

**Table S1 Primers used in qRT-PCR**

<b>gene ID</b>	<b>Gene description</b>	<b>F-primer</b>	<b>R-primer</b>
Dlo_033630.1	G-type lectin S-receptor-like serine/threonine-protein kinase B120 isoform X2	TTTGTGGTTTTGCTGGTCTG	ATTGCGGAAAAGGTTGAATG
Dlo_020951.2	Auxin response factor 3-like	CCAGCGGGTACTGTGGTATT	AATTTTCATGGCAACCAGCTC
Dlo_014365.1	Flowering locus T2	ACCAACATCGGGGATTCATA	CCGGAGATCCAAGGTTGTAA
Dlo_008881.1	UDP-glucosyltransferase	ACTGGATATTCTGCGGCATC	TGCTAATGCTCTCCATGCAC
Dlo_023607.1	Auxin response factor 2-like isoform X2	GGCTTCACTGCCAAAGAAAG	AAGAAGGGAACAAAGCAGCA
Dlo_030062.1	Receptor-like serine/threonine-protein kinase SD1-7	TGGAGAAGGTGGTTTTGGAG	TCCAAGCAAAAACCCAGAAG
Dlo_020508.1	Brassinosteroid insensitive 1-associated receptor kinase 1	TTTCATACCCCCAGCAGAAC	TTGTTGCAGCTTTGATTTGC
Dlo_029223.1	BRASSINOSTEROID INSENSITIVE 1- associated receptor kinase 1-like isoform X1	GTGACTCAGCCTCCACTTCC	CGAACTTTGGCTTGAGGATG
novel.3159	beta-Fructofuranosidase, insoluble isoenzyme CWINV1	GGGTGAAATTTTCTGGCAAT	GAATCGCCATTCTTGGTTA
novel.4880	Receptor-like protein kinase HSL1	AGCTCATCCATTGCTTGCTT	GGGATTTCTTCACGGTCAGA

**Table S2 KEGG annotation of genes in bisque4 module**

ID	KEGG	KEGG pathway
Dlo_016631.1	K02109 F-type H <sup>+</sup> -transporting ATPase subunit b   (RefSeq) ATP synthase subunit b', chloroplastic (A)	ko00190: Oxidative phosphorylation; ko00195: Photosynthesis
Dlo_021237.1	K08906 cytochrome c6   (RefSeq) cytochrome c6, chloroplastic (A)	ko00195: Photosynthesis
dlo_034184.1	K02704 photosystem II CP47 chlorophyll apoprotein   (RefSeq) uncharacterized protein LOC110789024 (A)	ko00195: Photosynthesis
dlo_034939.1	K02704 photosystem II CP47 chlorophyll apoprotein   (RefSeq) uncharacterized protein LOC110789024 (A)	ko00195: Photosynthesis
dlo_038117.1	K02704 photosystem II CP47 chlorophyll apoprotein   (RefSeq) uncharacterized protein LOC110789024 (A)	ko00195: Photosynthesis
Dlo_007361.1	K12118 cryptochrome 1   (RefSeq) cryptochrome-1 isoform X1 (A)	ko04712: Circadian rhythm - plant
Dlo_008062.1	K16222 Dof zinc finger protein DOF5.5   (RefSeq) cyclic dof factor 1 (A)	ko04712: Circadian rhythm - plant
Dlo_008466.1	K16222 Dof zinc finger protein DOF5.5   (RefSeq) cyclic dof factor 1 isoform X1 (A)	ko04712: Circadian rhythm - plant
Dlo_010292.1	K12127 pseudo-response regulator 1   (RefSeq) hypothetical protein (A)	ko04712: Circadian rhythm - plant
Dlo_013961.1	K12135 zinc finger protein CONSTANS   (RefSeq) zinc finger protein CONSTANS-LIKE 2-like (A)	ko04712: Circadian rhythm - plant
Dlo_016181.1	K16240 protein suppressor of PHYA-105 1   (RefSeq) protein SPA1-RELATED 4 isoform X1 (A)	ko04712: Circadian rhythm - plant
Dlo_019040.1	K12125 protein EARLY FLOWERING 3   (RefSeq) protein EARLY FLOWERING 3 (A)	ko04712: Circadian rhythm - plant
Dlo_019195.1	K12133 MYB-related transcription factor LHY   (RefSeq) uncharacterized protein LOC112280611 (A)	ko04712: Circadian rhythm - plant
Dlo_026237.1	K16221 transcription factor TCP21 (protein CCA1 HIKING EXPEDITION)   (RefSeq) transcription factor TCP7 (A)	ko04712: Circadian rhythm - plant

Dlo_034174.1	K12135 zinc finger protein CONSTANS   (RefSeq) zinc finger protein CONSTANS-like (A)	ko04712: Circadian rhythm - plant
Dlo_002040.1	K19893 glucan endo-1,3-beta-glucosidase 5/6 [EC:3.2.1.39]   (RefSeq) glucan endo-1,3-beta-glucosidase 6-like (A)	ko00500: Starch and sucrose metabolism
Dlo_004690.1	K00703 starch synthase [EC:2.4.1.21]   (RefSeq) glycogen synthase-like isoform X1 (A)	ko00500: Starch and sucrose metabolism
Dlo_004901.1	K19893 glucan endo-1,3-beta-glucosidase 5/6 [EC:3.2.1.39]   (RefSeq) glucan endo-1,3-beta-glucosidase 6-like (A)	ko00500: Starch and sucrose metabolism
Dlo_005793.1	K01176 alpha-amylase [EC:3.2.1.1]   (RefSeq) lectin-domain containing receptor kinase VI.3-like (A)	ko00500: Starch and sucrose metabolism
Dlo_007158.1	K00688 glycogen phosphorylase [EC:2.4.1.1]   (RefSeq) alpha-1,4 glucan phosphorylase L isozyme, chloroplastic/amyloplastic (A)	ko00500: Starch and sucrose metabolism
Dlo_008073.1	K00975 glucose-1-phosphate adenylyltransferase [EC:2.7.7.27]   (RefSeq) putative two-component response regulator ARR21 (A)	ko00500: Starch and sucrose metabolism; ko00520: Amino sugar and nucleotide sugar metabolism
Dlo_008102.1	K16055 trehalose 6-phosphate synthase/phosphatase [EC:2.4.1.15 3.1.3.12]   (RefSeq) probable alpha,alpha-trehalose-phosphate synthase [UDP-forming] 7 (A)	ko00500: Starch and sucrose metabolism
Dlo_008908.1	K19891 glucan endo-1,3-beta-glucosidase 1/2/3 [EC:3.2.1.39]   (RefSeq) glucan endo-1,3-beta-glucosidase 3-like (A)	ko00500: Starch and sucrose metabolism
Dlo_011114.2	K19893 glucan endo-1,3-beta-glucosidase 5/6 [EC:3.2.1.39]   (RefSeq) glucan endo-1,3-beta-glucosidase 6-like (A)	ko00500: Starch and sucrose metabolism
Dlo_011514.1	K01179 endoglucanase [EC:3.2.1.4]   (RefSeq) endoglucanase 6 isoform X2 (A)	ko00500: Starch and sucrose metabolism
Dlo_013090.1	K01176 alpha-amylase [EC:3.2.1.1]   (RefSeq) lectin-domain containing receptor kinase VI.3-like (A)	ko00500: Starch and sucrose metabolism
Dlo_013091.1	K01176 alpha-amylase [EC:3.2.1.1]   (RefSeq) lectin-domain containing receptor kinase VI.3-like (A)	ko00500: Starch and sucrose metabolism
Dlo_013092.1	K01176 alpha-amylase [EC:3.2.1.1]   (RefSeq) lectin-domain containing receptor kinase VI.3-like (A)	ko00500: Starch and sucrose metabolism
Dlo_013097.1	K00975 glucose-1-phosphate adenylyltransferase [EC:2.7.7.27]   (RefSeq) putative two-component response regulator ARR21 (A)	ko00500: Starch and sucrose metabolism; ko00520: Amino sugar and nucleotide sugar metabolism
Dlo_013135.1	K00975 glucose-1-phosphate adenylyltransferase [EC:2.7.7.27]   (RefSeq) putative two-component response regulator ARR21 (A)	ko00500: Starch and sucrose metabolism; ko00520: Amino sugar and nucleotide sugar metabolism

Dlo_013656.1	K01210 glucan 1,3-beta-glucosidase [EC:3.2.1.58]   (RefSeq) glucan 1,3-beta-glucosidase-like (A)	ko00500: Starch and sucrose metabolism
Dlo_015813.1	K00703 starch synthase [EC:2.4.1.21]   (RefSeq) starch synthase 1, chloroplastic/amyloplastic (A)	ko00500: Starch and sucrose metabolism
Dlo_015859.1	K16055 trehalose 6-phosphate synthase/phosphatase [EC:2.4.1.15 3.1.3.12]   (RefSeq) probable alpha,alpha-trehalose-phosphate synthase [UDP-forming] 11 (A)	ko00500: Starch and sucrose metabolism
Dlo_016152.1	K19891 glucan endo-1,3-beta-glucosidase 1/2/3 [EC:3.2.1.39]   (RefSeq) glucan endo-1,3-beta-glucosidase 1 (A)	ko00500: Starch and sucrose metabolism
Dlo_016697.3	K00975 glucose-1-phosphate adenylyltransferase [EC:2.7.7.27]   (RefSeq) putative two-component response regulator ARR21 (A)	ko00500: Starch and sucrose metabolism; ko00520: Amino sugar and nucleotide sugar metabolism
Dlo_016709.1	K16055 trehalose 6-phosphate synthase/phosphatase [EC:2.4.1.15 3.1.3.12]   (RefSeq) alpha,alpha-trehalose-phosphate synthase [UDP-forming] 5 isoform X1 (A)	ko00500: Starch and sucrose metabolism
Dlo_018095.1	K01179 endoglucanase [EC:3.2.1.4]   (RefSeq) basic cellulase (A)	ko00500: Starch and sucrose metabolism
Dlo_018543.1	K16055 trehalose 6-phosphate synthase/phosphatase [EC:2.4.1.15 3.1.3.12]   (RefSeq) hypothetical protein (A)	ko00500: Starch and sucrose metabolism
Dlo_019225.1	K01176 alpha-amylase [EC:3.2.1.1]   (RefSeq) alpha-amylase isozyme 2A (A)	ko00500: Starch and sucrose metabolism
Dlo_019355.1	K19891 glucan endo-1,3-beta-glucosidase 1/2/3 [EC:3.2.1.39]   (RefSeq) hypothetical protein (A)	ko00500: Starch and sucrose metabolism
Dlo_021114.1	K19893 glucan endo-1,3-beta-glucosidase 5/6 [EC:3.2.1.39]   (RefSeq) glucan endo-1,3-beta-glucosidase 6-like (A)	ko00500: Starch and sucrose metabolism
Dlo_022387.1	K01176 alpha-amylase [EC:3.2.1.1]   (RefSeq) lectin-domain containing receptor kinase VI.3-like (A)	ko00500: Starch and sucrose metabolism
Dlo_023622.1	K01176 alpha-amylase [EC:3.2.1.1]   (RefSeq) lectin-domain containing receptor kinase VI.3-like (A)	ko00500: Starch and sucrose metabolism
Dlo_024549.1	K19891 glucan endo-1,3-beta-glucosidase 1/2/3 [EC:3.2.1.39]   (RefSeq) hypothetical protein (A)	ko00500: Starch and sucrose metabolism
Dlo_024983.1	K19892 glucan endo-1,3-beta-glucosidase 4 [EC:3.2.1.39]   (RefSeq) glucan endo-1,3-beta-glucosidase 4 isoform X2 (A)	ko00500: Starch and sucrose metabolism
Dlo_025013.1	K19893 glucan endo-1,3-beta-glucosidase 5/6 [EC:3.2.1.39]   (RefSeq) glucan endo-1,3-beta-glucosidase 6-like (A)	ko00500: Starch and sucrose metabolism

