Table S1. Regions identified as significant under a 0.1% genome wide false discovery rate.

Test	**Base Pairs (Amhara)**	**Regions (distinct)**	**Genes**	**Base Pairs (Oromos)**	**Regions (distinct)**	**Genes**
S_f	7,928,000	99	88	7,858,000	95	99
S_π	8,018,000	98	89	8,740,000	114	110
F_{st}	6,824,000	78	71	6,442,000	68	49
PBS	7,670,000	93	79	7,406,000	88	80
Total	**23,950,000**	**261**	**272**	**24,744,000**	**260**	**271**