Supplemental Table 1: Genes significantly up-regulated in 3D (and ≥1.5 fold)

Gene	Fold change	Gene Name
GPNMB	9.51	glycoprotein (transmembrane) nmb
SERPINA3	7.43	serpin peptidase inhibitor, clade A, member 3
ALOX15B	4.80	arachidonate 15-lipoxygenase, type B
C1R	4.12	complement component 1, r subcomponent
MAOA	3.93	monoamine oxidase A
BTG1	3.28	B-cell translocation gene 1, anti-proliferative
HIST1H2BD	3.18	histone cluster 1, H2bd
TMSB15B	3.15	thymosin beta 15B
SEPP1	3.08	selenoprotein P, plasma, 1
SCNN1B	3.02	sodium channel, nonvoltage-gated 1, beta
GSTA4	2.92	glutathione S-transferase alpha 4
ANG	2.90	angiogenin, ribonuclease, RNase A family, 5
SLC22A18	2.86	solute carrier family 22, member 18
IGBP1	2.84	immunoglobulin (CD79A) binding protein 1
YPEL5	2.81	yippee-like 5 (Drosophila)
HIST3H2A	2.81	histone cluster 3, H2a
NFIL3	2.77	nuclear factor, interleukin 3 regulated
NUPR1	2.68	nuclear protein 1
TNNT1	2.67	troponin T type 1 (skeletal, slow)
ASS1	2.64	argininosuccinate synthetase 1
GM2A	2.57	GM2 ganglioside activator
HCFC1R1	2.56	host cell factor C1 regulator 1 (XPO1 dependent)
TRAPPC6A	2.55	trafficking protein particle complex 6A
FANCE	2.53	Fanconi anemia, complementation group E
COL2A1	2.51	collagen, type II, alpha 1
CSNK2A2	2.51	casein kinase 2, alpha prime polypeptide
UBE2L6	2.49	ubiquitin-conjugating enzyme E2L 6
C9orf16	2.44	chromosome 9 open reading frame 16
C6orf48	2.43	chromosome 6 open reading frame 48
NR1H3	2.43	nuclear receptor subfamily 1, group H, member 3
LOC391132	2.42	similar to hCG2041276
GLUL	2.40	glutamate-ammonia ligase (glutamine synthetase)

PFDN5	2.37	prefoldin subunit 5
PGLS	2.37	6-phosphogluconolactonase
PDPN	2.34	podoplanin
TMEM159	2.33	transmembrane protein 159
HS1BP3	2.31	HCLS1 binding protein 3
LETMD1	2.27	LETM1 domain containing 1
C3	2.25	complement component 3
HIST1H2BK	2.23	histone cluster 1, H2bk
BCKDHA	2.21	branched chain keto acid dehydrogenase E1, alpha
ATP5G2	2.21	ATP synthase, mitochondrial F0 complex, subunit C2
GRN	2.21	granulin
GLTSCR2	2.20	glioma tumor suppressor candidate region gene 2
CCNB1IP1	2.20	cyclin B1 interacting protein 1
GCHFR	2.16	GTP cyclohydrolase I feedback regulator
RPL36	2.15	ribosomal protein L36
MTSS1	2.14	metastasis suppressor 1
TSC2	2.14	tuberous sclerosis 2
TTLL1	2.14	tubulin tyrosine ligase-like family, member 1
VPS28	2.13	vacuolar protein sorting 28 homolog (S. cerevisiae)
C14orf159	2.13	chromosome 14 open reading frame 159
C21orf33	2.12	chromosome 21 open reading frame 33
HEBP1	2.12	heme binding protein 1
GPX4	2.10	glutathione peroxidase 4 (phospholipid hydroperoxidase)
CTSB	2.09	cathepsin B
CCDC51	2.08	coiled-coil domain containing 51
RGS10	2.08	regulator of G-protein signaling 10
CKB	2.06	creatine kinase, brain
EIF3G	2.06	eukaryotic translation initiation factor 3, subunit G
HDAC5	2.05	histone deacetylase 5
CTSF	2.04	cathepsin F
MGMT	2.04	O-6-methylguanine-DNA methyltransferase
CRYL1	2.04	crystallin, lambda 1
NME3	2.04	non-metastatic cells 3, protein expressed in
C2orf28	2.04	chromosome 2 open reading frame 28
TSC22D3	2.03	TSC22 domain family, member 3

