

**Table S5. Test for enrichment of peaks overlapping regions with inversions.** We tested for an enrichment of peaks in regions of the genome with inversions that are present in at least 10 strains in the Zambian and Raleigh data sets. To do so we performed a one-sided binomial test calculating the probability of at least the number of peaks observed to overlap assuming a uniform distribution of peaks along the autosomal arms. We observe an enrichment of peaks overlapping common inversions on chromosome 3R when performing the scan in windows of 801 SNPs down sampled to 401 SNPs in Zambian data and in windows of 401 SNPs in Raleigh data (low probabilities are highlighted in bold).

Inversion	Number of overlapping peaks in Zambia (scan performed in 801 SNPs windows down sampled to 401 SNPs)	Probability	Number of overlapping peaks in Raleigh (scan performed in 401 SNP windows)	Probability
In(2L)t	4	0.14	4	0.14
In(2R)ns	0	0.73	0	0.73
In(3L)Ok	3	0.20	-	-
In(3R)K	5	0.16	7	<b>0.02</b>
In(3R)Mo	-	-	2	0.31
In(3R)P	5	<b>0.02</b>	5	<b>0.02</b>