

**Table 1.** Sequencing and error statistics

Sample	Subset	No. of reads (% reads)	% nucleotides	Longest	Median	% subst.	% insert.	% deletions	% errors
WT	Complete sample	224,724 (100.0)	100.00	26,210	826	—	—	—	—
	HCoV-229E reference	74,783 (33.3)	42.52	26,210	1414	4.292	2.558	8.264	15.114
Mapped to	<i>H. sapiens</i>	106,618 (47.4)	46.37	9562	816	4.333	2.676	8.572	15.581
	<i>S. cerevisiae</i> ENO2	35,454 (15.8)	10.50	3482	636	3.752	2.384	6.359	<b>12.494</b>
Unmapped		7869 (3.5)	0.62	1157	186	—	—	—	—
SL2	Complete sample	180,906 (100.0)	100.00	25,885	1342	—	—	—	—
	HCoV-229E	64,995 (35.9)	48.83	25,885	1626	4.396	2.680	8.507	15.582
	w/SARS-CoV SL2								
Mapped to	<i>H. sapiens</i>	95,340 (52.7)	45.44	16,030	1023	4.513	2.783	8.775	16.071
	<i>S. cerevisiae</i> ENO2	18,530 (10.2)	5.58	3872	858	4.021	2.463	6.892	<b>13.376</b>
Unmapped		2041 (1.1)	0.15	928	200	—	—	—	—