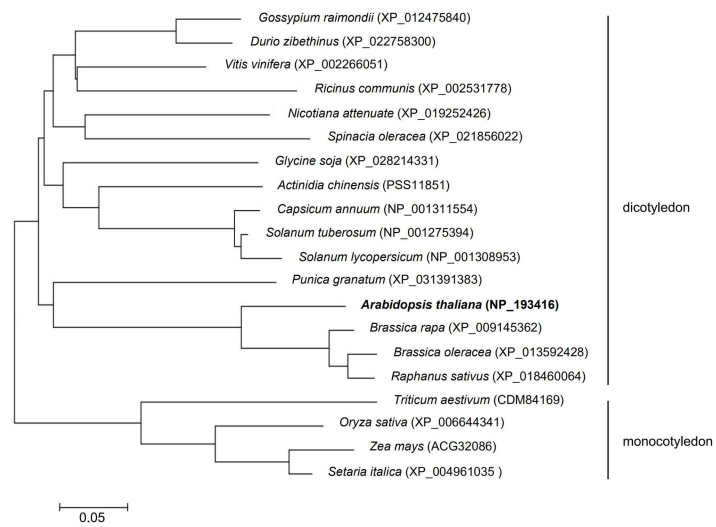
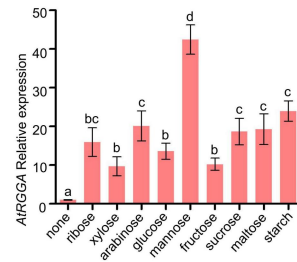
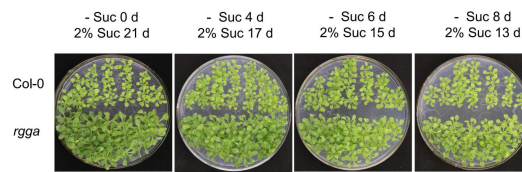




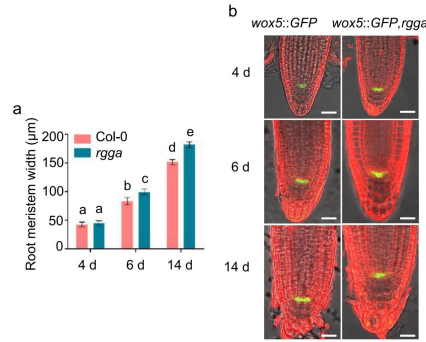
Supplementary Fig. 1 | Phylogenetic analysis of AtRGGA and its homologues from other species. The tree was generated in MEGA with the neighbor-joining algorithm (1000 replicates) using amino acid sequences.



Supplementary Fig. 2 | *AtRGGA* expression analysis of Col-0 and *rgga* plants by qPCR which were grown in the MS medium containing 2% ribose, xylose, arabinose, glucose, mannose, fructose, sucrose, maltose, and starch for 14 days.

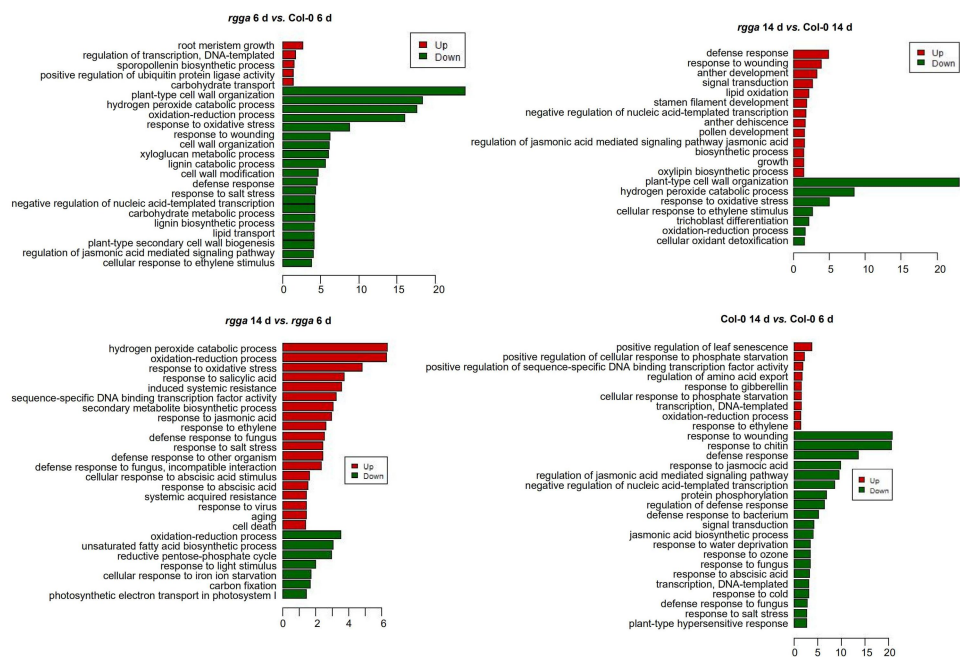


Supplementary Fig. 3 | *rgga* responses to sucrose within a relatively large time window. Col-0 and *rgga* were cultured in - Suc MS for different times (0, 4, 6, 8 d) respectively and then transferred to 2% Suc MS for continuing growth till 21 d age. Suc, sucrose; - Suc, no sucrose.



