Supplementary Table 3. Significance of differences in combined expression levels along each chromosome.

Chr	window size		
	10	50	100
1	0.0028	0.1760	0.0180
2	<0.0001	0.0022	0.0054
3	<0.0001	<0.0001	<0.0001
4	0.0008	0.0004	<0.0001
5	<0.0001	<0.0001	<0.0001

For each chromosome, sliding windows of different sizes were analyzed and compared to 10,000 permutations of each chromosome. The 95th percentile of the natural chromosome was compared to the permuted chromosomes. A two-tailed p-value was calculated by counting the occurrences where the 95th percentile of the permuted chromosome was greater than that of the natural chromosome, then dividing by the number of permutations, and multiplying by 2 for the two-tailed test.