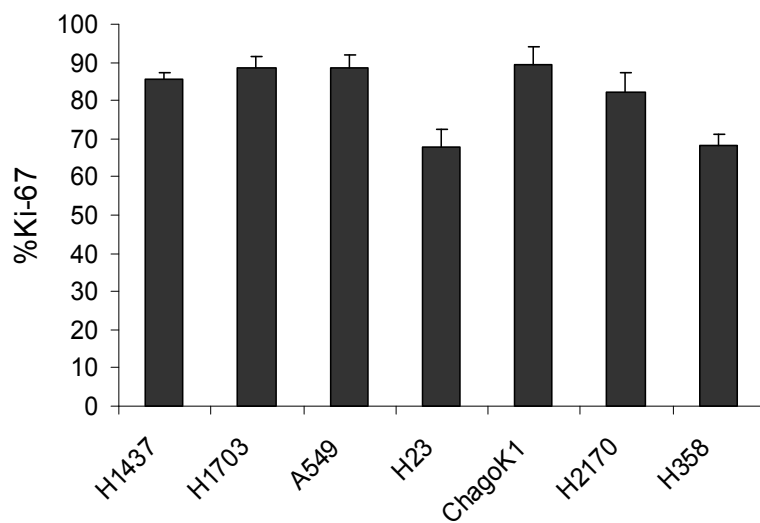


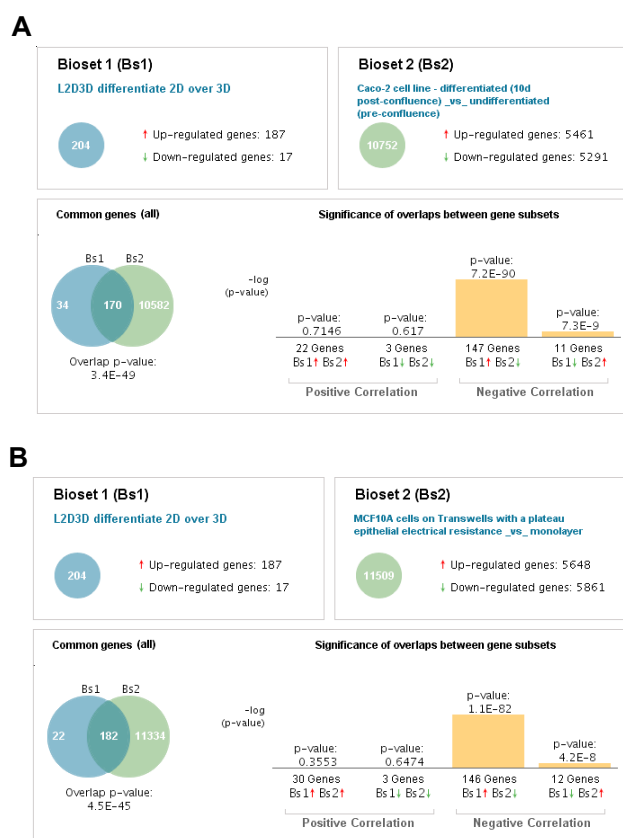
Supplemental Figure 1. Proliferation status of lung cancer cell lines in 3D IrECM.



Supplemental Figure 1. Proliferation status of lung cancer cell lines in 3D IrECM.

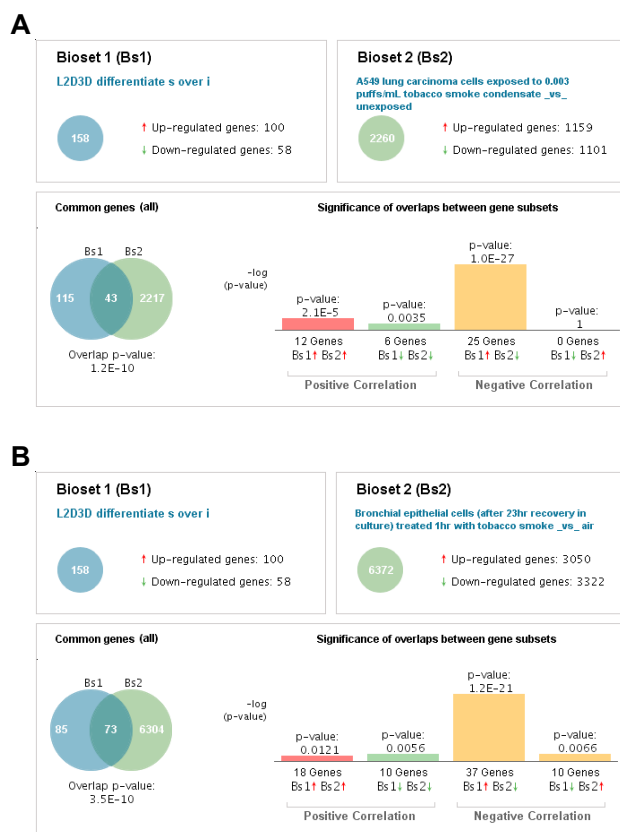
Lung cancer cell lines cultured in 3D IrECM for 5 d were analyzed for expression of Ki67 by immunofluorescence. Results represent means \pm SEM for three independent samples.

Supplemental Figure 2. Meta-analysis of transcripts differentially expressed between lung cancer cells grown in 2D and 3D.



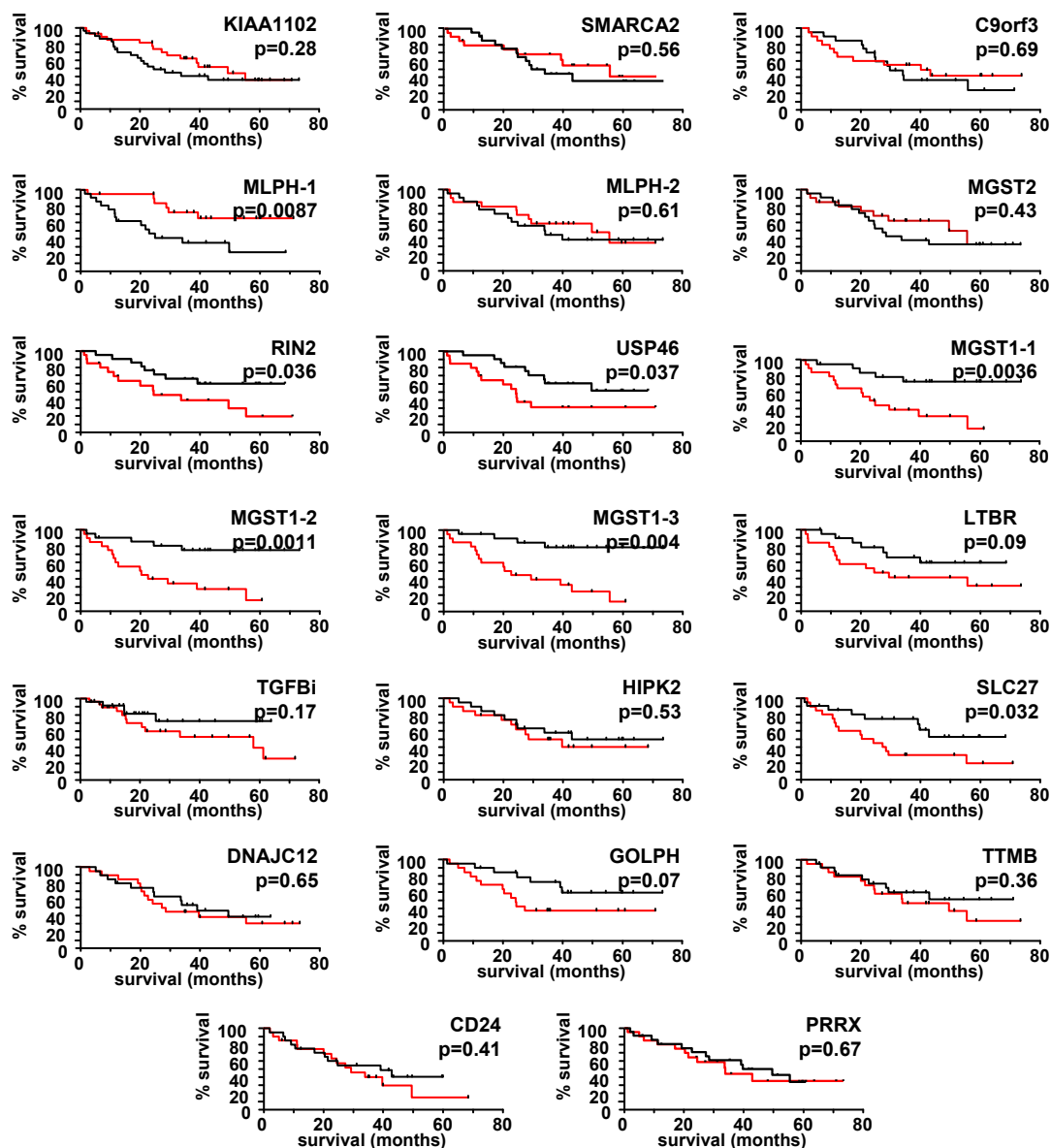
Supplemental Figure 2. Meta-analysis of transcripts differentially expressed between lung cancer cells grown in 2D and 3D. In each panel, Bioset #1 contains the 228 transcripts (representing 204 known genes) significantly differentially expressed ($p < 0.05$, ANOVA) between lung cancer cell lines grown on tissue culture plastic (2D) or in 3D IrECM (3D), in which the “Up-regulated” gene set showed increased expression in 2D relative to 3D, while the “Down-regulated genes” showed increased expression in 3D relative to 2D. Bioset #1 showed significant overlap ($p = 3.4e-49$) and was anticorrelated with a gene set in which differentiated Caco-2 cells were compared to undifferentiated Caco-2 cells (A) and significant overlap ($p = 4.5e-45$) and was anticorrelated with a gene set in which differentiated MCF10A cells were compared with undifferentiated MCF10A cells.

Supplemental Figure 3. Meta-analysis of transcripts differentially expressed between lung cancer cell lines showing smooth or branching morphology.



