



Supplementary Material S1. Genome-wide association analysis of pre-harvest sprouting (PHS) in the complete dataset (24 Indica and 253 Japonica rice accessions). Manhattan and Quantile-quantile plots were generated through the mixed linear model (MLM) with kinship matrix and principal components. Points above the blue and red threshold lines indicate significant association at $-\log_{10}(p)=5$ and 6, respectively.