Supplementary 1. Plot of frequency of mosquitoes not genotyped at each SNP marker. Plot shows results prior to filtering markers with <50% of individuals genotyped.

Supplementary 2. Frequency (decimal percent) of Log Posterior Density scores >10 from 1000 runs of Bayesian interval mapping, after randomly permuting the phenotype of saltwater-tolerant or susceptible.

Supplementary 3. Recombination rate for each chromosome, from 10 Mb sliding windows. Schematics depict positions of chromosome arms, with gray shading at the inversion 2Rop.

Supplementary 4. Genomic regions with random forests Variable Importance >0.002 and Bayesian Log Posterior Density >10.

Supplementary 5. List of all genes in the six QTL peak regions, with chromosomal locations.

Supplementary 6. Separate heatmaps of genotypes for male vs. female saltwater-tolerant and susceptible backcross progeny, showing SNP markers in the six QTL regions. Each row represents an individual mosquito, and each column a marker. Individual panels show (**A**) tolerant males, (**B**) susceptible males, (**C**) tolerant females, and (**D**) susceptible females. Blue color represents homozygosity for *An. merus*, or hemizygosity for *An. merus* on the X in males.

Supplementary 7. Mean (± 1 SE) Log Posterior Density for main effect contributions from each marker, from Bayesian interval mapping.

Supplementary 8. Mean (± 1 SE) Log Posterior Density for epistatic contributions from each marker, from Bayesian interval mapping.

Supplementary 9. Mean (± 1 SE) Log Posterior Density for gene-sex contributions from each marker, from Bayesian interval mapping.

Supplementary 10. List of select genes of interest within the QTL peaks.