

Table S2. Summary of mapped reads and depth of coverage for Seoul virus using next-generation sequencing in this study.

Sample	Total reads	Mapped reads/ Total reads (%)	L segment		M segment		S segment	
			Reads mapped to reference (%)	Depth of coverage	Reads mapped to reference (%)	Depth of coverage	Reads mapped to reference (%)	Depth of coverage
Rn18-1	2,057,486	1,023,268 (49.7)	117,462 (11.5)	2,076.0	426,755 (41.7)	12,578.9	479,051 (46.8)	27,824.2
Rn19-5	6,589,296	6,326,623 (96.0)	2,080,167 (32.9)	38,615.5	2,227,049 (35.2)	73,719.6	2,019,407 (31.9)	137,705.4
Average (%)	4,323,391	3,674,946 (85.0)	1,098,815 (29.9)	20,345.7	1,326,902 (36.1)	43,149.2	1,249,229 (34.0)	82,764.8

Rn, *Rattus norvegicus*; L, large; M, medium; S, small.

The depth of coverage was calculated using the number of mapped reads (read length × number of reads matching the reference/reference genome size).