Supplemental Figure S6. Breed-specific map data for the Arabian. Colored bars represent previously reported signatures of selection (green) (Petersen et al. 2013), unique recombination hotspots (red), and unique coldspots (blue).

Supplemental Figure S7. Breed-specific map data for the Belgian. Colored bars represent previously reported signatures of selection (green) (Petersen et al. 2013), unique recombination hotspots (red), and unique coldspots (blue).

Supplemental Figure S8. Breed-specific map data for the Franches-Montagnes. Colored bars represent the locations of previously reported signatures of selection (green) (Petersen et al. 2013), unique recombination hotspots (red), and unique coldspots (blue).

Supplemental Figure S9. Breed-specific map data for the French Trotter. Colored bars represent the locations of previously reported signatures of selection (green) (Petersen et al. 2013), unique recombination hotspots (red), and unique coldspots (blue).

Supplemental Figure S10. Breed-specific map data for the Icelandic. Colored bars represent the locations of previously reported signatures of selection (green) (Petersen et al. 2013), unique recombination hotspots (red), and unique coldspots (blue).
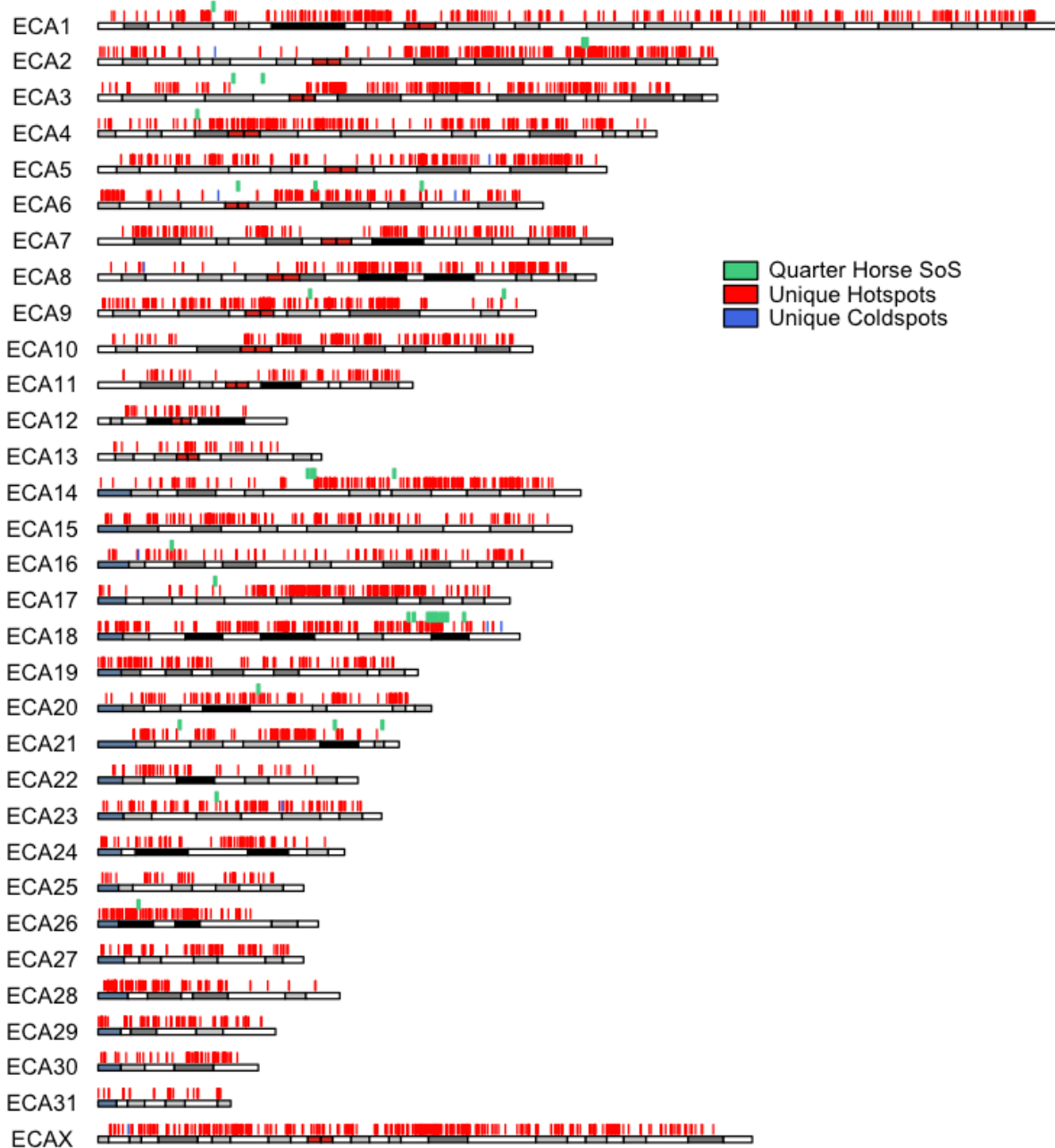
Supplemental Figure S11. Breed-specific map data for the Lusitano. Colored bars represent the locations of unique recombination hotspots (red) and unique coldspots (blue). Signatures of selection analyses were not performed for the Lusitano in Petersen et al. (2013).

