

Suppl. Table 1 : Genes altered during proliferation arrest in monolayer cultures

Probe ID	Gene Symbol	Chromosome	Transcript	Biological process	Molecular function	P value	Fold change	Shape
205064_at	SPRR1B	chr1q21-q22	g4507186	epidermis development	structural molecule activity	0.04724317	14.90160963	UP
204734_at	KRT15	chr17q21.2	g4504914	epidermis development	structural molecule activity	0.00163853	14.14475139	UP
					carbonate dehydratase			
209301_at	CA2	chr8q22	g179794	kidney development	activity	0.01107622	12.05347986	UP
202917_s_at	S100A8	chr1q21	g9845519	chemotaxis	calcium ion binding	0.01867846	9.884514329	UP
208650_s_at	CD24	chr6q21	Hs.286124.1	response to hypoxia	signal transducer activity	0.00411693	6.979471914	UP
266_s_at	CD24	chr6q21	L33930	response to hypoxia	signal transducer activity	0.0007097	6.854250486	UP
209771_x_at	CD24	chr6q21	Hs.286124.0	response to hypoxia	signal transducer activity	0.00371731	6.64308068	UP
209772_s_at	CD24	chr6q21	g396167	response to hypoxia	signal transducer activity	0.00360138	6.418304556	UP
204351_at	S100P	chr4p16	g5174662	endothelial cell migration	magnesium ion binding	0.03240656	5.904163882	UP
216379_x_at	CD24	chr6q21	Hs.332045.0	response to hypoxia	signal transducer activity	0.0010966	5.75918783	UP
209800_at	KRT16	chr17q21.2	g4091878	cytoskeleton organization	structural molecule activity	0.03590442	5.634181737	UP
208651_x_at	CD24	chr6q21	g180167	response to hypoxia	signal transducer activity	0.00432804	5.407119742	UP
203535_at	S100A9	chr1q21	g9845520	chemotaxis	signal transducer activity	0.03354197	5.404623779	UP
				regulation of translational				
201841_s_at	HSPB1	chr7q11.23	g4996892	initiation	protein binding	0.00069271	4.437596829	UP
205547_s_at	TAGLN	chr11q23.2	g12621918	muscle organ development	actin binding	0.0012673	4.152991515	UP
202489_s_at	FXYD3	chr19q13.12	g13528881	transport	ion channel activity	0.00059687	3.85517949	UP
207847_s_at	MUC1	chr1q21	g4505282	female pregnancy	NA	0.03500206	3.659692995	UP
					endopeptidase inhibitor			
203691_at	PI3	chr20q13.12	g4505786	copulation	activity	0.01671699	3.587142105	UP
				calcium-independent cell-cell				
202790_at	CLDN7	chr17p13	g10835007	adhesion	structural molecule activity	0.00059356	3.570325645	UP
				response to reactive oxygen				
202628_s_at	SERPINE1	chr7q21.3-q22	g10835158	species	protease binding	0.0001663	3.454999808	UP
					carbonate dehydratase			
205199_at	CA9	chr9p12	g9955947	response to hypoxia	activity	0.04687992	3.323767385	UP
205157_s_at	KRT17	chr17q21.2	g4557700	epidermis development	structural molecule activity	0.00061039	3.297775094	UP
202388_at	RGS2	chr1q31	g4506516	cell cycle	signal transducer activity	0.00291131	3.295745276	UP
					endopeptidase inhibitor			
41469_at	PI3	chr20q13.12	4862113_RC	copulation	activity	0.01429812	3.135199736	UP
219630_at	PDZK1IP1	chr1p33	g5031656	NA	NA	0.00334573	3.129679286	UP
213693_s_at	MUC1	chr1q21	Hs.89603.6	female pregnancy	NA	0.01883448	3.08972009	UP
200632_s_at	NDRG1	chr8q24.3	g5174656	response to metal ion	protein binding	0.02622175	3.078991889	UP
209118_s_at	TUBA1A	chr12q13.12	g4929133	microtubule-based process	nucleotide binding	0.00476844	3.0494502	UP

212657_s_at	IL1RN	chr2q14.2	Hs.81134.0	chronic inflammatory response to antigenic stimulus	receptor activity	0.02522971	2.976653359 UP
207935_s_at	KRT13	chr17q12-q21.2	g4504910	epidermis development	structural molecule activity	0.03387237	2.97097404 UP
205595_at	DSG3	chr18q12.1	g4503404	cell adhesion	calcium ion binding	0.0076782	2.883585674 UP
204597_x_at	STC1	chr8p21-p11.2	g4507264	ossification	hormone activity	0.01274316	2.729278281 UP
212236_x_at	KRT17	chr17q21.2	Hs.2785.1	epidermis development	structural molecule activity	0.00036246	2.723758429 UP
203021_at	SLPI	chr20q12	g4507064	NA	endopeptidase inhibitor activity	0.0008173	2.639304565 UP
203571_s_at	C10orf116	chr10q23.2	g5802975	NA	NA	0.00481734	2.591242646 UP
219127_at	PRR15L	chr17q21.32	g13236560	NA	NA	0.01451494	2.590789773 UP
205363_at	BBOX1	chr11p14.2	g4502368	carnitine biosynthetic process	iron ion binding	0.02731879	2.584098926 UP
206632_s_at	APOBEC3B	chr22q13.1-q13.2	g4758159	NA	RNA binding	0.00943469	2.461235198 UP
219476_at	C1orf116	chr1q32.1	g13129133	NA	receptor activity	0.04001345	2.451806207 UP
213293_s_at	TRIM22	chr11p15	Hs.295978.0	transcription	sequence-specific DNA binding transcription factor activity	0.00283426	2.408730537 UP
209008_x_at	KRT8	chr12q13	g1673574	cytoskeleton organization	structural molecule activity	0.01397969	2.33324953 UP
201170_s_at	BHLHE40	chr3p26	g4503298	transcription	DNA binding	0.02136551	2.330897501 UP
209373_at	MALL	chr2q13	g13112010	cholesterol homeostasis	protein binding	0.0258844	2.309204349 UP
221478_at	BNIP3L	chr8p21	Hs.132955.0	apoptosis	protein binding	0.02538764	2.251205677 UP
219534_x_at	CDKN1C	chr11p15.5	g4557440	regulation of cyclin-dependent protein kinase activity	protein kinase inhibitor activity	0.01972268	2.238519208 UP
221269_s_at	SH3BGRL3	chr1p36.11	g13775197	cell redox homeostasis	electron carrier activity	0.00032034	2.228448046 UP
201131_s_at	CDH1	chr16q22.1	g4757959	trophoblast cell differentiation	calcium ion binding	0.00901205	2.221594298 UP
202627_s_at	SERPINE1	chr7q21.3-q22	Hs.82085.0	response to reactive oxygen species	protease binding	0.00273167	2.220696768 UP
211695_x_at	MUC1	chr1q21	g13560650	female pregnancy	NA	0.02475333	2.201556379 UP
202022_at	ALDOC	chr17cen-q12	g4885062	response to hypoxia	catalytic activity	0.00082912	2.193002115 UP
202180_s_at	MVP	chr16p11.2	g9665254	transport	protein binding	0.00082723	2.186512072 UP
209531_at	GSTZ1	chr14q24.3	g12655190	L-phenylalanine catabolic process	catalytic activity	0.00075855	2.181610844 UP
221841_s_at	KLF4	chr9q31	Hs.7934.1	transcription	nucleic acid binding	0.04501805	2.171446129 UP
202023_at	EFNA1	chr1q21-q22	g4758245	activation of MAPK activity	receptor binding	6.08E-05	2.138278509 UP
213572_s_at	SERPINB1	chr6p25	Hs.183583.1	NA	serine-type endopeptidase inhibitor activity	0.00564888	2.132535714 UP
214370_at	S100A8	chr1q21	Hs.100000.1	chemotaxis	calcium ion binding	0.00227372	2.11837819 UP

215223_s_at	SOD2	chr6q25.3	Hs.318885.2	response to reactive oxygen species	superoxide dismutase activity	0.00092098	2.082114462	UP
213279_at	DHRS1	chr14q12	Hs.308467.0	metabolic process	catalytic activity	0.00398662	2.050002422	UP
212268_at	SERPINB1	chr6p25	Hs.183583.0	NA	serine-type endopeptidase inhibitor activity	0.00062214	2.016961573	UP
201720_s_at	LAPTM5	chr1p34	Hs.79356.0	transport	NA	0.01894611	2.013103847	UP
201721_s_at	LAPTM5	chr1p34	g5803055	transport	NA	0.01055726	2.009525022	UP
204858_s_at	TYMP	chr22q13 22q13.33	g7669488	mitochondrial genome maintenance	platelet-derived growth factor receptor binding	0.0035755	2.007250418	UP
201849_at	BNIP3	chr10q26.3	g7669480	response to hypoxia	protein binding	0.00596117	1.996006092	UP
202998_s_at	LOXL2	chr8p21.3	g4505010	protein modification process	scavenger receptor activity	0.01487211	1.990895326	UP
215034_s_at	TM4SF1	chr3q21-q25	Hs.306643.0	NA	NA	0.02442372	1.988397059	UP
204542_at	ST6GALNAC2	chr17q25.1	g5454091	protein glycosylation	sialyltransferase activity	0.00775359	1.987239402	UP
200696_s_at	GSN	chr9q33	g4504164	apoptosis	actin binding	0.00317581	1.985132443	UP
203108_at	GPRC5A	chr12p13-p12.3	g12056470	signal transduction	signal transducer activity	0.03359752	1.984151694	UP
202912_at	ADM	chr11p15.4	g4501944	response to hypoxia	receptor binding	0.00232102	1.983273616	UP
203964_at	NMI	chr2q23	g4758813	transcription from RNA polymerase II promoter	nucleotide binding	0.00363805	1.978107802	UP
215446_s_at	LOX	chr5q23.2	Hs.102267.3	blood vessel development	protein-lysine 6-oxidase activity	0.03419449	1.975490897	UP
217272_s_at	SERPINB13	chr18q21.3-q22	Hs.241407.2	response to UV	serine-type endopeptidase inhibitor activity	0.01863352	1.962423008	UP
205819_at	MARCO	chr2q14.2	g5803079	cell surface receptor linked signaling pathway	receptor activity	0.00388519	1.961501337	UP
204379_s_at	FGFR3	chr4p16.3	g13112046	MAPKKK cascade	nucleotide binding	0.02866581	1.957601618	UP
201015_s_at	JUP	chr17q21	g12056467	cell fate specification	transcription coactivator activity	0.02369083	1.951125164	UP
206884_s_at	SCEL	chr13q22	g4506798	epidermis development	protein binding	0.03812138	1.934220709	UP
208791_at	CLU	chr8p21-p12	g180619	release of cytochrome c from mitochondria	protein binding	0.00322229	1.93247815	UP
218531_at	TMEM134	chr11q13.2	g13376700	NA	NA	0.00070528	1.918497996	UP
201328_at	ETS2	chr21q22.3 21q22.2	Hs.85146.0	skeletal system development	DNA binding	0.00142081	1.913084408	UP
212099_at	RHOB	chr2p24	Hs.204354.0	angiogenesis	nucleotide binding	0.00212143	1.908214069	UP
202688_at	TNFSF10	chr3q26	g4507592	apoptosis	receptor binding	0.02560326	1.906873195	UP
210845_s_at	PLAUR	chr19q13	g517197	cellular component movement	receptor activity	0.01293699	1.899344941	UP
203585_at	ZNF185	chrXq28	g6005971	NA	zinc ion binding	0.00403861	1.891484175	UP
221588_x_at	ALDH6A1	chr14q24.3	Hs.293970.1	thymine catabolic process	acyl-CoA binding	0.01978282	1.880898005	UP
202130_at	RIOK3	chr18q11.2	Hs.209061.0	protein phosphorylation	nucleotide binding	0.00189021	1.879264162	UP
203227_s_at	TSPAN31	chr12q13.3	g5174666	positive regulation of cell proliferation	NA	0.00232443	1.870607826	UP

221477_s_at	SOD2	chr6q25.3	Hs.177781.0	response to reactive oxygen species	superoxide dismutase activity	0.00420038	1.858268176 UP
214433_s_at	SELENBP1	chr1q21.3	Hs.288973.1	transport	protein binding	0.0273699	1.857625041 UP
204470_at	CXCL1	chr4q21	g4504152	chemotaxis	receptor binding	0.00842643	1.854813572 UP
219888_at	SPAG4	chr20q11.21	g11037054	spermatogenesis cellular biogenic amine	structural molecule activity	0.04278436	1.854016578 UP
212741_at	MAOA	chrXp11.3	Hs.183109.1	metabolic process	protein binding	0.00553224	1.833733853 UP
212647_at	RRAS	chr19q13.3-qter	Hs.9651.0	signal transduction	nucleotide binding	0.00199884	1.833654346 UP
210785_s_at	C1orf38	chr1p35.3	g8272423	inflammatory response	NA	0.01335391	1.8286004 UP
205126_at	VRK2	chr2p16.1	g5454163	protein phosphorylation	nucleotide binding	5.53E-05	1.813643086 UP
206033_s_at	DSC3	chr18q12.1	g13435367	cell adhesion	calcium ion binding	9.39E-05	1.803750503 UP
33304_at	ISG20	chr15q26	4866504	DNA catabolic process, exonucleolytic	3'-5'-exoribonuclease activity	0.03284559	1.794009741 UP
205185_at	SPINK5	chr5q32	g5803218	epidermal cell differentiation	serine-type endopeptidase inhibitor activity	0.00765228	1.793741727 UP
211368_s_at	CASP1	chr11q23	g717045	response to hypoxia	cysteine-type endopeptidase activity	0.00298563	1.787505553 UP
202996_at	POLD4	chr11q13	g10863968	positive regulation of endothelial cell proliferation	DNA-directed DNA polymerase activity	0.00872433	1.777665471 UP
204290_s_at	ALDH6A1	chr14q24.3	g11095440	thymine catabolic process	acyl-CoA binding	0.01265244	1.77377393 UP
214453_s_at	IFI44	chr1p31.1	Hs.82316.2	response to virus	NA	0.02176279	1.770740102 UP
214093_s_at	FUBP1	chr1p31.1	Hs.22370.0	transcription	DNA binding	0.00188523	1.770016171 UP
209894_at	LEPR	chr1p31	g3236285	angiogenesis	receptor activity	0.01223844	1.768015275 UP
209386_at	TM4SF1	chr3q21-q25	Hs.3337.0	NA	NA	0.03557034	1.766601556 UP
211355_x_at	LEPR	chr1p31	g1279904	angiogenesis	receptor activity	0.03627748	1.759845495 UP
213667_at	SRCAP	chr16p11.2	Hs.87908.1	transcription	nucleotide binding	0.01037139	1.757800834 UP
209667_at	CES2	chr16q22.1	Hs.282975.0	catabolic process	carboxylesterase activity	0.00399657	1.748631295 UP
203986_at	FAM47E /// STBD1	chr4q21.1	g4503976	carbohydrate metabolic process	catalytic activity	0.00107632	1.740952202 UP
201310_s_at	C5orf13	chr5q22.1	g4758865	regulation of transforming growth factor beta receptor signaling pathway	protein binding	0.0019843	1.730375555 UP
201236_s_at	BTG2	chr1q32	g5802987	DNA repair	protein binding	0.03463072	1.720945895 UP
213698_at	LOC100130633 /// ZMYM6	chr1p34.2 /// chr1p34.3	Hs.301637.1	G-protein coupled receptor protein signaling pathway	nucleic acid binding	0.02592778	1.717540259 UP
204981_at	SLC22A18	chr11p15.5	g4505526	transport	drug transmembrane transporter activity	0.04060274	1.717339 UP
209463_s_at	TAF12	chr1p35.3	g1345403	transcription	DNA binding	0.00284485	1.714627326 UP
201315_x_at	IFITM2	chr11p15.5	g10835237	immune response cellular component	protein binding	0.00049492	1.711731918 UP
214866_at	PLAUR	chr19q13	Hs.179657.2	movement	receptor activity	0.01144091	1.70515559 UP

209034_at	PNRC1	chr6q15	g12751123	transcription	protein binding	0.03964706	1.704167216 UP
209387_s_at	TM4SF1	chr3q21-q25	g186803	NA	NA	0.0040358	1.699972689 UP
202488_s_at	FXYD3	chr19q13.12	g11612675	transport	ion channel activity	0.00116214	1.684519787 UP
201848_s_at	BNIP3	chr10q26.3	g558845	response to hypoxia	protein binding phospholipase inhibitor activity	0.02727737	1.683887256 UP
201302_at	ANXA4	chr2p13	g4809272	anti-apoptosis multicellular organismal development	NA	0.00097351	1.682875727 UP
201325_s_at	EMP1	chr12p12.3	g4503558	multicellular organismal development	NA	0.02306666	1.682290854 UP
218010_x_at	PPDPF	chr20q13.33	g13236523	development	NA	0.04037737	1.682225542 UP
202201_at	BLVRB	chr19q13.1-q13.2	g4502418	metabolic process	catalytic activity protein-methionine-R-oxide reductase activity	0.01503181	1.680194891 UP
218773_s_at	MSRB2	chr10p12	g6912591	protein repair	hydrolase activity	0.0163634	1.678223757 UP
204034_at	ETHE1	chr19q13.31	g7657686	NA	NA N4-(beta-N- acetylglucosaminy)-L- asparaginase activity	0.00533721	1.678179944 UP
216064_s_at	AGA	chr4q34.3	Hs.207776.1	protein deglycosylation	metalloendopeptidase activity	0.00673412	1.673411949 UP
219909_at	MMP28	chr17q21.1	g13236529	proteolysis	glutathione transferase activity	9.58E-05	1.667152504 UP
217751_at	GSTK1	chr7q35	g7705703	NA	activity	0.01004675	1.665088757 UP
201058_s_at	MYL9	chr20q11.23	g5174602	muscle contraction	motor activity	0.03610724	1.664870187 UP
201329_s_at	ETS2	chr21q22.3 21q22.2	g4885220	skeletal system development	DNA binding phospholipase inhibitor activity	0.02571267	1.664512593 UP
201301_s_at	ANXA4	chr2p13	g12652858	anti-apoptosis	cysteine-type endopeptidase activity	0.00017488	1.661702752 UP
211367_s_at	CASP1	chr11q23	g717043	response to hypoxia negative regulation of cytokine-mediated signaling pathway	phosphoprotein phosphatase activity	0.00391486	1.660886248 UP
200636_s_at	PTPRF	chr1p34	g4506310	calcium-independent cell-cell adhesion	transmembrane receptor activity	0.04572522	1.660729448 UP
201428_at	CLDN4	chr7q11.23	g4502876	adhesion	activity	0.01167854	1.660154961 UP
202411_at	IFI27	chr14q32	g5031780	apoptosis	NA	0.0114501	1.654789176 UP
219352_at	HERC6	chr4q22.1	g8923589	protein modification process	ligase activity	0.01383166	1.65274675 UP
202936_s_at	SOX9	chr17q23	g4557852	cartilage condensation	DNA binding	0.02363985	1.651717416 UP
210732_s_at	LGALS8	chr1q43	g13249300	NA	sugar binding	0.00399367	1.649854651 UP
210827_s_at	ELF3	chr1q32.2	g1841524	transcription	DNA binding	0.01824815	1.649747098 UP
206032_at	DSC3	chr18q12.1	Hs.41690.0	cell adhesion	calcium ion binding	0.00626878	1.649611357 UP
202597_at	IRF6	chr1q32.3-q41	Hs.11801.0	transcription	DNA binding	0.03301679	1.644689078 UP
206492_at	FHIT	chr3p14.2	g4503718	DNA replication	catalytic activity	0.01000708	1.642669846 UP
200811_at	CIRBP	chr19p13.3	g4502846	response to stress	nucleotide binding	0.00373498	1.638389675 UP

