

**Supplemental Materials to Li et al.:**

**Mutation of *OsGUN4* uncoupled the sucrose-dependent signals to regulate starch biosynthesis in rice**

**RICE**

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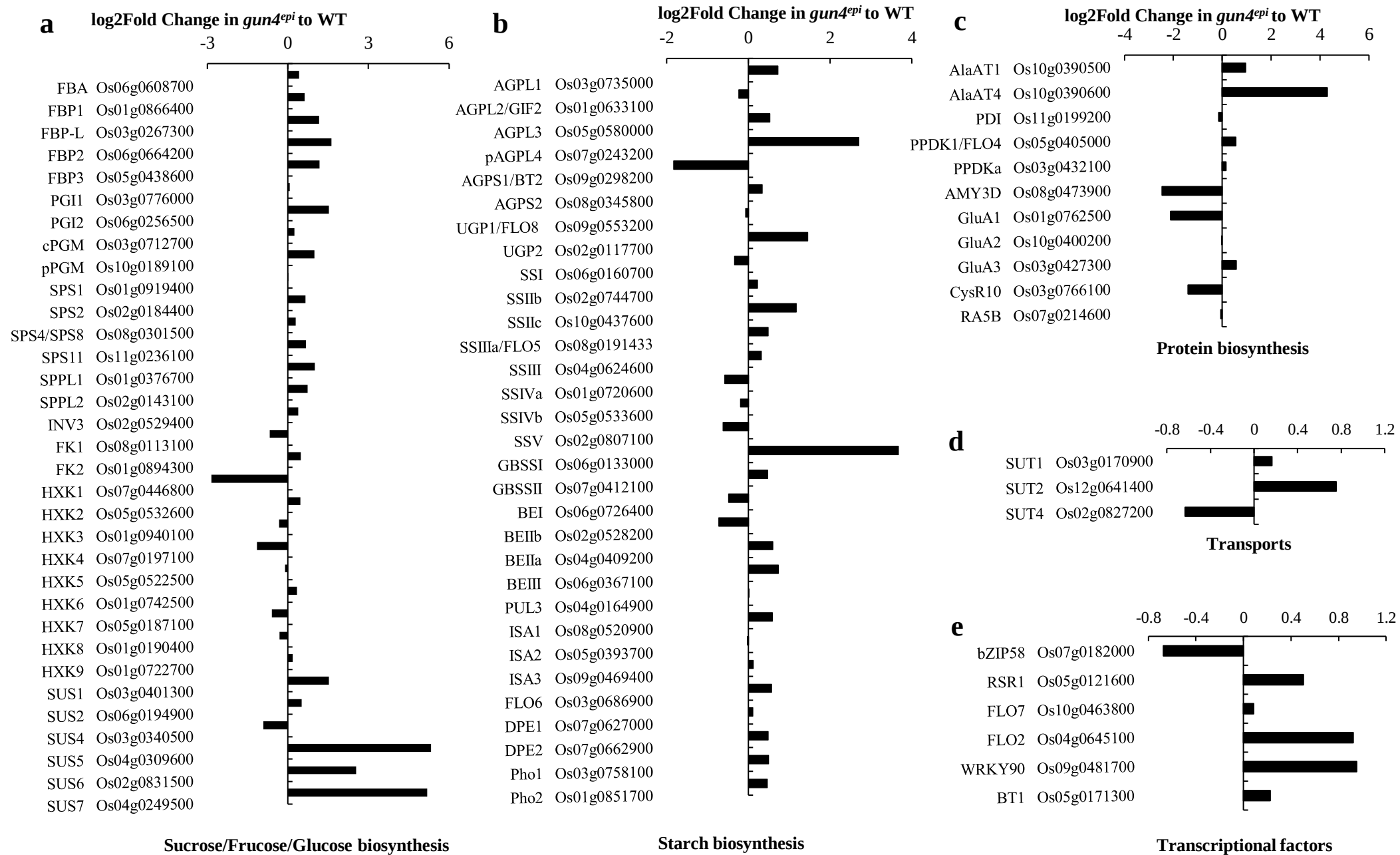
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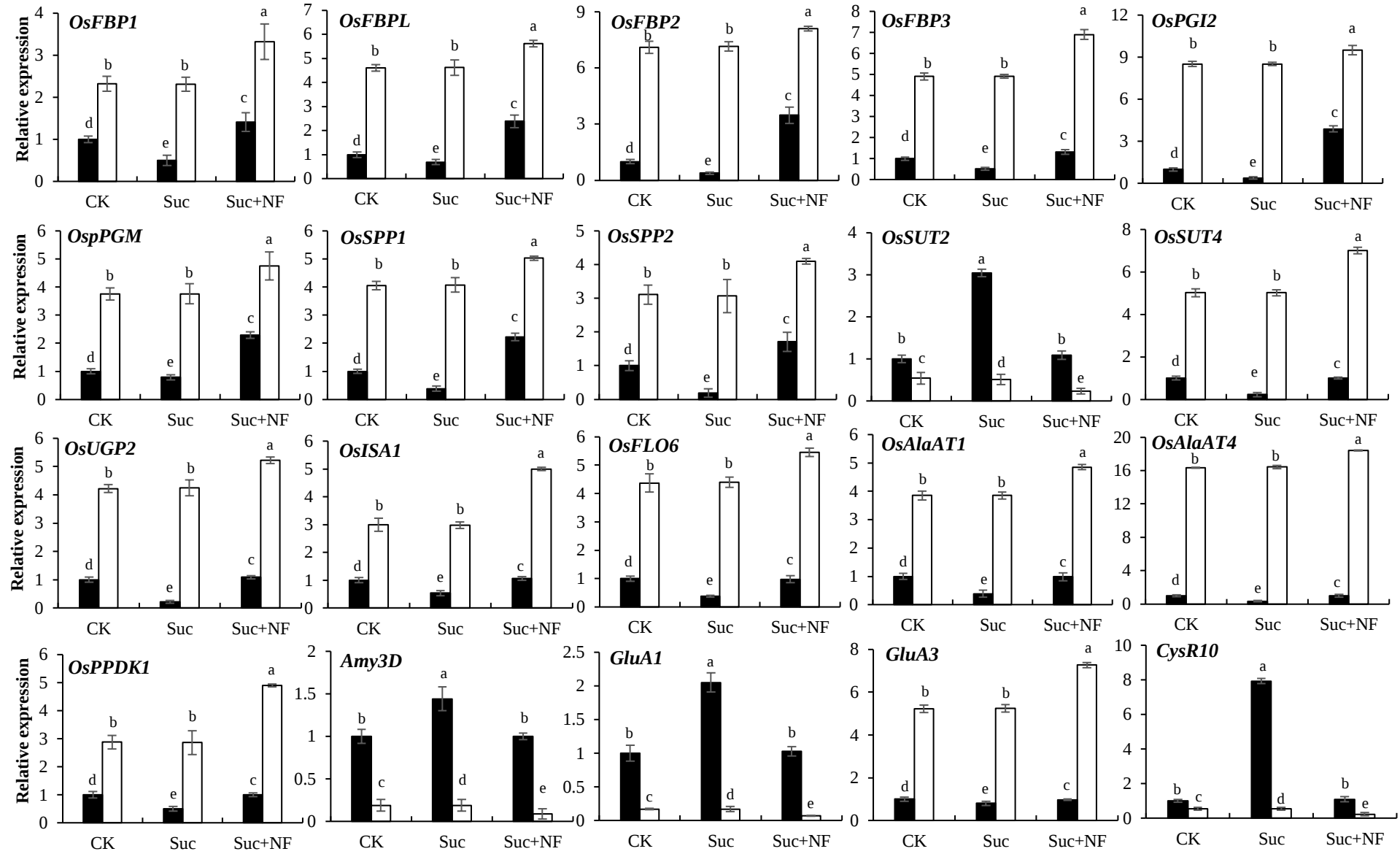
**Table S5** Two-way ANOVA test for expression levels of the genes involved in starch biosynthesis.

**Table S6** Two-way ANOVA test for reported sucrose-dependent signals.

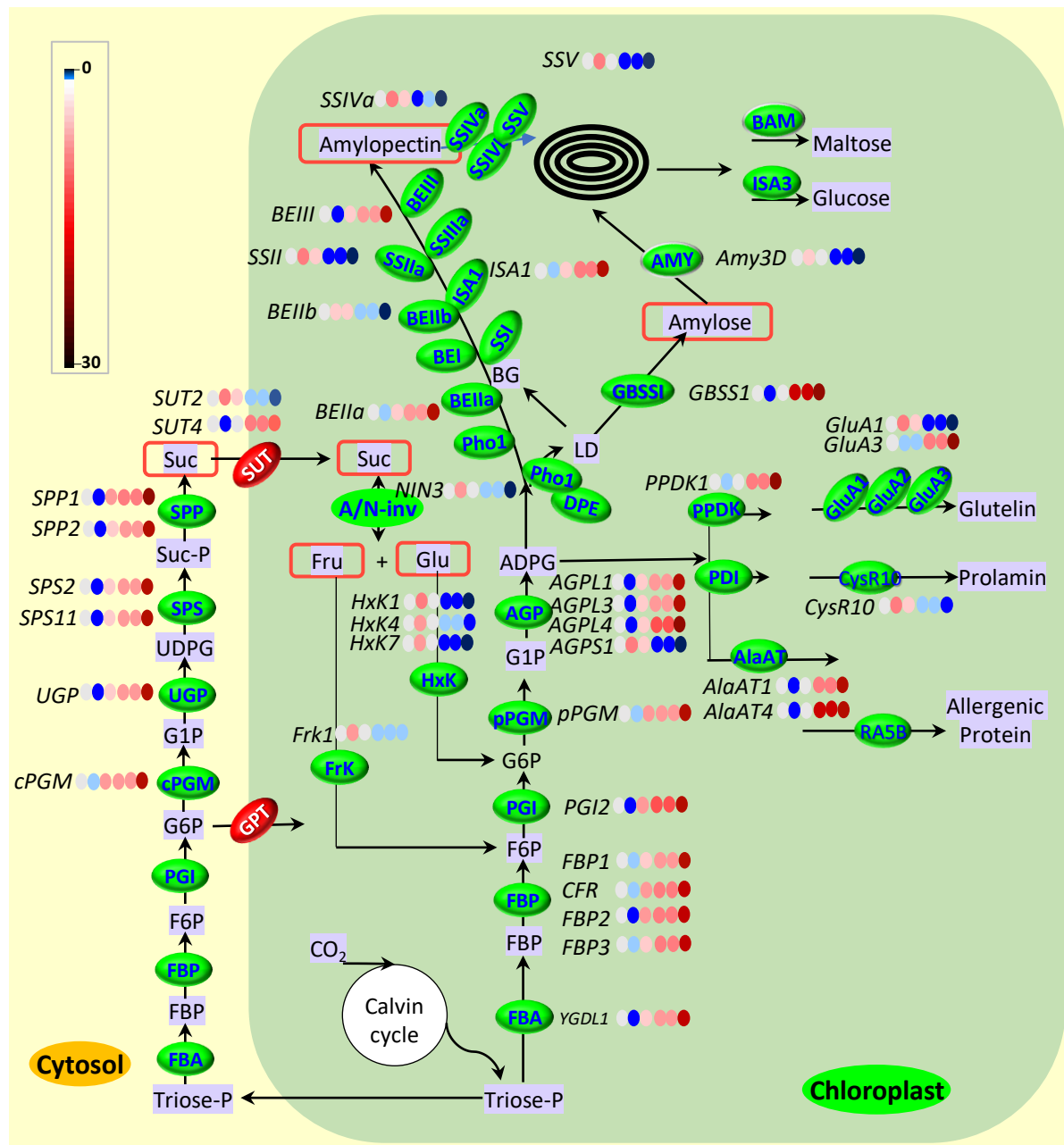


**Fig. S1** Different-expressed genes involved in starch biosynthesis by RNAseq in leaves. Genes involved in (a) sucrose biosynthesis, (b) starch biosynthesis, (c) protein biosynthesis, (d) sucrose transports and (e) transcriptional factors for starch biosynthesis.

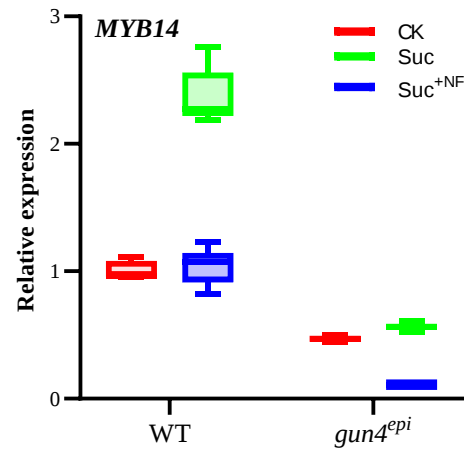
*Abbreviations:* FBA, Fructose-1,6-bisphosphate aldolase; FBP, Fructose 1,6-bisphosphate; PGI, Phosphoglucoseisomerase; PGM, Phosphoglucomutase; SPS, Sucrose-phosphate-synthase; SPP, Sucrose phosphate phosphatase; NIN3, Alkaline/neutral invertase; FrK, Fructokinase; HxK, Hexokinase; A/N-inv, alkaline/neutral invertase; SUS, Sucrose synthase; AGPL, ADP-glucose pyrophosphorylase large subunit; AGPS, ADP-glucose pyrophosphorylase small subunit; UGP, UDP-glucose pyrophosphorylase; SSI, II, III, IV, V, Soluble starch synthase I, II, III, IV, V; GBSSI, II, Granule bound starch synthase I, II; BE I, II, III, Starch branching enzyme I, II, III; PUL, pullulanase; ISA1, 2, 3, Isoamylase 1, 2, 3; FLO, Floury; DPE1, 2, Disproportionating enzyme; Pho1, 2, Plastidial starch phosphorylase1, 2; AlaAT1, 4, Alanine aminotransferase 1, 4; PDI, Protein disulfate isomerase; PPDK, Pyruvate orthophosphate dikinase; Amy3A, 3B, 3C,  $\alpha$ -amylase 3A, 3B, 3C; GluA1, GluA2, GluA3, glutelins A1, A2, A3; CysR10, prolamin; SUT, Sucrose transporter; BT, Brittle1; bZIP58, Basic leucine zipper transcription factor 58; RSR1, Rice starch regulator 1.



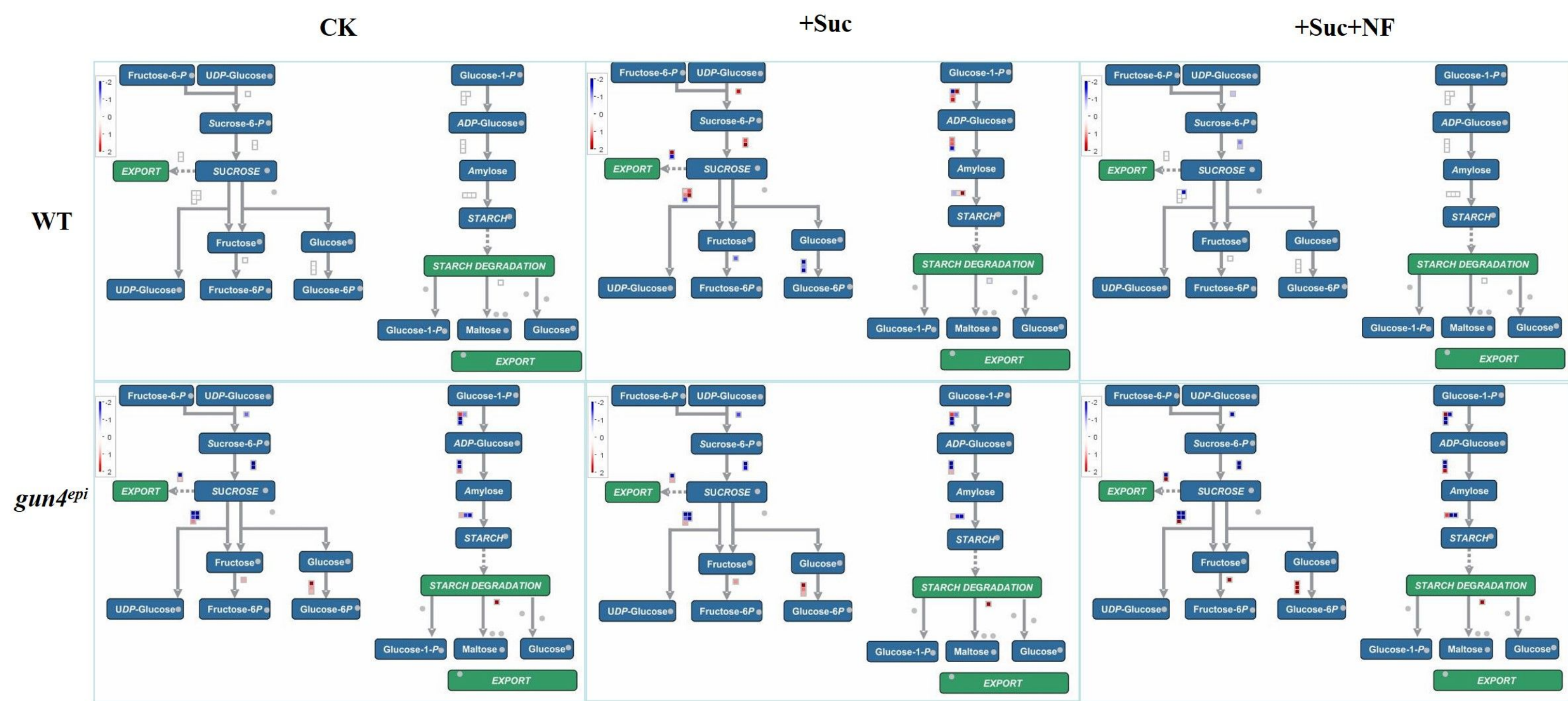
**Fig. S2** Expression of representative genes involved in sucrose biosynthesis, sucrose transports (SUT), starch biosynthesis, protein biosynthesis in leaves of wild-type (black bar) and *gun4<sup>epi</sup>* (blank bar) at 35 days-old-seedlings treated without (check, CK) or with 200  $\mu$ M sucrose (Suc) or Suc plus with 10  $\mu$ M norflurazon (Suc + NF).



