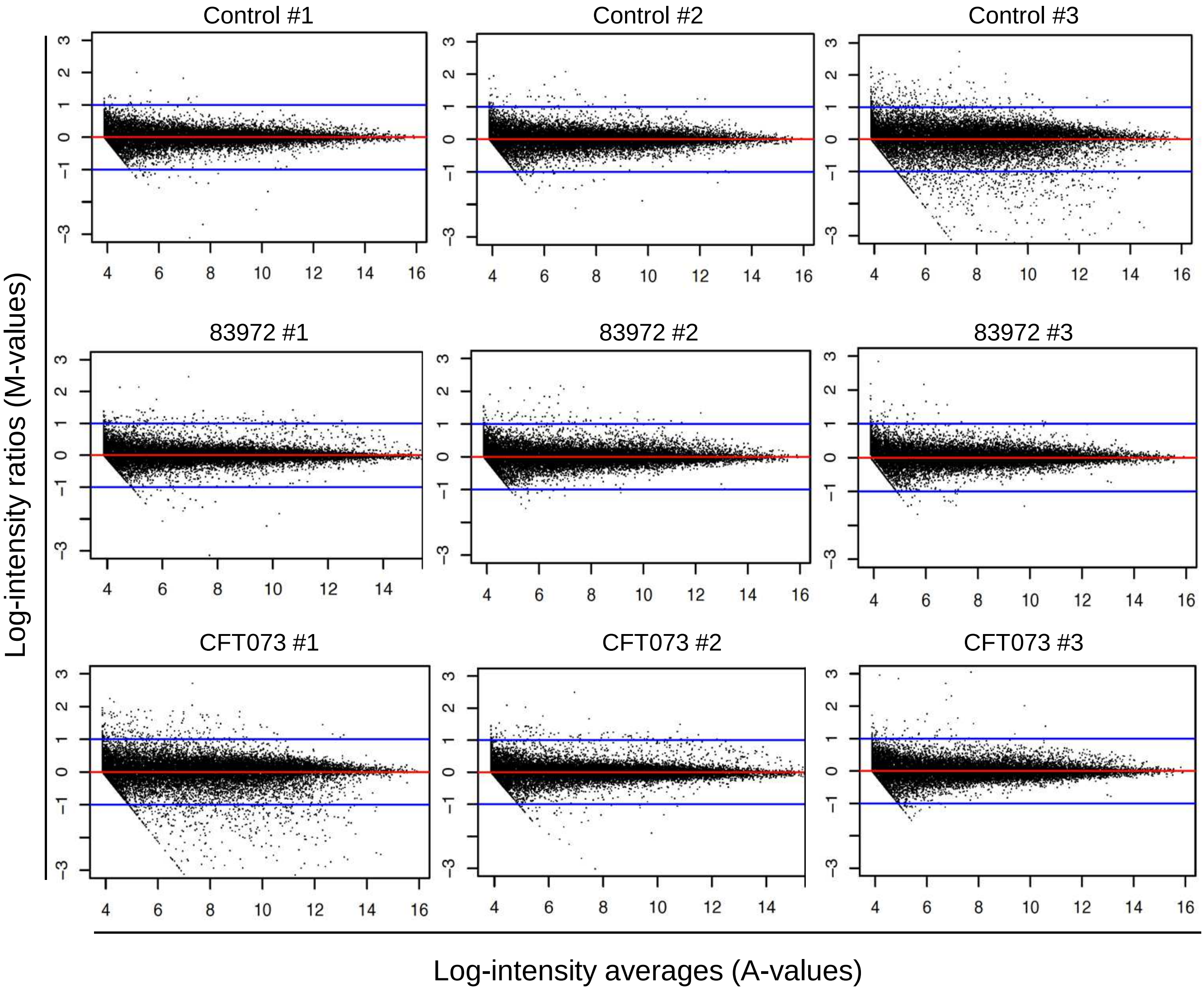
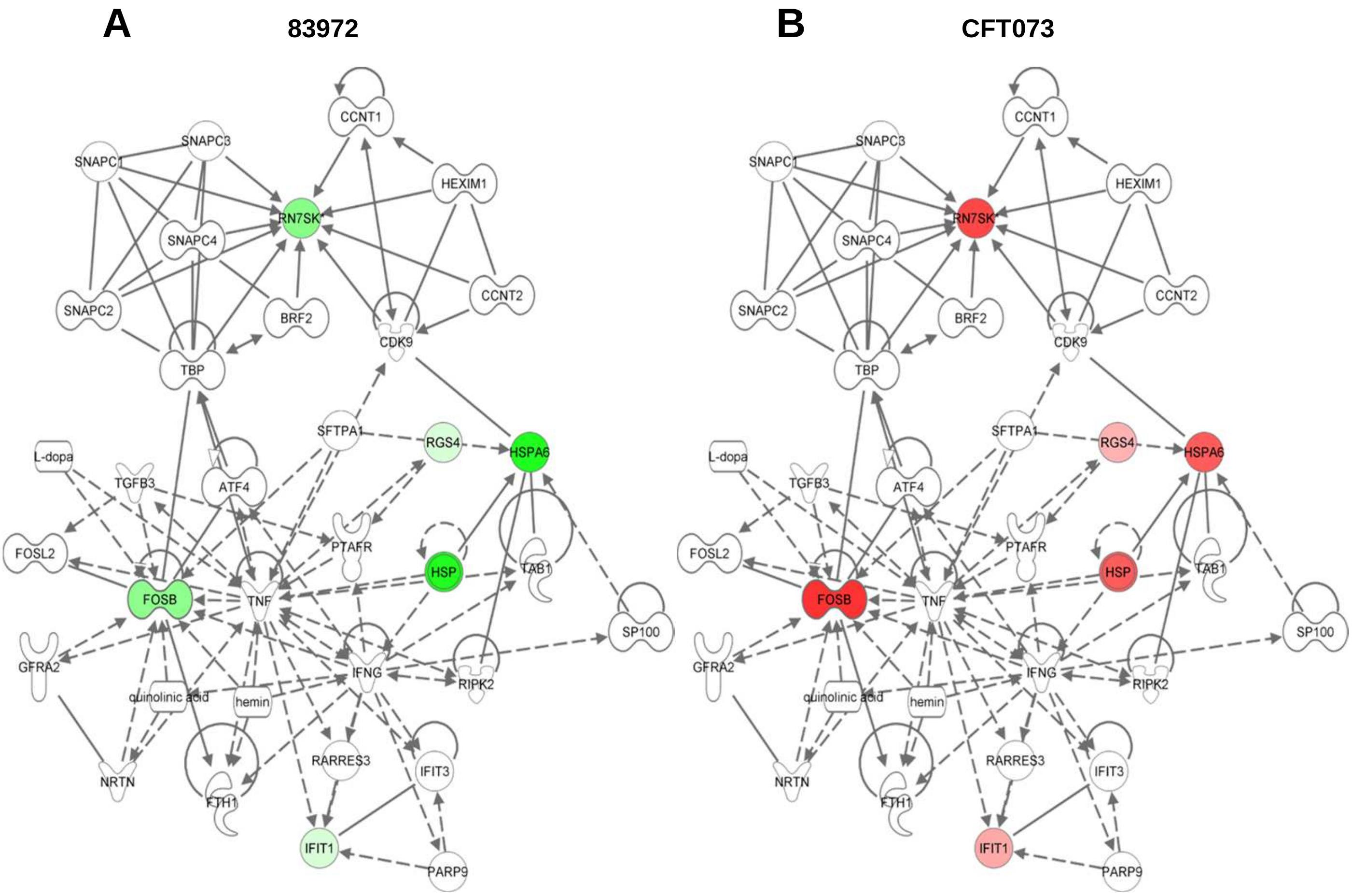


Supplemental Figure 1. MA-plots showing normalized raw data using cross-correlation.

The data was found to be of high quality with high replicate correlation (correlation>0.98) and with no systematic bias.



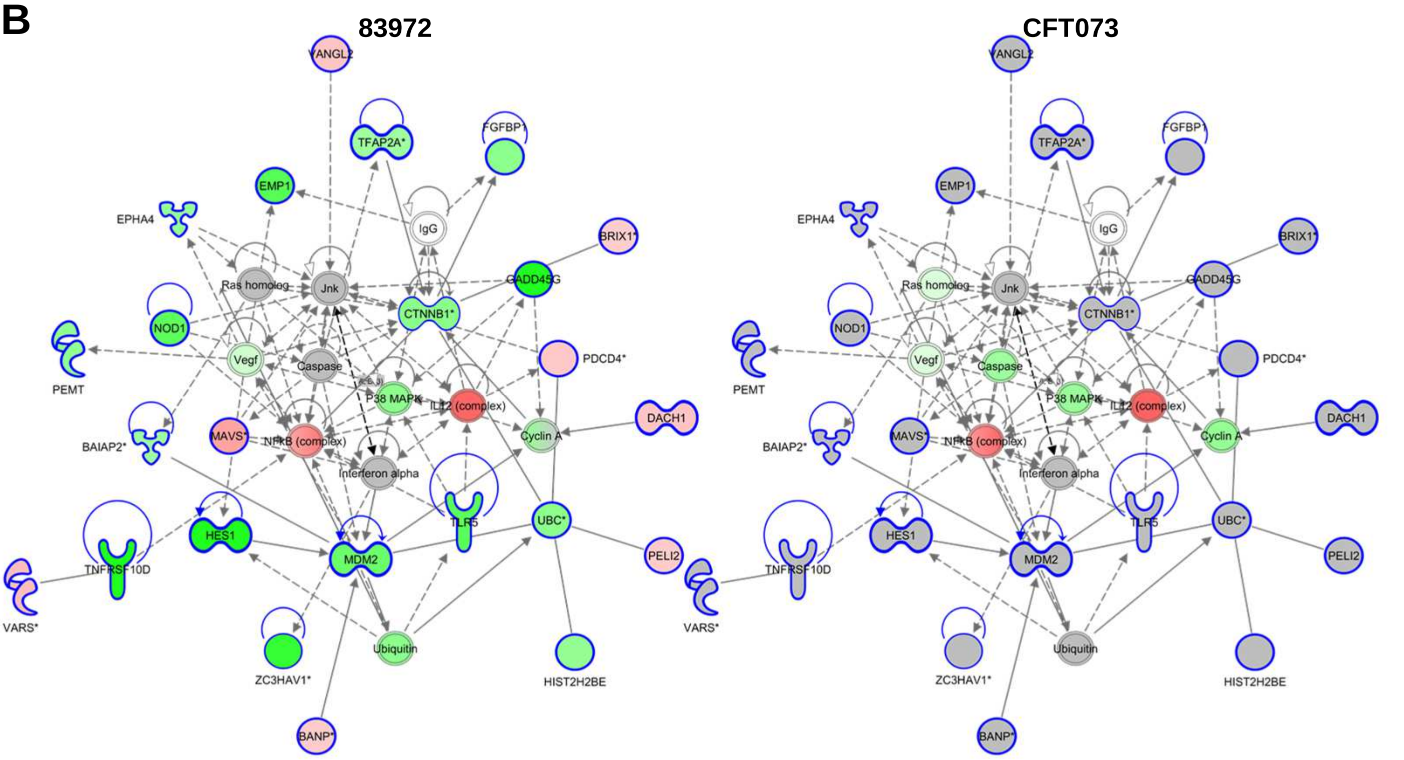
Supplemental Figure 2. Inversely regulated gene networks generated by IPA.

The five inversely regulated genes belonged to one functional network in which HSPA6, FOSB and RN7SK interact with TATA box binding protein (TBP), a general transcription factor required for RNA polymerase II activity. The ABU strain 83972 (**A**) suppressed *FOSB* and other genes in this network while the CFT073 strain (**B**) enhanced their expression. 83972 also suppressed *RGS4*, a negative regulator of G-protein-coupled receptor-induced signaling and *IFIT1*, a gene of the type I IFN signaling pathway essential for the antibacterial effector response.

A

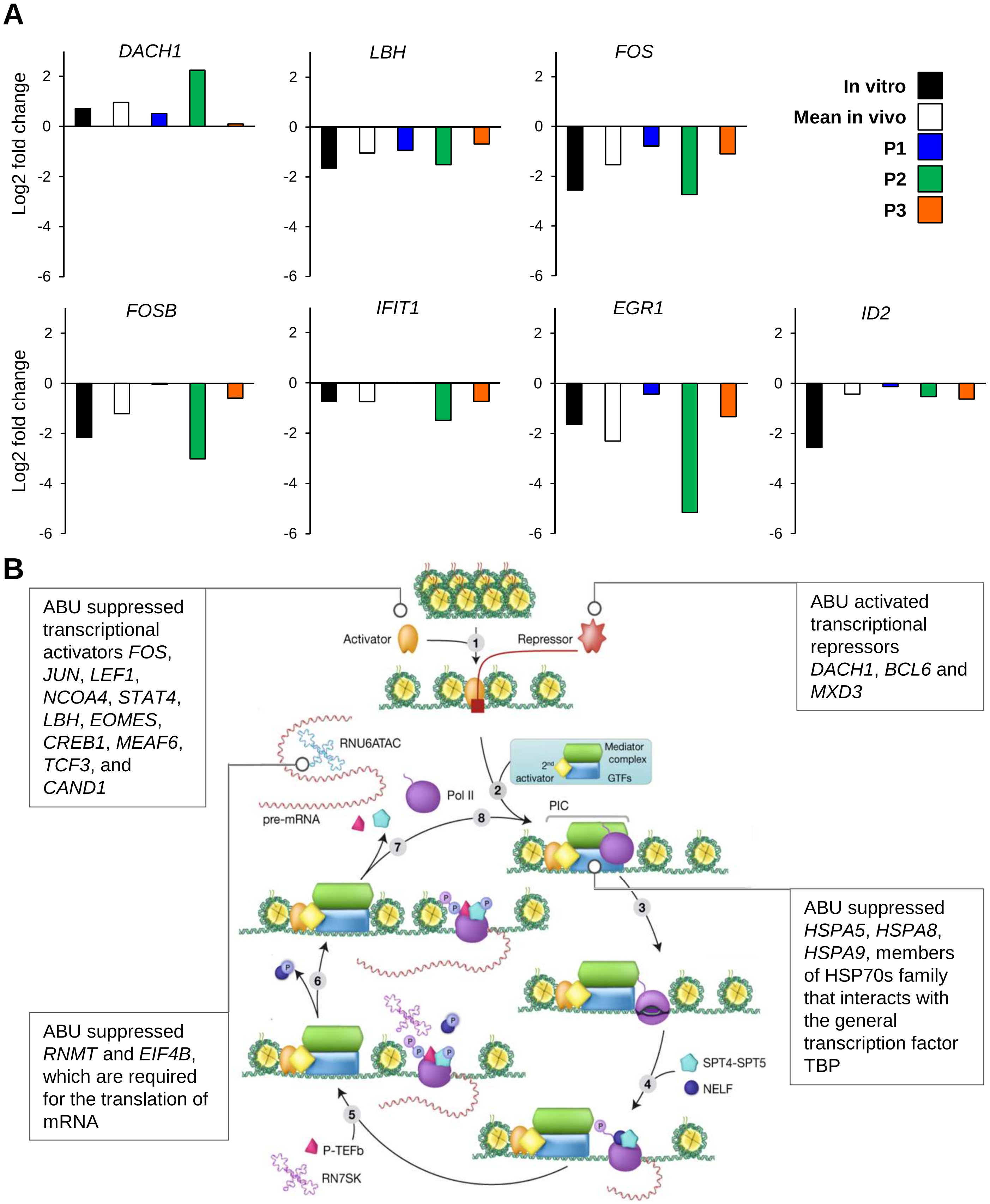
Network genes	Score	No of affected genes	Top functions
BAIAP2, BANP, BRIX1, Caspase, CTNNB1, Cyclin A, DACH1, EMP1, EPHA4, FGFBP1, GADD45G, HES1, HIST2H2BE, IgG, IL12, Interferon α, Jnk, MAVS, MDM2, NFkB, NOD1, P38 MAPK, PDCD4, PELI2, PEMT, Ras homolog, TFAP2A, TLR5, TNFRSF10D, UBC, Ubiquitin, VANGL2, VARS, Vegf, ZC3HAV1	51	24	Infection Mechanisms, Infectious Disease, Endocrine System Development and Function
AHCTF1, AKR1C2, ALOX5AP, ARL4A, BAMBI, BAZ2B, Bcl9-Cbp/p300-Ctnnb1-Lef/Tcf, BRF2, CA9, Ca2+, CNN2, CRIP1, CTNNB1, CTNNβ-LEF1, DDX20, DKK3, ECM1, EXOC1, FAM27E3, HIF1A, HIST1H2AC, MYC, OSR2, PDXDC2, PRNP, RCN1, RPL41, SOX4, SOX17, TAX1BP3, TCF4-CTNNβ, TGFB1, TRIM9, TRPM8, TYRP1	27	15	Small Molecule Biochemistry, Cellular Development, Cellular Growth and Proliferation
ARRDC3,CYP26B1,DBF4,DHCR24,E2F4,ETV3,FAM105A,FAM63A,FKBP3,FKBP9,LHX1,MT1L,MYCN,NAA38,POLA1,POLH,PRIM1,PRIM2,REST,RNF40,RPL11,RPL23,RPL26,RPS13,SMC2,TAGLN,TFAP4,TNF,TOP2B,TP53,TP53I3,TP53INP1,UBE2E3,ZBTB11,ZNF451	17	10	Infection Mechanisms, Cancer, Gene Expression
ARHGAP32, ARL4D, CALD1, CNPY2, Cofilin, DNAJA1, EIF3CL, EPHA2, ERBB2IP (includes EG:55914), HRAS, IL24, KRAS, KSR1, MBOAT2, Mrlc, MYH10, MYL12B, MYLIP, NFkB, PPFIBP1, PTPRJ, RABGEF1, Raf, RAP1GDS1, RARRES3, RASA1, RASGRF1, RASSF1, S100A4, SCNN1A, SHOC2, TCOF1, TNFRSF10A (includes EG:8797), TNFRSF10B, TOP2A	10	6	Cancer, Cell Morphology, Cellular Assembly and Organization

B



Supplemental Figure 3. 83972 specific networks.

(**A**) The top four networks are shown. (**B**) 83972-specific gene network of 24 genes including transcriptional repressors (*DACH1*, *PDCD4*, *BANP*), transcription factors (*HES1*, *MDM2*), innate immunity receptors (*TLR5*, *NOD1*), genes involved in TNF signaling (*TNFRSF10D*, *TFAP2A*), G-protein signaling (*BAIAP2*) and activators of MAPK signaling (*GADD45G*, *FGFBP1*). These genes were unaffected by the CFT073 strain (green=down-regulated, red=upregulated, grey=genes expressed at basal level, blue=83972 specific genes).



ABU suppressed transcriptional activators *FOS*, *JUN*, *LEF1*, *NCOA4*, *STAT4*, *LBH*, *EOMES*, *CREB1*, *MEAF6*, *TCF3*, and *CAND1*

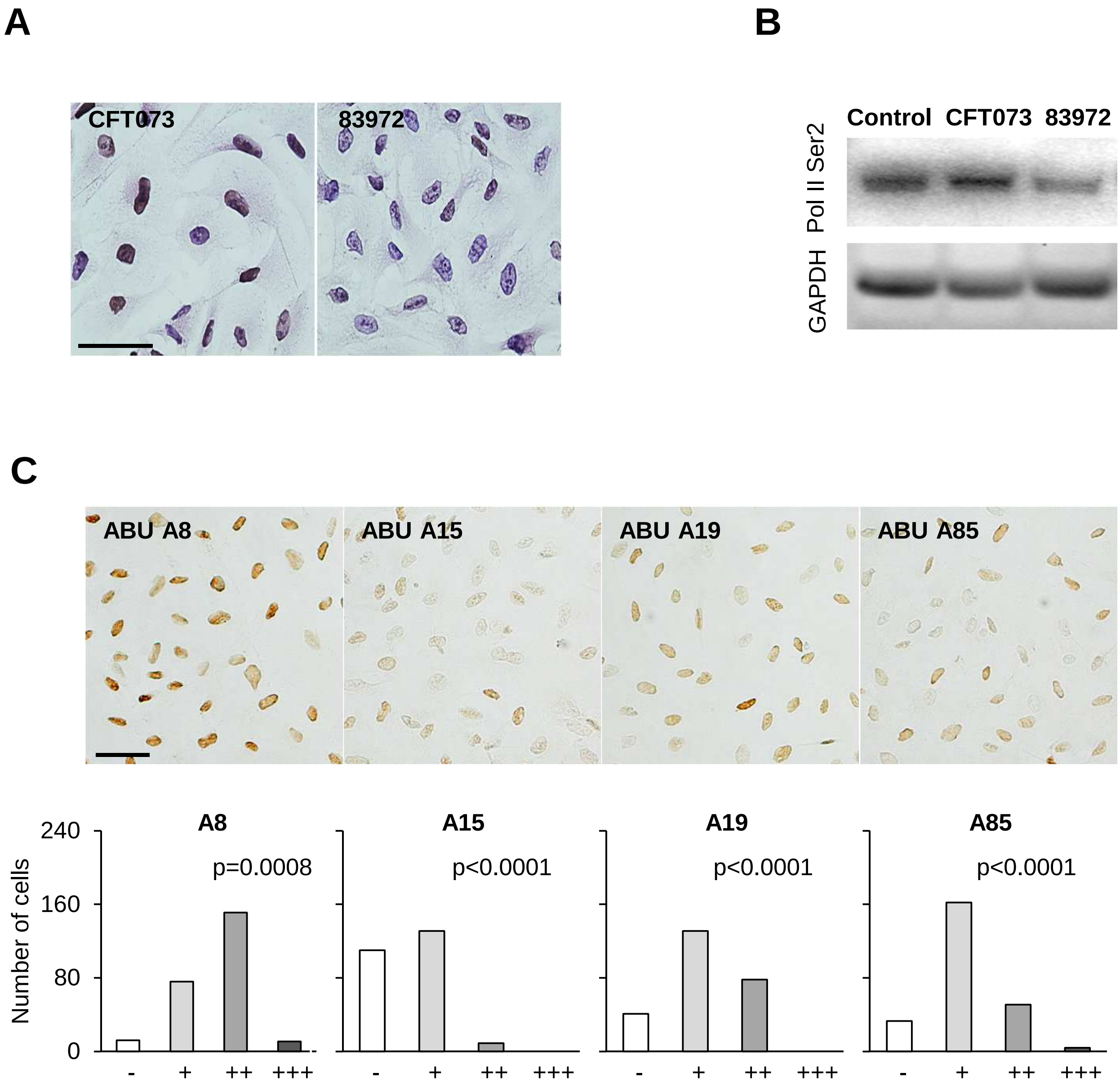
ABU activated transcriptional repressors *DACH1*, *BCL6* and *MXD3*

ABU suppressed *HSPA5*, *HSPA8*, *HSPA9*, members of HSP70s family that interacts with the general transcription factor TBP

ABU suppressed *RNMT* and *EIF4B*, which are required for the translation of mRNA

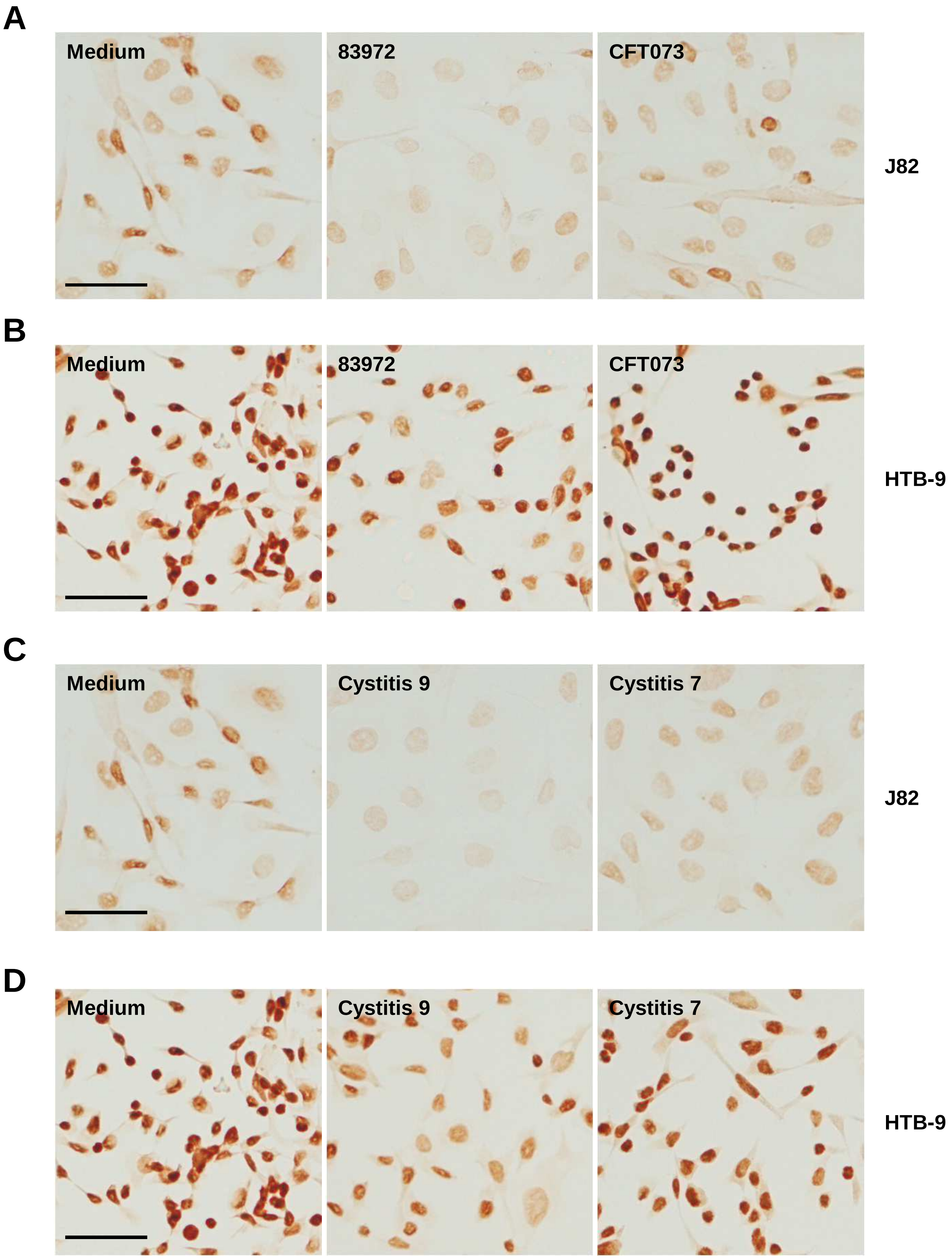
Supplemental Figure 4. Transcriptional regulation by the 83972 strain in vivo.