ORAI3	2.03	ORAI calcium release-activated calcium modulator 3
POLR1D	2.02	polymerase (RNA) I polypeptide D, 16kDa
CHI3L2	2.02	chitinase 3-like 2
PIGV	2.02	phosphatidylinositol glycan anchor biosynthesis, class V
UBXN1	2.00	UBX domain protein 1
LCMT1	2.00	leucine carboxyl methyltransferase 1
RPS28P6	1.99	ribosomal protein S28 pseudogene 6
GABARAP	1.98	GABA(A) receptor-associated protein
H2BFS	1.98	H2B histone family, member S
SURF1	1.98	surfeit 1
ERGIC3	1.96	ERGIC and golgi 3
TP53TG1	1.96	TP53 target 1 (non-protein coding)
PKIG	1.95	protein kinase (cAMP-dependent, catalytic) inhibitor gamma
RPL18AP6	1.94	ribosomal protein L18a pseudogene 6
APOE	1.89	apolipoprotein E
LYPD3	1.87	LY6/PLAUR domain containing 3
HIST1H2BE	1.87	histone cluster 1, H2be
C1orf66	1.87	chromosome 1 open reading frame 66
PRCP	1.87	prolylcarboxypeptidase (angiotensinase C)
RAMP1	1.85	receptor (G protein-coupled) activity modifying protein 1
BCAS3	1.83	breast carcinoma amplified sequence 3
SMPD1	1.83	sphingomyelin phosphodiesterase 1, acid lysosomal
NENF	1.83	neuron derived neurotrophic factor
PSME1	1.82	proteasome (prosome, macropain) activator subunit 1
NUDT2	1.82	nudix (nucleoside diphosphate linked moiety X)-type motif 2
PRKCZ	1.82	protein kinase C, zeta
TIMM9	1.81	translocase of inner mitochondrial membrane 9 homolog
COX7A2L	1.81	cytochrome c oxidase subunit VIIa polypeptide 2 like
PEX6	1.80	peroxisomal biogenesis factor 6
FHL3	1.78	four and a half LIM domains 3
NDUFB11	1.78	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 11
JUNB	1.78	jun B proto-oncogene
DDIT3	1.76	DNA-damage-inducible transcript 3
ZNF32	1.75	zinc finger protein 32
ZNF358	1.75	zinc finger protein 358

PRDX2	1.75	peroxiredoxin 2
CST3	1.75	cystatin C
RPS10P3	1.74	ribosomal protein S10 pseudogene 3
SSR4	1.74	signal sequence receptor, delta
CUTA	1.74	cutA divalent cation tolerance homolog (E. coli)
AIP	1.74	aryl hydrocarbon receptor interacting protein
HIST1H4J	1.73	histone cluster 1, H4j
HIGD2A	1.73	HIG1 domain family, member 2A
C12orf10	1.72	chromosome 12 open reading frame 10
RPL10L	1.72	ribosomal protein L10-like
MRPS18B	1.72	mitochondrial ribosomal protein S18B
RNASET2	1.72	ribonuclease T2
NFKBIL1	1.72	nuclear factor of kappa in B-cells inhibitor-like 1
ITPKC	1.72	inositol 1,4,5-trisphosphate 3-kinase C
EIF3F	1.71	eukaryotic translation initiation factor 3, subunit F
DNAJC12	1.71	DnaJ (Hsp40) homolog, subfamily C, member 12
NDUFA3	1.71	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 3
C11orf60	1.71	chromosome 11 open reading frame 60
WDR13	1.71	WD repeat domain 13
KLHDC4	1.71	kelch domain containing 4
KIAA0141	1.70	KIAA0141
RP3-377H14.5	1.70	hypothetical LOC285830
DEPDC6	1.70	DEP domain containing 6
CRTAP	1.70	cartilage associated protein
DCTN2	1.70	dynactin 2 (p50)
UBXN6	1.70	UBX domain protein 6
DNAL4	1.69	dynein, axonemal, light chain 4
TOM1	1.69	target of myb1 (chicken)
HBP1	1.69	HMG-box transcription factor 1
SUPT4H1	1.69	suppressor of Ty 4 homolog 1 (S. cerevisiae)
CORO1B	1.69	coronin, actin binding protein, 1B
THNSL2	1.69	threonine synthase-like 2 (S. cerevisiae)
MED16	1.69	mediator complex subunit 16
C19orf56	1.67	chromosome 19 open reading frame 56
PDCD4	1.66	programmed cell death 4