209398_at	HIST1H1C	chr6p21.3	g12803628	nucleosome assembly	DNA binding	0.01097293	1.633844799	UP
202121_s_at	CHMP2A	chr19q	g7656921	transport generation of precursor metabolites and energy	protein binding	0.01163151	1.632583928	UP
207813_s_at	FDXR	chr17q24-q25	g13435351	response to oxidative stress	catalytic activity	0.01691099	1.628894263	UP
219597_s_at	DUOX1	chr15q15.3	g8393276	NA	peroxidase activity	0.02349668	1.624914047	UP
221610_s_at	STAP2	chr19p13.3	g12653994	protein polyubiquitination	protein binding	0.0014485	1.620985151	UP
203409_at	DDB2	chr11p12-p11	g4557514	NA	DNA binding	0.00245757	1.619819052	UP
203153_at	IFIT1	chr10q23.31	g4504584	apoptosis	binding	0.01558039	1.611321766	UP
221479_s_at	BNIP3L	chr8p21 chr9q12- q21.2 9q21.13	g12001981	lipid metabolic process	protein binding phospholipase inhibitor activity	0.04998139	1.607905287	UP
201012_at	ANXA1		g4502100	inflammatory response cellular component	transmembrane receptor protein tyrosine kinase adaptor protein activity	0.00014435	1.606955375	UP
207655_s_at	BLNK	chr10q23.2-q23.33	g7019534	movement	protein binding	0.01339227	1.60652194	UP
201005_at	CD9	chr12p13.3	g4502692	ganglioside metabolic process	beta-N- acetylhexosaminidase activity	0.00323273	1.603135695	UP
215891_s_at	GM2A	chr5q33.1	Hs.289082.1	negative regulation of protein ubiquitination	protein binding	0.02348796	1.602593076	UP
212633_at	KIAA0776	chr6q16.1	Hs.5460.0	visual perception	catalytic activity	0.00502988	1.602397806	UP
204399_s_at	EML2	chr19q13.32	Hs.24178.0	regulation of cyclin- dependent protein kinase activity	activity	0.00688755	1.602386087	UP
203725_at	GADD45A	chr1p31.2	g9790904	liver development	protein binding	0.00159724	1.600219916	UP
208190_s_at	LSR	chr19q13.12	g7706247	immune response	receptor activity	0.01201514	1.596458396	UP
221291_at	ULBP2	chr6q25	g13376823	oxidation reduction cellular component	MHC class I receptor activity peptide-methionine-(S)-S- oxide reductase activity	0.00112914	1.594410256	UP
217783_s_at	YPEL5	chr2p23.1	g7706340	movement	nucleotide binding	0.00131197	1.591880359	UP
216388_s_at	LTB4R	chr14q11.2-q12	Hs.28408.2	steroid biosynthetic process	catalytic activity	0.00875907	1.590185073	UP
205829_at	HSD17B1	chr17q11-q21	g4504500	positive regulation of cell proliferation	NA	0.0141431	1.588034435	UP
203226_s_at	TSPAN31	chr12q13.3	Hs.50984.0	NA	NA	0.00323586	1.583676395	UP
209114_at	TSPAN1	chr1p34.1	g6434903	glycerol metabolic process	phosphoric diester hydrolase activity	0.00145489	1.582693506	UP
219722_s_at	GDPD3	chr16p11.2	g13236539	angiogenesis	receptor activity	0.022046	1.578174851	UP
211356_x_at	LEPR	chr1p31	g1519389	metabolic process	3-keto sterol reductase activity	0.02676462	1.577995387	UP
205379_at	CBR3	chr21q22.2	g7108334			0.00763837	1.577535269	UP

211911_x_at	HLA-B	chr6p21.3	g307236	stimulatory C-type lectin receptor signaling pathway retrograde vesicle-mediated	protein binding	0.00122334	1.577183895 UP
202296_s_at	RER1	chr1p36	g5902045	transport, Golgi to ER	NA	0.02556422	1.57228587 UP
211668_s_at	PLAU	chr10q24	g340155	angiogenesis	catalytic activity	0.01464054	1.572077779 UP
219147_s_at	C9orf95	chr9q21.13	g8923529	pyridine nucleotide biosynthetic process	nucleotide binding	0.01451819	1.57149606 UP
213540_at	HSD17B8	chr6p21.3	Hs.288354.0	fatty acid biosynthetic process	catalytic activity	0.01342279	1.571358396 UP
219104_at	RNF141	chr11p15.4	g7706776	regulation of transcription, DNA-dependent	DNA binding	0.04705965	1.567289832 UP
203882_at	IRF9	chr14q11.2	g5174474	protein polyubiquitination	DNA binding	0.00430184	1.56407644 UP
212136_at	ATP2B4	chr1q32.1	Hs.305923.2	ATP biosynthetic process	nucleotide binding	0.04202282	1.561000091 UP
202525_at	PRSS8	chr16p11.2	g4506152	proteolysis	catalytic activity	0.04164104	1.560994442 UP
204389_at	MAOA	chrXp11.3	g4557734	cellular biogenic amine metabolic process	protein binding	0.00383477	1.559904465 UP
202284_s_at	CDKN1A	chr6p21.2	g11386202	regulation of cyclin- dependent protein kinase activity	protein kinase inhibitor activity	0.00153505	1.559495432 UP
201009_s_at	TXNIP	chr1q21.1	Hs.179526.0	negative regulation of transcription from RNA polymerase II promoter	enzyme inhibitor activity	0.04400437	1.554307676 UP
204971_at	CSTA	chr3q21	g4885164	negative regulation of peptidase activity	protease binding	0.01662906	1.553774515 UP
200904_at	HLA-E	chr6p21.3	Hs.181392.0	antigen processing and presentation of peptide	MHC class I receptor activity	0.02119863	1.552444405 UP
208319_s_at	RBM3	chrXp11.2	g5803136	antigen via MHC class I RNA processing	nucleotide binding	0.01308874	1.552086439 UP
213895_at	EMP1	chr12p12.3	Hs.79368.1	multicellular organismal development	NA	0.01320548	1.54983348 UP
202833_s_at	SERPINA1	chr14q32.1	g4505792	response to hypoxia	protease binding	0.00043503	1.549217276 UP
212203_x_at	IFITM3	chr11p15.5	Hs.182241.2	immune response	NA	0.01146802	1.54913539 UP
219655_at	C7orf10	chr7p14.1	g13376041	metabolic process	catalytic activity	0.00201291	1.547063016 UP
204398_s_at	EML2	chr19q13.32	g6912355	visual perception	catalytic activity	0.00441355	1.545760635 UP
213010_at	PRKCDBP	chr11p15.4	Hs.85181.1	NA	protein kinase C binding	0.0108365	1.545509352 UP
218844_at	ACSF2	chr17q21.33	g13376740	lipid metabolic process	nucleotide binding	0.01788725	1.544790773 UP
220052_s_at	TINF2	chr14q12	g6912715	telomere maintenance	DNA binding	0.04115792	1.543689961 UP
212659_s_at	IL1RN	chr2q14.2	Hs.81134.0	chronic inflammatory response to antigenic stimulus	receptor activity	0.04181312	1.540273395 UP
218343_s_at	GTF3C3	chr2q33.1	g6912397	transcription	DNA binding	0.03198409	1.538778856 UP

210020_x_at	CALML3	chr10pter-p13	g189080	NA	calcium ion binding	0.01100541	1.53830535	UP
204698_at	ISG20	chr15q26	g6857799	NA	3'-5'-exoribonuclease	0.04707216	1.538302399	UP
217744_s_at	PERP	chr6q24	g11545842	exonucleolytic	activity	0.01559941	1.537961251	UP
204480_s_at	C9orf16	chr9q34.1	g13129127	apoptosis	NA	0.00248682	1.537667734	UP
216591_s_at	SDHC	chr1q23.3	Hs.247725.0	NA	succinate dehydrogenase	0.01616017	1.537001913	UP
202769_at	CCNG2	chr4q21.1	Hs.79069.0	tricarboxylic acid cycle	activity	0.00013863	1.536610133	UP
200622_x_at	CALM3	chr19q13.2-q13.3	Hs.141011.0	cell cycle checkpoint	NA	0.02853967	1.532707943	UP
209230_s_at	NUPR1	chr16p11.2	g5732669	muscle contraction	calcium ion binding	0.01940904	1.52776046	UP
211924_s_at	PLAUR	chr19q13	g13641308	induction of apoptosis	NA	0.01040002	1.524211674	UP
213509_x_at	CES2	chr16q22.1	Hs.282975.1	cellular component	receptor activity	0.02196529	1.523804444	UP
33646_g_at	GM2A	chr5q33.1	4819721	movement	carboxylesterase activity	0.03715897	1.519247195	UP
204462_s_at	SLC16A2	chrXq13.2	g5730044	catabolic process	beta-N-acetylhexosaminidase	0.00991272	1.518841954	UP
205076_s_at	MTMR11	chr1q12-q21	g5870890	ganglioside metabolic process	activity	0.00888834	1.514652449	UP
203828_s_at	IL32	chr16p13.3	g4758811	transport	transporter activity	0.01807272	1.51440081	UP
41047_at	C9orf16	chr9q34.1	4860579_RC	dephosphorylation	phosphatase activity	0.00139715	1.514152877	UP
200710_at	ACADVL	chr17p13.1	g4557234	defense response	cytokine activity	0.00016262	1.514069694	UP
211559_s_at	CCNG2	chr4q21.1	g1236234	NA	acyl-CoA dehydrogenase	0.04232358	1.513912394	UP
202447_at	DECR1	chr8q21.3	g4503300	temperature homeostasis	activity	0.00821675	1.513774773	UP
202644_s_at	TNFAIP3	chr6q23	g5454131	cell cycle checkpoint	NA	0.01064754	1.513489848	UP
216841_s_at	SOD2	chr6q25.3	Hs.318885.1	fatty acid beta-oxidation	catalytic activity	0.01925615	1.513301662	UP
202772_at	HMGCL	chr1p36.1-p35	g4504426	apoptosis	DNA binding	0.01628472	1.512898444	UP
209025_s_at	SYNCRIP	chr6q14-q15	g3037012	response to reactive oxygen species	superoxide dismutase activity	0.03651403	1.510477775	UP
218376_s_at	MICAL1	chr6q21	g12232438	nucleobase, nucleoside, nucleotide and nucleic acid	acyl-CoA binding	0.01084483	1.510206035	UP
209970_x_at	CASP1	chr11q23	g435598	metabolic process	acyl-CoA binding	0.0017896	1.510086987	UP
208729_x_at	HLA-B	chr6p21.3	g1871135	RNA processing	nucleotide binding	0.00026082	1.509576518	UP
202122_s_at	PLIN3	chr19p13.3	g5032182	cytoskeleton organization	nucleotide binding	0.02077263	1.508919907	UP
212841_s_at	PPFIBP2	chr11p15.4	Hs.12953.0	response to hypoxia	monooxygenase activity	0.01504713	1.508587366	UP
200810_s_at	CIRBP	chr19p13.3	g4502846	stimulatory C-type lectin	cysteine-type endopeptidase activity	0.00856382	1.507267569	UP
201850_at	CAPG	chr2p11.2	g4502560	receptor signaling pathway	protein binding	0.00836841	1.50675503	UP
215184_at	DAPK2	chr15q22.31	Hs.266662.0	transport	protein binding	0.04158848	1.505919365	UP
				cell communication	DNA binding			
				response to stress	nucleotide binding			
				protein complex assembly	actin binding			
				protein phosphorylation	nucleotide binding			

216894_x_at	CDKN1C	chr11p15.5	Hs.106070.3	regulation of cyclin-dependent protein kinase activity	protein kinase inhibitor activity	0.04572052	1.50429537 UP
218992_at	C9orf46	chr9p24.1	g8923931	NA	NA	0.01267102	1.501585164 UP
203594_at	RTCD1	chr1p21.2	g4506588	RNA processing	nucleotide binding	0.02964833	1.500417632 UP
201109_s_at	THBS1	chr15q15	Hs.87409.0	activation of MAPK activity	phosphatidylserine binding	0.04487543	3.055059648 DN
209101_at	CTGF	chr6q23.1	g180923	cartilage condensation carbohydrate metabolic process	fibronectin binding	0.00183674	3.005257713 DN
201272_at	AKR1B1	chr7q35	g4502048	process	aldehyde reductase activity	0.00034077	2.86573879 DN
222108_at	AMIGO2	chr12q13.11	Hs.121520.0	anti-apoptosis	protein binding sodium:potassium-exchanging ATPase activity	0.04638288	2.692082023 DN
201242_s_at	ATP1B1	chr1q24	g12652534	response to hypoxia	transporter activity	0.02334219	2.654414839 DN
219911_s_at	SLCO4A1	chr20q13.33	g7706516	transport	transporter activity	0.0047013	2.653750333 DN
205282_at	LRP8	chr1p34	g4758687	proteolysis	receptor activity	0.01335067	2.624476979 DN
203946_s_at	ARG2	chr14q24.1	g1763757	urea cycle	arginase activity	0.0015405	2.470943839 DN
209699_x_at	AKR1C2	chr10p15-p14	g531159	lipid metabolic process negative regulation of transcription from RNA polymerase II promoter	oxidoreductase activity	0.01454117	2.451292711 DN
208937_s_at	ID1	chr20q11	g464181	polymerase II promoter	protein binding	0.01558983	2.411252167 DN
203159_at	GLS	chr2q32-q34	g7662327	glutamine metabolic process protein import into nucleus,	glutaminase activity	0.0023157	2.346602725 DN
210793_s_at	NUP98	chr11p15.5	g1184172	docking	transporter activity	0.00101589	2.341428991 DN
204151_x_at	AKR1C1	chr10p15-p14	g5453542	lipid metabolic process	aldo-keto reductase activity	0.00281728	2.330425653 DN
202760_s_at	AKAP2	chr9q31.3	g6005708	regulation of cell shape	protein binding	0.03131807	2.258365358 DN
208433_s_at	LRP8	chr1p34	g8923799	proteolysis	receptor activity	0.00157043	2.233425871 DN
216594_x_at	AKR1C1	chr10p15-p14	Hs.306098.1	lipid metabolic process	aldo-keto reductase activity	0.00055356	2.171840536 DN
203158_s_at	GLS	chr2q32-q34	g6002672	glutamine metabolic process	glutaminase activity	0.03023614	2.143257797 DN
211653_x_at	AKR1C2	chr10p15-p14	g187444	lipid metabolic process	oxidoreductase activity	0.00235818	2.142822561 DN
203499_at	EPHA2	chr1p36	g4758277	skeletal system development	nucleotide binding epidermal growth factor receptor binding	0.00063794	2.138642752 DN
205767_at	EREG	chr4q13.3	g4557566	angiogenesis G1/S transition of mitotic cell cycle	receptor binding	0.0235911	2.115811672 DN
208712_at	CCND1	chr11q13	g179364	cycle	protein kinase activity ubiquitin-protein ligase activity	0.01310809	2.071947443 DN
218585_s_at	DTL	chr1q32	g7705575	protein polyubiquitination	activity	0.00369329	2.046226265 DN
202580_x_at	FOXM1	chr12p13	g11386144	regulation of cell growth	DNA binding	0.00095087	2.035325247 DN
204768_s_at	FEN1	chr11q12	g6325465	DNA replication	magnesium ion binding insulin-like growth factor binding	0.00706734	2.000566213 DN
210764_s_at	CYR61	chr1p22.3	g6649848	regulation of cell growth	binding	0.04168295	1.994223911 DN

219017_at	ETNK1	chr12p12.1	g10092614	phosphatidylethanolamine biosynthetic process	nucleotide binding	0.01968943	1.987789756 DN
201502_s_at	NFKBIA	chr14q13	Hs.81328.0	protein import into nucleus, translocation	protein binding cysteine-type	0.00610364	1.969263788 DN
210017_at	MALT1	chr18q21	Hs.180566.2	B-1 B cell differentiation	endopeptidase activity	0.00647218	1.965122896 DN
205968_at	KCNS3	chr2p24	g4504862	transport	ion channel activity	0.00723304	1.945615726 DN
219836_at	ZBED2	chr3q13.2	g13375643	NA	DNA binding	0.00972985	1.94249045 DN
210053_at	TAF5	chr10q24-q25.2	Hs.96103.0	transcription	DNA binding	0.01071407	1.940643184 DN
212464_s_at	FN1	chr2q34	Hs.287820.1	angiogenesis	protease binding	0.00818567	1.936590972 DN
219221_at	ZBTB38	chr3q23	g13376033	transcription	nucleic acid binding	0.03883131	1.915040469 DN
205899_at	CCNA1	chr13q12.3-q13	g4502610	cell cycle	protein binding	0.0152456	1.900695606 DN
204818_at	HSD17B2	chr16q24.1-q24.2	g4504502	steroid biosynthetic process	catalytic activity	0.01906486	1.891042152 DN
204962_s_at	CENPA	chr2p24-p21	g4585861	establishment of mitotic spindle orientation	DNA binding	0.00742626	1.88682344 DN
204604_at	CDK14	chr7q21-q22	g6912583	G2/M transition of mitotic cell cycle	nucleotide binding	0.01244238	1.850826837 DN
203967_at	CDC6	chr17q21.3	g1684902	DNA replication checkpoint	nucleotide binding	0.00699281	1.845476878 DN
220333_at	PAQR5	chr15q23	g8923182	multicellular organismal development	receptor activity	0.04780843	1.841488207 DN
216442_x_at	FN1	chr2q34	Hs.287820.2	angiogenesis	protease binding extracellular matrix	0.00348564	1.84060145 DN
211964_at	COL4A2	chr13q34	Hs.75617.0	angiogenesis	structural constituent	0.01712455	1.825848144 DN
204244_s_at	DBF4	chr7q21.3	g5729733	G1/S transition of mitotic cell cycle	nucleic acid binding	0.01677739	1.814304243 DN
220651_s_at	MCM10	chr10p13	g8924142	DNA replication	protein binding	0.0062812	1.813324355 DN
201540_at	FHL1	chrXq26	g4503720	multicellular organismal development	protein binding	0.00468205	1.805960382 DN
209946_at	VEGFC	chr4q34.3	g1373426	angiogenesis	growth factor activity	0.00521356	1.800592621 DN
203968_s_at	CDC6	chr17q21.3	g4502702	DNA replication checkpoint	nucleotide binding	0.00390767	1.798528565 DN
220234_at	CA8	chr8q11-q12	g5148943	one-carbon metabolic process	carbonate dehydratase activity	0.01177842	1.789713818 DN
211538_s_at	HSPA2	chr14q24.1	g4204879	response to stress	nucleotide binding	0.0004283	1.785104529 DN
221489_s_at	SPRY4	chr5q31.3	Hs.285814.0	multicellular organismal development	protein binding neurotransmitter	0.01254919	1.77350693 DN
206376_at	SLC6A15	chr12q21.3	g8922349	transport	transporter activity	0.00980224	1.768732489 DN
212944_at	SLC5A3	chr21q22.12	Hs.268016.0	inositol metabolic process	transporter activity	0.01801191	1.762610501 DN
202207_at	ARL4C	chr2q37.1	Hs.111554.0	transport	nucleotide binding	0.03307652	1.760910203 DN
210495_x_at	FN1	chr2q34	g11493493	angiogenesis	protease binding	0.02305029	1.755353625 DN
201984_s_at	EGFR	chr7p12	g4885198	activation of MAPKK activity	nucleotide binding	0.00054808	1.75404941 DN