(**A**) Comparison of in vitro and in vivo expression of Pol II related genes (**B**) Genes regulated after 24 hours in vivo by the 83972 strain are shown relative to specific steps in the Pol II transcription cycle (unadjusted p-values <0.05 and absolute log2 fold change >0.5).

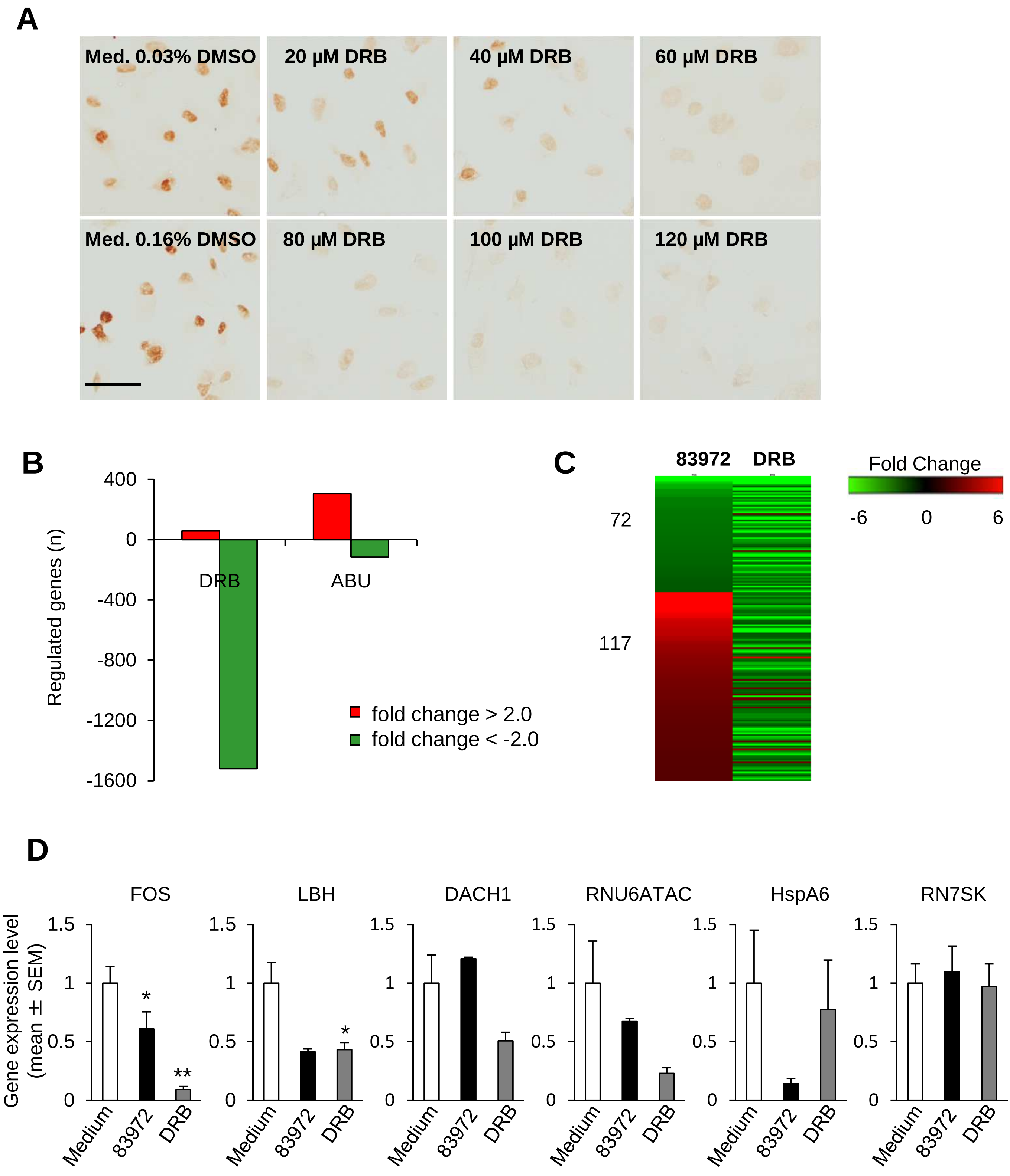


Supplemental Figure 5. Validation of proteomic results.

(**A**) Nuclear Pol II phosphorylation and Htx-eosin counter-staining of A498 kidney epithelial cells after stimulation with the 83972 and CFT073 strains. (**B**) Western-blot showing inhibition of Pol II Ser2 phosphorylation by the 83972 but not the CFT073 strain. (**C**) Pol II inhibition by four different *E. coli* strains isolated from asymptomatic carriers of the same epidemiological group (compared to uninfected cells, Chi-squared test for independence). Scale bars = 50 µm.

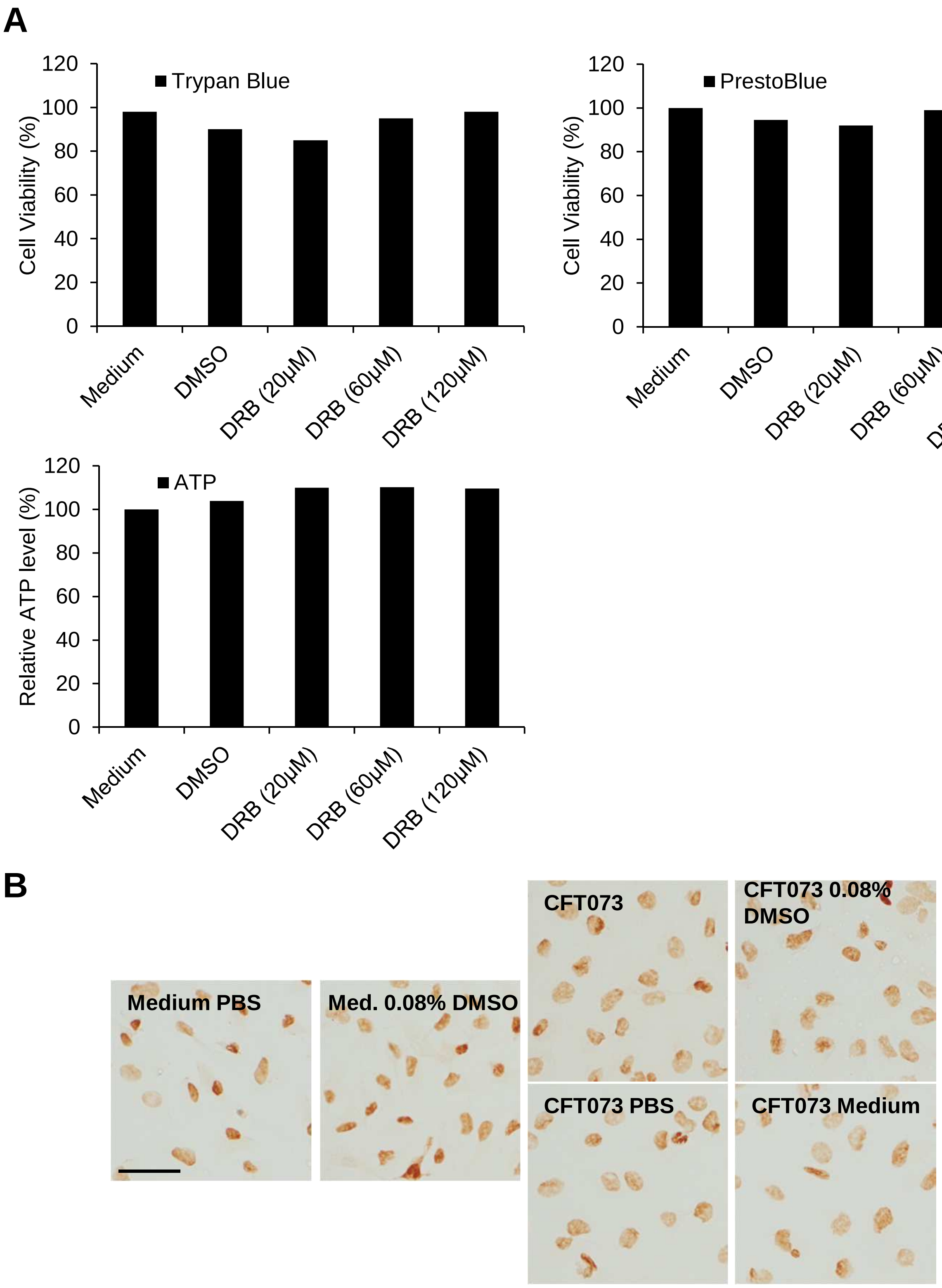


Supplemental Figure 6. Pol II inhibitor effect on bladder cancer cell lines in vitro . (**A**) Inhibition of Pol II by 83972 in J82 cells. (**B**) Inhibition of Pol II by 83972 in HTB-9 cells. (**C**) Pol II inhibition by inhibitory cystitis strain C9 compared to non-inhibitory cystitis strain C7 in J82 cells. (**D**) Pol II inhibition by inhibitory C9 strain compared to non-inhibitory C7 strain in HTB-9 cells. Scale bars = 50 µm.



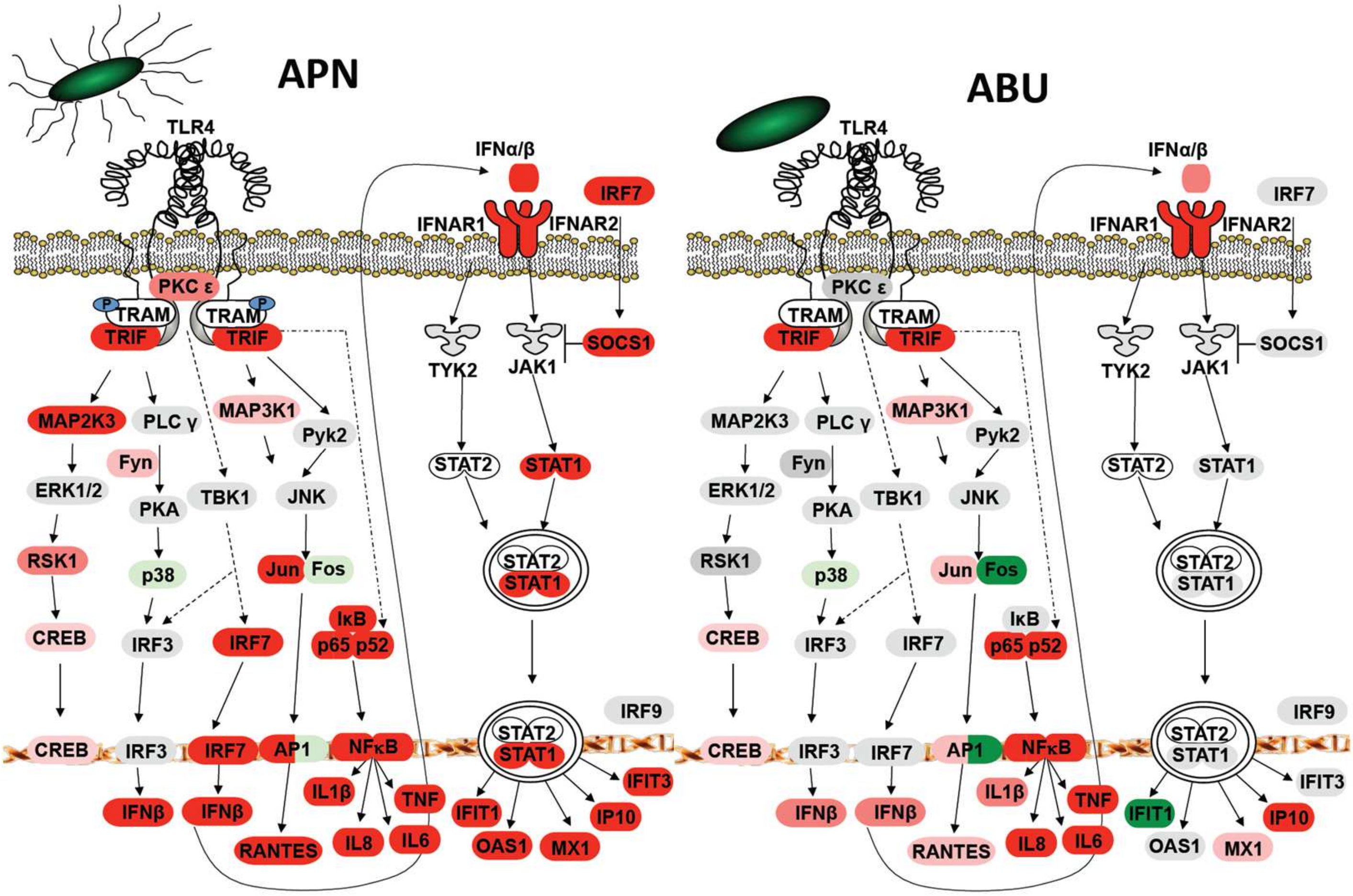
Supplemental Figure 7. Pol II inhibitor effect on A498 cells in vitro.

(**A**) Dose-dependent effect of DRB on Pol II phosphorylation. (**B**) Regulated genes by 83972 and DRB, cut-off with absolute fold change>2, red=upregulated, green=downregulated. (**C**) Heat-map of commonly regulated genes (**D**) RT-PCR verification of transcriptomic data (unpaired t-test compared to Medium, **p*<0.05, ***p*<0.01). Scale bar = 50 µm.



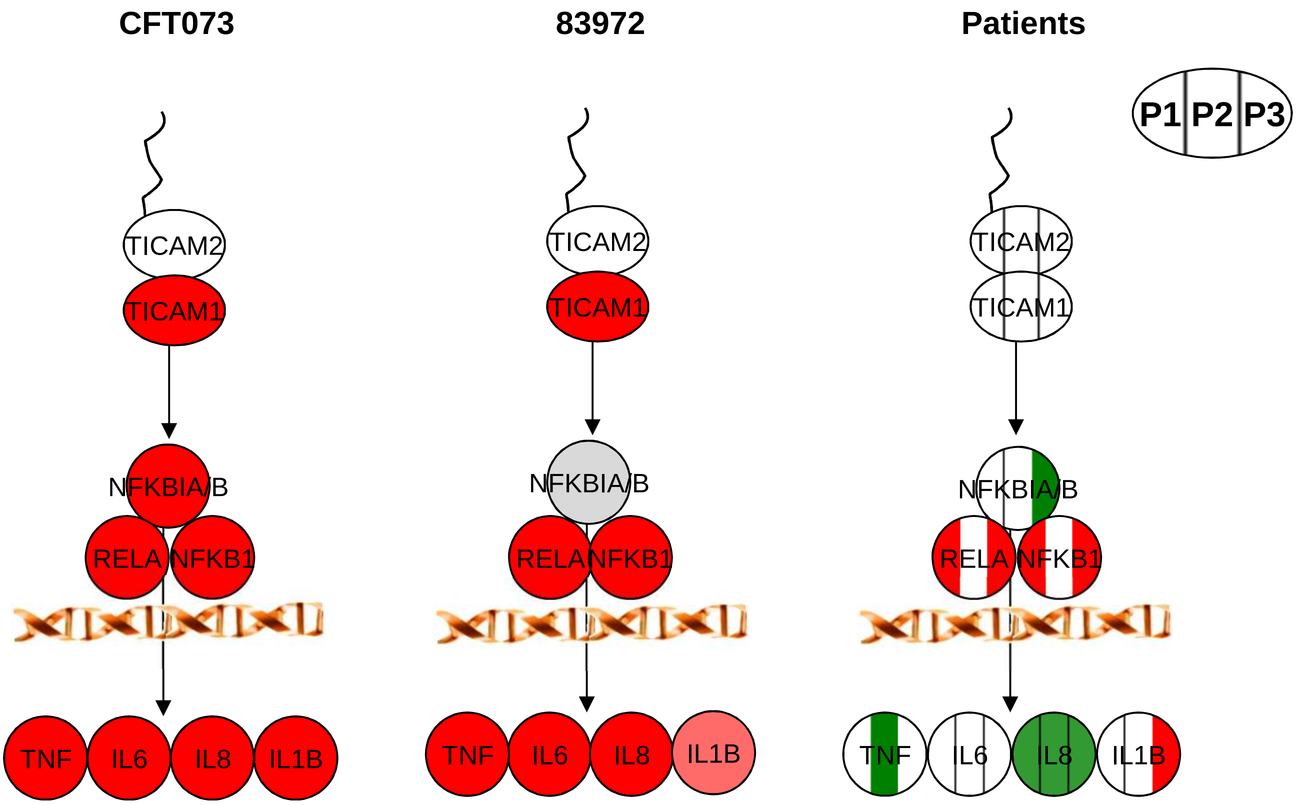
Supplemental Figure 8. Cell viability essays after DMSO and DRB treatment.

(**A**) A498 cells were exposed to DRB for four hours and changes in cell viability by Trypan blue and Prestoblue and cellular ATP level were measured. No significant change in cell death was observed even at high concentration of DRB (120µM), thus DRB at these concentrations is not causing cell death. A high concentration of DMSO (0.16%) was used as a control. (**B**) 0.08% of DMSO did not affect Pol II phosphorylation. This concentration of DMSO correspond to the amount used for 60µM of DRB. Scale bar = 50 µm.



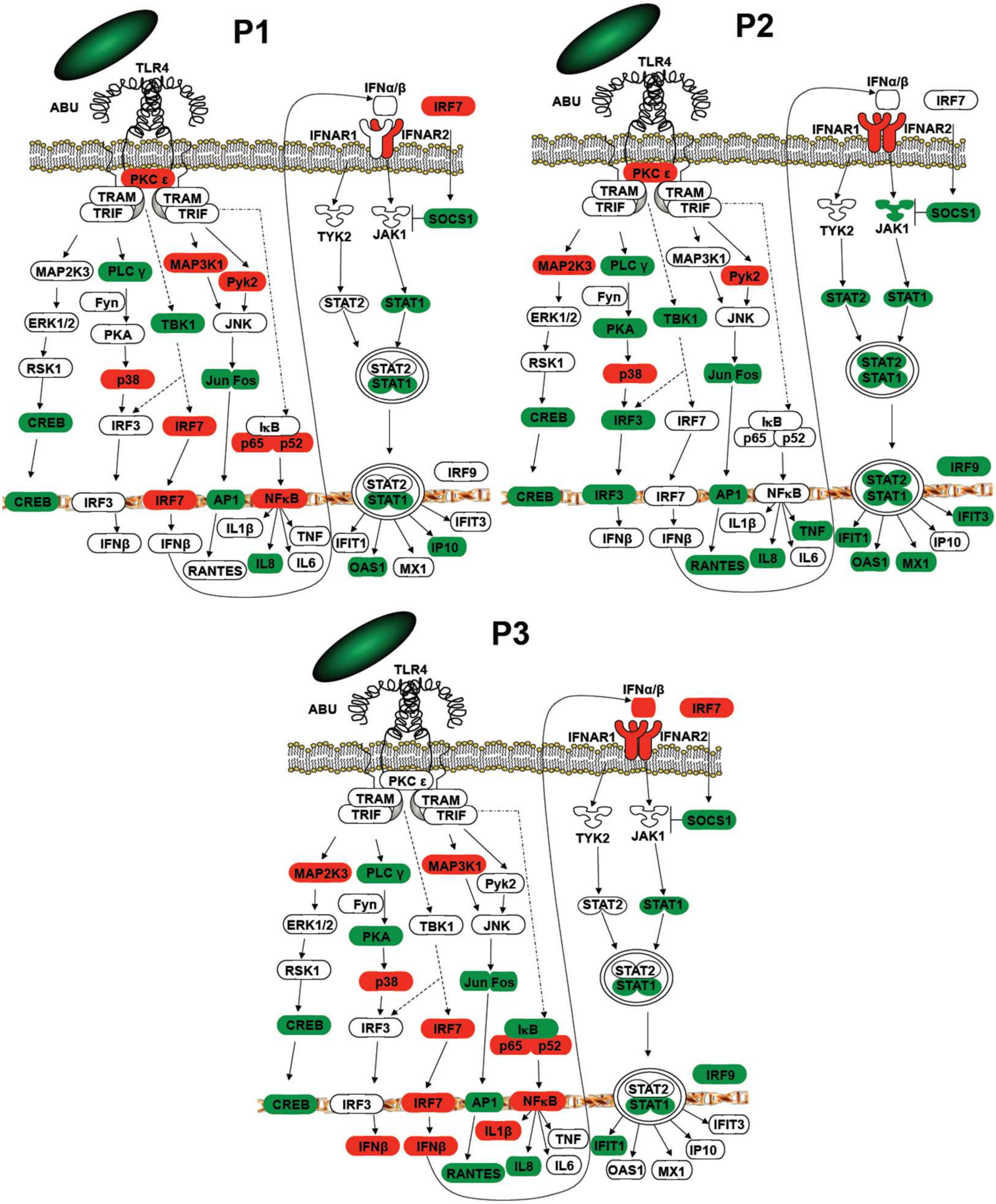
Supplemental Figure 9. Suppression by the 83972 strain of pathogen-specific signaling in infected A498 cells.