Dlo_025504.1	K19891 glucan endo-1,3-beta-glucosidase 1/2/3 [EC:3.2.1.39]   (RefSeq) glucan endo-1,3-beta-glucosidase 2 (A)	ko00500: Starch and sucrose metabolism
Dlo_026667.1	K00975 glucose-1-phosphate adenylyltransferase [EC:2.7.7.27]   (RefSeq) glucose-1-phosphate adenylyltransferase large subunit 1-like (A)	ko00500: Starch and sucrose metabolism; ko00520: Amino sugar and nucleotide sugar metabolism
Dlo_027521.1	K19893 glucan endo-1,3-beta-glucosidase 5/6 [EC:3.2.1.39]   (RefSeq) glucan endo-1,3-beta-glucosidase 6-like (A)	ko00500: Starch and sucrose metabolism
Dlo_029524.1	K01176 alpha-amylase [EC:3.2.1.1]   (RefSeq) lectin-domain containing receptor kinase VI.3-like (A)	ko00500: Starch and sucrose metabolism
Dlo_029589.1	K01176 alpha-amylase [EC:3.2.1.1]   (RefSeq) lectin-domain containing receptor kinase VI.3-like (A)	ko00500: Starch and sucrose metabolism
Dlo_029595.1	K01177 beta-amylase [EC:3.2.1.2]   (RefSeq) beta-amylase 1, chloroplastic (A)	ko00500: Starch and sucrose metabolism
Dlo_030455.1	K01176 alpha-amylase [EC:3.2.1.1]   (RefSeq) lectin-domain containing receptor kinase VI.3-like (A)	ko00500: Starch and sucrose metabolism
Dlo_031084.1	K00703 starch synthase [EC:2.4.1.21]   (RefSeq) hypothetical protein (A)	ko00500: Starch and sucrose metabolism
Dlo_031832.1	K19891 glucan endo-1,3-beta-glucosidase 1/2/3 [EC:3.2.1.39]   (RefSeq) hypothetical protein (A)	ko00500: Starch and sucrose metabolism
Dlo_032373.1	K01179 endoglucanase [EC:3.2.1.4]   (RefSeq) uncharacterized LOC100245045 (A)	ko00500: Starch and sucrose metabolism
novel.2267	K00695 sucrose synthase [EC:2.4.1.13]   (RefSeq) sucrose synthase 2-like (A)	ko00500: Starch and sucrose metabolism
novel.4817	K00695 sucrose synthase [EC:2.4.1.13]   (RefSeq) hypothetical protein (A)	ko00500: Starch and sucrose metabolism
novel.514	K00695 sucrose synthase [EC:2.4.1.13]   (RefSeq) sucrose synthase 2-like (A)	ko00500: Starch and sucrose metabolism
Dlo_001441.1	K16224 senescence-induced receptor-like serine/threonine-protein kinase   (RefSeq) senescence-induced receptor-like serine/threonine-protein kinase (A)	ko04016: MAPK signaling pathway - plant; ko04626: Plant-pathogen interaction
Dlo_003399.1	K13420 LRR receptor-like serine/threonine-protein kinase FLS2 [EC:2.7.11.1]   (RefSeq) LRR receptor-like serine/threonine-protein kinase FLS2 (A)	ko04016: MAPK signaling pathway - plant; ko04626: Plant-pathogen interaction
Dlo_003886.1	K13420 LRR receptor-like serine/threonine-protein kinase FLS2 [EC:2.7.11.1]   (RefSeq) LOC109747212; LRR receptor-like serine/threonine-protein kinase FLS2 (A)	ko04016: MAPK signaling pathway - plant; ko04626: Plant-pathogen interaction

Dlo_004435.1	K13424 WRKY transcription factor 33   (RefSeq) probable WRKY transcription factor 26 (A)	ko04016: MAPK signaling pathway - plant; ko04626: Plant-pathogen interaction
Dlo_004862.1	K13416 brassinosteroid insensitive 1-associated receptor kinase 1 [EC:2.7.10.1 2.7.11.1]   (RefSeq) BRASSINOSTEROID INSENSITIVE 1-associated receptor kinase 1-like isoform X1 (A)	ko04016: MAPK signaling pathway - plant; ko04075: Plant hormone signal transduction; ko04626: Plant-pathogen interaction
Dlo_004883.1	K13416 brassinosteroid insensitive 1-associated receptor kinase 1 [EC:2.7.10.1 2.7.11.1]   (RefSeq) somatic embryogenesis receptor kinase 4-like isoform X1 (A)	ko04016: MAPK signaling pathway - plant; ko04075: Plant hormone signal transduction; ko04626: Plant-pathogen interaction
Dlo_005200.1	K13420 LRR receptor-like serine/threonine-protein kinase FLS2 [EC:2.7.11.1]   (RefSeq) LRR receptor-like serine/threonine-protein kinase FLS2 (A)	ko04016: MAPK signaling pathway - plant; ko04626: Plant-pathogen interaction
Dlo_006713.1	K14498 serine/threonine-protein kinase SRK2 [EC:2.7.11.1]   (RefSeq) serine/threonine-protein kinase SRK2A (A)	ko04016: MAPK signaling pathway - plant; ko04075: Plant hormone signal transduction
Dlo_008501.1	K16224 senescence-induced receptor-like serine/threonine-protein kinase   (RefSeq) senescence-induced receptor-like serine/threonine-protein kinase (A)	ko04016: MAPK signaling pathway - plant; ko04626: Plant-pathogen interaction
Dlo_008502.1	K16224 senescence-induced receptor-like serine/threonine-protein kinase   (RefSeq) senescence-induced receptor-like serine/threonine-protein kinase (A)	ko04016: MAPK signaling pathway - plant; ko04626: Plant-pathogen interaction
Dlo_008508.1	K16224 senescence-induced receptor-like serine/threonine-protein kinase   (RefSeq) senescence-induced receptor-like serine/threonine-protein kinase (A)	ko04016: MAPK signaling pathway - plant; ko04626: Plant-pathogen interaction
Dlo_008665.1	K16224 senescence-induced receptor-like serine/threonine-protein kinase   (RefSeq) senescence-induced receptor-like serine/threonine-protein kinase (A)	ko04016: MAPK signaling pathway - plant; ko04626: Plant-pathogen interaction
Dlo_008668.1	K16224 senescence-induced receptor-like serine/threonine-protein kinase   (RefSeq) senescence-induced receptor-like serine/threonine-protein kinase (A)	ko04016: MAPK signaling pathway - plant; ko04626: Plant-pathogen interaction
Dlo_008723.1	K13416 brassinosteroid insensitive 1-associated receptor kinase 1 [EC:2.7.10.1 2.7.11.1]   (RefSeq) somatic embryogenesis receptor-like kinase-like protein (A)	ko04016: MAPK signaling pathway - plant; ko04075: Plant hormone signal transduction; ko04626: Plant-pathogen interaction
Dlo_008724.1	K13420 LRR receptor-like serine/threonine-protein kinase FLS2 [EC:2.7.11.1]   (RefSeq) LRR receptor-like serine/threonine-protein kinase FLS2 (A)	ko04016: MAPK signaling pathway - plant; ko04626: Plant-pathogen interaction
Dlo_009134.1	K13422 transcription factor MYC2   (RefSeq) transcription factor MYC2-like (A)	ko04016: MAPK signaling pathway - plant; ko04075: Plant hormone signal transduction

Dlo_009414.1	K20557 transcription factor VIP1   (RefSeq) transcription factor VIP1 (A)	ko04016: MAPK signaling pathway - plant
Dlo_009835.1	K02183 calmodulin   (RefSeq) LOC109751263; calmodulin-1-like (A)	ko04016: MAPK signaling pathway - plant; ko04070: Phosphatidylinositol signaling system; ko04626: Plant-pathogen interaction
Dlo_009969.1	K20606 mitogen-activated protein kinase kinase kinase ANP1 [EC:2.7.11.25]   (RefSeq) receptor-like serine/threonine-protein kinase SD1-7 isoform X1 (A)	ko04016: MAPK signaling pathway - plant
Dlo_009980.1	K20606 mitogen-activated protein kinase kinase kinase ANP1 [EC:2.7.11.25]   (RefSeq) receptor-like serine/threonine-protein kinase SD1-7 isoform X1 (A)	ko04016: MAPK signaling pathway - plant
Dlo_009981.1	K20606 mitogen-activated protein kinase kinase kinase ANP1 [EC:2.7.11.25]   (RefSeq) receptor-like serine/threonine-protein kinase SD1-7 isoform X1 (A)	ko04016: MAPK signaling pathway - plant
Dlo_010002.1	K20606 mitogen-activated protein kinase kinase kinase ANP1 [EC:2.7.11.25]   (RefSeq) receptor-like serine/threonine-protein kinase SD1-7 isoform X1 (A)	ko04016: MAPK signaling pathway - plant
Dlo_010510.1	K20606 mitogen-activated protein kinase kinase kinase ANP1 [EC:2.7.11.25]   (RefSeq) receptor-like serine/threonine-protein kinase SD1-7 isoform X1 (A)	ko04016: MAPK signaling pathway - plant
Dlo_010513.1	K20606 mitogen-activated protein kinase kinase kinase ANP1 [EC:2.7.11.25]   (RefSeq) receptor-like serine/threonine-protein kinase SD1-7 isoform X1 (A)	ko04016: MAPK signaling pathway - plant
Dlo_010613.3	K20606 mitogen-activated protein kinase kinase kinase ANP1 [EC:2.7.11.25]   (RefSeq) receptor-like serine/threonine-protein kinase SD1-7 isoform X1 (A)	ko04016: MAPK signaling pathway - plant
Dlo_010873.1	K13425 WRKY transcription factor 22   (RefSeq) WRKY transcription factor 22-like (A)	ko04016: MAPK signaling pathway - plant; ko04626: Plant-pathogen interaction
Dlo_011260.1	K20606 mitogen-activated protein kinase kinase kinase ANP1 [EC:2.7.11.25]   (RefSeq) receptor-like serine/threonine-protein kinase SD1-7 isoform X1 (A)	ko04016: MAPK signaling pathway - plant
Dlo_011424.1	K20718 LRR receptor-like serine/threonine-protein kinase ERECTA [EC:2.7.11.1]   (RefSeq) LRR receptor-like serine/threonine-protein kinase ERL1 (A)	ko04016: MAPK signaling pathway - plant
Dlo_011473.1	K14498 serine/threonine-protein kinase SRK2 [EC:2.7.11.1]   (RefSeq) Serine/threonine-protein kinase SAPK10 (A)	ko04016: MAPK signaling pathway - plant; ko04075: Plant hormone signal transduction