202800_at	SLC1A3	chr5p13	g4759125	neurotransmitter uptake	L-glutamate transmembrane transporter activity	0.01062962	1.751150389 DN
202491_s_at	IKBKAP	chr9q31	g4504628	transcription	DNA binding	0.00353782	1.750429109 DN
217427_s_at	HIRA	chr22q11.2 22q11.21	Hs.172350.1	transcription	chromatin binding	0.03689576	1.748241226 DN
202241_at	TRIB1	chr8q24.13	g13399327	protein phosphorylation	protein kinase activity	0.04275139	1.748186074 DN
204767_s_at	FEN1	chr11q12	g12653112	DNA replication	magnesium ion binding	0.0194221	1.7474038 DN
212771_at	FAM171A1	chr10p13	Hs.66762.0	NA	NA	0.00203726	1.743623966 DN
204318_s_at	GTSE1	chr22q13.2-q13.3	g7705291	G2 phase of mitotic cell cycle regulation of transcription,	NA	0.00884162	1.742865801 DN
203349_s_at	ETV5	chr3q28	g4758315	DNA-dependent	DNA binding	0.00064665	1.742852237 DN
211719_x_at	FN1	chr2q34	g13543399	angiogenesis	protease binding	0.01074906	1.738687213 DN
205284_at	URB2	chr1q42.13	g7661931	NA	NA	0.00571112	1.73854842 DN
212825_at	PAXIP1	chr7q36	Hs.173854.0	response to DNA damage stimulus	protein binding	0.01440567	1.72988327 DN
210119_at	KCNJ15	chr21q22.2	g1765984	transport	ion channel activity	0.01156063	1.72678716 DN
203139_at	DAPK1	chr9q34.1	g4826683	protein phosphorylation	nucleotide binding	0.01038931	1.724056644 DN
217678_at	SLC7A11	chr4q28-q32	Hs.284235.0	transport	amino acid transmembrane transporter activity	0.0152401	1.710319608 DN
204275_at	SOLH	chr16p13.3	Hs.55836.0	proteolysis	sequence-specific DNA binding transcription factor activity	0.01110999	1.707483159 DN
212660_at	PHF15	chr5q31.1	Hs.9729.1	histone H3 acetylation	protein binding	0.00108085	1.703964241 DN
205055_at	ITGAE	chr17p13	g6007850	cell adhesion	receptor activity	0.03106771	1.702444673 DN
212875_s_at	C2CD2	chr21q22.3	Hs.16007.0	NA	NA	0.00328167	1.697665605 DN
201983_s_at	EGFR	chr7p12	Hs.77432.0	activation of MAPKK activity	nucleotide binding	0.01469844	1.689595544 DN
201818_at	LPCAT1	chr5p15.33	g13376233	metabolic process	calcium ion binding	0.00178102	1.687709482 DN
203157_s_at	GLS	chr2q32-q34	g4240164	glutamine metabolic process	glutaminase activity	0.01733208	1.686431216 DN
202084_s_at	SEC14L1	chr17q25.2	g4506866	NA	binding	0.02623595	1.686205581 DN
214594_x_at	ATP8B1	chr18q21-q22 18q21.31	Hs.166196.0	ATP biosynthetic process	nucleotide binding	0.01117576	1.682117717 DN
206508_at	CD70	chr19p13	g4507604	induction of apoptosis	receptor binding	0.03987988	1.681071687 DN
209464_at	AURKB	chr17p13.1	g5688865	cytokinesis	nucleotide binding	0.0036425	1.678393842 DN
212665_at	TIPARP	chr3q25.31	Hs.12813.0	vasculogenesis	nucleic acid binding	0.00090365	1.674752879 DN
55081_at	MICALL1	chr22q13.1	4876617_RC	NA	zinc ion binding	0.00600872	1.672289858 DN
214771_x_at	MPRIIP	chr17p11.2	Hs.84883.2	NA	actin binding	0.00109145	1.668312772 DN
218627_at	DRAM1	chr12q23.2	g8922957	autophagy	NA	0.00250246	1.667401568 DN
219286_s_at	RBM15	chr1p13	g12232444	patterning of blood vessels	nucleotide binding	0.01381663	1.664247327 DN
212693_at	MDN1	chr6q15	Hs.76730.0	protein complex assembly	nucleotide binding	0.00339092	1.662500125 DN

202613_at	CTPS	chr1p34.1	g4503132	nucleobase, nucleoside, nucleotide and nucleic acid				
218875_s_at	FBXO5	chr6q25.2	g6912365	metabolic process	nucleotide binding	0.00732775	1.658203375	DN
213449_at	POP1	chr8q22.1	Hs.170114.0	mitotic metaphase	protein binding	0.04677225	1.642841881	DN
				tRNA 5'-leader removal	ribonuclease MRP activity	0.01488169	1.64060399	DN
				transforming growth factor beta receptor signaling pathway	frizzled binding	0.0437011	1.639477981	DN
203304_at	BAMBI	chr10p12.3-p11.2	g6912533		protein binding	0.011968	1.639201735	DN
209288_s_at	CDC42EP3	chr2p21	g6807668	signal transduction	cysteine-type			
				DNA repair	endopeptidase activity	0.02979949	1.638911615	DN
					inositol or phosphatidylinositol			
203211_s_at	MTMR2	chr11q22	Hs.181326.0	protein dephosphorylation	phosphatase activity	0.03633378	1.634465245	DN
					cysteine-type			
210018_x_at	MALT1	chr18q21	g5706377	B-1 B cell differentiation	endopeptidase activity	0.01956775	1.633678818	DN
212552_at	HPCAL1	chr2p25.1	Hs.3618.1	NA	calcium ion binding	0.00149939	1.632928503	DN
202082_s_at	SEC14L1	chr17q25.2	Hs.75232.0	NA	binding	0.00601004	1.631703991	DN
				polyamine biosynthetic process	adenosylmethionine decarboxylase activity	0.03878348	1.62972423	DN
201196_s_at	AMD1	chr6q21	g178517		sodium:potassium- exchanging ATPase activity	0.01589316	1.629194736	DN
201243_s_at	ATP1B1	chr1q24	g4502276	response to hypoxia	DNA binding	0.00418468	1.628878137	DN
200878_at	EPAS1	chr2p21-p16	Hs.8136.0	angiogenesis	nucleotide binding	0.00402995	1.623015357	DN
207746_at	POLQ	chr3q13.33	g7662545	DNA replication				
				microtubule-based movement	nucleotide binding	0.00083551	1.622172473	DN
219306_at	KIF15	chr3p21.31	g9910265	negative regulation of transcription from RNA				
				polymerase II promoter DNA synthesis involved in	DNA binding	0.02322196	1.620510165	DN
201697_s_at	DNMT1	chr19p13.2	g4503350	DNA repair				
204127_at	RFC3	chr13q13.2	g12803002		nucleotide binding	0.03080918	1.618758954	DN
					amino acid transmembrane transporter activity	0.04820972	1.613046984	DN
218041_x_at	SLC38A2	chr12q	g8924006	transport	sodium:potassium- exchanging ATPase activity	0.00683377	1.609172837	DN
208836_at	ATP1B3	chr3q23	g1522634	ATP biosynthetic process epithelial to mesenchymal transition	calcium ion binding	0.01893948	1.608302997	DN
203186_s_at	S100A4	chr1q21	g9845514		receptor activity	0.01015962	1.608105485	DN
212722_s_at	JMJD6	chr17q25	Hs.72660.0	blood vessel development	nucleic acid binding	0.0164354	1.598437895	DN
218866_s_at	POLR3K	chr16p13.3	g7706498	transcription				
				multicellular organismal development	protein binding	0.04597444	1.598057204	DN
201539_s_at	FHL1	chrXq26	g2078479					

213043_s_at	MED24	chr17q21.1	Hs.23106.1	transcription methionine metabolic process	transcription cofactor activity	0.03375559	1.596388594 DN
203200_s_at	MTRR	chr5p15.31	g13325067	process	iron ion binding	0.00168553	1.593984036 DN
213682_at	NUP50	chr22q13.31	Hs.169329.0	transport	protein binding	0.00396389	1.58933165 DN
212092_at	PEG10	chr7q21	Hs.137476.0	apoptosis	nucleic acid binding	0.0208295	1.58690693 DN
202214_s_at	CUL4B	chrXq23	g13270466	DNA repair regulation of cyclin- dependent protein kinase activity	protein binding	0.01338092	1.585777055 DN
204695_at	CDC25A	chr3p21	Hs.1634.0	in utero embryonic development	phosphoprotein phosphatase activity	0.04609403	1.584641689 DN
201611_s_at	ICMT	chr1p36.21	g6912429	development	protein C-terminal carboxyl O-methyltransferase activity	0.01354474	1.581767144 DN
205462_s_at	HPCAL1	chr2p25.1	g4504474	NA	calcium ion binding	0.00134592	1.580945654 DN
208309_s_at	MALT1	chr18q21	g5803077	B-1 B cell differentiation purine base metabolic process	endopeptidase activity	0.04475511	1.579756114 DN
212360_at	AMPD2	chr1p13.3	Hs.82927.0	microtubule-based movement	AMP deaminase activity	0.00260764	1.577889046 DN
206364_at	KIF14	chr1q32.1	g7661877	polyamine biosynthetic process	nucleotide binding	0.0288507	1.57769335 DN
201197_at	AMD1	chr6q21	g5209326	N-terminal protein amino acid acetylation	adenosylmethionine decarboxylase activity	0.00113626	1.576811492 DN
219378_at	NAA16	chr13q14.11	g13375728	NA	receptor activity	0.02733814	1.576487865 DN
200755_s_at	CALU	chr7q32.1	Hs.7753.0	blood vessel development	calcium ion binding	0.02103965	1.576193203 DN
212723_at	JMJD6	chr17q25	Hs.72660.0	early endosome to late endosome transport	receptor activity	0.02223644	1.575898284 DN
221522_at	ANKRD27	chr19q13.11	g12053080	interspecies interaction between organisms	guanyl-nucleotide exchange factor activity	0.01521704	1.575015991 DN
203119_at	CCDC86	chr11q12.2	g13129103	release of cytochrome c from mitochondria	NA	0.00880913	1.574546756 DN
204493_at	BID	chr22q11.1	g4557360	transport	death receptor binding	0.0220343	1.574021872 DN
202111_at	SLC4A2	chr7q35-q36	g4507022	NA	transporter activity	0.00675683	1.570496948 DN
212197_x_at	MPRIP	chr17p11.2	Hs.84883.0	NA	actin binding	0.02646358	1.568964715 DN
202412_s_at	USP1	chr1p31.3	Hs.35086.0	DNA repair	cysteine-type endopeptidase activity	0.01714399	1.568103084 DN
203276_at	LMNB1	chr5q23.2	g5031876	NA	structural molecule activity	0.00580873	1.565420282 DN
204254_s_at	VDR	chr12q13.11	g4507882	skeletal system development	DNA binding	0.00239394	1.563968019 DN
218016_s_at	POLR3E	chr16p12.2	g8922476	transcription	DNA-directed RNA polymerase activity	0.00413535	1.561785104 DN
209053_s_at	WHSC1	chr4p16.3	Hs.110457.3	transcription	DNA binding	0.0105477	1.561315996 DN
202521_at	CTCF	chr16q21-q22.3	g5729789	DNA methylation	nucleic acid binding	0.00428119	1.555559705 DN

201041_s_at	DUSP1	chr5q34	g7108342	protein dephosphorylation transcription from RNA	phosphoprotein phosphatase activity	0.00208103	1.553922733	DN
203250_at	RBM16	chr6q25.1-q25.3	g7662491	polymerase II promoter	nucleotide binding	0.01647229	1.553601517	DN
212094_at	PEG10	chr7q21	Hs.137476.0	apoptosis	nucleic acid binding	0.01445561	1.553598353	DN
209226_s_at	TNPO1	chr5q13.2	g1657775	protein import into nucleus, translocation	binding	0.01544034	1.548556565	DN
209225_x_at	TNPO1	chr5q13.2	Hs.168075.1	protein import into nucleus, translocation	binding	0.00298615	1.547673599	DN
210220_at	FZD2	chr17q21.1	g736678	signal transduction	signal transducer activity	0.00097152	1.545433509	DN
210640_s_at	GPER	chr7p22.3	g2656120	signal transduction	signal transducer activity	0.00753052	1.544888835	DN
201368_at	ZFP36L2	chr2p22.3-p21	Hs.78909.0	cell proliferation	nucleic acid binding	0.02929772	1.542594189	DN
204066_s_at	AGAP1	chr2q37	g7662483	transport	nucleotide binding	0.02429195	1.539467106	DN
205677_s_at	DLEU1	chr13q14.3	g5031858	NA	protein binding	0.03790138	1.538742644	DN
202715_at	CAD	chr2p22-p21	g4757895	'de novo' pyrimidine base biosynthetic process	nucleotide binding RNA 7-methylguanosine cap	0.0063993	1.53816611	DN
213310_at	EIF2C2	chr8q24	Hs.324504.1	transcription	binding	0.03157357	1.537430653	DN
219502_at	NEIL3	chr4q34.3	g8922721	DNA repair microtubule-based	bubble DNA binding	0.03116625	1.537112103	DN
203087_s_at	KIF2A	chr5q12-q13	g4758643	movement	nucleotide binding	0.0490348	1.534758633	DN
221020_s_at	SLC25A32	chr8q22.3	g13540550	transport	transporter activity	0.01022993	1.531071242	DN
208079_s_at	AURKA	chr20q13	g4507278	mitotic cell cycle	nucleotide binding	0.00187265	1.529332294	DN
209501_at	CDR2	chr16p12.3	Hs.75124.0	NA	protein binding	5.99E-05	1.526055365	DN
217833_at	SYNCRIP	chr6q14-q15	Hs.155489.0	RNA processing	nucleotide binding	0.00260188	1.525767976	DN
221779_at	MICALL1	chr22q13.1	Hs.8535.0	NA	zinc ion binding	0.02936283	1.52438726	DN
204113_at	CELF1	chr11p11	g5729793	mRNA splice site selection multicellular organismal	nucleotide binding	0.00045353	1.521408592	DN
210298_x_at	FHL1	chrXq26	g3851649	development regulation of the force of	protein binding	0.02013934	1.51997584	DN
220948_s_at	ATP1A1	chr1p21	g4502268	heart contraction	nucleotide binding transcription cofactor	0.00027967	1.51855952	DN
202642_s_at	TRRAP	chr7q21.2-q22.1	g4507690	transcription	activity	0.04796571	1.517333517	DN
218829_s_at	CHD7	chr8q12.2	g8923329	skeletal system development	nucleotide binding	0.00757222	1.51540893	DN
204682_at	LTBP2	chr14q24	g4557732	protein targeting	binding	0.00637172	1.513554101	DN
219320_at	MYO19	chr17q12	g13376680	NA	nucleotide binding	0.00602838	1.510945613	DN
213523_at	CCNE1	chr19q12	Hs.9700.0	G1/S transition of mitotic cell cycle	transcription coactivator activity	0.0365157	1.509641563	DN
211966_at	COL4A2	chr13q34	Hs.75617.0	angiogenesis	extracellular matrix structural constituent	0.03118893	1.507691858	DN
203755_at	BUB1B	chr15q15	g5729749	protein phosphorylation	nucleotide binding	0.03568129	1.505330749	DN

201129_at	SRSF7	chr2p22.1	g6857827	mRNA processing	nucleotide binding	0.03623973	1.505322645 DN
205870_at	BDKRB2	chr14q32.1-q32.2	g4557358	smooth muscle contraction	protease binding	0.02218647	1.502469867 DN
205053_at	PRIM1	chr12q13	g4506050	DNA replication	DNA primase activity	0.00544954	1.500351305 DN

Suppl. Table 2: Genes altered during proliferation in 3D culture

Probe ID	Gene symbol	Chromosome	Transcript ID	Biological process	Molecular function	P value	Fold change	Shape
213796_at	SPRR1A	chr1q21-q22	Hs.46320.0	epidermis development	structural molecule activity	0.0470852	11.16479432	UP
219434_at	TREM1	chr6p21.1	g8924261	humoral immune response	receptor activity	0.00117867	7.183657699	UP
205199_at	CA9	chr9p12	g9955947	response to hypoxia	carbonate dehydratase activity	0.01422686	5.712946413	UP
214549_x_at	SPRR1A	chr1q21-q22	Hs.211913.0	epidermis development	structural molecule activity	0.03229483	3.003405468	UP
205916_at	S100A7	chr1q21	g9845518	response to reactive oxygen species	calcium ion binding	0.04001287	2.989617687	UP
215734_at	IZUMO4	chr19p13.3	Hs.90010.1	NA	NA	0.00449753	2.918968812	UP
218990_s_at	SPRR3	chr1q21-q22	g4885606	epidermis development regulation of transforming growth factor beta receptor signaling pathway	structural molecule activity	0.00024275	2.639947612	UP
201310_s_at	C5orf13	chr5q22.1	g4758865	creatine metabolic process	protein binding	0.02095206	2.541172877	UP
202219_at	SLC6A8	chrXq28	g5032096	copulation	creatine transporter activity	0.00066909	2.450089324	UP
203691_at	PI3	chr20q13.12 chr12p13.3-	g4505786	response to hypoxia	endopeptidase inhibitor activity	0.04797757	2.418142287	UP
211600_at	PTPRO	p13.2 12p13-p12	g885925	peptidyl-proline hydroxylation to 4-hydroxy-L-proline	NADH dehydrogenase activity procollagen-proline 4-dioxygenase activity	0.00256033	2.349068487	UP
207543_s_at	P4HA1	chr10q21.3-q23.1	g4505564	response to metal ion	protein binding	2.82E-05	2.204261187	UP
200632_s_at	NDRG1	chr8q24.3	g5174656	response to stress	nucleotide binding	0.04845627	1.972403602	UP
200811_at	CIRBP	chr19p13.3	g4502846	NA	protein binding	0.00344116	1.95390981	UP
209049_s_at	ZMYND8	chr20q13.12	g12654362	cholesterol homeostasis	protein binding	0.04992623	1.910050475	UP
209373_at	MALL	chr2q13	g13112010	one-carbon metabolic process	carbonate dehydratase activity	0.01046543	1.902277346	UP
204508_s_at	CA12	chr15q22	g12654376	NA	protein kinase C binding	0.04345563	1.840705274	UP
213010_at	PRKCDBP	chr11p15.4	Hs.85181.1	NA	protein binding	0.01834214	1.818351087	UP
209048_s_at	ZMYND8	chr20q13.12	Hs.75871.0	one-carbon metabolic process	carbonate dehydratase activity	0.02543175	1.813848067	UP
203963_at	CA12	chr15q22	g9951924	mRNA processing	nucleotide binding	0.0072387	1.809732993	UP
201129_at	SRSF7	chr2p22.1	g6857827	DNA replication	protein binding	0.00609773	1.807306558	UP
221521_s_at	GINS2	chr16q24.1	g13112024	protein polyubiquitination	ubiquitin-protein ligase activity	0.00484257	1.794902026	UP
218585_s_at	DTL	chr1q32	g7705575	negative regulation of transcription from RNA polymerase II promoter	enzyme inhibitor activity	0.00017285	1.791053965	UP
201009_s_at	TXNIP	chr1q21.1	Hs.179526.0	transcription from RNA polymerase II promoter	binding	0.0254157	1.780684955	UP
207020_at	HSF2BP	chr21q22.3	g5901979					

