



Figure S12 Genetic interaction networks for six traits and phenotypic distributions in heading date. (A) Genetic interaction networks for plant height, tiller number, yield per plant, grain length, grain width and length width ratio. The name of QTLs and bin-markers are given. The genes in the brackets are inferred candidate genes for QTLs. (B) Phenotypic distributions of F_2 individuals with different combination of interacting alleles in four-locus network at *Hd1* locus in heading date. 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.