Supplementary Fig. 4 | Comparison of root apical meristems of *rgga* and Col-0.

WUSCHEL-RELATED HOMEODOMAIN (WOX5) gene is specifically expressed in the quiescent centre of *Arabidopsis* root. *WOX5::GFP*, *rgga* line was acquired by hybridizing *WOX5::GFP* and *rgga* lines. *wox5::GFP* and *wox5::GFP, rgga* were cultured in 2% sucrose MS for 4, 6, 14 d. **a**, Images of root apical meristems of *wox5::GFP* and *wox5::GFP, rgga*. Scale bar, 20μm. **B**, Root meristem width of *wox5::GFP* and *wox5::GFP, rgga*. n=50 plants. One-Way Anova, P<0.05, n=3 biologically independent samples.

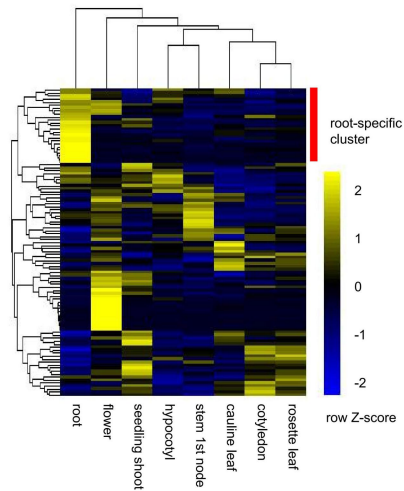


Supplementary Fig. 5 | Gene ontology (GO) analysis for the differentially expressed

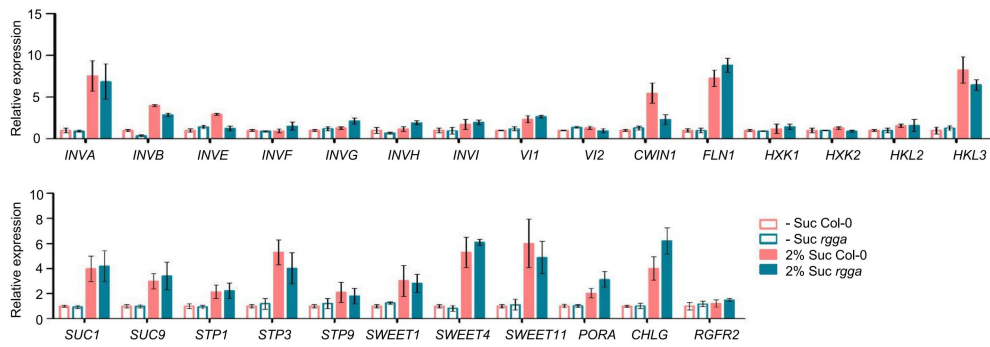
genes of *rgga* and Col-0. Samples for RNA sequencing are the whole seedlings of

Col-0 and *rgga* cultured in 2% sucrose MS for 6 d and 14 d respectively. The value of

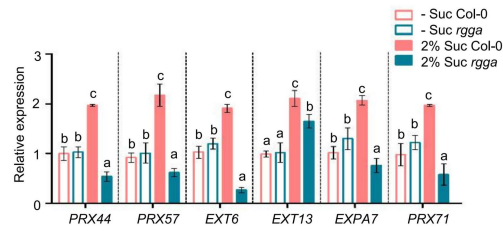
horizontal coordinate is $-\log_{10}(\text{p-value})$. Three biological replications were set.



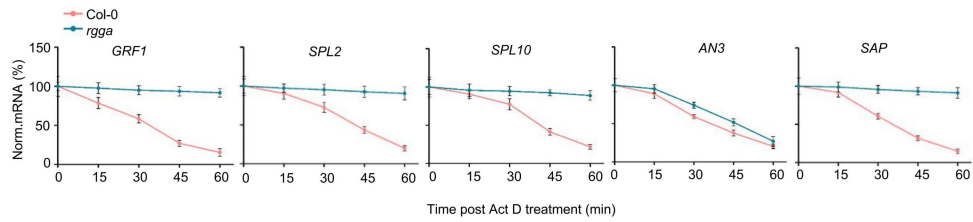
Supplementary Fig. 6 | 25/151 up-regulated differentially expressed genes (DEGs) in *rgga* 6 d vs. Col-0 6 d are specifically expressed in root, including *PLT1*, *PLT2*. *rgga* 6 d and Col-0 6 d are the seedlings of Col-0 and *rgga* cultured in 2% sucrose MS for 6 days. Data from eFP (electronic fluorescent pictograph) browser¹.