ECHDC3	1.65	enoyl Coenzyme A hydratase domain containing 3
RAB13	1.65	RAB13, member RAS oncogene family
TCEB2	1.65	transcription elongation factor B (SIII), polypeptide 2
EXOSC5	1.65	exosome component 5
CUEDC2	1.65	CUE domain containing 2
C14orf93	1.65	chromosome 14 open reading frame 93
TADA3L	1.64	transcriptional adaptor 3 (NGG1 homolog, yeast)-like
GMPR2	1.64	guanosine monophosphate reductase 2
STOM	1.64	stomatin
ERMAP	1.64	erythroblast membrane-associated protein
COX5B	1.63	cytochrome c oxidase subunit Vb
RPL29P11	1.63	ribosomal protein L29 pseudogene 11
VAT1	1.63	vesicle amine transport protein 1 homolog (T. californica)
LOC201229	1.63	hypothetical protein LOC201229
IFI6	1.63	interferon, alpha-inducible protein 6
RPS10P11	1.62	ribosomal protein S10 pseudogene 11
CRBN	1.61	cereblon
BTBD2	1.61	BTB (POZ) domain containing 2
PSAP	1.61	prosaposin
MANBA	1.61	mannosidase, beta A, lysosomal
ACSM3	1.60	acyl-CoA synthetase medium-chain family member 3
MYO1F	1.60	myosin IF
RARRES3	1.59	retinoic acid receptor responder (tazarotene induced) 3
SIRT2	1.59	sirtuin 2
CIDEB	1.59	cell death-inducing DFFA-like effector b
C1orf50	1.59	chromosome 1 open reading frame 50
ARL4D	1.58	ADP-ribosylation factor-like 4D
COX6B1	1.58	cytochrome c oxidase subunit Vib polypeptide 1
TMED1	1.57	transmembrane emp24 protein transport domain 1
ZNHIT1	1.57	zinc finger, HIT type 1
C11orf10	1.57	chromosome 11 open reading frame 10
ABHD14A	1.57	abhydrolase domain containing 14A
C4A	1.57	complement component 4A (Rodgers blood group)
HIST1H1D	1.56	histone cluster 1, H1d
RTN1	1.56	reticulon 1

GDI1	1.56	GDP dissociation inhibitor 1
RRAGD	1.56	Ras-related GTP binding D
RPL14	1.56	ribosomal protein L14
ZNF34	1.55	zinc finger protein 34
VPS11	1.54	vacuolar protein sorting 11 homolog (S. cerevisiae)
APH1B	1.53	anterior pharynx defective 1 homolog B (C. elegans)
NECAB3	1.53	N-terminal EF-hand calcium binding protein 3
LOC100129250	1.53	similar to hCG1811779
DYRK4	1.52	dual-specificity tyrosine-phosphorylation regulated kinase 4
UQCR	1.52	ubiquinol-cytochrome c reductase, 6.4kDa subunit
CPNE1	1.52	copine I
LRRC23	1.52	leucine rich repeat containing 23
TSPAN4	1.52	tetraspanin 4
TM9SF1	1.52	transmembrane 9 superfamily member 1
MAPK3	1.52	mitogen-activated protein kinase 3
C12orf39	1.51	chromosome 12 open reading frame 39
HIST1H2AE	1.51	histone cluster 1, H2ae
C19orf53	1.51	chromosome 19 open reading frame 53
MAN1B1	1.51	mannosidase, alpha, class 1B, member 1

Supplemental Table 2: Genes significantly down-regulated in 3D (and ≤0.5 fold)