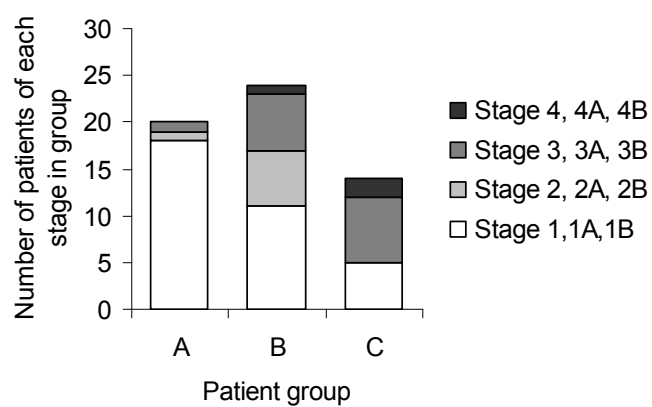
Supplemental Figure 3. Meta-analysis of transcripts differentially expressed between lung cancer cell lines showing smooth or branching morphology. In each panel, Bioset #1 contains the 200 transcripts (representing 204 known genes) significantly differentially expressed ($p < 1e-05$, ANOVA) between lung cancer cell lines showing smooth or branching morphology when grown in 3D IrECM, in which the “Up-regulated” gene set showed increased expression in smooth cell lines as compared to branching cell lines, while the “Down-regulated genes” showed increased expression in branching cell lines relative to smooth cell lines. Bioset #1 showed significant overlap ($p = 1.2e-10$) and anticorrelation with a gene set in which A549 lung carcinoma cells were exposed to tobacco smoke condensate vs unexposed (A) and significant overlap ($p = 3.5e-10$) and anticorrelation with a gene set in which isolated bronchial epithelial cells were exposed to tobacco smoke vs air (B).

Supplemental Figure 4. Association of individual transcripts in the 20-transcript set with survival in patients with lung adenocarcinoma.



Supplemental Figure 4. Association of individual transcripts in the 20-transcript set with survival in 59 patients with lung adenocarcinoma. Kaplan-Meier plots of individual genes of the 20-gene signature showing differences in disease-free survival. Patients were divided into two equally sized groups based upon gene expression (low gene expression, black line; high gene expression, red line).

Supplemental Figure 5. Distribution of cancer stage assignment within patient groups.



Supplemental Figure 5. Distribution of cancer stage assignment within patient groups.
Clinical cancer stage information for each patient in the Duke adenocarcinoma data set graphed for each group.

Supplemental Table 1: 228 transcripts significantly differentially expressed ($p < 0.05$, ANOVA) between lung cancer cell lines grown on tissue culture plastic (2D) and in 3D IrECM (3D)

Gene Symbol	Description	Affymetrix probe ID	average expression in 2D/average expression in 3D	p-value
SERPINB6	Serpin peptidase inhibitor, clade B (ovalbumin), member 6	231628_s_at	0.010428867	3.20E-11
MIDN	midnolin	225954_s_at	0.235220079	0.000304
DF	D component of complement (adipsin)	205382_s_at	0.318410953	0.0115
SPAG4	sperm associated antigen 4	219888_at	0.327814538	0.00365
BNIP3	BCL2/adenovirus E1B 19kDa interacting protein 3	201848_s_at	0.377144413	0.0178
LOC401152	HCV F-transactivated protein 1	224604_at	0.379857695	0.023
BNIP3	BCL2/adenovirus E1B 19kDa interacting protein 3	201849_at	0.414313529	0.0166
RAB11A	RAB11A, member RAS oncogene family	234998_at	0.440022181	0.0154
CA11	carbonic anhydrase XI	209726_at	0.448149786	0.0168
	CDNA clone IMAGE:5262734	228959_at	0.451228286	0.03
E2IG5	growth and transformation-dependent protein ; growth and transformati	224345_x_at	0.463079717	0.0178
E2IG5	growth and transformation-dependent protein	223193_x_at	0.4643751	0.0195
E2IG5	growth and transformation-dependent protein	220942_x_at	0.481163318	0.018
	Transcribed locus	235611_at	0.510025494	0.00365
RBM12	RNA binding motif protein 12	212170_at	0.514441563	0.0116
HSPA5	heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa)	230031_at	0.533775959	0.0132
LOC153222	adult retina protein	225956_at	0.534340876	0.012
SLC30A1	solute carrier family 30 (zinc transporter), member 1	228181_at	0.551045356	0.0387
PRO0149	PRO0149 protein	225197_at	0.597807363	0.0204
MSI2	Musashi homolog 2 (Drosophila)	226134_s_at	0.650543791	0.0234
ARID4B	AT rich interactive domain 4B (RBP1-like)	223111_x_at	1.176494994	0.044
ANAPC2	anaphase promoting complex subunit 2	218555_at	1.180256927	0.028
SUV39H1	suppressor of variegation 3-9 homolog 1 (Drosophila)	218619_s_at	1.243294832	0.0312
SNRPD3	small nuclear ribonucleoprotein D3 polypeptide 18kDa	202567_at	1.261067901	0.0296
NFATC3	nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 2	210555_s_at	1.285651819	0.0432
ZNF295	zinc finger protein 295	233952_s_at	1.305471351	0.00908
BOLA2	bolA-like 2 (E. coli)	209836_x_at	1.307337321	0.0344
LOC133619	hypothetical protein MGC12103	221734_at	1.310465037	0.0234
CBX5	Chromobox homolog 5 (HP1 alpha homolog, Drosophila)	212126_at	1.313315621	0.0302
SRGAP2	SLIT-ROBO Rho GTPase activating protein 2	232095_at	1.334641665	0.0271
PSMD1	proteasome (prosome, macropain) 26S subunit, non-ATPase, 1	201198_s_at	1.344201383	0.0344
	Similar to KIAA0160 gene product is novel	217704_x_at	1.347602604	0.042
UGCGL1	UDP-glucose ceramide glucosyltransferase-like 1	222569_at	1.353295684	0.0159
LUC7L2	LUC7-like 2 (S. cerevisiae)	243852_at	1.367044333	0.0211
ARHGAP11A	Rho GTPase activating protein 11A	204492_at	1.368609514	0.0132
ORC6L	origin recognition complex, subunit 6 homolog-like (yeast)	219105_x_at	1.376539354	0.0123
KIAA1271	KIAA1271 protein	231829_at	1.387244155	0.0371
PTPN11	protein tyrosine phosphatase, non-receptor type 11 (Noonan syndrome)	209895_at	1.388783884	0.0125
BLM	Bloom syndrome	205733_at	1.389806409	0.0249
MTHFD1	methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 1, meth	202309_at	1.393148256	0.0249
DDX18	DEAD (Asp-Glu-Ala-Asp) box polypeptide 18	208897_s_at	1.399347812	0.0132
C14orf156	chromosome 14 open reading frame 156 ; chromosome 14 open readin	221434_s_at	1.400943471	0.0151
FLJ20516	timeless-interacting protein	219258_at	1.405340426	0.00516
SFRS2IP	splicing factor, arginine/serine-rich 2, interacting protein	213850_s_at	1.408180017	0.00773
CDKN3	cyclin-dependent kinase inhibitor 3 (CDK2-associated dual specificity p	209714_s_at	1.416589372	0.00603
UGCGL1	UDP-glucose ceramide glucosyltransferase-like 1	218257_s_at	1.416942363	0.0444
PTPN11	protein tyrosine phosphatase, non-receptor type 11 (Noonan syndrome)	209896_s_at	1.421731732	0.00693
FLJ11301	hypothetical protein FLJ11301	223200_s_at	1.427365747	0.0129
MAP4K4	mitogen-activated protein kinase kinase kinase kinase 4	206571_s_at	1.428781442	0.00974
GART	phosphoribosylglycinamide formyltransferase, phosphoribosylglyciami	212378_at	1.429538657	0.016
BANP	BTG3 associated nuclear protein	219966_x_at	1.435121296	0.0242
E2F7	E2F transcription factor 7	228033_at	1.43727263	0.0382
PRC1	protein regulator of cytokinesis 1	218009_s_at	1.439382956	0.00974
RAD54B	RAD54 homolog B (S. cerevisiae)	219494_at	1.447694949	0.0387
FLJ20718	hypothetical protein FLJ20718	219289_at	1.451313625	0.0131
ARS2	arsenate resistance protein ARS2	201679_at	1.459184304	0.0131
NUP93	nucleoporin 93kDa	202188_at	1.467462804	0.00782
POLE2	polymerase (DNA directed), epsilon 2 (p59 subunit)	205909_at	1.475822965	0.00577
	CDNA FLJ30026 fis, clone 3NB692001123	1560048_at	1.476469282	0.0344
CLTB	clathrin, light polypeptide (Lcb)	205172_x_at	1.47839951	0.0284
CLTB	clathrin, light polypeptide (Lcb)	206284_x_at	1.478848601	0.0225
BRCA1	breast cancer 1, early onset	204531_s_at	1.480330563	0.0178
C15orf25	chromosome 15 open reading frame 25	229181_s_at	1.481627586	0.00154
BANP	BTG3 associated nuclear protein	228928_x_at	1.482231725	0.00802
DDX18	DEAD (Asp-Glu-Ala-Asp) box polypeptide 18	205763_s_at	1.482458931	0.0205
ATM	ataxia telangiectasia mutated (includes complementation groups A, C a	208442_s_at	1.483519036	0.0411
CGI-96 ; dJ222E	CGI-96 protein ; similar to CGI-96	214828_s_at	1.484956259	0.0413
KIAA1731	KIAA1731	1569302_at	1.486277482	0.0186
FBXL18	F-box and leucine-rich repeat protein 18	215068_s_at	1.488187618	0.0132
SDCCAG1	serologically defined colon cancer antigen 1	1557950_at	1.489962851	0.00723
PKMYT1	protein kinase, membrane associated tyrosine/threonine 1	204267_x_at	1.493546262	0.00669
C14orf145	chromosome 14 open reading frame 145	244033_at	1.494029645	0.0038
CNOT1	CCR4-NOT transcription complex, subunit 1	1554052_at	1.495147687	0.0249
SFRS12	splicing factor, arginine/serine-rich 12	244287_at	1.495696224	0.000504
LOC400506	similar to TSG118.1	213235_at	1.502716733	0.015
BICD2	bicaudal D homolog 2 (Drosophila)	209203_s_at	1.508318439	0.0166
CLTB	clathrin, light polypeptide (Lcb) ; clathrin, light polypeptide (Lcb)	211043_s_at	1.512815594	0.0262
ZNF294	zinc finger protein 294	233819_s_at	1.515650122	0.0178
DLEU1	deleted in lymphocytic leukemia, 1	205677_s_at	1.526710333	0.0358
WDHD1	WD repeat and HMG-box DNA binding protein 1	216228_s_at	1.52740861	0.0228

