

Fig. S1 Grouping of the 3K rice genotypes used in the study. **a** Pie chart with the percentage of each rice subgroups. **b** STRUCTURE plot. **c** Heatmap of the kinship matrix. **d** PCA plot. Kasalath (*aus*) and Swarna (*indica*) are highlighted (arrows). **e** Eigenvalue based scree plot. **f** MDS (MultiDimensional Scaling) plot downloaded from Rice SNP-seek database with red squares representing the genotypes used in this experiment.

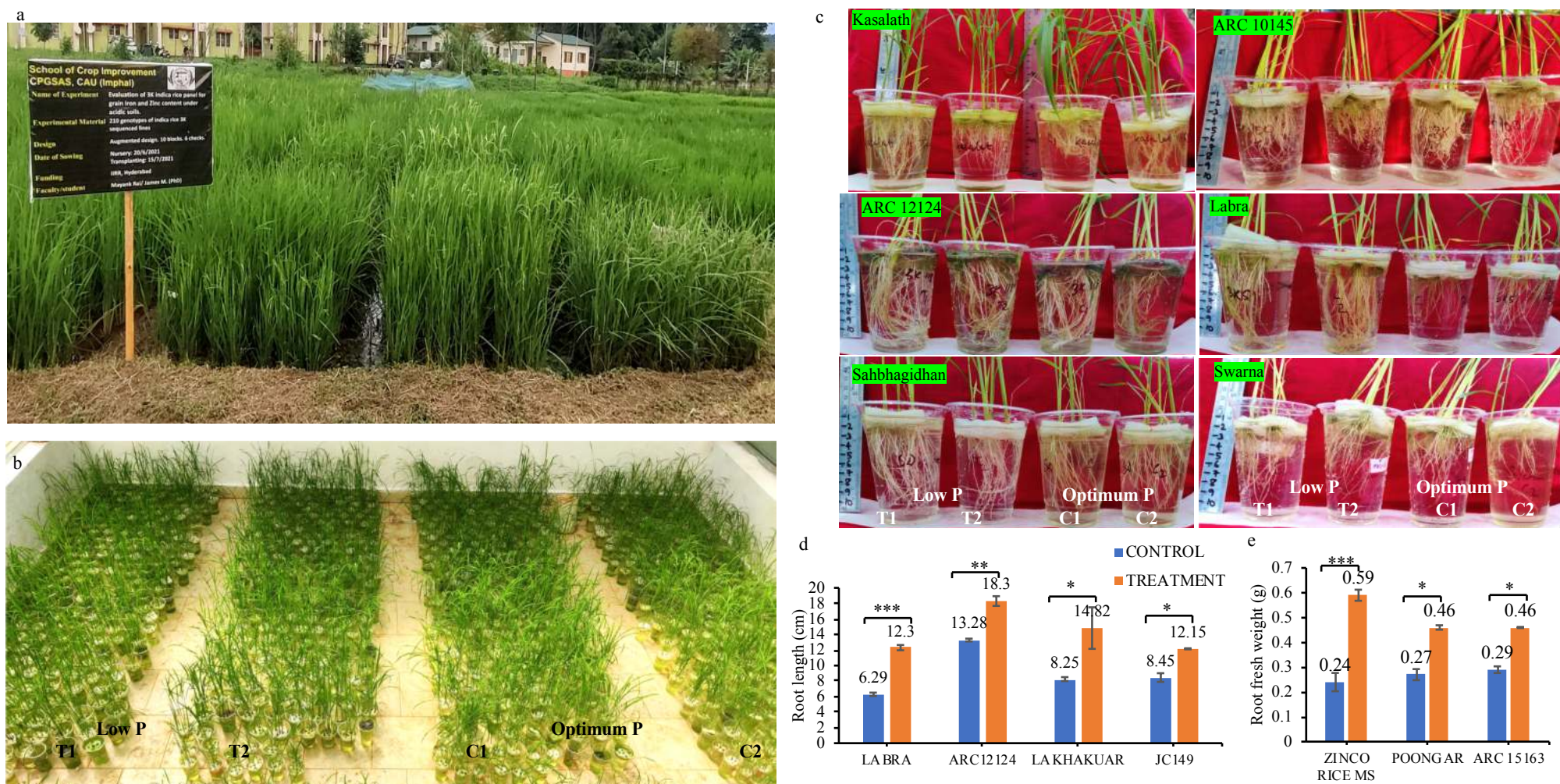
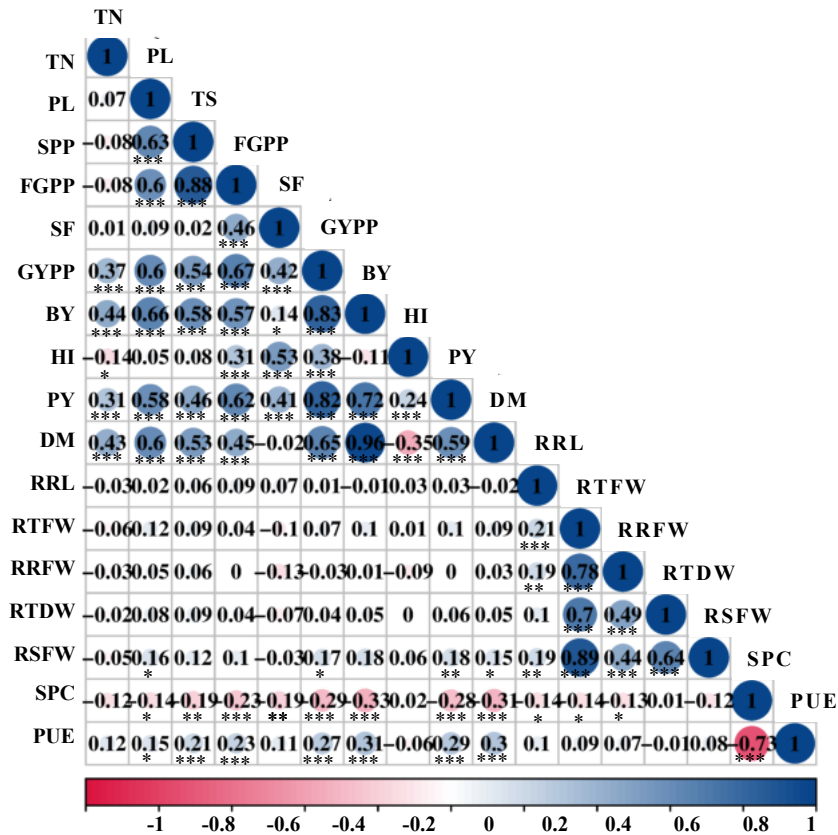


