A Mouse Diversity Array Analysis of B6.Line12-YPOS versus wild-derived strains
Mouse Diversity Array Analysis of B6.Line12-Y\textsuperscript{POS} vs other \textit{M. m. domesticus poschiavinus} strains

**Figure S3** Mouse Diversity array analysis of B6.Line12-Y\textsuperscript{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\textsuperscript{POS} protective congenic strain (2\textsuperscript{nd} 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 \textit{M. musculus}: \textit{domesticus}, \textit{musculus}, \textit{molossinus}, and \textit{castaneus} identified significant similarity between 3 other typed \textit{M. m. domesticus Poschiavinus} wild strains Tirano, Zalende, and RBFDnJ grouped under \textit{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](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 \textit{M. m. domesticus Poschiavinus} subspecies show significant similarity over the span of this non-coding region.