Development related transcripts_MapMan

BinCode	BinName
33.1	development.storage proteins
33.1	development.storage proteins
33.3	development.squamosa promoter binding like (SPL)
33.3	development.squamosa promoter binding like (SPL)
33.99	development.unspecified
33.99	development.unspecified
33.99	development.unspecified
33.99	development.unspecified
33.99	development.unspecified
33.99	development.unspecified
33.99	development.unspecified
33.99	development.unspecified
33.99	development.unspecified
33.99	development.unspecified
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33.99	development.unspecified
33.99	development.unspecified
33.99	development.unspecified
33.99	development.unspecified
33.99	development.unspecified

Cell division_MapMan

BinCode	BinName
31.2	cell.division
31.2	cell.division

31.2	cell.division

Biotic stress

BinCode	BinName
20.1	stress.biotic
20.1	stress.biotic
20.1	stress.biotic
20.1	stress.biotic
20.1	stress.biotic
20.1	stress.biotic
20.1	stress.biotic
20.1	stress.biotic
20.1	stress.biotic
20.1	stress.biotic
20.1	stress.biotic
20.1	stress.biotic
20.1	stress.biotic
20.1	stress.biotic
20.1	stress.biotic
20.1.2	stress.biotic.receptors
20.1.7	stress.biotic.PR-proteins
20.1.7	stress.biotic.PR-proteins

Heat Stress _MapMan

BinCode	BinName
20.2.1	stress.abiotic.heat
20.2.1	stress.abiotic.heat
20.2.1	stress.abiotic.heat
20.2.1	stress.abiotic.heat
20.2.1	stress.abiotic.heat
20.2.1	stress.abiotic.heat

Cell cycle transcripts

BinCode	BinName
31.3	cell.cycle
31.3	cell.cycle
31.3	cell.cycle
31.3	cell.cycle
31.3	cell.cycle

Cold Stress transcripts_MapMan

BinCode	BinName
20.2.2	stress.abiotic.cold
20.2.2	stress.abiotic.cold
20.2.2	stress.abiotic.cold
20.2.2	stress.abiotic.cold

Drought/Salt stress

BinCode	BinName
20.2.3	stress.abiotic.drought/salt

Cell organization_MapMan

BinCode	BinName
31.1	cell.organisation
31.1	cell.organisation
31.1	cell.organisation
31.1	cell.organisation
31.1	cell.organisation
31.1	cell.organisation
31.1	cell.organisation
31.1	cell.organisation
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31.1	cell.organisation
31.1	cell.organisation
31.1	cell.organisation
31.1	cell.organisation
31.1	cell.organisation
31.1	cell.organisation
31.1	cell.organisation

Unassigned ontology

BinCode	BinName
35.1	not assigned.no ontology
35.1	not assigned.no ontology
35.1	not assigned.no ontology
35.1	not assigned.no ontology
35.1	not assigned.no ontology
35.1	not assigned.no ontology

35.1	not assigned.no ontology
35.1	not assigned.no ontology
35.1	not assigned.no ontology
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35.1	not assigned.no ontology
35.1	not assigned.no ontology
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35.1	not assigned.no ontology
35.1	not assigned.no ontology
35.1	not assigned.no ontology
35.1	not assigned.no ontology
35.1	not assigned.no ontology

Protein Degradation

BinCode	BinName
29.5	protein.degradation
29.5.1	protein.degradation.subtilases
29.5.3	protein.degradation.cysteine protease
29.5.3	protein.degradation.cysteine protease
29.5.3	protein.degradation.cysteine protease
29.5.3	protein.degradation.cysteine protease
29.5.5	protein.degradation.serine protease
29.5.5	protein.degradation.serine protease
29.5.5	protein.degradation.serine protease
29.5.5	protein.degradation.serine protease
29.5.9	protein.degradation.AAA type
29.5.11	protein.degradation.ubiquitin
29.5.11.1	protein.degradation.ubiquitin.ubiquitin
29.5.11.3	protein.degradation.ubiquitin.E2
29.5.11.3	protein.degradation.ubiquitin.E2
29.5.11.4.2	protein.degradation.ubiquitin.E3.RING
29.5.11.4.2	protein.degradation.ubiquitin.E3.RING
29.5.11.4.2	protein.degradation.ubiquitin.E3.RING
29.5.11.4.2	protein.degradation.ubiquitin.E3.RING
29.5.11.4.2	protein.degradation.ubiquitin.E3.RING
29.5.11.4.2	protein.degradation.ubiquitin.E3.RING
29.5.11.4.2	protein.degradation.ubiquitin.E3.RING
29.5.11.4.2	protein.degradation.ubiquitin.E3.RING

29.5.11.4.2	protein.degradation.ubiquitin.E3.RING
29.5.11.4.2	protein.degradation.ubiquitin.E3.RING
29.5.11.4.2	protein.degradation.ubiquitin.E3.RING
29.5.11.4.2	protein.degradation.ubiquitin.E3.RING
29.5.11.4.2	protein.degradation.ubiquitin.E3.RING
29.5.11.4.2	protein.degradation.ubiquitin.E3.RING
29.5.11.4.2	protein.degradation.ubiquitin.E3.RING
29.5.11.4.2	protein.degradation.ubiquitin.E3.RING
29.5.11.4.3.2	protein.degradation.ubiquitin.E3.SCF.FBOX
29.5.11.4.3.2	protein.degradation.ubiquitin.E3.SCF.FBOX
29.5.11.4.3.2	protein.degradation.ubiquitin.E3.SCF.FBOX
29.5.11.4.3.2	protein.degradation.ubiquitin.E3.SCF.FBOX
29.5.11.4.3.2	protein.degradation.ubiquitin.E3.SCF.FBOX
29.5.11.4.3.2	protein.degradation.ubiquitin.E3.SCF.FBOX
29.5.11.4.3.2	protein.degradation.ubiquitin.E3.SCF.FBOX
29.5.11.4.3.2	protein.degradation.ubiquitin.E3.SCF.FBOX
29.5.11.4.3.2	protein.degradation.ubiquitin.E3.SCF.FBOX
29.5.11.4.3.2	protein.degradation.ubiquitin.E3.SCF.FBOX
29.5.11.4.3.2	protein.degradation.ubiquitin.E3.SCF.FBOX
29.5.11.4.3.2	protein.degradation.ubiquitin.E3.SCF.FBOX
29.5.11.4.3.2	protein.degradation.ubiquitin.E3.SCF.FBOX
29.5.11.4.3.2	protein.degradation.ubiquitin.E3.SCF.FBOX
29.5.11.4.3.2	protein.degradation.ubiquitin.E3.SCF.FBOX
29.5.11.4.3.2	protein.degradation.ubiquitin.E3.SCF.FBOX

Protein modification

BinCode	BinName
29.4	protein.postranslational modification
29.4	protein.postranslational modification
29.4	protein.postranslational modification
29.4	protein.postranslational modification
29.4	protein.postranslational modification
29.4	protein.postranslational modification
29.4	protein.postranslational modification
29.4	protein.postranslational modification
29.4	protein.postranslational modification
29.4	protein.postranslational modification
29.4	protein.postranslational modification
29.4	protein.postranslational modification
29.4	protein.postranslational modification

29.4	protein.postranslational modification
29.4	protein.postranslational modification

Regulation

BinCode	BinName
30.1	signalling.in sugar and nutrient physiology
30.1	signalling.in sugar and nutrient physiology
30.2.3	signalling.receptor kinases.leucine rich repeat III
30.2.8.2	signalling.receptor kinases.leucine rich repeat VIII.VIII-2
30.2.11	signalling.receptor kinases.leucine rich repeat XI
30.2.13	signalling.receptor kinases.leucine rich repeat XIII
30.2.17	signalling.receptor kinases.DUF 26
30.2.23	signalling.receptor kinases.RKF3 like
30.2.25	signalling.receptor kinases.wall associated kinase
30.2.99	signalling.receptor kinases.misc
30.2.99	signalling.receptor kinases.misc
30.2.99	signalling.receptor kinases.misc
30.2.99	signalling.receptor kinases.misc
30.2.99	signalling.receptor kinases.misc
30.3	signalling.calcium
30.3	signalling.calcium
30.3	signalling.calcium
30.3	signalling.calcium
30.3	signalling.calcium
30.3	signalling.calcium
30.3	signalling.calcium
30.3	signalling.calcium
30.4.1	signalling.phosphinositides.phosphatidylinositol-4-phosphate 5-kinase
30.5	signalling.G-proteins
30.5	signalling.G-proteins
30.5	signalling.G-proteins
30.5	signalling.G-proteins
30.5	signalling.G-proteins
30.6	signalling.MAP kinases
30.11	signalling.light
30.11	signalling.light

RNA Processing

BinCode	BinName
27.1	RNA.processing
27.1	RNA.processing
27.1	RNA.processing
27.1.1	RNA.processing.splicing
27.1.1	RNA.processing.splicing
27.1.1	RNA.processing.splicing
27.1.1	RNA.processing.splicing
27.1.1	RNA.processing.splicing
27.1.1	RNA.processing.splicing
27.1.2	RNA.processing.RNA helicase
27.1.3.17	RNA.processing.3' end processing.PabN
27.1.3.17	RNA.processing.3' end processing.PabN
27.1.19	RNA.processing.ribonucleases
27.1.19	RNA.processing.ribonucleases
27.1.19	RNA.processing.ribonucleases

Regulation of transcription

BinCode	BinName
27.3	RNA.regulation of transcription
27.3	RNA.regulation of transcription
27.3.1	RNA.regulation of transcription.ABI3/VP1-related B3-domain-containing tra
27.3.2	RNA.regulation of transcription.Alfin-like
27.3.3	RNA.regulation of transcription.AP2/EREBP, APETALA2/Ethylene-responsive
27.3.3	RNA.regulation of transcription.AP2/EREBP, APETALA2/Ethylene-responsive
27.3.3	RNA.regulation of transcription.AP2/EREBP, APETALA2/Ethylene-responsive
27.3.3	RNA.regulation of transcription.AP2/EREBP, APETALA2/Ethylene-responsive
27.3.3	RNA.regulation of transcription.AP2/EREBP, APETALA2/Ethylene-responsive
27.3.3	RNA.regulation of transcription.AP2/EREBP, APETALA2/Ethylene-responsive
27.3.3	RNA.regulation of transcription.AP2/EREBP, APETALA2/Ethylene-responsive
27.3.3	RNA.regulation of transcription.AP2/EREBP, APETALA2/Ethylene-responsive
27.3.3	RNA.regulation of transcription.AP2/EREBP, APETALA2/Ethylene-responsive
27.3.6	RNA.regulation of transcription.bHLH,Basic Helix-Loop-Helix family
27.3.6	RNA.regulation of transcription.bHLH,Basic Helix-Loop-Helix family
27.3.6	RNA.regulation of transcription.bHLH,Basic Helix-Loop-Helix family
27.3.6	RNA.regulation of transcription.bHLH,Basic Helix-Loop-Helix family
27.3.6	RNA.regulation of transcription.bHLH,Basic Helix-Loop-Helix family
27.3.6	RNA.regulation of transcription.bHLH,Basic Helix-Loop-Helix family
27.3.6	RNA.regulation of transcription.bHLH,Basic Helix-Loop-Helix family

27.3.7	RNA.regulation of transcription.C2C2(Zn) CO-like, Constans-like zinc finger f
27.3.7	RNA.regulation of transcription.C2C2(Zn) CO-like, Constans-like zinc finger f
27.3.7	RNA.regulation of transcription.C2C2(Zn) CO-like, Constans-like zinc finger f
27.3.7	RNA.regulation of transcription.C2C2(Zn) CO-like, Constans-like zinc finger f
27.3.8	RNA.regulation of transcription.C2C2(Zn) DOF zinc finger family
27.3.8	RNA.regulation of transcription.C2C2(Zn) DOF zinc finger family
27.3.8	RNA.regulation of transcription.C2C2(Zn) DOF zinc finger family
27.3.9	RNA.regulation of transcription.C2C2(Zn) GATA transcription factor family
27.3.9	RNA.regulation of transcription.C2C2(Zn) GATA transcription factor family
27.3.11	RNA.regulation of transcription.C2H2 zinc finger family
27.3.11	RNA.regulation of transcription.C2H2 zinc finger family
27.3.11	RNA.regulation of transcription.C2H2 zinc finger family
27.3.11	RNA.regulation of transcription.C2H2 zinc finger family
27.3.11	RNA.regulation of transcription.C2H2 zinc finger family
27.3.11	RNA.regulation of transcription.C2H2 zinc finger family
27.3.12	RNA.regulation of transcription.C3H zinc finger family
27.3.15	RNA.regulation of transcription.CCAAT box binding factor family, HAP3
27.3.20	RNA.regulation of transcription.G2-like transcription factor family, GARP
27.3.20	RNA.regulation of transcription.G2-like transcription factor family, GARP
27.3.21	RNA.regulation of transcription.GRAS transcription factor family
27.3.22	RNA.regulation of transcription.HB,Homeobox transcription factor family
27.3.22	RNA.regulation of transcription.HB,Homeobox transcription factor family
27.3.22	RNA.regulation of transcription.HB,Homeobox transcription factor family
27.3.22	RNA.regulation of transcription.HB,Homeobox transcription factor family
27.3.24	RNA.regulation of transcription.MADS box transcription factor family
27.3.24	RNA.regulation of transcription.MADS box transcription factor family
27.3.24	RNA.regulation of transcription.MADS box transcription factor family
27.3.24	RNA.regulation of transcription.MADS box transcription factor family
27.3.24	RNA.regulation of transcription.MADS box transcription factor family
27.3.25	RNA.regulation of transcription.MYB domain transcription factor family
27.3.25	RNA.regulation of transcription.MYB domain transcription factor family
27.3.25	RNA.regulation of transcription.MYB domain transcription factor family
27.3.25	RNA.regulation of transcription.MYB domain transcription factor family
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27.3.25	RNA.regulation of transcription.MYB domain transcription factor family
27.3.25	RNA.regulation of transcription.MYB domain transcription factor family
27.3.25	RNA.regulation of transcription.MYB domain transcription factor family
27.3.25	RNA.regulation of transcription.MYB domain transcription factor family
27.3.26	RNA.regulation of transcription.MYB-related transcription factor family

27.3.26	RNA.regulation of transcription.MYB-related transcription factor family
27.3.27	RNA.regulation of transcription.NAC domain transcription factor family
27.3.27	RNA.regulation of transcription.NAC domain transcription factor family
27.3.29	RNA.regulation of transcription.TCP transcription factor family
27.3.30	RNA.regulation of transcription.Trihelix, Triple-Helix transcription factor fan
27.3.30	RNA.regulation of transcription.Trihelix, Triple-Helix transcription factor fan
27.3.30	RNA.regulation of transcription.Trihelix, Triple-Helix transcription factor fan
27.3.30	RNA.regulation of transcription.Trihelix, Triple-Helix transcription factor fan
27.3.30	RNA.regulation of transcription.Trihelix, Triple-Helix transcription factor fan
27.3.30	RNA.regulation of transcription.Trihelix, Triple-Helix transcription factor fan
27.3.30	RNA.regulation of transcription.Trihelix, Triple-Helix transcription factor fan
27.3.30	RNA.regulation of transcription.Trihelix, Triple-Helix transcription factor fan
27.3.30	RNA.regulation of transcription.Trihelix, Triple-Helix transcription factor fan
27.3.30	RNA.regulation of transcription.Trihelix, Triple-Helix transcription factor fan
27.3.32	RNA.regulation of transcription.WRKY domain transcription factor family
27.3.32	RNA.regulation of transcription.WRKY domain transcription factor family
27.3.32	RNA.regulation of transcription.WRKY domain transcription factor family
27.3.32	RNA.regulation of transcription.WRKY domain transcription factor family
27.3.32	RNA.regulation of transcription.WRKY domain transcription factor family
27.3.32	RNA.regulation of transcription.WRKY domain transcription factor family
27.3.35	RNA.regulation of transcription.bZIP transcription factor family
27.3.35	RNA.regulation of transcription.bZIP transcription factor family
27.3.37	RNA.regulation of transcription.AS2,Lateral Organ Boundaries Gene Family
27.3.47	RNA.regulation of transcription.ELF3
27.3.51	RNA.regulation of transcription.General Transcription, TBP-binding protein
27.3.55	RNA.regulation of transcription.HDA
27.3.59	RNA.regulation of transcription.Methyl binding domain proteins
27.3.59	RNA.regulation of transcription.Methyl binding domain proteins
27.3.60	RNA.regulation of transcription.NIN-like bZIP-related family
27.3.64	RNA.regulation of transcription.PHOR1
27.3.67	RNA.regulation of transcription.putative transcription regulator
27.3.67	RNA.regulation of transcription.putative transcription regulator