201194_at	SEPW1	chr19q13.3	g4506886	cell redox homeostasis	selenium binding	0.00316891	1.76370618	UP
204839_at	POP5	chr12q24.31	g7705422	tRNA processing	ribonuclease P activity	0.02928385	1.715381402	UP
208804_s_a								
t	SRSF6	chr20q12-q13.1	Hs.6891.1	mRNA splice site selection	nucleotide binding	0.0167081	1.714845705	UP
59625_at	NOL3	chr16q22.1	4854714_RC	response to hypoxia	RNA binding	0.03960688	1.708885274	UP
211695_x_a								
t	MUC1	chr1q21	g13560650	female pregnancy	NA	0.0131656	1.705864749	UP
221567_at	NOL3	chr16q22.1	g3172418	response to hypoxia	RNA binding	0.00791388	1.702731091	UP
209668_x_a								
t	CES2	chr16q22.1	g2641989	catabolic process	carboxylesterase activity	0.04604651	1.699518963	UP
	CEL ///							
205910_s_a	LOC10050820							
t	6	chr9q34.3	g4502770	lipid metabolic process	catalytic activity	0.01295446	1.697115227	UP
212320_at	TUBB	chr6p21.33	Hs.179661.5	cellular component movement	nucleotide binding	0.00147298	1.695561715	UP
205076_s_a								
t	MTMR11	chr1q12-q21	g5870890	dephosphorylation	phosphatase activity	0.04316674	1.684615374	UP
218012_at	TSPYL2	chrXp11.2	g11545834	nucleosome assembly	rDNA binding	0.00052802	1.672636672	UP
221211_s_a								
t	C21orf7	chr21q22.3	g9910145	NA	protein binding	0.01497755	1.669100045	UP
202154_x_a								
t	TUBB3	chr16q24.3	g5174736	microtubule-based process	nucleotide binding	0.03736439	1.666813987	UP
208977_x_a								
t	TUBB2C	chr9q34	g13278848	cellular component movement	nucleotide binding	0.00261197	1.664885437	UP
204430_s_a								
t	SLC2A5	chr1p36.2	g4507012	carbohydrate metabolic process	transporter activity	0.01586505	1.662148519	UP
218717_s_a								
t	LEPREL1	chr3q28	g8922618	oxidation reduction	binding	0.00677108	1.661163332	UP
45714_at	HCFC1R1	chr16p13.3	4893136_RC	NA	NA	0.02513774	1.658637698	UP
206758_at	EDN2	chr1p34	g4503462	prostaglandin biosynthetic process	hormone activity	0.04850633	1.657610251	UP
218537_at	HCFC1R1	chr16p13.3	g8923535	NA	NA	0.01792936	1.654258448	UP
200953_s_a								
t	CCND2	chr12p13	g4502616	ovarian follicle development	protein binding	0.01486815	1.624723471	UP
209125_at	KRT6A	chr12q12-q13	Hs.111758.0	cytoskeleton organization	structural molecule activity	0.03237323	1.622205287	UP
210638_s_a								
t	FBXO9	chr6p12.3-p11.2	g6103646	protein ubiquitination	ubiquitin-protein ligase activity	0.04196354	1.621979692	UP
219737_s_a								
t	PCDH9	chr13q21.32	Hs.12450.0	cell adhesion	calcium ion binding	0.04622183	1.621170244	UP
218355_at	KIF4A	chrXq13.1	g7305204	organelle organization	nucleotide binding	0.01135347	1.614970926	UP
209365_s_a								
t	ECM1	chr1q21	g1488323	ossification	protease binding	0.00358371	1.61244329	UP
202708_s_a								
t	HIST2H2BE	chr1q21.2	g4504276	nucleosome assembly	DNA binding	0.0290849	1.610687558	UP

202729_s_a				negative regulation of transforming growth factor beta receptor signaling pathway by extracellular sequestering of TGFbeta	transforming growth factor beta receptor activity	0.02503867	1.607988802	UP
t	LTBP1	chr2p22-p21	g4557730					
211240_x_a				morphogenesis of a polarized epithelium	binding	9.03E-05	1.598214395	UP
t	CTNND1	chr11q11	g2224708					
203592_s_a				ossification	fibronectin binding	0.00338497	1.59771251	UP
t	FSTL3	chr19p13	g5031700					
209068_at	HNRPDL	chr4q21.22	g3218539	transcription	nucleotide binding	0.0020199	1.585478564	UP
212657_s_a				chronic inflammatory response to antigenic stimulus	receptor activity	0.03716357	1.575281937	UP
t	IL1RN	chr2q14.2	Hs.81134.0					
201251_at	PKM2	chr15q22	g4505838	glycolysis	nucleotide binding	0.00777456	1.564035895	UP
221591_s_a				NA	protein binding	0.01297957	1.563284738	UP
t	FAM64A	chr17p13.2	g13436475					
200646_s_a				NA	DNA binding	0.04012929	1.561567329	UP
t	NUCB1	chr19q13.33	g5453817					
212037_at	PNN	chr14q21.1	Hs.44499.3	transcription	DNA binding	0.00695029	1.552464734	UP
200075_s_a				purine nucleotide metabolic process	nucleotide binding	0.00598959	1.541146483	UP
t	GUK1	chr1q32-q41	g13623296					
206081_at	SLC24A1	chr15q22	g4759127	transport	protein binding	0.02376262	1.53948547	UP
201116_s_a				cardiac left ventricle morphogenesis	carboxypeptidase activity	0.00344995	1.531263553	UP
t	CPE	chr4q32.3	Hs.75360.0					
213867_x_a				cellular component movement	nucleotide binding	0.00956079	1.529859351	UP
t	ACTB	chr7p22	Hs.288061.2					
209182_s_a				NA	NA	0.00014876	1.519638541	UP
t	C10orf10	chr10q11.21	Hs.93675.0					
218726_at	HJURP	chr2q37.1	g8922180	cell cycle	DNA binding	0.00120917	1.507106182	UP
201090_x_a				microtubule-based process	nucleotide binding	0.01577548	1.50474017	UP
t	TUBA1B	chr12q13.12	g5174476					
217645_at	COX16	chr14q24.2	Hs.312076.0	NA	NA	0.03457178	1.504536527	UP
202338_at	TK1	chr17q23.2-q25.3	g4507518	nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	nucleotide binding	0.00856967	1.503570444	UP
215867_x_a				one-carbon metabolic process	carbonate dehydratase activity	0.01738627	1.500621624	UP
t	CA12	chr15q22	Hs.5344.2					
215223_s_a				response to reactive oxygen species	superoxide dismutase activity	0.01121611	5.573228162	DN
t	SOD2	chr6q25.3	Hs.318885.2					
216841_s_a				response to reactive oxygen species	superoxide dismutase activity	0.00034419	5.0153683	DN
t	SOD2	chr6q25.3	Hs.318885.1					
204818_at	HSD17B2	chr16q24.1-q24.2	g4504502	steroid biosynthetic process	catalytic activity	0.01464371	4.787749805	DN
222062_at	IL27RA	chr19p13.11	Hs.132781.1	positive regulation of T-helper 1 type immune response	receptor activity	0.00550158	4.350749176	DN
203946_s_a				urea cycle	arginase activity	7.52E-05	3.920730358	DN
t	ARG2	chr14q24.1	g1763757					
205899_at	CCNA1	chr13q12.3-q13	g4502610	cell cycle	protein binding	5.82E-05	3.837808433	DN

221477_s_at	SOD2	chr6q25.3	Hs.177781.0	response to reactive oxygen species positive regulation of immune system	superoxide dismutase activity	0.00721837	3.646296492	DN
39248_at	AQP3	chr9p13	4855867_RC	process	transporter activity	0.00735656	3.499812548	DN
210538_s_at	BIRC3	chr11q22	g1145290	apoptosis	ubiquitin-protein ligase activity	0.01112174	3.282091855	DN
201839_s_at	EPCAM	chr2p21	g4505058	ureteric bud development	protein binding	0.00637677	3.208840284	DN
201141_at	GNPMB	chr7p15	g4505404	osteoblast differentiation	integrin binding	0.01389104	3.029541728	DN
204224_s_at	GCH1	chr14q22.1-q22.2	g4503948	GTP catabolic process	nucleotide binding	0.02670599	2.972685994	DN
201272_at	AKR1B1	chr7q35	g4502048	carbohydrate metabolic process microtubule cytoskeleton	aldehyde reductase activity	0.00433341	2.920606803	DN
202289_s_at	TACC2	chr10q26	g11119413	organization protein import into nucleus, translocation	protein domain specific binding	0.00269222	2.909230414	DN
203140_at	BCL6	chr3q27	g4502382	transcription from RNA polymerase II promoter	nucleic acid binding	0.00102043	2.881890224	DN
207469_s_at	PIR	chrXp22.2	g4505822	transcription cofactor activity	transcription cofactor activity	0.00064676	2.862077019	DN
209774_x_at	CXCL2	chr4q21	g183626	chemotaxis	cytokine activity	0.0492251	2.809358298	DN
203914_x_at	HPGD	chr4q34-q35	g4504478	lipid metabolic process	catalytic activity	0.01925175	2.776123954	DN
201721_s_at	LAPTM5	chr1p34	g5803055	transport nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	NA	0.00052361	2.754185051	DN
205552_s_at	OAS1	chr12q24.1	g8051622	nucleotide binding	nucleotide binding	0.00109737	2.729407642	DN
209699_x_at	AKR1C2	chr10p15-p14	g531159	lipid metabolic process	oxidoreductase activity	3.23E-05	2.673789425	DN
212314_at	SEL1L3	chr4p15.2	Hs.49500.0	NA	binding	0.01036948	2.661259552	DN
212070_at	GPR56	chr16q13	Hs.6527.1	cell adhesion	signal transducer activity	0.00317779	2.628257114	DN
202833_s_at	SERPINA1	chr14q32.1	g4505792	response to hypoxia	protease binding	0.00013625	2.599077269	DN
201720_s_at	LAPTM5	chr1p34	Hs.79356.0	transport microtubule cytoskeleton	NA	0.00516505	2.540330795	DN
211382_s_at	TACC2	chr10q26	g7934571	organization	protein domain specific binding	0.00130945	2.525283597	DN
204279_at	PSMB9	chr6p21.3	g4506204	carbohydrate metabolic process	endopeptidase activity	0.00279127	2.5082324	DN
217739_s_at	NAMPT	chr7q22.3	g5031976	nicotinamide metabolic process	nicotinate-nucleotide diphosphorylase (carboxylating) activity	0.00413222	2.421967739	DN
216594_x_at	AKR1C1	chr10p15-p14	Hs.306098.1	lipid metabolic process positive regulation of T cell mediated	aldo-keto reductase activity	0.00015818	2.376838078	DN
202307_s_at	TAP1	chr6p21.3	g9665247	cytotoxicity	nucleotide binding	0.00029084	2.33506965	DN

204151_x_a									
t	AKR1C1	chr10p15-p14	g5453542	lipid metabolic process	aldo-keto reductase activity	8.75E-05	2.333874668	DN	
212902_at	SEC24A	chr5q31.1	Hs.211612.0	transport	protein binding	0.0033719	2.332092528	DN	
203827_at	WIPI1	chr17q24.2	g8922207	autophagy	receptor binding	0.01160138	2.324053599	DN	
219648_at	MREG	chr2q35	g8922236	melanocyte differentiation	NA	0.01171329	2.287547745	DN	
211429_s_a									
t	SERPINA1	chr14q32.1	g7770182	response to hypoxia	protease binding	0.00221535	2.261449099	DN	
219188_s_a									
t	MACROD1	chr11q11	g13569839	NA	NA	0.01415362	2.244412598	DN	
203634_s_a					carnitine O-palmitoyltransferase activity				
t	CPT1A	chr11q13.2	g4503020	glucose metabolic process	activity	0.00920946	2.235522061	DN	
212694_s_a									
t	PCCB	chr3q21-q22	Hs.63788.0	fatty acid biosynthetic process	nucleotide binding	0.00267635	2.22758	DN	
208146_s_a									
t	CPVL	chr7p15.1	g13786124	proteolysis	carboxypeptidase activity	0.03959927	2.220522167	DN	
213112_s_a				ubiquitin-dependent protein catabolic process	protein kinase C binding				
t	SQSTM1	chr5q35	Hs.279891.1	release of cytochrome c from mitochondria	death receptor binding	0.00176014	2.185053274	DN	
211725_s_a									
t	BID	chr22q11.1	g13543452			0.00016139	2.174335188	DN	
207275_s_a									
t	ACSL1	chr4q35	g4503650	lipid metabolic process	nucleotide binding	0.00974831	2.170163433	DN	
					carnitine O-palmitoyltransferase activity				
203633_at	CPT1A	chr11q13.2	Hs.259785.0	glucose metabolic process	activity	0.00177808	2.167571828	DN	
208700_s_a									
t	TKT	chr3p14.3	g388890	pentose-phosphate shunt	magnesium ion binding	0.00014843	2.166627715	DN	
211275_s_a									
t	GYG1	chr3q24-q25.1	g5814084	glycogen biosynthetic process	protein binding	0.01391749	2.147815781	DN	
219869_s_a					metal ion transmembrane transporter activity				
t	SLC39A8	chr4q22-q24	g11545899	transport	activity	0.01420496	2.133346824	DN	
206857_s_a					peptidyl-prolyl cis-trans isomerase activity				
t	FKBP1B	chr2p23.3	g4758379	regulation of heart rate	activity	0.00926	2.124510336	DN	
221675_s_a					diacylglycerol				
t	CHPT1	chr12q	g9502012	regulation of cell growth	cholinephosphotransferase activity	0.0007224	2.114612372	DN	
203414_at	MMD	chr17q	g6912507	cytolysis	receptor activity	0.03052956	2.107968377	DN	
				release of cytochrome c from mitochondria	death receptor binding				
204493_at	BID	chr22q11.1	g4557360			0.00229321	2.097643849	DN	
221985_at	KLHL24	chr3q27.1	Hs.246875.1	NA	protein binding	0.00010798	2.096599338	DN	
				very long-chain fatty acid metabolic process					
205769_at	SLC27A2	chr15q21.2	g4503652		nucleotide binding	0.04042651	2.095529446	DN	
211653_x_a									
t	AKR1C2	chr10p15-p14	g187444	lipid metabolic process	oxidoreductase activity	0.00054294	2.092140809	DN	
205960_at	PDK4	chr7q21.3	g4505692	carbohydrate metabolic process	two-component sensor activity	0.03756094	2.089678431	DN	
206508_at	CD70	chr19p13	g4507604	induction of apoptosis	receptor binding	0.03572922	2.088785127	DN	

202017_at	EPHX1	chr1q42.1	g4557560	cellular aromatic compound				
218627_at	DRAM1	chr12q23.2	g8922957	metabolic process	catalytic activity	0.0198322	2.080684315	DN
				autophagy	NA	0.01174067	2.075153897	DN
				response to molecule of bacterial origin				
201743_at	CD14	chr5q22-q32 5q31.1	g4557416		lipopolysaccharide binding	0.01592359	2.069115862	DN
210285_x_a								
t	WTAP	chr6q25-q27	g12653228	mRNA processing	NA	0.0052485	2.053515845	DN
206295_at	IL18	chr11q22.2-q22.3	g4504652	angiogenesis	signal transducer activity	0.00918927	2.050092548	DN
208691_at	TFRC	chr3q29	g12654696	response to hypoxia	receptor activity	0.01932544	2.049638652	DN
213836_s_a								
t	WIP1	chr17q24.2	Hs.279937.1	autophagy	receptor binding	0.00550884	2.040195901	DN
207332_s_a								
t	TFRC	chr3q29	g4507456	response to hypoxia	receptor activity	0.00640869	2.035533696	DN
206656_s_a								
t	C20orf3	chr20p11.2	g12653170	biosynthetic process	arylesterase activity	0.01336888	2.034028039	DN
201554_x_a								
t	GYG1	chr3q24-q25.1	g4758491	glycogen biosynthetic process	protein binding	6.32E-05	2.030678767	DN
205992_s_a								
t	IL15	chr4q31	g10835152	NK T cell proliferation	signal transducer activity	0.02901042	2.022977559	DN
201243_s_a					sodium:potassium-exchanging ATPase activity			
t	ATP1B1	chr1q24	g4502276	response to hypoxia	activity	0.01938636	2.017682667	DN
204059_s_a								
t	ME1	chr6q12	g13435400	carbohydrate metabolic process	catalytic activity	0.00369093	2.006207763	DN
208699_x_a								
t	TKT	chr3p14.3	Hs.89643.0	pentose-phosphate shunt	magnesium ion binding	0.00057158	2.002502194	DN
201790_s_a								
t	DHCR7	chr11q13.4	Hs.11806.0	blood vessel development	protein binding	0.00808537	1.996692088	DN
209616_s_a								
t	CES1	chr16q22.2	g688112	metabolic process	carboxylesterase activity	0.00441923	1.993194314	DN
202923_s_a								
t	GCLC	chr6p12	g4557624	cysteine metabolic process	nucleotide binding	0.00020483	1.992941982	DN
					inositol or phosphatidylinositol			
203126_at	IMPA2	chr18p11.2	g7657235	phosphate metabolic process	phosphatase activity	0.01356203	1.992744524	DN
201118_at	PGD	chr1p36.22	g4505758	pentose-phosphate shunt	catalytic activity	0.00409666	1.988553933	DN
215785_s_a								
t	CYFIP2	chr5q33.3	Hs.258503.2	apoptosis	protein binding	0.00033258	1.988198393	DN
201242_s_a					sodium:potassium-exchanging ATPase activity			
t	ATP1B1	chr1q24	g12652534	response to hypoxia	activity	0.0474456	1.984803632	DN
220937_s_a								
t	ST6GALNAC4	chr9q34	g7657622	protein glycosylation	sialyltransferase activity	0.01492231	1.983139415	DN
211548_s_a								
t	HPGD	chr4q34-q35	g1203981	lipid metabolic process	catalytic activity	0.01610898	1.976454395	DN
209529_at	PPAP2C	chr19p13	g2911497		NA	0.00762579	1.969412867	DN
209443_at	SERPINA5	chr14q32.1	g180549	spermatogenesis	protease binding	0.03160893	1.962282785	DN

204675_at	SRD5A1	chr5p15	g4507200	lipid metabolic process	3-oxo-5-alpha-steroid 4-dehydrogenase activity	0.01900823	1.961733651	DN
210663_s_a								
t	KYNU	chr2q22.2	g12654128	tryptophan catabolic process	catalytic activity	0.00431815	1.960261549	DN
202842_s_a		chr7q31 14q24.2-						
t	DNAJB9	q24.3	g5262493	protein folding	protein binding	0.00683844	1.956978819	DN
206377_at	FOXF2	chr6p25.3	g4557594	epithelial to mesenchymal transition	DNA binding	0.01856352	1.956300974	DN
212335_at	GNS	chr12q14	Hs.164036.0	glycosaminoglycan catabolic process	catalytic activity	0.00291429	1.947213445	DN
203139_at	DAPK1	chr9q34.1	g4826683	protein phosphorylation	nucleotide binding	0.00021022	1.944380103	DN
210298_x_a				multicellular organismal				
t	FHL1	chrXq26	g3851649	development	protein binding	0.0042861	1.941708824	DN
219093_at	PID1	chr2q36.3	g8923631	NA	NA	0.04269284	1.939606392	DN
209160_at	AKR1C3	chr10p15-p14	g6624210	prostaglandin metabolic process	aldo-keto reductase activity	0.0003125	1.937665571	DN
202587_s_a				nucleobase, nucleoside, nucleotide				
t	AK1	chr9q34.1	g12654562	and nucleic acid metabolic process	nucleotide binding	0.00121479	1.931933901	DN
202946_s_a								
t	BTBD3	chr20p12.2	g7662401	NA	protein binding	0.01849196	1.929563743	DN
210971_s_a				protein import into nucleus,				
t	ARNTL	chr11p15	g2094740	translocation	DNA binding	0.02621884	1.922803903	DN
213246_at	C14orf109	chr14q32.12	Hs.275352.0	NA	NA	0.00628824	1.91841819	DN
211564_s_a								
t	PDLIM4	chr5q31.1	g13111856	NA	protein binding	0.02643988	1.90313617	DN
214696_at	C17orf91	chr17p13.3	Hs.29206.0	NA	NA	0.00930131	1.896337893	DN
201963_at	ACSL1	chr4q35	g12669906	lipid metabolic process	nucleotide binding	0.01411763	1.887792098	DN
203925_at	GCLM	chr1p22.1	g4504010	cysteine metabolic process	glutamate-cysteine ligase activity	0.00292286	1.886328307	DN
218092_s_a								
t	AGFG1	chr2q36.3	g7262381	acrosome assembly	DNA binding	0.00561287	1.885181886	DN
219911_s_a								
t	SLCO4A1	chr20q13.33	g7706516	transport	transporter activity	0.03368462	1.884808326	DN
205449_at	SAC3D1	chr11q13.1	g9558738	cell cycle	protein binding	0.00626475	1.873455352	DN
205968_at	KCNS3	chr2p24	g4504862	transport	ion channel activity	0.004512	1.870488609	DN
200790_at	ODC1	chr2p25	g4505488	kidney development	catalytic activity	0.01153827	1.85622168	DN
202722_s_a					glutamine-fructose-6-phosphate			
t	GFPT1	chr2p13	g4503980	chondrocyte development	transaminase (isomerizing) activity	0.00093632	1.8536989	DN
200670_at	XBP1	chr22q12.1 22q12	g4827057	transcription	DNA binding	0.00221959	1.852252417	DN
212311_at	SEL1L3	chr4p15.2	Hs.49500.0	NA	binding	0.00166778	1.849790706	DN
					3-chloroallyl aldehyde dehydrogenase activity			
205623_at	ALDH3A1	chr17p11.2	g4502034	response to hypoxia		0.04936598	1.849134213	DN
210372_s_a								
t	TPD52L1	chr6q22-q23	g12246900	G2/M transition of mitotic cell cycle	protein binding	0.00057002	1.848123387	DN
218723_s_a				regulation of cyclin-dependent				
t	C13orf15	chr13q14.11	g7662650	protein kinase activity	protein binding	0.0071129	1.846549566	DN
201471_s_a				ubiquitin-dependent protein				
t	SQSTM1	chr5q35	g4505570	catabolic process	protein kinase C binding	0.00469829	1.844272173	DN