Dlo_011701.2	K14497 protein phosphatase 2C [EC:3.1.3.16]   (RefSeq) protein phosphatase 2C 16-like (A)	ko04016: MAPK signaling pathway - plant; ko04075: Plant hormone signal transduction
Dlo_011802.1	K20606 mitogen-activated protein kinase kinase kinase ANP1 [EC:2.7.11.25]   (RefSeq) receptor-like serine/threonine-protein kinase SD1-7 isoform X1 (A)	ko04016: MAPK signaling pathway - plant
Dlo_011865.1	K13420 LRR receptor-like serine/threonine-protein kinase FLS2 [EC:2.7.11.1]   (RefSeq) LRR receptor-like serine/threonine-protein kinase FLS2 (A)	ko04016: MAPK signaling pathway - plant; ko04626: Plant-pathogen interaction
Dlo_012200.1	K13420 LRR receptor-like serine/threonine-protein kinase FLS2 [EC:2.7.11.1]   (RefSeq) LRR receptor-like serine/threonine-protein kinase FLS2 (A)	ko04016: MAPK signaling pathway - plant; ko04626: Plant-pathogen interaction
Dlo_012202.1	K13420 LRR receptor-like serine/threonine-protein kinase FLS2 [EC:2.7.11.1]   (RefSeq) LRR receptor-like serine/threonine-protein kinase FLS2 (A)	ko04016: MAPK signaling pathway - plant; ko04626: Plant-pathogen interaction
Dlo_012775.1	K20718 LRR receptor-like serine/threonine-protein kinase ERECTA [EC:2.7.11.1]   (RefSeq) LRR receptor-like serine/threonine-protein kinase ERECTA (A)	ko04016: MAPK signaling pathway - plant
Dlo_013471.1	K20725 MAP kinase substrate 1   (RefSeq) nuclear speckle RNA-binding protein B (A)	ko04016: MAPK signaling pathway - plant
Dlo_014864.2	K14514 ethylene-insensitive protein 3   (RefSeq) protein ETHYLENE INSENSITIVE 3-like (A)	ko04016: MAPK signaling pathway - plant; ko04075: Plant hormone signal transduction
Dlo_015049.1	K13416 brassinosteroid insensitive 1-associated receptor kinase 1 [EC:2.7.10.1 2.7.11.1]   (RefSeq) somatic embryogenesis receptor kinase 4-like isoform X1 (A)	ko04016: MAPK signaling pathway - plant; ko04075: Plant hormone signal transduction; ko04626: Plant-pathogen interaction
Dlo_015121.1	K20600 mitogen-activated protein kinase 4 [EC:2.7.11.24]   (RefSeq) hypothetical protein (A)	ko04016: MAPK signaling pathway - plant; ko04626: Plant-pathogen interaction
Dlo_015204.1	K13420 LRR receptor-like serine/threonine-protein kinase FLS2 [EC:2.7.11.1]   (RefSeq) LRR receptor-like serine/threonine-protein kinase FLS2 (A)	ko04016: MAPK signaling pathway - plant; ko04626: Plant-pathogen interaction
Dlo_015373.1	K13420 LRR receptor-like serine/threonine-protein kinase FLS2 [EC:2.7.11.1]   (RefSeq) LRR receptor-like serine/threonine-protein kinase FLS2 (A)	ko04016: MAPK signaling pathway - plant; ko04626: Plant-pathogen interaction
Dlo_016082.1	K20599 NB-LRR protein SUMM2   (RefSeq) probable disease resistance protein At1g12280 (A)	ko04016: MAPK signaling pathway - plant



Dlo_016229.1	K16224 senescence-induced receptor-like serine/threonine-protein kinase   (RefSeq) senescence-induced receptor-like serine/threonine-protein kinase (A)	ko04016: MAPK signaling pathway - plant; ko04626: Plant-pathogen interaction
Dlo_016368.1	K20718 LRR receptor-like serine/threonine-protein kinase ERECTA [EC:2.7.11.1]   (RefSeq) LRR receptor-like serine/threonine-protein kinase ERECTA (A)	ko04016: MAPK signaling pathway - plant
Dlo_016768.1	K13420 LRR receptor-like serine/threonine-protein kinase FLS2 [EC:2.7.11.1]   (RefSeq) LRR receptor-like serine/threonine-protein kinase FLS2 (A)	ko04016: MAPK signaling pathway - plant; ko04626: Plant-pathogen interaction
Dlo_016968.1	K20606 mitogen-activated protein kinase kinase kinase ANP1 [EC:2.7.11.25]   (RefSeq) receptor-like serine/threonine-protein kinase SD1-7 isoform X1 (A)	ko04016: MAPK signaling pathway - plant
Dlo_017469.1	K16224 senescence-induced receptor-like serine/threonine-protein kinase   (RefSeq) FRK1; FLG22-induced receptor-like kinase 1 (A)	ko04016: MAPK signaling pathway - plant; ko04626: Plant-pathogen interaction
Dlo_017583.1	K13420 LRR receptor-like serine/threonine-protein kinase FLS2 [EC:2.7.11.1]   (RefSeq) LRR receptor-like serine/threonine-protein kinase FLS2 (A)	ko04016: MAPK signaling pathway - plant; ko04626: Plant-pathogen interaction
Dlo_018481.1	K13420 LRR receptor-like serine/threonine-protein kinase FLS2 [EC:2.7.11.1]   (RefSeq) LRR receptor-like serine/threonine-protein kinase FLS2 (A)	ko04016: MAPK signaling pathway - plant; ko04626: Plant-pathogen interaction
Dlo_018615.1	K20606 mitogen-activated protein kinase kinase kinase ANP1 [EC:2.7.11.25]   (RefSeq) receptor-like serine/threonine-protein kinase SD1-7 isoform X1 (A)	ko04016: MAPK signaling pathway - plant
Dlo_018775.1	K20606 mitogen-activated protein kinase kinase kinase ANP1 [EC:2.7.11.25]   (RefSeq) receptor-like serine/threonine-protein kinase SD1-7 isoform X1 (A)	ko04016: MAPK signaling pathway - plant
Dlo_020508.1	K13416 brassinosteroid insensitive 1-associated receptor kinase 1 [EC:2.7.10.1 2.7.11.1]   (RefSeq) BRASSINOSTEROID INSENSITIVE 1-associated receptor kinase 1-like isoform X1 (A)	ko04016: MAPK signaling pathway - plant; ko04075: Plant hormone signal transduction; ko04626: Plant-pathogen interaction
Dlo_020923.1	K20599 NB-LRR protein SUMM2   (RefSeq) probable disease resistance protein At1g12280 (A)	ko04016: MAPK signaling pathway - plant
Dlo_021624.1	K13416 brassinosteroid insensitive 1-associated receptor kinase 1 [EC:2.7.10.1 2.7.11.1]   (RefSeq) BRASSINOSTEROID INSENSITIVE 1-associated receptor kinase 1-like (A)	ko04016: MAPK signaling pathway - plant; ko04075: Plant hormone signal transduction; ko04626: Plant-pathogen interaction
Dlo_021800.1	K13416 brassinosteroid insensitive 1-associated receptor kinase 1 [EC:2.7.10.1 2.7.11.1]   (RefSeq) BRASSINOSTEROID INSENSITIVE 1-associated receptor kinase 1-like (A)	ko04016: MAPK signaling pathway - plant; ko04075: Plant hormone signal transduction; ko04626: Plant-pathogen interaction

Dlo_021916.1	K14497 protein phosphatase 2C [EC:3.1.3.16]   (RefSeq) hypothetical protein (A)	ko04016: MAPK signaling pathway - plant; ko04075: Plant hormone signal transduction
Dlo_022994.1	K13420 LRR receptor-like serine/threonine-protein kinase FLS2 [EC:2.7.11.1]   (RefSeq) LRR receptor-like serine/threonine-protein kinase FLS2 (A)	ko04016: MAPK signaling pathway - plant; ko04626: Plant-pathogen interaction
Dlo_022995.1	K13420 LRR receptor-like serine/threonine-protein kinase FLS2 [EC:2.7.11.1]   (RefSeq) LRR receptor-like serine/threonine-protein kinase FLS2 (A)	ko04016: MAPK signaling pathway - plant; ko04626: Plant-pathogen interaction
Dlo_023010.1	K13420 LRR receptor-like serine/threonine-protein kinase FLS2 [EC:2.7.11.1]   (RefSeq) LRR receptor-like serine/threonine-protein kinase FLS2 (A)	ko04016: MAPK signaling pathway - plant; ko04626: Plant-pathogen interaction
Dlo_023223.3	K13420 LRR receptor-like serine/threonine-protein kinase FLS2 [EC:2.7.11.1]   (RefSeq) LRR receptor-like serine/threonine-protein kinase FLS2 (A)	ko04016: MAPK signaling pathway - plant; ko04626: Plant-pathogen interaction
Dlo_023269.1	K14497 protein phosphatase 2C [EC:3.1.3.16]   (RefSeq) probable protein phosphatase 2C 75 (A)	ko04016: MAPK signaling pathway - plant; ko04075: Plant hormone signal transduction
Dlo_024204.1	K14515 EIN3-binding F-box protein   (RefSeq) EIN3-binding F-box protein 1 (A)	ko04016: MAPK signaling pathway - plant; ko04075: Plant hormone signal transduction
Dlo_024741.2	K20557 transcription factor VIP1   (RefSeq) hypothetical protein (A)	ko04016: MAPK signaling pathway - plant
Dlo_024951.1	K02183 calmodulin   (RefSeq) calmodulin (A)	ko04016: MAPK signaling pathway - plant; ko04070: Phosphatidylinositol signaling system; ko04626: Plant-pathogen interaction
Dlo_025188.1	K13424 WRKY transcription factor 33   (RefSeq) hypothetical protein (A)	ko04016: MAPK signaling pathway - plant; ko04626: Plant-pathogen interaction
Dlo_025907.1	K20728 vegetative storage protein 2   (RefSeq) vegetative storage protein 1-like (A)	ko04016: MAPK signaling pathway - plant
Dlo_026641.1	K20538 mitogen-activated protein kinase 8 [EC:2.7.11.24]   (RefSeq) mitogen-activated protein kinase 8-like isoform X1 (A)	ko04016: MAPK signaling pathway - plant
Dlo_027125.1	K20558 transcription factor SPEECHLESS   (RefSeq) transcription factor SPEECHLESS-like (A)	ko04016: MAPK signaling pathway - plant
Dlo_027716.1	K20606 mitogen-activated protein kinase kinase kinase ANP1 [EC:2.7.11.25]   (RefSeq) mitogen-activated protein kinase kinase	ko04016: MAPK signaling pathway - plant

kinase NPK1-like (A)		
Dlo_028021.1	K14509 ethylene receptor [EC:2.7.13.-]   (RefSeq) ethylene response sensor 1-like (A)	ko04016: MAPK signaling pathway - plant; ko04075: Plant hormone signal transduction
Dlo_029223.1	K13416 brassinosteroid insensitive 1-associated receptor kinase 1 [EC:2.7.10.1 2.7.11.1]   (RefSeq) BRASSINOSTEROID INSENSITIVE 1-associated receptor kinase 1-like isoform X1 (A)	ko04016: MAPK signaling pathway - plant; ko04075: Plant hormone signal transduction; ko04626: Plant-pathogen interaction
Dlo_029322.1	K13413 mitogen-activated protein kinase kinase 4/5 [EC:2.7.12.2]   (RefSeq) mitogen-activated protein kinase kinase 5-like (A)	ko04016: MAPK signaling pathway - plant; ko04075: Plant hormone signal transduction; ko04626: Plant-pathogen interaction
Dlo_030832.1	K14514 ethylene-insensitive protein 3   (RefSeq) hypothetical protein (A)	ko04016: MAPK signaling pathway - plant; ko04075: Plant hormone signal transduction
Dlo_030878.1	K13420 LRR receptor-like serine/threonine-protein kinase FLS2 [EC:2.7.11.1]   (RefSeq) probable LRR receptor-like serine/threonine-protein kinase At3g47570 isoform X1 (A)	ko04016: MAPK signaling pathway - plant; ko04626: Plant-pathogen interaction
Dlo_031405.1	K13420 LRR receptor-like serine/threonine-protein kinase FLS2 [EC:2.7.11.1]   (RefSeq) LRR receptor-like serine/threonine-protein kinase FLS2 (A)	ko04016: MAPK signaling pathway - plant; ko04626: Plant-pathogen interaction
Dlo_031620.1	K14516 ethylene-responsive transcription factor 1   (RefSeq) ethylene-responsive transcription factor 1B-like (A)	ko04016: MAPK signaling pathway - plant; ko04075: Plant hormone signal transduction
Dlo_031694.1	K20718 LRR receptor-like serine/threonine-protein kinase ERECTA [EC:2.7.11.1]   (RefSeq) LRR receptor-like serine/threonine-protein kinase ERL1 (A)	ko04016: MAPK signaling pathway - plant
Dlo_031746.1	K16224 senescence-induced receptor-like serine/threonine-protein kinase   (RefSeq) senescence-induced receptor-like serine/threonine-protein kinase (A)	ko04016: MAPK signaling pathway - plant; ko04626: Plant-pathogen interaction
Dlo_031894.1	K13420 LRR receptor-like serine/threonine-protein kinase FLS2 [EC:2.7.11.1]   (RefSeq) hypothetical protein (A)	ko04016: MAPK signaling pathway - plant; ko04626: Plant-pathogen interaction
Dlo_032194.1	K14498 serine/threonine-protein kinase SRK2 [EC:2.7.11.1]   (RefSeq) serine/threonine-protein kinase SAPK2-like (A)	ko04016: MAPK signaling pathway - plant; ko04075: Plant hormone signal transduction
Dlo_033234.1	K13420 LRR receptor-like serine/threonine-protein kinase FLS2 [EC:2.7.11.1]   (RefSeq) receptor kinase-like protein Xa21 isoform X1 (A)	ko04016: MAPK signaling pathway - plant; ko04626: Plant-pathogen interaction

