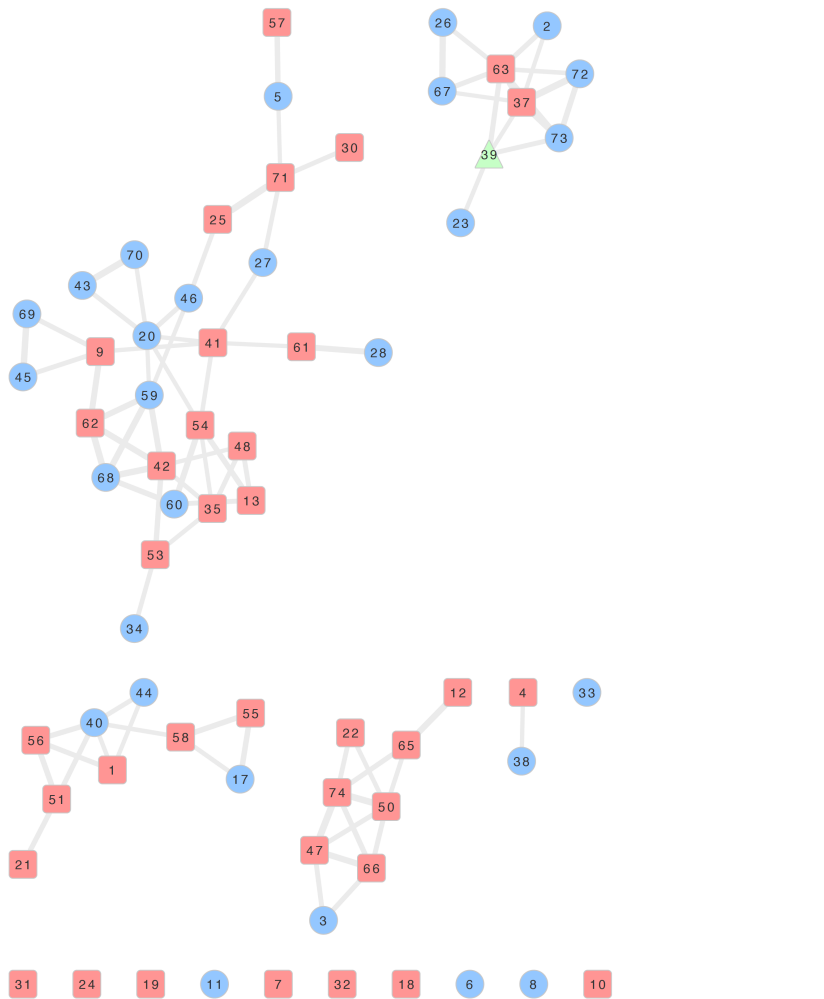


A]

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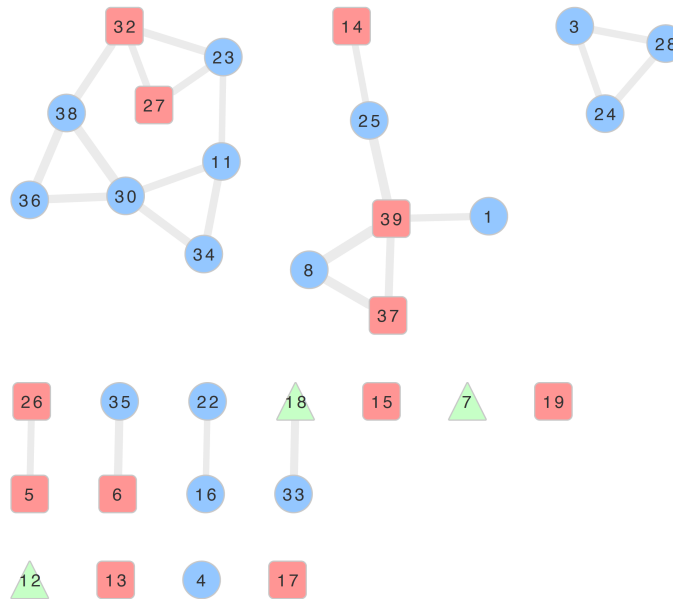


