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Supplementary Materials for

Single-cell morphology encodes metastatic potential

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The PDF file includes:

Other Supplementary Material for this manuscript includes the following:

(available at advances.sciencemag.org/cgi/content/full/6/4/eaaw6938/DC1)

Supplementary materials

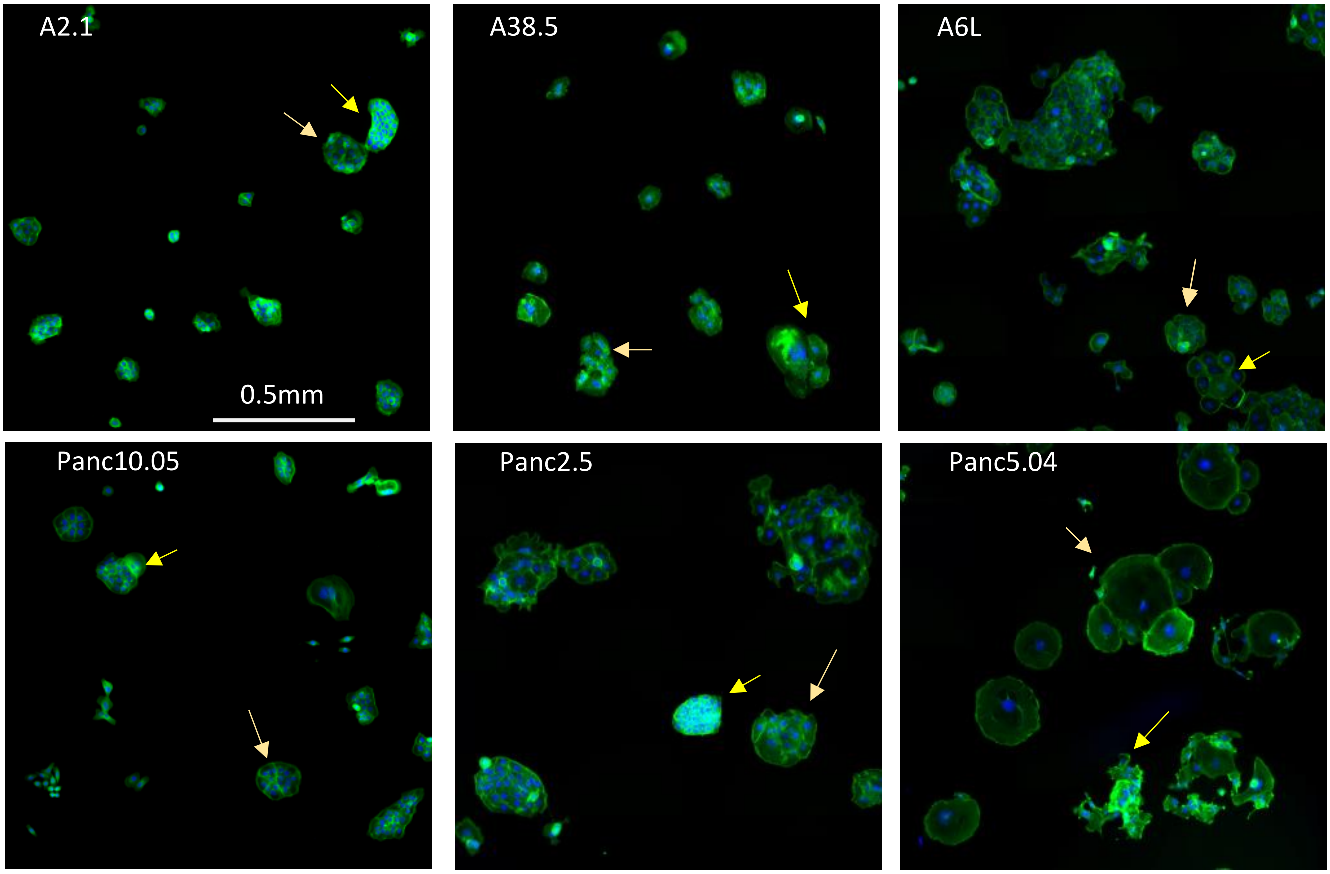


Fig. S1. Cell polymorphism in cancer cells derived from primary pancreatic tumors and metastases. Representative images of pancreatic cancer cells stained for their nucleus (blue) and F-actin (green) in the ultra low-density growth conditions. These include cancer cells derived from metastases that spread from pancreatic tumors (A2.1, A38.5 and A6L) and cells derived from primary pancreatic tumors (Panc10.05, Panc2.5 and Panc5.04). Cells formed several spatially and morphologically distinct progenies. Arrows highlight colonies with distinct cell morphology of the same type.

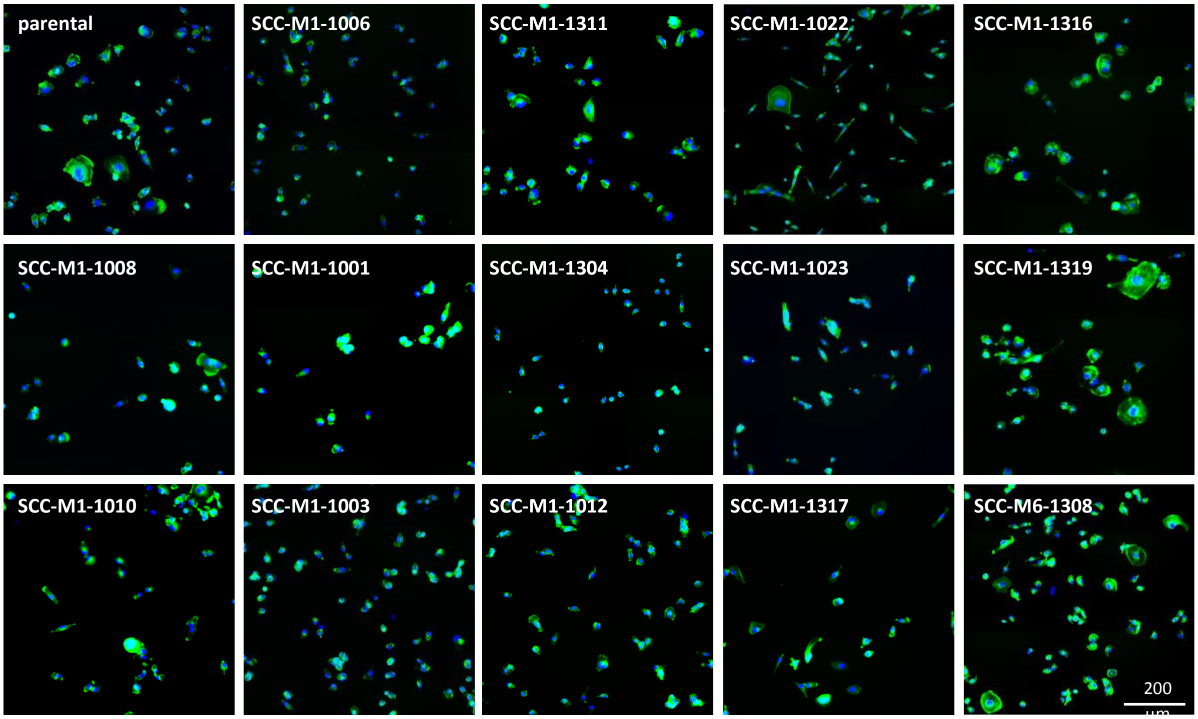


Fig. S2. Morphological spectrum of SCCs. Representative images of 14 different SCCs and their parental MDA-MB-231 breast cancer cells; nuclei and F-actin were stained and shown in blue and green, respectively.

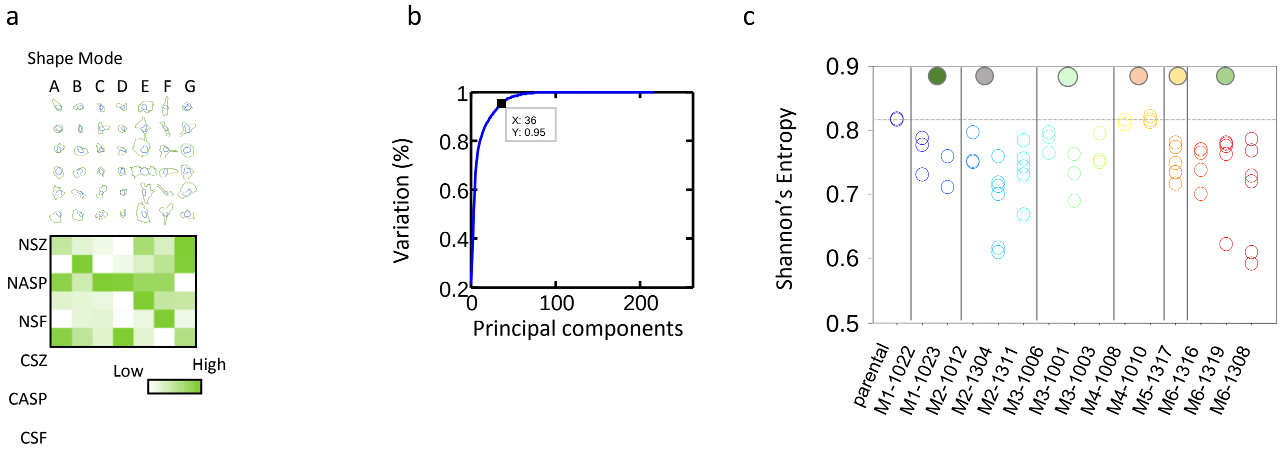


Fig. S3. Quantitative morphology analysis of metastasis of breast cancer cells. a. A heat map shows the average nucleus size (NSZ), the nucleus aspect ratio (NASP), the nucleus shape factor (NSF), the cell size (CSZ), the cell aspect ratio (CASP), and the cell shape factor (CSF) for the cell morph classes A-G. The aspect ratio is defined as the ratio between the lengths of the long axis and short axis. The shape factor was calculated using 4π x (Area)/(perimeter^2). **b**. Principal component analysis for cell morphology feature matrix of SCC cells shows that 95% of variations were covered by the first 36 eigenvectors. **c**. Shannon's entropy of CM distribution for different SCCs. The numbers at the bottom indicate the corresponding morpho-types of the SCCs.

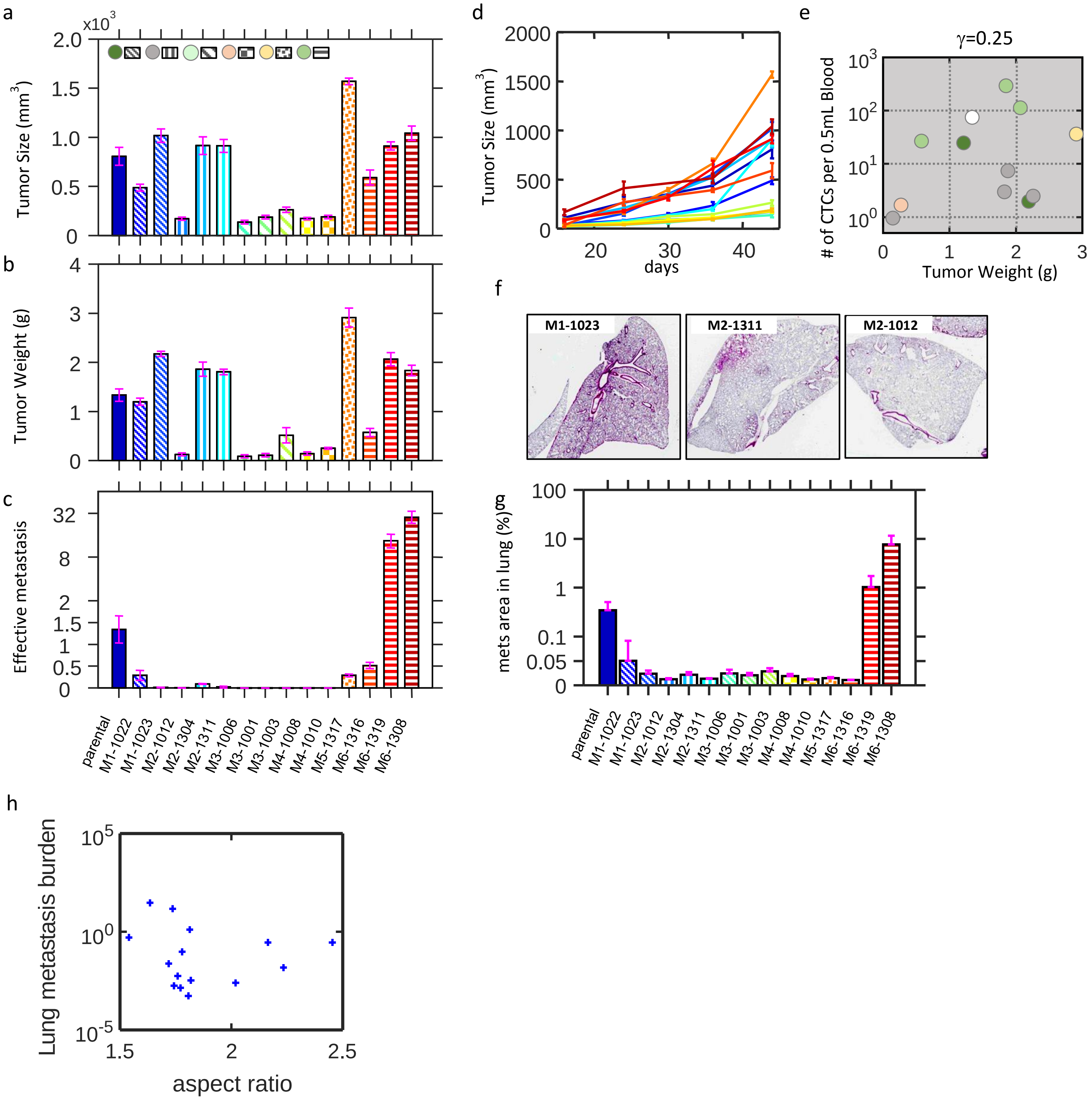


Fig. S4. SCCs derived from the same parental breast cancer cells show divergent invasive behavior in vivo. a-c. Bar graphs show the tumor size (a), tumor weight (b), and effective metastasis to the lung (c) after injecting different SCCs into the mammary pad of mice. **d**. Growth of tumors formed by different SCCs. **e**. Scatter plot shows that the CTC count and tumor weight of different SCCs are poorly correlated (Pearson correlation coefficient of 0.25). **f**. Histological sections of mice lung show metastatic lesion free are presented in SCC-1023, SCC-1311 and SCC-1012. At least four mice were tested for each SCC. **g**. Measurement of area ratio occupied by metastasized cancer cells in the tissue sections of lung of mice. **h**. A scatter plot shows the relationship between average cell aspect ratio and corresponding lung metastasis burden (measured by human DNA in the lung) among different SCCs. There is no clear correlation between the cell aspect ratio of SCCs and their metastatic potential, with a Pearson's correlation coefficient of 0.13. Error bars represent standard error of the mean.