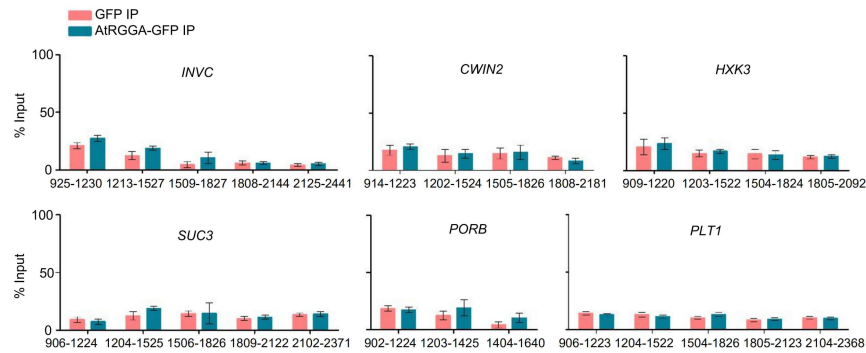
Supplementary Fig. 7 | The expression levels of growth-related genes. Gene expression analysis of Col-0 and *rrga* by qRT-PCR which cultured in - Suc MS and 2% sucrose MS for 14 days. The detected genes including NI, AI, HK and sucrose transporter encoded genes, chlorophyll synthesis related genes, root development related genes, and growth regulation TFs genes. One-Way Anova, $P < 0.05$, $n = 3$ biologically independent samples. Suc, sucrose; - Suc, no sucrose; NI, neutral invertase; AI, acid invertase; HK, hexokinase.



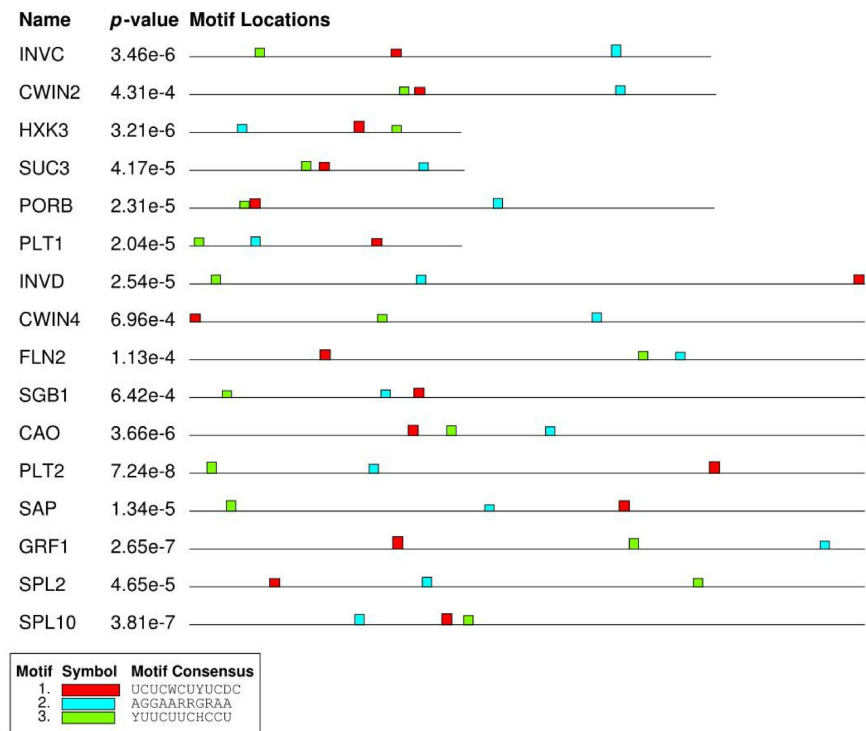
Supplementary Fig. 8 | Expression levels of the genes related to cell wall formation were analyzed by qPCR. Col-0 and *rgga* cultured in 2% Suc and - Suc MS MS for 14 days respectively were sampled. n=3 biologically independent samples. Suc, sucrose; - Suc, no sucrose.



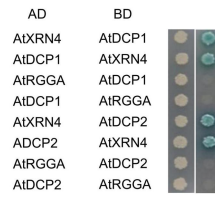
Supplementary Fig. 9 | mRNA stability analysis of the transcript factor genes (*GRF1*, *SPL2*, *SPL10*, *AN3*, *SAP*) in Col-0 and *rgga*. Seedlings grown in 2% sucrose MS for 14 days were treated with Act D and then sampled for qPCR analysis at 15, 30, 45, and 60 min post ActD treatment. min, minutes. The values of mRNA level before Act D treatment are set to 100%. n=3 biologically independent samples.



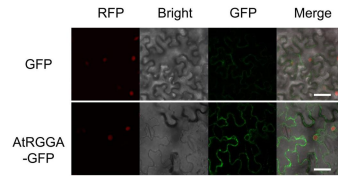
Supplementary Fig. 10| Binding region analysis of AtRGGA targeted mRNAs using RIP combined qPCR. *GFP* transgenic and *AtRGGA-GFP* transgenic *Arabidopsis* seedlings cultured in 2% sucrose MS for 14 days were sampled qPCR analysis with segmented primer pairs (each segment about 300bp). and other results were showed in **Fig. 4b**. One-Way Anova, $P < 0.05$, $n = 3$ biologically independent samples. RIP, RNA immunoprecipitation.



