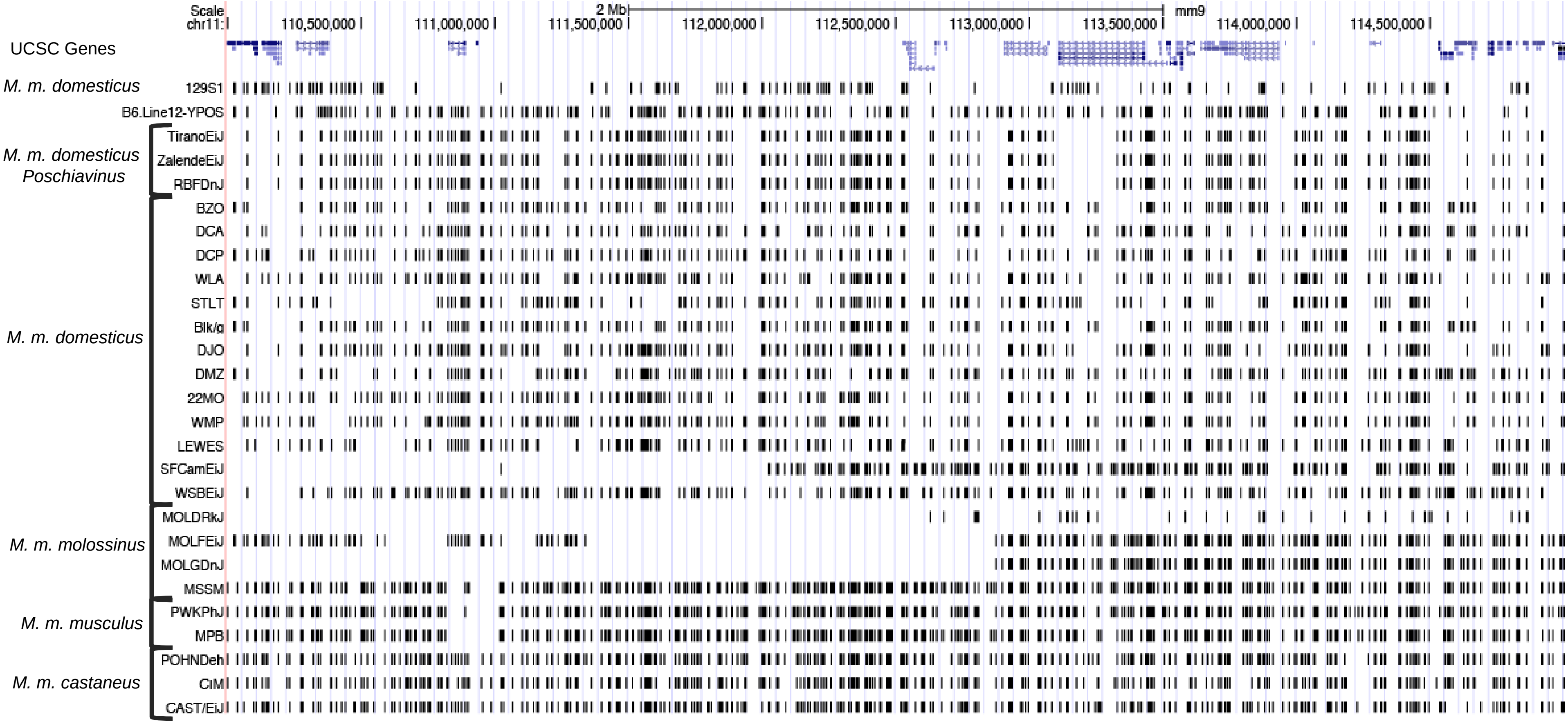
A

Mouse Diversity Array Analysis of B6.Line12-Y^{POS} versus wild-derived strains



B

Mouse Diversity Array Analysis of B6.Line12-Y^{POS} vs other *M. m. domesticus poschiavinus strains*

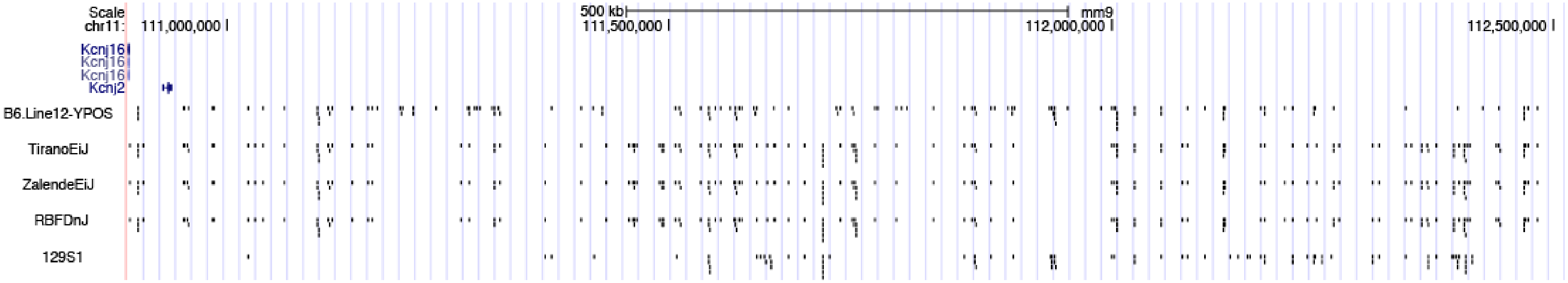


Figure S3 Mouse Diversity array analysis of B6.Line12-Y^{POS} versus wild-derived strains. A) To identify the potential origins of the protective region, we compared Diversity Array data from the data from the 129 strain (top line) to our LineB6/11-13-Y^{POS} protective congenic strain (2nd line), which contains only the 110 region, to and found that the Chromosome 11 110 region (shown here Chr11:110000000-115000000) is not derived from the 129 strain. Further analysis with array data from wild-derived strains of the 4 major subspecies of M. musuclus: *domesticus, musculus, molossinus, and castaneus* identified significant similarity between 3 other typed *M. m. domesticus Poschiavinus* wild strains *Tirano*, *Zalende*, and *RBFDnJ* grouped under *M. m. domesticus Poschiavinus*. SNP data for the 129 and wild derived strains is obtained from http://cgd.jax.org/datasets/popgen/diversityarray/yang2011.shtml. B) In-depth analysis of the minimal overlap protective region derived from sub110-1 and sub110-2 (chr11:110,887,739-112,514,446) of the protected strain LineB6/11-13 and 3 genotyped animals from the *M. m. domesticus Poschiavinus* subspecies show significant similarity over the span of this non-coding region.