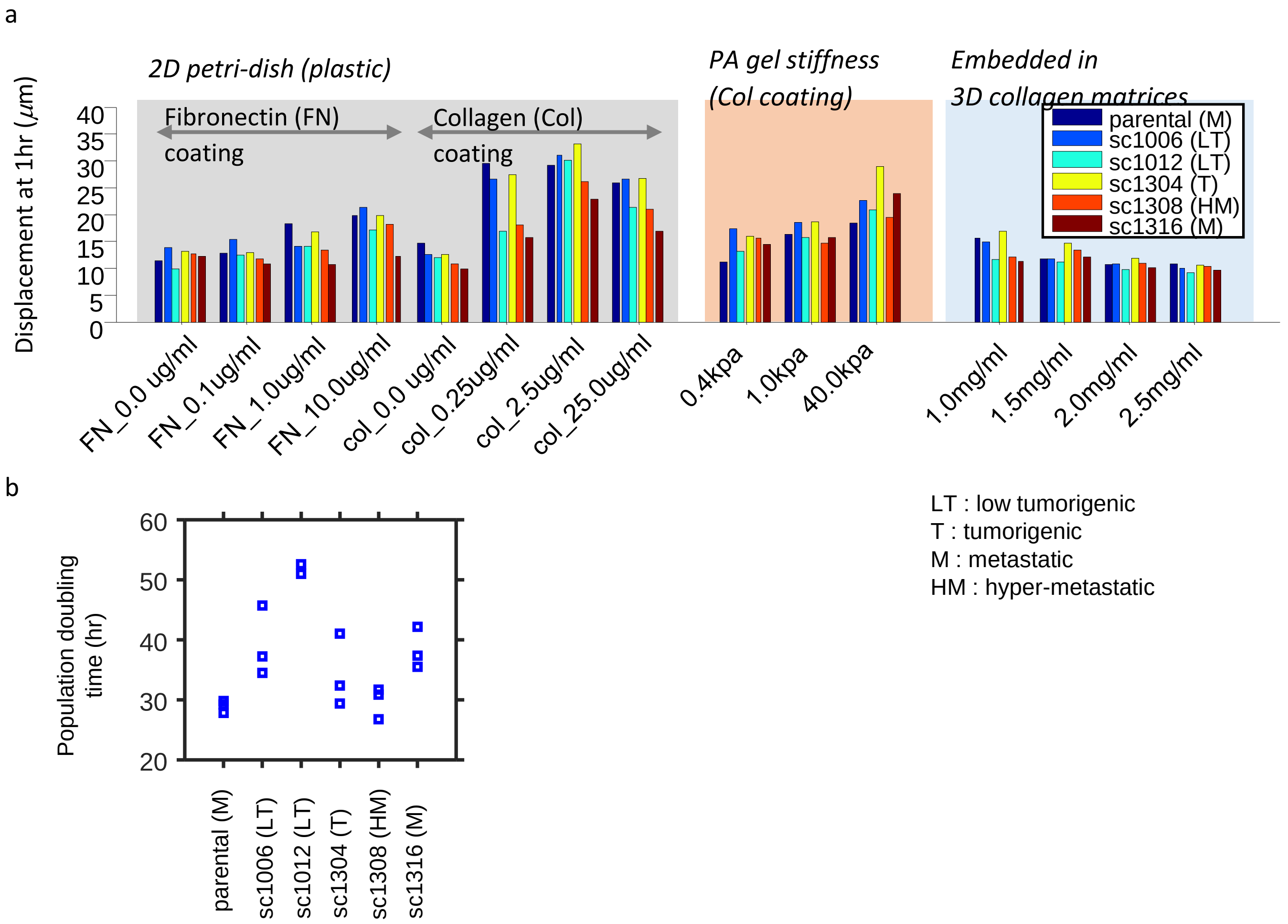


Fig. S5. Analysis of SCC with migration and proliferation assay. a. Migration speed of different SCCs under different culture models including 2D substrates with different concentration of fibronectin (FN) and collagen I (COL) coating on petri dishes, on 2D substrates of different stiffness (0.4kpa, 1.0kpa and 40.0kpa) and embedded in 3D collagen I matrices of four different collagen densities (1mg/ml, 1.5mg/ml, 2.0mg/ml and 2.5mg/ml). Overall the results show the metastatic SCCs, SC1308 and SC1316, do not display a more motile behavior than other SCCs in all *in vitro* models tested. **b**. Population doubling time of different SCCs. These results show little correlation between tumorigenicity (primary tumor growth) of SCCs *in vivo* and their doubling time *in vitro*.

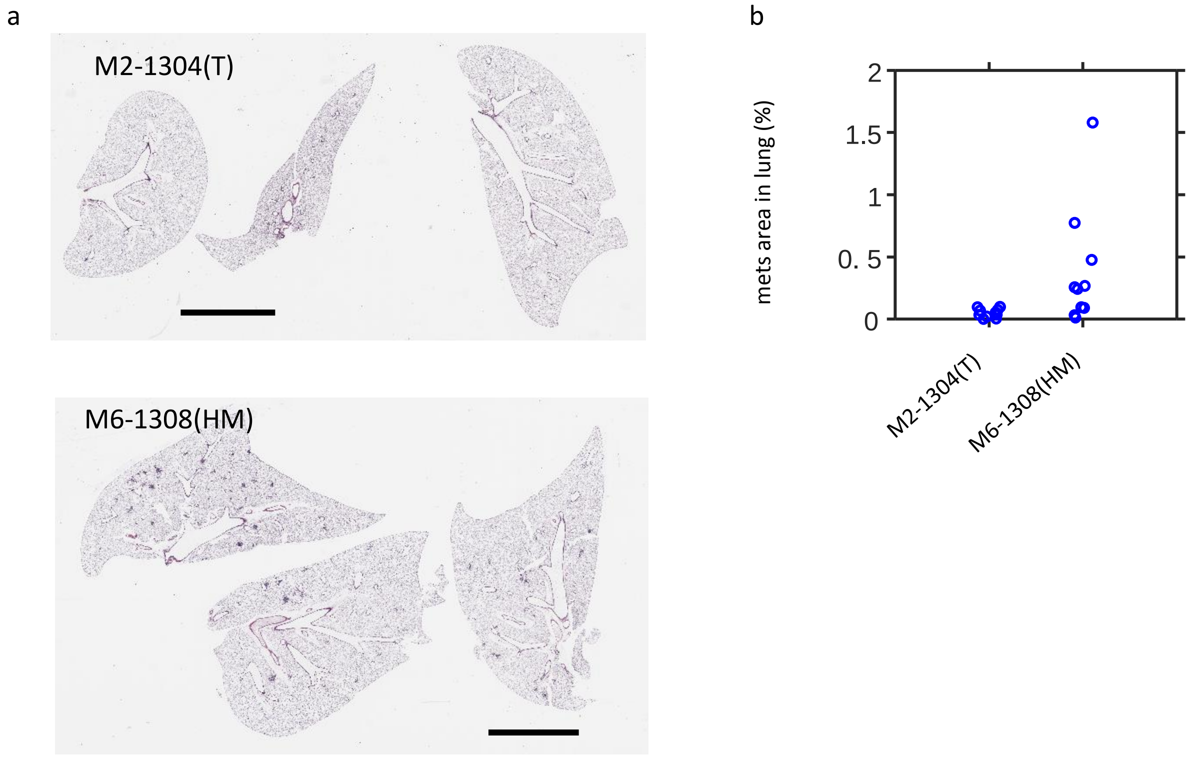


Fig. S6. Lung tissue sections in tail vein metastasis model for different SCCs. a. Histological sections of mice lung show there are multiple metastatic lesions in mice that were injected in the tail vein with SCC-1308 (HM) cells, but not with SCC-1304 (T) cells. **b**. Measurement of the area ratio occupied by metastasized tumor cells in the tissue sections of the lung of mice in these two samples.

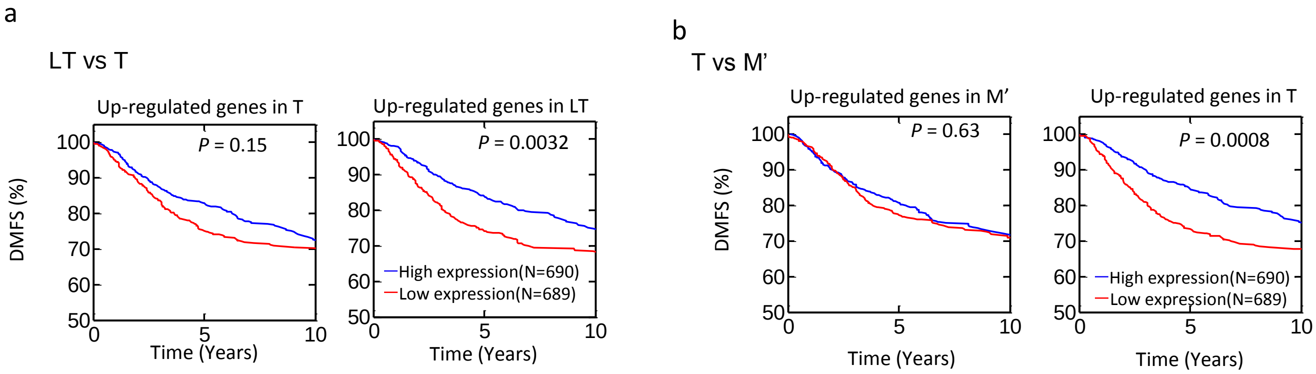
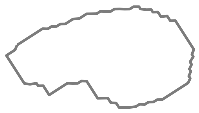


Fig. S7. Distinct gene expression profiles of SCCs reveal prognostic genes. a-b. Differentially expressed genes between LT-SCCs and T-SCCs (a) and between T-SCCs and M'-SCCs (b) were used to investigate the prognostication power. Patients with a higher expression of tumorigenic and metastatic suppressor genes (i.e. genes up-regulated in LT-SCCs compared to T-SCCs or genes up-regulated in T-SCCs compared to M-SCCs) have a significantly longer survival time than patients with low expression (*P* = 0.0032 and *P* = 0.0008 for LT vs. T and T vs. M'). For the genes that are up-regulated in the T-SCCs compared to LT-SCCs or T-SCCs compared to M'-SCCs, no significant prognostic power was found (*P* > 0.05). *P* value was calculated using log-rank test.

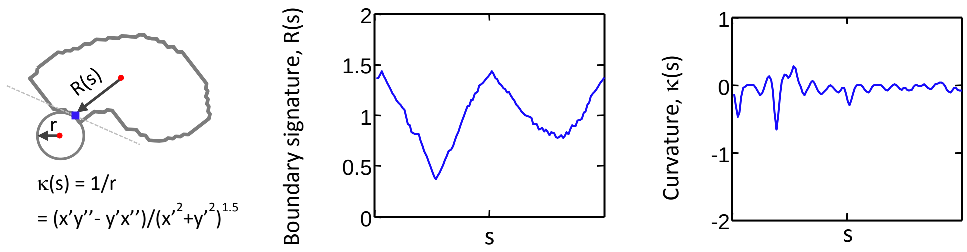
Category I : Basic morphological features



Features:

Area, perimeter, long axis, aspect ratio,…etc.

Category II & III : Boundary signature and curvature

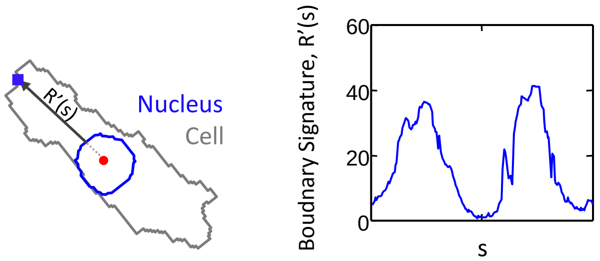


Features:

mean(R), median(R), std(R),

mean(κ), median(κ),std(κ)….etc

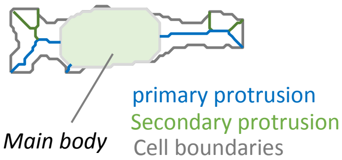
Category IV: N-C positioning signature



Features:

mean(R'), median(R'), std(R'), ….etc.

Category V: Protrusion



Features:

Protrusion numbers, <protrusion length> …etc.

Fig. S8. Morphological features. Schematic plots illustrating four major categories of morphological features that were extracted to quantitatively represent the morphology of individual cells.

Table S1. Summary of SCC information.

Cell name	Morphotype class	Gene expression profiles	Agressiveness grade	Tested mouse number	Xenograft mouse model			
					Turmor size(mm^3) (mean ± sem)	Turmor weight (g) (mean ± sem)	Effective metastasis (A.U.) (mean ± sem)	CTC counts (#/0.5ml blood) (mean ± sem)
parental	4	4	M	8	807.9 ± 257.2	1.34 ± 0.13	$1.3 \times 10^{0} \pm 1.3 \times 10^{-1}$	71.8 ± 8.17
SCC-1006	3	1	LT	4	137.0 ± 39.2	0.09 ± 0.03	$1.4 \times 10^{-3} \pm 4.5 \times 10^{-4}$	N.A.
SCC-1001	3	1	LT	4	188.0 ± 39.7	0.11 ± 0.04	$3.4 \times 10^{-3} \pm 5.7 \times 10^{-4}$	N.A.
SCC-1003	3	1	LT	4	263.2 ± 55.6	0.51 ± 0.16	$1.8 \times 10^{-3} \pm 4.2 \times 10^{-4}$	N.A.
SCC-1008	4	1	LT	4	174.3 ± 26.1	0.14 ± 0.04	$2.5 \times 10^{-3} \pm 8.9 \times 10^{-4}$	N.A.
SCC-1010	4	1	LT	4	189.6 ± 34.6	0.25 ± 0.02	$5.5 \times 10^{-4} \pm 1.2 \times 10^{-4}$	1.6 ± 0.4
SCC-1012	2	1	LT	4	172.0 ± 29.6	0.13 ± 0.03	$5.6 \times 10^{-3} \pm 1.2 \times 10^{-3}$	1.0 ± 0.0
SCC-1304	2	3	T	4	916.1 ± 180.4	1.86 ± 0.14	$9.6 \times 10^{-2} \pm 1.0 \times 10^{-2}$	7.4 ± 0.7
SCC-1311	2	3	T	4	912.8 ± 133.0	1.81 ± 0.06	$2.4 \times 10^{-2} \pm 1.9 \times 10^{-2}$	3.0 ± 1.3
SCC-1022	1	2	T	4	488.7 ± 71.4	1.20 ± 0.07	$2.9 \times 10^{-1} \pm 1.1 \times 10^{-1}$	24.6 ± 8.3
SCC-1023	1	2	T	4	1017.9 ± 136.8	2.18 ± 0.05	$1.5 \times 10^{-2} \pm 5.6 \times 10^{-3}$	2.0 ± 0.4
SCC-1317	5	3	T	4	1569.1 ± 65.3	2.92 ± 0.19	$2.9 \times 10^{-1} \pm 2.8 \times 10^{-2}$	35.8 ± 11.0
SCC-1316	6	4	M	4	590.5 ± 171.8	0.58 ± 0.08	$5.2 \times 10^{-1} \pm 7.0 \times 10^{-2}$	26.8 ± 4.9
SCC-1319	6	4	HM	4	912.5 ± 83.8	2.07 ± 0.13	$1.5 \times 10^{1} \pm 3.0 \times 10^{0}$	112.6 ± 28.7
SCC-1308	6	4	HM	4	1042.1 ± 145.0	1.84 ± 0.11	$3.0 \times 10^{1} \pm 5.5 \times 10^{0}$	293.0 ± 55.4

Table S2. Genes that are highly differentially expressed among SCP.

