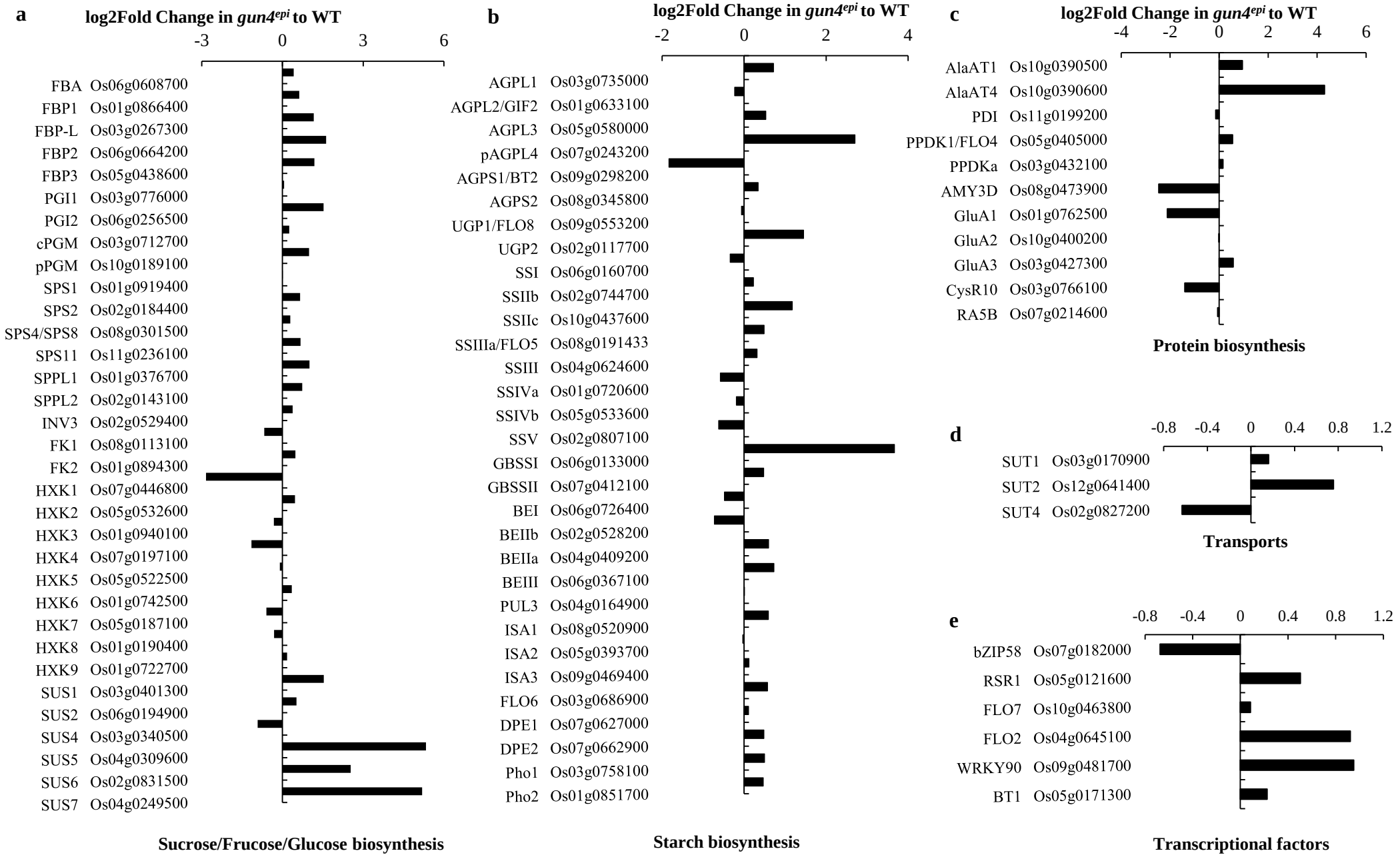
a
log2Fold Change in gun4epi to WT
-3
0
3
6
FBA Os06g0608700
FBP1 Os01g0866400
FBP-L Os03g0267300
FBP2 Os06g0664200
FBP3 Os05g0438600
PGI1 Os03g0776000
PGI2 Os06g0256500
cPGM Os03g0712700
pPGM Os10g0189100
SPS1 Os01g0919400
SPS2 Os02g0184400
SPS4/SPS8 Os08g0301500
SPS11 Os11g0236100
SPPL1 Os01g0376700
SPPL2 Os02g0143100
INV3 Os02g0529400
FK1 Os08g0113100
FK2 Os01g0894300
HXK1 Os07g0446800
HXK2 Os05g0532600
HXK3 Os01g0940100
HXK4 Os07g0197100
HXK5 Os05g0522500
HXK6 Os01g0742500
HXK7 Os05g0187100
HXK8 Os01g0190400
HXK9 Os01g0722700
SUS1 Os03g0401300
SUS2 Os06g0194900
SUS4 Os03g0340500
SUS5 Os04g0309600
SUS6 Os02g0831500
SUS7 Os04g0249500
Sucrose/Frucose/Glucose biosynthesis
b
log2Fold Change in gun4epi to WT
-2
0
2
4
AGPL1 Os03g0735000
AGPL2/GIF2 Os01g0633100
AGPL3 Os05g0580000
pAGPL4 Os07g0243200
AGPS1/BT2 Os09g0298200
AGPS2 Os08g0345800
UGP1/FLO8 Os09g0553200
UGP2 Os02g0117700
SSI Os06g0160700
SSIIb Os02g0744700
SSIIc Os10g0437600
SSIIIa/FLO5 Os08g0191433
SSIII Os04g0624600
SSIVa Os01g0720600
SSIVb Os05g0533600
SSV Os02g0807100
GBSSI Os06g0133000
GBSSII Os07g0412100
BEI Os06g0726400
BEIIb Os02g0528200
BEIIa Os04g0409200
BEIII Os06g0367100
PUL3 Os04g0164900
ISA1 Os08g0520900
ISA2 Os05g0393700
ISA3 Os09g0469400
FLO6 Os03g0686900
DPE1 Os07g0627000
DPE2 Os07g0662900
Pho1 Os03g0758100
Pho2 Os01g0851700
Starch biosynthesis
c
log2Fold Change in gun4epi to WT
-4
-2
0
2
4
6
AlaAT1 Os10g0390500
AlaAT4 Os10g0390600
PDI Os11g0199200
PPDK1/FLO4 Os05g0405000
PPDKa Os03g0432100
AMY3D Os08g0473900
GluA1 Os01g0762500
GluA2 Os10g0400200
GluA3 Os03g0427300
CysR10 Os03g0766100
RA5B Os07g0214600
Protein biosynthesis
d
-0.8
-0.4
0
0.4
0.8
1.2
SUT1 Os03g0170900
SUT2 Os12g0641400
SUT4 Os02g0827200
Transports
e
-0.8
-0.4
0
0.4
0.8
1.2
bZIP58 Os07g0182000
RSR1 Os05g0121600
FLO7 Os10g0463800
FLO2 Os04g0645100
WRKY90 Os09g0481700
BT1 Os05g0171300
Transcriptional factors

Fig. S1 Different-expressed genes involved in starch biosynthesis by RNAseq in leaves.
(A)Genes involved in (a) sucrose biosynthesis, (b) starch biosynthesis , (c) protein biosynthesis, (d) sucrose transports, (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, α-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.