

Supplemental Table S10. Permutation test results for the enrichment or depletion of different genomic features (TEs, genes, secretome/effector genes and allele-specific expressed genes) within different SV types conducted for whole genome. Statistical significance was assessed through two-tailed permutation tests, as described above for centromeric TE analysis.

Genomic feature	SV category	Observed feature coverage diff within vs outside of given SV category	permutation test p- value	permutation test p-value (FDR corrected)
Transposable element	All SVs	15.50793144	0	0
	Indel (>=50bp)	6.912209381	0	0
	Inversion	22.38842466	0	0
	Translocation	21.66703971	0	0
	Duplication	42.50530291	0	0
Gene	All SVs	-1.235425292	0	0
	Indel (>=50bp)	-5.105776541	0.0004	0.000571429
	Inversion	-14.38836517	0.0016	0.002133333
	Translocation	-14.13300059	0	0
	Duplication	-27.39173382	0	0
Secretome/effector genes	All SVs	-4.218475088	0	0
	Indel (>=50bp)	-0.628310186	0.1834	0.1834
	Inversion	-3.629882291	0.0082	0.009647059
	Translocation	-1.91632035	0	0
	Duplication	-3.969194811	0	0
Allele-specific expressed genes	All SVs	-30.26566839	0	0
	Indel (>=50bp)	0.453896011	0.1608	0.169263158
	Inversion	-1.997613073	0.0336	0.037333333
	Translocation	-0.716410851	0.0052	0.0065
	Duplication	-1.500616614	0	0