PNAS

Supporting Information for
Multi-omics of a rice population identifies genes and genomic regions in rice that bestow low glycemic index and high protein content

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Development of a F_2-derived F_3 population. The F_2-derived F_3 mapping population was developed by employing the hybridization between Samba Mahsuri (a superior grain quality line with dominant allele of *OsSBEIIb*) and IR36 amylose extender (IR36*ae*) line(recessive allele of *OsSBEIIb*), a high amylose line mutant created using the IR36 (1, 2). Samba Mahsuri, one of the parents, is one of the most popular varieties consumed mainly across India due to its excellent cooking and eating qualities. A total of ~5500 F2 progenies of IR36ae x Samba Mahsuri were raised. Upon examining the SNP variations existing in *SBEIIB* (LOC_Os02g32660) gene between both parents, one SNP (snp_02_19362520, G→A) previously reported by Butardo et al. (3), predicted to be located at the exon-intron junction (Exon 11 coordinates 19362521-19362640) was genotyped using Kompetitive allele specific PCR (KASP) assay. After assessing their fit to the Mendelian segregation ratio, a total of 369 F_2 progenies were selected and eventually self-pollinated until F_3 generation utilizing single seed descent (SSD) method and advanced to F_6 generation under open field conditions.

Measurement of Amylose and Protein Content. Seeds collected from F_3 generations of each family were bulk-harvested and dried until seed moisture content of 12-14% was attained. The samples were subjected to milling and the homogenized rice powder was subjected to amylose and protein estimation. The apparent amylose content (AC) was determined using an in-house validated method by the IRRI Service Laboratories (4) which was based on ISO 6647-2:2020 (Rice—Determination of Amylose Content—Part2: Routine Methods) (5) method. The apparent amylose content (AC) was determined using an in-house validated method by the IRRI Service Laboratories (4) which was based on ISO 6647-2:2020 (Rice—Determination of Amylose Content —Part2: Routine Methods) (5) method. The test solution is prepared by hot-dispersion with sodium hydroxide and analyzed using the San++ Segmented Flow Analyser (SFA) system (Skalar Analytical B.V., The Netherlands) and allowed to react with iodine to form amylose-iodine complex (K-I2). The absorbance of the iodine complex solution was determined at 620 nm wavelength and the AC (%) was quantified against the standard curves.

Crude protein content (PC) was measured using an in-house protocol of the IRRI Service Laboratories (54). A test portion of rice flour (50 mg) was digested in sulfuric acid (2 mL) with 1 g anhydrous potassium sulfate:selenium mixture (50:1, w/w) for 1 h at 380 °C. The sample was then cooled to room temperature, made up to volume (20 mL) with deionised water, and kept overnight to allow for sedimentation. The liberated ammonium in the digest was allowed to react with the solution consisting of sodium salicylate and sodium nitroprusside , and aqueous sodium hypochlorite through the glass transition lines in a Continuous Flow Analyser (CFA) system. The absorbance values of the ammonia-salicylate complex were determined at $\lambda = 660$ nm, and the % Kjeldahl N values of the samples were determined based on the non-linear relationship between absorbance and analyte concentration, following the Beer-Lambert Law based on a standard curve developed using ammonium sulfate solutions with different concentrations. Finally, the crude PC was calculated by multiplying the Kjeldahl N value by 5.95 (6).

***In-vitro* GI and resistance starch analysis.** The in vitro GI values of the milled rice samples of the F_5 derived F_6 RIL mapping populations was measured at the Commonwealth Scientific and Industrial Research Organisation (CSIRO), Adelaide, Australia using a predictive in vitro protocol that mimics the oral, gastric, pancreatic and intestinal digestion process in the human gut (7). The milled rice samples of T_0 homozygous lines of sbe2b genome edited lines and the corresponding wild type samples were subjected to the *in vitro* starch digestion was followed according to section 2.3.3 Method 3 described in Pautong et al. (8) with some modifications. Detailed method was described in the Supplementary information. In summary, the process involved cooking 300 ± 0.3 mg whole milled rice with a 1:2 rice-to-water ratio in a 50-ml tube over boiling water for 23 minutes. The sample was then left at room temperature for 5 minutes before it was transferred in a beaker fitted to the NutraScan GI20 Glycemic Index Analyser. It was added with 1mL of 0.05M sodium potassium phosphate buffer (pH 6.9) and the rice was minced using a stainless-steel spatula. The temperature was maintained at 37◦C. Subsequently, the 50-ml tube was washed with 4mL of the same buffer and the washing was also transferred to the beaker. To simulate the digestion process, the NutraScan GI20 Glycemic Index Analyser was used to dispense the necessary enzymes and buffers in the following manner: 2 mL of α-amylase in 0.05 M sodium potassium phosphate buffer (pH 6.9), 3 mL of aqueous HCl (pH ~1), then 3 mL of pepsin in 0.1 M sodium potassium phosphate buffer (pH 1.5). It was allowed to incubate for 30 minutes before the addition of 15 mL of aqueous NaOH (pH ~12.6). Following this, a 15 mL enzyme solution containing pancreatin and amyloglucosidase in 0.1 M sodium potassium phosphate buffer (pH 6.9) was added and was allowed to incubate for another 30 minutes. Duplicate aliquots (0.70 mL) were withdrawn at 0 minutes (just before pancreatin-AMG addition) and at 30 minutes (after pancreatin-AMG addition). The aliquots were placed on ice until centrifugation (13,500 rpm, 10 minutes, 4 ◦C). After which, a 1-µL aliquot of the supernatant was transferred to a 0.6-mL microfuge tube and added with 9 µL of AMG solution (33.3 U/mL in 0.4 M sodium acetate buffer, pH 5.0), vortexed, and incubated in a water bath (50 ◦C) for 20 minutes. Lastly, glucose in the mixture and reagent blank were measured by adding GOPOD reagent. The absorbance values at 510 nm for both the sample and glucose standard were corrected using a reagent blank. The corrected values were then converted into glucose concentrations (mg/ml of aliquot) following the equation described by Pautong et al.(8) in section 2.3.4 and the area under the curve (AUC) was calculated based on the trapezoidal rule. Finally, the predictive GI (pGI) of the samples were computed using the linear equation pGI = 0.07821 x AUC (corrected) + 47.8876.

Bulk generation, DNA isolation and whole genome sequencing. Based on the extreme phenotypes of grain quality phenotype including AC and PC, the 14-15 progenies per bulk were selected from either of the extreme phenotypes and bulk sets were created for each respective phenotype, constructing a total of four bulk sets. Bulk sets created for amylose content were confirmed for their contrasting glycaemic index values, i.e. high and low amylose bulk sets served as low and intermediate GI bulks, respectively. Genomic DNA was extracted from the selected bulk set individually using the cetyltrimethylammonium bromide (CTAB) method and purified using Qiagen DNeasy Plant Mini Kit. Qualitative analysis of DNA quality was done by running the samples on 1% agarose gel and by performing the DNA quantification through NanoDrop 2000. The final DNA concentration was adjusted to 100 ng/µL. The 30X- whole genome resequencing (WGS) was performed for all four bulk sets, aside from parental genotypes. Before library preparation, samples were ensured for the right concentration using fluorometer (Qubit Fluorometer, Invitrogen) and DNA sample integrity was assessed using agarose gel electrophoresis using 1% Agarose Gel (150 V for 40 min). 1µg genomic DNA was randomly fragmented, followed by purification and end repair performed using AxyPrep Mag PCR clean up Kit. The repair DNA were combined with A-tailing mix followed by incubation at 37℃ for 30 min while Illumina adapters were ligated to adenylate 3' ends of the DNA following incubation of 16℃ for 16h. Multiple rounds of PCR amplification were conducted to enrich the adapter-ligated DNA fragments. The 150 bp pair-end reads sequencing of qualified libraries was done using Illumina Hiseq X10 sequencer. The genotype data processing and QTL-seq analysis were detailed in Supplementary information.

Genotype data processing and QTL-seq analysis.
The clean reads from the extreme bulk sets for respective traits mapped onto the Nipponbare pseudomolecule reference (MSU version 7) and the variants were called. SNP calls with reference allele frequency of 0.2 in both bulks were filtered out and removed as these may be due to sequencing errors. Next Generation Sequencing (NGS)-based BSA analysis was performed following the earlier reports (9, 10). Briefly, SNP index was calculated as the ratio of the alternative allele reads to the total read depth in the individual bulk samples. Then, delta SNP index was calculated as per Takagi et al. (11). The genome wide G statistics (G value) was

calculated for each SNP by observed and expected allele depth of the reference and alternate allele assuming that the allele depth is equal for both resistance and susceptible bulks. G' value was calculated using a tricube smoothed G value by average weighted of the physical distance across the neighbouring SNPs within a given window that accounts for Linkage disequilibrium (LD) and also minimizes background noise attributed to SNP calling errors (9, 10). Both of the parents, IR36ae and Samba Mahsuri were used as references while calculating the key parameters of G', delta SNP, and P values, and only peaks identified contrasting in both parents were used for analysis.

QTL Seq analysis or Bulk segregant (Bulk Seq) was performed on bulk sets created based on extreme values of amylose content and protein content. Bulk Seq analysis was implemented using the G statistics, wherein G' has been adopted avoiding the background noise during analysis while accounting for linkage disequilibrium (LD) between SNPs. Significant QTLs associated with AC and GPC were identified based on -log10P, G' and delta SNP index based on the default thresholds setting of the pipeline. The genotyping-by-sequencing data was generated for F_5-derived F_6 population following the Elshire et al. (12) method and have incorporated the following changes: 100 ng of genomic DNA were used, 3.6 ng of total adapters were used, the genomic DNAs were restricted with ApeKI enzyme, and the library was amplified with 18 PCR cycles. The 150-bp paired end reads were sequenced using the NovaSeq sequencing platform. The ABH format genotype data was created using PLINK1.9 (13) with 20% missingness call rate resulting in 44,946 SNPs after filtering.

QTL mapping, targeted association and epistatic interaction analysis. QTL mapping analysis for protein and AC was performed for the F_5-derived F_6 recombinant inbred line population using composite interval mapping (CIM) method from the R/qtl package (14). Targeted association analysis of the candidate genes lying within the fine-mapped QTLs identified from BSA-seq and CIM analyses was conducted using PLINK1.9 (13) and EMMAX (15) and significant SNPs were filtered at 95% confidence level. Epistatic interactions among significant SNPs were also tested using PLINK1.9 at $p<0.05$. Candidate genes common to AC and PC based on either BSA-seq analysis or CIM analysis, and genes with multiple epistatic interactions were used to construct the association network summary using Cytoscape (16). The percent phenotypic variation explained by the markers were calculated using LDAK (17). The expression profiles of candidate genes common to AC and PC based on BSA-seq and targeted association analyses were checked in the Rice eFP Browser (http://bar.utoronto.ca/) and genes with absolute expression value > 1000 in developing embryos were selected and their significant SNPs were used to determine different allelic combinations showing distinct GI, AC, and PC values in the F_5-derived F_6 RILs visualized using the *ggstatsplot* (18) R package.

Sample Preparation and Extraction of Tissue Metabolites. Brown rice flour samples of QTL-seq pools of high amylose and low amylose, and high protein and low proteins were added with 800 µL of 80% methanol and homogenized for 90s. The homogenized samples were sonicated for 30 minutes at 4^{O}C. Samples were then kept at -40°C for 1h, vortex mixed for 30s and kept for another 30 min. This was followed by centrifugation at 12,000 rpm and 4°C for 15 mins. The supernatant was transferred to a vial for LC-MS analysis.

Metabolomic analysis of ultra-low, low, and high GI samples. The extraction and processing of the samples for metabolomic analyses were performed following the previous study (19, 20) . Briefly, 50 mg of the rice samples were extracted with 1.2 mL MTBE:methanol. The upper lipid-containing phase (500 µL) was dried in a SpeedVac concentrator and then resuspended in a 250 µL acetonitrile:2-propanol (7:3, v/v) solution. Then, a volume of 2 µL per sample was injected into a Waters Acquity ultra-performance LC system with an RP C8 column coupled with Fourier transform MS in positive ionization mode. The workflow included peak detection, retention time alignment, and removal of chemical noise. Identified lipids were confirmed through manual verification of the chromatograms using Xcalibur (version 3.0, Thermo-Fisher, Bremen, Germany). Mass spectra were acquired using an Orbitrap high-resolution mass spectrometer: Fourier-transform mass spectrometer (FT-MS) coupled with a linear ion trap (LTQ) Orbitrap XL (ThermoFisher Scientific, https://www.thermofisher.com). Chromatograms and mass spectra were evaluated using Chroma TOF 4.5 (Leco) and TagFinder 4.2 software. Metabolite data correlation was analyzed using Expressionist Analyst 14.0.5 (Genedata, Basel, Switzerland) (https://www.genedata.com/products/expressionist). The metabolite reporting checklist is given in Supplementary Table 5.

Mathematical Modeling for GI Classification, and Metabolomic Multivariate Statistical Analysis. To classify each rice line independently to three GI classes (Ultra-low, Low and Intermediate, and High), the peak SNPs, significant targeted association SNPs, and grain quality parameters were used as input traits through the models following the previous works on classification modeling in rice (21-23). The phenome-genome models were created using MATLAB® (version R2023b) using either Random Forest or Artificial Neural Network, whichever showed higher accuracy. The hyperparameters for both models were optimized using a built-in Bayesian Optimization option in the software. The data set (n = 386) was split into training and testing sets with a 70:30 training-testing split ratio. The models were validated using 10-fold cross-validation. The selected phenome-genome parameters were combined to further improve the accuracy of the model. The processed metabolomic datasets were imported into a web-based software package, MetaboAnalyst v5.0, for principal component analysis (PCA) and orthogonal partial least squares discriminant analysis (oPLS-DA) to visualize the differences in metabolite between the two groups (24). Variable Importance in Projection (VIP) analysis in the oPLS-DA model was used to identify those metabolites having the highest discrimination potential (VIP score ≥ 1). Pathway enrichment analysis was performed using the *O. sativa* japonica as the KEGG pathway reference (24).

Purification of rice protein isolate and quantification of amino acids. The protein concentrate was isolated from the rice samples using the alkali extraction method as described by de Souza et al. (25), with slight modifications. In brief, 300 g of rice samples were combined with 1500 mL of 0.18% NaOH and stirred continuously for 30 minutes. The sample was then centrifuged to collect the protein extract, and the pH was adjusted to 4.8 by adding 0.1 M HCl. The resulting protein concentrate was obtained, and after centrifugation to remove the supernatant, it was neutralized and dried to yield the protein powder. The amino acids were quantified using the method reported by Sekhar and Reddy (26) with slight modifications. For amino acid quantification, seeds from all varieties were ground into a fine powder for analysis. Approximately 0.5-1.0 grams of each sample were weighed and transferred to a hydrolysis tube, followed by the addition of 3 ml of 6 N HCl. The tubes were sealed and placed in an oven at 110 °C for 24 hours for hydrolysis. After hydrolysis, the samples were diluted to 15 ml with borate buffer to adjust the pH to 6.5-7.5. The resulting solution was kept in a water bath at 37°C for 1 hour, and then filtered through a 0.22 μm filter into a 1.5 ml HPLC vial for subsequent analysis. The vial was then prepared for analysis (26).

Vector construction and rice transformation. The single guide RNA (sgRNA) which specifically targets the 15th exon of *OsSBEIIb* was designed by using the CRISPR RGEN tools (http://www.rgenome.net/about/). The 20bp gRNA with 4bp-overhangings was prepared by oligomer duplex (Table S1). And then, the short DNA duplex was ligated into the CRISPR-Cas9 binary vector (pSR339) digested with *AarI* restriction enzyme. The pSR339 vector was developed at the IRRI for a PCR-free single step CRISPR vector construction and it contains three cassettes on its T-DNA region: *pZmUbi1-SpCas9-tNOS* for expressing Cas9 protein, *pOsU3*-AarI-*LacZ*-AarI-gRNA scaffold for expressing sgRNA, and *p35S-HPT-tCaMV* as plant selection marker. After insertion of the oligomer duplex into pSR339, the sequence of the construct was confirmed by Sanger sequencing with Tnos-F primer. The final construct was transformed into *Agrobacterium tumefaciens* LBA4404 strain by using freeze-thaw method. For the *OsSBEIIb* gene editing, a popular high-yielding *indica* variety (NSICRc222, IRRI designation-IRRI 154) was used as a background material. Rice transformation was conducted by using immature embryo based on an efficient *indica* rice transformation method (27). Through rice transformation, more than 80 T_0 plants were produced. Information of all the oligomers used in this study is presented in Table S1.

Sequence analysis of the *OsSBEIIb* target site. To confirm the sequence of the CRISPR target site, PCR and Sanger sequencing were performed. Briefly, DNAs were prepared from T_0 plants by using a simple DNA extraction method (28). PCRs were conducted with two PCR primer sets: pUbi-F3/Cas9-97-R primer set to check T-DNA presence and SBEIIb-TS-F1/R1 primer set to amplify the *OsSBEIIb* target site. All the T_0 plants generated possessed the T-DNA. Thus, the target site amplicon from randomly selected 10 T_0 plants were sequenced by AB3730 DNA sequencer through the Macrogen, Korea (https://dna.macrogen.com/main.do#). Chromatograms of the sequencing results were manually analyzed.

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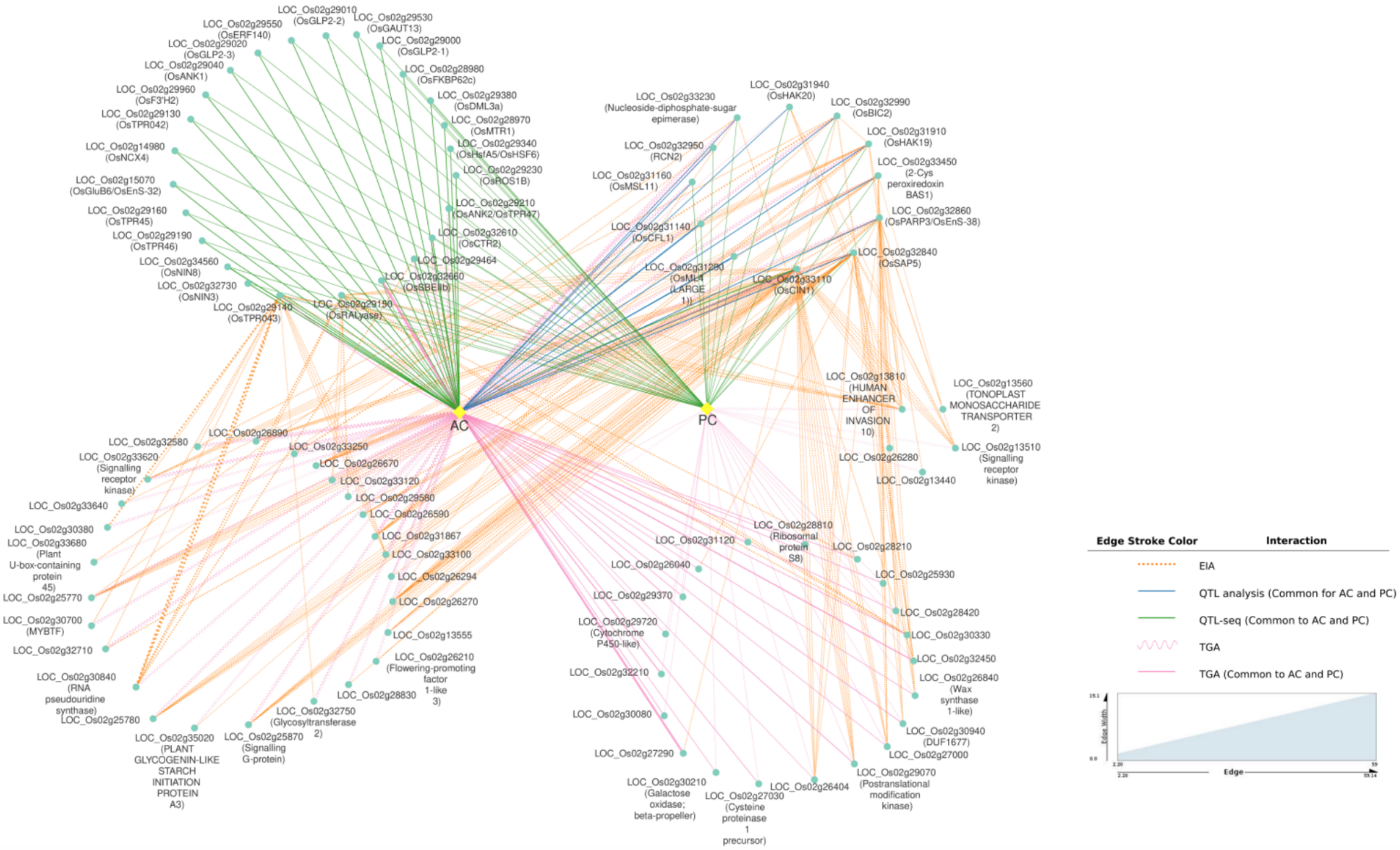
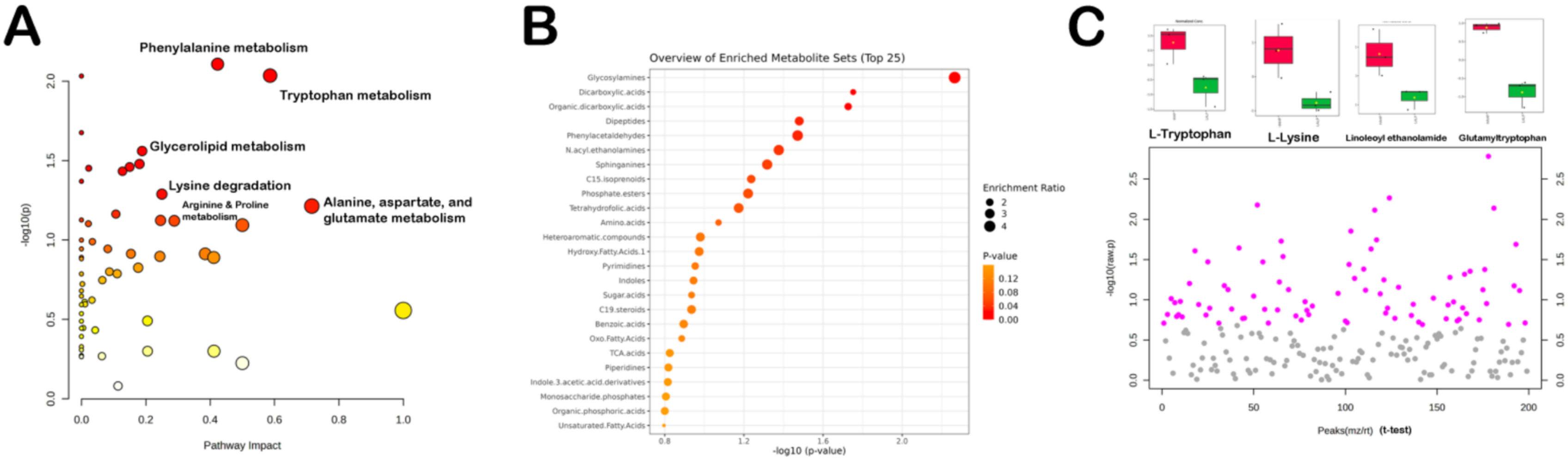
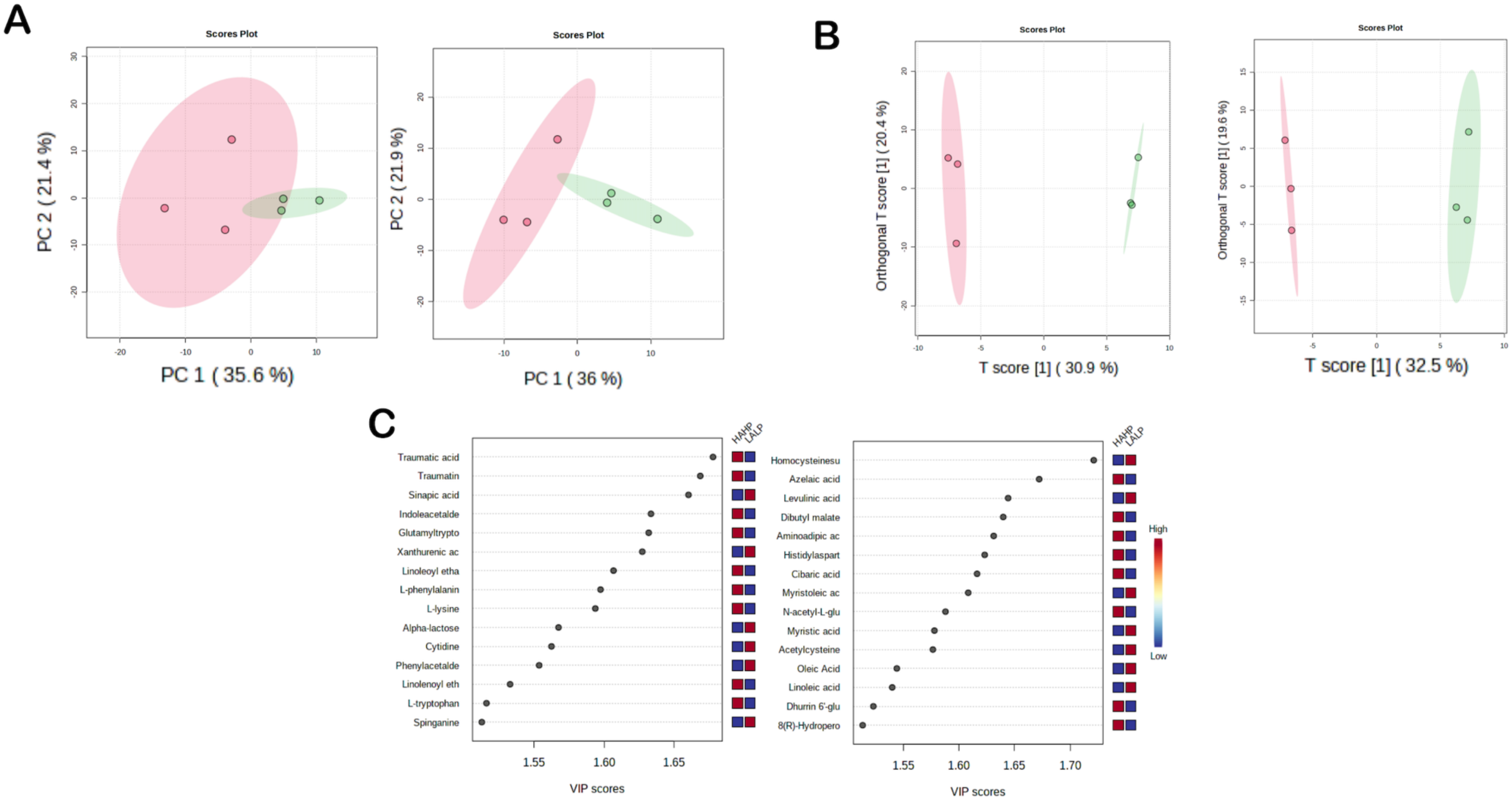


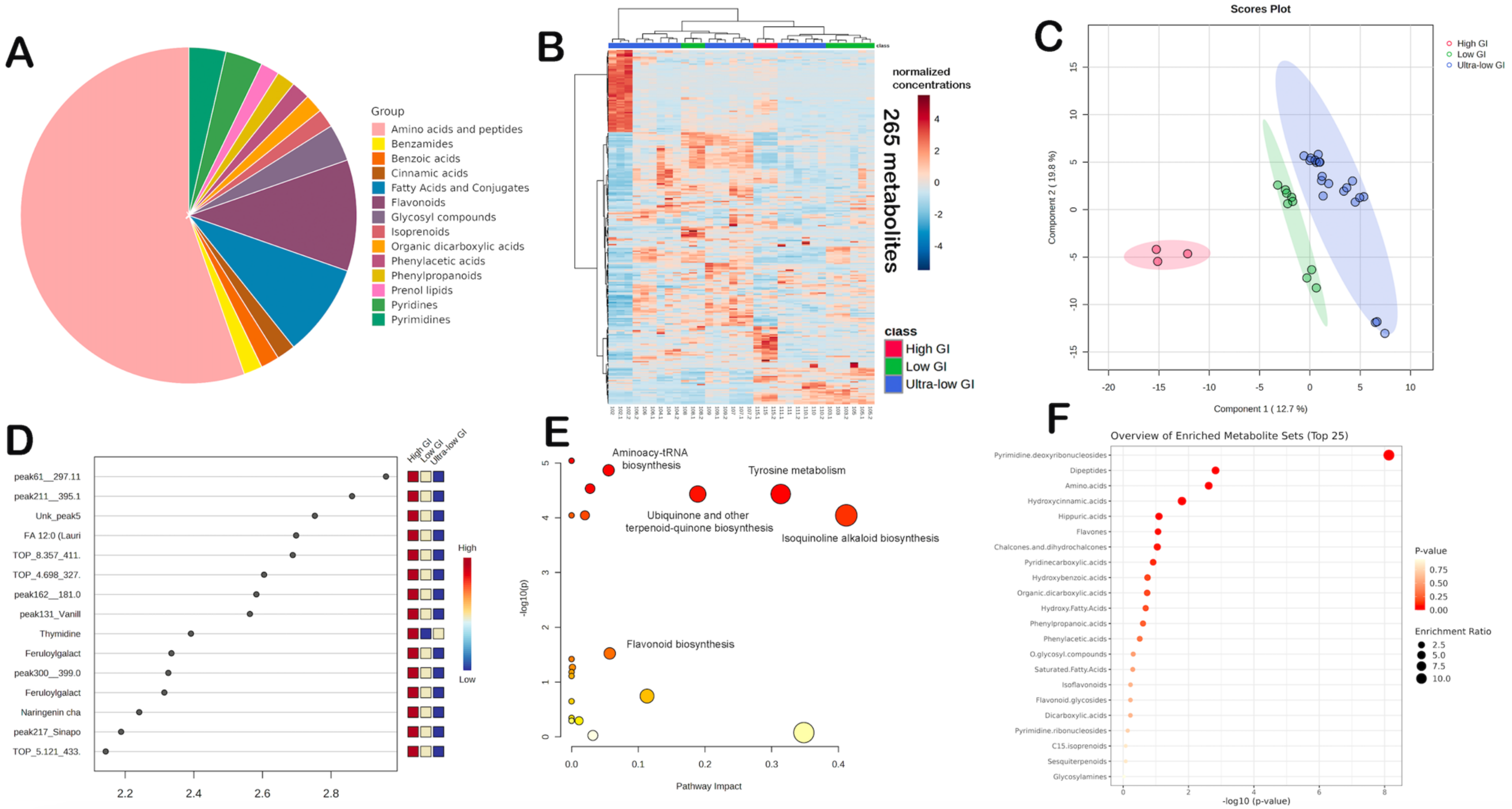
Supplementary Figure 1. Network analysis of genes resulted from QTL-seq and targeted association analyses



