

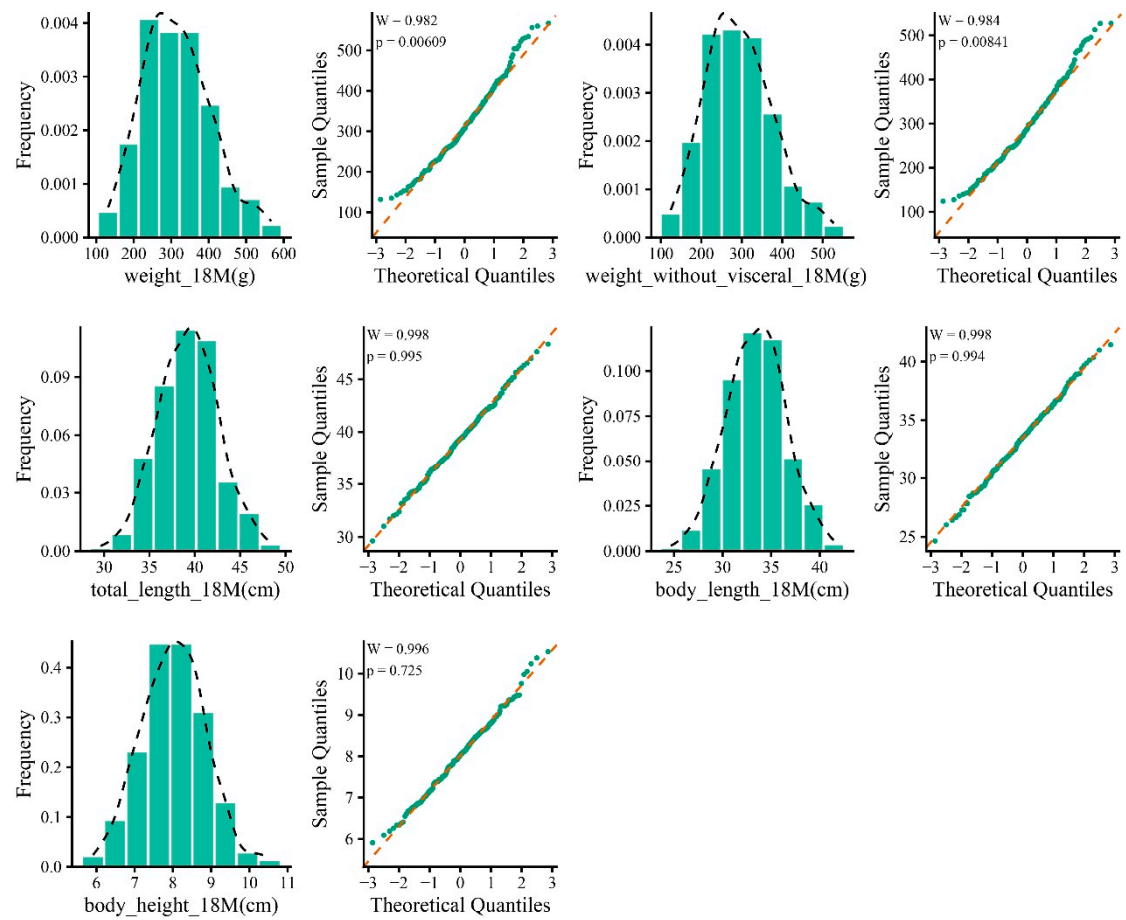


Figure S1. Phenotypic data distribution of five growth traits in topmouth culter at 18 mpf.

Left panels show frequency distribution histograms (overlaid with normal distribution curves), with the X-axis representing trait measurement values and the Y-axis representing frequency; right panels show Q-Q plots. BW: body weight; BWW: body weight without viscera; TL: total length; BL: body length; BH: body height.