Dlo_033445.1	K13416 brassinosteroid insensitive 1-associated receptor kinase 1 [EC:2.7.10.1 2.7.11.1]   (RefSeq) BRASSINOSTEROID INSENSITIVE 1-associated receptor kinase 1-like (A)	ko04016: MAPK signaling pathway - plant; ko04075: Plant hormone signal transduction; ko04626: Plant-pathogen interaction
Dlo_033455.1	K13416 brassinosteroid insensitive 1-associated receptor kinase 1 [EC:2.7.10.1 2.7.11.1]   (RefSeq) somatic embryogenesis receptor kinase 4-like isoform X1 (A)	ko04016: MAPK signaling pathway - plant; ko04075: Plant hormone signal transduction; ko04626: Plant-pathogen interaction
Dlo_033908.1	K13413 mitogen-activated protein kinase kinase 4/5 [EC:2.7.12.2]   (RefSeq) mitogen-activated protein kinase kinase 5-like (A)	ko04016: MAPK signaling pathway - plant; ko04075: Plant hormone signal transduction; ko04626: Plant-pathogen interaction
novel.2361	K20718 LRR receptor-like serine/threonine-protein kinase ERECTA [EC:2.7.11.1]   (RefSeq) LRR receptor-like serine/threonine-protein kinase ERL1 (A)	ko04016: MAPK signaling pathway - plant
novel.3139	K13420 LRR receptor-like serine/threonine-protein kinase FLS2 [EC:2.7.11.1]   (RefSeq) probable LRR receptor-like serine/threonine-protein kinase At3g47570 (A)	ko04016: MAPK signaling pathway - plant; ko04626: Plant-pathogen interaction
novel.3395	K16224 senescence-induced receptor-like serine/threonine-protein kinase   (RefSeq) senescence-induced receptor-like serine/threonine-protein kinase (A)	ko04016: MAPK signaling pathway - plant; ko04626: Plant-pathogen interaction
novel.4461	K13447 respiratory burst oxidase [EC:1.6.3.- 1.11.1.-]   (RefSeq) respiratory burst oxidase homolog protein D-like (A)	ko04016: MAPK signaling pathway - plant; ko04626: Plant-pathogen interaction
novel.2026	K13420 LRR receptor-like serine/threonine-protein kinase FLS2 [EC:2.7.11.1]   (RefSeq) probable LRR receptor-like serine/threonine-protein kinase At3g47570 (A)	ko04016: MAPK signaling pathway - plant; ko04626: Plant-pathogen interaction
Dlo_031760.1	K14432 ABA responsive element binding factor   (RefSeq) hypothetical protein (A)	ko04075: Plant hormone signal transduction
Dlo_018087.1	K14432 ABA responsive element binding factor   (RefSeq) hypothetical protein (A)	ko04075: Plant hormone signal transduction
Dlo_001095.1	K14486 auxin response factor   (RefSeq) uncharacterized protein LOC110640186 (A)	ko04075: Plant hormone signal transduction
Dlo_009455.1	K14484 auxin-responsive protein IAA   (RefSeq) uncharacterized protein LOC110708826 isoform X1 (A)	ko04075: Plant hormone signal transduction
Dlo_011077.1	K14486 auxin response factor   (RefSeq) auxin response factor 5 (A)	ko04075: Plant hormone signal transduction
Dlo_015422.1	K14484 auxin-responsive protein IAA   (RefSeq) auxin-responsive protein IAA29 (A)	ko04075: Plant hormone signal transduction

Dlo_016833.1	K14484 auxin-responsive protein IAA   (RefSeq) auxin-responsive protein IAA27-like (A)	ko04075: Plant hormone signal transduction
Dlo_019013.1	K14484 auxin-responsive protein IAA   (RefSeq) hypothetical protein (A)	ko04075: Plant hormone signal transduction
Dlo_023262.1	K14486 auxin response factor   (RefSeq) auxin response factor 19-like isoform X1 (A)	ko04075: Plant hormone signal transduction
Dlo_002258.1	K14488 SAUR family protein   (RefSeq) auxin-responsive protein SAUR50-like (A)	ko04075: Plant hormone signal transduction
Dlo_009661.1	K14488 SAUR family protein   (RefSeq) hypothetical protein (A)	ko04075: Plant hormone signal transduction
Dlo_002416.1	K13415 protein brassinosteroid insensitive 1 [EC:2.7.10.1 2.7.11.1]   (RefSeq) systemin receptor SR160-like (A)	ko04075: Plant hormone signal transduction
Dlo_003532.1	K13415 protein brassinosteroid insensitive 1 [EC:2.7.10.1 2.7.11.1]   (RefSeq) uncharacterized protein LOC103413440 isoform X1 (A)	ko04075: Plant hormone signal transduction
Dlo_005748.1	K13415 protein brassinosteroid insensitive 1 [EC:2.7.10.1 2.7.11.1]   (RefSeq) systemin receptor SR160-like (A)	ko04075: Plant hormone signal transduction
Dlo_017586.1	K13415 protein brassinosteroid insensitive 1 [EC:2.7.10.1 2.7.11.1]   (RefSeq) systemin receptor SR160-like (A)	ko04075: Plant hormone signal transduction
Dlo_017789.1	K13415 protein brassinosteroid insensitive 1 [EC:2.7.10.1 2.7.11.1]   (RefSeq) systemin receptor SR160 (A)	ko04075: Plant hormone signal transduction
Dlo_016769.1	K13415 protein brassinosteroid insensitive 1 [EC:2.7.10.1 2.7.11.1]   (RefSeq) systemin receptor SR160-like (A)	ko04075: Plant hormone signal transduction
Dlo_022711.1	K13415 protein brassinosteroid insensitive 1 [EC:2.7.10.1 2.7.11.1]   (RefSeq) systemin receptor SR160-like (A)	ko04075: Plant hormone signal transduction
Dlo_030023.1	K13415 protein brassinosteroid insensitive 1 [EC:2.7.10.1 2.7.11.1]   (RefSeq) systemin receptor SR160-like (A)	ko04075: Plant hormone signal transduction
Dlo_001733.2	K13415 protein brassinosteroid insensitive 1 [EC:2.7.10.1 2.7.11.1]   (RefSeq) uncharacterized protein LOC103413440 isoform X1 (A)	ko04075: Plant hormone signal transduction
Dlo_031916.2	K13415 protein brassinosteroid insensitive 1 [EC:2.7.10.1 2.7.11.1]   (RefSeq) uncharacterized protein LOC103413440 isoform X1 (A)	ko04075: Plant hormone signal transduction
Dlo_032239.1	K13415 protein brassinosteroid insensitive 1 [EC:2.7.10.1 2.7.11.1]   (RefSeq) uncharacterized protein LOC103413440 isoform X1 (A)	ko04075: Plant hormone signal transduction

Dlo_033285.1	K13415 protein brassinosteroid insensitive 1 [EC:2.7.10.1 2.7.11.1]   (RefSeq) systemin receptor SR160-like (A)	ko04075: Plant hormone signal transduction
novel.1772	K14500 BR-signaling kinase [EC:2.7.11.1]   (RefSeq) probable serine/threonine-protein kinase At4g35230 (A)	ko04075: Plant hormone signal transduction
Dlo_033808.1	K14493 gibberellin receptor GID1 [EC:3.-.-.]   (RefSeq) GID1b-1; hypothetical protein (A)	ko04075: Plant hormone signal transduction
Dlo_029937.1	K14494 DELLA protein   (RefSeq) DELLA protein RGL1 (A)	ko04075: Plant hormone signal transduction
Dlo_017418.1	K14494 DELLA protein   (RefSeq) hypothetical protein (A)	ko04075: Plant hormone signal transduction
Dlo_007688.1	K14494 DELLA protein   (RefSeq) DELLA protein GAI-like (A)	ko04075: Plant hormone signal transduction
Dlo_028846.1	K14489 arabidopsis histidine kinase 2/3/4 (cytokinin receptor) [EC:2.7.13.3]   (RefSeq) histidine kinase 3-like (A)	ko04075: Plant hormone signal transduction
dlo_038209.1	K12126 phytochrome-interacting factor 3   (RefSeq) transcription factor PIF3 (A)	ko04075: Plant hormone signal transduction; ko04712: Circadian rhythm - plant
Dlo_024133.1	K14485 transport inhibitor response 1   (RefSeq) protein TRANSPORT INHIBITOR RESPONSE 1 (A)	ko04075: Plant hormone signal transduction
Dlo_003553.2	K16189 phytochrome-interacting factor 4   (RefSeq) PIL5; putative HLH DNA-binding domain superfamily protein (A)	ko04075: Plant hormone signal transduction
Dlo_005334.1	K14431 transcription factor TGA   (RefSeq) transcription factor TGA1 (A)	ko04075: Plant hormone signal transduction
Dlo_000989.1	K14508 regulatory protein NPR1   (RefSeq) BTB/POZ domain and ankyrin repeat-containing protein NPR2 (A)	ko04075: Plant hormone signal transduction