**Fig. S3** Graphical representation for expression levels of genes involved in starch biosynthesis of 35 DAG seedlings in leaves. The small round balls represent the relative mRNA expression relative to WT and internal parameters. The depth of the color indicates the amount of expression. The orders of colored balls were WT, WT+suc, WT+suc+NF, MT, MT+suc, MT+suc+NF. Italics are genes Grey fonts represent metabolites. The large green and red balls represent enzymes and transports, respectively. *Abbreviations:* FBA, Fructose-1,6-bisphosphate aldolase; FBP, Fructose 1,6-bisphosphate; PGI, Phosphoglucose isomerase; PGM, Phosphoglucomutase; SPS, Sucrose-phosphate-synthase; SPP, Sucrose phosphate phosphatase; NIN3, Alkaline/neutral invertase; FrK, Fructokinase; HxK, Hexokinase; A/N-inv, alkaline/neutral invertase; SUS, Sucrose synthase; AGPL, ADP-glucose pyrophosphorylase large subunit; AGPS, ADP-glucose pyrophosphorylase small subunit; UGP, UDP-glucose pyrophosphorylase; SSI, II, III, IV, V, Soluble starch synthase I, II, III, IV, V; GBSSI, II, Granule bound starch synthase I, II; BE I, II, III, Starch branching enzyme I, II, III; PUL, pullulanase; ISA1, 2, 3, Isoamylase 1, 2, 3; FLO, Floury; DPE1, 2, Disproportionating enzyme; Pho1, 2, Plastidial starch phosphorylase 1, 2; AlaAT1, 4, Alanine aminotransferase 1, 4; PDI, Protein disulfate isomerase; PPDK, Pyruvate orthophosphate dikinase; Amy3D,  $\alpha$ -amylase 3D; GluA1, GluA3, glutelins A1, A3; CysR10, prolamin; SUT, Sucrose transporter; F6P, fructose-6-phosphate; G6P, glucose-6-phosphate; G1P, glucose-1-phosphate; ADPG, ADPglucose; UDPG, UDPglucose; Suc-P, sucrose-phosphate; LD, Linear dextrin; BG, Branched glucan; Suc, Sucrose; Fru, Fructose; Glu, Glucose; AAs, Amino acids.



**Fig. S4** Affection of *OsGUN4* mutation on *MYB14*. Expression levels of gene encoding transcriptional factors of MYB14 in wild-type (black bar) and *gun4<sup>epi</sup>* (blank bar) at 35 DAG seedlings treated without (check, CK) or with 200  $\mu$ M sucrose (Suc) or Suc plus with 10  $\mu$ M norflurazon (Suc+NF).



**Fig. S5** Comparisons of pathway involved in starch-sucrose between *gun4<sup>epi</sup>* and wild-type. The resulting file was loaded into the MapMan Image Annotator module to generate the metabolism overview map. On the logarithmic color scale, red represents downregulated and blue represents upregulated transcripts.

**Table S1** Primers for RT-q PCR and information of representative genes used in this study

| Name    | Accession NO. | Description                                   | Forward primer (5'→3') | Reverse primer (5'→3')  |
|---------|---------------|-----------------------------------------------|------------------------|-------------------------|
| OsGUN4  | AP014967      | Genome uncoupled 4                            | TTACCGGCAGGCCGACGAGA   | TGCCCAGGAGCTGTGTCCCT    |
| OsFBA   | AP014962      | Fructose-bisphosphate aldolase 5, cytosolic   | CTCATCTGCCAGGAGAACGG   | CAGGTCTTGATGTCGTGGGC    |
| OsFBP1  | AP014957      | Fructose-1,6-bisphosphatase 1                 | GTTCTGTCACGCTTGTTCTG   | TGAACTCCCCGAGAGATGGA    |
| OsFBP-L | AP014959      | Fructose-1,6-bisphosphatase like              | CAACTGCCTCAAATCGAGCG   | CACGATGTAGTTGCCCGAGT    |
| OsFBP2  | AP014961      | Fructose-1,6-bisphosphatase 2                 | CAAACAACGGGCCCTTGAAC   | CGTCATCATAGCTCCCCAGG    |
| OsFBP3  | AP008212      | Fructose-1,6-bisphosphatase 3                 | CCTTGATCCTTCCCTTG GGG  | TTGCATTGTTGAATCACAGACCT |
| OsPGI2  | AP014962      | Glucose-6-phosphate isomerase, cytosolic      | CCAATGGGCAACACAGCTTC   | CAAGTAAACGGGTGCTGGC     |
| OsPGM   | AP014966      | Phosphoglucomutase, chloroplastic             | TCAAGGGCTTGTTGTCTCGG   | AGGATCCGCATATGCACCAG    |
| OsSPS2  | AP014958      | Sucrose-phosphate synthase 2                  | CATTACGCATCACGTTCCC    | CGCCACTTTCACCAACAAGG    |
| OsSPS5  | AP014967      | Sucrose-phosphate synthase 5                  | GCGTCCAAGGTGAAGAAGGT   | GTGTAGACGAGGTTGCACCG    |
| OsSPPL1 | AP014957      | Sucrose-phosphatase 1                         | CCCTGCTGGCTTCCTGATAA   | CTTGAGGACTGCTCATCCG     |
| OsSPPL2 | AP014958      | Sucrose-phosphatase 2-like                    | TGGAAGGTGATGTGTGGTCG   | TGTGTTACCACGAAGCCCTC    |
| OsFrK1  | AP014964      | Fructokinase-2-like                           | TGACCTTGAAAAGCAACGGC   | GGATCAGGTCCAGGTTGAGC    |
| OsHXK1  | AP014963      | Hexokinase-1-like                             | TCCCATTGACGGAGTTTCGAC  | CTTCTCGTAGGTCTGCTCGC    |
| OsHXK4  | AP014963      | Hexokinase-4, chloroplastic-like              | GCGCTATGCAACAAGACACC   | CAGCAGAGAAGCTTG G GACA  |
| OsHXK7  | AP014961      | Cytosolic hexokinase                          | TGTGGCTGAAAACTTGCAGA   | AGGGAATACAGTTCAATGCTGGA |
| OsSUS1  | AP014959      | Sucrose synthase 1-like                       | TGAACGGAGTGTCTGGCTTC   | GGGTCTTCCTGGCACTTCTC    |
| OsSUS2  | AP014962      | Sucrose synthase 2-like                       | AGTCTTTGTCCAGCCTGCAT   | CCATGGCATGTTGCGATTGT    |
| OsSUS4  | AP014959      | Sucrose synthase 4-like                       | TTGGCTGGGGTTTATGGCTT   | CAAGATAGCGCCTGGTCTCC    |
| OsSUS5  | AP014960      | Sucrose synthase 5-like                       | GCTGGATCAAGGCACAGACT   | TGCAGGCTGAACAAATGCAC    |
| OsSUS6  | AP014958      | Sucrose synthase 6-like                       | CACAACCTACAGAGAGCGCA   | AGAATGGGCACACTTGCTT     |
| OsSUS7  | AP014960      | Sucrose synthase 7-like                       | GCTGGATCAAGGCACAGACT   | TGCAGGCTGAACAAATGCAC    |
| OsAGPL1 | AK100910      | ADP-glucose pyrophosphorylase large subunit 1 | AACAGCCACCGAGATTCAGC   | TGGCGGTAAGTTTCTCCGTG    |
| OsAGPL2 | AK071497      | ADP-glucose pyrophosphorylase large subunit 2 | GGAGCCGAGCTTCTGACTAT   | CCAAATCAGCACCTCTGGT     |
| OsAGPL3 | AK069296      | ADP-glucose pyrophosphorylase large subunit 3 | AGCGAGGGTGTCCAAGAAAG   | CCTTCCCGTCCTTGATGGTC    |

|          |          |                                                      |                          |                         |
|----------|----------|------------------------------------------------------|--------------------------|-------------------------|
| OsAGPL4  | AK121036 | ADP-glucose pyrophosphorylase large subunit 4        | AGTTTCCCATGGGTGCTTTCT    | GCACCCCGGTTCTAATCTT     |
| OsAGPS1  | AK073146 | ADP-glucose pyrophosphorylase small subunit 1        | GAAGGCGCAGTGATAGAGGA     | CCACCAGTCTCAGAAAGGGC    |
| OsAGPS2a | AK071826 | ADP-glucose pyrophosphorylase small subunit 2a       | AGGATGCTTTGCTCCCTAGC     | TTATAATGCCCCGCTGGTGC    |
| OsAGPS2b | AK103906 | ADP-glucose pyrophosphorylase small subunit 2b       | TACTTGCCCTTGACGACGTG     | CACGGAGGAGCTGAAGCATT    |
| OsUGP2   | AP014958 | UDP-glucosepyrophosphorylase 2                       | TACATATCTGTTCAACAATCAGC  | AGGTTTTAGTGACAAACGTTA   |
| OsGBSSI  | AK070431 | Granule-bound starch synthase 1                      | TGCAGGGGATGAGATACGGA     | AGTCTTGCCTTCGATGACCG    |
| OsGBSSII | AK067654 | Granule-bound starch synthase 2                      | GCTTCAACTGTCAAACGGGC     | AGCCATGCAGTTCTGAACCA    |
| OsSSI    | AK109458 | Soluble starch synthase I                            | TGGGCCTTCATGGATCAACC     | GGTCCTCGGAGAAATTCGCT    |
| OsSSIIa  | AK101978 | Soluble starch synthase IIa                          | GTGAAGAGACCATGTCCGCC     | CCAAGCTTCTTCAGGGAGGC    |
| OsSSIIb  | AK066446 | Soluble starch synthase IIb                          | TCGTCAAGGCCAAGTACCAG     | CAGAGCCGCCCTAGAGAAAA    |
| OsSSIIc  | AK072339 | Similar to Starch synthase II, chloroplast precursor | GTGGTCTTCGAGACACCGTT     | TCAGTCTGTTTGCCTCTGCC    |
| OsSSIIIa | AK061604 | Soluble starch synthase IIIa                         | TTGTTCTATGGTTTCTTTTGCGCT | CTCTTGCAAGGCATACACAGC   |
| OsSSIIIb | AK122098 | Soluble starch synthase IIIb                         | TGACGGCCTGTGTAGCTTTT     | GTTTGGTTCACGCTGCCAAT    |
| OsSSIVa  | AK103906 | Similar to Starch synthase IVa                       | CTATACCTGTGGAGCTGCGG     | GCTGAATGCCCTTTCCAAGC    |
| OsSSIVb  | AK067577 | Soluble starch synthase IVb                          | AGGCTAGTTCCTCAAAAGGGTG   | CTGGACTTGAGCCCAGAAGA    |
| OsSSV    | AP014958 | Similar to Starch synthase V                         | TCCTGAGGAAAGCTGAAGCAGA   | TATACTGCACCTGTCCATATTCT |
| OsBEI    | AK119436 | Starch branching enzyme I                            | GGAAGAAGGTTCACTCCCTGT    | GTGAGTGCTCATCTCCGAGC    |
| OsBEIIa  | AB023498 | Starch branching enzyme IIa                          | GCGTGCAGCTATTGACCAAC     | GCGGGTGAATCCAAGCTTTT    |
| OsBEIIb  | D16201   | starch branching enzyme IIb                          | AGCACTTCACTGCCGATTGT     | TCCGCTGGAGCATAGACAAC    |
| OsBEIII  | AP014962 | Similar to starch branching enzyme III               | GGGAGCTGACGAGCAATCAA     | CAATTCCAAGGAGTTGCGGC    |
| OsISA1   | AB093426 | Starch-debranching enzyme, Isoamylase 1              | CTGACTTGCAACGGTTCTGC     | AACCGTTGAGCTGTTGGGAA    |
| OsISA2   | AC132483 | Isoamylase 2                                         | GGAATCTTGCCTACAGATGACT   | TTGCAGAAGCAACTCCAAACT   |
| OsISA3   | AP005574 | Isoamylase 3                                         | CGACGATTTCTCGGTACGCA     | ACCATCTCACCTTTTGCGA     |
| PUL      | AB012915 | Pullulanase                                          | TGGGGCTTGAATTGCATCCT     | GAGACAACACTTCAACAACCTGG |
| Amy3E    | AK064300 | Alpha-amylase isozyme 3E                             | AGTAAGCGGAATGTACCCTGT    | TGCAAGTCTTTCTTGAGGATCG  |
| Amy3B    | AK241191 | Alpha-amylase isozyme 3B                             | CCAGTTGAACCCCTGGAAGA     | GCATAGCCTCAATGAGCAGC    |
| Amy3C    | AK101358 | Alpha-amylase isozyme 3C                             | CGGAGATGTCTACGTCGCAA     | GCCCACATCATAACCGAGTC    |
| Amy3D    | AK119761 | Alpha-amylase isozyme 3D precursor                   | CTCAACTGGCTCAAGTCCGA     | TCTTAGCGATGTCCGTGGAG    |
| OsPPDKB  | AK103898 | Pyruvate orthophosphate dikinase                     | GGCTGGGCTGGACTATGTTT     | GGGCGTCATCATCAGAGGAG    |

|               |              |                                                             |                         |                        |
|---------------|--------------|-------------------------------------------------------------|-------------------------|------------------------|
| PDI           | AK068268     | Protein disulfate isomerase                                 | GAGAGGGCATGGATGCTTGT    | TTGGCAAAATCTGGCGTTGG   |
| GluA1         | AK242245     | Glutelin type-A1 basic chain                                | GTAAGCAGCCAAGTGGCAAG    | AAACTGAGCCCGTGTTTCGAC  |
| GluA2         | AK107314     | Glutelin type-A2 precursor                                  | TTGTGTTCCCGTTCCAATGT    | AGATAAGGGAGGGTTGTCCA   |
| GluA3         | AK107271     | Glutelin type-A3 precursor                                  | TTCCATCTTCCGCGCACTT     | TGCTTGAGCCTCCTAGCTTC   |
| CysR10        | AP014959     | 10 kDa prolamin precursor                                   | CCATGGATCCGTGTAGGCAG    | CCATTGGCTGCGACATGAAC   |
| OsAlaAT1      | AP014966     | Alanine aminotransferase 1                                  | TCCCTCAGCTTAGTCTGCCA    | CGAGGAGACGAAGGGCATAG   |
| OsAlaAT4      | AP008216     | Alanine transaminase 4                                      | CACAGAGCCGGATGTGTTCT    | TGTCCAAACACTGAGCCAGG   |
| Globulin1     | AK105347     | Globulin1                                                   | GGCGGGGACGATCAATTACT    | AGGGACGGAGATGGTATGGA   |
| Globulin2     | AK121667     | Globulin2                                                   | GCAGCTGTGTGATCGAGAGG    | CCCCTTGGCTACACGTACAC   |
| 11s-Globulin  | AK121775     | 11s-Globulin                                                | GAGAAGCTGTTCGGTCCAA     | GACGCAATGGCAAAGGGAAG   |
| 10kD-Prolamin | AK108254     | 10kD-Prolamin                                               | CCATGGATCCGTGTAGGCAG    | CCATTGGCTGCGACATGAAC   |
| 13kD-Prolamin | AK242306     | 13kD-Prolamin                                               | GGACATTAACGTTGTCCAGGC   | TGAGCCAGATTCCGGTCAAT   |
| 17kD-Prolamin | AK242322     | 17kD-Prolamin                                               | GCAACAGGTGCAATTAGATGCT  | GACACCACACATGGAGGGTA   |
| 19kD-Globulin | AK287940     | 19kD-Globulin                                               | ACGACCCATAATGCCTGGTG    | AGATCCGCCAATTTTCAGGCT  |
| RA16          | AK242298     | Species of rice allergenic proteins                         | CGTTCTGCAACGTGGACATC    | GCTAGTAGCCAGTTCCTGGT   |
| RA17          | AK242340     | Species of rice allergenic proteins                         | TGTTGATGCATGAAGAAGAAA   | AGTAACATTACCATGCATAATC |
| RA5B          | AK242333     | Species of rice allergenic proteins                         | GAGGTGGTGTCTGCTACTGG    | CACACCACATACATGCACAGC  |
| RAG2          | AK107328     | Species of rice allergenic proteins                         | TGCTTTTCATTTGTCAGGAAGCA | TGCTACCCAATTGGCAAGATG  |
| RG21          | AK243000     | Species of rice allergenic proteins                         | TCGGTGCCTTCACTCCTAGA    | CACTCTGAGGCCTCGTTCTC   |
| OsbZIP58      | AP014963     | bZIP transcription factor 58                                | TGACCCAACAGATCCAGTGC    | ATTCATTCGAAGTTGCGCCG   |
| OsRSR1        | AP014961     | RICE STRACH REGULATOR 1                                     | TAGAGGCTGCAAGGGCTTATG   | CATCATATGTGCTGGGCTCG   |
| SnRK1A        | Os05g0530500 | Rice Snf1-related protein kinase1                           | GAGGTGATAGACACCCACAGC   | GGTGCTGCATAATTTGGGCT   |
| MYBS1         | Os01g0524500 | Transcription factor MYBS1                                  | ATGGACGGACATGAG         | GCTTTCACCGGGTGTA       |
| NAC36         | Os05g0426200 | No apical meristem (NAM) protein domain containing protein. | GGACAAATCGTTCCACACCAA   | CCCAATCAGTCCTGTTGCCTT  |
| MYB14         | Os01g0702700 | MYB transcription factor 14                                 | TGCGGTGGATCAACTACCTG    | CTAGGATCTCATGCAGGCCG   |
| FLO2          | AP014960     | FLOURY ENDOSPERM 2                                          | AACTGTTGGCACCACAGACA    | TCCTTTCCCTTTGCATGGGCT  |
| OsWRKY90      | AP014965     | SUSIBA2-like (WRKY transcription factor 90)                 | GAGGGGAAGCACAACCATGA    | AGCGTTTCCAGATCCAGAGC   |
| OsSUT2        | AP014968     | Sucrose transporter 2                                       | AACAACGCTACACAGGGACC    | TATCCGAGTCCTCCTTGGGT   |

