegin
A_23_P202448	0.896	0.000	0.006	CXCL12	chemokine (C-X-C motif) ligand 12
A_23_P200741	0.888	0.000	0.003	DPT	dermatopontin
A_23_P88404	0.884	0.002	0.018	TGFB3	transforming growth factor, beta 3
A_23_P358917	0.856	0.001	0.014	CYP3A7	cytochrome P450, family 3, subfamily A, polypeptide 7
A_24_P84396	0.853	0.000	0.004	KIAA1199	KIAA1199
A_32_P209230	0.851	0.000	0.002	CITED4	Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain, 4
A_23_P333498	0.847	0.000	0.002	EEPDI1	endonuclease/exonuclease/phosphatase family domain containing 1
A_24_P38276	0.847	0.000	0.002	FZD1	frizzled family receptor 1
A_32_P140489	0.845	0.000	0.004	GDF6	growth differentiation factor 6
A_33_P3354414	0.843	0.000	0.002	AOX1	aldehyde oxidase 1
A_24_P261567	0.838	0.000	0.002	GDPD5	glycerophosphodiester phosphodiesterase domain containing 5
A_24_P190472	0.831	0.000	0.004	SLPI	secretory leukocyte peptidase inhibitor
A_23_P430930	0.821	0.002	0.019	RSPO2	R-spondin 2
A_24_P319364	0.819	0.000	0.007	F11R	F11 receptor
A_24_P368575	0.813	0.000	0.003	SLC4A7	solute carrier family 4, sodium bicarbonate cotransporter, member 7
A_23_P163567	0.811	0.003	0.023	SMPD3	sphingomyelin phosphodiesterase 3, neutral membrane (neutral sphingomyelinase II)
A_32_P25050	0.809	0.000	0.001	RDH10	retinol dehydrogenase 10 (all-trans)
A_23_P102890	0.798	0.000	0.006	MRPS6	mitochondrial ribosomal protein S6
A_33_P3234697	0.787	0.000	0.002	LXN	latexin
A_23_P401700	0.785	0.000	0.003	APBB1IP	amyloid beta (A4) precursor protein-binding, family B, member 1 interacting protein
A_23_P75283	0.785	0.000	0.002	RBP4	retinol binding protein 4, plasma
A_23_P337270	0.783	0.000	0.005	NEK10	NIMA (never in mitosis gene a)- related kinase 10
A_23_P32233	0.773	0.003	0.022	KLF4	Kruppel-like factor 4 (gut)
A_24_P71468	0.771	0.000	0.002	QPCT	glutaminyl-peptide cyclotransferase
A_33_P3415052	0.764	0.001	0.012	NIPAL4	NIPA-like domain containing 4
A_23_P214011	0.763	0.000	0.004	CDH6	cadherin 6, type 2, K-cadherin (fetal kidney)
A_23_P8801	0.763	0.001	0.014	CYP3A5	cytochrome P450, family 3, subfamily A, polypeptide 5
A_23_P65307	0.763	0.003	0.022	SLITRK6	SLIT and NTRK-like family, member 6
A_23_P82929	0.753	0.000	0.002	NOV	nephroblastoma overexpressed gene
A_23_P126623	0.747	0.002	0.015	PGD	phosphogluconate dehydrogenase
A_24_P87036	0.744	0.001	0.009	ANO1	anoctamin 1, calcium activated chloride channel
A_23_P25674	0.740	0.001	0.015	CKB	creatine kinase, brain
A_24_P8371	0.738	0.001	0.012	SPNS2	spinster homolog 2 (Drosophila)
A_21_P0004807	0.726	0.000	0.005	XLOC_005935	K-EST0172083 L12JSHC0 Homo sapiens cDNA clone L12JSHC0-2-D12 5', mRNA sequence [CB123670]

A_33_P3239185	0.722	0.011	0.049	<i>SYT7</i>	synaptotagmin VII
A_33_P3272209	0.720	0.001	0.011	<i>MFSD6</i>	major facilitator superfamily domain containing 6
A_33_P3352019	0.711	0.000	0.004	<i>SCARA3</i>	scavenger receptor class A, member 3
A_24_P62530	0.706	0.009	0.043	<i>RHOU</i>	ras homolog gene family, member U
A_23_P34093	0.702	0.001	0.008	<i>G6PD</i>	glucose-6-phosphate dehydrogenase
A_23_P82651	0.702	0.008	0.040	<i>NPTX2</i>	neuronal pentraxin II
A_24_P145629	0.700	0.001	0.009	<i>SERINC2</i>	serine incorporator 2
A_23_P135722	0.691	0.001	0.009	<i>BTC</i>	betacellulin
A_23_P132763	0.687	0.000	0.001	<i>VGLL3</i>	vestigial like 3 (Drosophila)
A_23_P118065	0.686	0.000	0.006	<i>HSD17B2</i>	hydroxysteroid (17-beta) dehydrogenase 2
A_23_P157569	0.683	0.000	0.005	<i>ADHFE1</i>	alcohol dehydrogenase, iron containing, 1
A_23_P154526	0.683	0.004	0.025	<i>GRB14</i>	growth factor receptor-bound protein 14
A_23_P69573	0.680	0.000	0.006	<i>GUCY1A3</i>	guanylate cyclase 1, soluble, alpha 3
A_23_P88678	0.680	0.000	0.005	<i>C15orf27</i>	chromosome 15 open reading frame 27
A_24_P191781	0.669	0.000	0.002	<i>PARM1</i>	prostate androgen-regulated mucin-like protein 1
A_33_P3331307	0.667	0.000	0.003	<i>CDC42EP3</i>	CDC42 effector protein (Rho GTPase binding) 3
A_23_P421011	0.665	0.000	0.002	<i>KAZALD1</i>	Kazal-type serine peptidase inhibitor domain 1
A_23_P80040	0.664	0.001	0.011	<i>PROCR</i>	protein C receptor, endothelial
A_23_P373521	0.657	0.000	0.005	<i>HAND2</i>	heart and neural crest derivatives expressed 2
A_23_P149992	0.657	0.000	0.008	<i>PDLIM1</i>	PDZ and LIM domain 1
A_32_P40288	0.653	0.000	0.006	<i>TMEM200A</i>	transmembrane protein 200A
A_24_P355944	0.653	0.000	0.004	<i>EFNB2</i>	ephrin-B2
A_23_P431268	0.651	0.000	0.002	<i>PLEKHA6</i>	pleckstrin homology domain containing, family A member 6
A_33_P3287223	0.649	0.000	0.003	<i>DPP4</i>	dipeptidyl-peptidase 4
A_33_P3252286	0.643	0.004	0.026	<i>CRLF1</i>	cytokine receptor-like factor 1
A_23_P128574	0.640	0.000	0.003	<i>ENOX1</i>	ecto-NOX disulfide-thiol exchanger 1
A_23_P70398	0.640	0.010	0.046	<i>VEGFA</i>	vascular endothelial growth factor A
A_23_P215454	0.635	0.000	0.002	<i>ELN</i>	elastin
A_23_P122216	0.635	0.002	0.018	<i>LOX</i>	lysyl oxidase
A_23_P385067	0.626	0.001	0.013	<i>CLIC6</i>	chloride intracellular channel 6
A_23_P64879	0.618	0.000	0.002	<i>KCNJ8</i>	potassium inwardly-rectifying channel, subfamily J, member 8
A_23_P35725	0.614	0.001	0.013	<i>ANO3</i>	anoctamin 3
A_23_P42282	0.610	0.000	0.004	<i>C4B</i>	complement component 4B (Chido blood group)
A_23_P250274	0.609	0.000	0.005	<i>LRRC8A</i>	leucine rich repeat containing 8 family, member A
A_23_P257971	0.607	0.001	0.009	<i>AKR1C1</i>	aldo-keto reductase family 1, member C1 (dihydrodiol dehydrogenase 1; 20-alpha (3-alpha)-hydroxysteroid dehydrogenase)
A_24_P759477	0.607	0.000	0.006	<i>ITGB8</i>	integrin, beta 8
A_23_P137470	0.606	0.000	0.002	<i>SIPAIL2</i>	signal-induced proliferation-associated 1 like 2
A_24_P383609	0.603	0.001	0.012	<i>NANOS1</i>	nanos homolog 1 (Drosophila)
A_24_P62505	0.601	0.007	0.037	<i>GLT25D2</i>	glycosyltransferase 25 domain containing 2
A_24_P411749	0.597	0.003	0.023	<i>GPR126</i>	G protein-coupled receptor 126
A_24_P10137	0.594	0.001	0.015	<i>C13orf15</i>	chromosome 13 open reading frame 15
A_23_P360797	0.588	0.000	0.003	<i>NTF3</i>	neurotrophin 3
A_23_P51002	0.586	0.003	0.022	<i>SULT1C2</i>	sulfotransferase family, cytosolic, 1C, member 2
A_33_P3338121	0.586	0.000	0.004	<i>LAMB3</i>	laminin, beta 3
A_23_P92042	0.586	0.000	0.006	<i>ITPR1</i>	inositol 1,4,5-trisphosphate receptor, type 1

A_23_P331700	0.573	0.000	0.007	<i>SRRM3</i>	serine/arginine repetitive matrix 3
A_21_P0010854	0.573	0.002	0.017	<i>AKR1CL1</i>	aldo-keto reductase family 1, member C-like 1
A_24_P219378	0.572	0.007	0.036	<i>CASKIN1</i>	CASK interacting protein 1
A_23_P20494	0.571	0.001	0.009	<i>NDRG1</i>	N-myc downstream regulated 1
A_23_P76914	0.570	0.000	0.006	<i>SIX1</i>	SIX homeobox 1
A_24_P48723	0.565	0.000	0.007	<i>PTGIS</i>	prostaglandin I2 (prostacyclin) synthase
A_33_P3267186	0.564	0.001	0.011	<i>ATP2B1</i>	ATPase, Ca ⁺⁺ transporting, plasma membrane 1
A_23_P352266	0.560	0.000	0.003	<i>BCL2</i>	B-cell CLL/lymphoma 2
A_23_P135548	0.553	0.000	0.002	<i>DPYD</i>	dihydropyrimidine dehydrogenase
A_23_P381261	0.551	0.000	0.002	<i>ADCY4</i>	adenylate cyclase 4
A_32_P86739	0.550	0.003	0.021	<i>C10orf114</i>	chromosome 10 open reading frame 114
A_23_P320261	0.548	0.000	0.003	<i>DMKN</i>	dermokine
A_23_P310	0.544	0.000	0.004	<i>MARCKSL1</i>	MARCKS-like 1
A_23_P140748	0.541	0.003	0.020	<i>NDRG4</i>	NDRG family member 4
A_23_P79978	0.541	0.001	0.010	<i>SLC24A3</i>	solute carrier family 24 (sodium/potassium/calcium exchanger), member 3
A_23_P69362	0.537	0.000	0.004	<i>CCDC51</i>	coiled-coil domain containing 51
A_33_P3271111	0.534	0.003	0.024	<i>NINJI</i>	ninjurin 1
A_33_P3312601	0.532	0.000	0.006	<i>AADA4L4</i>	arylacetylamide deacetylase-like 4
A_24_P334130	0.532	0.002	0.017	<i>FN1</i>	fibronectin 1
A_23_P4353	0.529	0.000	0.007	<i>WSB1</i>	WD repeat and SOCS box containing 1
A_33_P3268892	0.528	0.000	0.002	<i>GDNF</i>	glial cell derived neurotrophic factor
A_32_P181103	0.527	0.001	0.015	<i>GGCX</i>	gamma-glutamyl carboxylase
A_23_P139123	0.526	0.000	0.002	<i>SERPING1</i>	serpin peptidase inhibitor, clade G (C1 inhibitor), member 1
A_33_P3407324	0.525	0.003	0.025	<i>GULP1</i>	GULP, engulfment adaptor PTB domain containing 1
A_23_P328323	0.523	0.001	0.013	<i>RAVER2</i>	ribonucleoprotein, PTB-binding 2
A_33_P3315134	0.523	0.001	0.014	<i>DIRC3</i>	disrupted in renal carcinoma 3
A_24_P321068	0.520	0.003	0.022	<i>SLC31A1</i>	solute carrier family 31 (copper transporters), member 1
A_23_P215956	0.518	0.000	0.005	<i>MYC</i>	v-myc myelocytomatosis viral oncogene homolog (avian)
A_33_P3236881	0.517	0.001	0.013	<i>C1orf151-NBL1</i>	C1orf151-NBL1 readthrough
A_23_P73493	0.517	0.000	0.007	<i>CETN2</i>	centrin, EF-hand protein, 2
A_23_P329261	0.513	0.002	0.016	<i>KCNJ2</i>	potassium inwardly-rectifying channel, subfamily J, member 2
A_21_P0001227	0.512	0.001	0.014	<i>XLOC_001215</i>	601566084F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3840837 5', mRNA sequence [BE735115]
A_23_P156687	0.512	0.000	0.002	<i>CFB</i>	complement factor B
A_23_P324327	0.511	0.000	0.003	<i>GPRC5B</i>	G protein-coupled receptor, family C, group 5, member B
A_33_P3372727	0.511	0.001	0.014	<i>SEMA5A</i>	sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic tail
A_24_P415150	0.511	0.000	0.008	<i>GNA14</i>	guanine nucleotide binding protein (G protein), alpha 14
A_24_P555066	0.510	0.001	0.009	<i>SMTNL2</i>	smoothelin-like 2
A_33_P3245922	0.507	0.002	0.017	<i>MAP3K4</i>	mitogen-activated protein kinase kinase kinase 4
A_23_P38677	0.506	0.000	0.003	<i>SLMO1</i>	slowmo homolog 1 (Drosophila)
A_33_P3404316	0.504	0.000	0.007	<i>MIR100HG</i>	mir-100-let-7a-2 cluster host gene (non-protein coding)
A_32_P101689	0.504	0.000	0.003	<i>FAM3C</i>	family with sequence similarity 3, member C
A_21_P0009140	0.501	0.000	0.006	<i>XLOC_012044</i>	BROAD Institute lincRNA (XLOC_012044), lincRNA [TCONS_00025084]
A_23_P19517	0.497	0.000	0.005	<i>ITPR3</i>	inositol 1,4,5-trisphosphate receptor, type 3
A_23_P149975	0.493	0.001	0.009	<i>FAM107B</i>	family with sequence similarity 107, member B
A_21_P0011081	0.491	0.001	0.009	<i>FAM86C1</i>	family with sequence similarity 86, member C1

A_23_P212050	0.491	0.001	0.009	BCHE	butyrylcholinesterase
A_32_P80850	0.490	0.002	0.015	COL14A1	collagen, type XIV, alpha 1
A_19_P00315649	0.490	0.003	0.023	LOC100507165	uncharacterized LOC100507165
A_32_P197561	0.488	0.001	0.009	EBF1	early B-cell factor 1
A_19_P00322310	0.486	0.002	0.018	LOC100505702	uncharacterized LOC100505702
A_23_P121564	0.485	0.003	0.022	GUCY1B3	guanylate cyclase 1, soluble, beta 3
A_23_P56703	0.485	0.000	0.006	C2orf89	chromosome 2 open reading frame 89
A_32_P107876	0.484	0.000	0.005	FRAS1	Fraser syndrome 1
A_33_P3216292	0.484	0.000	0.005	TBC1D2	TBC1 domain family, member 2
A_24_P178503	0.483	0.002	0.020	ABCC9	ATP-binding cassette, sub-family C (CFTR/MRP), member 9
A_33_P3275702	0.479	0.006	0.035	FMO2	flavin containing monooxygenase 2 (non-functional)
A_23_P204286	0.479	0.004	0.027	MGP	matrix Gla protein
A_23_P385105	0.479	0.000	0.005	PLCD4	phospholipase C, delta 4
A_33_P3265744	0.478	0.000	0.005	PTGER3	prostaglandin E receptor 3 (subtype EP3)
A_23_P150249	0.475	0.001	0.011	CCDC85B	coiled-coil domain containing 85B
A_23_P25030	0.473	0.009	0.042	HSD17B6	hydroxysteroid (17-beta) dehydrogenase 6 homolog (mouse)
A_23_P62081	0.473	0.001	0.012	SCG5	secretogranin V (7B2 protein)
A_33_P3246448	0.472	0.001	0.011	KCNE4	potassium voltage-gated channel, Isk-related family, member 4
A_23_P155666	0.466	0.001	0.014	NAAA	N-acylethanolamine acid amidase
A_23_P102391	0.465	0.000	0.006	SLC40A1	solute carrier family 40 (iron-regulated transporter), member 1
A_23_P15394	0.464	0.000	0.003	CD68	CD68 molecule
A_23_P257043	0.463	0.003	0.021	GEM	GTP binding protein overexpressed in skeletal muscle
A_23_P33759	0.462	0.001	0.011	DHRS3	dehydrogenase/reductase (SDR family) member 3
A_23_P134714	0.462	0.001	0.013	HRSP12	heat-responsive protein 12
A_23_P43164	0.457	0.001	0.012	SULF1	sulfatase 1
A_21_P0000731	0.457	0.001	0.011	LOC100507632	uncharacterized LOC100507632
A_33_P3421203	0.457	0.002	0.016	FLJ10661	family with sequence similarity 86, member A pseudogene
A_24_P38951	0.457	0.001	0.012	RELT	RELT tumor necrosis factor receptor
A_23_P325690	0.455	0.000	0.006	ANKRD35	ankyrin repeat domain 35
A_23_P156708	0.454	0.009	0.042	TNXB	tenascin XB
A_21_P0014017	0.451	0.000	0.003	LOC100652790	uncharacterized LOC100652790
A_32_P103695	0.451	0.002	0.016	FAM92A1	family with sequence similarity 92, member A1
A_33_P3303414	0.450	0.001	0.010	MAN1A1	mannosidase, alpha, class 1A, member 1
A_23_P142322	0.447	0.002	0.018	CIRBP	cold inducible RNA binding protein
A_23_P258136	0.447	0.002	0.019	MXRA5	matrix-remodelling associated 5
A_24_P419087	0.446	0.005	0.031	AVIL	advillin
A_23_P396858	0.446	0.002	0.020	FZD8	frizzled family receptor 8
A_23_P250294	0.444	0.000	0.004	ABHD5	abhydrolase domain containing 5
A_33_P3323074	0.442	0.000	0.006	AGPAT4	1-acylglycerol-3-phosphate O-acyltransferase 4 (lysophosphatidic acid acyltransferase, delta)
A_33_P3263533	0.441	0.004	0.027	SCN1A	sodium channel, voltage-gated, type I, alpha subunit
A_23_P145935	0.437	0.000	0.006	EPHB6	EPH receptor B6
A_23_P101374	0.432	0.000	0.005	CYP2S1	cytochrome P450, family 2, subfamily S, polypeptide 1
A_33_P3326904	0.431	0.000	0.006	LOC441268	uncharacterized LOC441268
A_23_P10121	0.431	0.001	0.014	SFRP1	secreted frizzled-related protein 1
A_33_P3344243	0.430	0.008	0.040	C4orf46	chromosome 4 open reading frame 46

A_23_P114883	0.430	0.000	0.006	FMOD	fibromodulin
A_32_P96036	0.429	0.000	0.004	MEX3A	mex-3 homolog A (C. elegans)
A_23_P200260	0.427	0.000	0.007	PCNXL2	pecanex-like 2 (Drosophila)
A_33_P3590259	0.426	0.003	0.021	CXCL14	chemokine (C-X-C motif) ligand 14
A_33_P3298425	0.422	0.001	0.014	LMO4	LIM domain only 4
A_23_P311150	0.421	0.010	0.045	SPTSSA	serine palmitoyltransferase, small subunit A
A_23_P19754	0.420	0.003	0.022	CPA4	carboxypeptidase A4
A_33_P3396891	0.419	0.000	0.005	AVPI1	arginine vasopressin-induced 1
A_23_P409093	0.419	0.001	0.014	ANO4	anoctamin 4
A_23_P434301	0.416	0.005	0.029	PTMA	prothymosin, alpha
A_23_P121064	0.411	0.004	0.027	PTX3	pentraxin 3, long
A_23_P55544	0.411	0.000	0.004	CCBE1	collagen and calcium binding EGF domains 1
A_33_P3222689	0.411	0.000	0.006	H2BFM	H2B histone family, member M
A_24_P911676	0.409	0.000	0.005	SOX4	SRY (sex determining region Y)-box 4
A_33_P3282489	0.409	0.001	0.011	GCNT1	glucosaminyl (N-acetyl) transferase 1, core 2
A_23_P166686	0.408	0.001	0.008	AMOTL2	angiominin like 2
A_23_P317465	0.407	0.007	0.036	RAB8B	RAB8B, member RAS oncogene family
A_21_P0008399	0.406	0.002	0.019	XLOC_010947	BROAD Institute lincRNA (XLOC_010947), lincRNA [TCONS_00022643]
A_21_P0013028	0.405	0.002	0.020	XLOC_I2_012605	BROAD Institute lincRNA (XLOC_I2_012605), lincRNA [TCONS_I2_00024286]
A_23_P167096	0.405	0.002	0.017	VEGFC	vascular endothelial growth factor C
A_19_P00318323	0.402	0.002	0.019	LINC00340	long intergenic non-protein coding RNA 340
A_33_P3227793	0.396	0.002	0.016	CGREF1	cell growth regulator with EF-hand domain 1
A_24_P149036	0.396	0.003	0.021	DPYSL3	dihydropyrimidinase-like 3
A_23_P304450	0.396	0.001	0.014	GATA6	GATA binding protein 6
A_23_P83028	0.394	0.005	0.029	RECK	reversion-inducing-cysteine-rich protein with kazal motifs
A_21_P0003863	0.394	0.000	0.006	XLOC_003784	DA915098 SKNSH2 Homo sapiens cDNA clone SKNSH2009915 5', mRNA sequence
A_24_P389415	0.393	0.000	0.006	PNMA2	paraneoplastic antigen MA2
A_33_P3367917	0.390	0.005	0.028	SSH2	slingshot homolog 2 (Drosophila)
A_33_P3376095	0.387	0.001	0.012	SYPL2	synaptophysin-like 2
A_23_P107587	0.387	0.009	0.045	NPC1	Niemann-Pick disease, type C1
A_23_P301855	0.384	0.001	0.010	LSAMP	limbic system-associated membrane protein
A_23_P342138	0.382	0.004	0.028	ADAMTSL1	ADAMTS-like 1
A_23_P65230	0.381	0.000	0.005	TMTC4	transmembrane and tetratricopeptide repeat containing 4
A_24_P90097	0.380	0.001	0.014	ADD3	adducin 3 (gamma)
A_24_P68079	0.379	0.001	0.009	TRANK1	tetratricopeptide repeat and ankyrin repeat containing 1
A_23_P123732	0.378	0.004	0.025	C9orf103	chromosome 9 open reading frame 103
A_21_P0014312	0.375	0.000	0.005	LOC100507303	uncharacterized LOC100507303
A_23_P94230	0.375	0.008	0.040	LY96	lymphocyte antigen 96
A_21_P0000653	0.374	0.004	0.028	LOC283104	uncharacterized LOC283104
A_33_P3287631	0.373	0.000	0.005	CTSB	cathepsin B
A_23_P218190	0.372	0.000	0.007	CAPN3	calpain 3, (p94)
A_23_P53363	0.370	0.002	0.017	XRCC6BP1	XRCC6 binding protein 1
A_24_P106542	0.368	0.006	0.033	RSPO3	R-spondin 3
A_33_P3230269	0.368	0.002	0.019	GRHL1	grainyhead-like 1 (Drosophila)
A_33_P3243907	0.367	0.000	0.004	CTSD	cathepsin D

A_33_P3404588	0.367	0.003	0.021	FGD4	FYVE, RhoGEF and PH domain containing 4
A_23_P116414	0.364	0.001	0.011	PLA2G16	phospholipase A2, group XVI
A_23_P127891	0.363	0.003	0.022	BDNF	brain-derived neurotrophic factor
A_33_P3418209	0.363	0.002	0.018	ITGBL1	integrin, beta-like 1 (with EGF-like repeat domains)
A_23_P58266	0.362	0.002	0.017	S100P	S100 calcium binding protein P
A_23_P160159	0.362	0.004	0.027	SLC2A5	solute carrier family 2 (facilitated glucose/fructose transporter), member 5
A_23_P71328	0.361	0.007	0.036	MATN2	matrilin 2
A_24_P295010	0.360	0.004	0.027	SERPINB9	serpin peptidase inhibitor, clade B (ovalbumin), member 9
A_33_P3708413	0.360	0.002	0.020	MFAP5	microfibrillar associated protein 5
A_33_P3257330	0.360	0.009	0.043	DCBLD1	discoidin, CUB and LCCL domain containing 1
A_33_P3329301	0.358	0.009	0.044	LOC646014	uncharacterized LOC646014
A_33_P3290343	0.358	0.008	0.039	CYP1B1	cytochrome P450, family 1, subfamily B, polypeptide 1
A_33_P3245178	0.358	0.000	0.004	BEX2	brain expressed X-linked 2
A_23_P14804	0.357	0.000	0.006	TSPAN3	tetraspanin 3
A_23_P10591	0.356	0.004	0.025	METRNL	meteorin, glial cell differentiation regulator-like
A_19_P00811940	0.355	0.011	0.049	XLOC_002759	UI-H-ED1-ayb-p-10-0-UI.s1 NCI_CGAP_ED1 Homo sapiens cDNA clone IMAGE:5836665 3', mRNA sequence [BQ]
A_33_P3315243	0.355	0.003	0.021	C17orf72	chromosome 17 open reading frame 72
A_23_P56734	0.355	0.002	0.018	HNMT	histamine N-methyltransferase
A_23_P162171	0.354	0.008	0.039	MCAM	melanoma cell adhesion molecule
A_23_P71530	0.354	0.011	0.049	TNFRSF11B	tumor necrosis factor receptor superfamily, member 11b
A_23_P21324	0.353	0.002	0.018	TWIST2	twist homolog 2 (Drosophila)
A_23_P39131	0.353	0.003	0.022	GLTSCR2	glioma tumor suppressor candidate region gene 2
A_32_P147078	0.352	0.001	0.015	SLC8A1	solute carrier family 8 (sodium/calcium exchanger), member 1
A_23_P415706	0.351	0.006	0.035	GPR133	G protein-coupled receptor 133
A_23_P252306	0.351	0.004	0.026	ID1	inhibitor of DNA binding 1, dominant negative helix-loop-helix protein
A_24_P246518	0.350	0.009	0.043	PKD1L2	polycystic kidney disease 1-like 2
A_33_P3318796	0.348	0.000	0.005	FSTL3	follistatin-like 3 (secreted glycoprotein)
A_23_P17855	0.348	0.001	0.011	TRIOBP	TRIO and F-actin binding protein
A_23_P254165	0.347	0.008	0.039	RAI2	retinoic acid induced 2
A_23_P133474	0.346	0.001	0.012	GPX3	glutathione peroxidase 3 (plasma)
A_24_P13083	0.344	0.004	0.027	TSPAN18	tetraspanin 18
A_19_P00319981	0.344	0.005	0.030	LOC100506119	uncharacterized LOC100506119
A_24_P46334	0.344	0.002	0.015	SCOC	short coiled-coil protein
A_24_P414371	0.339	0.000	0.007	PPP3CA	protein phosphatase 3, catalytic subunit, alpha isozyme
A_24_P382187	0.339	0.004	0.028	IGFBP4	insulin-like growth factor binding protein 4
A_23_P130376	0.339	0.002	0.019	PIEZO2	piezo-type mechanosensitive ion channel component 2
A_21_P0013105	0.339	0.006	0.032	XLOC_l2_013149	BROAD Institute lincRNA (XLOC_l2_013149), lincRNA [TCONS_l2_00025502]
A_24_P870620	0.338	0.000	0.005	PTN	pleiotrophin
A_33_P3262789	0.338	0.004	0.028	REEP6	receptor accessory protein 6
A_23_P106906	0.336	0.009	0.043	PPL	periplakin
A_23_P217098	0.335	0.001	0.014	VPS13A	vacuolar protein sorting 13 homolog A (S. cerevisiae)
A_33_P3333777	0.332	0.008	0.039	LOC100129387	uncharacterized LOC100129387
A_33_P3230166	0.330	0.004	0.026	NALCN	sodium leak channel, non-selective
A_24_P206047	0.330	0.000	0.005	SLC25A4	solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 4
A_24_P924862	0.329	0.001	0.014	RAPH1	Ras association (RalGDS/AF-6) and pleckstrin homology domains 1

A_21_P0000236	0.328	0.003	0.025	<i>SNORA64</i>	small nucleolar RNA, H/ACA box 64
A_19_P00322397	0.325	0.009	0.043	<i>LOC400550</i>	uncharacterized LOC400550
A_23_P7313	0.325	0.003	0.022	<i>SPP1</i>	secreted phosphoprotein 1
A_33_P3269740	0.324	0.005	0.030	<i>FAM86B2</i>	family with sequence similarity 86, member B2
A_23_P502312	0.323	0.006	0.033	<i>CD97</i>	CD97 molecule
A_23_P81973	0.323	0.007	0.039	<i>HSD17B8</i>	hydroxysteroid (17-beta) dehydrogenase 8
A_33_P3250963	0.320	0.006	0.034	<i>TP53TG1</i>	TP53 target 1 (non-protein coding)
A_23_P49338	0.320	0.002	0.016	<i>TNFRSF12A</i>	tumor necrosis factor receptor superfamily, member 12A
A_33_P3420204	0.319	0.004	0.027	<i>CRTC1</i>	CREB regulated transcription coactivator 1
A_23_P359245	0.319	0.001	0.012	<i>MET</i>	met proto-oncogene (hepatocyte growth factor receptor)
A_32_P37592	0.318	0.001	0.014	<i>SCARNA17</i>	small Cajal body-specific RNA 17
A_33_P3261902	0.318	0.000	0.006	<i>ENOSF1</i>	enolase superfamily member 1
A_21_P0013709	0.316	0.003	0.024	<i>XLOC_l2_015034</i>	Q4V9S2_HUMAN CXorf20 protein, partial (5%) [THC2653521]
A_23_P30666	0.314	0.001	0.014	<i>TNFRSF21</i>	tumor necrosis factor receptor superfamily, member 21
A_23_P316460	0.313	0.003	0.021	<i>C7orf29</i>	chromosome 7 open reading frame 29
A_24_P52697	0.312	0.001	0.014	<i>H19</i>	H19, imprinted maternally expressed transcript (non-protein coding)
A_23_P122174	0.311	0.001	0.008	<i>XRCC4</i>	X-ray repair complementing defective repair in Chinese hamster cells 4
A_23_P50081	0.311	0.001	0.010	<i>IMPA2</i>	inositol(myo)-1(or 4)-monophosphatase 2
A_33_P3328928	0.310	0.010	0.047	<i>BMP2K</i>	BMP2 inducible kinase
A_23_P144465	0.310	0.002	0.020	<i>PAPSS1</i>	3'-phosphoadenosine 5'-phosphosulfate synthase 1
A_33_P3406899	0.310	0.002	0.017	<i>TRAK1</i>	trafficking protein, kinesin binding 1
A_33_P3311956	0.307	0.001	0.012	<i>FEZ2</i>	fasciculation and elongation protein zeta 2 (zygin II)
A_23_P333683	0.306	0.001	0.014	<i>IGSF10</i>	immunoglobulin superfamily, member 10
A_33_P3289835	0.306	0.009	0.044	<i>OSBPL9</i>	oxysterol binding protein-like 9
A_23_P96041	0.306	0.000	0.006	<i>TMEM164</i>	transmembrane protein 164
A_23_P30294	0.305	0.001	0.011	<i>CDO1</i>	cysteine dioxygenase, type I
A_23_P164436	0.305	0.002	0.017	<i>ASPA</i>	aspartoacylase
A_23_P217901	0.305	0.002	0.016	<i>TSTD1</i>	thiosulfate sulfurtransferase (rhodanese)-like domain containing 1
A_23_P503200	0.304	0.003	0.020	<i>PHF10</i>	PHD finger protein 10
A_33_P3613516	0.300	0.010	0.046	<i>LOC254057</i>	uncharacterized LOC254057
A_23_P28420	0.299	0.004	0.025	<i>OLA1</i>	Obg-like ATPase 1
A_32_P69368	0.298	0.009	0.044	<i>ID2</i>	inhibitor of DNA binding 2, dominant negative helix-loop-helix protein
A_33_P3309551	0.298	0.005	0.030	<i>PTPRD</i>	protein tyrosine phosphatase, receptor type, D
A_23_P94819	0.297	0.005	0.028	<i>RPH3AL</i>	rabphilin 3A-like (without C2 domains)
A_23_P163143	0.297	0.002	0.019	<i>ACYP1</i>	acylphosphatase 1, erythrocyte (common) type
A_33_P3381454	0.296	0.001	0.010	<i>C1orf56</i>	chromosome 1 open reading frame 56
A_23_P81392	0.295	0.007	0.037	<i>WWC1</i>	WW and C2 domain containing 1
A_21_P0013285	0.295	0.002	0.018	<i>XLOC_l2_013734</i>	BROAD Institute lincRNA (XLOC_l2_013734), lincRNA [TCONS_l2_00026411]
A_23_P387184	0.293	0.003	0.024	<i>NHSL1</i>	NHS-like 1
A_23_P209700	0.293	0.007	0.038	<i>NMUR1</i>	neuromedin U receptor 1
A_33_P3323722	0.293	0.008	0.040	<i>ARL4C</i>	ADP-ribosylation factor-like 4C
A_23_P160318	0.293	0.006	0.033	<i>COL16A1</i>	collagen, type XVI, alpha 1
A_23_P422851	0.292	0.009	0.043	<i>CABLES1</i>	Cdk5 and Abl enzyme substrate 1
A_23_P428260	0.288	0.001	0.010	<i>STEAP2</i>	STEAP family member 2, metalloreductase
A_21_P0011047	0.288	0.005	0.028	<i>XLOC_l2_003021</i>	602250064F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4328318 5', mRNA sequence [BF789912]

A_24_P403734	0.288	0.004	0.026	ZNF385A	zinc finger protein 385A
A_23_P72117	0.287	0.002	0.018	SMPDL3A	sphingomyelin phosphodiesterase, acid-like 3A
A_21_P0000310	0.286	0.003	0.024	SNORA12	small nucleolar RNA, H/ACA box 12
A_33_P3209960	0.286	0.008	0.039	RASGRP2	RAS guanyl releasing protein 2 (calcium and DAG-regulated)
A_32_P100439	0.284	0.001	0.012	C7orf41	chromosome 7 open reading frame 41
A_23_P24535	0.283	0.002	0.018	TTC12	tetratricopeptide repeat domain 12
A_33_P3263890	0.282	0.002	0.018	PRRX1	paired related homeobox 1
A_23_P340722	0.282	0.006	0.034	XPOT	exportin, tRNA (nuclear export receptor for tRNAs)
A_23_P9458	0.282	0.003	0.024	POLR1E	polymerase (RNA) I polypeptide E, 53kDa
A_23_P135157	0.281	0.003	0.024	PLAA	phospholipase A2-activating protein
A_21_P0011496	0.281	0.009	0.042	CES1	carboxylesterase 1
A_24_P287756	0.279	0.002	0.016	NUDT21	nudix (nucleoside diphosphate linked moiety X)-type motif 21
A_21_P0008570	0.279	0.004	0.025	XLOC_011248	AGENCOURT_6822137 NIH_MGC_106 Homo sapiens cDNA clone IMAGE:5935069 5', mRNA sequence [BQ0533'
A_23_P252855	0.278	0.004	0.026	BRX1	BRX1, biogenesis of ribosomes, homolog (S. cerevisiae)
A_33_P3290567	0.278	0.001	0.014	WEE1	WEE1 homolog (S. pombe)
A_23_P210708	0.277	0.008	0.042	SIRPA	signal-regulatory protein alpha
A_24_P108311	0.277	0.005	0.030	NEDD4L	neural precursor cell expressed, developmentally down-regulated 4-like
A_23_P83579	0.276	0.003	0.023	ARNT2	aryl-hydrocarbon receptor nuclear translocator 2
A_23_P207058	0.273	0.002	0.018	SOCS3	suppressor of cytokine signaling 3
A_33_P3228271	0.272	0.006	0.033	CST3	cystatin C
A_33_P3288694	0.272	0.011	0.049	LOC100131607	uncharacterized LOC100131607
A_33_P3252781	0.271	0.009	0.043	PLAC9	placenta-specific 9
A_32_P216426	0.271	0.001	0.015	HNRNPA1L2	heterogeneous nuclear ribonucleoprotein A1-like 2
A_33_P3363271	0.267	0.002	0.020	CACNB2	calcium channel, voltage-dependent, beta 2 subunit
A_23_P23783	0.266	0.008	0.039	MYOC	myocilin, trabecular meshwork inducible glucocorticoid response
A_33_P3732466	0.264	0.002	0.019	DKFZp547G183	uncharacterized LOC55525
A_33_P3375476	0.263	0.002	0.020	KLHDC4	kelch domain containing 4
A_33_P3362611	0.260	0.002	0.019	ELTD1	EGF, latrophilin and seven transmembrane domain containing 1
A_24_P289178	0.259	0.004	0.028	C16orf74	chromosome 16 open reading frame 74
A_23_P4536	0.259	0.003	0.023	EPB41L3	erythrocyte membrane protein band 4.1-like 3
A_24_P418408	0.259	0.004	0.027	FAM89A	family with sequence similarity 89, member A
A_23_P84929	0.258	0.007	0.038	SLC38A5	solute carrier family 38, member 5
A_21_P0007694	0.257	0.003	0.022	LOC100506451	uncharacterized LOC100506451
A_23_P257201	0.256	0.003	0.021	RNF146	ring finger protein 146
A_23_P215525	0.256	0.007	0.038	OSBPL3	oxysterol binding protein-like 3
A_24_P264943	0.256	0.010	0.045	COMP	cartilage oligomeric matrix protein
A_19_P00317793	0.256	0.005	0.030	LOC388796	uncharacterized LOC388796
A_33_P3382412	0.256	0.007	0.039	ZNF468	zinc finger protein 468
A_23_P98218	0.255	0.005	0.030	CWC15	CWC15 spliceosome-associated protein homolog (S. cerevisiae)
A_23_P24716	0.252	0.003	0.022	TMEM132A	transmembrane protein 132A
A_23_P112260	0.251	0.004	0.027	GNG10	guanine nucleotide binding protein (G protein), gamma 10
A_23_P76159	0.250	0.008	0.041	EEA1	early endosome antigen 1
A_24_P854913	0.249	0.007	0.037	METTL21A	methyltransferase like 21A
A_33_P3220530	0.249	0.006	0.033	SRSF6	serine/arginine-rich splicing factor 6
A_21_P0001050	0.249	0.005	0.032	XLOC_000527	uncharacterized LOC100506696

A_33_P3369567	0.245	0.007	0.038	LSP1	lymphocyte-specific protein 1
A_33_P3240018	0.242	0.003	0.024	PDE3B	phosphodiesterase 3B, cGMP-inhibited
A_19_P00315550	0.242	0.006	0.034	LOC400043	uncharacterized LOC400043
A_21_P0000044	0.241	0.002	0.016	STEAP1B	STEAP family member 1B
A_23_P54144	0.241	0.008	0.040	BMP4	bone morphogenetic protein 4
A_21_P0009481	0.241	0.009	0.043	RAB27B	RAB27B, member RAS oncogene family
A_23_P258769	0.241	0.003	0.024	HLA-DPB1	major histocompatibility complex, class II, DP beta 1
A_32_P149432	0.241	0.003	0.022	EIF4A1	eukaryotic translation initiation factor 4A1
A_24_P309594	0.240	0.009	0.042	SLC48A1	solute carrier family 48 (heme transporter), member 1
A_19_P00320471	0.238	0.010	0.046	FLJ35024	uncharacterized LOC401491
A_23_P202104	0.238	0.005	0.031	PPIF	peptidylprolyl isomerase F
A_33_P3231670	0.235	0.009	0.043	RNF208	ring finger protein 208
A_23_P149259	0.234	0.005	0.031	TMEM79	transmembrane protein 79
A_21_P0011258	0.233	0.005	0.030	XLOC_l2_004315	BROAD Institute lincRNA (XLOC_l2_004315), lincRNA [TCONS_l2_00007925]
A_33_P3270509	0.232	0.005	0.031	SIAH1	seven in absentia homolog 1 (Drosophila)
A_32_P52153	0.230	0.008	0.041	LOC728978	uncharacterized LOC728978
A_32_P38467	0.228	0.002	0.019	SNHG8	small nucleolar RNA host gene 8 (non-protein coding)
A_23_P9603	0.227	0.007	0.037	PRKDC	protein kinase, DNA-activated, catalytic polypeptide
A_23_P122906	0.227	0.009	0.043	AUTS2	autism susceptibility candidate 2
A_23_P156402	0.227	0.006	0.033	NME5	non-metastatic cells 5, protein expressed in (nucleoside-diphosphate kinase)
A_21_P0011796	0.226	0.009	0.042	XLOC_l2_007271	BROAD Institute lincRNA (XLOC_l2_007271), lincRNA [TCONS_l2_00013558]
A_33_P3311493	0.225	0.006	0.032	LOC283392	uncharacterized LOC283392
A_33_P3343957	0.224	0.004	0.026	EHBPI	EH domain binding protein 1
A_33_P3389188	0.218	0.007	0.038	TFAM	transcription factor A, mitochondrial
A_23_P38505	0.218	0.010	0.045	CXCL16	chemokine (C-X-C motif) ligand 16
A_33_P3401301	0.218	0.011	0.050	RPL39	ribosomal protein L39
A_23_P24997	0.217	0.003	0.025	CDK4	cyclin-dependent kinase 4
A_23_P432591	0.214	0.010	0.047	CCDC125	coiled-coil domain containing 125
A_23_P75330	0.211	0.006	0.034	HNRNPF	heterogeneous nuclear ribonucleoprotein F
A_21_P0001550	0.209	0.011	0.049	LOC100131564	uncharacterized LOC100131564
A_33_P3362249	0.209	0.006	0.032	LOC100288292	putative uncharacterized protein FLJ44672-like
A_24_P354615	0.209	0.011	0.049	MTMR12	myotubularin related protein 12
A_21_P0008627	0.209	0.010	0.047	XLOC_011226	OIP5 antisense RNA 1
A_24_P160969	0.208	0.006	0.036	TP53I11	tumor protein p53 inducible protein 11
A_23_P157170	0.207	0.011	0.048	DNAJC30	DnaJ (Hsp40) homolog, subfamily C, member 30
A_33_P3349827	0.207	0.010	0.046	RBM3	RNA binding motif (RNP1, RRM) protein 3
A_23_P500956	0.205	0.006	0.033	B3GNT2	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 2
A_21_P0012979	0.204	0.008	0.042	XLOC_l2_011987	putative beta-glucuronidase-like protein FLJ75287 pseudogene
A_23_P28434	0.202	0.006	0.032	VAMP8	vesicle-associated membrane protein 8 (endobrevin)
A_21_P0013113	0.201	0.011	0.049	XLOC_l2_013189	BROAD Institute lincRNA (XLOC_l2_013189), lincRNA [TCONS_l2_00025009]
A_23_P20532	0.200	0.009	0.044	CNTNAP3B	contactin associated protein-like 3B
A_23_P201655	0.196	0.009	0.044	MYCBP	c-myc binding protein
A_33_P3419835	0.195	0.004	0.027	FBXL19-AS1	FBXL19 antisense RNA 1 (non-protein coding)
A_33_P3402763	0.194	0.007	0.038	MKI67IP	MKI67 (FHA domain) interacting nucleolar phosphoprotein
A_23_P88489	0.191	0.008	0.039	CATSPER2	cation channel, sperm associated 2