Transcriptomic analysis of genes involved in the TLR4/CREB/IRF3/7 pathway and the Type 1 IFN pathway as well as cytokine genes. Activation by the CFT073 strain of gene (left) expression versus suppression by the 83972 strain (right) of genes in these pathways is shown. For log fold change of individual genes, see Supplemental Table 5. Increased expression=red, reduced expression=green, no change=gray. The color intensity reflects the fold change.



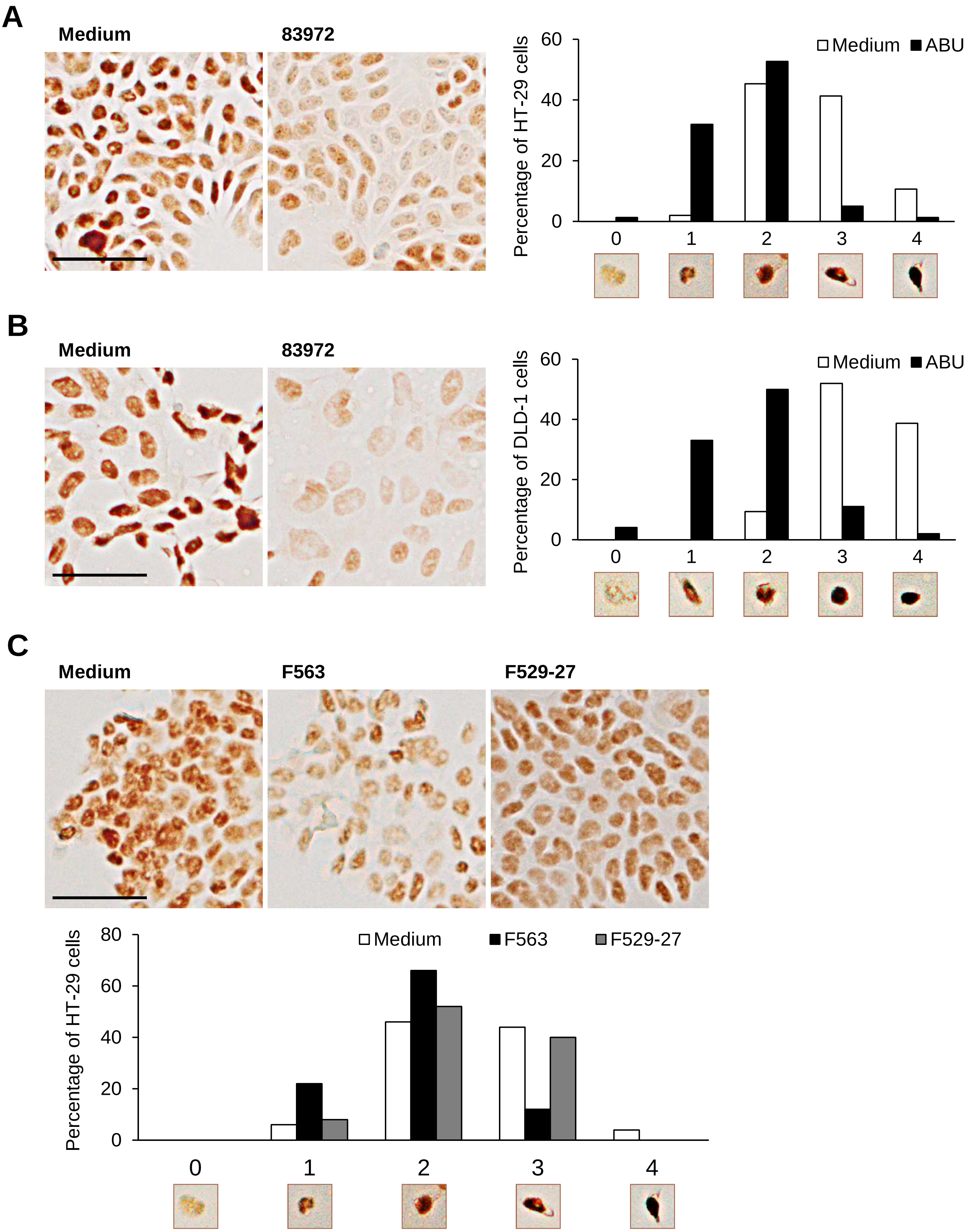
Supplemental Figure 10. NFKB signaling pathway.

Increased expression=red, reduced expression=green, no change=gray. For log fold change of individual genes, see Supplemental Tables 1 and 5.



Supplemental Figure 11. Suppression by the 83972 strain of pathogen-specific signaling in inoculated patients.

Inhibition of the TLR4/CREB/IRF3/7 pathway in inoculated patients and suppression of type I IFN signaling. Increased expression=red, reduced expression=green, no change=gray. For log fold change of individual genes, see Supplemental Table 1.



Supplemental Figure 12. Pol II inhibitor effect on colon cancer cells in vitro.

(**A**) Inhibition of Pol II by 83972 in HT-29 cells. (**B**) Inhibition of Pol II by 83972 in DLD-1 cells. (**C**) Pol II inhibition by inhibitory fecal strain F563 compared to non-inhibitory fecal strain F529-27 in HT-29 colon cancer cells. Scale bars = 50 µm.

Supplemental Table 1. Commonly regulated genes in all three patients after inoculation with *Escherichia coli* 83972.

Symbol	Entrez Gene Name	Log Ratio	Function
Transcriptional regulators			
a) Transcriptional repressors			
BCL6	B-cell CLL/lymphoma 6	1.20	Transcriptional repressor
SIN3A	SIN3 transcription regulator homolog A (yeast)	-0.70	Transcriptional repressor
SET	SET nuclear oncogene	-0.71	Negative regulation of histone acetylation
PBXIP1	Pre-B-cell leukemia homeobox interacting protein 1	-0.75	Transcriptional repressor
LETMD1	LETM1 domain containing 1	-0.83	Suppression of p53
b) Transcriptional activators			
RFX2	Regulatory factor X, 2 (influences HLA class II expression)	0.63	Transcriptional activator
CAND1	Cullin-associated and neddylation-dissociated 1	-0.60	Postive regulation of transcription, TATA-binding protein interacting (TIP20)
TRRAP	Transformation/transcription domain-associated protein	-0.60	Links HAT complexes to transcriptional activators
TCF3	Transcription factor 3 (E2A immunoglobulin enhancer binding factors E12/E47)	-0.70	Transcriptional activator
MEAF6	MYST/Esa1-associated factor 6	-0.71	Transcriptional activator
EOMES	Eomesodermin	-0.91	Transcriptional activator involved in immune responses
LBH	Limb bud and heart development homolog (mouse)	-1.04	Transcriptional activator
NCOA4	Nuclear receptor coactivator 4	-1.24	Androgen receptor transcriptional co-activator
LEF1	Lymphoid enhancer-binding factor 1	-1.30	Activates transcription of target genes in the presence of CTNNB1 and EP300
c) Zinc finger proteins, zinc-binding proteins			
ZNF195	zinc finger protein 195	-0.58	Krueppel C2H2-type zinc-finger protein family, transcription factor
DCTD	dCMP deaminase	-0.62	Deamination of dCMP to dUMP, zinc-binding protein
ZNF146	Zinc finger protein 146	-0.78	Transcription regulation
ZNF664	Zinc finger protein 664	-1.00	Transcriptional regulation
d) Transcriptional and translational regulation			
CNOT6L	CCR4-NOT transcription complex. Subunit 6-like	-0.57	RNA post-transcriptional modification
RSL1D1	Ribosomal L1 domain containing 1	-0.58	RNA binding, translation
WARS	Tryptophanyl-trna synthetase	-0.60	Aminoacylation of tRNA, linking amino acids with nucleotide triplets
GSPT1	G1 to S phase transition 1	-0.65	Translation termination in response to the termination codons
DDX24	DEAD (Asp-Glu-Ala-Asp) box polypeptide 24	-0.66	Translation initiation, nuclear and mitochondrial splicing, and ribosome

			and spliceosome assembly
SRSF10	Serine/arginine-rich splicing factor 10	-0.69	RNA splicing
RNMT	RNA (guanine-7-) methyltransferase	-0.71	mRNA capping
TNRC6A	Trinucleotide repeat containing 6A	-0.71	Post-transcriptional gene silencing, RNAi and microRNA pathways
CPSF6	Cleavage and polyadenylation specific factor 6, 68kda	-0.72	mRNA processing
ABCF1	ATP-binding cassette, sub-family F (GCN20), member 1	-0.78	Promotion of translation initiation
HNRNPA1	Heterogeneous nuclear ribonucleoprotein A1	-0.78	Pre-mRNA processing
RPL15	Ribosomal protein L15	-0.85	A component of the 60S subunit
SRPK2	SRSF protein kinase 2	-0.85	Regulation of splicing
THRA	Thyroid hormone receptor, alpha	-0.87	Receptor mediated signaling, transcription regulator
TRMT13	Trna methyltransferase 13 homolog (S. Cerevisiae)	-0.99	Methylation of guanosine-4 in tRNAs
NCBP2	Nuclear cap binding protein subunit 2, 20kda	-1.06	Nuclear cap-binding protein complex, mRNA capping
HNRPDL	Heterogeneous nuclear ribonucleoprotein D-like	-1.08	RNA binding protein, pre-mRNA processing
EIF4B	Eukaryotic translation initiation factor 4B	-1.28	Required for translation initiation
e) Transcription regulators of innate immune response			
CREB5	Camp responsive element binding protein 5	0.88	Activates transcription as a homodimer or a heterodimer with c-Jun or CRE-BP1
HMGB1	High mobility group box 1	-0.68	Regulate gene expression, activate cell signaling through TLRs
HSPA9	Heat shock 70kda protein 9 (mortalin)	-0.82	Protein folding, immune and stress response
CREB1	Camp responsive element binding protein 1	-0.84	TLR signaling, immune response, transcription, regulates FOS, CCND1, EGR1, etc.
HSPA8	Heat shock 70kda protein 8	-1.03	Protein folding, immune and stress response
STAT4	Signal transducer and activator of transcription 4	-1.06	Signal transductiona and transcription activation, mediates cytokine signaling
JUN	Jun proto-oncogene	-1.11	Component of the AP-1 transcription factor, innate immune response
FOS	FBJ murine osteosarcoma viral oncogene homolog	-1.60	Component of transcriptional regulators, component of AP1 transcriptional factor, innate immune response
f) Chromatin and DNA organization			
HMGN4	High mobility group nucleosomal binding domain 4	-0.55	Chromatin-modifying enzyme
HMGN1	High mobility group nucleosome binding domain 1	-0.61	Maintain an open chromatin configuration
RAD17	RAD17 homolog (S. Pombe)	-0.67	Maintenance of chromosomal stability
NUDCD3	Nudc domain containing 3	-0.68	Dynein stabilization during mitosis
PARP14	Poly (ADP-ribose) polymerase 1, member 14	-0.76	DNA-dependent polyADP-ribosylation of nuclear proteins, regulates transcription
RPAP3	RNA polymerase II associated protein 3	-0.81	Regulation of histone phosphorylation and RNA pol assembly
NAP1L1	Nucleosome assembly protein 1-like 1	-0.90	Nucleosome assembly protein

HDAC1	Histone deacetylase 1	-1.15	Positive regulation of transcription
RCBTB2	Regulator of chromosome condensation (RCC1) and BTB (POZ) domain containing protein 2	-1.30	Chromosome condensation
Innate immunity, inflammatory response			
PTPRC	Protein tyrosine phosphatase, receptor type, C	0.91	Signaling molecule, regulator of T- and B-cell antigen receptor signaling
CD55	CD55 molecule, decay accelerating factor for complement (Cromer blood group)	0.88	Complement cascade
JAK3	Janus kinase 3	0.71	Cytokine receptor-mediated signal transduction
CLEC2D	C-type lectin domain family 2, member D	-0.66	Regulation of NK-cell activity
KLRK1	Killer cell lectin-like receptor subfamily K, member 1	-0.90	Regulation of NK-cell activity
KLRD1	Killer cell lectin-like receptor subfamily D, member 1	-0.96	Regulation of NK-cell activity
KLRC3	Killer cell lectin-like receptor subfamily C, Member 3	-0.98	NK cell function
GZMK	Granzyme K (granzyme 3; tryptase II)	-1.00	NK- and CTL-mediated cell death
D6	CD6 molecule	-1.04	Cell adhesion molecule involved in T-cell activation
TAGAP	T-cell activation rhogtpase activating protein	-1.04	GTPase-activating protein, T-cell activation
BTN3A1	Butyrophilin, subfamily 3, member A1	-1.05	Production of Th1-cytokines
CD160	CD160 molecule	-1.10	Cytolisis of NK and T cells
TPD52	Tumor protein D52	-1.11	B cell differentiation
KLRF1	Killer cell lectin-like receptor subfamily F, member 1	-1.13	Regulation of NK-cell activity
CLEC7A	C-type lectin domain family 7, member A	-1.14	TLR2-mediated inflammatory response
KLRG1	Killer cell lectin-like receptor subfamily G, member 1	-1.16	Regulation of NK-cell activity
TRD@	T cell receptor delta locus	-1.16	T-cell antigen receptor
SH2D1A	SH2 domain containing 1A	-1.23	Inhibitor of the signaling lymphocyte-activation molecule in activated T, B and NK cells
GBP4	Guanylate binding protein 4	-1.38	Mediator of cytokine signaling
IL8	Interleukin 8	-2.16	Chemotactic mediator of the inflammatory response
Cell growth and proliferation, cellular organization			
SPATA13	Spermatogenesis associated 13	1.28	Regulation of Rho protein signal transduction
IGF1R	Insulin-like growth factor 1 receptor	1.15	Cell growth and survival control
LRP10	Low density lipoprotein receptor-related protein 10	1.15	Inhibitor of the Wnt/beta-catenin pathway
SSH1	Slingshot homolog 1 (Drosophila)	1.08	Regulation of actin dynamics
PHIP	Pleckstrin homology domain interacting protein	1.03	Stimulation of cell proliferation
TNFRSF10C	Tumor necrosis factor receptor superfamily, member 10c, decoy without an intracellular domain	0.88	TRAIL decoy receptor
NBEAL2	Neurobeachin-like 2	0.79	Platelet formation
AK3	Adenylate kinase 3	-0.57	Mikltochondrial ADP biosynthesis
KIF2A	Kinesin heavy chain member 2A	-0.58	Mitotic progression
VDAC3	Voltage-dependent anion channel 3	-0.60	Mitochondrial porin family
MTHFD1	Methylenetetrahydrofolate dehydrogenase	-0.62	One-carbon metabolism

	(NADP+ dependent) 1, methenyltetrahydrofolate cyclohydrolase, formyltetrahydrofolate synthetase		
ADH5	Alcohol dehydrogenase 5 (class III), chi polypeptide	-0.66	Oxidation
NUB1	Negative regulator of ubiquitin-like proteins 1	-0.67	Regulator of proteasomal degradation
ST6GAL1	ST6 beta-galactosamide alpha-2,6-sialyltranferase 1	-0.68	Glycosyltransferase
SLC37A4	Solute carrier family 37 (glucose-6-phosphate transporter), member 4	-0.69	Glucose-6-phosphate transport
CAPN7	Calpain 7	-0.70	cell fusion and cell motility, protein degradation
LPXN	Leupaxin	-0.71	Adaptor protein
AKAP11	A kinase (PRKA) anchor protein 11	-0.72	Cell cycle control
AMD1	Adenosylmethionine decarboxylase 1	-0.72	Polyamine biosynthesis, cellular proliferation
MAP3K4	Mitogen-activated protein kinase kinase kinase 4	-0.72	MAPKKK activity
ACSL5	Acyl-coa synthetase long-chain family member 5	-0.74	Lipid metabolism
DUSP5	Dual specificity phosphatase 5	-0.74	Negative regulator of cell proliferation, MAPK phosphatase
DNAJC9	Dnaj (Hsp40) homolog, subfamily C, member 9	-0.75	Protein folding
TPM1	Tropomyosin 1 (alpha)	-0.77	Stabilization of actin filaments
MAPRE2	Microtubule-associated protein. Rp/eb family, member 2	-0.81	Proliferative control
DDIT4	DNA-damage-inducible transcript 4	-0.82	Inhibition of cell proliferation
ADSS	Adenylosuccinate synthase	-0.83	Conversion of inosine monophosphate to adenosine monophosphate
AGK	Acylglycerol kinase	-0.85	Lipid metabolism
ALDH1A1	Aldehyde dehydrogenase 1 family, member A1	-0.88	Aldehyde metabolism, retinoic acid biosynthesis
INSIG1	Insulin induced gene 1	-0.90	Cell growth
BIN1	Bridging integrator 1	-0.92	Adaptor protein
PFKP	Phosphofructokinase, platelet	-0.92	Glycolysis
THBS1	Thrombospondin 1	-0.94	Cell-cell and cell-matrix interactions
GOLGA8A/ GOLGA8B	Golgin A8 family. Member B	-0.95	Maintainance of Golgi structure
RCSD1	RCSD domain containing 1	-1.00	Actin filament assembly
AQP3	Aquaporin 3 (Gill blood group)	-1.05	Transport of small nonionic solutes
DUSP1	Dual specificity phosphatase 1	-1.05	Negative regulator of cell proliferation, MAPK phosphatise, interacts with Pol II
BCL2	B-cell CLL/lymphoma 2	-1.06	Anti-apoptosis
CYB561	Cytochrome b-561	-1.07	Electron transport protein
STMN1	Stathmin 1	-1.09	Destabilization of microtubules
PDE4B	Phosphodiesterase 4B, camp-specific	-1.20	Signal transduction
IFIT2	Interferon-induced protein with tetratricopeptide repeats 2	-1.31	Microtubule-associated protein

Membrane functions

a) Lipid metabolism

MTMR12	Myotubularin related protein 12	-0.73	Adaptor protein

PAQR8	Progestin and adipoQ receptor family member VIII	-0.90	Steroid membrane receptor
ATP8B2	ATPase, class I, type 8B, member 2	-1.09	Transport of phospholipids
PLCG1	Phospholipase C, gamma 1	-1.47	Biosynthesis of DAG and IP3
b) Ion transport			
CNNM3	cyclin M3	-0.73	Metal transport
SGK1	Serum/glucocorticoid regulated kinase 1	-1.28	Activator of ion channels
c) Protein transport			
CYTH4	Cytohesin 4	0.89	Regulation of protein sorting and membrane trafficking
SNTB2	Syntrophin, beta 2 (dystrophin-associated protein A1, 59kDa, basic component 2)	0.89	Regulation of secretory granules
TAP2	Transporter 2. ATP-binding cassette. Sub-family B (MDR/TAP)	-0.60	Membrane-associated protein, superfamily of ATP-binding cassette (ABC) transporters
IPO5	Importin 5	-0.80	Nuclear import of proteins
SYTL2	Synaptotagmin-like 2	-1.03	Exocytosis
Ubiquitination			
VPRBP	Vpr (HIV-1) binding protein	-0.63	Adaptor protein to E3 ligase complexes
UBA2	Ubiquitin-like modifier activating enzyme 2	-0.67	SUMO-activating enzyme for the sumoylation of proteins
USP42	Ubiquitin specific peptidase 42	-0.67	Deubiquitinating enzyme
DDB2	Damage-specific DNA binding protein 2, 48kDa	-0.76	Ubiquitinylation of histone proteins, interacts with Pol II
UBXN1	UBX domain protein 1	-0.82	Ubiquitin-binding protein
G-protein signaling			
ARL11	ADP-ribosylation factor-like 11	0.71	Stimulation of apoptosis, small GTPase superfamily member
RABL2B	RAB, member of RAS oncogene family-like 2B	-0.71	Unknown, small GTPase superfamily member
RAPGEF6	Rap guanine nucleotide exchange factor (GEF) 6	-0.78	Ras protein signal transduction
DOCK10	Dedicator of cytokinesis 10	-0.93	Activator of Cdc42
CXCR4	Chemokine (C-X-C motif) receptor 4	-0.96	Chemotaxis
ARHGEF3	Rho guanine nucleotide exchange factor (GEF) 3	-0.99	Acceleration of the GTPase activity of Rho GTPases
P2RY10	Purinergic receptor P2Y, G-protein coupled, 10	-1.47	Lysophospholipid receptor
Pseudogens and others			
PHF20L1	PHD finger protein 20-like 1	1.24	Unknown
FAM126B	Family with sequence similarity 126, member B	1.02	Unknown
CASD1	CAS1 domain containing 1	-0.53	Membrane protein, putative glycosyltransferase
TSPYL4	TSPY-like 4	-0.63	Implicated in nucleosome assembly
PADI2	Peptidyl arginine deiminase. Type ii	0.67	Deimination of arginine residues of proteins
DNAJC10	Dnaj (Hsp40) homolog, subfamily C, member 10	-0.68	Recognizing and degrading misfolded proteins
LANCL1	Lanc lantibiotic synthetase component C-like 1 (bacterial)	-0.68	Implicated in peptide modification
RMND5A	Required for meiotic nuclear division 5 homolog A (S. Cerevisiae)	-0.68	Unknown
OXNAD1	Oxidoreductase NAD-binding domain	-0.69	Oxidoreductase activity

	containing 1		
CRY1	Cryptochrome 1 (photolyase-like)	-0.76	Regulation of circadian cycle
CTSC	Cathepsin C	-0.76	Chaperone
MFNG	MFNG O-fucosylpeptide 3-beta-N-acetylglucosaminyltransferase	-0.76	Positive regulation of Notch signaling pathway
BTN3A2	Butyrophilin, subfamily 3, member A2	-0.84	Unknown, MHC-associated gene
GLOD4	Glyoxalase domain containing 4	-0.91	Implicated in suppression of cell growth
XPO7	Exportin 7	-0.93	Nuclear export of proteins
ECE1	Endothelin converting enzyme 1	0.98	Proteolytic processing of endothelin precursors
MEI1	Meiosis inhibitor 1	-0.98	Meiotic chromosome synapsis
SH3BGRL2	SH3 domain binding glutamic acid-rich protein like 2	-1.04	Unknown
TJP2	Tight junction protein 2 (zona occludens 2)	-1.07	Component of tight junction barrier
BTN3A3	Butyrophilin, subfamily 3, member A3	-1.08	Unknown, MHC-associated gene
PRSS23	Protease, serine, 23	-1.17	Unknown
SAMD3	Sterile alpha motif domain containing 3	-1.42	Unknown

Supplemental Table 2. The networks of the genes regulated by *E. coli* 83972 in the patients.