- | | | |
|--|---|---|
| 1: response to reactive oxygen species | 28: double-strand break repair | 52: auxin-activated signaling pathway |
| 2: vacuolar transport | 29: double-strand break repair via homologous recombination | 53: glutamate biosynthesis |
| 3: phloem development | 30: proteolysis | 54: pyrimidine nucleotide biosynthesis |
| 4: cellulose microfibril organization | 31: response to karrikin | 55: response to bacterium |
| 5: protein peptidyl-prolyl isomerization | 32: response to wounding | 56: brassinosteroid mediated signaling pathway |
| 6: protein folding | 33: oxidation-reduction process | 57: peptidyl-diphthamide biosynthesis |
| 7: regulation of nitrogen utilization | 34: riboflavin biosynthesis | 58: response to molecule of bacterial origin |
| 8: carbohydrate metabolism | 35: tricarboxylic acid cycle | 59: allantoin catabolism |
| 9: mRNA splicing, via spliceosome | 36: mitochondrial electron transport, ubiquinol to cytochrome c | 60: Mo-molybdopterin cofactor biosynthesis |
| 10: primary metabolism | 37: metal ion transport | 61: RNA-directed DNA methylation |
| 11: nitric oxide biosynthesis | 38: tubulin complex assembly | 62: deadenylation-dependent decapping of nuclear-transcribed mRNA |
| 12: cytokinesis by cell plate formation | 39: drug transmembrane transport | 63: transport |
| 13: phosphatidylinositol dephosphorylation | 40: response to auxin | 64: transmembrane transport |
| 14: attachment of GPI anchor to protein | 41: regulation of transcription, DNA-templated | 65: male meiosis |
| 15: ceramide metabolism | 42: L-phenylalanine catabolism | 66: floral meristem determinacy |
| 16: sphingolipid biosynthesis | 43: cell redox homeostasis | 67: ER to Golgi vesicle-mediated transport |
| 17: response to insect | 44: response to cadmium ion | 68: chlorophyll catabolism |
| 18: L-arabinose metabolism | 45: charged-tRNA amino acid modification | 69: tRNA threonylcarbamoyladenosine modification |
| 19: microtubule-based process | 46: signal peptide processing | 70: regulation of pH |
| 20: regulation of translational fidelity | 47: procambium histogenesis | 71: protein ubiquitination |
| 21: regulation of vernalization response | 48: very long-chain fatty acid metabolism | 72: iron ion transport |
| 22: vasculature development | 49: fatty acid biosynthesis | 73: ATP hydrolysis coupled proton transport |
| 23: polyamine transport | 50: vegetative to reproductive phase transition of meristem | 74: embryo development ending in seed dormancy |
| 24: response to arsenic-containing substance | 51: regulation of auxin mediated signaling pathway | |
| 25: protein deubiquitination | | |
| 26: retrograde transport, endosome to Golgi | | |
| 27: protein glycosylation | | |

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B]

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- 1: nuclear division
- 2: mitotic sister chromatid segregation
- 3: drug transmembrane transport
- 4: metabolism
- 5: procambium histogenesis
- 6: regulation of cyclin-dependent protein serine/threonine kinase activity
- 7: carbohydrate metabolism
- 8: DNA repair
- 9: double-strand break repair via homologous recombination
- 10: base-excision repair
- 11: cellular amino acid metabolism
- 12: sucrose metabolism
- 13: proteolysis

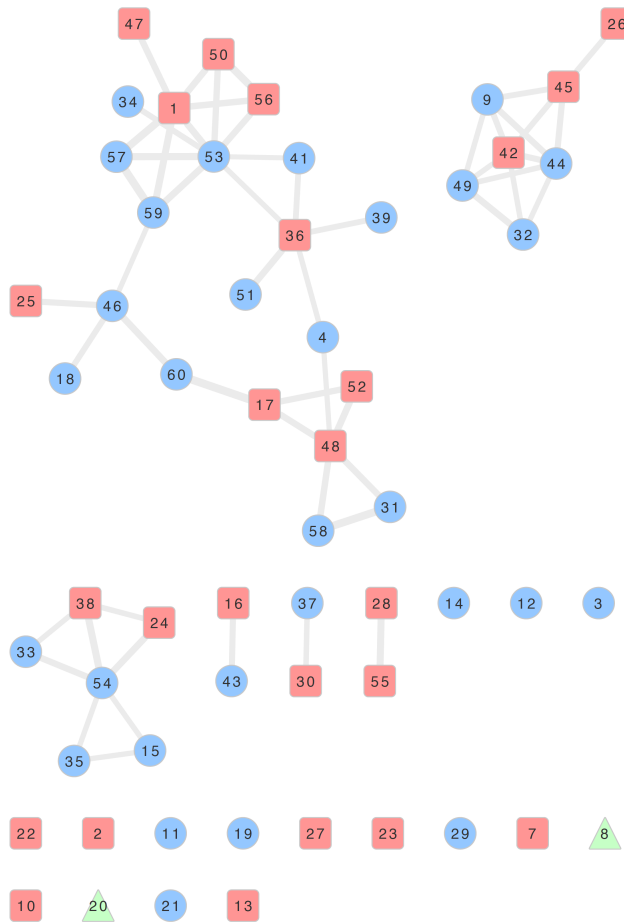
- 14: lipid storage
- 15: defense response to oomycetes
- 16: regulation of auxin mediated signaling pathway
- 17: response to wounding
- 18: response to heat
- 19: response to metal ion
- 20: response to water deprivation
- 21: response to cadmium ion
- 22: response to chitin
- 23: 'de novo' IMP biosynthesis
- 24: malate transport
- 25: cell redox homeostasis
- 26: vegetative to reproductive phase transition of meristem