A_33_P3275381	0.178	0.010	0.046	MAP9	microtubule-associated protein 9
A_33_P3246268	0.176	0.009	0.044	HOXD13	homeobox D13
A_23_P121250	0.171	0.011	0.050	EIF4A2	eukaryotic translation initiation factor 4A2
A_33_P3240392	-0.174	0.011	0.049	FOXO3	forkhead box O3
A_23_P18798	-0.185	0.011	0.049	PCDHB9	protocadherin beta 9
A_23_P135164	-0.189	0.010	0.046	UAP1L1	UDP-N-acetylglucosamine pyrophosphorylase 1-like 1
A_33_P3411925	-0.193	0.008	0.040	WDR18	WD repeat domain 18
A_23_P65481	-0.198	0.007	0.037	TEP1	telomerase-associated protein 1
A_23_P161190	-0.200	0.009	0.042	VIM	vimentin
A_24_P72518	-0.201	0.010	0.048	AHCYL2	adenosylhomocysteinase-like 2
A_23_P151529	-0.202	0.010	0.046	C14orf132	chromosome 14 open reading frame 132
A_32_P150891	-0.205	0.007	0.038	DIAPH3	diaphanous homolog 3 (Drosophila)
A_33_P3250083	-0.210	0.009	0.042	NFATC4	nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 4
A_23_P363255	-0.213	0.008	0.042	CCDC68	coiled-coil domain containing 68
A_21_P0010491	-0.214	0.010	0.045	LOC100507312	uncharacterized LOC100507312
A_21_P0000624	-0.215	0.010	0.045	SLC6A13	solute carrier family 6 (neurotransmitter transporter, GABA), member 13
A_23_P98686	-0.216	0.010	0.046	ATHL1	ATH1, acid trehalase-like 1 (yeast)
A_33_P3349444	-0.216	0.005	0.030	NAGA	N-acetylgalactosaminidase, alpha-
A_24_P303454	-0.217	0.009	0.043	TIAM2	T-cell lymphoma invasion and metastasis 2
A_23_P22614	-0.220	0.004	0.027	SEPT6	septin 6
A_21_P0014134	-0.220	0.006	0.034	EVC	Ellis van Creveld syndrome
A_33_P3319581	-0.222	0.008	0.040	FIGNL2	fidgetin-like 2
A_23_P27724	-0.223	0.005	0.029	SEPW1	selenoprotein W, 1
A_33_P3404052	-0.224	0.011	0.048	TNFAIP8	tumor necrosis factor, alpha-induced protein 8
A_33_P3238290	-0.225	0.009	0.044	FAM65C	family with sequence similarity 65, member C
A_23_P155868	-0.227	0.006	0.034	PGRMC2	progesterone receptor membrane component 2
A_23_P83939	-0.228	0.009	0.043	SYAP1	synapse associated protein 1
A_23_P74299	-0.231	0.004	0.028	ADORA1	adenosine A1 receptor
A_33_P3346193	-0.231	0.009	0.044	TPM3	tropomyosin 3
A_23_P408996	-0.232	0.003	0.022	MBOAT1	membrane bound O-acyltransferase domain containing 1
A_23_P387471	-0.232	0.009	0.044	MICB	MHC class I polypeptide-related sequence B
A_32_P222695	-0.233	0.009	0.042	ARHGEF37	Rho guanine nucleotide exchange factor (GEF) 37
A_23_P81048	-0.233	0.003	0.021	STIM2	stromal interaction molecule 2
A_21_P0000418	-0.234	0.008	0.040	SNORD114-21	small nucleolar RNA, C/D box 114-21
A_21_P0009964	-0.235	0.002	0.018	LOC100506053	uncharacterized LOC100506053
A_21_P0004354	-0.235	0.003	0.024	XLOC_004710	BROAD Institute lincRNA (XLOC_004710), lincRNA [TCONS_00010248]
A_33_P3295283	-0.240	0.006	0.034	LPCAT3	lysophosphatidylcholine acyltransferase 3
A_24_P709377	-0.241	0.005	0.030	LOC654433	uncharacterized LOC654433
A_33_P3284453	-0.242	0.010	0.047	C6orf174	chromosome 6 open reading frame 174
A_21_P0013238	-0.243	0.007	0.037	XLOC_12_013467	BROAD Institute lincRNA (XLOC_12_013467), lincRNA [TCONS_12_00025992]
A_21_P0000588	-0.244	0.004	0.027	LOC404266	uncharacterized LOC404266
A_23_P351667	-0.244	0.004	0.027	ADAM23	ADAM metallopeptidase domain 23
A_23_P213014	-0.245	0.004	0.026	SLC2A9	solute carrier family 2 (facilitated glucose transporter), member 9
A_21_P0013517	-0.245	0.010	0.046	XLOC_12_014549	BROAD Institute lincRNA (XLOC_12_014549), lincRNA [TCONS_12_00028240]
A_19_P00811440	-0.246	0.004	0.027	XLOC_002473	BROAD Institute lincRNA (XLOC_002473), lincRNA [TCONS_00004564]

A_23_P20427	-0.246	0.007	0.039	RHOBTB2	Rho-related BTB domain containing 2
A_33_P3629678	-0.247	0.008	0.039	COL5A1	collagen, type V, alpha 1
A_21_P0006970	-0.247	0.005	0.030	SFTA1P	surfactant associated 1, pseudogene
A_21_P0000491	-0.249	0.007	0.039	SNAR-G1	small ILF3/NF90-associated RNA G1
A_23_P218086	-0.249	0.009	0.042	TPCN1	two pore segment channel 1
A_19_P00320362	-0.250	0.006	0.034	LOC729177	uncharacterized LOC729177
A_21_P0009319	-0.250	0.007	0.038	XLOC_012457	ALU1_HUMAN (P39188) Alu subfamily J sequence contamination warning entry, partial (14%) [THC2665248]
A_33_P3253672	-0.251	0.009	0.044	KCNH3	potassium voltage-gated channel, subfamily H (eag-related), member 3
A_33_P3344282	-0.252	0.005	0.030	HS1BP3	HCLS1 binding protein 3
A_23_P109636	-0.252	0.006	0.033	LRIG1	leucine-rich repeats and immunoglobulin-like domains 1
A_33_P3360611	-0.252	0.011	0.049	MPP2	membrane protein, palmitoylated 2 (MAGUK p55 subfamily member 2)
A_23_P373119	-0.253	0.003	0.023	HMGB3P1	high mobility group box 3 pseudogene 1
A_24_P469641	-0.253	0.009	0.042	RNF216	ring finger protein 216
A_33_P3295578	-0.253	0.003	0.022	TCEAL8	transcription elongation factor A (SII)-like 8
A_33_P3227400	-0.254	0.007	0.039	COL4A4	collagen, type IV, alpha 4
A_23_P137173	-0.256	0.004	0.028	TMSB15A	thymosin beta 15a
A_33_P3293266	-0.256	0.005	0.030	TMEM175	transmembrane protein 175
A_19_P00801634	-0.257	0.008	0.040	NOP56	NOP56 ribonucleoprotein homolog (yeast)
A_24_P355626	-0.257	0.010	0.046	ABCG4	ATP-binding cassette, sub-family G (WHITE), member 4
A_21_P0011873	-0.257	0.002	0.017	XLOC_12_007767	09F_J17.2 Novel Promoters 5' RACE-PCR Homo sapiens cDNA 5', mRNA sequence [EL584821]
A_23_P15582	-0.259	0.004	0.028	XYLT2	xylosyltransferase II
A_23_P205489	-0.259	0.010	0.048	SLC7A8	solute carrier family 7 (amino acid transporter light chain, L system), member 8
A_23_P67661	-0.259	0.007	0.036	COX7A1	cytochrome c oxidase subunit VIIa polypeptide 1 (muscle)
A_24_P82880	-0.260	0.009	0.044	TPM4	tropomyosin 4
A_24_P71938	-0.261	0.003	0.022	SMAD1	SMAD family member 1
A_23_P51187	-0.262	0.008	0.040	PRKCZ	protein kinase C, zeta
A_23_P139500	-0.262	0.008	0.042	BHLHE41	basic helix-loop-helix family, member e41
A_23_P205074	-0.264	0.005	0.030	SLC46A3	solute carrier family 46, member 3
A_33_P3338152	-0.265	0.006	0.033	HIF3A	hypoxia inducible factor 3, alpha subunit
A_33_P3302428	-0.271	0.007	0.037	TNRC6C	trinucleotide repeat containing 6C
A_24_P192994	-0.271	0.009	0.043	FADS1	fatty acid desaturase 1
A_23_P18598	-0.271	0.005	0.030	PI4K2B	phosphatidylinositol 4-kinase type 2 beta
A_24_P135628	-0.272	0.009	0.043	LOC100652762	uncharacterized LOC100652762
A_24_P278747	-0.272	0.011	0.050	CCND2	cyclin D2
A_23_P170337	-0.272	0.004	0.026	ALDH4A1	aldehyde dehydrogenase 4 family, member A1
A_33_P3220475	-0.272	0.007	0.036	FLJ23867	uncharacterized protein FLJ23867
A_33_P3422170	-0.273	0.003	0.022	HNRNPA3	heterogeneous nuclear ribonucleoprotein A3
A_23_P147255	-0.273	0.007	0.037	PCBP3	poly(rC) binding protein 3
A_33_P3805090	-0.273	0.006	0.033	FNIP2	folliculin interacting protein 2
A_21_P0000409	-0.274	0.004	0.027	SNORD114-12	small nucleolar RNA, C/D box 114-12
A_23_P63660	-0.274	0.006	0.035	C10orf58	chromosome 10 open reading frame 58
A_23_P103672	-0.275	0.002	0.018	NES	nestin
A_23_P170186	-0.277	0.007	0.039	OPLAH	5-oxoprolinase (ATP-hydrolysing)
A_33_P3358898	-0.277	0.009	0.044	SSC5D	scavenger receptor cysteine rich domain containing (5 domains)
A_21_P0000424	-0.279	0.002	0.015	SNORD114-28	small nucleolar RNA, C/D box 114-28

A_23_P372923	-0.280	0.006	0.033	FGFR1	fibroblast growth factor receptor 1
A_23_P66481	-0.281	0.002	0.019	RTN4RL1	reticulon 4 receptor-like 1
A_19_P00811717	-0.282	0.001	0.010	LOC100652903	uncharacterized LOC100652903
A_21_P0000408	-0.283	0.009	0.042	SNORD114-11	small nucleolar RNA, C/D box 114-11
A_23_P140427	-0.283	0.002	0.019	EVL	Enah/Vasp-like
A_23_P348257	-0.283	0.009	0.043	NUAK1	NUAK family, SNF1-like kinase, 1
A_33_P3229032	-0.285	0.001	0.008	CLEC11A	C-type lectin domain family 11, member A
A_33_P3399433	-0.286	0.001	0.015	C20orf27	chromosome 20 open reading frame 27
A_24_P69053	-0.286	0.007	0.039	ODZ3	odz, odd Oz/ten-m homolog 3 (Drosophila)
A_21_P0000422	-0.286	0.002	0.017	SNORD114-26	small nucleolar RNA, C/D box 114-26
A_33_P3228564	-0.287	0.009	0.042	DOK3	docking protein 3
A_24_P371281	-0.289	0.003	0.021	TMEM22	transmembrane protein 22
A_33_P3424800	-0.289	0.007	0.038	HLA-B	major histocompatibility complex, class I, B
A_23_P161698	-0.289	0.004	0.028	MMP3	matrix metalloproteinase 3 (stromelysin 1, progelatinase)
A_33_P3342628	-0.289	0.002	0.019	HES4	hairy and enhancer of split 4 (Drosophila)
A_33_P3269218	-0.291	0.005	0.029	BAI2	brain-specific angiogenesis inhibitor 2
A_33_P3220837	-0.292	0.008	0.041	MAFB	v-maf musculoaponeurotic fibrosarcoma oncogene homolog B (avian)
A_33_P3324206	-0.292	0.003	0.022	HR	hairless homolog (mouse)
A_33_P3283480	-0.294	0.002	0.017	CTSC	cathepsin C
A_23_P88069	-0.294	0.005	0.030	LHFP	lipoma HMGIC fusion partner
A_32_P52911	-0.295	0.009	0.044	ADII	acireductone dioxygenase 1
A_24_P193295	-0.295	0.007	0.037	RAB15	RAB15, member RAS oncogene family
A_23_P56578	-0.295	0.006	0.035	VIT	vitrin
A_23_P200801	-0.295	0.006	0.034	PDE4DIP	phosphodiesterase 4D interacting protein
A_23_P78742	-0.296	0.001	0.012	FLT3LG	fms-related tyrosine kinase 3 ligand
A_33_P3308105	-0.296	0.004	0.026	GGH	gamma-glutamyl hydrolase (conjugase, foyl/polyglutamyl hydrolase)
A_33_P3226832	-0.297	0.004	0.027	F3	coagulation factor III (thromboplastin, tissue factor)
A_32_P207124	-0.298	0.005	0.030	CT47A11	cancer/testis antigen family 47, member A11
A_23_P32036	-0.299	0.002	0.019	C9orf95	chromosome 9 open reading frame 95
A_24_P23411	-0.300	0.002	0.017	ARMCX3	armadillo repeat containing, X-linked 3
A_23_P156890	-0.300	0.010	0.046	TCF21	transcription factor 21
A_23_P74088	-0.300	0.007	0.039	MMP23B	matrix metalloproteinase 23B
A_19_P00316398	-0.301	0.009	0.044	Q8NDX4	Q8NDX4_HUMAN PREBP1 protein, complete [THC2471066]
A_23_P64792	-0.301	0.005	0.030	KCNMB4	potassium large conductance calcium-activated channel, subfamily M, beta member 4
A_33_P3335920	-0.302	0.006	0.033	SYNE1	spectrin repeat containing, nuclear envelope 1
A_21_P0000412	-0.303	0.004	0.025	SNORD114-15	small nucleolar RNA, C/D box 114-15
A_23_P341532	-0.304	0.007	0.037	SETDB2	SET domain, bifurcated 2
A_23_P160849	-0.304	0.008	0.042	FCER1G	Fc fragment of IgE, high affinity I, receptor for; gamma polypeptide
A_23_P209564	-0.305	0.001	0.013	CYBRD1	cytochrome b reductase 1
A_33_P3387145	-0.305	0.004	0.025	SH3KBP1	SH3-domain kinase binding protein 1
A_23_P31143	-0.306	0.001	0.013	TPD52L1	tumor protein D52-like 1
A_24_P302374	-0.307	0.005	0.032	CLCN6	chloride channel 6
A_32_P313405	-0.308	0.003	0.022	LAMA1	laminin, alpha 1
A_23_P21976	-0.308	0.007	0.036	CSPG4	chondroitin sulfate proteoglycan 4
A_23_P316612	-0.308	0.001	0.011	GLIS1	GLIS family zinc finger 1

A_33_P3229863	-0.308	0.008	0.039	LOC100128714	uncharacterized LOC100128714
A_23_P94403	-0.309	0.009	0.043	TYRP1	tyrosinase-related protein 1
A_21_P0013166	-0.310	0.005	0.032	XLOC_12_013242	BROAD Institute lincRNA (XLOC_12_013242), lincRNA [TCONS_12_00025570]
A_24_P403561	-0.313	0.003	0.021	LRP4	low density lipoprotein receptor-related protein 4
A_23_P256158	-0.316	0.006	0.033	ADRA2C	adrenergic, alpha-2C-, receptor
A_24_P140475	-0.316	0.004	0.027	SORBS2	sorbin and SH3 domain containing 2
A_23_P205746	-0.316	0.005	0.030	EML1	echinoderm microtubule associated protein like 1
A_23_P349966	-0.316	0.002	0.017	TMEM130	transmembrane protein 130
A_23_P369899	-0.317	0.005	0.031	TMEM158	transmembrane protein 158 (gene/pseudogene)
A_33_P3312271	-0.317	0.007	0.037	FLJ41170	uncharacterized LOC440200
A_23_P377376	-0.318	0.003	0.025	ACTR2	ARP2 actin-related protein 2 homolog (yeast)
A_33_P3294524	-0.318	0.001	0.014	ANKRD12	ankyrin repeat domain 12
A_33_P3222380	-0.319	0.001	0.013	AHNAK2	AHNAK nucleoprotein 2
A_33_P3394809	-0.319	0.003	0.024	PCYT2	phosphate cytidyltransferase 2, ethanolamine
A_21_P0000420	-0.319	0.001	0.013	SNORD114-23	small nucleolar RNA, C/D box 114-23
A_23_P45999	-0.320	0.004	0.027	FBXO2	F-box protein 2
A_33_P3333455	-0.320	0.004	0.027	EMILIN1	elastin microfibril interfacier 1
A_23_P136573	-0.320	0.006	0.033	ST3GAL5	ST3 beta-galactoside alpha-2,3-sialyltransferase 5
A_21_P0005002	-0.320	0.011	0.050	XLOC_005617	BROAD Institute lincRNA (XLOC_005617), lincRNA [TCONS_00012087]
A_33_P3379886	-0.323	0.003	0.022	FGF2	fibroblast growth factor 2 (basic)
A_21_P0010415	-0.323	0.001	0.013	XLOC_014226	BROAD Institute lincRNA (XLOC_014226), lincRNA [TCONS_00029589]
A_33_P3394933	-0.323	0.005	0.030	P4HA2	prolyl 4-hydroxylase, alpha polypeptide II
A_23_P401904	-0.324	0.002	0.017	PHF19	PHD finger protein 19
A_21_P0000419	-0.325	0.002	0.016	SNORD114-22	small nucleolar RNA, C/D box 114-22
A_33_P3587376	-0.325	0.001	0.010	SNAR-A3	small ILF3/NF90-associated RNA A3
A_23_P342727	-0.328	0.004	0.025	STAR13	StAR-related lipid transfer (START) domain containing 13
A_32_P87013	-0.328	0.001	0.013	IL8	interleukin 8
A_24_P158089	-0.328	0.005	0.031	SERPINE1	serpin peptidase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 1
A_33_P3371089	-0.328	0.006	0.036	SGTB	small glutamine-rich tetratricopeptide repeat (TPR)-containing, beta
A_23_P113825	-0.329	0.002	0.017	NACC2	NACC family member 2, BEN and BTB (POZ) domain containing
A_33_P3271490	-0.329	0.002	0.018	RBMS1	RNA binding motif, single stranded interacting protein 1
A_23_P368154	-0.330	0.002	0.017	PODN	podocan
A_23_P371239	-0.331	0.008	0.041	CMIP	c-Maf inducing protein
A_23_P43810	-0.331	0.002	0.016	LTBP1	latent transforming growth factor beta binding protein 1
A_23_P420196	-0.332	0.004	0.025	SOCS1	suppressor of cytokine signaling 1
A_19_P00320729	-0.333	0.006	0.034	LOC100509498	uncharacterized LOC100509498
A_24_P942481	-0.334	0.001	0.014	GPR180	G protein-coupled receptor 180
A_23_P408095	-0.334	0.002	0.020	DSTN	destrin (actin depolymerizing factor)
A_33_P3277611	-0.334	0.010	0.047	TMEM8C	transmembrane protein 8C
A_23_P31273	-0.335	0.006	0.035	AMPH	amphiphysin
A_24_P402080	-0.335	0.010	0.045	MBP	myelin basic protein
A_33_P3221253	-0.336	0.006	0.035	LPP	LIM domain containing preferred translocation partner in lipoma
A_19_P00321202	-0.336	0.003	0.021	CRYBG3	beta-gamma crystallin domain containing 3
A_23_P303155	-0.337	0.000	0.006	TMEM87B	transmembrane protein 87B
A_23_P82868	-0.338	0.005	0.030	PLAT	plasminogen activator, tissue

A_23_P50907	-0.339	0.001	0.008	<i>ITGAV</i>	integrin, alpha V (vitronectin receptor, alpha polypeptide, antigen CD51)
A_23_P406330	-0.339	0.003	0.023	<i>SMAP2</i>	small ArfGAP2
A_24_P211565	-0.339	0.007	0.037	<i>CIQTNF6</i>	C1q and tumor necrosis factor related protein 6
A_33_P3341656	-0.340	0.002	0.017	<i>MEF2D</i>	myocyte enhancer factor 2D
A_24_P385313	-0.341	0.006	0.033	<i>PTPRF</i>	protein tyrosine phosphatase, receptor type, F
A_32_P79434	-0.342	0.005	0.029	<i>PTPRN2</i>	protein tyrosine phosphatase, receptor type, N polypeptide 2
A_32_P135348	-0.344	0.003	0.024	<i>TANC1</i>	tetratricopeptide repeat, ankyrin repeat and coiled-coil containing 1
A_21_P0000507	-0.345	0.001	0.013	<i>SNAR-B2</i>	small ILF3/NF90-associated RNA B2
A_33_P3308914	-0.345	0.001	0.009	<i>CIB2</i>	calcium and integrin binding family member 2
A_33_P3255209	-0.345	0.009	0.043	<i>MGAT5</i>	mannosyl (alpha-1,6-)-glycoprotein beta-1,6-N-acetyl-glucosaminyltransferase
A_23_P396666	-0.346	0.006	0.033	<i>TBC1D2B</i>	TBC1 domain family, member 2B
A_33_P3315719	-0.346	0.001	0.013	<i>PLEKHH2</i>	pleckstrin homology domain containing, family H (with MyTH4 domain) member 2
A_21_P0000399	-0.347	0.006	0.036	<i>SNORD114-2</i>	small nucleolar RNA, C/D box 114-2
A_24_P142743	-0.352	0.003	0.022	<i>CNN2</i>	calponin 2
A_33_P3253460	-0.352	0.003	0.022	<i>LOC100130654</i>	uncharacterized LOC100130654
A_33_P3253234	-0.353	0.001	0.011	<i>IQSEC2</i>	IQ motif and Sec7 domain 2
A_24_P50245	-0.354	0.002	0.018	<i>HLA-DMA</i>	major histocompatibility complex, class II, DM alpha
A_21_P0012078	-0.354	0.002	0.020	<i>LOC541471</i>	uncharacterized LOC541471
A_23_P360754	-0.354	0.002	0.018	<i>ADAMTS4</i>	ADAM metalloproteinase with thrombospondin type 1 motif, 4
A_33_P3405068	-0.356	0.004	0.027	<i>NAVI</i>	neuron navigator 1
A_24_P313186	-0.356	0.001	0.008	<i>CALM1</i>	calmodulin 1 (phosphorylase kinase, delta)
A_21_P0000511	-0.357	0.001	0.010	<i>SNAR-H</i>	small ILF3/NF90-associated RNA H
A_21_P0006166	-0.357	0.004	0.027	<i>XLOC_007433</i>	MR3-FN0206-020201-006-h05 FN0206 Homo sapiens cDNA, mRNA sequence [BI046002]
A_23_P85209	-0.358	0.001	0.013	<i>IL13RA2</i>	interleukin 13 receptor, alpha 2
A_21_P0000406	-0.358	0.001	0.011	<i>SNORD114-9</i>	small nucleolar RNA, C/D box 114-9
A_23_P107421	-0.359	0.001	0.008	<i>TK1</i>	thymidine kinase 1, soluble
A_32_P168464	-0.360	0.003	0.024	<i>CASK</i>	calcium/calmodulin-dependent serine protein kinase (MAGUK family)
A_23_P65674	-0.361	0.001	0.011	<i>TMOD3</i>	tropomodulin 3 (ubiquitous)
A_23_P12363	-0.362	0.003	0.024	<i>ROR1</i>	receptor tyrosine kinase-like orphan receptor 1
A_23_P205713	-0.362	0.001	0.009	<i>STXBP6</i>	syntaxin binding protein 6 (amisyn)
A_23_P201386	-0.363	0.006	0.034	<i>DDAH1</i>	dimethylarginine dimethylaminohydrolase 1
A_21_P0010663	-0.364	0.007	0.037	<i>XLOC_12_001206</i>	BROAD Institute lincRNA (XLOC_12_001206), lincRNA [TCONS_12_00001638]
A_32_P46214	-0.365	0.003	0.024	<i>SLC9A9</i>	solute carrier family 9 (sodium/hydrogen exchanger), member 9
A_21_P0006028	-0.365	0.002	0.017	<i>XLOC_007458</i>	TCERG1L antisense RNA 1
A_24_P173823	-0.366	0.004	0.027	<i>PBX1</i>	pre-B-cell leukemia homeobox 1
A_23_P38167	-0.366	0.001	0.008	<i>GPRC5C</i>	G protein-coupled receptor, family C, group 5, member C
A_33_P3399788	-0.369	0.001	0.013	<i>SERPINA3</i>	serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 3
A_33_P3389653	-0.369	0.002	0.019	<i>PDE4D</i>	phosphodiesterase 4D, cAMP-specific
A_23_P215484	-0.370	0.004	0.028	<i>CCL26</i>	chemokine (C-C motif) ligand 26
A_33_P3279379	-0.370	0.000	0.005	<i>DSTNP2</i>	destrin (actin depolymerizing factor) pseudogene 2
A_23_P342131	-0.370	0.001	0.009	<i>CYBASC3</i>	cytochrome b, ascorbate dependent 3
A_21_P0000508	-0.372	0.002	0.017	<i>SNAR-D</i>	small ILF3/NF90-associated RNA D
A_23_P11859	-0.372	0.002	0.018	<i>HSD17B7</i>	hydroxysteroid (17-beta) dehydrogenase 7
A_33_P3670415	-0.373	0.006	0.034	<i>NAT8L</i>	N-acetyltransferase 8-like (GCN5-related, putative)
A_33_P3265030	-0.374	0.005	0.029	<i>GP1BB</i>	glycoprotein Ib (platelet), beta polypeptide

A_21_P0001902	-0.375	0.001	0.010	<i>XLOC_001625</i>	uncharacterized LOC100507286
A_32_P181222	-0.378	0.000	0.005	<i>KCNMA1</i>	potassium large conductance calcium-activated channel, subfamily M, alpha member 1
A_23_P211252	-0.378	0.003	0.022	<i>LSS</i>	lanosterol synthase (2,3-oxidosqualene-lanosterol cyclase)
A_23_P154875	-0.380	0.000	0.006	<i>BACE2</i>	beta-site APP-cleaving enzyme 2
A_33_P3307197	-0.380	0.000	0.005	<i>PTGFRN</i>	prostaglandin F2 receptor negative regulator
A_23_P302005	-0.380	0.011	0.048	<i>STON1</i>	stonin 1
A_23_P28834	-0.383	0.002	0.018	<i>PHACTR3</i>	phosphatase and actin regulator 3
A_23_P68851	-0.384	0.000	0.007	<i>KREMEN1</i>	kringle containing transmembrane protein 1
A_21_P0011281	-0.384	0.008	0.042	<i>XLOC_I2_004306</i>	uncharacterized LOC100507257
A_23_P377434	-0.385	0.001	0.012	<i>TNRC18</i>	trinucleotide repeat containing 18
A_32_P53524	-0.387	0.002	0.017	<i>NTN1</i>	netrin 1
A_23_P73012	-0.389	0.003	0.022	<i>C9orf3</i>	chromosome 9 open reading frame 3
A_24_P202497	-0.389	0.000	0.006	<i>TWSG1</i>	twisted gastrulation homolog 1 (Drosophila)
A_33_P3393766	-0.389	0.000	0.005	<i>C17orf96</i>	chromosome 17 open reading frame 96
A_23_P82503	-0.390	0.000	0.006	<i>PEG10</i>	paternally expressed 10
A_33_P3295523	-0.391	0.001	0.015	<i>RAC3</i>	ras-related C3 botulinum toxin substrate 3 (rho family, small GTP binding protein Rac3)
A_32_P210202	-0.391	0.001	0.013	<i>E2F7</i>	E2F transcription factor 7
A_33_P3252146	-0.391	0.000	0.007	<i>HMX3</i>	H6 family homeobox 3
A_33_P3272773	-0.392	0.008	0.040	<i>ZNF217</i>	zinc finger protein 217
A_19_P00319398	-0.392	0.009	0.042	<i>ERVMER34-1</i>	endogenous retrovirus group MER34, member 1
A_23_P205031	-0.393	0.000	0.007	<i>COL4A2</i>	collagen, type IV, alpha 2
A_23_P128084	-0.393	0.002	0.020	<i>ITGA7</i>	integrin, alpha 7
A_23_P307844	-0.394	0.003	0.021	<i>PHYHD1</i>	phytanoyl-CoA dioxygenase domain containing 1
A_24_P326491	-0.395	0.000	0.005	<i>MKX</i>	mohawk homeobox
A_23_P48717	-0.395	0.005	0.029	<i>NPC2</i>	Niemann-Pick disease, type C2
A_23_P423695	-0.396	0.004	0.028	<i>MXD4</i>	MAX dimerization protein 4
A_23_P214459	-0.396	0.000	0.004	<i>PRPH2</i>	peripherin 2 (retinal degeneration, slow)
A_23_P63798	-0.397	0.004	0.028	<i>KLF6</i>	Kruppel-like factor 6
A_33_P3365878	-0.397	0.007	0.037	<i>BMP8B</i>	bone morphogenetic protein 8b
A_21_P0004481	-0.398	0.001	0.009	<i>XLOC_004244</i>	BROAD Institute lincRNA (XLOC_004244), lincRNA [TCONS_00010594]
A_33_P3405424	-0.398	0.010	0.045	<i>IL4I1</i>	interleukin 4 induced 1
A_23_P206280	-0.399	0.002	0.017	<i>GPR56</i>	G protein-coupled receptor 56
A_21_P0011949	-0.399	0.011	0.049	<i>XLOC_I2_008203</i>	BROAD Institute lincRNA (XLOC_I2_008203), lincRNA [TCONS_I2_00014793]
A_23_P7212	-0.405	0.000	0.003	<i>CFI</i>	complement factor I
A_24_P62659	-0.406	0.003	0.020	<i>TSPAN2</i>	tetraspanin 2
A_33_P3398912	-0.406	0.000	0.008	<i>SLC2A6</i>	solute carrier family 2 (facilitated glucose transporter), member 6
A_23_P108673	-0.406	0.007	0.039	<i>FAM176A</i>	family with sequence similarity 176, member A
A_24_P197964	-0.406	0.006	0.034	<i>TRIM14</i>	tripartite motif containing 14
A_23_P78108	-0.407	0.001	0.010	<i>ALDOC</i>	aldolase C, fructose-bisphosphate
A_23_P142075	-0.408	0.004	0.027	<i>ACP5</i>	acid phosphatase 5, tartrate resistant
A_23_P26124	-0.409	0.001	0.008	<i>RORA</i>	RAR-related orphan receptor A
A_33_P3218960	-0.409	0.005	0.032	<i>CACNA1H</i>	calcium channel, voltage-dependent, T type, alpha 1H subunit
A_21_P0014465	-0.409	0.003	0.022	<i>LOC100507286</i>	uncharacterized LOC100507286
A_23_P7636	-0.410	0.004	0.027	<i>PTTG1</i>	pituitary tumor-transforming 1
A_33_P3228322	-0.410	0.000	0.005	<i>IL18BP</i>	interleukin 18 binding protein

A_33_P3269844	-0.411	0.008	0.039	LRRC26	leucine rich repeat containing 26
A_33_P3255304	-0.412	0.001	0.009	GGT5	gamma-glutamyltransferase 5
A_24_P217904	-0.414	0.000	0.005	TRERF1	transcriptional regulating factor 1
A_33_P3287646	-0.415	0.001	0.012	HSPB1	heat shock 27kDa protein 1
A_21_P0007825	-0.416	0.007	0.038	XLOC_009677	BROAD Institute lincRNA (XLOC_009677), lincRNA [TCONS_00021084]
A_24_P89971	-0.416	0.003	0.024	SURF4	surfeit 4
A_23_P139418	-0.416	0.002	0.019	GALNTL4	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase-like 4
A_33_P3325978	-0.418	0.007	0.039	TRIB2	tribbles homolog 2 (Drosophila)
A_23_P161424	-0.418	0.007	0.037	PLXDC2	plexin domain containing 2
A_23_P327519	-0.419	0.001	0.014	STARD4	StAR-related lipid transfer (START) domain containing 4
A_23_P134744	-0.421	0.000	0.006	RNF122	ring finger protein 122
A_23_P380614	-0.423	0.000	0.006	ATP9A	ATPase, class II, type 9A
A_33_P3362321	-0.424	0.001	0.013	FHL2	four and a half LIM domains 2
A_23_P210900	-0.424	0.000	0.003	ACSS2	acyl-CoA synthetase short-chain family member 2
A_23_P340848	-0.426	0.009	0.043	PTGIR	prostaglandin I2 (prostacyclin) receptor (IP)
A_33_P3335030	-0.426	0.003	0.022	ANKRD36	ankyrin repeat domain 36
A_23_P253029	-0.426	0.000	0.006	BOK	BCL2-related ovarian killer
A_23_P71319	-0.427	0.001	0.011	FDFT1	farnesyl-diphosphate farnesyltransferase 1
A_23_P300150	-0.429	0.002	0.019	NFATC1	nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 1
A_33_P3242733	-0.430	0.001	0.013	PKDCC	protein kinase domain containing, cytoplasmic homolog (mouse)
A_23_P101905	-0.435	0.002	0.019	APC2	adenomatosis polyposis coli 2
A_33_P3262694	-0.435	0.001	0.009	LOC647086	chromosome 20 open reading frame 27 pseudogene
A_33_P3309034	-0.435	0.001	0.008	SEPT7L	septin 7-like
A_21_P0000630	-0.435	0.001	0.010	LOC643733	caspase 4, apoptosis-related cysteine peptidase pseudogene
A_24_P207139	-0.437	0.004	0.025	PML	promyelocytic leukemia
A_23_P213857	-0.438	0.005	0.030	C7	complement component 7
A_23_P171077	-0.438	0.001	0.014	EBP	emopamil binding protein (sterol isomerase)
A_23_P339818	-0.439	0.002	0.019	ARRDC4	arrestin domain containing 4
A_33_P3348164	-0.439	0.000	0.004	TTL7	tubulin tyrosine ligase-like family, member 7
A_23_P215048	-0.441	0.002	0.017	KIAA0408	KIAA0408
A_33_P3333033	-0.442	0.004	0.027	SGSM2	small G protein signaling modulator 2
A_23_P44466	-0.445	0.004	0.026	CCDC102B	coiled-coil domain containing 102B
A_21_P0003384	-0.446	0.008	0.039	XLOC_003631	BROAD Institute lincRNA (XLOC_003631), lincRNA [TCONS_00007582]
A_23_P83098	-0.446	0.001	0.015	ALDH1A1	aldehyde dehydrogenase 1 family, member A1
A_24_P260101	-0.447	0.003	0.023	MME	membrane metallo-endopeptidase
A_24_P232790	-0.447	0.004	0.028	C14orf162	chromosome 14 open reading frame 162
A_21_P0014880	-0.448	0.007	0.037	LOC100652751	uncharacterized LOC100652751
A_23_P329870	-0.448	0.000	0.007	RHBDP2	rhomboïd 5 homolog 2 (Drosophila)
A_33_P3295036	-0.450	0.001	0.010	LOC389676	uncharacterized LOC389676
A_23_P501822	-0.450	0.001	0.011	JUP	junction plakoglobin
A_19_P00321973	-0.452	0.004	0.027	Q29HP5	Q29HP5_DROPS (Q29HP5) GA14742-PA (Fragment), partial (9%) [THC2614488]
A_33_P3229156	-0.452	0.005	0.028	SLC17A9	solute carrier family 17, member 9
A_23_P389102	-0.452	0.000	0.007	MYO1D	myosin ID
A_24_P189533	-0.455	0.004	0.028	ENDOD1	endonuclease domain containing 1
A_21_P0008072	-0.456	0.003	0.022	XLOC_010411	BROAD Institute lincRNA (XLOC_010411), lincRNA [TCONS_00021811]

A_23_P53193	-0.456	0.010	0.046	<i>SYTL2</i>	synaptotagmin-like 2
A_23_P131846	-0.458	0.003	0.022	<i>SNAIL</i>	snail homolog 1 (Drosophila)
A_21_P0014015	-0.458	0.002	0.015	<i>LOC100652963</i>	putative uncharacterized protein encoded by NCRNA00269-like
A_23_P166280	-0.459	0.001	0.008	<i>ICOSLG</i>	inducible T-cell co-stimulator ligand
A_33_P3322363	-0.460	0.000	0.003	<i>HMSD</i>	histocompatibility (minor) serpin domain containing
A_23_P66017	-0.461	0.002	0.019	<i>PRRT2</i>	proline-rich transmembrane protein 2
A_23_P41804	-0.462	0.001	0.013	<i>NKD2</i>	naked cuticle homolog 2 (Drosophila)
A_23_P109269	-0.462	0.001	0.010	<i>LAMA5</i>	laminin, alpha 5
A_33_P3849275	-0.463	0.003	0.023	<i>FHL1</i>	four and a half LIM domains 1
A_23_P34233	-0.463	0.003	0.022	<i>QPRT</i>	quinolinate phosphoribosyltransferase
A_23_P207911	-0.463	0.003	0.024	<i>TRPV2</i>	transient receptor potential cation channel, subfamily V, member 2
A_33_P3392192	-0.464	0.010	0.045	<i>NRG1</i>	neuregulin 1
A_33_P3527721	-0.466	0.010	0.047	<i>LOC284219</i>	uncharacterized LOC284219
A_24_P229531	-0.469	0.003	0.021	<i>OBFC2A</i>	oligonucleotide/oligosaccharide-binding fold containing 2A
A_23_P314101	-0.469	0.000	0.006	<i>SUSD2</i>	sushi domain containing 2
A_23_P69109	-0.470	0.005	0.030	<i>PLSCR1</i>	phospholipid scramblase 1
A_23_P127911	-0.470	0.000	0.006	<i>PAMR1</i>	peptidase domain containing associated with muscle regeneration 1
A_23_P111701	-0.470	0.000	0.003	<i>GNG11</i>	guanine nucleotide binding protein (G protein), gamma 11
A_23_P24104	-0.475	0.004	0.026	<i>PLAU</i>	plasminogen activator, urokinase
A_21_P0002334	-0.476	0.007	0.037	<i>XLOC_001788</i>	BROAD Institute lincRNA (XLOC_001788), lincRNA [TCONS_00003974]
A_33_P3410589	-0.477	0.001	0.010	<i>FAM43A</i>	family with sequence similarity 43, member A
A_23_P426021	-0.477	0.000	0.004	<i>SEL1L3</i>	sel-1 suppressor of lin-12-like 3 (C. elegans)
A_23_P22350	-0.478	0.004	0.027	<i>GRAMD3</i>	GRAM domain containing 3
A_24_P921366	-0.479	0.007	0.037	<i>CALD1</i>	caldesmon 1
A_33_P3398917	-0.480	0.000	0.003	<i>C15orf59</i>	chromosome 15 open reading frame 59
A_33_P3713357	-0.481	0.000	0.003	<i>ALCAM</i>	activated leukocyte cell adhesion molecule
A_33_P3368830	-0.482	0.000	0.006	<i>LY9</i>	lymphocyte antigen 9
A_32_P20691	-0.483	0.008	0.040	<i>CLK3</i>	CDC-like kinase 3
A_23_P416395	-0.483	0.002	0.018	<i>STC2</i>	stanniocalcin 2
A_19_P00811460	-0.486	0.001	0.014	<i>VSTM4</i>	V-set and transmembrane domain containing 4
A_33_P3252394	-0.487	0.000	0.005	<i>GADD45G</i>	growth arrest and DNA-damage-inducible, gamma
A_23_P501007	-0.487	0.000	0.008	<i>EFEMP1</i>	EGF containing fibulin-like extracellular matrix protein 1
A_32_P198923	-0.490	0.000	0.003	<i>YWHAZ</i>	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, zeta polypeptide
A_33_P3281191	-0.490	0.000	0.006	<i>NID1</i>	nidogen 1
A_24_P122137	-0.490	0.004	0.026	<i>LIF</i>	leukemia inhibitory factor (cholinergic differentiation factor)
A_23_P74278	-0.491	0.007	0.037	<i>PDE4B</i>	phosphodiesterase 4B, cAMP-specific
A_33_P3282978	-0.491	0.004	0.028	<i>BAALC</i>	brain and acute leukemia, cytoplasmic
A_24_P220485	-0.491	0.007	0.036	<i>OLFML2A</i>	olfactomedin-like 2A
A_21_P0003493	-0.492	0.008	0.041	<i>XLOC_004050</i>	RST41900 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence [BG227980]
A_23_P156327	-0.492	0.000	0.006	<i>TGFBI</i>	transforming growth factor, beta-induced, 68kDa
A_23_P42695	-0.493	0.000	0.006	<i>GGCT</i>	gamma-glutamylcyclotransferase
A_23_P105251	-0.495	0.000	0.006	<i>GLI1</i>	GLI family zinc finger 1
A_33_P3225273	-0.495	0.001	0.010	<i>QSOX1</i>	quiescin Q6 sulfhydryl oxidase 1
A_33_P3369844	-0.497	0.008	0.041	<i>CD24</i>	CD24 molecule
A_23_P19182	-0.497	0.000	0.004	<i>REEP2</i>	receptor accessory protein 2

A_23_P33196	-0.499	0.000	0.003	<i>COL5A2</i>	collagen, type V, alpha 2
A_24_P323114	-0.502	0.004	0.026	<i>ANXA2P3</i>	annexin A2 pseudogene 3
A_24_P915692	-0.504	0.000	0.005	<i>PHLDA1</i>	pleckstrin homology-like domain, family A, member 1
A_23_P163306	-0.505	0.001	0.009	<i>CGNL1</i>	cingulin-like 1
A_33_P3316878	-0.506	0.000	0.006	<i>CHPF</i>	chondroitin polymerizing factor
A_23_P1331	-0.508	0.000	0.005	<i>COL13A1</i>	collagen, type XIII, alpha 1
A_23_P379475	-0.508	0.000	0.003	<i>DHCR24</i>	24-dehydrocholesterol reductase
A_23_P75529	-0.509	0.001	0.011	<i>PKNOX2</i>	PBX/knotted 1 homeobox 2
A_33_P3255434	-0.513	0.000	0.003	<i>MEG3</i>	maternally expressed 3 (non-protein coding)
A_21_P0013302	-0.516	0.000	0.002	<i>XLOC_12_013808</i>	Q59EY4_HUMAN CDC10 protein variant (Fragment), partial (89%) [THC2541514]
A_23_P94319	-0.517	0.001	0.010	<i>KBTBD11</i>	kelch repeat and BTB (POZ) domain containing 11
A_24_P557479	-0.519	0.005	0.030	<i>XAF1</i>	XIAP associated factor 1
A_23_P205177	-0.520	0.000	0.004	<i>F10</i>	coagulation factor X
A_32_P132317	-0.520	0.001	0.011	<i>GPR155</i>	G protein-coupled receptor 155
A_23_P166248	-0.525	0.001	0.009	<i>RCAN1</i>	regulator of calcineurin 1
A_33_P3329344	-0.527	0.000	0.003	<i>FASN</i>	fatty acid synthase
A_23_P44724	-0.530	0.007	0.037	<i>CSRP2</i>	cysteine and glycine-rich protein 2
A_23_P99063	-0.531	0.000	0.002	<i>LUM</i>	lumican
A_32_P95223	-0.533	0.001	0.010	<i>FDPSL2A</i>	MGC44478
A_23_P373708	-0.536	0.008	0.042	<i>KRT18P55</i>	keratin 18 pseudogene 55
A_32_P103669	-0.538	0.001	0.010	<i>GOLGA6C</i>	golgin A6 family, member C
A_23_P24444	-0.538	0.000	0.007	<i>DHCR7</i>	7-dehydrocholesterol reductase
A_33_P3307253	-0.539	0.000	0.003	<i>AK5</i>	adenylate kinase 5
A_23_P374695	-0.540	0.000	0.007	<i>TEK</i>	TEK tyrosine kinase, endothelial
A_23_P19291	-0.541	0.004	0.027	<i>TUBB2A</i>	tubulin, beta 2A class IIa
A_23_P406025	-0.542	0.002	0.020	<i>PRUNE2</i>	prune homolog 2 (Drosophila)
A_32_P52609	-0.543	0.000	0.002	<i>LPIN1</i>	lipin 1
A_23_P360964	-0.544	0.000	0.005	<i>DACT3</i>	dapper, antagonist of beta-catenin, homolog 3 (Xenopus laevis)
A_23_P360079	-0.547	0.000	0.006	<i>NCKAP5</i>	NCK-associated protein 5
A_23_P79803	-0.547	0.000	0.006	<i>VSTM2L</i>	V-set and transmembrane domain containing 2 like
A_33_P3221129	-0.548	0.005	0.029	<i>LRRN4CL</i>	LRRN4 C-terminal like
A_23_P77310	-0.549	0.000	0.004	<i>ZFP106</i>	zinc finger protein 106 homolog (mouse)
A_23_P361049	-0.549	0.000	0.007	<i>MYO1B</i>	myosin IB
A_32_P208120	-0.550	0.003	0.021	<i>CAMK1D</i>	calcium/calmodulin-dependent protein kinase ID
A_24_P140204	-0.557	0.000	0.007	<i>PXK</i>	PX domain containing serine/threonine kinase
A_24_P296508	-0.557	0.000	0.004	<i>SLC43A2</i>	solute carrier family 43, member 2
A_23_P69738	-0.557	0.002	0.017	<i>RASL11B</i>	RAS-like, family 11, member B
A_24_P192805	-0.557	0.000	0.002	<i>CARD17</i>	caspase recruitment domain family, member 17
A_24_P117029	-0.559	0.000	0.005	<i>LDLR</i>	low density lipoprotein receptor
A_23_P393620	-0.559	0.000	0.004	<i>TFPI2</i>	tissue factor pathway inhibitor 2
A_24_P48204	-0.562	0.000	0.004	<i>SECTM1</i>	secreted and transmembrane 1
A_19_P00317447	-0.562	0.003	0.023	<i>XLOC_002736</i>	uncharacterized LOC100506377
A_23_P204630	-0.565	0.002	0.018	<i>NTN4</i>	netrin 4
A_23_P201376	-0.565	0.007	0.038	<i>SSX2IP</i>	synovial sarcoma, X breakpoint 2 interacting protein
A_23_P33326	-0.565	0.006	0.035	<i>ADRA1B</i>	adrenergic, alpha-1B-, receptor