GART	phosphoribosylglycinamide formyltransferase, phosphoribosylglycinami	217445_s_at	1.528661275	0.00274
PX19	px19-like protein	224232_s_at	1.535687178	0.0444
FLJ10719	hypothetical protein FLJ10719	223785_at	1.537739469	0.015
		222606_at	1.537937837	0.000828
CSE1L	CSE1 chromosome segregation 1-like (yeast)	201111_at	1.538939263	0.0168
PPIL5	peptidylprolyl isomerase (cyclophilin)-like 5	235113_at	1.544682535	0.0264
TCOF1	Treacher Collins-Franceschetti syndrome 1	202384_s_at	1.545723589	0.0234
NAP1L4	nucleosome assembly protein 1-like 4	1560339_s_at	1.555883811	0.00297
FLJ37562	hypothetical protein FLJ37562	1553107_s_at	1.559768238	0.00782
FLJ30656	hypothetical protein FLJ30656	212529_at	1.560709815	0.0178
FLJ25416	hypothetical protein FLJ25416	228281_at	1.560861767	0.00266
NUPL1	Nucleoporin like 1	241425_at	1.564229569	0.0228
FAM72A	family with sequence similarity 72, member A	225834_at	1.566688586	0.00773
NUCKS1	nuclear casein kinase and cyclin-dependent kinase substrate 1	229353_s_at	1.567990041	0.00444
MDM4	Mdm4, transformed 3T3 cell double minute 4, p53 binding protein (mou	225742_at	1.571595706	0.0264
MTA1	metastasis associated 1	202247_s_at	1.576083635	0.00365
PCBP2	Poly(rC) binding protein 2	213517_at	1.577089121	0.0371
GPAM	glycerol-3-phosphate acyltransferase, mitochondrial	225420_at	1.580512879	0.0336
GART	phosphoribosylglycinamide formyltransferase, phosphoribosylglycinami	212379_at	1.580529965	0.00577
POLR3D	polymerase (RNA) III (DNA directed) polypeptide D, 44kDa	208361_s_at	1.590747197	0.0262
GAJ	GAJ protein	223700_at	1.590867073	0.0432
POLR3K	polymerase (RNA) III (DNA directed) polypeptide K, 12.3 kDa	218866_s_at	1.594473022	0.0228
RANBP1	RAN binding protein 1	202483_s_at	1.602862253	0.00616
TMPO	thymopoietin	203432_at	1.610908432	0.0125
HSPCA	heat shock 90kDa protein 1, alpha	211968_s_at	1.612744553	0.00297
HOMER3	homer homolog 3 (Drosophila)	215489_x_at	1.613677782	0.0239
GLE1L	GLE1 RNA export mediator-like (yeast)	206920_s_at	1.613890062	0.0125
UHMK1	U2AF homology motif (UHM) kinase 1	227740_at	1.615608756	0.0307
NCBP1	nuclear cap binding protein subunit 1, 80kDa	209520_s_at	1.619005921	0.0218
UHMK1	U2AF homology motif (UHM) kinase 1	235003_at	1.627165982	0.0371
NUCKS1	nuclear casein kinase and cyclin-dependent kinase substrate 1	222424_s_at	1.627556106	0.0161
ATAD3B	ATPase family, AAA domain containing 3B	223617_x_at	1.62845103	0.042
PRIM1	primase, polypeptide 1, 49kDa	205053_at	1.629674571	0.0228
CPSF2	cleavage and polyadenylation specific factor 2, 100kDa	233208_x_at	1.631434986	0.00159
CHEK1	CHK1 checkpoint homolog (S. pombe)	205393_s_at	1.63429277	0.0474
DKFZp547G183	hypothetical protein DKFZp547G183	220572_at	1.642141504	0.00723
IQGAP1	IQ motif containing GTPase activating protein 1	213446_s_at	1.642304459	0.00186
	CDNA clone IMAGE:6043059	228559_at	1.645866327	0.00272
CYCS	cytochrome c, somatic	244546_at	1.647678111	0.0368
KIF22	kinesin family member 22	216969_s_at	1.652209433	0.00274
SNRPF	small nuclear ribonucleoprotein polypeptide F	203832_at	1.655795734	0.0133
SRPRB	signal recognition particle receptor, B subunit	222532_at	1.655957499	0.0125
CSPG6	chondroitin sulfate proteoglycan 6 (bamacan)	209257_s_at	1.657434773	0.00266
TIMM44	translocase of inner mitochondrial membrane 44 homolog (yeast)	203093_s_at	1.667989993	0.0307
SMTN	smoothelin	207390_s_at	1.669023917	0.0278
TRIM14	tripartite motif-containing 14	203147_s_at	1.669123069	0.00583
DTYMK	deoxythymidylate kinase (thymidylate kinase)	203270_at	1.676734101	0.0101
EWSR1	Ewing sarcoma breakpoint region 1	229666_at	1.676928935	0.00159
BRCA1	breast cancer 1, early onset	211851_x_at	1.677300917	0.0113
C1orf112	chromosome 1 open reading frame 112	220840_s_at	1.68062383	0.0472
LOC23117 ; LOC KIAA0220-like protein ; hypothetical protein LOC440345 ; PI-3-kinase-n-231989_s_at		240247_at	1.68697125	0.00219
AHSA1	AHA1, activator of heat shock 90kDa protein ATPase homolog 1 (yeast)	201491_at	1.688231765	0.00723
DKFZp547E087	hypothetical gene LOC283846	235060_at	1.692501919	0.00655
	Transcribed locus	240247_at	1.693089016	0.00616
BANP	BTG3 associated nuclear protein	233186_s_at	1.693531258	0.00304
RSN	restin (Reed-Steinberg cell-expressed intermediate filament-associated	1558924_s_at	1.695229878	0.0101
MAZ	MYC-associated zinc finger protein (purine-binding transcription factor)	207824_s_at	1.69602149	0.023
	CDNA clone IMAGE:3929520	235134_at	1.701577718	0.0211
MALAT1	metastasis associated lung adenocarcinoma transcript 1 (non-coding R	226675_s_at	1.703934696	0.0168
ZWILCH	Zwilch, kinetochore associated, homolog (Drosophila)	218349_s_at	1.707235347	0.00051
CDC45L	CDC45 cell division cycle 45-like (S. cerevisiae)	204126_s_at	1.711229768	0.0387
RFWD3	ring finger and WD repeat domain 3	218564_at	1.711283987	0.0226
C20orf172	chromosome 20 open reading frame 172	219512_at	1.718093881	0.0317
CEBPZ	CCAAT/enhancer binding protein zeta	231819_at	1.719184092	0.0125
LIMS1	LIM and senescent cell antigen-like domains 1	207198_s_at	1.727183846	0.00842
LZIC	Leucine zipper and CTNBP1 domain containing	226081_at	1.734752401	0.00384
C9orf86	chromosome 9 open reading frame 86	225377_at	1.735983628	0.00264
JUB	jub, ajuba homolog (Xenopus laevis)	225806_at	1.738368617	0.0274
PPP1R10	protein phosphatase 1, regulatory subunit 10	201703_s_at	1.742043837	0.00203
MALAT1	metastasis associated lung adenocarcinoma transcript 1 (non-coding R	224567_x_at	1.753498038	0.00974
PPID	peptidylprolyl isomerase D (cyclophilin D)	204186_s_at	1.760919912	0.00773
UBN1	ubiquitin 1	209088_s_at	1.766555936	0.0133
EPRS	glutamyl-prolyl-tRNA synthetase	200841_s_at	1.767000831	0.0302
XRCC2	X-ray repair complementing defective repair in Chinese hamster cells 2	207598_x_at	1.771401553	0.00117
ESCO2	establishment of cohesion 1 homolog 2 (S. cerevisiae)	235588_at	1.776943204	0.00378
CYP51A1	cytochrome P450, family 51, subfamily A, polypeptide 1	216607_s_at	1.778417125	0.00583
	Transcribed locus	241879_at	1.79065997	0.0258
ZNF146	Zinc finger protein 146	1569312_at	1.794103975	0.0274
RAD51C	RAD51 homolog C (S. cerevisiae)	209849_s_at	1.800275666	0.00982
RANGAP1	Ran GTPase activating protein 1	212125_at	1.803853782	0.0373
HIST1H4C	histone 1, H4c	205967_at	1.806753491	0.00187
SPTBN1	spectrin, beta, non-erythrocytic 1	200672_x_at	1.808081753	0.0178
PKN2	protein kinase N2	212629_s_at	1.814840933	0.00987