probe ID	Gene Symbol	Gene title	S.D. of SCP gene expression (in log2)	range of SCP gene expression (in log2)	max diff gene exp relative to parental (in log2)
11738785_at	SPANXB2	SPANX family, member B2	4.09	10.10	1.57
11738786_x_at	SPANXB2	SPANX family, member B2	3.95	9.99	2.08
11731994_s_at	SPANXE	SPANX family, member E	3.83	9.66	2.79
11726177_s_at	SPANXB2	SPANX family, member B2	3.78	9.49	2.34
11734286_a_at	COX7B2	cytochrome c oxidase subunit VIIb2	3.42	7.62	0.97
11726339_s_at	MAGEA3	melanoma antigen family A, 3	3.14	7.76	1.73
11749461_a_at	CDH11	cadherin 11, type 2, OB-cadherin (osteoblast)	3.03	7.98	2.13
11728829_at	INHBB	inhibin, beta B	2.89	7.97	2.13
11724322_a_at	CST6	cystatin E/M	2.80	6.99	5.07
11728190_s_at	CXCR4	chemokine (C-X-C motif) receptor 4	2.77	7.40	0.72
11754662_s_at	ADAMTS1	ADAM metallopeptidase with thrombospondin type 1 motif, 1	2.75	6.90	0.00
11720146_a_at	DAPK1	death-associated protein kinase 1	2.71	7.08	1.92
11744581_a_at	KHDRBS3	KH domain containing, RNA binding, signal transduction associated 3	2.68	6.95	0.00
11742710_a_at	SRGN	serglycin	2.63	7.03	0.13
11747952_x_at	TNFSF10	tumor necrosis factor (ligand) superfamily, member 10	2.59	6.84	6.19
11729544_at	MAGEC1	melanoma antigen family C, 1	2.53	6.76	0.72
11715455_x_at	KISS1	KiSS-1 metastasis-suppressor	2.50	7.75	1.06
11724885_at	CLIC3	chloride intracellular channel 3	2.47	7.24	5.61
11715454_at	KISS1	KiSS-1 metastasis-suppressor	2.46	7.44	0.89
11748907_a_at	RARRES3	retinoic acid receptor responder (tazarotene induced) 3	2.46	6.91	6.10
11729543_a_at	MAGEC1	melanoma antigen family C, 1	2.46	6.65	1.00
11743730_at	TNFSF10	tumor necrosis factor (ligand) superfamily, member 10	2.46	6.39	6.19
11719692_a_at	RARRES3	retinoic acid receptor responder (tazarotene induced) 3	2.43	6.83	5.93
11726250_at	AGR2	anterior gradient 2 homolog (Xenopus laevis)	2.41	6.61	2.70
11719172_x_at	AKR1C1	aldo-keto reductase family 1, member C1	2.36	7.51	4.97
11743731_a_at	TNFSF10	tumor necrosis factor (ligand) superfamily, member 10	2.36	6.53	5.90
11719414_a_at	PBX1	pre-B-cell leukemia homeobox 1	2.36	6.48	4.58
11729495_at	FAM133A	family with sequence similarity 133, member A	2.35	6.47	1.99
11727844_a_at	KRT81	keratin 81	2.35	6.17	0.86
11740312_at	HAS2	hyaluronan synthase 2	2.35	6.79	0.46
11732318_a_at	KHDRBS3	KH domain containing, RNA binding, signal transduction associated 3	2.34	6.17	0.06
11754189_s_at	AKR1C1	aldo-keto reductase family 1, member C1	2.32	8.07	4.50
11755928_s_at	MMP1	matrix metallopeptidase 1 (interstitial collagenase)	2.32	6.91	1.84
11719171_a_at	AKR1C1	aldo-keto reductase family 1, member C1	2.31	7.19	4.89
11757871_s_at	PBX1	pre-B-cell leukemia homeobox 1	2.31	5.97	4.14
11729496_at	FAM133A	family with sequence similarity 133, member A	2.29	5.97	1.59
11728189_a_at	CXCR4	chemokine (C-X-C motif) receptor 4	2.29	6.52	1.06
11739696_s_at	AFF3	AF4/FMR2 family, member 3	2.24	5.53	0.24
11746283_s_at	KRTAP2-3	keratin associated protein 2-3	2.22	5.87	1.35
11754879_a_at	SDR16C5	short chain dehydrogenase/reductase family 16C, member 5	2.21	5.98	1.94
11758031_s_at	BHLHE41	basic helix-loop-helix family, member e41	2.21	5.65	0.51
11747096_a_at	KCNK1	potassium channel, subfamily K, member 1	2.18	4.99	0.10
11731538_a_at	GPR110	G protein-coupled receptor 110	2.17	6.23	3.26
11741223_s_at	FAM198B	family with sequence similarity 198, member B	2.17	5.70	5.45
11758102_s_at	TMEM163	transmembrane protein 163	2.17	6.39	2.53
11743350_a_at	C15orf48	chromosome 15 open reading frame 48	2.17	6.63	5.25
11719562_at	SOX4	SRY (sex determining region Y)-box 4	2.16	5.54	0.93
11726812_a_at	TFF1	trefoil factor 1	2.14	6.39	2.88
11721984_at	C7orf29	chromosome 7 open reading frame 29	2.14	5.82	5.42
11727690_at	IL11	interleukin 11	2.13	6.14	1.22
11715711_a_at	AKR1C3	aldo-keto reductase family 1, member C3	2.13	6.67	5.00
11733461_at	SUSD5	sushi domain containing 5	2.12	5.59	0.16
11736687_a_at	FGF5	fibroblast growth factor 5	2.11	5.46	0.81
11737331_at	PDE1C	phosphodiesterase 1C, calmodulin-dependent 70kDa	2.11	5.66	1.12
11757480_x_at	IFI27	interferon, alpha-inducible protein 27	2.10	6.27	3.51
11722888_s_at	EMB	embigin	2.09	5.76	0.54
11727984_at	TENM3	teneurin transmembrane protein 3	2.08	5.57	0.01
11719120_a_at	KYNU	kynureninase	2.07	6.17	1.77
11758227_s_at	ROBO1	roundabout, axon guidance receptor, homolog 1 (Drosophila)	2.06	5.22	0.22
11751833_a_at	BCHE	butyrylcholinesterase	2.06	5.95	1.28
11719384_at	PRSS3	protease, serine, 3	2.06	5.76	1.07
11716329_s_at	GJA1	gap junction protein, alpha 1, 43kDa	2.06	6.71	0.37
11744195_at	FAT3	FAT tumor suppressor homolog 3 (Drosophila)	2.05	5.61	1.02
11724795_at	ZG16B	zymogen granule protein 16B	2.04	5.57	4.19
11736688_x_at	FGF5	fibroblast growth factor 5	2.04	5.33	0.62
11732569_at	SLCO1B3	solute carrier organic anion transporter family, member 1B3	2.04	5.84	0.12

11716017_at	MAL2	mal, T-cell differentiation protein 2 (gene/pseudogene)	2.03	5.95	3.06
11763394_a_at	LOC100505946	uncharacterized LOC100505946	2.00	5.50	2.82
11757532_s_at	RBM47	RNA binding motif protein 47	2.00	5.43	4.58
11725057_s_at	NEDD9	neural precursor cell expressed, developmentally down-regulated 9	1.99	5.70	4.21
11746830_a_at	AGR2	anterior gradient 2 homolog (Xenopus laevis)	1.99	5.84	2.34
11728191_x_at	CXCR4	chemokine (C-X-C motif) receptor 4	1.99	5.54	0.89
11716665_s_at	GDF15	growth differentiation factor 15	1.98	5.92	3.38
11731995_x_at	SPANXC	SPANX family, member C	1.98	6.61	1.21
11751225_s_at	CSF2RA	colony stimulating factor 2 receptor, alpha, low-affinity (granulocyte-macrophage)	1.97	5.75	3.77
11754862_a_at	RARRES2	retinoic acid receptor responder (tazarotene induced) 2	1.97	5.31	4.86
11756473_a_at	CELF2	CUGBP, Elav-like family member 2	1.97	5.53	0.96
11740390_a_at	RBM47	RNA binding motif protein 47	1.96	5.64	4.35
11758525_s_at	SOX4	SRY (sex determining region Y)-box 4	1.96	5.21	1.09
11753942_a_at	UCA1	urothelial cancer associated 1 (non-protein coding)	1.95	5.75	2.64
11730442_s_at	FAM155A	family with sequence similarity 155, member A	1.95	5.37	0.23
11741897_a_at	MMP1	matrix metallopeptidase 1 (interstitial collagenase)	1.95	6.33	2.06
11735833_a_at	KIAA1199	KIAA1199	1.95	6.34	5.55
11757534_s_at	FAM198B	family with sequence similarity 198, member B	1.94	5.34	5.08
11748362_s_at	ABCC3	ATP-binding cassette, sub-family C (CFTR/MRP), member 3	1.94	5.03	4.36
11725521_x_at	GLUL	glutamate-ammonia ligase	1.93	6.86	1.69
11735148_a_at	SOCS2	suppressor of cytokine signaling 2	1.92	5.40	0.00
11758070_s_at	PBX1	pre-B-cell leukemia homeobox 1	1.91	4.75	4.43
11736730_a_at	RIMS2	regulating synaptic membrane exocytosis 2	1.90	5.02	1.15
11739809_at	TMEM156	transmembrane protein 156	1.90	4.63	0.09
11740091_s_at	TMEM163	transmembrane protein 163	1.89	5.94	2.78
11762533_a_at	RAP1A	RAP1A, member of RAS oncogene family	1.89	7.66	7.66
11717762_a_at	CPVL	carboxypeptidase, vitellogenic-like	1.89	5.76	0.92
11717803_a_at	NTN4	netrin 4	1.89	5.25	0.53
11717305_a_at	ADIRF	adipogenesis regulatory factor	1.88	6.15	3.12
11736729_a_at	RIMS2	regulating synaptic membrane exocytosis 2	1.87	4.92	1.25
11726188_at	SHISA3	shisa homolog 3 (Xenopus laevis)	1.87	4.67	0.25
11729647_s_at	ESM1	endothelial cell-specific molecule 1	1.87	5.97	0.82
11757702_s_at	DSC2	desmocollin 2	1.87	5.28	1.39
11723751_at	TFF2	trefoil factor 2	1.86	6.03	3.49
11734808_s_at	DTNA	dystrobrevin, alpha	1.85	4.69	0.69
11740311_at	HAS2	hyaluronan synthase 2	1.85	5.65	0.50
11723464_s_at	CELF2	CUGBP, Elav-like family member 2	1.84	5.70	1.02
11756085_a_at	MAGEC1	melanoma antigen family C, 1	1.84	5.10	0.85
11725517_x_at	ABCG1	ATP-binding cassette, sub-family G (WHITE), member 1	1.84	5.22	2.66
11736685_a_at	FGF5	fibroblast growth factor 5	1.84	4.95	0.92
11718230_a_at	HLA-F	major histocompatibility complex, class I, F	1.83	4.63	4.20
11756072_s_at	SAA1	serum amyloid A1	1.83	6.58	5.83
11754856_a_at	CA12	carbonic anhydrase XII	1.82	6.34	3.87
11740528_a_at	AFF3	AF4/FMR2 family, member 3	1.82	4.90	0.49
11720947_x_at	CA12	carbonic anhydrase XII	1.82	6.42	3.84
11757046_a_at	LOC100127888	uncharacterized LOC100127888	1.82	5.01	2.13
11754601_s_at	SPON2	spondin 2, extracellular matrix protein	1.81	5.09	4.80
11717885_a_at	CCDC3	coiled-coil domain containing 3	1.81	5.05	5.05
11717742_a_at	GPRC5C	G protein-coupled receptor, family C, group 5, member C	1.80	5.52	4.25
11743129_at	SORL1	sortilin-related receptor, L(DLR class) A repeats containing	1.80	5.22	4.14
11755523_a_at	RBM47	RNA binding motif protein 47	1.78	4.83	4.24
11721625_s_at	GLUL	glutamate-ammonia ligase	1.78	6.76	1.88
11734271_a_at	CDH18	cadherin 18, type 2	1.77	4.41	1.01
11744484_s_at	HLA-DRA	major histocompatibility complex, class II, DR alpha	1.77	5.53	2.98
11729020_at	ZNF804A	zinc finger protein 804A	1.76	4.70	0.50
11746149_x_at	BCHE	butyrylcholinesterase	1.76	4.97	1.20
11726192_at	TFAP2C	transcription factor AP-2 gamma (activating enhancer binding protein 2 gamma)	1.76	4.91	0.85
11726333_s_at	LEF1	lymphoid enhancer-binding factor 1	1.75	5.14	0.04
11753915_a_at	SEL1L3	sel-1 suppressor of lin-12-like 3 (C. elegans)	1.74	5.69	1.15
11715893_s_at	IFI27	interferon, alpha-inducible protein 27	1.74	5.49	3.31
11758166_s_at	KAL1	Kallmann syndrome 1 sequence	1.73	6.31	2.30
11730106_a_at	PLCB1	phospholipase C, beta 1 (phosphoinositide-specific)	1.72	4.66	1.44
11719827_a_at	QPCT	glutaminyl-peptide cyclotransferase	1.72	5.25	1.35
11759295_at	EHF	ets homologous factor	1.71	6.57	0.90
11755908_s_at	IGSF3	immunoglobulin superfamily, member 3	1.71	5.60	3.50
11732719_at	EREG	epiregulin	1.70	5.56	2.70

11738858_x_at	CSF2RA	colony stimulating factor 2 receptor, alpha, low-affinity (granulocyte-macrophage)	1.70	5.15	3.40
11717721_s_at	ST6GAL1	ST6 beta-galactosamide alpha-2,6-sialyltranferase 1	1.70	4.93	2.00
11721454_a_at	SERPINA1	serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 1	1.69	4.88	4.06
11743856_a_at	CTHRC1	collagen triple helix repeat containing 1	1.69	4.77	2.34
11728203_a_at	PHGDH	phosphoglycerate dehydrogenase	1.69	4.41	0.75
11719828_x_at	QPCT	glutaminyl-peptide cyclotransferase	1.68	5.09	1.42
11716666_a_at	ID3	inhibitor of DNA binding 3, dominant negative helix-loop-helix protein	1.67	5.28	2.57
11734938_x_at	CSF2RA	colony stimulating factor 2 receptor, alpha, low-affinity (granulocyte-macrophage)	1.67	4.96	3.00
11744776_a_at	NNMT	nicotinamide N-methyltransferase	1.67	5.70	3.61
11716663_a_at	GDF15	growth differentiation factor 15	1.67	4.82	3.14
11757396_s_at	ANXA8L2	annexin A8-like 2	1.67	5.14	3.18
11751612_a_at	SOCS2	suppressor of cytokine signaling 2	1.67	4.81	0.34
11715918_s_at	CD24	CD24 molecule	1.67	5.31	1.57
11730048_at	SLITRK5	SLIT and NTRK-like family, member 5	1.67	4.24	0.62
11722991_a_at	DMD	dystrophin	1.66	4.29	1.49
11715467_s_at	ARHGDIB	Rho GDP dissociation inhibitor (GDI) beta	1.66	6.44	0.39
11754796_a_at	SLCO3A1	solute carrier organic anion transporter family, member 3A1	1.66	4.64	3.38
11720409_s_at	CYP1B1	cytochrome P450, family 1, subfamily B, polypeptide 1	1.66	5.00	2.94
11727583_a_at	EPHA3	EPH receptor A3	1.66	4.95	1.10
11718506_at	TFF3	trefoil factor 3 (intestinal)	1.66	4.99	3.82
11732158_a_at	ADAMTS1	ADAM metallopeptidase with thrombospondin type 1 motif, 1	1.65	4.38	0.01
11746930_a_at	BHLHE41	basic helix-loop-helix family, member e41	1.65	4.43	0.81
11719198_s_at	CCND2	cyclin D2	1.65	4.53	1.30
11750552_s_at	CARD16	caspase recruitment domain family, member 16	1.65	5.45	1.58
11764166_s_at	EHF	ets homologous factor	1.65	6.42	0.98
11725515_a_at	ABCG1	ATP-binding cassette, sub-family G (WHITE), member 1	1.65	4.68	2.19
11725516_s_at	ABCG1	ATP-binding cassette, sub-family G (WHITE), member 1	1.65	4.74	3.11
11744718_a_at	CTHRC1	collagen triple helix repeat containing 1	1.64	4.22	1.79
11742850_x_at	HLA-DRA	major histocompatibility complex, class II, DR alpha	1.64	4.90	3.08
11751745_x_at	PRSS3	protease, serine, 3	1.64	4.58	1.11
11746094_a_at	MPP4	membrane protein, palmitoylated 4 (MAGUK p55 subfamily member 4)	1.63	4.56	2.18
11739094_a_at	CXCR4	chemokine (C-X-C motif) receptor 4	1.62	4.92	0.97
11732870_a_at	CASP1	caspase 1, apoptosis-related cysteine peptidase	1.62	4.48	0.87
11719561_s_at	SOX4	SRY (sex determining region Y)-box 4	1.62	5.25	1.96
11720277_a_at	OLFML2A	olfactomedin-like 2A	1.62	5.06	4.09
11733091_a_at	TSPAN8	tetraspanin 8	1.62	5.10	1.98
11741453_at	SPINK4	serine peptidase inhibitor, Kazal type 4	1.61	4.46	3.97
11718620_a_at	CHRDL1	chordin-like 1	1.61	4.45	1.32
11759905_a_at	EXD3	exonuclease 3'-5' domain containing 3	1.60	4.66	4.39
11726396_x_at	KAL1	Kallmann syndrome 1 sequence	1.60	5.80	2.29
11719447_s_at	GBP2	guanylate binding protein 2, interferon-inducible	1.59	4.63	3.07
11740782_a_at	RNF128	ring finger protein 128, E3 ubiquitin protein ligase	1.59	4.36	3.69
11743197_at	TLR4	toll-like receptor 4	1.59	4.81	1.60
11745722_x_at	FHL1	four and a half LIM domains 1	1.59	5.55	2.43
11715624_at	SH3BGRL	SH3 domain binding glutamic acid-rich protein like	1.59	6.73	0.80
11725058_a_at	NEDD9	neural precursor cell expressed, developmentally down-regulated 9	1.58	4.32	3.70
11726458_s_at	GSPT2	G1 to S phase transition 2	1.58	4.75	2.95
11738935_a_at	KLRC3	killer cell lectin-like receptor subfamily C, member 3	1.58	5.01	4.65
11744079_s_at	PRSS2	protease, serine, 2 (trypsin 2)	1.58	5.79	4.28
11746463_a_at	IL6	interleukin 6 (interferon, beta 2)	1.58	5.53	4.82
11747104_s_at	CYP1B1	cytochrome P450, family 1, subfamily B, polypeptide 1	1.58	4.49	3.13
11720410_s_at	CYP1B1	cytochrome P450, family 1, subfamily B, polypeptide 1	1.58	4.90	2.66
11718904_s_at	FILIP1L	filamin A interacting protein 1-like	1.58	5.96	2.17
11755282_a_at	SCNN1A	sodium channel, non-voltage-gated 1 alpha subunit	1.58	4.51	4.20
11732993_a_at	RGS4	regulator of G-protein signaling 4	1.58	5.30	1.31
11726559_s_at	LCP1	lymphocyte cytosolic protein 1 (L-plastin)	1.58	5.31	2.47
11730184_at	CST1	cystatin SN	1.58	5.16	3.45
11750623_a_at	FILIP1L	filamin A interacting protein 1-like	1.57	5.31	2.67
11731465_a_at	CTSC	cathepsin C	1.57	4.41	0.00
11744848_x_at	PRR16	proline rich 16	1.57	4.79	0.28
11755141_a_at	CACNA2D4	calcium channel, voltage-dependent, alpha 2/delta subunit 4	1.57	4.72	3.24
11718347_a_at	S100P	S100 calcium binding protein P	1.57	4.87	3.26
11758952_at	AGR2	anterior gradient 2 homolog (Xenopus laevis)	1.56	4.68	3.30
11742873_a_at	CDH11	cadherin 11, type 2, OB-cadherin (osteoblast)	1.56	4.71	2.14
11729348_at	HMGN5	high mobility group nucleosome binding domain 5	1.56	4.52	0.84
11742923_a_at	LAPTM5	lysosomal protein transmembrane 5	1.56	5.59	2.30
11726678_a_at	AFAP1L2	actin filament associated protein 1-like 2	1.56	5.53	2.95
11720411_s_at	CYP1B1	cytochrome P450, family 1, subfamily B, polypeptide 1	1.56	4.84	2.70