- 27: phosphatidylinositol dephosphorylation
- 28: potassium ion transmembrane transport
- 29: potassium ion transport
- 30: L-phenylalanine catabolism
- 31: tryptophan biosynthesis
- 32: Mo-molybdopterin cofactor biosynthesis
- 33: response to salt stress
- 34: cysteine biosynthesis from serine
- 35: cytokinesis by cell plate formation
- 36: allantoin catabolism
- 37: RNA-directed DNA methylation
- 38: chlorophyll catabolism
- 39: telomere maintenance

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C]

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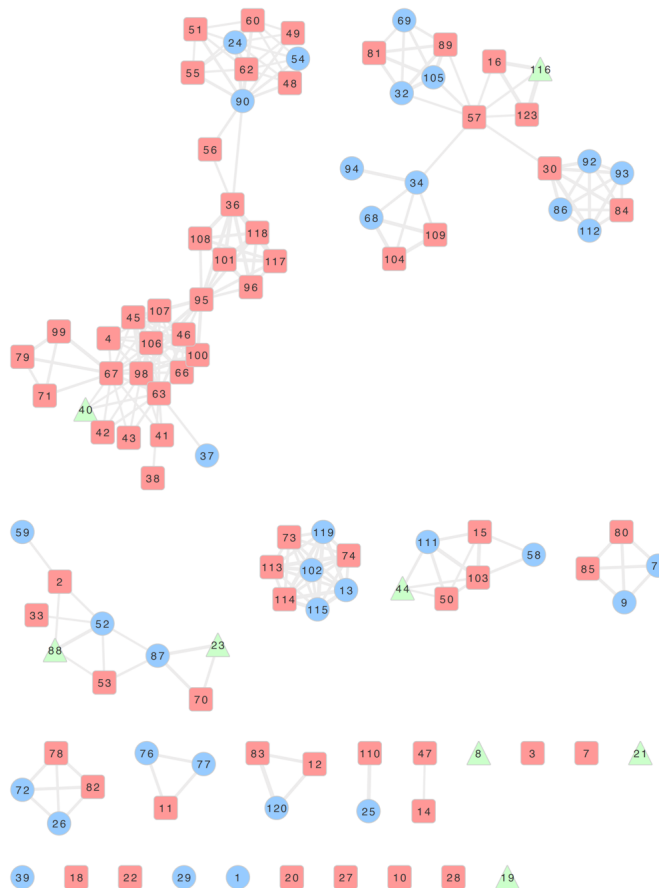
- | | | |
|---|---|---|
| 1: GPI anchor biosynthesis | 22: phloem or xylem histogenesis | 42: potassium ion transmembrane transport |
| 2: metabolism | 23: regulation of cyclin-dependent protein serine/threonine kinase activity | 43: protein peptidyl-prolyl isomerization |
| 3: superoxide metabolism | 24: regulation of systemic acquired resistance | 44: lipid transport |
| 4: cytokinin metabolism | 25: RNA processing | 45: transport |
| 5: tryptophan biosynthesis | 26: vacuolar transport | 46: regulation of transcription, DNA-templated |
| 6: cytokinin biosynthesis | 27: pollen tube growth | 47: carotenoid biosynthesis |
| 7: polarity specification of adaxial/abaxial axis | 28: xylan biosynthesis | 48: telomere maintenance |
| 8: carbohydrate metabolism | 29: aging | 49: nucleotide-sugar transport |
| 9: drug transmembrane transport | 30: response to abscisic acid | 50: thiamine diphosphate biosynthesis |
| 10: biosynthesis | 31: cellular glucose homeostasis | 51: salicylic acid metabolism |
| 11: positive regulation of cell proliferation | 32: basic amino acid transport | 52: base-excision repair |
| 12: nuclear-transcribed mRNA poly(A) tail shortening | 33: response to insect | 53: 'de novo' IMP biosynthesis |
| 13: tRNA wobble position uridine thiolation | 34: deoxyribonucleoside diphosphate metabolism | 54: defense response to fungus |
| 14: microtubule-based process | 35: response to oxidative stress | 55: sucrose metabolism |
| 15: response to salt stress | 36: cellular amino acid metabolism | 56: Mo-molybdopterin cofactor biosynthesis |
| 16: peptidyl-lysine modification to peptidyl-hypusine | 37: response to cadmium ion | 57: protein glycosylation |
| 17: RNA-directed DNA methylation | 38: defense response to oomycetes | 58: cellular iron ion homeostasis |
| 18: DNA-templated transcription, initiation | 39: arginine catabolism | 59: nucleotide-sugar biosynthesis |
| 19: phosphorelay signal transduction system | 40: glutamine metabolism | 60: negative regulation of transcription, DNA-templated |
| 20: proteolysis | 41: translational initiation | |
| 21: lipid metabolism | | |

