

**SUPPLEMENTAL TABLE 1 - TOP 50 GENES UP-REGULATED - BY FOLD-CHANGE**

Gene Symbol	Gene Name	Systematic Nomenclature	log <sub>2</sub> Fold Change	Adjusted p-Value
SEMA3D	Sema domain, cytoplasmic, similar to dynein	NM_152754	3.47	0.0245
REG4	Regenerating islet-derived family, member 4	NM_032044	3.09	0.0119
GBA2	Beta-2 glucosidase	NM_020944	2.94	0.0186
NUPR1	Nuclear protein-1	NM_001042483	2.77	0.0122
ATF3	Activating transcription factor 3	NM_001040619	2.70	0.0203
BBC3	BCL2 binding component 3	NM_014417	2.67	0.0091
AGR2	Anterior gradient homolog 2	NM_006408	2.65	0.0234
TRIB3	Tribbles homolog 3	NM_021158	2.58	0.0203
FAM20A	Family with sequence similarity 20, member A	NM_017565	2.53	0.0426
KIF26A	Kinesin family member 26A	BC009415	2.45	0.0152
KCNN4	Potassium intermediate/small conductance calcium-activated channel, subfamily N, member 4	NM_002250	2.38	0.0264
ARMC9	armadillo repeat containing 9	NM_025139	2.36	0.0125
DDIT3	DNA-damage-inducible transcript 3	NM_004083	2.34	0.0125
DDIT4	DNA-damage-inducible transcript 4	NM_019058	2.33	0.0119
JDP2	Jun dimerization protein 2	NM_130469	2.29	0.0185
HPGD	Hydroxyprostaglandin dehydrogenase 15-(NAD)	NM_000860	2.28	0.0125
MAPT	Microtubule-associated protein tau	NM_016835	2.26	0.0186
ASNS	Asparagine synthetase and olfactory receptor, family 7, subfamily E, member 38 pseudogene	NM_001673	2.25	0.0487
NUDT8	Nudix (nucleoside diphosphate linked moiety X)-type motif 8	NM_181843	2.23	0.0146
LFNG	O-fucosylpeptide 3-beta-N-acetyl-glucosaminyltransferase	NM_001040167	2.23	0.0221
TncRNA	Trophoblast-derived noncoding RNA	NR_002802	2.22	0.0178
KIAA1881	KIAA1881	AB067468	2.12	0.0321
PRAC	Small nuclear protein PRAC	NM_032391	2.12	0.0130
ZNF467	Zinc finger protein 467	BC038972	2.09	0.0286
CDH1	Cadherin 1, type 1, E-cadherin (epithelial)	NM_004360	2.08	0.0336
SLC7A11	Solute carrier family 7, (cationic amino acid transporter) member 11	NM_014331	2.03	0.0209
ATF4	Activating transcription factor 4	NM_001675	2.03	0.0176
SESN2	Sestrin 2	NM_031459	1.99	0.0206
FCGR2A	Fc fragment of IgG, low affinity IIa, receptor (CD32)	NM_021642	1.98	0.0334
CHRM3	Cholinergic receptor, muscarinic 3	NM_000740	1.97	0.0218
IFIT2	Interferon-induced protein with tetratricopeptide repeats 2	NM_001547	1.97	0.0396
KIAA1370	KIAA1370	NM_019600	1.96	0.0267
TRPM4	Transient receptor potential cation channel, subfamily M, member 4	NM_017636	1.92	0.0352
RBCK1	RanBP-type and C3HC4-type zinc finger containing	NM_031229	1.90	0.0344
KDR	Kinase insert domain receptor (a type III receptor tyrosine kinase)	NM_002253	1.89	0.0456
PCK2	Phosphoenolpyruvate carboxykinase 2	NM_004563	1.88	0.0295
CTH	Cystathionase (cystathionine gamma-lyase)	NM_001902	1.81	0.0320
SMARCD3	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily d, member 3	NM_003078	1.81	0.0337
PPL	Periplakin	NM_002705	1.80	0.0266
FGF13	Fibroblast growth factor 13	NM_004114	1.80	0.0270
RNASE4	Ribonuclease, RNase A family, 4	NM_194430	1.79	0.0493
KRT15	Keratin 15	NM_002275	1.77	0.0330
TFPI	Tissue factor pathway inhibitor	NM_001032281	1.75	0.0427
AXIIR	Annexin II receptor-like	NM_001014279	1.75	0.0186
KRT75	Keratin 75	NM_004693	1.74	0.0399
MITF	Microphthalmia-associated transcription factor	NM_198159	1.72	0.0264
SCD	Stearoyl-CoA desaturase (delta-9-desaturase)	NM_005063	1.71	0.0270
SARS	Seryl-tRNA synthetase	NM_006513	1.71	0.0329
RHOBTB1	Rho-related BTB domain containing 1	NM_014836	1.68	0.0393
NPNT	Nephronectin	NM_001033047	1.67	0.0372