Table S3. Differentially expressed genes among LT versus T versus M’.

probe ID	Gene Symbol	Gene title	LT vs T	LT vs T log2 (FC)	P-val	T vs M'	T vs M' log2 (FC)	P-val	LT vs M'	LT vs M' log2 (FC)	P-val	Find match for survival analysis
11748362_s_at	ABCC3	ATP-binding cassette, sub-family C (CFTR/MRP), member 3	LT>T	2.93	6.00E-05	T>M'	1.30	2.42E-02	LT>M'	4.24	4.74E-07	TRUE
11755873_a_at	ACSS1	acyl-CoA synthetase short-chain family member 1	LT>T	2.04	5.23E-04	T>M'	0.55	1.72E-01	LT>M'	2.59	2.96E-05	TRUE
11732158_a_at	ADAMTS1	ADAM metallopeptidase with thrombospondin type 1 motif, 1	T>LT	-0.53	4.05E-01	M'>T	-2.79	1.26E-04	M'>LT	-3.32	1.10E-03	TRUE
11754662_s_at	ADAMTS1	ADAM metallopeptidase with thrombospondin type 1 motif, 1	T>LT	-2.24	9.57E-02	M'>T	-3.15	1.78E-03	M'>LT	-5.39	2.71E-03	TRUE
11717305_a_at	ADIRF	adipogenesis regulatory factor	LT>T	0.99	1.93E-01	T>M'	2.62	2.68E-02	LT>M'	3.62	6.20E-04	TRUE
11717306_x_at	ADIRF	adipogenesis regulatory factor	LT>T	0.83	2.18E-01	T>M'	1.70	5.12E-02	LT>M'	2.53	4.48E-04	TRUE
11726678_a_at	AFAP1L2	actin filament associated protein 1-like 2	LT>T	1.12	6.75E-03	T>M'	2.27	5.35E-03	LT>M'	3.39	1.44E-04	TRUE
11749667_a_at	AFAP1L2	actin filament associated protein 1-like 2	LT>T	0.91	1.15E-02	T>M'	1.78	4.38E-04	LT>M'	2.69	3.18E-05	TRUE
11739696_s_at	AFF3	AF4/FMR2 family, member 3	T>LT	-2.63	4.38E-03	M'>T	-2.12	6.42E-02	M'>LT	-4.74	2.47E-06	FALSE
11740528_a_at	AFF3	AF4/FMR2 family, member 3	T>LT	-2.14	2.36E-03	M'>T	-1.66	7.89E-02	M'>LT	-3.80	3.04E-05	TRUE
11726250_at	AGR2	anterior gradient 2 homolog (Xenopus laevis)	T>LT	-4.01	4.13E-03	T>M'	2.43	1.59E-01	M'>LT	-1.57	6.38E-02	TRUE
11746830_a_at	AGR2	anterior gradient 2 homolog (Xenopus laevis)	T>LT	-2.93	1.70E-02	T>M'	1.68	2.79E-01	M'>LT	-1.26	7.25E-02	TRUE
11758952_at	AGR2	anterior gradient 2 homolog (Xenopus laevis)	T>LT	-2.42	1.64E-02	T>M'	1.89	1.15E-01	M'>LT	-0.52	4.07E-02	TRUE
11719171_a_at	AKR1C1	aldo-keto reductase family 1, member C1	LT>T	3.71	7.57E-03	M'>T	-0.76	3.58E-01	LT>M'	2.95	3.84E-02	FALSE
11719172_x_at	AKR1C1	aldo-keto reductase family 1, member C1	LT>T	3.77	7.15E-03	M'>T	-0.71	4.48E-01	LT>M'	3.06	3.21E-02	TRUE
11754189_s_at	AKR1C1	aldo-keto reductase family 1, member C1	LT>T	3.64	7.05E-03	M'>T	-0.65	5.66E-01	LT>M'	2.98	2.66E-02	TRUE
11715711_a_at	AKR1C3	aldo-keto reductase family 1, member C3	LT>T	3.47	6.46E-06	T>M'	0.75	3.77E-01	LT>M'	4.21	1.40E-04	TRUE
11757396_s_at	ANXA8L2	annexin A8 /// annexin A8-like 1 /// annexin A8-like 2	LT>T	1.17	1.52E-01	T>M'	1.90	6.01E-02	LT>M'	3.07	1.52E-03	TRUE
11756912_a_at	AOX1	aldehyde oxidase 1	T>LT	-0.36	4.25E-01	M'>T	-2.18	2.88E-03	M'>LT	-2.54	2.38E-05	TRUE
11715306_s_at	AREG	amphiregulin	LT>T	0.80	2.22E-01	T>M'	1.70	6.19E-02	LT>M'	2.50	5.16E-05	TRUE
11715466_at	ARHGDIB	Rho GDP dissociation inhibitor (GDI) beta	T>LT	-2.03	1.78E-02	M'>T	-0.72	5.08E-02	M'>LT	-2.75	6.58E-03	TRUE
11715467_s_at	ARHGDIB	Rho GDP dissociation inhibitor (GDI) beta	T>LT	-2.13	2.99E-02	M'>T	-0.63	4.36E-02	M'>LT	-2.76	1.64E-02	TRUE
11725232_at	ATP8B2	ATPase, aminophospholipid transporter, class I, type 8B, member 2	T>LT	-2.06	9.52E-04	M'>T	-0.42	4.31E-01	M'>LT	-2.48	2.47E-05	TRUE
11731841_a_at	B4GALT6	UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, polypeptide 6	T>LT	-1.51	1.72E-03	M'>T	-0.93	2.89E-02	M'>LT	-2.44	2.82E-05	FALSE
11746149_x_at	BCHE	butyrylcholinesterase	T>LT	-0.73	2.59E-01	M'>T	-2.78	1.66E-02	M'>LT	-3.52	3.30E-05	TRUE
11751833_a_at	BCHE	butyrylcholinesterase	T>LT	-0.80	1.85E-01	M'>T	-3.55	3.81E-03	M'>LT	-4.36	6.31E-06	TRUE
11746930_a_at	BHLHE41	basic helix-loop-helix family, member e41	T>LT	-0.01	9.34E-01	M'>T	-3.57	7.52E-07	M'>LT	-3.58	7.18E-08	TRUE
11758031_s_at	BHLHE41	basic helix-loop-helix family, member e41	LT>T	0.00	9.96E-01	M'>T	-4.75	7.28E-07	M'>LT	-4.74	5.52E-08	TRUE
11734013_a_at	BMP4	bone morphogenetic protein 4	LT>T	1.60	1.23E-04	T>M'	0.74	8.61E-02	LT>M'	2.34	1.74E-05	FALSE
11743350_a_at	C15orf48	chromosome 15 open reading frame 48	LT>T	2.98	2.98E-05	T>M'	1.88	6.87E-03	LT>M'	4.86	1.91E-06	TRUE
11721984_at	C7orf29	chromosome 7 open reading frame 29	LT>T	3.57	8.28E-05	T>M'	0.71	2.49E-01	LT>M'	4.28	3.20E-05	TRUE
11764157_s_at	C8orf42	chromosome 8 open reading frame 42	LT>T	1.48	4.98E-03	T>M'	1.17	5.09E-02	LT>M'	2.65	2.89E-06	TRUE
11755141_a_at	CACNA2D4	calcium channel, voltage-dependent, alpha 2/delta subunit 4	T>LT	-2.35	2.34E-02	T>M'	0.88	4.51E-01	M'>LT	-1.47	1.07E-04	TRUE
11750552_s_at	CARD16	caspase recruitment domain family, member 16	T>LT	-2.76	1.42E-03	M'>T	-0.13	8.50E-01	M'>LT	-2.88	1.87E-04	FALSE
11732870_a_at	CASP1	caspase 1, apoptosis-related cysteine peptidase	T>LT	-1.61	5.80E-02	M'>T	-1.41	1.82E-01	M'>LT	-3.02	1.32E-06	TRUE
11733359_a_at	CCDC19	coiled-coil domain containing 19	T>LT	-0.03	8.41E-01	M'>T	-2.37	3.39E-07	M'>LT	-2.40	2.10E-07	TRUE
11717885_a_at	CCDC3	coiled-coil domain containing 3	LT>T	2.85	4.78E-05	T>M'	0.98	8.09E-02	LT>M'	3.83	2.14E-06	FALSE
11715918_s_at	CD24	CD24 molecule	T>LT	-3.08	5.84E-04	T>M'	1.43	1.56E-01	M'>LT	-1.64	1.05E-02	TRUE
11734271_a_at	CDH18	cadherin 18, type 2	T>LT	-0.40	4.05E-01	M'>T	-3.37	8.51E-04	M'>LT	-3.77	4.60E-08	TRUE
11747423_a_at	CDH18	cadherin 18, type 2	T>LT	-0.21	4.05E-01	M'>T	-2.33	1.48E-03	M'>LT	-2.54	6.41E-05	TRUE
11743135_s_at	CEBPD	CCAAT/enhancer binding protein (C/EBP), delta	LT>T	1.84	5.99E-05	T>M'	0.87	3.15E-02	LT>M'	2.71	2.32E-07	TRUE
11743136_x_at	CEBPD	CCAAT/enhancer binding protein (C/EBP), delta	LT>T	1.79	5.24E-05	T>M'	0.88	1.88E-02	LT>M'	2.67	7.36E-07	TRUE
11752869_s_at	CEBPD	CCAAT/enhancer binding protein (C/EBP), delta	LT>T	1.82	1.02E-04	T>M'	0.84	6.10E-02	LT>M'	2.66	2.18E-06	TRUE
11723464_s_at	CELF2	CUGBP, Elav-like family member 2	T>LT	-2.77	1.76E-02	T>M'	0.30	3.97E-01	M'>LT	-2.46	4.48E-02	TRUE
11756473_a_at	CELF2	CUGBP, Elav-like family member 2	T>LT	-3.02	1.33E-02	T>M'	0.24	5.72E-01	M'>LT	-2.78	2.94E-02	TRUE
11733725_a_at	CFB	complement factor B	LT>T	1.84	9.50E-04	T>M'	0.64	2.19E-01	LT>M'	2.48	3.58E-05	TRUE
11718620_a_at	CHRDL1	chordin-like 1	T>LT	-1.14	1.48E-01	M'>T	-1.25	2.76E-01	M'>LT	-2.40	2.60E-02	TRUE
11758355_s_at	CLDN4	claudin 4	LT>T	0.78	3.28E-02	T>M'	1.77	1.45E-02	LT>M'	2.55	3.35E-04	TRUE
11724885_at	CLIC3	chloride intracellular channel 3	LT>T	2.60	2.22E-04	T>M'	3.13	6.31E-04	LT>M'	5.73	1.60E-06	TRUE
11756547_a_at	CLU	clusterin	LT>T	2.19	4.52E-03	T>M'	0.46	4.85E-01	LT>M'	2.65	1.47E-04	TRUE
11759207_at	CNKSR2	connector enhancer of kinase suppressor of Ras 2	T>LT	-0.98	5.55E-02	M'>T	-1.70	2.44E-02	M'>LT	-2.68	1.12E-06	TRUE
11722821_a_at	COCH	coagulation factor C homolog, cochlin (Limulus polyphemus)	LT>T	0.59	5.17E-01	T>M'	1.76	1.01E-01	LT>M'	2.35	6.64E-03	FALSE
11717275_s_at	COL5A1	collagen, type V, alpha 1	LT>T	1.77	2.41E-05	T>M'	0.56	7.96E-02	LT>M'	2.34	9.51E-05	FALSE
11734286_a_at	COX7B2	cytochrome c oxidase subunit VIIb2	T>LT	-0.49	7.71E-01	M'>T	-5.51	1.10E-02	M'>LT	-6.00	8.40E-04	TRUE
11717762_a_at	CPVL	carboxypeptidase, vitellogenic-like	T>LT	-2.48	4.57E-02	T>M'	0.06	8.82E-01	M'>LT	-2.42	7.30E-02	TRUE
11722970_a_at	CREB5	cAMP responsive element binding protein 5	T>LT	-1.50	5.75E-02	M'>T	-1.21	1.37E-01	M'>LT	-2.71	3.35E-04	TRUE
11734938_x_at	CSF2RA	colony stimulating factor 2 receptor, alpha, low-affinity (granulocyte-macrophage)	LT>T	1.44	4.48E-03	T>M'	2.28	3.58E-03	LT>M'	3.72	4.02E-05	TRUE
11738858_x_at	CSF2RA	colony stimulating factor 2 receptor, alpha, low-affinity (granulocyte-macrophage)	LT>T	1.46	5.55E-03	T>M'	2.34	2.53E-03	LT>M'	3.80	3.35E-05	TRUE
11749844_x_at	CSF2RA	colony stimulating factor 2 receptor, alpha, low-affinity (granulocyte-macrophage)	LT>T	1.57	3.03E-03	T>M'	1.73	1.87E-03	LT>M'	3.29	1.31E-05	TRUE
11751225_s_at	CSF2RA	colony stimulating factor 2 receptor, alpha, low-affinity (granulocyte-macrophage)	LT>T	1.75	4.71E-03	T>M'	2.66	3.59E-03	LT>M'	4.41	1.71E-05	FALSE
11732526_s_at	CSGALNACT1	chondroitin sulfate N-acetylgalactosaminyltransferase 1	T>LT	-0.35	5.41E-01	T>M'	2.38	6.96E-03	LT>M'	2.02	1.16E-03	TRUE
11724322_a_at	CST6	cystatin E/M	LT>T	3.74	3.16E-03	T>M'	1.99	1.39E-01	LT>M'	5.73	1.47E-06	TRUE
11743856_a_at	CTHRC1	collagen triple helix repeat containing 1	T>LT	-3.25	1.36E-04	T>M'	2.48	1.61E-02	M'>LT	-0.77	9.97E-02	TRUE
11744718_a_at	CTHRC1	collagen triple helix repeat containing 1	T>LT	-3.08	2.95E-04	T>M'	2.38	2.30E-02	M'>LT	-0.70	1.37E-01	TRUE
11731465_a_at	CTSC	cathepsin C	T>LT	-0.79	1.52E-01	M'>T	-2.57	3.34E-03	M'>LT	-3.36	1.56E-06	TRUE
11731466_a_at	CTSC	cathepsin C	T>LT	-0.45	2.82E-01	M'>T	-1.93	2.50E-03	M'>LT	-2.38	2.71E-05	TRUE
11728189_a_at	CXCR4	chemokine (C-X-C motif) receptor 4	T>LT	-2.39	9.90E-02	M'>T	-0.87	5.55E-01	M'>LT	-3.26	6.79E-03	TRUE
11728190_s_at	CXCR4	chemokine (C-X-C motif) receptor 4	T>LT	-2.79	1.06E-01	M'>T	-1.26	4.76E-01	M'>LT	-4.05	6.49E-03	TRUE
11728191_x_at	CXCR4	chemokine (C-X-C motif) receptor 4	T>LT	-1.91	1.36E-01	M'>T	-0.79	5.67E-01	M'>LT	-2.70	6.91E-03	TRUE
11720409_s_at	CYP1B1	cytochrome P450, family 1, subfamily B, polypeptide 1	LT>T	2.36	4.86E-03	T>M'	0.63	3.50E-01	LT>M'	3.00	2.36E-03	TRUE
11720410_s_at	CYP1B1	cytochrome P450, family 1, subfamily B, polypeptide 1	LT>T	2.23	5.37E-03	T>M'	0.54	4.35E-01	LT>M'	2.77	3.43E-03	TRUE
11720411_s_at	CYP1B1	cytochrome P450, family 1, subfamily B, polypeptide 1	LT>T	2.24	4.80E-03	T>M'	0.50	4.74E-01	LT>M'	2.74	2.47E-03	TRUE
11747104_s_at	CYP1B1	cytochrome P450, family 1, subfamily B, polypeptide 1	LT>T	2.53	1.59E-03	T>M'	0.34	4.71E-01	LT>M'	2.86	1.45E-03	TRUE
11755080_a_at	DAAM1	dishevelled associated activator of morphogenesis 1	LT>T	1.70	1.49E-03	T>M'	0.73	1.46E-01	LT>M'	2.44	2.52E-06	TRUE
11720146_a_at	DAPK1	death-associated protein kinase 1	LT>T	0.38	7.83E-01	M'>T	-4.47	7.59E-04	M'>LT	-4.09	2.54E-02	FALSE
11728342_at	DCLK1	doublecortin-like kinase 1	T>LT	-0.09	3.51E-01	M'>T	-2.77	5.63E-03	M'>LT	-2.86	1.90E-03	FALSE
11755291_a_at	DENND2D	DENN/MADD domain containing 2D	LT>T	0.92	2.04E-02	T>M'	1.62	6.08E-03	LT>M'	2.54	1.87E-04	TRUE
11716835_a_at	DHRS3	dehydrogenase/reductase (SDR family) member 3	LT>T	2.12	2.93E-03	T>M'	0.91	5.27E-02	LT>M'	3.02	2.30E-04	FALSE
11722991_a_at	DMD	dystrophin	T>LT	-0.38	6.65E-01	M'>T	-2.37	4.73E-02	M'>LT	-2.75	5.61E-04	FALSE
11743800_a_at	DNAH2	dynein, axonemal, heavy chain 2	LT>T	1.68	7.96E-04	T>M'	1.43	3.45E-02	LT>M'	3.11	1.08E-04	TRUE
11743801_at	DNAH2	dynein, axonemal, heavy chain 2	LT>T	1.48	2.43E-04	T>M'	0.93	3.36E-02	LT>M'	2.41	9.11E-05	TRUE
11723863_a_at	DOCK10	dedicator of cytokinesis 10	T>LT	-1.35	6.49E-04	M'>T	-1.14	1.84E-02	M'>LT	-2.49	8.42E-06	FALSE
11757702_s_at	DSC2	desmocollin 2	T>LT	-3.09	5.88E-03	T>M'	0.46	3.61E-01	M'>LT	-2.63	1.77E-02	TRUE
11734808_s_at	DTNA	dystrobrevin, alpha	T>LT	-2.89	2.24E-03	M'>T	-0.56	4.49E-01	M'>LT	-3.46	6.25E-05	TRUE
11729169_a_at	DUSP10	dual specificity phosphatase 10	LT>T	2.57	2.10E-04	M'>T	-0.47	3.50E-01	LT>M'	2.09	1.01E-04	FALSE
11729170_x_at	DUSP10	dual specificity phosphatase 10	LT>T	2.42	1.35E-04	M'>T	-0.34	4.20E-01	LT>M'	2.09	1.37E-04	FALSE
11722888_s_at	EMB	embigin	T>LT	-2.72	3.62E-02	M'>T	-0.39	5.19E-01	M'>LT	-3.11	2.85E-02	TRUE
11727583_a_at	EPHA3	EPH receptor A3	T>LT	-0.78	2.47E-01	M'>T	-1.74	1.97E-01	M'>LT	-2.51	1.70E-02	TRUE
11755166_a_at	ESAM	endothelial cell adhesion molecule	T>LT	-2.33	1.85E-04	T>M'	0.14	4.04E-01	M'>LT	-2.19	8.65E-04	TRUE
11729647_s_at	ESM1	endothelial cell-specific molecule 1	LT>T	0.00	9.66E-01	M'>T	-3.00	4.05E-02	M'>LT	-2.99	2.42E-02	TRUE
11732078_a_at	EVA1A	eva-1 homolog A (C. elegans)	LT>T	1.21	1.27E-01	M'>T	-2.66	2.06E-02	M'>LT	-1.45	2.49E-04	TRUE
11759905_a_at	EXD3	exonuclease 3'-5' domain containing 3	LT>T	2.15	1.24E-03	T>M'	1.27	4.44E-02	LT>M'	3.42	1.34E-05	FALSE
11729495_at	FAM133A	family with sequence similarity 133, member A	T>LT	-2.11	7.58E-02	M'>T	-1.74	3.11E-01	M'>LT	-3.85	2.30E-03	TRUE
11729496_at	FAM133A	family with sequence similarity 133, member A	T>LT	-1.87	1.05E-01	M'>T	-1.87	2.70E-01	M'>LT	-3.74	2.97E-03	FALSE
11730441_a_at	FAM155A	family with sequence similarity 155, member A	T>LT	-1.23	8.22E-06	M'>T	-1.74	9.33E-05	M'>LT	-2.96	2.19E-07	FALSE
11730442_s_at	FAM155A	family with sequence similarity 155, member A	T>LT	-2.57	2.93E-05	M'>T	-1.91	4.12E-04	M'>LT	-4.49	5.00E-07	TRUE
11746927_a_at	FAM155A	family with sequence similarity 155, member A	T>LT	-1.07	9.07E-05	M'>T	-1.53	1.81E-04	M'>LT	-2.60	4.50E-07	TRUE
11741223_s_at	FAM198B	family with sequence similarity 198, member B	LT>T	4.13	9.11E-06	M'>T	-0.05	7.27E-01	LT>M'	4.08	4.49E-05	TRUE
11757534_s_at	FAM198B	family with sequence similarity 198, member B	LT>T	3.63	4.94E-05	M'>T	-0.07	5.23E-01	LT>M'	3.56	2.33E-04	TRUE
11728600_at	FAM24B	family with sequence similarity 24, member B	T>LT	-2.20	2.44E-04	M'>T	-0.69	1.75E-01	M'>LT	-2.89	1.82E-05	FALSE
11719151_at	FAM83H	family with sequence similarity 83, member H	LT>T	1.31	1.78E-02	T>M'	1.15	3.87E-02	LT>M'	2.46	1.98E-04	TRUE
11744195_at	FAT3	FAT tumor suppressor homolog 3 (Drosophila)	T>LT	-1.76	1.21E-01	M'>T	-1.88	1.44E-01	M'>LT	-3.64	2.37E-04	TRUE
11736685_a_at	FGF5	fibroblast growth factor 5	T>LT	-2.73	3.71E-04	M'>T	-1.10	1.44E-01	M'>LT	-3.83	8.86E-07	TRUE
11736687_a_at	FGF5	fibroblast growth factor 5	T>LT	-3.27	9.08E-05	M'>T	-1.21	1.05E-01	M'>LT	-4.48	9.02E-08	TRUE
11736688_x_at	FGF5	fibroblast growth factor 5	T>LT	-3.07	2.05E-04	M'>T	-1.26	1.05E-01	M'>LT	-4.32	1.07E-07	TRUE
11730866_a_at	GALNT18	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 18	LT>T	1.11	8.22E-02	T>M'	1.62	8.17E-02	LT>M'	2.73	1.45E-04	TRUE
11719447_s_at	GBP2	guanylate binding protein 2, interferon-inducible	LT>T	1.54	1.13E-02	T>M'	1.87	2.80E-02	LT>M'	3.41	7.17E-06	TRUE
11716663_a_at	GDF15	growth differentiation factor 15	T>LT	-1.47	1.71E-01	T>M'	2.44	4.45E-02	LT>M'	0.97	2.46E-01	TRUE
11716329_s_at	GJA1	gap junction protein, alpha 1, 43kDa	T>LT	-2.41	5.68E-02	M'>T	-0.76	2.08E-01	M'>LT	-3.17	2.80E-02	FALSE
11727085_s_at	GJB2	gap junction protein, beta 2, 26kDa	T>LT	-0.05	8.70E-01	T>M'	2.50	1.41E-03	LT>M'	2.46	1.12E-03	TRUE