**Table S3 KEGG annotation of genes in darkorange2 module**

ID	KEGG	KEGG pathway
Dlo_003760.1	K08917 light-harvesting complex II chlorophyll a/b binding protein 6   (RefSeq) hypothetical protein (A)	ko00196: Photosynthesis - antenna proteins
Dlo_009388.1	K08917 light-harvesting complex II chlorophyll a/b binding protein 6   (RefSeq) hypothetical protein (A)	ko00196: Photosynthesis - antenna proteins
Dlo_012277.1	K08912 light-harvesting complex II chlorophyll a/b binding protein 1   (RefSeq) chlorophyll a-b binding protein of LHCII type 1 (A)	ko00196: Photosynthesis - antenna proteins
Dlo_012937.1	K08914 light-harvesting complex II chlorophyll a/b binding protein 3   (RefSeq) chlorophyll a-b binding protein 13, chloroplastic (A)	ko00196: Photosynthesis - antenna proteins
Dlo_014069.1	K02636 cytochrome b6-f complex iron-sulfur subunit [EC:1.10.9.1]   (RefSeq) cytochrome b6-f complex iron-sulfur subunit, chloroplastic (A)	ko00195: Photosynthesis
Dlo_021093.1	K02115 F-type H <sup>+</sup> -transporting ATPase subunit gamma   (RefSeq) ATP synthase gamma chain 1, chloroplastic (A)	ko00190: Oxidative phosphorylation; ko00195: Photosynthesis
Dlo_027744.1	K02692 photosystem I subunit II   (RefSeq) PSADB; PSI reaction center subunit II (A)	ko00195: Photosynthesis
Dlo_030363.1	K02113 F-type H <sup>+</sup> -transporting ATPase subunit delta   (RefSeq) hypothetical protein (A)	ko00190: Oxidative phosphorylation; ko00195: Photosynthesis
Dlo_031081.1	K08912 light-harvesting complex II chlorophyll a/b binding protein 1   (RefSeq) hypothetical protein (A)	ko00196: Photosynthesis - antenna proteins
Dlo_031082.1	K08912 light-harvesting complex II chlorophyll a/b binding protein 1   (RefSeq) hypothetical protein (A)	ko00196: Photosynthesis - antenna proteins
dlo_035474.1	K08903 photosystem II 13kDa protein   (RefSeq) hypothetical protein (A)	ko00195: Photosynthesis
dlo_035686.1	K02704 photosystem II CP47 chlorophyll apoprotein   (RefSeq) uncharacterized protein LOC110789024 (A)	ko00195: Photosynthesis
dlo_037508.1	K02704 photosystem II CP47 chlorophyll apoprotein   (RefSeq) uncharacterized protein LOC110789024 (A)	ko00195: Photosynthesis

dlo_037523.1	K02704 photosystem II CP47 chlorophyll apoprotein   (RefSeq) uncharacterized protein LOC110789024 (A)	ko00195: Photosynthesis
novel.2140	K02111 F-type H <sup>+</sup> /Na <sup>+</sup> -transporting ATPase subunit alpha [EC:7.1.2.2 7.2.2.1]   (RefSeq) LOW QUALITY PROTEIN: uncharacterized protein LOC114822316 (A)	ko00190: Oxidative phosphorylation; ko00195: Photosynthesis
novel.4239	K08909 light-harvesting complex I chlorophyll a/b binding protein 3   (RefSeq) chlorophyll a-b binding protein 8, chloroplastic (A)	ko00196: Photosynthesis - antenna proteins
novel.1074	K02111 F-type H <sup>+</sup> /Na <sup>+</sup> -transporting ATPase subunit alpha [EC:7.1.2.2 7.2.2.1]   (RefSeq) LOW QUALITY PROTEIN: uncharacterized protein LOC114822316 (A)	ko00190: Oxidative phosphorylation; ko00195: Photosynthesis
Dlo_000296.1	K16223 protein FLOWERING LOCUS T   (RefSeq) protein HEADING DATE 3A-like (A)	ko04712: Circadian rhythm - plant
Dlo_007957.1	K12118 cryptochrome 1   (RefSeq) cryptochrome-1 isoform X1 (A)	ko04712: Circadian rhythm - plant
Dlo_010015.1	K12135 zinc finger protein CONSTANS   (RefSeq) zinc finger protein CONSTANS-like (A)	ko04712: Circadian rhythm - plant
Dlo_012579.1	K16223 protein FLOWERING LOCUS T   (RefSeq) protein HEADING DATE 3A-like (A)	ko04712: Circadian rhythm - plant
Dlo_014365.1	K16223 protein FLOWERING LOCUS T   (RefSeq) protein HEADING DATE 3A-like (A)	ko04712: Circadian rhythm - plant
Dlo_014509.1	K12116 flavin-binding kelch repeat F-box protein 1   (RefSeq) adagio protein 3 (A)	ko04712: Circadian rhythm - plant
Dlo_015386.1	K16241 transcription factor HY5   (RefSeq) transcription factor HY5 (A)	ko04712: Circadian rhythm - plant
Dlo_029217.1	K12135 zinc finger protein CONSTANS   (RefSeq) zinc finger protein CONSTANS-like (A)	ko04712: Circadian rhythm - plant
Dlo_029296.1	K12135 zinc finger protein CONSTANS   (RefSeq) zinc finger protein CONSTANS isoform X2 (A)	ko04712: Circadian rhythm - plant
novel.246	K16240 protein suppressor of PHYA-105 1   (RefSeq) LOC109736903; protein SUPPRESSOR OF PHYA-105 1-like (A)	ko04712: Circadian rhythm - plant
novel.1023	K12129 pseudo-response regulator 7   (RefSeq) two-component response regulator-like APRR7 (A)	ko04712: Circadian rhythm - plant
Dlo_000502.1	K00703 starch synthase [EC:2.4.1.21]   (RefSeq) glycogen synthase (A)	ko00500: Starch and sucrose metabolism



Dlo_001164.2	K01176 alpha-amylase [EC:3.2.1.1]   (RefSeq) alpha-amylase (A)	ko00500: Starch and sucrose metabolism
Dlo_002486.1	K19891 glucan endo-1,3-beta-glucosidase 1/2/3 [EC:3.2.1.39]   (RefSeq) hypothetical protein (A)	ko00500: Starch and sucrose metabolism
Dlo_007747.1	K01176 alpha-amylase [EC:3.2.1.1]   (RefSeq) lectin-domain containing receptor kinase VI.3-like (A)	ko00500: Starch and sucrose metabolism
Dlo_007904.1	K19891 glucan endo-1,3-beta-glucosidase 1/2/3 [EC:3.2.1.39]   (RefSeq) hypothetical protein (A)	ko00500: Starch and sucrose metabolism
Dlo_009155.1	K01210 glucan 1,3-beta-glucosidase [EC:3.2.1.58]   (RefSeq) glucan 1,3-beta-glucosidase-like (A)	ko00500: Starch and sucrose metabolism
Dlo_010605.1	K01176 alpha-amylase [EC:3.2.1.1]   (RefSeq) lectin-domain containing receptor kinase VI.3-like (A)	ko00500: Starch and sucrose metabolism
Dlo_011377.1	K19893 glucan endo-1,3-beta-glucosidase 5/6 [EC:3.2.1.39]   (RefSeq) glucan endo-1,3-beta-glucosidase 5 (A)	ko00500: Starch and sucrose metabolism
Dlo_015310.1	K01176 alpha-amylase [EC:3.2.1.1]   (RefSeq) lectin-domain containing receptor kinase VI.3-like (A)	ko00500: Starch and sucrose metabolism
Dlo_016650.1	K00706 1,3-beta-glucan synthase [EC:2.4.1.34]   (RefSeq) hypothetical protein (A)	ko00500: Starch and sucrose metabolism
Dlo_017093.2	K01176 alpha-amylase [EC:3.2.1.1]   (RefSeq) lectin-domain containing receptor kinase VI.3-like (A)	ko00500: Starch and sucrose metabolism
Dlo_017545.1	K00695 sucrose synthase [EC:2.4.1.13]   (GenBank) sucrose synthase (A)	ko00500: Starch and sucrose metabolism
Dlo_020679.1	K00695 sucrose synthase [EC:2.4.1.13]   (GenBank) sucrose synthase (A)	ko00500: Starch and sucrose metabolism
Dlo_022164.1	K00696 sucrose-phosphate synthase [EC:2.4.1.14]   (RefSeq) probable sucrose-phosphate synthase 3 (A)	ko00500: Starch and sucrose metabolism
Dlo_022997.1	K19893 glucan endo-1,3-beta-glucosidase 5/6 [EC:3.2.1.39]   (RefSeq) glucan endo-1,3-beta-glucosidase 6-like (A)	ko00500: Starch and sucrose metabolism
Dlo_023359.1	K01087 trehalose 6-phosphate phosphatase [EC:3.1.3.12]   (RefSeq) trehalose-phosphate phosphatase A isoform X1 (A)	ko00500: Starch and sucrose metabolism
Dlo_025707.1	K01087 trehalose 6-phosphate phosphatase [EC:3.1.3.12]   (RefSeq) probable trehalose-phosphate phosphatase D (A)	ko00500: Starch and sucrose metabolism
Dlo_026404.2	K00688 glycogen phosphorylase [EC:2.4.1.1]   (RefSeq) glycogen phosphorylase 1-like (A)	ko00500: Starch and sucrose metabolism

Dlo_026568.1	K00688 glycogen phosphorylase [EC:2.4.1.1]   (RefSeq) glycogen phosphorylase 1-like (A)	ko00500: Starch and sucrose metabolism
Dlo_027026.1	K19893 glucan endo-1,3-beta-glucosidase 5/6 [EC:3.2.1.39]   (RefSeq) glucan endo-1,3-beta-glucosidase 6-like (A)	ko00500: Starch and sucrose metabolism
Dlo_027435.1	K19891 glucan endo-1,3-beta-glucosidase 1/2/3 [EC:3.2.1.39]   (RefSeq) hypothetical protein (A)	ko00500: Starch and sucrose metabolism
Dlo_033769.1	K01177 beta-amylase [EC:3.2.1.2]   (RefSeq) beta-amylase (A)	ko00500: Starch and sucrose metabolism
novel.2866	K00688 glycogen phosphorylase [EC:2.4.1.1]   (RefSeq) alpha-glucan phosphorylase, H isozyme (A)	ko00500: Starch and sucrose metabolism
novel.3344	K00688 glycogen phosphorylase [EC:2.4.1.1]   (RefSeq) alpha-glucan phosphorylase, H isozyme (A)	ko00500: Starch and sucrose metabolism
novel.3429	K01210 glucan 1,3-beta-glucosidase [EC:3.2.1.58]   (RefSeq) glucan 1,3-beta-glucosidase-like (A)	ko00500: Starch and sucrose metabolism
novel.1740	K00695 sucrose synthase [EC:2.4.1.13]   (GenBank) sucrose synthase (A)	ko00500: Starch and sucrose metabolism
novel.1741	K00695 sucrose synthase [EC:2.4.1.13]   (GenBank) sucrose synthase (A)	ko00500: Starch and sucrose metabolism
Dlo_000294.1	K20718 LRR receptor-like serine/threonine-protein kinase ERECTA [EC:2.7.11.1]   (RefSeq) LRR receptor-like serine/threonine-protein kinase ERECTA (A)	ko04016: MAPK signaling pathway - plant
Dlo_000694.1	K13420 LRR receptor-like serine/threonine-protein kinase FLS2 [EC:2.7.11.1]   (RefSeq) LRR receptor-like serine/threonine-protein kinase FLS2 (A)	ko04016: MAPK signaling pathway - plant; ko04626: Plant-pathogen interaction
Dlo_000710.1	K13416 brassinosteroid insensitive 1-associated receptor kinase 1 [EC:2.7.10.1 2.7.11.1]   (RefSeq) BRASSINOSTEROID INSENSITIVE 1-associated receptor kinase 1-like (A)	ko04016: MAPK signaling pathway - plant; ko04075: Plant hormone signal transduction; ko04626: Plant-pathogen interaction
Dlo_001414.2	K14498 serine/threonine-protein kinase SRK2 [EC:2.7.11.1]   (RefSeq) serine/threonine-protein kinase SRK2E (A)	ko04016: MAPK signaling pathway - plant; ko04075: Plant hormone signal transduction
Dlo_002644.1	K20606 mitogen-activated protein kinase kinase kinase ANP1 [EC:2.7.11.25]   (RefSeq) receptor-like serine/threonine-protein kinase SD1-7 isoform X1 (A)	ko04016: MAPK signaling pathway - plant
Dlo_004286.1	K13420 LRR receptor-like serine/threonine-protein kinase FLS2 [EC:2.7.11.1]   (RefSeq) LRR receptor-like serine/threonine-protein kinase FLS2 (A)	ko04016: MAPK signaling pathway - plant; ko04626: Plant-pathogen interaction