218182_s_a t	CLDN1	chr3q28-q29	g10863886	cell adhesion	structural molecule activity	0.01760066	1.844183419	DN
203973_s_a t	CEBPD	chr8p11.2-p11.1	g4885130	transcription multicellular organismal	DNA binding	0.00033827	1.843660617	DN
209829_at	FAM65B	chr6p22.3-p21.32	g2224712	development	binding	0.04972001	1.843211247	DN
213006_at	CEBPD	chr8p11.2-p11.1	Hs.76722.1	transcription	DNA binding	0.00366328	1.841146599	DN
200862_at	DHCR24	chr1p32.3	g13375617	steroid biosynthetic process	catalytic activity	0.0010459	1.837999544	DN
218532_s_a t	FAM134B	chr5p15.1	g9506660	sensory perception of pain	NA	0.00082058	1.837913467	DN
202748_at	GBP2	chr1p22.2	g6996011	immune response	nucleotide binding	0.03457358	1.831042295	DN
209835_x_a t	CD44	chr11p13	g13325117	regulation of cell growth	receptor activity	0.00508051	1.828529253	DN
201942_s_a t	CPD	chr17q11.2	g3641620	proteolysis	carboxypeptidase activity	0.00433411	1.826079392	DN
217168_s_a t	HERPUD1	chr16q13	Hs.146393.1	cellular calcium ion homeostasis multicellular organismal	protein binding	0.00145142	1.822262285	DN
201539_s_a t	FHL1	chrXq26	g2078479	development	protein binding	0.00094484	1.822093261	DN
207096_at	SAA4	chr11p15.1-p14	g10835094	acute-phase response	NA	0.04441883	1.819225813	DN
203913_s_a t	HPGD	chr4q34-q35	Hs.77348.0	lipid metabolic process	catalytic activity	0.01114103	1.810264603	DN
218651_s_a t	LARP6	chr15q23	g8922933	RNA processing	nucleotide binding	0.0415223	1.80653072	DN
207196_s_a t	TNIP1	chr5q32-q33.1	g5174608	translation	protein binding	0.02388755	1.79999197	DN
210136_at	MBP	chr18q23	Hs.69547.4	immune response	structural constituent of myelin sheath	0.01898452	1.796589837	DN
217388_s_a t	KYNU	chr2q22.2	Hs.169139.2	tryptophan catabolic process	catalytic activity zinc ion transmembrane transporter activity	0.04528046	1.796447508	DN
212110_at	SLC39A14	chr8p21.3	Hs.89868.0	transport	activity	0.00401985	1.79588525	DN
201791_s_a t	DHCR7	chr11q13.4	g4503320	blood vessel development multicellular organismal	protein binding	0.00755098	1.788812716	DN
218603_at	HECA	chr6q23-q24	g7706434	development	NA	0.02935009	1.787484947	DN
212508_at	MOAP1	chr14q32	Hs.24719.0	apoptosis	protein binding adenosine receptor activity, G-protein coupled	0.03791211	1.780655681	DN
205891_at	ADORA2B	chr17p12	g4501950	activation of MAPK activity	coupled	0.00358163	1.779753728	DN
212160_at	XPOT	chr12q14.2	Hs.85951.0	tRNA export from nucleus release of cytochrome c from mitochondria	tRNA binding	0.0016334	1.778119728	DN
208791_at	CLU	chr8p21-p12	g180619	mitochondria	protein binding glutamine-fructose-6-phosphate transaminase (isomerizing) activity	0.00786673	1.778110675	DN
205100_at	GFPT2	chr5q34-q35	g4826741	carbohydrate metabolic process	transaminase (isomerizing) activity	0.01524951	1.77745756	DN

205531_s_a								
t	GLS2	chr12q13	g7019388	cellular amino acid metabolic process	glutaminase activity	0.0312094	1.771580797	DN
209276_s_a								
t	GLRX	chr5q14	g5442445	transport	electron carrier activity	0.01292571	1.769730733	DN
215990_s_a				protein import into nucleus,				
t	BCL6	chr3q27	Hs.155024.1	translocation	nucleic acid binding	0.03219537	1.766846667	DN
209605_at	TST	chr22q13.1	g1877030	sulfate transport	thiosulfate sulfurtransferase activity	0.00588411	1.765243703	DN
204249_s_a								
t	LMO2	chr11p13	g6633806	blood vessel development	DNA binding	0.03717352	1.764923589	DN
221589_s_a	LOC10050651							
t	7	---	Hs.293970.1	NA	NA	0.03079668	1.762616481	DN
202238_s_a					nicotinamide N-methyltransferase			
t	NNMT	chr11q23.1	g5453789	NA	activity	0.00770725	1.762348186	DN
218412_s_a								
t	GTF2IRD1	chr7q11.23	g7705386	transcription	DNA binding	0.00405088	1.757582967	DN
211373_s_a								
t	PSEN2	chr1q31-q42	g1079575	response to hypoxia	endopeptidase activity	0.01996941	1.753780371	DN
201626_at	INSIG1	chr7q36	Hs.56205.0	lipid metabolic process	protein binding	0.00868535	1.743345574	DN
221582_at	HIST3H2A	chr1q42.13	g12654706	nucleosome assembly	DNA binding	0.02256542	1.743111246	DN
213187_x_a					cysteine-type endopeptidase inhibitor			
t	FTL	chr19q13.33	Hs.324746.2	skeletal system development	activity	0.00077436	1.741875252	DN
201925_s_a				complement activation, classical				
t	CD55	chr1q32	g10835142	pathway	NA	0.01461848	1.737884582	DN
217909_s_a								
t	MLX	chr17q21.1	Hs.78185.0	transcription	DNA binding	0.023982	1.734735747	DN
204470_at	CXCL1	chr4q21	g4504152	chemotaxis	receptor binding	0.01156711	1.734417663	DN
205770_at	GSR	chr8p21.1	g10835188	glutathione metabolic process	glutathione-disulfide reductase activity	0.01033249	1.727756506	DN
203124_s_a								
t	SLC11A2	chr12q13	g10835168	transition metal ion transport	transporter activity	0.01706323	1.725281495	DN
210299_s_a				multicellular organismal				
t	FHL1	chrXq26	g3859848	development	protein binding	2.06E-05	1.725003821	DN
				multicellular organismal				
201540_at	FHL1	chrXq26	g4503720	development	protein binding	0.01603302	1.716332245	DN
221986_s_a								
t	KLHL24	chr3q27.1	Hs.246875.1	NA	protein binding	0.00034548	1.715870842	DN
206376_at	SLC6A15	chr12q21.3	g8922349	transport	neurotransmitter transporter activity	0.00338086	1.715627282	DN
218764_at	PRKCH	chr14q23.1	g13129041	protein phosphorylation	nucleotide binding	0.00775238	1.714025741	DN
204497_at	ADCY9	chr16p13.3	Hs.20196.0	cAMP biosynthetic process	nucleotide binding	0.01983825	1.713540971	DN
217826_s_a				post-translational protein				
t	UBE2J1	chr6q15	g7706311	modification	nucleotide binding	0.04514101	1.710817674	DN
201468_s_a					NAD(P)H dehydrogenase (quinone)			
t	NQO1	chr16q22.1	g4505414	xenobiotic metabolic process	activity	0.00228336	1.710367994	DN
203042_at	LAMP2	chrXq24	g4504956	NA	NA	0.02285728	1.705683313	DN

210802_s_a					rRNA (adenine-N6,N6)-			
t	DIMT1L	chr5q12.1	g12803982	rRNA modification	dimethyltransferase activity	0.00823995	1.705626588	DN
45288_at	ABHD6	chr3p14.3	4890230_RC	NA	catalytic activity	0.02321196	1.705483153	DN
202679_at	NPC1	chr18q11-q12	g4557802	endocytosis	receptor activity	0.00781539	1.704473148	DN
203647_s_a				generation of precursor metabolites				
t	FDX1	chr11q22	g182493	and energy	iron ion binding	0.00730128	1.701526171	DN
214505_s_a				multicellular organismal				
t	FHL1	chrXq26	Hs.239069.2	development	protein binding	0.00516424	1.698461104	DN
208788_at	ELOVL5	chr6p21.1-p12.1	g12053372	fatty acid biosynthetic process	fatty acid elongase activity	0.00560792	1.692239154	DN
211337_s_a				microtubule cytoskeleton				
t	TUBGCP4	chr15q15	g12803021	organization	structural constituent of cytoskeleton	0.00014767	1.689922304	DN
219129_s_a								
t	SAP30L	chr5q33.2	g13375861	transcription	DNA binding	0.00891916	1.688138639	DN
202069_s_a								
t	IDH3A	chr15q25.1-q25.2	Hs.250616.0	carbohydrate metabolic process	magnesium ion binding	0.02732372	1.686095336	DN
209020_at	C20orf111	chr20q13.11	g7688970	NA	NA	0.00925471	1.682956923	DN
218196_at	OSTM1	chr6q21	g7661737	osteoclast differentiation	protein binding	0.00459602	1.682563894	DN
				cellular aromatic compound				
209218_at	SQLE	chr8q24.1	g4204674	metabolic process	monooxygenase activity	0.02263103	1.681756509	DN
217741_s_a								
t	ZFAND5	chr9q13-q21	Hs.3776.0	in utero embryonic development	DNA binding	0.03041625	1.679911879	DN
210220_at	FZD2	chr17q21.1	g736678	signal transduction	signal transducer activity	0.00555101	1.677720698	DN
					nicotinamide N-methyltransferase			
202237_at	NNMT	chr11q23.1	g5453789	NA	activity	0.02729749	1.677284019	DN
204908_s_a				protein import into nucleus,				
t	BCL3	chr19q13.1-q13.2	g4885086	translocation	DNA binding	0.04175199	1.676147695	DN
211071_s_a								
t	MLLT11	chr1q21	g13623686	NA	NA	0.01441052	1.673240149	DN
					electron-transferring-flavoprotein			
33494_at	ETFDH	chr4q32-q35	4839546_RC	transport	dehydrogenase activity	0.01104652	1.670430188	DN
221903_s_a								
t	CYLD	chr16q12.1	Hs.18827.0	translation	structural constituent of ribosome	1.73E-05	1.669861635	DN
201940_at	CPD	chr17q11.2	Hs.5057.0	proteolysis	carboxypeptidase activity	0.01414573	1.667953635	DN
202593_s_a								
t	GDE1	chr16p12-p11.2	g7706616	glycerol metabolic process	phosphoric diester hydrolase activity	0.03732201	1.664990333	DN
206662_at	GLRX	chr5q14	g4504024	transport	electron carrier activity	0.00101787	1.664750047	DN
204824_at	ENDOG	chr9q34.1	g4758269	in utero embryonic development	nucleic acid binding	0.01145638	1.663930942	DN
204285_s_a				release of cytochrome c from				
t	PMAIP1	chr18q21.32	Hs.96.0	mitochondria	protein binding	0.00113959	1.66324499	DN
203339_at	SLC25A12	chr2q24	Hs.179866.0	transport	transporter activity	0.01392445	1.659698662	DN
201467_s_a					NAD(P)H dehydrogenase (quinone)			
t	NQO1	chr16q22.1	Hs.80706.0	xenobiotic metabolic process	activity	0.01549103	1.659648122	DN
57082_at	LDLRAP1	chr1p36-p35	4888623	lipid metabolic process	phosphotyrosine binding	0.01956795	1.659130432	DN

203337_x_a								
t	ITGB1BP1	chr2p25.2	g4758577	cell-matrix adhesion	protein binding	7.37E-05	1.659044611	DN
221841_s_a								
t	KLF4	chr9q31	Hs.7934.1	transcription	nucleic acid binding	0.01837385	1.656532141	DN
214769_at	CLCN4	chrXp22.3	Hs.6932.0	transport	nucleotide binding	0.00032634	1.654518227	DN
202531_at	IRF1	chr5q31.1	g4504720	transcription	DNA binding	0.00746001	1.65295152	DN
212014_x_a								
t	CD44	chr11p13	Hs.169610.3	regulation of cell growth	receptor activity	0.01432552	1.651852474	DN
218949_s_a								
t	QRSL1	chr6q21	g8922807	translation	nucleotide binding	0.01701469	1.650945914	DN
213050_at	COBL	chr7p12.1	Hs.33010.0	neural tube closure	protein binding	0.00413678	1.648212834	DN
219377_at	FAM59A	chr18q12.1	g12232414	NA	NA	0.00108615	1.647847494	DN
202074_s_a								
t	OPTN	chr10p13	g11415041	protein targeting to Golgi	protein binding	0.00782713	1.643116222	DN
204566_at	PPM1D	chr17q23.2	g4505996	G2/M transition of mitotic cell cycle	catalytic activity	0.00903156	1.643074788	DN
210959_s_a								
t	SRD5A1	chr5p15	g6523818	lipid metabolic process	3-oxo-5-alpha-steroid 4-dehydrogenase activity	0.00383625	1.641886304	DN
204476_s_a								
t	PC	chr11q13.4-q13.5	g11761614	pyruvate metabolic process	nucleotide binding	0.00141916	1.641783883	DN
218170_at	ISOC1	chr5q22.1-q33.3	g7705613	metabolic process	catalytic activity	0.01613374	1.63921844	DN
205512_s_a								
t	AIFM1	chrXq26.1	g4757731	apoptotic nuclear change	DNA binding	0.00267392	1.636561357	DN
205309_at	SMPDL3B	chr1p35.3	g7656907	sphingomyelin catabolic process	sphingomyelin phosphodiesterase activity	0.04312979	1.631062057	DN
202436_s_a								
t	CYP1B1	chr2p21	Hs.154654.0	metabolic process	monooxygenase activity	0.04674095	1.630378323	DN
218780_at	HOOK2	chr19p13.2	g7019410	transport	protein binding	0.00011186	1.629897813	DN
206204_at	GRB14	chr2q22-q24	g4758477	signal transduction	receptor activity	0.00186283	1.627978414	DN
218217_at	SCPEP1	chr17q22	g11055991	proteolysis	carboxypeptidase activity	0.00072438	1.625896206	DN
203038_at	PTPRK	chr6q22.2-q22.3	g4506316	protein dephosphorylation	phosphoprotein phosphatase activity	0.0179708	1.622472974	DN
204385_at	KYNU	chr2q22.2	g4504936	tryptophan catabolic process	catalytic activity	0.00038549	1.622406155	DN
203041_s_a								
t	LAMP2	chrXq24	g186929	NA	NA	0.00168239	1.621978958	DN
201627_s_a								
t	INSIG1	chr7q36	g5031800	lipid metabolic process	protein binding	0.01969596	1.621895909	DN
204214_s_a								
t	RAB32	chr6q24.3	g5803132	small GTPase mediated signal transduction	nucleotide binding	0.02148708	1.621805687	DN
220225_at	IRX4	chr5p15.3	g7705554	regulation of transcription, DNA-dependent	DNA binding	0.00552083	1.62065641	DN
211549_s_a								
t	HPGD	chr4q34-q35	g2047312	lipid metabolic process	catalytic activity	0.00146905	1.616705672	DN
200911_s_a								
t	TACC1	chr8p11.22	g5454099	microtubule cytoskeleton organization	protein binding	0.01401751	1.614520134	DN

206247_at	MICB	chr6p21.3	g5174564	immune response-activating cell surface receptor signaling pathway	natural killer cell lectin-like receptor binding	0.03658741	1.614072013	DN
212875_s_a								
t	C2CD2	chr21q22.3	Hs.16007.0	NA	NA	7.45E-05	1.612857317	DN
202675_at	SDHB	chr1p36.1-p35	g9257241	tricarboxylic acid cycle	protein binding	0.00808479	1.612826929	DN
219959_at	MOCOS	chr18q12	g8923660	Mo-molybdopterin cofactor biosynthetic process	catalytic activity	0.03523082	1.611726155	DN
205109_s_a					guanyl-nucleotide exchange factor activity			
t	ARHGEF4	chr2q22	g9558722	apoptosis	activity	0.02468125	1.610699641	DN
202073_at	OPTN	chr10p13	Hs.278898.0	protein targeting to Golgi	protein binding	0.03567829	1.610212427	DN
221692_s_a								
t	MRPL34	chr19p13.1	g13559395	translation	structural constituent of ribosome	0.00069893	1.609817666	DN
201920_at	SLC20A1	chr2q11-q14	g7382462	phosphate metabolic process	signal transducer activity	0.04191032	1.604566744	DN
208928_at	POR	chr7q11.2	g9964002	positive regulation of monooxygenase activity	NADPH-hemoprotein reductase activity	0.02632073	1.604009789	DN
202323_s_a								
t	ACBD3	chr1q42.12	Hs.6831.0	steroid biosynthetic process	acyl-CoA binding	0.04566001	1.603669524	DN
213696_s_a								
t	MED8	chr1p34.2	Hs.301756.2	transcription	NA	0.02111172	1.603292745	DN
221552_at	ABHD6	chr3p14.3	g12804562	NA	catalytic activity	0.00325797	1.602849773	DN
204490_s_a								
t	CD44	chr11p13	g180196	regulation of cell growth	receptor activity	0.00784711	1.602276754	DN
202948_at	IL1R1	chr2q12	g4504658	immune response	signal transducer activity	0.00576616	1.600807454	DN
218989_x_a					zinc ion transmembrane transporter activity			
t	SLC30A5	chr5q12.1	g12597642	transport	activity	0.03297562	1.600103961	DN
57715_at	CALHM2	chr10pter-q26.12	4905541	NA	NA	0.00966101	1.599732159	DN
219284_at	HSPBAP1	chr3q21.1	g13375820	response to stress	NA	0.02162448	1.597739111	DN
218772_x_a								
t	TMEM38B	chr9q31.2	g8922460	transport	ion channel activity	0.02792664	1.597737805	DN
222108_at	AMIGO2	chr12q13.11	Hs.121520.0	anti-apoptosis	protein binding	0.02168422	1.596779403	DN
209514_s_a								
t	RAB27A	chr15q15-q21.1	Hs.50477.1	protein targeting	nucleotide binding	0.00709178	1.596104963	DN
209189_at	FOS	chr14q24.3	g13325363	conditioned taste aversion	DNA binding	0.0148723	1.594456271	DN
209018_s_a								
t	PINK1	chr1p36	Hs.6163.0	protein phosphorylation	nucleotide binding	0.00289827	1.590838719	DN
202146_at	IFRD1	chr7q31.1	Hs.7879.0	multicellular organismal development	binding	0.00576115	1.589801864	DN
208962_s_a								
t	FADS1	chr11q12.2-q13.1	Hs.132898.0	lipid metabolic process	C-5 sterol desaturase activity	0.00072081	1.588704366	DN
203252_at	CDK2AP2	chr11q13	g5031668	NA	kinase activity	0.0011592	1.587948891	DN
200924_s_a								
t	SLC3A2	chr11q13	g4505140	carbohydrate metabolic process	catalytic activity	0.00878704	1.584747068	DN
214175_x_a								
t	PDLIM4	chr5q31.1	Hs.79691.2	NA	protein binding	0.00284931	1.582005367	DN