Unkown Proteins

BinCode	BinName
35.2	not assigned.unknown
35.2	not assigned.unknown
35.2	not assigned.unknown
35.2	not assigned.unknown
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35.2	not assigned.unknown
35.2	not assigned.unknown

Redox_Trancripts

BinCode	BinName
21.2	redox.ascorbate and glutathione
21.2	redox.ascorbate and glutathione
21.2	redox.ascorbate and glutathione
21.2.1	redox.ascorbate and glutathione.ascorbate
21.2.1	redox.ascorbate and glutathione.ascorbate
21.2.1	redox.ascorbate and glutathione.ascorbate
21.4	redox.glutaredoxins
21.4	redox.glutaredoxins
21.4	redox.glutaredoxins
21.4	redox.glutaredoxins
21.4	redox.glutaredoxins
21.4	redox.glutaredoxins

Metal associated transcripts

BinCode	BinName
15.2	metal handling.binding, chelation and storage
15.3	metal handling.regulation
15.1	metal handling.acquisition
15.2	metal handling.binding, chelation and storage
15.2	metal handling.binding, chelation and storage
15.2	metal handling.binding, chelation and storage
15.2	metal handling.binding, chelation and storage
15.2	metal handling.binding, chelation and storage

Transport transcripts

BinCode	BinName
34	transport
34.1.3	transport.p- and v-ATPases.inhibitor
34.2	transport.sugars
34.2	transport.sugars
34.2	transport.sugars
34.3	transport.amino acids
34.3	transport.amino acids

34.8	transport.metabolite transporters at the envelope membrane
34.9	transport.metabolite transporters at the mitochondrial membrane
34.9	transport.metabolite transporters at the mitochondrial membrane
34.9	transport.metabolite transporters at the mitochondrial membrane
34.12	transport.metal
34.12	transport.metal
34.13	transport.peptides and oligopeptides
34.13	transport.peptides and oligopeptides
34.13	transport.peptides and oligopeptides
34.13	transport.peptides and oligopeptides
34.14	transport.unspecified cations
34.14	transport.unspecified cations
34.14	transport.unspecified cations
34.15	transport.potassium
34.16	transport.ABC transporters and multidrug resistance systems
34.16	transport.ABC transporters and multidrug resistance systems
34.16	transport.ABC transporters and multidrug resistance systems
34.19.1	transport.Major Intrinsic Proteins.PIP
34.21	transport.calcium
34.99	transport.misc
34.99	transport.misc
34.99	transport.misc
34.99	transport.misc
34.99	transport.misc
34.99	transport.misc
34.99	transport.misc
34.99	transport.misc

Cell wall_Arabinogalactan

BinCode	BinName
10.5.1.1	cell wall.cell wall proteins.AGPs.AGP
10.5.1.1	cell wall.cell wall proteins.AGPs.AGP
10.5.1.1	cell wall.cell wall proteins.AGPs.AGP
10.5.1.1	cell wall.cell wall proteins.AGPs.AGP
10.5.1.1	cell wall.cell wall proteins.AGPs.AGP
10.5.1.1	cell wall.cell wall proteins.AGPs.AGP
10.5.1.1	cell wall.cell wall proteins.AGPs.AGP
10.5.1.1	cell wall.cell wall proteins.AGPs.AGP
10.5.1.1	cell wall.cell wall proteins.AGPs.AGP

10.5.1.1	cell wall.cell wall proteins.AGPs.AGP
10.5.1.1	cell wall.cell wall proteins.AGPs.AGP
10.5.1.1	cell wall.cell wall proteins.AGPs.AGP
10.5.1.1	cell wall.cell wall proteins.AGPs.AGP
10.5.1.1	cell wall.cell wall proteins.AGPs.AGP
10.5.1.1	cell wall.cell wall proteins.AGPs.AGP
10.5.1.1	cell wall.cell wall proteins.AGPs.AGP

Cell wall_cellulose synthesis

BinCode	BinName
10.2	cell wall.cellulose synthesis
10.2	cell wall.cellulose synthesis
10.2	cell wall.cellulose synthesis
10.2.1	cell wall.cellulose synthesis.cellulose synthase
10.2.1	cell wall.cellulose synthesis.cellulose synthase

Cell wall_Polygalactouran Synthesis

BinCode	BinName
10.6.3	cell wall.degradation.pectate lyases and polygalacturonases
10.6.3	cell wall.degradation.pectate lyases and polygalacturonases
10.6.3	cell wall.degradation.pectate lyases and polygalacturonases
10.6.3	cell wall.degradation.pectate lyases and polygalacturonases
10.6.3	cell wall.degradation.pectate lyases and polygalacturonases
10.6.3	cell wall.degradation.pectate lyases and polygalacturonases

Cell wall_Xyloglucan synthesis

BinCode	BinName
10.7	cell wall.modification
10.7	cell wall.modification
10.7	cell wall.modification
10.7	cell wall.modification
10.7	cell wall.modification
10.7	cell wall.modification
10.7	cell wall.modification

Starch biosynthesis

BinCode	BinName

2.2.2.1.1	major CHO metabolism.degradation.starch.starch cleavage.alpha amylase
2.2.2.1.2	major CHO metabolism.degradation.starch.starch cleavage.beta amylase
2.2.2.6	major CHO metabolism.degradation.starch.transporter
2.2.2.8	major CHO metabolism.degradation.starch.ISA3

Sucrose biosynthesis

BinCode	BinName
2.2.1.3.1	major CHO metabolism.degradation.sucrose.invertases.neutral
2.2.1.3.3	major CHO metabolism.degradation.sucrose.invertases.vacuolar
2.2.1.4	major CHO metabolism.degradation.sucrose.hexokinase
2.2.1.4	major CHO metabolism.degradation.sucrose.hexokinase

Phenolics biosynthesis

BinCode	BinName
16.1	secondary metabolism.simple phenols
16.1	secondary metabolism.simple phenols
16.1	secondary metabolism.simple phenols
16.1	secondary metabolism.simple phenols
16.1	secondary metabolism.simple phenols
16.1	secondary metabolism.simple phenols

Phenylpropanoid biosynthesis

BinCode	BinName
16.2	secondary metabolism.phenylpropanoids
16.2	secondary metabolism.phenylpropanoids
16.2	secondary metabolism.phenylpropanoids
16.2.1.3	secondary metabolism.phenylpropanoids.lignin biosynthesis.4CL
16.2.1.3	secondary metabolism.phenylpropanoids.lignin biosynthesis.4CL
16.2.1.6	secondary metabolism.phenylpropanoids.lignin biosynthesis.CCoAOMT
16.2.1.10	secondary metabolism.phenylpropanoids.lignin biosynthesis.CAD
16.2.1.10	secondary metabolism.phenylpropanoids.lignin biosynthesis.CAD

Flavonoids biosynthesis

BinCode	BinName
16.8.1	secondary metabolism.flavonoids.anthocyanins
16.8.1	secondary metabolism.flavonoids.anthocyanins

16.8.1	secondary metabolism.flavonoids.anthocyanins
16.8.1	secondary metabolism.flavonoids.anthocyanins
16.8.1.21	secondary metabolism.flavonoids.anthocyanins.anthocyanin 5-aromatic ac
16.8.1.21	secondary metabolism.flavonoids.anthocyanins.anthocyanin 5-aromatic ac
16.8.3.1	secondary metabolism.flavonoids.dihydroflavonols.dihydroflavonol 4-reduc
16.8.4.3	secondary metabolism.flavonoids.flavonols.flavonol-3-O-rhamnosyltransfer
16.8.8.2	secondary metabolism.flavonoids.flavonoid glycosylations.flavonol-3-O-gly

Terpene biosynthesis

BinCode	BinName
16.1.1	secondary metabolism.isoprenoids.non-mevalonate pathway
16.1.1	secondary metabolism.isoprenoids.non-mevalonate pathway
16.1.1.10	secondary metabolism.isoprenoids.non-mevalonate pathway.geranylgeran
16.1.5	secondary metabolism.isoprenoids.terpenoids
16.1.5	secondary metabolism.isoprenoids.terpenoids
16.1.5	secondary metabolism.isoprenoids.terpenoids

N Misc_Glucosinolate synthesis

BinCode	BinName
16.5.1.1.1.1	secondary metabolism.sulfur-containing.glucosinolates.synthesis.aliphatic.
16.5.1.1.1.2	secondary metabolism.sulfur-containing.glucosinolates.synthesis.aliphatic.
16.5.1.1.1.7	secondary metabolism.sulfur-containing.glucosinolates.synthesis.aliphatic.
16.5.1.1.1.10	secondary metabolism.sulfur-containing.glucosinolates.synthesis.aliphatic.f
16.5.1.1.1.10	secondary metabolism.sulfur-containing.glucosinolates.synthesis.aliphatic.f
16.5.1.1.1.10	secondary metabolism.sulfur-containing.glucosinolates.synthesis.aliphatic.f
16.5.1.1.1.11	secondary metabolism.sulfur-containing.glucosinolates.synthesis.aliphatic.
16.5.1.1.1.13	secondary metabolism.sulfur-containing.glucosinolates.synthesis.aliphatic.
16.5.1.1.3.2	secondary metabolism.sulfur-containing.glucosinolates.synthesis.indole.CY
16.5.1.2.1	secondary metabolism.sulfur-containing.glucosinolates.regulation.aliphatic
16.5.1.2.1	secondary metabolism.sulfur-containing.glucosinolates.regulation.aliphatic
16.5.1.3.1	secondary metabolism.sulfur-containing.glucosinolates.degradation.myrosi
16.5.1.3.1	secondary metabolism.sulfur-containing.glucosinolates.degradation.myrosi
16.5.1.3.2.1	secondary metabolism.sulfur-containing.glucosinolates.degradation.nitriles
16.5.1.3.3	secondary metabolism.sulfur-containing.glucosinolates.degradation.nitrilas

DNA Synthesis

BinCode	BinName

28.1	DNA.synthesis/chromatin structure
28.1	DNA.synthesis/chromatin structure
28.1	DNA.synthesis/chromatin structure
28.1.1	DNA.synthesis/chromatin structure.retrotransposon/transposase
28.1.1	DNA.synthesis/chromatin structure.retrotransposon/transposase
28.1.1	DNA.synthesis/chromatin structure.retrotransposon/transposase
28.1.1	DNA.synthesis/chromatin structure.retrotransposon/transposase
28.1.1.3	DNA.synthesis/chromatin structure.retrotransposon/transposase.copia-like
28.1.1.3	DNA.synthesis/chromatin structure.retrotransposon/transposase.copia-like
28.1.1.3	DNA.synthesis/chromatin structure.retrotransposon/transposase.copia-like
28.1.1.4	DNA.synthesis/chromatin structure.retrotransposon/transposase.hat-like t
28.1.1.5	DNA.synthesis/chromatin structure.retrotransposon/transposase.CACTA-lik
28.1.3.1	DNA.synthesis/chromatin structure.histone.H1
28.1.3.2.1	DNA.synthesis/chromatin structure.histone.core.H2A
28.1.3.2.3	DNA.synthesis/chromatin structure.histone.core.H3
28.1.3.2.4	DNA.synthesis/chromatin structure.histone.core.H4

Lys biosynthesis

BinCode	BinName
13.2.3.5	amino acid metabolism.degradation.aspartate family.lysine

Arg_biosynthesis

BinCode	BinName
13.2.2.3	amino acid metabolism.degradation.glutamate family.arginine

Mitochondrial electron transport

BinCode	BinName
9.1.2	mitochondrial electron transport / ATP synthesis.NADH-DH.localisation not
9.1.2	mitochondrial electron transport / ATP synthesis.NADH-DH.localisation not
9.1.2	mitochondrial electron transport / ATP synthesis.NADH-DH.localisation not
9.9	mitochondrial electron transport / ATP synthesis.F1-ATPase

Light reactions

BinCode	BinName
1.1.1.2	PS.lightreaction.photosystem II.PSII polypeptide subunits
1.1.1.2	PS.lightreaction.photosystem II.PSII polypeptide subunits
1.1.1.2	PS.lightreaction.photosystem II.PSII polypeptide subunits
1.1.1.2	PS.lightreaction.photosystem II.PSII polypeptide subunits
1.1.2.2	PS.lightreaction.photosystem I.PSI polypeptide subunits
1.1.2.2	PS.lightreaction.photosystem I.PSI polypeptide subunits

1.1.2.2	PS.lightreaction.photosystem I.PSI polypeptide subunits
1.1.2.2	PS.lightreaction.photosystem I.PSI polypeptide subunits
1.1.3.4	PS.lightreaction.cytochrome b6/f.apocytochrome f (CYF)
1.1.6	PS.lightreaction.NADH DH

Auxin synthesis

BinCode	BinName
17.2.1	hormone metabolism.auxin.synthesis-degradation
17.2.1	hormone metabolism.auxin.synthesis-degradation
17.2.1	hormone metabolism.auxin.synthesis-degradation
17.2.1	hormone metabolism.auxin.synthesis-degradation
17.2.1	hormone metabolism.auxin.synthesis-degradation
17.2.1	hormone metabolism.auxin.synthesis-degradation
17.2.3	hormone metabolism.auxin.induced-regulated-responsive-activated
17.2.3	hormone metabolism.auxin.induced-regulated-responsive-activated
17.2.3	hormone metabolism.auxin.induced-regulated-responsive-activated
17.2.3	hormone metabolism.auxin.induced-regulated-responsive-activated

Abscisic acid biosynthesis transcripts_MapMan

BinCode	BinName
17.1.1.2.1	hormone metabolism.abscisic acid.synthesis-degradation.degradation.8-hy
17.1.2	hormone metabolism.abscisic acid.signal transduction
17.1.3	hormone metabolism.abscisic acid.induced-regulated-responsive-activated
17.1.3	hormone metabolism.abscisic acid.induced-regulated-responsive-activated
17.1.3	hormone metabolism.abscisic acid.induced-regulated-responsive-activated
17.1.3	hormone metabolism.abscisic acid.induced-regulated-responsive-activated
17.1.3	hormone metabolism.abscisic acid.induced-regulated-responsive-activated
17.1.3	hormone metabolism.abscisic acid.induced-regulated-responsive-activated

