Table S8 Estimates for per site crossing over rate ($C = 4N_er$) and additional summary statistics related to linkage disequilibrium for each sample coverage class where $n > 10$. Values in parentheses are 95% confidence intervals based on bootstrapping across loci (n = 10,000 replicates). Singletons were included.

Coverage	Loci	C	LD-half (bp)[a]	Z_{nS}	C/θ_π
18	898	0.026	102	0.266	9.107
		(0.017 – 0.042)	(63 – 154)	(0.246 – 0.289)	(7.161 – 17.585)
17	755	0.023	117	0.270	8.129
		(0.017 – 0.032)	(85 – 159)	(0.248 – 0.295)	(5.957 – 11.376)
16	559	0.007	386	0.271	2.317
		(0.001 – 0.025)	(110 – 1390)	(0.243 – 0.299)	(0.489 – 8.911)
15	374	0.021	137	0.286	5.740
		(0.011 – 0.041)	(69 – 255)	(0.253 – 0.319)	(3.577 – 13.717)
14	339	0.010	288	0.314	2.871
		(0.004 – 0.020)	(144 – 701)	(0.282 – 0.349)	(1.159 – 5.771)
13	278	0.008	360	0.308	2.564
		(0.001 – 0.031)	(95 – 1392)	(0.271 – 0.347)	(0.473 – 9.252)
12	276	0.006	496	0.327	1.426
		(0.001 – 0.015)	(193 - 1405)	(0.285 – 0.371)	(0.517 – 5.033)
11	236	0.012	274	0.361	3.039
		(0.004 – 0.028)	(111 – 807)	(0.319 – 0.403)	(0.910 – 6.856)

Abbreviations: bp, base pairs; LD, linkage disequilibrium; θ_π, nucleotide diversity from the average number of pairwise differences; Z_{nS}, Kelly's statistic representing the average pairwise LD among SNPs within an amplicon.

[a] The distance in bp where the expected value of allelic correlations (r^2) dropped to half its initial value.