OsSUT4

AP014958

Sucrose transporter 4

CCGCTTTTCTGGTTGCAGTT

AGCTCTGCAGGCTGTTACAA

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**Table S2** Two-way ANOVA test for contents of metabolites related to starch biosynthesis

| Difference          | SS          | df | MS          | F           | P-value     | F crit      |
|---------------------|-------------|----|-------------|-------------|-------------|-------------|
| <b>Sucrose</b>      |             |    |             |             |             |             |
| Genotype            | 2243.601    | 1  | 2243.601    | 8583.931    | 1.95E-38    | 4.170877    |
| Growth condition    | 209.8805    | 2  | 104.9402    | 401.4972    | 2.22E-22    | 3.31583     |
| Interaction         | 167.7829    | 2  | 83.89144    | 320.9654    | 5.58E-21    | 3.31583     |
| Interior            | 7.841167    | 30 | 0.261372    |             |             |             |
| Total               | 2629.106    | 35 |             |             |             |             |
| <b>Glucose</b>      |             |    |             |             |             |             |
| Genotype            | 88.42267778 | 1  | 88.42267778 | 1220.202855 | 7.35891E-26 | 4.170876786 |
| Growth condition    | 80.17243889 | 2  | 40.08621944 | 553.1761833 | 2.10923E-24 | 3.315829501 |
| Interaction         | 81.43077222 | 2  | 40.71538611 | 561.8584692 | 1.68008E-24 | 3.315829501 |
| Interior            | 2.173966667 | 30 | 0.072465556 |             |             |             |
| Total               | 252.1999    | 35 |             |             |             |             |
| <b>Fructose</b>     |             |    |             |             |             |             |
| Genotype            | 88.83063    | 1  | 88.83063    | 1823.434    | 2E-28       | 4.170877    |
| Growth condition    | 74.39202    | 2  | 37.19601    | 763.5258    | 1.87E-26    | 3.31583     |
| Interaction         | 81.47355    | 2  | 40.73678    | 836.2074    | 4.91E-27    | 3.31583     |
| Interior            | 1.461483    | 30 | 0.048716    |             |             |             |
| Total               | 246.1577    | 35 |             |             |             |             |
| <b>Total starch</b> |             |    |             |             |             |             |
| Genotype            | 224.0011    | 1  | 224.0011    | 2515.767    | 1.7E-30     | 4.170877    |
| Growth condition    | 66.16267    | 2  | 33.08134    | 371.5381    | 6.82E-22    | 3.31583     |
| Interaction         | 81.57954    | 2  | 40.78977    | 458.1118    | 3.29E-23    | 3.31583     |
| Interior            | 2.671167    | 30 | 0.089039    |             |             |             |
| Total               | 374.4145    | 35 |             |             |             |             |
| <b>Amylose</b>      |             |    |             |             |             |             |
| Genotype            | 53.26567    | 1  | 53.26567    | 408.8152    | 4.97E-19    | 4.170877    |
| Growth condition    | 16.07921    | 2  | 8.039603    | 61.70413    | 2.34E-11    | 3.31583     |
| Interaction         | 10.86191    | 2  | 5.430953    | 41.68268    | 2.19E-09    | 3.31583     |
| Interior            | 3.908783    | 30 | 0.130293    |             |             |             |
| Total               | 84.11556    | 35 |             |             |             |             |
| <b>Protein</b>      |             |    |             |             |             |             |
| Genotype            | 31.26674    | 1  | 31.26674    | 451.0746    | 1.25E-19    | 4.170877    |
| Growth condition    | 20.21902    | 2  | 10.10951    | 145.8464    | 3.51E-16    | 3.31583     |
| Interaction         | 22.79344    | 2  | 11.39672    | 164.4166    | 6.81E-17    | 3.31583     |
| Interior            | 2.079483    | 30 | 0.069316    |             |             |             |
| Total               | 76.35868    | 35 |             |             |             |             |

**Table S3** Two-way ANOVA test for activities of enzymes involved in starch biosynthesis

| Difference                                  | SS          | df | MS       | F        | P-value  | F crit   |
|---------------------------------------------|-------------|----|----------|----------|----------|----------|
| <b>Sucrose synthase (SS)</b>                |             |    |          |          |          |          |
| Genotype                                    | 1084.824    | 1  | 1084.824 | 2760.171 | 4.31E-31 | 4.170877 |
| Growth condition                            | 1193.247    | 2  | 596.6233 | 1518.018 | 7.21E-31 | 3.31583  |
| Interaction                                 | 1153.4      | 2  | 576.7    | 1467.326 | 1.19E-30 | 3.31583  |
| Interior                                    | 11.79083    | 30 | 0.393028 |          |          |          |
| Total                                       | 3443.261589 | 35 |          |          |          |          |
| <b>Sucrose phosphate synthase (SPS)</b>     |             |    |          |          |          |          |
| Genotype                                    | 119.0645    | 1  | 119.0645 | 3886.127 | 2.66E-33 | 4.170877 |
| Growth condition                            | 199.5529    | 2  | 99.77644 | 3256.588 | 8.32E-36 | 3.31583  |
| Interaction                                 | 201.5387    | 2  | 100.7693 | 3288.995 | 7.17E-36 | 3.31583  |
| Interior                                    | 0.91915     | 30 | 0.030638 |          |          |          |
| Total                                       | 521.0752    | 35 |          |          |          |          |
| <b>ADP-Glc pyrophosphorylase (AGPase)</b>   |             |    |          |          |          |          |
| Genotype                                    | 102.7858    | 1  | 102.7858 | 3106.823 | 7.43E-32 | 4.170877 |
| Growth condition                            | 30.91002    | 2  | 15.45501 | 467.1461 | 2.48E-23 | 3.31583  |
| Interaction                                 | 35.35529    | 2  | 17.67764 | 534.3279 | 3.5E-24  | 3.31583  |
| Interior                                    | 0.992517    | 30 | 0.033084 |          |          |          |
| Total                                       | 170.0436    | 35 |          |          |          |          |
| <b>Granule-bound starch synthase (GBSS)</b> |             |    |          |          |          |          |
| Genotype                                    | 19.1698     | 1  | 19.1698  | 226.9436 | 1.56E-15 | 4.170877 |
| Growth condition                            | 788.2894    | 2  | 394.1447 | 4666.122 | 3.86E-38 | 3.31583  |
| Interaction                                 | 808.3021    | 2  | 404.151  | 4784.583 | 2.65E-38 | 3.31583  |
| Interior                                    | 2.534083    | 30 | 0.084469 |          |          |          |
| Total                                       | 1618.295    | 35 |          |          |          |          |
| <b>Soluble starch synthase (SSS)</b>        |             |    |          |          |          |          |
| Genotype                                    | 8088.604    | 1  | 8088.604 | 49549.71 | 7.71E-50 | 4.170877 |
| Growth condition                            | 7246.68     | 2  | 3623.34  | 22196.1  | 2.77E-48 | 3.31583  |
| Interaction                                 | 7180.613    | 2  | 3590.307 | 21993.74 | 3.18E-48 | 3.31583  |
| Interior                                    | 4.897267    | 30 | 0.163242 |          |          |          |
| Total                                       | 22520.79    | 35 |          |          |          |          |
| <b>Starch branching enzyme (SBE)</b>        |             |    |          |          |          |          |
| Genotype                                    | 52.34523    | 1  | 52.34523 | 1036.642 | 7.98E-25 | 4.170877 |
| Growth condition                            | 31.95209    | 2  | 15.97604 | 316.3886 | 6.86E-21 | 3.31583  |
| Interaction                                 | 33.0398     | 2  | 16.5199  | 327.1591 | 4.25E-21 | 3.31583  |
| Interior                                    | 1.51485     | 30 | 0.050495 |          |          |          |
| Total                                       | 118.852     | 35 |          |          |          |          |

**Table S4** Differential expressed genes in *gun4<sup>epi</sup>* compared to wild-type

| Gene_id      | Readcount_<br><i>gun4<sup>epi</sup></i> | Readcount_<br>WT | log2Fold<br>Change | Gene name        | InterPro short description                                                         |
|--------------|-----------------------------------------|------------------|--------------------|------------------|------------------------------------------------------------------------------------|
| OS03G0382100 | 5.243124232                             | 123.9695056      | -4.56              |                  | 3-ktacl-CoA_syn                                                                    |
| OS04G0409900 | 34.37                                   | 5.47             | 2.65               |                  | 6-hairpin_glycosidase-like                                                         |
| OS04G0460300 | 7.380464301                             | 391.158247       | -5.73              | OSJNBA0072F16.7  | AA_transpt_TM                                                                      |
| OS01G0825800 | 480.2842383                             | 2853.219618      | -2.57              |                  | AA_transpt_TM                                                                      |
| OS06G0228500 | 276.56                                  | 52.51            | 2.40               |                  | AA_transpt_TM                                                                      |
| OS01G0612500 | 11.3830726                              | 252.7368816      | -4.47              |                  | AB_hydrolase                                                                       |
| OS07G0164900 | 615.30                                  | 139.70           | 2.14               | AAO              | ABA aldehyde oxidase                                                               |
| OS09G0332700 | 566.46                                  | 161.27           | 1.81               | OS09G0332700     | ABC_2_trans                                                                        |
| OS05G0189900 | 1.052732294                             | 205.8144172      | -7.61              |                  | Acid_phosphat_B                                                                    |
| OS06G0649800 | 15.90269832                             | 83.24402854      | -2.39              |                  | Adenine_glyco                                                                      |
| OS04G0604000 | 11.45837216                             | 53.27902553      | -2.22              | Os04g0604000     | ADF-H/Gelsolin-like_dom                                                            |
| OS04G0447700 | 40.64                                   | 7.72             | 2.40               | Os04g0447700     | Aldo/ket_red                                                                       |
| OS05G0565400 | 114.5821422                             | 576.5620764      | -2.33              |                  | Aldolase_TIM                                                                       |
| OS06G0354700 | 1816.26                                 | 554.23           | 1.71               | NYC3             | Alpha/beta hydrolase-fold family protein, Chlorophyll degradation during senescenc |
| OS11G0132600 | 154.85                                  | 36.20            | 2.10               |                  | Alpha-L-AF_C                                                                       |
| OS08G0245200 | 16.79421341                             | 106.6374364      | -2.67              | 4CL1             | AMP-dep_Synth/Lig                                                                  |
| OS05G0124000 | 46.1646835                              | 366.8103185      | -2.99              |                  | Ankyrin_rpt                                                                        |
| OS09G0328600 | 0                                       | 27.02682351      | Inf                |                  | Ankyrin_rpt                                                                        |
| OS02G0657000 | 0.246785383                             | 27.9786978       | -6.82              |                  | AP2/ERF_dom                                                                        |
| OS01G0141000 | 94.75637452                             | 2085.045057      | -4.46              | Os01g0141000     | AP2/ERF_dom                                                                        |
| OS07G0617000 | 136.142977                              | 621.4626832      | -2.19              |                  | AP2/ERF_dom                                                                        |
| OS09G0286600 | 901.681627                              | 3024.264071      | -1.75              |                  | AP2/ERF_dom                                                                        |
| OS09G0434500 | 3855.383198                             | 12586.15619      | -1.71              | OJ1081_G10.25    | AP2/ERF_dom                                                                        |
| OS01G0140700 | 0                                       | 57.61842447      | Inf                |                  | AP2/ERF_dom                                                                        |
| OS03G0150200 | 9.97                                    | 0.00             | #NAME?             |                  | AP2/ERF_dom                                                                        |
| OS09G0522100 | 910.73                                  | 169.46           | 2.43               | DREB1H           | AP2/ERF_dom                                                                        |
| OS02G0764700 | 122.98                                  | 23.84            | 2.37               |                  | AP2/ERF_dom                                                                        |
| OS05G0497200 | 440.06                                  | 105.16           | 2.07               |                  | AP2/ERF_dom                                                                        |
| OS05G0549800 | 254.02                                  | 70.14            | 1.86               | Os05g0549800     | AP2/ERF_dom                                                                        |
| OS09G0457900 | 1576.77                                 | 220.95           | 2.84               | ERF102           | AP2/ERF_dom, Regulation of the internode elongation                                |
| OS04G0650700 | 3514.17                                 | 1011.15          | 1.80               | ASNase2          | Asparaginase 2                                                                     |
| OS04G0469300 | 14.33131916                             | 212.9574612      | -3.89              | OSJNBA0016O02.20 | ATFP4. (Os04t0469300-01)                                                           |
| OS06G0229066 | 460.13                                  | 6.95             | 6.05               | Os06g0229066     | ATP-dependent zinc metalloprotease FTSH 6, chloroplastic.                          |
| OS08G0529000 | 22.13                                   | 0.00             | #NAME?             | OSPIN5C          | Auxin_eff                                                                          |