Ethylene Biosynthesis pathway

BinCode	BinName
17.5.1	hormone metabolism.ethylene.synthesis-degradation
17.5.2	hormone metabolism.ethylene.signal transduction
17.5.2	hormone metabolism.ethylene.signal transduction
17.5.2	hormone metabolism.ethylene.signal transduction
17.5.3	hormone metabolism.ethylene.induced-regulated-responsive-activated
17.5.3	hormone metabolism.ethylene.induced-regulated-responsive-activated

Overall hormone biosynthesis

BinCode	BinName
17.1.1.2.1	hormone metabolism.abscisic acid.synthesis-degradation.degradation.8-hy
17.1.2	hormone metabolism.abscisic acid.signal transduction
17.1.3	hormone metabolism.abscisic acid.induced-regulated-responsive-activated
17.1.3	hormone metabolism.abscisic acid.induced-regulated-responsive-activated
17.1.3	hormone metabolism.abscisic acid.induced-regulated-responsive-activated
17.1.3	hormone metabolism.abscisic acid.induced-regulated-responsive-activated
17.1.3	hormone metabolism.abscisic acid.induced-regulated-responsive-activated
17.1.3	hormone metabolism.abscisic acid.induced-regulated-responsive-activated
17.2.1	hormone metabolism.auxin.synthesis-degradation
17.2.1	hormone metabolism.auxin.synthesis-degradation
17.2.1	hormone metabolism.auxin.synthesis-degradation
17.2.1	hormone metabolism.auxin.synthesis-degradation
17.2.1	hormone metabolism.auxin.synthesis-degradation
17.2.1	hormone metabolism.auxin.synthesis-degradation
17.2.3	hormone metabolism.auxin.induced-regulated-responsive-activated
17.2.3	hormone metabolism.auxin.induced-regulated-responsive-activated
17.2.3	hormone metabolism.auxin.induced-regulated-responsive-activated
17.2.3	hormone metabolism.auxin.induced-regulated-responsive-activated
17.3.1.1.3	hormone metabolism.brassinosteroid.synthesis-degradation.BRs.CPD
17.3.1.1.99	hormone metabolism.brassinosteroid.synthesis-degradation.BRs.other
17.3.1.2.99	hormone metabolism.brassinosteroid.synthesis-degradation.sterols.other
17.4.1	hormone metabolism.cytokinin.synthesis-degradation
17.5.1	hormone metabolism.ethylene.synthesis-degradation
17.5.2	hormone metabolism.ethylene.signal transduction
17.5.2	hormone metabolism.ethylene.signal transduction
17.5.2	hormone metabolism.ethylene.signal transduction
17.5.3	hormone metabolism.ethylene.induced-regulated-responsive-activated
17.5.3	hormone metabolism.ethylene.induced-regulated-responsive-activated
17.6.1	hormone metabolism.gibberelin.synthesis-degradation
17.6.1.11	hormone metabolism.gibberelin.synthesis-degradation.GA20 oxidase
17.6.3	hormone metabolism.gibberelin.induced-regulated-responsive-activated
17.6.3	hormone metabolism.gibberelin.induced-regulated-responsive-activated
17.7.1.2	hormone metabolism.jasmonate.synthesis-degradation.lipoxygenase
17.7.1.5	hormone metabolism.jasmonate.synthesis-degradation.12-Oxo-PDA-reduct
17.7.1.10	hormone metabolism.jasmonate.synthesis-degradation.jasmonate-O-meth
17.7.3	hormone metabolism.jasmonate.induced-regulated-responsive-activated
17.7.3	hormone metabolism.jasmonate.induced-regulated-responsive-activated

17.7.3	hormone metabolism.jasmonate.induced-regulated-responsive-activated
17.8.1	hormone metabolism.salicylic acid.synthesis-degradation
17.8.1	hormone metabolism.salicylic acid.synthesis-degradation
17.8.1.1.7	hormone metabolism.salicylic acid.synthesis-degradation.synthesis.methyl-

id	Type
at5g24770	Transcript
at5g24780	Transcript
at2g42200	Transcript
at3g15270	Transcript
at1g01720	Transcript
at1g05420	Transcript
at1g12260	Transcript
at1g13245	Transcript
at1g19200	Transcript
at1g26600	Transcript
at1g52890	Transcript
at1g56200	Transcript
at1g69320	Transcript
at1g69970	Transcript
at1g71930	Transcript
at2g16660	Transcript
at2g41380	Transcript
at2g45330	Transcript
at3g03200	Transcript
at3g15400	Transcript
at3g53210	Transcript
at3g61190	Transcript
at4g24220	Transcript
at4g28190	Transcript
at4g35783	Transcript
at5g09805	Transcript
at5g15800	Transcript
at5g41090	Transcript
at5g43070	Transcript
at5g50800	Transcript
at5g60910	Transcript
at5g62210	Transcript
at5g64667	Transcript

id	type
at3g02510	Transcript
at5g43070	Transcript

at5g60870	Transcript

id	type
at1g19610	Transcript
at1g19670	Transcript
at1g20030	Transcript
at1g58848	Transcript
at1g66100	Transcript
at1g73620	Transcript
at1g77700	Transcript
at2g14610	Transcript
at4g09950	Transcript
at4g19810	Transcript
at4g19820	Transcript
at4g24180	Transcript
at4g37000	Transcript
at4g39030	Transcript
at5g40020	Transcript
at1g65390	Transcript
at1g58807	Transcript
at1g65870	Transcript

id	type
at1g07400	Transcript
at1g54050	Transcript
at1g56300	Transcript
at1g77020	Transcript
at3g62190	Transcript
at5g64360	Transcript

id	type
at1g77390	Transcript
at2g23430	Transcript
at2g42260	Transcript
at4g03270	Transcript
at5g65420	Transcript

id	type
at2g42530	Transcript
at2g42540	Transcript
at4g38680	Transcript
at5g52310	Transcript

id	type
at4g15910	Transcript

id	type
at1g06530	Transcript
at1g12710	Transcript
at1g43700	Transcript
at1g71790	Transcript
at2g02350	Transcript
at2g38750	Transcript
at2g38760	Transcript
at2g42170	Transcript
at3g60840	Transcript
at4g08580	Transcript
at4g14390	Transcript
at4g19150	Transcript
at5g15970	Transcript
at5g20110	Transcript
at5g52120	Transcript
at5g54720	Transcript
at5g64920	Transcript

id	type
at1g03620	Transcript
at1g05135	Transcript
at1g08160	Transcript
at1g10657	Transcript
at1g14880	Transcript
at1g15200	Transcript

at1g15405	Transcript
at1g21326	Transcript
at1g21880	Transcript
at1g24577	Transcript
at1g28815	Transcript
at1g29395	Transcript
at1g47578	Transcript
at1g50970	Transcript
at1g68230	Transcript
at1g72620	Transcript
at1g74290	Transcript
at1g74340	Transcript
at1g76560	Transcript
at1g77630	Transcript

id	type
at5g04200	Transcript
at1g04110	Transcript
at1g20850	Transcript
at3g48350	Transcript
at4g11320	Transcript
at4g35350	Transcript
at2g22980	Transcript
at2g23010	Transcript
at2g26390	Transcript
at5g27660	Transcript
at3g28510	Transcript
at2g47110	Transcript
at5g14360	Transcript
at1g63800	Transcript
at4g36410	Transcript
at1g02610	Transcript
at1g23980	Transcript
at1g49210	Transcript
at1g49230	Transcript
at1g60360	Transcript
at1g72175	Transcript
at2g34200	Transcript
at2g37580	Transcript

at3g11110	Transcript
at3g46620	Transcript
at4g08590	Transcript
at5g01520	Transcript
at5g01880	Transcript
at5g01980	Transcript
at5g15820	Transcript
at5g49665	Transcript
at1g10890	Transcript
at1g26930	Transcript
at1g27420	Transcript
at1g31350	Transcript
at1g77000	Transcript
at2g17036	Transcript
at2g27310	Transcript
at3g18320	Transcript
at3g23260	Transcript
at3g59940	Transcript
at4g03030	Transcript
at4g36840	Transcript
at4g39550	Transcript
at4g39600	Transcript
at5g26960	Transcript
at5g49000	Transcript

id	type
at1g13350	Transcript
at1g32640	Transcript
at1g66700	Transcript
at2g30360	Transcript
at2g32510	Transcript
at2g32960	Transcript
at3g05640	Transcript
at3g57740	Transcript
at4g13000	Transcript
at4g14580	Transcript
at4g17480	Transcript
at4g27800	Transcript
at4g28560	Transcript

at4g32950	Transcript
at5g67080	Transcript

id	type
at4g08950	Transcript
at5g52390	Transcript
at1g66830	Transcript
at3g14840	Transcript
at1g09970	Transcript
at1g78530	Transcript
at4g11521	Transcript
at2g48010	Transcript
at1g21240	Transcript
at1g33260	Transcript
at1g51820	Transcript
at2g33020	Transcript
at3g46280	Transcript
at4g10390	Transcript
at1g52410	Transcript
at2g33380	Transcript
at3g29000	Transcript
at3g52870	Transcript
at5g42380	Transcript
at5g54490	Transcript
at5g61900	Transcript
at5g62390	Transcript
at2g41210	Transcript
at1g52240	Transcript
at3g09910	Transcript
at3g59220	Transcript
at4g32990	Transcript
at5g56230	Transcript
at4g23050	Transcript
at5g02200	Transcript
at5g47800	Transcript

id	type
at1g19120	Transcript
at3g16380	Transcript
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id	type

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id	type
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id	type
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id	type
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id	type
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id	type
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id	type
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id	type
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at3g16460	Transcript

at3g16470	Transcript
at1g05680	Transcript
at5g38780	Transcript
at3g11480	Transcript

Description
Symbols: VSP2, ATVSP2 | VSP2 (VEGETATIVE STORAGE PROTEIN 2); acid phosphatase | chr5:8500476-
Symbols: VSP1, ATVSP1 | VSP1 (VEGETATIVE STORAGE PROTEIN 1); acid phosphatase/ transcription fa
Symbols: SPL9 | SPL9 (SQUAMOSA PROMOTER BINDING PROTEIN-LIKE 9); transcription factor | chr2:1
Symbols: SPL5 | SPL5 (SQUAMOSA PROMOTER BINDING PROTEIN-LIKE 5); DNA binding / transcription
Symbols: ATAF1, ANAC002 | ATAF1; transcription activator/ transcription factor | chr1:268330-26981
Symbols: ATOFP12, OFP12 | OFP12 (OVATE FAMILY PROTEIN 12) | chr1:1590073-1590753 FORWARD
Symbols: VND4, EMB2749, ANAC007 | ANAC007 (ARABIDOPSIS NAC 007); transcription factor | chr1:4
Symbols: RTFL17, DVL4 | RTFL17 (ROTUNDIFOLIA LIKE 17) | chr1:4525486-4526064 REVERSE
senescence-associated protein-related | chr1:6625020-6625856 REVERSE
Symbols: CLE9 | CLE9 (CLAVATA3/ESR-RELATED 9); protein binding / receptor binding | chr1:9191607-
Symbols: ANAC019 | ANAC019 (Arabidopsis NAC domain containing protein 19); transcription factor |
Symbols: emb1303 | emb1303 (embryo defective 1303) | chr1:21030794-21032078 FORWARD
Symbols: CLE10 | CLE10 (CLAVATA3/ESR-RELATED 10); protein binding / receptor binding | chr1:26061
Symbols: CLE26 | CLE26 (CLAVATA3/ESR-RELATED 26); protein binding / receptor binding | chr1:26353
Symbols: VND7, ANAC030 | VND7 (VASCULAR RELATED NAC-DOMAIN PROTEIN 7); transcription activa
nodulin family protein | chr2:7218706-7221625 REVERSE
embryo-abundant protein-related | chr2:17251941-17253057 FORWARD
Symbols: emb1067 | emb1067 (embryo defective 1067); tRNA 2'-phosphotransferase/ transferase, tra
Symbols: anac045 | anac045 (Arabidopsis NAC domain containing protein 45); transcription factor | ch
Symbols: ATA20 | ATA20 | chr3:5201644-5203197 FORWARD
nodulin MtN21 family protein | chr3:19720165-19721875 FORWARD
Symbols: BAP1 | BAP1 (BON ASSOCIATION PROTEIN 1); phospholipid binding / protein binding | chr3:2
Symbols: VEP1, AWI31 | VEP1 (VEIN PATTERNING 1); binding / catalytic | chr4:12564945-12566755 FO
Symbols: ULT1, ULT | ULT1 (ULTRAPETALA1); DNA binding | chr4:13985461-13987261 FORWARD
Symbols: RTFL6, DVL17 | RTFL6 (ROTUNDIFOLIA LIKE 6) | chr4:16952406-16952800 FORWARD
Symbols: IDL3 | IDL3 (INFLORESCENCE DEFICIENT IN ABSCISSION (IDA)-LIKE 3) | chr5:3047218-304751
Symbols: SEP1, AGL2 | SEP1 (SEPALLATA1); DNA binding / transcription factor | chr5:5151334-515415
Symbols: anac095 | anac095 (Arabidopsis NAC domain containing protein 95); transcription factor | ch
Symbols: WPP1 | WPP1 (WPP domain protein 1) | chr5:17289100-17289776 REVERSE
nodulin MtN3 family protein | chr5:20665077-20667304 REVERSE
Symbols: AGL8, FUL | AGL8 (agamous-like 8); transcription factor | chr5:24502482-24506143 REVERSE
embryo-specific protein-related | chr5:24986327-24987489 REVERSE
Symbols: IDL2 | IDL2 (INFLORESCENCE DEFICIENT IN ABSCISSION (IDA)-LIKE 2) | chr5:25850656-25851

description
regulator of chromosome condensation (RCC1) family protein | chr3:521794-524631 REVERSE
Symbols: WPP1 | WPP1 (WPP domain protein 1) | chr5:17289100-17289776 REVERSE

regulator of chromosome condensation (RCC1) family protein | chr5:24485655-24487784 REVERSE

description
Symbols: LCR78, PDF1.4 | PDF1.4 | chr1:6781483-6782039 REVERSE
Symbols: ATCLH1, CORI1, ATHCOR1 | ATCLH1 (ARABIDOPSIS THALIANA CORONATINE-INDUCED PROTE
pathogenesis-related thaumatin family protein | chr1:6945425-6947344 FORWARD
ATP binding / protein binding | chr1:21791783-21797050 FORWARD
thionin, putative | chr1:24605671-24606537 REVERSE
thaumatin-like protein, putative / pathogenesis-related protein, putative | chr1:27681408-27683130
pathogenesis-related thaumatin family protein | chr1:29204747-29206217 FORWARD
Symbols: PR1, PR 1, ATPR1 | PR1 (PATHOGENESIS-RELATED GENE 1) | chr2:6241704-6242463 REVERS
avirulence-responsive family protein / avirulence induced gene (AIG1) family protein | chr4:6234762-
glycosyl hydrolase family 18 protein | chr4:10763934-10765753 REVERSE
glycosyl hydrolase family 18 protein | chr4:10767436-10768614 REVERSE
FUNCTIONS IN: molecular_function unknown; INVOLVED IN: response to other organism; LOCATED IN:
Symbols: ACD2, ATRCCR | ACD2 (ACCELERATED CELL DEATH 2); red chlorophyll catabolite reductase |
Symbols: EDS5, SID1 | EDS5 (ENHANCED DISEASE SUSCEPTIBILITY 5); antiporter/ multidrug efflux pum
pathogenesis-related thaumatin family protein | chr5:16022753-16024316 REVERSE
Symbols: ATPP2-A5 | ATPP2-A5 (ARABIDOPSIS THALIANA PHLOEM PROTEIN 2 A5); carbohydrate bindi
disease resistance protein (CC-NBS-LRR class), putative / PRM1 homolog, putative | chr1:21780574-21
disease resistance-responsive family protein | chr1:24503624-24504193 FORWARD