Associated network functions	Molecules in network	Score	Regulated molecules
Drug Metabolism, Lipid Metabolism, Molecular Transport	AGK, ALDH1A1, Ap1, Ap2 alpha, AQP3, BIN1, CASD1, CD6, Ck2, CREB5, Creb, DUSP1, Dynamin, EIF4B, ERK1/2, estrogen receptor, F5, GRINA, HP, MAPK14, NAP1L1, NCOA4, NMDA Receptor, NUMB, PARP, PDE4B, PFKP, POR, Ppp2c, Rar, RETN, Rxr, Sapk, T3-TR-RXR, thyroid hormone receptor	40	20
Lipid Metabolism, Molecular Transport, Small Molecule Biochemistry	ABCF1, ACSL5, ADH5 (includes EG:11532), ARL11, ATP8B2, AZI1, BTN3A1, CYB561, DNAJB11, DNAJC9, DNAJC19, DTNB, FBXO33, FNIP1, GFPT2, GLOD4, GMPPA, HSD17B10, IPO5, KIDINS220, KLHDC10, LANCL1, LOC100505603/PNRC2, LRP10, MTHFD1, MTMR12, NUDCD3, PLEKHA1, PQLC1, RNMT, SLC27A6, SNTB2, SRP19, STEAP3, UBC	33	17
Cell Death, Cell-To-Cell Signaling and Interaction, Cellular Development	Angiotensin II receptor type 1, DDB2, DUSP5, EOMES, Fcer1, GAS7, GBP1, Glucocorticoid-GCR, Gm-csf, GZMK, HLA-DR, IFIT2, Ifn, IFN alpha/beta, IFN Beta, Ifn gamma, IFN TYPE 1, IL23, IL12 (complex), Interferon alpha, JINK1/2, JUN/JUNB/JUND, KLRD1, KLRG1, KLRK1, Laminin1, MHC Class I (complex), MHC CLASS I (family), NFkB (complex), NUB1, SLC37A4, STAT4, TJP2, Tlr, TNFRSF10C	28	15
DNA Replication, Recombination, and Repair, Cell Cycle, Connective Tissue Development and Function	26s Proteasome, Actin, ADCY, CAND1, CD3, chemokine, CREB1, CRY1, FSH, GNRH, Gpcr, HISTONE, Histone h3, Histone h4, Hsp70, HSPA9, IKK (complex), IL12 (family), Jnk, JUN, Lh, MXD3, PARP1, Pka, Ras homolog, RNA polymerase II, RNMT, SGK1, SMC3, Tnf, TPM1 (includes EG:22003), TRRAP, Ubiquitin, Vegf, VPRBP	22	13
Cell-To-Cell Signaling and Interaction, Hematological System Development and Function, Immune Cell Trafficking	AK3, ARFGAP3, BTN3A1, BTN3A2, BTN3A3, CD48, CD160, CD276, CD200R1, Cd55/Daf2, CLEC2D, COL16A1, COL1A2, CYTH4, DYSF, ENTPD5, GPR65, H60a, HP, IFNG (includes EG:15978), IL2, KLRB1, LILRA2, MYD88, PLA2G7, PMP2 (includes EG:100334189), PRSS23, RABL2B, Raet1b, RFX2, Tlr11, Tlr12, Tlr13, TMEM50B, TNF	19	11
Hematological System Development and Function, Hematopoiesis, Humoral Immune Response	Akt, BCL2, BCL6, BCR (complex), Calcineurin A, Calcineurin protein(s), caspase, CXCR4, Cyclin A, DOCK10, F Actin, hCG, Hdac, Hsp90, Ige, IgG1, IgG, Igm, IL8, Immunoglobulin, JAK3, LBH, LPXN, MAP2K1/2, Mek, Nfat (family), Notch, PP2A, Rap1, RPAP3, SLC25A37, SSH1 (includes	19	12

	EG:231637), ST6GAL1, Tgf beta, TSH		
Cell Death, Connective Tissue Development and Function, Embryonic Development	APC/APC2, Ca2+, CYSLTR1, FOS, FZD3, G protein alpha, Gpcr, GPR19, GPR65, GPR97, GPR137B, Gsk3, HMGN4, HNF4A, Insulin, KLRF1, LPAR3, LPAR4, MRVI1, NPS, NTSR1, OCM2, P2RY6, P2RY10, p85 (pik3r), PCNX, PLC, RBM6, SPATA13, STAT, Stat dimer, SYTL2, TOR2A, TSPYL4, ZNF146	17	10
Cell Death, Developmental Disorder, Hereditary Disorder	ADRB, Alp, ALPL, AMPK, calpain, Cdc2, Collagen type I, Cytochrome c, DDIT4, ERK, Fgf, Focal adhesion kinase, GBP4, Hsp27, IL1, Integrin, LDL, MAP3K4, Mapk, NADPH oxidase, NFAT (complex), P38 MAPK, Pdgf (complex), PDGF BB, PI3K (complex), Pkc(s), PLCG1, Rac, Ras, Rock, Sos, SRC (family), STAT5a/b, TCR, THBS1	9	6

Supplemental Table 3. Transcriptional regulation by the ABU strain, *Escherichia coli* 83972.

Symbol	Entrez Gene Name	Log2 FC	Function
Transcriptional activators			
SOX4	SRY (sex determining region Y)-box 4	0.75	Regulation of transcription, cell differentiation
TFAP2A	Transcription factor AP-2 alpha (activating enhancer binding protein 2 alpha)	-0.59	Transcription coactivator activity, transcription from RNA polymerase II promoter
MN1	Meningioma (disrupted in balanced translocation) 1	-0.63	Transcription, cell proliferation
CTNNB1	Catenin (cadherin-associated protein), beta 1, 88kDa	-0.73	Transcription, regulation of calcium ion import
LHX1	LIM homeobox 1	-0.83	RNA polymerase II transcription factor activity; regulation of transcription
OSR2	Odd-skipped related 2 (Drosophila)	-0.85	Cell proliferation; gene expression
*EGR1**	Early growth response 1	-1.64	Specific RNA polymerase II transcription factor activity, type I IFN signaling
LBH	Limb bud and heart development homolog (mouse)	-1.65	AP1 transcription
*SNAI1**	Snail homolog 1 (Drosophila)	-2.23	Positive and negative regulation of transcription; p53 induced SNAI degradation via MDM2-mediated ubiquitination
Transcriptional repressors			
DACH1	Dachshund homolog 1 (Drosophila)	0.71	Regulation of transcription from RNA polymerase II promoter
BANP	BTG3 associated nuclear protein	0.63	Transcription, cell cycle, negative regulation of p53, MDM2
DDX20	DEAD (Asp-Glu-Ala-Asp) box polypeptide 20	0.59	Transcription from RNA polymerase II promoter
MDM2	Mdm2 p53 binding protein homolog (mouse)	-0.92	Decreased expression after RNA polymerase II blocking, negative regulation of p53
Zinc finger proteins, zinc-binding proteins			
ZNF451	Zinc finger protein 451	1.30	Regulation of transcription
ZNF786	Zinc finger protein 786	0.83	Regulation of transcription
ZBTB11	Zinc finger and BTB domain containing 11	0.81	Regulation of transcription
HERC2P2	Hect domain and RLD 2 pseudogene 2	0.68	Zinc ion binding
BAZ2B	Bromodomain adjacent to zinc finger domain, 2B	0.65	Regulation of transcription
D2HGDH	D-2-hydroxyglutarate dehydrogenase	0.62	Response to zinc and cobalt; oxidation of D-2-hydroxyglutarate to alpha-ketoglutarate
ZNF280C	Zinc finger protein 280C	0.60	Regulation of transcription
ZFP112	Zinc finger protein 112 homolog (mouse)	-0.59	Regulation of transcription
ZC3HAV1	Zinc finger CCCH-type, antiviral 1	-1.26	Protein amino acid ADP-ribosylation

FAM90A15	Family with sequence similarity 90, member A15	-2.11	Nucleic acid binding, zinc ion binding
Transcriptional and translational regulation			
EIF3CL	Eukaryotic translation initiation factor 3, subunit C-like	1.51	Translational initiation
VARS	Valyl-tRNA synthetase	0.79	Linking amino acids with nucleotide triplets contained in tRNAs, aminoacyl-tRNA synthetases
SNORD36C	Small nucleolar RNA, C/D box 36C	0.69	Biogenesis (modification) of other small nuclear RNAs (snRNAs), 2'-O-ribose methylation guide
PDCD4	Programmed cell death 4 (neoplastic transformation inhibitor)	0.66	Repression of AP-1 activity, inhibits translation initiation and cap-dependent translation
BRIX1	BRX1, biogenesis of ribosomes, homolog (S. cerevisiae)	0.60	Ribosomal biogenesis
RN28S1	RNA, 28S ribosomal 1	-0.67	The portion of one rDNA repeat which encodes a 28S rRNA
BTG2	BTG family, member 2	-0.96	DNA repair, positive regulation of nuclear-transcribed mRNA poly(A) tail shortening
RPPH1	Ribonuclease P RNA component H1	-1.56	A component of the RNase P ribonucleoprotein, involved in maturation of tRNA
RN7SK	RNA, 7SK small nuclear	-2.27	Sequesters transcription elongation factor b P-TEFb
RNU6ATAC	RNA, U6atac small nuclear (U12-dependent splicing)	-4.14	Pol III dependent gene, pre-mRNA splicing
Transcriptional regulators of innate immune response			
*HES1**	Hairy and enhancer of split 1, (Drosophila)	-2.08	Expression of the genes that require a bHLH protein for their transcription, cellular differentiation, sustains NF-κB activity
FOSB	FBJ murine osteosarcoma viral oncogene homolog B	-2.15	Interacts with Jun proteins enhancing their DNA binding activity, innate immune response
*FOS**	FBJ murine osteosarcoma viral oncogene homolog	-2.56	Form AP1 transcriptional factor with Jun proteins, innate immune response
*ID2**	Inhibitor of DNA binding 2, dominant negative helix-loop-helix protein	-2.56	Inhibition of basic helix-loop-helix transcription factors (HES1); transcription activator activity
*ID1**	Inhibitor of DNA binding 1, dominant negative helix-loop-helix protein	-3.17	Inhibition of basic helix-loop-helix transcription factors (HES1); increases translocation of NF-κB p50
HSPA6	Heat shock 70kDa protein 6 (HSP70B')	-4.26	Protein folding, immune and stress response
Chromatin and DNA organization			
HIST2H2BE	Histone cluster 2, H2be	-0.66	Nucleosome assembly; defense response to bacterium
HIST1H2AC	Histone cluster 1, H2ac	-0.72	Chromosome organization and biogenesis, nucleosome assembly

Note: * - genes from common group, more suppressed by ABU (p<0.05, two times lower than APN)

Supplemental Table 4. ABU specific genes, other functional groups.

Symbol	Entrez Gene Name	Log FC ABU	Function
Innate immunity, inflammatory response			
AKR1C2	Aldo-keto reductase family 1, member C2	1.50	Prostaglandin metabolic process; steroid metabolic process; oxidation reduction
MAVS	Mitochondrial antiviral signaling protein	1.12	JNK; IκB kinase/NFκB cascade; innate immune response
FGFBP1	Fibroblast growth factor binding protein 1	-0.72	Fibroblast growth factor receptor signaling pathway; regulation of MAPK
ALOX5AP	Arachidonate 5-lipoxygenase-activating protein	-0.76	Leukotriene production involved in inflammatory response; cellular response to calcium ion
IFIT1	Interferon-induced protein with tetratricopeptide repeats 1	-0.73	Type I interferon-mediated signaling pathway
NOD1	Nucleotide-binding oligomerization domain containing 1	-1.01	Recognises bacterial diaminopimelic acid; initiates inflammatory response
TLR5	Toll-like receptor 5	-1.03	Recognizes bacterial flagellin; activates innate immune responses
TNFRSF10D	Tumor necrosis factor receptor superfamily, member 10d	-1.59	NFkB activation
Cell growth and proliferation, cellular organization			
FILIP1L	Filamin A interacting protein 1-like	1.57	Cell proliferation and migration
DDX12	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 12	1.54	Cell proliferation, nucleic acid metabolic process
CYR61	Cysteine-rich, angiogenic inducer, 61	0.81	Regulation of cell growth
STGC3	Hypothetical STGC3	0.72	Cell growth and regulation of the cell cycle
VANGL2	Vang-like 2 (van gogh, Drosophila)	0.72	Planar cell polarity, apical protein localization
TPM2	Tropomyosin 2 (beta)	0.64	A member of the actin filament binding protein family, regulation of ATPase activity
MASTL	Microtubule associated serine/threonine kinase-like	0.61	Protein phosphorylation, prometaphase, spindle checkpoint, cytokinesis, mitosis, G2 phase
COBL	Cordon-bleu homolog (mouse)	-0.62	The Actin-binding WH2 domain is found in 5 isoforms
CRIP1	Cysteine-rich protein 1 (intestinal)	-0.72	Zinc ion binding; cell proliferation
PPFIBP1	PTPRF interacting protein, binding protein 1 (liprin beta 1)	-0.96	Cell adhesion, DNA integration
FBN2	Fibrillin 2	-1.55	Extracellular matrix structural constituent, calcium ion binding
GADD45G	Growth arrest and DNA-damage-inducible, gamma	-1.76	MAPKKK activity
Membrane functions			
a) Lipid metabolism			
CYP26B1	Cytochrome P450, family 26, subfamily B, polypeptide 1	1.00	Synthesis of cholesterol, steroids and other lipids
MBOAT2	Membrane bound O-acyltransferase domain containing	0.80	Phospholipid biosynthetic process

	2		
CES2	Carboxylesterase 2 (intestine, liver)	0.67	Fatty acyl and cholesterol ester metabolism
PEMT	Phosphatidylethanolamine N-methyltransferase	-0.68	Convertion of phosphatidylethanolamine to phosphatidylcholine; positive regulation of lipoprotein metabolic process
b) Ion transport			
KCNG3	Potassium voltage-gated channel, subfamily G, member 3	0.99	Potassium ion transport
TRPM8	Transient receptor potential cation channel, subfamily M, member 8	-0.68	Release of Ca2+ from endoplasmic reticulum
c) Protein transport			
VAMP5	Vesicle-associated membrane protein 5 (myobrevin)	-0.60	Vesicle docking during exocytosis, vesicle-mediated transport
EXOC1	Exocyst complex component 1	-0.61	Exocytosis; protein transport
FKBP9	FK506 binding protein 9, 63 kDa	-0.63	Protein folding
EMP1	Epithelial membrane protein 1	-1.06	Regulates trafficking of surface proteins
Ubiquitination			
FBXO38	F-box protein 38	0.92	Ubiquitin cycle
SH3RF2	SH3 domain containing ring finger 2	0.78	Ubiquitin cycle
PELI2	Pellino homolog 2 (Drosophila)	0.63	Polyubiquitination
UBE2E3	Ubiquitin-conjugating enzyme E2E 3 (UBC4/5 homolog, yeast)	-0.71	Ubiquitin-protein ligase activity
UBC	Ubiquitin C	-0.72	Protein degradation, DNA repair, cell cycle regulation, kinase modification, endocytosis
MYLIP	Myosin regulatory light chain interacting protein	-1.23	Protein ubiquitination involved in ubiquitin-dependent protein catabolic process
G-protein signaling			
SIPA1L2	Signal-induced proliferation-associated 1 like 2	1.00	Regulation of small GTPase mediated signal transduction
SHOC2	Soc-2 suppressor of clear homolog (C. elegans)	0.67	Fibroblast growth factor receptor signaling pathway; Ras protein signal transduction
C6ORF170	Chromosome 6 open reading frame 170	0.62	Regulation of Rab GTPase activity
BAIAP2	BAI1-associated protein 2	-0.60	Adaptor protein for membrane bound G-proteins; formation of stress fibers and cytokinesis
ARRDC3	Arrestin domain containing 3	-0.62	Transcription, activity of GPCRs
EPHA4	EPH receptor A4	-0.65	Protein amino acid phosphorylation; small GTPase Rho
FAM105A	Family with sequence similarity 105, member A	-0.71	GTPase-activator protein (GAP) for Rho-like GTPases (hypothetical protein)
RGS4	Regulator of G-protein signaling 4	-0.74	Inhibits signal transduction by increasing the GTPase activity of G protein alpha subunits, inactivation of MAPK activity
RAB7B	RAB7B, member RAS oncogene family	-1.25	Small GTPase mediated signal transduction
ARL4D	ADP-ribosylation factor-like 4D	-1.32	Protein secretion, small GTPase mediated signal transduction

Supplemental Table 5. Commonly expressed genes in kidney epithelial cells (A498) after stimulation with the ABU strain, *Escherichia coli* 83972 and the APN strain, *Escherichia coli* CFT073.

Symbol	Entrez Gene Name	CFT Log FC	ABU Log FC	CFT/ABU
CSF2	colony stimulating factor 2 (granulocyte-macrophage)	7.105	6.431	1.10
CCL20	chemokine (C-C motif) ligand 20	5.894	5.481	1.08
PTX3	pentraxin 3, long	5.169	4.86	1.06
ICAM4)	intercellular adhesion molecule 4 (Landsteiner-Wiener blood group)	5.143	3.065	1.68
CCL2	chemokine (C-C motif) ligand 2	4.726	4.662	1.01
CXCL1	chemokine (C-X-C motif) ligand 1 (melanoma growth stimulating activity, alpha)	4.715	5.073	0.93
IFNB1	interferon, beta 1, fibroblast	4.688	3.753	1.25
TRAF1	TNF receptor-associated factor 1	4.674	4.02	1.16
MMP10	matrix metallopeptidase 10 (stromelysin 2)	4.634	2.135	2.17
TNFAIP3	tumor necrosis factor, alpha-induced protein 3	4.533	4.468	1.01
PTGS2	prostaglandin-endoperoxide synthase 2 (prostaglandin G/H synthase and cyclooxygenase)	4.456	3.113	1.43
IL8	interleukin 8	4.403	4.352	1.01
OLR1	oxidized low density lipoprotein (lectin-like) receptor 1	4.31	3.019	1.43
CX3CL1	chemokine (C-X3-C motif) ligand 1	4.105	3.309	1.24
IL6	interleukin 6 (interferon, beta 2)	4.087	3.952	1.03
LTB	lymphotoxin beta (TNF superfamily, member 3)	4.083	4.095	1.00
CXCL10	chemokine (C-X-C motif) ligand 10	4.004	3.429	1.17
UBD	ubiquitin D	3.823	2.691	1.42
PPAP2B	phosphatidic acid phosphatase type 2B	3.704	3	1.23
CHAC1	ChaC, cation transport regulator homolog 1 (E. coli)	3.65	3.564	1.02
VCAM1	vascular cell adhesion molecule 1	3.648	3.669	0.99
LIF	leukemia inhibitory factor (cholinergic differentiation factor)	3.631	3.178	1.14
SOD2	superoxide dismutase 2, mitochondrial	3.628	2.914	1.25
CXCL2	chemokine (C-X-C motif) ligand 2	3.615	3.851	0.94
G0S2	G0/G1switch 2	3.535	3.316	1.07
BDKRB1	bradykinin receptor B1	3.531	2.862	1.23
HBEGF	heparin-binding EGF-like growth factor	3.499	2.036	1.72
RNF144B	ring finger protein 144B	3.425	3.047	1.12
IL1B	interleukin 1, beta	3.412	2.508	1.36
ICAM1	intercellular adhesion molecule 1	3.3	2.668	1.24
BPGM	2,3-bisphosphoglycerate mutase	3.279	3.148	1.04
MAFF	v-maf musculoaponeurotic fibrosarcoma oncogene homolog F (avian)	3.279	2.589	1.27
IRAK2	interleukin-1 receptor-associated kinase 2	3.256	2.763	1.18
C15ORF48	chromosome 15 open reading frame 48	3.253	1.797	1.81
IRF1	interferon regulatory factor 1	3.244	2.76	1.18
NECAB1	N-terminal EF-hand calcium binding protein 1	3.211	1.923	1.67
NEDD9	neural precursor cell expressed, developmentally down-regulated 9	3.172	3.526	0.90
RASGRP3	RAS guanyl releasing protein 3 (calcium and DAG-regulated)	3.166	0.996	3.18
CLDN1	claudin 1	3.15	2.861	1.10
SLC26A9	solute carrier family 26, member 9	3.139	2.748	1.14
PDGFB	platelet-derived growth factor beta polypeptide (simian sarcoma viral (v-sis) oncogene homolog)	3.074	2.417	1.27
TNF	tumor necrosis factor	3.073	3.603	0.85

TNFAIP2	tumor necrosis factor, alpha-induced protein 2	3.064	2.495	1.23
BIRC3	baculoviral IAP repeat-containing 3	3.062	3.019	1.01
AQP9	aquaporin 9	2.993	1.807	1.66
IL1A	interleukin 1, alpha	2.989	2.849	1.05
GCH1	GTP cyclohydrolase 1	2.952	1.457	2.03
ABTB2	ankyrin repeat and BTB (POZ) domain containing 2	2.91	1.681	1.73
NFKBIA	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, alpha	2.904	2.812	1.03
C6ORF58	chromosome 6 open reading frame 58	2.901	2.99	0.97
NRG1	neuregulin 1	2.9	2.351	1.23
SLCO5A1	solute carrier organic anion transporter family, member 5A1	2.864	0.882	3.25
NFKBIE	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, epsilon	2.859	2.41	1.19
EGR2	early growth response 2	2.838	2.74	1.04
SESN2	sestrin 2	2.836	2.396	1.18
MMP3	matrix metallopeptidase 3 (stromelysin 1, progelatinase)	2.822	1.12	2.52
KIAA0247	KIAA0247	2.817	2.038	1.38
LINCR	neuralized homolog 3 (Drosophila) pseudogene	2.804	1.314	2.13
XAF1	XIAP associated factor 1	2.804	1.88	1.49
SPRY4	sprouty homolog 4 (Drosophila)	2.777	2.208	1.26
SAMD4A	sterile alpha motif domain containing 4A	2.752	1.191	2.31
PIM3	pim-3 oncogene	2.742	1.833	1.50
ADORA2A	adenosine A2a receptor	2.705	1.749	1.55
TNFRSF9	tumor necrosis factor receptor superfamily, member 9	2.704	2.122	1.27
TUBE1	tubulin, epsilon 1	2.687	2.496	1.08
ETS1	v-ets erythroblastosis virus E26 oncogene homolog 1 (avian)	2.681	1.83	1.47
NUAK2	NUAK family, SNF1-like kinase, 2	2.677	2.63	1.02
RCAN1	regulator of calcineurin 1	2.629	1.523	1.73
STX11	syntaxin 11	2.624	1.539	1.71
GDF15	growth differentiation factor 15	2.6	2.858	0.91
ZEB2	zinc finger E-box binding homeobox 2	2.526	2.147	1.18
KRT86	keratin 86	2.516	1.079	2.33
PGM2L1	phosphoglucomutase 2-like 1	2.448	0.942	2.60
RASEF	RAS and EF-hand domain containing	2.427	1.586	1.53
ECM2	extracellular matrix protein 2, female organ and adipocyte specific	2.421	1.74	1.39
ICOSLG	inducible T-cell co-stimulator ligand	2.412	1.668	1.45
STC2	stanniocalcin 2	2.409	2.158	1.12
RELB	v-rel reticuloendotheliosis viral oncogene homolog B	2.4	1.791	1.34
LOC644242	hypothetical LOC644242	2.386	1.664	1.43
C12ORF59	chromosome 12 open reading frame 59	2.373	1.934	1.23
ADAMTS9	ADAM metallopeptidase with thrombospondin type 1 motif, 9	2.369	1.229	1.93
TIFA	TRAF-interacting protein with forkhead-associated domain	2.364	2.73	0.87
PLEKHG1	pleckstrin homology domain containing, family G (with RhoGef domain) member 1	2.358	1.53	1.54
HIVEP1	human immunodeficiency virus type I enhancer binding protein 1	2.357	1.987	1.19
HDAC9	histone deacetylase 9	2.353	1.624	1.45
SERPINE1	serpin peptidase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 1	2.335	1.299	1.80
ADM2	adrenomedullin 2	2.325	2.014	1.15
SLC1A4	solute carrier family 1 (glutamate/neutral amino acid transporter), member 4	2.323	2.051	1.13