Gene	Fold change	Gene Name
ASPM	0.09	asp (abnormal spindle) homolog, microcephaly associated
CEP55	0.13	centrosomal protein 55kDa
PBK	0.15	PDZ binding kinase
KIF14	0.16	kinesin family member 14
CENPF	0.16	centromere protein F, 350/400ka (mitosin)
DLGAP5	0.18	discs, large (Drosophila) homolog-associated protein 5
HMMR	0.19	hyaluronan-mediated motility receptor (RHAMM)
ZWILCH	0.19	Zwilch, kinetochore associated, homolog (Drosophila)
ECT2	0.19	epithelial cell transforming sequence 2 oncogene
CCNA2	0.21	cyclin A2
SMC4	0.21	structural maintenance of chromosomes 4
KIF11	0.21	kinesin family member 11
HMGCS1	0.21	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 1
SLC26A2	0.22	solute carrier family 26 (sulfate transporter), member 2
CDKN3	0.22	cyclin-dependent kinase inhibitor 3
RRM2	0.22	ribonucleotide reductase M2 polypeptide
CDC2	0.23	cell division cycle 2, G1 to S and G2 to M
TTK	0.23	TTK protein kinase
MLF1IP	0.24	MLF1 interacting protein
ATAD2	0.25	ATPase family, AAA domain containing 2
HELLS	0.26	helicase, lymphoid-specific
CDC20	0.26	cell division cycle 20 homolog (S. cerevisiae)
GOLGA8A	0.26	golgi autoantigen, golgin subfamily a, 8A
KRT81	0.26	keratin 81
ELOVL6	0.26	ELOVL family member 6, elongation of long chain fatty acids
CENPE	0.26	centromere protein E, 312kDa
CDC6	0.27	cell division cycle 6 homolog (S. cerevisiae)
VCAN	0.27	versican
LMNB1	0.28	lamin B1
PRC1	0.28	protein regulator of cytokinesis 1
XIST	0.28	X (inactive)-specific transcript (non-protein coding)
BUB1B	0.28	budding uninhibited by benzimidazoles 1 homolog beta
CCNB1	0.29	cyclin B1
MKI67	0.29	antigen identified by monoclonal antibody Ki-67
ANP32E	0.29	acidic nuclear phosphoprotein 32 family, member E
SLC2A3P1	0.29	solute carrier family 2, member 3 pseudogene 1
ARHGAP29	0.30	Rho GTPase activating protein 29
NCAPG2	0.30	non-SMC condensin II complex, subunit G2
FBN2	0.30	fibrillin 2
NUSAP1	0.30	nucleolar and spindle associated protein 1
MAD2L1	0.30	MAD2 mitotic arrest deficient-like 1 (yeast)
NCAPG	0.30	non-SMC condensin I complex, subunit G
CASP8AP2	0.30	caspase 8 associated protein 2
TDG	0.31	thymine-DNA glycosylase
CCDC99	0.31	coiled-coil domain containing 99

MCM10	0.31	minichromosome maintenance complex component 10
GINS1	0.31	GINS complex subunit 1 (Psf1 homolog)
DHFR	0.31	dihydrofolate reductase
BARD1	0.31	BRCA1 associated RING domain 1
ARHGDIB	0.32	Rho GDP dissociation inhibitor (GDI) beta
PIK3C2A	0.32	phosphoinositide-3-kinase, class 2, alpha polypeptide
SHCBP1	0.32	SHC SH2-domain binding protein 1
USP1	0.32	ubiquitin specific peptidase 1
SMC2	0.32	structural maintenance of chromosomes 2
KPNA2	0.32	karyopherin alpha 2 (RAG cohort 1, importin alpha 1)
TPX2	0.32	TPX2, microtubule-associated, homolog (Xenopus laevis)
BUB1	0.33	budding uninhibited by benzimidazoles 1 homolog (yeast)
DEPDC1	0.33	DEP domain containing 1
SMC1A	0.33	structural maintenance of chromosomes 1A
OIP5	0.33	Opa interacting protein 5
SACS	0.33	spastic ataxia of Charlevoix-Saguenay (sacsin)
CHST6	0.33	carbohydrate (N-acetylglucosamine 6-O) sulfotransferase 6
NUDT15	0.33	nudix (nucleoside diphosphate linked moiety X)-type motif 15
SFRS7	0.34	splicing factor, arginine/serine-rich 7, 35kDa
KIF23	0.34	kinesin family member 23
GALNT7	0.34	N-acetylgalactosaminyltransferase 7 (GalNAc-T7)
HNRNPA2B1	0.34	heterogeneous nuclear ribonucleoprotein A2/B1
CHD1	0.34	chromodomain helicase DNA binding protein 1
AURKA	0.34	aurora kinase A
WHSC1	0.35	Wolf-Hirschhorn syndrome candidate 1
KIF18A	0.35	kinesin family member 18A
TOP2B	0.35	topoisomerase (DNA) II beta 180kDa
NETO2	0.35	neuropilin (NRP) and tolloid (TLL)-like 2
PHIP	0.35	pleckstrin homology domain interacting protein
MELK	0.35	maternal embryonic leucine zipper kinase
CDC7	0.35	cell division cycle 7 homolog (S. cerevisiae)
FAT1	0.35	FAT tumor suppressor homolog 1 (Drosophila)
C10orf18	0.35	chromosome 10 open reading frame 18
PLK1	0.35	polo-like kinase 1 (Drosophila)
VRK1	0.35	vaccinia related kinase 1
RFC3	0.36	replication factor C (activator 1) 3, 38kDa
MBNL1	0.36	muscleblind-like (Drosophila)
SLC30A1	0.36	solute carrier family 30 (zinc transporter), member 1
LBR	0.36	lamin B receptor
CCNB2	0.36	cyclin B2
DENND1B	0.36	DENN/MADD domain containing 1B
ARID4B	0.36	AT rich interactive domain 4B (RBP1-like)
CKS2	0.37	CDC28 protein kinase regulatory subunit 2
KIF4A	0.37	kinesin family member 4A
TMPO	0.37	thymopoietin
FANCI	0.37	Fanconi anemia, complementation group I
TYMS	0.38	thymidylate synthetase

