

Supplementary Table 1. Total number of reads and virus specific reads for each group

Virus	Cell Line	Hours Post Infection	Total Reads	Viral Reads	Viral Bases Sequenced (M)	Percentage Viral Reads	Average Genome Coverage
EBOV	Thp1	Mock	35,875,581	-			
		6	34,538,060	9,130	0.9	0.03%	48
		12	26,658,967	65,306	6.6	0.24%	343
		24	22,665,814	1,015,290	102.5	4.48%	5331
	Vero	Mock	28,579,380				
		6	33,067,403	18,338	1.9	0.06%	96
		12	28,395,974	256,835	25.9	0.90%	1349
		24	26,716,874	1,827,362	184.5	6.84%	9595
MARV	Thp1	Mock	44,281,028	-			
		6	45,396,771	1,424	0.1	0.00%	7
		12	30,550,458	10,811	1.1	0.04%	56
		24	27,096,435	396,021	39.9	1.46%	2055
	Vero	Mock	36,384,342	-			
		6	40,074,951	3,760	0.4	0.01%	20
		12	38,323,861	69,981	7.1	0.18%	363
		24	37,500,752	1,114,825	112.5	2.97%	5790