XPO7	exportin 7	208459_s_at	1.829446752	0.00383
CDT1	DNA replication factor	209832_s_at	1.830792334	0.0123
DKFZp547E087	hypothetical gene LOC283846	235167_at	1.831030939	0.00424
CDC6	CDC6 cell division cycle 6 homolog (S. cerevisiae)	203967_at	1.841135025	0.00916
THRAP3	thyroid hormone receptor associated protein 3	222439_s_at	1.856528409	0.00162
SMG1 ; LOC231	PI-3-kinase-related kinase SMG-1 ; KIAA0220-like protein ; hypotheticala	244766_at	1.857264184	0.00384
KIAA1212	KIAA1212	219387_at	1.880581571	0.0309
PHF5A	PHD finger protein 5A	225309_at	1.884835552	0.00377
C22orf18	chromosome 22 open reading frame 18	218741_at	1.891124533	0.0189
JUB	jub, ajuba homolog (Xenopus laevis)	1553764_a_at	1.897567643	0.0216
CSPG6	chondroitin sulfate proteoglycan 6 (bamacan)	209258_s_at	1.912786106	0.00159
CHD4	chromodomain helicase DNA binding protein 4	201182_s_at	1.931718807	0.0067
	CDNA FLJ11381 fis, clone HEMBA1000501	227349_at	1.934825397	0.00893
BAZ1B	Bromodomain adjacent to zinc finger domain, 1B	213336_at	1.936513215	0.00582
	CDNA FLJ14193 fis, clone NT2RP3001115	232569_at	1.944041119	0.000925
SMCHD1	structural maintenance of chromosomes flexible hinge domain containir	1558747_at	1.944204004	0.0125
H2AFX	H2A histone family, member X	212525_s_at	1.947110389	0.00304
PSME4	proteasome (prosome, macropain) activator subunit 4	212220_at	1.958019045	0.00297
DKFZP434A013	DKFZp434A0131 protein	235263_at	1.961496431	0.00741
FSHPRH1	FSH primary response (LRPR1 homolog, rat) 1	207590_s_at	1.972466328	0.0299
BPNT1	3'(2'), 5'-bisphosphate nucleotidase 1	1554575_a_at	1.994689549	0.0225
Cep290	centrosome protein cep290	221683_s_at	2.002488923	0.00227
HSPH1	heat shock 105kDa/110kDa protein 1	208744_x_at	2.006309952	0.00694
PMS2 ; PMS2CL	PMS2 postmeiotic segregation increased 2 (S. cerevisiae) ; PMS2-C te	209805_at	2.017477094	0.0162
	Similar to Formin binding protein 2 (srGAP2)	228628_at	2.031738028	0.000322
PLK1	polo-like kinase 1 (Drosophila)	202240_at	2.073045166	0.00162
GTSE1	G-2 and S-phase expressed 1	204315_s_at	2.082457236	0.00846
TOP1	topoisomerase (DNA) I	208900_s_at	2.127260183	0.0296
KIAA0220	Hypothetical protein LOC440345	238449_at	2.129871262	0.00154
CHORDC1	cysteine and histidine-rich domain (CHORD)-containing 1	218566_s_at	2.140310604	0.0001
BIRC5	baculoviral IAP repeat-containing 5 (survivin)	210334_x_at	2.151155922	0.0102
C1orf43	chromosome 1 open reading frame 43	1555225_at	2.162211254	0.0231
SYNJ2BP	Synaptojanin 2 binding protein	235722_at	2.178084173	0.00444
FSHPRH1	FSH primary response (LRPR1 homolog, rat) 1	214804_at	2.197443656	0.00868
WDR76	WD repeat domain 76	205519_at	2.212225379	0.0148
ITM1	integral membrane protein 1	202223_at	2.249964358	0.00305
		1554948_at	2.254284086	0.000925
	CDNA FLJ41369 fis, clone BRCAN2006117	242691_at	2.278201966	0.00366
UGCGL1	UDP-glucose ceramide glucosyltransferase-like 1	222568_at	2.28546268	0.00062
TOMM22	translocase of outer mitochondrial membrane 22 homolog (yeast)	217960_s_at	2.324919287	0.00916
FUS	fusion (involved in t(12;16) in malignant liposarcoma)	1565717_s_at	2.326397778	0.00096
15E1.2	hypothetical protein LOC283459	214711_at	2.356731619	0.00023
DDX17	DEAD (Asp-Glu-Ala-Asp) box polypeptide 17	230180_at	2.398399298	0.00297
U2AF2	U2 (RNU2) small nuclear RNA auxiliary factor 2	218382_s_at	2.4219434	0.000404
DNCH1	dynein, cytoplasmic, heavy polypeptide 1	229115_at	2.429919229	0.0133
ARHGDI1A	Rho GDP dissociation inhibitor (GDI) alpha	213606_s_at	2.505106949	0.0028
ARHGDI1B	Rho GDP dissociation inhibitor (GDI) alpha	201167_x_at	2.538267802	0.00218
GNL3L	guanine nucleotide binding protein-like 3 (nucleolar)-like	205010_at	2.549904163	0.00062
		228919_at	2.551476882	0.0156
NUTF2	nuclear transport factor 2	202397_at	2.564248854	0.000281
RBBP5	retinoblastoma binding protein 5	205169_at	2.567612463	9.46E-05
HNRPL	heterogeneous nuclear ribonucleoprotein L	202072_at	2.580962638	0.00908
TAOK1	TAO kinase 1	227454_at	2.60221469	0.000304
C13orf3	chromosome 13 open reading frame 3	227165_at	2.605341733	0.00159
		AFFX-HUMRGE/M100	2.731322615	0.00234
SLD5	SLD5 homolog ; SLD5 homolog	211767_at	2.766710461	0.00162
EP400	E1A binding protein p400	230629_s_at	2.869850874	0.00162
HNRPH1	heterogeneous nuclear ribonucleoprotein H1 (H)	213470_s_at	2.881569473	0.00782
SET ; LOC38916	SET translocation (myeloid leukemia-associated) ; similar to SET protei	215780_s_at	3.000097122	0.00082
NARG1	NMDA receptor regulated 1	222837_s_at	3.072662616	9.46E-05
C1orf33	Chromosome 1 open reading frame 33	235783_at	3.137221897	0.00203
C14orf111	chromosome 14 open reading frame 111	219927_at	3.170476231	0.00304
THOC4	THO complex 4	226319_s_at	3.726514709	0.000258
THOC4	THO complex 4	226320_at	3.868636423	0.000312
SRP68	signal recognition particle 68kDa	AFFX-HUMRGE/M100	4.01986808	0.0183

Supplemental Table 2: Gene Ontology categories for 228 transcripts significantly differentially expressed (p<0.05, ANOVA) between lung cancer cell lines grown on tissue culture plastic (2D) and in 3D iRECM (

Category	Genes in Category	% of Genes in Category	Genes in List in Category	% of Genes in List in Category	p-Value
GO:6259: DNA metabolism	1551	5.209	29	20.71	1.49E-10
GO:7049: cell cycle	1966	6.603	31	22.14	1.98E-09
GO:43283: biopolymer metabolism	7387	24.81	67	47.86	2.90E-09
GO:279: M phase	506	1.699	14	10	1.29E-07
GO:6139: nucleobase, nucleoside, nucleotide and nucleic acid metabolism	8303	27.89	66	47.14	9.37E-07
GO:51327: M phase of meiotic cell cycle	126	0.423	7	5	2.31E-06
GO:7126: meiosis	126	0.423	7	5	2.31E-06
GO:51321: meiotic cell cycle	126	0.423	7	5	2.31E-06
GO:6974: response to DNA damage stimulus	649	2.18	14	10	2.48E-06
GO:6281: DNA repair	567	1.904	13	9.286	2.99E-06
GO:9719: response to endogenous stimulus	681	2.287	14	10	4.32E-06
GO:76: DNA replication checkpoint	8	0.0269	3	2.143	5.60E-06
GO:31570: DNA integrity checkpoint	59	0.198	5	3.571	8.73E-06
GO:51084: posttranslational protein folding	28	0.094	4	2.857	8.78E-06
GO:278: mitotic cell cycle	545	1.83	12	8.571	1.09E-05
GO:51168: nuclear export	160	0.537	7	5	1.12E-05
GO:74: regulation of progression through cell cycle	1321	4.437	19	13.57	1.44E-05
GO:7052: mitotic spindle organization and biogenesis	34	0.114	4	2.857	1.95E-05
GO:16071: mRNA metabolism	680	2.284	13	9.286	2.07E-05
GO:6188: IMP biosynthesis	12	0.0403	3	2.143	2.17E-05
GO:6189: 'de novo' IMP biosynthesis	12	0.0403	3	2.143	2.17E-05
GO:46040: IMP metabolism	12	0.0403	3	2.143	2.17E-05
GO:43170: macromolecule metabolism	10889	36.57	75	53.57	2.94E-05
GO:6260: DNA replication	417	1.401	10	7.143	2.97E-05
GO:6310: DNA recombination	196	0.658	7	5	4.13E-05
GO:7051: spindle organization and biogenesis	43	0.144	4	2.857	5.01E-05
GO:9113: purine base biosynthesis	16	0.0537	3	2.143	5.45E-05
GO:45739: positive regulation of DNA repair	3	0.0101	2	1.429	6.56E-05
GO:46605: regulation of centrosome cycle	3	0.0101	2	1.429	6.56E-05
GO:46599: regulation of centriole replication	3	0.0101	2	1.429	6.56E-05
GO:46600: negative regulation of centriole replication	3	0.0101	2	1.429	6.56E-05
GO:46606: negative regulation of centrosome cycle	3	0.0101	2	1.429	6.56E-05
GO:7099: centriole replication	3	0.0101	2	1.429	6.56E-05
GO:6978: DNA damage response, signal transduction by p53 class mediator resulting in	3	0.0101	2	1.429	6.56E-05
GO:42772: DNA damage response, signal transduction resulting in transcription	3	0.0101	2	1.429	6.56E-05
GO:6144: purine base metabolism	18	0.0605	3	2.143	7.88E-05
GO:30330: DNA damage response, signal transduction by p53 class mediator	18	0.0605	3	2.143	7.88E-05
GO:51052: regulation of DNA metabolism	95	0.319	5	3.571	8.82E-05
GO:16070: RNA metabolism	1258	4.225	17	12.14	9.06E-05
GO:7067: mitosis	388	1.303	9	6.429	9.65E-05
GO:79: regulation of cyclin dependent protein kinase activity	97	0.326	5	3.571	9.74E-05
GO:16043: cell organization and biogenesis	4222	14.18	37	26.43	9.95E-05
GO:6913: nucleocytoplasmic transport	395	1.327	9	6.429	0.00011
GO:87: M phase of mitotic cell cycle	395	1.327	9	6.429	0.00011
GO:9292: genetic transfer	4	0.0134	2	1.429	0.000131
GO:9294: DNA mediated transformation	4	0.0134	2	1.429	0.000131
GO:51298: centrosome duplication	4	0.0134	2	1.429	0.000131
GO:6397: mRNA processing	605	2.032	11	7.857	0.000142
GO:6333: chromatin assembly or disassembly	346	1.162	8	5.714	0.000242
GO:6261: DNA-dependent DNA replication	185	0.621	6	4.286	0.00025
GO:75: cell cycle checkpoint	120	0.403	5	3.571	0.000264
GO:46907: intracellular transport	1785	5.995	20	14.29	0.000286
GO:51649: establishment of cellular localization	1800	6.045	20	14.29	0.000296
GO:6611: protein export from nucleus	28	0.094	3	2.143	0.000306
GO:51169: nuclear transport	359	1.206	8	5.714	0.00031
GO:9127: purine nucleoside monophosphate biosynthesis	29	0.0974	3	2.143	0.00034
GO:9168: purine ribonucleoside monophosphate biosynthesis	29	0.0974	3	2.143	0.00034
GO:9126: purine nucleoside monophosphate metabolism	29	0.0974	3	2.143	0.00034
GO:9167: purine ribonucleoside monophosphate metabolism	29	0.0974	3	2.143	0.00034
GO:51641: cellular localization	1821	6.116	20	14.29	0.000344
GO:46112: nucleobase biosynthesis	31	0.104	3	2.143	0.000415
GO:51276: chromosome organization and biogenesis	807	2.71	12	8.571	0.000446
GO:8380: RNA splicing	478	1.605	9	6.429	0.00045
GO:46825: regulation of protein export from nucleus	7	0.0235	2	1.429	0.000454
GO:42770: DNA damage response, signal transduction	79	0.265	4	2.857	0.000535
GO:9112: nucleobase metabolism	35	0.118	3	2.143	0.000596
GO:51054: positive regulation of DNA metabolism	9	0.0302	2	1.429	0.000773
GO:7001: chromosome organization and biogenesis (sensu Eukaryota)	772	2.593	11	7.857	0.00109
GO:51329: interphase of mitotic cell cycle	165	0.554	5	3.571	0.00112
GO:51325: interphase	165	0.554	5	3.571	0.00112
GO:9156: ribonucleoside monophosphate biosynthesis	44	0.148	3	2.143	0.00117
GO:9161: ribonucleoside monophosphate metabolism	44	0.148	3	2.143	0.00117
GO:6396: RNA processing	1039	3.49	13	9.286	0.00127
GO:6406: mRNA export from nucleus	104	0.349	4	2.857	0.0015
GO:9124: nucleoside monophosphate biosynthesis	49	0.165	3	2.143	0.0016
GO:9123: nucleoside monophosphate metabolism	49	0.165	3	2.143	0.0016
GO:51028: mRNA transport	109	0.366	4	2.857	0.00178
GO:51053: negative regulation of DNA metabolism	14	0.047	2	1.429	0.00192
GO:7062: sister chromatid cohesion	14	0.047	2	1.429	0.00192
GO:398: nuclear mRNA splicing, via spliceosome	380	1.276	7	5	0.0022
GO:375: RNA splicing, via transesterification reactions	380	1.276	7	5	0.0022
GO:377: RNA splicing, via transesterification reactions with bulged adenosine as nucle	380	1.276	7	5	0.0022
GO:6359: regulation of transcription from RNA polymerase III promoter	15	0.0504	2	1.429	0.00221
GO:6457: protein folding	601	2.018	9	6.429	0.00222
GO:18105: peptidyl-serine phosphorylation	16	0.0537	2	1.429	0.00252
GO:18209: peptidyl-serine modification	16	0.0537	2	1.429	0.00252
GO:46777: protein amino acid autophosphorylation	59	0.198	3	2.143	0.00273
GO:16540: protein autoprocessing	60	0.202	3	2.143	0.00286
GO:8630: DNA damage response, signal transduction resulting in induction of apoptosis	18	0.0605	2	1.429	0.0032
GO:6325: establishment and/or maintenance of chromatin architecture	643	2.16	9	6.429	0.00346
GO:7131: meiotic recombination	65	0.218	3	2.143	0.00359
GO:6383: transcription from RNA polymerase III promoter	66	0.222	3	2.143	0.00375
GO:6405: RNA export from nucleus	134	0.45	4	2.857	0.00375
GO:6323: DNA packaging	661	2.22	9	6.429	0.00415
GO:226: microtubule cytoskeleton organization and biogenesis	138	0.463	4	2.857	0.00416