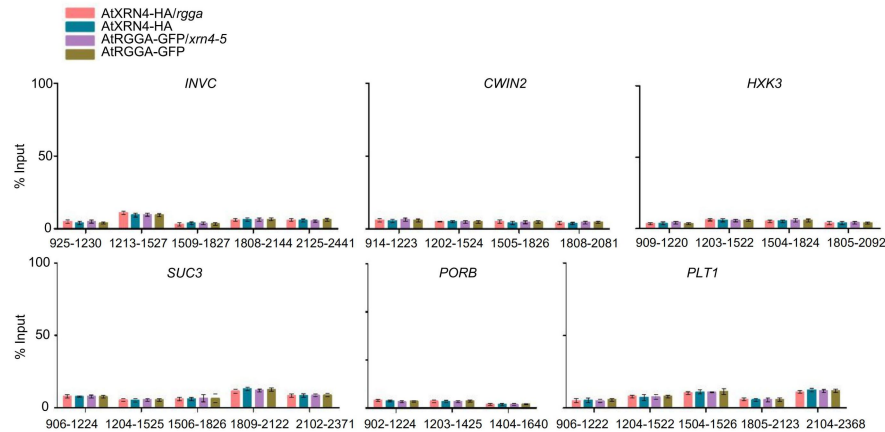
Supplementary Fig. 11 | Common motifs identified in the 5' terminus of the transcripts using MEME (Version 5.1.1). Analysis was performed on subsets of 6 transcripts (*INVC* 1-618, *CWIN2* 1-624, *HXK3* 1-322, *SUC3* 1-326, *PORB* 1-622, *PLT1* 1-323) of which AtRGGA binding regions were verified by RIP-qPCR and 10 transcripts (1-800) of which stability increased in *rgga*.



Supplementary Fig. 12 | Yeast two-hybrid (Y2H) assay of the interactions of AtDCP1, AtDCP2 with AtRGGA or AtXRN4. Transformed yeasts were spotted on control medium (DDO) or selective medium (QDO). Empty vector transformed yeasts were used as controls. BD, DNA binding domain vector; AD, activation domain vector. Yeast two-hybrid (Y2H) assay of AtXRN4 and AtRGGA.



Supplementary Fig. 13 | Subcellular localization analysis of *AtRGGA*. Co-infiltrated leaves of *RFP-H2B* transgenic *N. benthamiana* with *35S::GFP* and *35S::AtRGGA-GFP* at 48 hours post infiltration (hpi) were sampled for fluorescence observation. Scale bar, 20 μ m.



Supplementary Fig. 14 | AtRGGA addresses AtXRN4 to recognize target mRNAs.

The seedlings of *AtXRN4-HA/rgga*, *AtRGGA-GFP/xrn4-5*, *AtXRN4-HA* and *AtRGGA-GFP* grown in 2% sucrose MS for 14 d were sampled for binding region analysis for AtRGGA targets including *INVc*, *CWIN2*, *HXK3*, *SUC3*, *PORB* and *PLT1* mRNAs using RIP combined with qPCR. The enrichment of mRNA fragments was detected by the primer pairs each covering about 300bp. Only the results of 5' end of each target mRNA were showed here, and other results were showed in **Fig. 6a**. One-Way Anova, $P < 0.05$, $n = 3$ biological replicates. RIP, RNA immunoprecipitation assay.

Gene	Symbol	Name	Function	Description	Specifically expressed in root
AT4G26010	PRX44	peroxidase	root hair elongation	Mutants had shorter and ruptured root hairs ²	✓
AT5G64120	PRX71	peroxidase	negative regulation of growth; response to cell wall damage	AtPRX71 contributes to strengthen cell walls, therefore restricting cell expansion, during normal growth and in response to cell wall damage ³	
AT5G64100		peroxidase			✓
AT5G42180	PER64	peroxidase			
AT2G39040		peroxidase			✓
AT1G34510		peroxidase			✓
AT2G37130		peroxidase			
AT5G51890		peroxidase			
AT5G24070		peroxidase			✓
AT5G64110		peroxidase			
AT5G15180		peroxidase			✓
AT2G41480	PRX25	peroxidase			✓
AT1G30870		peroxidase			✓
AT2G24980	EXT6	extensin 6	root hair elongation	Mutants had shorter and irregular root hairs ⁴	✓
AT5G35190	EXT13	extensin 13	root hair elongation	Mutants had shorter and irregular root hairs ⁴	✓
AT1G21310	EXT3	extensin 3			✓
AT1G76930	EXT4	extensin 4			
AT5G06640	EXT10	extensin 10			✓
AT4G13390	EXT12	extensin 12			
AT1G12560	EXPA7	expansin A7	root hair elongation	Root hair-specific EXPANSIN A7 is required for root hair elongation in Arabidopsis ⁵	✓
AT1G62980	EXPA18	expansin A18			✓
AT3G54590	HRGP1	hydroxyproline-rich glycoprotein			✓
AT5G22410	RHS18	root hair specific 18			✓
AT3G29810	COBL2	COBRA-like protein 2			
AT5G06630		proline-rich extensin-like family protein			✓
AT1G26250		proline-rich extensin-like family protein			
AT2G21140	PRP2	proline-rich protein 2			
AT1G23720		proline-rich extensin-like family protein			✓
AT4G08410		proline-rich extensin-like family protein			✓
AT3G54580		proline-rich extensin-like family protein			

