

Table S5. Significantly up- and down-regulated gene ontology terms enriched in genes expressed by ARPE-19 human retinal pigment epithelial cells 24 hours following infection with EBOV.

	False discovery rate
Up-regulated gene ontology terms	
Type I interferon signaling pathway	2.29E-08
Cholesterol biosynthetic process	2.88E-08
Endoplasmic reticulum unfolded protein response	2.07E-07
Negative regulation of viral genome replication	5.60E-06
Defense response to virus	7.57E-06
Innate immune response	1.37E-05
Response to virus	1.71E-05
Activation of signaling protein activity involved in unfolded protein response	2.28E-05
ATP binding	2.92E-05
Cytokine-mediated signaling pathway	1.82E-04
Inactivation of MAPK activity	8.17E-04
tRNA aminoacylation for protein translation	0.00229
2'-5'-Oligoadenylate synthetase activity	0.00283
Aminoacyl-tRNA ligase activity	0.00358

Isoprenoid biosynthetic process	0.00367
Response to unfolded protein	0.00517
Post-embryonic camera-type eye development	0.00804
Proline transmembrane transport	0.00804
Regulation of signal transduction	0.00950
SREBP signaling pathway	0.0178
Circadian rhythm	0.0180
RNA polymerase II regulatory region sequence-specific	
DNA binding	0.0203
Endoplasmic reticulum	0.0208
MAP kinase tyrosine/serine/threonine phosphatase activity	0.0211
Middle ear morphogenesis	0.0214
Response to endoplasmic reticulum stress	0.0229
Intrinsic apoptotic signaling pathway in response to	
endoplasmic reticulum stress	0.0234
Cellular response to antibiotic	0.0250
Coenzyme binding	0.0255
Cytoplasm	0.0315
Organic cation transmembrane transporter activity	0.0387
Endoderm formation	0.0397
[Heparan sulfate]-glucosamine 3-sulfotransferase 3 activity	0.0406
Interleukin-8 receptor binding	0.0406
Regulation of ribonuclease activity	0.0406

Immune response	0.0413
Cellular response to hydrogen peroxide	0.0419
Small molecule metabolic process	0.0427
Cell morphogenesis	0.0428
Positive regulation of transcription from RNA polymerase II promoter	0.0442
Cellular response to interferon-alpha	0.0449
Proline transport	0.0449
Nucleotidyltransferase activity	0.0453

Down-regulated gene ontology terms

Cell fate commitment	0.0229
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