|              |             |             |        |                |                                                                                       |
|--------------|-------------|-------------|--------|----------------|---------------------------------------------------------------------------------------|
| OS12G0609600 | 0.797518091 | 190.0102142 | -7.9   |                | Auxin_inducible_ARG7                                                                  |
| OS02G0512000 | 0           | 14.58908028 | Inf    |                | Auxin_inducible_ARG7                                                                  |
| OS04G0662200 | 0           | 15.96664453 | Inf    |                | Auxin_inducible_ARG7                                                                  |
| OS01G0768333 | 98.30       | 16.08       | 2.61   | B1143G03.17    | Auxin_inducible_ARG7                                                                  |
| OS08G0524800 | 8.896521321 | 45.57325995 | -2.36  | OJ1191_A10.109 | bHLH_dom                                                                              |
| OS05G0139100 | 489.17      | 45.31       | 3.43   | APG            | bHLH_dom                                                                              |
| OS06G0493100 | 367.20      | 86.61       | 2.08   |                | Brown planthopper induced008a                                                         |
| OS11G0111900 | 2.654357496 | 48.30282945 | -4.19  |                | BTB/POZ-like                                                                          |
|              |             |             |        |                | B-type response regulator, Floral inducer to promote short-day (SD) flowering pathway |
| OS10G0463400 | 112.49      | 17.53       | 2.68   | EF1            | Butirosin_synth_BtrG-like                                                             |
| OS02G0465900 | 792.6748763 | 3765.609508 | -2.25  |                | Ca/CaM-dep_Ca-dep_prot_Kinase                                                         |
| OS11G0113700 | 113.0424994 | 609.8299513 | -2.43  | Os11g0113700   | Ca/CaM-dep_Ca-dep_prot_Kinase                                                         |
| OS12G0113500 | 260.3790859 | 957.9782711 | -1.88  | Os12g0113500   | CAAD_dom                                                                              |
| OS06G0217700 | 8.903320702 | 69.9874239  | -2.97  |                | Carbonic_anhydrase_a-class                                                            |
| OS08G0423500 | 1.012427994 | 1327.316082 | -10.36 |                | Carbonic_anhydrase_a-class                                                            |
| OS08G0423600 | 0.501999587 | 548.9905428 | -10.1  |                | CAT-like_dom                                                                          |
| OS01G0179000 | 4.704499945 | 32.65551329 | -2.8   |                | Chalcone_isomerase                                                                    |
| OS02G0778500 | 34.23662577 | 135.4200663 | -1.98  | OJ1293_A01.5   | Chloro_AB-bd_pln                                                                      |
| OS09G0439500 | 209.2772044 | 2820.612282 | -3.75  |                | Chloroa_b-bind                                                                        |
| OS04G0690800 | 167.2605693 | 815.4000824 | -2.29  |                | Cit_transptr-like_dom                                                                 |
| OS10G0447900 | 118.9554294 | 419.8546507 | -1.82  |                | Class_I_gatase-like                                                                   |
| OS09G0424200 | 71.2164361  | 618.1332478 | -3.12  |                | Class_I_gatase-like                                                                   |
| OS03G0685300 | 196.292029  | 723.4794647 | -1.88  |                | ClpA/B                                                                                |
| OS02G0526400 | 406.53      | 66.19       | 2.62   | CLPD1          | ConA-like_subgrp                                                                      |
| OS06G0697000 | 23.2526884  | 3610.290864 | -7.28  |                | ConA-like_subgrp                                                                      |
| OS09G0351700 | 0.757213791 | 111.3157747 | -7.2   | OS09G0351700   | ConA-like_subgrp                                                                      |
| OS06G0285400 | 1.076178955 | 18.66143016 | -4.12  | P0491D10.34    | ConA-like_subgrp                                                                      |
| OS07G0480800 | 6.900281935 | 55.73805031 | -3.01  | P0434A03.134   | ConA-like_subgrp                                                                      |
| OS07G0542600 | 42.90931981 | 190.1512671 | -2.15  |                | ConA-like_subgrp                                                                      |
| OS11G0539200 | 0           | 150.6562602 | Inf    |                | ConA-like_subgrp                                                                      |
| OS04G0632901 | 136.16      | 11.42       | 3.58   |                | ConA-like_subgrp                                                                      |
| OS09G0268000 | 302.05      | 54.12       | 2.48   | B1008E06.18    | ConA-like_subgrp                                                                      |
| OS10G0136400 | 104.84      | 24.42       | 2.10   |                | Conserved hypothetical protein                                                        |
| OS05G0521700 | 25.71071215 | 97.53850315 | -1.92  |                | Conserved hypothetical protein                                                        |
| OS09G0438100 | 480.5829163 | 1727.013882 | -1.85  |                | Conserved hypothetical protein                                                        |
| OS05G0516100 | 112.4086159 | 393.8220376 | -1.81  |                | Conserved hypothetical protein                                                        |
| OS11G0670900 | 58.05990302 | 195.8241402 | -1.75  |                | Conserved hypothetical protein                                                        |
| OS03G0826900 | 21.61       | 0.00        | #NAME? | OS03G0826900   | Conserved hypothetical protein                                                        |
| OS03G0124500 | 231.66      | 17.29       | 3.74   |                | Conserved hypothetical protein                                                        |
| OS03G0766600 | 151.04      | 14.72       | 3.36   | Os03g0766600   | Conserved hypothetical protein                                                        |
| OS05G0253200 | 203.51      | 27.51       | 2.89   | Os05g0253200   | Conserved hypothetical protein                                                        |

|              |             |             |       |                  |                                                   |
|--------------|-------------|-------------|-------|------------------|---------------------------------------------------|
| OS01G0959750 | 628.51      | 108.06      | 2.54  | Os01g0959750     | Conserved hypothetical protein                    |
| OS10G0516900 | 58.72       | 10.66       | 2.46  |                  | Conserved hypothetical protein                    |
| OS08G0351300 | 84.36       | 18.55       | 2.19  |                  | Conserved hypothetical protein                    |
| OS06G0133500 | 458.69      | 129.37      | 1.83  | P0679C08.32      | Conserved hypothetical protein                    |
| OS05G0181700 | 837.74      | 249.91      | 1.75  | Os05g0181700     | Conserved hypothetical protein                    |
| OS12G0516200 | 1313.55     | 414.81      | 1.66  |                  | Conserved hypothetical protein                    |
| OS06G0133400 | 1786.32     | 444.85      | 2.01  | Os06g0133400     | Conserved hypothetical protein.                   |
| OS01G0143900 | 31.22462825 | 349.8829924 | -3.49 |                  | Conserved hypothetical protein.                   |
| OS01G0838350 | 16.12731702 | 147.6369538 | -3.19 |                  | Conserved hypothetical protein.                   |
| OS02G0246900 | 5.84259006  | 58.39989927 | -3.32 |                  | Conserved hypothetical protein.                   |
| OS02G0261000 | 0.861269052 | 58.32446433 | -6.08 |                  | Conserved hypothetical protein.                   |
| OS02G0582900 | 0.246785383 | 72.8201029  | -8.2  |                  | Conserved hypothetical protein.                   |
| OS03G0118100 | 0.542303887 | 17.99787617 | -5.05 |                  | Conserved hypothetical protein.                   |
| OS03G0672400 | 0.246785383 | 13.85914163 | -5.81 |                  | Conserved hypothetical protein.                   |
| OS03G0713200 | 6.010606643 | 37.56977465 | -2.64 |                  | Conserved hypothetical protein.                   |
| OS03G0806800 | 2.677804157 | 92.77954919 | -5.11 |                  | Conserved hypothetical protein.                   |
| OS04G0382900 | 0           | 7.782629553 | Inf   | OSJNBA0072D21.16 | Conserved hypothetical protein.                   |
| OS05G0142400 | 5.919729422 | 49.79865191 | -3.07 |                  | Conserved hypothetical protein.                   |
| OS08G0474500 | 5.109033291 | 32.91165247 | -2.69 | P0451G12.14      | Conserved hypothetical protein.                   |
| OS09G0494500 | 5.723516959 | 38.02145416 | -2.73 |                  | Conserved hypothetical protein.                   |
| OS10G0128400 | 76.66278253 | 1812.727892 | -4.56 |                  | Conserved hypothetical protein.                   |
| OS10G0508900 | 0.255214204 | 26.14517868 | -6.68 |                  | Conserved hypothetical protein.                   |
| OS10G0509401 | 312.4848597 | 2938.265117 | -3.23 | OS10G0509401     | Conserved hypothetical protein.                   |
| OS12G0147200 | 2.128911249 | 79.36293124 | -5.22 | Os12g0147200     | Conserved hypothetical protein.                   |
| OS06G0674100 | 34.12       | 4.76        | 2.84  | Os06g0674100     | Conserved hypothetical protein.                   |
| OS03G0766800 | 4736.67     | 963.74      | 2.30  | OSJNBA0079B15.9  | Conserved hypothetical protein.                   |
| OS01G0183850 | 97.18       | 22.49       | 2.11  |                  | Conserved hypothetical protein.                   |
| OS11G0641800 | 0.829393571 | 632.2401545 | -9.57 | Os11g0641800     | Cu_oxidase_CS                                     |
| OS04G0208200 | 105.54      | 17.43       | 2.60  | Os04g0208200     | Cysteine proteinase.                              |
| OS11G0635300 | 1.363268639 | 26.99907993 | -4.31 |                  | Cyt_P450                                          |
| OS03G0602300 | 108.433815  | 791.4011338 | -2.87 | OS03G0602300     | Cyt_P450                                          |
| OS12G0139300 | 77.48416801 | 346.0445685 | -2.16 |                  | Cyt_P450                                          |
| OS10G0546600 | 261.0376713 | 900.073593  | -1.79 |                  | Cyt_P450                                          |
| OS09G0403300 | 64.83       | 2.86        | 4.50  |                  | Cyt_P450                                          |
| OS08G0507100 | 23.17       | 2.16        | 3.42  |                  | Cyt_P450                                          |
| OS11G0489250 | 1155.94     | 140.68      | 3.04  |                  | Cyt_P450                                          |
| OS02G0323600 | 151.47      | 19.63       | 2.95  |                  | Cyt_P450                                          |
| OS07G0518500 | 179.58      | 29.03       | 2.63  | Os07g0518500     | Cyt_P450                                          |
| OS03G0850200 | 41.57       | 8.09        | 2.36  | Os03g0850200     | Cyt_P450                                          |
| OS09G0522000 | 2115.83     | 390.73      | 2.44  |                  | Dehydration-responsive element-binding protein 1B |
| OS11G0645400 | 0.287089684 | 114.1977929 | -8.64 |                  | Disease-R_pln                                     |
| OS11G0214400 | 1.003999174 | 37.94106973 | -5.24 |                  | Disease-R_pln                                     |

|              |             |             |        |                      |                               |
|--------------|-------------|-------------|--------|----------------------|-------------------------------|
| OS07G0617100 | 22.50909119 | 300.8447186 | -3.74  |                      | Disease-R_pln                 |
| OS11G0644700 | 0           | 41.2131701  | Inf    |                      | Disease-R_pln                 |
| OS06G0650900 | 4340.31     | 1208.62     | 1.84   |                      | DnaJ_domain                   |
| OS09G0508500 | 2.367267812 | 192.7045947 | -6.35  | DRB5                 | dsRNA-bd_dom                  |
| OS01G0973100 | 10.03       | 0.00        | #NAME? | Os01g0973100         | DUF239                        |
| OS03G0310600 | 32.99610983 | 472.9498456 | -3.84  |                      | DUF247_pln                    |
| OS08G0356700 | 197.35      | 38.22       | 2.37   |                      | DUF247_pln                    |
| OS01G0678000 | 94.19       | 10.66       | 3.14   |                      | DUF2921                       |
| OS01G0678100 | 1432.20     | 340.46      | 2.07   |                      | DUF2921                       |
| OS03G0168200 | 911.54      | 291.55      | 1.64   |                      | DUF3110                       |
| OS07G0680600 | 3597.80     | 1051.90     | 1.77   | Os07g0680600         | DUF3133                       |
| OS01G0812900 | 324.930174  | 1077.587301 | -1.73  | P0425G02.34          | DUF3411_plant                 |
| OS06G0543601 | 57.27       | 10.88       | 2.40   | Os06g0543601         | DUF3778                       |
| OS03G0740200 | 12.14028639 | 141.6285114 | -3.54  |                      | DUF4228_plant                 |
| OS09G0493000 | 45.60       | 5.12        | 3.16   |                      | DUF4228_plant                 |
| OS05G0552800 | 1236.69     | 232.71      | 2.41   |                      | DUF4228_plant                 |
| OS02G0193300 | 1150.42     | 229.52      | 2.33   | P0437H03.120         | DUF4228_plant                 |
| OS02G0720400 | 6.326102568 | 62.22927346 | -3.3   |                      | DUF506_pln                    |
| OS10G0516701 | 12.99333698 | 73.42137304 | -2.5   |                      | DUF604                        |
| OS01G0611000 | 1.546303061 | 289.0803911 | -7.55  |                      | DUF642                        |
| OS05G0514400 | 1.108054435 | 219.6075357 | -7.63  | Os05g0514400         | DUF688                        |
| OS02G0229800 | 13.49349677 | 70.23518693 | -2.38  |                      | DUF761_pln                    |
| OS03G0272900 | 1287.57     | 274.62      | 2.23   |                      | DVL                           |
| OS03G0758500 | 87.73       | 11.88       | 2.89   | ENODL12              | early nodulin-like protein 12 |
| OS06G0254600 | 35.312384   | 287.7244851 | -3.03  |                      | EF_hand_dom                   |
| OS01G0955100 | 3400.11     | 797.62      | 2.09   | Os01g0955100         | EF_hand_dom                   |
| OS09G0471600 | 1.363268639 | 16.73848871 | -3.62  |                      | EG-like_dom                   |
| OS08G0508700 | 39.46317399 | 248.014153  | -2.65  | B1168A08.22          | Ethylene_insens-like_DNA-bd   |
| OS01G0823100 | 0.501999587 | 62.11427973 | -6.95  | EXPA2                | Expansin                      |
| OS05G0477600 | 0           | 42.68578031 | Inf    | Os05g0477600         | Expansin                      |
| OS10G0556100 | 1.331393158 | 95.35681978 | -6.16  | Os10g0556100         | Expansin/allergen_DPBB_dom    |
| OS10G0483500 | 31.47637321 | 220.6396772 | -2.81  | Os10g0483500         | FAD-bd_2_sub1                 |
| OS04G0578600 | 31.39       | 4.68        | 2.75   | Os04g0578600         | FAD-bd_8                      |
| OS01G0594800 | 15.72462348 | 144.3645408 | -3.2   | Os01g0594800         | FAD-dep_OxRdtase              |
| OS01G0668100 | 0.74878497  | 265.9353957 | -8.47  | OSJNBB0063G05.3<br>5 | FAS1_domain                   |
| OS04G0574200 | 1.586607362 | 23.65389138 | -3.9   |                      | FAS1_domain                   |
| OS10G0370500 | 6.272409866 | 69.98332311 | -3.48  |                      | Fascin                        |
| OS05G0244500 | 55.02112869 | 252.9774657 | -2.2   | Os05g0244500         | Fascin                        |
| OS05G0131500 | 30.3327637  | 175.3282614 | -2.53  | Os05g0131500         | Ferroportin-1                 |
| OS07G0112100 | 13.02705226 | 65.29988551 | -2.33  |                      | Flavin_mOase                  |
| OS07G0671000 | 1166.53     | 83.84       | 3.80   |                      | FPF1                          |
| OS04G0282400 | 17475.30    | 112.65      | 7.28   | Os04g0282400         | FPF1 protein-like (RAA1)      |
| OS06G0157700 | 86.51       | 16.64       | 2.38   | HD3A                 | FT                            |

|              |             |             |         |                      |                                                |
|--------------|-------------|-------------|---------|----------------------|------------------------------------------------|
| OS06G0229000 | 411.83      | 7.59        | 5.76    | Os06g0229000         | FtsH protease (VAR2) (Zinc dependent protease) |
| OS01G0883800 | 322.68      | 6.55        | 5.62    | 20OX2                | GA C20oxidase2                                 |
| OS03G0760800 | 0           | 41.90723259 | Inf     |                      | GASA                                           |
| Novel00135   | 11.83       | 0.36        | 5.06    | --                   | GATA zinc finger family protein                |
| OS01G0727100 | 0.255214204 | 37.31766724 | -7.19   | P0042A10.33          | GAUT                                           |
| OS04G0640700 | 0.287089684 | 197.4837146 | -9.43   |                      | Glyco_hydro_3                                  |
| OS01G0268600 | 234.2572123 | 810.5103497 | -1.79   |                      | Glyco_hydro_31                                 |
| OS01G0813700 | 0.246785383 | 43.56951591 | -7.46   | BGLU2                | Glyco_hydro_catalytic_dom                      |
| OS05G0375400 | 1659.22674  | 19127.88053 | -3.53   |                      | Glyco_hydro_catalytic_dom                      |
| OS02G0771700 | 21.62805508 | 214.0669897 | -3.31   |                      | Glyco_hydro_catalytic_dom                      |
| OS06G0179000 | 128.036333  | 853.0720723 | -2.74   |                      | Glyco_hydro_catalytic_dom                      |
| OS03G0703000 | 134.6494362 | 742.2929307 | -2.46   | Os03g0703000         | Glyco_hydro_catalytic_dom                      |
| OS01G0940800 | 20.0408879  | 87.74291709 | -2.13   |                      | Glyco_hydro_catalytic_dom                      |
| OS04G0474800 | 248.0140883 | 1045.693724 | -2.08   | Os04g0474800         | Glyco_hydro_catalytic_dom                      |
| OS06G0133000 | 6.376465127 | 81.05640959 | -3.67   | WAXY                 | Glyco_trans_1                                  |
| OS03G0692000 | 12.37205393 | 108.9301748 | -3.14   | OSJNBB0101N11.1<br>2 | Glyco_trans_14                                 |
| OS06G0573600 | 192.0340105 | 5879.946663 | -4.94   |                      | Glycoside_Hdrlase_35                           |
| OS06G0475400 | 121.93      | 25.21       | 2.27    | P0021H10.18          | Glycosyltransferase_AER61                      |
| OS10G0329900 | 42.50       | 5.11        | 3.05    |                      | GNK2                                           |
| OS04G0197100 | 823.24      | 224.71      | 1.87    |                      | GNK2                                           |
| OS03G0603600 | 133.8767838 | 755.846263  | -2.5    |                      | GP_PDE_dom                                     |
| OS03G0781000 | 154.197962  | 596.4257095 | -1.95   | OS03G0781000         | GTP_binding_domain                             |
| OS11G0267000 | 1945.540081 | 16788.81483 | -3.1093 |                      | GUN4-domain like                               |
| OS04G0496300 | 0.861269052 | 35.46696527 | -5.36   |                      | H0306B06.4 protein.                            |
| OS02G0526000 | 90.85775023 | 284.9570177 | -1.65   | Os02g0526000         | H0502B11.6 protein                             |
| OS05G0442550 | 447.09      | 65.11       | 2.78    |                      | H0801D08.16 protein                            |
| OS01G0186900 | 2388.75     | 563.72      | 2.08    | Os01g0186900         | HARBI1_dom                                     |
| OS09G0272000 | 233.13      | 59.53       | 1.97    | OS09G0272000         | Heavy metal transport/detoxification protein   |
| OS01G0927300 | 3.785858592 | 644.212645  | -7.41   | OSJNBA0093F16.2<br>8 | HeavyMe-assoc_HMA                              |
| OS04G0401000 | 53.27181379 | 2671.802259 | -5.65   | OSJNBB0014D23.1<br>6 | HeavyMe-assoc_HMA                              |
| OS01G0826000 | 153.78      | 37.47       | 2.04    | P0439E11.20          | HeavyMe-assoc_HMA                              |
| OS12G0415400 | 57.19       | 13.13       | 2.12    |                      | Histone H3                                     |
| OS02G0258200 | 1.027445834 | 16.08440316 | -3.97   | Os02g0258200         | HMG_box_dom                                    |
| OS03G0123500 | 2.622482016 | 151.0225492 | -5.85   | Os03g0123500         | Homeobox_dom                                   |
| OS05G0579300 | 52.48810482 | 330.5459129 | -2.65   | ZHD6                 | Homeodomain_ZF_HD                              |
| OS05G0530400 | 168.87      | 31.69       | 2.41    | Os05g0530400         | HSF_fam                                        |
| OS09G0445600 | 0           | 9.425801423 | Inf     | OJ1123_B08.25        | HSP20                                          |
| OS09G0379600 | 369.72      | 95.45       | 1.95    | OS09G0379600         | HTH_motif                                      |
| Novel00500   | 34.63       | 3.66        | 3.24    | --                   | hydroxyproline-rich glycoprotein               |