MAP3K8	mitogen-activated protein kinase kinase kinase 8	2.316	1.148	2.02
IL12A	interleukin 12A (natural killer cell stimulatory factor 1, cytotoxic lymphocyte maturation factor 1, p35)	2.307	1.855	1.24
PPP3CC	protein phosphatase 3, catalytic subunit, gamma isozyme	2.284	1.63	1.40
IL4I1	interleukin 4 induced 1	2.275	1.887	1.21
NCOA7	nuclear receptor coactivator 7	2.275	2.164	1.05
RND3	Rho family GTPase 3	2.274	1.952	1.16
CTH	cystathionase (cystathionine gamma-lyase)	2.264	1.791	1.26
ZC3H12A	zinc finger CCCH-type containing 12A	2.253	1.978	1.14
SLFN5	schlafen family member 5	2.251	1.428	1.58
SLC2A6	solute carrier family 2 (facilitated glucose transporter), member 6	2.246	1.654	1.36
NFKB2	nuclear factor of kappa light polypeptide gene enhancer in B-cells 2 (p49/p100)	2.239	1.623	1.38
STYK1	serine/threonine/tyrosine kinase 1	2.238	2.146	1.04
SLC39A14	solute carrier family 39 (zinc transporter), member 14	2.232	1.532	1.46
KRT75	keratin 75	2.223	0.848	2.62
PPP1R15B	protein phosphatase 1, regulatory (inhibitor) subunit 15B	2.223	1.887	1.18
CCL5	chemokine (C-C motif) ligand 5	2.222	0.891	2.49
DKFZP686O24166	hypothetical protein DKFZp686O24166	2.21	1.098	2.01
KLF6	Kruppel-like factor 6	2.209	1.978	1.12
GBP4 (includes EG:115361)	guanylate binding protein 4	2.198	0.658	3.34
IER3	immediate early response 3	2.193	2.411	0.91
SERTAD2	SERTA domain containing 2	2.188	1.479	1.48
USP54	ubiquitin specific peptidase 54	2.174	2.038	1.07
MSC	musculin	2.168	2.08	1.04
TNFAIP8	tumor necrosis factor, alpha-induced protein 8	2.162	1.578	1.37
DAAM1	dishevelled associated activator of morphogenesis 1	2.153	1.337	1.61
CD83	CD83 molecule	2.151	1.502	1.43
FUT4	fucosyltransferase 4 (alpha (1,3) fucosyltransferase, myeloid-specific)	2.14	1.663	1.29
ATF3	activating transcription factor 3	2.137	1.271	1.68
CD274	CD274 molecule	2.113	1.313	1.61
CEBPD	CCAAT/enhancer binding protein (C/EBP), delta	2.104	2.294	0.92
BDKRB2	bradykinin receptor B2	2.099	1.901	1.10
CREB5	cAMP responsive element binding protein 5	2.071	1.401	1.48
IFNAR2	interferon (alpha, beta and omega) receptor 2	2.066	1.819	1.14
STK40	serine/threonine kinase 40	2.063	1.453	1.42
IFNGR2	interferon gamma receptor 2 (interferon gamma transducer 1)	2.062	1.402	1.47
PIM1	pim-1 oncogene	2.061	1.957	1.05
FLJ46906	hypothetical protein LOC441172	2.046	1.296	1.58
AKAP2	A kinase (PRKA) anchor protein 2	2.042	1.061	1.92
PHLDB2	pleckstrin homology-like domain, family B, member 2	2.042	1.257	1.62
FOXO1	forkhead box O1	2.041	1.7	1.20
PPP1R15A	protein phosphatase 1, regulatory (inhibitor) subunit 15A	2.039	1.401	1.46
FLJ27255	hypothetical LOC401281	2.025	1.042	1.94
ABL2	v-abl Abelson murine leukemia viral oncogene homolog 2	2.023	2.143	0.94
ATP2B1	ATPase, Ca++ transporting, plasma membrane 1	2.022	1.096	1.84
SLC7A2	solute carrier family 7 (cationic amino acid transporter, y+ system), member 2	2.012	0.692	2.91
C10ORF47	chromosome 10 open reading frame 47	2.003	1.46	1.37
GFPT2	glutamine-fructose-6-phosphate transaminase 2	2.002	1.128	1.77
IFNGR1	interferon gamma receptor 1	2.001	2.063	0.97

PRIC285	peroxisomal proliferator-activated receptor A interacting complex 285	1.997	0.94	2.12
JUB	jub, ajuba homolog (Xenopus laevis)	1.994	1.995	1.00
LARP6	La ribonucleoprotein domain family, member 6	1.994	1.793	1.11
EPHA2	EPH receptor A2	1.99	1.461	1.36
CCDC93	coiled-coil domain containing 93	1.983	1.423	1.39
ST3GAL1	ST3 beta-galactoside alpha-2,3-sialyltransferase 1	1.971	1.159	1.70
RIPK2	receptor-interacting serine-threonine kinase 2	1.969	1.807	1.09
LAD1	ladinin 1	1.966	1.233	1.59
SOCS2	suppressor of cytokine signaling 2	1.956	1.507	1.30
PLD6	phospholipase D family, member 6	1.955	1.238	1.58
PPTC7	PTC7 protein phosphatase homolog (S. cerevisiae)	1.947	1.442	1.35
TRIM36	tripartite motif-containing 36	1.946	1.17	1.66
PMAIP1	phorbol-12-myristate-13-acetate-induced protein 1	1.944	1.668	1.17
RPA4	replication protein A4, 30kDa	1.938	1.564	1.24
CEBPG	CCAAT/enhancer binding protein (C/EBP), gamma	1.927	1.694	1.14
MTHFD2	methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 2, methenyltetrahydrofolate cyclohydrolase	1.926	1.543	1.25
ITPKA	inositol 1,4,5-trisphosphate 3-kinase A	1.925	1.1	1.75
NFKB1	nuclear factor of kappa light polypeptide gene enhancer in B-cells 1	1.924	1.269	1.52
PDXDC2	pyridoxal-dependent decarboxylase domain containing 2, pseudogene	1.919	2.048	0.94
WTAP	Wilms tumor 1 associated protein	1.917	1.383	1.39
ASNS	asparagine synthetase (glutamine-hydrolyzing)	1.911	1.603	1.19
CD55	CD55 molecule, decay accelerating factor for complement (Cromer blood group)	1.906	0.728	2.62
MX1	myxovirus (influenza virus) resistance 1, interferon-inducible protein p78 (mouse)	1.901	0.591	3.22
VDR	vitamin D (1,25- dihydroxyvitamin D3) receptor	1.896	1.037	1.83
PRO0628	hypothetical LOC29053	1.895	1.952	0.97
TRIB3	tribbles homolog 3 (Drosophila)	1.894	1.542	1.23
NFKBIZ	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, zeta	1.884	1.89	1.00
ITPRIP	inositol 1,4,5-triphosphate receptor interacting protein	1.874	1.379	1.36
B3GNT5	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 5	1.87	1.617	1.16
EFNA1	ephrin-A1	1.862	1.431	1.30
IL15RA	interleukin 15 receptor, alpha	1.856	0.816	2.27
FAS	Fas (TNF receptor superfamily, member 6)	1.85	1.41	1.31
TNIP1	TNFAIP3 interacting protein 1	1.848	1.276	1.45
ASAM	adipocyte-specific adhesion molecule	1.845	1.777	1.04
AHR	aryl hydrocarbon receptor	1.841	1.688	1.09
ZNFX1	zinc finger, NFX1-type containing 1	1.833	1.006	1.82
DUSP10	dual specificity phosphatase 10	1.831	2.113	0.87
DUSP8	dual specificity phosphatase 8	1.827	2.604	0.70
RGMB	RGM domain family, member B	1.826	1.398	1.31
SAT1	spermidine/spermine N1-acetyltransferase 1	1.814	1.437	1.26
RNF19B	ring finger protein 19B	1.799	0.896	2.01
TSC22D1	TSC22 domain family, member 1	1.787	1.48	1.21
ZSWIM4	zinc finger, SWIM-type containing 4	1.787	1.718	1.04
LMO4	LIM domain only 4	1.784	1.43	1.25
PCK2	phosphoenolpyruvate carboxykinase 2 (mitochondrial)	1.783	1.44	1.24
LOC285216	hypothetical protein LOC285216	1.777	1.476	1.20
SMOX	spermine oxidase	1.775	1.297	1.37
C17ORF68	chromosome 17 open reading frame 68	1.765	1.514	1.17

JUNB	jun B proto-oncogene	1.763	1.325	1.33
TNFRSF10B	tumor necrosis factor receptor superfamily, member 10b	1.763	1.44	1.22
P2RY2	purinergic receptor P2Y, G-protein coupled, 2	1.76	1.208	1.46
LRRC49	leucine rich repeat containing 49	1.756	1.28	1.37
BMP2	bone morphogenetic protein 2	1.737	0.997	1.74
SLC4A7	solute carrier family 4, sodium bicarbonate cotransporter, member 7	1.735	1.222	1.42
LRP12	low density lipoprotein receptor-related protein 12	1.733	1.184	1.46
ZBTB10	zinc finger and BTB domain containing 10	1.733	1.379	1.26
EHD1	EH-domain containing 1	1.732	0.655	2.64
ELL2	elongation factor, RNA polymerase II, 2	1.732	0.92	1.88
CFB	complement factor B	1.73	1.059	1.63
C7ORF40	chromosome 7 open reading frame 40	1.728	1.497	1.15
GBP1 (includes EG:2633)	guanylate binding protein 1, interferon-inducible, 67kDa	1.725	0.959	1.80
MXD1	MAX dimerization protein 1	1.72	0.967	1.78
KLF5	Kruppel-like factor 5 (intestinal)	1.71	0.96	1.78
TRAF4	TNF receptor-associated factor 4	1.704	1.245	1.37
FRMD6	FERM domain containing 6	1.696	1.065	1.59
DDIT3	DNA-damage-inducible transcript 3	1.686	1.598	1.06
NUP43	nucleoporin 43kDa	1.686	2.315	0.73
CITED4	Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain, 4	1.685	1.735	0.97
FGD6	FYVE, RhoGEF and PH domain containing 6	1.685	1.446	1.17
BIRC2	baculoviral IAP repeat-containing 2	1.678	1.312	1.28
CDC42EP2	CDC42 effector protein (Rho GTPase binding) 2	1.676	1.552	1.08
LACTB	lactamase, beta	1.663	1.219	1.36
CYLD	cylindromatosis (turban tumor syndrome)	1.659	1.049	1.58
ACHE	acetylcholinesterase	1.651	0.746	2.21
C9ORF72	chromosome 9 open reading frame 72	1.647	1.786	0.92
ASB6	ankyrin repeat and SOCS box-containing 6	1.645	1.132	1.45
PBX4	pre-B-cell leukemia homeobox 4	1.641	1.159	1.42
TRIB1	tribbles homolog 1 (Drosophila)	1.636	1.68	0.97
GABARAPL1	GABA(A) receptor-associated protein like 1	1.634	1.27	1.29
GEM	GTP binding protein overexpressed in skeletal muscle	1.627	1.128	1.44
CCRN4L	CCR4 carbon catabolite repression 4-like (S. cerevisiae)	1.625	1.409	1.15
SLC41A1	solute carrier family 41, member 1	1.623	1.079	1.50
C3ORF52	chromosome 3 open reading frame 52	1.622	0.956	1.70
C6ORF150	chromosome 6 open reading frame 150	1.621	1.614	1.00
CXCR7	chemokine (C-X-C motif) receptor 7	1.616	1.112	1.45
DUSP1	dual specificity phosphatase 1	1.616	1.715	0.94
ARL5B	ADP-ribosylation factor-like 5B	1.613	0.697	2.31
GPRC5A	G protein-coupled receptor, family C, group 5, member A	1.609	0.808	1.99
TNFAIP6	tumor necrosis factor, alpha-induced protein 6	1.608	1.264	1.27
PXK	PX domain containing serine/threonine kinase	1.607	1.695	0.95
TMEM217	transmembrane protein 217	1.606	0.753	2.13
CHIC2	cysteine-rich hydrophobic domain 2	1.604	1.038	1.55
DUSP5	dual specificity phosphatase 5	1.602	1.452	1.10
CYTH1	cytohesin 1	1.597	0.792	2.02
MFHAS1	malignant fibrous histiocytoma amplified sequence 1	1.594	1.018	1.57
SERPINA1	serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 1	1.594	0.952	1.67
ELOVL7	ELOVL family member 7, elongation of long chain fatty acids (yeast)	1.588	0.643	2.47
GTPBP2	GTP binding protein 2	1.58	1.442	1.10
ZFP42	zinc finger protein 42 homolog (mouse)	1.58	1.475	1.07

IFNE	interferon, epsilon	1.578	1.521	1.04
PPP1R14C	protein phosphatase 1, regulatory (inhibitor) subunit 14C	1.576	0.746	2.11
VEGFA	vascular endothelial growth factor A	1.576	1.409	1.12
RELA	v-rel reticuloendotheliosis viral oncogene homolog A (avian)	1.575	1.088	1.45
GLIS3	GLIS family zinc finger 3	1.563	0.906	1.73
SDC4	syndecan 4	1.561	0.931	1.68
USP53	ubiquitin specific peptidase 53	1.561	0.851	1.83
TRMT2B	TRM2 tRNA methyltransferase 2 homolog B (S. cerevisiae)	1.559	1.707	0.91
SHB	Src homology 2 domain containing adaptor protein B	1.558	0.907	1.72
PISD	phosphatidylserine decarboxylase	1.552	1.274	1.22
BCL3	B-cell CLL/lymphoma 3	1.548	1.31	1.18
DCLRE1B	DNA cross-link repair 1B	1.547	1.086	1.42
CLIP2	CAP-GLY domain containing linker protein 2	1.546	0.601	2.57
RBMS1	RNA binding motif, single stranded interacting protein 1	1.54	1.252	1.23
SLC22A4	solute carrier family 22 (organic cation/ergothioneine transporter), member 4	1.54	0.698	2.21
ALOXE3	arachidonate lipoxygenase 3	1.537	0.753	2.04
CBX4	chromobox homolog 4	1.536	0.88	1.75
GRPEL2	GrpE-like 2, mitochondrial (E. coli)	1.536	1.488	1.03
MBNL2	muscleblind-like 2 (Drosophila)	1.534	0.977	1.57
MAFG	v-maf musculoaponeurotic fibrosarcoma oncogene homolog G (avian)	1.533	1.088	1.41
NAV3	neuron navigator 3	1.52	0.857	1.77
C1QTNF1	C1q and tumor necrosis factor related protein 1	1.513	0.888	1.70
ARSJ	arylsulfatase family, member J	1.504	0.956	1.57
ZBTB46	zinc finger and BTB domain containing 46	1.504	1.106	1.36
MESDC1	mesoderm development candidate 1	1.498	1.263	1.19
TGFB2	transforming growth factor, beta 2	1.497	0.895	1.67
TNFRSF10A	tumor necrosis factor receptor superfamily, member 10a	1.496	1.067	1.40
CYP26A1	cytochrome P450, family 26, subfamily A, polypeptide 1	1.495	1.064	1.41
KIF21B	kinesin family member 21B	1.495	1.136	1.32
A4GALT	alpha 1,4-galactosyltransferase	1.494	1.112	1.34
GADD45A	growth arrest and DNA-damage-inducible, alpha	1.493	1.688	0.88
HKDC1	hexokinase domain containing 1	1.482	1.151	1.29
GPT2	glutamic pyruvate transaminase (alanine aminotransferase) 2	1.48	1.46	1.01
LONRF3	LON peptidase N-terminal domain and ring finger 3	1.478	0.917	1.61
SLC38A2	solute carrier family 38, member 2	1.478	1.451	1.02
DGKI	diacylglycerol kinase, iota	1.476	0.868	1.70
REPS2	RALBP1 associated Eps domain containing 2	1.476	0.823	1.79
RAB9A	RAB9A, member RAS oncogene family	1.473	1.18	1.25
GOLGA7B	golgin A7 family, member B	1.457	0.692	2.11
RAPH1	Ras association (RalGDS/AF-6) and pleckstrin homology domains 1	1.457	0.843	1.73
DUSP16	dual specificity phosphatase 16	1.452	1.514	0.96
ZBTB17	zinc finger and BTB domain containing 17	1.449	1.133	1.28
C3ORF59	chromosome 3 open reading frame 59	1.448	0.99	1.46
URGCP	upregulator of cell proliferation	1.448	1.239	1.17
CDV3	CDV3 homolog (mouse)	1.447	0.908	1.59
PRKCD	protein kinase C, delta	1.445	0.803	1.80
CDK6	cyclin-dependent kinase 6	1.439	0.775	1.86
NAV2	neuron navigator 2	1.438	0.702	2.05
KLF9	Kruppel-like factor 9	1.435	1.021	1.41
PSAT1	phosphoserine aminotransferase 1	1.435	1.187	1.21

TPM1	tropomyosin 1 (alpha)	1.435	2.269	0.63
JMY	junction mediating and regulatory protein, p53 cofactor	1.433	1.138	1.26
AFAP1	actin filament associated protein 1	1.43	0.812	1.76
DKFZP434K191	POM121 membrane glycoprotein-like 8 pseudogene	1.427	1.332	1.07
FAM84B	family with sequence similarity 84, member B	1.426	0.961	1.48
KYNU	kynureninase (L-kynurenine hydrolase)	1.422	1.041	1.37
PKDCC	protein kinase domain containing, cytoplasmic homolog (mouse)	1.421	1.064	1.34
DTX2	deltex homolog 2 (Drosophila)	1.42	1.126	1.26
STK10	serine/threonine kinase 10	1.417	0.678	2.09
NUPR1	nuclear protein, transcriptional regulator, 1	1.415	1.216	1.16
ZNF295	zinc finger protein 295	1.415	1.355	1.04
SLC7A1	solute carrier family 7 (cationic amino acid transporter, y+ system), member 1	1.409	0.889	1.58
NCEH1	neutral cholesterol ester hydrolase 1	1.405	0.915	1.54
NUAK1	NUAK family, SNF1-like kinase, 1	1.405	0.909	1.55
IL7R	interleukin 7 receptor	1.404	0.933	1.50
RBBP9	retinoblastoma binding protein 9	1.404	1.319	1.06
PHC2	polyhomeotic homolog 2 (Drosophila)	1.399	0.956	1.46
SH2D5	SH2 domain containing 5	1.394	0.63	2.21
TNIP3	TNFAIP3 interacting protein 3	1.393	1.385	1.01
CLCF1	cardiotrophin-like cytokine factor 1	1.392	1.086	1.28
FLJ40448	hypothetical protein FLJ40448	1.391	0.827	1.68
IFNAR1	interferon (alpha, beta and omega) receptor 1	1.391	1.017	1.37
CDC42EP3	CDC42 effector protein (Rho GTPase binding) 3	1.39	0.674	2.06
FCF1 (includes EG:51077)	FCF1 small subunit (SSU) processome component homolog (S. cerevisiae)	1.384	1.454	0.95
GJC1	gap junction protein, gamma 1, 45kDa	1.384	0.994	1.39
ITGAM	integrin, alpha M (complement component 3 receptor 3 subunit)	1.381	1.017	1.36
SMAD3	SMAD family member 3	1.379	1.086	1.27
STARD13	StAR-related lipid transfer (START) domain containing 13	1.375	1.459	0.94
CARS	cysteinyl-tRNA synthetase	1.366	1.008	1.36
LRRC8C	leucine rich repeat containing 8 family, member C	1.366	0.61	2.24
HAS3	hyaluronan synthase 3	1.364	0.617	2.21
CSGALNACT2	chondroitin sulfate N-acetylgalactosaminyltransferase 2	1.359	0.62	2.19
SPEN	spen homolog, transcriptional regulator (Drosophila)	1.357	0.949	1.43
PRICKLE3	prickle homolog 3 (Drosophila)	1.355	0.945	1.43
TBC1D10A	TBC1 domain family, member 10A	1.352	1.072	1.26
FOSL1	FOS-like antigen 1	1.351	1.013	1.33
H6PD	hexose-6-phosphate dehydrogenase (glucose 1-dehydrogenase)	1.351	0.833	1.62
SLC41A2	solute carrier family 41, member 2	1.349	0.705	1.91
TTC39B	tetratricopeptide repeat domain 39B	1.344	0.951	1.41
VEGFC	vascular endothelial growth factor C	1.342	0.887	1.51
RAB24	RAB24, member RAS oncogene family	1.333	0.73	1.83
NIPA1	non imprinted in Prader-Willi/Angelman syndrome 1	1.329	0.914	1.45
ARHGAP42	Rho GTPase activating protein 42	1.323	0.773	1.71
IL15	interleukin 15	1.318	0.748	1.76
SOCS3	suppressor of cytokine signaling 3	1.318	0.616	2.14
IFRD1	interferon-related developmental regulator 1	1.317	0.932	1.41
RGPD6	RANBP2-like and GRIP domain containing 6	1.317	1.816	0.73
TICAM1	toll-like receptor adaptor molecule 1	1.306	1.128	1.16
PVR	poliovirus receptor	1.304	0.847	1.54
CYTH2	cytohesin 2	1.303	0.915	1.42
TRIM47	tripartite motif-containing 47	1.302	0.681	1.91