A_23_P111995	-0.568	0.002	0.019	<i>LOXL2</i>	lysyl oxidase-like 2
A_23_P105592	-0.569	0.000	0.006	<i>MVK</i>	mevalonate kinase
A_24_P104407	-0.569	0.002	0.016	<i>SYNM</i>	synemin, intermediate filament protein
A_32_P116556	-0.577	0.002	0.015	<i>ZNF469</i>	zinc finger protein 469
A_21_P0011147	-0.577	0.000	0.006	<i>XLOC_12_003757</i>	Q8WZ85_HUMAN Olfactory-like receptor PJCG2 (Fragment), partial (81%) [THC2581448]
A_23_P218807	-0.578	0.000	0.001	<i>ZC3H7B</i>	zinc finger CCCH-type containing 7B
A_33_P3281795	-0.579	0.001	0.010	<i>MGLL</i>	monoglyceride lipase
A_23_P119196	-0.583	0.000	0.003	<i>KLF2</i>	Kruppel-like factor 2 (lung)
A_32_P300427	-0.587	0.000	0.004	<i>APCDD1L</i>	adenomatosis polyposis coli down-regulated 1-like
A_33_P3216059	-0.588	0.003	0.022	<i>ASPN</i>	asporin
A_33_P3313055	-0.592	0.002	0.017	<i>NOTCH3</i>	notch 3
A_24_P261417	-0.593	0.000	0.003	<i>DKK3</i>	dickkopf 3 homolog (Xenopus laevis)
A_24_P365180	-0.598	0.000	0.002	<i>DSEL</i>	dermatan sulfate epimerase-like
A_23_P34915	-0.601	0.000	0.003	<i>ATF3</i>	activating transcription factor 3
A_33_P3210488	-0.603	0.001	0.015	<i>COL6A3</i>	collagen, type VI, alpha 3
A_23_P205959	-0.607	0.004	0.028	<i>ALDH1A3</i>	aldehyde dehydrogenase 1 family, member A3
A_24_P416131	-0.609	0.001	0.010	<i>COTL1</i>	coactosin-like 1 (Dictyostelium)
A_32_P110390	-0.610	0.000	0.007	<i>TMEM171</i>	transmembrane protein 171
A_23_P110184	-0.610	0.000	0.004	<i>MSMO1</i>	methylsterol monooxygenase 1
A_21_P0011914	-0.611	0.001	0.009	<i>XLOC_12_008009</i>	BROAD Institute lincRNA (XLOC_12_008009), lincRNA [TCONS_12_00014564]
A_33_P3480395	-0.615	0.000	0.002	<i>FLJ30901</i>	uncharacterized protein FLJ30901
A_23_P148047	-0.615	0.001	0.009	<i>PTGER4</i>	prostaglandin E receptor 4 (subtype EP4)
A_23_P166566	-0.622	0.001	0.008	<i>CCDC48</i>	coiled-coil domain containing 48
A_23_P87013	-0.624	0.004	0.026	<i>TAGLN</i>	transgelin
A_23_P400449	-0.625	0.003	0.024	<i>VAT1L</i>	vesicle amine transport protein 1 homolog (T. californica)-like
A_24_P62783	-0.625	0.007	0.037	<i>FABP3</i>	fatty acid binding protein 3, muscle and heart (mammary-derived growth inhibitor)
A_23_P112798	-0.630	0.000	0.005	<i>CRIP2</i>	cysteine-rich protein 2
A_23_P337262	-0.631	0.001	0.013	<i>APCDD1</i>	adenomatosis polyposis coli down-regulated 1
A_23_P93282	-0.631	0.001	0.014	<i>HIST1H3J</i>	histone cluster 1, H3j
A_23_P429950	-0.634	0.001	0.009	<i>KAL1</i>	Kallmann syndrome 1 sequence
A_32_P151544	-0.636	0.004	0.027	<i>KRT18</i>	keratin 18
A_33_P3639068	-0.636	0.000	0.002	<i>GFRA1</i>	GDNF family receptor alpha 1
A_24_P128524	-0.640	0.000	0.004	<i>ICMT</i>	isoprenylcysteine carboxyl methyltransferase
A_23_P35414	-0.645	0.004	0.027	<i>PPP1R3C</i>	protein phosphatase 1, regulatory subunit 3C
A_21_P0012298	-0.646	0.000	0.008	<i>XLOC_12_009539</i>	BROAD Institute lincRNA (XLOC_12_009539), lincRNA [TCONS_12_00018033]
A_32_P101031	-0.649	0.005	0.029	<i>LYPD1</i>	LY6/PLAUR domain containing 1
A_23_P56505	-0.650	0.000	0.001	<i>ITGA4</i>	integrin, alpha 4 (antigen CD49D, alpha 4 subunit of VLA-4 receptor)
A_24_P46093	-0.657	0.001	0.014	<i>SLC6A6</i>	solute carrier family 6 (neurotransmitter transporter, taurine), member 6
A_24_P85775	-0.658	0.000	0.007	<i>C1orf38</i>	chromosome 1 open reading frame 38
A_24_P931443	-0.660	0.006	0.034	<i>GPR68</i>	G protein-coupled receptor 68
A_21_P0011867	-0.666	0.004	0.025	<i>XLOC_12_007656</i>	BROAD Institute lincRNA (XLOC_12_007656), lincRNA [TCONS_12_00014098]
A_24_P318656	-0.668	0.000	0.007	<i>ITGB3</i>	integrin, beta 3 (platelet glycoprotein IIIa, antigen CD61)
A_23_P31064	-0.669	0.001	0.010	<i>MOXD1</i>	monooxygenase, DBH-like 1
A_32_P144342	-0.672	0.000	0.003	<i>PARP4</i>	poly (ADP-ribose) polymerase family, member 4
A_21_P0000109	-0.672	0.000	0.007	<i>MTRNR2L9</i>	MT-RNR2-like 9 (pseudogene)

A_23_P8961	-0.672	0.000	0.002	IL7	interleukin 7
A_33_P3276713	-0.699	0.000	0.002	HGF	hepatocyte growth factor (hepapoietin A; scatter factor)
A_33_P3363245	-0.699	0.001	0.012	NXP4	neurexophilin 4
A_23_P213562	-0.706	0.000	0.001	F2R	coagulation factor II (thrombin) receptor
A_33_P3464555	-0.709	0.001	0.014	LOC283070	uncharacterized LOC283070
A_24_P114183	-0.710	0.000	0.002	FDPS	farnesyl diphosphate synthase
A_23_P146284	-0.710	0.000	0.007	SQLE	squalene epoxidase
A_24_P103886	-0.710	0.000	0.002	IDII	isopentenyl-diphosphate delta isomerase 1
A_33_P3296862	-0.712	0.000	0.001	C16orf89	chromosome 16 open reading frame 89
A_23_P350059	-0.713	0.003	0.022	PFN1P2	profilin 1 pseudogene 2
A_23_P136978	-0.717	0.000	0.007	SRPX2	sushi-repeat containing protein, X-linked 2
A_23_P146274	-0.718	0.000	0.006	STMN2	stathmin-like 2
A_33_P3231739	-0.718	0.000	0.002	ELOVL2	ELOVL fatty acid elongase 2
A_23_P69179	-0.728	0.001	0.013	LEPREL1	leprecan-like 1
A_23_P65240	-0.734	0.000	0.002	COL4A1	collagen, type IV, alpha 1
A_21_P0011522	-0.735	0.000	0.006	XLOC_12_005692	BROAD Institute lincRNA (XLOC_12_005692), lincRNA [TCONS_12_00010603]
A_33_P3312544	-0.740	0.001	0.014	GABRB1	gamma-aminobutyric acid (GABA) A receptor, beta 1
A_23_P167920	-0.751	0.000	0.005	DLL1	delta-like 1 (Drosophila)
A_23_P168403	-0.754	0.000	0.006	KCNH2	potassium voltage-gated channel, subfamily H (eag-related), member 2
A_23_P42257	-0.756	0.003	0.024	IER3	immediate early response 3
A_21_P0014365	-0.759	0.000	0.006	LOC100287082	uncharacterized LOC100287082
A_23_P124905	-0.763	0.000	0.003	NPTX1	neuronal pentraxin I
A_33_P3231953	-0.767	0.000	0.001	COL12A1	collagen, type XII, alpha 1
A_23_P76364	-0.768	0.000	0.007	CD9	CD9 molecule
A_23_P153676	-0.769	0.000	0.003	TLE2	transducin-like enhancer of split 2 (E(sp1) homolog, Drosophila)
A_24_P270460	-0.772	0.008	0.039	IFI27	interferon, alpha-inducible protein 27
A_33_P3325497	-0.778	0.005	0.031	FIBIN	fin bud initiation factor homolog (zebrafish)
A_23_P21560	-0.797	0.000	0.002	FAM49A	family with sequence similarity 49, member A
A_23_P303833	-0.811	0.000	0.005	SCN4B	sodium channel, voltage-gated, type IV, beta
A_33_P3314176	-0.814	0.001	0.011	FAM46C	family with sequence similarity 46, member C
A_23_P106617	-0.821	0.000	0.005	WFDC1	WAP four-disulfide core domain 1
A_23_P121533	-0.824	0.000	0.003	SPON2	spondin 2, extracellular matrix protein
A_21_P0009341	-0.826	0.000	0.006	LOC645638	WDM1-like pseudogene
A_23_P59888	-0.831	0.001	0.011	NACAP1	nascent-polypeptide-associated complex alpha polypeptide pseudogene 1
A_32_P86763	-0.841	0.000	0.005	TGM2	transglutaminase 2 (C polypeptide, protein-glutamine-gamma-glutamyltransferase)
A_24_P63522	-0.842	0.000	0.002	HMGCS1	3-hydroxy-3-methylglutaryl-CoA synthase 1 (soluble)
A_33_P3219651	-0.844	0.000	0.002	BMPER	BMP binding endothelial regulator
A_32_P148345	-0.863	0.003	0.024	ANXA2	annexin A2
A_23_P88303	-0.879	0.002	0.016	HSPA2	heat shock 70kDa protein 2
A_24_P41850	-0.885	0.000	0.001	MASP1	mannan-binding lectin serine peptidase 1 (C4/C2 activating component of Ra-reactive factor)
A_23_P32404	-0.889	0.000	0.004	ISG20	interferon stimulated exonuclease gene 20kDa
A_33_P3259135	-0.892	0.000	0.001	D4S234E	DNA segment on chromosome 4 (unique) 234 expressed sequence
A_23_P207456	-0.952	0.001	0.014	CCL8	chemokine (C-C motif) ligand 8
A_23_P152125	-0.974	0.000	0.001	MVD	mevalonate (diphospho) decarboxylase
A_23_P31135	-0.986	0.000	0.002	ACAT2	acetyl-CoA acetyltransferase 2

A_32_P142440	-0.986	0.000	0.003	PCSK9	proprotein convertase subtilisin/kexin type 9
A_23_P206022	-0.991	0.000	0.002	ITGA11	integrin, alpha 11
A_23_P76749	-0.995	0.000	0.001	GALNTL1	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase-like 1
A_23_P78037	-0.998	0.000	0.001	CCL7	chemokine (C-C motif) ligand 7
A_33_P3308347	-1.003	0.000	0.004	ADAMTS8	ADAM metalloproteinase with thrombospondin type 1 motif, 8
A_32_P74409	-1.005	0.000	0.002	C11orf96	chromosome 11 open reading frame 96
A_32_P8546	-1.020	0.000	0.005	LINC00473	long intergenic non-protein coding RNA 473
A_24_P183664	-1.039	0.006	0.033	TRIL	TLR4 interactor with leucine-rich repeats
A_32_P196263	-1.061	0.000	0.005	ADAMTS9	ADAM metalloproteinase with thrombospondin type 1 motif, 9
A_23_P94800	-1.121	0.000	0.002	S100A4	S100 calcium binding protein A4
A_33_P3560679	-1.139	0.000	0.002	LOC100287221	uncharacterized LOC100287221
A_23_P10647	-1.181	0.000	0.002	CYTL1	cytokine-like 1
A_23_P89431	-1.246	0.000	0.003	CCL2	chemokine (C-C motif) ligand 2
A_24_P125335	-1.324	0.000	0.007	CCL13	chemokine (C-C motif) ligand 13
A_24_P369232	-1.919	0.000	0.003	CCDC3	coiled-coil domain containing 3
A_23_P66635	-2.558	0.000	0.002	CCL11	chemokine (C-C motif) ligand 11

Supplementary Table S7 List of genes differentially-expressed in 1,25(OH)₂D₃- vs vehicle-treated human colon CAFs

Agilent ID	Log ₂ fold-change	p Value	Adjusted p Value	Gene symbol	Gene name
A_23_P28815	4.904	0.000	0.000	<i>CYP24A1</i>	cytochrome P450, family 24, subfamily A, polypeptide 1
A_23_P142424	1.765	0.000	0.000	<i>IGFLR1</i>	IGF-like family receptor 1
A_23_P86470	1.646	0.000	0.002	<i>CH25H</i>	cholesterol 25-hydroxylase
A_23_P129209	1.590	0.000	0.000	<i>IDH2</i>	isocitrate dehydrogenase 2 (NADP+), mitochondrial
A_23_P152055	1.577	0.000	0.001	<i>EFTUD1</i>	elongation factor Tu GTP binding domain containing 1
A_23_P215634	1.542	0.000	0.000	<i>IGFBP3</i>	insulin-like growth factor binding protein 3
A_23_P163087	1.459	0.000	0.001	<i>NID2</i>	nidogen 2 (osteonidogen)
A_23_P74609	1.407	0.001	0.007	<i>G0S2</i>	G0/G1switch 2
A_23_P132718	1.343	0.000	0.001	<i>SEMA3B</i>	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3B
A_23_P148990	1.291	0.000	0.001	<i>HMCN1</i>	hemicentin 1
A_23_P404494	1.258	0.000	0.001	<i>IL7R</i>	interleukin 7 receptor
A_23_P25706	1.240	0.000	0.002	<i>CLMN</i>	calmin (calponin-like, transmembrane)
A_23_P202448	1.211	0.000	0.002	<i>CXCL12</i>	chemokine (C-X-C motif) ligand 12
A_33_P3331491	1.168	0.001	0.006	<i>LOC728392</i>	uncharacterized LOC728392
A_33_P3511265	1.138	0.000	0.003	<i>POSTN</i>	periostin, osteoblast specific factor
A_24_P406132	1.080	0.001	0.006	<i>MAPK13</i>	mitogen-activated protein kinase 13
A_23_P1782	1.066	0.000	0.001	<i>CD82</i>	CD82 molecule
A_23_P401700	1.054	0.000	0.001	<i>APBB1IP</i>	amyloid beta (A4) precursor protein-binding, family B, member 1 interacting protein
A_23_P18078	1.043	0.000	0.001	<i>RARRES1</i>	retinoic acid receptor responder (tazarotene induced) 1
A_23_P26024	1.024	0.000	0.003	<i>C15orf48</i>	chromosome 15 open reading frame 48
A_23_P13907	1.014	0.000	0.001	<i>IGF1</i>	insulin-like growth factor 1 (somatomedin C)
A_23_P39237	1.011	0.000	0.001	<i>ZFP36</i>	zinc finger protein 36, C3H type, homolog (mouse)
A_23_P114947	0.976	0.004	0.025	<i>RGS2</i>	regulator of G-protein signaling 2, 24kDa
A_32_P108254	0.960	0.001	0.008	<i>FAM20A</i>	family with sequence similarity 20, member A
A_23_P105002	0.927	0.000	0.001	<i>ROM1</i>	retinal outer segment membrane protein 1
A_24_P87036	0.905	0.000	0.003	<i>ANO1</i>	anoctamin 1, calcium activated chloride channel
A_24_P168925	0.901	0.000	0.003	<i>CHRD1</i>	chordin-like 1
A_33_P3415052	0.886	0.000	0.001	<i>NIPAL4</i>	NIPA-like domain containing 4
A_23_P91390	0.881	0.001	0.009	<i>THBD</i>	thrombomodulin
A_23_P143981	0.871	0.000	0.000	<i>FBLN2</i>	fibulin 2
A_23_P18684	0.868	0.000	0.003	<i>CLGN</i>	calmegin
A_32_P452655	0.867	0.002	0.015	<i>LGALS9C</i>	lectin, galactoside-binding, soluble, 9C
A_23_P92042	0.867	0.000	0.001	<i>ITPR1</i>	inositol 1,4,5-trisphosphate receptor, type 1
A_23_P216361	0.867	0.000	0.001	<i>COL14A1</i>	collagen, type XIV, alpha 1
A_23_P134237	0.866	0.000	0.001	<i>RARRES2</i>	retinoic acid receptor responder (tazarotene induced) 2
A_23_P104318	0.864	0.000	0.004	<i>DDIT4</i>	DNA-damage-inducible transcript 4
A_21_P0005727	0.861	0.001	0.008	<i>XLOC_006850</i>	BROAD Institute lincRNA (XLOC_006850), lincRNA [TCONS_00014769]
A_23_P386320	0.855	0.000	0.005	<i>MF12</i>	antigen p97 (melanoma associated) identified by monoclonal antibodies 133.2 and 96.5
A_23_P70398	0.853	0.001	0.008	<i>VEGFA</i>	vascular endothelial growth factor A
A_24_P38276	0.851	0.000	0.004	<i>FZD1</i>	frizzled family receptor 1
A_23_P19624	0.845	0.012	0.048	<i>BMP6</i>	bone morphogenetic protein 6
A_33_P3243454	0.842	0.012	0.048	<i>IGFL3</i>	IGF-like family member 3

A_23_P68669	0.830	0.004	0.023	CHODL	chondrolectin
A_32_P117354	0.828	0.004	0.023	LIMCH1	LIM and calponin homology domains 1
A_24_P145629	0.827	0.000	0.003	SERINC2	serine incorporator 2
A_33_P3287223	0.817	0.000	0.005	DPP4	dipeptidyl-peptidase 4
A_32_P34444	0.796	0.000	0.002	FHOD3	formin homology 2 domain containing 3
A_24_P321068	0.796	0.000	0.004	SLC31A1	solute carrier family 31 (copper transporters), member 1
A_23_P50919	0.791	0.000	0.001	SERPINE2	serpin peptidase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 2
A_23_P216468	0.791	0.000	0.003	SLC1A1	solute carrier family 1 (neuronal/epithelial high affinity glutamate transporter, system Xag), member 1
A_33_P3289296	0.785	0.000	0.005	TMEM37	transmembrane protein 37
A_23_P63209	0.785	0.000	0.001	HSD11B1	hydroxysteroid (11-beta) dehydrogenase 1
A_23_P163567	0.774	0.005	0.029	SMPD3	sphingomyelin phosphodiesterase 3, neutral membrane (neutral sphingomyelinase II)
A_23_P62932	0.772	0.001	0.006	ATP1B1	ATPase, Na ⁺ /K ⁺ transporting, beta 1 polypeptide
A_33_P3236881	0.765	0.000	0.001	C1orf151-NBL1	C1orf151-NBL1 readthrough
A_23_P216340	0.763	0.000	0.002	SLA	Src-like-adaptor
A_21_P0010254	0.762	0.001	0.007	XLOC_013952	BROAD Institute lincRNA (XLOC_013952), lincRNA [TCONS_00029032]
A_23_P214011	0.762	0.000	0.001	CDH6	cadherin 6, type 2, K-cadherin (fetal kidney)
A_23_P25030	0.760	0.000	0.001	HSD17B6	hydroxysteroid (17-beta) dehydrogenase 6 homolog (mouse)
A_32_P25050	0.758	0.000	0.001	RDH10	retinol dehydrogenase 10 (all-trans)
A_23_P148879	0.755	0.001	0.006	ATP1A2	ATPase, Na ⁺ /K ⁺ transporting, alpha 2 polypeptide
A_24_P48723	0.752	0.003	0.019	PTGIS	prostaglandin I2 (prostacyclin) synthase
A_23_P333498	0.751	0.000	0.001	EEPD1	endonuclease/exonuclease/phosphatase family domain containing 1
A_33_P3295358	0.743	0.000	0.001	ANGPTL4	angiopoietin-like 4
A_23_P323272	0.739	0.001	0.010	OSR1	odd-skipped related 1 (Drosophila)
A_33_P3590259	0.729	0.001	0.010	CXCL14	chemokine (C-X-C motif) ligand 14
A_23_P256473	0.722	0.000	0.001	SEMA3C	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3C
A_23_P156708	0.718	0.000	0.001	TNXB	tenascin XB
A_21_P0013514	0.712	0.000	0.005	XLOC_12_014504	BROAD Institute lincRNA (XLOC_12_014504), lincRNA [TCONS_12_00028188]
A_23_P328323	0.710	0.000	0.002	RAVER2	ribonucleoprotein, PTB-binding 2
A_23_P250274	0.709	0.000	0.003	LRRC8A	leucine rich repeat containing 8 family, member A
A_32_P103695	0.707	0.000	0.003	FAM92A1	family with sequence similarity 92, member A1
A_23_P126623	0.703	0.000	0.002	PGD	phosphogluconate dehydrogenase
A_24_P80204	0.701	0.001	0.011	MALL	mal, T-cell differentiation protein-like
A_24_P40626	0.701	0.000	0.002	GREM2	gremlin 2
A_23_P32233	0.698	0.000	0.002	KLF4	Kruppel-like factor 4 (gut)
A_33_P3331307	0.686	0.000	0.003	CDC42EP3	CDC42 effector protein (Rho GTPase binding) 3
A_32_P66881	0.676	0.003	0.017	TLR4	toll-like receptor 4
A_23_P331700	0.676	0.000	0.004	SRRM3	serine/arginine repetitive matrix 3
A_24_P911676	0.675	0.000	0.002	SOX4	SRY (sex determining region Y)-box 4
A_19_P00315649	0.674	0.000	0.003	LOC100507165	uncharacterized LOC100507165
A_23_P139912	0.669	0.000	0.001	IGFBP6	insulin-like growth factor binding protein 6
A_33_P3337485	0.666	0.000	0.002	CD248	CD248 molecule, endosialin
A_23_P430930	0.664	0.000	0.005	RSPO2	R-spondin 2
A_23_P69573	0.662	0.001	0.010	GUCY1A3	guanylate cyclase 1, soluble, alpha 3
A_24_P383609	0.660	0.001	0.009	NANOS1	nanos homolog 1 (Drosophila)
A_33_P3310430	0.654	0.001	0.007	FAM86B2	family with sequence similarity 86, member B2

A_23_P14174	0.651	0.001	0.006	<i>TNFSF13B</i>	tumor necrosis factor (ligand) superfamily, member 13b
A_24_P55496	0.650	0.003	0.020	<i>OSR2</i>	odd-skipped related 2 (Drosophila)
A_23_P89780	0.648	0.001	0.007	<i>LAMA3</i>	laminin, alpha 3
A_23_P138760	0.647	0.000	0.001	<i>CLCF1</i>	cardiotrophin-like cytokine factor 1
A_33_P3272209	0.646	0.000	0.001	<i>MFSD6</i>	major facilitator superfamily domain containing 6
A_23_P304450	0.644	0.000	0.001	<i>GATA6</i>	GATA binding protein 6
A_23_P399078	0.633	0.000	0.002	<i>TIMP3</i>	TIMP metalloproteinase inhibitor 3
A_33_P3271111	0.631	0.001	0.008	<i>NINJI</i>	ninjurin 1
A_23_P210708	0.630	0.000	0.002	<i>SIRPA</i>	signal-regulatory protein alpha
A_23_P145114	0.630	0.002	0.014	<i>GCLC</i>	glutamate-cysteine ligase, catalytic subunit
A_24_P149036	0.624	0.000	0.001	<i>DPYSL3</i>	dihydropyrimidinase-like 3
A_23_P160318	0.623	0.000	0.005	<i>COL16A1</i>	collagen, type XVI, alpha 1
A_24_P353619	0.618	0.000	0.001	<i>ALPL</i>	alkaline phosphatase, liver/bone/kidney
A_23_P38677	0.618	0.000	0.002	<i>SLMO1</i>	slowmo homolog 1 (Drosophila)
A_23_P91114	0.616	0.000	0.002	<i>PREB</i>	prolactin regulatory element binding
A_23_P133438	0.616	0.003	0.017	<i>FAM105A</i>	family with sequence similarity 105, member A
A_33_P3391603	0.615	0.004	0.023	<i>LAMA4</i>	laminin, alpha 4
A_24_P402438	0.612	0.004	0.023	<i>TGFB2</i>	transforming growth factor, beta 2
A_24_P191781	0.609	0.000	0.002	<i>PARM1</i>	prostate androgen-regulated mucin-like protein 1
A_23_P128574	0.607	0.000	0.004	<i>ENOX1</i>	ecto-NOX disulfide-thiol exchanger 1
A_23_P369994	0.606	0.000	0.002	<i>DCLK1</i>	doublecortin-like kinase 1
A_23_P122216	0.602	0.001	0.007	<i>LOX</i>	lysyl oxidase
A_24_P261567	0.598	0.000	0.001	<i>GDPD5</i>	glycerophosphodiester phosphodiesterase domain containing 5
A_33_P3252286	0.596	0.002	0.016	<i>CRLF1</i>	cytokine receptor-like factor 1
A_33_P3303136	0.594	0.000	0.002	<i>SERPINB6</i>	serpin peptidase inhibitor, clade B (ovalbumin), member 6
A_23_P257043	0.594	0.005	0.028	<i>GEM</i>	GTP binding protein overexpressed in skeletal muscle
A_23_P120227	0.592	0.002	0.015	<i>LBH</i>	limb bud and heart development homolog (mouse)
A_33_P3227793	0.591	0.002	0.013	<i>CGREF1</i>	cell growth regulator with EF-hand domain 1
A_21_P0012224	0.586	0.011	0.047	<i>XLOC_12_009140</i>	uncharacterized LOC100652984
A_23_P149992	0.586	0.000	0.004	<i>PDLIM1</i>	PDZ and LIM domain 1
A_23_P135548	0.585	0.000	0.001	<i>DPYD</i>	dihydropyrimidine dehydrogenase
A_23_P138717	0.578	0.001	0.006	<i>RGS10</i>	regulator of G-protein signaling 10
A_23_P385067	0.577	0.005	0.027	<i>CLIC6</i>	chloride intracellular channel 6
A_23_P88404	0.576	0.009	0.041	<i>TGFB3</i>	transforming growth factor, beta 3
A_23_P76914	0.573	0.000	0.005	<i>SIX1</i>	SIX homeobox 1
A_23_P8913	0.567	0.006	0.029	<i>CA2</i>	carbonic anhydrase II
A_24_P62530	0.564	0.005	0.025	<i>RHOU</i>	ras homolog gene family, member U
A_23_P58676	0.564	0.001	0.010	<i>NPR3</i>	natriuretic peptide receptor C/guanylate cyclase C (atrionatriuretic peptide receptor C)
A_23_P127891	0.559	0.000	0.002	<i>BDNF</i>	brain-derived neurotrophic factor
A_23_P42282	0.557	0.001	0.010	<i>C4B</i>	complement component 4B (Chido blood group)
A_24_P10137	0.548	0.003	0.018	<i>C13orf15</i>	chromosome 13 open reading frame 15
A_19_P00322397	0.545	0.000	0.005	<i>LOC400550</i>	uncharacterized LOC400550
A_23_P126706	0.544	0.000	0.002	<i>ANGPTL1</i>	angiopoietin-like 1
A_32_P40288	0.543	0.003	0.019	<i>TMEM200A</i>	transmembrane protein 200A
A_23_P325690	0.539	0.000	0.004	<i>ANKRD35</i>	ankyrin repeat domain 35

A_23_P81973	0.536	0.009	0.041	HSD17B8	hydroxysteroid (17-beta) dehydrogenase 8
A_23_P65532	0.536	0.001	0.009	PELI2	pellino homolog 2 (Drosophila)
A_32_P197340	0.535	0.000	0.004	LOC285141	uncharacterized LOC285141
A_33_P3347452	0.534	0.006	0.030	RPS6KA2	ribosomal protein S6 kinase, 90kDa, polypeptide 2
A_24_P940149	0.533	0.002	0.012	C2CD2	C2 calcium-dependent domain containing 2
A_23_P4353	0.530	0.001	0.006	WSB1	WD repeat and SOCS box containing 1
A_23_P320261	0.526	0.000	0.001	DMKN	dermokine
A_23_P108501	0.526	0.005	0.028	EPHA4	EPH receptor A4
A_24_P390928	0.526	0.000	0.001	TRAPPC6A	trafficking protein particle complex 6A
A_33_P3234697	0.523	0.001	0.006	LXN	latexin
A_32_P69368	0.522	0.003	0.019	ID2	inhibitor of DNA binding 2, dominant negative helix-loop-helix protein
A_23_P159775	0.518	0.001	0.009	GABRE	gamma-aminobutyric acid (GABA) A receptor, epsilon
A_32_P101689	0.518	0.000	0.005	FAM3C	family with sequence similarity 3, member C
A_21_P0011081	0.517	0.000	0.004	FAM86C1	family with sequence similarity 86, member C1
A_23_P132763	0.517	0.000	0.002	VGLL3	vestigial like 3 (Drosophila)
A_23_P352266	0.515	0.001	0.007	BCL2	B-cell CLL/lymphoma 2
A_23_P157569	0.510	0.003	0.021	ADHFE1	alcohol dehydrogenase, iron containing, 1
A_23_P97365	0.508	0.000	0.002	LRRC8D	leucine rich repeat containing 8 family, member D
A_23_P156687	0.507	0.003	0.019	CFB	complement factor B
A_33_P3383226	0.504	0.000	0.003	GP9	glycoprotein IX (platelet)
A_32_P18824	0.504	0.000	0.002	BRD7	bromodomain containing 7
A_23_P118065	0.504	0.000	0.001	HSD17B2	hydroxysteroid (17-beta) dehydrogenase 2
A_24_P71468	0.502	0.001	0.008	QPCT	glutaminyl-peptide cyclotransferase
A_23_P112135	0.495	0.000	0.002	TRAM1	translocation associated membrane protein 1
A_21_P0008399	0.494	0.001	0.007	XLOC_010947	BROAD Institute lincRNA (XLOC_010947), lincRNA [TCONS_00022643]
A_23_P33759	0.492	0.002	0.013	DHRS3	dehydrogenase/reductase (SDR family) member 3
A_23_P324327	0.484	0.000	0.002	GPRC5B	G protein-coupled receptor, family C, group 5, member B
A_23_P396858	0.483	0.008	0.037	FZD8	frizzled family receptor 8
A_23_P69810	0.483	0.008	0.036	AGPAT9	1-acylglycerol-3-phosphate O-acyltransferase 9
A_23_P316460	0.480	0.001	0.007	C7orf29	chromosome 7 open reading frame 29
A_23_P363647	0.480	0.002	0.016	DDX26B	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 26B
A_23_P44505	0.480	0.000	0.002	KLF11	Kruppel-like factor 11
A_23_P211212	0.479	0.001	0.011	COL18A1	collagen, type XVIII, alpha 1
A_23_P76159	0.479	0.001	0.009	EEA1	early endosome antigen 1
A_24_P55295	0.477	0.001	0.007	GJA1	gap junction protein, alpha 1, 43kDa
A_23_P72117	0.475	0.002	0.015	SMPDL3A	sphingomyelin phosphodiesterase, acid-like 3A
A_24_P126139	0.474	0.007	0.035	RAB9B	RAB9B, member RAS oncogene family
A_23_P43141	0.471	0.000	0.001	EIF3E	eukaryotic translation initiation factor 3, subunit E
A_24_P290013	0.469	0.001	0.007	FLJ10661	family with sequence similarity 86, member A pseudogene
A_33_P3338121	0.468	0.001	0.006	LAMB3	laminin, beta 3
A_21_P0013057	0.466	0.003	0.020	XLOC_12_012847	BROAD Institute lincRNA (XLOC_12_012847), lincRNA [TCONS_12_00024571]
A_23_P121564	0.466	0.007	0.033	GUCY1B3	guanylate cyclase 1, soluble, beta 3
A_21_P0009140	0.464	0.002	0.013	XLOC_012044	BROAD Institute lincRNA (XLOC_012044), lincRNA [TCONS_00025084]
A_21_P0010854	0.463	0.006	0.031	AKR1CL1	aldo-keto reductase family 1, member C-like 1
A_23_P102391	0.460	0.001	0.006	SLC40A1	solute carrier family 40 (iron-regulated transporter), member 1

A_32_P209230	0.459	0.002	0.016	CITED4	Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain, 4
A_24_P206047	0.458	0.001	0.007	SLC25A4	solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 4
A_23_P373521	0.457	0.008	0.038	HAND2	heart and neural crest derivatives expressed 2
A_23_P3312	0.457	0.000	0.003	ISLR	immunoglobulin superfamily containing leucine-rich repeat
A_33_P3216890	0.454	0.001	0.010	PAG1	phosphoprotein associated with glycosphingolipid microdomains 1
A_24_P935986	0.450	0.004	0.025	BCAT1	branched chain amino-acid transaminase 1, cytosolic
A_23_P412577	0.450	0.003	0.020	ANKRD29	ankyrin repeat domain 29
A_23_P168368	0.449	0.006	0.031	C7orf69	chromosome 7 open reading frame 69
A_32_P219279	0.447	0.005	0.028	ELFN2	extracellular leucine-rich repeat and fibronectin type III domain containing 2
A_23_P33791	0.446	0.001	0.008	SSBP2	single-stranded DNA binding protein 2
A_23_P500892	0.443	0.000	0.003	TUB	tubby homolog (mouse)
A_23_P142322	0.442	0.000	0.002	CIRBP	cold inducible RNA binding protein
A_24_P261734	0.441	0.003	0.019	SLC38A1	solute carrier family 38, member 1
A_23_P20494	0.441	0.004	0.024	NDRG1	N-myc downstream regulated 1
A_24_P374634	0.441	0.001	0.006	STAU2	staufen, RNA binding protein, homolog 2 (Drosophila)
A_33_P3277110	0.441	0.002	0.012	SLC5A3	solute carrier family 5 (sodium/myo-inositol cotransporter), member 3
A_23_P79978	0.438	0.010	0.044	SLC24A3	solute carrier family 24 (sodium/potassium/calcium exchanger), member 3
A_23_P132536	0.438	0.000	0.005	TRAK1	trafficking protein, kinesin binding 1
A_24_P62505	0.435	0.008	0.037	GLT25D2	glycosyltransferase 25 domain containing 2
A_33_P3384462	0.431	0.006	0.030	THSD4	thrombospondin, type I, domain containing 4
A_23_P54144	0.429	0.000	0.005	BMP4	bone morphogenetic protein 4
A_23_P12884	0.428	0.008	0.036	GRK5	G protein-coupled receptor kinase 5
A_23_P42096	0.428	0.001	0.007	MAP3K4	mitogen-activated protein kinase kinase kinase 4
A_19_P00319981	0.427	0.000	0.002	LOC100506119	uncharacterized LOC100506119
A_23_P165624	0.427	0.000	0.002	TNFAIP6	tumor necrosis factor, alpha-induced protein 6
A_33_P3321657	0.424	0.001	0.007	HSPG2	heparan sulfate proteoglycan 2
A_23_P109143	0.424	0.001	0.006	PRNP	prion protein
A_33_P3329301	0.424	0.001	0.006	LOC646014	uncharacterized LOC646014
A_23_P117582	0.423	0.010	0.044	JDP2	Jun dimerization protein 2
A_23_P72025	0.422	0.000	0.006	SLC25A20	solute carrier family 25 (carnitine/acylcarnitine translocase), member 20
A_33_P3267186	0.421	0.000	0.002	ATP2B1	ATPase, Ca ⁺⁺ transporting, plasma membrane 1
A_23_P155666	0.420	0.002	0.016	NAAA	N-acylethanolamine acid amidase
A_33_P3363271	0.416	0.006	0.032	CACNB2	calcium channel, voltage-dependent, beta 2 subunit
A_33_P3226605	0.415	0.001	0.010	PSIP1	PC4 and SFRS1 interacting protein 1
A_24_P7594	0.415	0.000	0.003	APOL6	apolipoprotein L, 6
A_33_P3354414	0.415	0.002	0.015	AOX1	aldehyde oxidase 1
A_33_P3250963	0.413	0.000	0.002	TP53TG1	TP53 target 1 (non-protein coding)
A_23_P340722	0.413	0.001	0.010	XPOT	exportin, tRNA (nuclear export receptor for tRNAs)
A_23_P378690	0.412	0.003	0.018	TMEM64	transmembrane protein 64
A_23_P85783	0.410	0.009	0.041	PHGDH	phosphoglycerate dehydrogenase
A_23_P409093	0.409	0.001	0.011	ANO4	anoctamin 4
A_23_P252855	0.409	0.001	0.007	BRX1	BRX1, biogenesis of ribosomes, homolog (S. cerevisiae)
A_23_P503200	0.408	0.004	0.024	PHF10	PHD finger protein 10
A_24_P419087	0.407	0.003	0.017	AVIL	advillin
A_23_P23221	0.407	0.000	0.004	GADD45A	growth arrest and DNA-damage-inducible, alpha

A_23_P147641	0.406	0.000	0.003	<i>TCEA2</i>	transcription elongation factor A (SII), 2
A_24_P389415	0.405	0.001	0.007	<i>PNMA2</i>	paraneoplastic antigen MA2
A_33_P3368471	0.404	0.003	0.019	<i>NTSDC1</i>	5'-nucleotidase domain containing 1
A_23_P60002	0.404	0.007	0.033	<i>TTC35</i>	tetratricopeptide repeat domain 35
A_23_P140748	0.403	0.002	0.015	<i>NDRG4</i>	NDRG family member 4
A_23_P39131	0.403	0.000	0.002	<i>GLTSCR2</i>	glioma tumor suppressor candidate region gene 2
A_32_P141768	0.403	0.001	0.011	<i>AGPAT4</i>	1-acylglycerol-3-phosphate O-acyltransferase 4 (lysophosphatidic acid acyltransferase, delta)
A_19_P00320665	0.402	0.002	0.016	<i>FLJ46906</i>	uncharacterized LOC441172
A_23_P391506	0.402	0.000	0.005	<i>IVNS1ABP</i>	influenza virus NS1A binding protein
A_33_P3231297	0.402	0.000	0.003	<i>CREG1</i>	cellular repressor of E1A-stimulated genes 1
A_23_P64879	0.399	0.000	0.005	<i>KCNJ8</i>	potassium inwardly-rectifying channel, subfamily J, member 8
A_23_P385105	0.398	0.003	0.018	<i>PLCD4</i>	phospholipase C, delta 4
A_23_P101208	0.396	0.002	0.013	<i>CYB5A</i>	cytochrome b5 type A (microsomal)
A_32_P204205	0.395	0.000	0.005	<i>SIX4</i>	SIX homeobox 4
A_21_P0009481	0.394	0.003	0.019	<i>RAB27B</i>	RAB27B, member RAS oncogene family
A_19_P00326732	0.393	0.000	0.002	<i>C6orf228</i>	chromosome 6 open reading frame 228
A_33_P3228762	0.392	0.001	0.008	<i>SLC25A36</i>	solute carrier family 25, member 36
A_23_P162171	0.392	0.005	0.026	<i>MCAM</i>	melanoma cell adhesion molecule
A_23_P128817	0.391	0.006	0.031	<i>PCK2</i>	phosphoenolpyruvate carboxykinase 2 (mitochondrial)
A_33_P3353051	0.391	0.000	0.006	<i>C6orf48</i>	chromosome 6 open reading frame 48
A_33_P3230166	0.391	0.001	0.008	<i>NALCN</i>	sodium leak channel, non-selective
A_33_P3269636	0.388	0.006	0.031	<i>SBSN</i>	suprabasin
A_33_P3382412	0.388	0.002	0.013	<i>ZNF468</i>	zinc finger protein 468
A_33_P3217689	0.386	0.003	0.018	<i>JMY</i>	junction mediating and regulatory protein, p53 cofactor
A_32_P147078	0.386	0.002	0.013	<i>SLC8A1</i>	solute carrier family 8 (sodium/calcium exchanger), member 1
A_23_P159255	0.385	0.000	0.003	<i>PTPRM</i>	protein tyrosine phosphatase, receptor type, M
A_23_P215566	0.384	0.004	0.023	<i>AHR</i>	aryl hydrocarbon receptor
A_33_P3265749	0.382	0.006	0.031	<i>PTGER3</i>	prostaglandin E receptor 3 (subtype EP3)
A_33_P3248982	0.381	0.010	0.044	<i>FAIM2</i>	Fas apoptotic inhibitory molecule 2
A_33_P3423425	0.381	0.000	0.003	<i>ZNF770</i>	zinc finger protein 770
A_23_P58538	0.380	0.003	0.018	<i>EPB41L4A-AS1</i>	EPB41L4A antisense RNA 1 (non-protein coding)
A_23_P77328	0.378	0.000	0.004	<i>GCHFR</i>	GTP cyclohydrolase I feedback regulator
A_33_P3379644	0.377	0.007	0.035	<i>ALDH1A1</i>	aldehyde dehydrogenase 1 family, member A1
A_32_P96036	0.377	0.002	0.017	<i>MEX3A</i>	mex-3 homolog A (C. elegans)
A_23_P69362	0.376	0.001	0.006	<i>CCDC51</i>	coiled-coil domain containing 51
A_23_P151133	0.373	0.001	0.011	<i>TSPAN9</i>	tetraspanin 9
A_33_P3380693	0.372	0.002	0.013	<i>ADAM15</i>	ADAM metallopeptidase domain 15
A_23_P162449	0.371	0.000	0.004	<i>SRGAP1</i>	SLIT-ROBO Rho GTPase activating protein 1
A_23_P104025	0.371	0.000	0.005	<i>TSEN15</i>	tRNA splicing endonuclease 15 homolog (S. cerevisiae)
A_23_P55107	0.369	0.003	0.018	<i>ULK2</i>	unc-51-like kinase 2 (C. elegans)
A_21_P0013028	0.369	0.011	0.046	<i>XLOC_12_012605</i>	BROAD Institute lincRNA (XLOC_12_012605), lincRNA [TCONS_12_00024286]
A_23_P100141	0.369	0.006	0.031	<i>UNKL</i>	unkempt homolog (Drosophila)-like
A_23_P58390	0.366	0.007	0.034	<i>C4orf32</i>	chromosome 4 open reading frame 32
A_23_P70359	0.366	0.001	0.011	<i>AGPAT4-IT1</i>	AGPAT4 intronic transcript 1 (non-protein coding)
A_23_P58506	0.364	0.001	0.010	<i>ELL2</i>	elongation factor, RNA polymerase II, 2

A_23_P38567	0.364	0.002	0.014	<i>SPECCI</i>	sperm antigen with calponin homology and coiled-coil domains 1
A_23_P63896	0.363	0.002	0.013	<i>FAS</i>	Fas (TNF receptor superfamily, member 6)
A_23_P431268	0.362	0.004	0.025	<i>PLEKHA6</i>	pleckstrin homology domain containing, family A member 6
A_23_P67042	0.362	0.004	0.025	<i>MOCOS</i>	molybdenum cofactor sulfurase
A_23_P250982	0.361	0.012	0.048	<i>ISOCI</i>	isochorismatase domain containing 1
A_23_P421011	0.360	0.001	0.011	<i>KAZALDI</i>	Kazal-type serine peptidase inhibitor domain 1
A_23_P104224	0.360	0.006	0.029	<i>AICF</i>	APOBEC1 complementation factor
A_32_P8813	0.360	0.001	0.009	<i>LOC283663</i>	uncharacterized LOC283663
A_33_P3231277	0.359	0.003	0.021	<i>HIF1A</i>	hypoxia inducible factor 1, alpha subunit (basic helix-loop-helix transcription factor)
A_23_P320113	0.357	0.002	0.017	<i>SRXN1</i>	sulfiredoxin 1
A_23_P10591	0.356	0.009	0.041	<i>METRNL</i>	meteorin, glial cell differentiation regulator-like
A_33_P3209351	0.355	0.002	0.012	<i>IARS</i>	isoleucyl-tRNA synthetase
A_33_P3220470	0.355	0.003	0.020	<i>SMAD6</i>	SMAD family member 6
A_24_P368575	0.354	0.001	0.010	<i>SLC4A7</i>	solute carrier family 4, sodium bicarbonate cotransporter, member 7
A_24_P397515	0.354	0.002	0.013	<i>HMGN4</i>	high mobility group nucleosomal binding domain 4
A_23_P130376	0.354	0.003	0.019	<i>PIEZO2</i>	piezo-type mechanosensitive ion channel component 2
A_23_P41789	0.354	0.010	0.045	<i>SLC27A6</i>	solute carrier family 27 (fatty acid transporter), member 6
A_33_P3270509	0.353	0.000	0.005	<i>SLAH1</i>	seven in absentia homolog 1 (Drosophila)
A_24_P376391	0.353	0.006	0.030	<i>PLXND1</i>	plexin D1
A_23_P1691	0.351	0.006	0.031	<i>MMP1</i>	matrix metalloproteinase 1 (interstitial collagenase)
A_24_P542375	0.350	0.005	0.027	<i>PTMA</i>	prothymosin, alpha
A_24_P295963	0.350	0.004	0.023	<i>SLC38A2</i>	solute carrier family 38, member 2
A_33_P3394727	0.349	0.002	0.013	<i>KHDRBS3</i>	KH domain containing, RNA binding, signal transduction associated 3
A_23_P214222	0.348	0.001	0.009	<i>MARCKS</i>	myristoylated alanine-rich protein kinase C substrate
A_23_P252711	0.348	0.002	0.015	<i>LACTB2</i>	lactamase, beta 2
A_23_P388900	0.348	0.001	0.009	<i>SLC22A15</i>	solute carrier family 22, member 15
A_23_P34093	0.348	0.010	0.043	<i>G6PD</i>	glucose-6-phosphate dehydrogenase
A_33_P3348782	0.346	0.006	0.032	<i>CYP2S1</i>	cytochrome P450, family 2, subfamily S, polypeptide 1
A_23_P217098	0.345	0.000	0.005	<i>VPS13A</i>	vacuolar protein sorting 13 homolog A (S. cerevisiae)
A_23_P254165	0.345	0.010	0.044	<i>RAI2</i>	retinoic acid induced 2
A_23_P36700	0.344	0.000	0.005	<i>TAPBPL</i>	TAP binding protein-like
A_23_P205531	0.344	0.004	0.024	<i>RNASE4</i>	ribonuclease, RNase A family, 4
A_23_P39602	0.344	0.000	0.004	<i>NCOA1</i>	nuclear receptor coactivator 1
A_33_P3318796	0.344	0.003	0.017	<i>FSTL3</i>	follistatin-like 3 (secreted glycoprotein)
A_23_P324523	0.343	0.001	0.011	<i>IQCK</i>	IQ motif containing K
A_24_P339869	0.343	0.005	0.027	<i>ZNF295</i>	zinc finger protein 295
A_24_P158421	0.341	0.004	0.023	<i>SAR1A</i>	SAR1 homolog A (S. cerevisiae)
A_23_P113972	0.340	0.009	0.039	<i>EXOC1</i>	exocyst complex component 1
A_23_P87560	0.339	0.004	0.022	<i>BTG1</i>	B-cell translocation gene 1, anti-proliferative
A_23_P118254	0.339	0.003	0.019	<i>FOXF1</i>	forkhead box F1
A_21_P0005963	0.338	0.008	0.039	<i>LOC100507420</i>	uncharacterized LOC100507420
A_33_P3245178	0.337	0.000	0.005	<i>BEX2</i>	brain expressed X-linked 2
A_24_P115199	0.335	0.006	0.031	<i>FO XK1</i>	forkhead box K1
A_33_P3222689	0.334	0.005	0.029	<i>H2BFM</i>	H2B histone family, member M
A_23_P342709	0.334	0.001	0.007	<i>FBXO15</i>	F-box protein 15