206707_x_a				multicellular organismal				
t	FAM65B	chr6p22.3-p21.32	g7705341	development	binding	0.03404243	1.580704649	DN
203786_s_a								
t	TPD52L1	chr6q22-q23	g4507640	G2/M transition of mitotic cell cycle	protein binding	0.01440376	1.580491499	DN
212788_x_a								
t	FTL	chr19q13.33	Hs.111334.1	iron ion transport	binding inositol or phosphatidylinositol	0.00225466	1.578440694	DN
202797_at	SACM1L	chr3p21.3	g7662337	phosphoinositide dephosphorylation	phosphatase activity	0.0147471	1.577499143	DN
204262_s_a								
t	PSEN2	chr1q31-q42	g4506164	response to hypoxia	endopeptidase activity	0.0177911	1.576948827	DN
202218_s_a								
t	FADS2	chr11q12.2	g4758333	lipid metabolic process	stearoyl-CoA 9-desaturase activity NAD(P)H dehydrogenase (quinone)	0.00197952	1.575738573	DN
210519_s_a								
t	NQO1	chr16q22.1	g12654176	xenobiotic metabolic process	activity	0.00704081	1.574747691	DN
38241_at	BTN3A3	chr6p21.3	4853366	NA	NA	0.00669323	1.574121436	DN
219922_s_a								
t	LTBP3	chr11q13.1	g10835104	skeletal system development	binding guanyl-nucleotide exchange factor	0.00385693	1.572963376	DN
212895_s_a								
t	ABR	chr17p13.3	Hs.118021.2	apoptosis	activity	0.01027722	1.572596776	DN
203039_s_a								
t	NDUFS1	chr2q33-q34	g4826855	mitochondrial electron transport, NADH to ubiquinone	NADH dehydrogenase activity	0.04782466	1.570416229	DN
205768_s_a								
t	SLC27A2	chr15q21.2	g4503652	very long-chain fatty acid metabolic process	nucleotide binding	0.0109929	1.566931638	DN
221654_s_a								
t	USP3	chr15q22.3	g4689127	mitotic cell cycle	ubiquitin thiolesterase activity	0.04996582	1.562373376	DN
210793_s_a								
t	NUP98	chr11p15.5	g1184172	protein import into nucleus, docking	transporter activity	0.00761774	1.561916785	DN
210418_s_a								
t	IDH3B	chr20p13	g4103445	tricarboxylic acid cycle	magnesium ion binding	0.00511043	1.559567147	DN
215726_s_a								
t	CYB5A	chr18q23	Hs.83834.2	transport	aldo-keto reductase activity	0.00728119	1.558957232	DN
201502_s_a								
t	NFKBIA	chr14q13	Hs.81328.0	protein import into nucleus, translocation	protein binding	0.02425931	1.558089701	DN
216080_s_a								
t	FADS3	chr11q12-q13.1	Hs.21765.1	lipid metabolic process	iron ion binding	0.01136909	1.557631324	DN
201818_at	LPCAT1	chr5p15.33	g13376233	metabolic process	calcium ion binding	0.00843787	1.55707746	DN
206561_s_a								
t	AKR1B10	chr7q33	g13346507	cellular aldehyde metabolic process	aldo-keto reductase activity extracellular matrix structural	0.00049763	1.557064055	DN
203184_at	FBN2	chr5q23-q31	g4755135	anatomical structure morphogenesis	constituent	0.0115237	1.553782967	DN
218692_at	SYBU	chr8q23.2	g8923340	NA	NA	0.00759028	1.553382557	DN
202976_s_a								
t	RHOBTB3	chr5q15	g7662355	transport	nucleotide binding	0.02197306	1.551830748	DN
212510_at	GPD1L	chr3p22.3	Hs.82432.0	carbohydrate metabolic process	catalytic activity	0.00157267	1.551386406	DN

212276_at	LPIN1	chr2p25.1	Hs.81412.0	transcription	transcription coactivator activity	0.02391691	1.551366458	DN
210868_s_a					transferase activity, transferring acyl			
t	ELOVL6	chr4q25	g12654918	fatty acid biosynthetic process	groups other than amino-acyl groups	0.00704707	1.551235749	DN
209139_s_a								
t	PRKRA	chr2q31.2	g4927415	protein phosphorylation	RNA binding	0.03172408	1.550964512	DN
206074_s_a				DNA unwinding involved in				
t	HMGA1	chr6p21	g4504432	replication	DNA binding	0.01575496	1.550137156	DN
200999_s_a								
t	CKAP4	chr12q23.3	g5803112	NA	NA	0.04757418	1.549447053	DN
209307_at	SWAP70	chr11p15	Hs.153026.0	somatic cell DNA recombination	DNA binding	2.22E-05	1.548583841	DN
					sequence-specific DNA binding			
218225_at	ECSIT	chr19p13.2	g7706114	mesoderm formation	transcription factor activity	0.01081702	1.548462486	DN
218018_at	PDXK	chr21q22.3	Hs.4746.0	cell proliferation	nucleotide binding	0.03262781	1.547987902	DN
202084_s_a								
t	SEC14L1	chr17q25.2	g4506866	NA	binding	0.00764871	1.547574721	DN
209750_at	NR1D2	chr3p24.2	Hs.37288.0	transcription	DNA binding	3.91E-05	1.547178665	DN
204215_at	C7orf23	chr7q21.1-q21.2	g13236556	NA	NA	0.0094504	1.547082463	DN
210754_s_a								
t	LYN	chr8q13	g187270	protein phosphorylation	nucleotide binding	0.00716825	1.546798114	DN
215243_s_a								
t	GJB3	chr1p34	Hs.98485.1	in utero embryonic development	gap junction channel activity	0.03617682	1.546410191	DN
221020_s_a								
t	SLC25A32	chr8q22.3	g13540550	transport	transporter activity	0.00117278	1.544298157	DN
222173_s_a								
t	TBC1D2	chr9q22.33	Hs.135917.4	regulation of Rab GTPase activity	GTPase activator activity	0.01941633	1.544294854	DN
202431_s_a				branching involved in ureteric bud				
t	MYC	chr8q24.21	g12962934	morphogenesis	DNA binding	0.01340044	1.543868717	DN
217118_s_a								
t	C22orf9	chr22q13.31	Hs.13255.1	NA	protein binding	0.03712164	1.543747825	DN
209409_at	GRB10	chr7p12.2	g1503997	signal transduction	receptor activity	0.04802699	1.543208302	DN
219305_x_a								
t	FBXO2	chr1p36.22	g6912363	protein modification process	beta-amyloid binding	0.03160139	1.542533124	DN
206157_at	PTX3	chr3q25	g4506332	response to yeast	zymosan binding	4.87E-06	1.540798935	DN
					inositol or phosphatidylinositol			
202794_at	INPP1	chr2q32	g4755138	phosphate metabolic process	phosphatase activity	0.01958947	1.540371456	DN
202085_at	TJP2	chr9q13-q21	g4759341	response to organic substance	guanylate kinase activity	0.03048064	1.538895804	DN
222203_s_a								
t	RDH14	chr2p24.2	Hs.288880.1	metabolic process	catalytic activity	0.01302546	1.53836464	DN
210026_s_a								
t	CARD10	chr22q13.1	g13488606	protein complex assembly	protein binding	0.01402326	1.536835451	DN
219041_s_a								
t	REPIN1	chr7q36.1	g7656889	DNA replication	nucleic acid binding	0.01841314	1.536649833	DN
202491_s_a								
t	IKBKAP	chr9q31	g4504628	transcription	DNA binding	0.01406901	1.536636873	DN

207357_s_a t	GALNT10	chr5q33.2	g9055207	protein O-linked glycosylation	polypeptide N-acetylgalactosaminyltransferase activity	0.03659124	1.536606623	DN
208918_s_a t	NADK	chr1p36.33	Hs.220324.2	metabolic process	nucleotide binding	0.00737721	1.534740886	DN
214527_s_a t	PQBP1	chrXp11.23	Hs.30570.4	transcription	DNA binding serine-type endopeptidase inhibitor activity	0.01707822	1.533157528	DN
202826_at	SPINT1	chr15q15.1	g4504328	embryonic placenta development		0.01320876	1.532327112	DN
202802_at	DHPS	chr19p13	g7108341	translation	protein binding	0.00554293	1.531868568	DN
202375_at	SEC24D	chr4q26	g7662658	transport	protein binding	0.00792765	1.531748816	DN
204257_at	FADS3	chr11q12-q13.1	g13375615	lipid metabolic process ubiquitin-dependent protein	iron ion binding	0.00474087	1.53126336	DN
209943_at	FBXL4	chr6q16.1-q16.3	g6103636	catabolic process	NA	0.00052202	1.528595571	DN
214214_s_a t	C1QBP	chr17p13.3	Hs.78614.3	immune response	complement component C1q binding	0.0013571	1.527623316	DN
204679_at	KCNK1	chr1q42-q43	g4504846	transport	ion channel activity	0.00087186	1.526146102	DN
201538_s_a t	DUSP3	chr17q21	g4758207	inactivation of MAPK activity	phosphoprotein phosphatase activity	0.00552865	1.525199246	DN
201795_at	LBR	chr1q42.1	g4504960	NA	nucleic acid binding	0.03420201	1.524895721	DN
208510_s_a t	PPARG	chr3p25	g7705548	negative regulation of transcription from RNA polymerase II promoter	DNA binding	0.01223094	1.524731708	DN
202275_at	G6PD	chrXq28	g4503844	cytokine production	catalytic activity	0.01274762	1.523544061	DN
203125_x_a t	SLC11A2	chr12q13	g3170363	transition metal ion transport	transporter activity	0.01983646	1.523519775	DN
212445_s_a t	NEDD4L	chr18q21	Hs.12017.1	protein modification process regulation of transcription, DNA-dependent	ubiquitin-protein ligase activity RNA polymerase II transcription factor activity	0.01603652	1.523501863	DN
201200_at	CREG1	chr1q24	g4503036			0.00992522	1.522609046	DN
204836_at	GLDC	chr9p22	g4504012	cellular amino acid metabolic process negative regulation of transcription	catalytic activity	0.0457235	1.522328323	DN
212774_at	ZNF238	chr1q44-qter	Hs.69997.1	from RNA polymerase II promoter antigen processing and presentation of exogenous peptide antigen via MHC class II	nucleic acid binding	0.04777929	1.521963923	DN
201422_at	IFI30	chr19p13.1	g5453695		oxidoreductase activity	0.01740561	1.521262104	DN
202931_x_a t	BIN1	chr2q14	g4757747	endocytosis	protein binding	0.0342608	1.521225159	DN
211715_s_a t	BDH1	chr3q29	g13543366	metabolic process	catalytic activity	0.02461105	1.521145119	DN
221679_s_a t	ABHD6	chr3p14.3	g9963838	NA RNA splicing, via transesterification reactions	catalytic activity	0.00263233	1.518405345	DN
200071_at	SMNDC1	chr10q23	Hs.79968.0		nucleic acid binding	0.01959107	1.517263359	DN

203045_at	NINJ1	chr9q22	g4758809	cell adhesion	NA	0.04158461	1.517145906	DN
205219_s_at	GALK2	chr15q21.1-q21.2	g4503896	carbohydrate metabolic process	nucleotide binding calcium activated cation channel activity	0.04016164	1.516749159	DN
218375_at	NUDT9	chr4q22.1	g13129009	cation transport	activity	0.00753944	1.516628845	DN
219639_x_at	PARP6	chr15q23	g9910373	NA	NAD+ ADP-ribosyltransferase activity	0.01255366	1.515585762	DN
221571_at	TRAF3	chr14q32.32	Hs.297660.1	regulation of cytokine production	ubiquitin-protein ligase activity	0.02780444	1.515364861	DN
205171_at	PTPN4	chr2q14.2	g4506294	protein dephosphorylation	phosphoprotein phosphatase activity	0.01746427	1.515341177	DN
218093_s_at	ANKRD10	chr13q34	g8923103	NA	NA	0.0370273	1.511746628	DN
214746_s_at	ZNF467	chr7q36.1	Hs.112158.1	transcription	nucleic acid binding	0.04268511	1.51038572	DN
214437_s_at	SHMT2	chr12q12-q14	Hs.75069.0	glycine metabolic process	catalytic activity	0.04810032	1.509800421	DN
221551_x_at	ST6GALNAC4	chr9q34	g6468226	protein glycosylation	sialyltransferase activity	0.0213769	1.508487295	DN
209075_s_at	ISCU	chr12q24.1	g11545706	nitrogen fixation	iron ion binding	0.00073118	1.506841619	DN
202003_s_at	ACAA2	chr18q21.1	g5174428	lipid metabolic process post-translational protein modification	catalytic activity	0.02147958	1.506386568	DN
217823_s_at	UBE2J1	chr6q15	Hs.184325.0	modification	nucleotide binding platelet-derived growth factor receptor binding	0.00758218	1.504529225	DN
205463_s_at	PDGFA	chr7p22	g4505678	angiogenesis	binding	0.0031217	1.502882746	DN
31845_at	ELF4	chrXq26	4863928	natural killer cell proliferation	DNA binding	0.02881319	1.501480459	DN
210986_s_at	TPM1	chr15q22.1	g854188	in utero embryonic development	actin binding	0.02176398	1.50008469	DN

Suppl. Table 3: Genes and pathways representing differences between proliferating cells in 2D and 3D.

Total number of differentially expressed genes: 2126					
Pathway	Number Of Protein In Pathway	Protein From Sample	P-Value	FDR	IDs
M Phase(R)	88	46	9.981e-14	<1.000e-03	[AURKB, BIRC5, BUB1, BUB1B, BUB3, CCDC99, CDC20, CDCA8, CENPA, CENPC1, CENPE, CENPF, CENPI, CENPM, CENPN, CLASP2, FBXO5, KIF18A, KIF20A, KIF23, KIF2A, KIF2C, KNTC1, MAD2L1, MAPRE1, MIS12, MLF1IP, NDC80, NUDC, NUP107, NUP43, NUP85, NUP98, PAFAH1B1, PLK1, RAD21, RANBP2, SKA1, SMC1A, SMC3, SPC25, STAG1, STAG2, XPO1, ZWILCH, ZWINT]
G1/S Transition(R)	98	45	1.330e-11	<5.000e-04	[CCNB1, CCNE1, CCNE2, CDC25A, CDC6, CDC7, CDK2, CKS1B, DBF4, DHFR, E2F3, FBXO5, MCM10, MCM2, MCM3, MCM4, MCM5, MCM6, MCM7, PCNA, POLA1, POLA2, POLE2, PRIM1, PSMA3, PSMA4, PSMB10, PSMB4, PSMB8, PSMB9, PSMC2, PSMC3, PSMD1, PSMD11, PSMD12, PSMD14, PSMD4, PSME1, PSME3, PSMF1, RRM2, SKP1, TFDP1, TYMS, WEE1]
DNA Replication(R)	95	44	1.717e-11	<3.333e-04	[CDC6, CDC7, CDK2, DBF4, E2F3, FEN1, GINS1, GINS2, GINS4, GMNN, MCM10, MCM2, MCM3, MCM4, MCM5, MCM6, MCM7, PCNA, POLA1, POLA2, POLD3, POLD4, POLE2, PRIM1, PSMA3, PSMA4, PSMB10, PSMB4, PSMB8, PSMB9, PSMC2, PSMC3, PSMD1, PSMD11, PSMD12, PSMD14, PSMD4, PSME1, PSME3, PSMF1, RFC2, RFC3, RFC4, RFC5]
S Phase(R)	97	44	3.302e-11	<2.500e-04	[CCND1, CDC25A, CDC6, CDK2, CKS1B, FEN1, GINS1, GINS2, GINS4, MCM2, MCM3, MCM4, MCM5, MCM6, MCM7, PCNA, POLA1, POLA2, POLD3, POLD4, POLE2, PRIM1, PSMA3, PSMA4, PSMB10, PSMB4, PSMB8, PSMB9, PSMC2, PSMC3, PSMD1, PSMD11, PSMD12, PSMD14, PSMD4, PSME1, PSME3, PSMF1, RFC2, RFC3, RFC4, RFC5, SKP1,

					WEE1]
Cell Cycle Checkpoints(R)	108	46	8.934e-11	<2.000e-04	[ATR, BUB1B, BUB3, CCNB1, CCNB2, CDC20, CDC25A, CDC25C, CDC27, CDC6, CDC7, CDK2, CHEK1, DBF4, MAD2L1, MCM10, MCM2, MCM3, MCM4, MCM5, MCM6, MCM7, PSMA3, PSMA4, PSMB10, PSMB4, PSMB8, PSMB9, PSMC2, PSMC3, PSMD1, PSMD11, PSMD12, PSMD14, PSMD4, PSME1, PSME3, PSMF1, RAD1, RAD17, RFC2, RFC3, RFC4, RFC5, UBE2C, WEE1]
Cell cycle(K)	112	43	7.526e-09	<1.667e-04	[ATR, BUB1, BUB1B, BUB3, CCNA2, CCNB1, CCNB2, CCND1, CCND2, CCNE1, CCNE2, CDC20, CDC25A, CDC25C, CDC27, CDC6, CDC7, CDK2, CDKN1C, CHEK1, DBF4, E2F3, ESPL1, MAD2L1, MCM2, MCM3, MCM4, MCM5, MCM6, MCM7, PCNA, PKMYT1, PLK1, PRKDC, PTTG1, SKP1, SKP2, SMC1A, TFDP1, TGFB1, WEE1, YWHAH]
APC/C-mediated degradation of cell cycle proteins(R)	72	30	2.661e-07	<1.429e-04	[AURKA, AURKB, BUB1B, BUB3, CCNB1, CDC20, CDC27, CDK2, FBXO5, MAD2L1, PLK1, PSMA3, PSMA4, PSMB10, PSMB4, PSMB8, PSMB9, PSMC2, PSMC3, PSMD1, PSMD11, PSMD12, PSMD14, PSMD4, PSME1, PSME3, PSMF1, PTTG1, SKP1, UBE2C]
Aurora B signaling(N)	39	21	3.220e-07	<1.250e-04	[AURKA, AURKB, BIRC5, BUB1, CBX5, CDCA8, CENPA, KIF20A, KIF23, KIF2C, NCAPD2, NCAPG, NCAPH, NDC80, PSMA3, RACGAP1, RASA1, SMC2, SMC4, STMN1, TACC1]
Influenza Life Cycle(R)	187	53	2.066e-06	<1.111e-04	[CLTA, FUS, GRSF1, GTF2F1, HNRNPA2B1, HNRNPA3, HNRNPD, HNRNPM, HNRNPR, HNRNPU, HSP90AA1, IPO5, KPNB1, NCBP1, NUP107, NUP153, NUP155, NUP205, NUP43, NUP50, NUP62, NUP85, NUP88, NUP98, POLR2K, PTBP1, RANBP2, RBMX, RPL10, RPL14, RPL15, RPL17, RPL18A, RPL28, RPL29, RPL31, RPL36, RPL37A, RPS16, RPS17, RPS21, RPS4X, RPS9, SMC1A, SNRNP70, SNRPD1, SNRPF, SNRPG, SRRM1, TPR, U2AF1, XPO1, YBX1]
M/G1 Transition(R)	61	25	3.429e-06	<1.000e-04	[CDC6, E2F3, GMNN, MCM2, MCM3, MCM4, MCM5, MCM6, MCM7, PSMA3, PSMA4, PSMB10, PSMB4, PSMB8, PSMB9, PSMC2, PSMC3, PSMD1, PSMD11, PSMD12, PSMD14, PSMD4, PSME1, PSME3, PSMF1]
Host Interactions of HIV factors(R)	119	38	4.445e-06	<9.091e-05	[CUL5, HLA-A, KPNB1, NUP107, NUP153, NUP155, NUP205, NUP43, NUP50, NUP62, NUP85, NUP88, NUP98, PAK2, PSIP1, PSMA3, PSMA4, PSMB10, PSMB4, PSMB8, PSMB9, PSMC2, PSMC3, PSMD1, PSMD11, PSMD12, PSMD14, PSMD4, PSME1, PSME3, PSMF1, RANBP1, RANBP2, SKP1,

