



**Figure 3-figure supplement 9 :** **(a)** GWAS with two different SNP data sets, one encompassing all SNP from whole genome sequencing and one SNP set after removing repetitive sequences. The number of MTA identified by each analysis are given in the Ven diagram. **(b)** Comparison of GWAS analysis (Manhattan plots) of principal component PC1 between whole genome SNP set (WG) and repeat masked SNP set (RM). The blue horizontal line in the Manhattan plots indicates the suggestive threshold  $-\log_{10}(8.98E-7)$ . The red horizontal line indicates the significance threshold (Bonferroni correction)  $-\log_{10}(1.67e-8)$ . **(c)** Comparison of local Manhattan plots from region 8.04 – 8.14 Mb on chromosome Cq2A associated with days to flowering (DTF), days to maturity (DTM), plant height (PH), and panicle length (PL) between whole genome SNP set (WG) and repeat masked SNP set (RM).