description
17.8 kDa class I heat shock protein (HSP17.8-CI) | chr1:2274943-2275758 FORWARD
17.4 kDa class III heat shock protein (HSP17.4-CIII) | chr1:20179422-20180281 REVERSE
DNAJ heat shock N-terminal domain-containing protein | chr1:21078820-21080423 REVERSE
DNAJ heat shock N-terminal domain-containing protein | chr1:28944843-28947031 REVERSE
DNAJ heat shock N-terminal domain-containing protein | chr3:23021121-23023332 FORWARD
DNAJ heat shock N-terminal domain-containing protein | chr5:25737071-25738667 REVERSE

description
Symbols: CYCA1;2, CYCA1 | CYCA1;2 (CYCLIN A1;2); cyclin-dependent protein kinase regulator | chr1:2
Symbols: ICK1, KRP1 | ICK1; cyclin-dependent protein kinase inhibitor | chr2:9976746-9978021 REVER
Symbols: UVI4, PYM | UVI4 (UV-B-INSENSITIVE 4) | chr2:17601955-17603633 REVERSE
Symbols: CYCD6;1 | CYCD6;1 (Cyclin D6;1); cyclin-dependent protein kinase | chr4:1432375-1433691
Symbols: CYCD4;1 | CYCD4;1 (CYCLIN D4;1); cyclin-dependent protein kinase regulator | chr5:2614147

description
Symbols: COR15B | COR15B (COLD REGULATED 15B) | chr2:17709036-17709945 REVERSE
Symbols: COR15A, COR15 | COR15A (COLD-REGULATED 15A) | chr2:17711037-17712092 REVERSE
Symbols: GRP2, CSDP2, CSP2, ATCSP2 | GRP2 (GLYCINE RICH PROTEIN 2); double-stranded DNA bindin
Symbols: COR78, LTI78, RD29A, LTI140 | LTI78 (LOW-TEMPERATURE-INDUCED 78) | chr5:21240849-21

description
Symbols: ATDI21, DI21 | ATDI21 (ARABIDOPSIS THALIANA DROUGHT-INDUCED 21) | chr4:9028461-902

description
myosin heavy chain-related | chr1:2001594-2002596 FORWARD
Symbols: AtPP2-A12 | AtPP2-A12 (Phloem protein 2-A12); carbohydrate binding | chr1:4326739-4328
Symbols: VIP1 | VIP1 (VIRE2-INTERACTING PROTEIN 1); protein binding / transcription factor | chr1:16
F-actin capping protein beta subunit family protein | chr1:26996809-26998977 FORWARD
Symbols: SKIP3, AtPP2-B9 | SKIP3 (SKP1 INTERACTING PARTNER 3); carbohydrate binding | chr2:61780
Symbols: ANNAT4 | ANNAT4 (ANNEXIN ARABIDOPSIS 4); calcium ion binding / calcium-dependent pho
Symbols: ANNAT3 | ANNAT3 (ANNEXIN ARABIDOPSIS 3); calcium ion binding / calcium-dependent pho
actin, putative | chr2:17577714-17580392 FORWARD
Symbols: MAP65-4 | MAP65-4 (MICROTUBULE-ASSOCIATED PROTEIN 65-4) | chr3:22477573-2248046
FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN
ankyrin repeat family protein | chr4:8289644-8292083 FORWARD
ankyrin repeat family protein | chr4:10471331-10472742 REVERSE
Symbols: KIN2, COR6.6 | KIN2 | chr5:5211911-5212665 FORWARD
dynein light chain, putative | chr5:6791487-6793346 REVERSE
Symbols: AtPP2-A14 | AtPP2-A14 (Phloem protein 2-A14); carbohydrate binding | chr5:21176422-211
ankyrin repeat family protein | chr5:22232195-22232949 REVERSE
Symbols: CIP8 | CIP8 (COP1-INTERACTING PROTEIN 8); protein binding / zinc ion binding | chr5:25943

description
phagocytosis and cell motility protein ELMO1-related | chr1:904319-906013 REVERSE
pseudogene of unknown protein | chr1:1477500-1478821 REVERSE
harpin-induced protein-related / HIN1-related / harpin-responsive protein-related | chr1:2559487-256
unknown protein | chr1:3530467-3531821 FORWARD
unknown protein | chr1:5132535-5133716 REVERSE
protein-protein interaction regulator family protein | chr1:5228336-5231061 REVERSE

other RNA | chr1:5297875-5298166 REVERSE
VQ motif-containing protein | chr1:7469002-7469721 REVERSE
Symbols: LYM1 | LYM1 (LYSM DOMAIN GPI-ANCHORED PROTEIN 1 PRECURSOR) | chr1:7680481-76826
unknown protein | chr1:8712478-8713032 REVERSE
unknown protein | chr1:10095797-10096374 FORWARD
Symbols: COR414-TM1 | COR414-TM1 | chr1:10288197-10289621 REVERSE
Biotin/lipoate A/B protein ligase family; FUNCTIONS IN: octanoyltransferase activity, catalytic activity;
membrane trafficking VPS53 family protein | chr1:18896323-18900268 FORWARD
reticulon family protein (RTNLB14) | chr1:25572185-25572921 FORWARD
hydrolase, alpha/beta fold family protein | chr1:27341079-27342455 FORWARD
esterase/lipase/thioesterase family protein | chr1:27931836-27934268 FORWARD
dolichol phosphate-mannose biosynthesis regulatory protein-related | chr1:27948123-27951668 REVE
Symbols: CP12-3 | CP12-3 | chr1:28728253-28728853 FORWARD
peptidoglycan-binding LysM domain-containing protein | chr1:29173457-29175530 FORWARD

description
Symbols: AtMC9 | AtMC9 (metacaspase 9); cysteine-type peptidase | chr5:1153790-1155040 FORWAR
Symbols: SDD1 | SDD1 (STOMATAL DENSITY AND DISTRIBUTION); serine-type endopeptidase | chr1:10
Symbols: XCP2 | XCP2 (xylem cysteine peptidase 2); cysteine-type peptidase/ peptidase | chr1:725217
cysteine proteinase, putative | chr3:17905725-17907561 FORWARD
cysteine proteinase, putative | chr4:6887254-6889059 FORWARD
Symbols: XCP1 | XCP1 (XYLEM CYSTEINE PEPTIDASE 1); cysteine-type endopeptidase/ cysteine-type pe
Symbols: SCPL13 | serine-type carboxypeptidase | chr2:9778877-9783251 FORWARD
Symbols: SCPL9 | serine carboxypeptidase S10 family protein | chr2:9798843-9802674 FORWARD
serpin, putative / serine protease inhibitor, putative | chr2:11229087-11230491 REVERSE
catalytic/ protein binding / serine-type endopeptidase/ serine-type peptidase | chr5:9789899-979229
AAA-type ATPase family protein | chr3:10685524-10687364 FORWARD
Symbols: UBQ6 | UBQ6; protein binding | chr2:19344668-19345345 FORWARD
ubiquitin family protein | chr5:4630997-4631742 FORWARD
Symbols: UBC5 | UBC5 (ubiquitin-conjugating enzyme 5); ubiquitin-protein ligase | chr1:23667616-236
Symbols: UBC17 | UBC17 (UBIQUITIN-CONJUGATING ENZYME 17); small conjugating protein ligase/ ub
zinc finger (C3HC4-type RING finger) family protein | chr1:553181-555854 REVERSE
zinc finger (C3HC4-type RING finger) family protein | chr1:8484703-8486002 REVERSE
zinc finger (C3HC4-type RING finger) family protein | chr1:18201889-18202764 FORWARD
zinc finger (C3HC4-type RING finger) family protein | chr1:18209261-18210128 FORWARD
zinc finger (C3HC4-type RING finger) family protein | chr1:22242748-22243731 REVERSE
zinc finger (C3HC4-type RING finger) family protein | chr1:27157875-27159558 FORWARD
zinc finger (C3HC4-type RING finger) family protein | chr2:14440648-14442005 FORWARD
zinc finger (C3HC4-type RING finger) family protein | chr2:15764728-15765553 FORWARD

zinc finger (C3HC4-type RING finger) family protein | chr3:3479979-3480455 FORWARD
zinc finger (C3HC4-type RING finger) family protein | chr3:17178697-17180067 REVERSE
Symbols: ORL1, VIM6, ORTHL | ORTHL (ORTHRUS-LIKE); ubiquitin-protein ligase/ zinc ion binding | chr
zinc finger (C3HC4-type RING finger) family protein | chr5:206432-208611 FORWARD
zinc finger (C3HC4-type RING finger) family protein | chr5:338899-340253 FORWARD
zinc finger (C3HC4-type RING finger) family protein | chr5:375215-377208 FORWARD
zinc finger (C3HC4-type RING finger) family protein | chr5:5161724-5163030 FORWARD
zinc finger (C3HC4-type RING finger) family protein | chr5:20167002-20169474 REVERSE
unknown protein | chr1:3627726-3630765 FORWARD
kelch repeat-containing F-box family protein | chr1:9336057-9337786 REVERSE
kelch repeat-containing F-box family protein | chr1:9519108-9520520 FORWARD
F-box family protein | chr1:11221335-11222786 REVERSE
Symbols: ATSKP2;2, SKP2B | SKP2B; ubiquitin-protein ligase | chr1:28940750-28942596 FORWARD
F-box family protein | chr2:7403856-7405219 FORWARD
F-box family protein | chr2:11683862-11684967 REVERSE
F-box family protein | chr3:6289227-6290383 REVERSE
F-box family protein | chr3:8313334-8314422 FORWARD
kelch repeat-containing F-box family protein | chr3:22142900-22144439 FORWARD
kelch repeat-containing F-box family protein | chr4:1335729-1337368 REVERSE
FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN
kelch repeat-containing F-box family protein | chr4:18380526-18381905 REVERSE
kelch repeat-containing F-box family protein | chr4:18389436-18390539 REVERSE
kelch repeat-containing F-box family protein | chr5:9484734-9486149 REVERSE
FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN

description
protein kinase family protein | chr1:4572419-4576632 REVERSE
Symbols: ATMYC2, RD22BP1, JAI1, JIN1, MYC2, ZBF1 | MYC2; DNA binding / transcription activator/ tra
Symbols: PXMT1 | PXMT1; S-adenosylmethionine-dependent methyltransferase | chr1:24873291-248
Symbols: CIPK11, PKS5, SIP4, SNRK3.22 | SIP4 (SOS3-INTERACTING PROTEIN 4); kinase/ protein kinase
Symbols: MAPKKK17 | MAPKKK17; ATP binding / kinase/ protein kinase/ protein serine/threonine kina
tyrosine specific protein phosphatase family protein | chr2:13987767-13990976 FORWARD
protein phosphatase 2C, putative / PP2C, putative | chr3:1640393-1643253 REVERSE
protein kinase family protein | chr3:21392671-21393744 FORWARD
protein kinase family protein | chr4:7598093-7599257 REVERSE
Symbols: CIPK4, SnRK3.3 | CIPK4 (CBL-interacting protein kinase 4); ATP binding / kinase/ protein kinas
palmitoyl protein thioesterase family protein | chr4:9745006-9746966 REVERSE
protein phosphatase 2C PPH1 / PP2C PPH1 (PPH1) | chr4:13851862-13854191 REVERSE
Symbols: RIC7 | RIC7 (ROP-INTERACTIVE CRIB MOTIF-CONTAINING PROTEIN 7); protein binding | chr4:

protein phosphatase 2C, putative / PP2C, putative | chr4:15904444-15906010 REVERSE
Symbols: MAPKKK19 | MAPKKK19; ATP binding / kinase/ protein kinase/ protein serine/threonine kina

description
Symbols: EXO | EXO (EXORDIUM) | chr4:5740297-5741524 FORWARD
photoassimilate-responsive protein, putative | chr5:21263936-21265264 REVERSE
leucine-rich repeat transmembrane protein kinase, putative | chr1:24930665-24932918 REVERSE
leucine-rich repeat family protein / protein kinase family protein | chr3:4988107-4994058 FORWARD
Symbols: LRR XI-23 | LRR XI-23; ATP binding / kinase/ protein kinase/ protein serine/threonine kinase |
protein kinase family protein | chr1:29539089-29540709 REVERSE
LOCATED IN: endomembrane system; CONTAINS InterPro DOMAIN/s: Protein of unknown function DU
Symbols: RKF3 | RKF3 (RECEPTOR-LIKE KINASE IN IN FLOWERS 3); kinase/ receptor signaling protein se
Symbols: WAK3 | WAK3 (wall associated kinase 3); kinase/ protein serine/threonine kinase | chr1:743
protein kinase family protein | chr1:12064509-12066376 FORWARD
leucine-rich repeat protein kinase, putative | chr1:19237407-19241883 REVERSE
Symbols: AtRLP24 | AtRLP24 (Receptor Like Protein 24); kinase/ protein binding | chr2:14013874-1401
protein kinase-related | chr3:17005483-17008424 REVERSE
protein kinase family protein | chr4:6441673-6443435 REVERSE
Symbols: TSA1 | TSA1 (TSK-ASSOCIATING PROTEIN 1); calcium ion binding / protein binding | chr1:195
Symbols: RD20 | RD20 (RESPONSIVE TO DESSICATION 20); calcium ion binding | chr2:14144831-14146
calcium-binding EF hand family protein | chr3:11005779-11006414 FORWARD
calmodulin-binding family protein | chr3:19593173-19595822 REVERSE
Symbols: CML39, CML37 | CML37 (CALMODULIN LIKE 37); calcium ion binding | chr5:16942576-16943
Symbols: PBP1 | PBP1 (PINOID-BINDING PROTEIN 1); calcium ion binding / protein binding | chr5:2212
Symbols: BON1, CPN1, BON | BON1 (BONZAI 1); calcium-dependent phospholipid binding | chr5:2485
Symbols: ATBAG7 | ATBAG7 (ARABIDOPSIS THALIANA BCL-2-ASSOCIATED ATHANOGENE 7); calmoduli
Symbols: PIP5K5 | PIP5K5 (PHOSPHATIDYLINOSITOL- 4-PHOSPHATE 5-KINASE 5); 1-phosphatidylinosito
Symbols: ATROPGEF11, ROPGEF11 | ROPGEF11 (RHO GUANYL-NUCLEOTIDE EXCHANGE FACTOR 11); R
Symbols: ATRAB18C, ATRABC2B | ATRABC2B (ARABIDOPSIS RAB GTPASE HOMOLOG C2B); ATP binding
Symbols: PRN, PRN1, ATPIRIN1 | PRN (PIRIN); calmodulin binding | chr3:21894134-21895623 FORWA
nucleotide binding | chr4:15920230-15922658 FORWARD
Symbols: PRA1.G2 | PRA1.G2 (PRENYLATED RAB ACCEPTOR 1.G2) | chr5:22758768-22759371 REVERSE
protein kinase, putative | chr4:12080060-12084256 FORWARD
Symbols: FHL | FHL (FAR-RED-ELONGATED HYPOCOTYL1-LIKE); protein binding | chr5:437460-438894
phototropic-responsive NPH3 family protein | chr5:19353676-19356300 FORWARD