FSTL3	follistatin-like 3 (secreted glycoprotein)	1.294	0.62	2.09
KCTD13	potassium channel tetramerisation domain containing 13	1.294	0.973	1.33
OGT	O-linked N-acetylglucosamine (GlcNAc) transferase (UDP-N-acetylglucosamine:polypeptide-N-acetylglucosaminyl transferase)	1.294	1.016	1.27
SLC22A23	solute carrier family 22, member 23	1.294	0.708	1.83
SPSB1	splA/ryanodine receptor domain and SOCS box containing 1	1.291	0.619	2.09
USP12	ubiquitin specific peptidase 12	1.286	0.604	2.13
GABPB1	GA binding protein transcription factor, beta subunit 1	1.285	0.687	1.87
GOLGA8G	golgin A8 family, member G	1.282	1.182	1.08
LOC441124	hypothetical gene supported by AK093729; BX647918	1.281	1.079	1.19
BHLHE41	basic helix-loop-helix family, member e41	1.276	0.613	2.08
C3	complement component 3	1.275	1.12	1.14
FUBP3	far upstream element (FUSE) binding protein 3	1.273	1.295	0.98
PTGER4	prostaglandin E receptor 4 (subtype EP4)	1.273	1.294	0.98
CEBPB	CCAAT/enhancer binding protein (C/EBP), beta	1.272	1.238	1.03
F3	coagulation factor III (thromboplastin, tissue factor)	1.272	1.467	0.87
PPARD	peroxisome proliferator-activated receptor delta	1.272	0.874	1.46
HSPBAP1	HSPB (heat shock 27kDa) associated protein 1	1.264	0.88	1.44
PPAN	peter pan homolog (Drosophila)	1.264	1.065	1.19
FJX1	four jointed box 1 (Drosophila)	1.263	0.873	1.45
BAZ1A	bromodomain adjacent to zinc finger domain, 1A	1.257	0.922	1.36
CDC14A	CDC14 cell division cycle 14 homolog A (S. cerevisiae)	1.253	1.133	1.11
TNKS1BP1	tankyrase 1 binding protein 1, 182kDa	1.248	0.81	1.54
SOX9	SRY (sex determining region Y)-box 9	1.247	1.031	1.21
TNIP2	TNFAIP3 interacting protein 2	1.246	0.972	1.28
WWC1	WW and C2 domain containing 1	1.246	0.751	1.66
LONRF1	LON peptidase N-terminal domain and ring finger 1	1.244	1.106	1.12
NAB1	NGFI-A binding protein 1 (EGR1 binding protein 1)	1.243	0.867	1.43
TMEM156	transmembrane protein 156	1.243	0.84	1.48
TNFRSF12A	tumor necrosis factor receptor superfamily, member 12A	1.241	0.804	1.54
UBTD2	ubiquitin domain containing 2	1.241	0.739	1.68
ZXDA	zinc finger, X-linked, duplicated A	1.24	1.507	0.82
ELK4	ELK4, ETS-domain protein (SRF accessory protein 1)	1.238	0.908	1.36
MARS	methionyl-tRNA synthetase	1.237	0.965	1.28
MYO3B	myosin IIIB	1.233	1.586	0.78
ZMIZ2	zinc finger, MIZ-type containing 2	1.233	0.862	1.43
PPP1R3F	protein phosphatase 1, regulatory (inhibitor) subunit 3F	1.23	0.774	1.59
OTUD4	OTU domain containing 4	1.228	0.711	1.73
DDX21	DEAD (Asp-Glu-Ala-Asp) box polypeptide 21	1.227	0.928	1.32
DDX10	DEAD (Asp-Glu-Ala-Asp) box polypeptide 10	1.225	1.048	1.17
TNFAIP1	tumor necrosis factor, alpha-induced protein 1 (endothelial)	1.225	0.743	1.65
SUPV3L1	suppressor of var1, 3-like 1 (S. cerevisiae)	1.221	0.997	1.22
JUND	jun D proto-oncogene	1.22	1.086	1.12
CFLAR	CASP8 and FADD-like apoptosis regulator	1.218	1.035	1.18
GSG1L	GSG1-like	1.218	0.997	1.22
GPR125	G protein-coupled receptor 125	1.216	1.55	0.78
CYB5R2	cytochrome b5 reductase 2	1.215	0.792	1.53
AGPHD1	aminoglycoside phosphotransferase domain containing 1	1.214	1.574	0.77
SBNO2	strawberry notch homolog 2 (Drosophila)	1.209	0.896	1.35
TPRA1	transmembrane protein, adipocyte asscociated 1	1.209	0.605	2.00
FAM129A	family with sequence similarity 129, member A	1.207	0.595	2.03
LOC387895	hypothetical LOC387895	1.207	0.65	1.86
SH2B3	SH2B adaptor protein 3	1.205	0.617	1.95

ELF4	E74-like factor 4 (ets domain transcription factor)	1.204	0.688	1.75
GOLGA8F	golgin A8 family, member F	1.204	1.158	1.04
RFFL	ring finger and FYVE-like domain containing 1	1.204	1.014	1.19
STK17A	serine/threonine kinase 17a	1.198	1.252	0.96
SLC25A22	solute carrier family 25 (mitochondrial carrier: glutamate), member 22	1.196	0.612	1.95
E2F7	E2F transcription factor 7	1.195	0.725	1.65
APOL6	apolipoprotein L, 6	1.193	0.838	1.42
CPEB2	cytoplasmic polyadenylation element binding protein 2	1.192	0.916	1.30
RFTN1	raftlin, lipid raft linker 1	1.189	0.666	1.79
C9ORF150	chromosome 9 open reading frame 150	1.185	1.29	0.92
HRH1	histamine receptor H1	1.183	0.762	1.55
TRIM8	tripartite motif-containing 8	1.18	0.855	1.38
DDIT4	DNA-damage-inducible transcript 4	1.179	1.248	0.94
IL18BP	interleukin 18 binding protein	1.179	0.629	1.87
AKR1B15	aldo-keto reductase family 1, member B15	1.178	1.11	1.06
ALPK2	alpha-kinase 2	1.177	0.666	1.77
ROR1	receptor tyrosine kinase-like orphan receptor 1	1.175	0.653	1.80
ZFP36	zinc finger protein 36, C3H type, homolog (mouse)	1.175	0.629	1.87
INF2	inverted formin, FH2 and WH2 domain containing	1.173	1.05	1.12
TRIO	triple functional domain (PTPRF interacting)	1.171	0.61	1.92
ARID5A	AT rich interactive domain 5A (MRF1-like)	1.17	0.92	1.27
GNB4	guanine nucleotide binding protein (G protein), beta polypeptide 4	1.169	1.05	1.11
PHLDA1	pleckstrin homology-like domain, family A, member 1	1.167	1.35	0.86
ZNF609	zinc finger protein 609	1.165	1.195	0.97
CBS	cystathionine-beta-synthase	1.159	0.789	1.47
RBBP8	retinoblastoma binding protein 8	1.159	0.778	1.49
FAM65A	family with sequence similarity 65, member A	1.158	0.756	1.53
GOPC	golgi-associated PDZ and coiled-coil motif containing	1.156	1.223	0.95
ZNF296	zinc finger protein 296	1.153	0.67	1.72
PPIF	peptidylprolyl isomerase F	1.152	0.742	1.55
NOC3L	nucleolar complex associated 3 homolog (S. cerevisiae)	1.149	0.591	1.94
ENGASE	endo-beta-N-acetylglucosaminidase	1.148	1.046	1.10
MOBKL2C	MOB1, Mps One Binder kinase activator-like 2C (yeast)	1.148	0.605	1.90
TRIM56	tripartite motif-containing 56	1.146	0.596	1.92
CREB1	cAMP responsive element binding protein 1	1.144	1.116	1.03
SLC6A9	solute carrier family 6 (neurotransmitter transporter, glycine), member 9	1.143	0.779	1.47
MGC2752	hypothetical LOC65996	1.141	1.142	1.00
GRB7	growth factor receptor-bound protein 7	1.14	0.991	1.15
NFE2L1	nuclear factor (erythroid-derived 2)-like 1	1.14	0.835	1.37
AP1AR	adaptor-related protein complex 1 associated regulatory protein	1.135	0.952	1.19
XBP1	X-box binding protein 1	1.134	1.072	1.06
UGCG	UDP-glucose ceramide glucosyltransferase	1.131	1.352	0.84
LDLR	low density lipoprotein receptor	1.13	0.82	1.38
OBFC2A	oligonucleotide/oligosaccharide-binding fold containing 2A	1.13	1.113	1.02
LHFPL2	lipoma HMGIC fusion partner-like 2	1.127	0.596	1.89
RPL23AP13	ribosomal protein L23a pseudogene 32	1.126	1.209	0.93
YRDC	yrdC domain containing (E. coli)	1.117	1.18	0.95
SMURF1	SMAD specific E3 ubiquitin protein ligase 1	1.115	0.816	1.37
C10ORF12	chromosome 10 open reading frame 12	1.114	0.639	1.74
SRF	serum response factor (c-fos serum response element-binding transcription factor)	1.114	0.807	1.38
ARHGEF2	Rho/Rac guanine nucleotide exchange factor (GEF) 2	1.113	0.975	1.14

DENND4A	DENN/MADD domain containing 4A	1.113	0.614	1.81
MED13	mediator complex subunit 13	1.112	0.654	1.70
OSMR	oncostatin M receptor	1.112	0.644	1.73
TRIM65	tripartite motif-containing 65	1.111	1.328	0.84
LAMB3	laminin, beta 3	1.109	0.803	1.38
PAX8	paired box 8	1.109	0.72	1.54
HIVEP2	human immunodeficiency virus type I enhancer binding protein 2	1.108	0.712	1.56
CNNM4	cyclin M4	1.105	0.935	1.18
HELB	helicase (DNA) B	1.105	1.19	0.93
TRIP10	thyroid hormone receptor interactor 10	1.105	0.659	1.68
KIAA0355	KIAA0355	1.1	0.891	1.23
RASSF1	Ras association (RalGDS/AF-6) domain family member 1	1.099	0.766	1.43
NNMT	nicotinamide N-methyltransferase	1.098	0.701	1.57
RNF24	ring finger protein 24	1.096	0.63	1.74
PPP2R5B	protein phosphatase 2, regulatory subunit B', beta	1.095	0.792	1.38
PTPN1	protein tyrosine phosphatase, non-receptor type 1	1.095	0.598	1.83
CA2	carbonic anhydrase II	1.093	1.087	1.01
TLR1	toll-like receptor 1	1.093	1.261	0.87
PPAN-P2RY11	PPAN-P2RY11 readthrough	1.085	1.28	0.85
CCBE1	collagen and calcium binding EGF domains 1	1.083	1.257	0.86
LRRFIP2	leucine rich repeat (in FLII) interacting protein 2	1.083	0.902	1.20
ASPHD2	aspartate beta-hydroxylase domain containing 2	1.082	0.999	1.08
C14ORF82	chromosome 14 open reading frame 82	1.082	1.607	0.67
PRKAG2	protein kinase, AMP-activated, gamma 2 non-catalytic subunit	1.082	0.624	1.73
EYA4	eyes absent homolog 4 (Drosophila)	1.081	1.094	0.99
FAM176A	family with sequence similarity 176, member A	1.081	0.713	1.52
SKIL	SKI-like oncogene	1.081	1.01	1.07
KDM4A	lysine (K)-specific demethylase 4A	1.078	1.005	1.07
CSNK1E	casein kinase 1, epsilon	1.077	1.081	1.00
IL4R	interleukin 4 receptor	1.075	0.848	1.27
LOC653879	similar to Complement C3 precursor	1.075	0.932	1.15
PLIN5	perilipin 5	1.074	1.232	0.87
JUN	jun proto-oncogene	1.073	0.672	1.60
LOC648852	T cell receptor gamma variable 5	1.073	1.397	0.77
TBC1D22B	TBC1 domain family, member 22B	1.073	0.818	1.31
EIF1	eukaryotic translation initiation factor 1	1.072	0.674	1.59
RBM24	RNA binding motif protein 24	1.068	0.706	1.51
TFIP11	tuftelin interacting protein 11	1.066	0.731	1.46
GAB2	GRB2-associated binding protein 2	1.065	0.871	1.22
GINS4	GINS complex subunit 4 (Sld5 homolog)	1.065	1.435	0.74
FOXK1	forkhead box K1	1.059	0.734	1.44
OSGIN2	oxidative stress induced growth inhibitor family member 2	1.059	0.988	1.07
NFAT5	nuclear factor of activated T-cells 5, tonicity-responsive	1.055	0.718	1.47
XRCC2	X-ray repair complementing defective repair in Chinese hamster cells 2	1.052	1.34	0.79
PTPN12	protein tyrosine phosphatase, non-receptor type 12	1.049	0.85	1.23
MARK2	MAP/microtubule affinity-regulating kinase 2	1.047	0.734	1.43
WDR33	WD repeat domain 33	1.044	0.748	1.40
MLL	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila)	1.043	0.925	1.13
MLLT6	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 6	1.041	0.875	1.19
CSRNP2	cysteine-serine-rich nuclear protein 2	1.037	0.767	1.35
CCDC59	coiled-coil domain containing 59	1.035	0.766	1.35

COQ10B	coenzyme Q10 homolog B (S. cerevisiae)	1.031	0.797	1.29
IL1RAP	interleukin 1 receptor accessory protein	1.031	1.001	1.03
PIP5K1A	phosphatidylinositol-4-phosphate 5-kinase, type I, alpha	1.03	0.775	1.33
RBPMS	RNA binding protein with multiple splicing	1.03	0.684	1.51
RGS17	regulator of G-protein signaling 17	1.03	0.827	1.25
DDX52	DEAD (Asp-Glu-Ala-Asp) box polypeptide 52	1.029	0.975	1.06
ETV5	ets variant 5	1.029	0.781	1.32
CATSPER2	cation channel, sperm associated 2	1.027	1.219	0.84
ARHGAP29	Rho GTPase activating protein 29	1.026	1.027	1.00
FAM100B	family with sequence similarity 100, member B	1.026	0.723	1.42
SEMA3C	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3C	1.024	0.639	1.60
SEMA3E	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3E	1.024	1.206	0.85
WDR43	WD repeat domain 43	1.022	0.658	1.55
CCNJL	cyclin J-like	1.02	0.761	1.34
FCAR	Fc fragment of IgA, receptor for	1.02	1.098	0.93
TLK2	tousled-like kinase 2	1.02	0.736	1.39
DCBLD1	discoidin, CUB and LCCL domain containing 1	1.019	1.122	0.91
BMP2K	BMP2 inducible kinase	1.018	0.802	1.27
REL	v-rel reticuloendotheliosis viral oncogene homolog (avian)	1.018	1.434	0.71
C7ORF53	chromosome 7 open reading frame 53	1.017	0.746	1.36
TDRD1	tudor domain containing 1	1.017	1.066	0.95
RGNEF	190 kDa guanine nucleotide exchange factor	1.016	1.398	0.73
BID	BH3 interacting domain death agonist	1.014	0.753	1.35
TAB2	TGF-beta activated kinase 1/MAP3K7 binding protein 2	1.014	0.661	1.53
ZNF643	zinc finger protein 643	1.014	1.137	0.89
TLR6	toll-like receptor 6	1.011	0.952	1.06
STEAP1	six transmembrane epithelial antigen of the prostate 1	1.01	0.821	1.23
GATSL3	GATS protein-like 3	1.009	1.097	0.92
ADAM17	ADAM metallopeptidase domain 17	1.008	0.768	1.31
IKBKE	inhibitor of kappa light polypeptide gene enhancer in B-cells, kinase epsilon	1.007	0.841	1.20
MMD	monocyte to macrophage differentiation-associated	1.007	0.859	1.17
PILRA	paired immunoglobin-like type 2 receptor alpha	1.006	1.242	0.81
SSH1	slingshot homolog 1 (Drosophila)	1.006	0.827	1.22
WBP4	WW domain binding protein 4 (formin binding protein 21)	1.006	0.653	1.54
FOXC2	forkhead box C2 (MFH-1, mesenchyme forkhead 1)	1.005	0.836	1.20
RAB8B	RAB8B, member RAS oncogene family	1.003	0.799	1.26
ATF4	activating transcription factor 4 (tax-responsive enhancer element B67)	1	1.147	0.87
ANKRD11	ankyrin repeat domain 11	0.999	0.659	1.52
ARFRP1	ADP-ribosylation factor related protein 1	0.999	0.745	1.34
COL27A1	collagen, type XXVII, alpha 1	0.999	0.754	1.32
MICALL1	MICAL-like 1	0.999	0.672	1.49
ADO	2-aminoethanethiol (cysteamine) dioxygenase	0.993	0.784	1.27
IL6ST	interleukin 6 signal transducer (gp130, oncostatin M receptor)	0.991	0.738	1.34
BLZF1	basic leucine zipper nuclear factor 1	0.988	1.215	0.81
WDFY2	WD repeat and FYVE domain containing 2	0.987	0.676	1.46
INSIG2	insulin induced gene 2	0.986	0.594	1.66
GRIPAP1	GRIP1 associated protein 1	0.985	1.281	0.77
CLK4	CDC-like kinase 4	0.981	0.951	1.03
SLC5A8	solute carrier family 5 (iodide transporter), member 8	0.979	1.333	0.73
AKIRIN1	akirin 1	0.977	0.808	1.21
SHROOM4	shroom family member 4	0.977	1.155	0.85

C9ORF30	chromosome 9 open reading frame 30	0.976	0.664	1.47
WNT5A	wingless-type MMTV integration site family, member 5A	0.975	0.696	1.40
DCP1A	DCP1 decapping enzyme homolog A (S. cerevisiae)	0.974	0.75	1.30
NRIP1	nuclear receptor interacting protein 1	0.974	0.776	1.26
IL10RB	interleukin 10 receptor, beta	0.973	0.751	1.30
PLSCR1	phospholipid scramblase 1	0.973	0.733	1.33
CLK3	CDC-like kinase 3	0.972	0.964	1.01
GARS	glycyl-tRNA synthetase	0.972	0.784	1.24
IER5	immediate early response 5	0.972	0.618	1.57
UCN2	urocortin 2	0.972	1.006	0.97
FAM53C	family with sequence similarity 53, member C	0.971	0.908	1.07
FAM73A	family with sequence similarity 73, member A	0.971	1.237	0.78
CASK	calcium/calmodulin-dependent serine protein kinase (MAGUK family)	0.969	0.698	1.39
PUS1	pseudouridylate synthase 1	0.968	0.792	1.22
USP25	ubiquitin specific peptidase 25	0.967	0.76	1.27
BRAF	v-raf murine sarcoma viral oncogene homolog B1	0.965	0.646	1.49
ZFYVE27	zinc finger, FYVE domain containing 27	0.962	0.764	1.26
DEM1	defects in morphology 1 homolog (S. cerevisiae)	0.961	1.201	0.80
KIAA1751	KIAA1751	0.957	1.265	0.76
ARL13B	ADP-ribosylation factor-like 13B	0.955	0.938	1.02
SPDYE6	speedy homolog E6 (Xenopus laevis)	0.955	1.198	0.80
CHD1	chromodomain helicase DNA binding protein 1	0.954	0.871	1.10
TJAP1	tight junction associated protein 1 (peripheral)	0.952	0.813	1.17
C19ORF61	chromosome 19 open reading frame 61	0.951	0.736	1.29
ZNF549	zinc finger protein 549	0.948	1.264	0.75
MCART1	mitochondrial carrier triple repeat 1	0.946	1.193	0.79
POLR3D	polymerase (RNA) III (DNA directed) polypeptide D, 44kDa	0.946	0.699	1.35
TMEM17	transmembrane protein 17	0.946	1.343	0.70
SIAH1	seven in absentia homolog 1 (Drosophila)	0.945	0.969	0.98
SLC25A25	solute carrier family 25 (mitochondrial carrier; phosphate carrier), member 25	0.945	0.712	1.33
MYC	v-myc myelocytomatosis viral oncogene homolog (avian)	0.944	1.206	0.78
SLC30A1	solute carrier family 30 (zinc transporter), member 1	0.943	0.802	1.18
CYTSA	cytospin A	0.942	0.76	1.24
AXIN1	axin 1	0.941	0.703	1.34
C1ORF55	chromosome 1 open reading frame 55	0.941	0.738	1.28
CDC42EP1	CDC42 effector protein (Rho GTPase binding) 1	0.941	0.688	1.37
PLK2	polo-like kinase 2	0.941	1.472	0.64
NPC1	Niemann-Pick disease, type C1	0.939	0.809	1.16
CD44	CD44 molecule (Indian blood group)	0.938	0.674	1.39
MAGT1	magnesium transporter 1	0.938	1.196	0.78
KCMF1	potassium channel modulatory factor 1	0.936	0.61	1.53
EGLN2	egl nine homolog 2 (C. elegans)	0.935	0.791	1.18
TANK	TRAF family member-associated NFKB activator	0.935	0.86	1.09
ZNF14	zinc finger protein 14	0.935	1.413	0.66
PKD1	polycystic kidney disease 1 (autosomal dominant)	0.934	0.764	1.22
NAT9	N-acetyltransferase 9 (GCN5-related, putative)	0.93	0.676	1.38
ZNF774	zinc finger protein 774	0.929	1.619	0.57
ISM1	isthmin 1 homolog (zebrafish)	0.926	0.592	1.56
DUSP19	dual specificity phosphatase 19	0.925	1.07	0.86
LMOD3	leiomodin 3 (fetal)	0.925	1.46	0.63
RSL24D1	ribosomal L24 domain containing 1	0.925	0.658	1.41
GNA13	guanine nucleotide binding protein (G protein), alpha 13	0.922	0.695	1.33
INO80D	INO80 complex subunit D	0.918	0.677	1.36

KIF3C	kinesin family member 3C	0.918	0.663	1.38
SPN	sialophorin	0.917	1.146	0.80
C11ORF63	chromosome 11 open reading frame 63	0.915	1.021	0.90
C7ORF55	chromosome 7 open reading frame 55	0.915	1.222	0.75
PAWR	PRKC, apoptosis, WT1, regulator	0.913	0.663	1.38
FAM110A	family with sequence similarity 110, member A	0.912	0.946	0.96
NFIL3	nuclear factor, interleukin 3 regulated	0.912	1.232	0.74
EGLN1	egl nine homolog 1 (C. elegans)	0.911	0.614	1.48
CNOT4	CCR4-NOT transcription complex, subunit 4	0.91	0.965	0.94
FBXO11	F-box protein 11	0.91	0.753	1.21
LIMK2	LIM domain kinase 2	0.906	1.061	0.85
NAMPT	nicotinamide phosphoribosyltransferase	0.906	0.901	1.01
ANKRD44	ankyrin repeat domain 44	0.905	1.065	0.85
JAG1	jagged 1	0.903	0.91	0.99
MBTD1	mbt domain containing 1	0.903	1.493	0.60
MEX3C	mex-3 homolog C (C. elegans)	0.903	0.661	1.37
RNF19A	ring finger protein 19A	0.903	0.707	1.28
RUNX2	runt-related transcription factor 2	0.897	0.93	0.96
SATB2	SATB homeobox 2	0.896	0.658	1.36
SLC35E1	solute carrier family 35, member E1	0.894	0.989	0.90
HNRPDL	heterogeneous nuclear ribonucleoprotein D-like	0.893	0.642	1.39
FBRS	fibrosin	0.892	0.738	1.21
SARS	seryl-tRNA synthetase	0.892	0.601	1.48
SLC38A1	solute carrier family 38, member 1	0.892	0.648	1.38
TDP1	tyrosyl-DNA phosphodiesterase 1	0.892	1.131	0.79
ARIH1	ariadne homolog, ubiquitin-conjugating enzyme E2 binding protein, 1 (Drosophila)	0.891	0.679	1.31
CHRNA5	cholinergic receptor, nicotinic, alpha 5	0.891	1.174	0.76
GMEB2	glucocorticoid modulatory element binding protein 2	0.891	0.836	1.07
DNMT3B	DNA (cytosine-5-)-methyltransferase 3 beta	0.89	0.716	1.24
ZNF319	zinc finger protein 319	0.89	0.98	0.91
SH3PXD2B	SH3 and PX domains 2B	0.889	0.645	1.38
NDEL1	nudE nuclear distribution gene E homolog (A. nidulans)-like 1	0.888	0.684	1.30
VEZT	vezatin, adherens junctions transmembrane protein	0.887	0.587	1.51
TRIM13	tripartite motif-containing 13	0.886	0.936	0.95
NLK	nemo-like kinase	0.885	0.594	1.49
C3ORF34	chromosome 3 open reading frame 34	0.884	1.032	0.86
FAM131A	family with sequence similarity 131, member A	0.884	0.904	0.98
SLMO1	slowmo homolog 1 (Drosophila)	0.882	0.812	1.09
EBI3	Epstein-Barr virus induced 3	0.878	0.622	1.41
ZCCHC7	zinc finger, CCHC domain containing 7	0.878	0.636	1.38
QPCT (includes EG:25797)	glutaminyl-peptide cyclotransferase	0.877	0.664	1.32
ABL1	c-abl oncogene 1, non-receptor tyrosine kinase	0.876	0.618	1.42
KIAA1310	KIAA1310	0.875	0.683	1.28
ZNF669	zinc finger protein 669	0.874	0.797	1.10
MTMR3	myotubularin related protein 3	0.873	0.77	1.13
NPIPL3	nuclear pore complex interacting protein-like 3	0.873	0.734	1.19
TNS1	tensin 1	0.873	0.596	1.46
ZBTB7B	zinc finger and BTB domain containing 7B	0.869	0.909	0.96
CEP120	centrosomal protein 120kDa	0.867	0.864	1.00
WAC	WW domain containing adaptor with coiled-coil	0.867	0.76	1.14
SNAPC1	small nuclear RNA activating complex, polypeptide 1, 43kDa	0.861	0.864	1.00
NLRP8	NLR family, pyrin domain containing 8	0.86	1.174	0.73