TRIP13	0.38	thyroid hormone receptor interactor 13
SMC3	0.38	structural maintenance of chromosomes 3
DEK	0.38	DEK oncogene
SFRS2	0.38	splicing factor, arginine/serine-rich 2
SFRS18	0.38	splicing factor, arginine/serine-rich 18
POLR3G	0.38	polymerase (RNA) III (DNA directed) polypeptide G (32kD)
LARP4	0.38	La ribonucleoprotein domain family, member 4
SUZ12	0.38	suppressor of zeste 12 homolog (Drosophila)
TBL1XR1	0.39	transducin (beta)-like 1 X-linked receptor 1
KIAA0101	0.39	KIAA0101
TCERG1	0.39	transcription elongation regulator 1
KIF2A	0.39	kinesin heavy chain member 2A
UBE2S	0.39	ubiquitin-conjugating enzyme E2S
REV3L	0.39	REV3-like, catalytic subunit of DNA polymerase zeta (yeast)
ATR	0.39	ataxia telangiectasia and Rad3 related
NASP	0.39	nuclear autoantigenic sperm protein (histone-binding)
PLK4	0.39	polo-like kinase 4 (Drosophila)
KIF15	0.40	kinesin family member 15
BIRC5	0.40	baculoviral IAP repeat-containing 5
XPO1	0.40	exportin 1 (CRM1 homolog, yeast)
C3orf63	0.40	chromosome 3 open reading frame 63
TARDBP	0.40	TAR DNA binding protein
PRR11	0.41	proline rich 11
RAD51AP1	0.41	RAD51 associated protein 1
DDX21	0.41	DEAD (Asp-Glu-Ala-Asp) box polypeptide 21
PHACTR2	0.41	phosphatase and actin regulator 2
LMNB2	0.41	lamin B2
NCBP1	0.41	nuclear cap binding protein subunit 1, 80kDa
SEPHS1	0.41	selenophosphate synthetase 1
PRPF4B	0.41	PRP4 pre-mRNA processing factor 4 homolog B (yeast)
FKBP11	0.41	FK506 binding protein 11, 19 kDa
GGH	0.41	gamma-glutamyl hydrolase
FLRT2	0.42	fibronectin leucine rich transmembrane protein 2
DNAJA1	0.42	DnaJ (Hsp40) homolog, subfamily A, member 1
LDLR	0.42	low density lipoprotein receptor
HNRNPA3P1	0.42	heterogeneous nuclear ribonucleoprotein A3 pseudogene 1
CENPN	0.42	centromere protein N
PDSS1	0.42	prenyl (decaprenyl) diphosphate synthase, subunit 1
MYO5C	0.43	myosin VC
MCM7	0.43	minichromosome maintenance complex component 7
SLC38A1	0.43	solute carrier family 38, member 1
CCNE2	0.43	cyclin E2
CAPRIN2	0.43	caprin family member 2
RC3H2	0.43	ring finger and CCCH-type zinc finger domains 2
BCLAF1	0.43	BCL2-associated transcription factor 1
HNRNPR	0.43	heterogeneous nuclear ribonucleoprotein R
TOP1	0.43	topoisomerase (DNA) I