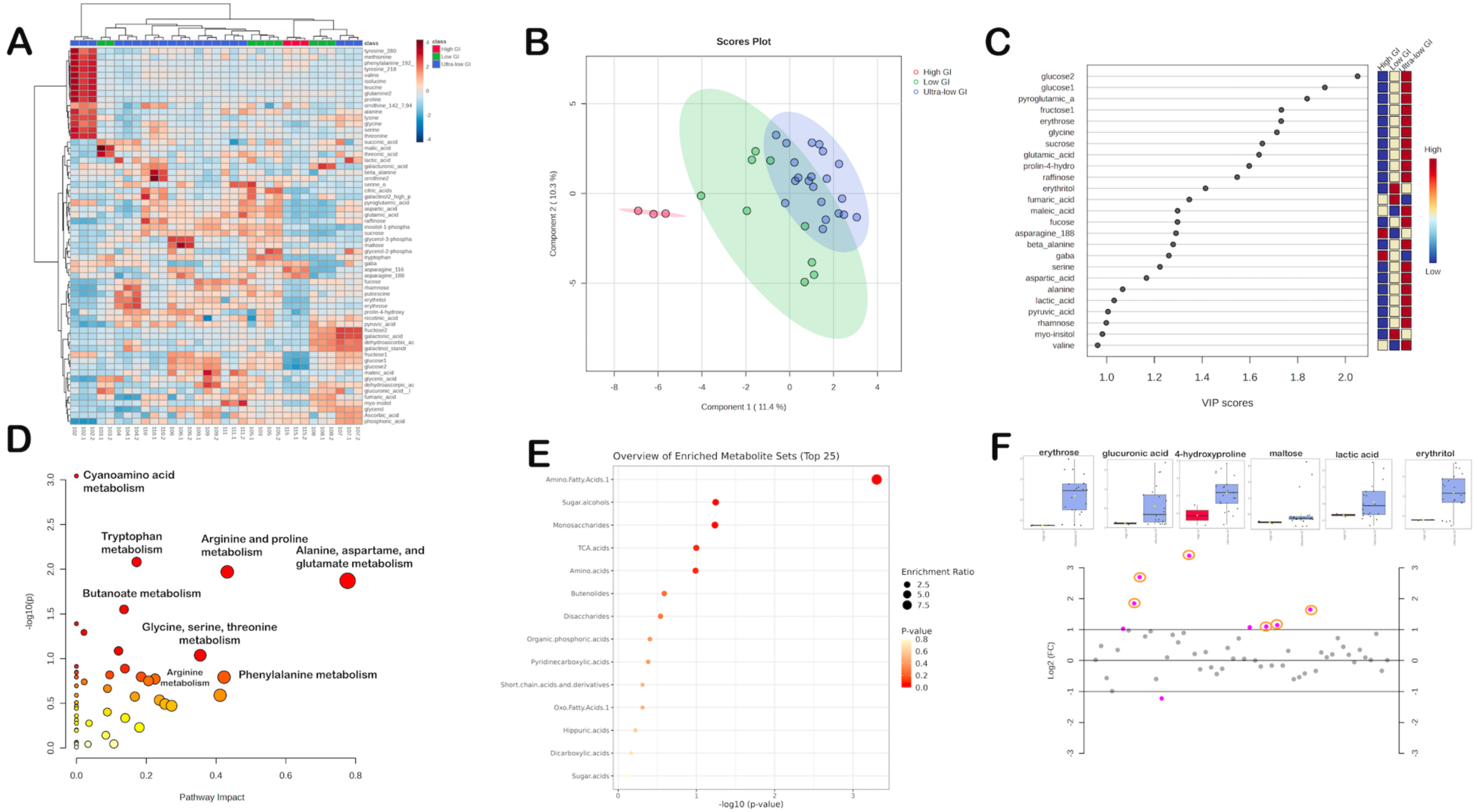
Supplementary Figure 2. Metabolomic analysis of high amylose high protein (HAHP) and low amylose low protein (LALP) in the positive ionization mode (A) Pathway impact showing amino acids and fatty acid metabolism were differentially accumulated between the two groups. (B) Enrichment analysis demonstrating the main class of compounds differentially accumulated between the two groups. (C) t-test analysis of metabolites demonstrating amino acids and dipeptides as accumulating in the HAHP lines.



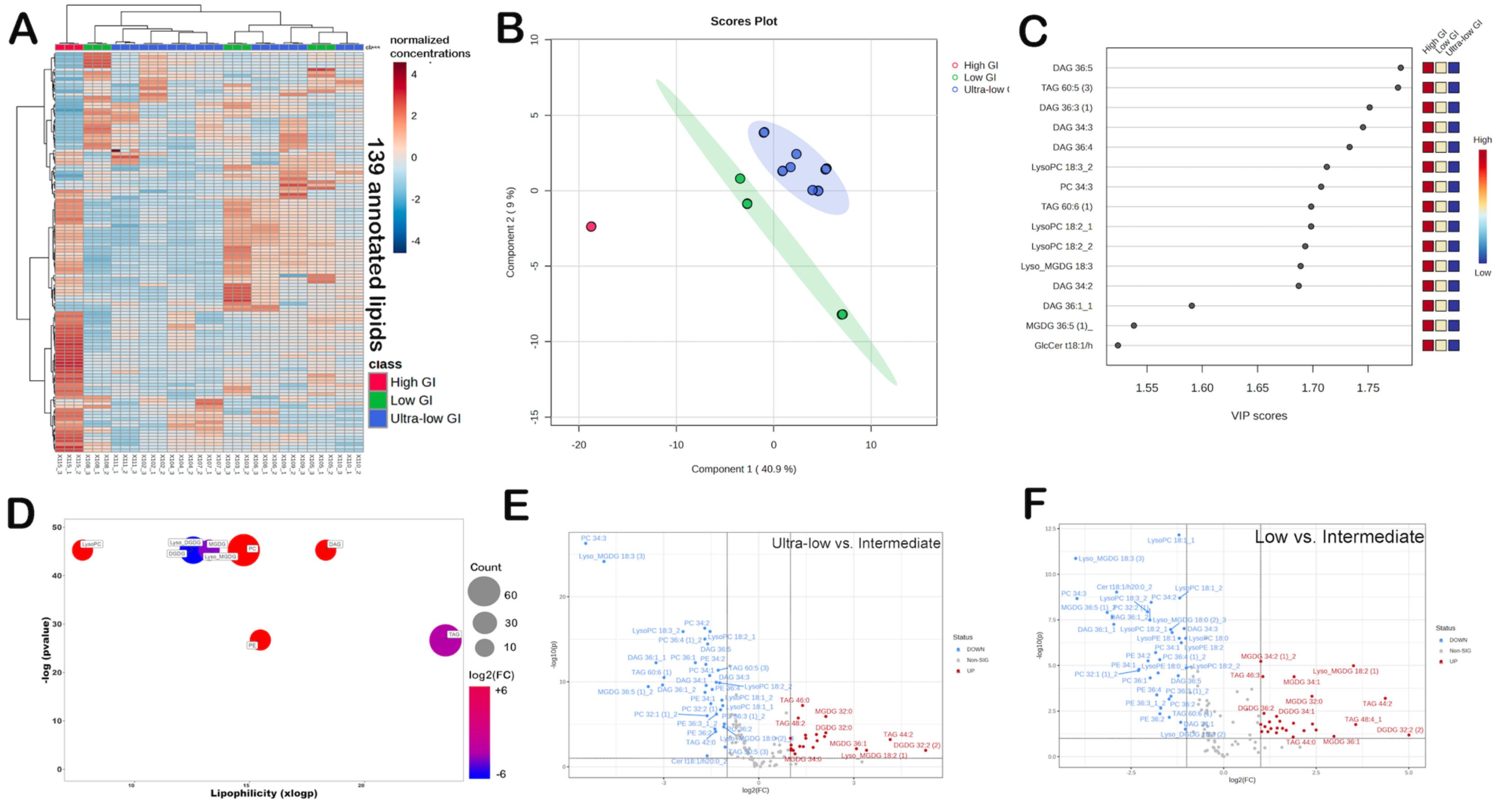
Supplementary Figure 3. Multivariate analysis of high amylose high protein (HAHP) and low amylose low protein (LALP) using the metabolomic data. (A) PCA distinguishing the HAHP and LALP in both negative and positive ionization modes. (B) PLS-DA model distinguishing the HAHP and LALP in both negative and positive ionization modes. (C) Top variable of important metabolites in both negative and positive ionization modes.



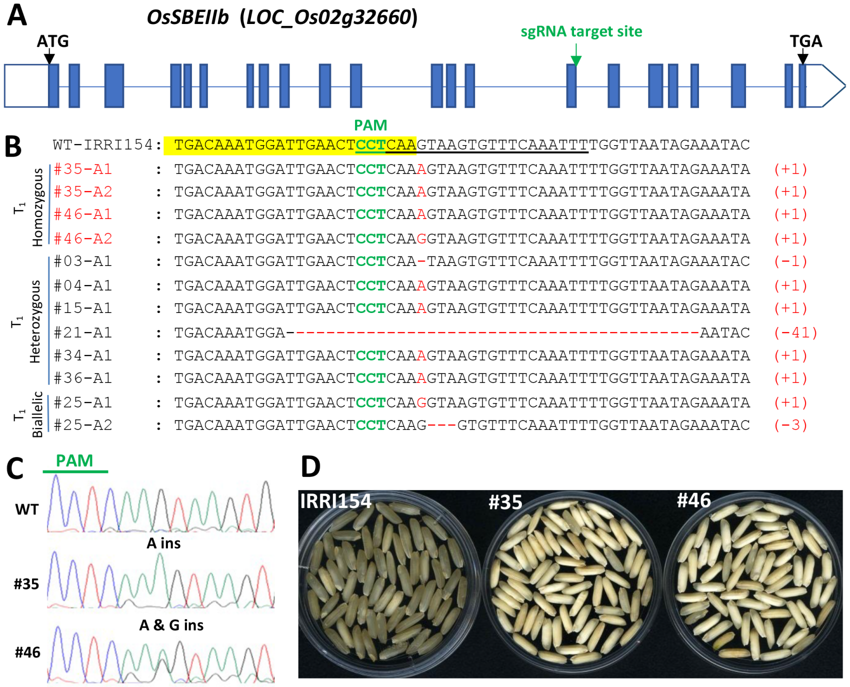
Supplementary Figure 4. Metabolomic analysis using methanolic extracts of high, low, and ultra-low GI rice lines. (A) Metabolite composition showing amino acid and dipeptides as predominant in the high, low, and ultra-low GI rice metabolome. (B) Heatmap distinguishing the high, low, and ultra-low GI rice lines using 265 metabolites. (C) PLS-DA model distinguishing the high, low, and ultra-low GI rice lines. (D) Top variable of important metabolites distinguishing the high, low, and ultra-low GI rice lines. (E) Pathway impact analysis showing amino acids and flavonoid biosynthesis as differentially accumulated among the groups. (F) Enrichment analysis showing the top classes of compounds differentially accumulating among high, low, and ultra-low GI rice lines.



Supplementary Figure 5. GC metabolite analysis of high, low, and ultra-low GI rice lines. (A) Heatmap distinguishing the high, low, and ultra-low GI rice lines using the primary metabolites through GC-TOF-MS. (B) PLS-DA model distinguishing the lipid profiles of high, low, and ultra-low GI rice lines using the primary metabolites. (C) Top variable of important primary metabolites distinguishing the high, low, and ultra-low GI rice lines. (D) Pathway impact analysis showing amino acids as differentially accumulated among the groups. (E) Enrichment analysis showing the amino acid and fatty acid pathways as differentially accumulated between ultra-low GI and high GI rice lines. (F) Specific metabolites that are highly accumulating in the low GI rice lines.



Supplementary Figure 6. Lipidomic analysis of high, low, and ultra-low GI rice lines. (A) Heatmap distinguishing the high, low, and ultralow GI rice lines using 139 annotated lipids. (B) PLS-DA model distinguishing the lipid profiles of high, low, and ultra-low GI rice lines. (C) Top variable of important lipids distinguishing the high, low, and ultra-low GI rice lines. (D) Lipid pathway analysis showing the main lipid classes differentially accumulated among the groups. (E) Volcano plot showing higher lipid accumulation in high GI compared to ultra-low rice lines. (F) Volcano plot showing higher lipid accumulation in high GI compared to low GI rice lines.



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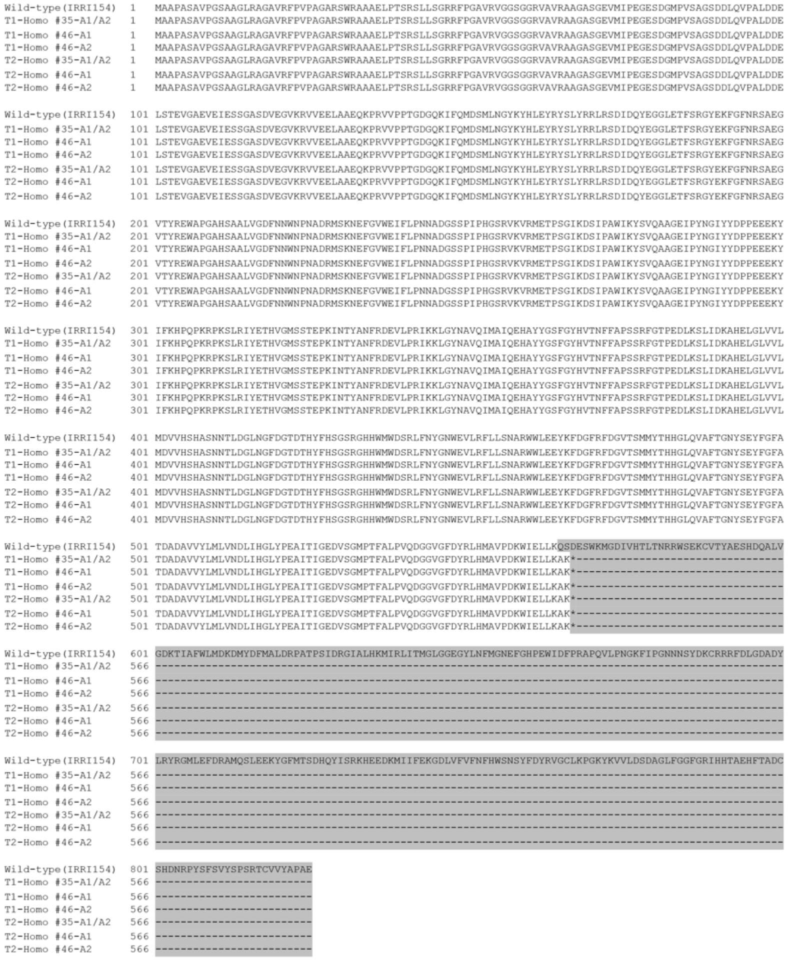
Event	Allele 1	Allele 2	Mutation	GI	RS%
Wild-type (IRRI154)	-	-	-	59±0.21[a]	0.18±0.00[a]
TC control (IRRI154)	-	-	-	58±0.75[a]	0.97±0.04[d]
T_1-Homo #35	A ins	A ins	Knock-out	55±0.50[b]	2.50±0.09[c]
T_1-Homo #46	A ins	G ins	Knock-out	54±0.35[c]	2.35±0.00[c]
T_2-Homo #35	A ins	A ins	Knock-out	53±0.05[c]	1.06±0.08[d]
T_2-Homo #46	A ins	G ins	Knock-out	50±0.30[d]	4.32±0.24[b]

Supplementary Figure 7: CRISPR/Cas9-mediated OsSBEIIb gene editing. (A) Schematic representation of the targeted gRNA site. (B) CRISPR/Cas9 induced mutations at donor-splicing site of 15th exon for SBEIIb gene in IRRI154 background. Yellow highlight:

exonic region, underlined: target gRNA with green Protospacer-adjacent motif (PAM) sequence, A1: Allele 1, A2: Allele 2, #: mutant line number. (C) Chromatograms for selected homozygous lines in comparison with wild-type (WT). (D) T0 plant derived T1 seed morphology. (E) In-vitro GI and Resistance Starch (RS) percent of T1 and T2 homozygous seeds derived from T0 and T1 plants respectively, TC control: Tissue-culture derived plant without Agrobacterium co-cultivation.

* a,b,c,d Duncan grouping code



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Wild-type(IRRI154)  1   MAAPASAVPGSAAGLRAGAVRFPVPAGARSWRAAAELPTSRSLLSGRRFPGAVRVGGSGGRVAVRAAGASGEVMIPEGESDGMPVSAGSDDLQVPALDDE
T1-Homo #35-A1/A2   1   MAAPASAVPGSAAGLRAGAVRFPVPAGARSWRAAAELPTSRSLLSGRRFPGAVRVGGSGGRVAVRAAGASGEVMIPEGESDGMPVSAGSDDLQVPALDDE
T1-Homo #46-A1      1   MAAPASAVPGSAAGLRAGAVRFPVPAGARSWRAAAELPTSRSLLSGRRFPGAVRVGGSGGRVAVRAAGASGEVMIPEGESDGMPVSAGSDDLQVPALDDE
T1-Homo #46-A2      1   MAAPASAVPGSAAGLRAGAVRFPVPAGARSWRAAAELPTSRSLLSGRRFPGAVRVGGSGGRVAVRAAGASGEVMIPEGESDGMPVSAGSDDLQVPALDDE
T2-Homo #35-A1/A2   1   MAAPASAVPGSAAGLRAGAVRFPVPAGARSWRAAAELPTSRSLLSGRRFPGAVRVGGSGGRVAVRAAGASGEVMIPEGESDGMPVSAGSDDLQVPALDDE
T2-Homo #46-A1      1   MAAPASAVPGSAAGLRAGAVRFPVPAGARSWRAAAELPTSRSLLSGRRFPGAVRVGGSGGRVAVRAAGASGEVMIPEGESDGMPVSAGSDDLQVPALDDE
T2-Homo #46-A2      1   MAAPASAVPGSAAGLRAGAVRFPVPAGARSWRAAAELPTSRSLLSGRRFPGAVRVGGSGGRVAVRAAGASGEVMIPEGESDGMPVSAGSDDLQVPALDDE

Wild-type(IRRI154)  101 LSTEVGAEVEIESSGASDVEGVKRVVEELAAEQKPRVVPPTGDGQKIFQMDSMLNGYKYHLEYRYSLYRRLRSDIDQYEGGLETFSRGYEKFGFNRSAEG
T1-Homo #35-A1/A2   101 LSTEVGAEVEIESSGASDVEGVKRVVEELAAEQKPRVVPPTGDGQKIFQMDSMLNGYKYHLEYRYSLYRRLRSDIDQYEGGLETFSRGYEKFGFNRSAEG
T1-Homo #46-A1      101 LSTEVGAEVEIESSGASDVEGVKRVVEELAAEQKPRVVPPTGDGQKIFQMDSMLNGYKYHLEYRYSLYRRLRSDIDQYEGGLETFSRGYEKFGFNRSAEG
T1-Homo #46-A2      101 LSTEVGAEVEIESSGASDVEGVKRVVEELAAEQKPRVVPPTGDGQKIFQMDSMLNGYKYHLEYRYSLYRRLRSDIDQYEGGLETFSRGYEKFGFNRSAEG
T2-Homo #35-A1/A2   101 LSTEVGAEVEIESSGASDVEGVKRVVEELAAEQKPRVVPPTGDGQKIFQMDSMLNGYKYHLEYRYSLYRRLRSDIDQYEGGLETFSRGYEKFGFNRSAEG
T2-Homo #46-A1      101 LSTEVGAEVEIESSGASDVEGVKRVVEELAAEQKPRVVPPTGDGQKIFQMDSMLNGYKYHLEYRYSLYRRLRSDIDQYEGGLETFSRGYEKFGFNRSAEG
T2-Homo #46-A2      101 LSTEVGAEVEIESSGASDVEGVKRVVEELAAEQKPRVVPPTGDGQKIFQMDSMLNGYKYHLEYRYSLYRRLRSDIDQYEGGLETFSRGYEKFGFNRSAEG

Wild-type(IRRI154)  201 VTYREWAPGAHSAALVGDFNNWNPNADRMSKNEFGVWEIFLPNNADGSSPIPHGSRVKVRMETPSGIKDSIPAWIKYSVQAAGEIPYNGIYYDPPEEEKY
T1-Homo #35-A1/A2   201 VTYREWAPGAHSAALVGDFNNWNPNADRMSKNEFGVWEIFLPNNADGSSPIPHGSRVKVRMETPSGIKDSIPAWIKYSVQAAGEIPYNGIYYDPPEEEKY
T1-Homo #46-A1      201 VTYREWAPGAHSAALVGDFNNWNPNADRMSKNEFGVWEIFLPNNADGSSPIPHGSRVKVRMETPSGIKDSIPAWIKYSVQAAGEIPYNGIYYDPPEEEKY
T1-Homo #46-A2      201 VTYREWAPGAHSAALVGDFNNWNPNADRMSKNEFGVWEIFLPNNADGSSPIPHGSRVKVRMETPSGIKDSIPAWIKYSVQAAGEIPYNGIYYDPPEEEKY
T2-Homo #35-A1/A2   201 VTYREWAPGAHSAALVGDFNNWNPNADRMSKNEFGVWEIFLPNNADGSSPIPHGSRVKVRMETPSGIKDSIPAWIKYSVQAAGEIPYNGIYYDPPEEEKY
T2-Homo #46-A1      201 VTYREWAPGAHSAALVGDFNNWNPNADRMSKNEFGVWEIFLPNNADGSSPIPHGSRVKVRMETPSGIKDSIPAWIKYSVQAAGEIPYNGIYYDPPEEEKY
T2-Homo #46-A2      201 VTYREWAPGAHSAALVGDFNNWNPNADRMSKNEFGVWEIFLPNNADGSSPIPHGSRVKVRMETPSGIKDSIPAWIKYSVQAAGEIPYNGIYYDPPEEEKY

Wild-type(IRRI154)  301 IFKHPQPKRPKSLRIYETHVGMSSTEPKINTYANFRDEVLPRIKKLGYNAVQIMAIQEHAYYGSFGYHVTNFFAPSSRFGTPEDLKSLIDKAHELGLVVL
T1-Homo #35-A1/A2   301 IFKHPQPKRPKSLRIYETHVGMSSTEPKINTYANFRDEVLPRIKKLGYNAVQIMAIQEHAYYGSFGYHVTNFFAPSSRFGTPEDLKSLIDKAHELGLVVL
T1-Homo #46-A1      301 IFKHPQPKRPKSLRIYETHVGMSSTEPKINTYANFRDEVLPRIKKLGYNAVQIMAIQEHAYYGSFGYHVTNFFAPSSRFGTPEDLKSLIDKAHELGLVVL
T1-Homo #46-A2      301 IFKHPQPKRPKSLRIYETHVGMSSTEPKINTYANFRDEVLPRIKKLGYNAVQIMAIQEHAYYGSFGYHVTNFFAPSSRFGTPEDLKSLIDKAHELGLVVL
T2-Homo #35-A1/A2   301 IFKHPQPKRPKSLRIYETHVGMSSTEPKINTYANFRDEVLPRIKKLGYNAVQIMAIQEHAYYGSFGYHVTNFFAPSSRFGTPEDLKSLIDKAHELGLVVL
T2-Homo #46-A1      301 IFKHPQPKRPKSLRIYETHVGMSSTEPKINTYANFRDEVLPRIKKLGYNAVQIMAIQEHAYYGSFGYHVTNFFAPSSRFGTPEDLKSLIDKAHELGLVVL
T2-Homo #46-A2      301 IFKHPQPKRPKSLRIYETHVGMSSTEPKINTYANFRDEVLPRIKKLGYNAVQIMAIQEHAYYGSFGYHVTNFFAPSSRFGTPEDLKSLIDKAHELGLVVL

Wild-type(IRRI154)  401 MDVVHSHASNNTLDGLNGFDGTDTHYFHSGSRGHHWMWDSRLFNYGNWEVLRFLLSNARWWLEEYKFDGFRFDGVTSMMYTHHGLQVAFTGNYSEYFGFA
T1-Homo #35-A1/A2   401 MDVVHSHASNNTLDGLNGFDGTDTHYFHSGSRGHHWMWDSRLFNYGNWEVLRFLLSNARWWLEEYKFDGFRFDGVTSMMYTHHGLQVAFTGNYSEYFGFA
T1-Homo #46-A1      401 MDVVHSHASNNTLDGLNGFDGTDTHYFHSGSRGHHWMWDSRLFNYGNWEVLRFLLSNARWWLEEYKFDGFRFDGVTSMMYTHHGLQVAFTGNYSEYFGFA
T1-Homo #46-A2      401 MDVVHSHASNNTLDGLNGFDGTDTHYFHSGSRGHHWMWDSRLFNYGNWEVLRFLLSNARWWLEEYKFDGFRFDGVTSMMYTHHGLQVAFTGNYSEYFGFA
T2-Homo #35-A1/A2   401 MDVVHSHASNNTLDGLNGFDGTDTHYFHSGSRGHHWMWDSRLFNYGNWEVLRFLLSNARWWLEEYKFDGFRFDGVTSMMYTHHGLQVAFTGNYSEYFGFA
T2-Homo #46-A1      401 MDVVHSHASNNTLDGLNGFDGTDTHYFHSGSRGHHWMWDSRLFNYGNWEVLRFLLSNARWWLEEYKFDGFRFDGVTSMMYTHHGLQVAFTGNYSEYFGFA
T2-Homo #46-A2      401 MDVVHSHASNNTLDGLNGFDGTDTHYFHSGSRGHHWMWDSRLFNYGNWEVLRFLLSNARWWLEEYKFDGFRFDGVTSMMYTHHGLQVAFTGNYSEYFGFA

Wild-type(IRRI154)  501 TDADAVVYLMLVNDLIHGLYPEAITIGEDVSGMPTFALPVQDGGVFDYRLHMAVPDKWIELLKQSDESWKMGDIVHTLTNRRWSEKCVTYAESHDQALV
T1-Homo #35-A1/A2   501 TDADAVVYLMLVNDLIHGLYPEAITIGEDVSGMPTFALPVQDGGVFDYRLHMAVPDKWIELLKAK*----------------------------------
T1-Homo #46-A1      501 TDADAVVYLMLVNDLIHGLYPEAITIGEDVSGMPTFALPVQDGGVFDYRLHMAVPDKWIELLKAK*----------------------------------
T1-Homo #46-A2      501 TDADAVVYLMLVNDLIHGLYPEAITIGEDVSGMPTFALPVQDGGVFDYRLHMAVPDKWIELLKAK*----------------------------------
T2-Homo #35-A1/A2   501 TDADAVVYLMLVNDLIHGLYPEAITIGEDVSGMPTFALPVQDGGVFDYRLHMAVPDKWIELLKAK*----------------------------------
T2-Homo #46-A1      501 TDADAVVYLMLVNDLIHGLYPEAITIGEDVSGMPTFALPVQDGGVFDYRLHMAVPDKWIELLKAK*----------------------------------
T2-Homo #46-A2      501 TDADAVVYLMLVNDLIHGLYPEAITIGEDVSGMPTFALPVQDGGVFDYRLHMAVPDKWIELLKAK*----------------------------------

Wild-type(IRRI154)  601 GDKTIAFWLMDKDMYDFMALDRPATPSIDRGIALHKMIRLITMGLGGEGYLNFMGNEFGHPEWIDFPRAPQVLPNGKFIPGNNNSYDKCRRRFDLGDADY
T1-Homo #35-A1/A2   566 ----------------------------------------------------------------------------------------------------
T1-Homo #46-A1      566 ----------------------------------------------------------------------------------------------------
T1-Homo #46-A2      566 ----------------------------------------------------------------------------------------------------
T2-Homo #35-A1/A2   566 ----------------------------------------------------------------------------------------------------
T2-Homo #46-A1      566 ----------------------------------------------------------------------------------------------------
T2-Homo #46-A2      566 ----------------------------------------------------------------------------------------------------

Wild-type(IRRI154)  701 LRYRGMLEFDRAMQSLEEKYGFMTSDHQYISRKHEEDKMIIFEKGDLVFVFNFHWSNSYFDYRVGCLKPGKYKVVLDSDAGLFGGFGRIHHTAEHFTADC
T1-Homo #35-A1/A2   566 ----------------------------------------------------------------------------------------------------
T1-Homo #46-A1      566 ----------------------------------------------------------------------------------------------------
T1-Homo #46-A2      566 ----------------------------------------------------------------------------------------------------
T2-Homo #35-A1/A2   566 ----------------------------------------------------------------------------------------------------
T2-Homo #46-A1      566 ----------------------------------------------------------------------------------------------------
T2-Homo #46-A2      566 ----------------------------------------------------------------------------------------------------

Wild-type(IRRI154)  801 SHDNRPYSFSVYSPSRTCVVYAPAE
T1-Homo #35-A1/A2   566 -------------------------
T1-Homo #46-A1      566 -------------------------
T1-Homo #46-A2      566 -------------------------
T2-Homo #35-A1/A2   566 -------------------------
T2-Homo #46-A1      566 -------------------------
T2-Homo #46-A2      566 -------------------------
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Supplementary Figure 8. Multiple sequence alignment of putative OsSBEIIb amino acids from the CRISPR/Cas9-induced KO lines of T1 and T2 seeds in comparison to wild-type of IRRI154 background.