description
small nuclear ribonucleoprotein, putative / snRNP, putative / Sm protein, putative | chr1:6608115-66
Symbols: PAB6 | PAB6 (POLY(A) BINDING PROTEIN 6); RNA binding / translation initiation factor | chr3
Symbols: U2.6 | U2.6; snRNA | chr3:21004259-21004809 FORWARD
splicing factor Prp18 family protein | chr1:754371-756303 REVERSE
Symbols: ATU2AF35A | ATU2AF35A; RNA binding / nucleic acid binding / nucleotide binding / zinc ion
Symbols: RSZ33, ATRSZ33 | RSZ33; nucleic acid binding / nucleotide binding / zinc ion binding | chr2:1
Symbols: SCL30 | SCL30; RNA binding / nucleic acid binding / nucleotide binding | chr3:20560808-205
Symbols: SRZ-22, SRZ22, RSZP22 | SRZ-22; protein binding | chr4:15306654-15308347 FORWARD
Symbols: ATU2AF35B, U2AF35B | U2AF35B; RNA binding / nucleic acid binding / nucleotide binding / z
RNA helicase, putative | chr4:9388071-9390774 REVERSE
polyadenylate-binding protein family protein / PABP family protein | chr5:3255434-3257807 REVERSE
polyadenylate-binding protein family protein / PABP family protein | chr5:26080231-26083017 REVER
Symbols: RNS3 | RNS3 (RIBONUCLEASE 3); RNA binding / endoribonuclease/ ribonuclease T2 | chr1:92
Symbols: RNS1, ATRNS1 | RNS1 (RIBONUCLEASE 1); endoribonuclease/ ribonuclease | chr2:873506-87
endoribonuclease L-PSP family protein | chr3:7109949-7111824 REVERSE

description
Symbols: PTAC6 | PTAC6 (PLASTID TRANSCRIPTIONALLY ACTIVE6) | chr1:7571185-7573846 REVERSE
BolA-like family protein | chr5:3057646-3058821 REVERSE
DNA-binding protein, putative | chr2:15148259-15151575 REVERSE
Symbols: AL4 | AL4 (ALFIN-LIKE 4); DNA binding / methylated histone residue binding | chr5:9158318-
Symbols: RAP2.6 | RAP2.6 (related to AP2 6); DNA binding / transcription factor | chr1:16263813-162
Symbols: RAP2.1 | RAP2.1 (related to AP2 1); DNA binding / transcription factor | chr1:17265701-172
Symbols: ORA47 | ORA47; DNA binding / transcription factor | chr1:28144132-28145049 FORWARD
AP2 domain-containing transcription factor | chr2:9443128-9444423 REVERSE
AP2 domain-containing transcription factor, putative | chr2:9937998-9938875 FORWARD
AP2 domain-containing transcription factor family protein | chr2:14258509-14260733 REVERSE
Symbols: RAP2.9 | RAP2.9 (related to AP2 9); DNA binding / transcription factor | chr4:4073962-40745
Symbols: RAP2.10 | RAP2.10 (related to AP2 10); DNA binding / transcription factor | chr4:17388814-1
Symbols: Rap2.6L | Rap2.6L (related to AP2 6L); DNA binding / transcription factor | chr5:4272060-427
transcription factor | chr1:3493940-3495144 REVERSE
DNA binding / transcription factor | chr1:3506186-3509006 FORWARD
basic helix-loop-helix (bHLH) family protein | chr1:13039916-13042102 FORWARD
Symbols: PIL1 | PIL1 (PHYTOCHROME INTERACTING FACTOR 3-LIKE 1); transcription factor | chr2:1929
transcription factor | chr3:1727306-1728296 FORWARD
Symbols: MUTE | MUTE (MUTE); DNA binding / transcription factor | chr3:1846531-1848230 FORWAR
Symbols: SPCH | SPCH (SPEECHLESS); DNA binding / transcription factor | chr5:21586606-21588941 R

zinc finger (B-box type) family protein | chr1:8933716-8935460 REVERSE
zinc finger (B-box type) family protein | chr1:9775528-9777810 REVERSE
zinc finger (B-box type) family protein | chr1:25709114-25710907 REVERSE
Symbols: ATCOL4, COL4 | zinc finger (B-box type) family protein | chr5:8589234-8591236 FORWARD
Dof-type zinc finger domain-containing protein | chr1:17525365-17526306 FORWARD
Dof-type zinc finger domain-containing protein | chr5:539249-541112 REVERSE
Symbols: OBP4 | OBP4; DNA binding / transcription factor | chr5:24480449-24481873 FORWARD
transcription factor | chr2:7982868-7984096 REVERSE
zinc finger (GATA type) family protein | chr4:17268906-17269743 REVERSE
zinc finger (CCCH-type) family protein | chr1:10344046-10345651 FORWARD
zinc finger (C2H2 type) family protein (ZAT11) | chr2:15706357-15707224 FORWARD
zinc finger (C2H2 type) family protein | chr5:880225-881305 FORWARD
Symbols: C2H2, CZF2, ZAT6 | ZAT6 (ZINC FINGER OF ARABIDOPSIS THALIANA 6); nucleic acid binding /
Symbols: AZF3 | AZF3 (ARABIDOPSIS ZINC-FINGER PROTEIN 3); DNA binding / nucleic acid binding / tra
Symbols: AZF1 | AZF1 (ARABIDOPSIS ZINC-FINGER PROTEIN 1); DNA binding / nucleic acid binding / tra
RNA recognition motif (RRM)-containing protein | chr3:17351141-17352822 REVERSE
Symbols: NF-YB11 | NF-YB11 (NUCLEAR FACTOR Y, SUBUNIT B11); transcription factor | chr2:1174498
Symbols: PCL1, LUX | PCL1 (PHYTOCLOCK 1); DNA binding / transcription factor | chr3:17183090-1718
myb family transcription factor | chr5:2103162-2105898 FORWARD
Symbols: RGL3 | RGL3 (RGA-LIKE PROTEIN 3); transcription factor | chr5:5764063-5766077 REVERSE
Homeobox-leucine zipper protein family; FUNCTIONS IN: sequence-specific DNA binding, transcription
Symbols: HAT9 | HAT9; DNA binding / transcription factor | chr2:9704706-9706150 REVERSE
transposable element gene | chr3:5814748-5816592 FORWARD
Symbols: WOX1 | WOX1 (WUSCHEL related homeobox 1); transcription factor | chr3:6161137-616327
Symbols: SEP3, AGL9 | SEP3 (SEPALLATA3); DNA binding / protein binding / transcription factor | chr1:
unknown protein | chr1:22061083-22061481 REVERSE
Symbols: SEP1, AGL2 | SEP1 (SEPALLATA1); DNA binding / transcription factor | chr5:5151334-515415
Symbols: AGL62 | AGL62 (Agamous-like 62); DNA binding / transcription factor | chr5:24306294-2430
Symbols: AGL31, MAF2 | AGL31 (AGAMOUS LIKE MADS-BOX PROTEIN 31); transcription factor | chr5:
Symbols: AtMYB47 | AtMYB47 (myb domain protein 47); DNA binding / transcription factor | chr1:645
Symbols: MYB95, ATMYB95, ATMYBCP66 | MYB95 (myb domain protein 95); DNA binding / transcripti
myb family transcription factor / ELM2 domain-containing protein | chr2:1045456-1047684 REVERSE
Symbols: AtMYB70 | AtMYB70 (myb domain protein 70); DNA binding / transcription factor | chr2:990
Symbols: ATMYB2, MYB2 | MYB2 (MYB DOMAIN PROTEIN 2); DNA binding / calmodulin binding / trans
Symbols: MYB15, ATY19, ATMYB15 | MYB15 (MYB DOMAIN PROTEIN 15); DNA binding / transcription
Symbols: MYB111, ATMYB48, PFG3, ATMYB48-3 | MYB111 (MYB DOMAIN PROTEIN 111); DNA binding
Symbols: MYB29, ATMYB29, PMG2 | ATMYB29 (ARABIDOPSIS THALIANA MYB DOMAIN PROTEIN 29);
Symbols: MYB76, AtMYB76 | MYB76 (myb domain protein 76); DNA binding / transcription factor | ch
Symbols: MYB59, ATMYB59-3 | MYB59 (MYB DOMAIN PROTEIN 59); DNA binding / transcription facto
Symbols: ATMYBR1, ATMYB44, MYBR1 | MYBR1 (MYB DOMAIN PROTEIN R1); DNA binding / transcript
Symbols: ETC1 | ETC1 (ENHANCER OF TRY AND CPC 1); DNA binding / transcription factor | chr1:1471

Symbols: ATRL3 | ATRL3 (ARABIDOPSIS RAD-LIKE 3); DNA binding / transcription factor | chr4:1725466
Symbols: anac045 | anac045 (Arabidopsis NAC domain containing protein 45); transcription factor | ch
Symbols: ATNAC3, ANAC055 | ANAC055 (ARABIDOPSIS NAC DOMAIN CONTAINING PROTEIN 55); trans
TCP family transcription factor, putative | chr2:18820242-18821889 REVERSE
Symbols: ASIL1 | ASIL1 (ARABIDOPSIS 6B-INTERACTING PROTEIN 1-LIKE 1); sequence-specific DNA bind
DNA-binding protein-related | chr2:16018357-16019500 FORWARD
transcription factor | chr2:18437333-18438565 REVERSE
transcription factor | chr3:3096415-3098071 REVERSE
transcription factor | chr3:3476187-3477405 REVERSE
transcription factor | chr3:4707113-4708848 REVERSE
hydroxyproline-rich glycoprotein family protein | chr3:9073623-9074682 FORWARD
glycine-rich protein | chr4:14307249-14307973 FORWARD
transcription factor | chr4:15183188-15184961 REVERSE
transcription factor | chr5:1639032-1640606 REVERSE
Symbols: WRKY63, ATWRKY63 | WRKY63; transcription factor | chr1:24848320-24849364 FORWARD
Symbols: WRKY45, ATWRKY45 | WRKY45; transcription factor | chr3:326397-327412 REVERSE
Symbols: WRKY69, ATWRKY69 | WRKY69; transcription factor | chr3:21715007-21716916 FORWARD
Symbols: WRKY29, ATWRKY29 | WRKY29; transcription factor | chr4:12291820-12293096 FORWARD
Symbols: WRKY13, ATWRKY13 | WRKY13; transcription factor | chr4:18332878-18334789 REVERSE
Symbols: WRKY30, ATWRKY30 | WRKY30; transcription factor | chr5:8153115-8154709 REVERSE
Symbols: EEL, ATBZIP12, DPBF4 | EEL (ENHANCED EM LEVEL); DNA binding / transcription factor | chr2
Symbols: GBF3 | GBF3 (G-BOX BINDING FACTOR 3); sequence-specific DNA binding / transcription facto
Symbols: LBD41 | LBD41 (LOB DOMAIN-CONTAINING PROTEIN 41) | chr3:536505-537998 REVERSE
Symbols: ELF3, PYK20 | ELF3 (EARLY FLOWERING 3); protein C-terminus binding / transcription factor |
Symbols: TAF14 | TAF14 (TBP-associated factor 14) | chr2:7829035-7830059 FORWARD
Symbols: HDA08, HDA8, ATHDA8 | HDA08; histone deacetylase | chr1:2672451-2674628 FORWARD
Symbols: MBD8 | MBD8; methyl-CpG binding | chr1:7881537-7883742 REVERSE
Symbols: MBD11, ATMBD11 | MBD11; DNA binding / methyl-CpG binding | chr3:5343016-5344700 FO
RWP-RK domain-containing protein | chr1:27993032-27994178 REVERSE
Symbols: PUB22 | PUB22 (PLANT U-BOX 22); ubiquitin-protein ligase | chr3:19440739-19442383 REVE
nucleic acid binding | chr1:7004879-7007651 REVERSE
Remorin family protein; CONTAINS InterPro DOMAIN/s: Remorin, C-terminal (InterPro:IPR005516); BES

description
unknown protein | chr1:99922-101834 FORWARD
FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN
unknown protein | chr1:773411-775344 FORWARD
nucleic acid binding / ribonuclease H | chr1:3263877-3264788 REVERSE
FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN

unknown protein | chr1:3670278-3671187 REVERSE
unknown protein | chr1:3740765-3744675 FORWARD
unknown protein | chr1:3832623-3834191 FORWARD
FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN
unknown protein | chr1:3870833-3871570 FORWARD
unknown protein | chr1:3945737-3946613 FORWARD
unknown protein | chr1:4378939-4379516 REVERSE
unknown protein | chr1:4794756-4796594 FORWARD
unknown protein | chr1:5242198-5243227 REVERSE
The protein encoded by this gene was identified as a part of pollen proteome by mass spec analysis. It
unknown protein | chr1:5448726-5450177 FORWARD
unknown protein | chr1:5639032-5640173 FORWARD
unknown protein | chr1:5786560-5787112 REVERSE
Symbols: JAZ5, TIFY11A | JAZ5 (JASMONATE-ZIM-DOMAIN PROTEIN 5) | chr1:5955488-5957212 REVEF
unknown protein | chr1:6135803-6138432 REVERSE
unknown protein | chr1:6282252-6283293 REVERSE
unknown protein | chr1:6710961-6711787 FORWARD
FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN
unknown protein | chr1:7106922-7107617 REVERSE
pseudogene of unknown protein | chr1:7537087-7537649 REVERSE
unknown protein | chr1:8911130-8912398 REVERSE
unknown protein | chr1:9067039-9068207 FORWARD
Symbols: KDR | KDR (KIDARI); transcription regulator | chr1:9351454-9352761 FORWARD
binding | chr1:9412820-9417504 REVERSE
unknown protein | chr1:9483157-9484368 FORWARD
INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN
unknown protein | chr1:9846884-9847923 REVERSE
nucleic acid binding / zinc ion binding | chr1:10332371-10335694 FORWARD
unknown protein | chr1:10355703-10356482 REVERSE
unknown protein | chr1:10993195-10994125 REVERSE
DNA binding | chr1:11163858-11164928 REVERSE
INVOLVED IN: N-terminal protein myristoylation; LOCATED IN: plasma membrane; EXPRESSED IN: 14 p
unknown protein | chr1:11797335-11798602 FORWARD
Leucine-rich repeat (LRR) family protein; LOCATED IN: endomembrane system; CONTAINS InterPro DO
FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN
unknown protein | chr1:12514106-12516521 REVERSE
unknown protein | chr1:14293064-14296191 REVERSE
transposable element gene | chr1:16470872-16471248 FORWARD
Symbols: TED6 | TED6 (TRACHEARY ELEMENT DIFFERENTIATION-RELATED 6) | chr1:16575895-165764
unknown protein | chr1:17154921-17159397 REVERSE
unknown protein | chr1:17687269-17688816 FORWARD