**SUPPLEMENTAL TABLE 2 - TOP 50 GENES DOWN-REGULATED - BY FOLD-CHANGE**

Gene Symbol	Gene Name	Systematic Nomenclature	log <sub>2</sub> Fold Change	Adjusted p-Value
GLIS3	GLIS family zinc finger 3	NM_001042413	-2.77	0.0395
E2F1	E2F transcription factor 1	NM_005225	-2.78	0.0389
DHFR	Dihydrofolate reductase	NM_000791	-2.79	0.0178
GINS2	GINS complex subunit 2 (Psf2 homolog)	NM_016095	-2.83	0.0223
TNFAIP2	Tumor necrosis factor, alpha-induced protein 2	NM_006291	-2.84	0.0091
ESCO2	Establishment of cohesion 1 homolog 2	NM_001017420	-2.86	0.0258
CDC2	Cell division cycle 2, G1 to S and G2 to M	NM_001786	-2.88	0.0332
PRIM1	Primase, polypeptide 1	NM_000946	-2.95	0.0158
ID1	Inhibitor of DNA binding 1, dominant negative helix-loop-helix protein	NM_002165	-2.96	0.0372
FAM54A	Family with sequence similarity 54, member A	NM_138419	-2.97	0.0122
PCNA	Proliferating cell nuclear antigen	NM_002592	-3.00	0.0091
G0S2	G0/G1 switch 2	NM_015714	-3.01	0.0091
KNTC2	Kinetochore complex component (NDC80 homolog)	NM_006101	-3.02	0.0146
DCC1	Defective in sister chromatid cohesion homolog 1	NM_024094	-3.03	0.0125
TFPI2	Tissue factor pathway inhibitor 2	NM_006528	-3.04	0.0170
ATAD2	ATPase family, AAA domain containing 2	NM_014109	-3.05	0.0426
ZWINT	ZW10 interactor	NM_001005414	-3.06	0.0091
CCDC74B	Coiled-coil domain containing 74B	NM_207310	-3.07	0.0091
UHRF1	Ubiquitin-like, containing PHD and RING finger domains, 1	NM_013282	-3.08	0.0122
AKR1B10	Aldose reductase family 1, member B10	NM_020299	-3.08	0.0270
LCP1	Lymphocyte cytosolic protein 1 (L-plastin)	NM_002298	-3.19	0.0245
NCAPG	Non-SMC condensin I complex, subunit G	NM_022346	-3.21	0.0119
SGK	Serum/glucocorticoid regulated kinase	NM_005627	-3.26	0.0146
NFKBIA	Nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, alpha.	NM_020529	-3.27	0.0091
MAD2L1	MAD2 mitotic arrest deficient-like 1	NM_002358	-3.29	0.0360
PI3	Peptidase inhibitor 3	NM_002638	-3.30	0.0134
CDC45L	CDC45 cell division cycle 45-like	NM_003504	-3.32	0.0342
RNF182	Ring finger protein 182	NM_152737	-3.32	0.0224
KIAA0101	KIAA0101 and casein kinase 1, gamma 1	NM_014736	-3.32	0.0334
RAD51	RAD51 homolog (RecA homolog)	NM_002875	-3.33	0.0099
SPBC25	SPC25, NDC80 kinetochore complex component, homolog	NM_020675	-3.35	0.0125
DTL	Denticleless homolog	NM_016448	-3.37	0.0144
PLAU	Plasminogen activator, urokinase	NM_002658	-3.40	0.0271
C3	Complement component 3	NM_000064	-3.43	0.0176
CDH11	Cadherin 11, type 2, OB-cadherin	NM_001797	-3.50	0.0447
TK1	Thymidine kinase 1, soluble	NM_003258	-3.57	0.0091
GJB2	Gap junction protein, beta 2	NM_004004	-3.60	0.0264
SAA1	Serum amyloid A1	NM_000331	-3.60	0.0237
BIRC3	Baculoviral IAP repeat-containing 3	NM_001165	-3.63	0.0152
RRM2	Ribonucleotide reductase M2 polypeptide	NM_001034	-3.65	0.0227
BEX1	Brain expressed, X-linked 1	NM_018476	-3.99	0.0423
SERPINB4	Serpin peptidase inhibitor, clade B, member 4	NM_002974	-4.09	0.0267
COL13A1	Collagen, type XIII, alpha 1	NM_005203	-4.09	0.0264
CXCL2	Chemokine (C-X-C motif) ligand 2	NM_002089	-4.13	0.0134
LCN2	Lipocalin 2 (oncogene 24p3)	NM_005564	-4.18	0.0178
CYB5R2	Cytochrome b5 reductase 2	NM_016229	-4.53	0.0122
TYMS	Thymidylate synthetase	NM_001071	-4.53	0.0237
IL1B	Interleukin 1, beta	NM_000576	-5.15	0.0091
SERPINB3	Serpin peptidase inhibitor, clade B, member 3	NM_006919	-5.56	0.0091
CXCL1	Chemokine (C-X-C motif) ligand 1	NM_001511	-6.18	0.0091