GO:50657: nucleic acid transport	139	0.467	4	2.857	0.00427
GO:50658: RNA transport	139	0.467	4	2.857	0.00427
GO:51236: establishment of RNA localization	139	0.467	4	2.857	0.00427
GO:6996: organelle organization and biogenesis	2248	7.55	20	14.29	0.00431
GO:50875: cellular physiological process	24283	81.55	126	90	0.00434
GO:45786: negative regulation of progression through cell cycle	545	1.83	8	5.714	0.00435
GO:6950: response to stress	2411	8.097	21	15	0.00439
GO:6450: regulation of translational fidelity	1	0.00336	1	0.714	0.0047
GO:6605: protein targeting	437	1.468	7	5	0.00473
GO:6282: regulation of DNA repair	22	0.0739	2	1.429	0.00477
GO:7098: centrosome cycle	22	0.0739	2	1.429	0.00477
GO:31023: microtubule organizing center organization and biogenesis	22	0.0739	2	1.429	0.00477
GO:51297: centrosome organization and biogenesis	22	0.0739	2	1.429	0.00477
GO:6403: RNA localization	146	0.49	4	2.857	0.00508
GO:7127: meiosis I	75	0.252	3	2.143	0.00537
GO:46483: heterocycle metabolism	155	0.521	4	2.857	0.00626
GO:15931: nucleobase, nucleoside, nucleotide and nucleic acid transport	161	0.541	4	2.857	0.00715
GO:7017: microtubule-based process	366	1.229	6	4.286	0.00784
GO:48523: negative regulation of cellular process	2058	6.912	18	12.86	0.008
GO:6275: regulation of DNA replication	30	0.101	2	1.429	0.00876
GO:44238: primary metabolism	17197	57.76	95	67.86	0.00898
GO:6164: purine nucleotide biosynthesis	174	0.584	4	2.857	0.00933
GO:9076: histidine family amino acid biosynthesis	2	0.00672	1	0.714	0.00938
GO:105: histidine biosynthesis	2	0.00672	1	0.714	0.00938
GO:6163: purine nucleotide metabolism	185	0.621	4	2.857	0.0115
GO:51223: regulation of protein transport	36	0.121	2	1.429	0.0125
GO:6334: nucleosome assembly	195	0.655	4	2.857	0.0137
GO:9165: nucleotide biosynthesis	299	1.004	5	3.571	0.0137
GO:48519: negative regulation of biological process	2181	7.325	18	12.86	0.014
GO:51243: negative regulation of cellular physiological process	1858	6.24	16	11.43	0.014
GO:8054: cyclin catabolism	3	0.0101	1	0.714	0.014
GO:46834: lipid phosphorylation	3	0.0101	1	0.714	0.014
GO:46854: phosphoinositide phosphorylation	3	0.0101	1	0.714	0.014
GO:48227: plasma membrane to endosome transport	3	0.0101	1	0.714	0.014
GO:22: mitotic spindle elongation	3	0.0101	1	0.714	0.014
GO:51231: spindle elongation	3	0.0101	1	0.714	0.014
GO:7292: female gamete generation	39	0.131	2	1.429	0.0145
GO:7162: negative regulation of cell adhesion	40	0.134	2	1.429	0.0152
GO:6473: protein amino acid acetylation	41	0.138	2	1.429	0.016
GO:30521: androgen receptor signaling pathway	114	0.383	3	2.143	0.0167
GO:43118: negative regulation of physiological process	1898	6.374	16	11.43	0.0168
GO:6270: DNA replication initiation	43	0.144	2	1.429	0.0175
GO:44237: cellular metabolism	17754	59.63	96	68.57	0.0179
GO:6433: prolyl-tRNA aminoacylation	4	0.0134	1	0.714	0.0187
GO:42026: protein refolding	4	0.0134	1	0.714	0.0187
GO:6369: transcription termination from RNA polymerase II promoter	4	0.0134	1	0.714	0.0187
GO:31497: chromatin assembly	215	0.722	4	2.857	0.0189
GO:6886: intracellular protein transport	1154	3.876	11	7.857	0.0206
GO:16485: protein processing	125	0.42	3	2.143	0.0213
GO:18193: peptidyl-amino acid modification	125	0.42	3	2.143	0.0213
GO:6626: protein targeting to mitochondrion	48	0.161	2	1.429	0.0215
GO:45893: positive regulation of transcription, DNA-dependent	337	1.132	5	3.571	0.0218
GO:45859: regulation of protein kinase activity	338	1.135	5	3.571	0.022
GO:51338: regulation of transferase activity	339	1.139	5	3.571	0.0223
GO:80: G1 phase of mitotic cell cycle	52	0.175	2	1.429	0.025
GO:51318: G1 phase	52	0.175	2	1.429	0.025
GO:77: DNA damage checkpoint	54	0.181	2	1.429	0.0268
GO:9139: pyrimidine nucleoside diphosphate biosynthesis	6	0.0202	1	0.714	0.0279
GO:9197: pyrimidine deoxyribonucleoside diphosphate biosynthesis	6	0.0202	1	0.714	0.0279
GO:6233: dTDP biosynthesis	6	0.0202	1	0.714	0.0279
GO:9148: pyrimidine nucleoside triphosphate biosynthesis	6	0.0202	1	0.714	0.0279
GO:9212: pyrimidine deoxyribonucleoside triphosphate biosynthesis	6	0.0202	1	0.714	0.0279
GO:6235: dTTP biosynthesis	6	0.0202	1	0.714	0.0279
GO:9202: deoxyribonucleoside triphosphate biosynthesis	6	0.0202	1	0.714	0.0279
GO:30174: regulation of DNA replication initiation	6	0.0202	1	0.714	0.0279
GO:46075: dTTP metabolism	6	0.0202	1	0.714	0.0279
GO:9196: pyrimidine deoxyribonucleoside diphosphate metabolism	6	0.0202	1	0.714	0.0279
GO:46072: dTDP metabolism	6	0.0202	1	0.714	0.0279
GO:46685: response to arsenic	6	0.0202	1	0.714	0.0279
GO:46822: regulation of nucleocytoplasmic transport	57	0.191	2	1.429	0.0296
GO:8629: induction of apoptosis by intracellular signals	59	0.198	2	1.429	0.0315
GO:8156: negative regulation of DNA replication	7	0.0235	1	0.714	0.0325
GO:35067: negative regulation of histone acetylation	7	0.0235	1	0.714	0.0325
GO:31057: negative regulation of histone modification	7	0.0235	1	0.714	0.0325
GO:320: re-entry into mitotic cell cycle	7	0.0235	1	0.714	0.0325
GO:45023: G0 to G1 transition	7	0.0235	1	0.714	0.0325
GO:6725: aromatic compound metabolism	260	0.873	4	2.857	0.0347
GO:6424: glutamyl-tRNA aminoacylation	8	0.0269	1	0.714	0.037
GO:9133: nucleoside diphosphate biosynthesis	8	0.0269	1	0.714	0.037
GO:9189: deoxyribonucleoside diphosphate biosynthesis	8	0.0269	1	0.714	0.037
GO:31571: G1 DNA damage checkpoint	8	0.0269	1	0.714	0.037
GO:6977: DNA damage response, signal transduction by p53 class mediator resulting in	8	0.0269	1	0.714	0.037
GO:30518: steroid hormone receptor signaling pathway	156	0.524	3	2.143	0.0375
GO:9893: positive regulation of metabolism	530	1.78	6	4.286	0.0396
GO:30522: intracellular receptor-mediated signaling pathway	161	0.541	3	2.143	0.0406
GO:59: protein import into nucleus, docking	68	0.228	2	1.429	0.0409
GO:42177: negative regulation of protein catabolism	9	0.0302	1	0.714	0.0415
GO:31056: regulation of histone modification	9	0.0302	1	0.714	0.0415
GO:35065: regulation of histone acetylation	9	0.0302	1	0.714	0.0415
GO:6474: N-terminal protein amino acid acetylation	9	0.0302	1	0.714	0.0415
GO:6273: lagging strand elongation	9	0.0302	1	0.714	0.0415
GO:6269: DNA replication, synthesis of RNA primer	9	0.0302	1	0.714	0.0415
GO:9211: pyrimidine deoxyribonucleoside triphosphate metabolism	9	0.0302	1	0.714	0.0415
GO:9200: deoxyribonucleoside triphosphate metabolism	9	0.0302	1	0.714	0.0415
GO:9152: purine ribonucleotide biosynthesis	166	0.558	3	2.143	0.0438
GO:7266: Rho protein signal transduction	71	0.238	2	1.429	0.0442
GO:7386: compartment specification	10	0.0336	1	0.714	0.046
GO:6353: transcription termination	10	0.0336	1	0.714	0.046

GO:45941: positive regulation of transcription

419

1.407

5

3.571 0.0483

(3D) for which p-value of association is less than 0.5

Supplemental Table 3: 200 transcripts significantly differentially expressed ($p < 1e-5$) between lung cancer cell lines showing smooth morphology vs branching morphology wher