A_23_P380881	0.334	0.008	0.036	<i>ANKRD13B</i>	ankyrin repeat domain 13B
A_32_P20523	0.334	0.003	0.021	<i>TIGD2</i>	tigger transposable element derived 2
A_23_P126752	0.334	0.001	0.009	<i>CAPZB</i>	capping protein (actin filament) muscle Z-line, beta
A_23_P379649	0.333	0.001	0.012	<i>BMF</i>	Bcl2 modifying factor
A_33_P3244122	0.332	0.002	0.014	<i>HAAO</i>	3-hydroxyanthranilate 3,4-dioxygenase
A_23_P137665	0.332	0.007	0.034	<i>CHI3L1</i>	chitinase 3-like 1 (cartilage glycoprotein-39)
A_23_P93431	0.332	0.001	0.010	<i>AIG1</i>	androgen-induced 1
A_23_P36753	0.331	0.003	0.018	<i>ALDH2</i>	aldehyde dehydrogenase 2 family (mitochondrial)
A_33_P3363620	0.331	0.006	0.031	<i>TMEM91</i>	transmembrane protein 91
A_21_P0003719	0.330	0.001	0.008	<i>XLOC_003881</i>	BROAD Institute lincRNA (XLOC_003881), lincRNA [TCONS_00008434]
A_32_P37592	0.329	0.002	0.014	<i>SCARNA17</i>	small Cajal body-specific RNA 17
A_23_P56734	0.328	0.003	0.018	<i>HNMT</i>	histamine N-methyltransferase
A_33_P3243907	0.328	0.003	0.018	<i>CTSD</i>	cathepsin D
A_33_P3412087	0.327	0.002	0.016	<i>C6orf97</i>	chromosome 6 open reading frame 97
A_23_P368126	0.326	0.011	0.046	<i>AHCYL1</i>	adenosylhomocysteinase-like 1
A_23_P114883	0.326	0.004	0.021	<i>FMOD</i>	fibromodulin
A_19_P00317108	0.326	0.004	0.024	<i>LOC647979</i>	uncharacterized LOC647979
A_23_P132595	0.326	0.002	0.015	<i>VGLL4</i>	vestigial like 4 (Drosophila)
A_33_P3363260	0.325	0.004	0.023	<i>PGM2L1</i>	phosphoglucomutase 2-like 1
A_23_P55998	0.325	0.011	0.045	<i>SLC1A5</i>	solute carrier family 1 (neutral amino acid transporter), member 5
A_23_P96872	0.324	0.001	0.010	<i>HSPB11</i>	heat shock protein family B (small), member 11
A_23_P49338	0.323	0.003	0.019	<i>TNFRSF12A</i>	tumor necrosis factor receptor superfamily, member 12A
A_33_P3349651	0.321	0.001	0.009	<i>SWAP70</i>	SWAP switching B-cell complex 70kDa subunit
A_23_P422851	0.320	0.004	0.023	<i>CABLES1</i>	Cdk5 and Abl enzyme substrate 1
A_33_P3362900	0.320	0.002	0.012	<i>LOC375190</i>	UPF0638 protein B
A_21_P0007694	0.320	0.002	0.015	<i>LOC100506451</i>	uncharacterized LOC100506451
A_24_P106112	0.319	0.001	0.007	<i>PKD2</i>	polycystic kidney disease 2 (autosomal dominant)
A_32_P213661	0.318	0.002	0.016	<i>CCDC122</i>	coiled-coil domain containing 122
A_23_P322845	0.318	0.004	0.023	<i>PPAPDC1B</i>	phosphatidic acid phosphatase type 2 domain containing 1B
A_24_P319736	0.318	0.006	0.030	<i>MEIS1</i>	Meis homeobox 1
A_23_P215024	0.318	0.009	0.040	<i>LRRC1</i>	leucine rich repeat containing 1
A_23_P251499	0.318	0.007	0.033	<i>PCOLCE</i>	procollagen C-endopeptidase enhancer
A_33_P3336642	0.317	0.005	0.028	<i>THOC3</i>	THO complex 3
A_23_P215956	0.317	0.005	0.026	<i>MYC</i>	v-myc myelocytomatosis viral oncogene homolog (avian)
A_32_P45009	0.317	0.002	0.012	<i>IDH1</i>	isocitrate dehydrogenase 1 (NADP+), soluble
A_23_P137097	0.316	0.002	0.015	<i>SLC16A2</i>	solute carrier family 16, member 2 (monocarboxylic acid transporter 8)
A_24_P65060	0.316	0.003	0.020	<i>MEX3B</i>	mex-3 homolog B (C. elegans)
A_33_P3371718	0.315	0.002	0.015	<i>SAT1</i>	spermidine/spermine N1-acetyltransferase 1
A_23_P162127	0.315	0.001	0.011	<i>CCDC90B</i>	coiled-coil domain containing 90B
A_21_P0003863	0.314	0.007	0.032	<i>XLOC_003784</i>	DA915098 SKNSH2 Homo sapiens cDNA clone SKNSH2009915 5', mRNA sequence
A_23_P4808	0.314	0.005	0.028	<i>PTGER1</i>	prostaglandin E receptor 1 (subtype EP1), 42kDa
A_23_P401106	0.314	0.011	0.047	<i>PDE2A</i>	phosphodiesterase 2A, cGMP-stimulated
A_23_P43095	0.313	0.011	0.046	<i>ZFHX4</i>	zinc finger homeobox 4
A_23_P23141	0.313	0.001	0.011	<i>H3F3A</i>	H3 histone, family 3A
A_33_P3368785	0.313	0.004	0.024	<i>FLJ35776</i>	uncharacterized LOC649446

A_24_P46334	0.313	0.002	0.014	<i>SCOC</i>	short coiled-coil protein
A_33_P3599591	0.312	0.002	0.014	<i>PAPPA</i>	pregnancy-associated plasma protein A, pappalysin 1
A_33_P3347132	0.311	0.006	0.031	<i>EXOSC2</i>	exosome component 2
A_33_P3404316	0.311	0.010	0.042	<i>MIR100HG</i>	mir-100-let-7a-2 cluster host gene (non-protein coding)
A_23_P10442	0.309	0.001	0.009	<i>OSBPL1A</i>	oxysterol binding protein-like 1A
A_23_P168882	0.309	0.008	0.038	<i>TP53INP1</i>	tumor protein p53 inducible nuclear protein 1
A_23_P149975	0.309	0.002	0.013	<i>FAM107B</i>	family with sequence similarity 107, member B
A_23_P216549	0.308	0.002	0.012	<i>RUSC2</i>	RUN and SH3 domain containing 2
A_23_P134925	0.307	0.004	0.022	<i>BNIP3L</i>	BCL2/adenovirus E1B 19kDa interacting protein 3-like
A_33_P3368139	0.307	0.007	0.032	<i>MAP3K1</i>	mitogen-activated protein kinase kinase kinase 1
A_33_P3363560	0.305	0.012	0.050	<i>TMEM51</i>	transmembrane protein 51
A_21_P0012767	0.305	0.003	0.021	<i>XLOC_12_011027</i>	family with sequence similarity 86, member E, pseudogene
A_23_P257201	0.305	0.001	0.011	<i>RNF146</i>	ring finger protein 146
A_23_P123732	0.304	0.012	0.050	<i>C9orf103</i>	chromosome 9 open reading frame 103
A_23_P156180	0.304	0.003	0.019	<i>SLC22A4</i>	solute carrier family 22 (organic cation/ergothioneine transporter), member 4
A_33_P3404588	0.303	0.002	0.013	<i>FGD4</i>	FYVE, RhoGEF and PH domain containing 4
A_23_P21134	0.303	0.002	0.013	<i>DDIT3</i>	DNA-damage-inducible transcript 3
A_23_P133474	0.302	0.003	0.020	<i>GPX3</i>	glutathione peroxidase 3 (plasma)
A_24_P506977	0.301	0.003	0.019	<i>C7orf40</i>	chromosome 7 open reading frame 40
A_33_P3303414	0.300	0.006	0.032	<i>MAN1A1</i>	mannosidase, alpha, class 1A, member 1
A_33_P3330114	0.300	0.005	0.027	<i>LOC100130417</i>	uncharacterized LOC100130417
A_23_P151820	0.299	0.006	0.029	<i>RIN3</i>	Ras and Rab interactor 3
A_24_P106910	0.299	0.006	0.030	<i>PTCH1</i>	patched 1
A_24_P305570	0.298	0.002	0.015	<i>RIN2</i>	Ras and Rab interactor 2
A_23_P376188	0.297	0.006	0.030	<i>BEND7</i>	BEN domain containing 7
A_32_P160561	0.296	0.005	0.027	<i>DOK6</i>	docking protein 6
A_24_P11315	0.295	0.003	0.018	<i>OLFML3</i>	olfactomedin-like 3
A_33_P3338733	0.291	0.003	0.017	<i>MITF</i>	microphthalmia-associated transcription factor
A_33_P3315243	0.291	0.004	0.021	<i>C17orf72</i>	chromosome 17 open reading frame 72
A_23_P302207	0.290	0.002	0.015	<i>ZNF853</i>	zinc finger protein 853
A_33_P3270451	0.290	0.006	0.030	<i>TXNDC5</i>	thioredoxin domain containing 5 (endoplasmic reticulum)
A_33_P3257714	0.290	0.003	0.019	<i>RPS23</i>	ribosomal protein S23
A_23_P89799	0.289	0.007	0.032	<i>ACAA2</i>	acetyl-CoA acyltransferase 2
A_23_P209449	0.289	0.006	0.029	<i>FZD7</i>	frizzled family receptor 7
A_23_P217704	0.289	0.007	0.035	<i>GYG2</i>	glycogenin 2
A_24_P916614	0.289	0.004	0.022	<i>PTBP3</i>	polypyrimidine tract binding protein 3
A_23_P344531	0.288	0.006	0.031	<i>SYNPO</i>	synaptopodin
A_23_P9603	0.288	0.002	0.016	<i>PRKDC</i>	protein kinase, DNA-activated, catalytic polypeptide
A_23_P168909	0.287	0.007	0.032	<i>ZFPM2</i>	zinc finger protein, multitype 2
A_23_P102508	0.286	0.002	0.013	<i>SLC5A6</i>	solute carrier family 5 (sodium-dependent vitamin transporter), member 6
A_32_P123629	0.286	0.005	0.028	<i>TTC39C</i>	tetratricopeptide repeat domain 39C
A_23_P11160	0.286	0.003	0.020	<i>MAP7D3</i>	MAP7 domain containing 3
A_33_P3271635	0.285	0.007	0.032	<i>HLA-DPB1</i>	major histocompatibility complex, class II, DP beta 1
A_23_P374351	0.285	0.007	0.032	<i>KCTD20</i>	potassium channel tetramerisation domain containing 20
A_21_P0003595	0.285	0.004	0.023	<i>XLOC_003501</i>	BROAD Institute lincRNA (XLOC_003501), lincRNA [TCONS_00008036]

A_23_P301855	0.284	0.009	0.039	LSAMP	limbic system-associated membrane protein
A_23_P59616	0.284	0.009	0.041	GTF2IRD2	GTF2I repeat domain containing 2
A_23_P46017	0.283	0.004	0.021	CCBL2	cysteine conjugate-beta lyase 2
A_33_P3353791	0.283	0.003	0.018	ITGA1	integrin, alpha 1
A_23_P111672	0.282	0.006	0.030	TES	testis derived transcript (3 LIM domains)
A_23_P132378	0.282	0.006	0.029	CELSR1	cadherin, EGF LAG seven-pass G-type receptor 1 (flamingo homolog, Drosophila)
A_23_P55518	0.282	0.006	0.030	SMAD7	SMAD family member 7
A_23_P74778	0.282	0.004	0.024	C1orf54	chromosome 1 open reading frame 54
A_21_P0000044	0.281	0.010	0.042	STEAP1B	STEAP family member 1B
A_33_P3403867	0.281	0.004	0.025	PMEP1A1	prostate transmembrane protein, androgen induced 1
A_32_P153071	0.280	0.006	0.030	VIPR2	vasoactive intestinal peptide receptor 2
A_23_P122906	0.280	0.003	0.021	AUTS2	autism susceptibility candidate 2
A_32_P5480	0.279	0.002	0.014	CERS6	ceramide synthase 6
A_23_P157007	0.279	0.010	0.043	TMEM176B	transmembrane protein 176B
A_23_P92154	0.278	0.006	0.031	MBD4	methyl-CpG binding domain protein 4
A_23_P416142	0.277	0.006	0.030	DLG1	discs, large homolog 1 (Drosophila)
A_33_P3235262	0.277	0.006	0.030	PIP5KLI1	phosphatidylinositol-4-phosphate 5-kinase-like 1
A_23_P56703	0.277	0.009	0.040	C2orf89	chromosome 2 open reading frame 89
A_23_P28434	0.276	0.004	0.024	VAMP8	vesicle-associated membrane protein 8 (endobrevin)
A_23_P95823	0.276	0.007	0.033	NSMCE1	non-SMC element 1 homolog (S. cerevisiae)
A_23_P170733	0.275	0.009	0.040	ANTXR2	anthrax toxin receptor 2
A_23_P163380	0.273	0.002	0.016	MTHFS	5,10-methenyltetrahydrofolate synthetase (5-formyltetrahydrofolate cyclo-ligase)
A_23_P250629	0.273	0.003	0.017	PSMB8	proteasome (prosome, macropain) subunit, beta type, 8 (large multifunctional peptidase 7)
A_23_P155257	0.272	0.005	0.028	FOXP1	forkhead box P1
A_23_P112478	0.269	0.004	0.024	NUDT2	nudix (nucleoside diphosphate linked moiety X)-type motif 2
A_24_P361457	0.269	0.004	0.024	ENDO V	endonuclease V
A_23_P58251	0.269	0.005	0.026	CPZ	carboxypeptidase Z
A_23_P122007	0.268	0.007	0.032	C5orf30	chromosome 5 open reading frame 30
A_23_P125829	0.268	0.004	0.024	PGK1	phosphoglycerate kinase 1
A_23_P32029	0.267	0.003	0.017	SLC35D2	solute carrier family 35, member D2
A_23_P169197	0.266	0.007	0.034	HSDL2	hydroxysteroid dehydrogenase like 2
A_23_P81121	0.266	0.006	0.032	EXOSC9	exosome component 9
A_23_P150365	0.265	0.006	0.031	REXO2	REX2, RNA exonuclease 2 homolog (S. cerevisiae)
A_23_P54846	0.265	0.004	0.023	HERPUD1	homocysteine-inducible, endoplasmic reticulum stress-inducible, ubiquitin-like domain member 1
A_23_P71752	0.264	0.007	0.034	ZFAND5	zinc finger, AN1-type domain 5
A_33_P3361257	0.264	0.005	0.026	NOP16	NOP16 nucleolar protein homolog (yeast)
A_21_P0005511	0.263	0.006	0.032	XLOC_006513	BROAD Institute lincRNA (XLOC_006513), lincRNA [TCONS_00013877]
A_21_P0014047	0.263	0.004	0.024	C4A	complement component 4A (Rodgers blood group)
A_23_P12733	0.263	0.003	0.020	H2AFY2	H2A histone family, member Y2
A_23_P434890	0.263	0.010	0.042	CARD10	caspase recruitment domain family, member 10
A_33_P3351120	0.263	0.010	0.044	TXNRD1	thioredoxin reductase 1
A_24_P160969	0.262	0.004	0.024	TP53I11	tumor protein p53 inducible protein 11
A_24_P242299	0.262	0.008	0.036	ZRANB2	zinc finger, RAN-binding domain containing 2
A_33_P3381265	0.261	0.006	0.030	CYB5R2	cytochrome b5 reductase 2
A_23_P404091	0.261	0.003	0.021	GRPEL2	GrpE-like 2, mitochondrial (E. coli)

A_32_P31618	0.260	0.008	0.036	GSR	glutathione reductase
A_23_P34176	0.260	0.006	0.030	WWC3	WWC family member 3
A_23_P123086	0.260	0.006	0.031	KIAA1908	uncharacterized LOC114796
A_23_P103968	0.259	0.007	0.035	AKR7A3	aldo-keto reductase family 7, member A3 (aflatoxin aldehyde reductase)
A_33_P3290562	0.258	0.009	0.040	GLI3	GLI family zinc finger 3
A_23_P157726	0.258	0.009	0.040	DENND4C	DENN/MADD domain containing 4C
A_23_P116235	0.258	0.008	0.038	MDK	midkine (neurite growth-promoting factor 2)
A_23_P119857	0.257	0.009	0.039	TTC32	tetratricopeptide repeat domain 32
A_32_P34116	0.256	0.006	0.030	NUS1	nuclear undecaprenyl pyrophosphate synthase 1 homolog (S. cerevisiae)
A_23_P502797	0.256	0.007	0.035	WDFY1	WD repeat and FYVE domain containing 1
A_33_P3272563	0.255	0.011	0.045	NMT2	N-myristoyltransferase 2
A_33_P3261902	0.255	0.008	0.036	ENOSF1	enolase superfamily member 1
A_24_P137897	0.255	0.012	0.048	IFRD1	interferon-related developmental regulator 1
A_21_P0010162	0.254	0.010	0.044	XLOC_013929	Q9BSD2_HUMAN C21orf105 protein (Fragment), partial (23%) [THC2633305]
A_23_P25003	0.253	0.011	0.048	CLIP1	CAP-GLY domain containing linker protein 1
A_19_P00315551	0.252	0.007	0.034	LOC400043	uncharacterized LOC400043
A_24_P356916	0.250	0.003	0.021	SLC13A3	solute carrier family 13 (sodium-dependent dicarboxylate transporter), member 3
A_33_P3378514	0.249	0.006	0.030	PDE5A	phosphodiesterase 5A, cGMP-specific
A_21_P0008570	0.249	0.011	0.045	XLOC_011248	AGENCOURT_6822137 NIH_MGC_106 Homo sapiens cDNA clone IMAGE:5935069 5', mRNA sequence [BQ05337]
A_24_P236235	0.247	0.006	0.031	FLRT2	fibronectin leucine rich transmembrane protein 2
A_24_P108291	0.247	0.011	0.047	IMPACT	Impact homolog (mouse)
A_21_P0000300	0.247	0.009	0.041	SNORA48	small nucleolar RNA, H/ACA box 48
A_19_P00322754	0.246	0.003	0.020	SNHG5	small nucleolar RNA host gene 5 (non-protein coding)
A_23_P153026	0.246	0.003	0.019	GAA	glucosidase, alpha; acid
A_19_P00317793	0.245	0.007	0.032	LOC388796	uncharacterized LOC388796
A_23_P149259	0.245	0.004	0.023	TMEM79	transmembrane protein 79
A_24_P418203	0.244	0.011	0.047	CNTNAP3	contactin associated protein-like 3
A_23_P40718	0.244	0.007	0.032	PARVB	parvin, beta
A_21_P0001550	0.243	0.008	0.037	LOC100131564	uncharacterized LOC100131564
A_24_P926960	0.243	0.008	0.038	MEGF6	multiple EGF-like-domains 6
A_33_P3302957	0.242	0.009	0.039	PLEKHG4	pleckstrin homology domain containing, family G (with RhoGef domain) member 4
A_23_P169576	0.239	0.009	0.042	EXOC6	exocyst complex component 6
A_23_P7282	0.239	0.010	0.042	ELMOD2	ELMO/CED-12 domain containing 2
A_33_P3384287	0.237	0.007	0.034	PALM	paralemmin
A_23_P139123	0.237	0.012	0.049	SERPING1	serpin peptidase inhibitor, clade G (C1 inhibitor), member 1
A_23_P105392	0.236	0.004	0.023	CCT2	chaperonin containing TCP1, subunit 2 (beta)
A_21_P0013556	0.235	0.009	0.039	XLOC_12_014711	BROAD Institute lincRNA (XLOC_12_014711), lincRNA [TCONS_12_00028630]
A_23_P339098	0.235	0.007	0.035	SLC35F2	solute carrier family 35, member F2
A_24_P89843	0.234	0.006	0.031	CYHR1	cysteine/histidine-rich 1
A_23_P73809	0.234	0.012	0.050	LRCH2	leucine-rich repeats and calponin homology (CH) domain containing 2
A_23_P201342	0.233	0.010	0.044	DVLI	dishevelled, dsh homolog 1 (Drosophila)
A_33_P3409099	0.233	0.011	0.045	ATXN1	ataxin 1
A_23_P252082	0.231	0.011	0.046	TMEM176A	transmembrane protein 176A
A_23_P71513	0.230	0.010	0.045	EFR3A	EFR3 homolog A (S. cerevisiae)
A_33_P3219785	0.228	0.008	0.035	ANKRD57	ankyrin repeat domain 57

A_23_P319583	0.228	0.006	0.031	RIMS3	regulating synaptic membrane exocytosis 3
A_33_P3367447	0.227	0.008	0.038	ALDH3B1	aldehyde dehydrogenase 3 family, member B1
A_23_P347632	0.226	0.011	0.047	MTSS1	metastasis suppressor 1
A_32_P163125	0.226	0.010	0.044	SGMS1	sphingomyelin synthase 1
A_24_P137434	0.226	0.008	0.037	DCBLD2	discoidin, CUB and LCCL domain containing 2
A_24_P149124	0.223	0.012	0.050	C5orf13	chromosome 5 open reading frame 13
A_33_P3361811	0.220	0.006	0.031	NAA16	N(alpha)-acetyltransferase 16, NatA auxiliary subunit
A_23_P110362	0.219	0.011	0.047	LAMTOR3	late endosomal/lysosomal adaptor, MAPK and MTOR activator 3
A_24_P350649	0.219	0.006	0.029	PDPR	pyruvate dehydrogenase phosphatase regulatory subunit
A_23_P2492	0.219	0.012	0.050	C1S	complement component 1, s subcomponent
A_23_P48070	0.218	0.012	0.049	ING4	inhibitor of growth family, member 4
A_23_P41359	0.216	0.007	0.032	ZNF330	zinc finger protein 330
A_23_P110167	0.215	0.008	0.037	MGST2	microsomal glutathione S-transferase 2
A_23_P131954	0.213	0.009	0.040	SNX5	sorting nexin 5
A_23_P9056	0.211	0.009	0.040	RBICC1	RB1-inducible coiled-coil 1
A_23_P207811	0.210	0.011	0.045	PAIP1	poly(A) binding protein interacting protein 1
A_21_P0001767	0.208	0.007	0.035	FONG	uncharacterized LOC348751
A_23_P63897	0.206	0.008	0.036	CTBP2	C-terminal binding protein 2
A_23_P208198	0.204	0.010	0.045	ZNF577	zinc finger protein 577
A_33_P3239347	0.203	0.010	0.045	NKX3-1	NK3 homeobox 1
A_33_P3418209	0.200	0.012	0.049	ITGBL1	integrin, beta-like 1 (with EGF-like repeat domains)
A_23_P19619	0.198	0.012	0.049	HIVEP1	human immunodeficiency virus type I enhancer binding protein 1
A_23_P117782	0.195	0.012	0.050	LARP6	La ribonucleoprotein domain family, member 6
A_33_P3226167	-0.200	0.011	0.047	FAM129B	family with sequence similarity 129, member B
A_19_P00320927	-0.204	0.010	0.044	LOC100292680	uncharacterized LOC100292680
A_23_P48717	-0.204	0.011	0.046	NPC2	Niemann-Pick disease, type C2
A_33_P3216232	-0.213	0.009	0.041	ITGB1BP1	integrin beta 1 binding protein 1
A_32_P220715	-0.213	0.008	0.036	MAP1LC3B	microtubule-associated protein 1 light chain 3 beta
A_24_P417526	-0.214	0.008	0.038	FRG1B	FSHD region gene 1 family, member B
A_24_P403561	-0.216	0.011	0.046	LRP4	low density lipoprotein receptor-related protein 4
A_23_P132226	-0.217	0.011	0.046	TPST2	tyrosylprotein sulfotransferase 2
A_23_P406131	-0.219	0.011	0.047	TMEM159	transmembrane protein 159
A_23_P23669	-0.222	0.012	0.049	PALMD	palmdelphin
A_32_P193822	-0.226	0.006	0.030	ZC3H11A	zinc finger CCCH-type containing 11A
A_33_P3263232	-0.226	0.009	0.039	LRRC3	leucine rich repeat containing 3
A_24_P330303	-0.228	0.011	0.046	FRMD6	FERM domain containing 6
A_24_P388786	-0.228	0.006	0.031	DNAH5	dynein, axonemal, heavy chain 5
A_23_P88909	-0.229	0.009	0.041	SYNGR3	synaptogyrin 3
A_33_P3285260	-0.230	0.009	0.039	C21orf33	chromosome 21 open reading frame 33
A_33_P3412294	-0.230	0.012	0.049	ZSCAN2	zinc finger and SCAN domain containing 2
A_33_P3328666	-0.234	0.008	0.038	CLTB	clathrin, light chain B
A_23_P167997	-0.236	0.007	0.035	HIST1H2BG	histone cluster 1, H2bg
A_23_P78664	-0.236	0.005	0.028	DDX39A	DEAD (Asp-Glu-Ala-Asp) box polypeptide 39A
A_23_P166459	-0.237	0.011	0.046	LGALS1	lectin, galactoside-binding, soluble, 1
A_33_P3221568	-0.237	0.008	0.038	ARMC5	armadillo repeat containing 5

A_23_P22134	-0.237	0.009	0.041	<i>BNC1</i>	basonuclin 1
A_23_P394836	-0.239	0.003	0.019	<i>INF2</i>	inverted formin, FH2 and WH2 domain containing
A_24_P55148	-0.243	0.007	0.035	<i>HIST1H2BJ</i>	histone cluster 1, H2bj
A_23_P34233	-0.244	0.008	0.038	<i>QPRT</i>	quinolinate phosphoribosyltransferase
A_33_P3278220	-0.246	0.010	0.043	<i>RABEPK</i>	Rab9 effector protein with kelch motifs
A_32_P47754	-0.246	0.007	0.032	<i>SLC2A14</i>	solute carrier family 2 (facilitated glucose transporter), member 14
A_21_P0013756	-0.247	0.005	0.027	<i>XLOC_12_015476</i>	BROAD Institute lincRNA (XLOC_12_015476), lincRNA [TCONS_12_00030169]
A_33_P3559138	-0.247	0.011	0.046	<i>FLJ42200</i>	FLJ42200 protein
A_23_P431933	-0.248	0.007	0.033	<i>CAMKK1</i>	calcium/calmodulin-dependent protein kinase kinase 1, alpha
A_21_P0000417	-0.248	0.007	0.035	<i>SNORD114-20</i>	small nucleolar RNA, C/D box 114-20
A_33_P3237135	-0.249	0.004	0.024	<i>MMP2</i>	matrix metalloproteinase 2 (gelatinase A, 72kDa gelatinase, 72kDa type IV collagenase)
A_32_P171328	-0.250	0.005	0.026	<i>UBE2S</i>	ubiquitin-conjugating enzyme E2S
A_33_P3367392	-0.250	0.009	0.040	<i>FAM167B</i>	family with sequence similarity 167, member B
A_23_P129695	-0.250	0.009	0.041	<i>VASN</i>	vasorin
A_23_P111701	-0.250	0.011	0.048	<i>GNG11</i>	guanine nucleotide binding protein (G protein), gamma 11
A_33_P3399433	-0.253	0.009	0.041	<i>C20orf27</i>	chromosome 20 open reading frame 27
A_24_P16124	-0.254	0.006	0.031	<i>IFITM4P</i>	interferon induced transmembrane protein 4 pseudogene
A_24_P142743	-0.255	0.004	0.023	<i>CNN2</i>	calponin 2
A_33_P3367438	-0.257	0.011	0.045	<i>NRXN3</i>	neurexin 3
A_23_P106773	-0.257	0.008	0.036	<i>SULT1A2</i>	sulfotransferase family, cytosolic, 1A, phenol-preferring, member 2
A_23_P81048	-0.257	0.005	0.028	<i>STIM2</i>	stromal interaction molecule 2
A_33_P3249976	-0.257	0.008	0.036	<i>JAM2</i>	junctional adhesion molecule 2
A_21_P0005787	-0.257	0.006	0.031	<i>XLOC_006978</i>	DA263654 BRCAN2 Homo sapiens cDNA clone BRCAN2016427 5', mRNA sequence
A_23_P45475	-0.258	0.005	0.026	<i>GLA</i>	galactosidase, alpha
A_23_P166336	-0.258	0.004	0.021	<i>TMEM191A</i>	transmembrane protein 191A
A_24_P658584	-0.258	0.005	0.025	<i>SASH1</i>	SAM and SH3 domain containing 1
A_23_P255331	-0.259	0.011	0.047	<i>C4orf49</i>	chromosome 4 open reading frame 49
A_24_P23411	-0.259	0.006	0.031	<i>ARMCX3</i>	armadillo repeat containing, X-linked 3
A_19_P00811533	-0.259	0.004	0.025	<i>FLJ32224</i>	uncharacterized LOC440584
A_33_P3213772	-0.259	0.003	0.019	<i>SRGAP2</i>	SLIT-ROBO Rho GTPase activating protein 2
A_24_P206776	-0.260	0.009	0.040	<i>CRYAB</i>	crystallin, alpha B
A_33_P3325306	-0.260	0.011	0.045	<i>HSPE1</i>	heat shock 10kDa protein 1 (chaperonin 10)
A_24_P173754	-0.261	0.005	0.027	<i>C1orf21</i>	chromosome 1 open reading frame 21
A_21_P0007572	-0.261	0.008	0.037	<i>XLOC_009788</i>	BROAD Institute lincRNA (XLOC_009788), lincRNA [TCONS_00020456]
A_23_P88626	-0.262	0.010	0.042	<i>ANPEP</i>	alanyl (membrane) aminopeptidase
A_24_P82880	-0.262	0.010	0.045	<i>TPM4</i>	tropomyosin 4
A_23_P500333	-0.262	0.009	0.040	<i>SSBP3</i>	single stranded DNA binding protein 3
A_24_P385313	-0.262	0.003	0.019	<i>PTPRF</i>	protein tyrosine phosphatase, receptor type, F
A_33_P3415097	-0.263	0.011	0.047	<i>CLCN4</i>	chloride channel 4
A_23_P55251	-0.263	0.009	0.041	<i>ITGA3</i>	integrin, alpha 3 (antigen CD49C, alpha 3 subunit of VLA-3 receptor)
A_23_P45999	-0.264	0.005	0.027	<i>FBXO2</i>	F-box protein 2
A_23_P400449	-0.264	0.011	0.046	<i>VAT1L</i>	vesicle amine transport protein 1 homolog (T. californica)-like
A_24_P20630	-0.265	0.007	0.033	<i>LEF1</i>	lymphoid enhancer-binding factor 1
A_33_P3221064	-0.265	0.006	0.032	<i>LTBP4</i>	latent transforming growth factor beta binding protein 4
A_23_P418031	-0.265	0.007	0.035	<i>IFFO2</i>	intermediate filament family orphan 2

A_23_P78099	-0.267	0.003	0.019	<i>VTN</i>	vitronectin
A_33_P3240996	-0.267	0.007	0.033	<i>LOC100134240</i>	uncharacterized LOC100134240
A_24_P206344	-0.269	0.005	0.028	<i>ZNF746</i>	zinc finger protein 746
A_33_P3336720	-0.270	0.008	0.036	<i>HAMP</i>	hepcidin antimicrobial peptide
A_33_P3296862	-0.271	0.006	0.031	<i>C16orf89</i>	chromosome 16 open reading frame 89
A_23_P369899	-0.273	0.003	0.018	<i>TMEM158</i>	transmembrane protein 158 (gene/pseudogene)
A_23_P145238	-0.273	0.006	0.030	<i>HIST1H2BK</i>	histone cluster 1, H2bk
A_33_P3258061	-0.274	0.009	0.041	<i>PALM3</i>	paralemmin 3
A_24_P283341	-0.275	0.004	0.021	<i>MICAL1</i>	microtubule associated monooxygenase, calponin and LIM domain containing 1
A_23_P211504	-0.277	0.002	0.012	<i>KDEL3</i>	KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 3
A_23_P418015	-0.277	0.005	0.025	<i>MAPRE2</i>	microtubule-associated protein, RP/EB family, member 2
A_23_P104073	-0.277	0.009	0.041	<i>S100A3</i>	S100 calcium binding protein A3
A_21_P0013776	-0.278	0.005	0.027	<i>XLOC_12_015578</i>	Q8K2R3_MOUSE A1448196 protein (Fragment), partial (39%) [THC2649310]
A_33_P3407299	-0.279	0.011	0.045	<i>ANP32E</i>	acidic (leucine-rich) nuclear phosphoprotein 32 family, member E
A_23_P131846	-0.279	0.006	0.030	<i>SNAIL</i>	snail homolog 1 (Drosophila)
A_23_P150018	-0.279	0.008	0.038	<i>DUSP5</i>	dual specificity phosphatase 5
A_33_P3833256	-0.279	0.009	0.041	<i>LOC440028</i>	uncharacterized LOC440028
A_24_P406060	-0.280	0.002	0.014	<i>RNF144B</i>	ring finger protein 144B
A_32_P313405	-0.280	0.003	0.018	<i>LAMA1</i>	laminin, alpha 1
A_21_P0005486	-0.281	0.011	0.045	<i>XLOC_006390</i>	Q3KII3_PSEPF Inner-membrane translocator, partial (6%) [THC2773766]
A_33_P3227716	-0.281	0.011	0.047	<i>GATSL3</i>	GATS protein-like 3
A_24_P318656	-0.281	0.005	0.028	<i>ITGB3</i>	integrin, beta 3 (platelet glycoprotein IIIa, antigen CD61)
A_23_P136573	-0.283	0.002	0.016	<i>ST3GAL5</i>	ST3 beta-galactoside alpha-2,3-sialyltransferase 5
A_21_P0000588	-0.283	0.006	0.031	<i>LOC404266</i>	uncharacterized LOC404266
A_32_P169179	-0.283	0.006	0.030	<i>MSX2P1</i>	msh homeobox 2 pseudogene 1
A_33_P3413840	-0.283	0.008	0.036	<i>GK</i>	glycerol kinase
A_23_P7636	-0.283	0.009	0.042	<i>PTTG1</i>	pituitary tumor-transforming 1
A_23_P106389	-0.283	0.007	0.034	<i>SEMA7A</i>	semaphorin 7A, GPI membrane anchor (John Milton Hagen blood group)
A_33_P3262575	-0.284	0.007	0.035	<i>BAIAP2L1</i>	BAI1-associated protein 2-like 1
A_21_P0004895	-0.284	0.009	0.041	<i>XLOC_005338</i>	BX360095 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA clone CS0DI065YP01 5-PRIME
A_33_P3404052	-0.285	0.006	0.031	<i>TNFAIP8</i>	tumor necrosis factor, alpha-induced protein 8
A_23_P342727	-0.286	0.004	0.023	<i>STARD13</i>	StAR-related lipid transfer (START) domain containing 13
A_33_P3334515	-0.286	0.008	0.038	<i>NDRG2</i>	NDRG family member 2
A_23_P325726	-0.287	0.004	0.021	<i>ACOT11</i>	acyl-CoA thioesterase 11
A_33_P3405285	-0.287	0.004	0.024	<i>GSG1</i>	germ cell associated 1
A_33_P3355014	-0.288	0.011	0.045	<i>TMEM229B</i>	transmembrane protein 229B
A_21_P0011841	-0.288	0.001	0.010	<i>PAFAH1B1</i>	platelet-activating factor acetylhydrolase 1b, regulatory subunit 1 (45kDa)
A_33_P3341499	-0.289	0.012	0.049	<i>WNT5A</i>	wingless-type MMTV integration site family, member 5A
A_24_P142095	-0.289	0.003	0.020	<i>AKAP13</i>	A kinase (PRKA) anchor protein 13
A_21_P0012398	-0.289	0.011	0.045	<i>XLOC_12_009888</i>	BROAD Institute lincRNA (XLOC_12_009888), lincRNA [TCONS_12_00018862]
A_21_P0000424	-0.289	0.002	0.013	<i>SNORD114-28</i>	small nucleolar RNA, C/D box 114-28
A_33_P3401243	-0.290	0.001	0.010	<i>OLFML2B</i>	olfactomedin-like 2B
A_33_P3375145	-0.290	0.004	0.022	<i>C9orf150</i>	chromosome 9 open reading frame 150
A_24_P214598	-0.291	0.005	0.025	<i>PPM1K</i>	protein phosphatase, Mg ²⁺ /Mn ²⁺ dependent, 1K
A_23_P82379	-0.291	0.005	0.028	<i>CACNA2D1</i>	calcium channel, voltage-dependent, alpha 2/delta subunit 1

A_23_P202837	-0.291	0.011	0.045	<i>CCND1</i>	cyclin D1
A_23_P379475	-0.292	0.005	0.029	<i>DHCR24</i>	24-dehydrocholesterol reductase
A_21_P0007176	-0.292	0.008	0.038	<i>XLOC_009067</i>	BROAD Institute lincRNA (XLOC_009067), lincRNA [TCONS_00019237]
A_24_P248185	-0.292	0.012	0.049	<i>C12orf53</i>	chromosome 12 open reading frame 53
A_33_P3301381	-0.292	0.002	0.016	<i>RBM43</i>	RNA binding motif protein 43
A_23_P411113	-0.293	0.002	0.016	<i>CNTNAP1</i>	contactin associated protein 1
A_33_P3393766	-0.293	0.006	0.032	<i>C17orf96</i>	chromosome 17 open reading frame 96
A_23_P397293	-0.293	0.009	0.041	<i>LY6K</i>	lymphocyte antigen 6 complex, locus K
A_23_P160226	-0.294	0.007	0.034	<i>HEATR8</i>	HEAT repeat containing 8
A_32_P186474	-0.294	0.004	0.025	<i>RACGAP1</i>	Rac GTPase activating protein 1
A_24_P416131	-0.294	0.012	0.049	<i>COTL1</i>	coactosin-like 1 (Dictyostelium)
A_33_P3335624	-0.294	0.005	0.028	<i>PSMD10</i>	proteasome (prosome, macropain) 26S subunit, non-ATPase, 10
A_21_P0005856	-0.294	0.008	0.037	<i>XLOC_007118</i>	BROAD Institute lincRNA (XLOC_007118), lincRNA [TCONS_00015037]
A_24_P273143	-0.297	0.012	0.049	<i>LINC00152</i>	long intergenic non-protein coding RNA 152
A_21_P0004054	-0.297	0.003	0.019	<i>XLOC_004528</i>	BROAD Institute lincRNA (XLOC_004528), lincRNA [TCONS_00009497]
A_33_P3244828	-0.297	0.004	0.024	<i>PPP2R5C</i>	protein phosphatase 2, regulatory subunit B', gamma
A_23_P119143	-0.297	0.003	0.019	<i>ICAM5</i>	intercellular adhesion molecule 5, telencephalin
A_21_P0009319	-0.297	0.010	0.044	<i>XLOC_012457</i>	ALU1_HUMAN (P39188) Alu subfamily J sequence contamination warning entry, partial (14%) [THC2665248]
A_33_P3259801	-0.299	0.001	0.009	<i>TMEM189</i>	transmembrane protein 189
A_23_P63736	-0.300	0.005	0.028	<i>LOC84856</i>	uncharacterized LOC84856
A_23_P67725	-0.301	0.002	0.013	<i>LMNB2</i>	lamin B2
A_21_P0011281	-0.301	0.001	0.010	<i>XLOC_12_004306</i>	uncharacterized LOC100507257
A_24_P261417	-0.301	0.003	0.018	<i>DKK3</i>	dickkopf 3 homolog (Xenopus laevis)
A_23_P50535	-0.302	0.003	0.021	<i>DMPK</i>	dystrophia myotonica-protein kinase
A_24_P522631	-0.302	0.008	0.037	<i>TMEM201</i>	transmembrane protein 201
A_21_P0002334	-0.302	0.004	0.024	<i>XLOC_001788</i>	BROAD Institute lincRNA (XLOC_001788), lincRNA [TCONS_00003974]
A_23_P16722	-0.303	0.005	0.026	<i>DOCK10</i>	dedicator of cytokinesis 10
A_23_P205370	-0.304	0.003	0.020	<i>ASB2</i>	ankyrin repeat and SOCS box containing 2
A_24_P282309	-0.304	0.007	0.034	<i>MYOF</i>	myoferlin
A_23_P33196	-0.304	0.001	0.009	<i>COL5A2</i>	collagen, type V, alpha 2
A_24_P4705	-0.304	0.006	0.031	<i>PPME1</i>	protein phosphatase methyltransferase 1
A_32_P135336	-0.305	0.002	0.013	<i>LOC388242</i>	coiled-coil domain containing 101 pseudogene
A_21_P0014664	-0.305	0.002	0.014	<i>LOC100505874</i>	uncharacterized LOC100505874
A_33_P3405022	-0.306	0.005	0.028	<i>LETM1</i>	leucine zipper-EF-hand containing transmembrane protein 1
A_23_P8961	-0.306	0.002	0.014	<i>IL7</i>	interleukin 7
A_33_P3290687	-0.308	0.003	0.021	<i>DNAJC1</i>	DnaJ (Hsp40) homolog, subfamily C, member 1
A_33_P3255914	-0.308	0.005	0.028	<i>MYLIP</i>	myosin regulatory light chain interacting protein
A_33_P3231572	-0.308	0.002	0.016	<i>LOC100130456</i>	uncharacterized LOC100130456
A_23_P3532	-0.309	0.001	0.010	<i>LITAF</i>	lipopolysaccharide-induced TNF factor
A_23_P383986	-0.309	0.005	0.028	<i>CHST15</i>	carbohydrate (N-acetylgalactosamine 4-sulfate 6-O) sulfotransferase 15
A_23_P85140	-0.309	0.009	0.041	<i>TCEAL2</i>	transcription elongation factor A (SII)-like 2
A_33_P3254666	-0.309	0.002	0.013	<i>LZTS2</i>	leucine zipper, putative tumor suppressor 2
A_24_P402080	-0.310	0.006	0.030	<i>MBP</i>	myelin basic protein
A_33_P3388501	-0.310	0.002	0.012	<i>CHIT1</i>	chitinase 1 (chitotriosidase)
A_33_P3214209	-0.310	0.003	0.020	<i>GUSBP1</i>	glucuronidase, beta pseudogene 1

A_33_P3255304	-0.311	0.008	0.038	GGT5	gamma-glutamyltransferase 5
A_23_P202520	-0.311	0.012	0.050	ABLIM1	actin binding LIM protein 1
A_23_P120594	-0.311	0.006	0.031	ACSS1	acyl-CoA synthetase short-chain family member 1
A_33_P3398634	-0.311	0.001	0.006	TFEB	transcription factor EB
A_23_P217114	-0.311	0.011	0.046	ALAD	aminolevulinatase dehydratase
A_33_P3527721	-0.311	0.001	0.007	LOC284219	uncharacterized LOC284219
A_33_P3374758	-0.312	0.005	0.027	DYNC1LI2	dynein, cytoplasmic 1, light intermediate chain 2
A_23_P329870	-0.313	0.002	0.015	RHBDF2	rhomboid 5 homolog 2 (Drosophila)
A_33_P3383326	-0.313	0.006	0.030	LPAR1	lysophosphatidic acid receptor 1
A_33_P3357678	-0.313	0.002	0.014	LCTL	lactase-like
A_21_P0014502	-0.313	0.007	0.035	LOC100287803	uncharacterized LOC100287803
A_24_P284353	-0.313	0.006	0.030	TMEM107	transmembrane protein 107
A_23_P21976	-0.314	0.002	0.014	CSPG4	chondroitin sulfate proteoglycan 4
A_23_P206022	-0.314	0.002	0.014	ITGA11	integrin, alpha 11
A_23_P14302	-0.314	0.001	0.009	LINC00341	long intergenic non-protein coding RNA 341
A_33_P3311267	-0.314	0.003	0.018	KRTAP19-2	keratin associated protein 19-2
A_33_P3409675	-0.315	0.009	0.042	LOC442132	golgin A6 family-like 1 pseudogene
A_23_P79069	-0.316	0.011	0.046	RASAL3	RAS protein activator like 3
A_21_P0014711	-0.316	0.005	0.025	LOC100507948	uncharacterized LOC100507948
A_23_P213336	-0.316	0.002	0.017	FGF1	fibroblast growth factor 1 (acidic)
A_23_P366394	-0.318	0.002	0.016	ZAK	sterile alpha motif and leucine zipper containing kinase AZK
A_24_P207139	-0.318	0.004	0.022	PML	promyelocytic leukemia
A_23_P88522	-0.319	0.006	0.030	NMB	neuromedin B
A_32_P79434	-0.321	0.008	0.038	PTPRN2	protein tyrosine phosphatase, receptor type, N polypeptide 2
A_21_P0011458	-0.322	0.003	0.018	XLOC_12_005415	BROAD Institute lincRNA (XLOC_12_005415), lincRNA [TCONS_12_00010039]
A_24_P208998	-0.323	0.003	0.019	TRIM23	tripartite motif containing 23
A_33_P3375613	-0.323	0.002	0.013	C8orf44-SGK3	C8orf44-SGK3 readthrough
A_23_P80473	-0.325	0.001	0.011	CHST13	carbohydrate (chondroitin 4) sulfotransferase 13
A_33_P3302428	-0.326	0.010	0.043	TNRC6C	trinucleotide repeat containing 6C
A_23_P1331	-0.326	0.009	0.039	COL13A1	collagen, type XIII, alpha 1
A_32_P150891	-0.326	0.005	0.027	DIAPH3	diaphanous homolog 3 (Drosophila)
A_23_P153676	-0.327	0.004	0.023	TLE2	transducin-like enhancer of split 2 (E(sp1) homolog, Drosophila)
A_23_P61371	-0.327	0.001	0.008	TMEM173	transmembrane protein 173
A_23_P54918	-0.327	0.005	0.026	LDHD	lactate dehydrogenase D
A_33_P3242075	-0.328	0.003	0.020	LOC100132339	uncharacterized LOC100132339
A_33_P3222380	-0.328	0.004	0.024	AHNAK2	AHNAK nucleoprotein 2
A_33_P3223495	-0.329	0.009	0.040	FRY	furry homolog (Drosophila)
A_23_P79803	-0.329	0.001	0.006	VSTM2L	V-set and transmembrane domain containing 2 like
A_23_P118392	-0.329	0.008	0.036	RASD1	RAS, dexamethasone-induced 1
A_23_P22350	-0.331	0.001	0.010	GRAMD3	GRAM domain containing 3
A_33_P3871347	-0.331	0.004	0.025	SNED1	sushi, nidogen and EGF-like domains 1
A_19_P00317653	-0.331	0.007	0.032	Q9N083	Q9N083_MACFA Unnamed portein product, partial (29%) [THC2524584]
A_24_P125335	-0.332	0.002	0.012	CCL13	chemokine (C-C motif) ligand 13
A_33_P3311717	-0.332	0.010	0.044	TGIF1	TGFB-induced factor homeobox 1
A_24_P140204	-0.332	0.001	0.011	PXK	PX domain containing serine/threonine kinase