**SUPPLEMENTAL TABLE 3 - BIOLOGICAL PROCESS GO TERMS THAT HAVE A SIGNIFICANT OVER-REPRESENTATION ( $P < 0.001$ ) OF GENES FOUND TO BE SIGNIFICANTLY DIFFERENTIALLY EXPRESSED BY *PRKCZ* KNOCKDOWN**

<b>GO ID</b>	<b><i>p</i>-value</b>	<b>Term</b>
GO:0022402	2.60E-26	cell cycle process
GO:0000279	1.67E-22	M phase
GO:0000278	9.22E-20	mitotic cell cycle
GO:0051301	9.25E-19	cell division
GO:0006260	1.61E-17	DNA replication
GO:0006281	7.17E-15	DNA repair
GO:0007067	1.21E-14	mitosis
GO:0007059	1.06E-10	chromosome segregation
GO:0006950	6.50E-09	response to stress
GO:0000724	6.64E-08	double-strand break repair via homologous recombination
GO:0006297	4.49E-07	nucleotide-excision repair, DNA gap filling
GO:0007051	9.54E-07	spindle organization and biogenesis
GO:0007093	1.12E-06	mitotic cell cycle checkpoint
GO:0007049	3.03E-06	cell cycle
GO:0051303	4.19E-06	establishment of chromosome localization
GO:0000070	1.10E-05	mitotic sister chromatid segregation
GO:0006996	1.41E-05	organelle organization and biogenesis
GO:0000075	3.15E-05	cell cycle checkpoint
GO:0007126	4.53E-05	meiosis
GO:0051052	4.53E-05	regulation of DNA metabolic process
GO:0006268	5.50E-05	DNA unwinding during replication
GO:0051321	5.58E-05	meiotic cell cycle
GO:0006270	5.93E-05	DNA replication initiation
GO:0007018	5.95E-05	microtubule-based movement
GO:0048015	0.000105762	phosphoinositide-mediated signaling
GO:0006139	0.000107285	nucleobase, nucleoside, nucleotide and nucleic acid metabolic process
GO:0032392	0.000107904	DNA geometric change
GO:0007088	0.000111507	regulation of mitosis
GO:0051329	0.000120198	interphase of mitotic cell cycle
GO:0031577	0.00012838	spindle checkpoint
GO:0042770	0.00018963	DNA damage response, signal transduction
GO:0031570	0.000190839	DNA integrity checkpoint
GO:0008156	0.00024533	negative regulation of DNA replication
GO:0007017	0.000247312	microtubule-based process
GO:0006310	0.000255543	DNA recombination
GO:0000079	0.000272498	regulation of cyclin-dependent protein kinase activity
GO:0006312	0.000349485	mitotic recombination
GO:0007079	0.000356715	mitotic chromosome movement towards spindle pole
GO:0030261	0.000581281	chromosome condensation
GO:0006261	0.00079167	DNA-dependent DNA replication

