



**Figure S10 Mapping causal gene for *qGL3-1* and *qGW5-2*.** (A) and (B) Traditional LOD score plot for *qGL3-1* and *qGW5-2* controlling grain shape on chromosome 3 and chromosome 5. (C) and (D) The causal score is calculated at each candidate locus via pairwise comparisons for each trait. (E) and (F) The up panels show the gene annotation of candidate region. The bottom panels show the number of individuals with recombinant genotypes and the phenotype of individuals with different genotypes at causal gene locus. MH, H and ZS represent the genotype of Minghui 63, heterozygous and Zhenshan 97, respectively. n.s. means not significant, \* means  $P < 0.05$ , \*\* means  $P < 0.01$ , \*\*\* means  $P < 0.001$ .