Table S1.1. Genomic regions identified significantly associated with amylose content based on QTL-seq of F2-derived F3 RILs and QTL analysis of F5-derived F6 RILs complemented with targeted association analysis (TGA)

Method	**QTL**	**Chr**	**Physical Position (Mb)**	**G' value or LOD score**	**Overlapping gene**	**Gene Name / Putative functions**	**PVE of significant SNPs after TGA**
QTL-seq	*qseqAC1.1*	1	6.02-6.18	6.81- 6.82	LOC_Os01g11250	*OsKAT2* (*SHAKER POTASSIUM CHANNEL 2*)	
					LOC_Os01g11260	Phospho-N-acetylmuramoyl-pentapeptide- transferase	
					LOC_Os01g12440	*OsERF53/AP2 (Ethylene Response Factor 53)*	
					LOC_Os01g12580	*OsEnS-2; Late embryogenesis abundant protein 5*	
QTL-seq	*qseqAC2.1*	2	7.74-8.61	14.21-16.07	LOC_Os02g14730	*OsLG1* (*LARGE GRAIN 1*)	
					LOC_Os02g14770	*PEPC-1*; glycolysis cytosolic branch (PEPC)	
					LOC_Os02g14840	*OsKAT3* (SHAKER POTASSIUM CHANNEL 3);	
					LOC_Os02g14900	1,3-beta-glucan synthase component domain containing protein	
					LOC_Os02g14980	*OsEFCAX2; Na+/Ca2+ Exchanger 4*	
					LOC_Os02g15070	*Glutelin B6; OsEnS-32*	
					LOC_Os02g15080	*RING-type E3 ubiquitin ligase 55*	
					LOC_Os02g15350	*OsEnS-34/OsDOF3*; prolamin box binding factor	
QTL-seq, TGA	*qseqAC2.2*	2	17.15-19.95	15.00-20.57	**LOC_Os02g28970**	*Microspore and tapetum regulator 1; secretory fasciclin glycoprotein*	
					LOC_Os02g29000	*Germin-like protein 2-1*	
					LOC_Os02g29010	*Germin-like protein 2-2*	
					LOC_Os02g29020	*Germin-like protein 2-3*	
					LOC_Os02g29040	*Ankyrin 1*	

					LOC_Os02g29070	*Probable cyclin-dependent/tyrosine/ lipopolysaccharide kinase-domain containing protein)*	18.02
					LOC_Os02g29110	*TPR2* (*TPR*: *Tetratricopeptide repeat-containing protein*; *ankyrin repeat family protein*)	
					LOC_Os02g29130	*TPR42* (*ankyrin repeat family protein*)	
					LOC_Os02g29140	*TPR43* (*ankyrin repeat family protein*)	16.48
					LOC_Os02g29150	*OsRALyase* (*Ribosomal RNA apurinic site specific lyase*)	8.75
					LOC_Os02g29160	*TPR45* (*ankyrin repeat family protein*)	
					LOC_Os02g29190	*TPR46* (*ankyrin repeat family protein*)	
					LOC_Os02g29210	*Ankyrin 2/TPR47*	14.44
					LOC_Os02g29340	*Heat stress transcription factor A5*	
					LOC_Os02g29370	*Mariner sub-class transposon*	15.3
					LOC_Os02g29530	*Galacturonosyltransferase 13*	
					LOC_Os02g29550	*P2/EREBP13* (*ethylene response factor 140*)	
					LOC_Os02g29960	*Flavonoid 3'-hydroxylase 2*	
					LOC_Os02g30210	*Galactose oxidase beta propeller*	12.7
					LOC_Os02g30940	*Uncharacterized DUF1677*	17.1
					LOC_Os02g30840	*Amino acid activation pseudouridylate synthase*	11.92
					LOC_Os02g32610	*CONSTITUTIVE TRIPLE-RESPONSE 2*; heading date and yield	19.44
					LOC_Os02g32660	*OsSBEIIb*: Major CHO metabolism-starch synthesis/branching	59.14
					LOC_Os02g32730	*OsNIN3* (neutral/alkaline invertase 3); Major CHO metabolism-degradation, sucrose invertases	
					LOC_Os02g33110	*CIN1*: Cell-wall invertase 1; Major	20.82

						CHO metabolism-starch synthesis/branching	
QTL analysis	*qAC-2.1*	2	18.62-19.95	10.92-19.70	**LOC_Os02g31140**	*OsCFL1* (*Curly Flag Leaf 1*)	
					LOC_Os02g31160	*OsMSL11 (trihelix transcription factor)*	18.63
					LOC_Os02g31210	*Putative glycosyltransferase*	16.48
					LOC_Os02g31220	*Similar to Topoisomerase II-associated protein PAT1 homolog 1*	16.09
					LOC_Os02g31290	*LARGE1*	
					LOC_Os02g31910	*High-affinity Potassium(K+) Transporter 19*	21.77
					LOC_Os02g31940	*High-affinity Potassium(K+) Transporter 20*	2.71
					LOC_Os02g32750	*Glycosyltransferase 2*	16.34
					LOC_Os02g32840	*OsSAP5* (*stress-associated protein 5*)	20.56
					LOC_Os02g32860	*OsEnS-38* (*poly(ADP-ribose) polymerase 3*)	18.42
					LOC_Os02g32950	*RICE CENTRORADIALIS 2*	18.24
					LOC_Os02g33090	*Fantastic Four meristem regulator-like protein*	19.04
					LOC_Os02g33110	*CIN1*: Cell-wall invertase 1; Major CHO metabolism-starch synthesis/branching	20.82
					LOC_Os02g33120	*Probable protein phosphatase 2C*	18.84
					LOC_Os02g33140	*Similar to 40S ribosomal protein S14*	12.34
					LOC_Os02g33230	*Nucleoside-diphosphate-sugar epimerase*	23.25
					LOC_Os02g33360	*Transposon Ty3-G Gag-Pol polyprotein*	15.5
					LOC_Os02g33450	*2-Cys peroxiredoxin BAS1*	
					LOC_Os02g33550	*Late embryogenesis abundant protein*	
QTL-seq	*qseqAC2.3*	2	20.72-	19.81-	**LOC_Os02g34560**	*OsNIN8* (neutral/alkaline invertase	

			21.90	20.42		8); Major CHO metabolism-degradation, sucrose invertases	
					LOC_Os02g34630	*MYB-related transcription factor*	11.8
					LOC_Os02g36140	*OsKS7* (terpene synthase; ent-kaurene synthase7)	
					LOC_Os02g36210	*OsCPS2* (ent-kaurene synthase; hormone metabolism- gibberellin synthesis)	11.64
					LOC_Os02g36220	*OsKS5* (ent-kaurene synthase; hormone metabolism-gibberellin synthesis/degradation)	13.22
					LOC_Os02g36264	*OsKS6* (ent-kaurene synthase; hormone metabolism-gibberellin synthesis/degradation)	
					LOC_Os02g51070	*Starch synthase-IIb*	
					LOC_Os02g51320	*Positive Regulator of Grain Length 2*	
QTL-seq	*qseqAC6.1*	6	28.83-29.67	7.31-7.64	LOC_Os06g47620	*AH7* (AMIDOHYDROLASE 7; Hormone metabolism-auxin synthesis/degradation)	
					LOC_Os06g48040	*OsMAR1* (microtubule-associated RING finger protein 1; protein degradation-ubiquitin E3-RING)	
					LOC_Os06g48640	RPN1B (19S REGULATORY PARTICLE NON-ATPASE SUBUNIT 1B; regulation of protein catabolic process)	
					LOC_Os06g48950	ARF7A (AUXIN RESPONSE FACTOR 7A; transcription regulation-ARF)	

Table S1.2. Genomic regions/QTLs significantly associated with grain protein content based on QTL-seq of F2-derived F3 RILs and QTL analysis of F5-derived F6 RILs complemented with targeted association analysis (TGA).

Method	QTL	Chr	Physical Position (Mb)	G' value or LOD score	Overlapping gene	Gene Name / Putative functions	PVE of significant SNPs filtered after TGA
QTL-seq, TGA	*qseqPC2.1*	2	7.06-8.44	9.00-9.03	LOC_Os02g13560	Tonoplast monosaccharide transporter 2	4.08
					LOC_Os02g13840	Citrate synthase	
					LOC_Os02g13810	*Human enhancer of invasion 10;* pollination, fertility, reciprocal meiotic recombination	3.41
					LOC_Os02g14980	*OsEFCAX2; Na+/Ca2+ Exchanger 4*	
					LOC_Os02g15070	*Glutelin B6; OsEnS-32*	
					LOC_Os02g15090	*Glutelin D*	
					LOC_Os02g15150	*Glutelin 7*	
QTL-analysis, TGA	*qPC2.1*	2	10.13-10.33	>3.009	LOC_Os02g17620	Isochorismatase	3.28
QTL-seq	*qseqPC2.2*	2	15.01-20.20	7.60-9.06	LOC_Os02g25860	*Glutelin A*	
					LOC_Os02g25930	*Retrotransposon*	3.83
					LOC_Os02g26160	*ABNORMAL POLLEN 1*	
					LOC_Os02g26290	*Fasciclin-like arabinogalactan protein 22*	
					LOC_Os02g26320	*Fasciclin-like arabinogalactan protein 20*	
					LOC_Os02g26650	*OsDHCR7 (7-dehydrocholesterol reductase)*	
					LOC_Os02g26800	*Aminotransferase-like, plant mobile domain domain containing protein*	
					LOC_Os02g26840	*Membrane-bound O-acyltransferase; similar to Wax synthase*	3.04

						isoform 1)	
					LOC_Os02g27000	*Microchidia protein 4*	5.51
					LOC_Os02g27030	*Cysteine proteinase 1 precursor*	2.64
					LOC_Os02g28420	*OsFBK7; Galactose oxidase, beta-propeller*	4.24
					LOC_Os02g28580	*OsEnS-37*	
					LOC_Os02g28970	*Microspore and tapetum regulator 1*	
					LOC_Os02g29000	*Germin-like protein 2-1*	
					LOC_Os02g29010	*Germin-like protein 2-2*	
					LOC_Os02g29020	*Germin-like protein 2-3*	
					LOC_Os02g29040	*Ankyrin 1*	
					LOC_Os02g29070	*Probable cyclin-dependent/tyrosine/ lipopolysaccharide kinase-domain containing protein)*	5.03
					LOC_Os02g29110	*TPR2* (*TPR*: *Tetratricopeptide repeat-containing protein*; *ankyrin repeat family protein*)	
					LOC_Os02g29130	*TPR42* (*ankyrin repeat family protein*)	
					LOC_Os02g29140	*TPR43* (*ankyrin repeat family protein*)	3.62
					LOC_Os02g29150	*OsRALyase* (*Ribosomal RNA apurinic site specific lyase*)	
					LOC_Os02g29160	*TPR45* (*ankyrin repeat family protein*)	
					LOC_Os02g29190	*TPR46* (*ankyrin repeat family protein*)	
					LOC_Os02g29210	*Ankyrin 2/TPR47*	
					LOC_Os02g29340	*Heat stress transcription factor A5*	
					LOC_Os02g29370	*Mariner sub-class transposon*	5.61
					LOC_Os02g29530	*Galacturonosyltransferase 13*	
					LOC_Os02g29550	*AP2/EREBP13* (*ethylene response factor 140*)	

					LOC_Os02g29960	*Flavonoid 3'-hydroxylase 2*	
					LOC_Os02g30714	*Short chain dehydrogenase/reductase (SDR)*	
					LOC_Os02g30840	*Amino acid activation pseudouridylate synthase*	
					LOC_Os02g30940	*Uncharacterized DUF1677*	3.96
					LOC_Os02g30630	*Acetolactate synthase 1*	
					LOC_Os02g30210	*Galactose oxidase beta propeller*	4.63
					LOC_Os02g31140	*OsCFL1* (*Curly Flag Leaf 1*)	
					LOC_Os02g31160	*OsMSL11 (trihelix transcription factor)*	
					LOC_Os02g31210	*Putative glycosyltransferase*	
					LOC_Os02g31220	*Similar to Topoisomerase II-associated protein PAT1 homolog 1*	
					LOC_Os02g31290	*LARGE1*	
					LOC_Os02g31910	*High-affinity Potassium(K+) Transporter 19*	
					LOC_Os02g31940	*High-affinity Potassium(K+) Transporter 20*	1.92
					LOC_Os02g32060	*Nudix Hydrolase 12*	
					LOC_Os02g32610	*CONSTITUTIVE TRIPLE-RESPONSE 2; heading date and yield*	
					LOC_Os02g32750	*Glycosyltransferase 2*	
					LOC_Os02g32430	*TRANSPARENT TESTA GLABRA 1B*	
					LOC_Os02g32520	*OsERD1*	
					LOC_Os02g32660	*Starch branching enzyme 3*	7.94
					LOC_Os02g32730	*OsNIN3 (neutral/alkaline invertase 3);* major CHO metabolism	
					LOC_Os02g32840	*OsSAP5 (stress-associated protein 5)*	
					LOC_Os02g32860	*OsEnS-38 (poly(ADP-ribose)*	

						polymerase 3)	
					LOC_Os02g32950	*RICE CENTRORADIALIS 2*	
					LOC_Os02g32980	*Germin-like protein 2-4*	
					LOC_Os02g33090	*Fantastic Four meristem regulator-like protein*	
					LOC_Os02g33110	*CIN1*: Cell-wall invertase 1; Major CHO metabolism-starch synthesis/branching	
					LOC_Os02g33120	*Probable protein phosphatase 2C*	
					LOC_Os02g33140	*Similar to 40S ribosomal protein S14*	
					LOC_Os02g33230	*Nucleoside-diphosphate-sugar epimerase*	
					LOC_Os02g33360	*Transposon Ty3-G Gag-Pol polyprotein*	
					LOC_Os02g33450	*2-Cys peroxiredoxin BAS1*	
					LOC_Os02g33550	*Late embryogenesis abundant protein 14*	
					LOC_Os02g33580	*Digalactosyldiacylglycerol synthase 1*	
					LOC_Os02g33600	*Valine-glutamine protein 8*	
					LOC_Os02g33610	*Green-revertible yellow79*	
						Myb/SANT-LIKE 12; Putative metallo-beta-lactamase-trihelix chimera	
QTL-seq	*qseqPC-2.3*	2	20.71-21.37	10.32-10.48	**LOC_Os02g34560**	*OsNIN8 (major CHO metabolism degradation sucrose invertases neutral)*	
					LOC_Os02g34630	*MYB-related transcription factor*	
					LOC_Os02g34990	Amino acid-binding ACT domain containing protein	
					LOC_Os02g35020	*OsPGSIP-A3 (Plant glycogenin-like starch initiation protein A3)*	
QTL-seq	*qseqPC3.1*	3	0.41-0.95	10.34-11.32	LOC_Os03g01880	*LOG LIKE phosphoribohydrolase 3*	
					LOC_Os03g01890	*OsHOX10/LATERAL FLORET 1*	

QTL-seq	*qseqPC4.1*	4	31.69	5.39	LOC_Os04g53210	*OsGLO3 (Glycolate oxidase 3)*	
QTL-seq	*qseqPC5.1*	5	0.86-1.00	5.95-5.99	LOC_Os05g02500	*GSN1 (Grain size and number 1)*	
					LOC_Os05g02770	*Glycine-rich cell-wall structural protein 1; Regulation of grain size and accumulation of seed storage protein and lipids*	
QTL-seq	*qseqPC8.1*	8	3.50-4.06	8.88-9.18	LOC_Os08g06380	*Cellulose synthase-like family F6; Nucleotide-diphospho-sugar transferase*	
					LOC_Os08g06550	*Acyl-CoA-binding protein*	
					LOC_Os08g06630	*Yellow-Green Leaf 13*	
					LOC_Os08g07010	*ATP-binding cassette transporter (control of long-distance transport of cytokinins from root to shoot; promotion of grain yield)*	
QTL-seq	*qseqPC8.2*	8	20.65-21.31	6.50-7.08	LOC_Os08g33200	*1-phosphatidylinositol-4-phosphate 5-kinase* (cellular protein metabolic process)	
					LOC_Os08g33488	*OsMADS23*	
					LOC_Os08g33540	*PLASTID CASEINOLYTIC PROTEASE S1*	
					LOC_Os08g33620	*Arginine decarboxylase 3*	
					LOC_Os08g33660	*OsMYB106*	
					LOC_Os08g33720	*lactate/malate dehydrogenase*	
					LOC_Os08g33810	*Lipoate-protein ligase A*	
					LOC_Os08g33820	*Delayed yellowing1*	
					LOC_Os08g33830	*Polypyrimidine tract-binding protein*	
					LOC_Os08g33850	*Nucleoside-triphosphatase*	
					LOC_Os08g33940	*R2R3-MYB Transcription Factor 78*	
Note: Loci in bold font were also associated with							

AC.							

Table S2.1 Significant loci associated with apparent amylose content of F2-derived F3 RILs with details of G prime (G'), delta SNP index and P values (only top 20 SNPs are shown)

QTL	CHR	SNP Position	REF	ALT	Gprime	deltaSNP	pvalue	qvalue	Region	Effect	Amino acid change	Overlapping gene
qseqAC1.1	1	6083091	A	C	6.82322191	0.21428571	3.7641E-05	0.0004414	upstream_gene_variant	MODIFIER	-	LOC_Os01g11340
	1	6083105	A	G	6.82322089	0.27759197	3.7641E-05	0.0004414	upstream_gene_variant	MODIFIER	-	LOC_Os01g11340
	1	6081178	G	A	6.82321285	0.3122807	3.7642E-05	0.0004414	upstream_gene_variant	MODIFIER	-	LOC_Os01g11340
	1	6081160	A	T	6.82320812	0.32246377	3.7642E-05	0.0004414	upstream_gene_variant	MODIFIER	-	LOC_Os01g11340
	1	6081158	A	T	6.82320759	0.35869565	3.7642E-05	0.0004414	upstream_gene_variant	MODIFIER	-	LOC_Os01g11340
	1	6081150	G	A	6.82320549	0.32712215	3.7642E-05	0.0004414	upstream_gene_variant	MODIFIER	-	LOC_Os01g11340
	1	6081129	A	T	6.82319997	0.4637037	3.7642E-05	0.0004414	upstream_gene_variant	MODIFIER	-	LOC_Os01g11340
	1	6081119	T	C	6.82319734	0.41666667	3.7643E-05	0.0004414	upstream_gene_variant	MODIFIER	-	LOC_Os01g11340
	1	6081100	C	G	6.82319235	0.43333333	3.7643E-05	0.0004414	upstream_gene_variant	MODIFIER	-	LOC_Os01g11340
	1	6081048	G	A	6.82317868	0.53571429	3.7644E-05	0.0004414	upstream_gene_variant	MODIFIER	-	LOC_Os01g11340
	1	6081034	G	A	6.823175	0.56043956	3.7644E-05	0.0004414	upstream_gene_variant	MODIFIER	-	LOC_Os01g11340
	1	6081030	A	G	6.82317395	0.5455665	3.7644E-05	0.0004414	upstream_gene_variant	MODIFIER	-	LOC_Os01g11340
	1	6080972	A	C	6.82315871	0.50854701	3.7645E-05	0.0004414	upstream_gene_variant	MODIFIER	-	LOC_Os01g11340
	1	6080908	G	A	6.82314189	0.56231884	3.7646E-05	0.0004414	upstream_gene_variant	MODIFIER	-	LOC_Os01g11340
	1	6080728	G	A	6.82309458	0.49333333	3.7649E-05	0.0004414	upstream_gene_variant	MODIFIER	-	LOC_Os01g11340
	1	6080717	T	C	6.82309169	0.51971326	3.7649E-05	0.0004414	upstream_gene_variant	MODIFIER	-	LOC_Os01g11340
	1	6080661	C	T	6.82307697	0.59425287	3.765E-05	0.0004414	upstream_gene_variant	MODIFIER	-	LOC_Os01g11340
	1	6080605	T	G	6.82306226	0.51015532	3.7651E-05	0.0004414	upstream_gene_variant	MODIFIER	-	LOC_Os01g11340
	1	6080598	G	A	6.82306042	0.48645161	3.7651E-05	0.0004414	upstream_gene_variant	MODIFIER	-	LOC_Os01g11340
	1	5712460	C	T	6.72631023	0.265	4.4081E-05	0.00048907	upstream_gene_variant	MODIFIER	-	LOC_Os01g10680

Table S2.2 Significant loci associated with protein content of F2-derived F3 RILs with details of G prime (G'), delta SNP index and P-values. (Only top 20 are shown)

QTL	CHR	SNP Position	REF	ALT	Gprime	deltaSNP	pvalue	qvalue	Region	Effect	Amino acid change	Overlapping gene
qseqPC2.1	2	7059407	C	A	9.0108	-0.4639	1.1115E-06	5.1569E-05	synonymous_variant	LOW	-	LOC_Os02g13250
	2	7059796	G	A	9.0110	-0.3111	1.1113E-06	5.1569E-05	upstream_gene_variant	MODIFIER	-	LOC_Os02g13260
	2	7059806	A	G	9.0110	-0.2995	1.1113E-06	5.1569E-05	upstream_gene_variant	MODIFIER	-	LOC_Os02g13260
	2	7059809	A	G	9.0110	-0.3016	1.1113E-06	5.1569E-05	upstream_gene_variant	MODIFIER	-	LOC_Os02g13260
	2	7059818	G	A	9.0110	-0.3137	1.1113E-06	5.1569E-05	upstream_gene_variant	MODIFIER	-	LOC_Os02g13260
	2	7060358	A	G	9.0112	-0.6177	1.111E-06	5.1569E-05	synonymous_variant	LOW	-	LOC_Os02g13250
	2	7060420	A	G	9.0112	-0.5371	1.1109E-06	5.1569E-05	upstream_gene_variant	MODIFIER	-	LOC_Os02g13260
	2	7060421	G	A	9.0112	-0.4519	1.1109E-06	5.1569E-05	upstream_gene_variant	MODIFIER	-	LOC_Os02g13260
	2	7060428	G	A	9.0112	-0.4881	1.1109E-06	5.1569E-05	upstream_gene_variant	MODIFIER	-	LOC_Os02g13260
	2	7060486	G	T	9.0112	-0.3306	1.1109E-06	5.1569E-05	upstream_gene_variant	MODIFIER	-	LOC_Os02g13260
	2	7060559	C	T	9.0112	-0.4058	1.1109E-06	5.1569E-05	upstream_gene_variant	MODIFIER	-	LOC_Os02g13260
	2	7060560	G	A	9.0112	-0.4375	1.1109E-06	5.1569E-05	upstream_gene_variant	MODIFIER	-	LOC_Os02g13260
	2	7060803	T	C	9.0113	-0.4074	1.1107E-06	5.1569E-05	upstream_gene_variant	MODIFIER	-	LOC_Os02g13260
	2	7060814	A	G	9.0113	-0.5135	1.1107E-06	5.1569E-05	upstream_gene_variant	MODIFIER	-	LOC_Os02g13260
	2	7060863	C	T	9.0113	-0.3551	1.1107E-06	5.1569E-05	upstream_gene_variant	MODIFIER	-	LOC_Os02g13260
	2	7061123	C	T	9.0114	-0.2946	1.1106E-06	5.1569E-05	upstream_gene_variant	MODIFIER	-	LOC_Os02g13260
	2	7061126	A	G	9.0114	-0.3312	1.1106E-06	5.1569E-05	upstream_gene_variant	MODIFIER	-	LOC_Os02g13260
	2	7061366	T	A	9.0115	-0.5369	1.1104E-06	5.1569E-05	upstream_gene_variant	MODIFIER	-	LOC_Os02g13260
	2	7061625	T	C	9.0116	-0.5337	1.1103E-06	5.1569E-05	upstream_gene_variant	MODIFIER	-	LOC_Os02g13260

Table S3. Significant QTLs identified using composite interval mapping of F5-derived F6 recombinant inbred lines.

QTL name	Chr	Region (Mb)	Associated Trait	SNP ID	LOD score	Position	locus	bp	ref	alt	type_of_aa_change
qPC2.1	2	10.13-10.33	PC	snp_02_10141997	3.0093	intronic	LOC_Os02g17620	10141997	G	A	NA
				snp_02_10142042	3.0098	intronic		10142042	T	A	NA
				snp_02_10142047	3.0099	intronic		10142047	A	C	NA
				snp_02_10142051	3.0099	intronic		10142051	C	T	NA
				snp_02_10328456	3.5173	intergenic	LOC_Os02g17840(dist=8445), LOC_Os02g17850(dist=2237)	10328456	A	C	NA
				snp_02_10328456	3.8913	intergenic	LOC_Os02g17840(dist=8445), LOC_Os02g17850(dist=2237)	10328456	A	C	NA
qAC2.1	2	18.62-19.96	AC	snp_02_18615462	10.9165	intergenic	LOC_Os02g31120, LOC_Os02g31140	NA	NA	NA	NA
				snp_02_18615470	11.6130	intergenic		NA	NA	NA	NA
				snp_02_18615488	11.6144	intergenic		NA	NA	NA	NA
				snp_02_18615515	11.6167	intergenic		NA	NA	NA	NA
				snp_02_18615519	11.6170	intergenic		NA	NA	NA	NA
				snp_02_18624558	13.3778	intergenic		NA	NA	NA	NA
				snp_02_18637200	13.8433	intergenic	LOC_Os02g31120(dist=28112), LOC_Os02g31140(dist=1936)	18637200	C	T	NA
				snp_02_18660414	13.6031	intronic	LOC_Os02g31160	18660414	T	C	NA
				snp_02_18694437	13.6975	upstream	LOC_Os02g31210	18694437	C	T	NA
				snp_02_18711010	14.4694	NA	NA	NA	NA	NA	NA
				snp_02_18711211	14.4708	exonic	LOC_Os02g31220	18711211	C	T	synonymous SNV
				snp_02_18752798	14.7581	NA	NA	NA	NA	NA	NA
				snp_02_18767486	14.8544	intergenic	LOC_Os02g31280(dist=19661), LOC_Os02g31290(dist=2233)	18767486	A	C	NA
				snp_02_18845763	16.1763	exonic	LOC_Os02g31910	18845763	T	C	synonymous SNV
				snp_02_18845781	16.1829	exonic	LOC_Os02g31910	18845781	G	T	synonymous SNV
				snp_02_18846101	16.6442	exonic	LOC_Os02g31910	18846101	A	C	synonymous SNV
				snp_02_18846852	15.8462	exonic	LOC_Os02g31910	18846852	C	T	synonymous SNV
				snp_02_18848592	15.8550	exonic	LOC_Os02g31910	18848592	A	G	synonymous SNV
				snp_02_18856082	15.0076	intergenic	LOC_Os02g31910(dist=4240), LOC_Os02g31920(dist=3152)	18856082	G	A	NA
				snp_02_18871604	13.0832	downstream	LOC_Os02g31940	18871604	T	C	NA

				snp_02_18871693	13.0838	downstream	LOC_Os02g31940	18871693	T	C	NA
				snp_02_18889427	16.6462	downstream	LOC_Os02g31960	18889427	T	C	NA
				snp_02_19028834	18.4855	intronic	LOC_Os02g32210	19028834	G	A	NA
				snp_02_19062328	18.7305	exonic	LOC_Os02g32280	19062328	A	G	synonymous SNV
				snp_02_19163651	18.3261	downstream	LOC_Os02g32410	19163651	T	C	NA
				snp_02_19186685	18.9878	exonic	LOC_Os02g32450	19186685	A	G	synonymous SNV
				snp_02_19186913	19.3720	exonic	LOC_Os02g32450	19186913	A	G	synonymous SNV
				snp_02_19262151	19.1389	UTR3	LOC_Os02g32540(LOC_Os02g32540.1:c.*383T>A)	19262151	T	A	NA
				snp_02_19290185	19.6953	NA	NA	NA	NA	NA	NA
				snp_02_19304020	19.3508	exonic	LOC_Os02g32580	19304020	T	C	nonsynonymous SNV
				snp_02_19304085	19.3510	intronic	LOC_Os02g32580	19304085	G	C	NA
				snp_02_19449660	17.7522	downstream	LOC_Os02g32750	19449660	A	G	NA
				snp_02_19449785	17.7502	downstream	LOC_Os02g32750	19449785	C	T	NA
				snp_02_19456018	18.4127	intronic	LOC_Os02g32760	19456018	A	G	NA
				snp_02_19487646	17.2205	upstream	LOC_Os02g32840	19487646	T	G	NA
				snp_02_19487768	15.1417	upstream	LOC_Os02g32840	19487768	G	C	NA
				snp_02_19513808	16.6774	exonic	LOC_Os02g32860	19513808	C	A	synonymous SNV
				snp_02_19564705	15.3388	exonic	LOC_Os02g32940	19564705	C	T	synonymous SNV
				snp_02_19564792	15.3355	exonic	LOC_Os02g32940	19564792	G	A	synonymous SNV
				snp_02_19564801	15.3352	exonic	LOC_Os02g32940	19564801	G	A	synonymous SNV
				snp_02_19564806	15.3351	exonic	LOC_Os02g32940	19564806	A	T	synonymous SNV
				snp_02_19568752	14.6837	exonic	LOC_Os02g32950	19568752	A	G	synonymous SNV
				snp_02_19568814	14.6837	UTR5	LOC_Os02g32950(LOC_Os02g32950.1:c.-18A>T)	19568814	T	A	NA
				snp_02_19614069	13.9317	UTR5	LOC_Os02g32990(LOC_Os02g32990.1:c.-178C>G)	19614069	C	G	NA
				snp_02_19654273	14.2251	exonic	LOC_Os02g33090	19654273	T	C	synonymous SNV
				snp_02_19654332	14.2243	exonic	LOC_Os02g33090	19654332	G	T	synonymous SNV
				snp_02_19682485	15.1420	upstream	LOC_Os02g33110	19682485	A	C	NA
				snp_02_19685411	14.9157	exonic	LOC_Os02g33110	19685411	A	C	synonymous SNV
				snp_02_19685437	14.9155	exonic	LOC_Os02g33110	19685437	A	T	synonymous SNV
				snp_02_19685438	14.9155	exonic	LOC_Os02g33110	19685438	G	T	synonymous SNV
				snp_02_19685439	14.9155	exonic	LOC_Os02g33110	19685439	C	T	synonymous SNV
				snp_02_19703249	14.3647	downstream	LOC_Os02g33120	19703249	C	T	NA
				snp_02_19713122	14.0198	intronic	LOC_Os02g33140	19713122	T	C	NA