PML	promyelocytic leukemia	0.859	0.699	1.23
ZNF787	zinc finger protein 787	0.858	0.622	1.38
CHST15	carbohydrate (N-acetylgalactosamine 4-sulfate 6-O) sulfotransferase 15	0.857	0.685	1.25
LOC646463	ubiquitin-conjugating enzyme E2H (UBC8 homolog, yeast) pseudogene 1	0.857	0.784	1.09
ZNF160	zinc finger protein 160	0.857	1.092	0.78
RPL37	ribosomal protein L37	0.856	0.795	1.08
HECA	headcase homolog (Drosophila)	0.855	0.869	0.98
DDX51	DEAD (Asp-Glu-Ala-Asp) box polypeptide 51	0.854	1.16	0.74
GTPBP4	GTP binding protein 4	0.853	0.646	1.32
EID3	EP300 interacting inhibitor of differentiation 3	0.852	0.928	0.92
ULK1	unc-51-like kinase 1 (C. elegans)	0.849	0.914	0.93
N4BP2	NEDD4 binding protein 2	0.848	1.014	0.84
METRNL	meteorin, glial cell differentiation regulator-like	0.847	0.619	1.37
ZNF394	zinc finger protein 394	0.846	1.056	0.80
ARID1A	AT rich interactive domain 1A (SWI-like)	0.843	0.591	1.43
C7ORF41	chromosome 7 open reading frame 41	0.843	0.587	1.44
CBL	Cas-Br-M (murine) ecotropic retroviral transforming sequence	0.841	0.892	0.94
FKBP14	FK506 binding protein 14, 22 kDa	0.839	1.171	0.72
KCNH6	potassium voltage-gated channel, subfamily H (eag-related), member 6	0.839	0.971	0.86
BTN2A1	butyrophilin, subfamily 2, member A1	0.837	0.971	0.86
MYO1B	myosin IB	0.835	0.635	1.31
GCNT2	glucosaminyl (N-acetyl) transferase 2, I-branching enzyme (I blood group)	0.834	0.692	1.21
IGFN1	immunoglobulin-like and fibronectin type III domain containing 1	0.833	0.714	1.17
PLAGL2	pleiomorphic adenoma gene-like 2	0.833	0.652	1.28
NFX1	nuclear transcription factor, X-box binding 1	0.832	1.157	0.72
ZNF483	zinc finger protein 483	0.83	1.167	0.71
MTAP	methylthioadenosine phosphorylase	0.828	0.878	0.94
HINT3	histidine triad nucleotide binding protein 3	0.826	0.795	1.04
ZNF707	zinc finger protein 707	0.826	0.937	0.88
PDE8A	phosphodiesterase 8A	0.825	0.681	1.21
CSNK1G3	casein kinase 1, gamma 3	0.824	0.607	1.36
LOC728734	similar to NPIP-like protein ENSP00000283050	0.823	0.609	1.35
LRRFIP1	leucine rich repeat (in FLII) interacting protein 1	0.823	0.795	1.04
XPO5	exportin 5	0.823	0.61	1.35
CDKN2AIPNL	CDKN2A interacting protein N-terminal like	0.821	1.095	0.75
USP49	ubiquitin specific peptidase 49	0.821	1.035	0.79
UBE2H	ubiquitin-conjugating enzyme E2H (UBC8 homolog, yeast)	0.82	0.836	0.98
E2F5	E2F transcription factor 5, p130-binding	0.818	0.963	0.85
SLC25A20	solute carrier family 25 (carnitine/acylcarnitine translocase), member 20	0.818	1.184	0.69
TMEM92	transmembrane protein 92	0.817	0.702	1.16
C15ORF63	chromosome 15 open reading frame 63	0.816	1.039	0.79
TLE3	transducin-like enhancer of split 3 (E(sp1) homolog, Drosophila)	0.816	0.89	0.92
FAM110B	family with sequence similarity 110, member B	0.815	1.004	0.81
ZNF282	zinc finger protein 282	0.815	0.749	1.09
PDP1	pyruvate dehyrogenase phosphatase catalytic subunit 1	0.814	0.763	1.07
KCTD15	potassium channel tetramerisation domain containing 15	0.812	0.68	1.19
RNF44	ring finger protein 44	0.812	0.869	0.93
RUSC2	RUN and SH3 domain containing 2	0.812	0.692	1.17

ITPK1AS	ITPK1 antisense RNA (non-protein coding)	0.808	1.031	0.78
LIG4	ligase IV, DNA, ATP-dependent	0.807	0.989	0.82
MGC87042	STEAP family protein MGC87042	0.807	0.762	1.06
NCRNA00219	non-protein coding RNA 219	0.807	0.704	1.15
INADL	InaD-like (Drosophila)	0.806	0.628	1.28
URB2	URB2 ribosome biogenesis 2 homolog (S. cerevisiae)	0.806	0.65	1.24
ZCCHC8	zinc finger, CCHC domain containing 8	0.806	0.872	0.92
SIAH2	seven in absentia homolog 2 (Drosophila)	0.804	0.665	1.21
ZNF335	zinc finger protein 335	0.802	0.739	1.09
AMMECR1L	AMME chromosomal region gene 1-like	0.801	0.899	0.89
GSDMB	gasdermin B	0.801	1.146	0.70
GALNT4	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 4 (GalNAc-T4)	0.8	0.653	1.23
ZNF140	zinc finger protein 140	0.799	0.679	1.18
BCL2	B-cell CLL/lymphoma 2	0.798	0.687	1.16
RNF41	ring finger protein 41	0.797	0.829	0.96
C14ORF153	chromosome 14 open reading frame 153	0.796	1.022	0.78
SLC16A9	solute carrier family 16, member 9 (monocarboxylic acid transporter 9)	0.796	0.742	1.07
SNRK	SNF related kinase	0.796	0.74	1.08
SPIRE1	spire homolog 1 (Drosophila)	0.795	0.61	1.30
TLE4	transducin-like enhancer of split 4 (E(sp1) homolog, Drosophila)	0.795	0.825	0.96
FAM119A	family with sequence similarity 119, member A	0.794	1.106	0.72
DMC1	DMC1 dosage suppressor of mck1 homolog, meiosis-specific homologous recombination (yeast)	0.793	1.126	0.70
FOSL2	FOS-like antigen 2	0.79	0.967	0.82
SENP5	SUMO1/sentrin specific peptidase 5	0.79	0.905	0.87
AARS	alanyl-tRNA synthetase	0.788	0.735	1.07
MID1IP1	MID1 interacting protein 1 (gastrulation specific G12 homolog (zebrafish))	0.788	0.689	1.14
FAM89A	family with sequence similarity 89, member A	0.787	0.616	1.28
SETD8	SET domain containing (lysine methyltransferase) 8	0.787	0.662	1.19
ASB7	ankyrin repeat and SOCS box-containing 7	0.786	0.696	1.13
ST3GAL4	ST3 beta-galactoside alpha-2,3-sialyltransferase 4	0.786	0.601	1.31
PPA2	pyrophosphatase (inorganic) 2	0.783	0.926	0.85
PTGR2	prostaglandin reductase 2	0.78	1.09	0.72
LEP	leptin	0.777	1.132	0.69
ZGPAT	zinc finger, CCCH-type with G patch domain	0.776	0.604	1.28
APBA3	amyloid beta (A4) precursor protein-binding, family A, member 3	0.775	0.597	1.30
EID2B	EP300 interacting inhibitor of differentiation 2B	0.775	1.093	0.71
NCK1	NCK adaptor protein 1	0.775	0.86	0.90
ARHGAP31	Rho GTPase activating protein 31	0.774	0.801	0.97
GMIP	GEM interacting protein	0.773	0.645	1.20
ZNF773	zinc finger protein 773	0.773	0.835	0.93
ZNF577	zinc finger protein 577	0.772	0.98	0.79
ERAP2	endoplasmic reticulum aminopeptidase 2	0.771	1.097	0.70
DAXX	death-domain associated protein	0.77	0.709	1.09
FMNL2	formin-like 2	0.77	0.619	1.24
PSMD12	proteasome (prosome, macropain) 26S subunit, non-ATPase, 12	0.77	0.862	0.89
EVI5	ecotropic viral integration site 5	0.769	0.738	1.04
PLEKHH3	pleckstrin homology domain containing, family H (with MyTH4 domain) member 3	0.769	0.897	0.86
STEAP2	six transmembrane epithelial antigen of the prostate 2	0.769	1.091	0.70

RCHY1	ring finger and CHY zinc finger domain containing 1	0.766	0.599	1.28
C19ORF48	chromosome 19 open reading frame 48	0.765	0.884	0.87
MCL1	myeloid cell leukemia sequence 1 (BCL2-related)	0.763	0.723	1.06
TXNRD1	thioredoxin reductase 1	0.76	0.587	1.29
SLC7A5	solute carrier family 7 (cationic amino acid transporter, y+ system), member 5	0.756	0.625	1.21
GLI1	GLI family zinc finger 1	0.755	0.627	1.20
ST7L	suppression of tumorigenicity 7 like	0.754	0.717	1.05
CCNB1IP1	cyclin B1 interacting protein 1	0.753	0.594	1.27
WNK1	WNK lysine deficient protein kinase 1	0.753	0.86	0.88
FAM40A	family with sequence similarity 40, member A	0.752	0.598	1.26
UTP15	UTP15, U3 small nucleolar ribonucleoprotein, homolog (S. cerevisiae)	0.75	0.627	1.20
RBM3	RNA binding motif (RNP1, RRM) protein 3	0.748	1.037	0.72
DMTF1	cyclin D binding myb-like transcription factor 1	0.747	0.605	1.23
GALNT3	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 3 (GalNAc-T3)	0.747	0.753	0.99
CXCR4	chemokine (C-X-C motif) receptor 4	0.744	1.065	0.70
ZMYND11	zinc finger, MYND domain containing 11	0.743	0.757	0.98
ZNF682	zinc finger protein 682	0.742	0.967	0.77
KRAS	v-Ki-ras2 Kirsten rat sarcoma viral oncogene homolog	0.741	0.592	1.25
CNST	consortin, connexin sorting protein	0.74	0.757	0.98
ZNF641	zinc finger protein 641	0.74	0.594	1.25
SRC	v-src sarcoma (Schmidt-Ruppin A-2) viral oncogene homolog (avian)	0.739	0.642	1.15
NCRNA00114	non-protein coding RNA 114	0.738	1.022	0.72
ZFP36L1	zinc finger protein 36, C3H type-like 1	0.738	1.091	0.68
ZNF600	zinc finger protein 600	0.737	0.833	0.88
WDR52	WD repeat domain 52	0.732	0.688	1.06
ING5	inhibitor of growth family, member 5	0.73	0.757	0.96
SNAPC4	small nuclear RNA activating complex, polypeptide 4, 190kDa	0.73	0.813	0.90
CRAMP1L	Crm, cramped-like (Drosophila)	0.729	0.666	1.09
SLC12A4	solute carrier family 12 (potassium/chloride transporters), member 4	0.727	0.686	1.06
BSDC1	BSD domain containing 1	0.724	0.632	1.15
FAM115C	family with sequence similarity 115, member C	0.722	0.996	0.72
TNFSF14	tumor necrosis factor (ligand) superfamily, member 14	0.718	0.859	0.84
FAM40B	family with sequence similarity 40, member B	0.714	0.869	0.82
WSB1	WD repeat and SOCS box-containing 1	0.713	0.856	0.83
NKIRAS1	NFKB inhibitor interacting Ras-like 1	0.709	0.823	0.86
PHAX	phosphorylated adaptor for RNA export	0.709	0.759	0.93
PCDHB9	protocadherin beta 9	0.708	0.926	0.76
PLA2G2D	phospholipase A2, group IID	0.706	1.048	0.67
C15ORF52	chromosome 15 open reading frame 52	0.705	0.721	0.98
LRIG2	leucine-rich repeats and immunoglobulin-like domains 2	0.705	0.925	0.76
RHBDL2	rhomboid, veinlet-like 2 (Drosophila)	0.705	0.875	0.81
RDH10	retinol dehydrogenase 10 (all-trans)	0.704	0.804	0.88
CSF1	colony stimulating factor 1 (macrophage)	0.703	0.815	0.86
GOSR1	golgi SNAP receptor complex member 1	0.703	0.881	0.80
PDE7A	phosphodiesterase 7A	0.703	1.041	0.68
RGPD8	RANBP2-like and GRIP domain containing 8	0.702	0.874	0.80
PTP4A2	protein tyrosine phosphatase type IVA, member 2	0.698	0.899	0.78
C7ORF43	chromosome 7 open reading frame 43	0.697	0.746	0.93
C1ORF109	chromosome 1 open reading frame 109	0.695	0.652	1.07
CCNL1	cyclin L1	0.695	0.634	1.10

MIER2	mesoderm induction early response 1, family member 2	0.694	0.794	0.87
GJB2	gap junction protein, beta 2, 26kDa	0.693	0.607	1.14
POGK	pogo transposable element with KRAB domain	0.691	0.595	1.16
VPS37A	vacuolar protein sorting 37 homolog A (S. cerevisiae)	0.691	0.631	1.10
ERCC4	excision repair cross-complementing rodent repair deficiency, complementation group 4	0.69	0.859	0.80
LOC652634	similar to fem-1 homolog a (C.elegans)	0.689	0.686	1.00
ZNF24	zinc finger protein 24	0.689	0.73	0.94
ABCA1	ATP-binding cassette, sub-family A (ABC1), member 1	0.687	0.586	1.17
SAV1	salvador homolog 1 (Drosophila)	0.687	0.594	1.16
LOC100132979	golgin A8 family, member D (pseudogene)	0.686	0.603	1.14
TGIF1	TGFB-induced factor homeobox 1	0.685	0.681	1.01
IL17RD	interleukin 17 receptor D	0.683	0.971	0.70
CRCP	CGRP receptor component	0.681	1.077	0.63
RGPD3	RANBP2-like and GRIP domain containing 3	0.681	0.824	0.83
IPPK	inositol 1,3,4,5,6-pentakisphosphate 2-kinase	0.68	0.869	0.78
HNRNPU	heterogeneous nuclear ribonucleoprotein U (scaffold attachment factor A)	0.679	0.974	0.70
LOC338758	hypothetical LOC338758	0.678	0.64	1.06
ZNF69	zinc finger protein 69	0.675	0.952	0.71
ERN1	endoplasmic reticulum to nucleus signaling 1	0.674	0.885	0.76
GOLGA8A	golgin A8 family, member A	0.674	0.79	0.85
TMEM79	transmembrane protein 79	0.673	0.948	0.71
ZRANB1	zinc finger, RAN-binding domain containing 1	0.673	0.622	1.08
SIRT1	sirtuin 1	0.671	0.585	1.15
HSD17B7	hydroxysteroid (17-beta) dehydrogenase 7	0.669	0.931	0.72
COL7A1	collagen, type VII, alpha 1	0.668	0.712	0.94
ADAMTS1	ADAM metallopeptidase with thrombospondin type 1 motif, 1	0.667	1.096	0.61
KLF11	Kruppel-like factor 11	0.667	0.662	1.01
NXT1	NTF2-like export factor 1	0.667	0.649	1.03
ZCCHC6	zinc finger, CCHC domain containing 6	0.667	0.595	1.12
C8ORF45	chromosome 8 open reading frame 45	0.665	1.02	0.65
C9ORF80	chromosome 9 open reading frame 80	0.663	0.848	0.78
SPTLC1	serine palmitoyltransferase, long chain base subunit 1	0.662	0.942	0.70
STK38L	serine/threonine kinase 38 like	0.662	0.648	1.02
XPNPEP3	X-prolyl aminopeptidase (aminopeptidase P) 3, putative	0.66	0.736	0.90
OCIAD1	OCIA domain containing 1	0.655	0.897	0.73
SSTR2	somatostatin receptor 2	0.655	1.12	0.58
MGC12760	ciliary rootlet coiled-coil, rootletin pseudogene 2	0.654	1.392	0.47
ZNF460	zinc finger protein 460	0.65	0.984	0.66
HIATL2	hippocampus abundant transcript-like 2	0.648	1.066	0.61
GCLC	glutamate-cysteine ligase, catalytic subunit	0.647	0.821	0.79
KCNH1	potassium voltage-gated channel, subfamily H (eag-related), member 1	0.646	0.614	1.05
KCNG1	potassium voltage-gated channel, subfamily G, member 1	0.639	0.617	1.04
APH1B	anterior pharynx defective 1 homolog B (C. elegans)	0.636	0.59	1.08
PDP2	pyruvate dehyrogenase phosphatase catalytic subunit 2	0.632	1.169	0.54
ADNP2	ADNP homeobox 2	0.629	0.649	0.97
LOC731275	hypothetical LOC731275	0.629	0.679	0.93
CSF2RA	colony stimulating factor 2 receptor, alpha, low-affinity (granulocyte-macrophage)	0.628	0.813	0.77
ZNF223	zinc finger protein 223	0.628	0.832	0.75
COL8A1	collagen, type VIII, alpha 1	0.626	1.313	0.48
TNFSF15	tumor necrosis factor (ligand) superfamily, member 15	0.626	0.712	0.88
ZBTB41	zinc finger and BTB domain containing 41	0.626	0.653	0.96

E2F3	E2F transcription factor 3	0.625	0.611	1.02
TDG	thymine-DNA glycosylase	0.625	0.597	1.05
SGSH	N-sulfoglucosamine sulfohydrolase	0.624	0.603	1.03
TMEM63A	transmembrane protein 63A	0.624	0.724	0.86
INTS6	integrator complex subunit 6	0.623	0.794	0.78
MAK16	MAK16 homolog (S. cerevisiae)	0.622	0.635	0.98
AKAP8L	A kinase (PRKA) anchor protein 8-like	0.621	0.745	0.83
MAP3K1	mitogen-activated protein kinase kinase kinase 1	0.62	0.722	0.86
NCRNA00152	non-protein coding RNA 152	0.62	1.34	0.46
TCF20	transcription factor 20 (AR1)	0.617	0.673	0.92
C5ORF28	chromosome 5 open reading frame 28	0.615	0.903	0.68
ATXN2L	ataxin 2-like	0.614	0.869	0.71
CTSC	cathepsin C	0.614	1.075	0.57
CCR6	chemokine (C-C motif) receptor 6	0.611	0.716	0.85
ZNF93	zinc finger protein 93	0.61	0.658	0.93
LILRB1	leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 1	0.607	0.657	0.92
LOC643509	dihydrofolate reductase pseudogene 1	0.606	0.824	0.74
SLC3A2	solute carrier family 3 (activators of dibasic and neutral amino acid transport), member 2	0.606	0.589	1.03
UBAP1	ubiquitin associated protein 1	0.605	0.603	1.00
ALPP	alkaline phosphatase, placental	0.604	0.895	0.67
KLF3	Kruppel-like factor 3 (basic)	0.604	0.591	1.02
CRYZL1	crystallin, zeta (quinone reductase)-like 1	0.603	0.769	0.78
ERRFI1	ERBB receptor feedback inhibitor 1	0.602	1.084	0.56
PPM1K	protein phosphatase, Mg2+/Mn2+ dependent, 1K	0.601	0.861	0.70
TAF1A	TATA box binding protein (TBP)-associated factor, RNA polymerase I, A, 48kDa	0.601	0.717	0.84
LUZP1	leucine zipper protein 1	0.598	0.683	0.88
IL10	interleukin 10	0.596	0.823	0.72
NUBPL	nucleotide binding protein-like	0.596	0.907	0.66
RIF1	RAP1 interacting factor homolog (yeast)	0.595	0.635	0.94
C12ORF65	chromosome 12 open reading frame 65	0.594	0.674	0.88
LIN54	lin-54 homolog (C. elegans)	0.593	0.688	0.86
RBM14	RNA binding motif protein 14	0.593	0.981	0.60
ANKRD20A5	ankyrin repeat domain 20 family, member A5	0.587	0.733	0.80
ZNF679	zinc finger protein 679	-0.587	-0.617	0.95
FAN1	FANCD2/FANCI-associated nuclease 1	-0.599	-0.644	0.93
ASTE1	asteroid homolog 1 (Drosophila)	-0.609	-0.586	1.04
CYFIP2	cytoplasmic FMR1 interacting protein 2	-0.61	-0.6	1.02
ZSCAN5A	zinc finger and SCAN domain containing 5A	-0.616	-0.635	0.97
PKIB	protein kinase (cAMP-dependent, catalytic) inhibitor beta	-0.617	-0.594	1.04
SNX7	sorting nexin 7	-0.62	-0.619	1.00
CCNA1	cyclin A1	-0.621	-0.659	0.94
ALG14	asparagine-linked glycosylation 14 homolog (S. cerevisiae)	-0.629	-0.822	0.77
IRX5	iroquois homeobox 5	-0.634	-0.976	0.65
SPATA18	spermatogenesis associated 18 homolog (rat)	-0.634	-0.617	1.03
DGCR14	DiGeorge syndrome critical region gene 14	-0.635	-0.66	0.96
C3ORF55	chromosome 3 open reading frame 55	-0.637	-0.685	0.93
NINJ2	ninjurin 2	-0.641	-0.816	0.79
TXNDC5	thioredoxin domain containing 5 (endoplasmic reticulum)	-0.643	-0.764	0.84
MEIS1	Meis homeobox 1	-0.646	-0.612	1.06
ORAI3	ORAI calcium release-activated calcium modulator 3	-0.655	-0.673	0.97
TMEM45A	transmembrane protein 45A	-0.657	-0.605	1.09
CLDND2	claudin domain containing 2	-0.665	-0.678	0.98

