

Description of Additional Supplementary Data

Title: Supplementary data 1

Description: For the AL population, genomic regions putatively under positive selection based on the locus-specific branch length statistic. Regions contain a minimum of 3 SNPs in top 0.1% of the genome-wide distribution within 50Kb of one another and under high linkage disequilibrium ($r^2 \geq 0.9$).

Title: Supplementary data 2

Description: For the TN population, genomic regions putatively under positive selection based on the locus-specific branch length statistic. Regions contain a minimum of 3 SNPs in top 0.1% of the genome-wide distribution within 50Kb of one another and under high linkage disequilibrium ($r^2 \geq 0.9$).

Title: Supplementary data 3

Description: For the AR population, genomic regions putatively under positive selection based on the locus-specific branch length statistic. Regions contain a minimum of 3 SNPs in top 0.1% of the genome-wide distribution within 50Kb of one another and under high linkage disequilibrium ($r^2 \geq 0.9$).

Title: Supplementary data 4

Description: Genomic regions putatively under positive selection in the AL population based on at least two of three statistics: Tajima's D (top 0.5% of the genome-wide distribution), saltitassi Λ (top 0.5% of the genome-wide distribution), and locus-specific branch lengths (top 0.1% of the genome wide distribution with a minimum of three SNPs within 50Kb of one another and $r^2 \geq 0.9$).

Title: Supplementary data 5

Description: Gene ontology enrichment table for regions putatively under positive selection in the AL population based on at least two of three selection statistics ($\pm 25Kb$). Terms are significant at $FDR \leq 0.05$.

Title: Supplementary data 6

Description: Gene ontology enrichment table for regions putatively under positive selection in the AL population based on the Tajima's D statistic ($\pm 25\text{Kb}$). Terms are significant at $\text{FDR} \leq 0.05$.

Title: Supplementary data 7

Description: Gene ontology enrichment table for regions putatively under positive selection in the AL population based on the saltilassi $\wedge$ statistic ($\pm 25\text{Kb}$). Terms are significant at $\text{FDR} \leq 0.05$.

Title: Supplementary data 8

Description: Gene ontology enrichment table for regions putatively under positive selection in the TN population based on at least two of three selection statistics ($\pm 25\text{Kb}$). Terms are significant at $\text{FDR} \leq 0.05$.

Title: Supplementary data 9

Description: Gene ontology enrichment table for regions putatively under positive selection in the TN population based on the Tajima's D statistic ($\pm 25\text{Kb}$). Terms are significant at $\text{FDR} \leq 0.05$.

Title: Supplementary data 10

Description: Gene ontology enrichment table for regions putatively under positive selection in the TN population based on the saltilassi $\wedge$ statistic ($\pm 25\text{Kb}$). Terms are significant at $\text{FDR} \leq 0.05$.

Title: Supplementary data 11

Description: Gene ontology enrichment table for regions putatively under positive selection in the AR population based on the Tajima's D statistic ($\pm 25\text{Kb}$). Terms are significant at $\text{FDR} \leq 0.05$.

Title: Supplementary data 12

Description: Gene ontology enrichment table for regions putatively under positive selection in the AR population based on the saltilassi $\wedge$ statistic ($\pm 25\text{Kb}$). Terms are significant at $\text{FDR} \leq 0.05$.

Title: Supplementary data 13

Description: Gene ontology enrichment table for regions significantly associated with hind limb length in the AL population accounting for body length, sex, and principal components 1 through 4 of a principal components analysis for population genetic differences. Significant regions ($\pm 25\text{Kb}$) contain a minimum of three SNPs at $P < 1\text{e-}6$ within 50Kb of one another and at high linkage disequilibrium ($r^2 \leq 0.9$). Gene ontology terms are significant at $\text{FDR} \leq 0.05$.