				snp_02_19747480	13.9551	intergenic	LOC_Os02g33210(dist=2873),LOC_Os02g33220(dist=1414)	19747480	T	C	NA
				snp_02_19755401	13.8661	downstream	LOC_Os02g33230	19755401	T	A	NA
				snp_02_19764769	14.0697	downstream	LOC_Os02g33250	19764769	C	T	NA
				snp_02_19764801	14.0714	downstream	LOC_Os02g33250	19764801	T	G	NA
				snp_02_19819816	14.1633	upstream	LOC_Os02g33360	19819816	A	G	NA
				snp_02_19819844	14.1634	upstream	LOC_Os02g33360	19819844	A	C	NA
				snp_02_19882260	14.3320	exonic	LOC_Os02g33450	19882260	G	C	synonymous SNV
				snp_02_19884468	14.1060	intronic	LOC_Os02g33450	19884468	T	A	NA
				snp_02_19884473	14.1060	intronic	LOC_Os02g33450	19884473	G	T	NA
				snp_02_19952595	15.5417	intergenic	LOC_Os02g33540(dist=4225), LOC_Os02g33550(dist=1958)	19952595	T	A	NA
qGI1.1	1	7.68-8.30	GI	snp_01_7680341	3.0481	intronic	LOC_Os01g13730	7680341	T	A	NA
				snp_01_7743691	3.2254	upstream;downstream	LOC_Os01g13810; LOC_Os01g13800	7743691	G	C	NA
				snp_01_8300940	3.0263	exonic	LOC_Os01g14840	8300940	T	C	synonymous SNV
qGI2.1	2	18.63-19.97	GI	snp_02_18637200	13.9449	intergenic	LOC_Os02g31120(dist=28112), LOC_Os02g31140(dist=1936)	18637200	C	T	NA
				snp_02_18660414	13.6286	intronic	LOC_Os02g31160	18660414	T	C	NA
				snp_02_18694437	13.2933	upstream	LOC_Os02g31210	18694437	C	T	NA
				snp_02_18711010	13.8502	NA	NA	NA	NA	NA	NA
				snp_02_18711211	13.8527	exonic	LOC_Os02g31220	18711211	C	T	synonymous SNV
				snp_02_18752798	15.0857	NA	NA	NA	NA	NA	NA
				snp_02_18767486	15.3346	intergenic	LOC_Os02g31280(dist=19661), LOC_Os02g31290(dist=2233)	18767486	A	C	NA
				snp_02_18845763	17.2704	exonic	LOC_Os02g31910	18845763	T	C	synonymous SNV
				snp_02_18845781	17.2819	exonic	LOC_Os02g31910	18845781	G	T	synonymous SNV
				snp_02_18846101	17.9607	exonic	LOC_Os02g31910	18846101	A	C	synonymous SNV
				snp_02_18846852	16.7854	exonic	LOC_Os02g31910	18846852	C	T	synonymous SNV
				snp_02_18848592	16.7999	exonic	LOC_Os02g31910	18848592	A	G	synonymous SNV
				snp_02_18856082	16.5213	intergenic	LOC_Os02g31910(dist=4240), LOC_Os02g31920(dist=3152)	18856082	G	A	NA
				snp_02_18871604	15.5857	downstream	LOC_Os02g31940	18871604	T	C	NA
				snp_02_18871693	15.5862	downstream	LOC_Os02g31940	18871693	T	C	NA
				snp_02_18889427	19.2889	downstream	LOC_Os02g31960	18889427	T	C	NA
				snp_02_19028834	20.4901	intronic	LOC_Os02g32210	19028834	G	A	NA
				snp_02_19062328	20.0805	exonic	LOC_Os02g32280	19062328	A	G	synonymous SNV

				snp_02_19163651	18.6761	downstream	LOC_Os02g32410	19163651	T	C	NA
				snp_02_19186685	19.9661	exonic	LOC_Os02g32450	19186685	A	G	synonymous SNV
				snp_02_19186913	20.5500	exonic	LOC_Os02g32450	19186913	A	G	synonymous SNV
				snp_02_19262151	20.9667	UTR3	LOC_Os02g32540(LOC_Os02g32540.1:c.*383T>A)	19262151	T	A	NA
				snp_02_19290185	21.7909	NA	NA	NA	NA	NA	NA
				snp_02_19304020	22.1614	exonic	LOC_Os02g32580	19304020	T	C	nonsynonymous SNV
				snp_02_19304085	22.1620	intronic	LOC_Os02g32580	19304085	G	C	NA
				snp_02_19449660	19.8780	downstream	LOC_Os02g32750	19449660	A	G	NA
				snp_02_19449785	19.8764	downstream	LOC_Os02g32750	19449785	C	T	NA
				snp_02_19456018	21.1766	intronic	LOC_Os02g32760	19456018	A	G	NA
				snp_02_19487646	20.2737	upstream	LOC_Os02g32840	19487646	T	G	NA
				snp_02_19487768	18.1903	upstream	LOC_Os02g32840	19487768	G	C	NA
				snp_02_19513808	19.3748	exonic	LOC_Os02g32860	19513808	C	A	synonymous SNV
				snp_02_19564705	17.1122	exonic	LOC_Os02g32940	19564705	C	T	synonymous SNV
				snp_02_19564792	17.1093	exonic	LOC_Os02g32940	19564792	G	A	synonymous SNV
				snp_02_19564801	17.1091	exonic	LOC_Os02g32940	19564801	G	A	synonymous SNV
				snp_02_19564806	17.1089	exonic	LOC_Os02g32940	19564806	A	T	synonymous SNV
				snp_02_19568752	16.9065	exonic	LOC_Os02g32950	19568752	A	G	synonymous SNV
				snp_02_19568814	16.9064	UTR5	LOC_Os02g32950(LOC_Os02g32950.1:c.-18A>T)	19568814	T	A	NA
				snp_02_19614069	16.1325	UTR5	LOC_Os02g32990(LOC_Os02g32990.1:c.-178C>G)	19614069	C	G	NA
				snp_02_19654273	17.1803	exonic	LOC_Os02g33090	19654273	T	C	synonymous SNV
				snp_02_19654332	17.1796	exonic	LOC_Os02g33090	19654332	G	T	synonymous SNV
				snp_02_19682485	17.3465	upstream	LOC_Os02g33110	19682485	A	C	NA
				snp_02_19685411	16.9319	exonic	LOC_Os02g33110	19685411	A	C	synonymous SNV
				snp_02_19685437	16.9318	exonic	LOC_Os02g33110	19685437	A	T	synonymous SNV
				snp_02_19685438	16.9318	exonic	LOC_Os02g33110	19685438	G	T	synonymous SNV
				snp_02_19685439	16.9318	exonic	LOC_Os02g33110	19685439	C	T	synonymous SNV
				snp_02_19703249	16.2676	downstream	LOC_Os02g33120	19703249	C	T	NA
				snp_02_19713122	15.4760	intronic	LOC_Os02g33140	19713122	T	C	NA
				snp_02_19747480	15.4325	intergenic	LOC_Os02g33210(dist=2873), LOC_Os02g33220(dist=1414)	19747480	T	C	NA
				snp_02_19755401	15.3455	downstream	LOC_Os02g33230	19755401	T	A	NA
				snp_02_19764769	15.5479	downstream	LOC_Os02g33250	19764769	C	T	NA

				snp_02_19764801	15.5487	downstream	LOC_Os02g33250	19764801	T	G	NA
				snp_02_19819816	16.2372	upstream	LOC_Os02g33360	19819816	A	G	NA
				snp_02_19819844	16.2375	upstream	LOC_Os02g33360	19819844	A	C	NA
				snp_02_19882260	16.7145	exonic	LOC_Os02g33450	19882260	G	C	synonymous SNV
				snp_02_19884468	16.7242	intronic	LOC_Os02g33450	19884468	T	A	NA
				snp_02_19884473	16.7242	intronic	LOC_Os02g33450	19884473	G	T	NA
				snp_02_19952595	17.0587	intergenic	LOC_Os02g33540(dist=4225), LOC_Os02g33550(dist=1958)	19952595	T	A	NA
				snp_02_19966766	15.9175	exonic	LOC_Os02g33560	19966766	C	A	synonymous SNV

Table S4.1 Top non-redundant significant SNPs of candidate genes for AC and PC and the corresponding percent phenotypic variation values after targeted association analysis.

Trait	Locus	Top_predictor_SNP	PVE (%)	Beta	SE	P	SNP_position	type_of_aa_change
AC	LOC_Os02g31940	snp_02_18871604	2.7059	-0.2496813	0.0895939	0.0056779	downstream	NA
	LOC_Os02g27820	snp_02_16470322	4.093	-0.2338043	0.1027517	0.0236525	upstream	NA
		snp_02_16470423		-0.2548106	0.1020179	0.0130868	upstream	NA
		snp_02_16473118		-0.2807654	0.1051098	0.0080112	intronic	NA
		snp_02_16476369		-0.2326566	0.0995812	0.0201941	exonic	nonsynonymous SNV
	LOC_Os02g33790	snp_02_20158379	5.566	-0.2699648	0.0858029	0.0018176	NA	NA
	LOC_Os02g31860	snp_02_18817478	5.6418	-0.271653	0.0881512	0.0022528	downstream	NA
	LOC_Os02g33680	snp_02_20082377	5.9607	-0.318248	0.0752921	3.155E-05	exonic	synonymous SNV
		snp_02_20082383		-0.3269196	0.0771692	3.031E-05	exonic	synonymous SNV
		snp_02_20082386		-0.3138427	0.0767654	5.594E-05	exonic	synonymous SNV
		snp_02_20082615		-0.3523073	0.0781482	9.408E-06	exonic	synonymous SNV
		snp_02_20082638		-0.3307687	0.0768051	2.253E-05	exonic	synonymous SNV
	LOC_Os02g27570	snp_02_16328549	6.1284	-0.2095184	0.0900559	0.0206405	intronic	NA
	LOC_Os02g30640	snp_02_18240771	7.4833	-0.1923224	0.0899662	0.0333092	intronic	NA
		snp_02_18240912		-0.2016606	0.0929755	0.0308332	intronic	NA
		snp_02_18240951		-0.182452	0.089563	0.0424721	intronic	NA
		snp_02_20037230	8.4618	-0.3596161	0.0792434	8.272E-06	downstream	NA
	LOC_Os02g29150	snp_02_17271281	8.7481	-0.2315067	0.0925521	0.0128555	UTR3	NA
		snp_02_17271333		-0.2297509	0.0920955	0.0130948	UTR3	NA
	LOC_Os02g27110	snp_02_15935358	9.2727	-0.2434529	0.0927715	0.0091051	exonic	nonsynonymous SNV
	LOC_Os02g35020	snp_02_21016307	9.4002	-0.2145302	0.0785878	0.0067568	exonic	synonymous SNV
	LOC_Os02g31120	snp_02_18607827	9.5262	-0.2028861	0.0994635	0.042354	intronic	NA
		snp_02_18608900		-0.281371	0.0919841	0.0024474	exonic	synonymous SNV
	LOC_Os02g26210	snp_02_15400132	10.0115	-0.2661052	0.0928429	0.004435	intergenic	NA
		snp_02_15400183		-0.2288284	0.0917003	0.0130948	intergenic	NA
	LOC_Os02g26480	snp_02_15558985	10.3981	-0.2631198	0.0960642	0.0065058	upstream	NA
	LOC_Os02g34990	snp_02_20993759	10.7379	-0.1702304	0.0742835	0.0225741	exonic	synonymous SNV
	LOC_Os02g26404	snp_02_15512248	10.8923	-0.2196673	0.094231	0.0203777	intronic	NA

	LOC_Os02g29720	snp_02_17677857	11.0241	-0.4007358	0.1039591	0.000143	exonic	nonsynonymous SNV
		snp_02_17677866		-0.3921394	0.1035425	0.0001856	exonic	nonsynonymous SNV
		snp_02_17677891		-0.3424444	0.1013892	0.0008325	NA	NA
		snp_02_17677905		-0.3319083	0.1014127	0.0011949	exonic	synonymous SNV
	LOC_Os02g28670	snp_02_16962209	11.3181	-0.1987687	0.0934355	0.0341996	upstream	A
	LOC_Os02g30114	snp_02_17889038	11.3767	-0.1822559	0.0924387	0.0496044	intronic	NA
	LOC_Os02g36210	snp_02_21847256	11.6421	-0.2071832	0.0790528	0.0092248	exonic	synonymous SNV
	LOC_Os02g34630	snp_02_20767401	11.801	-0.203963	0.0829839	0.0145576	exonic	synonymous SNV
	LOC_Os02g34630	snp_02_20767410		-0.2171867	0.0835944	0.0098496	exonic	synonymous SNV
	LOC_Os02g30840	snp_02_18385163	11.9192	-0.2171347	0.0915202	0.0182928	upstream	NA
	LOC_Os02g28550	snp_02_16888902	11.9425	-0.1723502	0.0854377	0.0444975	upstream	NA
	LOC_Os02g28830	snp_02_17046347	12.0659	-0.1871919	0.0935519	0.0462964	downstream	NA
	LOC_Os02g28340	snp_02_16750570	12.1885	-0.2072022	0.0974476	0.0342687	exonic	synonymous SNV
	LOC_Os02g33140	snp_02_19713122	12.3447	-0.2281211	0.0796934	0.0045085	intronic	NA
	LOC_Os02g30210	snp_02_17959252	12.6964	-0.2223272	0.0908844	0.0149918	exonic	nonsynonymous SNV
	LOC_Os02g26040	snp_02_15286516	12.8776	-0.3159265	0.0988278	0.0015319	exonic	synonymous SNV
	LOC_Os02g26294	snp_02_15442082	12.9897	-0.2330438	0.1022529	0.0233219	UTR5	T
	LOC_Os02g26349	snp_02_15470192	13.0041	-0.23784	0.0970422	0.0148266	intronic	NA
	LOC_Os02g26349	snp_02_15478472		-0.3393868	0.0945643	0.0003882	NA	NA
	LOC_Os02g27000	snp_02_15876071	13.0116	-0.2881341	0.0961656	0.002957	UTR3	NA
	LOC_Os02g27490	snp_02_16268167	13.0877	-0.1925149	0.0955722	0.0447972	intronic	NA
	LOC_Os02g28180	snp_02_16683168	13.1065	-0.1928752	0.0944425	0.0419865	downstream	NA
	LOC_Os02g36220	snp_02_21860560	13.2155	-0.2116404	0.0755675	0.0053938	intronic	NA
	LOC_Os02g27220	snp_02_16010382	13.4403	-0.2103679	0.0926	0.0237797	exonic	synonymous SNV
	LOC_Os02g29030	snp_02_17191079	13.5423	-0.238207	0.0948965	0.0125899	exonic	synonymous SNV
	LOC_Os02g30440	snp_02_18130541	13.6012	-0.2560959	0.0881004	0.0039147	upstream	NA
	LOC_Os02g27850	snp_02_16487977	13.7209	-0.2252007	0.0976505	0.021753	UTR3	NA
	LOC_Os02g29464	snp_02_17503963	13.7233	-0.2304891	0.094271	0.0150092	exonic	synonymous SNV
	LOC_Os02g26590	snp_02_15613607	13.7633	-0.196311	0.0949926	0.0395338	downstream	NA
	LOC_Os02g28810	snp_02_17037081	13.9401	-0.2314143	0.0918942	0.0122589	intronic	NA
	LOC_Os02g30380	snp_02_18092703	14.0897	-0.2163315	0.0904192	0.0172777	UTR3	NA
	LOC_Os02g29890	snp_02_17781288	14.1627	-0.1764079	0.0845072	0.0376224	UTR5	NA
	LOC_Os02g29210	snp_02_17336504	14.4415	-0.3132494	0.0997934	0.0018641	upstream	NA

	LOC_Os02g33890	snp_02_20199340	14.4914	-0.1913142	0.0781318	0.0148912	intergenic	NA
		snp_02_20199396		-0.2058169	0.0774193	0.0082544	NA	NA
	LOC_Os02g26840	snp_02_15760177	14.6813	-0.2055468	0.0913236	0.0251041	exonic	nonsynonymous SNV
		snp_02_15760221		-0.2450721	0.0939244	0.0095156	exonic	synonymous SNV
	LOC_Os02g26310	snp_02_15452898	14.7417	-0.2552927	0.0953161	0.007774	downstream	NA
	LOC_Os02g33450	snp_02_19882259	14.7946	-0.3454082	0.0814981	3.022E-05	exonic	synonymous SNV
		snp_02_19882260		-0.3783352	0.0792032	2.82E-06	exonic	synonymous SNV
		snp_02_19882295		-0.3522878	0.0824884	2.635E-05	exonic	synonymous SNV
		snp_02_19884473		-0.3100916	0.079624	0.000122	intronic	NA
	LOC_Os02g26670	snp_02_15659575	14.8556	-0.2320342	0.0903014	0.0106204	exonic	nonsynonymous SNV
	LOC_Os02g33100	snp_02_19659783	14.9409	-0.3241262	0.0758768	2.578E-05	downstream	NA
	LOC_Os02g25780	snp_02_15106052	14.981	-0.307755	0.1009296	0.0024984	upstream	G
		snp_02_15106300	14.981	-0.2801449	0.0954131	0.0035796	upstream	T
	LOC_Os02g26600	snp_02_15615777	15.0742	-0.4025086	0.096451	3.838E-05	exonic	synonymous SNV
	LOC_Os02g26270	snp_02_15428873	15.0961	-0.3657917	0.1092079	0.0009232	exonic	nonsynonymous SNV
		snp_02_15430884		-0.2870265	0.1093195	0.0091365	intronic	NA
	LOC_Os02g29580	snp_02_17600915	15.1336	-0.2744189	0.0901466	0.0025395	upstream	NA
	LOC_Os02g26890	snp_02_15789691	15.2734	-0.2915884	0.0977039	0.0030658	exonic	synonymous SNV
	LOC_Os02g29370	snp_02_17446176	15.297	-0.2653853	0.0931134	0.004661	upstream	NA
		snp_02_17446330		-0.2252922	0.0868042	0.0098945	upstream	NA
	LOC_Os02g27030	snp_02_15892404	15.337	-0.2150778	0.0951594	0.0245464	intronic	NA
		snp_02_15894520		-0.2761097	0.1010738	0.0066833	intronic	NA
	LOC_Os02g30080	snp_02_17862881	15.3506	-0.2808568	0.0943863	0.0031619	intronic	NA
	LOC_Os02g28420	snp_02_16810236	15.3939	-0.3048177	0.0946423	0.0014002	exonic	nonsynonymous SNV
	LOC_Os02g31230	snp_02_18715998	15.4344	-0.2751576	0.0848747	0.0013127	intronic	NA
	LOC_Os02g28210	snp_02_16699586	15.4616	-0.3120053	0.0975565	0.0015563	exonic	synonymous SNV
		snp_02_16699608		-0.2911468	0.1040518	0.0055298	downstream	NA
	LOC_Os02g33360	snp_02_19819816	15.5044	-0.3797412	0.0867723	1.72E-05	upstream	NA
	LOC_Os02g28400	snp_02_16794771	15.5978	-0.2601503	0.0909517	0.004514	intergenic	NA
		snp_02_16794908		-0.2850102	0.090992	0.0018971	intergenic	NA
	LOC_Os02g29320	snp_02_17416587	15.6218	-0.2000323	0.091125	0.0288251	exonic	synonymous SNV
	LOC_Os02g33420	snp_02_19860601	15.6276	-0.3288402	0.0748264	1.56E-05	exonic	synonymous SNV
	LOC_Os02g25930	snp_02_15219832	15.6599	-0.2344815	0.0996219	0.0192733	exonic	nonsynonymous SNV

		snp_02_15219922		-0.2398298	0.0936162	0.0109319	exonic	nonsynonymous SNV
		snp_02_15220376		-0.2625664	0.0964478	0.0068854	exonic	nonsynonymous SNV
	LOC_Os02g27160	snp_02_15990619	15.745	-0.2337577	0.0996861	0.0196908	upstream	NA
	LOC_Os02g30250	snp_02_17986683	16.0392	-0.2481768	0.0980193	0.0118252	downstream	NA
		snp_02_17986693		-0.2305408	0.0977858	0.0189984	downstream	NA
	LOC_Os02g30420	snp_02_18120796	16.0725	-0.2758964	0.0878918	0.001843	exonic	synonymous SNV
	LOC_Os02g31220	snp_02_18711010	16.0944	-0.2478896	0.0858962	0.0041621	NA	NA
		snp_02_18711211		-0.2345987	0.0855321	0.0064272	exonic	synonymous SNV
	LOC_Os02g26940	snp_02_15825151	16.1595	-0.2958317	0.0957918	0.0021765	exonic	nonsynonymous SNV
	LOC_Os02g31874	snp_02_18828442	16.2266	-0.3176977	0.0861913	0.0002678	intronic	NA
	LOC_Os02g30700	snp_02_18290410	16.2772	-0.3086269	0.084701	0.0003103	exonic	nonsynonymous SNV
		snp_02_18290444		-0.2910881	0.082421	0.0004693	exonic	synonymous SNV
	LOC_Os02g25870	snp_02_15160683	16.3433	-0.2940255	0.100472	0.0037215	upstream	NA
		snp_02_15160853		-0.2658278	0.0928104	0.0045102	upstream	NA
		snp_02_15160883		-0.2373843	0.0939969	0.01213	upstream	NA
		snp_02_15161482		-0.1922748	0.0957852	0.0457122	exonic	nonsynonymous SNV
	LOC_Os02g32750	snp_02_19449660	16.344	-0.4088015	0.0771209	2.107E-07	downstream	NA
	LOC_Os02g29140	snp_02_17258929	16.4805	-0.2784701	0.0997626	0.0055989	exonic	synonymous SNV
		snp_02_17258984		-0.2505226	0.1045114	0.0171612	exonic	synonymous SNV
		snp_02_17259650		-0.2327744	0.0924513	0.0123494	intronic	NA
	LOC_Os02g31210	snp_02_18694437	16.4834	-0.2720503	0.0893305	0.0025311	upstream	NA
	LOC_Os02g33610	snp_02_20009271	16.4992	-0.2676018	0.0792534	0.0008228	intronic	NA
	LOC_Os02g29570	snp_02_17591726	16.5297	-0.2518142	0.0957381	0.0089743	exonic	synonymous SNV
		snp_02_17593523		-0.2843169	0.0988565	0.0043162	intronic	NA
	LOC_Os02g27990	snp_02_16574548	16.7955	-0.3052371	0.0965874	0.0017475	NA	NA
		snp_02_16576923		-0.2665729	0.0997276	0.0079538	intergenic	NA
	LOC_Os02g30330	snp_02_18067425	16.8005	-0.2398572	0.0952749	0.0123373	upstream	NA
		snp_02_18068119		-0.3388238	0.0977798	0.0006069	upstream	NA
		snp_02_18068141		-0.3591177	0.0971424	0.0002594	upstream	NA
	LOC_Os02g30940	snp_02_18481164	17.1042	-0.2149057	0.0874166	0.0144655	exonic	nonsynonymous SNV
		snp_02_18481190		-0.1664532	0.084151	0.0487519	exonic	synonymous SNV
		snp_02_18481231		-0.2261135	0.0883325	0.0109157	exonic	nonsynonymous SNV
	LOC_Os02g30390	snp_02_18098101	17.1567	-0.3421414	0.0904437	0.000183	downstream	NA

	LOC_Os02g25770	snp_02_15101212	17.296	-0.3499909	0.1033495	0.0008231	exonic	synonymous SNV
		snp_02_15106052		-0.3838338	0.1071628	0.0004106	upstream	G
		snp_02_15106300		-0.3072649	0.1021294	0.0028951	upstream	T
	LOC_Os02g30150	snp_02_17911664	17.3588	-0.3383896	0.094536	0.0004054	exonic	nonsynonymous SNV
	LOC_Os02g32760	snp_02_19456018	17.4827	-0.3670807	0.0773251	3.107E-06	intronic	NA
	LOC_Os02g31960	snp_02_19456018	17.7699	-0.3253285	0.0860782	0.0001891	downstream	NA
	LOC_Os02g33560	snp_02_19966766	17.8038	-0.2953282	0.0761861	0.0001272	exonic	synonymous SNV
	LOC_Os02g31950	snp_02_18882574	18.0123	-0.3404448	0.0892825	0.0001673	exonic	nonsynonymous SNV
	LOC_Os02g29070	snp_02_17218097	18.0165	-0.2620866	0.1063228	0.0142949	exonic	synonymous SNV
		snp_02_17218127		-0.2417751	0.1036431	0.0203614	exonic	synonymous SNV
	LOC_Os02g32950	snp_02_19568752	18.241	-0.3582707	0.0802276	1.146E-05	exonic	synonymous SNV
		snp_02_19568814		-0.3750768	0.0782522	2.63E-06	UTR5	NA
	LOC_Os02g31867	snp_02_18825659	18.3184	-0.3135617	0.0833194	0.0001994	exonic	synonymous SNV
		snp_02_18825660		-0.3267268	0.0827402	9.662E-05	exonic	synonymous SNV
		snp_02_18825730		-0.2902216	0.083561	0.0005851	exonic	synonymous SNV
	LOC_Os02g32860	snp_02_19513808	18.421	-0.4278437	0.0797901	1.671E-07	exonic	synonymous SNV
	LOC_Os02g28360	snp_02_16761557	18.4526	-0.2642847	0.0999795	0.0086438	upstream	NA
	LOC_Os02g31160	snp_02_18660414	18.6266	-0.3197427	0.0887839	0.0003649	intronic	NA
	LOC_Os02g33120	snp_02_19703249	18.8352	-0.3518469	0.0739515	3.017E-06	downstream	NA
	LOC_Os02g32504	snp_02_19226636	19.0301	-0.3961946	0.080205	1.276E-06	intronic	NA
	LOC_Os02g33090	snp_02_19654273	19.0398	-0.3524366	0.0765273	6.179E-06	exonic	synonymous SNV
		snp_02_19654332		-0.4042113	0.080191	8.199E-07	exonic	synonymous SNV
	LOC_Os02g33230	snp_02_19755401	19.1843	-0.3628553	0.0794964	7.008E-06	downstream	NA
	LOC_Os02g32610	snp_02_19329803	19.4398	-0.4168413	0.0796346	3.092E-07	intronic	NA
	LOC_Os02g32710	snp_02_19429943	19.4602	-0.3674158	0.0786558	4.281E-06	downstream	NA
	LOC_Os02g33250	snp_02_19764675	19.4939	-0.4128278	0.0777738	2.06E-07	downstream	NA
		snp_02_19764769		-0.4068304	0.077418	2.69E-07	downstream	NA
	LOC_Os02g32990	snp_02_19614069	19.8444	-0.373173	0.0763212	1.601E-06	UTR5	NA
	LOC_Os02g33330	snp_02_19798665	20.4076	-0.3849273	0.0795753	2.008E-06	UTR5	NA
	LOC_Os02g30690	snp_02_18286380	20.4629	-0.2695603	0.0925109	0.0038218	intronic	NA
	LOC_Os02g32840	snp_02_19487646	20.561	-0.4214823	0.0773641	1.113E-07	upstream	NA
		snp_02_19488040		-0.4673511	0.0802386	1.564E-08	upstream	NA
		snp_02_19488084		-0.4544572	0.0800975	3.472E-08	upstream	NA