11744896_a_at	GPSM3	G-protein signaling modulator 3	T>LT	-1.17	9.95E-04	M'>T	-1.21	1.05E-02	M'>LT	-2.38	3.96E-05	TRUE
11723329_a_at	GSN	gelsolin	LT>T	1.68	1.32E-03	T>M'	1.39	1.12E-02	LT>M'	3.07	5.07E-07	TRUE
11726458_s_at	GSPT2	G1 to S phase transition 2	LT>T	1.38	4.07E-02	T>M'	1.64	1.07E-01	LT>M'	3.02	5.34E-04	TRUE
11718578_a_at	GSTM3	glutathione S-transferase mu 3 (brain)	LT>T	0.30	1.97E-01	T>M'	2.24	9.61E-03	LT>M'	2.53	1.46E-03	TRUE
11740311_at	HAS2	hyaluronan synthase 2	T>LT	-1.59	1.12E-01	M'>T	-1.74	1.34E-01	M'>LT	-3.32	3.01E-04	TRUE
11740312_at	HAS2	hyaluronan synthase 2	T>LT	-2.22	8.11E-02	M'>T	-2.06	1.21E-01	M'>LT	-4.28	6.76E-04	FALSE
11720922_a_at	HCP5	HLA complex P5 (non-protein coding)	LT>T	2.37	8.75E-06	T>M'	0.45	1.56E-01	LT>M'	2.82	2.25E-06	FALSE
11755933_x_at	HLA-B	major histocompatibility complex, class I, B	LT>T	1.99	1.71E-05	T>M'	0.77	8.65E-02	LT>M'	2.76	7.84E-06	TRUE
11755966_x_at	HLA-B	major histocompatibility complex, class I, B	LT>T	1.78	8.13E-06	T>M'	0.72	7.57E-02	LT>M'	2.50	6.06E-06	TRUE
11742850_x_at	HLA-DRA	major histocompatibility complex, class II, DR alpha	LT>T	0.88	3.58E-01	T>M'	1.66	1.17E-01	LT>M'	2.53	9.83E-03	FALSE
11744484_s_at	HLA-DRA	major histocompatibility complex, class II, DR alpha	LT>T	0.84	3.53E-01	T>M'	2.13	6.72E-02	LT>M'	2.97	4.62E-03	TRUE
11718230_a_at	HLA-F	major histocompatibility complex, class I, F	LT>T	2.79	7.65E-05	T>M'	1.19	4.11E-02	LT>M'	3.98	4.52E-08	TRUE
11718231_x_at	HLA-F	major histocompatibility complex, class I, F	LT>T	2.37	1.46E-05	T>M'	0.94	2.23E-02	LT>M'	3.31	9.49E-08	TRUE
11734530_x_at	HLA-F	major histocompatibility complex, class I, F	LT>T	2.43	4.42E-05	T>M'	0.93	4.42E-02	LT>M'	3.36	5.10E-07	TRUE
11740290_a_at	HOXC6	homeobox C6	T>LT	-1.80	1.89E-02	M'>T	-0.92	1.82E-01	M'>LT	-2.72	3.15E-04	TRUE
11732999_a_at	ICAM1	intercellular adhesion molecule 1	LT>T	1.69	6.72E-03	T>M'	0.98	5.42E-02	LT>M'	2.67	4.54E-04	FALSE
11733000_at	ICAM1	intercellular adhesion molecule 1	LT>T	1.55	1.45E-02	T>M'	0.80	1.50E-01	LT>M'	2.35	9.70E-04	FALSE
11721687_at	ID4	inhibitor of DNA binding 4, dominant negative helix-loop-helix protein	T>LT	-1.80	2.78E-02	M'>T	-0.81	3.91E-01	M'>LT	-2.61	5.56E-06	TRUE
11721688_at	ID4	inhibitor of DNA binding 4, dominant negative helix-loop-helix protein	T>LT	-1.93	1.58E-02	M'>T	-0.92	3.15E-01	M'>LT	-2.85	3.16E-06	TRUE
11715893_s_at	IFI27	interferon, alpha-inducible protein 27	LT>T	2.08	6.30E-03	T>M'	1.44	1.14E-01	LT>M'	3.52	3.46E-05	FALSE
11757480_x_at	IFI27	interferon, alpha-inducible protein 27	LT>T	2.49	7.75E-03	T>M'	1.70	1.40E-01	LT>M'	4.19	4.54E-05	FALSE
11724346_a_at	IFIH1	interferon induced with helicase C domain 1	LT>T	2.32	5.96E-03	T>M'	0.30	6.86E-01	LT>M'	2.61	2.10E-04	TRUE
11756820_a_at	IFIT1	interferon-induced protein with tetratricopeptide repeats 1	LT>T	1.58	4.89E-02	T>M'	1.13	1.79E-01	LT>M'	2.71	3.30E-04	TRUE
11721874_at	IFIT2	interferon-induced protein with tetratricopeptide repeats 2	LT>T	0.72	3.43E-01	T>M'	1.76	9.73E-02	LT>M'	2.48	1.28E-05	FALSE
11739787_a_at	IGF2	insulin-like growth factor 2 (somatomedin A)	T>LT	-0.83	1.17E-01	M'>T	-2.04	2.82E-02	M'>LT	-2.86	1.57E-04	FALSE
11717473_s_at	IGFBP1	insulin-like growth factor binding protein 1	T>LT	-1.50	3.58E-03	M'>T	-0.91	1.48E-03	M'>LT	-2.41	3.63E-04	FALSE
11727690_at	IL11	interleukin 11	T>LT	-3.50	1.69E-04	M'>T	-0.76	2.94E-01	M'>LT	-4.25	2.14E-05	TRUE
11751797_a_at	IL11	interleukin 11	T>LT	-2.11	1.79E-03	M'>T	-0.40	5.04E-01	M'>LT	-2.51	4.88E-05	TRUE
11718025_at	IL1R1	interleukin 1 receptor, type I	LT>T	2.03	3.61E-04	T>M'	0.95	3.07E-02	LT>M'	2.99	3.94E-05	FALSE
11746463_a_at	IL6	interleukin 6 (interferon, beta 2)	LT>T	1.04	2.38E-01	T>M'	1.71	2.12E-02	LT>M'	2.75	8.38E-03	TRUE
11733187_a_at	IL7R	interleukin 7 receptor	T>LT	-0.75	5.46E-02	M'>T	-1.77	2.29E-02	M'>LT	-2.52	6.26E-04	TRUE
11745624_s_at	INADL	InaD-like (Drosophila)	LT>T	1.90	1.55E-04	T>M'	0.45	1.46E-01	LT>M'	2.35	2.50E-05	TRUE
11728829_at	INHBB	inhibin, beta B	T>LT	-4.83	3.86E-03	T>M'	0.88	6.17E-01	M'>LT	-3.95	1.01E-04	TRUE
11725001_at	IRX3	iroquois homeobox 3	LT>T	2.24	4.65E-04	T>M'	0.57	2.18E-01	LT>M'	2.81	1.45E-04	FALSE
11725002_x_at	IRX3	iroquois homeobox 3	LT>T	2.29	2.08E-04	T>M'	0.62	1.58E-01	LT>M'	2.92	1.43E-04	TRUE
11758166_s_at	KAL1	Kallmann syndrome 1 sequence	LT>T	2.40	4.52E-02	M'>T	-1.11	4.03E-01	LT>M'	1.29	4.18E-03	TRUE
11747096_a_at	KCNK1	potassium channel, subfamily K, member 1	T>LT	-4.22	5.08E-07	T>M'	0.13	7.00E-01	M'>LT	-4.09	1.10E-05	TRUE
11732318_a_at	KHDRBS3	KH domain containing, RNA binding, signal transduction associated 3	T>LT	-3.42	2.10E-03	M'>T	-1.27	6.54E-03	M'>LT	-4.69	5.86E-04	TRUE
11744581_a_at	KHDRBS3	KH domain containing, RNA binding, signal transduction associated 3	T>LT	-3.93	3.41E-03	M'>T	-1.28	2.06E-02	M'>LT	-5.21	1.21E-03	TRUE
11735833_a_at	KIAA1199	KIAA1199	LT>T	2.73	6.97E-04	T>M'	1.43	6.96E-04	LT>M'	4.16	1.66E-04	TRUE
11731663_a_at	KIAA1217	KIAA1217	LT>T	2.04	2.47E-05	T>M'	1.08	2.41E-02	LT>M'	3.12	1.42E-06	TRUE
11715454_at	KISS1	KiSS-1 metastasis-suppressor	T>LT	-1.01	1.83E-01	M'>T	-4.27	2.61E-04	M'>LT	-5.28	6.62E-05	FALSE
11715455_x_at	KISS1	KiSS-1 metastasis-suppressor	T>LT	-1.04	1.70E-01	M'>T	-4.34	3.05E-04	M'>LT	-5.38	6.53E-05	TRUE
11738935_a_at	KLRC3	killer cell lectin-like receptor subfamily C, member 3	LT>T	0.83	3.92E-01	T>M'	1.59	1.68E-01	LT>M'	2.42	1.05E-03	FALSE
11727844_a_at	KRT81	keratin 81	T>LT	-2.28	1.23E-01	M'>T	-0.78	6.69E-01	M'>LT	-3.06	2.58E-03	FALSE
11746283_s_at	KRTAP2-3	keratin associated protein 2-3	T>LT	-1.81	8.06E-02	M'>T	-2.62	4.93E-02	M'>LT	-4.43	1.17E-05	TRUE
11719120_a_at	KYNU	kynureninase	T>LT	-3.20	6.06E-03	M'>T	-0.08	9.40E-01	M'>LT	-3.28	8.71E-04	TRUE
11716162_at	LBH	limb bud and heart development	LT>T	1.91	4.59E-03	T>M'	0.48	3.19E-01	LT>M'	2.38	4.75E-04	TRUE
11726559_s_at	LCP1	lymphocyte cytosolic protein 1 (L-plastin)	T>LT	-0.56	1.98E-01	M'>T	-2.71	1.54E-03	M'>LT	-3.27	3.48E-04	TRUE
11726333_s_at	LEF1	lymphoid enhancer-binding factor 1	T>LT	-2.48	3.54E-03	M'>T	-0.98	6.03E-02	M'>LT	-3.46	4.68E-04	FALSE
11757046_a_at	LOC100127888	uncharacterized LOC100127888	T>LT	-2.38	4.30E-02	T>M'	0.15	9.00E-01	M'>LT	-2.23	1.07E-02	TRUE
11763394_a_at	LOC100505946	uncharacterized LOC100505946	T>LT	-3.63	1.06E-03	T>M'	1.98	1.25E-01	M'>LT	-1.64	1.85E-02	TRUE
11727440_at	LOXL4	lysyl oxidase-like 4	LT>T	1.70	3.12E-03	T>M'	1.21	8.78E-02	LT>M'	2.91	4.50E-05	TRUE
11741749_x_at	LRRC2	leucine rich repeat containing 2	T>LT	-0.21	1.11E-01	M'>T	-3.02	9.81E-06	M'>LT	-3.24	6.60E-07	TRUE
11739798_a_at	LY6K	lymphocyte antigen 6 complex, locus K	T>LT	-2.84	3.24E-04	T>M'	2.50	8.03E-03	M'>LT	-0.34	3.81E-01	TRUE
11729543_a_at	MAGEC1	melanoma antigen family C, 1	T>LT	-0.17	6.23E-02	M'>T	-4.90	6.75E-04	M'>LT	-5.07	1.63E-04	TRUE
11729544_at	MAGEC1	melanoma antigen family C, 1	T>LT	-0.17	4.22E-01	M'>T	-5.04	7.46E-04	M'>LT	-5.21	1.38E-04	TRUE
11756085_a_at	MAGEC1	melanoma antigen family C, 1	T>LT	-0.13	3.19E-01	M'>T	-3.42	5.26E-03	M'>LT	-3.55	1.79E-03	TRUE
11716017_at	MAL2	mal, T-cell differentiation protein 2 (gene/pseudogene)	T>LT	-1.69	1.43E-01	T>M'	3.33	1.42E-02	LT>M'	1.64	1.67E-01	TRUE
11733832_a_at	MAP2	microtubule-associated protein 2	LT>T	2.44	1.44E-03	M'>T	-0.90	2.09E-02	LT>M'	1.54	3.41E-02	TRUE
11736559_a_at	MAP2	microtubule-associated protein 2	LT>T	2.36	1.14E-03	M'>T	-0.92	2.52E-02	LT>M'	1.44	2.93E-02	TRUE
11757815_s_at	METTL7A	methyltransferase like 7A	LT>T	1.06	7.95E-02	T>M'	1.62	5.35E-02	LT>M'	2.68	9.98E-05	TRUE
11757698_s_at	MIG7	mig-7	T>LT	-2.52	1.12E-02	T>M'	1.75	1.27E-01	M'>LT	-0.77	1.20E-02	TRUE
11741897_a_at	MMP1	matrix metallopeptidase 1 (interstitial collagenase)	T>LT	-2.60	1.15E-02	M'>T	-0.88	4.33E-01	M'>LT	-3.48	7.97E-05	TRUE
11755928_s_at	MMP1	matrix metallopeptidase 1 (interstitial collagenase)	T>LT	-3.04	1.28E-02	M'>T	-1.17	3.63E-01	M'>LT	-4.22	1.18E-04	TRUE
11746094_a_at	MPP4	membrane protein, palmitoylated 4 (MAGUK p55 subfamily member 4)	T>LT	-1.32	3.43E-02	M'>T	-1.98	4.97E-02	M'>LT	-3.30	9.75E-05	TRUE
11716167_a_at	MX1	myxovirus (influenza virus) resistance 1, interferon-inducible protein p78 (mouse)	LT>T	1.52	5.28E-02	T>M'	0.92	2.66E-01	LT>M'	2.44	5.43E-04	TRUE
11723823_a_at	MYO5C	myosin VC	T>LT	-2.33	1.09E-03	T>M'	0.60	1.54E-01	M'>LT	-1.73	5.90E-03	TRUE
11723824_s_at	MYO5C	myosin VC	T>LT	-2.36	1.08E-03	T>M'	0.41	3.87E-01	M'>LT	-1.95	2.05E-03	TRUE
11720611_a_at	NAP1L5	nucleosome assembly protein 1-like 5	T>LT	-1.61	5.14E-02	M'>T	-0.84	2.91E-01	M'>LT	-2.44	9.06E-04	FALSE
11720612_x_at	NAP1L5	nucleosome assembly protein 1-like 5	T>LT	-1.69	4.92E-02	M'>T	-0.87	2.98E-01	M'>LT	-2.56	6.91E-04	FALSE
11725057_s_at	NEDD9	neural precursor cell expressed, developmentally down-regulated 9	LT>T	2.57	1.64E-02	T>M'	0.79	4.60E-01	LT>M'	3.36	3.27E-03	TRUE
11725058_a_at	NEDD9	neural precursor cell expressed, developmentally down-regulated 9	LT>T	2.06	1.63E-02	T>M'	0.70	3.19E-01	LT>M'	2.76	3.66E-03	TRUE
11724820_a_at	NEK6	NIMA-related kinase 6	LT>T	1.48	1.64E-03	T>M'	1.09	1.93E-02	LT>M'	2.57	5.28E-06	TRUE
11725182_a_at	NEK6	NIMA-related kinase 6	LT>T	1.52	3.55E-03	T>M'	1.17	2.39E-02	LT>M'	2.69	2.41E-05	FALSE
11744776_a_at	NNMT	nicotinamide N-methyltransferase	LT>T	3.11	3.04E-04	M'>T	-1.04	2.32E-01	LT>M'	2.07	5.69E-03	FALSE
11728488_a_at	NRXN3	neurexin 3	T>LT	-0.68	8.32E-02	M'>T	-1.90	4.01E-03	M'>LT	-2.58	3.40E-07	TRUE
11755324_a_at	NRXN3	neurexin 3	T>LT	-0.65	6.65E-02	M'>T	-1.82	5.83E-03	M'>LT	-2.47	9.08E-06	FALSE
11717803_a_at	NTN4	netrin 4	T>LT	-3.22	6.62E-06	M'>T	-0.72	6.55E-02	M'>LT	-3.94	4.56E-06	TRUE
11720277_a_at	OLFML2A	olfactomedin-like 2A	LT>T	2.23	1.74E-04	T>M'	1.30	1.60E-02	LT>M'	3.53	2.07E-05	FALSE
11728587_a_at	PARD6B	par-6 partitioning defective 6 homolog beta (C. elegans)	LT>T	0.89	1.87E-01	T>M'	2.23	1.90E-02	LT>M'	3.12	1.54E-05	TRUE
11719414_a_at	PBX1	pre-B-cell leukemia homeobox 1	LT>T	1.87	4.50E-02	T>M'	3.13	1.77E-02	LT>M'	5.00	2.98E-06	TRUE
11757871_s_at	PBX1	pre-B-cell leukemia homeobox 1	LT>T	2.05	2.08E-02	T>M'	2.92	1.83E-02	LT>M'	4.97	3.02E-06	TRUE
11758070_s_at	PBX1	pre-B-cell leukemia homeobox 1	LT>T	1.89	2.14E-02	T>M'	2.17	2.79E-02	LT>M'	4.06	1.15E-06	TRUE
11737331_at	PDE1C	phosphodiesterase 1C, calmodulin-dependent 70kDa	T>LT	-0.88	1.05E-01	M'>T	-3.77	6.70E-04	M'>LT	-4.65	2.72E-07	TRUE
11757985_s_at	PDE7B	phosphodiesterase 7B	LT>T	1.70	3.81E-03	T>M'	1.53	1.76E-02	LT>M'	3.23	2.03E-06	TRUE
11732925_s_at	PEAR1	platelet endothelial aggregation receptor 1	T>LT	-2.07	5.71E-04	M'>T	-1.30	3.55E-02	M'>LT	-3.37	1.39E-07	TRUE
11733060_a_at	PELI1	pellino E3 ubiquitin protein ligase 1	T>LT	-0.36	7.71E-03	M'>T	-2.07	7.48E-07	M'>LT	-2.43	3.82E-09	TRUE
11724068_at	PELI2	pellino E3 ubiquitin protein ligase family member 2	T>LT	-2.43	8.75E-07	T>M'	1.22	2.13E-02	M'>LT	-1.20	4.47E-03	TRUE
11719512_s_at	PHC1	polyhomeotic homolog 1 (Drosophila)	T>LT	-1.03	1.35E-03	M'>T	-1.35	1.56E-03	M'>LT	-2.38	7.46E-07	TRUE
11728203_a_at	PHGDH	phosphoglycerate dehydrogenase	T>LT	-1.57	8.86E-02	M'>T	-1.43	2.21E-01	M'>LT	-3.00	4.12E-06	TRUE
11730106_a_at	PLCB1	phospholipase C, beta 1 (phosphoinositide-specific)	T>LT	-2.23	2.30E-02	M'>T	-0.67	5.49E-01	M'>LT	-2.90	6.07E-06	TRUE
11743841_at	PLCXD2	phosphatidylinositol-specific phospholipase C, X domain containing 2	T>LT	-1.29	9.65E-03	M'>T	-1.26	6.87E-03	M'>LT	-2.55	1.90E-04	TRUE
11728184_a_at	PLEKHA7	pleckstrin homology domain containing, family A member 7	LT>T	1.64	2.10E-02	T>M'	0.86	1.95E-01	LT>M'	2.50	2.19E-03	TRUE
11758396_s_at	POLR3G	polymerase (RNA) III (DNA directed) polypeptide G (32kD)	T>LT	-1.55	3.33E-03	M'>T	-1.01	3.53E-02	M'>LT	-2.56	3.03E-04	TRUE
11737479_a_at	PON2	paraoxonase 2	LT>T	1.30	3.03E-02	T>M'	1.27	8.94E-02	LT>M'	2.57	6.34E-07	TRUE
11737480_x_at	PON2	paraoxonase 2	LT>T	1.15	3.74E-02	T>M'	1.23	7.69E-02	LT>M'	2.38	3.96E-07	FALSE
11741354_a_at	PON2	paraoxonase 2	LT>T	1.30	3.14E-02	T>M'	1.29	8.70E-02	LT>M'	2.59	8.69E-07	TRUE
11763834_a_at	PPP1R1C	protein phosphatase 1, regulatory (inhibitor) subunit 1C	LT>T	1.16	4.61E-02	T>M'	1.33	8.22E-02	LT>M'	2.50	1.24E-05	TRUE
11737620_a_at	PRR16	proline rich 16	LT>T	1.15	6.07E-02	M'>T	-3.23	8.96E-04	M'>LT	-2.08	2.68E-03	TRUE
11744848_x_at	PRR16	proline rich 16	LT>T	1.21	6.98E-02	M'>T	-3.34	1.20E-03	M'>LT	-2.13	1.74E-03	TRUE
11719384_at	PRSS3	protease, serine, 3	T>LT	-3.25	2.14E-03	M'>T	-0.47	5.33E-01	M'>LT	-3.72	7.06E-04	FALSE
11751745_x_at	PRSS3	protease, serine, 3	T>LT	-2.63	1.24E-03	M'>T	-0.34	6.02E-01	M'>LT	-2.98	2.66E-04	FALSE
11754526_a_at	PTGES	prostaglandin E synthase	T>LT	-0.83	2.67E-01	T>M'	2.49	3.40E-02	LT>M'	1.66	3.10E-02	FALSE
11719827_a_at	QPCT	glutaminyl-peptide cyclotransferase	T>LT	-2.92	8.02E-04	T>M'	0.01	9.87E-01	M'>LT	-2.90	3.42E-04	TRUE
11719828_x_at	QPCT	glutaminyl-peptide cyclotransferase	T>LT	-2.82	9.25E-04	T>M'	0.02	9.78E-01	M'>LT	-2.79	4.90E-04	TRUE
11731817_s_at	RAB17	RAB17, member RAS oncogene family	LT>T	1.44	8.18E-02	T>M'	1.27	1.60E-02	LT>M'	2.72	7.43E-03	TRUE
11754862_a_at	RARRES2	retinoic acid receptor responder (tazarotene induced) 2	LT>T	3.03	4.71E-06	T>M'	1.37	2.07E-03	LT>M'	4.40	1.67E-07	FALSE
11719692_a_at	RARRES3	retinoic acid receptor responder (tazarotene induced) 3	LT>T	2.97	5.27E-03	T>M'	2.15	5.60E-02	LT>M'	5.12	3.06E-06	TRUE
11748907_a_at	RARRES3	retinoic acid receptor responder (tazarotene induced) 3	LT>T	2.98	5.70E-03	T>M'	2.21	5.74E-02	LT>M'	5.19	2.12E-06	TRUE
11740390_a_at	RBM47	RNA binding motif protein 47	LT>T	2.34	2.43E-03	T>M'	1.91	2.57E-02	LT>M'	4.24	6.74E-06	TRUE
11755523_a_at	RBM47	RNA binding motif protein 47	LT>T	2.44	1.51E-03	T>M'	1.33	6.70E-02	LT>M'	3.77	2.71E-06	TRUE
11757532_s_at	RBM47	RNA binding motif protein 47	LT>T	2.39	1.78E-03	T>M'	2.02	1.64E-02	LT>M'	4.42	9.37E-07	TRUE