unknown protein | chr1:17847356-17848564 FORWARD
unknown protein | chr1:18310494-18311634 FORWARD
unknown protein | chr1:18388792-18390496 REVERSE
unknown protein | chr1:19418306-19419853 FORWARD
unknown protein | chr1:19579886-19580686 REVERSE
unknown protein | chr1:19706085-19706706 FORWARD
Symbols: ATMRD1, MRD1 | unknown protein | chr1:19963214-19964712 REVERSE
unknown protein | chr1:20014410-20014923 REVERSE
unknown protein | chr1:20122426-20122866 REVERSE
unknown protein | chr1:20207020-20207540 FORWARD
unknown protein | chr1:20617313-20618005 FORWARD
Symbols: NDF5 | carbohydrate binding / catalytic | chr1:20674783-20676351 FORWARD
unknown protein | chr1:21191121-21192217 REVERSE
unknown protein | chr1:21580417-21580641 REVERSE
Symbols: MEE9 | MEE9 (maternal effect embryo arrest 9) | chr1:22409472-22410654 FORWARD
unknown protein | chr1:22729816-22731182 FORWARD
FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN
pseudogene of S-adenosylmethionine-dependent methyltransferase/rRNA (adenine-N6,N6-)-dimethyl
Unknown gene | chr1:23984011-23984795 FORWARD
unknown protein | chr1:24036021-24037401 FORWARD
unknown protein | chr1:24038034-24039177 FORWARD
FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN
FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN
FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; EXPRESSED
unknown protein | chr1:25614197-25615403 REVERSE
unknown protein | chr1:25711869-25712238 REVERSE
unknown protein | chr1:25892086-25892798 FORWARD
Symbols: AFP1 | AFP1 (ABI FIVE BINDING PROTEIN) | chr1:26039048-26040720 FORWARD
unknown protein | chr1:26072284-26076254 REVERSE
Symbols: JAZ9, TIFY7 | TIFY7 | chr1:26654768-26657064 FORWARD
unknown protein | chr1:26789236-26790160 REVERSE
unknown protein | chr1:26809841-26811842 REVERSE
unknown protein | chr1:27528052-27530946 REVERSE
unknown protein | chr1:27849230-27849812 FORWARD
unknown protein | chr1:28219382-28220227 FORWARD
unknown protein | chr1:28274588-28275990 FORWARD
unknown protein | chr1:28593250-28594742 FORWARD
FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN
unknown protein | chr1:30014361-30015078 FORWARD
unknown protein | chr1:30139101-30140204 FORWARD
unknown protein | chr1:30397128-30398210 FORWARD

unknown protein | chr2:6571-6672 FORWARD
FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN
unknown protein | chr2:332194-332781 REVERSE
unknown protein | chr2:421624-422626 REVERSE
FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN
unknown protein | chr2:1933272-1934212 REVERSE
transposable element gene | chr2:2297816-2298721 FORWARD
unknown protein | chr2:3246037-3246366 REVERSE
unknown protein | chr2:4304947-4305887 REVERSE
unknown protein | chr2:4805684-4807310 REVERSE
unknown protein | chr2:5049953-5050087 REVERSE
unknown protein | chr2:6947309-6947688 FORWARD
unknown protein | chr2:7545538-7546374 REVERSE
unknown protein | chr2:7573835-7575939 REVERSE
unknown protein | chr2:7584505-7588008 REVERSE
LOCATED IN: cellular_component unknown; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 1
unknown protein | chr2:8830565-8831533 REVERSE
Symbols: EPF1 | EPF1 (EPIDERMAL PATTERNING FACTOR 1) | chr2:8983074-8983612 REVERSE
unknown protein | chr2:9386516-9388183 FORWARD
unknown protein | chr2:9695932-9696909 FORWARD
unknown protein | chr2:10906428-10907288 FORWARD
FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN
FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN
LOCATED IN: chloroplast; EXPRESSED IN: 21 plant structures; EXPRESSED DURING: 13 growth stages; C
unknown protein | chr2:13580600-13581112 FORWARD
unknown protein | chr2:13581581-13582126 FORWARD
unknown protein | chr2:14152706-14154530 REVERSE
unknown protein | chr2:14324309-14325192 REVERSE
unknown protein | chr2:14387421-14390230 REVERSE
Symbols: JAZ7, TIFY5B | JAZ7 (JASMONATE-ZIM-DOMAIN PROTEIN 7) | chr2:14573080-14573856 FOR
unknown protein | chr2:14783291-14784710 FORWARD
unknown protein | chr2:15286498-15288990 FORWARD
unknown protein | chr2:15554917-15556831 REVERSE
unknown protein | chr2:15686758-15688003 FORWARD
FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; EXPRESSED
unknown protein | chr2:16224072-16225296 FORWARD
unknown protein | chr2:16541084-16543338 FORWARD
transferase, transferring glycosyl groups | chr2:17360491-17362535 FORWARD
unknown protein | chr2:17428098-17428812 FORWARD
FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; EXPRESSED
Symbols: LSH10 | LSH10 (LIGHT SENSITIVE HYPOCOTYLS 10) | chr2:17747917-17750440 FORWARD

Symbols: CPuORF17 | CPuORF17 (Conserved peptide upstream open reading frame 17) | chr2:178915
Symbols: ARL | ARL (ARGOS-LIKE) | chr2:18237152-18238173 FORWARD
unknown protein | chr2:18382070-18383513 FORWARD
FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN
unknown protein | chr2:18755045-18756302 REVERSE
unknown protein | chr2:18921024-18922179 REVERSE
unknown protein | chr2:19148730-19150995 FORWARD
unknown protein | chr2:19485875-19486553 FORWARD
FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN
unknown protein | chr3:324581-325087 REVERSE
unknown protein | chr3:488780-489471 FORWARD
INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; CONTAINS Int
FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN
unknown protein | chr3:822937-824546 REVERSE
unknown protein | chr3:1347646-1349202 FORWARD
Encodes a defensin-like (DEFL) family protein. | chr3:1693552-1694138 FORWARD
unknown protein | chr3:1823099-1824216 REVERSE
unknown protein | chr3:2167730-2169222 FORWARD
nucleic acid binding | chr3:2223001-2225254 REVERSE
unknown protein | chr3:2807667-2808268 REVERSE
unknown protein | chr3:3069231-3071429 FORWARD
unknown protein | chr3:3645022-3647542 REVERSE
3'-5' exonuclease/ nucleic acid binding | chr3:3954695-3955423 REVERSE
unknown protein | chr3:4392956-4393961 REVERSE
unknown protein | chr3:4710483-4711969 FORWARD
unknown protein | chr3:4851696-4851812 FORWARD
unknown protein | chr3:5045110-5045328 FORWARD
unknown protein | chr3:5258876-5259082 FORWARD
unknown protein | chr3:5451864-5452316 REVERSE
unknown protein | chr3:5676829-5677921 FORWARD
unknown protein | chr3:5681419-5682331 FORWARD
unknown protein | chr3:5852152-5853080 FORWARD
FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN
unknown protein | chr3:6479688-6480378 FORWARD
FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN
unknown protein | chr3:6825521-6826006 REVERSE
unknown protein | chr3:6965647-6967248 FORWARD
unknown protein | chr3:7591483-7592322 REVERSE
unknown protein | chr3:8410433-8412193 FORWARD
unknown protein | chr3:8646892-8647908 FORWARD
FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN

unknown protein | chr3:8952006-8952572 FORWARD
FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN
unknown protein | chr3:9276845-9278629 FORWARD
unknown protein | chr3:9463316-9464283 REVERSE
unknown protein | chr3:9676982-9679900 FORWARD
unknown protein | chr3:9972508-9974225 REVERSE
FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; EXPRESSED
unknown protein | chr3:10045186-10047343 REVERSE
unknown protein | chr3:10061545-10062731 FORWARD
transcription regulator | chr3:10855632-10856624 REVERSE
Symbols: AFP3 | AFP3 (ABI FIVE BINDING PROTEIN 3) | chr3:11382214-11384004 REVERSE
unknown protein | chr3:11452942-11453037 REVERSE
unknown protein | chr3:17650260-17651765 REVERSE
unknown protein | chr3:17707918-17708909 REVERSE
unknown protein | chr3:17772057-17774739 FORWARD
unknown protein | chr3:19273494-19275269 REVERSE
unknown protein | chr3:19312718-19313224 FORWARD
unknown protein | chr3:19323332-19323827 FORWARD
unknown protein | chr3:19323772-19325668 REVERSE
Overexpression leads to PEL (Pseudo-Etiolation in Light) phenotype. | chr3:20473541-20474763 REVE
Symbols: ESK1 | ESK1 (ESKIMO 1) | chr3:20780315-20783233 FORWARD
unknown protein | chr3:20896481-20897593 FORWARD
Symbols: ARGOS | ARGOS (AUXIN-REGULATED GENE INVOLVED IN ORGAN SIZE) | chr3:22129726-2213
unknown protein | chr3:22281916-22282017 REVERSE
FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN
unknown protein | chr3:22922550-22922940 FORWARD
unknown protein | chr3:22932496-22933362 REVERSE
unknown protein | chr3:23333513-23334034 REVERSE
Unknown gene | chr3:23459182-23459800 REVERSE
unknown protein | chr4:466391-468294 REVERSE
unknown protein | chr4:711192-712643 REVERSE
unknown protein | chr4:1119849-1119989 REVERSE
unknown protein | chr4:2327044-2328264 REVERSE
unknown protein | chr4:2506163-2506786 FORWARD
unknown protein.
unknown protein | chr4:5448133-5448523 FORWARD
FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN
unknown protein | chr4:6872151-6873541 REVERSE
FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN
unknown protein | chr4:7594944-7595463 REVERSE
Symbols: CLE44 | CLE44 (CLAVATA3/ESR-RELATED 44) | chr4:7662371-7663177 REVERSE

unknown protein | chr4:7753311-7754086 FORWARD
Symbols: SMAP1 | SMAP1 (SMALL ACIDIC PROTEIN 1) | chr4:7864394-7864924 FORWARD
unknown protein | chr4:7866719-7868742 FORWARD
unknown protein | chr4:7869874-7870750 FORWARD
Protein containing PAM2 motif which mediates interaction with the PABC domain of polyadenyl bindir
pseudogene, hypothetical protein, similar to putative reverse transcriptase | chr4:8458474-8458755 R
unknown protein | chr4:9179244-9179833 REVERSE
unknown protein | chr4:9192336-9192568 REVERSE
unknown protein | chr4:9311355-9315813 FORWARD
unknown protein | chr4:9749728-9751709 REVERSE
unknown protein | chr4:9924698-9926372 REVERSE
binding | chr4:9965742-9966969 FORWARD
unknown protein | chr4:10181334-10182140 REVERSE
unknown protein | chr4:10209174-10209733 FORWARD
FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN
unknown protein | chr4:10598445-10599151 REVERSE
unknown protein | chr4:11545926-11546434 FORWARD
unknown protein | chr4:11636084-11636473 REVERSE
unknown protein | chr4:12414230-12415049 FORWARD
unknown protein | chr4:12519932-12520813 REVERSE
unknown protein | chr4:13090209-13091798 REVERSE
other RNA | chr4:13293941-13296465 FORWARD
unknown protein | chr4:13813044-13813516 FORWARD
unknown protein | chr4:13933232-13935315 REVERSE
unknown protein | chr4:13960032-13960483 FORWARD
unknown protein | chr4:14011844-14012583 REVERSE
unknown protein | chr4:14713518-14713661 REVERSE
unknown protein | chr4:14806345-14807425 FORWARD
unknown protein | chr4:15202296-15203431 FORWARD
unknown protein | chr4:15276180-15277219 REVERSE
EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; BEST Arabidopsis thaliana p
unknown protein | chr4:16135400-16135914 FORWARD
Symbols: MAPKKK21 | MAPKKK21; ATP binding / protein kinase/ protein serine/threonine kinase | chr
unknown protein | chr4:17433643-17437069 REVERSE
FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN
unknown protein | chr4:17936921-17938728 REVERSE
unknown protein | chr5:5256-5891 REVERSE
unknown protein | chr5:412031-412698 REVERSE
unknown protein | chr5:573054-573558 REVERSE
FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN
unknown protein | chr5:762787-763321 REVERSE

FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN
unknown protein | chr5:1557037-1557998 REVERSE
DNA binding | chr5:1576982-1578754 REVERSE
unknown protein | chr5:1757098-1760666 REVERSE
unknown protein | chr5:1876034-1876637 REVERSE
unknown protein | chr5:1884928-1887121 REVERSE
Symbols: CPuORF21 | CPuORF21 (Conserved peptide upstream open reading frame 21) | chr5:299591
unknown protein | chr5:3058997-3061970 FORWARD
unknown protein | chr5:3241518-3242266 REVERSE
FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN
unknown protein | chr5:4234486-4235346 FORWARD
unknown protein | chr5:4263493-4265337 FORWARD
unknown protein | chr5:4277939-4279446 REVERSE
unknown protein | chr5:4442014-4444935 FORWARD
unknown protein | chr5:4553964-4554176 REVERSE
FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN
unknown protein | chr5:4646781-4647444 REVERSE
unknown protein | chr5:4898737-4900581 FORWARD
unknown protein | chr5:5260604-5262840 REVERSE
unknown protein | chr5:5572576-5573070 FORWARD
FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN
unknown protein | chr5:5978678-5980376 FORWARD
unknown protein | chr5:6310064-6310846 FORWARD
unknown protein | chr5:6470129-6471062 FORWARD
unknown protein | chr5:6718341-6718995 FORWARD
unknown protein | chr5:6740777-6743773 REVERSE
unknown protein | chr5:6797440-6798899 FORWARD
unknown protein | chr5:6993114-6993873 REVERSE
ubiquitin thiolesterase | chr5:7261600-7263513 FORWARD
unknown protein | chr5:7433790-7434935 FORWARD
unknown protein | chr5:7483253-7483811 FORWARD
unknown protein | chr5:7668229-7669315 REVERSE
other RNA | chr5:7794142-7795010 FORWARD
FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN
Symbols: LSU4 | LSU4 (RESPONSE TO LOW SULFUR 4) | chr5:8440694-8441218 REVERSE
other RNA | chr5:8468331-8469262 REVERSE
unknown protein | chr5:8723958-8725771 FORWARD
FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN
unknown protein | chr5:9874824-9876464 REVERSE
transposable element gene | chr5:12971144-12973180 FORWARD
other RNA | chr5:13085037-13086565 FORWARD