|              |             |             |        |                      |                                                   |
|--------------|-------------|-------------|--------|----------------------|---------------------------------------------------|
|              |             |             |        |                      | family protein                                    |
| OS11G0707100 | 81.26       | 4.98        | 4.03   | OS11G0707100         | Hypothetical conserved gene                       |
| OS01G0195300 | 141.43      | 32.83       | 2.11   |                      | Hypothetical conserved gene                       |
| OS06G0678500 | 662.25      | 185.83      | 1.83   | B1153E06.42          | Hypothetical conserved gene                       |
| OS02G0231000 | 0           | 16.55820263 | Inf    | Os02g0231000         | Hypothetical conserved gene.                      |
| OS03G0642450 | 7.563498724 | 38.91658681 | -2.36  | Os03g0642450         | Hypothetical conserved gene.                      |
| OS06G0531751 | 27.00364081 | 362.8079173 | -3.75  | Os06g0531751         | Hypothetical conserved gene.                      |
| OS10G0128502 | 11.10257193 | 261.8571792 | -4.56  | Os06g0531751         | Hypothetical conserved gene.                      |
| OS11G0264500 | 68.8270016  | 2772.463053 | -5.33  |                      | Hypothetical conserved gene.                      |
| OS07G0695700 | 74.05       | 11.80       | 2.65   |                      | Hypothetical conserved gene.                      |
| OS02G0124866 | 725.8305626 | 3327.395535 | -2.2   |                      | Hypothetical gene                                 |
| OS09G0449700 | 87.27       | 24.56       | 1.83   | Os09g0449700         | Hypothetical gene                                 |
| OS11G0699532 | 77.45       | 2.89        | 4.74   |                      | Hypothetical gene.                                |
| OS05G0202800 | 3446.72     | 135.97      | 4.66   | MT3B                 | Hypothetical gene.                                |
| OS03G0195475 | 230.413632  | 805.6223215 | -1.81  | Os03g0195475         | Hypothetical protein                              |
| OS06G0263450 | 31.60       | 0.00        | #NAME? |                      | Hypothetical protein                              |
| OS04G0447950 | 32.99       | 1.08        | 4.93   |                      | Hypothetical protein                              |
| OS08G0200750 | 29.95       | 1.81        | 4.05   | Os08g0200750         | Hypothetical protein                              |
| OS01G0602466 | 67.36       | 5.04        | 3.74   | Os01g0602466         | Hypothetical protein                              |
| OS02G0571000 | 50.12       | 7.89        | 2.67   |                      | Hypothetical protein                              |
| OS01G0341750 | 271.94      | 57.20       | 2.25   | Os01g0341750         | Hypothetical protein                              |
| Novel00654   | 33.48       | 3.10        | 3.43   | --                   | hypothetical protein                              |
| Novel00450   | 183.03      | 42.98       | 2.09   | --                   | hypothetical protein                              |
| Novel00223   | 100.43      | 20.09       | 2.32   | --                   | hypothetical protein                              |
|              |             |             |        |                      | LOC_Os12g42830                                    |
| Novel00564   | 1.569749722 | 18.64961496 | -3.57  | --                   | hypothetical protein OsI_21960                    |
| Novel00767   | 18.37239195 | 205.8569975 | -3.49  | --                   | hypothetical protein OsI_31134                    |
| Novel00097   | 55.96       | 9.86        | 2.50   | --                   | hypothetical protein OsI_32666                    |
| Novel00144   | 86.90       | 16.10       | 2.43   | --                   | hypothetical protein OsJ_17646                    |
| Novel00787   | 21.58       | 1.45        | 3.89   | --                   | hypothetical protein OsJ_28778                    |
| OS03G0206150 | 4.757982285 | 29.32106004 | -2.62  |                      | Hypothetical protein.                             |
| OS03G0782200 | 265.437978  | 39188.95367 | -7.21  |                      | Hypothetical protein.                             |
| OS06G0220100 | 0           | 9.918294188 | Inf    | Os06g0220100         | Hypothetical protein.                             |
| OS08G0411250 | 0.255214204 | 9.829115447 | -5.27  |                      | Hypothetical protein.                             |
| OS11G0291475 | 0.255214204 | 138.861567  | -9.09  | Os11g0291475         | Hypothetical protein.                             |
| OS07G0131001 | 168.30      | 10.88       | 3.95   | Os07g0131001         | Hypothetical protein.                             |
| OS02G0767300 | 0.829393571 | 53.19513303 | -6     |                      | IPNS-like                                         |
| OS04G0581100 | 8.913589323 | 68.22088216 | -2.94  | OSJNBA0064M23.<br>15 | IPNS-like                                         |
| OS03G0752800 | 34.53       | 1.27        | 4.76   |                      | Isoform 2 of MADS-box<br>transcription factor 14  |
| OS01G0841700 | 1025.84     | 216.46      | 2.24   | ERG1                 | Isoform ERG1b of<br>Elicitor-responsive protein 1 |
| OS01G0896400 | 1.658787143 | 22.78298185 | -3.78  |                      | JHL23J11.5 protein.                               |

|              |             |             |       |                 |                                                            |
|--------------|-------------|-------------|-------|-----------------|------------------------------------------------------------|
| OS11G0547000 | 27.50932    | 105.8439718 | -1.94 |                 | Kelch-typ_b-propeller                                      |
| OS06G0627500 | 0.861269052 | 24.86190484 | -4.85 |                 | L_dom-like                                                 |
| OS10G0127900 | 5.755392439 | 34.48241029 | -2.58 | OS10G0127900    | L_dom-like                                                 |
| OS07G0568700 | 0           | 82.66429803 | Inf   | FOR1            | L_dom-like                                                 |
| OS02G0156633 | 76.18       | 16.51       | 2.21  | Os02g0156633    | L_dom-like                                                 |
| OS04G0685400 | 9.581555331 | 50.44519761 | -2.4  |                 | LEA-14                                                     |
| OS09G0268100 | 255.82      | 55.67       | 2.20  |                 | Lectin-like receptor kinase 7.                             |
| OS04G0480500 | 60.23       | 13.34       | 2.18  | OSJNBB0011N17.1 | Leucine-rich repeat                                        |
| OS05G0399800 | 47.40       | 3.66        | 3.69  |                 | Leucine-rich repeat, N-terminal domain containing protein. |
| OS08G0509100 | 612.98      | 114.69      | 2.42  | Os08g0509100    | LipOase                                                    |
| OS02G0194700 | 7282.16     | 2074.98     | 1.81  | OJ1225_F07.1    | LipOase                                                    |
| OS08G0508800 | 151.71      | 9.93        | 3.93  | CM-LOX1         | Lipoxygenase, chloroplast precursor                        |
| OS06G0218900 | 1.371697459 | 13.90448623 | -3.34 |                 | LMBR1-like_membr_prot                                      |
| OS03G0609500 | 264.21      | 86.15       | 1.62  |                 | LOB                                                        |
| OS10G0555900 | 6.299325766 | 502.2589068 | -6.32 | EXPB3           | LolPI                                                      |
| OS06G0157500 | 180.88      | 48.05       | 1.91  | HD3B            | lorigen, Flowering time, Long-day promotion                |
| OS04G0373400 | 1033.61     | 278.14      | 1.89  | Os04g0373400    | MATE                                                       |
| OS12G0571100 | 3.535603969 | 178.1953497 | -5.66 | MT4C            | Metalthion_15p                                             |
| OS05G0231700 | 61.09825662 | 468.9663424 | -2.94 | Os05g0231700    | MIP                                                        |
| OS06G0336200 | 2508.357096 | 11269.09247 | -2.17 | TIP2-2          | MIP                                                        |
| OS01G0225000 | 35.14       | 6.22        | 2.50  |                 | Mit_carrier                                                |
| OS04G0554200 | 1.242355737 | 45.03349399 | -5.18 |                 | MSP_dom                                                    |
| OS10G0419400 | 32.58570763 | 205.7983273 | -2.66 | ARD1            | MTCBP-1_eukaryotes                                         |
| OS11G0303800 | 491.6006793 | 3379.405939 | -2.78 |                 | Myb_DNA-bind_5                                             |
| OS02G0104500 | 33.29148924 | 180.3899406 | -2.44 |                 | Myb-like_dom                                               |
| OS02G0742700 | 3.411571287 | 51.37326694 | -3.91 | OJ1734_E02.2    | MYC/MYB_N                                                  |
| OS07G0566500 | 24.43       | 2.13        | 3.52  | ONAC010         | NAC-dom                                                    |
| OS01G0675800 | 409.56      | 85.24       | 2.26  |                 | NAC-dom                                                    |
| OS01G0106300 | 0.789089271 | 147.4237552 | -7.55 |                 | NAD(P)-bd_dom                                              |
| OS01G0106400 | 114.8165622 | 3355.802877 | -4.87 |                 | NAD(P)-bd_dom                                              |
| OS07G0598000 | 0.757213791 | 16.48578859 | -4.44 |                 | NAD(P)-bd_dom                                              |
| OS02G0178800 | 6.999377616 | 91.4557995  | -3.71 |                 | NAD(P)-bd_dom                                              |
| OS06G0299100 | 8.688410799 | 95.96390051 | -3.47 |                 | NAD(P)-bd_dom                                              |
| OS09G0426800 | 213.3427332 | 1947.218343 | -3.19 |                 | NAD(P)-bd_dom                                              |
| OS07G0601600 | 4.885694567 | 41.5557231  | -3.09 | OJ2013_G04.118  | NAD(P)-bd_dom                                              |
| OS08G0476300 | 81.92609455 | 341.5800457 | -2.06 |                 | NAD(P)-bd_dom                                              |
| OS06G0129100 | 158.92      | 23.38       | 2.77  |                 | NAD(P)-bd_dom                                              |
| OS10G0114300 | 90.65       | 16.94       | 2.42  |                 | NADPH-dependent codeinone reductase                        |
| OS01G0862800 | 174.54      | 44.13       | 1.98  | NAC59           | NAM ATAF1/2 CUC2) transcription factor, Early and          |

|              |             |             |       |                                |                                                 |
|--------------|-------------|-------------|-------|--------------------------------|-------------------------------------------------|
|              |             |             |       |                                | transient regulator of abiotic stress responses |
| OS07G0117300 | 65.07       | 7.41        | 3.13  |                                | NB-ARC                                          |
| OS08G0539700 | 323.16      | 17.76       | 4.19  | PIBH8                          | NB-ARC domain containing protein.               |
| OS11G0492300 | 25.34       | 1.45        | 4.12  | Os11g0492300                   | NB-ARC domain containing protein.               |
| OS08G0155400 | 82.00       | 17.33       | 2.24  | NRT1.1A                        | Nitrate/chlorate transporter                    |
| OS01G0777900 | 15.55164731 | 83.11218936 | -2.42 | -/-                            | Non-protein coding transcript                   |
| OS02G0716600 | 31.59642685 | 219.0370874 | -2.79 | -/-                            | Non-protein coding transcript                   |
| OS04G0641101 | 14.56068708 | 385.4460027 | -4.73 | -/-                            | Non-protein coding transcript                   |
| OS08G0251000 | 0.574179368 | 20.99154284 | -5.19 | -/-                            | Non-protein coding transcript                   |
| OS11G0173100 | 2.335392332 | 20.38624093 | -3.13 | -/-                            | Non-protein coding transcript                   |
| OS12G0115050 | 1.856839405 | 94.23003945 | -5.67 | -/-                            | Non-protein coding transcript                   |
| OS02G0166200 | 1548.49     | 289.10      | 2.42  | -/-                            | Non-protein coding transcript                   |
| OS04G0271450 | 78.41       | 15.61       | 2.33  | -/-                            | Non-protein coding transcript                   |
| OS11G0288350 | 29.15       | 3.62        | 3.01  | -/-                            | Non-protein coding transcript.                  |
| OS05G0195101 | 475.00      | 68.22       | 2.80  | -/-                            | Non-protein coding transcript.                  |
| OS12G0136500 | 623.91      | 135.13      | 2.21  | -/-                            | Non-protein coding transcript.                  |
| OS10G0562900 | 156.90      | 41.73       | 1.91  | Non-protein coding transcript. | Non-protein coding transcript.                  |
| OS07G0634600 | 57.22922947 | 503.4113523 | -3.14 | Os07g0634600                   | NOTUM                                           |
| OS05G0342100 | 3.841391093 | 124.9533864 | -5.02 |                                | NTF2-like_dom                                   |
| OS05G0342000 | 41.38334363 | 194.1409548 | -2.23 |                                | NTF2-like_dom                                   |
| OS03G0291500 | 10.80358419 | 3993.085745 | -8.53 |                                | Ntn_hydrolases_N                                |
| OS04G0457500 | 360.6030396 | 1154.107695 | -1.68 |                                | Ntn_hydrolases_N                                |
| OS09G0279500 | 242.4818242 | 830.1947525 | -1.78 |                                | Nucleotide-bd_a/b_plait                         |
| OS07G0694400 | 0.287089684 | 114.8336723 | -8.64 |                                | Nucleotide-diphossugar_trans                    |
| OS12G0555600 | 1.809946085 | 34.08722883 | -4.24 | Os12g0555600                   | Nucleotide-diphossugar_trans                    |
| OS02G0192500 | 0           | 28.86527974 | Inf   | CSLA1                          | Nucleotide-diphossugar_trans                    |
| OS12G0601400 | 0.246785383 | 35.67197405 | -7.18 | IAA31                          | OPR_PB1                                         |
| OS01G0286900 | 6.950854856 | 52.41541226 | -2.91 |                                | OPR_PB1                                         |
| OS02G0723400 | 36.88234409 | 142.4895343 | -1.95 | IAA8                           | OPR_PB1                                         |
| Novel00416   | 4.751393265 | 30.80414957 | -2.7  | --                             | unknown protein                                 |
| Novel00437   | 59.00       | 11.69       | 2.34  | --                             | unknown protein                                 |
| Novel00612   | 1.824963925 | 17.28235547 | -3.24 | --                             | unknown protein                                 |
| Novel00794   | 20.340086   | 131.5009331 | -2.69 | --                             | unknown protein                                 |
| OS09G0359500 | 40.47       | 0.71        | 5.83  |                                | OsD305                                          |
| OS02G0460200 | 10678.45    | 129.01      | 6.37  |                                | OSIGBa0131F24.5 protein.                        |
| OS04G0445900 | 0.74035615  | 67.38517464 | -6.51 | Os04g0445900                   | OSIGBa0140O07.10 protein.<br>(Os04t0445900-00)  |
| OS11G0471300 | 0.501999587 | 44.58097817 | -6.47 | OS11G0471300                   | OSIGBa0145N07.3 protein.<br>(Os11t0471300-01)   |
| OS04G0598000 | 3531.94     | 876.91      | 2.01  |                                | OSJNb0093F12.14 protein.                        |

