Table S4. Significantly up- and down-regulated pathways enriched in genes expressed by ARPE-19 human retinal pigment epithelial cells 24 hours following infection with EBOV.

	False discovery rate
Up-regulated pathways	
Interferon alpha/beta signaling	1.34E-08
Cholesterol biosynthesis	3.85E-07
Cytosolic tRNA aminoacylation	2.27E-05
Interferon Signaling	2.87E-05
Regulation of cholesterol biosynthesis by SREBP (SREBF)	7.16E-05
Cytokine signaling in immune system	2.08E-04
Steroid metabolism	2.11E-04
Activation of gene expression by SREBF (SREBP)	3.30E-04
PERK regulates gene expression	4.20E-04
Unfolded Protein Response (UPR)	5.32E-04
tRNA aminoacylation	6.54E-04
Aminoacyl-tRNA biosynthesis	0.00102
HIF-1-alpha transcription factor network	0.00203
Protein processing in endoplasmic reticulum	0.00211
Steroid biosynthesis	0.00562

Terpenoid backbone biosynthesis	0.00856
Scavenging by Class F Receptors	0.0121
AP-1 transcription factor network	0.0124
Glycine serine metabolism	0.0133
ATF4 activates genes	0.0136
ATF-2 transcription factor network	0.0186
Norepinephrine neurotransmitter release cycle	0.0226
Transport of inorganic cations/anions and amino acids/oligopeptides	0.0232
Amino acid transport across the plasma membrane	0.0240
Jak-STAT signaling pathway	0.0244
Hepatitis C	0.0245
ATF6-alpha activates chaperone genes	0.0290
Regulation of map kinase pathways through dual specificity phosphatases	0.0290
Negative regulators of RIG-I/MDA5 signaling	0.0335
Kit receptor	0.0337
RANKL	0.0338
Immune System	0.0366
Antiviral mechanism by IFN-stimulated genes	0.0367
ISG15 antiviral mechanism	0.0367
Alanine aspartate asparagine metabolism	0.0400
Keratinocyte differentiation	0.0411

ATF6-alpha activates chaperones	0.0415
BMAL1:CLOCK, NPAS2 activates circadian gene expression	0.0431
SLC-mediated transmembrane transport	0.0475

Down-regulated pathways

Tryptophan metabolism	0.00454
Defective AMN causes hereditary megaloblastic anemia 1	0.0172
Defective BTD causes biotidinase deficiency	0.0172
Defective CD320 causes methylmalonic aciduria	0.0172
Defective CUBN causes hereditary megaloblastic anemia 1	0.0172
Defective GIF causes intrinsic factor deficiency	0.0172
Defective HLCS causes multiple carboxylase deficiency	0.0172
Defective LMBRD1 causes methylmalonic aciduria and homocystinuria type cblF	0.0172
Defective MMAA causes methylmalonic aciduria type cblA	0.0172
Defective MMAB causes methylmalonic aciduria type cblB	0.0172
Defective MMACHC causes methylmalonic aciduria and homocystinuria type cblC	0.0172
Defective MMADHC causes methylmalonic aciduria and homocystinuria type cblD	0.0172
Defective MTR causes methylmalonic aciduria and homocystinuria type cblG	0.0172
Defective MTRR causes methylmalonic aciduria and	0.0172

homocystinuria type cblE	
Defective MUT causes methylmalonic aciduria mut type	0.0172
Defective TCN2 causes hereditary megaloblastic anemia	0.0172
Defects in biotin (Btn) metabolism	0.0172
Defects in cobalamin (B12) metabolism	0.0172
Defects in vitamin and cofactor metabolism	0.0172
Metabolism of vitamins and cofactors	0.0172
Metabolism of water-soluble vitamins and cofactors	0.0172
Tryptophan degradation	0.0200
BMP2 signaling	0.0210
Alk in cardiac myocytes	0.0236
Wnt signaling pathway	0.0259
Synthesis of prostaglandins (PG) and thromboxanes (TX)	0.0283
GRB7 events in ERBB2 signaling	0.0284
Metabolism of xenobiotics by cytochrome P450	0.0356
cGMP effects	0.0478