

Table S3. Genes differentially-regulated by PT pretreatment in influenza virus-infected mice at 36 h post-inoculation.

Symbol	Gene Annotation ^a	Fold Change	P-value	Accession ^b
<i>ELN</i>	elastin	1.71	1.71E-05	NM_007925
<i>ZBTB16</i>	zinc finger and BTB domain containing 16	1.71	2.84E-09	NM_001033324
<i>NME2</i>	non-metastatic cells 2, protein (NM23B) expressed in	1.61	4.56E-06	NM_001077529
<i>EIF4EBP2</i>	eukaryotic translation initiation factor 4E binding protein 2	1.51	4.04E-02	NM_010124
<i>SOX4</i>	SRY (sex determining region Y)-box 4	1.51	6.26E-03	NM_009238
<i>CCL5</i>	chemokine (C-C motif) ligand 5	-1.51	1.19E-02	NM_013653
<i>CXCR2</i>	chemokine (C-X-C motif) receptor 2	-1.51	1.06E-02	NM_009909
<i>GPR146</i>	G protein-coupled receptor 146	-1.51	2.50E-03	NM_001038703
<i>HCK</i>	hemopoietic cell kinase	-1.51	6.18E-03	NM_010407
<i>IL18BP</i>	interleukin 18 binding protein	-1.51	5.63E-07	NM_010531
<i>IRGM</i>	immunity-related GTPase family, M	-1.51	2.37E-02	NM_008326
<i>NAMPT</i>	nicotinamide phosphoribosyltransferase	-1.51	1.08E-02	NM_021524
<i>PLAUR</i>	plasminogen activator, urokinase receptor	-1.51	2.70E-04	NM_011113
<i>TGFB1</i>	transforming growth factor, beta-induced, 68kDa	-1.51	4.57E-02	NM_009369
<i>TNFAIP3</i>	tumor necrosis factor, alpha-induced protein 3	-1.51	2.05E-03	NM_009397
<i>VCAM1</i>	vascular cell adhesion molecule 1	-1.51	4.16E-02	NM_011693
<i>CCL9</i>	chemokine (C-C motif) ligand 9	-1.61	2.73E-02	NM_011338
<i>CH25H</i>	cholesterol 25-hydroxylase	-1.61	6.82E-03	NM_009890
<i>DUSP1</i>	dual specificity phosphatase 1	-1.61	1.79E-02	NM_013642
<i>F13A1</i>	coagulation factor XIII, A1 polypeptide	-1.61	3.96E-04	NM_028784
<i>HLA-E</i>	major histocompatibility complex, class I, E	-1.61	4.41E-04	NM_010398
<i>LCP2</i>	lymphocyte cytosolic protein 2 (SH2 domain containing leukocyte protein of 76kDa)	-1.61	3.50E-04	NM_010696
<i>MX1</i>	myxovirus (influenza virus) resistance 1, interferon-inducible protein p78 (mouse)	-1.61	2.17E-02	NR_003508
<i>PLAC8</i>	placenta-specific 8	-1.61	6.18E-03	NM_139198
<i>SLFN5</i>	schlafen family member 5	-1.61	9.74E-06	NM_183201
<i>CD300LF</i>	CD300 molecule-like family member f	-1.71	1.04E-02	NM_145634
<i>CLECT7A</i>	C-type lectin domain family 7, member A	-1.71	1.33E-03	NM_020008
<i>CMPK2</i>	cytidine monophosphate (UMP-CMP) kinase 2, mitochondrial	-1.71	1.82E-03	NM_020557
<i>CXCL10</i>	chemokine (C-X-C motif) ligand 10	-1.71	6.00E-03	NM_021274
<i>IGTP</i>	interferon gamma induced GTPase	-1.71	3.20E-03	NM_018738
<i>ITGAM</i>	integrin, alpha M (complement component 3 receptor 3 subunit)	-1.71	4.00E-02	NM_001082960
<i>TAP1</i>	transporter 1, ATP-binding cassette, sub-family B (MDR/TAP)	-1.71	4.29E-03	NM_013683
<i>ANKRD1</i>	ankyrin repeat domain 1 (cardiac muscle)	-1.81	2.01E-04	NM_013468
<i>APOBEC1</i>	apolipoprotein B mRNA editing enzyme, catalytic polypeptide 1	-1.81	1.43E-02	NM_031159
<i>CA13</i>	carbonic anhydrase XIII	-1.81	2.43E-02	NM_024495
<i>GBP2</i>	guanylate binding protein 2, interferon-inducible	-1.81	9.92E-03	NM_010260
<i>HSPA8</i>	heat shock 70kDa protein 8	-1.81	4.48E-08	M13967

<i>IL1RN</i>	interleukin 1 receptor antagonist	-1.81	1.17E-03	NM_031167
<i>IFI44L</i>	interferon-induced protein 44-like	-1.91	3.23E-02	NM_031367
<i>IFIT2</i>	interferon-induced protein with tetratricopeptide repeats 2	-1.91	1.20E-02	NM_008332
<i>IIGP1</i>	interferon inducible GTPase 1	-1.91	4.25E-04	NM_021792
<i>LILRA6</i>	leukocyte immunoglobulin-like receptor, subfamily A (with TM domain), member 6	-1.91	5.83E-04	NM_011088
<i>OAS3</i>	2'-5'-oligoadenylate synthetase 3, 100kDa	-1.91	4.30E-02	NM_145226
<i>PFKFB3</i>	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 3	-1.91	7.03E-03	NM_133232
<i>CD274</i>	CD274 molecule	-2.01	1.00E-02	NM_021893
<i>THBS1</i>	thrombospondin 1	-2.01	2.65E-03	NM_011580
<i>FCGR1A</i>	Fc fragment of IgG, high affinity Ia, receptor (CD64)	-2.11	7.65E-03	NM_010186
<i>FGL2</i>	fibrinogen-like 2	-2.11	4.31E-03	NM_008013
<i>GBP5</i>	guanylate binding protein 5	-2.11	1.54E-05	NM_153564
<i>SELP</i>	selectin P (granule membrane protein 140kDa, antigen CD62)	-2.11	2.98E-02	NM_011347
<i>RSAD2</i>	radical S-adenosyl methionine domain containing 2	-2.21	5.10E-03	NM_021384

^a Genes with a fold change greater than 1.5 or more ($P < 0.05$) of experimental group over controls.

^b GenBank accession number.