Fig. S2 Representative pictures at different stages of the experiment- **a** rice field with 3K genotypes showing variation in kharif 2021. **b** hydroponics experiment in greenhouse. **c** representative picture of checks and few genotypes showing difference in root length and biomass. **d-e** Difference in the phenotypic means for traits root length (RL) and root fresh weight (RFW) in hydroponics experiment. Asterisks * ($P < 0.05$), ** ($P < 0.01$) and *** ($P < 0.001$) on the top of bars indicate significant difference in phenotypic values between control and treatment.

a



b

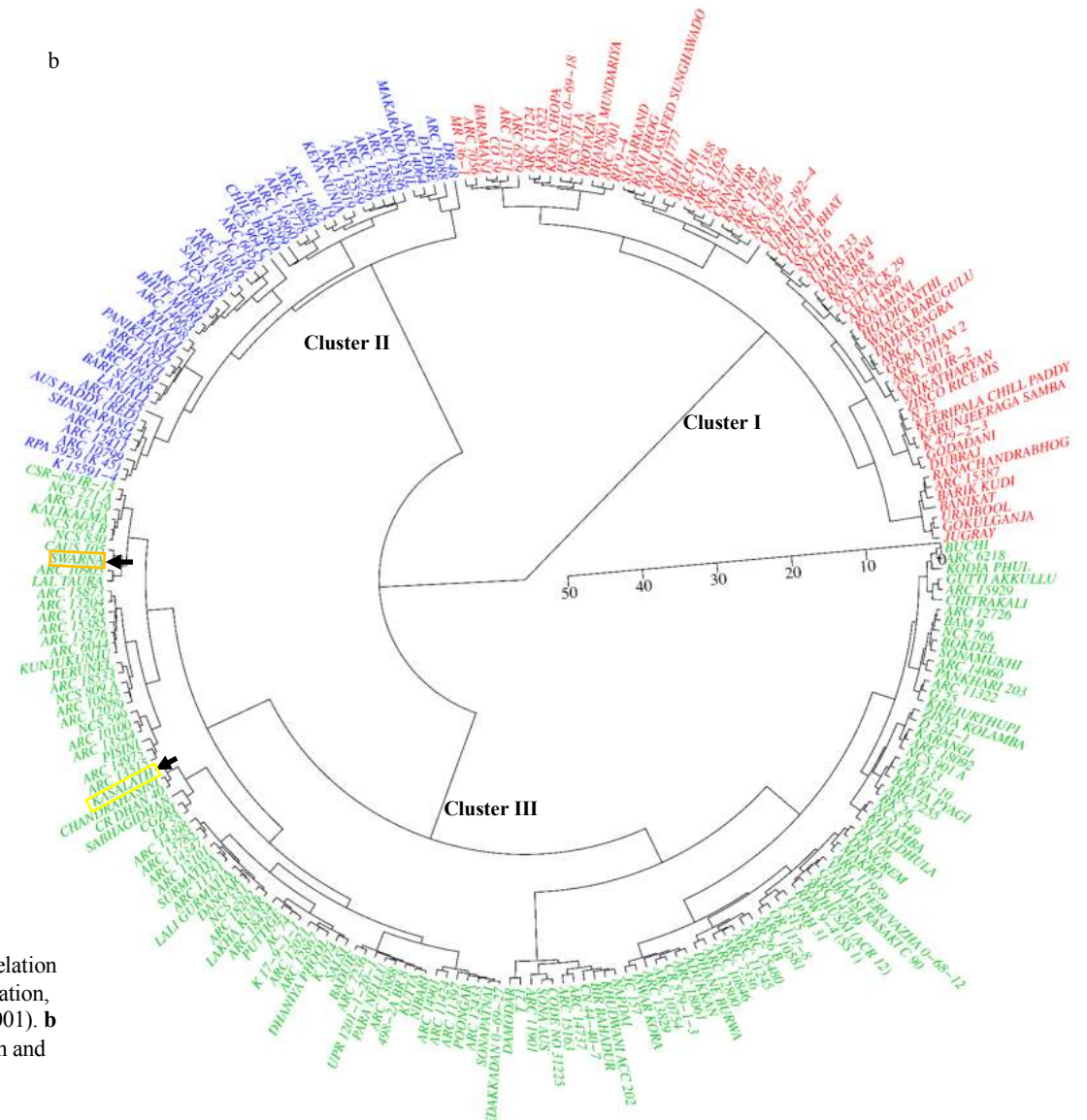


Fig. S3 Correlation matrix and clustering of genotypes. **a** Heatmap showing phenotypic correlation between all the traits studied with blue and red colour indicating positive and negative correlation, respectively. Significant values are indicated by * ($P < 0.05$), ** ($P < 0.01$) and *** ($P < 0.001$). **b** Grouping of genotypes based on Euclidean distance (Wards clustering). Positions of Kasalath and Swarna are highlighted.