|              |             |             |        |               |                                                    |
|--------------|-------------|-------------|--------|---------------|----------------------------------------------------|
| OS11G0614500 | 0           | 12.52582969 | Inf    | OS11G0614500  | Patatin/PLipase_A2-rel                             |
| OS11G0658800 | 84.46       | 19.64       | 2.10   |               | Pectin_lyas_fold                                   |
| OS01G0312500 | 0           | 17.98455052 | Inf    | Os01g0312500  | Pectinesterase_Asp_AS                              |
| OS10G0508700 | 42.74370285 | 2598.722957 | -5.93  |               | Pectinesterase_inhib_dom                           |
|              |             |             |        |               | Penicillin-binding protein,                        |
| OS11G0463700 | 85.69248552 | 310.1197074 | -1.86  | OS11G0463700  | transpeptidase fold domain                         |
|              |             |             |        |               | containing protein                                 |
| OS03G0729000 | 2101.09     | 514.94      | 2.03   | EGY3          | Peptidase                                          |
| OS01G0140100 | 3.403142467 | 44.69077881 | -3.72  |               | PEPTIDASE_A1                                       |
| OS01G0378100 | 0.829393571 | 2057.997242 | -11.28 |               | Peroxidase_pln                                     |
| OS10G0109300 | 16.42120609 | 6573.713061 | -8.65  | Os10g0109300  | Peroxidase_pln                                     |
| OS01G0294700 | 14.67040084 | 3387.964041 | -7.85  |               | Peroxidase_pln                                     |
| OS06G0547400 | 5.10223391  | 876.6830778 | -7.42  |               | Peroxidase_pln                                     |
| OS03G0234900 | 1.793088445 | 155.7990918 | -6.44  | PRX39         | Peroxidase_pln                                     |
| OS06G0681600 | 17.74451988 | 1154.878818 | -6.02  | P0547F09.20-1 | Peroxidase_pln                                     |
| OS05G0134400 | 26.4396588  | 1348.911855 | -5.67  | Os05g0134400  | Peroxidase_pln                                     |
| OS06G0522300 | 2.813945259 | 66.87642914 | -4.57  |               | Peroxidase_pln                                     |
| OS04G0434800 | 445.31      | 108.97      | 2.03   | Os04g0434800  | Peroxidase_pln/fun/bac                             |
| OS06G0220000 | 0.255214204 | 78.91547046 | -8.27  | Os06g0220000  | Phosphate-induced_prot1                            |
| OS04G0517500 | 124.16      | 21.76       | 2.51   | Os04g0517500  | Phosphoenolpyruvate carboxylase<br>kinase          |
| OS05G0518000 | 342.34      | 15.93       | 4.43   | Os05g0518000  | Phosphotidylethanolamine-bd_CS                     |
| OS04G0445700 | 75.38140248 | 359.2159331 | -2.25  |               | PKS_Beta-ketoAc_synthase_dom                       |
| OS12G0260500 | 0           | 11.92094593 | Inf    |               | PKS_KR                                             |
| OS11G0115350 | 166.4990449 | 7443.41076  | -5.48  | LTP2-A        | Plant_LTP                                          |
| OS03G0280400 | 84.68       | 0.36        | 7.90   |               | plant-specific domain TIGR01589<br>family protein. |
| OS02G0823100 | 3088.50     | 738.54      | 2.06   | PIP1;3        | Plasma membrane intrinsic<br>protein               |
| OS01G0281600 | 2.543502854 | 181.2583405 | -6.16  |               | Plcyanin-like                                      |
| OS08G0137400 | 10.59377296 | 397.0194696 | -5.23  |               | Plcyanin-like                                      |
| OS07G0635900 | 508.6160422 | 1712.484955 | -1.75  | LTI6A         | PMP3                                               |
| OS04G0441800 | 26.75210621 | 111.8932399 | -2.06  |               | POT_fam                                            |
| OS04G0691400 | 52.01246131 | 184.0622533 | -1.82  |               | POT_fam                                            |
| OS01G0934350 | 26.69678407 | 131.5095652 | -2.3   | Os01g0934350  | predicted protein.<br>(Os01t0934350-00)            |
| OS09G0520550 | 5.8191434   | 84.30787567 | -3.86  |               | predicted protein.<br>(Os09t0520550-01)            |
| OS12G0555000 | 690.93      | 197.42      | 1.81   | OsPR10a       | Probenazole-inducible protein<br>PBZ1              |
| OS03G0113000 | 4.289697979 | 135.7549167 | -4.98  |               | Prot_kinase_dom                                    |
| OS12G0603700 | 158.4006727 | 679.7062394 | -2.1   | Os12g0603700  | Prot_kinase_dom                                    |
| OS02G0623932 | 25.99       | 3.29        | 2.98   |               | Prot_kinase_dom                                    |
| OS10G0142600 | 99.65       | 25.59       | 1.96   | OS10G0142600  | Prot_kinase_dom                                    |

|              |             |             |        |                      |                                                                    |
|--------------|-------------|-------------|--------|----------------------|--------------------------------------------------------------------|
| OS05G0258400 | 65.53       | 1.45        | 5.50   |                      | Protein kinase, catalytic domain domain containing protein         |
| OS02G0215700 | 41.05       | 2.15        | 4.26   | Os02g0215700         | Protein kinase, catalytic domain domain containing protein.        |
| OS01G0116900 | 461.26      | 56.40       | 3.03   |                      | Protein kinase, catalytic domain domain containing protein.        |
| OS06G0241100 | 83.38       | 10.23       | 3.03   | OSJNBA0001B11.1<br>2 | Protein kinase, catalytic domain domain containing protein.        |
| OS01G0885700 | 20.05       | 0.71        | 4.82   |                      | Protein kinase-like domain containing protein                      |
| OS02G0182600 | 1.595036182 | 38.32351826 | -4.59  |                      | Protein kinase-like protein (Fragment).                            |
| OS07G0114000 | 704.82      | 126.41      | 2.48   | Os07g0114000         | Protein_Pase_2C                                                    |
| OS01G0124100 | 89.84       | 20.69       | 2.12   | RBBI3-2              | Proteinase inhibitor I12                                           |
| OS08G0393600 | 36.02128539 | 137.2927261 | -1.93  | Os08g0393600         | Protein-tyrosine phosphatase-like, PTPLA domain containing protein |
| OS03G0747700 | 138.2548203 | 590.0764316 | -2.09  |                      | PSII_Pbs27                                                         |
| OS07G0147500 | 16906.08    | 22.85       | 9.53   | PsbR                 | PSII_PsbR                                                          |
| OS07G0147550 | 76.17       | 2.77        | 4.78   | Os07g0147550         | PSII_PsbR                                                          |
| OS01G0748800 | 61.79       | 0.00        | #NAME? |                      | PtdEtn-bd_prot_PEBP                                                |
| OS07G0564500 | 168.15      | 30.77       | 2.45   |                      | Pyr_nucl-diS_OxRdtase_FAD/NAD                                      |
| OS01G0192900 | 1.299517678 | 110.6920921 | -6.41  | Os01g0192900         | PyrdxIP-dep_Trfase_major_sub2                                      |
| OS10G0517500 | 153.5858814 | 563.8766952 | -1.88  |                      | PyrdxIP-dep_Trfase_major_sub2                                      |
| OS01G0645400 | 6.493908789 | 45.29156177 | -2.8   |                      | Pyridine_nuc-diS_OxRdtase_2                                        |
| OS12G0189300 | 7065.244164 | 34272.14419 | -2.28  |                      | Pyrv/PenolPyrv_Kinase-like_dom                                     |
| OS01G0115600 | 39.09       | 5.23        | 2.90   | RLCK11               | Receptor-like Cytoplasmic Kinase 11                                |
| OS09G0471400 | 191.41      | 57.01       | 1.75   | WAK81                | Receptor-like Cytoplasmic Kinase 273                               |
| OS11G0667700 | 103.33      | 17.74       | 2.54   | RLCK348              | Receptor-like Cytoplasmic Kinase                                   |
| OS03G0111200 | 0           | 170.567784  | Inf    |                      | Remorin_C                                                          |
| Novel00503   | 43.89972022 | 397.8329771 | -3.18  | --                   | retrotransposon protein, putative, unclassified                    |
| OS08G0554300 | 0           | 18.2357402  | Inf    | Os08g0554300         | RG-lyase_III                                                       |
| OS02G0102300 | 14.94049379 | 481.7776283 | -5.01  | Os02g0102300         | Rhodanese-like_dom                                                 |
| OS03G0751400 | 45.29542416 | 286.6639467 | -2.66  |                      | Ribosomal_L6                                                       |
| OS05G0568300 | 71.73254425 | 357.6257146 | -2.32  |                      | Ribosomal_L7/12                                                    |
| OS10G0490100 | 2.080178129 | 31.91678034 | -3.94  |                      | RlpA-like_DPBB                                                     |
| OS04G0684900 | 1909.00     | 516.75      | 1.89   | OSJNBA0088H09.<br>11 | RNase_CAF1                                                         |
| OS12G0117400 | 81.29       | 11.62       | 2.81   |                      | RPT2                                                               |
| OS12G0274700 | 14318.78195 | 54211.05511 | -1.92  | RBCS                 | RuBisCO_sc_dom                                                     |

|              |             |             |       |                      |                                                                                                           |
|--------------|-------------|-------------|-------|----------------------|-----------------------------------------------------------------------------------------------------------|
| OS10G0422200 | 1.035874654 | 14.05124292 | -3.76 |                      | S_MeTrfase                                                                                                |
| OS07G0689600 | 159.4755751 | 1236.76673  | -2.96 | NAS3                 | SAM-dependent_MTases-like                                                                                 |
| OS04G0104900 | 65.45       | 12.32       | 2.41  |                      | SAM-dependent_MTases-like                                                                                 |
| OS08G0169300 | 54.65       | 12.66       | 2.11  | Os08g0169300         | SAM-dependent_MTases-like                                                                                 |
| OS05G0140100 | 1.610054022 | 190.4389126 | -6.89 |                      | SANT/Myb                                                                                                  |
| OS01G0975300 | 877.94      | 241.90      | 1.86  | P0459B04.21          | SANT/Myb                                                                                                  |
|              |             |             |       |                      | Serine/threonine protein                                                                                  |
| OS04G0127500 | 20.47       | 2.05        | 3.32  | WAK29                | kinase-related domain containing protein                                                                  |
|              |             |             |       |                      | serine/threonine-protein kinase receptor.                                                                 |
| OS12G0611100 | 416.54      | 110.95      | 1.91  | RLCK373              |                                                                                                           |
| OS11G0424400 | 60.79       | 12.06       | 2.33  |                      | Ser-tRNA-synth_1_N                                                                                        |
|              |             |             |       |                      | SG1 (SHORT GRAIN1)-related protein, Brassinosteroid signaling, Regulation of seed and panicle development |
| OS02G0762600 | 2.18423339  | 85.1372978  | -5.28 | P0486G03.21          |                                                                                                           |
|              |             |             |       |                      |                                                                                                           |
| OS06G0351500 | 11.68518012 | 922.0214008 | -6.3  | OSJNBB0014G01.3<br>1 | SGNH_hydro                                                                                                |
| OS06G0531600 | 27.04557455 | 1568.333146 | -5.86 |                      | SGNH_hydro                                                                                                |
| OS05G0209600 | 2.860838579 | 26.09036565 | -3.19 |                      | SGNH_hydro                                                                                                |
| OS06G0156600 | 0           | 99.26757688 | Inf   |                      | SGNH_hydro                                                                                                |
| OS08G0203201 | 9.742423074 | 54.67637537 | -2.49 |                      | SHR5-receptor-like kinase (Fragment). (Os08t0203201-00)                                                   |
|              |             |             |       |                      |                                                                                                           |
| OS01G0667600 | 212.60      | 57.51       | 1.89  | OSJNBB0063G05.2<br>7 | Small_GTPase                                                                                              |
| OS02G0140400 | 485.43      | 82.89       | 2.55  | OsOSC4               | SQ_cyclase_C                                                                                              |
| OS05G0201700 | 5.004767669 | 38.49457949 | -2.94 |                      | START-like_dom                                                                                            |
| OS01G0827800 | 0           | 14.45413879 | Inf   |                      | START-like_dom                                                                                            |
| OS12G0555500 | 2510.77     | 584.45      | 2.10  |                      | START-like_dom                                                                                            |
| OS02G0271000 | 31.82       | 2.15        | 3.89  | SUB17                | Subtilase                                                                                                 |
| OS11G0261600 | 31.62       | 1.84        | 4.10  | OS11G0261600         | Subtilisin-like serine proteinase                                                                         |
| OS11G0637100 | 22.59       | 1.10        | 4.36  | Os11g0637100         | Sugar/inositol_transpt                                                                                    |
| OS03G0218400 | 7054.61     | 1980.75     | 1.83  | OsMST4               | Sugar/inositol_transpt                                                                                    |
|              |             |             |       |                      |                                                                                                           |
| OS03G0736500 | 0.510428407 | 18.75253751 | -5.2  | OSJNBB0016H12.1<br>5 | T_SNARE_dom                                                                                               |
|              |             |             |       |                      |                                                                                                           |
| OS12G0106300 | 0.574179368 | 110.1581237 | -7.58 |                      | TBL                                                                                                       |
| OS01G0652800 | 4.209089378 | 67.70215625 | -4.01 |                      | TBL                                                                                                       |
| OS01G0217000 | 7.633838705 | 58.43794761 | -2.94 | P0515G01.44-1        | TBL                                                                                                       |
| OS12G0491800 | 61.48       | 1.10        | 5.81  | Os12g0491800         | Terpene_synth_N                                                                                           |
| OS04G0345400 | 153.36      | 24.22       | 2.66  |                      | Terpene_synth_N                                                                                           |
| OS02G0570900 | 122.91      | 26.80       | 2.20  |                      | Terpene_synth_N                                                                                           |
| OS02G0571300 | 118.22      | 30.48       | 1.96  | Os02g0571300         | Terpene_synth_N                                                                                           |
| OS02G0571800 | 988.14      | 271.38      | 1.86  | Os02g0571800         | Terpene_synth_N                                                                                           |
| OS02G0571100 | 807.26      | 262.10      | 1.62  | CPS2                 | Terpene_synthase_metal-bd                                                                                 |

|              |             |             |       |                 |                                                       |
|--------------|-------------|-------------|-------|-----------------|-------------------------------------------------------|
| OS03G0647600 | 477.96      | 129.26      | 1.89  |                 | TF_CBFb                                               |
| OS05G0500600 | 3.124481603 | 90.19572551 | -4.85 |                 | TF_GRAS                                               |
| OS03G0215400 | 44.96       | 4.85        | 3.21  | LHS1            | TF_MADSbox                                            |
| OS08G0112700 | 84.29       | 22.99       | 1.87  | Os08g0112700    | TF_MADSbox                                            |
| OS03G0243900 | 0.287089684 | 99.47637384 | -8.44 | OS03G0243900    | Thaumatococcus                                        |
| OS07G0529600 | 1927.924829 | 6907.982488 | -1.84 |                 | Thi4_fam                                              |
| OS03G0165900 | 37.14698889 | 669.369457  | -4.17 |                 | TPR-like_helical                                      |
| OS01G0783100 | 82.57110245 | 305.8603803 | -1.89 |                 | TPR-like_helical                                      |
| OS06G0606700 | 4119.98     | 1229.21     | 1.74  |                 | TPR-like_helical                                      |
| OS02G0189400 | 8.214817453 | 101.4121296 | -3.63 | OSJNBB0031B09.7 | TypeIII_acyltransferase                               |
| OS01G0907200 | 0.510428407 | 29.52883373 | -5.85 | Os01g0907200    | Ubiquitin-rel_dom                                     |
| OS03G0757100 | 15.29976325 | 78.89408127 | -2.37 | OSJNBA0040E01.2 | UDP-glucosyltransferase                               |
|              |             |             |       | 1               |                                                       |
| OS08G0404000 | 55.10       | 4.59        | 3.58  | Os08g0404000    | UDP-glucosyltransferase                               |
| OS04G0321100 | 153.96      | 31.50       | 2.29  | Os04g0321100    | UDP-glucosyltransferase                               |
| OS04G0272200 | 70.64       | 15.11       | 2.22  | OSJNBB0056F09.1 | UDP-glucosyltransferase                               |
|              |             |             |       | 2               |                                                       |
| OS03G0830300 | 178.34      | 38.31       | 2.22  |                 | Uncharacterised_Cys-rich                              |
| OS03G0830400 | 289.11      | 77.64       | 1.90  | PGPS/D12        | Uncharacterised_Cys-rich                              |
| Novel00701   | 57.84       | 12.95       | 2.16  | --              | unnamed protein product [Oryza sativa Japonica Group] |
| OS11G0649600 | 16.84953555 | 82.41611685 | -2.29 |                 | UPF0497_TM_pln_subgr                                  |
| OS03G0196400 | 330.18      | 42.75       | 2.95  | OS03G0196400    | UPF0497_TM_pln_subgr                                  |
| OS05G0355400 | 1191.77     | 122.16      | 3.29  | UspA            | UspA domain containing protein.                       |
| OS06G0142500 | 4902.28     | 433.30      | 3.50  | Os06g0142500    | Wall-associated kinase 3.                             |
| OS01G0208000 | 5.553870937 | 33.66371106 | -2.6  |                 | WAT1-related                                          |
| OS09G0426500 | 458.3773017 | 1802.428551 | -1.98 |                 | WAT1-related                                          |
| OS04G0422600 | 33.43       | 2.97        | 3.49  |                 | WAT1-related                                          |
| OS05G0106200 | 97.37       | 22.40       | 2.12  | OSJNBB0035J08.1 | WAT1-related                                          |
|              |             |             |       | 3               |                                                       |
| OS02G0468100 | 21.31       | 1.47        | 3.86  | Os02g0468100    | Wax_synthase_dom                                      |
| OS01G0186000 | 33.5915466  | 209.996881  | -2.64 | Os01g0186000    | WRKY_DNA-bd                                           |
| OS01G0821600 | 1810.60     | 220.68      | 3.04  |                 | WRKY_DNA-bd                                           |
| OS11G0117500 | 54.08       | 11.32       | 2.26  |                 | WRKY_DNA-bd                                           |
| OS03G0756300 | 10.49651708 | 86.02221951 | -3.03 |                 | X8                                                    |
| OS09G0385700 | 603.84      | 109.23      | 2.47  | SAP17           | Znf_AN1                                               |
| OS05G0195200 | 999.74      | 178.69      | 2.48  |                 | Znf_CCCH                                              |
| OS05G0155400 | 41.31314275 | 176.4884083 | -2.09 |                 | Znf_NHR/GATA                                          |
| OS09G0268600 | 348.56      | 93.87       | 1.89  | OS09G0268600    | Znf_PMZ                                               |
| OS01G0555100 | 386.1236466 | 2343.519372 | -2.6  | B1110C07.45     | Znf_RanBP2                                            |
| OS06G0141200 | 1274.278264 | 5859.949952 | -2.2  |                 | Znf_RanBP2                                            |
| OS02G0690600 | 1.833392745 | 49.12587306 | -4.74 |                 | Znf_RING/FYVE/PHD                                     |
| OS07G0686300 | 10.4091091  | 173.6487262 | -4.06 | OJ1200_C08.113  | Znf_RING/FYVE/PHD                                     |
| OS06G0534800 | 7.30991396  | 81.40892995 | -3.48 | OSJNBA0001B21.1 | Znf_RING/FYVE/PHD                                     |