					SLC25A6, TCEB2, TPR, XPO1]
Signaling by Aurora kinases(N)	94	31	1.822e-05	1.667e-04	[AURKA, AURKB, BIRC2, BIRC5, BUB1, CBX5, CDCA8, CENPA, DLGAP5, KIF20A, KIF23, KIF2C, MALT1, NCAPD2, NCAPG, NCAPH, NDC80, NFKB2, PIK3CA, PSMA3, RACGAP1, RASA1, RELB, SMC2, SMC4, STMN1, TACC1, TACC3, TNFAIP3, TPX2, XPO1]
eukaryotic protein translation(B)	13	10	2.171e-05	2.308e-04	[EIF2S1, EIF2S2, EIF4A1, EIF4A2, EIF4E, EIF4G1, EIF4G2, EIF4G3, EIF5, EIF5B]
BARD1 signaling events(N)	29	15	2.376e-05	2.143e-04	[ATR, BARD1, CCNE1, CDK2, FANCA, FANCE, FANCL, MRE11A, NBN, PCNA, PRKDC, RAD50, RAD51, RBBP8, TOPBP1]
FOXO1 transcription factor network(N)	38	17	4.252e-05	2.667e-04	[AURKB, BIRC5, BRCA2, CCNB1, CCNB2, CCND1, CCNE1, CDK2, CENPA, CENPF, CKS1B, ETV5, FOS, FOXO1, NEK2, PLK1, SKP2]
G2/M Transition(R)	81	27	5.190e-05	3.125e-04	[AKAP9, CCNA2, CCNB1, CCNB2, CDC25A, CDC25C, CEP135, CEP76, CSNK1D, DCTN2, FGFR1OP, HSP90AA1, MAPRE1, NEK2, PAFAH1B1, PCNT, PKMYT1, PLK1, PLK4, TUBA4A, TUBB, TUBB2C, TUBG1, TUBGCP3, WEE1, XPO1, YWHAE]
Signaling by Wnt(R)	50	19	1.299e-04	7.647e-04	[APC, CSNK1A1, PSMA3, PSMA4, PSMB10, PSMB4, PSMB8, PSMB9, PSMC2, PSMC3, PSDM1, PSDM11, PSDM12, PSDM14, PSDM4, PSME1, PSME3, PSMF1, SKP1]
Transport of Mature Transcript to Cytoplasm(R)	55	20	1.553e-04	1.000e-03	[CPSF1, EIF4E, MAGOH, NCBP1, NUP107, NUP153, NUP155, NUP205, NUP43, NUP50, NUP62, NUP85, NUP88, NUP98, RANBP2, RBM8A, SRRM1, TPR, U2AF1, UPF3B]
role of brca1 brca2 and atr in cancer susceptibility(B)	20	11	1.671e-04	1.000e-03	[ATR, BRCA2, FANCA, FANCE, MAPK3, MRE11A, NBN, RAD1, RAD17, RAD50, RAD51]
Apoptosis(R)	124	34	2.509e-04	1.700e-03	[APC, BBC3, BIRC2, CASP9, CYCS, FAS, FNTA, GSN, KPNB1, LMNA, LMNB1, MST4, PAK2, PMAIP1, PPP3CC, PSMA3, PSMA4, PSMB10, PSMB4, PSMB8, PSMB9, PSMC2, PSMC3, PSDM1, PSDM11, PSDM12, PSDM14, PSDM4, PSME1, PSME3, PSMF1, ROCK1, TFDP1, TJP1]
Formation and Maturation of mRNA Transcript(R)	152	39	3.364e-04	2.619e-03	[CPSF1, CPSF7, FUS, GTF2F1, HNRNPA2B1, HNRNPA3, HNRNPD, HNRNPM, HNRNPR, HNRNPU, MAGOH, METTL3, NCBP1, PAPOLA, POLR2K, PTBP1, RBM8A, RBMX, RNGTT, SF3B1, SF3B3, SMC1A, SNRNP70, SNRPA1, SNRPD1, SNRPF, SNRPG, SRRM1, SUPT16H, SUPT4H1, TAF10, TAF12, TAF5, TAF9, TCEB2, TCEB3, U2AF1, UPF3B, YBX1]
Telomere	30	13	4.388e-04	3.182e-03	[FEN1, PCNA, POLA1, POLA2, POLD3, POLD4, POLE2,

Maintenance(R)					PRIM1, RFC2, RFC3, RFC4, RFC5, TERF1]
HIV Life Cycle(R)	103	29	4.612e-04	3.087e-03	[CXCR4, FEN1, GTF2F1, NCBP1, NUP107, NUP153, NUP155, NUP205, NUP43, NUP50, NUP62, NUP85, NUP88, NUP98, POLR2K, PSIP1, RANBP1, RANBP2, RNGTT, SUPT16H, SUPT4H1, TAF10, TAF12, TAF5, TAF9, TCEB2, TCEB3, TPR, XPO1]
Metabolism of proteins(R)	187	45	4.717e-04	3.042e-03	[ACTB, CCT2, DHPS, DPM3, EEF2, EIF1AX, EIF2S1, EIF2S2, EIF3D, EIF3F, EIF3G, EIF3H, EIF3K, EIF4A1, EIF4A2, EIF4B, EIF4E, EIF4G1, EIF5, EIF5A, EIF5B, PFDN5, PIGH, PIGT, RPL10, RPL14, RPL15, RPL17, RPL18A, RPL28, RPL29, RPL31, RPL36, RPL37A, RPS16, RPS17, RPS21, RPS4X, RPS9, TUBA1B, TUBA1C, TUBA4A, TUBB2C, TUBB3, VBP1]
DNA Repair(R)	84	25	5.121e-04	3.320e-03	[BRCA2, DDB1, DDB2, FEN1, H2AFX, MBD4, MGMT, MPG, MRE11A, NBN, PCNA, POLD3, POLD4, POLE2, POLR2K, PRKDC, RAD50, RAD51, REV1, RFC2, RFC3, RFC4, RFC5, TDG, XPC]
Metabolism of non-coding RNA(R)	49	17	7.827e-04	5.308e-03	[NCBP1, NUP107, NUP153, NUP155, NUP205, NUP43, NUP50, NUP62, NUP85, NUP88, NUP98, RANBP2, SNRPD1, SNRPF, SNRPG, TPR, WDR77]
Metabolism of amino acids(R)	97	27	8.409e-04	5.370e-03	[AZIN1, BCAT2, BCKDHA, CKB, DBT, FAH, GAMT, GLUD1, PSMA3, PSMA4, PSMB10, PSMB4, PSMB8, PSMB9, PSMC2, PSMC3, PSMD1, PSMD11, PSMD12, PSMD14, PSMD4, PSME1, PSME3, PSMF1, SLC7A11, SLC7A5, SLC7A6]
Translation(R)	119	31	1.041e-03	6.357e-03	[EEF2, EIF1AX, EIF2S1, EIF2S2, EIF3D, EIF3F, EIF3G, EIF3H, EIF3K, EIF4A1, EIF4A2, EIF4B, EIF4E, EIF4G1, EIF5, EIF5B, RPL10, RPL14, RPL15, RPL17, RPL18A, RPL28, RPL29, RPL31, RPL36, RPL37A, RPS16, RPS17, RPS21, RPS4X, RPS9]
EphrinB-EPHB pathway(N)	53	17	1.784e-03	1.179e-02	[CRK, EFNB2, EFNB3, EPHB3, ITSN1, KRAS, MAP2K4, MAP3K7, MAPK3, PIK3CA, PTPN13, PXN, RASA1, ROCK1, RRAS, TIAM1, YES1]
VEGFR1 specific signals(N)	27	11	1.896e-03	1.230e-02	[CALM1, CAV1, CD2AP, HSP90AA1, MAPK3, NRP1, PGF, PIK3CA, PTPN11, RASA1, VEGFB]
control of gene expression by vitamin d receptor(B)	16	8	2.261e-03	1.435e-02	[ARID1A, BAZ1B, CHAF1A, MED1, SMARCC1, SUPT16H, TOP2B, TSC2]
Metablism of nucleotides(R)	56	17	3.106e-03	2.113e-02	[ADA, APRT, CAD, CTPS, DPYS, GLRX, NME3, PAICS, PPAT, RRM1, RRM2, SLC25A6, TK1, TXNRD1, TYMP, TYMS, UMPS]
IL6-mediated signaling	47	15	3.372e-03	2.270e-02	[CEBPD, FOS, GAB2, HSP90B1, IL6R, IRF1, JUNB, MAP2K4,

events(N)					MAPK11, PIK3CA, PTPN11, SOCS3, SOS1, STAT3, TIMP1]
Regulation of Telomerase(N)	67	19	3.816e-03	2.591e-02	[BLM, CCND1, EGFR, FOS, HSP90AA1, IRF1, MAPK3, MRE11A, NBN, PARP2, PTGES3, RAD1, RAD50, RBBP7, RPS6KB1, SAP30, TERF1, UBE3A, YWHAE]
cdk regulation of dna replication(B)	18	8	4.558e-03	3.091e-02	[CCNE1, CDC6, MCM2, MCM3, MCM4, MCM5, MCM6, MCM7]
Metabolism of carbohydrates(R)	106	26	5.464e-03	3.736e-02	[AGL, CALM1, ENO1, NUP107, NUP153, NUP155, NUP205, NUP43, NUP50, NUP62, NUP85, NUP88, NUP98, PC, PFKM, PGLS, PGM1, PKM2, PRPS1, RANBP2, SLC16A3, SLC25A12, SLC25A13, SLC2A1, TKT, TPR]
mechanism of protein import into the nucleus(B)	12	6	7.748e-03	5.337e-02	[KPNA2, KPNB1, NUP153, NUP62, RANBP1, RANBP2]
role of ran in mitotic spindle regulation(B)	12	6	7.748e-03	5.337e-02	[KIF15, KPNA2, KPNB1, RANBP1, RANBP2, TPX2]
chromatin remodeling by hswi/snf atp-dependent complexes(B)	16	7	8.379e-03	5.692e-02	[ACTB, ARID1A, GTF2F1, NF1, NR3C1, POLR1D, SMARCC1]
EPHB forward signaling(N)	38	12	8.859e-03	5.749e-02	[CRK, EFNB2, EFNB3, EPHB3, ITS1N1, KRAS, MAPK3, PIK3CA, PXN, RASA1, ROCK1, RRAS]
Signaling events mediated by HDAC Class II(N)	38	12	8.859e-03	5.749e-02	[BCL6, HDAC5, HSP90AA1, NR3C1, NUP153, NUP62, RANBP2, RFXANK, SUMO1, TUBA1B, XPO1, YWHAE]
Arf6 signaling events(N)	139	31	9.573e-03	5.859e-02	[ACAP1, ADRB2, ASAP1, ASAP2, CAV1, CD59, CLTA, CRK, EGFR, EXOC3, GNAQ, INPP5D, ITGA2B, JUP, MAPK3, PIK3CA, PLD1, PLD2, PRKCI, PRKCZ, PTPN11, PXN, RAB11A, RASA1, RPS6KB1, SDC1, SOS1, TBC1D4, TIAM1, YWHAE, YWHAH]
Insulin Pathway(N)	139	31	9.573e-03	5.859e-02	[ACAP1, ADRB2, ASAP1, ASAP2, CAV1, CD59, CLTA, CRK, EGFR, EXOC3, GNAQ, INPP5D, ITGA2B, JUP, MAPK3, PIK3CA, PLD1, PLD2, PRKCI, PRKCZ, PTPN11, PXN, RAB11A, RASA1, RPS6KB1, SDC1, SOS1, TBC1D4, TIAM1, YWHAE, YWHAH]
Arf6 trafficking events(N)	139	31	9.573e-03	5.859e-02	[ACAP1, ADRB2, ASAP1, ASAP2, CAV1, CD59, CLTA, CRK, EGFR, EXOC3, GNAQ, INPP5D, ITGA2B, JUP, MAPK3, PIK3CA, PLD1, PLD2, PRKCI, PRKCZ, PTPN11, PXN, RAB11A, RASA1, RPS6KB1, SDC1, SOS1, TBC1D4, TIAM1, YWHAE, YWHAH]
p53 signaling	54	15	1.122e-02	7.078e-02	[ATR, BBC3, CCNB1, CCNB2, CHEK1, CYCS, DDB2, FAS,

pathway(K)					GTSE1, PERP, PMAIP1, RRM2, STEAP3, THBS1, TP73]
FAS signaling pathway (CD95)(N)	35	11	1.228e-02	7.726e-02	[ARHGDI1B, FAF1, FAIM3, FAS, GSN, LMNA, MAP2K4, MAP3K7, PAK2, PRKDC, PTPN13]
Integrins in angiogenesis(N)	65	17	1.253e-02	7.772e-02	[CD44, FN1, FOS, GSN, HSP90AA1, IGF1R, MAPK3, MFGE8, PIK3C2A, PIK3CA, PTPN11, PXN, ROCK1, ROCK2, RPS6KB1, SDC1, TGFBR2]
il-2 receptor beta chain in t cell activation(B)	45	13	1.307e-02	7.977e-02	[CCNB1, CCND1, CCND2, CCNE1, FAS, FOS, MAPK3, PCNA, PIK3CA, RPS6KB1, SOCS3, SOS1, TFDP1]
cell cycle: g1/s check point(B)	22	8	1.406e-02	8.496e-02	[ATR, CCND1, CCNE1, DHFR, MAPK3, PTPN11, TFDP1, TGFB1]
Signaling events mediated by VEGFR1 and VEGFR2(N)	66	17	1.432e-02	8.502e-02	[CALM1, CAV1, CD2AP, HSP90AA1, HSPB1, MAPK11, MAPK3, NRP1, PGF, PIK3CA, PTPN11, PXN, RASA1, ROCK1, SOS1, VEGFB, YES1]
Small cell lung cancer(K)	61	16	1.474e-02	8.631e-02	[CASP9, CCND1, CCNE1, CCNE2, CDK2, CKS1B, COL4A1, COL4A2, CYCS, FN1, ITGA2B, LAMA5, LAMB1, LAMC2, SKP2, TRAF5]
internal ribosome entry pathway(B)	18	7	1.510e-02	8.688e-02	[CASP9, EIF4A1, EIF4E, EIF4G1, EIF4G2, EIF4G3, PTBP1]
IGF1 pathway(N)	150	32	1.528e-02	8.623e-02	[ACAP1, ADRB2, ASAP1, ASAP2, CAV1, CD59, CLTA, CRK, EGFR, EXOC3, GNAQ, IGF1R, INPP5D, ITGA2B, JUP, MAPK3, PIK3CA, PLD1, PLD2, PRKCI, PRKCZ, PTPN11, PXN, RAB11A, RASA1, RPS6KB1, SDC1, SOS1, TBC1D4, TIAM1, YWHAE, YWHAH]
IL2-mediated signaling events(N)	111	25	1.671e-02	9.530e-02	[BIRC2, CALM1, CCNA2, CCND2, FOS, GAB2, HSP90AA1, KRAS, MALT1, MAPK11, MAPK3, NFKB2, PIK3CA, PRKCZ, PTPN11, RASA1, RELB, RPS6KB1, SMPD1, SOCS3, SOS1, STAT3, TNFAIP3, UGCG, XPO1]
Aurora A signaling(N)	62	16	1.686e-02	9.451e-02	[AURKA, AURKB, BIRC2, BIRC5, CENPA, DLGAP5, MALT1, NFKB2, PIK3CA, RASA1, RELB, TACC1, TACC3, TNFAIP3, TPX2, XPO1]
Signaling events activated by Hepatocyte Growth Factor Receptor (c-Met)(N)	169	35	1.723e-02	9.543e-02	[ACAP1, ADRB2, ASAP1, ASAP2, CAV1, CD59, CLTA, CRK, EGFR, EXOC3, FOS, GLMN, GNAQ, INPP5D, ITGA2B, JUP, MAP2K4, MAPK3, PIK3CA, PLD1, PLD2, PRKCI, PRKCZ, PTPN11, PXN, RAB11A, RASA1, RPS6KB1, SDC1, SOS1, STAT3, TBC1D4, TIAM1, YWHAE, YWHAH]

Suppl. Table: 4: Genes and pathways representing differences between proliferation-arrested cells in 2D and 3D.

Total number of differentially expressed genes: 1801					
Pathway	Number Of Protein In Pathway	Protein From Sample	P-Value	FDR	IDs
M Phase(R)	88	38	2.838e-11	<1.000e-03	[AHCTF1, AURKB, BIRC5, BUB1, BUB1B, BUB3, CCDC99, CDC20, CENPA, CENPE, CENPF, CENPN, CLIP1, FBXO5, KIF18A, KIF20A, KIF23, KIF2A, KIF2C, MAD2L1, MAPRE1, MLF1IP, NDC80, NUP107, NUP37, PAFAH1B1, PLK1, RAD21, RANBP2, RANGAP1, SMC1A, SMC3, SPC25, STAG1, STAG2, XPO1, ZWILCH, ZWINT]
Cell cycle(K)	112	40	1.972e-09	<5.000e-04	[ANAPC5, ATM, ATR, BUB1, BUB1B, BUB3, CCNA2, CCNB1, CCNB2, CCND2, CCNE2, CDC20, CDC25A, CDC25C, CDC27, CDC6, CDC7, CDK2, CHEK1, DBF4, GSK3B, MAD2L1, MCM3, MCM4, MCM5, MCM6, MCM7, MDM2, PCNA, PLK1, PRKDC, PTTG1, RB1, SKP2, SMAD4, SMC1A, TFDP1, TGFB1, YWHAB, YWHAH]
Cell Cycle Checkpoints(R)	108	38	7.415e-09	<3.333e-04	[ANAPC5, ATM, ATR, BUB1B, BUB3, CCNB1, CCNB2, CDC20, CDC25A, CDC25C, CDC27, CDC6, CDC7, CDK2, CHEK1, DBF4, MAD2L1, MCM10, MCM3, MCM4, MCM5, MCM6, MCM7, MDM2, PSMA3, PSMA4, PSMC2, PSMC3, PSMD1, PSMD11, PSMD12, PSMD14, PSME1, PSME3, RFC3, RFC4, RFC5, UBE2C]
Aurora B signaling(N)	39	19	4.467e-07	<2.500e-04	[AURKA, AURKB, BIRC5, BUB1, CBX5, CENPA, KIF20A, KIF23, KIF2C, NCAPD2, NCAPG, NCAPH, NDC80, PSMA3, RACGAP1, RASA1, SMC2, SMC4, TACC1]
G1/S Transition(R)	98	32	5.702e-07	<2.000e-04	[CCNB1, CCNE2, CDC25A, CDC6, CDC7, CDK2, DBF4, DHFR, FBXO5, MCM10, MCM3, MCM4, MCM5, MCM6, MCM7, PCNA, POLA1, POLE2, PSMA3, PSMA4, PSMC2, PSMC3, PSMD1, PSMD11, PSMD12, PSMD14, PSME1, PSME3, RB1, RRM2, TFDP1, TYMS]
Signaling by Aurora kinases(N)	94	31	6.969e-07	<1.667e-04	[ATM, AURKA, AURKB, BIRC2, BIRC5, BUB1, CBX5, CENPA, CHUK, DLGAP5, GSK3B, IKBKB, KIF20A, KIF23, KIF2C, MALT1, MDM2, NCAPD2, NCAPG,

