Description of Additional Supplementary Files

Supplementary Data 1: The phenomics data including macro-phenome and traits used for BSA.

Supplementary Data 2: The summary of genetic mapping including pQTLs, eQTLs and mQTLs.

Supplementary Data 3: The actual wavelengths corresponding to the trait IDs.

Supplementary Data 4: The prediction accuracy of yield, dry matter and well-predicted metabolites using tuber hyperspectral imaging data.

Supplementary Data 5: The correlation between traits and gene expression in tuber.

Supplementary Data 6: Triple relationships of bins, genes and traits.

Supplementary Data 7: Genes with dominant or overdominant QTLs.

Supplementary Data 8: The possible off-target sites of *PME* gene.