	LOC_Os02g33110	snp_02_19682485	20.8193	-0.3308169	0.0816124	6.561E-05	upstream	NA
		snp_02_19685411		-0.4372862	0.0846335	4.561E-07	exonic	synonymous SNV
		snp_02_19685438		-0.4405478	0.0842281	3.34E-07	exonic	synonymous SNV
		snp_02_19685439		-0.4372862	0.0846335	4.561E-07	exonic	synonymous SNV
	LOC_Os02g33600	snp_02_20000687	21.196	-0.3491836	0.0816252	2.523E-05	upstream	NA
		snp_02_20000944		-0.3170674	0.0782985	6.506E-05	upstream	NA
	LOC_Os02g32580	snp_02_19304020	21.4916	-0.4617526	0.0784587	1.096E-08	exonic	nonsynonymous SNV
		snp_02_19304085		-0.5125892	0.0793919	4.501E-10	intronic	NA
	LOC_Os02g31910	snp_02_18845763	21.766	-0.2952812	0.0856607	0.0006382	exonic	synonymous SNV
		snp_02_18845781		-0.2772627	0.0876414	0.0016997	exonic	synonymous SNV
		snp_02_18846101		-0.3384471	0.0865765	0.0001119	exonic	synonymous SNV
		snp_02_18846852		-0.2822202	0.0779932	0.0003416	exonic	synonymous SNV
		snp_02_18848592		-0.2008092	0.086646	0.0210689	exonic	synonymous SNV
	LOC_Os02g32280	snp_02_19062328	21.7711	-0.4164403	0.0778365	1.658E-07	exonic	synonymous SNV
	LOC_Os02g32340	snp_02_19091002	21.9644	-0.3817222	0.0870178	1.612E-05	UTR3	NA
	LOC_Os02g32410	snp_02_19163651	22.0995	-0.4505461	0.0807526	5.614E-08	downstream	NA
	LOC_Os02g32540	snp_02_19262151	22.7247	-0.3588753	0.0857476	3.892E-05	UTR3	NA
		snp_02_19262334		-0.4961297	0.083948	1.061E-08	upstream	A
		snp_02_19262345		-0.460496	0.0820524	5.078E-08	upstream	C
	LOC_Os02g32210	snp_02_19028834	23.4863	-0.4394506	0.0798167	7.57E-08	intronic	NA
	LOC_Os02g33620	snp_02_20017292	23.6596	-0.3606042	0.0784134	6.314E-06	exonic	synonymous SNV
		snp_02_20017408		-0.4336722	0.0826505	2.957E-07	exonic	synonymous SNV
		snp_02_20017433		-0.37272	0.0779283	2.734E-06	intronic	NA
		snp_02_20017486		-0.2998652	0.0781191	0.0001514	intronic	NA
		snp_02_20019434		-0.3377835	0.0800442	3.256E-05	exonic	synonymous SNV
	LOC_Os02g32940	snp_02_19564705	25.6342	-0.4079305	0.0780478	3.183E-07	exonic	synonymous SNV
		snp_02_19564739		-0.3935499	0.0786211	9.368E-07	exonic	synonymous SNV
		snp_02_19564801		-0.4220426	0.0792856	1.966E-07	exonic	synonymous SNV
		snp_02_19564806		-0.3841168	0.078531	1.615E-06	exonic	synonymous SNV
		snp_02_19564894		-0.3998679	0.079327	7.912E-07	upstream	NA
	LOC_Os02g32450	snp_02_19186685	26.1547	-0.4343471	0.0822019	2.649E-07	exonic	synonymous SNV
		snp_02_19186803		-0.5353054	0.0854886	1.536E-09	exonic	synonymous SNV
		snp_02_19186913		-0.4634065	0.0849368	1.121E-07	exonic	synonymous SNV

	LOC_Os02g28770	snp_02_17022010	32.8808	-0.2832151	0.1132753	0.012969	exonic	synonymous SNV
		snp_02_17022047		-0.2842365	0.1123121	0.0119156	exonic	synonymous SNV
		snp_02_17022059		-0.297465	0.1119247	0.008308	exonic	nonsynonymous SNV
		snp_02_17022102		-0.2897635	0.1036114	0.0055126	exonic	synonymous SNV
		snp_02_17022157		-0.2994564	0.1021918	0.003658	intronic	NA
	LOC_Os02g25710	snp_02_15056267	42.255	-0.2607821	0.0996205	0.0093156	intronic	NA
	LOC_Os02g27290	snp_02_16074185	45.4603	-0.2280966	0.0980096	0.0205676	intronic	NA
	LOC_Os02g32660	snp_02_19362520	59.1407	-0.8237682	0.0440969	3.941E-54	exon-intron junction	NA
PC		snp_02_19362520	7.9419	-0.3205192	0.0626063	5.128E-07	exon-intron junction	NA
	LOC_Os02g13440	snp_02_7178016	5.6283	-0.2206234	0.071961	0.0023626	exonic	synonymous SNV
	LOC_Os02g13520	snp_02_7249337	2.5957	-0.1766115	0.072736	0.0157557	upstream	NA
	LOC_Os02g13555	snp_02_7266399	3.1026	-0.1563146	0.0732168	0.0335746	UTR3	NA
	LOC_Os02g13560	snp_02_7275897	4.0757	-0.1892387	0.0774826	0.0151917	intronic	NA
	LOC_Os02g13510	snp_02_7222404	4.3657	-0.1849309	0.0774068	0.0175366	exonic	synonymous SNV
	LOC_Os02g13810	snp_02_7470132	3.412	-0.1743107	0.0714718	0.0153309	intronic	NA
	LOC_Os02g14370	snp_02_7892495	3.1723	-0.1970196	0.0731626	0.0074926	intergenic	NA
	LOC_Os02g14310	snp_02_7857480	3.1564	-0.1880927	0.0747315	0.0124917	exonic	nonsynonymous SNV
	LOC_Os02g14170	snp_02_7761476	5.0769	-0.1512886	0.0754935	0.0458827	exonic	synonymous SNV
		snp_02_7761675		-0.1874537	0.0765588	0.0148624	intronic	NA
	LOC_Os02g29070	snp_02_17217858	5.0289	-0.1836375	0.0835314	0.0287283	exonic	nonsynonymous SNV
	LOC_Os02g31120	snp_02_18607827	3.4527	-0.1916545	0.0761899	0.0124744	intronic	NA
		snp_02_18608900		-0.1999582	0.074129	0.0074324	exonic	synonymous SNV
	LOC_Os02g29720	snp_02_17677905	3.4356	-0.2256466	0.0888821	0.0116543	exonic	synonymous SNV
	LOC_Os02g26404	snp_02_15512248	3.3343	-0.1903982	0.0745953	0.011171	intronic	NA
	LOC_Os02g30210	snp_02_17959252	4.6291	-0.187093	0.0795387	0.0192885	exonic	nonsynonymous SNV
	LOC_Os02g17620	snp_02_10141997	3.2781	-0.1900723	0.0813882	0.0202126	intronic	NA
		snp_02_10142051		-0.187037	0.0816184	0.0226528	intronic	NA
	LOC_Os02g27030	snp_02_15894520	2.6428	-0.1648113	0.0795599	0.0391865	intronic	NA
	LOC_Os02g26294	snp_02_15442082	2.8244	-0.1697842	0.0807981	0.0363953	UTR5	T
	LOC_Os02g27000	snp_02_15876071	5.5138	-0.251306	0.0843091	0.0031059	UTR3	NA
	LOC_Os02g25930	snp_02_15220376	3.8316	-0.2291882	0.0829282	0.0060914	exonic	nonsynonymous SNV
	LOC_Os02g26280	snp_02_15430882	4.0532	-0.193078	0.0919928	0.0367463	intronic	NA
	LOC_Os02g29140	snp_02_17259533	3.6213	-0.1664154	0.0838382	0.0480943	intronic	NA

	LOC_Os02g29464	snp_02_17503963	3.1301	-0.1911858	0.0837656	0.0231022	exonic	synonymous SNV
	LOC_Os02g28810	snp_02_17037081	3.9408	-0.1819401	0.0792495	0.0223052	intronic	NA
	LOC_Os02g26840	snp_02_15760177	3.0375	-0.1619807	0.0796025	0.0427173	exonic	nonsynonymous SNV
		snp_02_15760221		-0.1603946	0.0811094	0.0488725	exonic	synonymous SNV
	LOC_Os02g28210	snp_02_16699331	4.0952	-0.1776446	0.0796018	0.0264997	exonic	synonymous SNV
		snp_02_16699586		-0.2623303	0.0819198	0.0015352	exonic	synonymous SNV
		snp_02_16699608		-0.2399951	0.083053	0.0041857	downstream	NA
	LOC_Os02g30330	snp_02_18067425	4.3335	-0.2258443	0.0855088	0.0086931	upstream	NA
	LOC_Os02g30940	snp_02_18481164	3.9592	-0.1756016	0.0783611	0.0256914	exonic	nonsynonymous SNV
		snp_02_18481231		-0.16741	0.0792362	0.0353643	exonic	nonsynonymous SNV
	LOC_Os02g32210	snp_02_19028834	2.6529	-0.1639332	0.0716847	0.0228584	intronic	NA
	LOC_Os02g32450	snp_02_19186803	2.2018	-0.1811085	0.0832239	0.0304301	exonic	synonymous SNV
	LOC_Os02g29370	snp_02_17446176	5.611	-0.2752391	0.0851535	0.0013594	upstream	NA
		snp_02_17446330		-0.2758242	0.0814282	0.0007962	upstream	NA
	LOC_Os02g30080	snp_02_17862881	3.8594	-0.1727934	0.0872446	0.0485537	intronic	NA
	LOC_Os02g28420	snp_02_16810236	4.2435	-0.1669523	0.0834572	0.0462347	exonic	nonsynonymous SNV

Table S4.2 Epistatic interactions of significant SNPs associated to AC and PC of F5-derived F6 RILs.

SNP1	SNP2	BETA_INT	STAT	P-value
snp_02_7178016	snp_02_16699331	0.234191	9.09574	0.002562
snp_02_7178016	snp_02_17046347	0.212126	7.68788	0.005559
snp_02_7178016	snp_02_17416587	0.203802	8.20813	0.00417
snp_02_7178016	snp_02_17593523	0.21078	7.6981	0.005528
snp_02_7178016	snp_02_17781288	0.182464	6.65504	0.009888
snp_02_7178016	snp_02_18067425	0.194334	7.64009	0.005709
snp_02_7178016	snp_02_18098101	0.219394	9.52801	0.002024
snp_02_7178016	snp_02_18286380	0.186255	6.85787	0.008825
snp_02_7178016	snp_02_18481190	0.212523	9.73094	0.001812
snp_02_7178016	snp_02_18607827	0.263658	12.5354	0.0003994
snp_02_7178016	snp_02_19062328	0.196031	9.39957	0.00217
snp_02_7178016	snp_02_19186803	0.195329	9.44347	0.002119
snp_02_7178016	snp_02_19226636	0.190025	7.91647	0.004899
snp_02_7178016	snp_02_19449660	0.179811	8.0703	0.0045
snp_02_7178016	snp_02_19513808	0.206228	9.15643	0.002479
snp_02_7178016	snp_02_19659783	0.190947	8.85497	0.002923
snp_02_7178016	snp_02_20000944	0.201357	9.67681	0.001866
snp_02_7178016	snp_02_20017486	0.185217	7.9009	0.004941
snp_02_7178016	snp_02_21860560	0.190758	9.81235	0.001734
snp_02_7222404	snp_02_16699331	0.240531	8.97331	0.00274
snp_02_7222404	snp_02_17781288	0.206323	8.63402	0.0033
snp_02_7222404	snp_02_18067425	0.210936	9.0118	0.002683
snp_02_7222404	snp_02_18290410	0.186756	6.95802	0.008345
snp_02_7222404	snp_02_18290444	0.189806	7.36022	0.006668
snp_02_7222404	snp_02_18607827	0.21937	9.19146	0.002432
snp_02_7222404	snp_02_18871693	0.185442	6.89029	0.008667

snp_02_7222404	snp_02_19062328	0.22456	12.181	0.0004829
snp_02_7222404	snp_02_19186803	0.171796	7.23446	0.007152
snp_02_7222404	snp_02_19488040	0.195792	9.41408	0.002153
snp_02_7222404	snp_02_19488084	0.184892	8.51062	0.003531
snp_02_7222404	snp_02_19513808	0.177405	7.88959	0.004972
snp_02_7222404	snp_02_19659783	0.177035	7.4281	0.006421
snp_02_7222404	snp_02_19682485	0.186933	7.87206	0.005021
snp_02_7222404	snp_02_19685411	0.1988	9.89082	0.001661
snp_02_7222404	snp_02_19685438	0.202762	10.2565	0.001362
snp_02_7222404	snp_02_19685439	0.196774	9.78845	0.001756
snp_02_7222404	snp_02_19703249	0.208972	10.3106	0.001323
snp_02_7222404	snp_02_20082377	0.179479	7.84706	0.00509
snp_02_7222404	snp_02_20082386	0.183295	8.01967	0.004627
snp_02_7222404	snp_02_20082615	0.178254	7.53059	0.006066
snp_02_7222404	snp_02_20082638	0.174152	7.36813	0.006639
snp_02_7266399	snp_02_16699331	0.214185	7.94745	0.004816
snp_02_7266399	snp_02_19062328	0.170327	7.19892	0.007295
snp_02_7266399	snp_02_19186803	0.197788	10.4114	0.001253
snp_02_7266399	snp_02_19226636	0.170418	6.65336	0.009897
snp_02_7266399	snp_02_19304020	0.188219	7.90581	0.004928
snp_02_7266399	snp_02_19449660	0.173411	7.77699	0.005292
snp_02_7266399	snp_02_19456018	0.177239	7.03823	0.007979
snp_02_7266399	snp_02_19487646	0.176291	7.56999	0.005935
snp_02_7266399	snp_02_19488040	0.165808	6.76849	0.009278
snp_02_7266399	snp_02_19488084	0.165784	6.8007	0.009112
snp_02_7266399	snp_02_19513808	0.193632	9.0214	0.002669
snp_02_7266399	snp_02_19659783	0.235625	13.9912	0.0001837
snp_02_7266399	snp_02_19685411	0.161649	6.695	0.009668
snp_02_7266399	snp_02_19685438	0.162108	6.64356	0.009952

snp_02_7266399	snp_02_19685439	0.161649	6.695	0.009668
snp_02_7266399	snp_02_19713122	0.227053	10.9	0.0009618
snp_02_7266399	snp_02_20082377	0.16864	7.15772	0.007464
snp_02_7266399	snp_02_20082386	0.171209	7.37898	0.006599
snp_02_7266399	snp_02_20082615	0.165504	6.95238	0.008371
snp_02_7275897	snp_02_16699331	0.217285	8.02209	0.004621
snp_02_7275897	snp_02_18067425	0.233046	11.3871	0.0007397
snp_02_7275897	snp_02_19186803	0.168931	7.82099	0.005164
snp_02_7275897	snp_02_19513808	0.194519	9.3822	0.002191
snp_02_7275897	snp_02_19713122	0.188969	7.81026	0.005195
snp_02_7275897	snp_02_19884473	0.162691	6.91424	0.008551
snp_02_7470132	snp_02_7743222	0.318297	6.76204	0.009312
snp_02_7470132	snp_02_7761476	0.352294	9.89923	0.001654
snp_02_7470132	snp_02_7761675	0.343945	8.97441	0.002738
snp_02_7470132	snp_02_15056267	0.215604	7.14461	0.007519
snp_02_7470132	snp_02_15160683	0.257572	10.8234	0.001002
snp_02_7470132	snp_02_15160853	0.215024	7.04274	0.007959
snp_02_7470132	snp_02_15161482	0.266484	10.9342	0.0009442
snp_02_7470132	snp_02_15220376	0.22724	8.32651	0.003907
snp_02_7470132	snp_02_15286516	0.2402	8.61435	0.003335
snp_02_7470132	snp_02_15613607	0.211135	7.23161	0.007163
snp_02_7470132	snp_02_15659575	0.19744	6.97732	0.008255
snp_02_7470132	snp_02_15760177	0.218313	7.85148	0.005078
snp_02_7470132	snp_02_15760221	0.211642	7.24732	0.007101
snp_02_7470132	snp_02_15825151	0.215871	7.35532	0.006687
snp_02_7470132	snp_02_15876071	0.238764	8.1228	0.004371
snp_02_7470132	snp_02_15894520	0.241747	8.7404	0.003112
snp_02_7470132	snp_02_16074185	0.213712	6.74532	0.009399
snp_02_7470132	snp_02_16268167	0.212588	7.30775	0.006866

snp_02_7470132	snp_02_16476369	0.220421	9.00241	0.002696
snp_02_7470132	snp_02_16487977	0.206351	7.24093	0.007126
snp_02_7470132	snp_02_16574548	0.221472	7.73739	0.005409
snp_02_7470132	snp_02_16699331	0.327758	16.5554	4.727E-05
snp_02_7470132	snp_02_16699586	0.216093	7.2748	0.006993
snp_02_7470132	snp_02_16750570	0.19959	6.79955	0.009118
snp_02_7470132	snp_02_16810236	0.206607	6.91407	0.008552
snp_02_7470132	snp_02_17037081	0.194533	6.96792	0.008298
snp_02_7470132	snp_02_17191079	0.22995	9.29937	0.002292
snp_02_7470132	snp_02_17218097	0.237277	9.61259	0.001933
snp_02_7470132	snp_02_17218127	0.246489	10.5943	0.001134
snp_02_7470132	snp_02_17258929	0.272274	12.2374	0.0004685
snp_02_7470132	snp_02_17258984	0.248807	10.0213	0.001547
snp_02_7470132	snp_02_17271281	0.20872	7.18601	0.007347
snp_02_7470132	snp_02_17271333	0.219524	7.80044	0.005223
snp_02_7470132	snp_02_17416587	0.28569	14.959	0.0001099
snp_02_7470132	snp_02_17503963	0.198565	6.89355	0.008651
snp_02_7470132	snp_02_17591726	0.240073	10.6671	0.001091
snp_02_7470132	snp_02_17600915	0.245092	10.6253	0.001116
snp_02_7470132	snp_02_17781288	0.293069	16.2808	5.464E-05
snp_02_7470132	snp_02_17911664	0.192104	6.76751	0.009283
snp_02_7470132	snp_02_17959252	0.209927	7.10091	0.007705
snp_02_7470132	snp_02_17986683	0.202098	7.13726	0.00755
snp_02_7470132	snp_02_17986693	0.198489	6.92753	0.008488
snp_02_7470132	snp_02_18067425	0.270437	14.3882	0.0001488
snp_02_7470132	snp_02_18068119	0.232825	9.55704	0.001992
snp_02_7470132	snp_02_18068141	0.229775	9.44999	0.002112
snp_02_7470132	snp_02_18092703	0.257946	11.8887	0.0005648
snp_02_7470132	snp_02_18098101	0.309169	18.1199	2.076E-05

snp_02_7470132	snp_02_18120796	0.248195	11.9194	0.0005556
snp_02_7470132	snp_02_18130541	0.234313	9.80289	0.001743
snp_02_7470132	snp_02_18240771	0.23404	9.99614	0.001569
snp_02_7470132	snp_02_18240912	0.238593	10.316	0.001319
snp_02_7470132	snp_02_18240951	0.243134	10.9454	0.0009385
snp_02_7470132	snp_02_18290410	0.220476	9.68882	0.001854
snp_02_7470132	snp_02_18290444	0.228295	10.5613	0.001155
snp_02_7470132	snp_02_18385163	0.220711	8.16596	0.004269
snp_02_7470132	snp_02_18607827	0.273607	13.3289	0.0002614
snp_02_7470132	snp_02_18846101	0.199825	8.39349	0.003766
snp_02_7470132	snp_02_18848592	0.227862	10.7105	0.001065
snp_02_7470132	snp_02_18871604	0.211855	8.86864	0.002901
snp_02_7470132	snp_02_18871693	0.21496	9.19543	0.002426
snp_02_7470132	snp_02_18889427	0.187287	6.9762	0.00826
snp_02_7470132	snp_02_19062328	0.219967	10.8952	0.0009643
snp_02_7470132	snp_02_19091002	0.190362	7.2327	0.007159
snp_02_7470132	snp_02_19186803	0.185824	8.03536	0.004587
snp_02_7470132	snp_02_19262334	0.189802	8.20451	0.004179
snp_02_7470132	snp_02_19262345	0.200073	9.48459	0.002072
snp_02_7470132	snp_02_19304020	0.175575	6.78795	0.009178
snp_02_7470132	snp_02_19449660	0.175594	7.63077	0.005738
snp_02_7470132	snp_02_19513808	0.214758	10.3294	0.001309
snp_02_7470132	snp_02_19659783	0.20539	9.6267	0.001918
snp_02_7470132	snp_02_19685411	0.201984	9.82577	0.001721
snp_02_7470132	snp_02_19685438	0.205767	10.1654	0.001431
snp_02_7470132	snp_02_19685439	0.200081	9.76173	0.001782
snp_02_7743222	snp_02_15220376	0.218818	8.15087	0.004304
snp_02_7743222	snp_02_16487977	0.216815	7.92472	0.004877
snp_02_7743222	snp_02_16699331	0.317987	17.441	2.965E-05

snp_02_7743222	snp_02_17416587	0.206275	7.67224	0.005608
snp_02_7743222	snp_02_17781288	0.20254	7.76089	0.005339
snp_02_7743222	snp_02_18067425	0.210835	8.59424	0.003372
snp_02_7743222	snp_02_18098101	0.225565	9.54758	0.002002
snp_02_7743222	snp_02_18120796	0.189714	7.15638	0.00747
snp_02_7743222	snp_02_18290444	0.180428	6.68408	0.009728
snp_02_7743222	snp_02_18607827	0.203376	7.67716	0.005593
snp_02_7743222	snp_02_20082377	0.170338	7.23168	0.007163
snp_02_7743222	snp_02_20082383	0.191785	9.1265	0.002519
snp_02_7743222	snp_02_20082386	0.166792	6.7666	0.009288
snp_02_7761476	snp_02_16699331	0.316689	16.0415	6.2E-05
snp_02_7761476	snp_02_17781288	0.216561	8.82141	0.002977
snp_02_7761476	snp_02_17959252	0.203529	6.6657	0.009829
snp_02_7761476	snp_02_18067425	0.202245	7.55691	0.005978
snp_02_7761476	snp_02_19186803	0.17731	7.9199	0.00489
snp_02_7761476	snp_02_20037230	0.165679	7.04563	0.007946
snp_02_7761675	snp_02_16699331	0.306558	14.7095	0.0001255
snp_02_7761675	snp_02_17781288	0.198906	7.11949	0.007625
snp_02_7761675	snp_02_19186803	0.170234	7.18133	0.007367
snp_02_7857480	snp_02_19091002	0.19001	7.09991	0.007709
snp_02_7892495	snp_02_16699331	0.26385	10.6431	0.001105
snp_02_7892495	snp_02_20017486	0.182144	6.95722	0.008348
snp_02_10142051	snp_02_16699331	0.287376	10.0143	0.001553
snp_02_15101212	snp_02_17677891	-0.337436	7.82032	0.005166
snp_02_15101212	snp_02_19429943	0.204928	7.10575	0.007684
snp_02_15101212	snp_02_19568814	0.212368	7.09836	0.007716
snp_02_15106052	snp_02_18130541	0.286877	6.89712	0.008634
snp_02_15106052	snp_02_18385163	0.291197	6.64721	0.009931
snp_02_15106052	snp_02_19304020	0.198386	6.97839	0.00825

snp_02_15106052	snp_02_19429943	0.194168	6.75273	0.009361
snp_02_15106052	snp_02_19685411	0.193963	6.93328	0.008461
snp_02_15106052	snp_02_19685438	0.197371	7.16449	0.007436
snp_02_15106052	snp_02_19685439	0.189054	6.68944	0.009699
snp_02_15106300	snp_02_15789691	0.440386	8.01312	0.004644
snp_02_15106300	snp_02_18130541	0.257671	6.67232	0.009792
snp_02_15106300	snp_02_19429943	0.218735	8.47375	0.003603
snp_02_15106300	snp_02_19449660	0.204329	7.63085	0.005738
snp_02_15106300	snp_02_19513808	0.197274	7.6831	0.005574
snp_02_15106300	snp_02_19659783	0.193533	7.48724	0.006214
snp_02_15106300	snp_02_19685411	0.208922	8.34078	0.003877
snp_02_15106300	snp_02_19685438	0.212252	8.59086	0.003379
snp_02_15106300	snp_02_19685439	0.204104	8.08946	0.004452
snp_02_15106300	snp_02_19703249	0.196143	7.64846	0.005682
snp_02_15106300	snp_02_20017486	0.195179	7.09549	0.007728
snp_02_15106300	snp_02_21016307	0.181998	7.1139	0.007649
snp_02_15160683	snp_02_19062328	0.185998	6.7053	0.009613
snp_02_15160683	snp_02_19429943	0.194258	7.47669	0.00625
snp_02_15160683	snp_02_19659783	0.190357	8.05108	0.004548
snp_02_15160683	snp_02_19703249	0.207217	8.73914	0.003115
snp_02_15160683	snp_02_20017486	0.187507	7.04266	0.007959
snp_02_15160853	snp_02_16470423	0.316091	7.89508	0.004957
snp_02_15160853	snp_02_17600915	0.273207	7.94104	0.004833
snp_02_15160853	snp_02_17781288	0.27269	8.99756	0.002704
snp_02_15160853	snp_02_18092703	0.252349	7.5213	0.006097
snp_02_15160853	snp_02_18120796	0.27272	9.61742	0.001928
snp_02_15160853	snp_02_18385163	0.294889	9.07106	0.002597
snp_02_15160853	snp_02_19226636	0.216687	9.48467	0.002072
snp_02_15160853	snp_02_19429943	0.193458	7.36163	0.006663

snp_02_15160853	snp_02_19449660	0.183116	6.90203	0.00861
snp_02_15160853	snp_02_19456018	0.184265	6.93555	0.00845
snp_02_15160853	snp_02_19488040	0.215762	9.2591	0.002343
snp_02_15160853	snp_02_19488084	0.198166	7.60533	0.00582
snp_02_15160853	snp_02_19685411	0.188929	7.47246	0.006265
snp_02_15160853	snp_02_19685438	0.194254	7.85917	0.005056
snp_02_15160853	snp_02_19685439	0.184026	7.20803	0.007258
snp_02_15160853	snp_02_20037230	0.174494	6.84032	0.008912
snp_02_15160883	snp_02_15558985	0.295619	6.79142	0.00916
snp_02_15160883	snp_02_15894520	0.293255	6.83829	0.008922
snp_02_15160883	snp_02_16470322	0.385047	12.0346	0.0005223
snp_02_15160883	snp_02_16470423	0.420292	14.5603	0.0001358
snp_02_15160883	snp_02_16794771	0.252352	7.0438	0.007954
snp_02_15160883	snp_02_16962209	0.271129	6.79737	0.009129
snp_02_15160883	snp_02_17046347	0.268774	6.84867	0.008871
snp_02_15160883	snp_02_17593523	0.261111	7.04195	0.007962
snp_02_15160883	snp_02_17781288	0.296118	10.7165	0.001062
snp_02_15160883	snp_02_17959252	0.279361	7.33067	0.006779
snp_02_15160883	snp_02_18067425	0.227015	7.08454	0.007775
snp_02_15160883	snp_02_18092703	0.240076	6.73352	0.009462
snp_02_15160883	snp_02_18120796	0.245721	7.56676	0.005946
snp_02_15160883	snp_02_18290410	0.240652	8.21324	0.004159
snp_02_15160883	snp_02_18290444	0.240818	8.36076	0.003834
snp_02_15160883	snp_02_18385163	0.30443	8.88639	0.002873
snp_02_15160883	snp_02_18607827	0.261334	8.22545	0.004131
snp_02_15160883	snp_02_19226636	0.229235	10.5343	0.001172
snp_02_15160883	snp_02_19488040	0.231749	10.6938	0.001075
snp_02_15160883	snp_02_19488084	0.213654	8.84817	0.002934
snp_02_15160883	snp_02_20009271	0.179958	6.68978	0.009697

snp_02_15219832	snp_02_16699331	0.331876	6.75866	0.009329
snp_02_15219832	snp_02_19513808	0.225004	8.83805	0.00295
snp_02_15219832	snp_02_19703249	0.190197	7.14157	0.007532
snp_02_15286516	snp_02_16750570	0.334074	8.16422	0.004273
snp_02_15286516	snp_02_18067425	0.278735	7.26826	0.007018
snp_02_15286516	snp_02_18385163	0.309698	8.44519	0.00366
snp_02_15286516	snp_02_19513808	0.213011	7.01596	0.008079
snp_02_15286516	snp_02_19659783	0.194336	6.83844	0.008922
snp_02_15286516	snp_02_19703249	0.23178	9.31194	0.002277
snp_02_15400132	snp_02_19513808	0.206791	7.34268	0.006734
snp_02_15428873	snp_02_17600915	0.322758	7.82296	0.005159
snp_02_15428873	snp_02_18067425	0.266862	6.829	0.008969
snp_02_15428873	snp_02_19028834	0.206783	6.71824	0.009543
snp_02_15428873	snp_02_19062328	0.239185	10.2306	0.001381
snp_02_15428873	snp_02_19186685	0.190734	6.90829	0.00858
snp_02_15428873	snp_02_19186803	0.194112	7.06399	0.007865
snp_02_15428873	snp_02_19226636	0.200628	7.29971	0.006897
snp_02_15428873	snp_02_19304020	0.21695	8.23833	0.004102
snp_02_15428873	snp_02_19304085	0.202611	7.05489	0.007905
snp_02_15428873	snp_02_19429943	0.251812	11.6683	0.0006359
snp_02_15428873	snp_02_19449660	0.212595	9.26334	0.002338
snp_02_15428873	snp_02_19456018	0.211888	8.21572	0.004153
snp_02_15428873	snp_02_19487646	0.190902	7.06451	0.007863
snp_02_15428873	snp_02_19488040	0.200164	7.42941	0.006417
snp_02_15428873	snp_02_19488084	0.209176	8.05931	0.004527
snp_02_15428873	snp_02_19513808	0.193246	6.95203	0.008372
snp_02_15428873	snp_02_19659783	0.243346	12.5971	0.0003864
snp_02_15428873	snp_02_19682485	0.222868	8.63111	0.003305
snp_02_15428873	snp_02_19685411	0.233579	10.8128	0.001008