A_33_P3338693	-0.333	0.005	0.026	<i>SNAP25</i>	synaptosomal-associated protein, 25kDa
A_24_P417007	-0.334	0.000	0.004	<i>POLR2F</i>	polymerase (RNA) II (DNA directed) polypeptide F
A_21_P0009855	-0.334	0.011	0.046	<i>XLOC_013567</i>	BX094767 Soares_testis_NHT Homo sapiens cDNA clone IMAGp998G084495, mRNA sequence
A_33_P3280385	-0.334	0.001	0.010	<i>COL6A3</i>	collagen, type VI, alpha 3
A_32_P208120	-0.335	0.003	0.018	<i>CAMK1D</i>	calcium/calmodulin-dependent protein kinase ID
A_33_P3346483	-0.336	0.002	0.016	<i>SYNPO2L</i>	synaptopodin 2-like
A_33_P3449097	-0.336	0.003	0.017	<i>TSPAN10</i>	tetraspanin 10
A_33_P3302312	-0.336	0.004	0.021	<i>IER5L</i>	immediate early response 5-like
A_33_P3325349	-0.336	0.011	0.045	<i>TSPAN5</i>	tetraspanin 5
A_21_P0012150	-0.336	0.003	0.019	<i>LOC149773</i>	uncharacterized LOC149773
A_23_P319859	-0.337	0.005	0.028	<i>EYA2</i>	eyes absent homolog 2 (Drosophila)
A_24_P9321	-0.337	0.001	0.010	<i>HIST1H3I</i>	histone cluster 1, H3i
A_21_P0009382	-0.337	0.009	0.042	<i>XLOC_012142</i>	BROAD Institute lincRNA (XLOC_012142), lincRNA [TCONS_00025864]
A_33_P3380837	-0.338	0.003	0.020	<i>AMZ1</i>	archaelysin family metallopeptidase 1
A_19_P00329806	-0.338	0.006	0.030	<i>HOTAIR</i>	HOX transcript antisense RNA
A_21_P0006970	-0.338	0.001	0.007	<i>SFTA1P</i>	surfactant associated 1, pseudogene
A_33_P3267482	-0.338	0.005	0.029	<i>KIAA1804</i>	mixed lineage kinase 4
A_33_P3344127	-0.338	0.002	0.014	<i>HIST1H2AC</i>	histone cluster 1, H2ac
A_33_P3394213	-0.338	0.002	0.012	<i>GRIN3B</i>	glutamate receptor, ionotropic, N-methyl-D-aspartate 3B
A_23_P310022	-0.339	0.003	0.017	<i>KIAA1217</i>	KIAA1217
A_24_P217834	-0.339	0.003	0.019	<i>HIST1H3D</i>	histone cluster 1, H3d
A_21_P0007799	-0.339	0.004	0.023	<i>XLOC_010257</i>	BROAD Institute lincRNA (XLOC_010257), lincRNA [TCONS_00020993]
A_33_P3343175	-0.339	0.006	0.031	<i>CXCL10</i>	chemokine (C-X-C motif) ligand 10
A_23_P74114	-0.340	0.001	0.011	<i>ZNF713</i>	zinc finger protein 713
A_23_P372923	-0.340	0.006	0.030	<i>FGFR1</i>	fibroblast growth factor receptor 1
A_24_P321525	-0.340	0.005	0.025	<i>RERG</i>	RAS-like, estrogen-regulated, growth inhibitor
A_23_P134935	-0.340	0.001	0.009	<i>DUSP4</i>	dual specificity phosphatase 4
A_24_P922631	-0.340	0.009	0.039	<i>C5orf58</i>	chromosome 5 open reading frame 58
A_33_P3325634	-0.341	0.003	0.019	<i>C19orf69</i>	chromosome 19 open reading frame 69
A_23_P416314	-0.341	0.010	0.043	<i>HRASLS5</i>	HRAS-like suppressor family, member 5
A_21_P0008544	-0.342	0.002	0.015	<i>XLOC_011081</i>	Q6F9Y7_ACIAD 30S ribosomal protein S1, partial (3%) [THC2622816]
A_33_P3537875	-0.343	0.005	0.028	<i>MGC10814</i>	uncharacterized protein MGC10814
A_33_P3325110	-0.343	0.001	0.007	<i>SOX13</i>	SRY (sex determining region Y)-box 13
A_33_P3378284	-0.343	0.003	0.018	<i>COX6B2</i>	cytochrome c oxidase subunit VIb polypeptide 2 (testis)
A_33_P3422654	-0.344	0.009	0.040	<i>LOC100133985</i>	uncharacterized LOC100133985
A_21_P0005360	-0.344	0.010	0.044	<i>XLOC_006009</i>	de0_012341 SARS-Cov infected lung tissue Homo sapiens cDNA clone de0_012341 5', mRNA sequence [GD263047]
A_21_P0005323	-0.344	0.001	0.007	<i>XLOC_006559</i>	RST29330 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence [BG209803]
A_21_P0002768	-0.344	0.001	0.006	<i>XLOC_002802</i>	603075994F1 NIH_MGC_119 Homo sapiens cDNA clone IMAGE:5168014 5', mRNA sequence [BI826287]
A_24_P239177	-0.346	0.000	0.005	<i>MUC4</i>	mucin 4, cell surface associated
A_21_P0013222	-0.346	0.007	0.035	<i>XLOC_12_013457</i>	BROAD Institute lincRNA (XLOC_12_013457), lincRNA [TCONS_12_00025956]
A_23_P61406	-0.346	0.000	0.005	<i>SHC3</i>	SHC (Src homology 2 domain containing) transforming protein 3
A_23_P136978	-0.346	0.001	0.009	<i>SRPX2</i>	sushi-repeat containing protein, X-linked 2
A_21_P0000135	-0.348	0.001	0.008	<i>ANKHD1</i>	ankyrin repeat and KH domain containing 1
A_21_P0007309	-0.349	0.001	0.008	<i>XLOC_009345</i>	BROAD Institute lincRNA (XLOC_009345), lincRNA [TCONS_00019550]
A_33_P3408844	-0.350	0.001	0.007	<i>LOC100133091</i>	uncharacterized LOC100133091

A_19_P00805840	-0.350	0.001	0.011	<i>ZNF37BP</i>	zinc finger protein 37B, pseudogene
A_23_P53137	-0.350	0.009	0.041	<i>HBG1</i>	hemoglobin, gamma A
A_33_P3363515	-0.350	0.001	0.010	<i>XRCC3</i>	X-ray repair complementing defective repair in Chinese hamster cells 3
A_23_P330070	-0.351	0.000	0.005	<i>TFPI</i>	tissue factor pathway inhibitor (lipoprotein-associated coagulation inhibitor)
A_33_P3320393	-0.351	0.002	0.013	<i>MRPS16</i>	mitochondrial ribosomal protein S16
A_24_P363896	-0.351	0.002	0.014	<i>COL27A1</i>	collagen, type XXVII, alpha 1
A_23_P45324	-0.351	0.003	0.020	<i>TMEM35</i>	transmembrane protein 35
A_23_P69179	-0.352	0.002	0.014	<i>LEPREL1</i>	leprecan-like 1
A_21_P0001790	-0.352	0.003	0.019	<i>XLOC_002129</i>	BROAD Institute lincRNA (XLOC_002129), lincRNA [TCONS_00002754]
A_33_P3274164	-0.354	0.002	0.013	<i>DOTIL</i>	DOT1-like, histone H3 methyltransferase (<i>S. cerevisiae</i>)
A_23_P401606	-0.354	0.002	0.014	<i>EDIL3</i>	EGF-like repeats and discoidin I-like domains 3
A_21_P0012357	-0.354	0.001	0.011	<i>XLOC_12_009510</i>	BROAD Institute lincRNA (XLOC_12_009510), lincRNA [TCONS_12_00018380]
A_24_P820037	-0.355	0.011	0.047	<i>SLC6A17</i>	solute carrier family 6, member 17
A_32_P168464	-0.355	0.001	0.009	<i>CASK</i>	calcium/calmodulin-dependent serine protein kinase (MAGUK family)
A_23_P356330	-0.356	0.001	0.010	<i>PPPDE2</i>	PPPDE peptidase domain containing 2
A_19_P00315581	-0.357	0.006	0.030	<i>FLJ30838</i>	uncharacterized LOC400955
A_23_P92730	-0.357	0.008	0.039	<i>HSPB3</i>	heat shock 27kDa protein 3
A_24_P71938	-0.358	0.005	0.025	<i>SMAD1</i>	SMAD family member 1
A_33_P3219720	-0.359	0.002	0.012	<i>ZNF248</i>	zinc finger protein 248
A_23_P389102	-0.359	0.001	0.009	<i>MYO1D</i>	myosin ID
A_23_P309381	-0.359	0.004	0.024	<i>HIST2H2AA4</i>	histone cluster 2, H2aa4
A_21_P0011831	-0.360	0.010	0.044	<i>XLOC_12_007456</i>	BROAD Institute lincRNA (XLOC_12_007456), lincRNA [TCONS_12_00013854]
A_33_P3282181	-0.360	0.005	0.027	<i>ARHGAP4</i>	Rho GTPase activating protein 4
A_21_P0003135	-0.360	0.008	0.036	<i>XLOC_003175</i>	BROAD Institute lincRNA (XLOC_003175), lincRNA [TCONS_00006552]
A_23_P108673	-0.361	0.001	0.007	<i>FAM176A</i>	family with sequence similarity 176, member A
A_33_P3594214	-0.362	0.005	0.027	<i>OR7E12P</i>	olfactory receptor, family 7, subfamily E, member 12 pseudogene
A_33_P3252146	-0.362	0.002	0.012	<i>HMX3</i>	H6 family homeobox 3
A_23_P85209	-0.362	0.003	0.020	<i>IL13RA2</i>	interleukin 13 receptor, alpha 2
A_21_P0000630	-0.363	0.010	0.043	<i>LOC643733</i>	caspase 4, apoptosis-related cysteine peptidase pseudogene
A_33_P3421984	-0.363	0.002	0.016	<i>HYAL4</i>	hyaluronoglucosaminidase 4
A_23_P55749	-0.363	0.005	0.027	<i>COL5A3</i>	collagen, type V, alpha 3
A_21_P0005689	-0.363	0.006	0.029	<i>XLOC_006775</i>	BROAD Institute lincRNA (XLOC_006775), lincRNA [TCONS_00014676]
A_23_P144531	-0.363	0.003	0.018	<i>ALPK1</i>	alpha-kinase 1
A_32_P162187	-0.364	0.002	0.016	<i>C2</i>	complement component 2
A_23_P46222	-0.365	0.001	0.009	<i>TRIM46</i>	tripartite motif containing 46
A_33_P3354464	-0.365	0.003	0.017	<i>LOXL1</i>	lysyl oxidase-like 1
A_33_P3222139	-0.365	0.000	0.004	<i>SREBF1</i>	sterol regulatory element binding transcription factor 1
A_33_P3299110	-0.366	0.004	0.023	<i>ARHGAP42</i>	Rho GTPase activating protein 42
A_33_P3351934	-0.366	0.000	0.005	<i>MSTO2P</i>	misato homolog 2 pseudogene
A_33_P3313055	-0.367	0.001	0.007	<i>NOTCH3</i>	notch 3
A_21_P0000507	-0.368	0.006	0.029	<i>SNAR-B2</i>	small ILF3/NF90-associated RNA B2
A_33_P3405424	-0.368	0.010	0.044	<i>IL4II</i>	interleukin 4 induced 1
A_23_P361049	-0.369	0.001	0.006	<i>MYO1B</i>	myosin IB
A_23_P251232	-0.370	0.001	0.010	<i>TTY14</i>	testis-specific transcript, Y-linked 14 (non-protein coding)
A_33_P3346193	-0.371	0.010	0.042	<i>TPM3</i>	tropomyosin 3

A_33_P3392000	-0.371	0.002	0.015	LOC100506190	uncharacterized LOC100506190
A_33_P3629131	-0.371	0.002	0.012	CDRT3	CMT1A duplicated region transcript 3
A_33_P3382493	-0.372	0.004	0.022	SIGLEC14	sialic acid binding Ig-like lectin 14
A_23_P154875	-0.372	0.002	0.013	BACE2	beta-site APP-cleaving enzyme 2
A_33_P3224878	-0.374	0.004	0.022	ITGA4	integrin, alpha 4 (antigen CD49D, alpha 4 subunit of VLA-4 receptor)
A_23_P30799	-0.375	0.005	0.029	HIST1H3F	histone cluster 1, H3f
A_24_P342632	-0.375	0.000	0.005	AK5	adenylate kinase 5
A_23_P201376	-0.375	0.001	0.008	SSX2IP	synovial sarcoma, X breakpoint 2 interacting protein
A_33_P3290955	-0.375	0.001	0.006	KIAA1875	KIAA1875
A_21_P0014099	-0.376	0.002	0.014	LOC100507554	uncharacterized LOC100507554
A_23_P69738	-0.376	0.001	0.009	RASL11B	RAS-like, family 11, member B
A_21_P0002446	-0.377	0.002	0.013	XLOC_002111	BROAD Institute lincRNA (XLOC_002111), lincRNA [TCONS_00004269]
A_21_P0005228	-0.378	0.002	0.015	XLOC_006069	601652062F1 NIH_MGC_82 Homo sapiens cDNA clone IMAGE:3935391 5', mRNA sequence [BE972828]
A_32_P116556	-0.379	0.001	0.006	ZNF469	zinc finger protein 469
A_23_P136196	-0.379	0.000	0.004	TBC1D19	TBC1 domain family, member 19
A_23_P138125	-0.379	0.004	0.022	FAIM3	Fas apoptotic inhibitory molecule 3
A_21_P0010376	-0.379	0.005	0.028	XLOC_014338	BROAD Institute lincRNA (XLOC_014338), lincRNA [TCONS_00029466]
A_33_P3396459	-0.379	0.002	0.016	POLR2H	polymerase (RNA) II (DNA directed) polypeptide H
A_23_P31064	-0.380	0.002	0.013	MOXD1	monooxygenase, DBH-like 1
A_33_P3424861	-0.380	0.002	0.013	FAM118A	family with sequence similarity 118, member A
A_33_P3287113	-0.381	0.002	0.015	KIAA1530	KIAA1530
A_23_P121533	-0.381	0.008	0.038	SPON2	spondin 2, extracellular matrix protein
A_21_P0006903	-0.382	0.002	0.017	XLOC_008586	BROAD Institute lincRNA (XLOC_008586), lincRNA [TCONS_00018312]
A_33_P3357651	-0.383	0.001	0.006	KRTAP10-12	keratin associated protein 10-12
A_33_P3262580	-0.383	0.000	0.003	ENTPDI	ectonucleoside triphosphate diphosphohydrolase 1
A_33_P3283061	-0.383	0.001	0.009	LOC100128348	uncharacterized LOC100128348
A_33_P3254946	-0.383	0.000	0.003	PLEKHH3	pleckstrin homology domain containing, family H (with MyTH4 domain) member 3
A_23_P352535	-0.383	0.001	0.009	PPP1R16B	protein phosphatase 1, regulatory subunit 16B
A_33_P3247534	-0.383	0.001	0.010	LOC389834	ankyrin repeat domain 57 pseudogene
A_21_P0014940	-0.384	0.001	0.011	LOC100653236	uncharacterized LOC100653236
A_33_P3248900	-0.384	0.000	0.003	FLJ45445	uncharacterized LOC399844
A_23_P76622	-0.384	0.006	0.030	DCT	dopachrome tautomerase (dopachrome delta-isomerase, tyrosine-related protein 2)
A_33_P3724155	-0.384	0.001	0.007	DERL3	Der1-like domain family, member 3
A_23_P109269	-0.385	0.001	0.006	LAMA5	laminin, alpha 5
A_33_P3255499	-0.387	0.007	0.034	MCART1	mitochondrial carrier triple repeat 1
A_24_P197964	-0.388	0.005	0.026	TRIM14	tripartite motif containing 14
A_24_P192805	-0.388	0.004	0.024	CARD17	caspase recruitment domain family, member 17
A_33_P3219697	-0.389	0.002	0.016	ANKRD45	ankyrin repeat domain 45
A_33_P3249349	-0.390	0.002	0.013	PRAME	preferentially expressed antigen in melanoma
A_33_P3244347	-0.390	0.000	0.003	PC	pyruvate carboxylase
A_23_P94921	-0.392	0.000	0.005	SLC20A2	solute carrier family 20 (phosphate transporter), member 2
A_33_P3283237	-0.393	0.006	0.029	YY2	YY2 transcription factor
A_33_P3221303	-0.393	0.001	0.006	CCR10	chemokine (C-C motif) receptor 10
A_33_P3639068	-0.394	0.001	0.008	GFRA1	GDNF family receptor alpha 1
A_24_P296698	-0.394	0.000	0.005	MAP2K3	mitogen-activated protein kinase kinase 3

A_33_P3358957	-0.394	0.005	0.029	<i>PAPL</i>	iron/zinc purple acid phosphatase-like protein
A_21_P0003756	-0.394	0.007	0.035	<i>XLOC_004049</i>	BROAD Institute lincRNA (XLOC_004049), lincRNA [TCONS_00008550]
A_24_P46093	-0.394	0.001	0.010	<i>SLC6A6</i>	solute carrier family 6 (neurotransmitter transporter, taurine), member 6
A_23_P14649	-0.395	0.001	0.011	<i>ANP32A-IT1</i>	ANP32A intronic transcript 1 (non-protein coding)
A_21_P0000508	-0.396	0.003	0.018	<i>SNAR-D</i>	small ILF3/NF90-associated RNA D
A_21_P0000511	-0.396	0.003	0.021	<i>SNAR-H</i>	small ILF3/NF90-associated RNA H
A_23_P125233	-0.397	0.003	0.017	<i>CNN1</i>	calponin 1, basic, smooth muscle
A_23_P501822	-0.397	0.001	0.010	<i>JUP</i>	junction plakoglobin
A_21_P0010982	-0.398	0.001	0.009	<i>MALAT1</i>	metastasis associated lung adenocarcinoma transcript 1 (non-protein coding)
A_33_P3295523	-0.398	0.005	0.026	<i>RAC3</i>	ras-related C3 botulinum toxin substrate 3 (rho family, small GTP binding protein Rac3)
A_23_P82503	-0.398	0.000	0.005	<i>PEG10</i>	paternally expressed 10
A_23_P74278	-0.400	0.002	0.013	<i>PDE4B</i>	phosphodiesterase 4B, cAMP-specific
A_23_P380857	-0.401	0.001	0.007	<i>APOL4</i>	apolipoprotein L, 4
A_23_P32707	-0.401	0.003	0.018	<i>ESPL1</i>	extra spindle pole bodies homolog 1 (<i>S. cerevisiae</i>)
A_21_P0006334	-0.401	0.001	0.009	<i>XLOC_007895</i>	BROAD Institute lincRNA (XLOC_007895), lincRNA [TCONS_00016511]
A_33_P3318646	-0.401	0.008	0.037	<i>CALY</i>	calcyon neuron-specific vesicular protein
A_33_P3212665	-0.402	0.001	0.008	<i>HTATSF1P2</i>	HIV-1 Tat specific factor 1 pseudogene 2
A_21_P0002398	-0.402	0.011	0.047	<i>XLOC_001974</i>	BROAD Institute lincRNA (XLOC_001974), lincRNA [TCONS_00004131]
A_21_P0013340	-0.402	0.001	0.008	<i>XLOC_12_013931</i>	BROAD Institute lincRNA (XLOC_12_013931), lincRNA [TCONS_12_00026781]
A_21_P0009366	-0.403	0.002	0.012	<i>XLOC_012586</i>	BROAD Institute lincRNA (XLOC_012586), lincRNA [TCONS_00025779]
A_24_P84880	-0.404	0.005	0.028	<i>LOC148709</i>	actin pseudogene
A_23_P416395	-0.404	0.006	0.031	<i>STC2</i>	stanniocalcin 2
A_23_P360964	-0.404	0.005	0.025	<i>DACT3</i>	dapper, antagonist of beta-catenin, homolog 3 (<i>Xenopus laevis</i>)
A_33_P3319640	-0.404	0.000	0.003	<i>HDGFRP2</i>	hepatoma-derived growth factor-related protein 2
A_23_P74668	-0.404	0.001	0.010	<i>C1orf158</i>	chromosome 1 open reading frame 158
A_23_P255376	-0.405	0.000	0.003	<i>CCDC109B</i>	coiled-coil domain containing 109B
A_23_P377376	-0.405	0.002	0.013	<i>ACTR2</i>	ARP2 actin-related protein 2 homolog (yeast)
A_23_P166248	-0.405	0.011	0.047	<i>RCAN1</i>	regulator of calcineurin 1
A_21_P0003244	-0.407	0.005	0.027	<i>XLOC_002730</i>	MTCSSXX <i>Ceratotherium simum</i> complete mitochondrial DNA sequence, partial (5%) [THC2492281]
A_24_P304154	-0.407	0.001	0.006	<i>AMPD3</i>	adenosine monophosphate deaminase 3
A_33_P3233459	-0.407	0.006	0.031	<i>LOC100287879</i>	uncharacterized LOC100287879
A_23_P124905	-0.407	0.008	0.038	<i>NPTX1</i>	neuronal pentraxin I
A_23_P168403	-0.407	0.001	0.007	<i>KCNH2</i>	potassium voltage-gated channel, subfamily H (eag-related), member 2
A_33_P3713357	-0.407	0.004	0.022	<i>ALCAM</i>	activated leukocyte cell adhesion molecule
A_21_P0011684	-0.407	0.002	0.015	<i>XLOC_12_006665</i>	BROAD Institute lincRNA (XLOC_12_006665), lincRNA [TCONS_12_00012419]
A_33_P3587376	-0.407	0.006	0.030	<i>SNAR-A3</i>	small ILF3/NF90-associated RNA A3
A_33_P3415191	-0.408	0.001	0.008	<i>ATP8B1</i>	ATPase, aminophospholipid transporter, class I, type 8B, member 1
A_24_P913716	-0.408	0.001	0.009	<i>B3GNT7</i>	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 7
A_23_P304897	-0.408	0.001	0.011	<i>BDKRB2</i>	bradykinin receptor B2
A_23_P333228	-0.408	0.007	0.034	<i>MARCH4</i>	membrane-associated ring finger (C3HC4) 4
A_33_P3222932	-0.409	0.002	0.013	<i>SHISA8</i>	shisa homolog 8 (<i>Xenopus laevis</i>)
A_23_P409386	-0.410	0.001	0.006	<i>SLC25A22</i>	solute carrier family 25 (mitochondrial carrier: glutamate), member 22
A_21_P0004261	-0.410	0.001	0.006	<i>XLOC_004415</i>	BROAD Institute lincRNA (XLOC_004415), lincRNA [TCONS_00009989]
A_33_P3294524	-0.410	0.005	0.028	<i>ANKRD12</i>	ankyrin repeat domain 12
A_23_P109026	-0.411	0.000	0.003	<i>KCNK15</i>	potassium channel, subfamily K, member 15

A_33_P3461633	-0.411	0.000	0.005	LOC284454	uncharacterized LOC284454
A_33_P3281613	-0.411	0.003	0.019	KCNT1	potassium channel, subfamily T, member 1
A_23_P360209	-0.411	0.006	0.030	ND3	NADH dehydrogenase, subunit 3 (complex I)
A_21_P0001152	-0.411	0.000	0.005	XLOC_000918	BROAD Institute lincRNA (XLOC_000918), lincRNA [TCONS_00000566]
A_21_P0004341	-0.412	0.006	0.030	HMP19	HMP19 protein
A_19_P00331618	-0.412	0.010	0.045	LOC100507645	uncharacterized LOC100507645
A_33_P3387145	-0.412	0.002	0.013	SH3KBP1	SH3-domain kinase binding protein 1
A_23_P167920	-0.413	0.000	0.004	DLL1	delta-like 1 (Drosophila)
A_21_P0011235	-0.413	0.001	0.009	XLOC_12_004115	603079729F1 NIH_MGC_119 Homo sapiens cDNA clone IMAGE:5171431 5', mRNA sequence [BI829679]
A_23_P119362	-0.415	0.008	0.038	EMP3	epithelial membrane protein 3
A_23_P150407	-0.417	0.002	0.013	CREB3L1	cAMP responsive element binding protein 3-like 1
A_21_P0001837	-0.417	0.000	0.005	XLOC_001370	BROAD Institute lincRNA (XLOC_001370), lincRNA [TCONS_00002839]
A_33_P3291454	-0.418	0.002	0.016	C10orf96	chromosome 10 open reading frame 96
A_23_P142096	-0.418	0.007	0.034	GPR32	G protein-coupled receptor 32
A_23_P350754	-0.418	0.001	0.007	OR7E14P	olfactory receptor, family 7, subfamily E, member 14 pseudogene
A_33_P3321369	-0.419	0.000	0.003	LOC145757	uncharacterized LOC145757
A_21_P0009305	-0.419	0.009	0.040	XLOC_012416	BROAD Institute lincRNA (XLOC_012416), lincRNA [TCONS_00025586]
A_23_P11005	-0.419	0.000	0.005	ADAMTS7	ADAM metallopeptidase with thrombospondin type 1 motif, 7
A_23_P139500	-0.420	0.000	0.003	BHLHE41	basic helix-loop-helix family, member e41
A_33_P3210622	-0.420	0.009	0.041	ASB13	ankyrin repeat and SOCS box containing 13
A_21_P0008919	-0.421	0.001	0.007	XLOC_011682	BROAD Institute lincRNA (XLOC_011682), lincRNA [TCONS_00024360]
A_33_P3309365	-0.421	0.001	0.006	FLJ40434	solute carrier family 25 (mitochondrial carrier; phosphate carrier), member 3 pseudogene
A_23_P373724	-0.421	0.001	0.009	PPF1BP1	PTPRF interacting protein, binding protein 1 (liprin beta 1)
A_33_P3410849	-0.421	0.000	0.005	C8orf58	chromosome 8 open reading frame 58
A_23_P211428	-0.422	0.005	0.027	SMTN	smoothelin
A_33_P3327158	-0.422	0.004	0.022	LOC100131432	uncharacterized LOC100131432
A_21_P0010348	-0.423	0.002	0.013	XLOC_014192	BROAD Institute lincRNA (XLOC_014192), lincRNA [TCONS_00029387]
A_33_P3570228	-0.423	0.000	0.004	LOC644962	trinucleotide repeat containing 18 pseudogene
A_23_P75529	-0.424	0.000	0.003	PKNOX2	PBX/knotted 1 homeobox 2
A_23_P151267	-0.425	0.001	0.010	LIMA1	LIM domain and actin binding 1
A_21_P0005606	-0.425	0.006	0.031	XLOC_006491	BROAD Institute lincRNA (XLOC_006491), lincRNA [TCONS_00014334]
A_33_P3326812	-0.425	0.006	0.031	LOC100130152	uncharacterized LOC100130152
A_33_P3452003	-0.425	0.000	0.005	LOC143286	uncharacterized LOC143286
A_33_P3294603	-0.426	0.001	0.010	SLC22A31	solute carrier family 22, member 31
A_33_P3312802	-0.426	0.001	0.011	RPL13AP17	ribosomal protein L13a pseudogene 17
A_32_P224666	-0.426	0.002	0.014	CAPZA2	capping protein (actin filament) muscle Z-line, alpha 2
A_19_P00812608	-0.426	0.000	0.003	Q442D3	Q442D3_SOLUS RND efflux system, outer membrane lipoprotein, NodT, partial (5%) [THC2510388]
A_33_P3338793	-0.427	0.001	0.009	KCNC3	potassium voltage-gated channel, Shaw-related subfamily, member 3
A_23_P53193	-0.427	0.002	0.016	SYTL2	synaptotagmin-like 2
A_24_P931443	-0.428	0.000	0.004	GPR68	G protein-coupled receptor 68
A_23_P152406	-0.428	0.004	0.024	CAPNS2	calpain, small subunit 2
A_21_P0012477	-0.429	0.000	0.002	XLOC_12_010493	BROAD Institute lincRNA (XLOC_12_010493), lincRNA [TCONS_12_00019671]
A_33_P3245248	-0.429	0.002	0.014	TERC	telomerase RNA component
A_33_P3391496	-0.430	0.004	0.022	SLIT3	slit homolog 3 (Drosophila)
A_24_P41850	-0.431	0.009	0.041	MASPI1	mannan-binding lectin serine peptidase 1 (C4/C2 activating component of Ra-reactive factor)

A_33_P3220152	-0.432	0.000	0.003	<i>SBNO2</i>	strawberry notch homolog 2 (Drosophila)
A_21_P0014051	-0.432	0.003	0.018	<i>LOC100132273</i>	uncharacterized LOC100132273
A_23_P146274	-0.432	0.000	0.003	<i>STMN2</i>	stathmin-like 2
A_33_P3397795	-0.434	0.000	0.005	<i>C14orf135</i>	chromosome 14 open reading frame 135
A_21_P0010927	-0.434	0.001	0.008	<i>XLOC_12_001683</i>	BROAD Institute lincRNA (XLOC_12_001683), lincRNA [TCONS_12_00004022]
A_23_P30204	-0.434	0.001	0.010	<i>HMHBI</i>	histocompatibility (minor) HB-1
A_33_P3499102	-0.435	0.000	0.003	<i>RBM10</i>	RNA binding motif protein 10
A_33_P3544887	-0.435	0.000	0.003	<i>TTC28</i>	tetratricopeptide repeat domain 28
A_33_P3343845	-0.436	0.005	0.026	<i>CBX7</i>	chromobox homolog 7
A_21_P0004638	-0.436	0.001	0.008	<i>XLOC_005225</i>	HLA complex group 14
A_23_P105251	-0.437	0.002	0.016	<i>GLI1</i>	GLI family zinc finger 1
A_23_P78037	-0.437	0.001	0.009	<i>CCL7</i>	chemokine (C-C motif) ligand 7
A_23_P205489	-0.437	0.000	0.004	<i>SLC7A8</i>	solute carrier family 7 (amino acid transporter light chain, L system), member 8
A_33_P3307886	-0.438	0.000	0.004	<i>TBXA2R</i>	thromboxane A2 receptor
A_21_P0011266	-0.439	0.005	0.028	<i>XLOC_12_004381</i>	long intergenic non-protein coding RNA 639
A_33_P3269408	-0.439	0.001	0.007	<i>FOXI2</i>	forkhead box I2
A_33_P3386132	-0.440	0.000	0.002	<i>C2orf49</i>	chromosome 2 open reading frame 49
A_23_P160559	-0.441	0.000	0.003	<i>ECM1</i>	extracellular matrix protein 1
A_33_P3377194	-0.442	0.001	0.010	<i>ADRA1A</i>	adrenergic, alpha-1A-, receptor
A_24_P48204	-0.442	0.002	0.016	<i>SECTM1</i>	secreted and transmembrane 1
A_33_P3231739	-0.442	0.007	0.032	<i>ELOVL2</i>	ELOVL fatty acid elongase 2
A_21_P0001900	-0.442	0.007	0.033	<i>XLOC_001620</i>	DB077273 TESTI4 Homo sapiens cDNA clone TESTI4021828 5', mRNA sequence
A_23_P31945	-0.442	0.001	0.008	<i>IL33</i>	interleukin 33
A_33_P3319581	-0.442	0.000	0.002	<i>FIGNL2</i>	fidgetin-like 2
A_33_P3281795	-0.443	0.004	0.022	<i>MGLL</i>	monoglyceride lipase
A_19_P00318915	-0.443	0.002	0.016	<i>Q9EPR2</i>	PG12A_MOUSE (Q9EPR2) Group XIIA secretory phospholipase A2 precursor (Phosphatidylcholine 2-acylhydrolase C
A_21_P0014885	-0.443	0.000	0.005	<i>LOC100506257</i>	uncharacterized LOC100506257
A_21_P0010126	-0.444	0.001	0.008	<i>XLOC_013826</i>	BROAD Institute lincRNA (XLOC_013826), lincRNA [TCONS_00028717]
A_19_P00801634	-0.444	0.005	0.027	<i>NOP56</i>	NOP56 ribonucleoprotein homolog (yeast)
A_33_P3678883	-0.444	0.000	0.005	<i>KIAA1654</i>	KIAA1654 protein
A_33_P3392123	-0.444	0.001	0.010	<i>LOC100233209</i>	uncharacterized LOC100233209
A_33_P3235432	-0.445	0.000	0.004	<i>ESYT3</i>	extended synaptotagmin-like protein 3
A_21_P0002865	-0.447	0.004	0.024	<i>XLOC_003176</i>	BROAD Institute lincRNA (XLOC_003176), lincRNA [TCONS_00005798]
A_21_P0010899	-0.447	0.002	0.013	<i>XLOC_12_002076</i>	BROAD Institute lincRNA (XLOC_12_002076), lincRNA [TCONS_12_00003732]
A_33_P3236441	-0.447	0.000	0.003	<i>LDHAL6A</i>	lactate dehydrogenase A-like 6A
A_24_P278747	-0.448	0.001	0.006	<i>CCND2</i>	cyclin D2
A_33_P3259135	-0.448	0.001	0.006	<i>D4S234E</i>	DNA segment on chromosome 4 (unique) 234 expressed sequence
A_33_P3415491	-0.450	0.003	0.017	<i>WDR90</i>	WD repeat domain 90
A_21_P0011028	-0.450	0.000	0.005	<i>XLOC_12_002502</i>	BROAD Institute lincRNA (XLOC_12_002502), lincRNA [TCONS_12_00005340]
A_33_P3337719	-0.451	0.000	0.003	<i>LOC100134868</i>	uncharacterized LOC100134868
A_19_P00318813	-0.451	0.000	0.003	<i>XLOC_012335</i>	DB297613 BRACE2 Homo sapiens cDNA clone BRACE2023991 3', mRNA sequence
A_19_P00316629	-0.452	0.001	0.010	<i>PIEZO1</i>	piezo-type mechanosensitive ion channel component 1
A_33_P3287646	-0.452	0.000	0.005	<i>HSPB1</i>	heat shock 27kDa protein 1
A_21_P0008530	-0.453	0.008	0.039	<i>XLOC_010979</i>	BROAD Institute lincRNA (XLOC_010979), lincRNA [TCONS_00023086]
A_24_P784765	-0.454	0.000	0.002	<i>CD59</i>	CD59 molecule, complement regulatory protein

A_23_P303833	-0.454	0.000	0.003	<i>SCN4B</i>	sodium channel, voltage-gated, type IV, beta
A_21_P0001995	-0.454	0.000	0.004	<i>XLOC_001954</i>	BROAD Institute lincRNA (XLOC_001954), lincRNA [TCONS_00003165]
A_21_P0011702	-0.454	0.001	0.010	<i>XLOC_12_006789</i>	BROAD Institute lincRNA (XLOC_12_006789), lincRNA [TCONS_12_00012635]
A_23_P316850	-0.454	0.000	0.003	<i>ODF3L2</i>	outer dense fiber of sperm tails 3-like 2
A_19_P00328190	-0.455	0.003	0.021	<i>FLJ39653</i>	uncharacterized FLJ39653
A_23_P205959	-0.455	0.006	0.029	<i>ALDH1A3</i>	aldehyde dehydrogenase 1 family, member A3
A_33_P3337627	-0.455	0.001	0.011	<i>TRPC6</i>	transient receptor potential cation channel, subfamily C, member 6
A_23_P215484	-0.456	0.002	0.014	<i>CCL26</i>	chemokine (C-C motif) ligand 26
A_21_P0007407	-0.456	0.000	0.002	<i>XLOC_009575</i>	BROAD Institute lincRNA (XLOC_009575), lincRNA [TCONS_00019776]
A_23_P256663	-0.457	0.003	0.020	<i>GALR3</i>	galanin receptor 3
A_33_P3341970	-0.457	0.006	0.029	<i>NEGR1</i>	neuronal growth regulator 1
A_21_P0003432	-0.457	0.004	0.025	<i>XLOC_003776</i>	BROAD Institute lincRNA (XLOC_003776), lincRNA [TCONS_00007680]
A_33_P3260053	-0.458	0.002	0.015	<i>AIF1L</i>	allograft inflammatory factor 1-like
A_21_P0014874	-0.458	0.003	0.017	<i>LOC100653008</i>	uncharacterized LOC100507904
A_33_P3332382	-0.459	0.000	0.003	<i>LOC100129406</i>	uncharacterized LOC100129406
A_33_P3351259	-0.459	0.000	0.004	<i>LOC100130560</i>	uncharacterized LOC100130560
A_23_P115064	-0.459	0.009	0.040	<i>CRABP2</i>	cellular retinoic acid binding protein 2
A_23_P34915	-0.460	0.000	0.002	<i>ATF3</i>	activating transcription factor 3
A_33_P3411885	-0.460	0.006	0.031	<i>LOC100128851</i>	uncharacterized LOC100128851
A_21_P0009578	-0.460	0.005	0.027	<i>XLOC_012880</i>	BROAD Institute lincRNA (XLOC_012880), lincRNA [TCONS_00026559]
A_33_P3276068	-0.460	0.001	0.008	<i>BET3L</i>	BET3 like (S. cerevisiae)
A_33_P3236591	-0.460	0.000	0.004	<i>RLTPR</i>	RGD motif, leucine rich repeats, tropomodulin domain and proline-rich containing
A_23_P140967	-0.460	0.001	0.007	<i>MEFV</i>	Mediterranean fever
A_33_P3258699	-0.461	0.001	0.011	<i>DUX4</i>	double homeobox 4
A_33_P3287348	-0.461	0.001	0.006	<i>CHN2</i>	chimerin (chimaerin) 2
A_33_P3362933	-0.461	0.000	0.003	<i>GYP A</i>	glycophorin A (MNS blood group)
A_33_P3363310	-0.462	0.002	0.015	<i>KRTAP5-10</i>	keratin associated protein 5-10
A_21_P0014135	-0.462	0.003	0.018	<i>LOC100505937</i>	uncharacterized LOC100505937
A_33_P3518572	-0.463	0.000	0.001	<i>LOC100287314</i>	uncharacterized LOC100287314
A_33_P3363245	-0.463	0.000	0.005	<i>NXPH4</i>	neurexophilin 4
A_33_P3265606	-0.464	0.000	0.002	<i>GCLM</i>	glutamate-cysteine ligase, modifier subunit
A_21_P0011566	-0.464	0.002	0.013	<i>XLOC_12_005952</i>	BROAD Institute lincRNA (XLOC_12_005952), lincRNA [TCONS_12_00011050]
A_21_P0014334	-0.465	0.001	0.008	<i>LOC100506521</i>	uncharacterized LOC100506521
A_21_P0013201	-0.465	0.002	0.016	<i>XLOC_12_013420</i>	BROAD Institute lincRNA (XLOC_12_013420), lincRNA [TCONS_12_00025900]
A_19_P00316401	-0.465	0.001	0.007	<i>XLOC_007052</i>	DKFZp779O0656_r1 779 (synonym: hnce1) Homo sapiens cDNA clone DKFZp779O0656 5', mRNA sequence [BX500
A_33_P3383912	-0.465	0.002	0.013	<i>HLA-DRB3</i>	major histocompatibility complex, class II, DR beta 3
A_24_P412734	-0.466	0.003	0.018	<i>PRSS36</i>	protease, serine, 36
A_32_P52330	-0.466	0.001	0.006	<i>LOC113230</i>	uncharacterized LOC113230
A_33_P3262555	-0.468	0.003	0.019	<i>MEX3D</i>	mex-3 homolog D (C. elegans)
A_23_P153022	-0.468	0.000	0.005	<i>KRTAP2-4</i>	keratin associated protein 2-4
A_21_P0007327	-0.470	0.004	0.024	<i>XLOC_009394</i>	O95074_HUMAN Bax epsilon (Fragment), partial (55%) [THC2712168]
A_33_P3257910	-0.471	0.008	0.036	<i>C3orf80</i>	chromosome 3 open reading frame 80
A_23_P213857	-0.471	0.000	0.004	<i>C7</i>	complement component 7
A_23_P420196	-0.471	0.005	0.026	<i>SOCS1</i>	suppressor of cytokine signaling 1
A_21_P0007239	-0.472	0.000	0.003	<i>XLOC_009223</i>	BROAD Institute lincRNA (XLOC_009223), lincRNA [TCONS_00019400]

A_23_P2283	-0.472	0.001	0.010	<i>TAC3</i>	tachykinin 3
A_24_P416961	-0.472	0.002	0.014	<i>ARVCF</i>	armadillo repeat gene deleted in velocardiofacial syndrome
A_33_P3385765	-0.472	0.000	0.002	<i>ZNF763</i>	zinc finger protein 763
A_24_P76854	-0.472	0.008	0.039	<i>KRTAP2-1</i>	keratin associated protein 2-1
A_21_P0013714	-0.473	0.001	0.007	<i>XLOC_12_015100</i>	CR746865 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGp998F174536 ; IMAGE:1853584 5', mRNA seq
A_24_P89971	-0.473	0.001	0.010	<i>SURF4</i>	surfeit 4
A_21_P0014365	-0.474	0.001	0.007	<i>LOC100287082</i>	uncharacterized LOC100287082
A_23_P218505	-0.475	0.001	0.010	<i>LHB</i>	luteinizing hormone beta polypeptide
A_32_P86150	-0.475	0.000	0.003	<i>CTRB2</i>	chymotrypsinogen B2
A_33_P3231953	-0.476	0.004	0.023	<i>COL12A1</i>	collagen, type XII, alpha 1
A_21_P0011372	-0.476	0.009	0.039	<i>LOC100505648</i>	uncharacterized LOC100505648
A_32_P110390	-0.477	0.003	0.020	<i>TMEM171</i>	transmembrane protein 171
A_33_P3279379	-0.477	0.001	0.009	<i>DSTNP2</i>	destrin (actin depolymerizing factor) pseudogene 2
A_33_P3329187	-0.477	0.000	0.004	<i>DNMT1</i>	DNA (cytosine-5-)-methyltransferase 1
A_23_P18246	-0.478	0.003	0.020	<i>XCR1</i>	chemokine (C motif) receptor 1
A_23_P366812	-0.479	0.004	0.024	<i>AQP5</i>	aquaporin 5
A_33_P3609431	-0.479	0.000	0.005	<i>ERVFRD-2</i>	endogenous retrovirus group FRD, member 2
A_33_P3363016	-0.482	0.003	0.020	<i>BRF1</i>	BRF1 homolog, subunit of RNA polymerase III transcription initiation factor IIIB (S. cerevisiae)
A_33_P3420446	-0.482	0.000	0.002	<i>LRRD1</i>	leucine-rich repeats and death domain containing 1
A_33_P3362952	-0.483	0.000	0.003	<i>LRRC37BP1</i>	leucine rich repeat containing 37B pseudogene 1
A_21_P0006584	-0.484	0.001	0.008	<i>NKAPP1</i>	NFKB activating protein pseudogene 1
A_33_P3395743	-0.484	0.000	0.002	<i>VWAI</i>	von Willebrand factor A domain containing 1
A_24_P144499	-0.485	0.008	0.037	<i>PPIAL4A</i>	peptidylprolyl isomerase A (cyclophilin A)-like 4A
A_32_P40547	-0.486	0.000	0.002	<i>MEG3</i>	maternally expressed 3 (non-protein coding)
A_33_P3317623	-0.487	0.000	0.001	<i>LOC284379</i>	solute carrier family 7 (cationic amino acid transporter, y+ system), member 3 pseudogene
A_23_P119593	-0.487	0.001	0.006	<i>EPHX3</i>	epoxide hydrolase 3
A_32_P46214	-0.487	0.000	0.001	<i>SLC9A9</i>	solute carrier family 9 (sodium/hydrogen exchanger), member 9
A_21_P0010313	-0.487	0.010	0.042	<i>XLOC_013949</i>	BROAD Institute lincRNA (XLOC_013949), lincRNA [TCONS_00029224]
A_33_P3343090	-0.489	0.002	0.012	<i>MAP1S</i>	microtubule-associated protein 1S
A_23_P39223	-0.489	0.000	0.001	<i>ZNF2</i>	zinc finger protein 2
A_33_P3294961	-0.491	0.000	0.003	<i>LAT2</i>	linker for activation of T cells family, member 2
A_33_P3262694	-0.492	0.000	0.002	<i>LOC647086</i>	chromosome 20 open reading frame 27 pseudogene
A_24_P242036	-0.492	0.000	0.002	<i>RRP7B</i>	ribosomal RNA processing 7 homolog B (S. cerevisiae)
A_21_P0011562	-0.492	0.001	0.010	<i>XLOC_12_005933</i>	BROAD Institute lincRNA (XLOC_12_005933), lincRNA [TCONS_12_00011027]
A_33_P3464555	-0.492	0.000	0.004	<i>LOC283070</i>	uncharacterized LOC283070
A_33_P3416503	-0.493	0.000	0.005	<i>NUDT8</i>	nudix (nucleoside diphosphate linked moiety X)-type motif 8
A_21_P0011874	-0.493	0.001	0.008	<i>XLOC_12_007767</i>	09F_J17.2 Novel Promoters 5' RACE-PCR Homo sapiens cDNA 5', mRNA sequence [EL584821]
A_33_P3209321	-0.494	0.000	0.004	<i>LOC729558</i>	uncharacterized LOC729558
A_23_P94319	-0.495	0.010	0.045	<i>KBTBD11</i>	kelch repeat and BTB (POZ) domain containing 11
A_21_P0014785	-0.496	0.010	0.045	<i>LOC100652935</i>	uncharacterized LOC100652935
A_33_P3222069	-0.496	0.001	0.007	<i>SPHK1</i>	sphingosine kinase 1
A_33_P3238074	-0.497	0.000	0.003	<i>SMCR7L</i>	Smith-Magenis syndrome chromosome region, candidate 7-like
A_33_P3260605	-0.497	0.010	0.044	<i>CTNNA1</i>	catenin (cadherin-associated protein), alpha-like 1
A_23_P49674	-0.500	0.001	0.008	<i>ARHGEF15</i>	Rho guanine nucleotide exchange factor (GEF) 15
A_24_P220485	-0.501	0.000	0.002	<i>OLFML2A</i>	olfactomedin-like 2A