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D]

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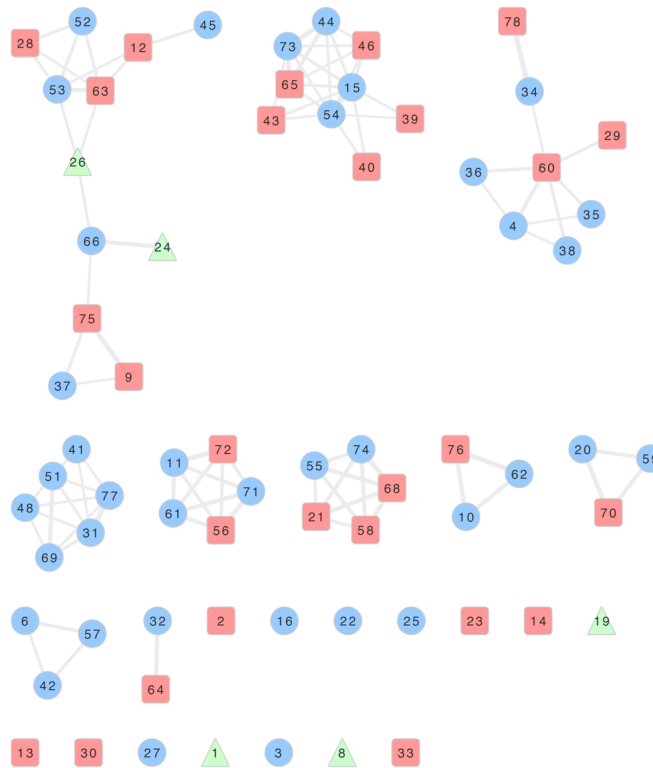
- 1: transcription factor activity, sequence-specific DNA binding
- 2: translation initiation factor activity
- 3: catalytic activity
- 4: pyruvate dehydrogenase (acetyl-transferring) activity
- 5: oxidoreductase activity, acting on the aldehyde or oxo group of donors, NAD or NADP as acceptor
- 6: oxoglutarate dehydrogenase (succinyl-transferring) activity
- 7: structural molecule activity
- 8: transporter activity
- 9: RNA ligase (ATP) activity
- 10: tocopherol cyclase activity
- 11: 5-methyltetrahydropteroyltriglutamate-homocysteine S-methyltransferase activity
- 12: inositol-3-phosphate synthase activity
- 13: glyoxalase III activity
- 14: protein dimerization activity
- 15: copper ion binding
- 16: serine-type carboxypeptidase activity
- 17: serine-type peptidase activity
- 18: deaminase activity
- 19: oxidoreductase activity
- 20: steroid binding
- 21: hydrolase activity
- 22: supercoiled DNA binding
- 23: GTP binding
- 24: DNA-directed 5'-3' RNA polymerase activity
- 25: glutaminase activity
- 26: adenine phosphoribosyltransferase activity
- 27: protein prenyltransferase activity
- 28: profilin binding
- 29: MAP-kinase scaffold activity
- 30: polygalacturonase activity
- 31: hydrolase activity, hydrolyzing O-glycosyl compounds
- 32: microtubule motor activity
- 33: core promoter binding
- 34: protein serine/threonine phosphatase activity
- 35: phosphoprotein phosphatase activity
- 36: transferase activity, transferring acyl groups other than amino-acyl groups
- 37: homogentisate 1,2-dioxygenase activity
- 38: L-aspartate oxidase activity
- 39: ubiquitin binding
- 40: NADPH-hemoprotein reductase activity
- 41: ribonucleoside-diphosphate reductase activity, thioredoxin disulfide as acceptor
- 42: 4-hydroxy-tetrahydrodipicolinate reductase
- 43: thiol oxidase activity
- 44: magnesium ion binding
- 45: UDP-glucose 6-dehydrogenase activity
- 46: alternative oxidase activity
- 47: protein domain specific binding
- 48: glycerol kinase activity
- 49: thymidylate kinase activity
- 50: calcium ion binding
- 51: inositol-1,4,5-trisphosphate 3-kinase activity
- 52: DNA binding
- 53: nucleic acid binding
- 54: diacylglycerol cholinephosphotransferase activity
- 55: aspartate kinase activity
- 56: transferase activity, transferring glycosyl groups
- 57: hydrolase activity, acting on ester bonds
- 58: molybdenum ion binding
- 59: mRNA 3'-UTR binding
- 60: ribokinase activity
- 61: 6-phosphofructokinase activity
- 62: 1-phosphatidylinositol 4-kinase activity