AT4G08400	proline-rich extensin-like family protein
AT3G28550	proline-rich extensin-like family protein

259 **Supplementary Tab. 2 | Oligonucleotides used in this study**

Designations	Sequence	Description
AtRGGa-His-F	5'-TCTAGAATGGCAACTTTGAACCCTTT-3'	PCR
AtRGGa-His-R	5'-GTCGACATGGTGATGGTGATGATGTTACTTGCCCCCAAGAGAT-3'	PCR
qAtRGGa-F	5'-CACTTCAATCATTAACTACC-3'	qPCR
qAtRGGa-R	5'-CTTCTTAGCCTTCTCTTC-3'	qPCR
LBa	5'-TGGTTCACGTAGTGGGCCATCG-3'	PCR
LP	5'-CTTCCTCCTGCTCAAGCCG-3'	PCR
RP	5'-GAGAGAGGCAAGGAGTGATG-3'	PCR
qActin-F	5'-CAGCAGAGCGGGAAATTGTAAGAG-3'	qPCR
qActin-R	5'-TTCCTTTCAGGTGGTGCAACGAC-3'	qPCR
XRN4-F	5'-GGATCCATGGGAGTACCGCGTTCTAC-3'	PCR
XRN4-R	5'-GAGCTCTCACAAGTTTGACCTCGATG-3'	PCR
qXRN4-F	5'-TGTCCTGCCAAACACTCTC-3'	qPCR
qXRN4-R	5'-CGTCGGTTGCTATTGTCTTC-3'	qPCR
INVA-F	5'-GAAGAGTATTCCACGGATGC-3'	qPCR
INVA-R	5'-CATTCTGCTTTGGTGATGCC-3'	qPCR
INVB-F	5'-CGACCTCAAATAGCAAGACG-3'	qPCR
INVB-R	5'-CTAAGTATCCTGCGACTGACC-3'	qPCR
INVC-F	5'-GGCTAAAGGAAGATGAGTGG-3'	qPCR
INVC-R	5'-CCCAGAACAAGAGTGATGC-3'	qPCR
INVD-F	5'-CGACCCTAAGAATACTCGTTG-3'	qPCR
INVD-R	5'-TTCCGATGAACCTTCCTG-3'	qPCR
INVE-F	5'-GGTAAACAGGCACGGCTAT-3'	qPCR
INVE-R	5'-CTCAAATCCGAATCCTCTTC-3'	qPCR
INVF-F	5'-ACTAACGGCGGCAAGCATA-3'	qPCR
INVF-R	5'-CGATGAATCTTCCAGACTTTCC-3'	qPCR
INVG-F	5'-AATACTCTCACACGGCGGT-3'	qPCR
INVG-R	5'-GAGGCATCTCACCTACAAGC-3'	qPCR
INVH-F	5'-TTGGGTTCTGAAAGTCCT-3'	qPCR
INVH-R	5'-GCCACTCTGAAGATTCTAAAGC-3'	qPCR
INVI-F	5'-CCTTTCTTCCTTGCAACT-3'	qPCR
INVI-R	5'-TCAGCGTCCACAGCAATAC-3'	qPCR
CWIN1-F	5'-GAATCTTCAAAGCCCGTCA-3'	qPCR
CWIN1-R	5'-AGGGATAGTGGTTGGTGAGG-3'	qPCR
CWIN2-F	5'-GGTGGATGTGGATGTGACA-3'	qPCR
CWIN2-R	5'-TTAGGCTTGTGGATGCG-3'	qPCR
CWIN4-F	5'-CATTAGCGACTCCTGATTG-3'	qPCR
CWIN4-R	5'-GCTTCACTGGATACACTCTTG-3'	qPCR