A_33_P3314176	-0.501	0.000	0.002	<i>FAM46C</i>	family with sequence similarity 46, member C
A_32_P156851	-0.502	0.000	0.002	<i>RCAN2</i>	regulator of calcineurin 2
A_21_P0000492	-0.503	0.000	0.002	<i>SNAR-F</i>	small ILF3/NF90-associated RNA F
A_24_P131580	-0.504	0.000	0.002	<i>ALPPL2</i>	alkaline phosphatase, placental-like 2
A_21_P0000139	-0.507	0.000	0.003	<i>DKK1L</i>	dickkopf-like 1
A_33_P3296067	-0.507	0.003	0.018	<i>CDC14C</i>	CDC14 cell division cycle 14 homolog C (S. cerevisiae)
A_33_P3312682	-0.507	0.000	0.002	<i>REXO1</i>	REX1, RNA exonuclease 1 homolog (S. cerevisiae)
A_33_P3391375	-0.508	0.001	0.008	<i>LANCL3</i>	LanC lantibiotic synthetase component C-like 3 (bacterial)
A_33_P3641714	-0.509	0.000	0.002	<i>C19orf66</i>	chromosome 19 open reading frame 66
A_24_P202497	-0.510	0.000	0.004	<i>TWSG1</i>	twisted gastrulation homolog 1 (Drosophila)
A_33_P3229863	-0.510	0.000	0.003	<i>LOC100128714</i>	uncharacterized LOC100128714
A_24_P127719	-0.511	0.000	0.002	<i>MAFA</i>	v-maf musculoaponeurotic fibrosarcoma oncogene homolog A (avian)
A_21_P0005573	-0.511	0.000	0.003	<i>XLOC_006200</i>	BROAD Institute lincRNA (XLOC_006200), lincRNA [TCONS_00014191]
A_33_P3670415	-0.511	0.003	0.017	<i>NAT8L</i>	N-acetyltransferase 8-like (GCN5-related, putative)
A_23_P103672	-0.512	0.003	0.020	<i>NES</i>	nestin
A_23_P137046	-0.512	0.000	0.002	<i>NYX</i>	nyctalopin
A_19_P00320966	-0.513	0.000	0.004	<i>XLOC_12_014645</i>	BROAD Institute lincRNA (XLOC_12_014645), lincRNA [TCONS_12_00028401]
A_33_P3229156	-0.513	0.000	0.002	<i>SLC17A9</i>	solute carrier family 17, member 9
A_33_P3333038	-0.513	0.000	0.002	<i>PTMS</i>	parathyrosin
A_33_P3347343	-0.517	0.007	0.034	<i>CCDC102B</i>	coiled-coil domain containing 102B
A_24_P169073	-0.518	0.001	0.008	<i>FAM131C</i>	family with sequence similarity 131, member C
A_24_P66932	-0.518	0.000	0.002	<i>LOC729080</i>	glycine cleavage system protein H (aminomethyl carrier) pseudogene
A_24_P161144	-0.518	0.005	0.026	<i>ZNF843</i>	zinc finger protein 843
A_21_P0012880	-0.518	0.000	0.002	<i>BRD9</i>	bromodomain containing 9
A_23_P121945	-0.520	0.000	0.002	<i>SNCB</i>	synuclein, beta
A_23_P255968	-0.520	0.001	0.008	<i>TAAR5</i>	trace amine associated receptor 5
A_21_P0011147	-0.521	0.002	0.016	<i>XLOC_12_003757</i>	Q8WZ85_HUMAN Olfactory-like receptor PJCG2 (Fragment), partial (81%) [THC2581448]
A_23_P142075	-0.521	0.001	0.007	<i>ACP5</i>	acid phosphatase 5, tartrate resistant
A_23_P131139	-0.521	0.000	0.002	<i>DIRC1</i>	disrupted in renal carcinoma 1
A_21_P0014676	-0.523	0.000	0.002	<i>LOC100509541</i>	uncharacterized LOC100509541
A_23_P128744	-0.525	0.002	0.016	<i>BDKRB1</i>	bradykinin receptor B1
A_33_P3376478	-0.527	0.004	0.022	<i>CYP17A1</i>	cytochrome P450, family 17, subfamily A, polypeptide 1
A_33_P3323559	-0.528	0.007	0.032	<i>CRYAA</i>	crystallin, alpha A
A_33_P3719214	-0.529	0.000	0.002	<i>LINC00355</i>	long intergenic non-protein coding RNA 355
A_33_P3228739	-0.529	0.001	0.008	<i>LRRC3C</i>	leucine rich repeat containing 3C
A_21_P0013293	-0.530	0.000	0.002	<i>XLOC_12_013765</i>	BROAD Institute lincRNA (XLOC_12_013765), lincRNA [TCONS_12_00027302]
A_33_P3275801	-0.531	0.000	0.002	<i>DES</i>	desmin
A_21_P0013671	-0.531	0.000	0.002	<i>XLOC_12_015295</i>	Q4C1A2_CROWT Rhodanese-like, partial (8%) [THC2746386]
A_24_P827491	-0.531	0.001	0.008	<i>PA2G4</i>	proliferation-associated 2G4, 38kDa
A_21_P0000754	-0.531	0.000	0.002	<i>LOC100507091</i>	uncharacterized LOC100507091
A_21_P0013302	-0.531	0.001	0.006	<i>XLOC_12_013808</i>	Q59EY4_HUMAN CDC10 protein variant (Fragment), partial (89%) [THC2541514]
A_21_P0004402	-0.532	0.000	0.002	<i>XLOC_004842</i>	BROAD Institute lincRNA (XLOC_004842), lincRNA [TCONS_00010353]
A_33_P3322430	-0.532	0.000	0.001	<i>CTNS</i>	cystinosin, lysosomal cystine transporter
A_23_P109133	-0.532	0.003	0.018	<i>AVP</i>	arginine vasopressin
A_33_P3252695	-0.533	0.000	0.004	<i>CYTL1</i>	cytokine-like 1

A_24_P295999	-0.533	0.000	0.002	CD4	CD4 molecule
A_33_P3410925	-0.534	0.000	0.003	KLF1	Kruppel-like factor 1 (erythroid)
A_33_P3286302	-0.536	0.004	0.023	TNFRSF14	tumor necrosis factor receptor superfamily, member 14
A_33_P3398998	-0.537	0.003	0.020	C2orf50	chromosome 2 open reading frame 50
A_19_P00317318	-0.537	0.004	0.022	RFX8	regulatory factor X, 8
A_21_P0010894	-0.537	0.000	0.002	XLOC_12_002049	BROAD Institute lincRNA (XLOC_12_002049), lincRNA [TCONS_12_00003697]
A_33_P3374952	-0.538	0.002	0.014	KLF17	Kruppel-like factor 17
A_32_P24376	-0.538	0.011	0.045	LOC730755	keratin associated protein 2-4-like
A_21_P0011573	-0.539	0.001	0.006	XLOC_12_006013	BROAD Institute lincRNA (XLOC_12_006013), lincRNA [TCONS_12_00011128]
A_24_P21770	-0.539	0.003	0.017	YPEL4	yippee-like 4 (Drosophila)
A_32_P300427	-0.540	0.000	0.003	APCDD1L	adenomatosis polyposis coli down-regulated 1-like
A_24_P270460	-0.541	0.001	0.009	IFI27	interferon, alpha-inducible protein 27
A_24_P68631	-0.541	0.000	0.001	HIST2H2AB	histone cluster 2, H2ab
A_23_P26294	-0.542	0.000	0.002	TPSG1	tryptase gamma 1
A_21_P0009093	-0.543	0.000	0.004	XLOC_011645	BROAD Institute lincRNA (XLOC_011645), lincRNA [TCONS_00024807]
A_33_P3316913	-0.544	0.006	0.030	LOC441698	ras-related protein Rap-2c-like
A_23_P35414	-0.544	0.000	0.004	PPP1R3C	protein phosphatase 1, regulatory subunit 3C
A_33_P3441583	-0.545	0.001	0.011	SRGAP2P1	SLIT-ROBO Rho GTPase activating protein 2 pseudogene 1
A_23_P111092	-0.545	0.000	0.003	OR2H1	olfactory receptor, family 2, subfamily H, member 1
A_33_P3387170	-0.545	0.000	0.001	LOC100129196	uncharacterized LOC100129196
A_33_P3285868	-0.546	0.000	0.003	CYGB	cytoglobin
A_33_P3222019	-0.547	0.001	0.006	WSCD2	WSC domain containing 2
A_33_P3420852	-0.548	0.000	0.002	KIRREL2	kin of IRRE like 2 (Drosophila)
A_21_P0003579	-0.548	0.000	0.005	XLOC_003463	BROAD Institute lincRNA (XLOC_003463), lincRNA [TCONS_00008000]
A_21_P0006850	-0.549	0.002	0.013	XLOC_008429	BROAD Institute lincRNA (XLOC_008429), lincRNA [TCONS_00018150]
A_33_P3257513	-0.549	0.000	0.002	FAT3	FAT tumor suppressor homolog 3 (Drosophila)
A_33_P3365747	-0.549	0.003	0.018	LINC00265	long intergenic non-protein coding RNA 265
A_24_P941322	-0.549	0.000	0.002	QKI	QKI, KH domain containing, RNA binding
A_33_P3312504	-0.549	0.001	0.010	PSD4	pleckstrin and Sec7 domain containing 4
A_21_P0011589	-0.549	0.001	0.006	ZNF385C	zinc finger protein 385C
A_33_P3245489	-0.549	0.001	0.006	ADAMTSL5	ADAMTS-like 5
A_21_P0007586	-0.550	0.004	0.021	XLOC_009810	BROAD Institute lincRNA (XLOC_009810), lincRNA [TCONS_00020478]
A_33_P3870056	-0.550	0.000	0.002	LOC283335	uncharacterized LOC283335
A_33_P3283669	-0.551	0.000	0.003	ATPIA3	ATPase, Na ⁺ /K ⁺ transporting, alpha 3 polypeptide
A_23_P404685	-0.552	0.000	0.003	LCE1A	late cornified envelope 1A
A_19_P00321670	-0.553	0.000	0.005	XLOC_005730	zt85h04.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:729175 5', mRNA sequence [AA397666]
A_24_P366122	-0.553	0.008	0.036	ACBD4	acyl-CoA binding domain containing 4
A_33_P3322859	-0.554	0.001	0.011	HES6	hairy and enhancer of split 6 (Drosophila)
A_33_P3409580	-0.555	0.000	0.004	LOC100129722	uncharacterized LOC100129722
A_19_P00321658	-0.556	0.000	0.003	LOC100131551	uncharacterized LOC100131551
A_24_P215804	-0.558	0.003	0.017	CKLF	chemokine-like factor
A_21_P0009551	-0.558	0.000	0.001	XLOC_012829	BROAD Institute lincRNA (XLOC_012829), lincRNA [TCONS_00026503]
A_33_P3370364	-0.558	0.000	0.002	PRLHR	prolactin releasing hormone receptor
A_33_P3272291	-0.559	0.004	0.023	AKRIC4	aldo-keto reductase family 1, member C4 (chlordecone reductase; 3-alpha hydroxysteroid dehydrogenase, type I; dihydr
A_33_P3250348	-0.559	0.000	0.003	PCDH18	protocadherin 18

A_24_P122137	-0.559	0.005	0.028	<i>LIF</i>	leukemia inhibitory factor (cholinergic differentiation factor)
A_33_P3272539	-0.560	0.000	0.005	<i>PLEKHG5</i>	pleckstrin homology domain containing, family G (with RhoGef domain) member 5
A_19_P00805950	-0.560	0.000	0.004	<i>XLOC_12_001196</i>	BROAD Institute lincRNA (XLOC_12_001196), lincRNA [TCONS_12_00001622]
A_23_P375524	-0.561	0.000	0.001	<i>LCE1D</i>	late cornified envelope 1D
A_33_P3419180	-0.561	0.000	0.001	<i>LOC283547</i>	uncharacterized LOC283547
A_21_P0012379	-0.562	0.001	0.007	<i>DUX4L9</i>	double homeobox 4 like 9
A_23_P74330	-0.562	0.001	0.006	<i>MGC4473</i>	uncharacterized LOC79100
A_33_P3546363	-0.563	0.002	0.013	<i>LOC400128</i>	uncharacterized LOC400128
A_21_P0012616	-0.565	0.000	0.005	<i>XLOC_12_010854</i>	BROAD Institute lincRNA (XLOC_12_010854), lincRNA [TCONS_12_00020780]
A_21_P0011802	-0.565	0.000	0.004	<i>XLOC_12_007310</i>	Q3SWU9_HUMAN MSH6 protein (Fragment), partial (8%) [THC2519945]
A_33_P3335920	-0.567	0.000	0.003	<i>SYNE1</i>	spectrin repeat containing, nuclear envelope 1
A_33_P3378659	-0.568	0.000	0.002	<i>TARP</i>	TCR gamma alternate reading frame protein
A_33_P3325195	-0.568	0.000	0.001	<i>IGSF9B</i>	immunoglobulin superfamily, member 9B
A_21_P0013704	-0.572	0.000	0.005	<i>XLOC_12_014931</i>	BX119021 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGp998K034258, mRNA sequence
A_33_P3292478	-0.574	0.001	0.008	<i>CCL16</i>	chemokine (C-C motif) ligand 16
A_33_P3309034	-0.574	0.000	0.002	<i>SEPT7L</i>	septin 7-like
A_33_P3334398	-0.574	0.001	0.011	<i>CA6</i>	carbonic anhydrase VI
A_21_P0014853	-0.574	0.002	0.016	<i>LOC100652791</i>	uncharacterized LOC100652791
A_33_P3373185	-0.576	0.000	0.001	<i>LOC399744</i>	uncharacterized LOC399744
A_21_P0014473	-0.578	0.006	0.031	<i>LOC100506338</i>	uncharacterized LOC100506338
A_21_P0000662	-0.579	0.000	0.001	<i>LOC100131320</i>	uncharacterized LOC100131320
A_33_P3408203	-0.579	0.002	0.014	<i>TGFA</i>	transforming growth factor, alpha
A_32_P87013	-0.581	0.008	0.038	<i>IL8</i>	interleukin 8
A_33_P3415698	-0.582	0.000	0.002	<i>TMIGD2</i>	transmembrane and immunoglobulin domain containing 2
A_24_P350228	-0.583	0.000	0.002	<i>SLC22A23</i>	solute carrier family 22, member 23
A_32_P78681	-0.584	0.007	0.034	<i>GLP2R</i>	glucagon-like peptide 2 receptor
A_21_P0011822	-0.585	0.005	0.026	<i>XLOC_12_007449</i>	BROAD Institute lincRNA (XLOC_12_007449), lincRNA [TCONS_12_00013837]
A_21_P0000910	-0.589	0.000	0.002	<i>LOC284628</i>	uncharacterized LOC284628
A_33_P3248863	-0.589	0.001	0.009	<i>KRBA2</i>	KRAB-A domain containing 2
A_33_P3264444	-0.589	0.001	0.006	<i>PFDN6</i>	prefoldin subunit 6
A_21_P0005640	-0.590	0.001	0.009	<i>XLOC_006680</i>	BROAD Institute lincRNA (XLOC_006680), lincRNA [TCONS_00014570]
A_33_P3340649	-0.590	0.000	0.003	<i>KRTAP19-8</i>	keratin associated protein 19-8
A_24_P104512	-0.591	0.000	0.004	<i>EVPL</i>	envoplakin
A_21_P0002073	-0.592	0.000	0.001	<i>XLOC_002217</i>	DB092709 TESTI4 Homo sapiens cDNA clone TESTI4042421 5', mRNA sequence
A_21_P0007502	-0.593	0.000	0.002	<i>LINC00173</i>	long intergenic non-protein coding RNA 173
A_21_P0009195	-0.593	0.000	0.005	<i>XLOC_012507</i>	BROAD Institute lincRNA (XLOC_012507), lincRNA [TCONS_00025234]
A_23_P72584	-0.593	0.000	0.003	<i>ACBD7</i>	acyl-CoA binding domain containing 7
A_33_P3308456	-0.594	0.000	0.003	<i>HOXB13-ASI</i>	HOXB13 antisense RNA 1 (non-protein coding)
A_33_P3267263	-0.594	0.006	0.030	<i>RNU1-5</i>	RNA, U1 small nuclear 5
A_33_P3812815	-0.595	0.000	0.002	<i>PKD1</i>	polycystic kidney disease 1 (autosomal dominant)
A_33_P3421219	-0.596	0.000	0.005	<i>LOC647070</i>	uncharacterized LOC647070
A_33_P3393537	-0.597	0.001	0.009	<i>PTAFR</i>	platelet-activating factor receptor
A_21_P0001897	-0.598	0.000	0.003	<i>XLOC_001619</i>	full-length cDNA clone CS0DD009YK02 of Neuroblastoma Cot 50-normalized of Homo sapiens (human) [CR626349]
A_23_P215491	-0.598	0.000	0.001	<i>CCL24</i>	chemokine (C-C motif) ligand 24
A_33_P3296169	-0.599	0.000	0.002	<i>CDC47</i>	cell division cycle associated 7

A_33_P3359012	-0.599	0.000	0.001	DUSP8	dual specificity phosphatase 8
A_21_P0013656	-0.599	0.000	0.002	XLOC_12_015213	BROAD Institute lincRNA (XLOC_12_015213), lincRNA [TCONS_12_00029360]
A_24_P111054	-0.603	0.001	0.008	SLC2A5	solute carrier family 2 (facilitated glucose/fructose transporter), member 5
A_23_P162547	-0.603	0.002	0.016	MYL2	myosin, light chain 2, regulatory, cardiac, slow
A_33_P3244843	-0.604	0.000	0.001	PRKAG3	protein kinase, AMP-activated, gamma 3 non-catalytic subunit
A_24_P183664	-0.604	0.003	0.019	TRIL	TLR4 interactor with leucine-rich repeats
A_33_P3285715	-0.605	0.000	0.002	GLI4	GLI family zinc finger 4
A_23_P160849	-0.605	0.000	0.001	FCER1G	Fc fragment of IgE, high affinity I, receptor for; gamma polypeptide
A_23_P138881	-0.606	0.000	0.003	ACTN3	actinin, alpha 3
A_33_P3560679	-0.607	0.000	0.002	LOC100287221	uncharacterized LOC100287221
A_33_P3278347	-0.608	0.001	0.007	C21orf88	chromosome 21 open reading frame 88
A_23_P28707	-0.608	0.000	0.002	OGFR	opioid growth factor receptor
A_19_P00321461	-0.609	0.000	0.002	XLOC_12_011204	BROAD Institute lincRNA (XLOC_12_011204), lincRNA [TCONS_12_00021934]
A_23_P372834	-0.609	0.000	0.004	AQP1	aquaporin 1 (Colton blood group)
A_33_P3213419	-0.610	0.000	0.002	LOC100129447	uncharacterized LOC100129447
A_23_P40192	-0.610	0.000	0.001	CDH22	cadherin 22, type 2
A_33_P3355717	-0.610	0.006	0.030	ZFP36L1	zinc finger protein 36, C3H type-like 1
A_33_P3283906	-0.610	0.001	0.007	NIP7	nuclear import 7 homolog (S. cerevisiae)
A_21_P0008917	-0.611	0.000	0.005	XLOC_011676	BROAD Institute lincRNA (XLOC_011676), lincRNA [TCONS_00024354]
A_33_P3370076	-0.613	0.000	0.001	TFE3	transcription factor binding to IGHM enhancer 3
A_23_P213562	-0.613	0.000	0.001	F2R	coagulation factor II (thrombin) receptor
A_33_P3321678	-0.615	0.001	0.007	RNF180	ring finger protein 180
A_21_P0004621	-0.615	0.001	0.010	XLOC_005938	Q73NU6_TREDE Conserved domain protein, partial (6%) [THC2628112]
A_33_P3270636	-0.616	0.000	0.005	SHISA5	shisa homolog 5 (Xenopus laevis)
A_33_P3253672	-0.618	0.000	0.001	KCNH3	potassium voltage-gated channel, subfamily H (eag-related), member 3
A_33_P3344574	-0.619	0.000	0.001	SFTPA2	surfactant protein A2
A_21_P0014892	-0.620	0.004	0.023	LOC100506027	uncharacterized LOC100506027
A_33_P3255949	-0.620	0.000	0.001	TYMP	thymidine phosphorylase
A_19_P00321722	-0.621	0.000	0.002	XLOC_006555	BROAD Institute lincRNA (XLOC_006555), lincRNA [TCONS_00013220]
A_32_P159445	-0.624	0.000	0.001	IQSEC2	IQ motif and Sec7 domain 2
A_33_P3349552	-0.624	0.000	0.002	CASKIN1	CASK interacting protein 1
A_19_P00808072	-0.626	0.000	0.004	XLOC_011130	BROAD Institute lincRNA (XLOC_011130), lincRNA [TCONS_00022876]
A_33_P3352687	-0.629	0.000	0.004	LOC100133161	uncharacterized LOC100133161
A_33_P3383524	-0.630	0.000	0.002	LOC91948	uncharacterized LOC91948
A_32_P74409	-0.631	0.000	0.001	C11orf96	chromosome 11 open reading frame 96
A_19_P00329086	-0.631	0.000	0.001	XLOC_005832	BROAD Institute lincRNA (XLOC_005832), lincRNA [TCONS_00012277]
A_24_P203953	-0.632	0.001	0.009	LOC439951	uncharacterized LOC439951
A_21_P0002876	-0.632	0.006	0.030	XLOC_003245	BROAD Institute lincRNA (XLOC_003245), lincRNA [TCONS_00005826]
A_24_P280497	-0.632	0.000	0.004	FBRSL1	fibrosin-like 1
A_33_P3376762	-0.633	0.000	0.003	LOC388152	uncharacterized LOC388152
A_19_P00320749	-0.633	0.000	0.004	PVT1	Pvt1 oncogene (non-protein coding)
A_33_P3366903	-0.634	0.000	0.001	CHST6	carbohydrate (N-acetylglucosamine 6-O) sulfotransferase 6
A_33_P3287119	-0.635	0.001	0.007	FAM178B	family with sequence similarity 178, member B
A_23_P51679	-0.636	0.000	0.001	MEF2D	myocyte enhancer factor 2D
A_33_P3387756	-0.638	0.002	0.016	C20orf201	chromosome 20 open reading frame 201

A_24_P296508	-0.640	0.000	0.001	<i>SLC43A2</i>	solute carrier family 43, member 2
A_23_P76749	-0.642	0.000	0.002	<i>GALNTL1</i>	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase-like 1
A_33_P3347040	-0.643	0.000	0.001	<i>LOC100131094</i>	uncharacterized LOC100131094
A_21_P0007151	-0.643	0.000	0.002	<i>XLOC_009339</i>	DA270978 BRCAN2 Homo sapiens cDNA clone BRCAN2025386 5', mRNA sequence
A_33_P3287661	-0.645	0.005	0.026	<i>LOC100130430</i>	uncharacterized LOC100130430
A_33_P3394599	-0.646	0.005	0.026	<i>HMG20B</i>	high mobility group 20B
A_21_P0014803	-0.646	0.000	0.003	<i>LOC100652974</i>	superoxide dismutase [Cu-Zn]-like
A_32_P144342	-0.646	0.000	0.005	<i>PARP4</i>	poly (ADP-ribose) polymerase family, member 4
A_21_P0011354	-0.648	0.000	0.001	<i>XLOC_12_004844</i>	ALU1_HUMAN (P39188) Alu subfamily J sequence contamination warning entry, partial (8%) [THC2500351]
A_23_P16415	-0.648	0.000	0.005	<i>LRP3</i>	low density lipoprotein receptor-related protein 3
A_33_P3236798	-0.649	0.001	0.009	<i>SRMS</i>	src-related kinase lacking C-terminal regulatory tyrosine and N-terminal myristylation sites
A_23_P32404	-0.656	0.000	0.001	<i>ISG20</i>	interferon stimulated exonuclease gene 20kDa
A_23_P134433	-0.658	0.000	0.003	<i>EN2</i>	engrailed homeobox 2
A_19_P00319633	-0.664	0.000	0.002	<i>LOC100294145</i>	uncharacterized LOC100294145
A_33_P3327663	-0.668	0.002	0.012	<i>SUSD4</i>	sushi domain containing 4
A_33_P3247082	-0.671	0.000	0.002	<i>SLC6A10P</i>	solute carrier family 6 (neurotransmitter transporter, creatine), member 10, pseudogene
A_23_P109907	-0.673	0.000	0.002	<i>ILDR1</i>	immunoglobulin-like domain containing receptor 1
A_21_P0010088	-0.674	0.000	0.001	<i>LOC100130157</i>	uncharacterized LOC100130157
A_33_P3241489	-0.674	0.000	0.002	<i>LOC100505876</i>	uncharacterized LOC100505876
A_32_P60065	-0.674	0.000	0.001	<i>F2RL2</i>	coagulation factor II (thrombin) receptor-like 2
A_33_P3384710	-0.674	0.008	0.038	<i>C17orf63</i>	chromosome 17 open reading frame 63
A_33_P3350202	-0.674	0.001	0.006	<i>MOCS3</i>	molybdenum cofactor synthesis 3
A_21_P0001457	-0.675	0.000	0.001	<i>XLOC_000676</i>	zt79d07.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:728557 5', mRNA sequence [AA397625]
A_32_P207124	-0.677	0.000	0.003	<i>CT47A11</i>	cancer/testis antigen family 47, member A11
A_23_P115261	-0.677	0.004	0.023	<i>AGT</i>	angiotensinogen (serpin peptidase inhibitor, clade A, member 8)
A_21_P0000494	-0.677	0.000	0.002	<i>SNORA16B</i>	small nucleolar RNA, H/ACA box 16B
A_23_P69497	-0.680	0.000	0.002	<i>CLEC3B</i>	C-type lectin domain family 3, member B
A_33_P3272347	-0.681	0.000	0.001	<i>LOC100128107</i>	uncharacterized LOC100128107
A_33_P3294217	-0.682	0.000	0.001	<i>UTF1</i>	undifferentiated embryonic cell transcription factor 1
A_23_P66241	-0.684	0.000	0.001	<i>MT1M</i>	metallothionein 1M
A_33_P3235400	-0.685	0.000	0.002	<i>HDGF</i>	hepatoma-derived growth factor
A_21_P0003278	-0.685	0.000	0.004	<i>XLOC_003052</i>	BROAD Institute lincRNA (XLOC_003052), lincRNA [TCONS_00007118]
A_23_P154771	-0.685	0.000	0.001	<i>DUSP15</i>	dual specificity phosphatase 15
A_33_P3304312	-0.686	0.000	0.002	<i>CELF6</i>	CUGBP, Elav-like family member 6
A_33_P3276713	-0.686	0.000	0.002	<i>HGF</i>	hepatocyte growth factor (hepapoietin A; scatter factor)
A_33_P3326025	-0.687	0.000	0.005	<i>KANK3</i>	KN motif and ankyrin repeat domains 3
A_21_P0009926	-0.688	0.000	0.002	<i>XLOC_013436</i>	BROAD Institute lincRNA (XLOC_013436), lincRNA [TCONS_00028091]
A_21_P0011390	-0.690	0.006	0.029	<i>PRKXP1</i>	protein kinase, X-linked, pseudogene 1
A_23_P258381	-0.690	0.000	0.001	<i>SPSB4</i>	spla/ryanodine receptor domain and SOCS box containing 4
A_33_P3223678	-0.691	0.002	0.012	<i>LHX3</i>	LIM homeobox 3
A_21_P0005002	-0.691	0.000	0.002	<i>XLOC_005617</i>	BROAD Institute lincRNA (XLOC_005617), lincRNA [TCONS_00012087]
A_23_P163711	-0.692	0.000	0.003	<i>FAM57B</i>	family with sequence similarity 57, member B
A_21_P0006911	-0.692	0.002	0.014	<i>XLOC_008610</i>	BROAD Institute lincRNA (XLOC_008610), lincRNA [TCONS_00018332]
A_21_P0006569	-0.692	0.000	0.001	<i>XLOC_008047</i>	BROAD Institute lincRNA (XLOC_008047), lincRNA [TCONS_00017454]
A_24_P419028	-0.693	0.000	0.004	<i>MOP-1</i>	MOP-1

A_33_P3411848	-0.694	0.000	0.002	<i>CNFN</i>	cornifelin
A_33_P3301620	-0.699	0.001	0.010	<i>RNF32</i>	ring finger protein 32
A_33_P3271196	-0.700	0.002	0.012	<i>AMOTL1</i>	angiomin like 1
A_23_P164341	-0.700	0.000	0.001	<i>VAMP2</i>	vesicle-associated membrane protein 2 (synaptobrevin 2)
A_21_P0003886	-0.702	0.000	0.001	<i>XLOC_003863</i>	BROAD Institute lincRNA (XLOC_003863), lincRNA [TCONS_00009017]
A_21_P0014015	-0.702	0.000	0.002	<i>LOC100652963</i>	putative uncharacterized protein encoded by NCRNA00269-like
A_24_P37887	-0.704	0.000	0.004	<i>GPR150</i>	G protein-coupled receptor 150
A_33_P3261353	-0.705	0.001	0.008	<i>BCORP1</i>	BCL6 corepressor pseudogene 1
A_21_P0000760	-0.706	0.000	0.004	<i>LOC100526771</i>	uncharacterized LOC100526771
A_23_P107735	-0.708	0.000	0.001	<i>CD79A</i>	CD79a molecule, immunoglobulin-associated alpha
A_24_P338788	-0.708	0.000	0.002	<i>CSNK1A1L</i>	casein kinase 1, alpha 1-like
A_33_P3232038	-0.710	0.000	0.004	<i>RBAK-LOC389458</i>	RBAK-LOC389458 readthrough
A_21_P0007168	-0.710	0.002	0.014	<i>XLOC_009021</i>	Q2DDM0_ACICY MiaB-like tRNA modifying enzyme, partial (4%) [THC2607848]
A_33_P3210379	-0.711	0.000	0.002	<i>SCGB3A1</i>	secretoglobin, family 3A, member 1
A_33_P3454968	-0.714	0.000	0.001	<i>LOC645553</i>	uncharacterized LOC645553
A_33_P3209476	-0.714	0.000	0.001	<i>CCM2</i>	cerebral cavernous malformation 2
A_33_P3399443	-0.714	0.000	0.002	<i>SH3TC1</i>	SH3 domain and tetratricopeptide repeats 1
A_33_P3331882	-0.716	0.000	0.001	<i>CRTC1</i>	CREB regulated transcription coactivator 1
A_33_P3359223	-0.717	0.000	0.001	<i>C9orf173</i>	chromosome 9 open reading frame 173
A_33_P3288649	-0.720	0.000	0.004	<i>HOXA10</i>	homeobox A10
A_23_P78734	-0.722	0.000	0.001	<i>MYH14</i>	myosin, heavy chain 14, non-muscle
A_21_P0003384	-0.723	0.000	0.003	<i>XLOC_003631</i>	BROAD Institute lincRNA (XLOC_003631), lincRNA [TCONS_00007582]
A_24_P292470	-0.724	0.002	0.014	<i>UCP3</i>	uncoupling protein 3 (mitochondrial, proton carrier)
A_24_P83738	-0.725	0.000	0.001	<i>ASTN2</i>	astrotactin 2
A_33_P3209581	-0.727	0.000	0.002	<i>IQSEC3</i>	IQ motif and Sec7 domain 3
A_21_P0005878	-0.728	0.000	0.000	<i>XLOC_007171</i>	BROAD Institute lincRNA (XLOC_007171), lincRNA [TCONS_00015115]
A_33_P3273000	-0.731	0.000	0.001	<i>PTK2B</i>	PTK2B protein tyrosine kinase 2 beta
A_32_P103669	-0.731	0.000	0.001	<i>GOLGA6C</i>	golgin A6 family, member C
A_24_P275073	-0.735	0.000	0.001	<i>ADAMTS14</i>	ADAM metallopeptidase with thrombospondin type 1 motif, 14
A_33_P3313411	-0.735	0.000	0.002	<i>ARHGAP33</i>	Rho GTPase activating protein 33
A_23_P59099	-0.736	0.001	0.006	<i>OR11A1</i>	olfactory receptor, family 11, subfamily A, member 1
A_33_P3285354	-0.739	0.001	0.011	<i>C11orf95</i>	chromosome 11 open reading frame 95
A_33_P3395823	-0.739	0.001	0.009	<i>KCNQ2</i>	potassium voltage-gated channel, KQT-like subfamily, member 2
A_24_P135628	-0.739	0.000	0.001	<i>LOC100652762</i>	uncharacterized LOC100652762
A_24_P251599	-0.741	0.003	0.018	<i>CAV3</i>	caveolin 3
A_33_P3224020	-0.743	0.000	0.001	<i>ARAF2P</i>	v-raf murine sarcoma 3611 viral oncogene homolog 2, pseudogene
A_21_P0003493	-0.744	0.000	0.001	<i>XLOC_004050</i>	RST41900 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence [BG227980]
A_33_P3273534	-0.749	0.000	0.002	<i>KRT81</i>	keratin 81
A_21_P0000107	-0.750	0.005	0.027	<i>MTRNR2L7</i>	MT-RNR2-like 7
A_21_P0006395	-0.755	0.002	0.017	<i>XLOC_007858</i>	BROAD Institute lincRNA (XLOC_007858), lincRNA [TCONS_00016872]
A_23_P164927	-0.761	0.001	0.011	<i>SYNGR4</i>	synaptogyrin 4
A_33_P3324454	-0.761	0.000	0.001	<i>TPPI</i>	tripeptidyl peptidase I
A_19_P00800638	-0.761	0.000	0.001	<i>LOC100505875</i>	uncharacterized LOC100505875
A_21_P0005187	-0.761	0.003	0.020	<i>XLOC_005944</i>	BROAD Institute lincRNA (XLOC_005944), lincRNA [TCONS_00012836]
A_33_P3210848	-0.762	0.000	0.002	<i>ELFN1</i>	extracellular leucine-rich repeat and fibronectin type III domain containing 1

A_33_P3355266	-0.763	0.000	0.001	<i>TINAGL1</i>	tubulointerstitial nephritis antigen-like 1
A_19_P00318152	-0.765	0.001	0.009	<i>SNHG11</i>	small nucleolar RNA host gene 11
A_33_P3303031	-0.766	0.000	0.001	<i>FLJ40606</i>	uncharacterized LOC643549
A_21_P0007825	-0.766	0.000	0.001	<i>XLOC_009677</i>	BROAD Institute lincRNA (XLOC_009677), lincRNA [TCONS_00021084]
A_24_P57898	-0.773	0.000	0.005	<i>BHLHE23</i>	basic helix-loop-helix family, member e23
A_33_P3335682	-0.774	0.000	0.003	<i>PPP1R14A</i>	protein phosphatase 1, regulatory (inhibitor) subunit 14A
A_21_P0002619	-0.774	0.000	0.001	<i>XLOC_001747</i>	BROAD Institute lincRNA (XLOC_001747), lincRNA [TCONS_00004944]
A_21_P0009830	-0.776	0.000	0.001	<i>XLOC_013470</i>	BROAD Institute lincRNA (XLOC_013470), lincRNA [TCONS_00027906]
A_21_P0005571	-0.777	0.000	0.001	<i>XLOC_006188</i>	BROAD Institute lincRNA (XLOC_006188), lincRNA [TCONS_00014180]
A_24_P118376	-0.779	0.000	0.003	<i>CEACAM20</i>	carcinoembryonic antigen-related cell adhesion molecule 20
A_21_P0002932	-0.779	0.000	0.001	<i>XLOC_002580</i>	BROAD Institute lincRNA (XLOC_002580), lincRNA [TCONS_00005950]
A_21_P0011149	-0.782	0.000	0.004	<i>XLOC_12_003758</i>	BROAD Institute lincRNA (XLOC_12_003758), lincRNA [TCONS_12_00006892]
A_33_P3325497	-0.783	0.000	0.004	<i>FIBIN</i>	fin bud initiation factor homolog (zebrafish)
A_23_P132139	-0.784	0.000	0.001	<i>C21orf58</i>	chromosome 21 open reading frame 58
A_24_P152468	-0.785	0.000	0.002	<i>LOC100134663</i>	uncharacterized LOC100134663
A_33_P3238390	-0.785	0.000	0.001	<i>SETP20</i>	SET pseudogene 20
A_23_P48455	-0.786	0.000	0.001	<i>AMN</i>	amniotless homolog (mouse)
A_33_P3321507	-0.786	0.000	0.001	<i>TNRC18</i>	trinucleotide repeat containing 18
A_33_P3253634	-0.787	0.000	0.001	<i>LOC390660</i>	FLJ00317 protein
A_24_P256155	-0.790	0.001	0.006	<i>NKX1-2</i>	NK1 homeobox 2
A_33_P3807268	-0.791	0.000	0.002	<i>DNAJA1P5</i>	DnaJ (Hsp40) homolog, subfamily A, member 1 pseudogene 5
A_33_P3263851	-0.793	0.001	0.011	<i>FLJ46020</i>	FLJ46020 protein
A_33_P3279009	-0.795	0.000	0.003	<i>HMX1</i>	H6 family homeobox 1
A_33_P3219870	-0.795	0.000	0.001	<i>PNPLA2</i>	patatin-like phospholipase domain containing 2
A_19_P00317242	-0.795	0.000	0.001	<i>LOC388210</i>	apolipoporphins-like
A_21_P0011406	-0.796	0.000	0.001	<i>XLOC_12_004817</i>	ALU5_HUMAN (P39192) Alu subfamily SC sequence contamination warning entry, partial (5%) [THC2638933]
A_23_P42257	-0.800	0.001	0.007	<i>IER3</i>	immediate early response 3
A_24_P108738	-0.801	0.000	0.003	<i>SCARF2</i>	scavenger receptor class F, member 2
A_23_P303891	-0.803	0.000	0.001	<i>LCE1C</i>	late cornified envelope 1C
A_33_P3378707	-0.803	0.000	0.002	<i>LOC646214</i>	p21 protein (Cdc42/Rac)-activated kinase 2 pseudogene
A_24_P317450	-0.808	0.000	0.001	<i>OSTCP1</i>	oligosaccharyltransferase complex subunit pseudogene 1
A_33_P3292896	-0.808	0.000	0.001	<i>SFXN5</i>	sideroflexin 5
A_24_P232790	-0.810	0.000	0.001	<i>C14orf162</i>	chromosome 14 open reading frame 162
A_24_P659122	-0.811	0.004	0.024	<i>LOC401357</i>	uncharacterized LOC401357
A_33_P3219651	-0.811	0.000	0.001	<i>BMPER</i>	BMP binding endothelial regulator
A_23_P129629	-0.812	0.000	0.001	<i>MT3</i>	metallothionein 3
A_21_P0011914	-0.812	0.000	0.001	<i>XLOC_12_008009</i>	BROAD Institute lincRNA (XLOC_12_008009), lincRNA [TCONS_12_00014564]
A_33_P3419970	-0.819	0.001	0.006	<i>NPB</i>	neuropeptide B
A_33_P3279124	-0.820	0.000	0.001	<i>FAM21C</i>	family with sequence similarity 21, member C
A_21_P0000103	-0.820	0.000	0.001	<i>MTRNR2L3</i>	MT-RNR2-like 3
A_33_P3318946	-0.824	0.000	0.003	<i>HAPLN2</i>	hyaluronan and proteoglycan link protein 2
A_32_P34	-0.825	0.000	0.000	<i>LOC100131581</i>	uncharacterized LOC100131581
A_33_P3297930	-0.833	0.000	0.001	<i>COL8A2</i>	collagen, type VIII, alpha 2
A_21_P0014791	-0.834	0.005	0.027	<i>LOC100652804</i>	uncharacterized LOC100652804
A_23_P48307	-0.835	0.000	0.003	<i>PABPC3</i>	poly(A) binding protein, cytoplasmic 3

A_33_P3415859	-0.835	0.000	0.001	<i>NLR3</i>	NLR family, CARD domain containing 3
A_33_P3417222	-0.840	0.000	0.001	<i>CD72</i>	CD72 molecule
A_33_P3379886	-0.848	0.001	0.007	<i>FGF2</i>	fibroblast growth factor 2 (basic)
A_33_P3362153	-0.851	0.000	0.001	<i>TMEM238</i>	transmembrane protein 238
A_21_P0014422	-0.852	0.000	0.001	<i>LOC646513</i>	VLGN1945
A_21_P0012298	-0.852	0.000	0.001	<i>XLOC_12_009539</i>	BROAD Institute lincRNA (XLOC_12_009539), lincRNA [TCONS_12_00018033]
A_33_P3282978	-0.853	0.000	0.002	<i>BAALC</i>	brain and acute leukemia, cytoplasmic
A_21_P0002061	-0.855	0.000	0.002	<i>XLOC_002140</i>	BROAD Institute lincRNA (XLOC_002140), lincRNA [TCONS_00003313]
A_33_P3399064	-0.871	0.001	0.012	<i>RN5-8S1</i>	RNA, 5.8S ribosomal 1
A_21_P0003882	-0.874	0.000	0.000	<i>XLOC_003849</i>	BROAD Institute lincRNA (XLOC_003849), lincRNA [TCONS_00009003]
A_33_P3216448	-0.874	0.000	0.002	<i>COL11A2</i>	collagen, type XI, alpha 2
A_33_P3274009	-0.877	0.000	0.002	<i>LOC100132966</i>	uncharacterized LOC100132966
A_21_P0006274	-0.880	0.000	0.002	<i>XLOC_007725</i>	BROAD Institute lincRNA (XLOC_007725), lincRNA [TCONS_00016344]
A_23_P405282	-0.886	0.000	0.001	<i>MGC45922</i>	uncharacterized LOC284365
A_33_P3387561	-0.886	0.000	0.002	<i>OSCAR</i>	osteoclast associated, immunoglobulin-like receptor
A_19_P00321628	-0.893	0.000	0.001	<i>LOC100505687</i>	uncharacterized LOC100505687
A_21_P0012887	-0.902	0.000	0.002	<i>XLOC_12_011911</i>	ALU1_HUMAN (P39188) Alu subfamily J sequence contamination warning entry, partial (20%) [THC2501992]
A_24_P631848	-0.907	0.001	0.006	<i>LOC100132147</i>	uncharacterized LOC100132147
A_33_P3246613	-0.912	0.000	0.001	<i>CCDC78</i>	coiled-coil domain containing 78
A_21_P0006463	-0.912	0.000	0.001	<i>XLOC_008236</i>	Q3TS54_MOUSE In vitro fertilized eggs cDNA, RIKEN full-length enriched library, clone:7420485E05 product:zinc fi
A_33_P3399468	-0.914	0.000	0.000	<i>LOC728054</i>	uncharacterized LOC728054
A_21_P0009166	-0.914	0.000	0.002	<i>XLOC_012176</i>	BROAD Institute lincRNA (XLOC_012176), lincRNA [TCONS_00025167]
A_33_P3368560	-0.916	0.000	0.002	<i>AHSA2</i>	AHA1, activator of heat shock 90kDa protein ATPase homolog 2 (yeast)
A_33_P3384900	-0.918	0.000	0.001	<i>SNRPD2P2</i>	small nuclear ribonucleoprotein D2 pseudogene 2
A_33_P3291459	-0.918	0.000	0.005	<i>LOC100507547</i>	uncharacterized LOC100507547
A_21_P0000108	-0.918	0.001	0.010	<i>MTRNR2L8</i>	MT-RNR2-like 8
A_33_P3221129	-0.919	0.000	0.005	<i>LRRN4CL</i>	LRRN4 C-terminal like
A_33_P3235132	-0.920	0.000	0.001	<i>LOC400968</i>	uncharacterized LOC400968
A_33_P3263284	-0.925	0.000	0.003	<i>LOC100130238</i>	uncharacterized LOC100130238
A_24_P142495	-0.927	0.000	0.001	<i>KRTAPI-3</i>	keratin associated protein 1-3
A_33_P3338152	-0.927	0.000	0.002	<i>HIF3A</i>	hypoxia inducible factor 3, alpha subunit
A_33_P3411315	-0.930	0.000	0.000	<i>KRTAP3-3</i>	keratin associated protein 3-3
A_33_P3318861	-0.933	0.000	0.001	<i>DYTN</i>	dystrotelin
A_33_P3211078	-0.934	0.001	0.010	<i>HMG2</i>	high mobility group AT-hook 2
A_21_P0011522	-0.937	0.000	0.002	<i>XLOC_12_005692</i>	BROAD Institute lincRNA (XLOC_12_005692), lincRNA [TCONS_12_00010603]
A_33_P3218797	-0.938	0.000	0.001	<i>PPDPF</i>	pancreatic progenitor cell differentiation and proliferation factor homolog (zebrafish)
A_33_P3274134	-0.938	0.000	0.002	<i>TMEM151B</i>	transmembrane protein 151B
A_24_P323114	-0.939	0.001	0.008	<i>ANXA2P3</i>	annexin A2 pseudogene 3
A_23_P89431	-0.941	0.008	0.036	<i>CCL2</i>	chemokine (C-C motif) ligand 2
A_24_P384397	-0.942	0.000	0.002	<i>RAVER1</i>	ribonucleoprotein, PTB-binding 1
A_24_P128524	-0.944	0.000	0.001	<i>ICMT</i>	isoprenylcysteine carboxyl methyltransferase
A_33_P3331687	-0.945	0.000	0.001	<i>GPSM1</i>	G-protein signaling modulator 1
A_21_P0013768	-0.951	0.000	0.001	<i>XLOC_12_015542</i>	BROAD Institute lincRNA (XLOC_12_015542), lincRNA [TCONS_12_00030232]
A_24_P917866	-0.957	0.000	0.003	<i>SET</i>	SET nuclear oncogene
A_33_P3245674	-0.959	0.000	0.001	<i>ZNF329</i>	zinc finger protein 329