Dlo_004288.1	K13416 brassinosteroid insensitive 1-associated receptor kinase 1 [EC:2.7.10.1 2.7.11.1]   (RefSeq) BRASSINOSTEROID INSENSITIVE 1-associated receptor kinase 1-like (A)	ko04016: MAPK signaling pathway - plant; ko04075: Plant hormone signal transduction; ko04626: Plant-pathogen interaction
Dlo_005414.1	K13422 transcription factor MYC2   (RefSeq) transcription factor MYC2-like (A)	ko04016: MAPK signaling pathway - plant; ko04075: Plant hormone signal transduction
Dlo_005847.1	K16224 senescence-induced receptor-like serine/threonine-protein kinase   (RefSeq) hypothetical protein (A)	ko04016: MAPK signaling pathway - plant; ko04626: Plant-pathogen interaction
Dlo_007884.1	K02183 calmodulin   (RefSeq) probable calcium-binding protein CML30 (A)	ko04016: MAPK signaling pathway - plant; ko04070: Phosphatidylinositol signaling system; ko04626: Plant-pathogen interaction
Dlo_008108.1	K13420 LRR receptor-like serine/threonine-protein kinase FLS2 [EC:2.7.11.1]   (RefSeq) receptor kinase-like protein Xa21 (A)	ko04016: MAPK signaling pathway - plant; ko04626: Plant-pathogen interaction
Dlo_008262.1	K20606 mitogen-activated protein kinase kinase kinase ANP1 [EC:2.7.11.25]   (RefSeq) receptor-like serine/threonine-protein kinase SD1-7 isoform X1 (A)	ko04016: MAPK signaling pathway - plant
Dlo_008543.1	K20606 mitogen-activated protein kinase kinase kinase ANP1 [EC:2.7.11.25]   (RefSeq) receptor-like serine/threonine-protein kinase SD1-7 isoform X1 (A)	ko04016: MAPK signaling pathway - plant
Dlo_009177.1	K13420 LRR receptor-like serine/threonine-protein kinase FLS2 [EC:2.7.11.1]   (RefSeq) LRR receptor-like serine/threonine-protein kinase FLS2 (A)	ko04016: MAPK signaling pathway - plant; ko04626: Plant-pathogen interaction
Dlo_009183.1	K13420 LRR receptor-like serine/threonine-protein kinase FLS2 [EC:2.7.11.1]   (RefSeq) LRR receptor-like serine/threonine-protein kinase FLS2 (A)	ko04016: MAPK signaling pathway - plant; ko04626: Plant-pathogen interaction
Dlo_010203.1	K13420 LRR receptor-like serine/threonine-protein kinase FLS2 [EC:2.7.11.1]   (RefSeq) LRR receptor-like serine/threonine-protein kinase FLS2 (A)	ko04016: MAPK signaling pathway - plant; ko04626: Plant-pathogen interaction
Dlo_010606.1	K20606 mitogen-activated protein kinase kinase kinase ANP1 [EC:2.7.11.25]   (RefSeq) receptor-like serine/threonine-protein kinase SD1-7 isoform X1 (A)	ko04016: MAPK signaling pathway - plant
Dlo_013098.1	K20557 transcription factor VIP1   (RefSeq) transcription factor VIP1-like isoform X1 (A)	ko04016: MAPK signaling pathway - plant
Dlo_013704.1	K13447 respiratory burst oxidase [EC:1.6.3.- 1.11.1.-]   (RefSeq) respiratory burst oxidase homolog protein E (A)	ko04016: MAPK signaling pathway - plant; ko04626: Plant-pathogen interaction

Dlo_013731.1	K13420 LRR receptor-like serine/threonine-protein kinase FLS2 [EC:2.7.11.1]   (RefSeq) LRR receptor-like serine/threonine-protein kinase FLS2 (A)	ko04016: MAPK signaling pathway - plant; ko04626: Plant-pathogen interaction
Dlo_014807.1	K14509 ethylene receptor [EC:2.7.13.-]   (RefSeq) protein EIN4 (A)	ko04016: MAPK signaling pathway - plant; ko04075: Plant hormone signal transduction
Dlo_015045.1	K13416 brassinosteroid insensitive 1-associated receptor kinase 1 [EC:2.7.10.1 2.7.11.1]   (RefSeq) somatic embryogenesis receptor kinase 4-like isoform X1 (A)	ko04016: MAPK signaling pathway - plant; ko04075: Plant hormone signal transduction; ko04626: Plant-pathogen interaction
Dlo_016122.1	K13416 brassinosteroid insensitive 1-associated receptor kinase 1 [EC:2.7.10.1 2.7.11.1]   (RefSeq) SERK3, SERK3A; BRASSINOSTEROID INSENSITIVE 1-associated receptor kinase 1-like (A)	ko04016: MAPK signaling pathway - plant; ko04075: Plant hormone signal transduction; ko04626: Plant-pathogen interaction
Dlo_017192.1	K20599 NB-LRR protein SUMM2   (RefSeq) probable disease resistance protein Atlg12280 (A)	ko04016: MAPK signaling pathway - plant
Dlo_018293.1	K13420 LRR receptor-like serine/threonine-protein kinase FLS2 [EC:2.7.11.1]   (RefSeq) LRR receptor-like serine/threonine-protein kinase FLS2 (A)	ko04016: MAPK signaling pathway - plant; ko04626: Plant-pathogen interaction
Dlo_020436.1	K20718 LRR receptor-like serine/threonine-protein kinase ERECTA [EC:2.7.11.1]   (RefSeq) LRR receptor-like serine/threonine-protein kinase ERL1 (A)	ko04016: MAPK signaling pathway - plant
Dlo_020505.1	K13416 brassinosteroid insensitive 1-associated receptor kinase 1 [EC:2.7.10.1 2.7.11.1]   (RefSeq) BRASSINOSTEROID INSENSITIVE 1-associated receptor kinase 1-like isoform X1 (A)	ko04016: MAPK signaling pathway - plant; ko04075: Plant hormone signal transduction; ko04626: Plant-pathogen interaction
Dlo_021225.1	K20558 transcription factor SPEECHLESS   (RefSeq) transcription factor SPEECHLESS (A)	ko04016: MAPK signaling pathway - plant
Dlo_021262.3	K13447 respiratory burst oxidase [EC:1.6.3.- 1.11.1.-]   (RefSeq) respiratory burst oxidase homolog protein D (A)	ko04016: MAPK signaling pathway - plant; ko04626: Plant-pathogen interaction
Dlo_021476.1	K20726 transmembrane protein 222   (RefSeq) hypothetical protein (A)	ko04016: MAPK signaling pathway - plant
Dlo_022440.1	K13420 LRR receptor-like serine/threonine-protein kinase FLS2 [EC:2.7.11.1]   (RefSeq) receptor kinase-like protein Xa21 (A)	ko04016: MAPK signaling pathway - plant; ko04626: Plant-pathogen interaction
Dlo_022844.1	K20718 LRR receptor-like serine/threonine-protein kinase ERECTA [EC:2.7.11.1]   (RefSeq) LRR receptor-like serine/threonine-protein kinase ERECTA (A)	ko04016: MAPK signaling pathway - plant
Dlo_023043.1	K13416 brassinosteroid insensitive 1-associated receptor kinase 1 [EC:2.7.10.1 2.7.11.1]   (RefSeq) BRASSINOSTEROID	ko04016: MAPK signaling pathway - plant; ko04075: Plant hormone

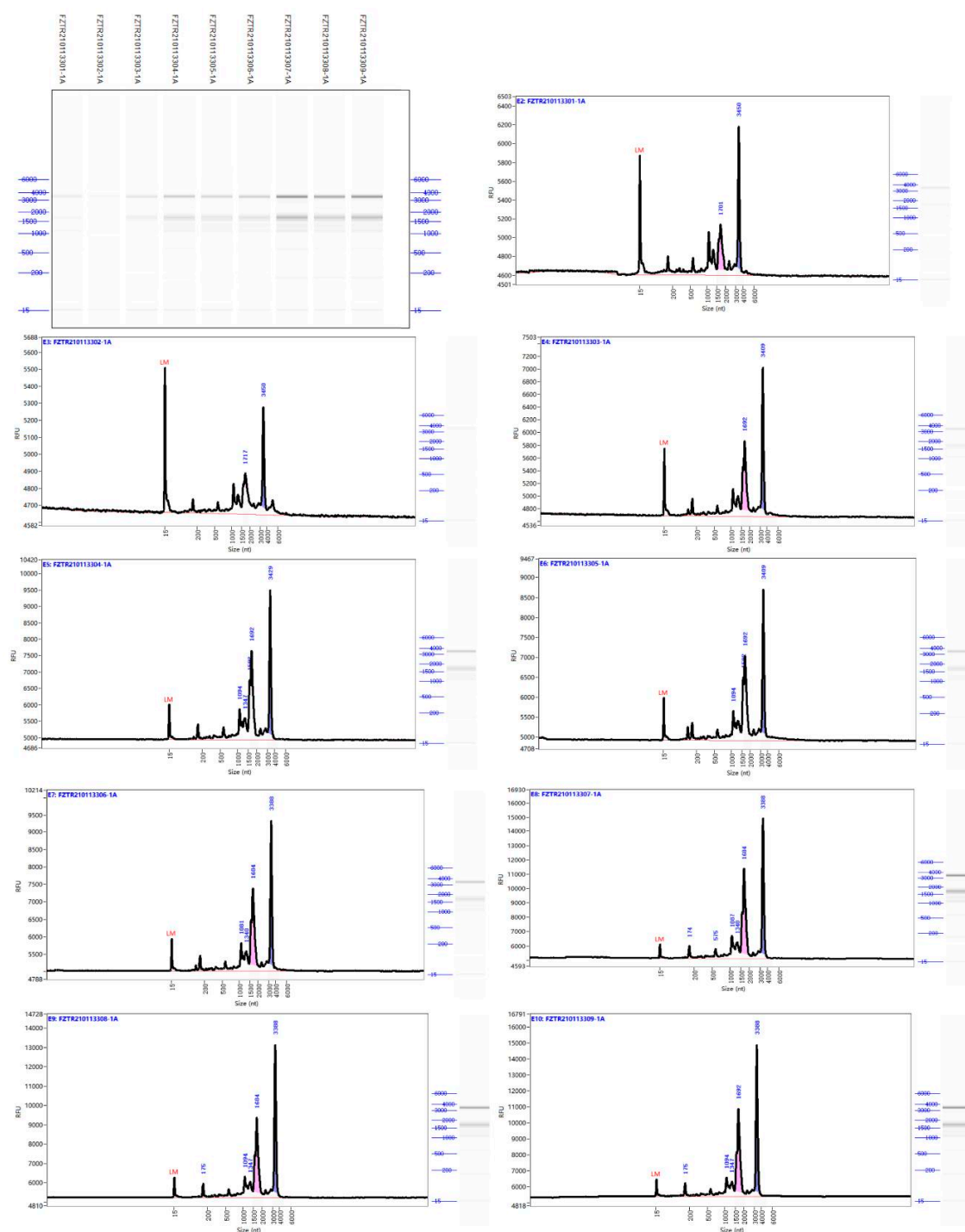
	INSENSITIVE 1-associated receptor kinase 1-like (A)	signal transduction; ko04626: Plant-pathogen interaction
Dlo_023156.1	K13420 LRR receptor-like serine/threonine-protein kinase FLS2 [EC:2.7.11.1]   (RefSeq) putative receptor-like protein kinase At3g47110 (A)	ko04016: MAPK signaling pathway - plant; ko04626: Plant-pathogen interaction
Dlo_023607.1	K14496 abscisic acid receptor PYR/PYL family   (RefSeq) abscisic acid receptor PYR1-like (A)	ko04016: MAPK signaling pathway - plant; ko04075: Plant hormone signal transduction
Dlo_025230.1	K14514 ethylene-insensitive protein 3   (RefSeq) putative ETHYLENE INSENSITIVE 3-like 4 protein (A)	ko04016: MAPK signaling pathway - plant; ko04075: Plant hormone signal transduction
Dlo_025974.1	K13425 WRKY transcription factor 22   (RefSeq) probable WRKY transcription factor 27 (A)	ko04016: MAPK signaling pathway - plant; ko04626: Plant-pathogen interaction
Dlo_026173.2	K14514 ethylene-insensitive protein 3   (RefSeq) hypothetical protein (A)	ko04016: MAPK signaling pathway - plant; ko04075: Plant hormone signal transduction
Dlo_026983.1	K20718 LRR receptor-like serine/threonine-protein kinase ERECTA [EC:2.7.11.1]   (RefSeq) LRR receptor-like serine/threonine-protein kinase ERECTA isoform X1 (A)	ko04016: MAPK signaling pathway - plant
Dlo_027394.1	K13422 transcription factor MYC2   (RefSeq) transcription factor MYC2-like (A)	ko04016: MAPK signaling pathway - plant; ko04075: Plant hormone signal transduction
Dlo_027765.1	K13420 LRR receptor-like serine/threonine-protein kinase FLS2 [EC:2.7.11.1]   (RefSeq) LRR receptor-like serine/threonine-protein kinase FLS2 (A)	ko04016: MAPK signaling pathway - plant; ko04626: Plant-pathogen interaction
Dlo_027984.2	K13420 LRR receptor-like serine/threonine-protein kinase FLS2 [EC:2.7.11.1]   (RefSeq) probable LRR receptor-like serine/threonine-protein kinase At3g47570 (A)	ko04016: MAPK signaling pathway - plant; ko04626: Plant-pathogen interaction
Dlo_029626.1	K20557 transcription factor VIP1   (RefSeq) transcription factor VIP1 (A)	ko04016: MAPK signaling pathway - plant
Dlo_029842.1	K13414 mitogen-activated protein kinase kinase kinase 1 [EC:2.7.11.25]   (RefSeq) mitogen-activated protein kinase kinase kinase 1 (A)	ko04016: MAPK signaling pathway - plant; ko04626: Plant-pathogen interaction
Dlo_030644.1	K14509 ethylene receptor [EC:2.7.13.-]   (RefSeq) ethylene receptor 2 isoform X1 (A)	ko04016: MAPK signaling pathway - plant; ko04075: Plant hormone signal transduction
Dlo_031170.1	K13416 brassinosteroid insensitive 1-associated receptor kinase 1 [EC:2.7.10.1 2.7.11.1]   (RefSeq) BRASSINOSTEROID	ko04016: MAPK signaling pathway - plant; ko04075: Plant hormone