Symbols: WSD1 | WSD1; diacylglycerol O-acyltransferase/ long-chain-alcohol O-fatty-acyltransferase | transposable element gene | chr5:15561465-15562122 FORWARD
unknown protein | chr5:16414038-16414504 FORWARD
unknown protein | chr5:16414848-16415220 REVERSE
FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN
unknown protein | chr5:18421744-18421962 FORWARD
unknown protein | chr5:18556975-18558097 REVERSE
unknown protein | chr5:19403173-19404088 REVERSE
FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN
unknown protein | chr5:20097040-20097486 REVERSE
unknown protein | chr5:20489094-20489727 REVERSE
DNA binding | chr5:20724578-20726479 FORWARD
unknown protein | chr5:20877967-20878464 REVERSE
unknown protein | chr5:21009592-21010345 FORWARD
FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN
unknown protein | chr5:21595994-21598224 FORWARD
unknown protein | chr5:21811633-21814908 FORWARD
unknown protein | chr5:21848135-21850111 FORWARD
unknown protein | chr5:21872794-21873303 REVERSE
RNA binding | chr5:22293325-22295144 FORWARD
FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN
unknown protein | chr5:22885192-22886541 FORWARD
unknown protein | chr5:23098959-23099368 FORWARD
unknown protein | chr5:23126922-23127654 REVERSE
FUNCTIONS IN: molecular_function unknown; INVOLVED IN: N-terminal protein myristoylation; LOCAT
FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN
unknown protein | chr5:23485500-23486818 FORWARD
unknown protein | chr5:23793129-23794245 FORWARD
antiporter/ drug transporter | chr5:24301633-24303068 FORWARD
unknown protein | chr5:24418229-24422234 REVERSE
FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN
FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN
unknown protein | chr5:25541576-25542893 FORWARD
unknown protein | chr5:25748202-25748297 REVERSE
unknown protein | chr5:26052245-26052644 REVERSE
unknown protein | chr5:26095147-26095771 REVERSE
unknown protein | chr5:26207654-26207962 FORWARD
unknown protein | chr5:26462585-26464131 FORWARD
unknown protein | chr5:26934153-26934952 REVERSE
unknown protein | chr5:26964770-26965996 REVERSE
Symbols: YCF10 | hypothetical protein | chrC:60741-61430 FORWARD

description
2-oxoglutarate-dependent dioxygenase, putative | chr1:2025601-2027271 FORWARD
2-oxoglutarate-dependent dioxygenase, putative | chr1:2032338-2034018 FORWARD
LOCATED IN: endomembrane system, integral to membrane; EXPRESSED IN: 16 plant structures; EXPRE
Symbols: DHAR1, ATDHAR1 | DHAR1 (dehydroascorbate reductase); copper ion binding / glutathione c
Symbols: MDHAR, ATMDAR3 | MDHAR (MONODEHYDROASCORBATE REDUCTASE); monodehydroasco
Symbols: APX5 | APX5 (ASCORBATE PEROXIDASE 5); L-ascorbate peroxidase/ heme binding / peroxidas
Symbols: GRX480 | GRX480; electron carrier/ protein disulfide oxidoreductase | chr1:10013474-10014
glutaredoxin family protein | chr1:11858211-11859292 FORWARD
glutaredoxin family protein | chr1:23953233-23954492 FORWARD
glutaredoxin family protein | chr3:10848669-10850122 FORWARD
glutaredoxin family protein | chr3:23268710-23269324 FORWARD
glutaredoxin family protein | chr4:8925806-8926310 FORWARD

description
Symbols: GL22 | GL22 (GERMIN-LIKE PROTEIN SUBFAMILY 2 MEMBER 2 PRECURSOR.); manganese ion
Symbols: ILR2 | ILR2 (IAA-LEUCINE RESISTANT 2) | chr3:6341918-6343178 REVERSE
cytochrome c oxidase copper chaperone family protein | chr1:19760001-19761452 REVERSE
Symbols: CUTA | CUTA; copper ion binding | chr2:14269581-14271723 FORWARD
copper-binding family protein | chr3:18152288-18153375 REVERSE
heavy-metal-associated domain-containing protein / copper chaperone (CCH)-related | chr4:16685720
Symbols: MT1C | MT1C; copper ion binding | chr1:2341542-2342123 FORWARD
metal ion binding | chr2:7920508-7922326 REVERSE

description
LOCATED IN: membrane; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF250 (InterP
F1F0-ATPase inhibitor protein, putative | chr5:1372147-1373619 FORWARD
nucleotide-sugar transmembrane transporter | chr1:2242256-2244428 REVERSE
sugar transporter family protein | chr1:2848348-2852270 FORWARD
OST3/OST6 family protein | chr1:22814390-22815430 FORWARD
amino acid transporter family protein | chr1:2583654-2586744 REVERSE
amino acid transporter family protein | chr5:427833-430695 FORWARD

Symbols: RCP1, MEX1 | RCP1 (ROOT CAP 1); maltose transmembrane transporter | chr5:5772583-577
mitochondrial phosphate transporter, putative | chr3:18114526-18116499 REVERSE
unknown protein | chr3:23168061-23169187 FORWARD
mitochondrial substrate carrier family protein | chr5:25958025-25960644 REVERSE
cation efflux family protein | chr1:5578431-5580693 FORWARD
Symbols: COPT2 | COPT2; copper ion transmembrane transporter/ high affinity copper ion transmemb
proton-dependent oligopeptide transport (POT) family protein | chr1:6520748-6523368 FORWARD
proton-dependent oligopeptide transport (POT) family protein | chr1:12127389-12130407 REVERSE
proton-dependent oligopeptide transport (POT) family protein | chr1:21968071-21972411 FORWARD
proton-dependent oligopeptide transport (POT) family protein | chr2:15864396-15866408 REVERSE
Symbols: NHX4, ATNHX4 | NHX4 (SODIUM HYDROGEN EXCHANGER 4); sodium ion transmembrane tra
ChaC-like family protein | chr4:15185886-15188484 FORWARD
magnesium transporter CorA-like family protein (MRS2-2) | chr5:25806769-25809641 REVERSE
potassium channel tetramerisation domain-containing protein | chr4:15054873-15056826 FORWARD
Symbols: ATNAP5 | ATNAP5; ATPase, coupled to transmembrane movement of substances / transport
ABC transporter family protein | chr3:19399378-19402953 FORWARD
MATE efflux protein-related | chr4:14368919-14370892 FORWARD
Symbols: PIP2F, PIP2;4 | PIP2;4 (PLASMA MEMBRANE INTRINSIC PROTEIN 2;4); water channel | chr5:2
Symbols: CXIP4 | CXIP4 (CAX INTERACTING PROTEIN 4); nucleic acid binding / zinc ion binding | chr2:1
choline transporter-related | chr1:8955308-8957949 REVERSE
AWPM-19-like membrane family protein | chr1:10323655-10324743 FORWARD
MATE efflux family protein | chr1:24901978-24904443 FORWARD
antiporter/ drug transporter/ transporter | chr2:1353755-1355790 REVERSE
auxin efflux carrier family protein | chr2:7606757-7609261 FORWARD
MATE efflux family protein | chr4:11625362-11629337 REVERSE
Symbols: ATTIL, TIL | TIL (TEMPERATURE-INDUCED LIPOCALIN); binding / transporter | chr5:23500061-
metal ion binding | chr5:26430202-26430912 FORWARD

description
Symbols: FLA9 | FLA9 (FASCICLIN-LIKE ARABINOOGALACTAN 9) | chr1:982506-983540 REVERSE
Symbols: AGP5 | AGP5 (ARABINOGALACTAN-PROTEIN 5) | chr1:12917149-12917763 FORWARD
Symbols: AGP19, ATAGP19 | AGP19 (ARABINOGALACTAN-PROTEIN 19) | chr1:25809298-25810130 FO
Symbols: FLA7 | FLA7 (FASCICLIN-LIKE ARABINOOGALACTAN 7) | chr2:1676742-1678455 FORWARD
Symbols: AGP17, ATAGP17 | AGP17 (ARABINOGALACTAN PROTEIN 17) | chr2:9844350-9845385 FORW
Symbols: FLA8, AGP8 | FLA8 (FASCICLIN-LIKE ARABINOGALACTAN PROTEIN 8) | chr2:18742540-187441
Symbols: AGP10, ATAGP10 | AGP10 (ARABINOGALACTAN PROTEIN 10) | chr4:5792207-5792790 FORW
arabinogalactan-protein family | chr4:9556978-9557812 FORWARD
Symbols: AGP18, ATAGP18 | AGP18 (ARABINOGALACTAN PROTEIN 18) | chr4:17605758-17606755 RE

Symbols: AGP3 | AGP3 (arabinogalactan-protein 3) | chr4:18580838-18581585 REVERSE
Symbols: FLA17 | FLA17 (FASCICLIN-LIKE ARABINOGALACTAN PROTEIN 17 PRECURSOR) | chr5:195285
Symbols: AGP25, ATAGP25 | AGP25 (ARABINOGALACTAN PROTEINS 25) | chr5:6233519-6234206 REV
Symbols: AGP14, ATAGP14 | AGP14 (ARABINOGALACTAN PROTEIN 14) | chr5:22893151-22893642 FO
Symbols: FLA12 | FLA12 | chr5:24325727-24326702 REVERSE
Symbols: AGP1, ATAGP1 | AGP1 (ARABINOGALACTAN PROTEIN 1) | chr5:25721933-25722646 FORWA
Symbols: AGP7 | AGP7 | chr5:26128584-26129338 REVERSE

description
Symbols: ATCSLA10, CSLA10 | ATCSLA10; cellulose synthase/ transferase, transferring glycosyl groups
Symbols: ATCSLA15, CSLA15 | ATCSLA15; cellulose synthase/ transferase, transferring glycosyl groups
Symbols: ATCSLA01, CSLA01, ATCSLA1 | ATCSLA01; cellulose synthase/ glucosyltransferase/ transferas
Symbols: CESA8, IRX1, ATCESA8, LEW2 | IRX1 (IRREGULAR XYLEM 1); cellulose synthase/ transferase, t
Symbols: ATCSLG2, CSLG2 | ATCSLG2; cellulose synthase/ transferase/ transferase, transferring glycos

description
polygalacturonase | chr1:3515365-3517888 REVERSE
polygalacturonase | chr1:8327312-8329622 FORWARD
pseudogene, polygalacturonase (pectinase), putative, similar to polygalacturonase (Cucumis sativus) G
BURP domain-containing protein / polygalacturonase, putative | chr1:22247474-22249636 REVERSE
glycoside hydrolase family 28 protein / polygalacturonase (pectinase) family protein | chr3:5325290-5
polygalacturonase, putative / pectinase, putative | chr5:4724450-4726513 FORWARD

description
Symbols: ATEXPA10, AT-EXP10, ATEXP10, ATHEXP ALPHA 1.1, EXP10 | ATEXPA10 (ARABIDOPSIS THALI
Symbols: ATXTH17, XTH17 | XTH17 (XYLOGLUCAN ENDOTRANSGLUCOSYLASE/HYDROLASE 17); hydrol
xyloglucan:xyloglucosyl transferase, putative / xyloglucan endotransglycosylase, putative / endo-xylogl
xyloglucan:xyloglucosyl transferase, putative / xyloglucan endotransglycosylase, putative / endo-xylogl
Symbols: ATEXLB1, EXPR, AT-EXPR, ATEXPR1, ATHEXP BETA 3.1 | ATEXLB1 (ARABIDOPSIS THALIANA EX
Symbols: EXGT-A4 | EXGT-A4 (ENDOXYLOGLUCAN TRANSFERASE A4); hydrolase, acting on glycosyl bon
Symbols: XTR3 | XTR3 (XYLOGLUCAN ENDOTRANSGLYCOSYLASE 3); hydrolase, acting on glycosyl bond

description

Symbols: ATAMY1, AMY1 | AMY1 (ALPHA-AMYLASE-LIKE); alpha-amylase | chr4:12851969-12853845
Symbols: ATBETA-AMY, AT-BETA-AMY, RAM1, BMY1, BAM5 | BAM5 (BETA-AMYLASE 5); beta-amylase
Symbols: RCP1, MEX1 | RCP1 (ROOT CAP 1); maltose transmembrane transporter | chr5:5772583-577
Symbols: ATISA3, ISA3 | ISA3 (ISOAMYLASE 3); alpha-amylase/ isoamylase | chr4:5784074-5789002 F

description
beta-fructofuranosidase, putative / invertase, putative / saccharase, putative / beta-fructosidase, puta
beta-fructosidase (BFRUCT3) / beta-fructofuranosidase / invertase, vacuolar | chr1:23199718-232037
Symbols: HKL1 | HKL1 (HEXOKINASE-LIKE 1); ATP binding / fructokinase/ glucokinase/ hexokinase | chr
Symbols: ATHXK4, HKL2 | ATHXK4; ATP binding / fructokinase/ glucokinase/ hexokinase | chr3:699489

description
O-methyltransferase family 2 protein | chr1:28822186-28823673 REVERSE
Symbols: LAC2, ATLAC2 | LAC2 (laccase 2); laccase | chr2:12524889-12527747 REVERSE
Symbols: IRX12, LAC4 | IRX12 (IRREGULAR XYLEM 12); laccase | chr2:15934460-15937616 FORWARD
Symbols: LAC10 | LAC10 (laccase 10); laccase | chr5:72392-74756 FORWARD
Symbols: LAC11 | LAC11 (laccase 11); laccase | chr5:777021-779424 REVERSE
Symbols: LAC17, ATLAC17 | LAC17 (laccase 17); laccase | chr5:24167996-24170462 FORWARD

description
Symbols: ATPRR1, PRR1 | PRR1 (PINORESINOL REDUCTASE 1); pinoresinol reductase | chr1:11546338-
transferase family protein | chr3:18637854-18639185 FORWARD
transferase family protein | chr5:5365669-5367385 REVERSE
Symbols: 4CL3 | 4CL3; 4-coumarate-CoA ligase | chr1:24167202-24171502 REVERSE
4-coumarate--CoA ligase family protein / 4-coumaroyl-CoA synthase family protein | chr5:15213765-1
Symbols: ATTSM1, TSM1 | TSM1; N1,N5,N10-tris-(5-hydroxyferuloyl)spermidine O-methyltransferase/
Symbols: CAD5, ATCAD5, CAD-5 | ATCAD5 (CINNAMYL ALCOHOL DEHYDROGENASE 5); cinnamyl-alcoh
Symbols: ELI3-2, ELI3, ATCAD8, CAD-B2 | ELI3-2 (ELICITOR-ACTIVATED GENE 3-2); aryl-alcohol dehydro

description
Symbols: PAP1, MYB75, SIAA1, ATMYB75 | PAP1 (PRODUCTION OF ANTHOCYANIN PIGMENT 1); DNA b
oxidoreductase, 2OG-Fe(II) oxygenase family protein | chr2:16012535-16014753 REVERSE

oxidoreductase, 2OG-Fe(II) oxygenase family protein | chr3:20766735-20769324 REVERSE
oxidoreductase, 2OG-Fe(II) oxygenase family protein | chr5:1672120-1674739 FORWARD
transferase family protein | chr1:1009542-1011056 REVERSE
Symbols: AACT1 | AACT1 (anthocyanin 5-aromatic acyltransferase 1); transferase/ transferase, transfe
dihydroflavonol 4-reductase family / dihydrokaempferol 4-reductase family | chr4:16833933-1683561
Symbols: UGT78D2 | UGT78D2 (UDP-GLUCOSYL TRANSFERASE 78D2); UDP-glycosyltransferase/ antho
UDP-glucoronosyl/UDP-glucosyl transferase family protein | chr1:1820308-1821894 REVERSE

description
geranylgeranyl transferase type II beta subunit, putative / RAB geranylgeranyltransferase beta subunit
geranylgeranyl transferase alpha subunit-related / RAB geranylgeranyltransferase alpha subunit-relate
Symbols: GGPS6 | GGPS6 (geranylgeranyl pyrophosphate synthase 6); farnesyltranstransferase | chr1:
Symbols: TPS10 | TPS10 (terpene synthase 10); (E)-beta-ocimene synthase/ myrcene synthase | chr2:1
Symbols: LAS1 | LAS1; lanosterol synthase | chr3:16512271-16517522 REVERSE
Symbols: ATTPS03 | ATTPS03; (E)-beta-ocimene synthase/ myrcene synthase | chr4:9407768-9410877

description
Symbols: BCAT4 | BCAT4 (BRANCHED-CHAIN AMINOTRANSFERASE4); catalytic/ methionine-oxo-acid tr
Symbols: MAM1, IMS3 | MAM1 (METHYLTHIOALKYLMALATE SYNTHASE 1); 2-isopropylmalate synthase
Symbols: CYP83A1, REF2 | CYP83A1 (CYTOCHROME P450 83A1); oxidoreductase, acting on paired don
Symbols: FMO GS-OX2 | FMO GS-OX2 (FLAVIN-MONOOXYGENASE GLUCOSINOLATE S-OXYGENASE 2);
Symbols: FMO GS-OX3 | FMO GS-OX3 (FLAVIN-MONOOXYGENASE GLUCOSINOLATE S-OXYGENASE 3);
Symbols: FMO GS-OX1 | FMO GS-OX1 (FLAVIN-MONOOXYGENASE GLUCOSINOLATE S-OXYGENASE 1);
Symbols: AOP2 | AOP2 (ALKENYL HYDROXALKYL PRODUCING 2); oxidoreductase, acting on paired don
2-oxoglutarate-dependent dioxygenase, putative | chr2:10829916-10831655 REVERSE
Symbols: CYP79B3 | CYP79B3; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxy
Symbols: MYB29, ATMYB29, PMG2 | ATMYB29 (ARABIDOPSIS THALIANA MYB DOMAIN PROTEIN 29);
Symbols: MYB76, AtMYB76 | MYB76 (myb domain protein 76); DNA binding / transcription factor | ch
Symbols: MBP1, ATMBP | MBP1 (MYROSINASE-BINDING PROTEIN 1); protein binding | chr1:19350375
myrosinase-associated protein, putative | chr1:20158664-20160815 REVERSE
Symbols: ESP, TASTY | ESP (EPITHIOSPECIFIER PROTEIN); enzyme regulator | chr1:20170715-20173949
Symbols: NIT2 | NIT2 (nitrilase 2); indole-3-acetonitrile nitrilase/ indole-3-acetonitrile nitrile hydratase