CWIN5-F	5'-CAGGTTTAGGTCCATTCGG-3'	qPCR
CWIN5-R	5'-ACTTGATGTGCTTTGGTCAC-3'	qPCR
VI1-F	5'-GCATTGTTTGATGTTGGGTC-3'	qPCR
VI1-R	5'-TCTCTCTTGTTCTTGTACAC-3'	qPCR
VI2-F	5'-CGATAGTAGAAGCATTGCGAC-3'	qPCR
VI2-R	5'-CTGTAAACGACGCCGTAAAC-3'	qPCR
FLN1-F	5'-CACCAGAGGAAATCAAGTCA-3'	qPCR
FLN1-R	5'-CAACAGCATCACCAGAACC-3'	qPCR
FLN2-F	5'-CTTGTTTGACCAATGGC-3'	qPCR
FLN2-R	5'-ATCTGGCTGAACCGTAAGC-3'	qPCR
HKL1-F	5'-GGGAGAAGCAGAAGTGAATC-3'	qPCR
HKL1-R	5'-TGTAAGAGGCAACGAGGA-3'	qPCR
HKL2-F	5'-GGAAGGAGAAGCGATAAGC-3'	qPCR
HKL2-R	5'-TGAACACTTTGTGACGAAGC-3'	qPCR
HKL3-F	5'-GAGCAGGAATAGTTGGGATG-3'	qPCR
HKL3-R	5'-AGAATCTTGATGACCGTCG-3'	qPCR
HXK1-F	5'-CTGCTGCTGGAATCTATGG-3'	qPCR
HXK1-R	5'-CATCATTGGAGTGAGTGACTTC-3'	qPCR
HXK2-F	5'-GATGTCGTTGTCGCAGTTAT-3'	qPCR
HXK2-R	5'-CTCTACGCAAGATTTCTCCC-3'	qPCR
HXK3-F	5'-TCCACTCCTTGCGACTCAG-3'	qPCR
HXK3-R	5'-TTCCACCACTCTCCTCTTG-3'	qPCR
SUC1-F	5'-GTTGAATGGATTGGTCGG-3'	qPCR
SUC1-R	5'-TCCTAATGAAAGTCCTTGGC-3'	qPCR
SUC3-F	5'-CTCGCAATCGTTATTCCC-3'	qPCR
SUC3-R	5'-GGTGGACTTGAAAGAACTCG-3'	qPCR
SUC4-F	5'-TCAACTGTTTGAGGTTGGG-3'	qPCR
SUC4-R	5'-GAATCCTTGTCGTGGAAG-3'	qPCR
SUC7-F	5'-GGATGCTACTAATCGTCACGG-3'	qPCR
SUC7-R	5'-CAAACACACGGCGAGAAT-3'	qPCR
SUC9-F	5'-CCTACCAATGCCATCAGAG-3'	qPCR
SUC9-R	5'-GTTTCCACCTCCAAATAACG-3'	qPCR
SGB1-F	5'-GTTTGTCTTGCCGTTCACT-3'	qPCR
SGB1-R	5'-GCTCTTCTTTAGTCTCAACC-3'	qPCR
STP1-F	5'-GAAAGGGATTCCGATAGAGG-3'	qPCR
STP1-R	5'-GCTTGGTTACTGTTCTTGCC-3'	qPCR
STP3-F	5'-CCGATGTTGTGTAAGTTTCG-3'	qPCR
STP3-R	5'-CCAATGCTTCTCCCAAAG-3'	qPCR
STP9-F	5'-CACGATGCTTTGCCACAT-3'	qPCR
STP9-R	5'-GCTTCCATACTTCTCCCATTC-3'	qPCR
SWEET1-F	5'-TCTATGGTCTAATCGGTCGTG-3'	qPCR
SWEET1-R	5'-TCATCTTCTGAGCATCTGC-3'	qPCR
SWEET4-F	5'-GCCATTCTCTCTCACTTGC-3'	qPCR
SWEET4-R	5'-ACTGCTCCTGATACCGTTCC-3'	qPCR