	INSENSITIVE 1-associated receptor kinase 1-like isoform X1 (A)	signal transduction; ko04626: Plant-pathogen interaction
Dlo_031466.1	K13425 WRKY transcription factor 22   (RefSeq) WRKY transcription factor 22 (A)	ko04016: MAPK signaling pathway - plant; ko04626: Plant-pathogen interaction
Dlo_032589.1	K02183 calmodulin   (RefSeq) calmodulin-4 (A)	ko04016: MAPK signaling pathway - plant; ko04070: Phosphatidylinositol signaling system; ko04626: Plant-pathogen interaction
Dlo_032624.1	K13422 transcription factor MYC2   (RefSeq) transcription factor MYC4-like (A)	ko04016: MAPK signaling pathway - plant; ko04075: Plant hormone signal transduction
Dlo_033071.1	K16224 senescence-induced receptor-like serine/threonine-protein kinase   (RefSeq) senescence-induced receptor-like serine/threonine-protein kinase (A)	ko04016: MAPK signaling pathway - plant; ko04626: Plant-pathogen interaction
dlo_037203.1	K16224 senescence-induced receptor-like serine/threonine-protein kinase   (RefSeq) senescence-induced receptor-like serine/threonine-protein kinase (A)	ko04016: MAPK signaling pathway - plant; ko04626: Plant-pathogen interaction
novel.3268	K13416 brassinosteroid insensitive 1-associated receptor kinase 1 [EC:2.7.10.1 2.7.11.1]   (RefSeq) BRASSINOSTEROID INSENSITIVE 1-associated receptor kinase 1-like (A)	ko04016: MAPK signaling pathway - plant; ko04075: Plant hormone signal transduction; ko04626: Plant-pathogen interaction
novel.1457	K16224 senescence-induced receptor-like serine/threonine-protein kinase   (RefSeq) FRK1; FLG22-induced receptor-like kinase 1 (A)	ko04016: MAPK signaling pathway - plant; ko04626: Plant-pathogen interaction
Dlo_021352.1	K14432 ABA responsive element binding factor   (RefSeq) hypothetical protein (A)	ko04075: Plant hormone signal transduction
Dlo_002610.1	K14486 auxin response factor   (RefSeq) auxin response factor 3 (A)	ko04075: Plant hormone signal transduction
Dlo_020951.2	K14486 auxin response factor   (RefSeq) auxin response factor 3-like (A)	ko04075: Plant hormone signal transduction
Dlo_023230.3	K14488 SAUR family protein   (RefSeq) uncharacterized protein LOC106757509 (A)	ko04075: Plant hormone signal transduction
Dlo_024347.1	K14488 SAUR family protein   (RefSeq) auxin-responsive protein SAUR23-like (A)	ko04075: Plant hormone signal transduction
Dlo_029638.1	K14488 SAUR family protein   (RefSeq) indole-3-acetic acid-induced protein ARG7-like (A)	ko04075: Plant hormone signal transduction

Dlo_030377.1	K14488 SAUR family protein   (RefSeq) auxin-responsive protein SAUR32-like (A)	ko04075: Plant hormone signal transduction
Dlo_013702.1	K14488 SAUR family protein   (RefSeq) uncharacterized protein LOC112019881 (A)	ko04075: Plant hormone signal transduction
Dlo_001199.1	K13415 protein brassinosteroid insensitive 1 [EC:2.7.10.1 2.7.11.1]   (RefSeq) protein BRASSINOSTEROID INSENSITIVE 1 (A)	ko04075: Plant hormone signal transduction
Dlo_005703.1	K13415 protein brassinosteroid insensitive 1 [EC:2.7.10.1 2.7.11.1]   (RefSeq) protein BRASSINOSTEROID INSENSITIVE 1 isoform X1 (A)	ko04075: Plant hormone signal transduction
Dlo_008080.1	K13415 protein brassinosteroid insensitive 1 [EC:2.7.10.1 2.7.11.1]   (RefSeq) brassinosteroid LRR receptor kinase BRI1 (A)	ko04075: Plant hormone signal transduction
Dlo_020375.1	K13415 protein brassinosteroid insensitive 1 [EC:2.7.10.1 2.7.11.1]   (RefSeq) protein BRASSINOSTEROID INSENSITIVE 1 (A)	ko04075: Plant hormone signal transduction
Dlo_027889.1	K13415 protein brassinosteroid insensitive 1 [EC:2.7.10.1 2.7.11.1]   (RefSeq) uncharacterized protein LOC103413440 isoform X1 (A)	ko04075: Plant hormone signal transduction
Dlo_000103.1	K14503 brassinosteroid resistant 1/2   (RefSeq) BES1/BZR1 homolog protein 2-like (A)	ko04075: Plant hormone signal transduction
Dlo_010565.1	K14503 brassinosteroid resistant 1/2   (RefSeq) protein BRASSINAZOLE-RESISTANT 1 (A)	ko04075: Plant hormone signal transduction
Dlo_029469.1	K14500 BR-signaling kinase [EC:2.7.11.1]   (RefSeq) probable serine/threonine-protein kinase At5g41260 (A)	ko04075: Plant hormone signal transduction
Dlo_006433.1	K14491 two-component response regulator ARR-B family   (RefSeq) two-component response regulator ORR22 (A)	ko04075: Plant hormone signal transduction
Dlo_012378.2	K14492 two-component response regulator ARR-A family   (RefSeq) two-component response regulator ARR5-like (A)	ko04075: Plant hormone signal transduction
Dlo_015798.1	K14494 DELLA protein   (RefSeq) DELLA protein GAIP-B-like (A)	ko04075: Plant hormone signal transduction
Dlo_016250.2	K14489 arabidopsis histidine kinase 2/3/4 (cytokinin receptor) [EC:2.7.13.3]   (RefSeq) histidine kinase 4 (A)	ko04075: Plant hormone signal transduction
Dlo_017979.1	K14494 DELLA protein   (RefSeq) DELLA protein RGL1 (A)	ko04075: Plant hormone signal transduction
Dlo_018031.1	K14493 gibberellin receptor GID1 [EC:3.-.-.]   (RefSeq) gibberellin receptor GID1B-like (A)	ko04075: Plant hormone signal transduction

