Figure S13 Phenotypic distributions of F₂ individuals with different combination of interacting alleles in four-locus network at *qPH1-2* locus in plant height. (A) The box plot is shown for each of the 81 subpopulation. Color indicates the genotype at the hub QTL (cyan/gray/green boxes for MH63/Heterozygous/ZS97 genotypes, respectively). The *x* axis represents the four-locus genotype classes, where blue/yellow/red dots indicate phenotypic value increasing/heterozygous/decreasing alleles at the interacting loci. The regression lines illustrate the fit for linear additive (black) and interaction (red) models. The number above the *x* axis is the number of individuals in each genotype class. (B) The box plot represents a group of individuals that have the same number of plant height increasing alleles at the interacting loci. The individuals are divided and colored based on the genotype at the *qPH1-2* locus. The *x* axis gives the number of plant height increasing alleles at the interacting loci and the number of individuals in each group. The regression lines illustrate the fit of linear additive model.