SWEET11-F	5'-GCACTCCAAATGATACTCTACG-3'	qPCR
SWEET11-R	5'-TTGACGAACCACTGAGATTG-3'	qPCR
CAO-F	5'-GGAGACATTTGCTGAACAG-3'	qPCR
CAO-R	5'-GGTAGTTTATCATGCCACG-3'	qPCR
CHLG-F	5'-TGGGTTAGGAATAGCCATTG-3'	qPCR
CHLG-R	5'-CAACGCCAACGCATAATAAG-3'	qPCR
PORA-F	5'-TCGGTGTTCACCTTCGG-3'	qPCR
PORA-R	5'-TGCCATTACCTGTCTCGG-3'	qPCR
PORB-F	5'-TTCCGAGAGCACATTCCT-3'	qPCR
PORB-R	5'-GAAGCCGAAGCATTGTTC-3'	qPCR
PORC-F	5'-ATACCGCTGTTTCGGCTT-3'	qPCR
PORC-R	5'-CCAATACACTCCTGACTTCCC-3'	qPCR
PLT1-F	5'-ACTTCATCTCCACCAACAGAC-3'	qPCR
PLT1-R	5'-GGACCCAATACCAATACCG-3'	qPCR
PLT2-F	5'-CGAGAGGAAATGATAGCCC-3'	qPCR
PLT2-R	5'-GCTGATGATGATGAAGATGC-3'	qPCR
RGFR-F	5'-TCCAATACCCGAAGACAGG-3'	qPCR
RGFR-R	5'-AGACGCAGAGAACTCGTG-3'	qPCR
INVC-P1	5'-CCATTTATTCAGACAACAA-3'	RIP
INVC-P2	5'-GAGAAAAACCGAAAAGCGAG-3'	RIP
INVC-P3	5'-CTCGCTTTTCGGTTTTTCTC-3'	RIP
INVC-P4	5'-CTTCACAAACATACTCTC-3'	RIP
INVC-P5	5'-GAGAGTATGTTTGTGAAG-3'	RIP
INVC-P6	5'-CTCCCCTTCTCCATCAAGC-3'	RIP
INVC-P7	5'-GCTTGATGGAGAAGGGGAG-3'	RIP
INVC-P8	5'-CTTGATCCCTGTTTGAAC-3'	RIP
INVC-P9	5'-GTTCAAACAGGGATCAAG-3'	RIP
INVC-P10	5'-CTCCTCTGTGTTGAACGG-3'	RIP
INVC-P11	5'-CCGGTGATTATTCGCCATTC-3'	RIP
INVC-P12	5'-GACTATCAGCTGCTGCTCGAGAC-3'	RIP
INVC-P13	5'-GTCTCGAGCAGCTGATAGTC-3'	RIP
INVC-P14	5'-CCTGAATCTGGTTTTATTTA-3'	RIP
CWIN2-P1	5'-CTATATCTTTACGAAAAC-3'	RIP
CWIN2-P2	5'-GTAGAGCATTGGAGATATGTTG-3'	RIP
CWIN2-P3	5'-CAACATATCTCCAATGCTCTAC-3'	RIP
CWIN2-P4	5'-CGTCTGGCTTTATCCATGTC-3'	RIP
CWIN2-P5	5'-GACATGGATAAAGCCAGACG-3'	RIP
CWIN2-P6	5'-CCTTCAACACATGCTTGCGC-3'	RIP
CWIN2-P7	5'-CGCCAAGCATGTGTTGAAGG-3'	RIP
CWIN2-P8	5'-CACGAGTTGCTTACCGCTAGAG-3'	RIP
CWIN2-P9	5'-CTCTAGCGGTAAGCAACTCGTG-3'	RIP
CWIN2-P10	5'-CTCTAAAGAAAACAGGAGTG-3'	RIP
CWIN2-P11	5'-CACTCCTGTTTTCTTTAGAG-3'	RIP
CWIN2-P12	5'-CACAGGTTGTGAGCCGTTG-3'	RIP

CWIN2-P13	5'-CAACGGCTCACAACTGTG-3'	RIP
CWIN2-P14	5'-ATGAAACACGTCTCCTAATC-3'	RIP
HXK3-P1	5'-CTTTGCATTCAAGGAAAAAC-3'	RIP
HXK3-P2	5'-CGGGTTGTGGTTGCAGCG-3'	RIP
HXK3-P3	5'-CGCTGCAACCACAACCGC-3'	RIP
HXK3-P4	5'-CCCGGAAGTTGGTTCC-3'	RIP
HXK3-P5	5'-GGAACCAACTCCGGG-3'	RIP
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HXK3-P8	5'-CCCAGGATTGATGCTAGC-3'	RIP
HXK3-P9	5'-GCTAGCATCAATCCTGGG-3'	RIP
HXK3-P10	5'-GCACCGGCTAAGCGTCCAG-3'	RIP
HXK3-P11	5'-CTGGACGCTTAGCCGGTGC-3'	RIP
HXK3-P12	5'-CATGGCAAATAGTTTTTCCC-3'	RIP
HXK3-P13	5'-GGGAAAACTATTGCCATG-3'	RIP
HXK3-P14	5'-GAATATAAGATCATACCACTG-3'	RIP
SUC3-P1	5'-GTTTTGATCCGATCAAATC-3'	RIP
SUC3-P2	5'-CATCGTCCTCAACACACAG-3'	RIP
SUC3-P3	5'-CTGTGTGTTGAGGACGATG-3'	RIP
SUC3-P4	5'-CCAAATAAACGAAGAAAAAGC-3'	RIP
SUC3-P5	5'-GCTTTTCTTCGTTTATTGG-3'	RIP
SUC3-P6	5'-GAAGAGCACGAGCAGGTCC-3'	RIP
SUC3-P7	5'-GGACCTGCTCGTGCTCTTC-3'	RIP
SUC3-P8	5'-GATCATCCAACAAAGGTGCAG-3'	RIP
SUC3-P9	5'-CTGCACCTTTGTTGGATGATC-3'	RIP
SUC3-P10	5'-GTTGGATCCCATGGTAAAC-3'	RIP
SUC3-P11	5'-GTTTACCATGGGGATCCAAC-3'	RIP
SUC3-P12	5'-GGGAAAACCAAGGAGTGC-3'	RIP
SUC3-P13	5'-GCACTCCTTGGTTTTCCC-3'	RIP
SUC3-P14	5'-GTGGTATAAAGATTTTAGCCG-3'	RIP
SUC3-P15	5'-CGGCTAAAATCTTTATACCAC-3'	RIP
SUC3-P16	5'-CAAACCTCAATAGTCCAATC-3'	RIP
PORB-P1	5'-CTCATTTGCTAGTACATAAAC-3'	RIP
PORB-P2	5'-GGGCTTGAACTCGAGCGG-3'	RIP
PORB-P3	5'-CCGCTGCGACTTCAAGCCC-3'	RIP
PORB-P4	5'-CATTGCAGACCAAAACATCGA-3'	RIP
PORB-P5	5'-TCGATGTTTTGGTCTGCAATG-3'	RIP
PORB-P6	5'-GCACCGTCGAAATCTCTC-3'	RIP
PORB-P7	5'-GAGGAGATTCGACGGTGC-3'	RIP
PORB-P8	5'-CTCAAAGAAGCCGAAGCATTG-3'	RIP
PORB-P9	5'-CAATGCTTCGGCTTCTTTGAG-3'	RIP
PORB-P10	5'-CTAATAAGGGATAAAAAAATTC-3'	RIP
PORB-P11	5'-GAAGTTTTTTTATCCTTATTAG-3'	RIP
PORB-P12	5'-GCAAAAAAATGTTCTCTAC-3'	RIP