description

Symbols: BFN1, ENDO1 | BFN1 (BIFUNCTIONAL NUCLEASE I); T/G mismatch-specific endonuclease/ en
transducin family protein / WD-40 repeat family protein | chr1:18305541-18307557 FORWARD
transposable element gene | chr4:2189515-2193763 FORWARD
Symbols: SADHU1-1 | transposable element gene | chr2:4005995-4007044 REVERSE
Symbols: SADHU6-1 | transposable element gene | chr3:525370-526255 FORWARD
Symbols: SADHU3-2 | transposable element gene | chr3:14749400-14750294 REVERSE
Symbols: SADHU4-1 | transposable element gene | chr5:10933823-10934730 REVERSE
transposable element gene | chr2:2936239-2938827 FORWARD
transposable element gene | chr3:7375158-7376420 FORWARD
transposable element gene | chr3:15598179-15600798 FORWARD
transposable element gene | chr5:25855347-25857377 REVERSE
transposable element gene | chr3:15677383-15678009 REVERSE
Symbols: HIS1-3 | HIS1-3 (HISTONE H1-3); DNA binding / nucleosomal DNA binding | chr2:7846050-78
Symbols: HTA4 | HTA4; DNA binding | chr4:7884516-7885664 FORWARD
histone H3 | chr1:2971593-2972199 REVERSE
histone H4 | chr1:2368837-2369734 FORWARD

description
lysine-ketoglutarate reductase/saccharopine dehydrogenase bifunctional enzyme | chr4:15985189-15

description
arginase, putative | chr4:5646439-5648727 REVERSE

description
pseudogene, similar to NADH dehydrogenase subunit 5, blastp match of 97% identity and 2.2e-244 P-v
NADH-ubiquinone oxidoreductase-related | chr3:23223061-23224308 REVERSE
NADH-ubiquinone oxidoreductase-related | chr5:21413646-21415006 FORWARD
Symbols: ATP9 | subunit 9 of mitochondrial F0-ATPase | chrM:278649-279152 FORWARD

description
Symbols: PSBP-2 | PSBP-2 (photosystem II subunit P-2); calcium ion binding | chr2:13119047-1312009
Symbols: PSBA | Encodes chlorophyll binding protein D1, a part of the photosystem II reaction center
Symbols: PSBC | chloroplast gene encoding a CP43 subunit of the photosystem II reaction center. prom
Symbols: PSBB | encodes for CP47, subunit of the photosystem II reaction center. | chrC:72371-73897
Symbols: PSAB | Encodes the D1 subunit of photosystem I and II reaction centers. | chrC:37375-39579
Symbols: PSAA | Encodes psaA protein comprising the reaction center for photosystem I along with ps

Symbols: PSAJ | Encodes subunit J of photosystem I. | chrC:66929-67063 FORWARD
Symbols: PSAC | Encodes the PsaC subunit of photosystem I. | chrC:117318-117563 REVERSE
Symbols: PETA | Encodes cytochrome f apoprotein; involved in photosynthetic electron transport chai
Symbols: NDHG | NADH dehydrogenase ND6 | chrC:118377-118907 REVERSE

description
Symbols: UGT1, UGT75B1 | UGT75B1 (UDP-GLUCOSYLTRANSFERASE 75B1); UDP-glucose:4-aminobenz
Symbols: ILL6 | ILL6; IAA-amino acid conjugate hydrolase/ metallopeptidase | chr1:16834210-1683828
Symbols: IAR3, JR3 | IAR3 (IAA-ALANINE RESISTANT 3); IAA-Ala conjugate hydrolase/ metallopeptidase
Symbols: ILL5 | ILL5; IAA-amino acid conjugate hydrolase/ metallopeptidase | chr1:19204512-1920658
Symbols: ILR1 | ILR1 (IAA-LEUCINE RESISTANT 1); IAA-Leu conjugate hydrolase/ IAA-Phe conjugate hyd
Symbols: NIT2 | NIT2 (nitrilase 2); indole-3-acetonitrile nitrilase/ indole-3-acetonitrile nitrile hydratase
auxin-responsive family protein | chr1:6872794-6873255 REVERSE
auxin-responsive protein-related | chr2:18641566-18642704 FORWARD
auxin-responsive family protein | chr4:16592397-16592717 REVERSE
auxin-responsive family protein | chr4:16596860-16597144 FORWARD

description
Symbols: CYP707A1 | CYP707A1; (+)-abscisic acid 8'-hydroxylase/ oxygen binding | chr4:10521379-105
Symbols: ABF3, DPBF5 | ABF3 (ABSCISIC ACID RESPONSIVE ELEMENTS-BINDING FACTOR 3); DNA bindi
Symbols: HVA22K | HVA22K (HVA22-LIKE PROTEIN K) | chr4:17307769-17309867 FORWARD
GRAM domain-containing protein / ABA-responsive protein-related | chr5:2686245-2687251 REVERSE
Symbols: KIN1 | KIN1 | chr5:5209898-5210727 FORWARD
GRAM domain-containing protein / ABA-responsive protein-related | chr5:7858253-7859387 REVERSE
GRAM domain-containing protein / ABA-responsive protein-related | chr5:7863331-7864271 REVERSE
protein phosphatase 2C, putative / PP2C, putative | chr5:23894404-23896619 REVERSE

description
2-oxoglutarate-dependent dioxygenase, putative | chr2:10829916-10831655 REVERSE
Symbols: ATERF13, EREBP, ERF13 | ERF13 (ETHYLENE-RESPONSIVE ELEMENT BINDING FACTOR 13); DN
DNA binding / transcription factor | chr4:2667990-2669364 REVERSE
Symbols: ERF104 | ethylene-responsive element-binding family protein | chr5:24766386-24767430 RE
universal stress protein (USP) family protein | chr3:23135984-23137173 FORWARD
Symbols: ATMES9, MES9 | MES9 (METHYL ESTERASE 9); hydrolase, acting on ester bonds / methyl ind

description
Symbols: CYP707A1 | CYP707A1; (+)-abscisic acid 8'-hydroxylase/ oxygen binding | chr4:10521379-105
Symbols: ABF3, DPBF5 | ABF3 (ABSCISIC ACID RESPONSIVE ELEMENTS-BINDING FACTOR 3); DNA bindi
Symbols: HVA22K | HVA22K (HVA22-LIKE PROTEIN K) | chr4:17307769-17309867 FORWARD
GRAM domain-containing protein / ABA-responsive protein-related | chr5:2686245-2687251 REVERSE
Symbols: KIN1 | KIN1 | chr5:5209898-5210727 FORWARD
GRAM domain-containing protein / ABA-responsive protein-related | chr5:7858253-7859387 REVERSE
GRAM domain-containing protein / ABA-responsive protein-related | chr5:7863331-7864271 REVERSE
protein phosphatase 2C, putative / PP2C, putative | chr5:23894404-23896619 REVERSE
Symbols: UGT1, UGT75B1 | UGT75B1 (UDP-GLUCOSYLTRANSFERASE 75B1); UDP-glucose:4-aminobenz
Symbols: ILL6 | ILL6; IAA-amino acid conjugate hydrolase/ metallopeptidase | chr1:16834210-1683828
Symbols: IAR3, JR3 | IAR3 (IAA-ALANINE RESISTANT 3); IAA-Ala conjugate hydrolase/ metallopeptidase
Symbols: ILL5 | ILL5; IAA-amino acid conjugate hydrolase/ metallopeptidase | chr1:19204512-1920658
Symbols: ILR1 | ILR1 (IAA-LEUCINE RESISTANT 1); IAA-Leu conjugate hydrolase/ IAA-Phe conjugate hyd
Symbols: NIT2 | NIT2 (nitrilase 2); indole-3-acetonitrile nitrilase/ indole-3-acetonitrile nitrile hydratase
auxin-responsive family protein | chr1:6872794-6873255 REVERSE
auxin-responsive protein-related | chr2:18641566-18642704 FORWARD
auxin-responsive family protein | chr4:16592397-16592717 REVERSE
auxin-responsive family protein | chr4:16596860-16597144 FORWARD
Symbols: CPD, CYP90A, CYP90, CBB3, DWF3, CYP90A1 | CPD (CONSTITUTIVE PHOTOMORPHOGENIC D
Symbols: ROT3 | ROT3 (ROTUNDIFOLIA 3); oxidoreductase, acting on paired donors, with incorporatio
squalene monooxygenase, putative / squalene epoxidase, putative | chr5:8180118-8181027 REVERSE
Symbols: CKX5, ATCKX5, ATCKX6 | CKX5 (CYTOKININ OXIDASE 5); cytokinin dehydrogenase | chr1:2831
2-oxoglutarate-dependent dioxygenase, putative | chr2:10829916-10831655 REVERSE
Symbols: ATERF13, EREBP, ERF13 | ERF13 (ETHYLENE-RESPONSIVE ELEMENT BINDING FACTOR 13); DN
DNA binding / transcription factor | chr4:2667990-2669364 REVERSE
Symbols: ERF104 | ethylene-responsive element-binding family protein | chr5:24766386-24767430 RE
universal stress protein (USP) family protein | chr3:23135984-23137173 FORWARD
Symbols: ATMES9, MES9 | MES9 (METHYL ESTERASE 9); hydrolase, acting on ester bonds / methyl ind
Symbols: AOP2 | AOP2 (ALKENYL HYDROXALKYL PRODUCING 2); oxidoreductase, acting on paired don
Symbols: GA5, GA20OX1, AT2301, ATGA20OX1 | GA20OX1; gibberellin 20-oxidase | chr4:12990884-12
gibberellin-responsive protein, putative | chr1:8027298-8028125 FORWARD
gibberellin-regulated family protein | chr5:24111324-24112020 FORWARD
Symbols: LOX2, ATLOX2 | LOX2 (LIPOXYGENASE 2); lipoxygenase | chr3:16525410-16529352 FORWAR
Symbols: OPR3 | OPR3 (OPDA-REDUCTASE 3); 12-oxophytodienoate reductase | chr2:2359115-236218
Symbols: JMT | JMT (JASMONIC ACID CARBOXYL METHYLTRANSFERASE); jasmonate O-methyltransfer
Symbols: ESP, TASTY | ESP (EPITHIOSPECIFIER PROTEIN); enzyme regulator | chr1:20170715-20173949
jacalin lectin family protein | chr3:5592582-5595710 FORWARD

Symbols: JR1 | JR1 | chr3:5595938-5598044 REVERSE

UDP-glucoronosyl/UDP-glucosyl transferase family protein | chr1:1703092-1704691 REVERSE

S-adenosyl-L-methionine:carboxyl methyltransferase family protein | chr5:15530015-15531522 FORW

Symbols: BSMT1, ATBSMT1 | BSMT1; S-adenosylmethionine-dependent methyltransferase | chr3:3614

log2_fold change
3.15638
3.12987
1.20839
1.50469
1.09387
-1.98766
-1.62434
1.02536
1.00219
-1.58521
2.20315
1.12764
-1.52125
-1.13795
-1.11131
1.03622
1.08253
1.08363
-1.22059
1.50898
1.10344
1.16651
1.01699
1.22913
2.14935
-2.89875
1.70725
inf
-1.04128
-1.21937
1.88121
-1.46358
-1.16083

log2_fold change
1.46289
-1.04128

	1.04403
log2_fold change	
	2.03939
	1.5608
	1.53978
	1.29601
	1.20016
	-1.21617
	-1.66602
	-2.40485
	-1.35058
	-1.9121
	-1.12992
	-1.64285
	1.12311
	1.09045
	-1.28473
	-1.15905
	1.11664
	-1.73882
log2_fold change	
	1.99185
	1.90882
	1.44351
	-1.06727
	1.0113
	1.0287
log2_fold change	
	-1.37709
	1.05064
	1.20131
	-1.40933
	1.18572

log2_fold change
1.43547
2.12301
1.06675
1.16667

log2_fold change
1.51773

log2_fold change
1.04038
1.12758
1.06009
1.25943
1.91681
1.75456
2.07282
1.19261
-1.10517
1.20524
-1.32013
1.3889
1.54072
1.56587
1.13025
-1.17728
1.082

log2_fold change
1.89947
1.7897
-1.3483
1.01001
-1.25187
1.18288

2.39344
-1.84919
-1.29049
-1.32498
1.59569
1.08713
-2.12416
1.14552
-1.66756
1.14574
-1.14282
-1.03287
1.20873
-1.20249

log2_fold change
-2.3909
-1.33388
-1.66461
1.38988
2.92822
-1.35554
1.01463
1.60405
-1.89174
1.27661
-2.49273
3.63877
1.22586
1.08961
-1.6778
1.02479
1.19772
-1.57327
-1.37158
-1.64586
1.37268
1.06131
1.1002

1.16035
1.03134
1.15115
1.10128
1.89472
1.04571
1.07052
2.03639
1.0873
1.3461
1.40055
1.27874
1.13058
1.09587
1.70307
1.15621
1.31732
1.20071
1.7448
1.01861
1.47988
1.09688
1.31274
1.01556

log2_fold change
1.147
1.83347
-1.03356
1.86233
2.09352
-1.16717
1.43642
-1.37473
-1.45975
1.16184
1.03028
1.04823
-1.13457

-1.90806
2.23363

log2_fold change
-1.74198
1.34978
-1.236
-1.65376
0.313837
-1.00524
-1.03028
1.1814
-1.13069
1.1054
-1.12591
1.24686
2.38942
1.42175
1.00595
1.43225
1.06147
1.09206
1.21267
1.09545
1.0296
1.00362
1.13903
1.58068
3.04564
2.70247
1.43914
-1.58505
1.20054
1.52682
-1.07091

log2_fold change
1.03274
1.71604
Inf
1.04518
1.08867
1.02624
1.01309
1.01722
1.1342
1.01023
1.1927
1.06778
-2.64418
2.96913
1.05889

log2_fold change
1.05331
1.40825
1.03882
1.30651
1.77261
1.13429
1.35594
1.72533
1.14835
-1.28413
1.21607
1.46958
2.28145
3.14301
1.27682
1.32599
-1.37855
1.49228
-1.3742
-1.16366

1.1068
1.59055
1.47686
1.22618
1.135
-1.13789
1.00092
-1.15863
-2.39598
1.22396
1.07592
-1.06011
1.01558
1.08569
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log2_fold change
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log2_fold change

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log2_fold change
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log2_fold change
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log2_fold change
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log2_fold change
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log2_fold change

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log2_fold change
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log2_fold change
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log2_fold change
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log2_fold change
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Upregulated_Downregulated_MIOX4_5.0_Mapman.txt
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