11722348_a_at	REPS2	RALBP1 associated Eps domain containing 2	LT>T	2.01	1.12E-03	T>M'	0.32	5.89E-01	LT>M'	2.33	1.38E-06	TRUE
11732625_a_at	RIMS1	regulating synaptic membrane exocytosis 1	T>LT	-0.50	4.59E-02	M'>T	-1.85	2.82E-04	M'>LT	-2.35	3.51E-08	TRUE
11736729_a_at	RIMS2	regulating synaptic membrane exocytosis 2	T>LT	0.00	1.00E+00	M'>T	-3.15	1.21E-02	M'>LT	-3.15	7.87E-04	TRUE
11736730_a_at	RIMS2	regulating synaptic membrane exocytosis 2	LT>T	0.24	7.91E-01	M'>T	-3.34	9.85E-03	M'>LT	-3.10	9.81E-04	TRUE
11757347_s_at	RNF144A	ring finger protein 144A	LT>T	2.47	3.31E-03	T>M'	0.01	9.54E-01	LT>M'	2.48	6.37E-03	TRUE
11758227_s_at	ROBO1	roundabout, axon guidance receptor, homolog 1 (Drosophila)	T>LT	-3.04	3.23E-03	M'>T	-0.93	2.16E-02	M'>LT	-3.98	1.40E-03	TRUE
11718347_a_at	S100P	S100 calcium binding protein P	T>LT	-2.38	1.58E-02	T>M'	2.04	9.46E-02	M'>LT	-0.35	2.59E-01	TRUE
11733442_x_at	SAA1	serum amyloid A1	LT>T	0.61	4.54E-01	T>M'	1.79	3.47E-02	LT>M'	2.40	6.18E-03	TRUE
11756072_s_at	SAA1	serum amyloid A1	LT>T	0.69	4.23E-01	T>M'	2.66	1.61E-02	LT>M'	3.35	1.31E-03	TRUE
11755282_a_at	SCNN1A	sodium channel, non-voltage-gated 1 alpha subunit	LT>T	1.33	9.16E-02	T>M'	1.73	3.95E-02	LT>M'	3.06	3.41E-04	TRUE
11754879_a_at	SDR16C5	short chain dehydrogenase/reductase family 16C, member 5	T>LT	-3.86	2.67E-03	T>M'	1.23	3.70E-01	M'>LT	-2.63	4.36E-04	TRUE
11753915_a_at	SEL1L3	sel-1 suppressor of lin-12-like 3 (C. elegans)	T>LT	-1.38	1.35E-01	M'>T	-1.53	1.79E-01	M'>LT	-2.91	3.50E-03	TRUE
11730390_at	SEMA3A	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3A	T>LT	-1.77	1.13E-02	M'>T	-0.56	3.30E-01	M'>LT	-2.33	3.63E-03	TRUE
11721454_a_at	SERPINA1	serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 1	LT>T	2.11	3.99E-02	T>M'	0.58	4.50E-01	LT>M'	2.69	8.76E-03	TRUE
11721455_s_at	SERPINA1	serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 1	LT>T	1.82	2.94E-02	T>M'	0.52	4.10E-01	LT>M'	2.34	5.20E-03	TRUE
11744315_at	SGK223	homolog of rat pragma of Rnd2	LT>T	0.27	2.86E-01	T>M'	2.21	2.82E-03	LT>M'	2.48	2.72E-04	TRUE
11718447_s_at	SH3BGRL2	SH3 domain binding glutamic acid-rich protein like 2	T>LT	-1.60	2.96E-03	M'>T	-1.23	3.56E-02	M'>LT	-2.82	3.06E-07	FALSE
11726188_at	SHISA3	shisa homolog 3 (Xenopus laevis)	T>LT	-2.83	2.08E-03	M'>T	-0.62	5.24E-01	M'>LT	-3.45	1.17E-05	TRUE
11729140_x_at	SLAMF7	SLAM family member 7	T>LT	-3.20	1.38E-06	T>M'	2.13	2.46E-03	M'>LT	-1.08	1.14E-02	TRUE
11749023_a_at	SLC16A4	solute carrier family 16, member 4 (monocarboxylic acid transporter 5)	LT>T	2.63	1.18E-03	M'>T	-0.04	6.66E-01	LT>M'	2.58	3.47E-03	TRUE
11749024_x_at	SLC16A4	solute carrier family 16, member 4 (monocarboxylic acid transporter 5)	LT>T	2.36	2.71E-03	T>M'	0.04	6.24E-01	LT>M'	2.40	6.11E-03	TRUE
11733491_a_at	SLC44A5	solute carrier family 44, member 5	T>LT	-2.12	5.61E-03	M'>T	-0.54	5.10E-01	M'>LT	-2.66	2.29E-06	TRUE
11733492_s_at	SLC44A5	solute carrier family 44, member 5	T>LT	-2.30	3.01E-03	M'>T	-0.31	7.06E-01	M'>LT	-2.62	7.93E-05	FALSE
11747964_a_at	SLC4A7	solute carrier family 4, sodium bicarbonate cotransporter, member 7	T>LT	-1.72	1.56E-03	M'>T	-0.98	1.04E-01	M'>LT	-2.70	9.29E-04	TRUE
11733042_at	SLC7A2	solute carrier family 7 (cationic amino acid transporter, y+ system), member 2	T>LT	-1.11	4.80E-02	M'>T	-1.24	7.87E-02	M'>LT	-2.36	1.41E-04	TRUE
11732569_at	SLCO1B3	solute carrier organic anion transporter family, member 1B3	T>LT	-2.88	3.19E-03	M'>T	-1.21	3.29E-02	M'>LT	-4.08	4.32E-04	TRUE
11754796_a_at	SLCO3A1	solute carrier organic anion transporter family, member 3A1	LT>T	1.77	3.20E-02	T>M'	1.50	1.28E-01	LT>M'	3.27	4.59E-07	TRUE
11758172_s_at	SLCO3A1	solute carrier organic anion transporter family, member 3A1	LT>T	1.18	1.52E-02	T>M'	1.25	2.82E-02	LT>M'	2.43	1.17E-06	TRUE
11730048_at	SLITRK5	SLIT and NTRK-like family, member 5	T>LT	-1.84	2.61E-02	M'>T	-1.43	1.05E-01	M'>LT	-3.28	3.99E-05	TRUE
11725808_x_at	SNCAIP	synuclein, alpha interacting protein	T>LT	-0.19	5.04E-01	M'>T	-2.29	3.42E-03	M'>LT	-2.48	1.47E-03	TRUE
11747095_x_at	SNCAIP	synuclein, alpha interacting protein	T>LT	-0.10	7.08E-01	M'>T	-2.56	2.79E-03	M'>LT	-2.66	1.12E-03	TRUE
11750730_x_at	SNCAIP	synuclein, alpha interacting protein	T>LT	-0.11	6.83E-01	M'>T	-2.40	3.70E-03	M'>LT	-2.51	1.11E-03	TRUE
11735148_a_at	SOCS2	suppressor of cytokine signaling 2	T>LT	-3.02	8.86E-04	M'>T	-0.76	8.50E-02	M'>LT	-3.78	3.29E-04	TRUE
11751612_a_at	SOCS2	suppressor of cytokine signaling 2	T>LT	-2.58	1.02E-03	M'>T	-0.71	1.19E-01	M'>LT	-3.29	2.86E-04	FALSE
11735570_a_at	SORBS2	sorbin and SH3 domain containing 2	LT>T	0.59	3.43E-01	T>M'	1.98	9.55E-03	LT>M'	2.57	5.67E-04	TRUE
11758588_s_at	SORCS2	sortilin-related VPS10 domain containing receptor 2	LT>T	2.85	2.87E-08	T>M'	0.35	8.22E-02	LT>M'	3.20	3.25E-09	FALSE
11743129_at	SORL1	sortilin-related receptor, L(DLR class) A repeats containing	LT>T	1.97	1.75E-04	T>M'	2.19	9.35E-04	LT>M'	4.16	6.25E-07	FALSE
11743130_a_at	SORL1	sortilin-related receptor, L(DLR class) A repeats containing	LT>T	1.77	9.93E-05	T>M'	1.80	1.10E-03	LT>M'	3.57	1.69E-07	TRUE
11719560_at	SOX4	SRY (sex determining region Y)-box 4	T>LT	-2.89	2.54E-04	T>M'	1.20	4.93E-02	M'>LT	-1.69	4.13E-03	TRUE
11719561_s_at	SOX4	SRY (sex determining region Y)-box 4	T>LT	-3.16	2.96E-04	T>M'	1.12	5.33E-02	M'>LT	-2.04	5.65E-03	TRUE
11719562_at	SOX4	SRY (sex determining region Y)-box 4	T>LT	-4.17	7.58E-05	T>M'	0.66	1.74E-01	M'>LT	-3.51	6.32E-04	TRUE
11757741_s_at	SOX4	SRY (sex determining region Y)-box 4	T>LT	-2.40	4.98E-05	T>M'	0.63	1.01E-01	M'>LT	-1.78	5.62E-04	TRUE
11758525_s_at	SOX4	SRY (sex determining region Y)-box 4	T>LT	-3.81	9.37E-05	T>M'	0.75	9.33E-02	M'>LT	-3.06	1.05E-03	FALSE
11726177_s_at	SPANXB2	SPANX family, member B2	T>LT	-6.74	1.52E-05	T>M'	0.34	8.42E-01	M'>LT	-6.40	7.02E-04	TRUE
11738785_at	SPANXB2	SPANX family, member B2	T>LT	-7.69	1.27E-06	T>M'	0.48	7.33E-01	M'>LT	-7.20	2.46E-04	FALSE
11738786_x_at	SPANXB2	SPANX family, member B2	T>LT	-7.21	5.43E-06	T>M'	0.34	8.33E-01	M'>LT	-6.87	3.69E-04	FALSE
11731995_x_at	SPANXC	SPANX family, member C	T>LT	-1.20	8.77E-04	M'>T	-2.78	2.92E-02	M'>LT	-3.98	1.98E-03	FALSE
11731130_at	SPANXE	SPANX family, member E	T>LT	-0.62	4.61E-02	M'>T	-1.94	8.02E-02	M'>LT	-2.57	1.41E-02	TRUE
11731994_s_at	SPANXE	SPANX family, member E	T>LT	-2.39	1.09E-01	M'>T	-5.59	1.71E-02	M'>LT	-7.97	6.16E-07	TRUE
11759051_x_at	SPANXE	SPANX family, member E	T>LT	-0.60	1.01E-01	M'>T	-1.90	7.19E-02	M'>LT	-2.49	9.32E-03	TRUE
11741453_at	SPINK4	serine peptidase inhibitor, Kazal type 4	LT>T	1.94	4.84E-03	T>M'	1.51	4.60E-02	LT>M'	3.45	4.54E-07	TRUE
11754601_s_at	SPON2	spondin 2, extracellular matrix protein	LT>T	2.92	3.07E-03	T>M'	0.18	4.67E-01	LT>M'	3.10	4.95E-03	TRUE
11742710_a_at	SRGN	serglycin	T>LT	-3.97	1.06E-03	M'>T	-1.37	4.31E-02	M'>LT	-5.34	1.64E-04	FALSE
11717721_s_at	ST6GAL1	ST6 beta-galactosamide alpha-2,6-sialyltranferase 1	T>LT	-2.94	1.55E-03	T>M'	0.73	4.08E-01	M'>LT	-2.21	9.59E-03	TRUE
11716055_s_at	STMN3	stathmin-like 3	LT>T	1.33	1.67E-02	T>M'	1.10	3.92E-02	LT>M'	2.42	1.44E-04	FALSE
11733461_at	SUSD5	sushi domain containing 5	T>LT	-2.84	3.14E-03	M'>T	-1.40	1.77E-01	M'>LT	-4.24	2.68E-05	TRUE
11717301_at	TACSTD2	tumor-associated calcium signal transducer 2	LT>T	1.96	6.44E-04	T>M'	1.40	9.50E-03	LT>M'	3.36	2.79E-06	TRUE
11727984_at	TENM3	teneurin transmembrane protein 3	T>LT	-2.56	3.97E-02	M'>T	-0.85	2.26E-01	M'>LT	-3.41	1.27E-02	TRUE
11726192_at	TFAP2C	transcription factor AP-2 gamma (activating enhancer binding protein 2 gamma)	T>LT	-1.59	8.94E-02	M'>T	-1.68	1.27E-01	M'>LT	-3.27	3.48E-05	TRUE
11726812_a_at	TFF1	trefoil factor 1	T>LT	-3.19	1.49E-02	T>M'	2.39	1.53E-01	M'>LT	-0.80	2.42E-01	TRUE
11723751_at	TFF2	trefoil factor 2	T>LT	-2.44	2.64E-02	T>M'	2.86	4.47E-02	LT>M'	0.42	5.47E-01	TRUE
11718506_at	TFF3	trefoil factor 3 (intestinal)	T>LT	-2.54	1.23E-02	T>M'	2.54	4.20E-02	M'>LT	0.00	9.98E-01	TRUE
11728302_at	TGFA	transforming growth factor, alpha	LT>T	0.57	6.78E-02	T>M'	1.77	1.03E-02	LT>M'	2.34	8.76E-04	TRUE
11734548_a_at	TGFBI	transforming growth factor, beta-induced, 68kDa	LT>T	1.29	2.94E-02	T>M'	1.14	6.49E-02	LT>M'	2.44	1.11E-03	TRUE
11734549_s_at	TGFBI	transforming growth factor, beta-induced, 68kDa	LT>T	1.21	5.38E-02	T>M'	1.22	1.04E-01	LT>M'	2.42	2.80E-03	TRUE
11734550_x_at	TGFBI	transforming growth factor, beta-induced, 68kDa	LT>T	1.24	4.26E-02	T>M'	1.27	7.53E-02	LT>M'	2.51	1.47E-03	TRUE
11743197_at	TLR4	toll-like receptor 4	T>LT	-3.05	1.16E-04	T>M'	0.50	2.32E-01	M'>LT	-2.55	7.18E-04	FALSE
11731603_at	TMEM154	transmembrane protein 154	T>LT	-1.31	1.03E-02	M'>T	-1.24	1.59E-03	M'>LT	-2.55	5.68E-04	TRUE
11758583_s_at	TMEM154	transmembrane protein 154	T>LT	-1.42	2.41E-02	M'>T	-1.05	1.65E-02	M'>LT	-2.48	2.89E-03	TRUE
11739809_at	TMEM156	transmembrane protein 156	T>LT	-3.40	2.57E-06	M'>T	-0.48	2.51E-01	M'>LT	-3.88	3.90E-08	TRUE
11740091_s_at	TMEM163	transmembrane protein 163	T>LT	-2.22	6.20E-02	M'>T	-0.55	6.90E-01	M'>LT	-2.77	1.48E-05	TRUE
11758102_s_at	TMEM163	transmembrane protein 163	T>LT	-2.72	3.90E-02	M'>T	-0.71	6.32E-01	M'>LT	-3.42	3.30E-06	TRUE
11743730_at	TNFSF10	tumor necrosis factor (ligand) superfamily, member 10	LT>T	3.31	8.67E-05	T>M'	2.27	4.90E-03	LT>M'	5.57	1.50E-08	TRUE
11743731_a_at	TNFSF10	tumor necrosis factor (ligand) superfamily, member 10	LT>T	3.17	1.75E-05	T>M'	2.26	5.61E-04	LT>M'	5.43	1.35E-07	FALSE
11747952_x_at	TNFSF10	tumor necrosis factor (ligand) superfamily, member 10	LT>T	3.41	1.06E-04	T>M'	2.48	4.95E-03	LT>M'	5.89	1.51E-08	FALSE
11733091_a_at	TSPAN8	tetraspanin 8	T>LT	-3.09	2.49E-04	T>M'	0.73	1.96E-01	M'>LT	-2.35	1.54E-03	TRUE
11755851_a_at	UBR4	ubiquitin protein ligase E3 component n-recognin 4	T>LT	-1.04	8.16E-03	M'>T	-1.33	4.35E-03	M'>LT	-2.37	4.41E-05	TRUE
11758628_s_at	ULK2	unc-51-like kinase 2 (C. elegans)	LT>T	1.80	6.52E-03	T>M'	0.70	2.86E-01	LT>M'	2.50	1.27E-03	FALSE
11732465_a_at	USP44	ubiquitin specific peptidase 44	T>LT	-1.15	9.18E-03	M'>T	-1.29	1.14E-02	M'>LT	-2.44	4.19E-06	TRUE
11740301_a_at	USP44	ubiquitin specific peptidase 44	T>LT	-1.33	1.78E-03	M'>T	-1.31	9.22E-03	M'>LT	-2.64	4.26E-07	TRUE
11724795_at	ZG16B	zymogen granule protein 16B	T>LT	-3.58	3.74E-03	T>M'	2.74	5.15E-02	M'>LT	-0.84	4.88E-04	TRUE
11729410_a_at	ZNF415	zinc finger protein 415	LT>T	0.80	7.29E-02	T>M'	1.61	4.06E-02	LT>M'	2.41	9.09E-04	FALSE
11729020_at	ZNF804A	zinc finger protein 804A	T>LT	-2.03	2.04E-04	M'>T	-2.06	9.23E-04	M'>LT	-4.09	6.38E-08	FALSE