PLT1-P1	5'-CACAAATATCTTCTCCTTTG-3'	RIP
PLT1-P2	5'-CATTTTCTTCTTTTGAGTC-3'	RIP
PLT1-P3	5'-GACTCAAAAAGAAGAAAATG-3'	RIP
PLT1-P4	5'-CGACATCGTTTGATTGGAC-3'	RIP
PLT1-P5	5'-GTCCAATCAAACGATGTCG-3'	RIP
PLT1-P6	5'-CTATTATCCCATAGATGAGC-3'	RIP
PLT1-P7	5'-GCTCATCTATGGGATAATAG-3'	RIP
PLT1-P8	5'-CCGATCCTTGCTTGCCTAC-3'	RIP
PLT1-P9	5'-GATGGCAAGCAAGGATCGG-3'	RIP
PLT1-P10	5'-GAGCCAGAGCCTGTGCTCG-3'	RIP
PLT1-P11	5'-CGAGCACAGGCTCTGGCTC-3'	RIP
PLT1-P12	5'-ATTGTTATTATTGTTGTCAACG-3'	RIP
PLT1-P13	5'-CGTTGACAACAATAACAAT-3'	RIP
PLT1-P14	5'-GAAATAAAAATTGAGAGTAG-3'	RIP
PLT1-P15	5'-CTACTCTCAATTTTATTTC-3'	RIP
PLT1-P16	5'-GATGTTTTCTCTAGCTCTT-3'	RIP
GRF1-F	5'-GTCAATCCCTATGGCTCCA-3'	qPCR
GRF1-R	5'-GGTCAAGAAACTCGGTGTTG-3'	qPCR
SPL2-F	5'-GACTGAGATTTCCGATACCG-3'	qPCR
SPL2-R	5'-GACAGAAGAGAGAGAGCACCA-3'	qPCR
SPL10-F	5'-CAAACATCTGGTGGGTTCTC-3'	qPCR
SPL10-R	5'-ATCCCTTGTGAATCCGAAG-3'	qPCR
AN3-F	5'-GGGAGAAGGAGGGTCACACTA-3'T	qPCR
AN3-R	5'-TTGCTGATGCTGAAGCGT-3'	qPCR
SAP-F	5'-TGGTAGATTTCACTGGCTGTG-3'	qPCR
SAP-R	5'-CCACCGACGAATGTTGCT-3'	qPCR
PRX44-F	5'-TTGCCACAAGAGACTCGGT-3'	qPCR
PRX44-R	5'-GGGTAAGTTCACATCATTGGG-3'	qPCR
PRX57-F	5'-CAGTTCTTCAAGCAAATCCG-3'	qPCR
PRX57-R	5'-GCTCCCATCTTACCATTG-3'	qPCR
EXT6-F	5'-TATTGCGGCTACGGTGACA-3'	qPCR
EXT6-R	5'-CCTTTGGCGATGGAGTGTA-3'	qPCR
EXT13-F	5'-GAGAAGGTGAAGGAAGATGTGA-3'	qPCR
EXT13-R	5'-GGAAACAGAGGCTGGCATA-3'	qPCR
EXPA7-F	5'-TCACAGCCACCAATCTTTG-3'	qPCR
EXPA7-R	5'-CCTCCAGTAAGCGAGTTTCAT-3'	qPCR
PRX71-F	5'-ACAACAACCTAAGCCGTGG-3'	qPCR
PRX71-R	5'-CATTGACCTCGAACTCA-3'	qPCR

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