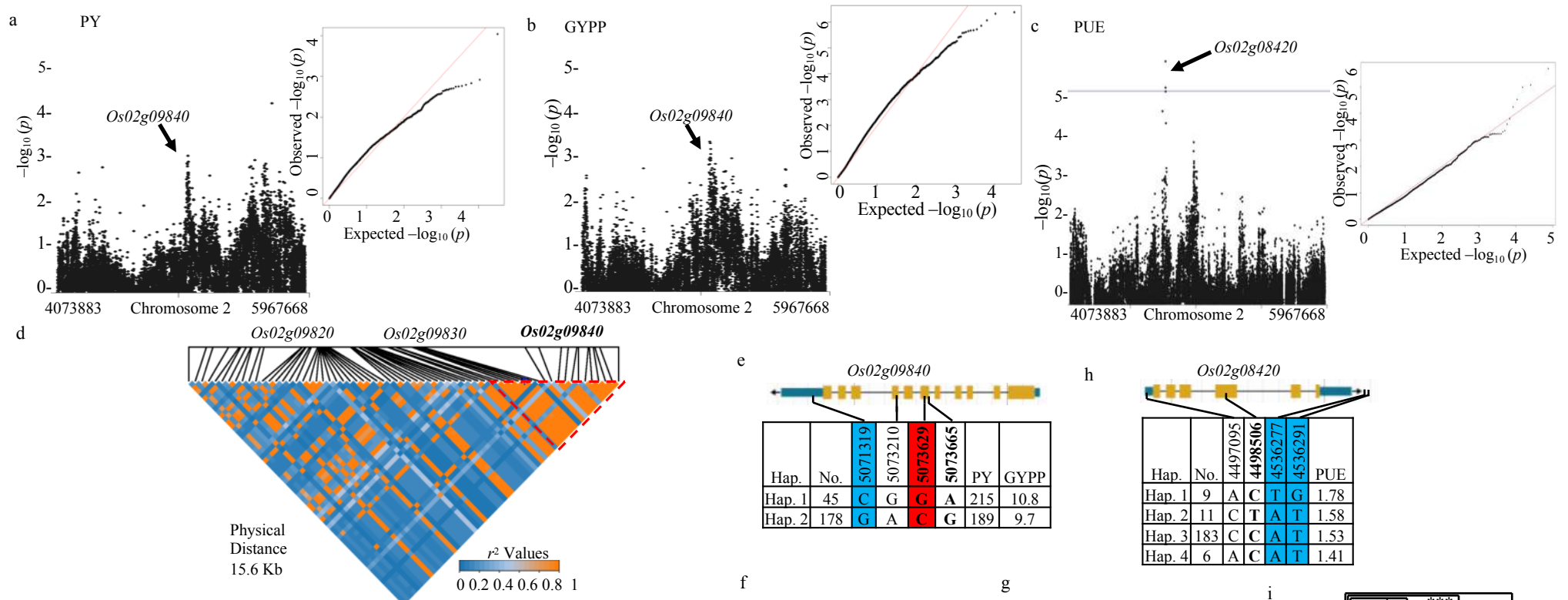
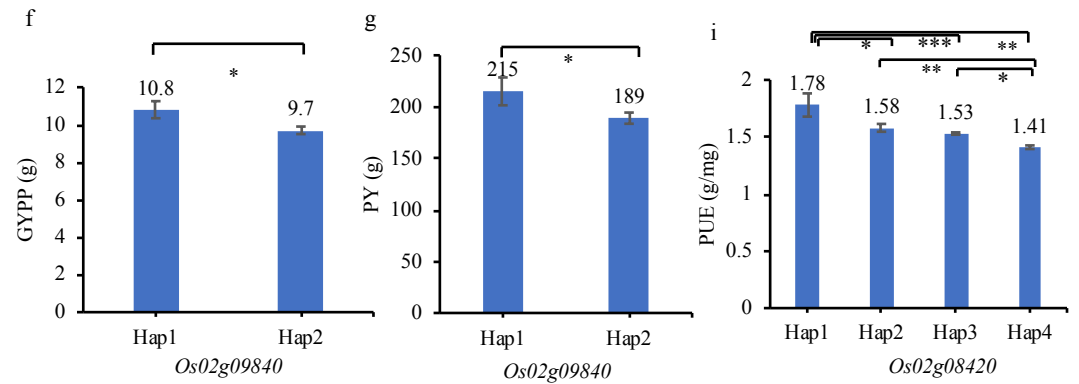


Fig. S4 Identification of candidate genes associated with PY, GYPP and PUE in the previously reported region on chromosome 2. **a-c** Manhattan plot and Q-Q plot of PY, GYPP and PUE with EMMAX model showing QTNs and associated candidate genes (highlighted with arrows). **d** Zoom in SNP likelihood LD (Linkage Disequilibrium) heatmap showing the position of candidate gene *Os02g09840* within dotted red triangle. Gene structure of candidate genes- **e** *Os02g09840*; **h** *Os02g08420* with haplotype analysis of peak SNPs. Orange, blue and white colour represent exons, UTR and introns, respectively. Nonsynonymous SNPs are in bold; blue and red-coloured columns represent peak, and deleterious SNP (SIFT score < 0.05), respectively. Average value for a particular haplotype (hap.) for GYPP, PY and PUE along with number of genotypes (no.) is indicated. **f-g; i** Phenotypic variation among haplotypes for GYPP, PY and PUE with significant values (t test) indicated by * ($P < 0.05$), ** ($P < 0.01$) and *** ($P < 0.001$), respectively for candidate genes.



