**Genetic basis of host resistance to *Sparicotyle chrysophrii* in farmed gilthead sea bream (*Sparus aurata*) population**

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**Figure S1.1:** Distribution of parasite count and the log transformed parasite count phenotypes.



**Figure S1.2:** Distribution of number of sibs per family along with the distribution of phenotype across full-sib families.



Panel **A)** is a distribution of sibs in full-fib families, panel **B)** is a distribution of parasite count across different full-sib families, and **C)** is a distribution of log transformed parasite count across different full-sib families.

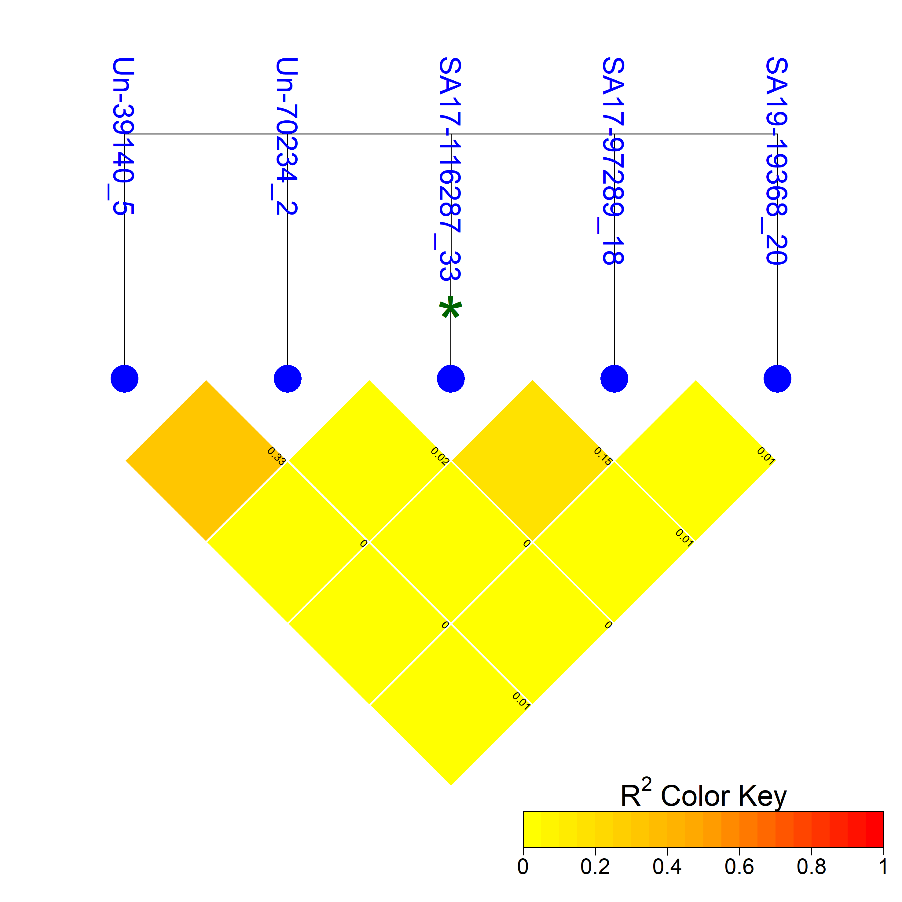
**Figure S1.3:** Plot of linkage maps with distribution of markers across different linkage groups.

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**Figure S1.4:** Pattern of linkage disequilibrium decay along the length (cM) of linkage groups.



**Figure S1.5:** Heat map of Linkage disequilibrium values for the top 5 significant markers in GWAS analysis.



**\*** is a chromosome-wide significant.