|                        |             |             |        |             |                   |
|------------------------|-------------|-------------|--------|-------------|-------------------|
| OS05G0355300           | 13.3760531  | 81.19620677 | -2.6   |             | Znf_RING/FYVE/PHD |
| OS12G0209200           | 15.25633917 | 61.75547399 | -2.02  |             | Znf_RING/FYVE/PHD |
| OS08G0492500           | 113.58      | 21.89       | 2.38   | P0686H11.17 | Znf_RING/FYVE/PHD |
| Novel00588             | 1.067750135 | 129.887165  | -6.93  | -/-         |                   |
| EPIOSAG0000<br>0018034 | 0.246785383 | 11.17919209 | -5.5   | -/-         |                   |
| EPIOSAG0000<br>0023434 | 2.112053609 | 30.4416488  | -3.85  | -/-         |                   |
| EPIOSAG0000<br>0012502 | 4.135069797 | 44.78749739 | -3.44  | -/-         |                   |
| Novel00263             | 0           | 16.24599595 | Inf    | -/-         |                   |
| EPIOSAG0000<br>0025431 | 229.29      | 0.00        | #NAME? | -/-         |                   |
| Novel00435             | 97.57       | 0.00        | #NAME? | -/-         |                   |
| Novel00454             | 312.98      | 4.39        | 6.16   | -/-         |                   |
| OS03G0203451           | 102.00      | 16.87       | 2.60   | -/-         |                   |
| Novel00808             | 55.54       | 10.18       | 2.45   | -/-         |                   |
| Novel00132             | 80.30       | 14.76       | 2.44   | -/-         |                   |

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**Table S5** Two-way ANOVA test for expression levels of the genes involved in starch biosynthesis

| Difference            | SS       | df | MS       | F        | P-value  | F crit   |
|-----------------------|----------|----|----------|----------|----------|----------|
| <b><i>OsFBA</i></b>   |          |    |          |          |          |          |
| Genotype              | 27.8784  | 1  | 27.8784  | 835.0438 | 1.85E-23 | 4.170877 |
| Growth condition      | 8.617267 | 2  | 4.308633 | 129.0568 | 1.83E-15 | 3.31583  |
| Interaction           | 2.235267 | 2  | 1.117633 | 33.47655 | 2.28E-08 | 3.31583  |
| Interior              | 1.001567 | 30 | 0.033386 |          |          |          |
| Total                 | 39.7325  | 35 |          |          |          |          |
| <b><i>OsFBP1</i></b>  |          |    |          |          |          |          |
| Genotype              | 21.6225  | 1  | 21.6225  | 954.87   | 2.64E-24 | 4.170877 |
| Growth condition      | 6.130872 | 2  | 3.065436 | 135.3725 | 9.63E-16 | 3.31583  |
| Interaction           | 1.940717 | 2  | 0.970358 | 42.85194 | 1.61E-09 | 3.31583  |
| Interior              | 0.679333 | 30 | 0.022644 |          |          |          |
| Total                 | 30.37342 | 35 |          |          |          |          |
| <b><i>OsFBP-L</i></b> |          |    |          |          |          |          |
| Genotype              | 38.13063 | 1  | 38.13063 | 699.509  | 2.4E-22  | 4.170877 |
| Growth condition      | 6.918239 | 2  | 3.459119 | 63.45779 | 1.67E-11 | 3.31583  |
| Interaction           | 3.462117 | 2  | 1.731058 | 31.75639 | 3.92E-08 | 3.31583  |
| Interior              | 1.635317 | 30 | 0.054511 |          |          |          |
| Total                 | 50.1463  | 35 |          |          |          |          |
| <b><i>OsFBP2</i></b>  |          |    |          |          |          |          |
| Genotype              | 68.31023 | 1  | 68.31023 | 1056.643 | 6.04E-25 | 4.170877 |
| Growth condition      | 17.1266  | 2  | 8.5633   | 132.4597 | 1.29E-15 | 3.31583  |
| Interaction           | 13.5242  | 2  | 6.7621   | 104.5982 | 2.99E-14 | 3.31583  |
| Interior              | 1.93945  | 30 | 0.064648 |          |          |          |
| Total                 | 100.9005 | 35 |          |          |          |          |
| <b><i>OsFBP3</i></b>  |          |    |          |          |          |          |
| Genotype              | 63.09654 | 1  | 63.09654 | 3420.073 | 1.78E-32 | 4.170877 |
| Growth condition      | 5.033839 | 2  | 2.516919 | 136.4266 | 8.68E-16 | 3.31583  |
| Interaction           | 1.631072 | 2  | 0.815536 | 44.20516 | 1.14E-09 | 3.31583  |
| Interior              | 0.553467 | 30 | 0.018449 |          |          |          |
| Total                 | 70.31492 | 35 |          |          |          |          |
| <b><i>OsPGI2</i></b>  |          |    |          |          |          |          |
| Genotype              | 78.08668 | 1  | 78.08668 | 2298.244 | 6.51E-30 | 4.170877 |
| Growth condition      | 18.53271 | 2  | 9.266353 | 272.727  | 5.71E-20 | 3.31583  |
| Interaction           | 15.14924 | 2  | 7.574619 | 222.9359 | 9.87E-19 | 3.31583  |
| Interior              | 1.0193   | 30 | 0.033977 |          |          |          |
| Total                 | 112.7879 | 35 |          |          |          |          |
| <b><i>OsPGM</i></b>   |          |    |          |          |          |          |
| Genotype              | 27.12674 | 1  | 27.12674 | 644.179  | 7.84E-22 | 4.170877 |
| Growth condition      | 5.954689 | 2  | 2.977344 | 70.70304 | 4.43E-12 | 3.31583  |
| Interaction           | 2.250956 | 2  | 1.125478 | 26.72674 | 2.16E-07 | 3.31583  |

|                  |          |    |          |          |          |          |
|------------------|----------|----|----------|----------|----------|----------|
| Interior         | 1.263317 | 30 | 0.042111 |          |          |          |
| Total            | 36.5957  | 35 |          |          |          |          |
| <b>OsSPS2</b>    |          |    |          |          |          |          |
| Genotype         | 31.41603 | 1  | 31.41603 | 1022.047 | 9.82E-25 | 4.170877 |
| Growth condition | 13.35971 | 2  | 6.679853 | 217.3134 | 1.41E-18 | 3.31583  |
| Interaction      | 7.299617 | 2  | 3.649808 | 118.738  | 5.59E-15 | 3.31583  |
| Interior         | 0.92215  | 30 | 0.030738 |          |          |          |
| Total            | 52.9975  | 35 |          |          |          |          |
| <b>OsSPS11</b>   |          |    |          |          |          |          |
| Genotype         | 36.02    | 1  | 36.02    | 1737.16  | 4.08E-28 | 4.170877 |
| Growth condition | 5.023617 | 2  | 2.511808 | 121.1386 | 4.28E-15 | 3.31583  |
| Interaction      | 0.012606 | 2  | 0.006303 | 0.303968 | 0.74013  | 3.31583  |
| Interior         | 0.62205  | 30 | 0.020735 |          |          |          |
| Total            | 41.67828 | 35 |          |          |          |          |
| <b>OsSPPL1</b>   |          |    |          |          |          |          |
| Genotype         | 43.80234 | 1  | 43.80234 | 1460.862 | 5.24E-27 | 4.170877 |
| Growth condition | 12.13029 | 2  | 6.065144 | 202.2801 | 3.86E-18 | 3.31583  |
| Interaction      | 7.662689 | 2  | 3.831344 | 127.7801 | 2.1E-15  | 3.31583  |
| Interior         | 0.899517 | 30 | 0.029984 |          |          |          |
| Total            | 64.49483 | 35 |          |          |          |          |
| <b>OsSPPL2</b>   |          |    |          |          |          |          |
| Genotype         | 48.23303 | 1  | 48.23303 | 669.1338 | 4.54E-22 | 4.170877 |
| Growth condition | 20.46162 | 2  | 10.23081 | 141.9314 | 5.08E-16 | 3.31583  |
| Interaction      | 13.42455 | 2  | 6.712275 | 93.11898 | 1.36E-13 | 3.31583  |
| Interior         | 2.162483 | 30 | 0.072083 |          |          |          |
| Total            | 84.28168 | 35 |          |          |          |          |
| <b>OsFrK1</b>    |          |    |          |          |          |          |
| Genotype         | 38.1718  | 1  | 38.1718  | 794.8687 | 3.79E-23 | 4.170877 |
| Growth condition | 12.72137 | 2  | 6.360686 | 132.4514 | 1.29E-15 | 3.31583  |
| Interaction      | 4.700439 | 2  | 2.350219 | 48.93968 | 3.59E-10 | 3.31583  |
| Interior         | 1.440683 | 30 | 0.048023 |          |          |          |
| Total            | 57.0343  | 35 |          |          |          |          |
| <b>OsHXX1</b>    |          |    |          |          |          |          |
| Genotype         | 150.8393 | 1  | 150.8393 | 6785.904 | 6.53E-37 | 4.170877 |
| Growth condition | 39.0296  | 2  | 19.5148  | 877.9246 | 2.39E-27 | 3.31583  |
| Interaction      | 15.39549 | 2  | 7.697744 | 346.3033 | 1.88E-21 | 3.31583  |
| Interior         | 0.66685  | 30 | 0.022228 |          |          |          |
| Total            | 205.9313 | 35 |          |          |          |          |
| <b>OsHXX4</b>    |          |    |          |          |          |          |
| Genotype         | 34.08614 | 1  | 34.08614 | 3690.973 | 5.73E-33 | 4.170877 |
| Growth condition | 13.78082 | 2  | 6.890411 | 746.1192 | 2.63E-26 | 3.31583  |
| Interaction      | 5.975089 | 2  | 2.987544 | 323.5024 | 4.99E-21 | 3.31583  |
| Interior         | 0.27705  | 30 | 0.009235 |          |          |          |
| Total            | 54.1191  | 35 |          |          |          |          |

**OsHXX7**

|                  |          |    |          |          |          |          |
|------------------|----------|----|----------|----------|----------|----------|
| Genotype         | 29.8298  | 1  | 29.8298  | 1370.68  | 1.34E-26 | 4.170877 |
| Growth condition | 4.672817 | 2  | 2.336408 | 107.358  | 2.12E-14 | 3.31583  |
| Interaction      | 2.034772 | 2  | 1.017386 | 46.74891 | 6.05E-10 | 3.31583  |
| Interior         | 0.652883 | 30 | 0.021763 |          |          |          |
| Total            | 37.19028 | 35 |          |          |          |          |

**OsSUS1**

|                  |          |    |          |          |          |          |
|------------------|----------|----|----------|----------|----------|----------|
| Genotype         | 41.79623 | 1  | 41.79623 | 1809.143 | 2.24E-28 | 4.170877 |
| Growth condition | 18.11721 | 2  | 9.058603 | 392.1002 | 3.13E-22 | 3.31583  |
| Interaction      | 11.26745 | 2  | 5.633725 | 243.8549 | 2.79E-19 | 3.31583  |
| Interior         | 0.693083 | 30 | 0.023103 |          |          |          |
| Total            | 71.87396 | 35 |          |          |          |          |

**OsSUS2**

|                  |          |    |          |          |          |          |
|------------------|----------|----|----------|----------|----------|----------|
| Genotype         | 30.17671 | 1  | 30.17671 | 1734.072 | 4.19E-28 | 4.170877 |
| Growth condition | 5.77805  | 2  | 2.889025 | 166.0147 | 5.97E-17 | 3.31583  |
| Interaction      | 1.921772 | 2  | 0.960886 | 55.21629 | 8.81E-11 | 3.31583  |
| Interior         | 0.522067 | 30 | 0.017402 |          |          |          |
| Total            | 38.3986  | 35 |          |          |          |          |

**OsSUS4**

|                  |          |    |          |          |          |          |
|------------------|----------|----|----------|----------|----------|----------|
| Genotype         | 31.64063 | 1  | 31.64063 | 1278.61  | 3.71E-26 | 4.170877 |
| Growth condition | 10.16569 | 2  | 5.082844 | 205.3997 | 3.11E-18 | 3.31583  |
| Interaction      | 3.451467 | 2  | 1.725733 | 69.73756 | 5.25E-12 | 3.31583  |
| Interior         | 0.742383 | 30 | 0.024746 |          |          |          |
| Total            | 46.00016 | 35 |          |          |          |          |

**OsSUS5**

|                  |          |    |          |          |          |          |
|------------------|----------|----|----------|----------|----------|----------|
| Genotype         | 281.9041 | 1  | 281.9041 | 2284.639 | 7.11E-30 | 4.170877 |
| Growth condition | 2.299372 | 2  | 1.149686 | 9.317414 | 0.000712 | 3.31583  |
| Interaction      | 0.916617 | 2  | 0.458308 | 3.714273 | 0.036205 | 3.31583  |
| Interior         | 3.701733 | 30 | 0.123391 |          |          |          |
| Total            | 288.8218 | 35 |          |          |          |          |

**OsSUS6**

|                  |          |    |          |          |          |          |
|------------------|----------|----|----------|----------|----------|----------|
| Genotype         | 108.5764 | 1  | 108.5764 | 4398.576 | 4.21E-34 | 4.170877 |
| Growth condition | 9.189572 | 2  | 4.594786 | 186.141  | 1.23E-17 | 3.31583  |
| Interaction      | 6.959817 | 2  | 3.479908 | 140.9758 | 5.57E-16 | 3.31583  |
| Interior         | 0.740533 | 30 | 0.024684 |          |          |          |
| Total            | 125.4663 | 35 |          |          |          |          |

**OsSUS7**

|                  |          |    |          |          |          |          |
|------------------|----------|----|----------|----------|----------|----------|
| Genotype         | 359.9241 | 1  | 359.9241 | 9141.446 | 7.6E-39  | 4.170877 |
| Growth condition | 14.9114  | 2  | 7.4557   | 189.3618 | 9.67E-18 | 3.31583  |
| Interaction      | 9.200556 | 2  | 4.600278 | 116.839  | 6.93E-15 | 3.31583  |
| Interior         | 1.181183 | 30 | 0.039373 |          |          |          |
| Total            | 385.2173 | 35 |          |          |          |          |

