

Mutation region	Mutation type	No chr1 end exclusion	No Repeat-Masker exclusion	< 30 bp from ligation site exclusion	< 35 bp from ligation site exclusion	< 40 bp from ligation site exclusion	Consensus > 0.9
All	All	(-4.217, 0.411)	(-5.977, -0.319)	(-3.938, 1.035)	(-4.217, 0.402)	(-4.071, 0.582)	(-4.574, 0.149)
	Substitutions	(-0.9868, 2.3260)	(-3.379, 1.574)	(-0.9209, 2.2083)	(-0.9869, 2.3319)	(-1.0631, 2.4955)	(-1.3502, 2.1322)
	Deletions	(-4.261, -0.240)	(-3.691, -0.109)	(-3.717, -0.065)	(-4.302, -0.263)	(-3.797, -0.042)	(-4.288, -0.381)
Gene	All	(-4.706, -0.616)	(-7.877, -0.997)	(-5.063, 0.061)	(-4.699, -0.610)	(-4.552, -0.588)	(-4.839, -1.207)
	Substitutions	(-1.1541, 1.2442)	(-4.573, 0.706)	(-1.0882, 1.1664)	(-1.1573, 1.2575)	(-1.2511, 1.3488)	(-1.3227, 1.0442)
	Deletions	(-4.493, -0.979)	(-4.154, -0.915)	(-4.455, -0.977)	(-4.492, -0.971)	(-3.914, -1.048)	(-4.482, -1.349)
Non-Gene	All	(-5.175, 9.817)	(-6.079, 7.729)	(-3.343, 9.905)	(-5.226, 9.782)	(-5.617, 10.468)	(-5.194, 9.766)
	Substitutions	(-2.142, 6.604)	(-4.1403, 5.3516)	(-1.981, 6.274)	(-2.139, 6.638)	(-2.277, 7.125)	(-2.127, 6.621)
	Deletions	(-4.2128, 12.1267)	(-4.3319, 9.2752)	(-3.424, 10.850)	(-4.2221, 12.0721)	(-4.5561, 13.2281)	(-4.1994, 12.0676)

Supplemental Table S2. Bootstrapped confidence intervals for average difference between mated and unmated mutation rate.

Intervals highlighted in bold do not contain zero, indicating a significant mutation rate difference. Each column shows a variation in analysis settings; the last three columns correspond to variations in minimum distance between Q2 mutation candidate and closest adapter ligation site. Results reported in other Figs of the manuscript correspond to shaded column.