*** Threshold value for Fold difference is 2.32 in log2 and P < 0.05; Genes that have significant difference between Groups are highlighted in red**

Table S4. List of genes affiliated with regulation of cell shape.

CLU(LT>M')	clusterin
COCH(LT>M')	coagulation factor C homolog, cochlin (Limulus polyphemus)
DCLK1(M'>T,M'>LT)	doublecortin-like kinase 1
DOCK10(M'>LT)	dedicator of cytokinesis 10
GJA1(M'>LT)	gap junction protein, alpha 1, 43kDa
HAS2(M'>LT)	hyaluronan synthase 2
ICAM1(LT>M')	intercellular adhesion molecule 1
IL6(LT>M')	interleukin 6 (interferon, beta 2)
IL7R(M'>LT)	interleukin 7 receptor
LEF1(T>LT,M'>LT)	lymphoid enhancer-binding factor 1
MAP2(LT>T)	microtubule-associated protein 2
NRXN3(M'>LT)	neurexin 3
NTN4(T>LT,M'>LT)	netrin 4
PARD6B(LT>M')	par-6 partitioning defective 6 homolog beta (C. elegans)
RIMS1(M'>LT)	regulating synaptic membrane exocytosis 1
RIMS2(M'>T,M'>LT)	regulating synaptic membrane exocytosis 2
ROBO1(T>LT,M'>LT)	roundabout, axon guidance receptor, homolog 1 (Drosophila)
SEMA3A(M'>LT)	sema domain, immunoglobulin domain (Ig), short basic domain, secr
SLITRK5(M'>LT)	SLIT and NTRK-like family, member 5
SPON2(LT>T,LT>M')	spondin 2, extracellular matrix protein
TACSTD2(LT>M')	tumor-associated calcium signal transducer 2
ULK2(LT>M')	unc-51-like kinase 2 (C. elegans)

Table S5. Summary of CM features.