**OsAGPL1**

|          |          |   |          |          |          |          |
|----------|----------|---|----------|----------|----------|----------|
| Genotype | 55.27923 | 1 | 55.27923 | 2012.878 | 4.63E-29 | 4.170877 |
|----------|----------|---|----------|----------|----------|----------|

|                  |          |    |          |          |          |         |
|------------------|----------|----|----------|----------|----------|---------|
| Growth condition | 7.590772 | 2  | 3.795386 | 138.2011 | 7.29E-16 | 3.31583 |
| Interaction      | 4.724817 | 2  | 2.362408 | 86.02219 | 3.76E-13 | 3.31583 |
| Interior         | 0.823883 | 30 | 0.027463 |          |          |         |
| Total            | 68.4187  | 35 |          |          |          |         |

#### **OsAGPL3**

|                  |          |    |          |          |          |          |
|------------------|----------|----|----------|----------|----------|----------|
| Genotype         | 36.10007 | 1  | 36.10007 | 1854.614 | 1.55E-28 | 4.170877 |
| Growth condition | 10.45872 | 2  | 5.229358 | 268.6544 | 7.07E-20 | 3.31583  |
| Interaction      | 6.019339 | 2  | 3.009669 | 154.6195 | 1.58E-16 | 3.31583  |
| Interior         | 0.58395  | 30 | 0.019465 |          |          |          |
| Total            | 53.16208 | 35 |          |          |          |          |

#### **OsAPGL4**

|                  |          |    |          |          |          |          |
|------------------|----------|----|----------|----------|----------|----------|
| Genotype         | 118.1931 | 1  | 118.1931 | 7020.679 | 3.93E-37 | 4.170877 |
| Growth condition | 3.201106 | 2  | 1.600553 | 95.07293 | 1.04E-13 | 3.31583  |
| Interaction      | 2.427406 | 2  | 1.213703 | 72.09402 | 3.48E-12 | 3.31583  |
| Interior         | 0.50505  | 30 | 0.016835 |          |          |          |
| Total            | 124.3267 | 35 |          |          |          |          |

#### **OsAGPS1**

|                  |          |    |          |          |          |          |
|------------------|----------|----|----------|----------|----------|----------|
| Genotype         | 59.05923 | 1  | 59.05923 | 970.7391 | 2.08E-24 | 4.170877 |
| Growth condition | 15.55184 | 2  | 7.775919 | 127.8105 | 2.09E-15 | 3.31583  |
| Interaction      | 7.872317 | 2  | 3.936158 | 64.69747 | 1.32E-11 | 3.31583  |
| Interior         | 1.825183 | 30 | 0.060839 |          |          |          |
| Total            | 84.30856 | 35 |          |          |          |          |

#### **OsUGP2**

|                  |          |    |          |          |          |          |
|------------------|----------|----|----------|----------|----------|----------|
| Genotype         | 74.07471 | 1  | 74.07471 | 3424.452 | 1.75E-32 | 4.170877 |
| Growth condition | 11.73776 | 2  | 5.868878 | 271.3165 | 6.15E-20 | 3.31583  |
| Interaction      | 8.884422 | 2  | 4.442211 | 205.3621 | 3.12E-18 | 3.31583  |
| Interior         | 0.648933 | 30 | 0.021631 |          |          |          |
| Total            | 95.34582 | 35 |          |          |          |          |

#### **OsGBSSI**

|                  |          |    |          |          |          |          |
|------------------|----------|----|----------|----------|----------|----------|
| Genotype         | 194.9281 | 1  | 194.9281 | 16286.99 | 1.34E-42 | 4.170877 |
| Growth condition | 3.752622 | 2  | 1.876311 | 156.773  | 1.31E-16 | 3.31583  |
| Interaction      | 2.970022 | 2  | 1.485011 | 124.0784 | 3.11E-15 | 3.31583  |
| Interior         | 0.35905  | 30 | 0.011968 |          |          |          |
| Total            | 202.0098 | 35 |          |          |          |          |

#### **OsSSIIc**

|                  |          |    |          |          |          |          |
|------------------|----------|----|----------|----------|----------|----------|
| Genotype         | 55.62674 | 1  | 55.62674 | 867.218  | 1.07E-23 | 4.170877 |
| Growth condition | 6.650339 | 2  | 3.325169 | 51.83922 | 1.84E-10 | 3.31583  |
| Interaction      | 2.747639 | 2  | 1.373819 | 21.41778 | 1.67E-06 | 3.31583  |
| Interior         | 1.924317 | 30 | 0.064144 |          |          |          |
| Total            | 66.94903 | 35 |          |          |          |          |

#### **OsSSIVa**

|                  |          |   |          |          |          |          |
|------------------|----------|---|----------|----------|----------|----------|
| Genotype         | 29.28614 | 1 | 29.28614 | 2937.917 | 1.71E-31 | 4.170877 |
| Growth condition | 9.305489 | 2 | 4.652744 | 466.7525 | 2.51E-23 | 3.31583  |
| Interaction      | 3.390156 | 2 | 1.695078 | 170.0463 | 4.29E-17 | 3.31583  |

|                  |          |    |          |          |          |          |
|------------------|----------|----|----------|----------|----------|----------|
| Interior         | 0.29905  | 30 | 0.009968 |          |          |          |
| Total            | 42.28083 | 35 |          |          |          |          |
| <b>OsSSV</b>     |          |    |          |          |          |          |
| Genotype         | 44.66694 | 1  | 44.66694 | 3507.875 | 1.22E-32 | 4.170877 |
| Growth condition | 11.13051 | 2  | 5.565253 | 437.0617 | 6.51E-23 | 3.31583  |
| Interaction      | 7.661206 | 2  | 3.830603 | 300.8327 | 1.41E-20 | 3.31583  |
| Interior         | 0.382    | 30 | 0.012733 |          |          |          |
| Total            | 63.84066 | 35 |          |          |          |          |
| <b>OsBEIIa</b>   |          |    |          |          |          |          |
| Genotype         | 32.98588 | 1  | 32.98588 | 2205.594 | 1.2E-29  | 4.170877 |
| Growth condition | 2.378439 | 2  | 1.189219 | 79.5169  | 1.02E-12 | 3.31583  |
| Interaction      | 0.740339 | 2  | 0.370169 | 24.7513  | 4.48E-07 | 3.31583  |
| Interior         | 0.448667 | 30 | 0.014956 |          |          |          |
| Total            | 36.55332 | 35 |          |          |          |          |
| <b>OsBEIIb</b>   |          |    |          |          |          |          |
| Genotype         | 16.37551 | 1  | 16.37551 | 1284.242 | 3.48E-26 | 4.170877 |
| Growth condition | 3.476822 | 2  | 1.738411 | 136.3341 | 8.76E-16 | 3.31583  |
| Interaction      | 1.313622 | 2  | 0.656811 | 51.51011 | 1.99E-10 | 3.31583  |
| Interior         | 0.382533 | 30 | 0.012751 |          |          |          |
| Total            | 21.54849 | 35 |          |          |          |          |
| <b>OsBEIII</b>   |          |    |          |          |          |          |
| Genotype         | 61.57018 | 1  | 61.57018 | 2189.205 | 1.34E-29 | 4.170877 |
| Growth condition | 11.69887 | 2  | 5.849436 | 207.9841 | 2.61E-18 | 3.31583  |
| Interaction      | 8.403372 | 2  | 4.201686 | 149.3962 | 2.53E-16 | 3.31583  |
| Interior         | 0.843733 | 30 | 0.028124 |          |          |          |
| Total            | 82.51616 | 35 |          |          |          |          |
| <b>OsISA1</b>    |          |    |          |          |          |          |
| Genotype         | 39.39654 | 1  | 39.39654 | 2411.377 | 3.2E-30  | 4.170877 |
| Growth condition | 4.41395  | 2  | 2.206975 | 135.0842 | 9.92E-16 | 3.31583  |
| Interaction      | 1.233672 | 2  | 0.616836 | 37.7552  | 6.42E-09 | 3.31583  |
| Interior         | 0.490133 | 30 | 0.016338 |          |          |          |
| Total            | 45.5343  | 35 |          |          |          |          |
| <b>OsFLO6</b>    |          |    |          |          |          |          |
| Genotype         | 61.51788 | 1  | 61.51788 | 2060.67  | 3.28E-29 | 4.170877 |
| Growth condition | 3.763089 | 2  | 1.881544 | 63.02628 | 1.81E-11 | 3.31583  |
| Interaction      | 3.722756 | 2  | 1.861378 | 62.35075 | 2.06E-11 | 3.31583  |
| Interior         | 0.8956   | 30 | 0.029853 |          |          |          |
| Total            | 69.89932 | 35 |          |          |          |          |
| <b>OsAlaAT1</b>  |          |    |          |          |          |          |
| Genotype         | 57.02767 | 1  | 57.02767 | 2614.815 | 9.62E-31 | 4.170877 |
| Growth condition | 4.85555  | 2  | 2.427775 | 111.3176 | 1.32E-14 | 3.31583  |
| Interaction      | 3.078572 | 2  | 1.539286 | 70.57888 | 4.53E-12 | 3.31583  |
| Interior         | 0.654283 | 30 | 0.021809 |          |          |          |
| Total            | 65.61608 | 35 |          |          |          |          |

**OsAlaAT4**

|                  |          |    |          |          |          |          |
|------------------|----------|----|----------|----------|----------|----------|
| Genotype         | 189.7965 | 1  | 189.7965 | 10749.96 | 6.73E-40 | 4.170877 |
| Growth condition | 5.066872 | 2  | 2.533436 | 143.4923 | 4.38E-16 | 3.31583  |
| Interaction      | 4.102439 | 2  | 2.051219 | 116.1798 | 7.47E-15 | 3.31583  |
| Interior         | 0.529667 | 30 | 0.017656 |          |          |          |
| Total            | 199.4955 | 35 |          |          |          |          |

**OsPPDK1**

|                  |          |    |          |          |          |          |
|------------------|----------|----|----------|----------|----------|----------|
| Genotype         | 38.72988 | 1  | 38.72988 | 856.056  | 1.29E-23 | 4.170877 |
| Growth condition | 4.23245  | 2  | 2.116225 | 46.77544 | 6.01E-10 | 3.31583  |
| Interaction      | 1.541906 | 2  | 0.770953 | 17.04056 | 1.14E-05 | 3.31583  |
| Interior         | 1.357267 | 30 | 0.045242 |          |          |          |
| Total            | 45.8615  | 35 |          |          |          |          |

**OsAMY3D**

|                  |          |    |          |          |          |          |
|------------------|----------|----|----------|----------|----------|----------|
| Genotype         | 74.6208  | 1  | 74.6208  | 10387.24 | 1.12E-39 | 4.170877 |
| Growth condition | 3.711606 | 2  | 1.855803 | 258.3284 | 1.23E-19 | 3.31583  |
| Interaction      | 1.586439 | 2  | 0.793219 | 110.4164 | 1.47E-14 | 3.31583  |
| Interior         | 0.215517 | 30 | 0.007184 |          |          |          |
| Total            | 80.13436 | 35 |          |          |          |          |

**OsGluA1**

|                  |          |    |          |          |          |          |
|------------------|----------|----|----------|----------|----------|----------|
| Genotype         | 99.13521 | 1  | 99.13521 | 2448.589 | 2.55E-30 | 4.170877 |
| Growth condition | 6.8094   | 2  | 3.4047   | 84.09435 | 5.02E-13 | 3.31583  |
| Interaction      | 2.583089 | 2  | 1.291544 | 31.90049 | 3.75E-08 | 3.31583  |
| Interior         | 1.2146   | 30 | 0.040487 |          |          |          |
| Total            | 109.7423 | 35 |          |          |          |          |

**OsGluA3**

|                  |         |    |          |          |          |          |
|------------------|---------|----|----------|----------|----------|----------|
| Genotype         | 64.1601 | 1  | 64.1601  | 4994.299 | 6.33E-35 | 4.170877 |
| Growth condition | 0.87245 | 2  | 0.436225 | 33.95628 | 1.97E-08 | 3.31583  |
| Interaction      | 0.42395 | 2  | 0.211975 | 16.50039 | 1.47E-05 | 3.31583  |
| Interior         | 0.3854  | 30 | 0.012847 |          |          |          |
| Total            | 65.8419 | 35 |          |          |          |          |

**OsCysR10**

|                  |          |    |          |          |          |          |
|------------------|----------|----|----------|----------|----------|----------|
| Genotype         | 48.37203 | 1  | 48.37203 | 4145.187 | 1.02E-33 | 4.170877 |
| Growth condition | 26.45374 | 2  | 13.22687 | 1133.462 | 5.49E-29 | 3.31583  |
| Interaction      | 13.53645 | 2  | 6.768225 | 579.9955 | 1.06E-24 | 3.31583  |
| Interior         | 0.350083 | 30 | 0.011669 |          |          |          |
| Total            | 112.244  | 35 |          |          |          |          |

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**Table S6** Two-way ANOVA test for reported sucrose-dependent signals

| Difference                       | SS          | df | MS       | F        | P-value  | F crit   |
|----------------------------------|-------------|----|----------|----------|----------|----------|
| <b><sup>1</sup>O<sub>2</sub></b> |             |    |          |          |          |          |
| Genotype                         | 41294078    | 1  | 41294078 | 278.3155 | 1.01E-16 | 4.170877 |
| Growth condition                 | 11850166    | 2  | 5925083  | 39.93411 | 3.5E-09  | 3.31583  |
| Interaction                      | 5255426     | 2  | 2627713  | 17.71036 | 8.34E-06 | 3.31583  |
| Interior                         | 4451145     | 30 | 148371.5 |          |          |          |
| Total                            | 62850814.24 | 35 |          |          |          |          |
| <b>Proto</b>                     |             |    |          |          |          |          |
| Genotype                         | 0.615725    | 1  | 0.615725 | 304.0117 | 3.01E-17 | 4.170877 |
| Growth condition                 | 0.181842    | 2  | 0.090921 | 44.89193 | 9.57E-10 | 3.31583  |
| Interaction                      | 0.631903    | 2  | 0.315951 | 155.9996 | 1.4E-16  | 3.31583  |
| Interior                         | 0.06076     | 30 | 0.002025 |          |          |          |
| Total                            | 1.49023     | 35 |          |          |          |          |
| <b>OsZIP58</b>                   |             |    |          |          |          |          |
| Genotype                         | 68.31023    | 1  | 68.31023 | 6002.363 | 4.08E-36 | 4.170877 |
| Growth condition                 | 12.73302    | 2  | 6.366508 | 559.4198 | 1.79E-24 | 3.31583  |
| Interaction                      | 5.766217    | 2  | 2.883108 | 253.3363 | 1.63E-19 | 3.31583  |
| Interior                         | 0.341417    | 30 | 0.011381 |          |          |          |
| Total                            | 87.15088    | 35 |          |          |          |          |
| <b>OsNAC36</b>                   |             |    |          |          |          |          |
| Genotype                         | 12.92921    | 1  | 12.92921 | 326.7762 | 1.12E-17 | 4.170877 |
| Growth condition                 | 7.474882    | 2  | 3.737441 | 94.46106 | 1.13E-13 | 3.31583  |
| Interaction                      | 5.721308    | 2  | 2.860654 | 72.30091 | 3.36E-12 | 3.31583  |
| Interior                         | 1.186978    | 30 | 0.039566 |          |          |          |
| Total                            | 27.31238004 | 35 |          |          |          |          |
| <b>MYB14</b>                     |             |    |          |          |          |          |
| Genotype                         | 10.67051    | 1  | 10.67051 | 849.4146 | 1.45E-23 | 4.170877 |
| Growth condition                 | 5.433329    | 2  | 2.716664 | 216.2572 | 1.51E-18 | 3.31583  |
| Interaction                      | 2.526789    | 2  | 1.263394 | 100.5712 | 5E-14    | 3.31583  |
| Interior                         | 0.376866    | 30 | 0.012562 |          |          |          |
| Total                            | 19.00749118 | 35 |          |          |          |          |
| <b>SnRK1A</b>                    |             |    |          |          |          |          |
| Genotype                         | 1.670234    | 1  | 1.670234 | 11.67237 | 0.001842 | 4.170877 |
| Growth condition                 | 139.2915    | 2  | 69.64577 | 486.7171 | 1.36E-23 | 3.31583  |
| Interaction                      | 19.04049    | 2  | 9.520247 | 66.53192 | 9.36E-12 | 3.31583  |
| Interior                         | 4.292787    | 30 | 0.143093 |          |          |          |
| Total                            | 164.2950504 | 35 |          |          |          |          |
| <b>MYBS1</b>                     |             |    |          |          |          |          |
| Genotype                         | 1.527661    | 1  | 1.527661 | 13.31315 | 0.000993 | 4.170877 |
| Growth condition                 | 108.7838    | 2  | 54.3919  | 474.0107 | 2E-23    | 3.31583  |
| Interaction                      | 14.85154    | 2  | 7.425771 | 64.71358 | 1.31E-11 | 3.31583  |

|          |             |    |          |
|----------|-------------|----|----------|
| Interior | 3.442448    | 30 | 0.114748 |
| Total    | 128.6054558 | 35 |          |

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