Supplemental Figure S12. Breed-specific map data for the Maremmano. Colored bars represent the locations of unique recombination hotspots (red) and unique coldspots (blue). Signatures of selection analyses were not performed for the Maremmano in Petersen et al. (2013).

Supplemental Figure S13. Breed-specific map data for the Morgan. Colored bars represent the locations of previously reported signatures of selection (green) (Petersen et al. 2013), unique recombination hotspots (red), and unique coldspots (blue).

Supplemental Figure S14. Breed-specific map data for the Quarter Horse. Colored bars represent the locations of previously reported signatures of selection (green) (Petersen et al. 2013), unique recombination hotspots (red), and unique coldspots (blue).
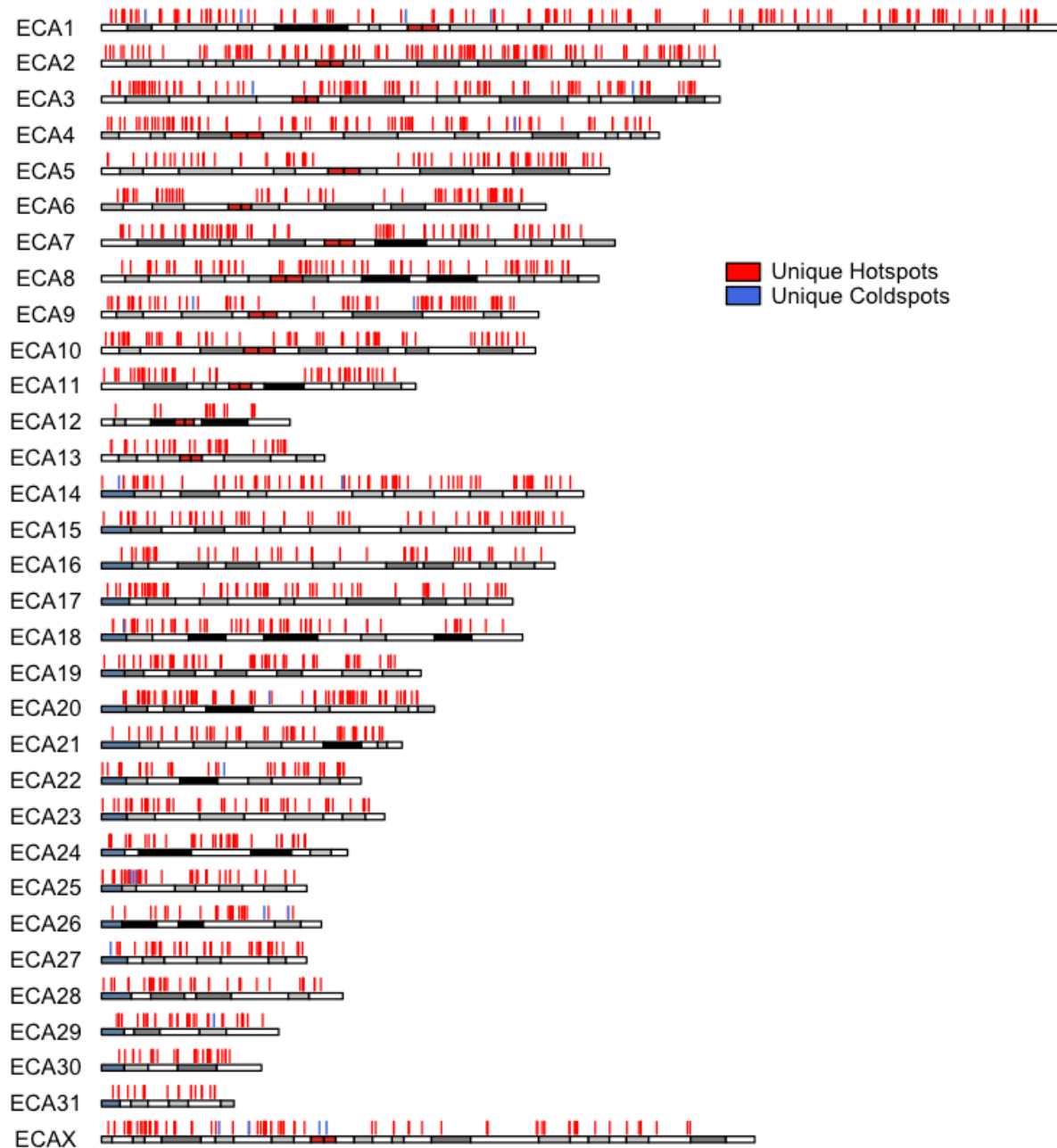
Supplemental Figure S15. Breed-specific map data for the Standardbred. Colored bars represent the locations of previously reported signatures of selection (green) (Petersen et al. 2013), unique recombination hotspots (red), and unique coldspots (blue).

Supplemental Figure S16. Breed-specific map data for the Thoroughbred. Colored bars represent the locations of previously reported signatures of selection (green) (Petersen et al. 2013), unique recombination hotspots (red), and unique coldspots (blue).

Supplemental Figure S17. Breed-specific map data for the Welsh Pony. Colored bars represent the locations of unique recombination hotspots (red), and unique coldspots (blue). Signatures of selection analyses were not performed for the Welsh Pony in Petersen et al. (2013).