CIT	0.43	citron (rho-interacting, serine/threonine kinase 21)
PUS7	0.43	pseudouridylate synthase 7 homolog (S. cerevisiae)
CDCA3	0.44	cell division cycle associated 3
UCHL5	0.44	ubiquitin carboxyl-terminal hydrolase L5
BAT2D1	0.44	BAT2 domain containing 1
TMEM194A	0.44	transmembrane protein 194A
TMEM41B	0.44	transmembrane protein 41B
PTPRG	0.44	protein tyrosine phosphatase, receptor type, G
ASXL2	0.44	additional sex combs like 2 (Drosophila)
ACAT2	0.44	acetyl-Coenzyme A acetyltransferase 2
SPAG5	0.45	sperm associated antigen 5
SLC43A3	0.45	solute carrier family 43, member 3
EIF4E	0.45	eukaryotic translation initiation factor 4E
FNBP4	0.45	formin binding protein 4
PSMD11	0.45	proteasome 26S subunit, non-ATPase, 11
LPGAT1	0.45	lysophosphatidylglycerol acyltransferase 1
GRAMD3	0.45	GRAM domain containing 3
HERC2P2	0.45	hect domain and RLD 2 pseudogene 2
LOC152719	0.46	hypothetical protein LOC152719
DHX29	0.46	DEAH (Asp-Glu-Ala-His) box polypeptide 29
ATP2B1	0.46	ATPase, Ca++ transporting, plasma membrane 1
EDEM3	0.46	ER degradation enhancer, mannosidase alpha-like 3
LOC100134401	0.46	hypothetical protein LOC100134401
MCM6	0.46	minichromosome maintenance complex component 6
RBBP8	0.46	retinoblastoma binding protein 8
SLTM	0.46	SAFB-like, transcription modulator
FBXW12	0.46	F-box and WD repeat domain containing 12
AKAP9	0.47	A kinase (PRKA) anchor protein (yotiao) 9
PCNA	0.47	proliferating cell nuclear antigen
ORC6L	0.47	origin recognition complex, subunit 6 like (yeast)
HMGB1	0.47	high-mobility group box 1
MPHOSPH9	0.47	M-phase phosphoprotein 9
CSE1L	0.47	CSE1 chromosome segregation 1-like (yeast)
NOL8	0.47	nucleolar protein 8
C21orf66	0.47	chromosome 21 open reading frame 66
UBP1	0.47	upstream binding protein 1 (LBP-1a)
KIF5B	0.47	kinesin family member 5B
CHSY1	0.47	chondroitin sulfate synthase 1
C1orf112	0.47	chromosome 1 open reading frame 112
TJP1	0.48	tight junction protein 1 (zona occludens 1)
TROVE2	0.48	TROVE domain family, member 2
CCNL1	0.48	cyclin L1
SSB	0.48	Sjogren syndrome antigen B (autoantigen La)
POLE2	0.48	polymerase (DNA directed), epsilon 2 (p59 subunit)
ZMPSTE24	0.48	zinc metallopeptidase (STE24 homolog, S. cerevisiae)
TOPBP1	0.48	topoisomerase (DNA) II binding protein 1
NUP107	0.48	nucleoporin 107kDa

RANBP1	0.48	RAN binding protein 1
ATAD2B	0.48	ATPase family, AAA domain containing 2B
CDC25C	0.49	cell division cycle 25 homolog C (S. pombe)
ZNF131	0.49	zinc finger protein 131
OXCT1	0.49	3-oxoacid CoA transferase 1
ZC3H11A	0.49	zinc finger CCCH-type containing 11A
SEPT11	0.49	septin 11
SYNCRIP	0.49	synaptotagmin binding, cytoplasmic RNA interacting protein
SFRP1	0.49	secreted frizzled-related protein 1
RBBP7	0.49	retinoblastoma binding protein 7
FAM13B	0.49	family with sequence similarity 13, member B
RBM25	0.49	RNA binding motif protein 25
HSP90AA1	0.49	heat shock protein 90kDa alpha (cytosolic), class A member 1
H2AFZ	0.49	H2A histone family, member Z
SETD5	0.49	SET domain containing 5
TLK1	0.49	tousled-like kinase 1
NBPF14	0.50	neuroblastoma breakpoint family, member 14
TK1	0.50	thymidine kinase 1, soluble
CNOT6	0.50	CCR4-NOT transcription complex, subunit 6
RAD51C	0.50	RAD51 homolog C (S. cerevisiae)
MTF2	0.50	metal response element binding transcription factor 2
PSMD14	0.50	proteasome 26S subunit, non-ATPase, 14
DCLRE1C	0.50	DNA cross-link repair 1C (PSO2 homolog, S. cerevisiae)

Supplemental Table 3: Myc target genes significantly up-regulated in 3D (and ≥1.5 fold)