- 63: peroxidase activity
- 64: catalase activity
- 65: thioredoxin-disulfide reductase activity
- 66: squalene monooxygenase activity
- 67: cytochrome-c oxidase activity
- 68: pectin acetyltransferase activity
- 69: acylphosphatase activity
- 70: ADP binding
- 71: auxin influx transmembrane transporter activity
- 72: galactoside 2-alpha-L-fucosyltransferase activity
- 73: N6-(1,2-dicarboxyethyl)AMP AMP-lyase (fumarate-forming) activity
- 74: uroporphyrinogen decarboxylase activity
- 75: adenylosuccinate synthase activity
- 76: 3-methyl-2-oxobutanoate hydroxymethyltransferase activity
- 77: protein-L-isoaspartate (D-aspartate) O-methyltransferase activity
- 78: alpha-1,2-mannosyltransferase activity
- 79: allantoin uptake transmembrane transporter activity
- 80: NEDD8 activating enzyme activity
- 81: DNA clamp loader activity
- 82: galactosylgalactosylxyloprotein 3-beta-glucuronosyltransferase activity
- 83: glucose-6-phosphate isomerase activity
- 84: alpha,alpha-trehalase activity
- 85: threonine-tRNA ligase activity
- 86: poly(ADP-ribose) glycohydrolase activity
- 87: nucleotide binding
- 88: RNA binding
- 89: DNA helicase activity
- 90: protein serine/threonine kinase activity
- 91: protein kinase activity
- 92: alpha-L-fucosidase activity
- 93: beta-N-acetylhexosaminidase activity
- 94: histidinol-phosphatase activity
- 95: 3-oxoacyl-[acyl-carrier-protein] reductase (NADPH) activity
- 96: hydroxymethylglutaryl-CoA synthase activity
- 97: citrate (Si)-synthase activity
- 98: D-arabinono-1,4-lactone oxidase activity
- 99: iron ion transmembrane transporter activity
- 100: 3-hydroxyacyl-CoA dehydrogenase activity
- 101: acetyl-CoA C-acetyltransferase activity
- 102: dihydroonepterin aldolase activity
- 103: zinc ion binding
- 104: phospholipase A2 activity
- 105: GTPase activity
- 106: glycerol-3-phosphate dehydrogenase [NAD+] activity
- 107: isocitrate dehydrogenase (NAD+) activity
- 108: gamma-glutamyltransferase activity
- 109: aminoacyl-tRNA editing activity
- 110: asparaginase activity
- 111: metal ion binding
- 112: beta-galactosidase activity
- 113: diphosphomevalonate decarboxylase activity
- 114: fumarate hydratase activity
- 115: 4-hydroxy-tetrahydrodipicolinate synthase
- 116: aspartic-type endopeptidase activity
- 117: dihydroilpoillysine-residue acetyltransferase activity
- 118: peptide alpha-N-acetyltransferase activity
- 119: tryptophan synthase activity
- 120: dodecenoyl-CoA delta-isomerase activity
- 121: protein disulfide isomerase activity
- 122: isopentenyl-diphosphate delta-isomerase activity
- 123: metalloendopeptidase activity



