**Fig. S5. eQTL analysis using pan-SVs.**

a. Manhattan plot of the association between the pan-SV dataset and the expression levels of the HGW (LOC_Os06g06530) gene.

b. Haplotypes of the HGW gene in Osi and Osj. Osi, Osji, and Osj refer to O. sativa indica and O. sativa japonica, respectively. c. Validation of the INS in HGW gene.

d. Breakpoint of the 127 bp INS in HGW gene in Os identified by mapping ONT reads to the Nipponbare reference genome. Os refer to O. sativa. e. Expression of the HGW gene in accessions with or without the INS (against the Nipponbare reference genome). ** P < 0.01. Wilcoxon tests.

f. 1,000-grain weights of accessions with or without the INS in OsNaPRT1 gene. ** P < 0.01. Two-tailed t-tests.

g. Breakpoint of the 1.3 kb DEL in OsNaPRT1 gene in Os identified by mapping ONT reads to the Nipponbare reference genome. Os refer to O. sativa. h. Expression of the OsNaPRT1 gene in accessions with or without the DEL. ** P < 0.01. Two-tailed t-tests.

i. Validation of the DEL in OsNaPRT1 gene. j. Breakpoint of the 1.8 kb DEL in OsNaPRT1 gene in Os identified by mapping ONT reads to the Nipponbare reference genome. Os refer to O. sativa. k. Expression of the OsNaPRT1 gene in accessions with or without the DEL. ** P < 0.01. Two-tailed t-tests.

l. 1,000-grain weights of accessions with or without the DEL in OsNaPRT1 gene. ** P < 0.01. Wilcoxon tests.

m. Phylogeny of 251 accessions based on SVs. Different colors indicate accessions in different sub-populations.

n. The distribution pattern of SVs of functional genes. Osi, Aus, Osji, Or, Og, and Ob refer to O. sativa indica, O. sativa aus, O. sativa japonica, O. rufipogon, O. glaberrima, and O. barthii, respectively.