Gene	Fold change	Response to Myc	Function
BTG1	3.28	Up-regulated	Tumor Suppressor
IGBP1	2.84	-	Receptor
NFIL3	2.77	-	Transcription factor
RRAS	2.67	-	-
LOX	2.61	Down-regulated	Extracellular matrix
GM2A	2.57	Down-regulated	Metabolism
NDRG1	2.40	Down-regulated	Differentiation, Proliferation
ADM	2.33	Down-regulated	Ligand, Stress Response
GBP2	2.23	Down-regulated	Signal Transduction
BCKDHA	2.21	-	Metabolism
ATP5G2	2.21	-	-
TSC2	2.14	-	Signal Transduction
HEBP1	2.12	-	-
CTSB	2.09	Down-regulated	Protein degradation
CTSF	2.04	-	Protease inhibitor , Protease
CRYAB	2.01	Down-regulated	Chaperones, Protein folding, Apoptosis
GABARAP	1.98	-	Cell structure
H2BFS	1.98	-	Chromatin
LAMP2	1.93	Down-regulated	Nucleolus, Immune response
FAH	1.92	-	Metabolism, Amino Acid
MXI1	1.91	Up-regulated	Transcription
GAA	1.90	Down-regulated	Carbohydrate degradation, Metabolism
HIST1H2BE	1.87	-	Chromatin
HSPB1	1.85	Down-regulated	Apoptosis, Protein folding
SRD5A1	1.83	-	Steroid, Metabolism
TIMM9	1.81	-	-
COX7A2L	1.81	-	Metabolism
ISG20	1.81	-	Miscellaneous
PEX6	1.80	-	-
JUNB	1.78	-	Transcription factor
MAN2B1	1.77	Down-regulated	Golgi processing enzyme, Metabolism
HIST1H2BH	1.76	-	Chromatin
POLD4	1.76	-	DNA replication
DDIT3	1.76	Down-regulated	Cell Proliferation
NFKBIL1	1.72	-	Signal Transduction
HBP1	1.69	-	Chromatin
SARS	1.68	-	Protein Synthesis
AKR7A2	1.67	-	Metabolism
SRRM2	1.66	-	-
MAP2K5	1.65	-	Signal Transduction
EXOSC5	1.65	Up-regulated	Metabolism, RNA
PTOV1	1.65	-	-
MEIS1	1.65	-	Transcription factor
DGCR6	1.62	-	Cell adhesion
PFKM	1.62	Up-regulated	Metabolism, Glycolysis

HIST2H2BE	1.61	-	Chromatin
PSAP	1.61	-	Lipid , Metabolism
SLC2A1	1.60	Up-regulated	Metabolism, Transport, Glycolysis
HIST1H2BI	1.59	-	Chromatin
HADHB	1.59	-	Metabolism
EEF2	1.58	Up-regulated	Protein Synthesis
HIST1H2BF	1.57	-	Chromatin
GDI1	1.56	Down-regulated	Signal Transduction
AP4M1	1.55	-	Transport
COX15	1.54	-	-
MAP4	1.53	Up-regulated	Cell structure
RAC2	1.53	-	Signal Transduction
MAPK3	1.52	Down-regulated	Signal Transduction
DDB1	1.51	-	DNA repair
ACYP2	1.51	-	Metabolism
PTPRF	1.51	-	Signal Transduction

Supplemental Table 4: Myc target genes significantly down-regulated in 3D (and ≤0.5 fold)