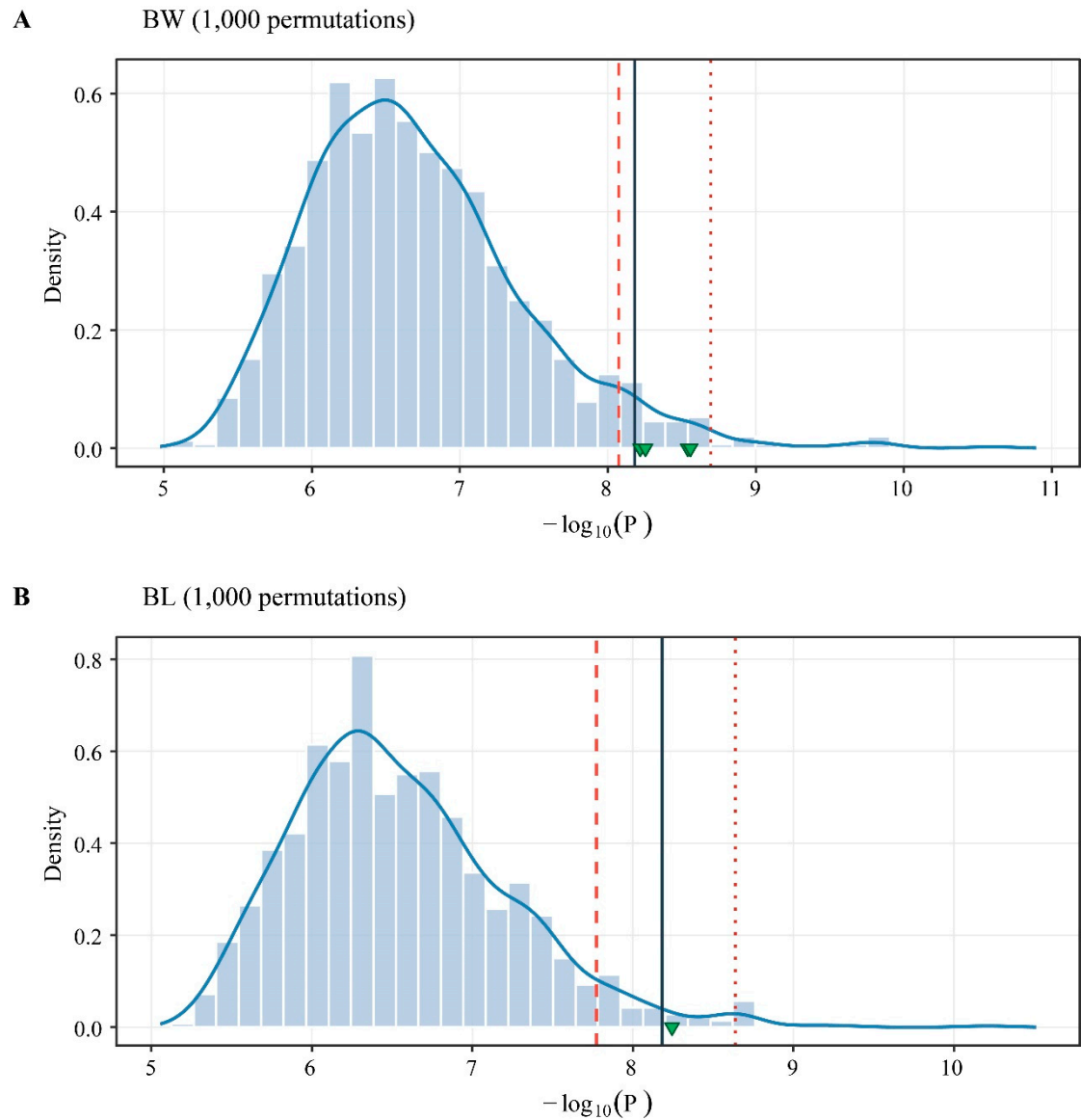


Figure S2. Empirical null distributions of minimum P -values from 1,000 permutations for body weight (A) and body length (B) in *Culter alburnus*. Histograms with density overlays show the distribution of minimum $-\log_{10}P$ values across permutations. The solid vertical line marks the Bonferroni genome-wide significance threshold ($-\log_{10}P = 8.182$); the dashed and dotted lines mark the empirical thresholds at $\alpha = 0.05$ and $\alpha = 0.01$, corresponding to the 5th and 1st percentiles of the permutation distribution, respectively. Green triangles indicate the observed $-\log_{10}P$ values of the genome-wide significant SNPs from the original GWAS. All six SNPs exceeded the empirical $\alpha = 0.05$ threshold, supporting the robustness of the associations.