snp_02_15428873	snp_02_19685438	0.237118	11.1159	0.000856
snp_02_15428873	snp_02_19685439	0.227834	10.4519	0.001225
snp_02_15428873	snp_02_19703249	0.23063	10.8429	0.0009919
snp_02_15428873	snp_02_19713122	0.203717	7.28066	0.00697
snp_02_15428873	snp_02_19755401	0.196961	7.62223	0.005765
snp_02_15428873	snp_02_19764675	0.182038	6.78574	0.009189
snp_02_15428873	snp_02_19764769	0.181678	6.81473	0.009041
snp_02_15428873	snp_02_20037230	0.190433	7.67091	0.005612
snp_02_15428873	snp_02_21016307	0.181488	7.41404	0.006472
snp_02_15430882	snp_02_19062328	0.226352	8.3614	0.003833
snp_02_15430882	snp_02_19186685	0.245929	9.23285	0.002377
snp_02_15430882	snp_02_19226636	0.217148	7.33834	0.00675
snp_02_15430882	snp_02_19429943	0.20826	6.98392	0.008225
snp_02_15430882	snp_02_19449660	0.232632	8.80003	0.003012
snp_02_15430882	snp_02_19488040	0.229495	8.00959	0.004653
snp_02_15430882	snp_02_19488084	0.233142	8.34445	0.003869
snp_02_15430882	snp_02_19659783	0.217805	8.51724	0.003518
snp_02_15430884	snp_02_19062328	0.244019	9.62322	0.001921
snp_02_15430884	snp_02_19186685	0.260857	10.2401	0.001374
snp_02_15430884	snp_02_19226636	0.230857	8.15537	0.004294
snp_02_15430884	snp_02_19429943	0.227976	8.21438	0.004156
snp_02_15430884	snp_02_19449660	0.2467	9.7108	0.001832
snp_02_15430884	snp_02_19488040	0.244207	8.87039	0.002898
snp_02_15430884	snp_02_19488084	0.247706	9.22494	0.002388
snp_02_15430884	snp_02_19659783	0.233768	9.76662	0.001777
snp_02_15430884	snp_02_19764675	0.202408	7.50113	0.006166
snp_02_15430884	snp_02_19764769	0.202926	7.65164	0.005672
snp_02_15442082	snp_02_19062328	0.226125	9.83395	0.001713
snp_02_15442082	snp_02_19429943	0.205945	7.64382	0.005697

snp_02_15442082	snp_02_19488040	0.203908	7.65047	0.005676
snp_02_15442082	snp_02_19659783	0.186808	7.51814	0.006108
snp_02_15442082	snp_02_19703249	0.222587	10.4364	0.001236
snp_02_15452898	snp_02_19062328	0.198349	8.00212	0.004672
snp_02_15452898	snp_02_19226636	0.188937	6.75678	0.009339
snp_02_15452898	snp_02_19703249	0.199607	8.85837	0.002918
snp_02_15452898	snp_02_20037230	0.218228	10.0874	0.001493
snp_02_15512248	snp_02_16750570	0.303214	6.92686	0.008491
snp_02_15512248	snp_02_17416587	0.283258	6.79793	0.009126
snp_02_15512248	snp_02_18067425	0.276129	9.41729	0.00215
snp_02_15512248	snp_02_18290410	0.229682	6.76338	0.009305
snp_02_15512248	snp_02_18290444	0.222271	6.72054	0.009531
snp_02_15512248	snp_02_18385163	0.377249	14.53	0.000138
snp_02_15512248	snp_02_19429943	0.223965	8.88802	0.002871
snp_02_15512248	snp_02_19488040	0.201614	7.26088	0.007047
snp_02_15512248	snp_02_19488084	0.200066	7.21458	0.007231
snp_02_15512248	snp_02_19513808	0.183387	6.85383	0.008845
snp_02_15512248	snp_02_19685411	0.199083	8.14345	0.004322
snp_02_15512248	snp_02_19685438	0.202373	8.39206	0.003769
snp_02_15512248	snp_02_19685439	0.195025	7.94046	0.004834
snp_02_15512248	snp_02_19703249	0.188048	7.61213	0.005798
snp_02_15558985	snp_02_18385163	0.323113	9.85137	0.001697
snp_02_15558985	snp_02_19429943	0.213714	7.86221	0.005048
snp_02_15558985	snp_02_19659783	0.183535	6.85245	0.008852
snp_02_15558985	snp_02_19703249	0.186075	7.15722	0.007466
snp_02_15613607	snp_02_19186685	0.18982	7.10819	0.007673
snp_02_15613607	snp_02_19456018	0.185107	6.73666	0.009445
snp_02_15613607	snp_02_19488040	0.207949	8.8357	0.002954
snp_02_15613607	snp_02_19488084	0.208907	8.84632	0.002937

snp_02_15613607	snp_02_19685411	0.183391	7.03923	0.007974
snp_02_15613607	snp_02_19685438	0.186372	7.25288	0.007079
snp_02_15613607	snp_02_19685439	0.180045	6.88118	0.008711
snp_02_15613607	snp_02_19703249	0.175123	6.65644	0.00988
snp_02_15613607	snp_02_20009271	0.187894	7.42569	0.00643
snp_02_15659575	snp_02_16574548	0.309734	7.23755	0.00714
snp_02_15659575	snp_02_19429943	0.22965	10.4744	0.001211
snp_02_15659575	snp_02_19449660	0.199617	8.20402	0.00418
snp_02_15659575	snp_02_19456018	0.180737	6.673	0.009788
snp_02_15659575	snp_02_19488040	0.203792	8.51645	0.00352
snp_02_15659575	snp_02_19488084	0.201847	8.2762	0.004017
snp_02_15659575	snp_02_19513808	0.22439	10.5497	0.001162
snp_02_15659575	snp_02_19659783	0.19273	8.56071	0.003435
snp_02_15659575	snp_02_19685411	0.191223	7.8368	0.005119
snp_02_15659575	snp_02_19685438	0.193992	8.04814	0.004555
snp_02_15659575	snp_02_19685439	0.185755	7.53505	0.006051
snp_02_15659575	snp_02_19703249	0.222722	11.3607	0.0007503
snp_02_15659575	snp_02_19882259	0.198493	8.03985	0.004576
snp_02_15659575	snp_02_19882295	0.193837	7.70698	0.005501
snp_02_15659575	snp_02_19884473	0.18769	7.96644	0.004765
snp_02_15659575	snp_02_19966766	0.174073	6.77578	0.00924
snp_02_15659575	snp_02_20017433	0.200661	7.68502	0.005568
snp_02_15659575	snp_02_20017486	0.190408	7.75043	0.00537
snp_02_15659575	snp_02_20037230	0.209065	10.2899	0.001338
snp_02_15659575	snp_02_20082383	0.178413	7.12344	0.007608
snp_02_15760177	snp_02_16574548	0.322202	7.51114	0.006132
snp_02_15760177	snp_02_18290410	0.247126	7.20746	0.00726
snp_02_15760177	snp_02_18290444	0.243696	7.40827	0.006493
snp_02_15760177	snp_02_18825660	0.237867	7.13691	0.007551

snp_02_15760177	snp_02_19062328	0.215117	9.26723	0.002333
snp_02_15760177	snp_02_19186685	0.19211	7.60806	0.005811
snp_02_15760177	snp_02_19186803	0.215646	9.44494	0.002117
snp_02_15760177	snp_02_19226636	0.193971	7.47414	0.006259
snp_02_15760177	snp_02_19304020	0.193757	6.84345	0.008897
snp_02_15760177	snp_02_19304085	0.200076	7.2255	0.007188
snp_02_15760177	snp_02_19429943	0.196331	7.3526	0.006697
snp_02_15760177	snp_02_19488040	0.19571	7.49186	0.006198
snp_02_15760177	snp_02_19488084	0.19669	7.50233	0.006162
snp_02_15760177	snp_02_19513808	0.198645	7.884	0.004988
snp_02_15760177	snp_02_19659783	0.209876	9.55475	0.001994
snp_02_15760177	snp_02_19703249	0.191154	7.9121	0.004911
snp_02_15760177	snp_02_19966766	0.175105	6.71575	0.009557
snp_02_15760177	snp_02_20009271	0.177675	6.8698	0.008767
snp_02_15760177	snp_02_20017408	0.1988	7.76928	0.005314
snp_02_15760177	snp_02_20017433	0.207657	8.28339	0.004001
snp_02_15760177	snp_02_20037230	0.214141	10.1999	0.001405
snp_02_15760221	snp_02_19186803	0.204524	8.39376	0.003765
snp_02_15760221	snp_02_19513808	0.189057	7.15901	0.007459
snp_02_15760221	snp_02_19659783	0.195159	8.09826	0.004431
snp_02_15760221	snp_02_19703249	0.181967	7.10768	0.007676
snp_02_15760221	snp_02_20037230	0.189745	7.7963	0.005235
snp_02_15760221	snp_02_21016307	0.183913	7.97548	0.004742
snp_02_15789691	snp_02_16750570	0.316727	6.8568	0.008831
snp_02_15789691	snp_02_19186685	0.199601	8.02336	0.004618
snp_02_15789691	snp_02_19226636	0.199946	6.96877	0.008295
snp_02_15789691	snp_02_19304020	0.244095	10.3464	0.001297
snp_02_15789691	snp_02_19304085	0.231056	9.12674	0.002519
snp_02_15789691	snp_02_19429943	0.22654	9.12336	0.002524

snp_02_15789691	snp_02_19449660	0.207146	8.08362	0.004467
snp_02_15789691	snp_02_19488040	0.204567	7.43928	0.006382
snp_02_15789691	snp_02_19488084	0.202824	7.23561	0.007147
snp_02_15789691	snp_02_19659783	0.206791	8.885	0.002875
snp_02_15789691	snp_02_19685411	0.200772	8.17171	0.004255
snp_02_15789691	snp_02_19685438	0.203628	8.29909	0.003967
snp_02_15789691	snp_02_19685439	0.195855	7.79016	0.005253
snp_02_15789691	snp_02_19703249	0.202718	8.18706	0.004219
snp_02_15789691	snp_02_19764675	0.188581	7.35876	0.006674
snp_02_15789691	snp_02_19764769	0.186045	7.24832	0.007097
snp_02_15789691	snp_02_20017486	0.214186	8.77389	0.003056
snp_02_15789691	snp_02_20037230	0.193821	7.75892	0.005345
snp_02_15789691	snp_02_21016307	0.220355	11.295	0.0007773
snp_02_15876071	snp_02_16750570	0.343109	7.35405	0.006691
snp_02_15876071	snp_02_18067425	0.249828	6.78149	0.009211
snp_02_15876071	snp_02_19062328	0.281273	13.154	0.000287
snp_02_15876071	snp_02_19186685	0.209094	8.03873	0.004579
snp_02_15876071	snp_02_19304020	0.223612	7.82956	0.00514
snp_02_15876071	snp_02_19304085	0.23213	8.38841	0.003776
snp_02_15876071	snp_02_19429943	0.203779	7.36157	0.006663
snp_02_15876071	snp_02_19449660	0.204764	7.955	0.004796
snp_02_15876071	snp_02_19513808	0.240139	10.0936	0.001488
snp_02_15876071	snp_02_19659783	0.205921	8.60083	0.00336
snp_02_15876071	snp_02_19685411	0.204011	7.46753	0.006282
snp_02_15876071	snp_02_19685438	0.20749	7.70421	0.005509
snp_02_15876071	snp_02_19685439	0.200036	7.2727	0.007001
snp_02_15876071	snp_02_19703249	0.250963	12.348	0.0004415
snp_02_15876071	snp_02_19764675	0.185178	6.7907	0.009163
snp_02_15876071	snp_02_19764769	0.203964	8.38978	0.003773

snp_02_15876071	snp_02_19882259	0.196272	7.14211	0.00753
snp_02_15876071	snp_02_19882295	0.200952	7.52718	0.006078
snp_02_15894520	snp_02_19186685	0.206473	7.84986	0.005083
snp_02_15894520	snp_02_19429943	0.209799	7.83779	0.005117
snp_02_15894520	snp_02_19659783	0.218811	9.6574	0.001886
snp_02_15935358	snp_02_18130541	0.270268	8.16668	0.004267
snp_02_15990619	snp_02_18130541	0.268966	6.94872	0.008388
snp_02_16074185	snp_02_17218097	0.308757	7.07445	0.007819
snp_02_16074185	snp_02_19062328	0.235705	9.99005	0.001574
snp_02_16074185	snp_02_19186803	0.195956	6.6448	0.009945
snp_02_16074185	snp_02_19429943	0.211975	7.06665	0.007853
snp_02_16074185	snp_02_19614069	0.198448	7.35219	0.006698
snp_02_16074185	snp_02_19703249	0.24234	11.5396	0.0006814
snp_02_16074185	snp_02_20017408	0.194214	7.28498	0.006953
snp_02_16074185	snp_02_20017433	0.20463	7.87508	0.005012
snp_02_16074185	snp_02_20017486	0.201766	7.72515	0.005446
snp_02_16074185	snp_02_20037230	0.183186	6.81327	0.009048
snp_02_16328549	snp_02_18067425	0.276327	7.25502	0.00707
snp_02_16328549	snp_02_19304020	0.196844	7.03426	0.007997
snp_02_16328549	snp_02_19449660	0.204842	8.02734	0.004608
snp_02_16328549	snp_02_19659783	0.178969	6.69075	0.009691
snp_02_16473086	snp_02_19429943	0.198388	6.9564	0.008352
snp_02_16473118	snp_02_19429943	0.195708	6.75769	0.009335
snp_02_16487977	snp_02_19429943	0.232684	8.7946	0.003021
snp_02_16487977	snp_02_19659783	0.193548	7.0147	0.008084
snp_02_16699331	snp_02_17271333	0.283677	7.21507	0.007229
snp_02_16699331	snp_02_19186685	0.192164	7.23128	0.007165
snp_02_16699331	snp_02_19429943	0.203581	6.71272	0.009573
snp_02_16699331	snp_02_19703249	0.202972	8.12046	0.004377

snp_02_16699586	snp_02_19186685	0.21489	7.74772	0.005378
snp_02_16699586	snp_02_19659783	0.188762	6.99707	0.008164
snp_02_16699608	snp_02_19659783	0.181134	7.16739	0.007424
snp_02_16699608	snp_02_20017486	0.18925	6.98546	0.008218
snp_02_16810236	snp_02_19186685	0.192986	7.16816	0.007421
snp_02_16810236	snp_02_19429943	0.207627	8.01249	0.004646
snp_02_16810236	snp_02_19513808	0.215827	8.24844	0.004079
snp_02_16810236	snp_02_19659783	0.181619	7.0892	0.007755
snp_02_17022010	snp_02_18385163	0.349286	7.06902	0.007843
snp_02_17022047	snp_02_18385163	0.35627	7.38036	0.006594
snp_02_17037081	snp_02_19429943	0.228561	8.53107	0.003491
snp_02_17046347	snp_02_19186685	0.213323	7.88876	0.004974
snp_02_17046347	snp_02_19487646	0.231591	8.38815	0.003777
snp_02_17046347	snp_02_19659783	0.191677	7.10505	0.007687
snp_02_17046347	snp_02_19966766	0.226178	9.49138	0.002065
snp_02_17046347	snp_02_20009271	0.256381	12.3051	0.0004518
snp_02_17217858	snp_02_19186685	0.223818	8.9579	0.002763
snp_02_17218097	snp_02_17593523	0.451765	12.0519	0.0005175
snp_02_17218097	snp_02_17600915	0.342426	8.00314	0.00467
snp_02_17218097	snp_02_17781288	0.416933	11.7679	0.0006027
snp_02_17218097	snp_02_17959252	0.342107	7.48159	0.006233
snp_02_17218097	snp_02_17986693	0.354564	7.44024	0.006378
snp_02_17218097	snp_02_18092703	0.360932	9.98657	0.001577
snp_02_17218097	snp_02_18098101	0.320177	6.96154	0.008328
snp_02_17218097	snp_02_18120796	0.301014	8.04381	0.004566
snp_02_17218097	snp_02_18290410	0.285377	6.96994	0.008289
snp_02_17218097	snp_02_18385163	0.363507	9.24164	0.002366
snp_02_17218097	snp_02_19685411	0.200973	7.64347	0.005698
snp_02_17218097	snp_02_19685438	0.203131	7.66546	0.005629

snp_02_17218097	snp_02_19685439	0.195134	7.21856	0.007215
snp_02_17218127	snp_02_17593523	0.419843	10.7267	0.001056
snp_02_17218127	snp_02_17600915	0.306386	6.76095	0.009317
snp_02_17218127	snp_02_17781288	0.397662	11.1066	0.0008603
snp_02_17218127	snp_02_17959252	0.322561	7.03354	0.008
snp_02_17218127	snp_02_17986693	0.360931	8.32363	0.003913
snp_02_17218127	snp_02_18092703	0.365397	10.6594	0.001095
snp_02_17218127	snp_02_18098101	0.33533	7.64324	0.005699
snp_02_17218127	snp_02_18120796	0.296068	8.23915	0.0041
snp_02_17218127	snp_02_18385163	0.361922	9.66187	0.001881
snp_02_17218127	snp_02_19429943	0.202728	6.66966	0.009807
snp_02_17218127	snp_02_19685411	0.199695	7.73255	0.005424
snp_02_17218127	snp_02_19685438	0.201855	7.75312	0.005362
snp_02_17218127	snp_02_19685439	0.193806	7.29595	0.006911
snp_02_17258929	snp_02_18092703	0.419356	7.52735	0.006077
snp_02_17258929	snp_02_18290444	0.287833	6.86841	0.008773
snp_02_17258929	snp_02_18385163	0.509566	10.8066	0.001011
snp_02_17258929	snp_02_19659783	0.190494	6.79645	0.009134
snp_02_17258984	snp_02_18385163	0.478193	9.68524	0.001858
snp_02_17258984	snp_02_19659783	0.196507	7.0825	0.007784
snp_02_17259533	snp_02_18067425	0.290783	7.91165	0.004912
snp_02_17259533	snp_02_19659783	0.197316	7.94987	0.004809
snp_02_17259650	snp_02_19304020	0.216046	7.50843	0.006141
snp_02_17259650	snp_02_19429943	0.221836	7.15873	0.00746
snp_02_17259650	snp_02_19449660	0.190918	6.81044	0.009063
snp_02_17259650	snp_02_19659783	0.226871	10.7926	0.001019
snp_02_17259650	snp_02_20017486	0.212543	8.90796	0.002839
snp_02_17271281	snp_02_18067425	0.278902	7.5499	0.006001
snp_02_17271281	snp_02_18385163	0.327344	7.85558	0.005067

snp_02_17271281	snp_02_19685411	0.200707	7.66603	0.005627
snp_02_17271281	snp_02_19685438	0.203431	7.85633	0.005064
snp_02_17271281	snp_02_19685439	0.195857	7.42652	0.006427
snp_02_17271281	snp_02_19703249	0.196421	7.74982	0.005372
snp_02_17271333	snp_02_17600915	0.299069	7.11293	0.007653
snp_02_17271333	snp_02_18067425	0.306676	8.72876	0.003132
snp_02_17271333	snp_02_18385163	0.308328	7.15489	0.007476
snp_02_17271333	snp_02_19685438	0.185529	6.65707	0.009876
snp_02_17271333	snp_02_19703249	0.197809	7.92662	0.004871
snp_02_17416587	snp_02_17593523	0.310519	6.75371	0.009355
snp_02_17446176	snp_02_17600915	0.341103	9.48012	0.002077
snp_02_17446176	snp_02_18067425	0.319694	7.47705	0.006249
snp_02_17446176	snp_02_19429943	0.218075	8.80916	0.002997
snp_02_17446176	snp_02_19449660	0.196023	7.36961	0.006634
snp_02_17446176	snp_02_19659783	0.186126	7.26528	0.00703
snp_02_17446176	snp_02_21016307	0.175492	7.00762	0.008116
snp_02_17446330	snp_02_17600915	0.30903	9.68288	0.00186
snp_02_17446330	snp_02_18067425	0.287077	7.47849	0.006244
snp_02_17446330	snp_02_18385163	0.278851	7.07202	0.00783
snp_02_17446330	snp_02_19429943	0.209103	8.47152	0.003608
snp_02_17446330	snp_02_19449660	0.193553	7.45957	0.00631
snp_02_17446330	snp_02_19659783	0.181224	7.20103	0.007286
snp_02_17503963	snp_02_18385163	0.317446	6.92722	0.008489
snp_02_17600915	snp_02_19062328	0.22273	7.41618	0.006464
snp_02_17600915	snp_02_19703249	0.189375	6.76579	0.009292
snp_02_17677857	snp_02_17677891	-0.477266	7.02282	0.008048
snp_02_17677891	snp_02_17677905	-0.548226	8.03874	0.004579
snp_02_17677891	snp_02_18240771	-0.504732	7.43294	0.006404
snp_02_17677891	snp_02_18240912	-0.513	7.67122	0.005611

snp_02_17889038	snp_02_19304020	0.221489	6.70461	0.009616
snp_02_17959252	snp_02_18067425	0.332635	7.12184	0.007615
snp_02_17959252	snp_02_19429943	0.221099	7.76716	0.005321
snp_02_17959252	snp_02_19659783	0.195435	7.12856	0.007587
snp_02_18067425	snp_02_19186685	0.267364	12.6243	0.0003808
snp_02_18067425	snp_02_19703249	0.203232	7.7202	0.005461
snp_02_18067425	snp_02_19860601	0.208081	8.02423	0.004616
snp_02_18098101	snp_02_19860601	0.192025	7.01883	0.008066
snp_02_18098101	snp_02_19966766	0.187912	7.29198	0.006926
snp_02_18120796	snp_02_19186685	0.246261	10.2738	0.001349
snp_02_18290410	snp_02_18385163	0.345928	6.81874	0.009021
snp_02_18290410	snp_02_19429943	0.210183	6.99627	0.008168
snp_02_18290410	snp_02_19703249	0.197629	7.59478	0.005854
snp_02_18290444	snp_02_18385163	0.341594	6.91592	0.008543
snp_02_18290444	snp_02_19703249	0.190154	7.1876	0.007341
snp_02_18385163	snp_02_19304020	0.22542	7.28801	0.006942
snp_02_18385163	snp_02_19304085	0.217331	6.69066	0.009692
snp_02_18481164	snp_02_19882259	0.197089	6.73213	0.009469
snp_02_18481164	snp_02_20017433	0.197132	7.14137	0.007533
snp_02_18481164	snp_02_20037230	0.207717	7.95661	0.004791
snp_02_18481231	snp_02_19186685	0.204586	7.4302	0.006414
snp_02_18481231	snp_02_19487646	0.20165	6.74454	0.009404
snp_02_18481231	snp_02_19882259	0.208148	7.49265	0.006195
snp_02_18481231	snp_02_20017433	0.207133	7.7486	0.005376
snp_02_18481231	snp_02_20037230	0.212278	8.2511	0.004073
snp_02_18711010	snp_02_19186685	0.231048	8.67812	0.003221
snp_02_18711211	snp_02_19186685	0.221671	7.82277	0.005159
snp_02_18817286	snp_02_20017433	0.213995	6.96504	0.008312
snp_02_18817478	snp_02_19186685	0.211109	6.77725	0.009233

snp_02_18817478	snp_02_20017433	0.22116	7.43563	0.006395
snp_02_18825659	snp_02_18825730	0.42191	6.72878	0.009487
snp_02_18825659	snp_02_19429943	0.241384	7.93862	0.004839
snp_02_18825659	snp_02_19882295	0.201768	6.73092	0.009476
snp_02_18825659	snp_02_20017433	0.224715	8.17149	0.004256
snp_02_18825659	snp_02_20019434	0.215085	6.70253	0.009628
snp_02_18825659	snp_02_20037230	0.219671	8.4256	0.0037
snp_02_18825660	snp_02_18846852	0.277229	7.00597	0.008124
snp_02_18825660	snp_02_19091002	0.326886	7.44942	0.006346
snp_02_18825730	snp_02_18845763	0.306788	6.7607	0.009319
snp_02_18825730	snp_02_19091002	0.298523	6.76	0.009322
snp_02_18825730	snp_02_19186685	0.227418	7.8619	0.005049
snp_02_18825730	snp_02_19429943	0.274052	10.1784	0.001421
snp_02_18825730	snp_02_19614069	0.234714	8.3533	0.00385
snp_02_18825730	snp_02_19659783	0.208657	8.1983	0.004193
snp_02_18825730	snp_02_19882259	0.204266	6.68266	0.009736
snp_02_18825730	snp_02_19882260	0.200727	6.66802	0.009816
snp_02_18825730	snp_02_19882295	0.215318	7.52128	0.006098
snp_02_18825730	snp_02_20017433	0.242918	9.71999	0.001823
snp_02_18825730	snp_02_20017486	0.204851	7.487	0.006215
snp_02_18825730	snp_02_20019434	0.219004	6.90899	0.008576
snp_02_18825730	snp_02_20037230	0.234346	9.57356	0.001974
snp_02_18825730	snp_02_21016307	0.177239	6.94744	0.008394
snp_02_18845763	snp_02_20037230	0.206412	7.62628	0.005752
snp_02_18845763	snp_02_21016307	0.175245	6.86705	0.00878
snp_02_18846101	snp_02_20017433	0.207454	7.2979	0.006904
snp_02_18846852	snp_02_19614069	0.209206	7.53765	0.006042
snp_02_18846852	snp_02_20017433	0.194843	6.71613	0.009555
snp_02_18846852	snp_02_20017486	0.218617	9.35205	0.002227

snp_02_18848592	snp_02_20017433	0.224692	7.89882	0.004947
snp_02_19163651	snp_02_19186685	0.293386	7.80289	0.005216
snp_02_19186685	snp_02_19487646	0.259301	7.52121	0.006098
snp_02_19186685	snp_02_19614069	0.266706	8.73714	0.003118
snp_02_19186685	snp_02_19659783	0.228795	6.71715	0.009549
snp_02_19186685	snp_02_19755401	0.232457	6.69495	0.009669
snp_02_19186685	snp_02_20082377	0.227971	8.0259	0.004611
snp_02_19186685	snp_02_20082383	0.22866	8.32243	0.003916
snp_02_19186685	snp_02_20082386	0.238601	9.02683	0.002661
snp_02_19304020	snp_02_19614069	0.256676	7.08978	0.007753
snp_02_19304020	snp_02_19764675	0.273969	8.63915	0.00329
snp_02_19429943	snp_02_19513808	0.299214	7.22609	0.007185
snp_02_19429943	snp_02_20767401	0.223135	7.32203	0.006812
snp_02_19429943	snp_02_20767410	0.226915	7.41334	0.006474
snp_02_19449660	snp_02_20767401	0.226239	7.40287	0.006512
snp_02_19449660	snp_02_20767410	0.230613	7.6909	0.00555
snp_02_19456018	snp_02_20082383	0.228135	6.99701	0.008165
snp_02_19456018	snp_02_20082386	0.240865	7.81711	0.005176
snp_02_19614069	snp_02_19764675	0.3529	9.88318	0.001668
snp_02_19659783	snp_02_20082377	0.284894	9.41222	0.002156
snp_02_19659783	snp_02_20082383	0.253947	7.64984	0.005678
snp_02_19659783	snp_02_20082386	0.26543	8.70715	0.00317
snp_02_19659783	snp_02_20082615	0.229539	7.14191	0.00753
snp_02_19755401	snp_02_20082386	0.256965	7.1013	0.007703
snp_02_19860601	snp_02_20082386	0.261596	6.80002	0.009116
snp_02_20009271	snp_02_20082377	0.329039	10.0437	0.001529
snp_02_20009271	snp_02_20082383	0.317478	9.51938	0.002033
snp_02_20009271	snp_02_20082386	0.33627	10.8706	0.0009772
snp_02_20009271	snp_02_20082615	0.289318	8.26809	0.004035

snp_02_20017292	snp_02_20037230	0.340956	9.26805	0.002332

Table S5. Candidate genes from significant QTLs based on BSA-seq analysis and targeted association analysis of recombinant inbred lines.