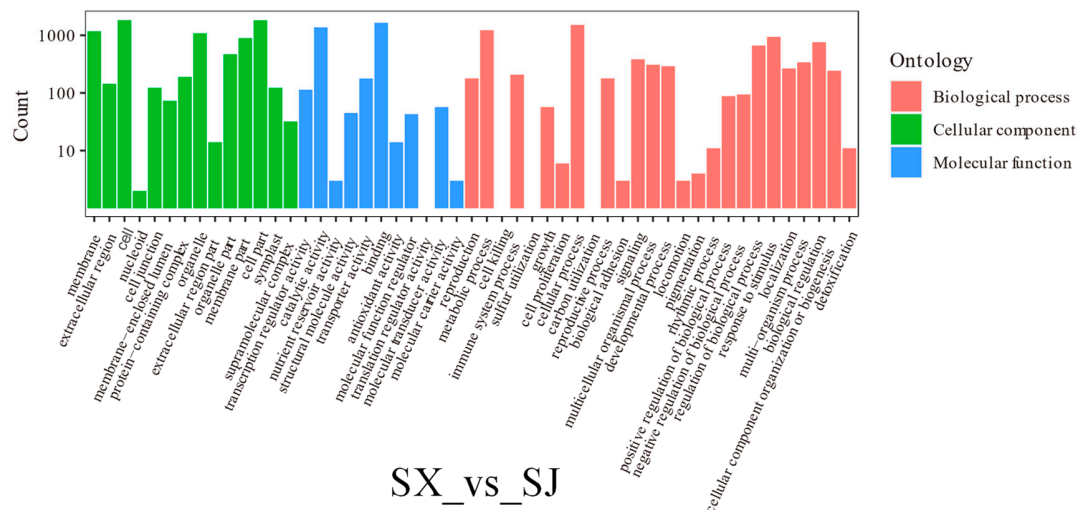
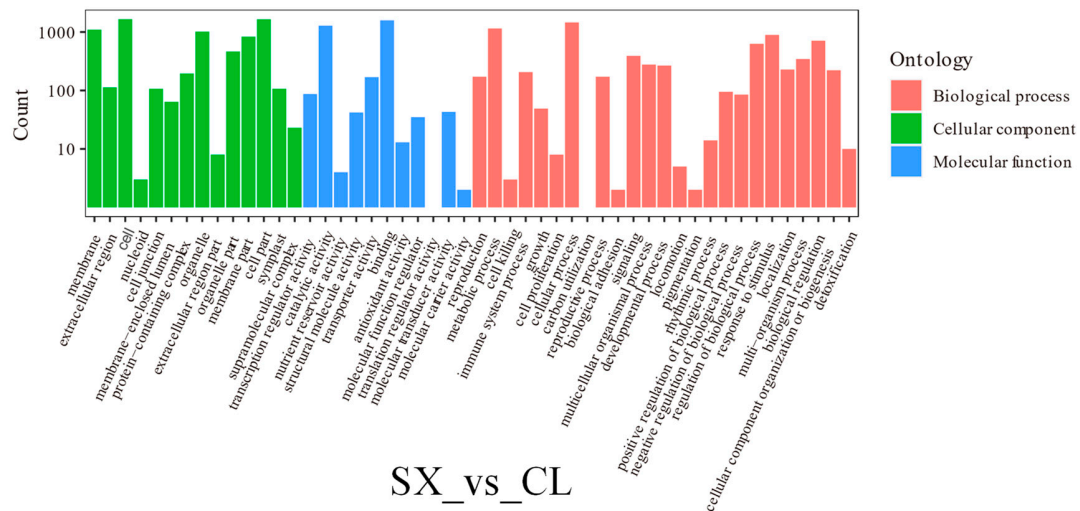
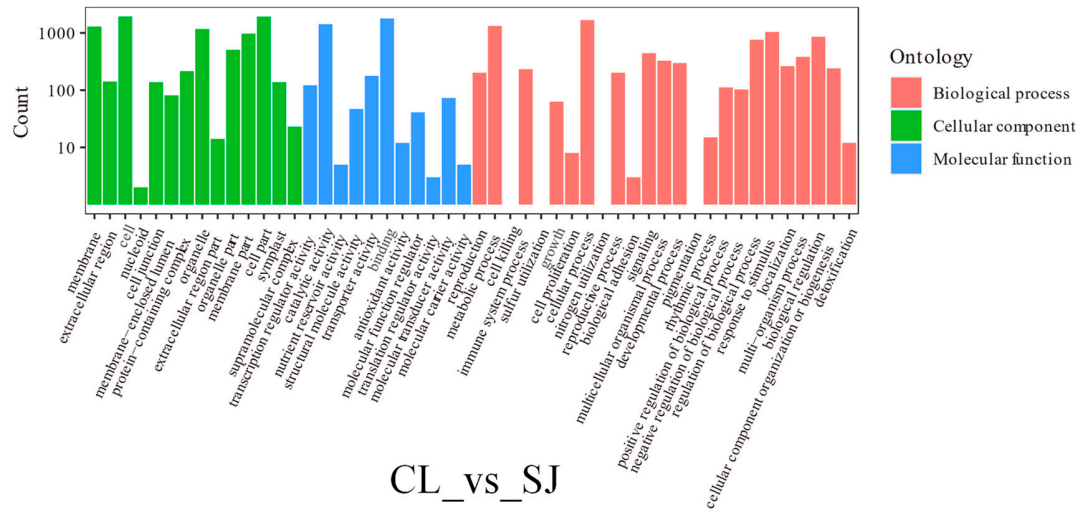
Dlo_018793.1	K14493 gibberellin receptor GID1 [EC:3.-.-.]   (RefSeq) gibberellin receptor GID1B-like isoform X1 (A)	ko04075: Plant hormone signal transduction
Dlo_004061.1	K14494 DELLA protein   (RefSeq) DELLA protein GAIP (A)	ko04075: Plant hormone signal transduction
Dlo_006628.1	K14493 gibberellin receptor GID1 [EC:3.-.-.]   (RefSeq) GID1b-1; hypothetical protein (A)	ko04075: Plant hormone signal transduction
Dlo_012860.1	K14495 F-box protein GID2   (RefSeq) GID2a-1; hypothetical protein (A)	ko04075: Plant hormone signal transduction
Dlo_023611.1	K14493 gibberellin receptor GID1 [EC:3.-.-.]   (RefSeq) gibberellin receptor GID1C-like (A)	ko04075: Plant hormone signal transduction
novel.3290	K14493 gibberellin receptor GID1 [EC:3.-.-.]   (RefSeq) gibberellin receptor GID1B-like (A)	ko04075: Plant hormone signal transduction
novel.924	K14493 gibberellin receptor GID1 [EC:3.-.-.]   (RefSeq) gibberellin receptor GID1B-like (A)	ko04075: Plant hormone signal transduction
Dlo_020626.1	K14431 transcription factor TGA   (RefSeq) bZIP transcription factor TGA10 (A)	ko04075: Plant hormone signal transduction
Dlo_028817.1	K12126 phytochrome-interacting factor 3   (RefSeq) transcription factor PIF3 isoform X1 (A)	ko04075: Plant hormone signal transduction; ko04712: Circadian rhythm - plant



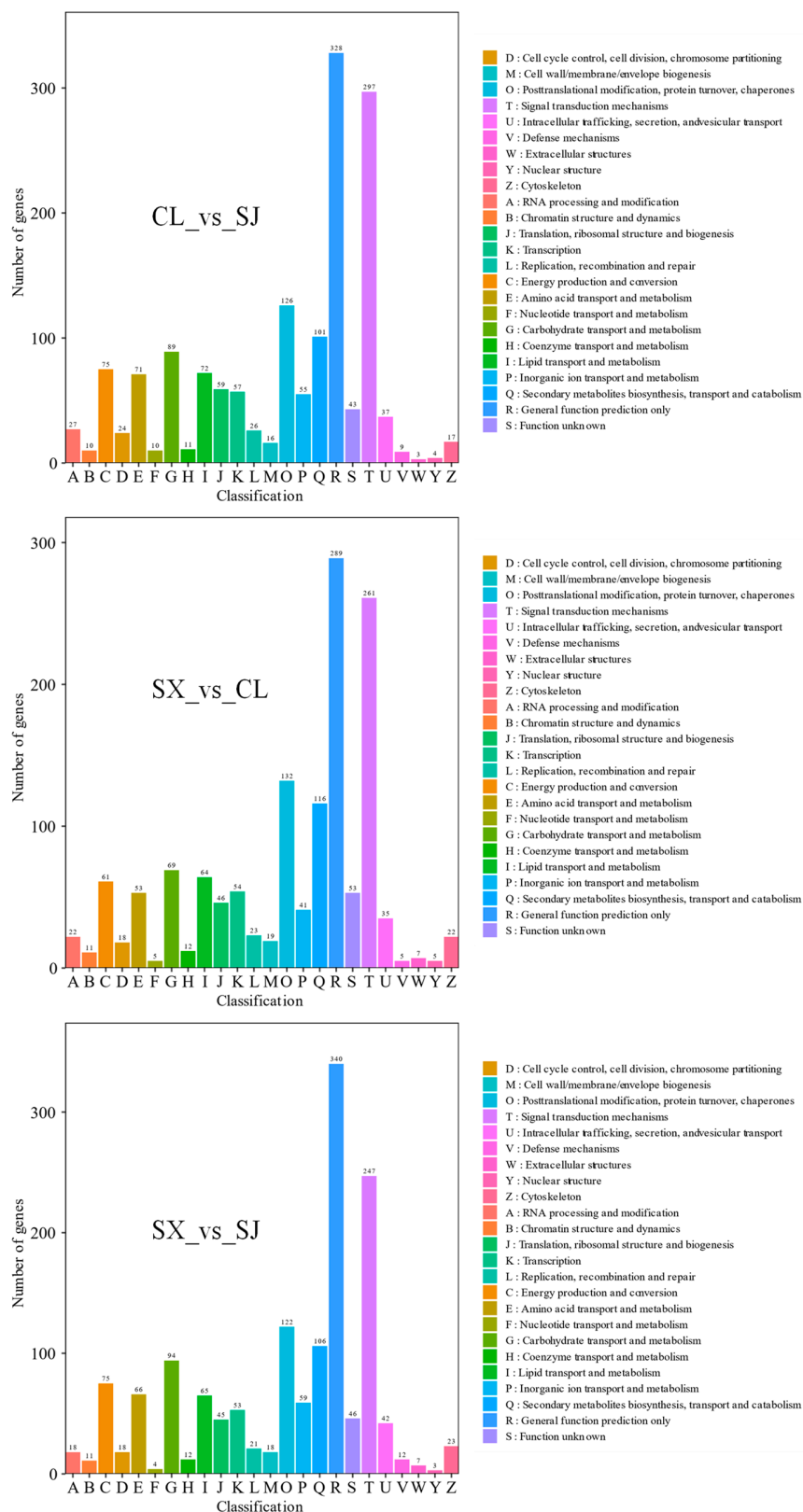


**Figure S1 RNA electropherogram of nine samples**

FZTR210113301-1A to FZTR210113309-1A: SX1, SX2, SX3, SJ1, SJ2, SJ3, CL1, CL2, CL3



### Figure S2 GO annotation of DEGs



**Figure S3 KOG annotation of DEGs**

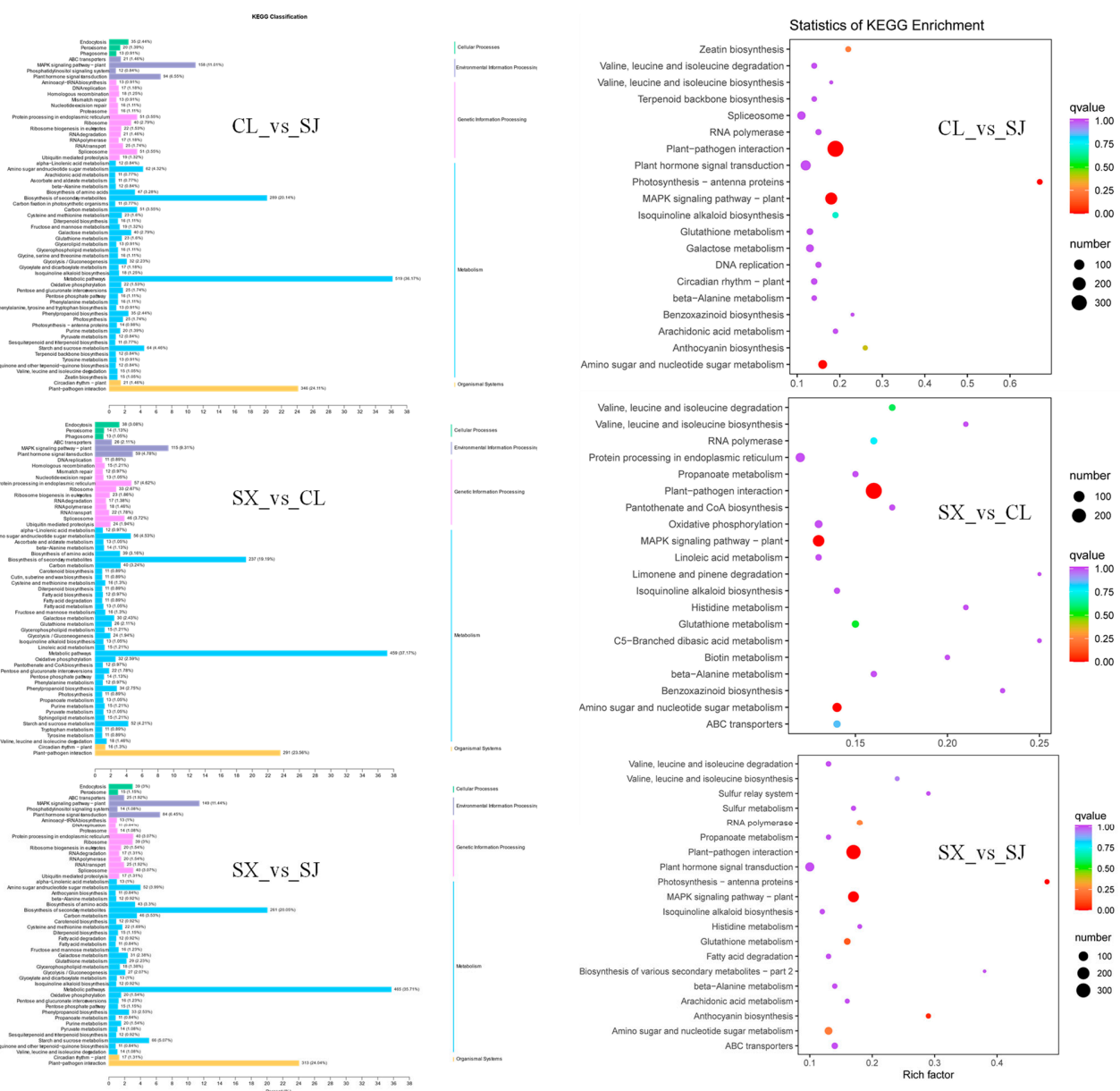


Figure S4 KEGG annotation of DEGs