Gene	Fold change	Response to Myc	Function
HMMR	0.19	-	Receptor
CCNA2	0.21	Up-regulated	Cell Cycle
CDC2	0.23	Up-regulated	Cell Cycle
CDC6	0.27	-	Cell Cycle
FOXM1	0.27	-	Transcription factor
SFRS1	0.28	Up-regulated	RNA Processing
KIF20A	0.29	-	-
CCNB1	0.29	Up-regulated	Cell Cycle
FBN2	0.30	Up-regulated	Cell adhesion
MAD2L1	0.30	-	Cell Cycle
CASP8AP2	0.30	-	Apoptosis
DHFR	0.31	Up-regulated	Metabolism, DNA
BARD1	0.31	-	Signal Transduction
ARHGDIB	0.32	Up-regulated	Signal Transduction
USP1	0.32	-	Protein degradation
SLC20A1	0.33	Up-regulated	Transport
SFRS7	0.34	Up-regulated	Transcription, Splicing
LRP8	0.35	Up-regulated	Metabolism, Lipid
VRK1	0.35	Up-regulated	Nucleotide, DNA synthesis, Metabolism
COL4A2	0.36	-	Extracellular matrix, Cell adhesion
LBR	0.36	-	Nuclear regulatory factors
CKS2	0.37	Up-regulated	Cell Cycle
TYMS	0.38	Up-regulated	Metabolism
SFRS2	0.38	Up-regulated	RNA Processing
ATR	0.39	Up-regulated	DNA damage repair, Cell cycle checkpoint
MSH2	0.39	Up-regulated	Metabolism, DNA repair
ADAM9	0.39	Up-regulated	Signal Transduction
CD2AP	0.40	-	Cytoskeletal protein
DDX21	0.41	Up-regulated	Nucleolus, RNA binding proteins
PRKDC	0.41	-	DNA repair, Chromatin
TFRC	0.41	Up-regulated	Transport, Metabolism, Iron
NCBP1	0.41	-	RNA binding proteins
GGH	0.41	Up-regulated	Protein degradation
ITGA6	0.42	-	Cell adhesion, Extracellular matrix
PPP1R12A	0.42	-	-
MCM7	0.43	-	Chromatin, DNA repair
TOP1	0.43	Up-regulated	DNA modification, DNA repair
MAP4K5	0.44	-	Signal Transduction
H2AFX	0.45	-	Chromatin
PMS1	0.45	-	DNA repair
EIF4E	0.45	Up-regulated	Translation, Protein Synthesis
IER3	0.46	Down-regulated	Apoptosis
RFC4	0.46	Up-regulated	Nucleotide, Metabolism, DNA synthesis
EXO1	0.46	-	-
MCM6	0.46	Up-regulated	DNA replication

RBBP8	0.46	-	Cell Cycle
FBXO5	0.46	-	-
CUL5	0.46	-	-
AKAP9	0.47	-	Signal Transduction
DCK	0.47	-	Nucleotide, Metabolism
PCNA	0.47	Up-regulated	Cell Cycle
AGPS	0.47	-	Metabolism
SCD	0.47	-	Metabolism, Lipid
MCM3	0.47	-	DNA replication
SSB	0.48	-	RNA Processing
FASN	0.48	Up-regulated	Lipid , Metabolism
ZMPSTE24	0.48	-	Membrane protein
TOPBP1	0.48	-	DNA modification
RANBP1	0.48	Up-regulated	RNA transport, Protein
MCM4	0.48	Up-regulated	Metabolism, DNA synthesis, Nucleotide
CDC25C	0.49	Up-regulated	Cell Cycle
MAN2A1	0.49	-	Metabolism
MCM5	0.49	-	DNA replication
HNRPDL	0.49	-	RNA binding proteins, Nucleolus
H2AFZ	0.49	Up-regulated	Chromatin
THBS1	0.49	Down-regulated	Angiogenesis, Metastasis
UBE2C	0.49	Up-regulated	Protein Synthesis, Degradation
TK1	0.50	Up-regulated	DNA enzyme, Metabolism
SUCLA2	0.50	Down-regulated	Metabolism
MYO1B	0.50	Down-regulated	Cytoskeletal protein
EEF1E1	0.50	-	Protein Synthesis
TFAM	0.50	Up-regulated	Immune response

Supplemental Table 5: Calculation of Myc overexpression in 3D relative to 2D

Sample	IR Signal (Normalized to Acti	Femtomoles per 10^5 cell	Molecules per cel	Fold overexpression
Lane 1: lacZ	0	0	0	0
Lane 2: WT Myc	64.8	33.0	198817	7.1
Lane 3: T58A Myc	90.7	46.2	278174	9.9
Lane 4: S62A Myc	114.3	58.2	350600	12.4
Lane 5: T58A S62A Myc	123.8	63.0	379505	13.5
Lane 6: ΔCPD Myc	81.4	41.4	249555	8.9
Lane 7: ΔMBII Myc	50.3	25.6	154293	5.5
Lane 8: ΔMBIII Myc	53.0	27.0	162457	5.8
Standard Curve (signal/femtomole)	2.0			
0 femtomoles	0			
50 femtomoles	96.4			
100 femtomoles	198.2			
2D endogenous Myc (Adeno-lacZ)	0.26	4.7	28178	1
Standard Curve (signal/femtomole)	0.06			
0 femtomoles	0			
100 femtomoles	5.7			
200 femtomoles	11.0			