QTL	Locus	Annotation	PVE (%) after targeted association analysis			Top SNPs	SNP position	Superior allele/s			Inferior allele/s		
			GI	AC	PC			Low GI	Low AC	High PC	High GI	High AC	Low PC
qseqPC2.2	LOC_Os02g25930	retrotransposon			3.8316	snp_02_15220376	exonic (nonsynonymous)	TGG	CAC	C/TGG or TGG	CA/GG or CAC	TGG	CGC/G
				15.6599		snp_02_15219832 snp_02_15219922 snp_02_15220376							
			10.2007			snp_02_15219832							
qseqPC2.2	LOC_Os02g26840	Membrane-bound O-acyltransferase; similar to Wax synthase isoform 1			3.0375	snp_02_15760177 snp_02_15760221	exonic (nonsynonymous) exonic (synonymous)	GG	TA or T/GA/G	GG	TA or T/GA/G	GG	TA
				14.6813									
			11.0165										
qseqPC2.2	LOC_Os02g27000	OsMORC4; microchidia protein 4			5.5138	snp_02_15876071	UTR3	T	C	T	C	T	C
				13.0116									
			11.4974										
qseqPC2.2	LOC_Os02g28420	Pong sub-class transposon			4.2435	snp_02_16810236	exonic (nonsynonymous)	T	C	T	C or C/T	T	C
				15.3939									
			11.9259										
qseqAC2.2, qseqPC2.2	LOC_Os02g29070	cyclin-dependent kinase; tyrosine or lipopolysaccharide kinase			5.0289	snp_02_17217858	exonic (nonsynonymous)	CTGC	TCAT	CC/TA/ GT/C or CTGC	TCAT	CTGC	CCAT or TCAT
				18.0165		snp_02_17218097 snp_02_17218127	exonic (synonymous)						
			10.7473			snp_02_17218076 snp_02_17218097 snp_02_17218127	exonic (synonymous)						

qseqAC2.2, qseqPC2.2	LOC_Os02g29370	Mariner sub-class transposon			5.611	snp_02_17446176 snp_02_17446330	upstream	CT	TC	CT	TT, TC, or T/CC/T	CT	TC
				15.297									
			13.5987										
qseqAC2.2, qseqPC2.2	LOC_Os02g30210	*OsFBK7*; Galactose oxidase, beta-propeller			4.6291	snp_02_17959252	exonic (nonsynonymous)	A	C	A	C	A	C
				12.6964									
			11.6581										
qseqAC2.2, qseqPC2.2	LOC_Os02g30940	Uncharacterized DUF1677			3.9592	snp_02_18481164 snp_02_18481231	exonic (nonsynonymous)	AGT	C/ AGC/T or CAC	AGT	CAC	AGT	CA/GC
				17.1042		snp_02_18481164 snp_02_18481190 snp_02_18481231	exonic (nonsynonymous) exonic (nonsynonymous exonic (synonymous)						
			14.0331				exonic						
qGI2.1, qseqAC2.2, qseqPC2.2	LOC_Os02g32660	OsSBEIIb; starch branching enzyme IIb	57.82	59.1407	7.9419	snp_02_19362520	exon-intron junction	A	G	A	G	A	G

Table S6.1 Putative metabolites detected in negative mode for HAHP and LALP F5-derived F6 RILs.

m/z	RT [min]	Molecular Weight	Compound name	QC_1	QC_2	QC_3	HAHP1	HAHP2	HAHP3	LALP1	LALP2	LALP3
87.0074	0.812	88.01485	Pyruvic acid	2971.1014	2943.7646	2869.0883	1570.2205	2603.6087	1410.9737	3028.6423	3355.6461	4274.7051
89.02305	0.815	90.03048	L-Lactic acid	367.78657	374.42063	330.86793	416.90908	396.22568	309.32433	282.03002	267.00506	369.72788
94.97953	0.863	95.98686	Silicic acid	35.598277	32.685672	39.431852	34.5227	37.624354	47.294076	45.72856	59.386825	57.608275
96.96827	0.865	97.97556	Phosphate	4963.1768	5101.8622	4931.5414	4664.1113	5020.8519	4536.8525	4095.3354	4657.0094	6024.1997
103.00237	0.837	104.00976	Malonic acid	139.23454	132.88352	128.3369	207.40363	182.51301	202.20415	123.01623	235.64482	141.65202
111.00747	1.217	112.01475	2-Furoic acid	296.55319	292.68581	322.45888	439.60179	250.99798	272.68987	119.08194	169.4565	171.3057
111.01866	0.817	112.0263	Uracil	321.87315	296.11879	308.67385	396.52976	429.63923	279.80492	194.09741	249.97114	228.03387
114.0548	0.806	115.06231	L-Proline	65.357202	71.196062	65.918851	69.71384	78.464255	70.297523	90.8045	66.038249	71.983189
115.00239	0.812	116.00969	Maleic acid	128.85513	128.64123	109.14247	74.722673	161.36703	139.8161	171.2778	143.67144	176.6485
115.03882	1.995	116.04611	Levulinic acid	57.787785	68.551073	50.33577	50.75918	46.215611	61.31359	200.83936	114.90877	147.09463
116.07045	14.557	117.07773	L-Valine	70.422818	72.531744	70.265138	80.737279	69.546846	117.89148	54.906214	87.326268	89.942625
117.01816	1.425	118.02538	Methylmalonic acid	225.79782	233.57242	237.87793	282.36873	239.47878	197.2025	338.55249	244.11206	216.55508
117.05446	3.18	118.06177	2-Methyl-3-hydroxybutyric acid	73.039728	71.730663	72.585133	59.275106	52.305928	42.877159	40.696796	52.841544	36.759259
119.03374	0.8	120.04139	Erythrose	663.96274	515.51702	681.14391	497.25725	756.70134	360.99727	241.87504	253.83259	672.2797
119.04906	4.617	120.05632	Phenylacetaldehyde	88.811898	89.998295	81.727189	68.30627	99.844701	70.851511	112.53598	94.736341	82.01818
121.02831	4.381	122.0356	Benzoic acid	341.84572	383.6249	277.78545	268.59997	514.58366	461.9026	358.17219	445.05358	265.55656
122.02354	1.231	123.0308	Nicotinic acid	169.97061	125.47412	141.84126	223.78068	107.50263	119.03374	79.12494	153.84941	147.79006
128.03409	1.231	129.04139	Pyroglutamic acid	1121.5522	1074.6007	1172.5273	1742.3257	1358.0421	1179.0854	782.88707	1005.65	1130.9562
129.01816	0.8	130.02538	Citraconic acid	1421.593	1564.3772	1270.0418	1794.2587	1452.6469	1427.1539	716.12911	1113.8485	1228.3653
130.0498	0.81	131.05733	N-Acetyl-L-alanine	143.49904	145.0819	130.62515	181.43953	156.70903	137.6985	136.57353	158.32796	133.63996
130.08614	1.331	131.09345	Leucine	178.06962	174.22467	177.26872	360.40768	207.89997	159.11642	120.25805	129.24256	140.70768
131.04504	0.729	132.05232	L-Asparagine	1910.0191	2119.6111	1933.1324	1727.2512	2009.7071	2958.0112	1538.7412	1898.3222	2197.3282
131.07025	4.301	132.07751	6-Hydroxycaproic acid	338.59199	342.13	311.57719	236.98006	175.23747	115.05906	121.45137	161.11266	139.91503
132.02902	0.876	133.03629	L-Aspartic acid	801.65791	199.33602	1002.4597	2453.4246	2353.9716	1674.901	874.0577	1522.1866	1508.4412
133.01309	0.811	134.02038	Malic acid	3026.0816	3001.8825	2929.0189	1529.6452	2694.9041	1476.1396	3181.4465	3456.808	4416.1273
179.05531	0.802	134.05709	Deoxyribose	603.07008	470.37418	575.79065	443.32217	698.19649	325.04648	219.48214	222.9208	632.23818
134.04596	1.505	135.05333	Adenine	56.919528	54.56575	51.945123	89.257249	55.145963	66.946224	49.815941	72.887614	60.432366
135.02876	0.841	136.03641	Threonic acid	6902.3685	7635.3792	7956.2956	7341.8832	10183.682	8557.6049	6560.9179	9658.1997	9584.9591
137.02328	5.457	138.0306	Salicylic acid	583.95988	642.49348	554.63253	821.47099	454.44042	490.1333	454.2676	552.20339	592.78957
137.03455	1.258	138.0418	Urocanic acid	13.550317	11.875058	15.725494	15.514168	14.165584	22.1778	12.241563	17.020604	17.759108

144.0291	0.845	145.03644	2-Keto-glutaramic acid	198.20914	205.42312	201.10856	259.1076	188.41701	251.21298	154.4724	210.45636	176.97248
144.06551	0.794	145.07322	Allysine	111.28408	107.15768	104.58588	129.2896	112.67887	105.52374	115.61596	121.18207	130.21257
145.01311	0.799	146.02078	Oxoglutaric acid	27626.545	28296.085	22846.902	46998.593	28734.384	29938.321	13160.095	23226.68	26768.106
145.04953	3.137	146.05685	Adipic acid	167.80032	180.19336	154.31866	152.01426	131.19577	183.40575	196.88597	156.95332	180.6561
146.04478	0.785	147.05206	L-Glutamic acid	1168.4692	970.6961	1159.1361	1864.8593	1334.1595	1720.6557	1674.7489	1099.8114	1042.8004
147.02884	0.8	148.03617	Citramalic acid	210.64539	216.48242	193.91685	185.51942	159.9473	153.7226	144.72557	111.07648	169.02387
147.06526	1.53	148.07254	Mevalonic acid	61.634341	68.819681	58.528421	49.02953	30.676902	61.684176	34.598987	38.711475	34.253247
148.04272	1.231	149.05	L-Methionine	23.405296	21.242899	23.665229	34.639125	24.345014	26.013847	17.979852	17.88894	19.817875
149.00818	14.684	150.01543	Tartaric acid	131.97912	88.173065	124.65053	168.03326	118.235	172.82186	77.961555	174.3156	172.73225
149.04437	0.773	150.05201	Xylose	6868.3525	7797.5203	8081.4547	7407.3218	10289.927	8646.5879	6705.4283	9780.8004	9684.3952
151.03903	4.727	152.04635	Vanillin	84.083549	87.472	88.161903	159.89998	123.01026	85.772334	89.858023	68.349449	106.48399
151.06015	0.798	152.06754	L-Arabitol	450.9738	562.62403	375.43484	429.95153	101.71002	902.96271	211.48909	107.79461	276.12038
153.01833	4.22	154.02563	Gentisic acid	274.5955	252.18155	284.20248	386.14236	239.2667	315.25288	307.99397	280.51884	261.78774
154.06111	0.72	155.06847	L-Histidine	169.66624	185.8478	167.06947	255.37738	191.3574	184.58851	78.129256	154.08255	157.55854
157.03574	0.814	158.04297	Allantoin	935.71063	895.93897	941.48863	1199.4603	1086.8292	943.81097	593.36832	883.18284	895.20364
159.02879	0.797	160.03648	Oxoadipic acid	281.04868	287.91077	274.47229	193.50033	321.18152	265.14049	276.9595	297.96221	315.7605
159.06535	3.896	160.07263	Pimelic acid	261.70281	196.2688	299.29014	229.23452	243.91034	275.04373	244.80001	388.41568	264.38997
160.06061	0.811	161.0679	Aminoadipic acid	211.71132	209.43125	233.56416	239.82696	254.46546	240.84705	201.06552	197.40513	216.34612
162.01863	1.458	163.02648	Acetylcysteine	1887.6946	1943.3276	1917.8971	761.19193	1174.5639	1441.944	3109.29	2463.6756	2526.2534
164.07074	2.311	165.07805	L-Phenylalanine	326.32124	197.41967	212.33298	288.95313	216.90471	207.32557	169.68573	333.33779	189.3344
165.01839	3.909	166.02567	Phthalic acid	57.081956	52.975612	49.778641	40.598977	123.86844	4810.8465	118.64119	98.516409	80.169905
165.03946	0.765	166.0468	L-Xylonic acid	1534.5928	1277.6538	1641.6516	655.15524	1441.2686	1117.7263	1155.8386	1193.6298	1235.6946
165.05478	4.756	166.06205	3-Phenyllactic acid	53.021062	54.696381	51.852798	11.214254	9.7055531	8.3836269	10.964253	7.228318	9.7246214
165.07597	0.817	166.08314	Rhamnitol	12.993282	15.921097	10.932744	9.5112537	12.745106	8.7392965	12.95766	12.962153	8.6842312
166.01697	0.864	167.02429	Homocysteinesulfinic acid	114.95268	88.852128	144.13871	106.55695	114.64693	107.47808	171.40951	173.04224	180.299
169.01331	14.491	170.02056	Gallic acid	23.268607	13.671524	29.080252	29.870421	14.510236	19.285161	16.124395	18.676256	21.689504
171.00551	0.857	172.01273	Glycerol 3-phosphate	276.14409	270.91643	275.79154	325.0219	322.72185	350.96212	300.75155	401.89838	361.87995
171.10175	5.935	172.10908	Butyl levulinate	174.52765	154.59337	210.52956	164.96142	400.11778	350.2693	161.59576	143.27218	116.06543
172.06068	0.824	173.0681	N-Acetyl-L-glutamate 5-semialdehyde	121.66687	122.77357	123.67634	127.322	137.10042	135.14848	111.07717	120.05265	109.73152
173.00822	0.801	174.01556	Dehydroascorbic acid	460.96005	376.10761	535.47227	741.48805	540.31279	507.71949	267.10918	317.60368	424.2712
173.08109	4.619	174.08836	Suberic acid	198.58641	205.66798	194.99315	282.47549	292.72758	348.32004	289.09694	222.59964	223.96387
173.10347	0.709	174.11082	L-Arginine	318.01111	329.48819	306.34915	553.39424	370.13421	327.72659	202.4214	350.25198	314.6999
173.11751	5.447	174.12475	3-Hydroxynonanoic acid	85.320118	81.542401	88.710796	117.97175	244.21486	104.99295	57.625203	84.210314	95.307894

174.05519	5.575	175.0625	Indoleacetic acid	55.217724	53.116613	58.063599	28.131387	41.836755	41.722142	51.287065	63.229216	56.602076
175.06058	1.232	176.0679	2-Isopropylmalic acid	12.974952	12.045703	12.919397	12.075729	13.312797	15.163717	12.483998	14.59385	15.430834
177.03957	0.799	178.0472	Gluconolactone	658.19365	594.73878	635.71541	643.66757	728.80856	593.58499	553.90323	594.06674	587.87167
179.03416	4.009	180.04149	Caffeic acid	326.28063	309.55932	325.29192	793.43123	69.163872	412.21528	171.22065	271.7774	244.78902
179.05534	0.798	180.06257	D-Glucose	579.06958	441.46778	562.93036	396.39425	672.13946	327.15371	203.25275	215.93474	596.8571
181.0499	6.461	182.05718	Hydroxyphenyllactic acid	73.042785	74.239395	72.222385	15.870016	68.027322	83.365315	78.235858	53.447479	58.602106
181.07097	0.778	182.07825	Mannitol	639.4032	871.33888	511.97949	875.85756	707.19366	1385.383	289.827	595.94129	822.56072
182.04507	1.686	183.05248	4-Pyridoxic acid	73.283008	73.274581	70.820296	66.033913	68.612925	54.937924	71.296329	74.225301	73.615242
183.10187	7.394	184.10919	Oleuropeic acid	71.30507	69.758085	71.408905	72.148315	71.043177	61.112702	64.616595	72.38196	69.298248
187.09674	5.314	188.1041	Azelaic acid	895.65422	929.82462	883.06322	1514.1574	1838.9722	1896.4192	1064.9206	916.24439	946.80279
187.13322	8.067	188.1405	3-Hydroxydecanoic acid	8.0064699	8.4027148	7.5107607	22.179068	11.877907	20.258518	11.435166	12.791122	12.303342
188.05586	1.256	189.06305	N-Acetyl-L-glutamic acid	81.877487	77.384491	77.810135	78.184073	80.0481	59.659986	44.874366	54.531698	54.922344
191.01891	0.8	192.02626	Citric acid	27825.605	28380.433	23140.073	47496.574	28982.199	30178.279	13208.889	23187.295	26902.77
191.05531	10.343	192.06263	Quinic acid	1850.2905	1503.0099	367.30164	2062.6988	1702.9312	1608.2194	1185.2795	1945.4251	2357.7103
193.04994	4.854	194.05724	Ferulic acid	1077.8968	1070.9371	1044.1572	1013.1219	1073.2793	836.39203	921.65132	1088.8162	1065.8025
195.05038	0.761	196.05757	Gluconic acid	6808.2304	7506.0057	7853.6329	7162.6319	10035.447	8418.2654	6461.1648	9519.0079	9412.7953
198.03217	3.214	199.03941	DL-o-Chlorophenylalanine	5608.7924	5788.108	5458.3842	7356.9722	5046.0462	6797.3156	5004.3278	6424.9564	5839.6168
203.0191	0.816	204.02643	Daucic acid	280.72963	285.30833	267.87484	277.24466	255.18839	242.84256	391.35517	308.17582	227.54491
203.08191	3.175	204.08921	L-Tryptophan	1526.1036	1501.3611	1636.4586	1829.48	1519.1915	1306.9144	498.75536	899.29861	997.5456
204.06601	4.968	205.07333	Indolelactic acid	119.40895	122.06415	119.44662	4.4163903	4.3290622	3.2141619	4.4235587	4.6537589	5.9672536
209.0296	0.825	210.03688	Glucaric acid	114.19727	119.48101	115.61219	159.02185	157.32557	113.34638	59.802648	73.361009	103.65303
209.06606	0.798	210.07336	D-manno-2-Heptulose	162.62741	157.01741	144.6462	159.86615	180.68081	140.07033	166.73266	182.98304	172.77542
211.1335	7.71	212.14078	Traumatin	10.722026	12.958499	9.2280754	11.893454	27.71439	17.885887	16.673988	8.9025586	14.08247
213.01665	0.848	214.02418	5-Deoxyribose-1-phosphate	827.17594	857.51283	869.18126	911.44906	833.77528	667.7104	983.0402	654.26685	1018.6402
214.07147	3.225	215.0788	Kinetin	20.615557	19.105016	19.828014	8.927841	12.415637	14.904622	20.340152	17.228302	14.706277
214.14445	5.605	215.15171	N-Nonanoylglycine	8.8704268	9.6579917	8.6819703	100.49034	8.4851842	243.00514	86.2502	117.36495	27.243026
215.12836	6.622	216.13566	Undecanedioic acid	78.158386	77.03754	73.822521	118.97629	68.489999	120.00366	157.46195	94.815269	103.73992
216.05099	0.762	217.05826	Lycoperdic acid	1018.3661	724.40421	1161.2015	1382.4291	822.60369	1642.8442	47.834432	1432.2782	1275.4606
218.10292	2.754	219.11021	Pantothenic acid	1081.0644	1094.1518	1069.2989	684.88668	1147.2643	870.61771	1436.3631	1094.5749	1187.991
219.07695	1.656	220.08425	5-Hydroxy-L-tryptophan	142.75311	148.22093	132.49233	137.5748	122.41004	97.926549	206.16343	146.9552	152.56555
220.08218	0.795	221.08973	N-Acetyl-D-glucosamine	670.26127	611.13092	602.16664	589.90057	995.00171	462.90317	793.96275	566.4081	628.47841
221.06619	0.797	222.07392	Ethyl glucuronide	2142.9485	2450.3117	2046.1449	2114.6511	1878.6876	1830.4864	2041.3872	2505.0409	2178.9235
223.06078	4.832	224.06808	Sinapic acid	162.77527	166.96751	153.50997	93.9728	45.625486	122.04069	179.18565	176.48779	179.90165

223.13351	7.922	224.14079	Methyl jasmonate	10.97513	10.502272	11.196838	12.716152	18.555006	11.632954	12.188403	13.531763	8.4635084
225.18562	11.664	226.19284	Myristoleic acid	35.645231	40.944141	37.962323	28.709347	25.378914	29.09034	47.046721	42.813694	61.820291
227.12852	5.741	228.13578	Traumatic acid	21.439978	22.053742	21.093512	20.986459	49.961136	26.710034	16.010433	12.86856	10.755225
227.20119	12.355	228.20845	Myristic acid	117.04771	125.67015	116.82202	104.63019	81.336639	98.2344	137.83297	145.61437	180.85647
228.16017	6.207	229.16745	N-Decanoylglycine	15.454622	15.713923	15.008827	91.275189	10.745141	141.66904	35.951286	53.752648	17.719315
229.14427	7.24	230.15155	Dodecanedioic acid	15.665348	16.781383	14.389765	16.736729	14.22851	20.361601	19.725904	17.773174	17.951927
236.07733	0.791	237.08484	Fructoseglycine	684.30483	681.17455	691.36477	560.53219	686.37488	603.5315	606.09354	535.15983	550.16883
239.07695	0.763	240.08424	D-glycero-L-galacto-Octulose	465.31625	429.99228	453.53924	428.3222	495.18052	462.40587	335.2716	371.16826	448.82048
242.07954	0.782	243.08706	Cytidine	326.78922	196.34248	734.73861	196.4353	923.96049	1120.1306	905.03644	224.70901	840.91267
242.17589	6.781	243.18318	N-Undecanoylglycine	167.09664	169.17929	161.52938	1527.2149	118.8701	4273.3874	1297.1965	1663.878	254.40566
243.06187	1.232	244.06941	Uridine	368.1088	374.46445	359.2512	446.96875	340.82174	329.36973	373.0007	401.28697	476.58128
243.19633	10.474	244.20362	2-Hydroxymyristic acid	117.75764	130.7863	114.14842	130.61223	119.79613	106.28177	123.03593	135.80027	142.57583
245.04295	0.747	246.05029	Glycerophosphoglycerol	724.21014	754.01019	831.45753	803.07275	569.45426	972.00895	713.64562	842.92949	435.85555
245.13933	4.718	246.1466	Dibutyl malate	26.282186	27.188694	25.77327	31.244515	91.541704	68.347654	9.6118883	7.672293	10.788776
247.11867	4.374	248.1259	Prenyl glucoside	20.785507	23.425512	18.596733	22.820965	51.860129	33.885821	19.112324	18.128932	33.180174
253.21713	12.58	254.22442	Palmitoleic acid	185.88025	214.00132	205.43859	116.55726	146.63137	125.63648	272.3361	155.84967	220.41223
255.05096	3.457	256.0583	Piscidic acid	28.481297	28.572917	31.121041	66.41668	30.600855	30.770798	11.894793	26.950647	29.224844
255.23293	14.52	256.24018	Palmitic acid	1019.0985	1058.3708	997.01778	826.31184	818.61987	789.08778	1229.4855	952.55362	1332.0493
256.13016	1.569	257.13748	Coumaperine	29.007675	29.638321	28.414232	26.365476	27.131789	29.137566	34.06794	27.050653	31.22328
257.17581	8.414	258.18311	Tetradecanedioic acid	10.284325	12.851303	9.3704111	7.0518532	6.4330398	7.8103947	5.780667	6.5138323	6.8556182
257.21213	11.612	258.21942	3-hydroxypentadecanoic acid	10.059174	13.636116	9.8514033	4.9872891	5.7672083	6.5040624	10.926876	1.9100532	9.194699
258.03815	0.844	259.04569	Glucosamine 6-phosphate	63.977285	60.699048	62.795392	60.25702	72.648346	55.297597	48.530649	48.131213	76.107193
259.02234	0.848	260.02962	Glucose 1-phosphate	784.03379	806.71848	829.80407	856.089	775.2565	550.91313	810.10564	464.9829	920.35318
260.02347	1.299	261.03069	2-Methoxyacetaminophen sulfate	17.077493	17.334187	17.140098	19.927484	14.224255	16.400059	10.726992	16.879458	13.458706
263.09735	1.159	264.10454	Phenylacetylglutamine	54.555151	59.797827	45.116416	51.790087	53.403821	52.99205	52.63108	62.590818	70.284319
263.129	5.997	264.13624	Abscisic acid	17.377439	17.108095	17.237209	22.422235	7.3179847	47.211615	9.199438	11.868915	6.5622099
265.14795	11.048	266.15521	4'-Dihydroabscisic acid	524.96952	533.79156	593.72112	419.40128	416.86195	349.95549	522.3369	386.30465	937.49734
269.08792	0.742	270.0952	Histidylaspartic acid	59.953319	66.626063	60.242081	66.31998	68.249438	88.134699	34.733982	36.789795	46.29741
269.21222	10.905	270.21956	3-Oxohexadecanoic acid	264.23719	281.01615	270.41443	133.18633	194.36006	180.75755	220.84713	213.20755	314.75875
271.22791	10.011	272.23522	16-Hydroxyhexadecanoic acid	407.65903	401.78491	410.54721	509.85309	569.78697	408.13135	565.67666	516.04196	452.62754
274.10449	1.227	275.11187	N-gamma-Glutamylglutamine	16.410822	20.233925	16.741963	34.069613	21.724563	21.34744	11.36162	26.001556	15.651984
275.10388	4.404	276.11123	N-lactoyl-Tryptophan	58.759989	60.546552	60.909778	78.913074	29.812022	38.97216	45.073123	69.632871	35.914411
277.21704	12.225	278.22444	alpha-Linolenic acid	2940.2279	3007.4159	3057.3561	2750.8989	2397.0373	1946.7633	3934.8957	2394.1952	3302.8609

278.10349	4.556	279.11076	Niazirin	5.6867056	6.1037403	5.0768416	3.0549011	2.6325881	7.146062	5.8966497	18.027496	4.7184228
279.10864	2.864	280.11587	Asparenyol	23.470485	22.967755	23.224878	27.624822	21.890644	27.639116	12.473602	20.374624	21.300593
279.23291	12.835	280.24013	Linoleic acid	3305.4104	3786.156	3828.1061	2925.1578	2348.1074	2362.2563	3545.6723	3201.2572	3385.3004
281.08777	0.806	282.09515	Xylobiose	7864.4763	7777.1128	7592.3038	6817.7619	6888.0964	6486.3124	6366.4834	6899.1419	6505.2488
281.2486	14.523	282.25586	Oleic acid	2430.8364	2467.5246	2177.3173	2049.1005	1604.7074	1825.8551	2849.4882	2318.3787	2950.2356
282.08438	1.491	283.0917	Guanosine	97.142201	96.35028	101.37267	212.08812	85.995763	77.74972	78.736998	88.444462	93.086057
283.26419	10.483	284.27152	Stearic acid	1986.6034	2385.5405	1926.05	1233.8796	1668.9527	1494.7282	1360.3817	501.47131	1673.9835
285.20703	9.596	286.21431	Hexadecanedioic acid	111.25389	119.20951	107.99435	47.894001	53.685345	41.241122	65.877213	43.414806	74.448552
287.22284	7.153	288.23018	(S)-10,16-Dihydroxyhexadecanoic acid	314.07055	340.68039	281.9935	321.16324	376.97502	312.00725	506.19551	339.95957	432.12622
289.07196	4.053	290.07922	Catechin	23.002116	22.137209	21.978806	28.735487	21.844277	53.499685	17.745748	94.50062	27.525004
297.24332	10.56	298.25069	Ricinoleic acid	2432.8739	2542.1084	2569.7025	2992.9742	2583.0326	2133.6818	3937.1152	2890.9174	2684.8512
299.20178	11.56	300.20894	all-trans-Retinoic acid	438.6118	500.23531	437.62402	548.59403	307.54999	506.7546	434.43034	449.33296	463.11944
299.25903	11.543	300.26633	12-Hydroxystearic acid	103.64465	102.43262	102.74426	105.08453	120.41844	89.595579	92.157852	115.04443	180.35094
300.99905	4.622	302.00634	Ellagic acid	42.253364	41.006471	37.746691	39.498834	40.474232	57.520181	33.936243	58.900733	48.868671
301.20209	6.993	302.20937	8-Hydroxyhexadecanedioic acid	67.567125	68.346985	65.003218	45.354179	83.591346	52.501418	67.277539	25.069819	39.918956
303.11975	0.798	304.12701	2'-Deoxymugineic acid	653.72353	651.70441	763.93565	1297.7675	873.133	1002.7619	166.31311	458.01283	850.2082
306.07666	0.8	307.08395	Glutathione	418.36092	487.25502	467.87133	391.55824	220.96742	233.08775	434.83205	301.12291	331.26565
309.27994	11.342	310.28726	9Z-Eicosenoic acid	1518.6156	2169.8929	1411.7621	884.52561	1011.1358	987.2093	704.37091	1121.7425	1287.9238
311.09857	0.799	312.10579	4-O-beta-D-Galactopyranosyl-D-xylose	4411.8868	4541.3322	4450.6245	4068.2418	3667.5425	3813.4151	3778.7891	3397.5345	3875.8536
311.16879	12.566	312.17607	N-Undecylbenzenesulfonic acid	94.305434	120.62914	110.64903	40.074822	44.851182	97.140607	65.824354	80.759906	62.0056
311.22293	10.652	312.23018	8(R)-Hydroperoxylinoleic acid	1884.9151	1749.3549	2319.1268	1866.4693	2598.3057	2325.1135	1392.7702	1665.3416	1568.2751
311.2955	14.086	312.30284	Arachidic acid	70.786076	80.246203	70.280991	45.331376	47.584734	39.929694	41.65245	50.847351	57.449395
317.05475	0.849	318.06206	Melanin	55.225463	58.633061	31.930087	50.773751	55.770808	52.140341	68.194872	46.925637	76.680785
323.18649	6.181	324.19376	Cibaric acid	11.278597	11.582342	12.138305	14.988127	51.586307	41.563604	3.2985601	5.5586295	4.5601856
327.21786	8.431	328.22513	Corchorifatty acid F	563.69928	569.158	608.90206	488.53125	792.06967	739.77902	421.26933	444.2448	498.58118
332.12546	3.95	333.13265	Glutamyltryptophan	15.359657	13.410491	16.72919	24.768608	13.725717	16.62619	2.5309589	7.4174901	6.8972249
333.05933	0.837	334.06661	Glycerophosphoinositol	502.49841	506.9112	503.53039	467.01021	639.43136	558.96963	423.12082	646.27348	536.86666
339.32669	12.423	340.33401	Behenic acid	64.715438	58.414779	59.456538	101.97969	2.6976909	65.064284	91.533109	83.913958	66.256199
341.10889	0.8	342.11588	Maltose	79311.077	55356.383	90323.208	62007.286	83284.338	92093.006	99927.259	93029.791	72430.424
343.12454	1.238	344.13214	Lactitol	46.705047	22.047379	66.615824	24.279946	71.013071	20.229807	24.642949	55.145724	19.778272
358.25198	11.511	359.25923	2-Hydroxylauroylcarnitine	476.18976	517.1018	522.85352	465.33726	519.09024	334.65793	295.37575	318.44354	367.60143
380.25732	10.483	381.2646	Sphinganine 1-phosphate	29.324643	35.774857	27.522006	31.168653	27.221392	25.811146	26.897739	24.988847	33.93157
393.13058	4.096	394.13786	N-Acetylserotonin glucuronide	4.5966849	4.2622236	4.7158124	3.3638662	1.6744821	3.0326213	10.607967	8.0975351	4.0058453

413.25443	9.007	414.26185	Ascorbyl palmitate	26.7427	27.880279	27.457241	48.387986	30.376233	12.222053	19.401076	20.432289	20.162054
417.28595	11.059	418.29317	Palmitoyl glucuronide	47.148139	48.366764	50.968381	45.188611	45.390654	22.090267	45.296548	43.389995	43.222814
441.07227	0.907	442.07956	3-Galloylcatechin	109.56823	116.97156	107.38494	155.90502	110.61669	32.357679	151.59591	116.44111	138.04948
452.27768	10.081	453.28463	LysoPE(16:0/0:0)	11684.193	11468.926	12779.223	12789.771	10791.031	10642.464	10959.699	10977.478	10654.411
472.14545	2.969	473.15299	Dhurrin 6'-glucoside	24.098336	25.125405	25.846789	36.527954	10.195317	28.406012	3.723905	4.9595774	5.8232066
472.15869	3.094	473.16593	Folinic acid	136.3422	130.59314	140.75803	231.95954	122.50267	109.44542	88.707495	77.170685	104.6214
476.27777	9.666	477.28504	LysoPE(18:2(9Z,12Z)/0:0)	13724.999	14986.55	13267.652	13288.797	10915.383	10927.171	12423.345	11721.227	13145.872
478.2934	10.428	479.30067	LysoPE(18:1(11Z)/0:0)	3142.7804	3330.0427	3374.9157	2512.0815	2789.6109	2982.5863	3885.4484	3268.3838	2598.3532
492.12802	3.195	493.1353	Malvidin 3-glucoside	35.788846	37.995524	35.449981	49.550659	35.965088	39.560336	35.672134	27.270872	38.911471
503.16187	0.793	504.16921	Raffinose	2753.5452	3174.1581	2558.0772	4303.3758	2027.9939	2021.2529	2779.9771	2824.3865	2680.0892
511.30392	14.47	512.31142	1-Stearoylglycerophosphoglycerol	145.29152	157.0434	110.79747	128.47731	109.17783	128.27604	97.422098	65.841222	101.6791
580.15228	3.978	581.15948	Cyanidin 3-sambubioside	93.697683	99.470567	98.469571	103.41054	82.719002	77.181245	76.867645	73.397145	76.110949

Table S6.2 Label and designation of the samples

Label	Designation	Remarks	Generation
HAHP1	IR 122297-B	Parent: High amylose and protein content	Parent 1
HAHP2	IR 122297-B-4130-1-1 RGA-B	High amylose content bulk	F6
HAHP3	IR 122297-B-4110-1-1 RGA-B	High protein content bulk	F6
LALP1	SAMBA MAHSURI::IRGC 117377-1	Parent: Lower amylose and protein content	Parent 2
LALP2	IR 122297-B-4323-1-1 RGA-B	Low amylose content bulk	F6
LALP3	IR 122297-B-4356-1-1 RGA-B	Low protein content bulk	F6

Table S7.1 Color parameters of HAHP_101 and Samba Mahsuri.