**SUPPLEMENTAL TABLE 4 - MOLECULAR FUNCTION GO TERMS THAT HAVE A SIGNIFICANT OVER-REPRESENTATION ( $P < 0.001$ ) OF GENES FOUND TO BE SIGNIFICANTLY DIFFERENTIALLY EXPRESSED BY *PRKC-Z* KNOCKDOWN**

<b>GO ID</b>	<b><i>p</i>-value</b>	<b>Term</b>
GO:0046870	7.24E-06	cadmium ion binding
GO:0005515	3.25E-05	protein binding
GO:0003689	5.89E-05	DNA clamp loader activity
GO:0005524	6.13E-05	ATP binding
GO:0030554	6.34E-05	adenyl nucleotide binding
GO:0008094	6.67E-05	DNA-dependent ATPase activity
GO:0003777	7.26E-05	microtubule motor activity
GO:0005507	0.000196362	copper ion binding
GO:0016725	0.000200742	oxidoreductase activity, acting on CH or CH2 groups
GO:0003680	0.000333573	AT DNA binding
GO:0004360	0.000333573	glutamine-fructose-6-phosphate transaminase (isomerizing) activity
GO:0003678	0.000408806	DNA helicase activity
GO:0043142	0.000988605	single-stranded DNA-dependent ATPase activity

**SUPPLEMENTAL TABLE 5 - TOP FOUR NETWORKS AFFECTED BY siRNA KNOCKDOWN**

<b>ID</b>	<b>MOLECULES IN NETWORK</b>	<b>SCORE</b>	<b>FOCUS MOLECULES</b>	<b>TOP FUNCTIONS</b>
1	ACAT1, ADFP, Angiotensin II receptor type 1, APOBEC3F, APOBEC3G, ATF3, BIRC2, BIRC3, C8, CCL20, CXCL10, GBP1 (includes EG:2633), ICAM1, Ifn gamma, IKK, IL1B, INDO, Interferon alpha, IRF7, LCP1, LDL, MAP4K4, MHC Class II, MX1, NDN, NFE2L1, Nfkb-RelA, P2RX7, PMAIP1, S100A8, S100A9, Sod, SYK/ZAP, TYROBP, UAP1	42	25	Cell-To-Cell Signaling and Interaction, Hematological System Development and Function, Immune and Lymphatic System Development and Function
2	ARRB1, ASB2, B2M, Cbp/p300, CCDC90B, CDKN2C, Ck2, CRCT1, DNAJC10, EEF1A1, EGR1, Histone h3, Hsp70, Hsp90, HSPA5, Jnk, MAGEA11, MAOB, MCFD2, MRE11A, NFKBIA, NPM1 (includes EG:4869), PDGF BB, POLR1E, Proteasome, PRSS35, PSMB8, PSMB9, RNA polymerase II, SGK1, STC2, TPM4, UBD, Ubiquitin, ZNF259	42	25	Cancer, Cell Death, Cellular Growth and Proliferation
3	ADRA2C, CAMK2N1, CCL2, COL13A1, CXCL3, DPYSL2, ERK, Fibrin, FN1, HTRA1, IL1, IL8, INHBA, Interferon beta, LCN2, LOXL1, Mac1, Mmp, MMP1 (includes EG:4312), MTSS1, NAMPT, Pdgf, PDGFC, PLAT, PLAU, PTPRR, RANBP9, SAA1, SAA2, SAA4, SAA@, Sos, SP100, STAT, Tgf beta	39	24	Cardiovascular Disease, Digestive System Development and Function, Hepatic System Development and Function
4	B4GALT1, BEX1 (includes EG:55859), C3, C1q, CFB, Complement component 1, CXCL2, CXCL6, DBT, ETS, GBP2, HLA-C, HLA-G, I kappa b kinase, IFN Beta, IgG, Igm, IHPK2, IL12, IL32, KYNU, LMO2, LTB, NF-&kappa;B, NFkB, peptidase, PI3, PPP2R5C, PTX3, ROBO4, S100A4, SLIT2, Tlr, TNIP1, VISA	37	23	Protein Synthesis, Cellular Growth and Proliferation, Hematological System Development and Function

A score of  $x$  is  $p=10^{-x}$ .  $x$ : score,  $p$ :  $p$ -value.