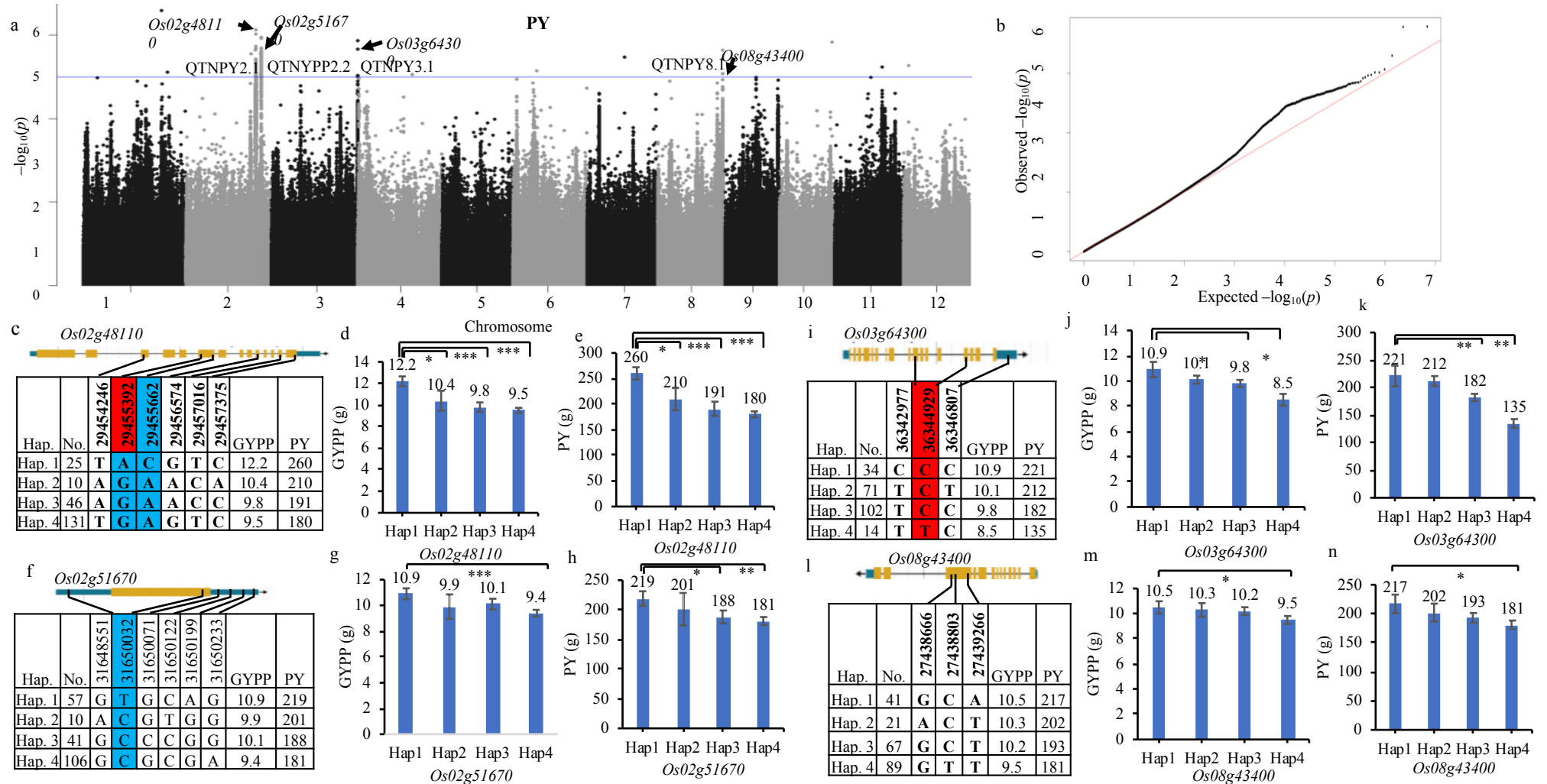


Fig. S5 Identification of candidate genes associated with plot yield (PY) in lowland acidic field. **a** Manhattan plot of PY with EMMAX model showing QTNs and associated candidate genes (highlighted with arrows). Solid blue line depicts the threshold P value for peak SNPs/QTNs. **b** Q-Q plot for PY. Gene structure of candidate genes- **c** *Os02g48110*; **f** *Os02g51670* and **i** *Os03g64300* and **l** *Os08g43400* with haplotype analysis of peak SNPs. Orange, blue and white colour represent exons, UTR and introns, respectively. Nonsynonymous SNPs are in bold; blue and red-coloured columns represent peak, and deleterious SNP (SIFT score < 0.05), respectively. Average value for a particular haplotype (hap.) for GYPP and PY along with number of genotypes (no.) is indicated. Phenotypic variation among haplotypes for GYPP and PY with significant values (t test) indicated by * ($P < 0.05$), ** ($P < 0.01$) and *** ($P < 0.001$), respectively for candidate genes- **d** and **e** *Os02g48110*; **g** and **h** *Os02g51670*; **j** and **k** *Os03g64300*; **m** and **n** *Os08g43400*