Gene Symbol	Description	Affymetrix probe ID	average expression smooth/average expression branching	p-value
FLJ10781	hypothetical protein FLJ10781	218824_at	0.026522763	9.70E-08
WT1	Wilms tumor 1	206067_s_at	0.027970246	1.14E-06
TCF7L1	transcription factor 7-like 1 (T-cell specific, HMG-box) ; tran	221016_s_at	0.035459787	9.24E-07
KIF1A	kinesin family member 1A	225482_at	0.036202831	9.04E-06
TTMB	cDNA DKFZp434C184 gene	227386_s_at	0.045406296	2.14E-10
LHX2	LIM homeobox 2	211219_s_at	0.064920075	6.14E-07
NPTX2	neuronal pentraxin II	213479_at	0.076148159	1.26E-06
FBXO27	F-box protein 27	235169_at	0.086044946	1.10E-06
LOC90557 ; DKF	hypothetical protein BC016861 ; hypothetical protein DKFZ	227966_s_at	0.091358528	2.01E-07
	CDNA clone IMAGE:5300488	228422_at	0.093227684	4.36E-09
BMP7	bone morphogenetic protein 7 (osteogenic protein 1)	209591_s_at	0.096329407	3.39E-06
BTG3	BTG family, member 3	215425_at	0.102131223	6.14E-07
TLE2	transducin-like enhancer of split 2 (E(sp1) homolog, Drosop	40837_at	0.105190168	5.38E-06
TLE2	transducin-like enhancer of split 2 (E(sp1) homolog, Drosop	204431_at	0.111191948	3.74E-06
FBXO2	F-box protein 2	219305_x_at	0.11138998	5.73E-06
	LOC440476	1555976_s_at	0.114294077	8.76E-06
MICB	MHC class I polypeptide-related sequence B	206247_at	0.119330158	1.95E-06
CRMP1	collapsin response mediator protein 1	202517_at	0.121865367	4.02E-06
RAB6B	RAB6B, member RAS oncogene family	225259_at	0.130417863	5.13E-09
PLCXD1	phosphatidylinositol-specific phospholipase C, X domain co	218951_s_at	0.132606522	5.73E-06
MGC11082	Hypothetical protein MGC11082	1560019_at	0.137276259	1.50E-06
PHC1	polyhomeotic-like 1 (Drosophila)	218338_at	0.140347167	5.56E-06
MRPS30	mitochondrial ribosomal protein S30	218398_at	0.144295795	3.12E-07
CXADR	coxsackie virus and adenovirus receptor	1555716_a_at	0.150127637	6.65E-07
GOLGA8A	golgi autoantigen, golgin subfamily a, 8A	208798_x_at	0.154733571	4.93E-06
CD40	CD40 antigen (TNF receptor superfamily member 5)	215346_at	0.160868314	8.04E-06
PRRX2	paired related homeobox 2	219729_at	0.172400255	2.14E-10
AOF1	amine oxidase (flavin containing) domain 1	1553150_at	0.173976928	1.86E-06
CTSL2	cathepsin L2	210074_at	0.191967293	2.02E-06
DCUN1D4	DCN1, defective in cullin neddylation 1, domain containing	212855_at	0.206726968	1.20E-08
CXADR	coxsackie virus and adenovirus receptor	203917_at	0.218793286	1.63E-08
CSPG5	chondroitin sulfate proteoglycan 5 (neuroglycan C)	39966_at	0.225707946	6.03E-06
LATS2	LATS, large tumor suppressor, homolog 2 (Drosophila)	227013_at	0.226314921	3.48E-06
	Full-length cDNA clone CS0DF012YG01 of Fetal brain of H	226374_at	0.234492395	1.20E-08
USP46	ubiquitin specific peptidase 46	203869_at	0.236243962	3.58E-11
MTMR12	myotubularin related protein 12	225232_at	0.262227867	7.25E-06
FGFR1OP2	FGFR1 oncogene partner 2	233898_s_at	0.26317747	1.24E-06
LPHN1	latrophilin 1	203488_at	0.265328673	3.62E-06
ARID3A	AT rich interactive domain 3A (BRIGHT- like)	205865_at	0.265996333	3.69E-06
DZIP3	zinc finger DAZ interacting protein 3	207231_at	0.26830175	1.77E-06
HDAC5	histone deacetylase 5	202455_at	0.269512982	5.05E-06
STAT3	signal transducer and activator of transcription 3 (acute-ph	208991_at	0.272629212	3.20E-08
C12orf11	chromosome 12 open reading frame 11	221652_s_at	0.275087269	6.65E-06
DZIP3	zinc finger DAZ interacting protein 3	207232_s_at	0.275847649	8.28E-06
STAT3	signal transducer and activator of transcription 3 (acute-ph	208992_s_at	0.282720127	3.03E-08
RAB23	RAB23, member RAS oncogene family	229504_at	0.283935678	1.93E-06
FLJ32363	FLJ32363 protein	229886_at	0.28770019	9.06E-06
LOC255783	hypothetical protein LOC255783	227325_at	0.29425867	5.38E-06
PCBP4	poly(rC) binding protein 4	209361_s_at	0.30365814	5.83E-06
C1orf108	chromosome 1 open reading frame 108	222459_at	0.311138055	3.38E-06
	PREDICTED: Homo sapiens olfactory receptor, family 7, su	217499_x_at	0.324882561	3.96E-06
FLJ30596	hypothetical protein FLJ30596	228594_at	0.329882488	8.28E-06
FLJ38984	hypothetical protein FLJ38984	212791_at	0.345549778	5.79E-06
MGC33584	hypothetical protein MGC33584	228226_s_at	0.348472219	4.88E-06
PPT2 ; EGFL8	palmitoyl-protein thioesterase 2 ; EGF-like-domain, multiple	209826_at	0.354236356	4.88E-06
CD83	CD83 antigen (activated B lymphocytes, immunoglobulin su	204440_at	0.36212833	1.29E-06
	CDNA clone IMAGE:6615994	228389_at	0.367848154	8.36E-06
	Transcribed locus, weakly similar to XP_496299.1 PREDIC	227547_at	0.370268713	5.47E-06
TEX27	testis expressed sequence 27	222493_s_at	0.378664323	3.62E-06
LOC285636	hypothetical protein LOC285636	226159_at	0.437053481	1.50E-06
	Transcribed locus	240170_at	0.448017997	6.65E-06
CCHCR1	coiled-coil alpha-helical rod protein 1	209698_at	0.480069913	4.37E-06
CCHCR1	coiled-coil alpha-helical rod protein 1	37425_g_at	0.520910728	6.65E-06
LOC51234	hypothetical protein LOC51234	223857_x_at	1.572233676	5.60E-06
FLJ10803	hypothetical protein FLJ10803	209445_x_at	1.622308994	4.99E-07
SFRS9	Splicing factor, arginine/serine-rich 9	225430_at	1.730202538	8.30E-06
FAM96A	family with sequence similarity 96, member A	224779_s_at	1.815121405	4.02E-06
NUDT9	nudix (nucleoside diphosphate linked moiety X)-type motif	218375_at	1.820523692	2.90E-06
NAT5	N-acetyltransferase 5 (ARD1 homolog, S. cerevisiae)	223040_at	2.111132201	1.50E-06
C20orf18	chromosome 20 open reading frame 18	207713_s_at	2.146510999	1.66E-06
GSPT1	G1 to S phase transition 1	240452_at	2.248460758	7.57E-07
PPP2R5C	protein phosphatase 2, regulatory subunit B (B56), gamma	213305_s_at	2.342143	3.49E-06
PPP2R5C	protein phosphatase 2, regulatory subunit B (B56), gamma	1554365_a_at	2.383422255	2.78E-06
CASK	calcium/calmodulin-dependent serine protein kinase (MAGI	211208_s_at	2.383746451	5.27E-06
ATBF1	AT-binding transcription factor 1	242738_s_at	2.42039374	1.96E-07
UQCRCB	ubiquinol-cytochrome c reductase binding protein	209065_at	2.474904852	5.27E-06