Feature name	Feature category	shape type	Feature description
f1	Basic	Nucleus	area
f2	Basic	Nucleus	perimeter
f3	Basic	Nucleus	long axis length
f4	Basic	Nucleus	short axis length
f5	Basic	Nucleus	angle
f6	Basic	Nucleus	soliditity
f7	Basic	Nucleus	equi diameter
f8	Basic	Nucleus	aspect ratio
f9	Basic	Nucleus	circularity
f10	Basic	Nucleus	roundness
f11	Basic	Cell	area
f12	Basic	Cell	perimeter
f13	Basic	Cell	long axis length
f14	Basic	Cell	short axis length
f15	Basic	Cell	angle
f16	Basic	Cell	soliditity
f17	Basic	Cell	equi diameter
f18	Basic	Cell	aspect ratio
f19	Basic	Cell	circularity
f20	Basic	Cell	roundness
f21	Boundary signature	Nucleus	mean(R) $(\equiv \langle R\rangle)$
f22	Boundary signature	Nucleus	median(R)
f23	Boundary signature	Nucleus	mode(R)
f24	Boundary signature	Nucleus	maR(R)
f25	Boundary signature	Nucleus	min(R)
f26	Boundary signature	Nucleus	25% percentile (R)
f27	Boundary signature	Nucleus	75% percentile (R)
f28	Boundary signature	Nucleus	mean(R(R >f27));
f29	Boundary signature	Nucleus	mean(R(R < f26));
f30	Boundary signature	Nucleus	$\Sigma(R)$
f31	Boundary signature	Nucleus	harmonic mean(R)
f32	Boundary signature	Nucleus	3% trimmed mean(R)
f33	Boundary signature	Nucleus	5% trimmed mean(R)
f34	Boundary signature	Nucleus	15% trimmed mean(R)
f35	Boundary signature	Nucleus	25% trimmed mean(R)
f36	Boundary signature	Nucleus	standard deviation(R) $(\equiv\sigma_R)$
f37	Boundary signature	Nucleus	$\sigma_R/\lvert\langle R\rangle\rvert$
f38	Boundary signature	Nucleus	$\sigma_R/\lvert\text{median}(R)\rvert$
f39	Boundary signature	Nucleus	$\sigma_R/\lvert\text{mode}(R)\rvert$
f40	Boundary signature	Nucleus	skewness(R)
f41	Boundary signature	Nucleus	kurtosis(R)
f42	Boundary signature	Nucleus	$\text{mean}(\lvert R-\langle R\rangle\rvert)$
f43	Boundary signature	Nucleus	range(X)
f44	Boundary signature	Nucleus	interquartile range (X)
f45	Boundary signature	Nucleus	$\Sigma(R^2)$
f46	Boundary signature	Nucleus	$\Sigma(R^3)$
f47	Boundary signature	Nucleus	$\text{mean}(R^2)$
f48	Boundary signature	Nucleus	$\text{mean}(R^3)$
f49	Boundary signature	Nucleus	$\text{mean}(R^4)$
f50	Boundary signature	Nucleus	$\text{mean}(R^5)$
f51	Boundary signature	Nucleus	$\Sigma(\lvert R-\langle R\rangle\rvert^2)$
f52	Boundary signature	Nucleus	$\Sigma(\lvert R-\langle R\rangle\rvert^3)$
f53	Boundary signature	Nucleus	$\text{mean}(\lvert R-\langle R\rangle\rvert^2)$
f54	Boundary signature	Nucleus	$\text{mean}(\lvert R-\langle R\rangle\rvert^3)$
f55	Boundary signature	Nucleus	$\text{mean}(\lvert R-\langle R\rangle\rvert^4)$
f56	Boundary signature	Nucleus	$\text{mean}(\lvert R-\langle R\rangle\rvert^5)$
f57	Boundary signature	Nucleus	number of peaks
f58	Boundary signature	Nucleus	gini coefficient (R)
f59	Boundary signature	Cell	mean(R) $(\equiv \langle R\rangle)$
f60	Boundary signature	Cell	median(R)
f61	Boundary signature	Cell	mode(R)
f62	Boundary signature	Cell	maR(R)
f63	Boundary signature	Cell	min(R)
f64	Boundary signature	Cell	25% percentile (R)
f65	Boundary signature	Cell	75% percentile (R)
f66	Boundary signature	Cell	mean(R(R >f65));
f67	Boundary signature	Cell	mean(R(R < f64));
f68	Boundary signature	Cell	$\Sigma(R)$

f69	Boundary signature	Cell	harmonic mean(R)
f70	Boundary signature	Cell	3% trimmed mean(R)
f71	Boundary signature	Cell	5% trimmed mean(R)
f72	Boundary signature	Cell	15% trimmed mean(R)
f73	Boundary signature	Cell	25% trimmed mean(R)
f74	Boundary signature	Cell	standard deviation(R) $(\equiv\sigma_R)$
f75	Boundary signature	Cell	$\sigma_R/\lvert\langle R\rangle\rvert$
f76	Boundary signature	Cell	$\sigma_R/\lvert\text{median}(R)\rvert$
f77	Boundary signature	Cell	$\sigma_R/\lvert\text{mode}(R)\rvert$
f78	Boundary signature	Cell	skewness(R)
f79	Boundary signature	Cell	kurtosis(R)
f80	Boundary signature	Cell	$\text{mean}(\lvert R-\langle R\rangle\rvert)$
f81	Boundary signature	Cell	range(X)
f82	Boundary signature	Cell	interquartile range (X)
f83	Boundary signature	Cell	$\Sigma(R^2)$
f84	Boundary signature	Cell	$\Sigma(R^3)$
f85	Boundary signature	Cell	$\text{mean}(R^2)$
f86	Boundary signature	Cell	$\text{mean}(R^3)$
f87	Boundary signature	Cell	$\text{mean}(R^4)$
f88	Boundary signature	Cell	$\text{mean}(R^5)$
f89	Boundary signature	Cell	$\Sigma(\lvert R-\langle R\rangle\rvert^2)$
f90	Boundary signature	Cell	$\Sigma(\lvert R-\langle R\rangle\rvert^3)$
f91	Boundary signature	Cell	$\text{mean}(\lvert R-\langle R\rangle\rvert^2)$
f92	Boundary signature	Cell	$\text{mean}(\lvert R-\langle R\rangle\rvert^3)$
f93	Boundary signature	Cell	$\text{mean}(\lvert R-\langle R\rangle\rvert^4)$
f94	Boundary signature	Cell	$\text{mean}(\lvert R-\langle R\rangle\rvert^5)$
f95	Boundary signature	Cell	number of peaks
f96	Boundary signature	Cell	gini coefficient (R)
f97	Curvature	Nucleus	$\text{mean}(\kappa)$ $(\equiv\langle\kappa\rangle)$
f98	Curvature	Nucleus	$\text{median}(\kappa)$
f99	Curvature	Nucleus	$\text{mode}(\kappa)$
f100	Curvature	Nucleus	$\max(\kappa)$
f101	Curvature	Nucleus	$\min(\kappa)$
f102	Curvature	Nucleus	25% percentile (κ)
f103	Curvature	Nucleus	75% percentile (κ)
f104	Curvature	Nucleus	$\text{mean}(\kappa(\kappa > \text{f103}))$;
f105	Curvature	Nucleus	$\text{mean}(\kappa(\kappa < \text{f102}))$;
f106	Curvature	Nucleus	$\Sigma(\kappa)$
f107	Curvature	Nucleus	harmonic mean(κ)
f108	Curvature	Nucleus	3% trimmed mean(κ)
f109	Curvature	Nucleus	5% trimmed mean(κ)
f110	Curvature	Nucleus	15% trimmed mean(κ)
f111	Curvature	Nucleus	25% trimmed mean(κ)
f112	Curvature	Nucleus	standard deviation(κ) $(\equiv\sigma_\kappa)$
f113	Curvature	Nucleus	$\sigma_\kappa/\lvert\langle\kappa\rangle\rvert$
f114	Curvature	Nucleus	$\sigma_\kappa/\lvert\text{median}(\kappa)\rvert$
f115	Curvature	Nucleus	$\sigma_\kappa/\lvert\text{mode}(\kappa)\rvert$
f116	Curvature	Nucleus	skewness(κ)
f117	Curvature	Nucleus	kurtosis(κ)
f118	Curvature	Nucleus	$\text{mean}(\lvert\kappa-\langle\kappa\rangle\rvert)$
f119	Curvature	Nucleus	range(k)
f120	Curvature	Nucleus	interquartile range (κ)
f121	Curvature	Nucleus	$\Sigma(\kappa^2)$
f122	Curvature	Nucleus	$\Sigma(\kappa^3)$
f123	Curvature	Nucleus	$\text{mean}(\kappa^2)$
f124	Curvature	Nucleus	$\text{mean}(\kappa^3)$
f125	Curvature	Nucleus	$\text{mean}(\kappa^4)$
f126	Curvature	Nucleus	$\text{mean}(\kappa^5)$
f127	Curvature	Nucleus	$\Sigma(\lvert\kappa-\langle\kappa\rangle\rvert^2)$
f128	Curvature	Nucleus	$\Sigma(\lvert\kappa-\langle\kappa\rangle\rvert^3)$
f129	Curvature	Nucleus	$\text{mean}(\lvert\kappa-\langle\kappa\rangle\rvert^2)$
f130	Curvature	Nucleus	$\text{mean}(\lvert\kappa-\langle\kappa\rangle\rvert^3)$
f131	Curvature	Nucleus	$\text{mean}(\lvert\kappa-\langle\kappa\rangle\rvert^4)$
f132	Curvature	Nucleus	$\text{mean}(\lvert\kappa-\langle\kappa\rangle\rvert^5)$
f133	Curvature	Nucleus	number of peaks
f134	Curvature	Nucleus	gini coefficient (κ)
f135	Curvature	Cell	$\text{mean}(\kappa)$ $(\equiv\langle\kappa\rangle)$

f136	Curvature	Cell	median(κ)
f137	Curvature	Cell	mode(κ)
f138	Curvature	Cell	max(κ)
f139	Curvature	Cell	min(κ)
f140	Curvature	Cell	25% percentile (κ)
f141	Curvature	Cell	75% percentile (κ)
f142	Curvature	Cell	mean(κ(κ >f141));
f143	Curvature	Cell	mean(κ(κ < f140));
f144	Curvature	Cell	Σ(κ)
f145	Curvature	Cell	harmonic mean(κ)
f146	Curvature	Cell	3% trimmed mean(κ)
f147	Curvature	Cell	5% trimmed mean(κ)
f148	Curvature	Cell	15% trimmed mean(κ)
f149	Curvature	Cell	25% trimmed mean(κ)
f150	Curvature	Cell	standard deviation(κ) (≡ σ_κ)
f151	Curvature	Cell	$\sigma_\kappa/\vert<\kappa>\vert$
f152	Curvature	Cell	$\sigma_\kappa/\vert\mathrm{median}(\kappa)\vert$
f153	Curvature	Cell	$\sigma_\kappa/\vert\mathrm{mode}(\kappa)\vert$
f154	Curvature	Cell	skewness(κ)
f155	Curvature	Cell	kurtosis(κ)
f156	Curvature	Cell	$\mathrm{mean}(\vert\kappa-<\kappa>\vert)$
f157	Curvature	Cell	range(k)
f158	Curvature	Cell	interquartile range (κ)
f159	Curvature	Cell	$\Sigma(\kappa^2)$
f160	Curvature	Cell	$\Sigma(\kappa^3)$
f161	Curvature	Cell	$\mathrm{mean}(\kappa^2)$
f162	Curvature	Cell	$\mathrm{mean}(\kappa^3)$
f163	Curvature	Cell	$\mathrm{mean}(\kappa^4)$
f164	Curvature	Cell	$\mathrm{mean}(\kappa^5)$
f165	Curvature	Cell	$\Sigma(\vert\kappa-<\kappa>\vert^2)$
f166	Curvature	Cell	$\Sigma(\vert\kappa-<\kappa>\vert^3)$
f167	Curvature	Cell	$\mathrm{mean}(\vert\kappa-<\kappa>\vert^2)$
f168	Curvature	Cell	$\mathrm{mean}(\vert\kappa-<\kappa>\vert^3)$
f169	Curvature	Cell	$\mathrm{mean}(\vert\kappa-<\kappa>\vert^4)$
f170	Curvature	Cell	$\mathrm{mean}(\vert\kappa-<\kappa>\vert^5)$
f171	Curvature	Cell	number of peaks
f172	Curvature	Cell	gini coefficient (κ)
f173	NC-positioning signature	Nucleus & Cell	mean(R') (≡ <R'>)
f174	NC-positioning signature	Nucleus & Cell	median(R')
f175	NC-positioning signature	Nucleus & Cell	mode(R')
f176	NC-positioning signature	Nucleus & Cell	maR'(R')
f177	NC-positioning signature	Nucleus & Cell	min(R')
f178	NC-positioning signature	Nucleus & Cell	25% percentile (R')
f179	NC-positioning signature	Nucleus & Cell	75% percentile (R')
f180	NC-positioning signature	Nucleus & Cell	Σ(R')
f181	NC-positioning signature	Nucleus & Cell	harmonic mean(R')
f182	NC-positioning signature	Nucleus & Cell	3% trimmed mean(R')
f183	NC-positioning signature	Nucleus & Cell	5% trimmed mean(R')
f184	NC-positioning signature	Nucleus & Cell	15% trimmed mean(R')
f185	NC-positioning signature	Nucleus & Cell	25% trimmed mean(R')
f186	NC-positioning signature	Nucleus & Cell	standard deviation(R') (≡ $\sigma_{R'}$)
f187	NC-positioning signature	Nucleus & Cell	$\mathrm{mean}(\vert R'-<R'>\vert)$
f188	NC-positioning signature	Nucleus & Cell	range(R')
f189	NC-positioning signature	Nucleus & Cell	interquartile range (R')
f190	NC-positioning signature	Nucleus & Cell	$\Sigma(R'^2)$
f191	NC-positioning signature	Nucleus & Cell	$\Sigma(R'^3)$
f192	NC-positioning signature	Nucleus & Cell	$\mathrm{mean}(R'^2)$
f193	NC-positioning signature	Nucleus & Cell	$\mathrm{mean}(R'^3)$
f194	NC-positioning signature	Nucleus & Cell	$\mathrm{mean}(R'^4)$
f195	NC-positioning signature	Nucleus & Cell	$\mathrm{mean}(R'^5)$
f196	NC-positioning signature	Nucleus & Cell	$\Sigma(\vert R'-<R'>\vert^2)$
f197	NC-positioning signature	Nucleus & Cell	$\Sigma(\vert R'-<R'>\vert^3)$
f198	NC-positioning signature	Nucleus & Cell	$\mathrm{mean}(\vert R'-<R'>\vert^2)$
f199	NC-positioning signature	Nucleus & Cell	$\mathrm{mean}(\vert R'-<R'>\vert^3)$
f200	NC-positioning signature	Nucleus & Cell	$\mathrm{mean}(\vert R'-<R'>\vert^4)$
f201	NC-positioning signature	Nucleus & Cell	$\mathrm{mean}(\vert R'-<R'>\vert^5)$
f202	NC-positioning signature	Nucleus & Cell	number of peaks
f203	NC-positioning signature	Nucleus & Cell	correlation coefficient between nucleus boundary signature and cell boundary signature

f204	Protrusion	Cell	mean protrusion length
f205	Protrusion	Cell	max protrusion length
f206	Protrusion	Cell	number of protrusion
f207	Protrusion	Cell	number of primary protrusion
f208	Protrusion	Cell	number of secondary protrusion
f209	Protrusion	Cell	Branching index (=f208/f207)
f210	Protrusion	Cell	mean primary protrusion length
f211	Protrusion	Cell	max primary protrusion length
f212	Protrusion	Cell	standard deviation of primary protrusion length
f213	Protrusion	Cell	mean secondary protrusion length
f214	Protrusion	Cell	max secondary protrusion length
f215	Protrusion	Cell	standard deviation of secondary protrusion length