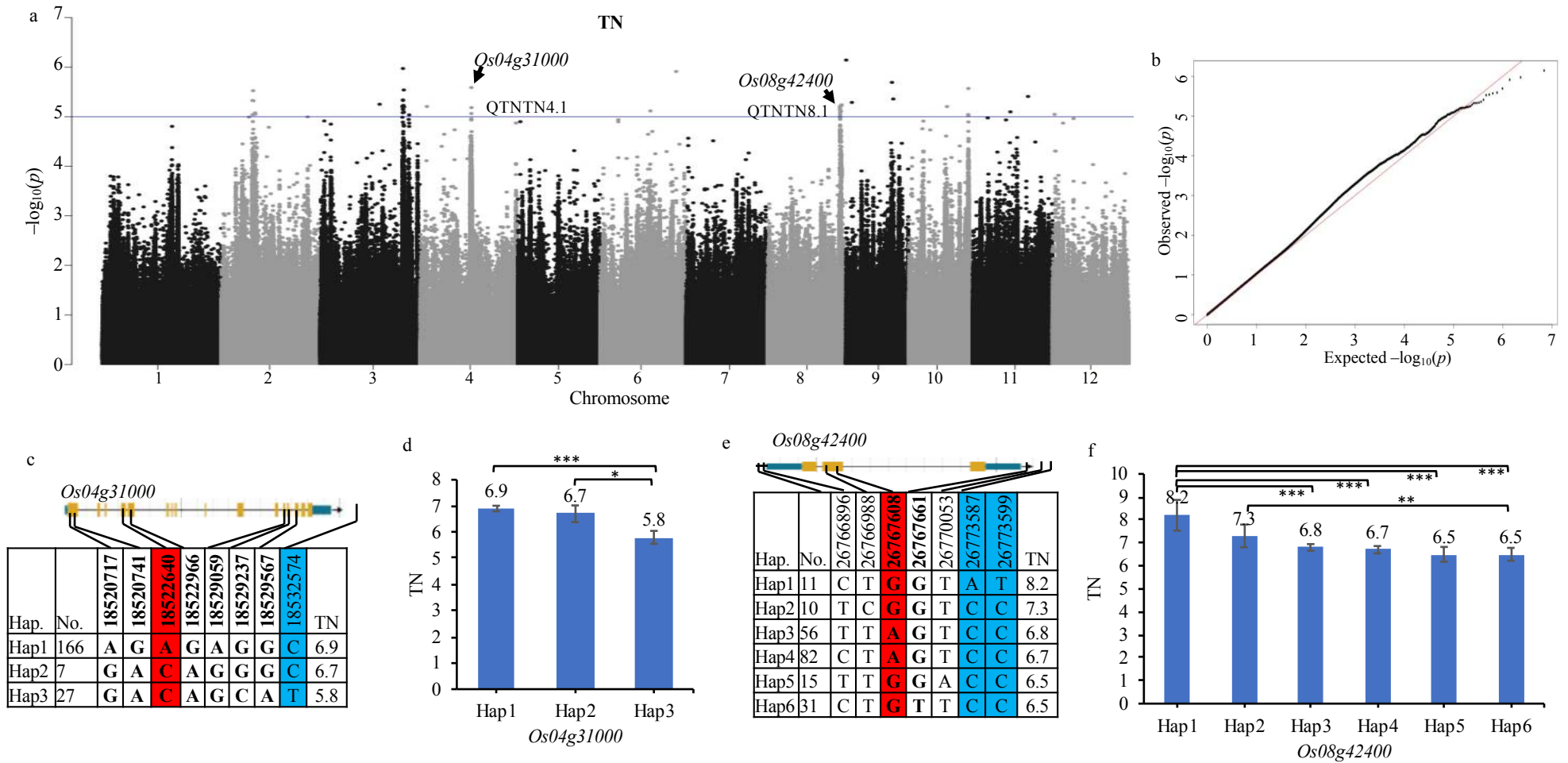


Fig. S6 Identification of candidate genes associated with TN. **a-b** Manhattan plot and Q-Q plot of TN with EMMAX model showing QTNs and associated candidate genes (highlighted with arrows). Gene structure of candidate genes- **c** *Os04g31000*; **e** *Os08g42400*; with haplotype analysis of peak SNPs. Orange, blue and white colour represent exons, UTR and introns, respectively. Nonsynonymous SNPs are in bold; blue coloured columns represent peak SNP. Average value for a particular haplotype (hap.) for TN along with number of genotypes (no.) is indicated. **d, f** Phenotypic variation among haplotypes for TN with significant values (t test) indicated by * ($P < 0.05$), ** ($P < 0.01$) and *** ($P < 0.001$), respectively for candidate genes