A_33_P3269844	-0.973	0.000	0.001	<i>LRRC26</i>	leucine rich repeat containing 26
A_19_P00317447	-0.977	0.000	0.003	<i>XLOC_002736</i>	uncharacterized LOC100506377
A_24_P368943	-0.981	0.000	0.002	<i>EVXI</i>	even-skipped homeobox 1
A_19_P00801735	-0.982	0.000	0.001	<i>XLOC_12_013783</i>	BROAD Institute lincRNA (XLOC_12_013783), lincRNA [TCONS_12_00026509]
A_21_P0011116	-0.993	0.001	0.007	<i>FEM1A</i>	fem-1 homolog a (C. elegans)
A_23_P78526	-0.994	0.000	0.002	<i>CEACAM19</i>	carcinoembryonic antigen-related cell adhesion molecule 19
A_33_P3239143	-0.995	0.001	0.009	<i>ZNF497</i>	zinc finger protein 497
A_23_P367071	-0.996	0.000	0.003	<i>UBE2DNL</i>	ubiquitin-conjugating enzyme E2D N-terminal like (pseudogene)
A_33_P3308347	-1.002	0.000	0.000	<i>ADAMTS8</i>	ADAM metallopeptidase with thrombospondin type 1 motif, 8
A_33_P3308626	-1.013	0.000	0.002	<i>MON1B</i>	MON1 homolog B (yeast)
A_21_P0009377	-1.016	0.000	0.001	<i>XLOC_012097</i>	BROAD Institute lincRNA (XLOC_012097), lincRNA [TCONS_00025825]
A_33_P3250148	-1.020	0.000	0.001	<i>SP8</i>	Sp8 transcription factor
A_21_P0005309	-1.036	0.000	0.001	<i>XLOC_006446</i>	BROAD Institute lincRNA (XLOC_006446), lincRNA [TCONS_00013173]
A_23_P94800	-1.053	0.000	0.000	<i>S100A4</i>	S100 calcium binding protein A4
A_33_P3418194	-1.066	0.000	0.005	<i>LYNX1</i>	Ly6/neurotoxin 1
A_33_P3275835	-1.083	0.000	0.000	<i>TOR2A</i>	torsin family 2, member A
A_21_P0009341	-1.094	0.001	0.006	<i>LOC645638</i>	WDNM1-like pseudogene
A_23_P350059	-1.098	0.000	0.002	<i>PFN1P2</i>	profilin 1 pseudogene 2
A_21_P0014808	-1.108	0.000	0.002	<i>LOC100288420</i>	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 4, 15kDa pseudogene
A_33_P3667484	-1.111	0.000	0.001	<i>LOC648740</i>	actin, gamma 2, smooth muscle, enteric pseudogene
A_23_P93282	-1.117	0.000	0.001	<i>HIST1H3J</i>	histone cluster 1, H3j
A_21_P0011867	-1.124	0.000	0.002	<i>XLOC_12_007656</i>	BROAD Institute lincRNA (XLOC_12_007656), lincRNA [TCONS_12_00014098]
A_23_P26468	-1.128	0.000	0.001	<i>RHBDL1</i>	rhomboid, veinlet-like 1 (Drosophila)
A_21_P0004484	-1.131	0.000	0.001	<i>LOC255167</i>	uncharacterized LOC255167
A_21_P0013961	-1.142	0.001	0.010	<i>LOC100506447</i>	uncharacterized protein LOC100506447
A_23_P255827	-1.148	0.000	0.002	<i>FKSG2</i>	tumor protein, translationally-controlled 1 pseudogene
A_33_P3397150	-1.157	0.000	0.003	<i>FLJ22184</i>	putative uncharacterized protein FLJ22184
A_19_P00801042	-1.157	0.000	0.003	<i>ZNF90</i>	zinc finger protein 90
A_21_P0004121	-1.166	0.000	0.001	<i>XLOC_004774</i>	BROAD Institute lincRNA (XLOC_004774), lincRNA [TCONS_00009634]
A_33_P3222769	-1.167	0.000	0.002	<i>PRR25</i>	proline rich 25
A_33_P3495962	-1.193	0.000	0.001	<i>SNORA71A</i>	small nucleolar RNA, H/ACA box 71A
A_21_P0005262	-1.201	0.000	0.004	<i>XLOC_006260</i>	BROAD Institute lincRNA (XLOC_006260), lincRNA [TCONS_00013082]
A_33_P3382944	-1.211	0.000	0.003	<i>YJEFN3</i>	YjeF N-terminal domain containing 3
A_33_P3318444	-1.216	0.000	0.001	<i>RNF222</i>	ring finger protein 222
A_21_P0001811	-1.228	0.000	0.004	<i>XLOC_001320</i>	BROAD Institute lincRNA (XLOC_001320), lincRNA [TCONS_00003548]
A_24_P56689	-1.230	0.000	0.002	<i>ZNF205</i>	zinc finger protein 205
A_24_P831309	-1.231	0.000	0.001	<i>C1orf229</i>	chromosome 1 open reading frame 229
A_24_P307289	-1.240	0.000	0.002	<i>TMEM95</i>	transmembrane protein 95
A_33_P3349252	-1.258	0.000	0.001	<i>DKFZP547L112</i>	uncharacterized protein DKFZp547L112
A_21_P0007137	-1.346	0.000	0.001	<i>XLOC_009023</i>	long intergenic non-protein coding RNA 1150
A_24_P14731	-1.354	0.000	0.002	<i>PCSK1N</i>	proprotein convertase subtilisin/kexin type 1 inhibitor
A_33_P3403082	-1.359	0.000	0.001	<i>LINC00176</i>	long intergenic non-protein coding RNA 176
A_21_P0000109	-1.374	0.000	0.001	<i>MTRNR2L9</i>	MT-RNR2-like 9 (pseudogene)
A_23_P59888	-1.378	0.000	0.001	<i>NACAPI</i>	nascent-polypeptide-associated complex alpha polypeptide pseudogene 1
A_33_P3255131	-1.387	0.000	0.001	<i>KCTD19</i>	potassium channel tetramerisation domain containing 19

A_19_P00316159	-1.411	0.000	0.002	<i>XLOC_12_007876</i>	BROAD Institute lincRNA (XLOC_12_007876), lincRNA [TCONS_12_00015692]
A_24_P369232	-1.418	0.000	0.001	<i>CCDC3</i>	coiled-coil domain containing 3
A_21_P0008252	-1.523	0.000	0.004	<i>XLOC_010588</i>	BROAD Institute lincRNA (XLOC_010588), lincRNA [TCONS_00022267]
A_23_P68910	-1.552	0.001	0.009	<i>SSTR3</i>	somatostatin receptor 3
A_23_P140527	-1.556	0.000	0.002	<i>FOXB1</i>	forkhead box B1
A_32_P148345	-1.600	0.000	0.001	<i>ANXA2</i>	annexin A2
A_23_P66635	-1.890	0.000	0.004	<i>CCL11</i>	chemokine (C-C motif) ligand 11

Supplementary Table S8 Comparison of 1,25(OH)₂D₃-regulated genes in NFs and CAFs

Genes exclusively regulated by 1,25(OH)₂D₃ in NFs (538 genes)	Genes exclusively regulated by 1,25(OH)₂D₃ in CAFs (1069 genes)	Genes commonly regulated by 1,25(OH)₂D₃ in NFs and CAFs (416 genes)	Genes inversely regulated by 1,25(OH)₂D₃ in NFs and CAFs (4 genes)
<i>CILP</i>	<i>RGS2</i>	<i>CYP24A1</i>	<i>CASKIN1</i>
<i>FIGF</i>	<i>RARRES2</i>	<i>CH25H</i>	<i>SLC2A5</i>
<i>IGFBP2</i>	<i>DDIT4</i>	<i>IGFLR1</i>	<i>CRTC1</i>
<i>CRIP1</i>	<i>BMP6</i>	<i>CHRD1</i>	<i>ALDH1A1</i>
<i>LOC100652760</i>	<i>IGFL3</i>	<i>CLMN</i>	
<i>OAF</i>	<i>CHODL</i>	<i>TMEM37</i>	
<i>NFE2</i>	<i>LIMCH1</i>	<i>EFTUD1</i>	
<i>DPT</i>	<i>SLA</i>	<i>OSR2</i>	
<i>CYP3A7</i>	<i>XLOC_013952</i>	<i>NPR3</i>	
<i>KIAA1199</i>	<i>ANGPTL4</i>	<i>POSTN</i>	
<i>GDF6</i>	<i>OSR1</i>	<i>G0S2</i>	
<i>SLPI</i>	<i>XLOC_12_014504</i>	<i>ATP1A2</i>	
<i>F11R</i>	<i>MALL</i>	<i>ROM1</i>	
<i>MRPS6</i>	<i>GREM2</i>	<i>NID2</i>	
<i>RBP4</i>	<i>TLR4</i>	<i>ATP1B1</i>	
<i>NEK10</i>	<i>LAMA3</i>	<i>CD82</i>	
<i>CYP3A5</i>	<i>CLCF1</i>	<i>C15orf48</i>	
<i>SLITRK6</i>	<i>GCLC</i>	<i>IGFBP3</i>	
<i>NOV</i>	<i>ALPL</i>	<i>HMCN1</i>	
<i>CKB</i>	<i>PREB</i>	<i>SEMA3B</i>	
<i>SPNS2</i>	<i>FAM105A</i>	<i>TNFSF13B</i>	
<i>XLOC_005935</i>	<i>LAMA4</i>	<i>XLOC_006850</i>	
<i>SYT7</i>	<i>TGFB2</i>	<i>IDH2</i>	
<i>SCARA3</i>	<i>SERPINB6</i>	<i>LGALS9C</i>	
<i>NPTX2</i>	<i>LBH</i>	<i>IGF1</i>	
<i>BTC</i>	<i>XLOC_12_009140</i>	<i>TIMP3</i>	
<i>GRB14</i>	<i>RGS10</i>	<i>ZFP36</i>	
<i>C15orf27</i>	<i>CA2</i>	<i>HSD11B1</i>	
<i>PROCR</i>	<i>ANGPTL1</i>	<i>CD248</i>	
<i>EFNB2</i>	<i>PELI2</i>	<i>RARRES1</i>	
<i>ELN</i>	<i>LOC285141</i>	<i>THBD</i>	
<i>ANO3</i>	<i>RPS6KA2</i>	<i>IGFBP6</i>	
<i>AKR1C1</i>	<i>C2CD2</i>	<i>LOC728392</i>	
<i>ITGB8</i>	<i>EPHA4</i>	<i>FBLN2</i>	
<i>SIPA1L2</i>	<i>TRAPPC6A</i>	<i>SBSN</i>	
<i>GPR126</i>	<i>GABRE</i>	<i>IL7R</i>	
<i>NTF3</i>	<i>LRRC8D</i>	<i>FHOD3</i>	
<i>SULT1C2</i>	<i>GP9</i>	<i>DCLK1</i>	
<i>ADCY4</i>	<i>BRD7</i>	<i>MFI2</i>	
<i>C10orf114</i>	<i>TRAM1</i>	<i>FAM20A</i>	
<i>MARCKSL1</i>	<i>AGPAT9</i>	<i>SEMA3C</i>	
<i>AADA4</i>	<i>DDX26B</i>	<i>MAPK13</i>	
<i>FN1</i>	<i>KLF11</i>	<i>SLC5A3</i>	
<i>GDNF</i>	<i>COL18A1</i>	<i>SERPINE2</i>	
<i>GGCX</i>	<i>GJA1</i>	<i>SLC1A1</i>	
<i>GULP1</i>	<i>RAB9B</i>	<i>CLGN</i>	
<i>DIRC3</i>	<i>EIF3E</i>	<i>CXCL12</i>	
<i>CETN2</i>	<i>XLOC_12_012847</i>	<i>TGFB3</i>	
<i>KCNJ2</i>	<i>ISLR</i>	<i>CITED4</i>	
<i>XLOC_001215</i>	<i>PAG1</i>	<i>EEPDI</i>	
<i>SEMA5A</i>	<i>BCAT1</i>	<i>FZD1</i>	
<i>GNA14</i>	<i>ANKRD29</i>	<i>AOX1</i>	
<i>SMTNL2</i>	<i>C7orf69</i>	<i>GDPD5</i>	
<i>ITPR3</i>	<i>ELFN2</i>	<i>RSPO2</i>	
<i>BCHE</i>	<i>SSBP2</i>	<i>SLC4A7</i>	

<i>EBF1</i>	<i>TUB</i>	<i>SMPD3</i>
<i>LOC100505702</i>	<i>SLC38A1</i>	<i>RDH10</i>
<i>FRAS1</i>	<i>STAU2</i>	<i>LXN</i>
<i>TBC1D2</i>	<i>THSD4</i>	<i>APBB1IP</i>
<i>ABCC9</i>	<i>GRK5</i>	<i>KLF4</i>
<i>FMO2</i>	<i>TNFAIP6</i>	<i>QPCT</i>
<i>MGP</i>	<i>HSPG2</i>	<i>NIPAL4</i>
<i>CCDC85B</i>	<i>PRNP</i>	<i>CDH6</i>
<i>SCG5</i>	<i>JDP2</i>	<i>PGD</i>
<i>KCNE4</i>	<i>SLC25A20</i>	<i>ANO1</i>
<i>CD68</i>	<i>PSIP1</i>	<i>MFSD6</i>
<i>HRSP12</i>	<i>APOL6</i>	<i>RHOA</i>
<i>SULF1</i>	<i>TMEM64</i>	<i>G6PD</i>
<i>LOC100507632</i>	<i>PHGDH</i>	<i>SERINC2</i>
<i>RELT</i>	<i>GADD45A</i>	<i>VGLL3</i>
<i>LOC100652790</i>	<i>TCEA2</i>	<i>HSD17B2</i>
<i>MXRA5</i>	<i>NT5DC1</i>	<i>ADHFE1</i>
<i>ABHD5</i>	<i>TTC35</i>	<i>GUCY1A3</i>
<i>SCN1A</i>	<i>FLJ46906</i>	<i>PARM1</i>
<i>EPHB6</i>	<i>IVNSIABP</i>	<i>CDC42EP3</i>
<i>LOC441268</i>	<i>CREG1</i>	<i>KAZALD1</i>
<i>SFRP1</i>	<i>CYB5A</i>	<i>HAND2</i>
<i>C4orf46</i>	<i>SIX4</i>	<i>PDLIM1</i>
<i>PCNXL2</i>	<i>C6orf228</i>	<i>TMEM200A</i>
<i>LMO4</i>	<i>SLC25A36</i>	<i>PLEKHA6</i>
<i>SPTSSA</i>	<i>PCK2</i>	<i>DPP4</i>
<i>CPA4</i>	<i>C6orf48</i>	<i>CRLF1</i>
<i>AVP11</i>	<i>JMY</i>	<i>ENOX1</i>
<i>PTX3</i>	<i>PTPRM</i>	<i>VEGFA</i>
<i>CCBE1</i>	<i>AHR</i>	<i>LOX</i>
<i>GCNT1</i>	<i>FAIM2</i>	<i>CLIC6</i>
<i>AMOTL2</i>	<i>ZNF770</i>	<i>KCNJ8</i>
<i>RAB8B</i>	<i>EPB41L4A-AS1</i>	<i>C4B</i>
<i>VEGFC</i>	<i>GCHFR</i>	<i>LRRC8A</i>
<i>LINC00340</i>	<i>TSPAN9</i>	<i>NANOS1</i>
<i>RECK</i>	<i>ADAM15</i>	<i>GLT25D2</i>
<i>SSH2</i>	<i>SRGAP1</i>	<i>C13orf15</i>
<i>SYPL2</i>	<i>TSEN15</i>	<i>LAMB3</i>
<i>NPC1</i>	<i>ULK2</i>	<i>ITPR1</i>
<i>ADAMTSL1</i>	<i>UNKL</i>	<i>SRRM3</i>
<i>TMTC4</i>	<i>C4orf32</i>	<i>AKR1CL1</i>
<i>ADD3</i>	<i>AGPAT4-IT1</i>	<i>NDRG1</i>
<i>TRANK1</i>	<i>ELL2</i>	<i>SIX1</i>
<i>LOC100507303</i>	<i>SPECC1</i>	<i>PTGIS</i>
<i>LY96</i>	<i>FAS</i>	<i>ATP2B1</i>
<i>LOC283104</i>	<i>MOCOS</i>	<i>BCL2</i>
<i>CTSB</i>	<i>ISOC1</i>	<i>DPYD</i>
<i>CAPN3</i>	<i>AICF</i>	<i>DMKN</i>
<i>XRCC6BP1</i>	<i>LOC283663</i>	<i>NDRG4</i>
<i>RSPO3</i>	<i>HIF1A</i>	<i>SLC24A3</i>
<i>GRHL1</i>	<i>SRXN1</i>	<i>CCDC51</i>
<i>PLA2G16</i>	<i>IARS</i>	<i>NINJ1</i>
<i>S100P</i>	<i>SMAD6</i>	<i>WSB1</i>
<i>MATN2</i>	<i>HMGN4</i>	<i>SERPING1</i>
<i>SERPINB9</i>	<i>SLC27A6</i>	<i>RAVER2</i>
<i>MFAP5</i>	<i>PLXND1</i>	<i>SLC31A1</i>
<i>DCBLD1</i>	<i>MMP1</i>	<i>MYC</i>
<i>CYP1B1</i>	<i>SLC38A2</i>	<i>C1orf151-NBL1</i>
<i>TSPAN3</i>	<i>KHDRBS3</i>	<i>CFB</i>
<i>XLOC_002759</i>	<i>MARCKS</i>	<i>GPRC5B</i>
<i>TNFRSF11B</i>	<i>LACTB2</i>	<i>MAP3K4</i>

<i>TWIST2</i>	<i>SLC22A15</i>	<i>SLMO1</i>
<i>GPR133</i>	<i>TAPBP1</i>	<i>MIR100HG</i>
<i>ID1</i>	<i>RNASE4</i>	<i>FAM3C</i>
<i>PKD1L2</i>	<i>NCOA1</i>	<i>XLOC_012044</i>
<i>TRIOBP</i>	<i>IQCK</i>	<i>FAM107B</i>
<i>TSPAN18</i>	<i>ZNF295</i>	<i>FAM86C1</i>
<i>PPP3CA</i>	<i>SAR1A</i>	<i>COL14A1</i>
<i>IGFBP4</i>	<i>EXOC1</i>	<i>LOC100507165</i>
<i>XLOC_12_013149</i>	<i>BTG1</i>	<i>GUCY1B3</i>
<i>PTN</i>	<i>FOXF1</i>	<i>C2orf89</i>
<i>REEP6</i>	<i>LOC100507420</i>	<i>PLCD4</i>
<i>PPL</i>	<i>FOXK1</i>	<i>PTGER3</i>
<i>LOC100129387</i>	<i>FBXO15</i>	<i>HSD17B6</i>
<i>RAPH1</i>	<i>ANKRD13B</i>	<i>NAAA</i>
<i>SNORA64</i>	<i>TIGD2</i>	<i>SLC40A1</i>
<i>SPP1</i>	<i>CAPZB</i>	<i>GEM</i>
<i>CD97</i>	<i>BMF</i>	<i>DHRS3</i>
<i>MET</i>	<i>HAAO</i>	<i>FLJ10661</i>
<i>XLOC_12_015034</i>	<i>CHI3L1</i>	<i>ANKRD35</i>
<i>TNFRSF21</i>	<i>AIG1</i>	<i>TNXB</i>
<i>H19</i>	<i>ALDH2</i>	<i>FAM92A1</i>
<i>XRCC4</i>	<i>TMEM91</i>	<i>MAN1A1</i>
<i>IMPA2</i>	<i>XLOC_003881</i>	<i>CIRBP</i>
<i>BMP2K</i>	<i>C6orf97</i>	<i>AVIL</i>
<i>PAPSS1</i>	<i>AHCYL1</i>	<i>FZD8</i>
<i>FEZ2</i>	<i>LOC647979</i>	<i>AGPAT4</i>
<i>IGSF10</i>	<i>VGLL4</i>	<i>CYP2S1</i>
<i>OSBPL9</i>	<i>PGM2L1</i>	<i>FMOD</i>
<i>TMEM164</i>	<i>SLC1A5</i>	<i>MEX3A</i>
<i>CDO1</i>	<i>HSPB11</i>	<i>CXCL14</i>
<i>ASPA</i>	<i>SWAP70</i>	<i>ANO4</i>
<i>TSTD1</i>	<i>LOC375190</i>	<i>PTMA</i>
<i>LOC254057</i>	<i>PKD2</i>	<i>H2BFM</i>
<i>OLA1</i>	<i>CCDC122</i>	<i>SOX4</i>
<i>PTPRD</i>	<i>PPAPDC1B</i>	<i>XLOC_010947</i>
<i>RPH3AL</i>	<i>MEIS1</i>	<i>XLOC_12_012605</i>
<i>ACYP1</i>	<i>LRRC1</i>	<i>CGREF1</i>
<i>C1orf56</i>	<i>PCOLCE</i>	<i>DPYSL3</i>
<i>WWC1</i>	<i>THOC3</i>	<i>GATA6</i>
<i>XLOC_12_013734</i>	<i>IDH1</i>	<i>XLOC_003784</i>
<i>NHSL1</i>	<i>SLC16A2</i>	<i>PNMA2</i>
<i>NMUR1</i>	<i>MEX3B</i>	<i>LSAMP</i>
<i>ARL4C</i>	<i>SAT1</i>	<i>C9orf103</i>
<i>STEAP2</i>	<i>CCDC90B</i>	<i>CTSD</i>
<i>XLOC_12_003021</i>	<i>PTGER1</i>	<i>FGD4</i>
<i>ZNF385A</i>	<i>PDE2A</i>	<i>BDNF</i>
<i>SNORA12</i>	<i>ZFHX4</i>	<i>ITGBL1</i>
<i>RASGRP2</i>	<i>H3F3A</i>	<i>LOC646014</i>
<i>C7orf41</i>	<i>FLJ35776</i>	<i>BEX2</i>
<i>TTC12</i>	<i>PAPPA</i>	<i>METRNL</i>
<i>PRRX1</i>	<i>EXOSC2</i>	<i>C17orf72</i>
<i>POLR1E</i>	<i>OSBPL1A</i>	<i>HNMT</i>
<i>PLAA</i>	<i>TP53INP1</i>	<i>MCAM</i>
<i>CES1</i>	<i>RUSC2</i>	<i>GLTSCR2</i>
<i>NUDT21</i>	<i>BNIP3L</i>	<i>SLC8A1</i>
<i>WEE1</i>	<i>MAP3K1</i>	<i>FSTL3</i>
<i>NEDD4L</i>	<i>TMEM51</i>	<i>RAI2</i>
<i>ARNT2</i>	<i>XLOC_12_011027</i>	<i>GPX3</i>
<i>SOCS3</i>	<i>SLC22A4</i>	<i>LOC100506119</i>
<i>CST3</i>	<i>DDIT3</i>	<i>SCOC</i>
<i>LOC100131607</i>	<i>C7orf40</i>	<i>PIEZO2</i>

<i>PLAC9</i>	<i>LOC100130417</i>	<i>VPS13A</i>
<i>HNRNPA1L2</i>	<i>RIN3</i>	<i>NALCN</i>
<i>MYOC</i>	<i>PTCH1</i>	<i>SLC25A4</i>
<i>DKFZp547G183</i>	<i>RIN2</i>	<i>LOC400550</i>
<i>KLHDC4</i>	<i>BEND7</i>	<i>FAM86B2</i>
<i>ELTD1</i>	<i>DOK6</i>	<i>HSD17B8</i>
<i>C16orf74</i>	<i>OLFML3</i>	<i>TP53TG1</i>
<i>EPB41L3</i>	<i>MITF</i>	<i>TNFRSF12A</i>
<i>FAM89A</i>	<i>ZNF853</i>	<i>SCARNA17</i>
<i>SLC38A5</i>	<i>TXNDC5</i>	<i>ENOSF1</i>
<i>OSBPL3</i>	<i>RPS23</i>	<i>C7orf29</i>
<i>COMP</i>	<i>ACAA2</i>	<i>TRAK1</i>
<i>CWC15</i>	<i>FZD7</i>	<i>PHF10</i>
<i>TMEM132A</i>	<i>GYG2</i>	<i>ID2</i>
<i>GNG10</i>	<i>PTBP3</i>	<i>COL16A1</i>
<i>METTL21A</i>	<i>SYNPO</i>	<i>CABLES1</i>
<i>SRSF6</i>	<i>ZFPM2</i>	<i>SMPDL3A</i>
<i>XLOC_000527</i>	<i>SLC5A6</i>	<i>XPOT</i>
<i>LSP1</i>	<i>TTC39C</i>	<i>XLOC_011248</i>
<i>PDE3B</i>	<i>MAP7D3</i>	<i>BRIX1</i>
<i>EIF4A1</i>	<i>KCTD20</i>	<i>SIRPA</i>
<i>SLC48A1</i>	<i>XLOC_003501</i>	<i>CACNB2</i>
<i>FLJ35024</i>	<i>GTF2IRD2</i>	<i>LOC100506451</i>
<i>PPIF</i>	<i>CCBL2</i>	<i>RNF146</i>
<i>RNF208</i>	<i>ITGA1</i>	<i>LOC388796</i>
<i>XLOC_12_004315</i>	<i>TES</i>	<i>ZNF468</i>
<i>LOC728978</i>	<i>CELSR1</i>	<i>EEA1</i>
<i>SNHG8</i>	<i>SMAD7</i>	<i>LOC400043</i>
<i>NME5</i>	<i>C1orf54</i>	<i>STEAP1B</i>
<i>XLOC_12_007271</i>	<i>PMEP1</i>	<i>BMP4</i>
<i>LOC283392</i>	<i>VIPR2</i>	<i>RAB27B</i>
<i>EHBP1</i>	<i>CERS6</i>	<i>HLA-DPB1</i>
<i>TFAM</i>	<i>TMEM176B</i>	<i>TMEM79</i>
<i>CXCL16</i>	<i>MBD4</i>	<i>SLAH1</i>
<i>RPL39</i>	<i>DLG1</i>	<i>PRKDC</i>
<i>CDK4</i>	<i>PIP5K1I</i>	<i>AUTS2</i>
<i>CCDC125</i>	<i>NSMCE1</i>	<i>LOC100131564</i>
<i>HNRNPF</i>	<i>ANTXR2</i>	<i>TP53I11</i>
<i>LOC100288292</i>	<i>MTHFS</i>	<i>VAMP8</i>
<i>MTMR12</i>	<i>PSMB8</i>	<i>DIAPH3</i>
<i>XLOC_011226</i>	<i>FOXP1</i>	<i>FIGNL2</i>
<i>DNAJC30</i>	<i>NUDT2</i>	<i>TNFAIP8</i>
<i>RBM3</i>	<i>ENDOV</i>	<i>TPM3</i>
<i>B3GNT2</i>	<i>CPZ</i>	<i>STIM2</i>
<i>XLOC_12_011987</i>	<i>C5orf30</i>	<i>LOC404266</i>
<i>XLOC_12_013189</i>	<i>PGK1</i>	<i>SFTA1P</i>
<i>CNTNAP3B</i>	<i>SLC35D2</i>	<i>XLOC_012457</i>
<i>MYCBP</i>	<i>HSDL2</i>	<i>KCNH3</i>
<i>FBXL19-AS1</i>	<i>EXOSC9</i>	<i>NOP56</i>
<i>MKI67IP</i>	<i>REXO2</i>	<i>XLOC_12_007767</i>
<i>CATSPER2</i>	<i>HERPUD1</i>	<i>SLC7A8</i>
<i>MAP9</i>	<i>ZFAND5</i>	<i>TPM4</i>
<i>HOXD13</i>	<i>NOP16</i>	<i>SMAD1</i>
<i>EIF4A2</i>	<i>XLOC_006513</i>	<i>BHLHE41</i>
<i>FOXO3</i>	<i>C4A</i>	<i>HIF3A</i>
<i>PCDHB9</i>	<i>H2AFY2</i>	<i>TNRC6C</i>
<i>UAP1L1</i>	<i>CARD10</i>	<i>LOC100652762</i>
<i>WDR18</i>	<i>TXNRD1</i>	<i>CCND2</i>
<i>TEP1</i>	<i>ZRANB2</i>	<i>NES</i>
<i>VIM</i>	<i>CYB5R2</i>	<i>SNORD114-28</i>
<i>AHCYL2</i>	<i>GRPEL2</i>	<i>FGFR1</i>

<i>C14orf132</i>	<i>GSR</i>	<i>C20orf27</i>
<i>NFATC4</i>	<i>WWC3</i>	<i>CT47A11</i>
<i>CCDC68</i>	<i>KIAA1908</i>	<i>ARMCX3</i>
<i>LOC100507312</i>	<i>AKR7A3</i>	<i>SYNE1</i>
<i>SLC6A13</i>	<i>GLI3</i>	<i>FCER1G</i>
<i>ATHL1</i>	<i>DENND4C</i>	<i>SH3KBP1</i>
<i>NAGA</i>	<i>MDK</i>	<i>LAMA1</i>
<i>TIAM2</i>	<i>TTC32</i>	<i>CSPG4</i>
<i>SEPT6</i>	<i>NUS1</i>	<i>LOC100128714</i>
<i>EVC</i>	<i>WDFY1</i>	<i>LRP4</i>
<i>SEPW1</i>	<i>NMT2</i>	<i>TMEM158</i>
<i>FAM65C</i>	<i>IFRD1</i>	<i>ACTR2</i>
<i>PGRMC2</i>	<i>XLOC_013929</i>	<i>ANKRD12</i>
<i>SYAP1</i>	<i>CLIP1</i>	<i>AHNAK2</i>
<i>ADORA1</i>	<i>SLC13A3</i>	<i>FBXO2</i>
<i>MBOAT1</i>	<i>PDE5A</i>	<i>ST3GAL5</i>
<i>MICB</i>	<i>FLRT2</i>	<i>XLOC_005617</i>
<i>ARHGEF37</i>	<i>IMPACT</i>	<i>FGF2</i>
<i>SNORD114-21</i>	<i>SNORA48</i>	<i>SNAR-A3</i>
<i>LOC100506053</i>	<i>SNHG5</i>	<i>STARD13</i>
<i>XLOC_004710</i>	<i>GAA</i>	<i>IL8</i>
<i>LPCAT3</i>	<i>CNTNAP3</i>	<i>SOCS1</i>
<i>LOC654433</i>	<i>PARVB</i>	<i>MBP</i>
<i>C6orf174</i>	<i>MEGF6</i>	<i>MEF2D</i>
<i>XLOC_12_013467</i>	<i>PLEKHG4</i>	<i>PTPRF</i>
<i>ADAM23</i>	<i>EXOC6</i>	<i>PTPRN2</i>
<i>SLC2A9</i>	<i>ELMOD2</i>	<i>SNAR-B2</i>
<i>XLOC_12_014549</i>	<i>PALM</i>	<i>CNN2</i>
<i>XLOC_002473</i>	<i>CCT2</i>	<i>IQSEC2</i>
<i>RHOBTB2</i>	<i>XLOC_12_014711</i>	<i>SNAR-H</i>
<i>COL5A1</i>	<i>SLC35F2</i>	<i>IL13RA2</i>
<i>SNAR-G1</i>	<i>CYHR1</i>	<i>CASK</i>
<i>TPCN1</i>	<i>LRCH2</i>	<i>SLC9A9</i>
<i>LOC729177</i>	<i>DVLI</i>	<i>CCL26</i>
<i>HS1BP3</i>	<i>ATXN1</i>	<i>DSTNP2</i>
<i>LRIG1</i>	<i>TMEM176A</i>	<i>SNAR-D</i>
<i>MPP2</i>	<i>EFR3A</i>	<i>NAT8L</i>
<i>HMGB3P1</i>	<i>ANKRD57</i>	<i>BACE2</i>
<i>RNF216</i>	<i>RIMS3</i>	<i>XLOC_12_004306</i>
<i>TCEAL8</i>	<i>ALDH3B1</i>	<i>TNRC18</i>
<i>COL4A4</i>	<i>MTSS1</i>	<i>TWSG1</i>
<i>TMSB15A</i>	<i>SGMS1</i>	<i>C17orf96</i>
<i>TMEM175</i>	<i>DCBLD2</i>	<i>PEG10</i>
<i>ABCG4</i>	<i>C5orf13</i>	<i>RAC3</i>
<i>XYLT2</i>	<i>NAA16</i>	<i>HMX3</i>
<i>COX7A1</i>	<i>LAMTOR3</i>	<i>NPC2</i>
<i>PRKCZ</i>	<i>PDPR</i>	<i>IL4I1</i>
<i>SLC46A3</i>	<i>C1S</i>	<i>FAM176A</i>
<i>FADS1</i>	<i>ING4</i>	<i>TRIM14</i>
<i>PI4K2B</i>	<i>ZNF330</i>	<i>ACP5</i>
<i>ALDH4A1</i>	<i>MGST2</i>	<i>PTTG1</i>
<i>FLJ23867</i>	<i>SNX5</i>	<i>LRRC26</i>
<i>HNRNPA3</i>	<i>RB1CC1</i>	<i>GGT5</i>
<i>PCBP3</i>	<i>PAIP1</i>	<i>HSPB1</i>
<i>FNIP2</i>	<i>FONG</i>	<i>XLOC_009677</i>
<i>SNORD114-12</i>	<i>CTBP2</i>	<i>SURF4</i>
<i>C10orf58</i>	<i>ZNF577</i>	<i>LOC647086</i>
<i>OPLAH</i>	<i>NKX3-1</i>	<i>SEPT7L</i>
<i>SSC5D</i>	<i>HIVEP1</i>	<i>LOC643733</i>
<i>RTN4RL1</i>	<i>LARP6</i>	<i>PML</i>
<i>LOC100652903</i>	<i>FAM129B</i>	<i>C7</i>

<i>SNORD114-11</i>	<i>LOC100292680</i>	<i>CCDC102B</i>
<i>EVL</i>	<i>ITGB1BP1</i>	<i>XLOC_003631</i>
<i>NUAK1</i>	<i>MAP1LC3B</i>	<i>C14orf162</i>
<i>CLEC11A</i>	<i>FRG1B</i>	<i>RHBDF2</i>
<i>ODZ3</i>	<i>TPST2</i>	<i>JUP</i>
<i>SNORD114-26</i>	<i>TMEM159</i>	<i>SLC17A9</i>
<i>DOK3</i>	<i>PALMD</i>	<i>MYO1D</i>
<i>TMEM22</i>	<i>ZC3H11A</i>	<i>SYTL2</i>
<i>HLA-B</i>	<i>LRRC3</i>	<i>SNAI1</i>
<i>MMP3</i>	<i>FRMD6</i>	<i>LOC100652963</i>
<i>HES4</i>	<i>DNAH5</i>	<i>LAMA5</i>
<i>BAI2</i>	<i>SYNGR3</i>	<i>QPRT</i>
<i>MAFB</i>	<i>C21orf33</i>	<i>LOC284219</i>
<i>HR</i>	<i>ZSCAN2</i>	<i>GNG11</i>
<i>CTSC</i>	<i>CLTB</i>	<i>XLOC_001788</i>
<i>LHFP</i>	<i>HIST1H2BG</i>	<i>GRAMD3</i>
<i>ADII</i>	<i>DDX39A</i>	<i>ALCAM</i>
<i>RAB15</i>	<i>LGALS1</i>	<i>STC2</i>
<i>VIT</i>	<i>ARMC5</i>	<i>LIF</i>
<i>PDE4DIP</i>	<i>BNC1</i>	<i>PDE4B</i>
<i>FLT3LG</i>	<i>INF2</i>	<i>BAALC</i>
<i>GGH</i>	<i>HIST1H2BJ</i>	<i>OLFML2A</i>
<i>F3</i>	<i>RABEPK</i>	<i>XLOC_004050</i>
<i>C9orf95</i>	<i>SLC2A14</i>	<i>GLI1</i>
<i>TCF21</i>	<i>XLOC_12_015476</i>	<i>COL5A2</i>
<i>MMP23B</i>	<i>FLJ42200</i>	<i>ANXA2P3</i>
<i>Q8NDX4</i>	<i>CAMKK1</i>	<i>COL13A1</i>
<i>KCNMB4</i>	<i>SNORD114-20</i>	<i>DHCR24</i>
<i>SNORD114-15</i>	<i>MMP2</i>	<i>PKNOX2</i>
<i>SETDB2</i>	<i>UBE2S</i>	<i>MEG3</i>
<i>CYBRD1</i>	<i>FAM167B</i>	<i>XLOC_12_013808</i>
<i>TPD52L1</i>	<i>VASN</i>	<i>KBTBD11</i>
<i>CLCN6</i>	<i>IFITM4P</i>	<i>RCAN1</i>
<i>GLIS1</i>	<i>NRXN3</i>	<i>GOLGA6C</i>
<i>TYRP1</i>	<i>SULT1A2</i>	<i>AK5</i>
<i>XLOC_12_013242</i>	<i>JAM2</i>	<i>DACT3</i>
<i>ADRA2C</i>	<i>XLOC_006978</i>	<i>VSTM2L</i>
<i>SORBS2</i>	<i>GLA</i>	<i>LRRN4CL</i>
<i>EML1</i>	<i>TMEM191A</i>	<i>MYO1B</i>
<i>TMEM130</i>	<i>SASH1</i>	<i>CAMK1D</i>
<i>FLJ41170</i>	<i>C4orf49</i>	<i>PXK</i>
<i>PCYT2</i>	<i>FLJ32224</i>	<i>SLC43A2</i>
<i>SNORD114-23</i>	<i>SRGAP2</i>	<i>RASL11B</i>
<i>EMILIN1</i>	<i>CRYAB</i>	<i>CARD17</i>
<i>XLOC_014226</i>	<i>HSPE1</i>	<i>SECTM1</i>
<i>P4HA2</i>	<i>C1orf21</i>	<i>XLOC_002736</i>
<i>PHF19</i>	<i>XLOC_009788</i>	<i>SSX2IP</i>
<i>SNORD114-22</i>	<i>ANPEP</i>	<i>ZNF469</i>
<i>SERPINE1</i>	<i>SSBP3</i>	<i>XLOC_12_003757</i>
<i>SGTB</i>	<i>CLCN4</i>	<i>MGLL</i>
<i>NACC2</i>	<i>ITGA3</i>	<i>APCDD1L</i>
<i>RBMS1</i>	<i>LEF1</i>	<i>NOTCH3</i>
<i>PODN</i>	<i>LTBP4</i>	<i>DKK3</i>
<i>CMIP</i>	<i>IFFO2</i>	<i>ATF3</i>
<i>LTBP1</i>	<i>VTN</i>	<i>COL6A3</i>
<i>LOC100509498</i>	<i>LOC100134240</i>	<i>ALDH1A3</i>
<i>GPR180</i>	<i>ZNF746</i>	<i>COTL1</i>
<i>DSTN</i>	<i>HAMP</i>	<i>TMEM171</i>
<i>TMEM8C</i>	<i>HIST1H2BK</i>	<i>XLOC_12_008009</i>
<i>AMPH</i>	<i>PALM3</i>	<i>VAT1L</i>
<i>LPP</i>	<i>MICAL1</i>	<i>HIST1H3J</i>

<i>CRYBG3</i>	<i>KDELR3</i>	<i>GFRA1</i>
<i>TMEM87B</i>	<i>MAPRE2</i>	<i>ICMT</i>
<i>PLAT</i>	<i>S100A3</i>	<i>PPP1R3C</i>
<i>ITGAV</i>	<i>XLOC_12_015578</i>	<i>XLOC_12_009539</i>
<i>SMAP2</i>	<i>ANP32E</i>	<i>ITGA4</i>
<i>C1QTNF6</i>	<i>DUSP5</i>	<i>SLC6A6</i>
<i>TANC1</i>	<i>LOC440028</i>	<i>GPR68</i>
<i>CIB2</i>	<i>RNF144B</i>	<i>XLOC_12_007656</i>
<i>MGAT5</i>	<i>XLOC_006390</i>	<i>ITGB3</i>
<i>TBC1D2B</i>	<i>GATSL3</i>	<i>MOXD1</i>
<i>PLEKHH2</i>	<i>MSX2P1</i>	<i>PARP4</i>
<i>SNORD114-2</i>	<i>GK</i>	<i>MTRNR2L9</i>
<i>LOC100130654</i>	<i>SEMA7A</i>	<i>IL7</i>
<i>HLA-DMA</i>	<i>BAIAP2L1</i>	<i>HGF</i>
<i>LOC541471</i>	<i>XLOC_005338</i>	<i>NXP4</i>
<i>ADAMTS4</i>	<i>NDRG2</i>	<i>F2R</i>
<i>NAV1</i>	<i>ACOT11</i>	<i>LOC283070</i>
<i>CALM1</i>	<i>GSG1</i>	<i>C16orf89</i>
<i>XLOC_007433</i>	<i>TMEM229B</i>	<i>PFN1P2</i>
<i>SNORD114-9</i>	<i>PAFAH1B1</i>	<i>SRPX2</i>
<i>TK1</i>	<i>WNT5A</i>	<i>STMN2</i>
<i>TMOD3</i>	<i>AKAP13</i>	<i>ELOVL2</i>
<i>ROR1</i>	<i>XLOC_12_009888</i>	<i>LEPREL1</i>
<i>STXBP6</i>	<i>OLFML2B</i>	<i>XLOC_12_005692</i>
<i>DDAH1</i>	<i>C9orf150</i>	<i>DLL1</i>
<i>XLOC_12_001206</i>	<i>PPM1K</i>	<i>KCNH2</i>
<i>XLOC_007458</i>	<i>CACNA2D1</i>	<i>IER3</i>
<i>PBX1</i>	<i>CCND1</i>	<i>LOC100287082</i>
<i>GPRC5C</i>	<i>XLOC_009067</i>	<i>NPTX1</i>
<i>SERPINA3</i>	<i>C12orf53</i>	<i>COL12A1</i>
<i>PDE4D</i>	<i>RBM43</i>	<i>TLE2</i>
<i>CYBASC3</i>	<i>CNTNAP1</i>	<i>IFI27</i>
<i>HSD17B7</i>	<i>LY6K</i>	<i>FIBIN</i>
<i>GP1BB</i>	<i>HEATR8</i>	<i>SCN4B</i>
<i>XLOC_001625</i>	<i>RACGAP1</i>	<i>FAM46C</i>
<i>KCNMA1</i>	<i>PSMD10</i>	<i>SPON2</i>
<i>LSS</i>	<i>XLOC_007118</i>	<i>LOC645638</i>
<i>PTGFRN</i>	<i>LINC00152</i>	<i>NACAP1</i>
<i>STON1</i>	<i>XLOC_004528</i>	<i>BMPER</i>
<i>PHACTR3</i>	<i>PPP2R5C</i>	<i>ANXA2</i>
<i>KREMEN1</i>	<i>ICAM5</i>	<i>MASP1</i>
<i>NTN1</i>	<i>TMEM189</i>	<i>ISG20</i>
<i>C9orf3</i>	<i>LOC84856</i>	<i>D4S234E</i>
<i>E2F7</i>	<i>LMNB2</i>	<i>ITGA11</i>
<i>ZNF217</i>	<i>DMPK</i>	<i>GALNTL1</i>
<i>ERVMER34-1</i>	<i>TMEM201</i>	<i>CCL7</i>
<i>COL4A2</i>	<i>DOCK10</i>	<i>ADAMTS8</i>
<i>ITGA7</i>	<i>ASB2</i>	<i>C11orf96</i>
<i>PHYHD1</i>	<i>MYOF</i>	<i>TRIL</i>
<i>MKX</i>	<i>PPME1</i>	<i>S100A4</i>
<i>MXD4</i>	<i>LOC388242</i>	<i>LOC100287221</i>
<i>PRPH2</i>	<i>LOC100505874</i>	<i>CYTL1</i>
<i>KLF6</i>	<i>LETM1</i>	<i>CCL2</i>
<i>BMP8B</i>	<i>DNAJC1</i>	<i>CCL13</i>
<i>XLOC_004244</i>	<i>MYLIP</i>	<i>CCDC3</i>
<i>GPR56</i>	<i>LOC100130456</i>	<i>CCL11</i>
<i>XLOC_12_008203</i>	<i>LITAF</i>	
<i>CFI</i>	<i>CHST15</i>	
<i>TSPAN2</i>	<i>TCEAL2</i>	
<i>SLC2A6</i>	<i>LZTS2</i>	
<i>ALDOC</i>	<i>CHIT1</i>	