GSDMA	gasdermin A	-0.669	-1.076	0.62
CARD6	caspase recruitment domain family, member 6	-0.676	-0.952	0.71
DEDD2	death effector domain containing 2	-0.678	-0.612	1.11
EIF1AD	eukaryotic translation initiation factor 1A domain containing	-0.685	-0.808	0.85
IQCG	IQ motif containing G	-0.688	-0.712	0.97
C17ORF81	chromosome 17 open reading frame 81	-0.694	-0.601	1.15
CTSZ	cathepsin Z	-0.694	-0.755	0.92
LOC729264	similar to TP53 target 3	-0.695	-0.637	1.09
NT5DC2	5'-nucleotidase domain containing 2	-0.695	-0.699	0.99
SALL1	sal-like 1 (Drosophila)	-0.697	-0.988	0.71
ID3	inhibitor of DNA binding 3, dominant negative helix-loop-helix protein	-0.698	-0.682	1.02
SYNGR4	synaptogyrin 4	-0.702	-0.987	0.71
MLYCD	malonyl-CoA decarboxylase	-0.705	-0.61	1.16
TBCC	tubulin folding cofactor C	-0.706	-0.928	0.76
FAM172A	family with sequence similarity 172, member A	-0.715	-0.711	1.01
HOXA5	homeobox A5	-0.716	-1.311	0.55
PPID	peptidylprolyl isomerase D	-0.718	-1.003	0.72
ANG	angiogenin, ribonuclease, RNase A family, 5	-0.72	-0.814	0.88
C5ORF13	chromosome 5 open reading frame 13	-0.72	-0.784	0.92
RALGDS	ral guanine nucleotide dissociation stimulator	-0.724	-0.904	0.80
KRT19	keratin 19	-0.728	-0.751	0.97
CDKN2C	cyclin-dependent kinase inhibitor 2C (p18, inhibits CDK4)	-0.729	-0.696	1.05
ALKBH4	alkB, alkylation repair homolog 4 (E. coli)	-0.73	-0.675	1.08
ENC1	ectodermal-neural cortex 1 (with BTB-like domain)	-0.731	-1.055	0.69
MTMR12	myotubularin related protein 12	-0.735	-0.772	0.95
SNAI1	snail homolog 1 (Drosophila)	-0.736	-2.228	0.33
FOXO4	forkhead box O4	-0.737	-0.593	1.24
GCSH	glycine cleavage system protein H (aminomethyl carrier)	-0.739	-0.616	1.20
KIAA1009	KIAA1009	-0.739	-0.615	1.20
KCNMB4	potassium large conductance calcium-activated channel, subfamily M, beta member 4	-0.741	-0.617	1.20
ELOVL6	ELOVL family member 6, elongation of long chain fatty acids (FEN1/Elo2, SUR4/Elo3-like, yeast)	-0.746	-0.63	1.18
LGR6	leucine-rich repeat-containing G protein-coupled receptor 6	-0.746	-0.683	1.09
KCTD12	potassium channel tetramerisation domain containing 12	-0.747	-0.622	1.20
DNAJB1	DnaJ (Hsp40) homolog, subfamily B, member 1	-0.75	-0.765	0.98
SERTAD4	SERTA domain containing 4	-0.753	-0.821	0.92
ZCCHC5	zinc finger, CCHC domain containing 5	-0.755	-1.195	0.63
FMO4	flavin containing monooxygenase 4	-0.756	-0.667	1.13
BRMS1L	breast cancer metastasis-suppressor 1-like	-0.76	-0.603	1.26
FLJ45244	hypothetical locus FLJ45244	-0.761	-1.035	0.74
PXMP4	peroxisomal membrane protein 4, 24kDa	-0.761	-0.59	1.29
LOC286254	hypothetical protein LOC286254	-0.764	-0.888	0.86
PDZK1	PDZ domain containing 1	-0.765	-0.993	0.77
TAF5L	TAF5-like RNA polymerase II, p300/CBP-associated factor (PCAF)-associated factor, 65kDa	-0.766	-1.015	0.75
KRT15	keratin 15	-0.769	-0.704	1.09
GAD1	glutamate decarboxylase 1 (brain, 67kDa)	-0.77	-0.653	1.18
IFFO1	intermediate filament family orphan 1	-0.77	-0.684	1.13
SLC47A2	solute carrier family 47, member 2	-0.773	-0.776	1.00
SAMD11	sterile alpha motif domain containing 11	-0.776	-0.702	1.11
KBTBD11	kelch repeat and BTB (POZ) domain containing 11	-0.777	-1.103	0.70
FAM46B	family with sequence similarity 46, member B	-0.786	-0.805	0.98

MAPK14	mitogen-activated protein kinase 14	-0.787	-0.705	1.12
RASAL1	RAS protein activator like 1 (GAP1 like)	-0.788	-0.766	1.03
CD24	CD24 molecule	-0.795	-0.663	1.20
RHOBTB2	Rho-related BTB domain containing 2	-0.8	-0.625	1.28
ANKRD36B	ankyrin repeat domain 36B	-0.806	-0.675	1.19
EGR1	early growth response 1	-0.811	-1.635	0.50
VRK3	vaccinia related kinase 3	-0.812	-0.907	0.90
ANGPT1	angiopoietin 1	-0.814	-0.593	1.37
TP53TG1	TP53 target 1 (non-protein coding)	-0.818	-0.672	1.22
SCRN3	secernin 3	-0.82	-0.6	1.37
TCFL5	transcription factor-like 5 (basic helix-loop-helix)	-0.821	-0.635	1.29
PLAA	phospholipase A2-activating protein	-0.822	-0.672	1.22
AGPAT5	1-acylglycerol-3-phosphate O-acyltransferase 5 (lysophosphatidic acid acyltransferase, epsilon)	-0.823	-0.668	1.23
ARID3A	AT rich interactive domain 3A (BRIGHT-like)	-0.827	-0.924	0.90
IGSF5	immunoglobulin superfamily, member 5	-0.829	-1.098	0.76
PEX1	peroxisomal biogenesis factor 1	-0.832	-0.764	1.09
RDH5	retinol dehydrogenase 5 (11-cis/9-cis)	-0.833	-0.951	0.88
HNF1B	HNF1 homeobox B	-0.84	-1.099	0.76
TSPAN8	tetraspanin 8	-0.843	-0.895	0.94
ZNF138	zinc finger protein 138	-0.845	-0.652	1.30
NR2F2	nuclear receptor subfamily 2, group F, member 2	-0.848	-0.616	1.38
SFT2D3	SFT2 domain containing 3	-0.849	-0.618	1.37
WDR81	WD repeat domain 81	-0.849	-0.956	0.89
LPCAT1	lysophosphatidylcholine acyltransferase 1	-0.852	-0.912	0.93
AFMID	arylformamidase	-0.857	-1.128	0.76
TARBP2	TAR (HIV-1) RNA binding protein 2	-0.858	-0.659	1.30
HOXA9	homeobox A9	-0.859	-1.097	0.78
C5ORF39	chromosome 5 open reading frame 39	-0.86	-1.085	0.79
HOXD1	homeobox D1	-0.863	-1.175	0.73
PIAS2	protein inhibitor of activated STAT, 2	-0.867	-0.963	0.90
METTL7B	methyltransferase like 7B	-0.871	-0.948	0.92
ZNF174	zinc finger protein 174	-0.874	-0.631	1.39
BCDIN3D	BCDIN3 domain containing	-0.879	-0.655	1.34
RPS26	ribosomal protein S26	-0.883	-0.802	1.10
CHCHD7	coiled-coil-helix-coiled-coil-helix domain containing 7	-0.886	-0.811	1.09
ANKRD36	ankyrin repeat domain 36	-0.888	-0.597	1.49
C1ORF103	chromosome 1 open reading frame 103	-0.89	-0.615	1.45
FZD1	frizzled homolog 1 (Drosophila)	-0.894	-0.812	1.10
UBL3	ubiquitin-like 3	-0.894	-1.17	0.76
TRIM9	tripartite motif-containing 9	-0.895	-0.712	1.26
ZMAT3	zinc finger, matrin type 3	-0.895	-1.023	0.87
HSPA1A	heat shock 70kDa protein 1A	-0.903	-1.233	0.73
FGFR1	fibroblast growth factor receptor 1	-0.911	-0.605	1.51
TM2D2	TM2 domain containing 2	-0.913	-0.728	1.25
B3GNT1	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 1	-0.914	-0.597	1.53
EFNA4	ephrin-A4	-0.914	-0.637	1.43
DLEU1	deleted in lymphocytic leukemia 1 (non-protein coding)	-0.915	-0.785	1.17
WDR37	WD repeat domain 37	-0.915	-1.184	0.77
C7ORF57	chromosome 7 open reading frame 57	-0.918	-0.771	1.19
GLI2	GLI family zinc finger 2	-0.925	-1.06	0.87
NUDT6	nudix (nucleoside diphosphate linked moiety X)-type motif 6	-0.927	-0.721	1.29
PYROXD2	pyridine nucleotide-disulphide oxidoreductase domain 2	-0.935	-0.744	1.26
RIN1	Ras and Rab interactor 1	-0.937	-0.743	1.26

C21ORF58	chromosome 21 open reading frame 58	-0.938	-0.784	1.20
ID2	inhibitor of DNA binding 2, dominant negative helix-loop-helix protein	-0.944	-2.563	0.37
FARP1	FERM, RhoGEF (ARHGEF) and pleckstrin domain protein 1 (chondrocyte-derived)	-0.945	-0.762	1.24
ZNF341	zinc finger protein 341	-0.946	-1.093	0.87
TEK	TEK tyrosine kinase, endothelial	-0.948	-0.884	1.07
RANBP6	RAN binding protein 6	-0.957	-0.792	1.21
MEIG1	meiosis expressed gene 1 homolog (mouse)	-0.959	-0.707	1.36
BCL7C	B-cell CLL/lymphoma 7C	-0.96	-0.641	1.50
FOS	FBJ murine osteosarcoma viral oncogene homolog	-0.96	-2.555	0.38
ACPL2	acid phosphatase-like 2	-0.964	-0.826	1.17
SMPX	small muscle protein, X-linked	-0.965	-0.932	1.04
PEX11A	peroxisomal biogenesis factor 11 alpha	-0.966	-0.619	1.56
IER5L	immediate early response 5-like	-0.967	-0.862	1.12
MTERF	mitochondrial transcription termination factor	-0.971	-0.843	1.15
NDRG4	NDRG family member 4	-0.973	-0.646	1.51
MAPKAP1	mitogen-activated protein kinase associated protein 1	-0.976	-0.869	1.12
BRD8	bromodomain containing 8	-0.978	-0.6	1.63
RBM4B	RNA binding motif protein 4B	-0.981	-0.731	1.34
RASSF9	Ras association (RalGDS/AF-6) domain family (N-terminal) member 9	-0.986	-0.702	1.40
SIRT4	sirtuin 4	-0.987	-1.172	0.84
FLJ35934	FLJ35934	-0.991	-0.936	1.06
LHX8	LIM homeobox 8	-0.996	-0.591	1.69
ZNF616	zinc finger protein 616	-1.006	-1.008	1.00
HSPA1B	heat shock 70kDa protein 1B	-1.008	-1.646	0.61
LOC652726	similar to ankyrin repeat domain 36	-1.015	-0.761	1.33
ENPP2	ectonucleotide pyrophosphatase/phosphodiesterase 2	-1.019	-0.724	1.41
C8ORF51	chromosome 8 open reading frame 51	-1.02	-0.693	1.47
TMEM37	transmembrane protein 37	-1.022	-0.616	1.66
TMEM143	transmembrane protein 143	-1.025	-0.9	1.14
INHBB	inhibin, beta B	-1.026	-0.641	1.60
NCRNA00256A	non-protein coding RNA 256A	-1.028	-0.712	1.44
C18ORF55	chromosome 18 open reading frame 55	-1.029	-0.741	1.39
SPATA7	spermatogenesis associated 7	-1.036	-0.812	1.28
ZKSCAN4	zinc finger with KRAB and SCAN domains 4	-1.038	-1.366	0.76
ZKSCAN3	zinc finger with KRAB and SCAN domains 3	-1.039	-0.637	1.63
STARD5	StAR-related lipid transfer (START) domain containing 5	-1.041	-1.196	0.87
LOC93622	hypothetical LOC93622	-1.049	-0.725	1.45
CCDC15	coiled-coil domain containing 15	-1.054	-0.632	1.67
HOXC13	homeobox C13	-1.061	-0.619	1.71
GMCL1	germ cell-less homolog 1 (Drosophila)	-1.071	-0.713	1.50
KIFC1	kinesin family member C1	-1.081	-0.609	1.78
ZNF792	zinc finger protein 792	-1.081	-1.145	0.94
CITED2	Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain, 2	-1.085	-0.746	1.45
SLC29A3	solute carrier family 29 (nucleoside transporters), member 3	-1.094	-0.901	1.21
PCTP	phosphatidylcholine transfer protein	-1.097	-1.09	1.01
FOXQ1	forkhead box Q1	-1.098	-0.847	1.30
WRB	tryptophan rich basic protein	-1.106	-0.863	1.28
RAD9A	RAD9 homolog A (S. pombe)	-1.109	-0.637	1.74
ZNF823	zinc finger protein 823	-1.123	-0.701	1.60
RGS2	regulator of G-protein signaling 2, 24kDa	-1.124	-1.914	0.59
SNORD14C	small nucleolar RNA, C/D box 14C	-1.124	-0.714	1.57

CEL	carboxyl ester lipase (bile salt-stimulated lipase)	-1.13	-1.051	1.08
MUM1	melanoma associated antigen (mutated) 1	-1.13	-0.658	1.72
OSGEPL1	O-sialoglycoprotein endopeptidase-like 1	-1.137	-0.667	1.70
HNRNPA0	heterogeneous nuclear ribonucleoprotein A0	-1.14	-0.82	1.39
GAS1	growth arrest-specific 1	-1.141	-0.735	1.55
VWA5A	von Willebrand factor A domain containing 5A	-1.142	-1	1.14
C12ORF76	chromosome 12 open reading frame 76	-1.152	-0.716	1.61
RAB26	RAB26, member RAS oncogene family	-1.156	-1.267	0.91
GPAM	glycerol-3-phosphate acyltransferase, mitochondrial	-1.159	-0.942	1.23
ABCB9	ATP-binding cassette, sub-family B (MDR/TAP), member 9	-1.164	-0.589	1.98
FLJ22184	hypothetical protein FLJ22184	-1.165	-0.854	1.36
HOXB5	homeobox B5	-1.178	-1.128	1.04
RSBN1L	round spermatid basic protein 1-like	-1.178	-1.138	1.04
HMGCR	3-hydroxy-3-methylglutaryl-CoA reductase	-1.184	-0.827	1.43
RAB4A	RAB4A, member RAS oncogene family	-1.191	-0.972	1.23
MEF2C	myocyte enhancer factor 2C	-1.192	-0.77	1.55
C17ORF97	chromosome 17 open reading frame 97	-1.199	-0.794	1.51
GALM	galactose mutarotase (aldose 1-epimerase)	-1.208	-0.759	1.59
NFIA	nuclear factor I/A	-1.211	-0.682	1.78
ZNF254	zinc finger protein 254	-1.215	-1.092	1.11
PITX2	paired-like homeodomain 2	-1.219	-0.795	1.53
TMCC1	transmembrane and coiled-coil domain family 1	-1.225	-0.939	1.30
C9ORF169	chromosome 9 open reading frame 169	-1.227	-1.004	1.22
POLH	polymerase (DNA directed), eta	-1.229	-0.64	1.92
PUS7L	pseudouridylate synthase 7 homolog (S. cerevisiae)-like	-1.231	-0.765	1.61
ALDH3A1	aldehyde dehydrogenase 3 family, member A1	-1.254	-0.648	1.94
FZD4	frizzled homolog 4 (Drosophila)	-1.263	-0.883	1.43
HOXA6	homeobox A6	-1.264	-1.361	0.93
SORBS1	sorbin and SH3 domain containing 1	-1.276	-0.995	1.28
DEPDC7	DEP domain containing 7	-1.286	-0.724	1.78
SP8	Sp8 transcription factor	-1.286	-0.727	1.77
KANK2	KN motif and ankyrin repeat domains 2	-1.287	-0.614	2.10
SLC2A12	solute carrier family 2 (facilitated glucose transporter), member 12	-1.287	-0.668	1.93
FAM81A	family with sequence similarity 81, member A	-1.289	-0.841	1.53
MEX3B	mex-3 homolog B (C. elegans)	-1.3	-1.005	1.29
EPOR	erythropoietin receptor	-1.302	-0.627	2.08
PIM2	pim-2 oncogene	-1.308	-0.976	1.34
TP53INP1	tumor protein p53 inducible nuclear protein 1	-1.31	-1.415	0.93
ZNF30	zinc finger protein 30	-1.31	-0.874	1.50
DMRT1	doublesex and mab-3 related transcription factor 1	-1.316	-0.811	1.62
SESN1	sestrin 1	-1.316	-1.488	0.88
SPHAR	S-phase response (cyclin related)	-1.316	-0.868	1.52
CLDN2	claudin 2	-1.317	-0.615	2.14
PSRC1	proline/serine-rich coiled-coil 1	-1.318	-0.984	1.34
HOXA10	homeobox A10	-1.321	-1.001	1.32
SPC25	SPC25, NDC80 kinetochore complex component, homolog (S. cerevisiae)	-1.326	-0.889	1.49
C6ORF165	chromosome 6 open reading frame 165	-1.331	-0.824	1.62
CSTF1	cleavage stimulation factor, 3' pre-RNA, subunit 1, 50kDa	-1.331	-0.636	2.09
FABP5L3	fatty acid binding protein 5-like 3 (pseudogene)	-1.352	-1.129	1.20
OSBPL7	oxysterol binding protein-like 7	-1.352	-1.032	1.31
C13ORF34	chromosome 13 open reading frame 34	-1.358	-0.71	1.91
EPCAM	epithelial cell adhesion molecule	-1.358	-0.905	1.50
JAKMIP2	janus kinase and microtubule interacting protein 2	-1.36	-0.627	2.17

MXD3	MAX dimerization protein 3	-1.364	-0.811	1.68
BAG3	BCL2-associated athanogene 3	-1.383	-1.035	1.34
MAT2B	methionine adenosyltransferase II, beta	-1.409	-0.657	2.14
FAM102B	family with sequence similarity 102, member B	-1.413	-1.09	1.30
SRPK2	SRSF protein kinase 2	-1.413	-0.807	1.75
PCDH7	protocadherin 7	-1.415	-0.691	2.05
APLN	apelin	-1.42	-0.616	2.31
KIAA1804	mixed lineage kinase 4	-1.425	-0.755	1.89
RNASEL	ribonuclease L (2',5'-oligoisoadenylate synthetase-dependent)	-1.426	-0.976	1.46
MEGF9	multiple EGF-like-domains 9	-1.427	-0.602	2.37
TRIM6	tripartite motif-containing 6	-1.439	-0.791	1.82
ALDH5A1	aldehyde dehydrogenase 5 family, member A1	-1.446	-0.801	1.81
ADORA1	adenosine A1 receptor	-1.449	-0.746	1.94
TRIM16L	tripartite motif-containing 16-like	-1.454	-1.436	1.01
HSPA1L	heat shock 70kDa protein 1-like	-1.458	-1.523	0.96
FAM78B	family with sequence similarity 78, member B	-1.468	-0.817	1.80
EFCAB7	EF-hand calcium binding domain 7	-1.471	-0.619	2.38
KANK1	KN motif and ankyrin repeat domains 1	-1.49	-0.948	1.57
SCN2A	sodium channel, voltage-gated, type II, alpha subunit	-1.494	-0.872	1.71
TTC30B	tetratricopeptide repeat domain 30B	-1.503	-0.996	1.51
LFNG	LFNG O-fucosylpeptide 3-beta-N-acetylglucosaminyltransferase	-1.51	-1.696	0.89
NR2F1	nuclear receptor subfamily 2, group F, member 1	-1.513	-0.921	1.64
DPYSL4	dihydropyrimidinase-like 4	-1.529	-0.688	2.22
NKX3-2	NK3 homeobox 2	-1.545	-1.089	1.42
MFNG	MFNG O-fucosylpeptide 3-beta-N-acetylglucosaminyltransferase	-1.55	-0.959	1.62
FAM83D	family with sequence similarity 83, member D	-1.574	-0.614	2.56
BMP4	bone morphogenetic protein 4	-1.577	-1.119	1.41
RTN4RL1	reticulon 4 receptor-like 1	-1.583	-0.781	2.03
VASH2	vasohibin 2	-1.583	-0.706	2.24
REEP1	receptor accessory protein 1	-1.585	-1.211	1.31
C1ORF116	chromosome 1 open reading frame 116	-1.633	-1.963	0.83
ORC1L	origin recognition complex, subunit 1-like (S. cerevisiae)	-1.646	-0.701	2.35
C9ORF100	chromosome 9 open reading frame 100	-1.658	-0.886	1.87
SGK223	homolog of rat pragma of Rnd2	-1.668	-1.422	1.17
CCDC110	coiled-coil domain containing 110	-1.671	-1.505	1.11
NFATC3	nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 3	-1.681	-0.712	2.36
AQP11	aquaporin 11	-1.704	-1.19	1.43
HOXA11	homeobox A11	-1.713	-1.866	0.92
CPM	carboxypeptidase M	-1.725	-1.651	1.04
ZNF114	zinc finger protein 114	-1.725	-1.582	1.09
DFFB	DNA fragmentation factor, 40kDa, beta polypeptide (caspase-activated DNase)	-1.74	-0.741	2.35
ZNF395	zinc finger protein 395	-1.742	-1.181	1.48
BCMO1	beta-carotene 15,15'-monooxygenase 1	-1.749	-1.266	1.38
LOC285419	hypothetical LOC285419	-1.758	-1.272	1.38
AXIN2	axin 2	-1.774	-1.502	1.18
LMCD1	LIM and cysteine-rich domains 1	-1.81	-1.129	1.60
PASK	PAS domain containing serine/threonine kinase	-1.814	-0.762	2.38
HEXIM2	hexamthylene bis-acetamide inducible 2	-1.828	-1.432	1.28
ID1	inhibitor of DNA binding 1, dominant negative helix-loop-helix protein	-1.83	-3.169	0.58
NRG4	neuregulin 4	-1.831	-0.98	1.87

GPR19	G protein-coupled receptor 19	-1.847	-1.14	1.62
ARHGEF37	Rho guanine nucleotide exchange factor (GEF) 37	-1.852	-1.24	1.49
C20ORF177	chromosome 20 open reading frame 177	-1.855	-1.427	1.30
HSPA2	heat shock 70kDa protein 2	-1.855	-1.161	1.60
HSPA2	heat shock 70kDa protein 2	-1.861	-1.208	1.54
CXXC4	CXXC finger 4	-1.883	-1.271	1.48
C21ORF122	chromosome 21 open reading frame 122	-1.896	-1.489	1.27
MAP2K6	mitogen-activated protein kinase kinase 6	-1.897	-1.138	1.67
FAM46C	family with sequence similarity 46, member C	-1.922	-2.098	0.92
EPN3	epsin 3	-1.929	-0.828	2.33
E2F8	E2F transcription factor 8	-1.952	-1.369	1.43
TEX19	testis expressed 19	-1.966	-1.078	1.82
LOC158376	hypothetical LOC158376	-1.969	-1.541	1.28
TRIM59	tripartite motif-containing 59	-1.969	-0.749	2.63
SKP2	S-phase kinase-associated protein 2 (p45)	-1.992	-1.291	1.54
RPRM	reprimo, TP53 dependent G2 arrest mediator candidate	-2.005	-1.932	1.04
CSRNP3	cysteine-serine-rich nuclear protein 3	-2.011	-1.4	1.44
HSPA8	heat shock 70kDa protein 8	-2.014	-0.903	2.23
ARMCX2	armadillo repeat containing, X-linked 2	-2.064	-1.228	1.68
PANK1	pantothenate kinase 1	-2.091	-1.427	1.47
GCNT1	glucosaminyl (N-acetyl) transferase 1, core 2	-2.145	-1.518	1.41
SUOX	sulfite oxidase	-2.145	-1.139	1.88
S1PR5	sphingosine-1-phosphate receptor 5	-2.182	-1.491	1.46
MAGEE1	melanoma antigen family E, 1	-2.265	-0.795	2.85
KBTBD7	kelch repeat and BTB (POZ) domain containing 7	-2.277	-1.735	1.31
PDK4	pyruvate dehydrogenase kinase, isozyme 4	-2.277	-1.343	1.70
HRCT1	histidine rich carboxyl terminus 1	-2.384	-1.503	1.59
EEPD1	endonuclease/exonuclease/phosphatase family domain containing 1	-2.478	-1.328	1.87
GPER	G protein-coupled estrogen receptor 1	-2.49	-1.073	2.32
DMRT2	doublesex and mab-3 related transcription factor 2	-2.558	-1.695	1.51
OTX1	orthodenticle homeobox 1	-2.56	-1.562	1.64
PPP1R3C	protein phosphatase 1, regulatory (inhibitor) subunit 3C	-2.681	-2.876	0.93
VAV3	vav 3 guanine nucleotide exchange factor	-2.703	-1.612	1.68
PLCH1	phospholipase C, eta 1	-2.708	-0.962	2.81