**Table S2.** Alignment statistics for RNA sequencing on total RNA extracted from ARPE-19 human retinal pigment epithelialcells 24 hours following infection with EBOV or mock-infection.

Isolate Paired reads	Paired reads aligning to genome (%)	Paired reads aligning unambiguously to annotated genes (%)
38,703,899	36,552,879 (94)	20,848,916 (57)
43,369,278	40,004,946 (92)	22,051,815 (55)
50,947,987	40,987,678 (80)	23,104,561 (56)
37,194,232	29,264,883 (79)	15,833,538 (54)
59,771,257	47,674,511 (80)	25,207,324 (53)
46,676,746	40,257,134 (87)	22,216,365 (55)
	50,073,823 38,703,899 43,369,278 50,947,987 37,194,232 59,771,257	genome (%)   50,073,823 47,057,907 (94)   38,703,899 36,552,879 (94)   43,369,278 40,004,946 (92)   50,947,987 40,987,678 (80)   37,194,232 29,264,883 (79)   59,771,257 47,674,511 (80)