					NCAPH, NDC80, PIK3CA, PSMA3, RACGAP1, RASA1, SMC2, SMC4, TACC1, TACC3, TPX2, XPO1]
DNA Replication(R)	95	31	8.661e-07	<1.429e-04	[CDC6, CDC7, CDK2, DBF4, FEN1, GINS1, GINS2, GMNN, MCM10, MCM3, MCM4, MCM5, MCM6, MCM7, PCNA, POLA1, POLE2, PSMA3, PSMA4, PSMC2, PSMC3, PSMD1, PSMD11, PSMD12, PSMD14, PSME1, PSME3, RB1, RFC3, RFC4, RFC5]
APC/C-mediated degradation of cell cycle proteins(R)	72	24	1.041e-05	1.250e-04	[ANAPC5, AURKA, AURKB, BUB1B, BUB3, CCNB1, CDC20, CDC27, CDK2, FBXO5, MAD2L1, PLK1, PSMA3, PSMA4, PSMC2, PSMC3, PSMD1, PSMD11, PSMD12, PSMD14, PSME1, PSME3, PTTG1, UBE2C]
FOXO1 transcription factor network(N)	38	16	2.094e-05	1.111e-04	[AURKB, BIRC5, BRCA2, CCNB1, CCNB2, CDK2, CENPA, CENPF, CREBBP, FOS, FOXM1, NEK2, PLK1, RB1, SKP2, XRCC1]
S Phase(R)	97	28	2.616e-05	2.000e-04	[CDC25A, CDC6, CDK2, FEN1, GINS1, GINS2, MCM3, MCM4, MCM5, MCM6, MCM7, PCNA, POLA1, POLE2, PSMA3, PSMA4, PSMC2, PSMC3, PSMD1, PSMD11, PSMD12, PSMD14, PSME1, PSME3, RB1, RFC3, RFC4, RFC5]
BARD1 signaling events(N)	29	13	6.564e-05	5.455e-04	[ATM, ATR, BARD1, CDK2, FANCE, FANCL, MRE11A, PCNA, PRKDC, RAD50, RBBP8, TOPBP1, XRCC5]
Host Interactions of HIV factors(R)	119	30	1.498e-04	1.167e-03	[ARF1, CUL5, HMGA1, KPNB1, NUP107, NUP153, NUP155, NUP205, NUP37, NUP50, NUP88, NUPL1, PAK2, PSIP1, PSMA3, PSMA4, PSMC2, PSMC3, PSMD1, PSMD11, PSMD12, PSMD14, PSME1, PSME3, RANBP1, RANBP2, RANGAP1, TCEB2, TPR, XPO1]
Influenza Life Cycle(R)	187	41	2.008e-04	1.615e-03	[CANX, DHX9, DNAJC3, FUS, GRSF1, HNRNPA2B1, HNRNPA3, HNRNPD, HNRNPH1, HNRNPK, HNRNPM, HNRNPR, HSP90AA1, KPNB1, NCBP1, NUP107, NUP153, NUP155, NUP205, NUP37, NUP50, NUP88, NUPL1, PCBP2, POLR2K, RANBP2, RPL15, RPL18A, RPL28, RPL29, RPL31, RPL36, RPL37A, RPS17, RPS21, SMC1A, SNRPD1, SNRPF, SNRPG, TPR, XPO1]
HIV Life Cycle(R)	103	26	3.961e-04	3.714e-03	[FEN1, HMGA1, NCBP1, NUP107, NUP153, NUP155, NUP205, NUP37, NUP50, NUP88, NUPL1, POLR2K, PSIP1, RANBP1, RANBP2, RANGAP1, RGTG, SSRP1, SUPT16H, SUPT4H1, TAF9, TCEB2, TPR, XPO1, XRCC4, XRCC5]
G2/M Transition(R)	81	22	4.199e-04	3.667e-03	[AKAP9, ALMS1, CCNA2, CCNB1, CCNB2, CDC25A, CDC25C, CEP76, FGFR1OP, HSP90AA1, MAPRE1, NEK2,

					PAFAH1B1, PCM1, PLK1, PLK4, TUBA4A, TUBB, TUBB2C, TUBGCP3, TUBGCP4, XPO1]
Apoptosis(R)	124	29	6.299e-04	5.250e-03	[APC, BIRC2, CASP3, CDH1, CFLAR, CYCS, DSG2, KPNB1, LMNB1, MAPT, MST4, OCLN, PAK2, PMAIP1, PSMA3, PSMA4, PSMC2, PSMC3, PSMD1, PSMD11, PSMD12, PSMD14, PSME1, PSME3, ROCK1, TFDP1, TJP1, TNFRSF10B, YWHAB]
Aurora A signaling(N)	62	18	6.466e-04	5.059e-03	[ATM, AURKA, AURKB, BIRC2, BIRC5, CENPA, CHUK, DLGAP5, GSK3B, IKBKB, MALT1, MDM2, PIK3CA, RASA1, TACC1, TACC3, TPX2, XPO1]
DNA Repair(R)	84	22	6.733e-04	5.222e-03	[ATM, BRCA2, ERCC1, FEN1, H2AFX, MBD4, MGMT, MRE11A, PCNA, POLE2, POLR2K, PRKDC, RAD23B, RAD50, REV1, RFC3, RFC4, RFC5, TDG, XRCC1, XRCC4, XRCC5]
role of ran in mitotic spindle regulation(B)	12	7	7.070e-04	5.368e-03	[KIF15, KPNA2, KPNB1, RANBP1, RANBP2, RANGAP1, TPX2]
Signaling events mediated by HDAC Class II(N)	38	13	8.414e-04	6.250e-03	[GNB1, HDAC5, HSP90AA1, NCOR2, NR3C1, NUP153, RANBP2, RANGAP1, SUMO1, TUBA1B, UBE2I, XPO1, YWHAB]
eukaryotic protein translation(B)	13	7	1.119e-03	9.095e-03	[EIF2S2, EIF4A1, EIF4E, EIF4G1, EIF4G2, EIF4G3, EIF5]
TNF alpha/NF-kB(C)	136	30	1.263e-03	1.050e-02	[ACTL6A, BIRC2, CASP3, CFLAR, CHUK, CREBBP, CSNK2A2, DDX3X, GSK3B, HSP90AA1, IKBKAP, IKBKB, KPNA2, KPNA3, KTN1, MAP2K5, MCM5, MCM7, POLR1D, PRKCZ, PSMC2, PSMC3, PSMD1, PSMD12, PTPN11, RPS6KB1, TRAF5, YWHAB, YWHAH, ZFAND5]
FAS signaling pathway (CD95)(N)	35	12	1.288e-03	1.052e-02	[ARHGDIB, CASP3, CFLAR, CHUK, FAIM3, MAP2K4, MAP3K7, MET, PAK2, PRKDC, PTPN13, RB1]
M/G1 Transition(R)	61	17	1.389e-03	1.088e-02	[CDC6, GMNN, MCM3, MCM4, MCM5, MCM6, MCM7, PSMA3, PSMA4, PSMC2, PSMC3, PSMD1, PSMD11, PSMD12, PSMD14, PSME1, PSME3]
internal ribosome entry pathway(B)	18	8	1.700e-03	1.272e-02	[CASP1, CASP3, EIF4A1, EIF4E, EIF4G1, EIF4G2, EIF4G3, PTBP2]
TNF receptor signaling pathway(N)	272	50	2.102e-03	1.615e-02	[AIFM1, APP, ARHGDIB, ATM, BIRC2, CALM1, CASP1, CASP3, CHUK, CREB1, CREBBP, CSNK1A1, CYCS, DDIT3, EIF4E, ELK4, FKBP1A, FOS, GDI1, GSK3B, IKBKB, IL8, KPNA2, KPNB1, LMNB1, LMNB2, MALT1, MAP2K4,

					MAP3K7, MAP4K3, MAP4K5, MAPKAPK5, NFATC1, PAK2, PAWR, PIK3CA, PLA2G4A, PRKCI, PRKCZ, PTPRK, RALA, RB1, SLK, SMPD1, TOP1, TSC2, XPO1, YES1, YWHAB, YWHAH]
Sumoylation by RanBP2 regulates transcriptional repression(N)	15	7	2.488e-03	1.926e-02	[MDM2, NUP153, RANBP2, RANGAP1, SUMO1, UBE2I, XPO1]
Class I PI3K signaling events mediated by Akt(N)	94	22	2.687e-03	2.111e-02	[ATM, BIRC2, CHUK, CREBBP, EEF2, EIF4A1, EIF4E, EIF4G1, FKBP1A, GSK3B, HSP90AA1, IKBKB, MALT1, MDM2, PIK3CA, PRKDC, RPS6KB1, TBC1D4, TSC2, XPO1, YWHAB, YWHAH]
Metabolism of non-coding RNA(R)	49	14	2.840e-03	2.152e-02	[NCBP1, NUP107, NUP153, NUP155, NUP205, NUP37, NUP50, NUP88, NUPL1, RANBP2, SNRPD1, SNRPF, SNRPG, TPR]
Transport of Mature Transcript to Cytoplasm(R)	55	15	3.149e-03	2.357e-02	[EIF4E, MAGOH, NCBP1, NUP107, NUP153, NUP155, NUP205, NUP37, NUP50, NUP88, NUPL1, RANBP2, SLBP, TPR, UPF3B]
IL1-mediated signaling events(N)	204	39	3.319e-03	2.406e-02	[ATM, BIRC2, CALM1, CASP1, CASP3, CHUK, CREB1, CREBBP, CSNK1A1, DDIT3, EIF4E, ELK4, FKBP1A, FOS, GDI1, GSK3B, IKBKB, IL1R1, IL8, KPNA2, KPNB1, MALT1, MAP2K4, MAP3K7, MAPKAPK5, NFATC1, PAK2, PIK3CA, PLA2G4A, PRKCI, PRKCZ, PTPRK, RALA, TSC2, UBE2N, XPO1, YES1, YWHAB, YWHAH]
control of gene expression by vitamin d receptor(B)	16	7	3.534e-03	2.475e-02	[ACTL6A, ARID1A, MED1, SMARCC1, SUPT16H, TOP2B, TSC2]
mechanism of protein import into the nucleus(B)	12	6	3.573e-03	2.424e-02	[KPNA2, KPNB1, NUP153, RANBP1, RANBP2, RANGAP1]
Metabolism of amino acids(R)	97	22	3.870e-03	2.626e-02	[BCKDHA, CKB, DBT, DLD, FAH, GLUD1, MAT2A, NQO1, ODC1, PSMA3, PSMA4, PSMC2, PSMC3, PSMD1, PSMD11, PSMD12, PSMD14, PSME1, PSME3, SLC7A11, SLC7A5, SLC7A8]
Metabolism of carbohydrates(R)	106	23	5.355e-03	3.766e-02	[AGL, CALM1, DLAT, DLD, ENO1, GYG1, MDH2, NUP107, NUP153, NUP155, NUP205, NUP37, NUP50, NUP88, NUPL1, PDHX, PFKM, PGD, PGLS, PRPS1, RANBP2, SLC16A3, TPR]
TRAIL signaling	323	55	6.150e-03	4.319e-02	[AIFM1, APP, ARF1, ARHGDI, ATM, BIRC2, CALM1, CASP1, CASP3, CFLAR,

pathway(N)					CHUK, CREBBP, CSNK1A1, CYCS, EEF2, EIF4A1, EIF4E, EIF4G1, FKBP1A, FOS, GSK3B, HSP90AA1, IBTK, IKBKB, IL8, KPNA2, KPNB1, KRAS, LMNB1, LMNB2, MALT1, MAP2K4, MAP3K7, MDM2, NFATC1, PAWR, PIK3CA, PPP3CA, PRKCZ, PRKDC, PTPRK, RASA1, RB1, RPS6KB1, SLK, SMPD1, SOS1, TBC1D4, TNFRSF10B, TOP1, TSC2, XPO1, YES1, YWHAB, YWHAH]
Regulation of cytoplasmic and nuclear SMAD2/3 signaling(N)	289	50	6.619e-03	4.333e-02	[ATM, CALM1, CASP3, CBFB, CDK2, CREB1, CREBBP, CSNK1A1, CTBP1, DDIT3, DYNLRB1, EIF4E, ELK4, FKBP1A, FOS, GDI1, GSK3B, HSPA8, IL8, KPNA2, KPNB1, MAP2K4, MAP3K7, MAPK13, MAPKAPK5, MAPT, NFATC1, NR3C1, NUP153, OCLN, PAK2, PLA2G4A, PPP2CA, PRKCZ, PTPRK, RALA, RBBP7, RPS6KB1, SAP30, SMAD4, SMURF2, SOS1, SPTBN1, TGFB2, TSC2, UBE2I, YAP1, YES1, YWHAB, YWHAH]
Regulation of nuclear SMAD2/3 signaling(N)	289	50	6.619e-03	4.333e-02	[ATM, CALM1, CASP3, CBFB, CDK2, CREB1, CREBBP, CSNK1A1, CTBP1, DDIT3, DYNLRB1, EIF4E, ELK4, FKBP1A, FOS, GDI1, GSK3B, HSPA8, IL8, KPNA2, KPNB1, MAP2K4, MAP3K7, MAPK13, MAPKAPK5, MAPT, NFATC1, NR3C1, NUP153, OCLN, PAK2, PLA2G4A, PPP2CA, PRKCZ, PTPRK, RALA, RBBP7, RPS6KB1, SAP30, SMAD4, SMURF2, SOS1, SPTBN1, TGFB2, TSC2, UBE2I, YAP1, YES1, YWHAB, YWHAH]
TGF-beta receptor signaling(N)	289	50	6.619e-03	4.333e-02	[ATM, CALM1, CASP3, CBFB, CDK2, CREB1, CREBBP, CSNK1A1, CTBP1, DDIT3, DYNLRB1, EIF4E, ELK4, FKBP1A, FOS, GDI1, GSK3B, HSPA8, IL8, KPNA2, KPNB1, MAP2K4, MAP3K7, MAPK13, MAPKAPK5, MAPT, NFATC1, NR3C1, NUP153, OCLN, PAK2, PLA2G4A, PPP2CA, PRKCZ, PTPRK, RALA, RBBP7, RPS6KB1, SAP30, SMAD4, SMURF2, SOS1, SPTBN1, TGFB2, TSC2, UBE2I, YAP1, YES1, YWHAB, YWHAH]
Signaling by Wnt(R)	50	13	8.351e-03	5.710e-02	[APC, CSNK1A1, GSK3B, PSMA3, PSMA4, PSMC2, PSMC3, PSMD1, PSMD11, PSMD12, PSMD14, PSME1, PSME3]
Metablism of nucleotides(R)	56	14	8.753e-03	5.937e-02	[AK2, APRT, DCK, DGUOK, HPRT1, NME3, NME4, PAICS, RRM1, RRM2, TK1, TXNRD1, TYMS, UPP1]
IFN-gamma pathway(N)	373	61	9.140e-03	6.107e-02	[ATM, CALM1, CASP1, CASP3, CBFB, CDK2, CREB1, CREBBP, CSNK1A1, CTBP1, DDIT3, DYNLRB1, EEF2, EIF4A1, EIF4E, EIF4G1, ELK4, FCER2, FKBP1A, FOS, GDI1, GSK3B, HMGA1, HSPA8, IL13RA1, IL8, IRF9, KPNA2, KPNB1,

					MAP2K4, MAP3K7, MAPK13, MAPKAPK5, MAPT, MYBL1, NFATC1, NR3C1, NUP153, OCLN, PAK2, PIK3CA, PLA2G4A, PPP2CA, PRKCZ, PTPN11, PTPRK, RALA, RBBP7, RPS6KB1, SAP30, SMAD4, SMURF2, SOS1, SPTBN1, TGFBR2, TSC2, UBE2I, YAP1, YES1, YWHAB, YWHAH]
Alpha6Beta4Integrin(C)	45	12	9.160e-03	5.986e-02	[CASP3, DST, EGFR, EIF4E, ERBB2IP, ITGA6, ITGB4, MET, PIK3CA, YES1, YWHAB, YWHAH]
mechanism of gene regulation by peroxisome proliferators via ppara(B)	40	11	9.958e-03	6.427e-02	[CPT1A, CREBBP, DUT, FAT1, HSP90AA1, ME1, MED1, NCOR2, NR1H3, NRIP1, RB1]
Formation and Maturation of mRNA Transcript(R)	152	29	1.069e-02	6.769e-02	[DHX9, FUS, HNRNPA2B1, HNRNPA3, HNRNPD, HNRNPH1, HNRNPK, HNRNPM, HNRNPR, MAGOH, METTL3, NCBP1, NHP2L1, PAPOLA, PCBP2, POLR2K, RNGTT, SF3B1, SMC1A, SNRPA1, SNRPD1, SNRPF, SNRPG, SSRP1, SUPT16H, SUPT4H1, TAF9, TCEB2, UPF3B]
FoxO family signaling(N)	46	12	1.074e-02	6.674e-02	[CCNB1, CDK2, CREBBP, CSNK1A1, PLK1, RALA, SKP2, USP7, XPO1, YWHAB, YWHAH, ZFAND5]
Glypican 1 network(N)	436	69	1.154e-02	7.096e-02	[APP, ARF1, ATM, BIRC2, CALM1, CASP3, CBF3, CDK2, CHUK, CREB1, CREBBP, CSNK1A1, CTBP1, DDIT3, DYNLRB1, EEF2, EIF4A1, EIF4E, EIF4G1, ELK4, FKBP1A, FOS, GDI1, GSK3B, HSP90AA1, HSPA8, IBTK, IKBKB, IL8, KPNA2, KPNB1, KRAS, MALT1, MAP2K4, MAP3K7, MAPK13, MAPKAPK5, MAPT, MDM2, NFATC1, NR3C1, NUP153, OCLN, PAK2, PIK3CA, PLA2G4A, PPP2CA, PPP3CA, PRKCZ, PRKDC, PTPRK, RALA, RASA1, RBBP7, RPS6KB1, SAP30, SMAD4, SMURF2, SOS1, SPTBN1, TBC1D4, TGFBR2, TSC2, UBE2I, XPO1, YAP1, YES1, YWHAB, YWHAH]
a6b1 and a6b4 Integrin signaling(N)	47	12	1.252e-02	7.623e-02	[CASP3, CDH1, EGFR, ITGA6, ITGB4, LAMA5, LAMB1, MET, PIK3CA, RPS6KB1, YWHAB, YWHAH]
IL2 signaling events mediated by PI3K(N)	65	15	1.330e-02	8.014e-02	[ATM, BIRC2, CALM1, CHUK, HSP90AA1, IKBKB, MALT1, PIK3CA, PRKCZ, PTPN11, RPS6KB1, SMPD1, SOS1, UGCG, XPO1]
chromatin remodeling by hswi/snf atp-	16	6	1.354e-02	8.010e-02	[ACTB, ARID1A, NF1, NR3C1, POLR1D, SMARCC1]

dependent complexes(B)					
nfbk activation by nontypeable hemophilus influenzae(B)	26	8	1.427e-02	8.404e-02	[CHUK, IKBKB, IL8, MAP3K7, NR3C1, SMAD4, TGFB1, TGFB2]
Signaling events mediated by HDAC Class I(N)	97	20	1.484e-02	8.658e-02	[CREBBP, GNB1, HDAC5, HSP90AA1, MBD2, NCOR2, NR3C1, NUP153, RANBP2, RANGAP1, RBBP7, SAP30, SIRT2, STAT3, SUMO1, TUBA1B, UBE2I, XPO1, YWHAB, YY1]
Glypican pathway(N)	472	73	1.543e-02	8.889e-02	[APC, APP, ARF1, ATM, BIRC2, CALM1, CASP3, CBF3, CDK2, CHUK, CREB1, CREBBP, CSNK1A1, CTBP1, DDIT3, DYNLRB1, EEF2, EIF4A1, EIF4E, EIF4G1, ELK4, FKBP1A, FOS, FZD6, GDI1, GNB1, GSK3B, HSP90AA1, HSPA8, IBTK, IKBKB, IL8, KPNA2, KPNB1, KRAS, MACF1, MALT1, MAP2K4, MAP3K7, MAPK13, MAPKAPK5, MAPT, MDM2, NFATC1, NR3C1, NUP153, OCLN, PAK2, PIK3CA, PLA2G4A, PPP2CA, PPP3CA, PRKCZ, PRKDC, PTPRK, RALA, RASA1, RBBP7, RPS6KB1, SAP30, SMAD4, SMURF2, SOS1, SPTBN1, TBC1D4, TGFB2, TSC2, UBE2I, XPO1, YAP1, YES1, YWHAB, YWHAH]
IL2-mediated signaling events(N)	111	22	1.649e-02	9.467e-02	[ATM, BIRC2, CALM1, CCNA2, CCND2, CHUK, FOS, HSP90AA1, IKBKB, KRAS, MALT1, PIK3CA, PRKCZ, PTPN11, RASA1, RPS6KB1, SMPD1, SOS1, STAM2, STAT3, UGCG, XPO1]