FTSJ1	FtsJ homolog 1 (E. coli)	205324_s_at	2.528614964	8.30E-06
B4GALT1	UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, poly	201883_s_at	2.598716443	8.52E-06
AP3S2	adaptor-related protein complex 3, sigma 2 subunit	202399_s_at	2.63225635	1.42E-06
EBP	emopamil binding protein (sterol isomerase)	202735_at	2.699804141	1.20E-07
EBP	emopamil binding protein (sterol isomerase)	213787_s_at	2.769268309	1.29E-06
TES	testis derived transcript (3 LIM domains)	202720_at	2.791997723	5.90E-06
CUTL1	cut-like 1, CCAAT displacement protein (Drosophila)	202367_at	2.82453316	1.95E-06
TCTE1L	t-complex-associated-testis-expressed 1-like	203303_at	2.830855748	4.15E-07
FLJ90013	hypothetical protein FLJ90013	227407_at	2.928864174	9.40E-06
PTPRU	protein tyrosine phosphatase, receptor type, U	211320_s_at	2.968832142	8.97E-06
IMPA2	inositol(myo)-1(or 4)-monophosphatase 2	203126_at	3.049890533	8.33E-07
B4GALT1	UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, poly	228498_at	3.276874057	5.87E-06
TSPAN3	tetraspanin 3	200972_at	3.277571063	2.65E-07
KIAA1815	KIAA1815	218342_s_at	3.311686426	4.02E-06
TBC1D2	TBC1 domain family, member 2	222173_s_at	3.424179873	1.29E-06
CST3	cystatin C (amyloid angiopathy and cerebral hemorrhage)	201360_at	3.43755114	2.54E-06
	Full length insert cDNA YH77E09	213750_at	3.531593757	4.46E-07
PDXK	pyridoxal (pyridoxine, vitamin B6) kinase	218019_s_at	3.557504217	7.63E-06
TSPAN3	tetraspanin 3	200973_s_at	3.775396944	2.08E-07
ABCC3	ATP-binding cassette, sub-family C (CFTR/MRP), member	239217_x_at	3.977203866	8.88E-09
FLJ31842	Transmembrane protein 56	237515_at	4.096655367	6.65E-06
RPL13	Ribosomal protein L13	229590_at	4.469971976	5.27E-06
MFSD3	major facilitator superfamily domain containing 3	227296_at	4.48378551	2.90E-06
ASAH1	N-acylsphingosine amidohydrolase (acid ceramidase) 1	1555419_a_at	4.547002556	8.30E-06
DSG2	desmoglein 2	1553105_s_at	4.667432604	8.93E-06
TREX1	three prime repair exonuclease 1	34689_at	4.95109193	1.23E-08
NFKBIZ	nuclear factor of kappa light polypeptide gene enhancer in f	223217_s_at	5.30407433	5.36E-07
KIAA0992	palladin	200906_s_at	5.78765253	6.49E-06
ARSD	arylsulfatase D	232423_at	5.806278059	4.02E-06
LRRC54	leucine rich repeat containing 54	218245_at	6.074117685	6.69E-06
NFKBIZ	nuclear factor of kappa light polypeptide gene enhancer in f	223218_s_at	6.443526521	6.65E-07
CREG1	cellular repressor of E1A-stimulated genes 1	201200_at	6.512848657	4.02E-06
KIAA0992	palladin	200897_s_at	6.564571491	1.72E-07
RPH3AL	rabphilin 3A-like (without C2 domains)	221614_s_at	6.71948824	6.50E-07
RAI17	retinoic acid induced 17	212124_at	6.737375502	2.11E-06
KIAA0992	palladin	200907_s_at	6.771293213	1.17E-07
HIPK2	homeodomain interacting protein kinase 2	219028_at	6.820318953	6.96E-09
HIPK2	Homeodomain interacting protein kinase 2	225115_at	7.097917973	1.84E-09
TREX1	three prime repair exonuclease 1	205875_s_at	7.104319452	2.80E-06
FLJ20245	hypothetical protein FLJ20245	219620_x_at	7.90901697	1.06E-07
TRIM38	tripartite motif-containing 38	203568_s_at	8.265726258	5.83E-06
GOLPH2	golgi phosphoprotein 2	217771_at	10.6698893	6.54E-12
UGDH	UDP-glucose dehydrogenase	203343_at	10.71894866	1.98E-07
CTSC	cathepsin C	231234_at	10.7699814	6.86E-06
HIPK2	Homeodomain interacting protein kinase 2	225097_at	11.09353557	9.07E-08
NEDD9	neural precursor cell expressed, developmentally down-reg	202150_s_at	12.2867792	5.13E-09
VEGFC	vascular endothelial growth factor C	209946_at	12.4054093	3.52E-06
C9orf3	chromosome 9 open reading frame 3	212848_s_at	14.17804523	2.20E-10
HIPK2	Homeodomain interacting protein kinase 2	225116_at	15.32774269	7.84E-09
TUBA1	tubulin, alpha 1 (testis specific)	212242_at	15.55305203	8.28E-09
HIPK2	Homeodomain interacting protein kinase 2	225368_at	15.66112711	4.36E-09
KITLG	KIT ligand	226534_at	15.73313065	3.00E-06
VLDLR	very low density lipoprotein receptor	209822_s_at	16.11466049	7.63E-06
EDN1	endothelin 1	222802_at	17.22332376	6.38E-06
SMARCA2	SWI/SNF related, matrix associated, actin dependent regul	206542_s_at	17.44627514	8.55E-08
ALDH3B1	aldehyde dehydrogenase 3 family, member B1	205640_at	18.61394235	2.59E-06
MAML3	mastermind-like 3 (Drosophila)	242794_at	19.40889968	8.30E-06
SMARCA2	SWI/SNF related, matrix associated, actin dependent regul	206544_x_at	19.46402383	3.71E-10
CTSC	cathepsin C	225647_s_at	19.48223399	6.69E-06
TPD52L1	tumor protein D52-like 1	203786_s_at	20.711499	1.66E-06
CPEB2	cytoplasmic polyadenylation element binding protein 2	226939_at	21.12773417	6.96E-06
SMARCA2	SWI/SNF related, matrix associated, actin dependent regul	217707_x_at	21.24528863	2.75E-08
RBPM5	RNA binding protein with multiple splicing	209488_s_at	21.32693626	6.49E-06
CTSC	cathepsin C	201487_at	21.91940186	8.83E-07
KRT8	Keratin 8	229879_at	22.23350294	6.43E-08
FLJ14054	hypothetical protein FLJ14054	219054_at	24.42077345	3.35E-08
TRIM16 ; LOC14	tripartite motif-containing 16 ; similar to tripartite moti	204341_at	24.71430968	2.04E-06
CARD6	caspase recruitment domain family, member 6 ; caspase re	224414_s_at	26.3276415	3.84E-08
SERPINB1	Serpin peptidase inhibitor, clade B (ovalbumin), member 1	228726_at	27.51500265	1.56E-08
GLIS3	GLIS family zinc finger 3	229435_at	28.69269938	1.45E-07
MGST2	microsomal glutathione S-transferase 2	204168_at	29.58147572	1.84E-09
MLPH	Melanophilin	229150_at	30.17823672	1.17E-11
TRIP6	thyroid hormone receptor interactor 6	209129_at	30.68028503	7.63E-06
DHRS3	dehydrogenase/reductase (SDR family) member 3	202481_at	31.67322322	1.45E-06
TRIM38	tripartite motif-containing 38	203567_s_at	34.00765267	3.17E-08
CD24	CD24 antigen (small cell lung carcinoma cluster 4 antigen)	209772_s_at	38.07335939	1.18E-09
NTN4	netrin 4	223315_at	38.29795836	5.83E-06
S100A13	S100 calcium binding protein A13	202598_at	41.09486998	9.50E-08
SERPINB1	serpin peptidase inhibitor, clade B (ovalbumin), member 1	213572_s_at	41.14050738	1.00E-06

SLC27A2	solute carrier family 27 (fatty acid transporter), member 2	205768_s_at	43.3017856	4.36E-09
PTGS2	prostaglandin-endoperoxide synthase 2 (prostaglandin G/H	204748_at	44.83580873	5.31E-06
CD24	CD24 antigen (small cell lung carcinoma cluster 4 antigen)	208650_s_at	46.83420411	1.79E-06
RIN2	Ras and Rab interactor 2	209684_at	48.07121424	5.74E-10
GLRX	glutaredoxin (thioltransferase)	209276_s_at	48.87772539	5.51E-06
SERPINB1	serpin peptidase inhibitor, clade B (ovalbumin), member 1	212268_at	51.28625449	7.12E-07
DNAJC12	DnaJ (Hsp40) homolog, subfamily C, member 12	223721_s_at	51.84365115	1.99E-08
CD24	CD24 antigen (small cell lung carcinoma cluster 4 antigen)	208651_x_at	52.91719504	3.35E-08
OAS1	2',5'-oligoadenylate synthetase 1, 40/46kDa	202869_at	57.68830975	3.93E-07
S100A4	S100 calcium binding protein A4 (calcium protein, calvascu	203186_s_at	58.67246312	1.88E-06
SLC27A2	solute carrier family 27 (fatty acid transporter), member 2	205769_at	58.80188792	9.66E-10
MYO5B	myosin VB	225301_s_at	59.3791451	2.49E-08
TNFAIP2	tumor necrosis factor, alpha-induced protein 2	202510_s_at	61.2726663	4.51E-09
CD24	CD24 antigen (small cell lung carcinoma cluster 4 antigen)	209771_x_at	70.66946762	1.38E-07
LXN	latexin	218729_at	72.7345426	2.80E-06
CD24	CD24 antigen (small cell lung carcinoma cluster 4 antigen)	216379_x_at	74.8943026	6.34E-08
MALL	mal, T-cell differentiation protein-like	209373_at	75.07077701	6.96E-09
LTBR	lymphotoxin beta receptor (TNFR superfamily, member 3)	203005_at	80.00537889	2.02E-13
CD24	CD24 antigen (small cell lung carcinoma cluster 4 antigen)	266_s_at	82.86617221	2.63E-08
OAS1	2',5'-oligoadenylate synthetase 1, 40/46kDa	205552_s_at	88.01083109	7.84E-09
IGFBP3	insulin-like growth factor binding protein 3	210095_s_at	88.08326331	2.90E-06
IFI16	interferon, gamma-inducible protein 16	206332_s_at	89.78885213	1.66E-06
		242037_at	91.31399888	8.55E-08
LGALS3BP	lectin, galactoside-binding, soluble, 3 binding protein	200923_at	91.68115595	1.07E-07
IGFBP3	insulin-like growth factor binding protein 3	212143_s_at	92.3467298	8.30E-06
KIAA1102	KIAA1102 protein	212325_at	93.31526999	6.36E-09
S100A16	S100 calcium binding protein A16	227998_at	96.03697605	3.84E-08
IFI16	interferon, gamma-inducible protein 16	208966_x_at	102.6027702	8.97E-07
MLPH	melanophilin	218211_s_at	104.5594108	1.55E-14
MTUS1	mitochondrial tumor suppressor 1	212096_s_at	104.6736829	3.74E-06
NEDD9	neural precursor cell expressed, developmentally down-reg	202149_at	105.7604841	4.36E-09
KIAA1102	KIAA1102 protein	212327_at	113.7305373	2.86E-08
KIAA1102	KIAA1102 protein	212328_at	117.837851	1.85E-09
DNAJC12	DnaJ (Hsp40) homolog, subfamily C, member 12	218976_at	134.1442363	3.89E-10
MGST1	microsomal glutathione S-transferase 1	224918_x_at	177.3489846	5.34E-13
FN1	fibronectin 1	210495_x_at	178.0356735	6.36E-07
TGFBI	transforming growth factor, beta-induced, 68kDa	201506_at	179.7186986	2.02E-13
MGST1	microsomal glutathione S-transferase 1	231736_x_at	184.8884099	7.30E-13
FN1	fibronectin 1	216442_x_at	191.3480731	6.65E-07
MGST1	microsomal glutathione S-transferase 1	1565162_s_at	198.3338149	1.11E-10
FN1	fibronectin 1 ; fibronectin 1	211719_x_at	218.1831898	6.67E-07
FN1	fibronectin 1	212464_s_at	228.6701518	5.17E-07
AGR2	anterior gradient 2 homolog (Xenopus laevis)	209173_at	315.1409425	1.20E-07
KRT19	keratin 19	201650_at	851.8034326	3.10E-07
AKR1C3	aldo-keto reductase family 1, member C3 (3-alpha hydroxy;	209160_at	1645.129695	5.23E-06

γ grown in 3D IrECM

Supplemental Table 4: Gene Ontology categories for 200 transcripts significantly differentially expressed ($p < 1e-5$) between lung cancer cell lines showing smooth morphology vs branching morphology when g

