

Table S1 Summary statistics across sample coverage classes.

Coverage class ^a	Count	L_{total} (bp)	L_{mean} (bp)	Masked Bases ^b	Masked SNPs ^b	S_{total}	S_{mean}	r	L_{total}/S_{total}	Indels
18	898	295869	329	324	1	3032	3.38	0.359	97.58	137
17	755	258801	343	613	4	2989	3.96	0.395	86.58	147
16	559	195733	350	526	3	2162	3.87	0.297	90.53	105
15	374	135247	362	462	3	1611	4.31	0.401	83.95	77
14	339	125825	371	670	1	1602	4.73	0.283	78.54	84
13	278	105873	381	579	4	1313	4.72	0.339	80.63	69
12	276	105623	383	729	3	1158	4.20	0.304	91.21	58
11	236	88298	374	744	2	1181	5.00	0.203	74.76	47
10	215	83498	388	791	4	967	4.50	0.273	86.34	47
9	186	73161	393	522	4	988	5.31	0.168	74.05	36
8	199	76123	383	470	4	969	4.87	0.268	78.55	45
7	170	65349	384	405	3	943	5.55	0.351	69.30	50
6	169	68561	406	779	6	1048	6.20	0.264	65.42	40
5	177	69670	394	695	9	762	4.31	0.122	91.43	37
4	178	71503	402	575	0	715	4.02	0.178	100.00	35
3	197	82293	418	686	2	704	3.57	0.216	116.89	36
2	250	105399	422	899	0	835	3.34	0.113	126.23	30
1	316	132942	421	753	NA	NA	NA	NA	NA	NA

Abbreviations: bp, base pairs; Indels, insertion-deletion events; L , length; r , Pearson's correlation coefficient between the number of segregating sites and the length of the amplicon (bp); S , segregating sites; SNPs, single nucleotide polymorphisms.

^aSample size in the alignment (i.e. the number of sequences).

^bMasked bases are the number of aligned sites with at least one base masked due to its quality score < 30.