**SUPPLEMENTAL TABLE 6**

**PREVIOUS siRNA KNOCKDOWN STUDIES AND TARGETS FOR *PRKC-ζ***

<b>Human cell-line</b>	<b>siRNA source</b>	<b>Published DNA target or siRNA sequence employed</b>	<b>Exon location within human <i>PRKC-ζ</i></b>	<b>Human <i>PRKC-ζ</i><sup>+</sup> variants</b>	<b>Other genes identified</b>	<b>Reference</b>
18Co	Ambion	5'-AAGACGACACATGTCTCTCACCTGTCTC-3'	8	a,b,h,l,vf,vl	<i>MARKLOY</i> <i>ZFYVE26</i>	(Di Mari <i>et al</i> , 2003)
786-O	Bespoke	5'-GTGAGAGACATGTGTCGTCTTCAA-3'	8	a,b,h,l,vf,vl	<i>KITARI</i>	(Datta <i>et al</i> , 2004)
HUVECs	Upstate*	<i>[Sequence not defined]</i>	-	-	-	(Reese <i>et al</i> , 2005)
MRC-5	Invitrogen*	<i>[Sequence not defined]</i>	-	-	-	(Hernandez-Pigeon <i>et al</i> , 2005)
TSU-pr1 <sup>*P</sup>	Dharmacon*	<i>[Sequence not defined]</i>	-	-	-	(Even-Faitelson <i>et al</i> , 2006)
L6 myotubes	Dharmacon	5'-GAACGAUGGUGUAGACCUU-3'	N/I	N/A	N/A	(Sajan <i>et al</i> , 2006)
		5'-GGAAACAUGACAAUAUCAA-3'	N/I	N/A	<i>REYCHARBY</i>	
		5'-GCUGAGAUCUGUAUCGCUC-3'	N/I	N/A	N/A	
		5'-GCAUGCCGAUGGACACAAUU-3'	N/I	N/A	N/A	
Caco-2	Ambion	5'-GGAAGUGAGAGAACAUGUGU-5'	N/I	N/A	<i>KERARA</i>	(Mustafi <i>et al</i> , 2006)
HeLa	Dharmacon*	<i>[Sequence not defined]</i>	-	-	-	(Liu <i>et al</i> , 2006)
JAR	Ambion*	<i>[Sequence not defined]</i>	-	-	-	(Zhang <i>et al</i> , 2006)
A431	Bespoke	5'-GTGAGAGACATGTGTCGTCTTCAA-3'	8	a,b,h,l,vf,vl	<i>KITARI</i>	(Singh <i>et al</i> , 2007)

Chondrocytes	Bespoke	5'-GAGAAGCACGTGTTTGAGC-3'	8	a,b,c,d,f,g,h,p,va,- b	CD93	(Chockalingam <i>et al</i> , 2007)
HUVECs	Santa Cruz*	[Sequence not defined]	-	-	-	(Choi <i>et al</i> , 2008)
Caco-2	Bespoke	5'-AUGAUCAGAUCUAUGCCAUGA-3'	N/I	N/A	N/A	(Frankenberg <i>et al</i> , 2008)
Huh7	Ambion*	[Sequence not defined]	-	-	-	(Prudencio <i>et al</i> , 2008)
LN-229	Bespoke	5'-GAGGAAGTGAGAGACATGTGT-3'	8	a,b,h,l,vf,vl	None	(Guo <i>et al</i> , 2009a)
THP-1	Bespoke	5'-GAGGAAGTGAGAGACATGTGT-3'		a,b,h,l,vf,vl	None	(Guo <i>et al</i> , 2009b)
Caco-2	Bespoke	5'-GACGACAAGAACGAGGACG-3'	50	a,b,c,d,f,g,h,k,p,t,- b,vc,vd,vh,vj,vo,vr	None	(Thongon <i>et al</i> , 2009)
AKI	Invitrogen*	[Sequence not defined]	-	-	-	(Kai <i>et al</i> , 2009)
PC3-M <sup>*P</sup>	Bespoke	5'-GTGAGAGACATGTGTCGTCTT-3'	8	a,b,h,l,vf,vl	None	(Yao, 2010)

**KEY:** \*P : Prostatic carcinoma cells  
N/I : Not identified  
N/A : Not applicable  
† : AceView Release 36, April 2007  
\* : Sequence could not be identified or accurately predicted from information provided