Category	Genes in Category	% of Genes in Category	Genes in List in Category	% of Genes in List in Category	p-Value
GO:8629: induction of apoptosis by intracellular signals	59	0.198	8	5.674	3.74E-10
GO:30511: positive regulation of transforming growth factor beta receptor signaling pat	10	0.0336	5	3.546	5.48E-10
GO:9613: response to pest, pathogen or parasite	1084	3.641	23	16.31	1.68E-09
GO:43207: response to external biotic stimulus	1123	3.772	23	16.31	3.28E-09
GO:19048: virus-host interaction	16	0.0537	5	3.546	9.29E-09
GO:6955: immune response	1705	5.726	27	19.15	2.84E-08
GO:46330: positive regulation of JNK cascade	21	0.0705	5	3.546	4.25E-08
GO:6952: defense response	1897	6.371	28	19.86	6.63E-08
GO:17015: regulation of transforming growth factor beta receptor signaling pathway	24	0.0806	5	3.546	8.77E-08
GO:9607: response to biotic stimulus	1986	6.67	28	19.86	1.71E-07
GO:6953: acute-phase response	52	0.175	6	4.255	1.72E-07
GO:46328: regulation of JNK cascade	35	0.118	5	3.546	6.42E-07
GO:9605: response to external stimulus	1545	5.189	23	16.31	1.02E-06
GO:44403: symbiosis, mutualism through parasitism	83	0.279	6	4.255	2.83E-06
GO:44404: symbiotic interaction between host and other organism	83	0.279	6	4.255	2.83E-06
GO:44419: interaction between organisms	84	0.282	6	4.255	3.04E-06
GO:9967: positive regulation of signal transduction	273	0.917	9	6.383	6.54E-06
GO:6959: humoral immune response	339	1.139	9	6.383	3.62E-05
GO:9966: regulation of signal transduction	642	2.156	12	8.511	5.80E-05
GO:6950: response to stress	2411	8.097	26	18.44	6.08E-05
GO:7179: transforming growth factor beta receptor signaling pathway	92	0.309	5	3.546	7.83E-05
GO:8630: DNA damage response, signal transduction resulting in induction of apoptosi	18	0.0605	3	2.128	8.05E-05
GO:30330: DNA damage response, signal transduction by p53 class mediator	18	0.0605	3	2.128	8.05E-05
GO:31032: actomyosin structure organization and biogenesis	19	0.0638	3	2.128	9.53E-05
GO:48522: positive regulation of cellular process	1516	5.092	19	13.48	1.02E-04
GO:43065: positive regulation of apoptosis	483	1.622	10	7.092	1.07E-04
GO:43068: positive regulation of programmed cell death	487	1.636	10	7.092	1.14E-04
GO:6928: cell motility	586	1.968	11	7.801	1.15E-04
GO:51674: localization of cell	586	1.968	11	7.801	1.15E-04
GO:40011: locomotion	586	1.968	11	7.801	1.15E-04
GO:7626: locomotory behavior	605	2.032	11	7.801	1.51E-04
GO:7243: protein kinase cascade	844	2.835	13	9.22	1.96E-04
GO:42771: DNA damage response, signal transduction by p53 class mediator resulting	5	0.0168	2	1.418	2.21E-04
GO:7610: behavior	751	2.522	12	8.511	2.50E-04
GO:38: very-long-chain fatty acid metabolism	6	0.0202	2	1.418	3.30E-04
GO:7178: transmembrane receptor protein serine/threonine kinase signaling pathway	126	0.423	5	3.546	3.42E-04
GO:45663: positive regulation of myoblast differentiation	7	0.0235	2	1.418	4.60E-04
GO:7167: enzyme linked receptor protein signaling pathway	585	1.965	10	7.092	4.92E-04
GO:16032: viral life cycle	138	0.463	5	3.546	5.19E-04
GO:7254: JNK cascade	144	0.484	5	3.546	6.30E-04
GO:31098: stress-activated protein kinase signaling pathway	144	0.484	5	3.546	6.30E-04
GO:48518: positive regulation of biological process	1763	5.921	19	13.48	6.73E-04
GO:6917: induction of apoptosis	428	1.437	8	5.674	0.00103
GO:12502: induction of programmed cell death	428	1.437	8	5.674	0.00103
GO:51242: positive regulation of cellular physiological process	1277	4.289	15	10.64	0.0011
GO:45661: regulation of myoblast differentiation	11	0.0369	2	1.418	0.00119
GO:6631: fatty acid metabolism	344	1.155	7	4.965	0.0013
GO:43119: positive regulation of physiological process	1315	4.416	15	10.64	0.00147
GO:50896: response to stimulus	4365	14.66	34	24.11	0.00199
GO:50874: organismal physiological process	4074	13.68	32	22.7	0.00243
GO:16477: cell migration	294	0.987	6	4.255	0.00284
GO:42981: regulation of apoptosis	870	2.922	11	7.801	0.00293
GO:43067: regulation of programmed cell death	879	2.952	11	7.801	0.00317
GO:1558: regulation of cell growth	317	1.065	6	4.255	0.0041
GO:9312: oligosaccharide biosynthesis	21	0.0705	2	1.418	0.00441
GO:9615: response to virus	140	0.47	4	2.837	0.00449
GO:46399: glucuronate biosynthesis	1	0.00336	1	0.709	0.00474
GO:6065: UDP-glucuronate biosynthesis	1	0.00336	1	0.709	0.00474
GO:51017: actin filament bundle formation	22	0.0739	2	1.418	0.00483
GO:6915: apoptosis	1377	4.625	14	9.929	0.00585
GO:12501: programmed cell death	1386	4.655	14	9.929	0.00618
GO:42770: DNA damage response, signal transduction	79	0.265	3	2.128	0.00632
GO:40008: regulation of growth	350	1.175	6	4.255	0.00658
GO:6690: icosanoid metabolism	82	0.275	3	2.128	0.00701
GO:30154: cell differentiation	1285	4.316	13	9.22	0.00815
GO:19371: cyclooxygenase pathway	2	0.00672	1	0.709	0.00945
GO:8219: cell death	1464	4.917	14	9.929	0.00977
GO:74: regulation of progression through cell cycle	1321	4.437	13	9.22	0.0101
GO:165: MAPKKK cascade	275	0.924	5	3.546	0.0101
GO:16265: death	1472	4.944	14	9.929	0.0102
GO:40007: growth	514	1.726	7	4.965	0.0115
GO:30224: monocyte differentiation	35	0.118	2	1.418	0.012
GO:19221: cytokine and chemokine mediated signaling pathway	37	0.124	2	1.418	0.0133
GO:122: negative regulation of transcription from RNA polymerase II promoter	193	0.648	4	2.837	0.0136
GO:6011: UDP-glucose metabolism	3	0.0101	1	0.709	0.0141
GO:6063: uronic acid metabolism	3	0.0101	1	0.709	0.0141
GO:19585: glucuronate metabolism	3	0.0101	1	0.709	0.0141
GO:46398: UDP-glucuronate metabolism	3	0.0101	1	0.709	0.0141
GO:7010: cytoskeleton organization and biogenesis	1084	3.641	11	7.801	0.0142
GO:9311: oligosaccharide metabolism	40	0.134	2	1.418	0.0154
GO:44255: cellular lipid metabolism	1102	3.701	11	7.801	0.0159
GO:7155: cell adhesion	1726	5.797	15	10.64	0.0169
GO:8361: regulation of cell size	435	1.461	6	4.255	0.0177
GO:16049: cell growth	435	1.461	6	4.255	0.0177
GO:7613: memory	4	0.0134	1	0.709	0.0188
GO:7249: I-kappaB kinase/NF-kappaB cascade	325	1.092	5	3.546	0.0195
GO:48534: hemopoietic or lymphoid organ development	217	0.729	4	2.837	0.02
GO:30097: hemopoiesis	217	0.729	4	2.837	0.02
GO:6692: prostanoid metabolism	46	0.154	2	1.418	0.0201
GO:6693: prostaglandin metabolism	46	0.154	2	1.418	0.0201
GO:7222: frizzled signaling pathway	46	0.154	2	1.418	0.0201
GO:45892: negative regulation of transcription, DNA-dependent	331	1.112	5	3.546	0.0209
GO:43123: positive regulation of I-kappaB kinase/NF-kappaB cascade	226	0.759	4	2.837	0.0228

GO:6357: regulation of transcription from RNA polymerase II promoter	869	2.919	9	6.383	0.0228
GO:46456: icosanoid biosynthesis	52	0.175	2	1.418	0.0253
GO:7015: actin filament organization	53	0.178	2	1.418	0.0262
GO:45005: maintenance of fidelity during DNA-dependent DNA replication	54	0.181	2	1.418	0.0271
GO:6298: mismatch repair	54	0.181	2	1.418	0.0271
GO:16053: organic acid biosynthesis	137	0.46	3	2.128	0.0275
GO:46394: carboxylic acid biosynthesis	137	0.46	3	2.128	0.0275
GO:6122: mitochondrial electron transport, ubiquinol to cytochrome c	6	0.0202	1	0.709	0.0281
GO:8588: release of cytoplasmic sequestered NF-kappaB	6	0.0202	1	0.709	0.0281
GO:6629: lipid metabolism	1361	4.571	12	8.511	0.0285
GO:45597: positive regulation of cell differentiation	56	0.188	2	1.418	0.029
GO:48513: organ development	1524	5.118	13	9.22	0.0291
GO:43122: regulation of I-kappaB kinase/NF-kappaB cascade	245	0.823	4	2.837	0.0294
GO:6929: substrate-bound cell migration	7	0.0235	1	0.709	0.0327
GO:45445: myoblast differentiation	60	0.202	2	1.418	0.033
GO:7519: striated muscle development	149	0.5	3	2.128	0.034
GO:82: G1/S transition of mitotic cell cycle	62	0.208	2	1.418	0.035
GO:8283: cell proliferation	1406	4.722	12	8.511	0.0352
GO:6695: cholesterol biosynthesis	63	0.212	2	1.418	0.036
GO:31571: G1 DNA damage checkpoint	8	0.0269	1	0.709	0.0373
GO:6977: DNA damage response, signal transduction by p53 class mediator resulting in	8	0.0269	1	0.709	0.0373
GO:42692: muscle cell differentiation	68	0.228	2	1.418	0.0414
GO:19369: arachidonic acid metabolism	9	0.0302	1	0.709	0.0418
GO:9611: response to wounding	823	2.764	8	5.674	0.0425
GO:8217: regulation of blood pressure	70	0.235	2	1.418	0.0436
GO:30099: myeloid cell differentiation	72	0.242	2	1.418	0.0459
GO:46824: positive regulation of nucleocytoplasmic transport	10	0.0336	1	0.709	0.0464
GO:42307: positive regulation of protein import into nucleus	10	0.0336	1	0.709	0.0464
GO:42993: positive regulation of transcription factor import into nucleus	10	0.0336	1	0.709	0.0464
GO:42346: positive regulation of NF-kappaB import into nucleus	10	0.0336	1	0.709	0.0464
GO:51222: positive regulation of protein transport	10	0.0336	1	0.709	0.0464
GO:8203: cholesterol metabolism	173	0.581	3	2.128	0.0493