Sample	Parameter	Technical replicate			Average
		1	2	3	
ULGI SI 101	L*	78.36	78.36	78.51	78.41
ULGI SI 101	a*	1.73	1.75	1.72	1.73
ULGI SI 101	b*	17.04	17.03	17.1	17.06
Samba Mahsuri	L*	81.72	81.74	81.76	81.74
Samba Mahsuri	a*	0.76	0.78	0.8	0.78
Samba Mahsuri	b*	15.62	15.63	15.61	15.62

Table S7.2 Amino acid profile of Samba Mahsuri and HAHP.

AMINO ACID	**Samba Mahsuri (g/100 g)**					**HAHP_101 (g/100 g)**				
	A1_1	A1_2	A1_3	AVE	SD	B1_1	B1_2	B1_3	AVE	SD
Alanine	1.293	1.301	1.397	1.330	0.058	1.117	1.153	1.112	1.127	0.022
Arginine	2.663	2.699	2.859	2.740	0.104	2.869	2.884	2.906	2.886	0.019
Aspartic acid	13.879	14.188	14.603	14.223	0.363	2.766	2.883	2.881	2.843	0.067
Cysteine	0.000	0.177	0.587	0.255	0.301	0.000	0.211	0.000	0.070	0.122
Glutamic acid	5.125	5.097	5.065	5.096	0.030	3.321	3.500	3.266	3.362	0.123
Glycine	7.193	7.505	8.062	7.587	0.440	1.711	1.337	1.098	1.382	0.309
Histidine	3.112	3.225	3.271	3.203	0.082	3.462	3.433	3.411	3.436	0.026
Isoleucine	2.577	2.750	2.625	2.651	0.089	2.913	2.990	2.984	2.962	0.043
Leucine	1.923	2.052	1.959	1.978	0.066	2.173	2.231	2.226	2.210	0.032
Lysine	11.841	12.222	12.543	12.202	0.351	14.240	14.203	14.135	14.193	0.053
Methionine	2.368	2.455	2.404	2.409	0.044	2.569	2.612	2.534	2.572	0.039
Phenylalanine	2.660	2.727	2.669	2.686	0.036	2.956	2.908	2.986	2.950	0.039
Proline	2.353	2.362	2.363	2.359	0.005	2.525	2.602	2.605	2.577	0.046
Serine	8.651	8.634	8.617	8.634	0.017	3.052	3.230	3.092	3.125	0.093
Threonine	4.036	4.077	4.221	4.111	0.098	1.074	1.170	1.122	1.122	0.048
Tyrosine	4.887	5.027	5.044	4.986	0.086	5.395	5.584	5.613	5.530	0.118
Valine	2.494	2.553	2.416	2.488	0.069	2.656	2.637	2.720	2.671	0.044

Table S8. Metabolomics of low, ultra-low, and high glycemic index rice

Experiment title: Metabolomics of low, ultra-low, and high glycemic index rice
Organism/Plant species: Rice
Organ/tissue: Seed
Analytical tool: LC-MS

Peak no.- number referenced back to the main text
Ret . Time- Retention time, in minutes (difference in Ret.Time between ES(+) and ES(-) modes was less than XX minutes)
Putative Name- putative identification of the metabolite
Mol. Formula- molecular formula of the metabolite or its FA adduct;
Theor. m/z- theoretical monoisotopic mass calculated for the ion $(M-H)^-$, $(M+H)^+$ or $(M+FA)^-$
Found m/z- mass detected in the experiment
m/z error (ppm)- difference between theoretical and found m/z values in ppm
MSMS fragments- fragments, obtained from the ion $(M-H)^-$, $(M+H)^+$ or $(M+FA)^-$
MS/MS CE (eV)- collision energy used for fragmentation optional
UV/Vis- UV/ Vis absorbance maxima
() FA- formic acid adduct
(S)- identification confirmed by a standard compound
I, II, III- different isomers
Identification level (A; B; C)- (A) standard or NMR; (B(i)) confident match based on MS/MS and (B(ii)) confident match using in-silico MS/MS approaches and (B(iii)) partial match based on MS/MS and (C(i)) confident match based on MS^n and (C(ii)) confident match using in-silico MS^n approaches and (C(iii)) partial match based on $MS^{n;}$ (D) MS only
International identifie (*optional): identifier from database such such as: HMDB, KEGG, PubChem, KNApSAcK, ect.

Peak no.	Ret._Time	Putative_metabolite_name	ES_Found_m.z	Identification level (A-D)
1	2.72529445	(S)-6-Oxo-2-piperidinecarboxylic acid	142.050097	B(i)
2	6.43453719	1-methoxy-3-indolylmethyl-glucosinolate	477.068091	B(i)
3	4.53091078	12-Crown-4	175.096841	B(i)
4	12.6038491	13-HPODE	311.222948	B(i)

5	4.75966341	2-Isopropylmalic acid	175.060445	B(i)
6	4.75751301	2,3-Dimethylsuccinic acid	145.04969	B(i)
7	2.53234992	2'-Deoxyuridine	227.067216	B(i)
8	2.25681461	3-Hydroxy-3-Methylglutaric acid	161.044804	B(i)
9	4.09466238	3-Methylglutaric acid	145.049859	B(i)
10	5.27737796	3,4-Dihydroxyhydrocinnamic acid	181.047543	B(i)
11	2.0568386	3,4-Dihydroxyphenylacetic acid	167.03423	B(i)
12	9.49353689	3,4,5triCQA	677.151494	B(i)
13	2.88110634	4-Hydroxy-3-Methoxymandelic acid	197.045155	B(i)
14	4.19533369	4-Hydroxymethyl-3-methoxyphenoxyacetic acid	211.060722	B(i)
15	6.43453719	4-Methoxyglucobrassicin	477.068091	B(i)
16	6.38690289	4-O-pcoumaroylshikimic acid	319.046041	B(i)
17	4.28737062	4,8-Dihydroxyquinoline-2-carboxylic acid	204.029813	B(i)
18	5.50283917	5,6-Dimethylbenzimidazole	145.086049	B(i)
19	12.8809071	5,7-Dihydroxy-4'-methoxyisoflavone	283.061475	B(i)
20	2.57172644	6-Hydroxynicotinic acid	138.01869	B(i)
21	2.8774067	6,7 Dimethylrihityl lumazine	325.107874	B(i)
22	14.1216174	9-hydroxy-(10E, 12Z, 15Z)-octadecatrienoic acid	295.227742	B(i)
23	2.74057875	Adenosine 3',5'-cyclic monophosphate	328.045613	B(i)
24	4.18805087	Adipic acid	145.049552	A
25	3.33102927	Alanyisoleucine	201.123959	B(i)
26	3.61562546	Alanyleucine	201.124006	B(i)
27	2.24380784	Alanymethionine	219.081268	B(i)
28	4.31841546	Alanyphenylalanine	235.108663	B(i)
29	5.0777297	Alanytryptophan	274.120156	B(i)
30	2.95429225	Alanytyrosine	251.103872	B(i)
31	1.85406146	Alanyvaline	187.108231	B(i)
32	14.6454736	alpha-Tocopherol acetate	471.380526	A
33	6.02590311	Ampelopsin	319.046244	B(i)
34	10.8902895	Aphidicolin	337.238526	B(i)

35	10.4941687	Apigenin	269.045757	A
36	7.81596589	Apigenin-7-O-glucoside	431.098568	A
37	3.14501039	Arginyphenylalanine	320.173017	B(i)
38	3.21716531	AsparaginyIsoleucine	244.129918	B(i)
39	3.46352684	asparaginyleucine	244.130234	B(i)
40	1.99141419	Asparaginymethionine	262.087264	B(i)
41	4.12912955	Asparaginyphenylalanine	278.114746	B(i)
42	4.95802566	AsparaginyTryptophan	317.125812	B(i)
43	3.04313943	Asparaginytyrosine	294.109854	B(i)
44	3.7086634	Aspartyleucine	245.114409	B(i)
45	4.38822911	Aspartyphenylalanine	279.098776	B(i)
46	5.19591044	Aspartytryptophan	318.109605	B(i)
47	3.07818743	Aspartytyrosine	295.093785	B(i)
48	1.99056767	Aspartyvaline	231.098688	B(i)
49	8.27541874	Astragalin	447.093894	B(i)
50	12.1391813	beta-hydroxycapric acid	187.133259	B(i)
51	13.4475872	beta-Hydroxylauric acid	215.164606	B(i)
52	12.4567497	beta-Hydroxypalmitic acid	271.228155	B(i)
53	5.83403076	Biotin	243.084768	A
54	9.85556035	C-hexosyl-luteolin O-hexoside	611.329103	B(i)
55	5.38127025	Caffeic acid	179.026154	A
56	11.1120426	Caffeoyl spermidine derivative	242.176123	B(i)
57	5.47869715	caffeoylquinic acid dervitives	515.130826	B(i)
58	4.41902283	CafHex1_3.87_341.0879	341.08794	B(i)
59	4.63143777	CafHex2_4.09_341.0879	341.087942	B(i)
60	4.89495677	Catechin	289.072057	A
61	4.85770639	chlorgenic acid_Saleh_standards_353.088_4.91	353.087933	A
62	5.1927152	Chlorogenic acid derv.	353.088225	B(i)
63	5.59093995	Chrysoeriol 5-O-hexoside	461.109508	A
64	14.7367607	cinnamic acid derivative	265.146947	B(i)

65	1.86167464	Citramalic acid	147.029072	B(i)
66	7.35216396	coumarin derivatives	147.044224	B(i)
67	5.01535338	Cyanidin-3-O-glucoside	465.103942	A
68	4.75430451	Cyanidin-3-O-sophoroside	609.146915	A
69	4.41066121	Delphinidin-3-O-galactoside	463.088828	A
70	4.75430451	delphinidin-3-O-rutinoside chloride_Saleh_standards_609.15_4.74	609.146915	A
71	6.54869795	Desthiobiotin	213.124014	B(i)
72	11.0711162	Dexamethasone	391.189622	B(i)
73	14.0940057	dieonic acid derivatives	311.222867	B(i)
74	5.74934953	Dihydromyricetin	319.045877	A
75	13.1058569	dihydroxy-octadecenoic acid II	311.222986	B(i)
76	9.69737368	FA 12:0 (Lauric acid=	181.049919	B(i)
77	5.21183889	FerHex2_4.65_355.1031	355.103642	B(i)
78	5.7503605	FerHex3_5.17_355.1031	355.103639	B(i)
79	7.13681361	Ferulic acid	193.049957	A
80	4.4939367	feruloyl-O-sinapoyl-O-caffeoylquinic acid	735.158898	B(i)
81	4.70386835	Flavine adenine dinucleotide (FAD)	784.151209	B(i)
82	9.92357716	fragment ofC-hexosyl-luteolin O-hexoside	299.019889	B(i)
83	3.63341359	GABA	143.118098	A
84	2.60648638	gallic acid	169.013505	A
85	12.1413753	Gibberellin A4	331.15537	A
86	3.55265226	Glutaminyleucine	258.146201	B(i)
87	4.20843846	GlutaminyPhenylalanine	292.130656	B(i)
88	5.00472612	Glutaminytryptophan	331.141281	B(i)
89	3.02682628	Glutaminytyrosine	308.125812	B(i)
90	1.92297999	Glutaminyvaline	244.130292	B(i)
91	3.51478795	Glutamyisoleucine	259.130282	B(i)
92	3.77559307	Glutamyleucine	259.130178	B(i)
93	2.56043077	Glutamymethionine	277.086737	B(i)

94	5.20380932	Glutamytryptophan	332.125569	B(i)
95	3.43040928	Glycyl-L-isoleucine	187.108176	B(i)
96	2.06959861	Glycyl-L-methionine	205.064828	B(i)
97	4.26147104	Glycyl-L-phenylalanine	221.092698	B(i)
98	5.01658724	Glycyl-L-tryptophan	260.104187	B(i)
99	2.93102129	Glycyl-L-tyrosine	237.088025	B(i)
100	1.9577088	Glycyl-L-valine	173.092582	B(i)
101	2.71607965	Guanosine	282.084832	A
102	4.34617828	H5FeruGlc1_3.92_371.0983	371.098832	B(i)
103	8.29240829	Hesperetin-7-O-glucoside	463.125275	A
104	7.88811867	hesperidine_Saleh_standards_609.18_7.93	609.183252	A
105	13.8741927	Hexadecanoic acid	315.254081	A
106	9.43998208	Homoeriodictyol	301.035633	A
107	3.27123969	Homogentisic acid	167.034124	A
108	8.00933224	Hydroxygallic acid derivatives	187.096804	B(i)
109	6.26089284	Indole-3-acetamide	173.080928	B(i)
110	2.71629754	Inosine	267.073755	A
111	7.71706352	Is3G_7.29_477.103	477.104293	B(i)
112	7.24686956	Is3G2-A_6.79_609.1467	609.146819	B(i)
113	7.52703643	Is3G6-R_7.02_623.1614	623.162698	B(i)
114	5.68157823	Is3G6-R7G_5.22_785.2141	785.215684	B(i)
115	1.85100139	Isoleucine	130.086372	A
116	2.67895298	Isoleucyalanine	201.124024	B(i)
117	1.96672713	Isoleucyaspartic acid	245.114519	B(i)
118	2.61506614	Isoleucyglutamic acid	259.130175	B(i)
119	2.03880042	Isoleucyglutamine	258.146169	B(i)
120	5.02183202	Isoleucyisoleucine	243.171436	B(i)
121	5.43993065	Isoleucyleucine	243.171449	B(i)
122	4.39092519	Isoleucymethionine	261.127875	B(i)
123	6.16207074	Isoleucyphenylalanine	277.155849	B(i)

124	2.04579083	Isoleucythreonine	231.134934	B(i)
125	6.45597315	Isoleucytryptophan	316.166867	B(i)
126	3.9446567	Isoleucyvaline	229.155489	B(i)
127	10.9635509	isorhamentin	315.051321	B(i)
128	7.71706352	Isorhamnetin-3-O-glucoside_Saleh_standards_477.1_7.81	477.104293	B(i)
129	7.52703643	Isorhamnetin-3-O-rutinoside	623.162698	B(i)
130	7.52703643	Isorhamnetin-3-O-rutinoside_Saleh_standards_623.16_7.54	623.162698	B(i)
131	7.71706352	isorhamnetin-o-glucoside	477.104293	A
132	6.91752695	isovitexin_Saleh_standards_431.1_6.93	431.098589	A
133	7.69817172	K3G_7.13_447.0926	447.093657	B(i)
134	6.68207521	K3G7G_6.14_609.1462	609.147028	B(i)
135	9.20042743	Kaempferol	287.056376	A
136	6.54597124	Kaempferol 3-O-glucoside 7-O-rhamnoside	593.151735	A
137	5.70166373	Kaempferol 3-O-rhamnoside-7-O-glucoside	593.150449	B(i)
138	7.46133783	Kaempferol-3-O-?-rutinoside_Saleh_standards_593.15_7.4	593.151717	B(i)
139	7.69817172	Kaempferol-3-O-Glucoside_Saleh_standards_447.09_7.66	447.093657	B(i)
140	9.41690576	kaempferol-3-rhamnosyhexose	593.130534	B(i)
141	7.69817172	Kaempferol-7-O-Glucoside_Saleh_standards_447.09_7.76	447.093657	B(i)
142	9.41690576	kaempferol-glycosides derv.	593.130534	B(i)
143	7.59907709	kaempferol-glycosides dervi	755.185127	B(i)
144	8.35098004	KGRAFer_7.93_901.2408	901.241381	B(i)
145	2.72474289	Leu-Gly-Gly	244.130244	B(i)
146	2.04427217	Leucine	130.086352	A
147	2.84300894	Leucyalanine	201.124031	B(i)
148	2.12818065	Leucyaspartic acid	245.114516	B(i)
149	2.76016579	Leucyglutamic acid	259.130302	B(i)

150	5.31548417	Leucyisoleucine	243.171593	B(i)
151	5.73086931	Leucyleucine	243.171426	B(i)
152	2.92202581	Leucylglycine	187.108237	B(i)
153	4.73291997	Leucymethionine	261.12455	B(i)
154	2.35612468	Leucythreonine	231.13491	B(i)
155	6.75092152	Leucytryptophan	316.166878	B(i)
156	4.56365792	Leucytyrosine	293.151094	B(i)
157	4.1893087	Leucyvaline	229.155474	B(i)
158	10.8156861	Luteolin 6-C glucoside	449.275567	A
159	6.71820466	Luzonoid	479.120067	B(i)
160	13.9245211	Lyso PC 18:2	564.330891	B(i)
161	13.3209169	LysoPC 14:0	512.299609	B(i)
162	14.3843877	LysoPC 18:1	566.346616	B(i)
163	1.93526213	Lysyleucine	258.18257	B(i)
164	2.90343754	Lysyphenylalanine	292.167295	B(i)
165	3.78214219	Lysytryptophan	331.170871	B(i)
166	5.13791647	Methionyleucine	261.128622	B(i)
167	1.82579097	Methionylglycine	205.073135	B(i)
168	4.10622795	Methionymethionine	279.084951	B(i)
169	4.13046646	Methionytyrosine	311.107467	B(i)
170	3.76994147	Methionyvaline	247.112291	B(i)
171	13.0685159	Methyl jasmonate	223.133506	B(i)
172	2.7379693	Mevalonic acid lactone	129.054462	B(i)
173	8.86250012	Morin	301.035697	B(i)
174	8.32661769	Myricetin	317.066708	A
175	2.69404157	N-Acetyl-L-Cysteine	162.018199	B(i)
176	4.49168272	N-Acetyl-L-Methionine	190.053721	B(i)
177	4.52281823	N-Acetyl-L-Tyrosine	222.077063	B(i)
178	2.4885891	N-Acetylmuramic acid	292.104333	B(i)
179	4.03404838	N-Formyl-L-Methionine	176.038083	B(i)

180	10.381224	Naringenin chalcone	271.061363	A
181	7.83597261	Naringin	579.172302	A
182	8.11347108	Neohesperidin	609.18307	A
183	7.8473711	NG1_7.39_433.1136	433.114106	B(i)
184	15.5273905	oleic acid derivatives	339.233002	B(i)
185	7.03743964	P35GG_6.64_597.18	597.183188	A
186	13.7225105	Palmitic acid or Hexadeconate	315.254111	B(i)
187	3.78344614	Panthenol	204.123712	A
188	3.64898002	Pantothenic acid (Vitamine B5)	218.103081	A
189	3.4432793	peak107_Gentesic acid-glucoside_315.0720515_3.55	315.072292	A
190	3.71769583	Coumaroylgalactarate_355.067_3.73	355.070719	B(i)
191	3.7407738	Phaseoloidin_329.0875_3.74	329.087627	B(i)
192	3.71537603	Phenylalanyalanine	235.108642	B(i)
193	2.56168142	Phenylalanyarginine	320.173171	B(i)
194	2.80002789	Phenylalanyasparagine	278.114917	B(i)
195	3.19410439	Phenylalanyaspartatic acid	279.098758	B(i)
196	3.19410439	Phenylalanyaspartatic acid	279.098758	B(i)
197	3.13653008	Phenylalanyglutamine	292.130717	B(i)
198	5.93891412	Phenylalanyisoleucine	277.155864	B(i)
199	6.5214702	Phenylalanyleucine	277.155856	B(i)
200	6.46064502	Phenylalanyleucine	277.155948	B(i)
201	3.72488297	Phenylalanylglycine	221.092797	B(i)
202	5.44434947	Phenylalanymethionine	295.112314	B(i)
203	6.89790931	Phenylalanyphenylalanine	311.140352	B(i)
204	2.95429225	Phenylalanyserine	251.103872	B(i)
205	3.17092938	Phenylalanythreonine	265.119493	B(i)
206	7.22899356	Phenylalanytryptophan	350.151298	B(i)
207	5.18660281	Phenylalanytyrosine	327.135365	B(i)
208	4.86059598	Phenylalanyvaline	263.14028	B(i)

209	8.52802166	phosphatidylethanolamine-derivatives	603.078566	B(i)
210	13.1503924	Phytosphingosine	316.285624	B(i)
211	4.80100848	procyanidin B1	577.136064	A
212	3.71290323	Prolyisoleucine	227.140017	B(i)
213	2.85262963	Prolymethionine	245.09657	B(i)
214	4.73291997	Prolyphenylalanine	261.12455	B(i)
215	5.38150626	Prolytryptophan	300.135577	B(i)
216	5.30712742	Prolytryptophan	300.135641	B(i)
217	3.27371929	Prolytyrosine	277.11964	B(i)
218	2.42135073	Prolyvaline	213.124254	B(i)
219	5.10467629	Propanoic acid, 3-(2,4-dihydroxyphenyl)-	181.050033	B(i)
220	13.0211121	Prostaglandin A(2) solution	333.20776	B(i)
221	3.74263384	Protocatechuic acid	153.018473	A
222	10.0994278	pseudochelerythrine	331.082724	B(i)
223	13.1474674	Psychosine	460.328571	B(i)
224	2.7137586	Pyridoxic acid	182.045261	B(i)
225	6.62652161	Q3G2-A_6.19_595.1315	595.130278	B(i)
226	6.81673254	Q3G6-R_6.33_609.1458	609.147076	B(i)
227	6.09974838	Q3G7G_5.68_625.1412	625.142223	B(i)
228	6.94929725	Quercelin-3-unk._Saleh_standards_463.09_7.04	463.088544	B(i)
229	7.02759519	Quercetin	301.035685	A
230	6.94929725	Quercetin-3-?-D-Glucoside	463.088544	B(i)
231	6.94929725	Quercetin-3-beta-D-glucoside	463.088544	B(i)
232	7.04764478	Quercetin-3-D-galactoside_Saleh_standards_463.098_6.98	463.088746	B(i)
233	5.26659153	quercetin-7-O-hexoside	465.104093	B(i)
234	6.62652161	Quercetin-apiosyl-galactose	595.130278	B(i)
235	6.91628834	Quercetine -glucosides derv.	625.142398	B(i)
236	7.7848956	Quercitrin	447.093847	A
237	5.75849002	Riboflavin	375.131051	A

238	6.81673254	Rutin	609.147076	A
239	2.39926448	S-Adenosyl-L-Homocysteine	383.114636	B(i)
240	4.37698247	Salicin	285.095957	B(i)
241	12.4346051	Secoisolariciresinol	361.166095	B(i)
242	3.2080926	Seryisoleucine	217.119063	B(i)
243	3.40800083	Seryleucine	217.119156	B(i)
244	2.03103124	Serymethionine	235.072309	B(i)
245	1.90745891	Serymethionine	235.076094	B(i)
246	4.07512761	Seryphenylalanine	251.103793	B(i)
247	4.90216259	Serytryptophan	290.11476	B(i)
248	2.8583113	Serytyrosine	267.098985	B(i)
249	2.8583113	Serytyrosine	267.098985	B(i)
250	5.59681576	Sinapoylglucose	385.114372	B(i)
251	5.8009771	SinGlc_5.24_385.1133	385.114702	B(i)
252	5.93495392	SinGlciso2_5.47_385.1133	385.114399	B(i)
253	14.8008903	Stearic acid or hexadecanoic acid	311.201838	B(i)
254	4.27818888	Theophylline, anhydrous	179.056689	B(i)
255	4.55041379	threo-3-isopropylmalic acid	175.060457	B(i)
256	3.45442259	Threonyisoleucine	231.134842	B(i)
257	3.67013011	Threonyleucine	231.134818	B(i)
258	2.43048702	Threonymethionine	249.091544	B(i)
259	4.3500164	Threonyphenylalanine	265.119413	B(i)
260	5.1047045	Threonytryptophan	304.130535	B(i)
261	3.07321524	Threonytyrosine	281.114673	B(i)
262	2.03566317	Threonyvaline	217.119168	B(i)
263	3.36124183	Thymidine	241.082931	B(i)
264	5.21449764	trans-Cyclohexane-1,2-dicarboxylic acid	171.065676	B(i)
265	3.84908562	trans-zeatin-O-glucoside	380.156528	B(i)
266	10.6363828	Tricetin	301.071857	B(i)
267	11.5544366	tricin	329.233475	A

268	11.2135108	trihydroxy-octadecadienoic acid	327.217954	B(i)
269	4.47618925	Tryptophyalanine	274.120102	B(i)
270	3.55535774	Tryptophyasparagine	317.125972	B(i)
271	3.95396487	Tryptophyaspartic acid	318.112354	B(i)
272	4.23833348	Tryptophyglutamic acid	332.12517	B(i)
273	2.82507846	Tryptophyhistidine	340.141626	B(i)
274	6.75092152	Tryptophyisoleucine	316.166878	B(i)
275	7.16165321	Tryptophyleucine	316.166862	B(i)
276	4.45851662	Tryptophylglycine	260.104405	B(i)
277	2.8681586	Tryptophylysine	331.178086	B(i)
278	2.86799599	Tryptophylysine	331.178381	B(i)
279	7.60600922	Tryptophyphenylalanine	350.151147	B(i)
280	5.97294588	Tryptophyproline	300.135599	B(i)
281	3.70121264	Tryptophyserine	290.114948	B(i)
282	3.88829073	Tryptophythreonine	304.130561	B(i)
283	7.86825169	Tryptophytryptophan	389.161904	B(i)
284	5.9217862	Tryptophytyrosine	366.146076	B(i)
285	5.75244988	Tryptophyvaline	302.151169	B(i)
286	5.67346677	Tryptophyvaline	302.151194	B(i)
287	1.89002412	Tyrosine	180.066018	A
288	2.61929228	Tyrosyalanine	251.103798	B(i)
289	1.90752559	Tyrosyaspartic acid	295.093831	B(i)
290	2.52234437	Tyrosyglutamic acid	309.10951	B(i)
291	1.95853715	Tyrosyglutamine	308.125793	B(i)
292	4.75206145	Tyrosyisoleucine	293.151066	B(i)
293	5.13016311	Tyrosyleucine	293.151125	B(i)
294	2.67238086	Tyrosylglycine	237.088051	B(i)
295	5.71461066	Tyrosyphenylalanine	327.135175	B(i)
296	3.84110172	Tyrosyproline	277.119664	B(i)
297	1.95730166	TyrosyThreonine	281.114566	B(i)

298	6.12932267	Tyrosytryptophan	366.145931	B(i)
299	4.19287591	Tyrosytyrosine	343.130156	B(i)
300	1.89699736	Uridine	243.062221	A
301	4.1893087	Valyisoleucine	229.155474	B(i)
302	4.56413141	Valyleucine	229.155532	B(i)
303	3.50224187	Valymethionine	247.112292	B(i)
304	5.26327185	Valyphenylalanine	263.140409	B(i)
305	3.21705032	Valyproline	213.123859	B(i)
306	3.66422518	Valytyrosine	279.135224	B(i)
307	3.73959003	Valytyrosine	279.135237	B(i)
308	7.27336927	vanillic acid	167.034181	A
309	6.90688148	Vitexin-2"-O-rhamnoside	577.156451	A

Table S9. The oligomers used in this study.

No.	Oligomer name	Sequence (5´ to 3´)	Purpose
1	U3-SBEIIb-CDS-T1-F	GGCAAATTTGAAACACTTACTTG	Oligomer-duplex for expressing gRNA. The underlined sequence was added for making overlapping with the pSR339-*AarI* digestion for ligation.
2	U3-SBEIIb-CDS-T1-R	AAACCAAGTAAGTGTTTCAAATT	
3	Tnos-F	GCATGACGTTATTTATGAGATGG	Vector sequence confirmation after insertion oligomer duplex into pSR339
4	pUbi-F3	GATATACTTGGATGATGGCAT	Confirmation of T-DNA presence in T_0 plants
5	Cas9-97-R	CAACTGAGTTCGTCCCGATGT	
6	SBEIIb-TS1- F1	CCTGTATGGTCTAGAGTTGCA	Amplification of target site for Sanger sequencing
7	SBEIIb-TS1- R1	CAAGGGCAGGAGTTATGCCA	