<i>RORA</i>	<i>GUSBP1</i>
<i>CACNA1H</i>	<i>ABLIM1</i>
<i>LOC100507286</i>	<i>ACSS1</i>
<i>IL18BP</i>	<i>TFEB</i>
<i>TRERF1</i>	<i>ALAD</i>
<i>GALNTL4</i>	<i>DYNC1LI2</i>
<i>TRIB2</i>	<i>LPAR1</i>
<i>PLXDC2</i>	<i>LCTL</i>
<i>STARD4</i>	<i>LOC100287803</i>
<i>RNF122</i>	<i>TMEM107</i>
<i>ATP9A</i>	<i>LINC00341</i>
<i>FHL2</i>	<i>KRTAP19-2</i>
<i>ACSS2</i>	<i>LOC442132</i>
<i>PTGIR</i>	<i>RASAL3</i>
<i>ANKRD36</i>	<i>LOC100507948</i>
<i>BOK</i>	<i>FGF1</i>
<i>FDFT1</i>	<i>ZAK</i>
<i>NFATC1</i>	<i>NMB</i>
<i>PKDCC</i>	<i>XLOC_12_005415</i>
<i>APC2</i>	<i>TRIM23</i>
<i>EBP</i>	<i>C8orf44-SGK3</i>
<i>ARRDC4</i>	<i>CHST13</i>
<i>TTL7</i>	<i>TMEM173</i>
<i>KIAA0408</i>	<i>LDHD</i>
<i>SGSM2</i>	<i>LOC100132339</i>
<i>MME</i>	<i>FRY</i>
<i>LOC100652751</i>	<i>RASD1</i>
<i>LOC389676</i>	<i>SNED1</i>
<i>Q29HP5</i>	<i>Q9N083</i>
<i>ENDOD1</i>	<i>TGIF1</i>
<i>XLOC_010411</i>	<i>SNAP25</i>
<i>ICOSLG</i>	<i>POLR2F</i>
<i>HMSD</i>	<i>XLOC_013567</i>
<i>PRRT2</i>	<i>SYNPO2L</i>
<i>NKD2</i>	<i>TSPAN10</i>
<i>FHL1</i>	<i>IER5L</i>
<i>TRPV2</i>	<i>TSPAN5</i>
<i>NRG1</i>	<i>LOC149773</i>
<i>OBFC2A</i>	<i>EYA2</i>
<i>SUSD2</i>	<i>HIST1H3I</i>
<i>PLSCR1</i>	<i>XLOC_012142</i>
<i>PAMR1</i>	<i>AMZ1</i>
<i>PLAU</i>	<i>HOTAIR</i>
<i>FAM43A</i>	<i>KIAA1804</i>
<i>SELIL3</i>	<i>HIST1H2AC</i>
<i>CALD1</i>	<i>GRIN3B</i>
<i>C15orf59</i>	<i>KIAA1217</i>
<i>LY9</i>	<i>HIST1H3D</i>
<i>CLK3</i>	<i>XLOC_010257</i>
<i>VSTM4</i>	<i>CXCL10</i>
<i>GADD45G</i>	<i>ZNF713</i>
<i>EFEMP1</i>	<i>REERG</i>
<i>YWHAZ</i>	<i>DUSP4</i>
<i>NID1</i>	<i>C5orf58</i>
<i>TGFBI</i>	<i>C19orf69</i>
<i>GGCT</i>	<i>HRASLS5</i>
<i>QSOX1</i>	<i>XLOC_011081</i>
<i>CD24</i>	<i>MGC10814</i>
<i>REEP2</i>	<i>SOX13</i>
<i>PHLDA1</i>	<i>COX6B2</i>
<i>CGNL1</i>	<i>LOC100133985</i>

<i>CHPF</i>	<i>XLOC_006009</i>
<i>XAF1</i>	<i>XLOC_006559</i>
<i>F10</i>	<i>XLOC_002802</i>
<i>GPR155</i>	<i>MUC4</i>
<i>FASN</i>	<i>XLOC_l2_013457</i>
<i>CSRP2</i>	<i>SHC3</i>
<i>LUM</i>	<i>ANKHD1</i>
<i>FDPSL2A</i>	<i>XLOC_009345</i>
<i>KRT18P55</i>	<i>LOC100133091</i>
<i>DHCR7</i>	<i>ZNF37BP</i>
<i>TEK</i>	<i>HBG1</i>
<i>TUBB2A</i>	<i>XRCC3</i>
<i>PRUNE2</i>	<i>TFPI</i>
<i>LPIN1</i>	<i>MRPS16</i>
<i>NCKAP5</i>	<i>COL27A1</i>
<i>ZFP106</i>	<i>TMEM35</i>
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<i>ADRA1B</i>	<i>XLOC_l2_009510</i>
<i>LOXL2</i>	<i>SLC6A17</i>
<i>MVK</i>	<i>PPPDE2</i>
<i>SYNM</i>	<i>FLJ30838</i>
<i>ZC3H7B</i>	<i>HSPB3</i>
<i>KLF2</i>	<i>ZNF248</i>
<i>ASPN</i>	<i>HIST2H2AA4</i>
<i>DSEL</i>	<i>XLOC_l2_007456</i>
<i>MSMO1</i>	<i>ARHGAP4</i>
<i>FLJ30901</i>	<i>XLOC_003175</i>
<i>PTGER4</i>	<i>OR7E12P</i>
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<i>TAGLN</i>	<i>COL5A3</i>
<i>FABP3</i>	<i>XLOC_006775</i>
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<i>APCDD1</i>	<i>C2</i>
<i>KALI</i>	<i>TRIM46</i>
<i>KRT18</i>	<i>LOXL1</i>
<i>LYPD1</i>	<i>SREBF1</i>
<i>C1orf38</i>	<i>ARHGAP42</i>
<i>FDPS</i>	<i>MSTO2P</i>
<i>SQLE</i>	<i>TTY14</i>
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<i>GABRB1</i>	<i>SIGLEC14</i>
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<i>FAM49A</i>	<i>KIAA1875</i>
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	<i>ENTPD1</i>
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FOXB1

Supplementary Table S9 Functional enrichment analysis of 1,25(OH)₂D₃-regulated genes in human colon NFs

		1,25(OH) ₂ D ₃ -upregulated genes				
Category	Term	Count	%	p Value	Fold enrichment	FDR
GOTERM_BP_ALL	GO:0065008~regulation of biological quality	65	15.815	1.50E-07	1.958	2.61E-06
GOTERM_BP_ALL	GO:0001501~skeletal system development	24	5.839	9.41E-07	3.329	1.64E-05
GOTERM_BP_ALL	GO:0009605~response to external stimulus	44	10.706	3.39E-06	2.130	5.90E-05
GOTERM_BP_ALL	GO:0048731~system development	84	20.438	7.59E-06	1.595	1.32E-04
GOTERM_BP_ALL	GO:0042221~response to chemical stimulus	54	13.139	9.77E-06	1.865	1.70E-04
GOTERM_BP_ALL	GO:0035295~tube development	18	4.380	1.03E-05	3.621	1.79E-04
GOTERM_BP_ALL	GO:0033273~response to vitamin	10	2.433	1.60E-05	6.705	2.78E-04
GOTERM_BP_ALL	GO:0048856~anatomical structure development	88	21.411	1.63E-05	1.541	2.84E-04
GOTERM_BP_ALL	GO:0007584~response to nutrient	14	3.406	1.66E-05	4.425	2.89E-04
GOTERM_BP_ALL	GO:0050793~regulation of developmental process	34	8.273	2.32E-05	2.232	4.04E-04
GOTERM_BP_ALL	GO:0007275~multicellular organismal development	96	23.358	2.65E-05	1.483	4.62E-04
GOTERM_BP_ALL	GO:0031667~response to nutrient levels	16	3.893	4.07E-05	3.594	7.09E-04
GOTERM_BP_ALL	GO:0032502~developmental process	102	24.818	5.23E-05	1.434	9.09E-04
GOTERM_BP_ALL	GO:0001503~ossification	12	2.920	5.65E-05	4.617	9.83E-04
GOTERM_BP_ALL	GO:0051302~regulation of cell division	8	1.946	7.99E-05	7.532	1.39E-03
GOTERM_BP_ALL	GO:0048754~branching morphogenesis of a tube	9	2.190	1.00E-04	6.127	1.75E-03
GOTERM_BP_ALL	GO:0060348~bone development	12	2.920	1.04E-04	4.317	1.81E-03
GOTERM_BP_ALL	GO:0009991~response to extracellular stimulus	16	3.893	1.42E-04	3.218	2.46E-03
GOTERM_BP_ALL	GO:0048513~organ development	63	15.328	1.43E-04	1.604	2.49E-03
GOTERM_BP_ALL	GO:0030001~metal ion transport	25	6.083	1.43E-04	2.379	2.49E-03
GOTERM_BP_ALL	GO:0009611~response to wounding	27	6.569	1.71E-04	2.254	2.97E-03
GOTERM_BP_ALL	GO:0006950~response to stress	61	14.842	1.97E-04	1.602	3.42E-03
GOTERM_BP_ALL	GO:0009653~anatomical structure morphogenesis	47	11.436	2.35E-04	1.737	4.08E-03
GOTERM_BP_ALL	GO:0001763~morphogenesis of a branching structure	9	2.190	2.52E-04	5.382	4.37E-03
GOTERM_BP_ALL	GO:0002320~lymphoid progenitor cell differentiation	4	0.973	3.71E-04	25.286	6.43E-03
GOTERM_BP_ALL	GO:0009888~tissue development	30	7.299	5.21E-04	1.996	9.03E-03
GOTERM_BP_ALL	GO:0032501~multicellular organismal process	125	30.414	5.27E-04	1.292	9.13E-03
GOTERM_BP_ALL	GO:0030198~extracellular matrix organization	10	2.433	5.62E-04	4.255	9.74E-03
GOTERM_BP_ALL	GO:0035239~tube morphogenesis	11	2.676	5.97E-04	3.833	1.03E-02
GOTERM_BP_ALL	GO:0006811~ion transport	33	8.029	5.99E-04	1.901	1.04E-02
GOTERM_BP_ALL	GO:0015674~di-, tri-valent inorganic cation transport	13	3.163	6.47E-04	3.269	1.12E-02
GOTERM_BP_ALL	GO:0010033~response to organic substance	31	7.543	8.98E-04	1.903	1.55E-02
GOTERM_BP_ALL	GO:0002252~immune effector process	11	2.676	9.06E-04	3.633	1.57E-02
GOTERM_BP_ALL	GO:0006928~cell motion	23	5.596	1.17E-03	2.143	2.01E-02
GOTERM_BP_ALL	GO:0042060~wound healing	13	3.163	1.33E-03	3.012	2.29E-02
GOTERM_BP_ALL	GO:0048878~chemical homeostasis	24	5.839	1.34E-03	2.074	2.30E-02
GOTERM_BP_ALL	GO:0060548~negative regulation of cell death	19	4.623	1.38E-03	2.335	2.37E-02
GOTERM_BP_ALL	GO:0002244~hemopoietic progenitor cell differentiation	4	0.973	1.63E-03	16.091	2.81E-02
GOTERM_BP_ALL	GO:0006812~cation transport	25	6.083	1.68E-03	2.000	2.89E-02
GOTERM_BP_ALL	GO:0009725~response to hormone stimulus	19	4.623	1.70E-03	2.291	2.93E-02

GOTERM_BP_ALL	GO:0001944~vasculature development	15	3.650	1.71E-03	2.644	2.93E-02
GOTERM_BP_ALL	GO:0051781~positive regulation of cell division	6	1.460	1.73E-03	6.808	2.96E-02
GOTERM_BP_ALL	GO:0030278~regulation of ossification	8	1.946	1.85E-03	4.539	3.18E-02
GOTERM_BP_ALL	GO:0045597~positive regulation of cell differentiation	14	3.406	2.12E-03	2.705	3.62E-02
GOTERM_BP_ALL	GO:0009719~response to endogenous stimulus	20	4.866	2.12E-03	2.185	3.63E-02
GOTERM_BP_ALL	GO:0008202~steroid metabolic process	13	3.163	2.14E-03	2.848	3.67E-02
GOTERM_BP_ALL	GO:0030154~cell differentiation	55	13.382	2.50E-03	1.487	4.27E-02
GOTERM_BP_ALL	GO:0006916~anti-apoptosis	13	3.163	2.51E-03	2.793	4.28E-02
GOTERM_BP_ALL	GO:0050896~response to stimulus	102	24.818	2.78E-03	1.289	4.72E-02
GOTERM_BP_ALL	GO:0043066~negative regulation of apoptosis	18	4.380	2.83E-03	2.250	4.81E-02
GOTERM_CC_ALL	GO:0044421~extracellular region part	62	15.085	1.46E-14	2.995	1.93E-13
GOTERM_CC_ALL	GO:0005576~extracellular region	93	22.628	5.75E-13	2.146	7.56E-12
GOTERM_CC_ALL	GO:0005615~extracellular space	42	10.219	2.90E-09	2.844	3.82E-08
GOTERM_CC_ALL	GO:0031012~extracellular matrix	28	6.813	7.51E-09	3.764	9.86E-08
GOTERM_CC_ALL	GO:0005578~proteinaceous extracellular matrix	26	6.326	2.85E-08	3.768	3.74E-07
GOTERM_CC_ALL	GO:0044420~extracellular matrix part	13	3.163	8.15E-06	5.153	1.07E-04
GOTERM_CC_ALL	GO:0031093~platelet alpha granule lumen	7	1.703	2.25E-04	7.918	2.95E-03
GOTERM_CC_ALL	GO:0042598~vesicular fraction	16	3.893	2.68E-04	3.041	3.52E-03
GOTERM_CC_ALL	GO:0005626~insoluble fraction	35	8.516	2.96E-04	1.935	3.88E-03
GOTERM_CC_ALL	GO:0005624~membrane fraction	34	8.273	3.21E-04	1.949	4.20E-03
GOTERM_CC_ALL	GO:0060205~cytoplasmic membrane-bounded vesicle lumen	7	1.703	3.35E-04	7.378	4.39E-03
GOTERM_CC_ALL	GO:0031983~vesicle lumen	7	1.703	4.29E-04	7.058	5.62E-03
GOTERM_CC_ALL	GO:0005792~microsome	15	3.650	6.38E-04	2.935	8.36E-03
GOTERM_CC_ALL	GO:0000267~cell fraction	40	9.732	1.08E-03	1.713	1.41E-02
GOTERM_CC_ALL	GO:0031091~platelet alpha granule	7	1.703	1.24E-03	5.797	1.62E-02
GOTERM_CC_ALL	GO:0030141~secretory granule	12	2.920	1.81E-03	3.092	2.35E-02
GOTERM_MF_ALL	GO:0008083~growth factor activity	14	3.406	4.75E-05	4.015	7.04E-04
GOTERM_MF_ALL	GO:0005520~insulin-like growth factor binding	6	1.460	1.70E-04	11.080	2.51E-03
GOTERM_MF_ALL	GO:0005509~calcium ion binding	38	9.246	1.93E-04	1.909	2.86E-03
GOTERM_MF_ALL	GO:0008201~heparin binding	10	2.433	3.87E-04	4.482	5.72E-03
GOTERM_MF_ALL	GO:0005488~binding	293	71.290	5.65E-04	1.079	8.34E-03
GOTERM_MF_ALL	GO:0016614~oxidoreductase activity, acting on CH-OH group of donors	10	2.433	9.21E-04	3.980	1.36E-02
GOTERM_MF_ALL	GO:0005515~protein binding	205	49.878	9.89E-04	1.161	1.46E-02
GOTERM_MF_ALL	GO:0016616~oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor	9	2.190	1.85E-03	3.995	2.72E-02
GOTERM_MF_ALL	GO:0030247~polysaccharide binding	11	2.676	1.90E-03	3.298	2.78E-02
GOTERM_MF_ALL	GO:0001871~pattern binding	11	2.676	1.90E-03	3.298	2.78E-02
GOTERM_MF_ALL	GO:0019838~growth factor binding	9	2.190	1.97E-03	3.957	2.88E-02
GOTERM_MF_ALL	GO:0033764~steroid dehydrogenase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor	5	1.217	2.53E-03	8.550	3.69E-02
GOTERM_MF_ALL	GO:0005201~extracellular matrix structural constituent	8	1.946	2.57E-03	4.295	3.74E-02
GOTERM_MF_ALL	GO:0050327~testosterone 17-beta-dehydrogenase activity	3	0.730	2.71E-03	34.626	3.95E-02
GOTERM_MF_ALL	GO:0005172~vascular endothelial growth factor receptor binding	3	0.730	2.71E-03	34.626	3.95E-02
GOTERM_MF_ALL	GO:0005539~glycosaminoglycan binding	10	2.433	3.38E-03	3.298	4.90E-02

1,25(OH)₂D₃-downregulated genes

Category	Term	Count	%	p Value	Fold enrichment	FDR
GOTERM_BP_ALL	GO:0048731~system development	102	22.768	9.83E-11	1.867	1.70E-09
GOTERM_BP_ALL	GO:0048856~anatomical structure development	106	23.661	4.31E-10	1.789	7.48E-09
GOTERM_BP_ALL	GO:0006695~cholesterol biosynthetic process	10	2.232	4.12E-09	16.403	7.15E-08
GOTERM_BP_ALL	GO:0016126~sterol biosynthetic process	11	2.455	4.65E-09	13.403	8.07E-08
GOTERM_BP_ALL	GO:0009611~response to wounding	37	8.259	8.94E-09	2.977	1.55E-07
GOTERM_BP_ALL	GO:0006694~steroid biosynthetic process	15	3.348	9.41E-09	7.526	1.63E-07
GOTERM_BP_ALL	GO:0048513~organ development	76	16.964	7.15E-08	1.865	1.24E-06
GOTERM_BP_ALL	GO:0008610~lipid biosynthetic process	26	5.804	1.65E-07	3.433	2.87E-06
GOTERM_BP_ALL	GO:0032502~developmental process	115	25.670	1.83E-07	1.558	3.18E-06
GOTERM_BP_ALL	GO:0008203~cholesterol metabolic process	14	3.125	2.09E-07	6.490	3.62E-06
GOTERM_BP_ALL	GO:0007275~multicellular organismal development	106	23.661	4.13E-07	1.578	7.17E-06
GOTERM_BP_ALL	GO:0016125~sterol metabolic process	14	3.125	6.31E-07	5.911	1.10E-05
GOTERM_BP_ALL	GO:0042127~regulation of cell proliferation	42	9.375	1.19E-06	2.276	2.06E-05
GOTERM_BP_ALL	GO:0009605~response to external stimulus	45	10.045	3.82E-06	2.100	6.63E-05
GOTERM_BP_ALL	GO:0009653~anatomical structure morphogenesis	54	12.054	4.19E-06	1.924	7.27E-05
GOTERM_BP_ALL	GO:0051239~regulation of multicellular organismal process	45	10.045	7.28E-06	2.048	1.26E-04
GOTERM_BP_ALL	GO:0042060~wound healing	17	3.795	1.08E-05	3.796	1.87E-04
GOTERM_BP_ALL	GO:0050793~regulation of developmental process	35	7.813	2.03E-05	2.215	3.53E-04
GOTERM_BP_ALL	GO:0008202~steroid metabolic process	17	3.795	2.17E-05	3.589	3.76E-04
GOTERM_BP_ALL	GO:0030154~cell differentiation	65	14.509	2.18E-05	1.693	3.79E-04
GOTERM_BP_ALL	GO:0006954~inflammatory response	22	4.911	2.66E-05	2.887	4.62E-04
GOTERM_BP_ALL	GO:0048869~cellular developmental process	66	14.732	4.15E-05	1.650	7.20E-04
GOTERM_BP_ALL	GO:0007155~cell adhesion	35	7.813	4.38E-05	2.132	7.60E-04
GOTERM_BP_ALL	GO:0022610~biological adhesion	35	7.813	4.44E-05	2.129	7.71E-04
GOTERM_BP_ALL	GO:0008299~isoprenoid biosynthetic process	6	1.339	7.87E-05	12.794	1.36E-03
GOTERM_BP_ALL	GO:0065008~regulation of biological quality	58	12.946	8.26E-05	1.684	1.43E-03
GOTERM_BP_ALL	GO:0008284~positive regulation of cell proliferation	24	5.357	1.16E-04	2.472	2.02E-03
GOTERM_BP_ALL	GO:0050878~regulation of body fluid levels	13	2.902	1.17E-04	3.932	2.03E-03
GOTERM_BP_ALL	GO:0050817~coagulation	11	2.455	1.35E-04	4.599	2.34E-03
GOTERM_BP_ALL	GO:0007596~blood coagulation	11	2.455	1.35E-04	4.599	2.34E-03
GOTERM_BP_ALL	GO:0042221~response to chemical stimulus	51	11.384	2.09E-04	1.698	3.62E-03
GOTERM_BP_ALL	GO:0007599~hemostasis	11	2.455	2.17E-04	4.344	3.76E-03
GOTERM_BP_ALL	GO:0007154~cell communication	36	8.036	2.36E-04	1.931	4.09E-03
GOTERM_BP_ALL	GO:0007399~nervous system development	45	10.045	2.44E-04	1.764	4.23E-03
GOTERM_BP_ALL	GO:0007267~cell-cell signaling	29	6.473	4.04E-04	2.061	6.99E-03
GOTERM_BP_ALL	GO:0007517~muscle organ development	15	3.348	4.49E-04	3.032	7.77E-03
GOTERM_BP_ALL	GO:0006720~isoprenoid metabolic process	7	1.563	5.21E-04	6.785	8.99E-03
GOTERM_BP_ALL	GO:0032501~multicellular organismal process	129	28.795	5.54E-04	1.285	9.58E-03
GOTERM_BP_ALL	GO:0030198~extracellular matrix organization	10	2.232	7.32E-04	4.101	1.26E-02
GOTERM_BP_ALL	GO:0042592~homeostatic process	33	7.366	7.57E-04	1.874	1.31E-02
GOTERM_BP_ALL	GO:0009887~organ morphogenesis	27	6.027	7.77E-04	2.042	1.34E-02

GOTERM_BP_ALL	GO:0031099~regeneration	8	1.786	1.12E-03	4.945	1.92E-02
GOTERM_BP_ALL	GO:0048519~negative regulation of biological process	63	14.063	1.19E-03	1.483	2.05E-02
GOTERM_BP_ALL	GO:0007229~integrin-mediated signaling pathway	8	1.786	1.21E-03	4.874	2.09E-02
GOTERM_BP_ALL	GO:0009719~response to endogenous stimulus	21	4.688	1.40E-03	2.211	2.39E-02
GOTERM_BP_ALL	GO:0030155~regulation of cell adhesion	11	2.455	1.42E-03	3.424	2.43E-02
GOTERM_BP_ALL	GO:0008219~cell death	31	6.920	1.53E-03	1.839	2.62E-02
GOTERM_BP_ALL	GO:0043062~extracellular structure organization	12	2.679	1.57E-03	3.140	2.70E-02
GOTERM_BP_ALL	GO:0016265~death	31	6.920	1.71E-03	1.826	2.93E-02
GOTERM_BP_ALL	GO:0006928~cell motion	23	5.134	1.87E-03	2.065	3.19E-02
GOTERM_BP_ALL	GO:0048771~tissue remodeling	7	1.563	1.89E-03	5.331	3.24E-02
GOTERM_BP_ALL	GO:0048878~chemical homeostasis	24	5.357	2.15E-03	1.999	3.67E-02
GOTERM_BP_ALL	GO:0001944~vasculature development	15	3.348	2.39E-03	2.549	4.06E-02
GOTERM_BP_ALL	GO:0006629~lipid metabolic process	33	7.366	2.74E-03	1.731	4.65E-02
GOTERM_BP_ALL	GO:0045595~regulation of cell differentiation	23	5.134	2.80E-03	1.994	4.75E-02
GOTERM_CC_ALL	GO:0044421~extracellular region part	59	13.170	3.05E-11	2.600	4.13E-10
GOTERM_CC_ALL	GO:0031012~extracellular matrix	32	7.143	1.78E-10	3.924	2.41E-09
GOTERM_CC_ALL	GO:0005578~proteinaceous extracellular matrix	30	6.696	5.75E-10	3.966	7.80E-09
GOTERM_CC_ALL	GO:0005576~extracellular region	85	18.973	8.05E-08	1.789	1.09E-06
GOTERM_CC_ALL	GO:0044420~extracellular matrix part	15	3.348	6.55E-07	5.424	8.88E-06
GOTERM_CC_ALL	GO:0005581~collagen	9	2.009	1.19E-06	10.879	1.62E-05
GOTERM_CC_ALL	GO:0005604~basement membrane	10	2.232	8.87E-05	5.424	1.20E-03
GOTERM_CC_ALL	GO:0005615~extracellular space	33	7.366	1.86E-04	2.038	2.52E-03
GOTERM_CC_ALL	GO:0044459~plasma membrane part	78	17.411	2.06E-04	1.498	2.78E-03
GOTERM_CC_ALL	GO:0031226~intrinsic to plasma membrane	48	10.714	5.27E-04	1.671	7.13E-03
GOTERM_CC_ALL	GO:0009897~external side of plasma membrane	13	2.902	7.16E-04	3.235	9.66E-03
GOTERM_CC_ALL	GO:0031233~intrinsic to external side of plasma membrane	4	0.893	1.38E-03	16.923	1.85E-02
GOTERM_CC_ALL	GO:0000267~cell fraction	41	9.152	3.18E-03	1.602	4.23E-02
GOTERM_MF_ALL	GO:0005201~extracellular matrix structural constituent	12	2.679	5.54E-06	5.886	8.27E-05
GOTERM_MF_ALL	GO:0005102~receptor binding	42	9.375	2.92E-05	2.000	4.36E-04
GOTERM_MF_ALL	GO:0008092~cytoskeletal protein binding	28	6.250	6.81E-05	2.343	1.02E-03
GOTERM_MF_ALL	GO:0005515~protein binding	228	50.893	1.34E-04	1.179	1.99E-03
GOTERM_MF_ALL	GO:0004175~endopeptidase activity	22	4.911	2.42E-04	2.475	3.60E-03
GOTERM_MF_ALL	GO:0008009~chemokine activity	7	1.563	7.06E-04	6.419	1.05E-02
GOTERM_MF_ALL	GO:0003779~actin binding	19	4.241	7.94E-04	2.458	1.18E-02
GOTERM_MF_ALL	GO:0042379~chemokine receptor binding	7	1.563	9.93E-04	6.026	1.47E-02

Supplementary Table S10 Functional enrichment analysis of 1,25(OH)₂D₃-regulated genes in human colon CAFs

1,25(OH) ₂ D ₃ -upregulated genes						
Category	Term	Count	%	p Value	Fold enrichment	FDR
GOTERM_BP_ALL	GO:0007507~heart development	22	4.603	2.63E-07	3.862	4.63E-06
GOTERM_BP_ALL	GO:0065008~regulation of biological quality	72	15.063	3.08E-07	1.850	5.42E-06
GOTERM_BP_ALL	GO:0035295~tube development	20	4.184	6.14E-06	3.431	1.08E-04
GOTERM_BP_ALL	GO:0048731~system development	95	19.874	9.37E-06	1.539	1.65E-04
GOTERM_BP_ALL	GO:0010941~regulation of cell death	43	8.996	2.52E-05	1.991	4.43E-04
GOTERM_BP_ALL	GO:0048856~anatomical structure development	99	20.711	2.97E-05	1.479	5.23E-04
GOTERM_BP_ALL	GO:0048513~organ development	74	15.481	3.37E-05	1.607	5.94E-04
GOTERM_BP_ALL	GO:0007275~multicellular organismal development	109	22.803	3.39E-05	1.436	5.97E-04
GOTERM_BP_ALL	GO:0048754~branching morphogenesis of a tube	10	2.092	4.93E-05	5.807	8.69E-04
GOTERM_BP_ALL	GO:0002252~immune effector process	14	2.929	5.48E-05	3.943	9.65E-04
GOTERM_BP_ALL	GO:0032502~developmental process	116	24.268	6.86E-05	1.391	1.21E-03
GOTERM_BP_ALL	GO:0006950~response to stress	71	14.854	7.13E-05	1.590	1.26E-03
GOTERM_BP_ALL	GO:0009888~tissue development	36	7.531	8.26E-05	2.043	1.45E-03
GOTERM_BP_ALL	GO:0042981~regulation of apoptosis	41	8.577	8.82E-05	1.925	1.55E-03
GOTERM_BP_ALL	GO:0070482~response to oxygen levels	14	2.929	9.28E-05	3.748	1.63E-03
GOTERM_BP_ALL	GO:0043067~regulation of programmed cell death	41	8.577	1.06E-04	1.906	1.87E-03
GOTERM_BP_ALL	GO:0035239~tube morphogenesis	13	2.720	1.36E-04	3.863	2.39E-03
GOTERM_BP_ALL	GO:0001763~morphogenesis of a branching structure	10	2.092	1.38E-04	5.100	2.44E-03
GOTERM_BP_ALL	GO:0001666~response to hypoxia	13	2.720	2.26E-04	3.662	3.97E-03
GOTERM_BP_ALL	GO:0001944~vasculature development	18	3.766	3.76E-04	2.707	6.60E-03
GOTERM_BP_ALL	GO:0055114~oxidation reduction	33	6.904	4.05E-04	1.949	7.11E-03
GOTERM_BP_ALL	GO:0007155~cell adhesion	35	7.322	4.56E-04	1.887	8.01E-03
GOTERM_BP_ALL	GO:0022610~biological adhesion	35	7.322	4.68E-04	1.884	8.21E-03
GOTERM_BP_ALL	GO:0060537~muscle tissue development	12	2.510	4.75E-04	3.623	8.34E-03
GOTERM_BP_ALL	GO:0009790~embryonic development	30	6.276	5.49E-04	1.993	9.63E-03
GOTERM_BP_ALL	GO:0030334~regulation of cell migration	14	2.929	5.55E-04	3.127	9.74E-03
GOTERM_BP_ALL	GO:0060541~respiratory system development	11	2.301	5.71E-04	3.844	1.00E-02
GOTERM_BP_ALL	GO:0048519~negative regulation of biological process	71	14.854	6.12E-04	1.479	1.07E-02
GOTERM_BP_ALL	GO:0006814~sodium ion transport	12	2.510	6.63E-04	3.484	1.16E-02
GOTERM_BP_ALL	GO:0048523~negative regulation of cellular process	66	13.808	6.99E-04	1.501	1.22E-02
GOTERM_BP_ALL	GO:0009653~anatomical structure morphogenesis	51	10.669	7.85E-04	1.608	1.37E-02
GOTERM_BP_ALL	GO:0001568~blood vessel development	17	3.556	8.22E-04	2.619	1.44E-02
GOTERM_BP_ALL	GO:0050793~regulation of developmental process	33	6.904	9.76E-04	1.848	1.71E-02
GOTERM_BP_ALL	GO:0002377~immunoglobulin production	6	1.255	1.04E-03	7.549	1.81E-02
GOTERM_BP_ALL	GO:0042221~response to chemical stimulus	53	11.088	1.17E-03	1.562	2.04E-02
GOTERM_BP_ALL	GO:0002440~production of molecular mediator of immune response	6	1.255	1.21E-03	7.305	2.11E-02

GOTERM_BP_ALL	GO:0014706~striated muscle tissue development	11	2.301	1.22E-03	3.489	2.12E-02
GOTERM_BP_ALL	GO:0030324~lung development	10	2.092	1.22E-03	3.812	2.12E-02
GOTERM_BP_ALL	GO:0043009~chordate embryonic development	20	4.184	1.32E-03	2.281	2.29E-02
GOTERM_BP_ALL	GO:0009792~embryonic development ending in birth or egg hatching	20	4.184	1.46E-03	2.260	2.54E-02
GOTERM_BP_ALL	GO:0060548~negative regulation of cell death	21	4.393	1.47E-03	2.202	2.56E-02
GOTERM_BP_ALL	GO:0048514~blood vessel morphogenesis	15	3.138	1.47E-03	2.683	2.56E-02
GOTERM_BP_ALL	GO:0007517~muscle organ development	15	3.138	1.47E-03	2.683	2.56E-02
GOTERM_BP_ALL	GO:0030323~respiratory tube development	10	2.092	1.50E-03	3.700	2.61E-02
GOTERM_BP_ALL	GO:0008285~negative regulation of cell proliferation	21	4.393	1.54E-03	2.196	2.67E-02
GOTERM_BP_ALL	GO:0007178~transmembrane receptor protein serine/threonine kinase signaling pathway	10	2.092	1.61E-03	3.664	2.80E-02
GOTERM_BP_ALL	GO:0033273~response to vitamin	8	1.674	1.73E-03	4.575	3.01E-02
GOTERM_BP_ALL	GO:0040012~regulation of locomotion	14	2.929	1.80E-03	2.752	3.12E-02
GOTERM_BP_ALL	GO:0051270~regulation of cell motion	14	2.929	1.88E-03	2.738	3.26E-02
GOTERM_BP_ALL	GO:0048568~embryonic organ development	13	2.720	2.07E-03	2.853	3.59E-02
GOTERM_BP_ALL	GO:0009605~response to external stimulus	40	8.368	2.08E-03	1.652	3.61E-02
GOTERM_BP_ALL	GO:0022603~regulation of anatomical structure morphogenesis	15	3.138	2.09E-03	2.585	3.61E-02
GOTERM_BP_ALL	GO:0001501~skeletal system development	19	3.975	2.12E-03	2.248	3.68E-02
GOTERM_BP_ALL	GO:0001655~urogenital system development	10	2.092	2.53E-03	3.431	4.37E-02
GOTERM_BP_ALL	GO:0043066~negative regulation of apoptosis	20	4.184	2.83E-03	2.132	4.88E-02
GOTERM_BP_ALL	GO:0010942~positive regulation of cell death	23	4.812	2.83E-03	1.996	4.88E-02
GOTERM_BP_ALL	GO:0042592~homeostatic process	34	7.113	2.89E-03	1.709	4.97E-02
GOTERM_CC_ALL	GO:0031012~extracellular matrix	27	5.649	8.16E-07	3.074	1.09E-05
GOTERM_CC_ALL	GO:0044421~extracellular region part	50	10.460	2.36E-06	2.046	3.16E-05
GOTERM_CC_ALL	GO:0005578~proteinaceous extracellular matrix	25	5.230	2.37E-06	3.069	3.17E-05
GOTERM_CC_ALL	GO:0005576~extracellular region	83	17.364	7.49E-06	1.622	1.00E-04
GOTERM_CC_ALL	GO:0044420~extracellular matrix part	13	2.720	4.24E-05	4.364	5.66E-04
GOTERM_CC_ALL	GO:0005604~basement membrane	9	1.883	8.02E-04	4.532	1.07E-02
GOTERM_CC_ALL	GO:0005615~extracellular space	32	6.695	1.38E-03	1.835	1.83E-02
GOTERM_MF_ALL	GO:0016614~oxidoreductase activity, acting on CH-OH group of donors	14	2.929	7.18E-06	4.772	1.08E-04
GOTERM_MF_ALL	GO:0016616~oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor	13	2.720	1.20E-05	4.942	1.80E-04
GOTERM_MF_ALL	GO:0005488~binding	346	72.385	1.66E-05	1.092	2.49E-04
GOTERM_MF_ALL	GO:0016491~oxidoreductase activity	35	7.322	1.50E-04	2.008	2.26E-03
GOTERM_MF_ALL	GO:0031402~sodium ion binding	12	2.510	1.81E-04	4.055	2.71E-03
GOTERM_MF_ALL	GO:0046983~protein dimerization activity	27	5.649	1.35E-03	1.970	2.00E-02
GOTERM_MF_ALL	GO:0050661~NADP or NADPH binding	6	1.255	1.97E-03	6.590	2.92E-02
GOTERM_MF_ALL	GO:0015293~symporter activity	11	2.301	2.49E-03	3.175	3.67E-02
GOTERM_MF_ALL	GO:0005515~protein binding	234	48.954	2.56E-03	1.135	3.78E-02

1,25(OH)₂D₃-downregulated genes

Category	Term	Count	%	p Value	Fold enrichment	FDR
GOTERM_BP_ALL	GO:0007155~cell adhesion	49	7.270	1.20E-06	2.116	2.10E-05
GOTERM_BP_ALL	GO:0022610~biological adhesion	49	7.270	1.27E-06	2.113	2.23E-05
GOTERM_BP_ALL	GO:0048731~system development	115	17.062	5.06E-06	1.492	8.87E-05
GOTERM_BP_ALL	GO:0048856~anatomical structure development	122	18.101	6.53E-06	1.459	1.15E-04
GOTERM_BP_ALL	GO:0007160~cell-matrix adhesion	14	2.077	6.68E-06	4.755	1.17E-04
GOTERM_BP_ALL	GO:0031589~cell-substrate adhesion	14	2.077	1.95E-05	4.318	3.42E-04
GOTERM_BP_ALL	GO:0048513~organ development	87	12.908	6.66E-05	1.513	1.17E-03
GOTERM_BP_ALL	GO:0009653~anatomical structure morphogenesis	65	9.644	7.60E-05	1.641	1.33E-03
GOTERM_BP_ALL	GO:0007275~multicellular organismal development	128	18.991	1.49E-04	1.350	2.61E-03
GOTERM_BP_ALL	GO:0055065~metal ion homeostasis	19	2.819	1.57E-04	2.802	2.75E-03
GOTERM_BP_ALL	GO:0032502~developmental process	137	20.326	2.56E-04	1.315	4.48E-03
GOTERM_BP_ALL	GO:0006875~cellular metal ion homeostasis	18	2.671	2.74E-04	2.776	4.79E-03
GOTERM_BP_ALL	GO:0030154~cell differentiation	79	11.721	4.96E-04	1.459	8.67E-03
GOTERM_BP_ALL	GO:0006954~inflammatory response	24	3.561	5.10E-04	2.232	8.90E-03
GOTERM_BP_ALL	GO:0009887~organ morphogenesis	35	5.193	5.24E-04	1.876	9.14E-03
GOTERM_BP_ALL	GO:0006935~chemotaxis	15	2.226	8.51E-04	2.834	1.48E-02
GOTERM_BP_ALL	GO:0042330~taxis	15	2.226	8.51E-04	2.834	1.48E-02
GOTERM_BP_ALL	GO:0008544~epidermis development	16	2.374	1.17E-03	2.628	2.03E-02
GOTERM_BP_ALL	GO:0000165~MAPKKK cascade	16	2.374	1.17E-03	2.628	2.03E-02
GOTERM_BP_ALL	GO:0051246~regulation of protein metabolic process	33	4.896	1.22E-03	1.827	2.12E-02
GOTERM_BP_ALL	GO:0055080~cation homeostasis	21	3.116	1.34E-03	2.219	2.33E-02
GOTERM_BP_ALL	GO:0048869~cellular developmental process	79	11.721	1.65E-03	1.400	2.85E-02
GOTERM_BP_ALL	GO:0030003~cellular cation homeostasis	19	2.819	1.97E-03	2.261	3.39E-02
GOTERM_BP_ALL	GO:0032268~regulation of cellular protein metabolic process	29	4.303	2.12E-03	1.849	3.66E-02
GOTERM_BP_ALL	GO:0030198~extracellular matrix organization	11	1.632	2.28E-03	3.197	3.92E-02
GOTERM_BP_ALL	GO:0030199~collagen fibril organization	6	0.890	2.37E-03	6.254	4.07E-02
GOTERM_BP_ALL	GO:0050801~ion homeostasis	26	3.858	2.37E-03	1.922	4.07E-02
GOTERM_BP_ALL	GO:0007398~ectoderm development	16	2.374	2.53E-03	2.430	4.34E-02
GOTERM_BP_ALL	GO:0007243~protein kinase cascade	24	3.561	2.81E-03	1.961	4.81E-02
GOTERM_BP_ALL	GO:0009611~response to wounding	31	4.599	2.88E-03	1.768	4.94E-02
GOTERM_CC_ALL	GO:0044421~extracellular region part	65	9.644	7.93E-08	2.028	1.09E-06
GOTERM_CC_ALL	GO:0005578~proteinaceous extracellular matrix	31	4.599	3.44E-07	2.902	4.72E-06
GOTERM_CC_ALL	GO:0031012~extracellular matrix	32	4.748	5.55E-07	2.779	7.62E-06
GOTERM_CC_ALL	GO:0005625~soluble fraction	25	3.709	1.34E-04	2.393	1.84E-03
GOTERM_CC_ALL	GO:0005576~extracellular region	95	14.095	3.66E-04	1.416	5.02E-03
GOTERM_CC_ALL	GO:0005615~extracellular space	41	6.083	4.14E-04	1.793	5.67E-03
GOTERM_CC_ALL	GO:0044420~extracellular matrix part	13	1.929	5.28E-04	3.329	7.22E-03

GOTERM_CC_ALL	GO:0005887~integral to plasma membrane	61	9.050	7.90E-04	1.538	1.08E-02
GOTERM_CC_ALL	GO:0031226~intrinsic to plasma membrane	62	9.199	8.24E-04	1.529	1.13E-02
GOTERM_CC_ALL	GO:0005581~collagen	7	1.039	9.47E-04	5.992	1.29E-02
GOTERM_MF_ALL	GO:0005102~receptor binding	61	9.050	7.87E-08	2.085	1.19E-06
GOTERM_MF_ALL	GO:0001664~G-protein-coupled receptor binding	17	2.522	6.92E-07	4.638	1.04E-05
GOTERM_MF_ALL	GO:0008009~chemokine activity	10	1.484	1.58E-05	6.584	2.38E-04
GOTERM_MF_ALL	GO:0042379~chemokine receptor binding	10	1.484	2.70E-05	6.181	4.07E-04
GOTERM_MF_ALL	GO:0008092~cytoskeletal protein binding	35	5.193	6.36E-05	2.103	9.57E-04
GOTERM_MF_ALL	GO:0003779~actin binding	25	3.709	2.11E-04	2.323	3.18E-03
GOTERM_MF_ALL	GO:0042277~peptide binding	18	2.671	4.07E-04	2.685	6.11E-03
GOTERM_MF_ALL	GO:0005201~extracellular matrix structural constituent	11	1.632	5.18E-04	3.874	7.77E-03
GOTERM_MF_ALL	GO:0001871~pattern binding	15	2.226	5.75E-04	2.950	8.63E-03
GOTERM_MF_ALL	GO:0030247~polysaccharide binding	15	2.226	5.75E-04	2.950	8.63E-03
GOTERM_MF_ALL	GO:0008201~heparin binding	11	1.632	2.10E-03	3.234	3.12E-02
GOTERM_MF_ALL	GO:0005539~glycosaminoglycan binding	13	1.929	2.30E-03	2.812	3.41E-02
GOTERM_MF_ALL	GO:0030246~carbohydrate binding	23	3.412	3.39E-03	1.968	4.98E-02

Supplementary Table S11 Forty-eight genes that comprise the 1,25(OH)₂D₃-gene signature established with the genes most differentially regulated (FDR<0.05, -1>log₂ fold-change>1) by 1,25(OH)₂D₃ in human colon CAFs

<i>ADAMTS8</i>	<i>DKFZP547L112</i>	<i>LINC00176</i>	<i>S100A4</i>
<i>ANXA2</i>	<i>EFTUD1</i>	<i>LOC728392</i>	<i>SEMA3B</i>
<i>APBB1IP</i>	<i>FLJ22184</i>	<i>LYNX1</i>	<i>SNORA71A</i>
<i>C15orf48</i>	<i>FOXB1</i>	<i>MAPK13</i>	<i>SP8</i>
<i>CCDC3</i>	<i>G0S2</i>	<i>MON1B</i>	<i>SSTR3</i>
<i>CCL11</i>	<i>HMCN1</i>	<i>NACAP1</i>	<i>TMEM95</i>
<i>CD14</i>	<i>IDH2</i>	<i>NID2</i>	<i>TOR2A</i>
<i>CD82</i>	<i>IGF1</i>	<i>NPTX2</i>	<i>YJEFN3</i>
<i>CH25H</i>	<i>IGFBP3</i>	<i>PCSK1N</i>	<i>ZFP36</i>
<i>CLMN</i>	<i>IGFLR1</i>	<i>POSTN</i>	<i>ZNF205</i>
<i>CXCL12</i>	<i>IL7R</i>	<i>RARRES1</i>	<i>ZNF205-AS1</i>
<i>CYP24A1</i>	<i>KCTD19</i>	<i>RHBDL1</i>	<i>ZNF90</i>