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E]

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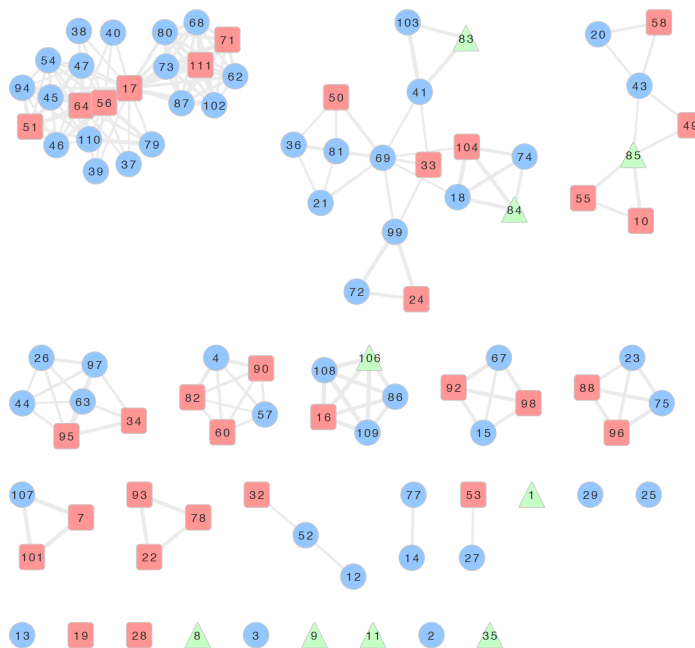


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|--|---|--|
| 1: transcription factor activity, sequence-specific DNA binding | 27: palmitoyl hydrolase activity | 53: DNA binding |
| 2: structural constituent of ribosome | 28: single-stranded DNA binding | 54: N,N-dimethylaniline monooxygenase activity |
| 3: catalytic activity | 29: ubiquitin-protein transferase activity | 55: galactoside 2-alpha-L-fucosyltransferase activity |
| 4: ribokinase activity | 30: DNA helicase activity | 56: dihydropyrimidin aldolase activity |
| 5: galactokinase activity | 31: protein serine/threonine phosphatase activity | 57: magnesium ion transmembrane transporter activity |
| 6: intracellular cAMP activated cation channel activity | 32: polygalacturonase activity | 58: galactosylgalactosylxylosylprotein 3-beta-glucuronosyltransferase activity |
| 7: ionotropic glutamate receptor activity | 33: heat shock protein binding | 59: tRNA methyltransferase activity |
| 8: binding | 34: glutathione transferase activity | 60: protein kinase activity |
| 9: iron ion binding | 35: phosphomevalonate kinase activity | 61: carbon-sulfur lyase activity |
| 10: chorismate mutase activity | 36: phosphatidate cytidyltransferase activity | 62: UDP-glucose 4-epimerase activity |
| 11: glyoxalase III activity | 37: magnesium ion binding | 63: RNA binding |
| 12: translation initiation factor activity | 38: riboflavin kinase activity | 64: beta-N-acetylhexosaminidase activity |
| 13: threonine-tRNA ligase activity | 39: dihydroorotate dehydrogenase activity | 65: long-chain-alcohol oxidase activity |
| 14: protein dimerization activity | 40: succinate-semialdehyde dehydrogenase [NAD(P)+] activity | 66: ATP binding |
| 15: peroxidase activity | 41: single-stranded DNA 5'-3' exodeoxyribonuclease activity | 67: nucleotide binding |
| 16: serine-type carboxypeptidase activity | 42: inorganic phosphate transmembrane transporter activity | 68: cellulose synthase (UDP-forming) activity |
| 17: serine-type endopeptidase activity | 43: methylenetetrahydrofolate reductase (NAD(P)H) activity | 69: aminoacyl-tRNA hydrolase activity |
| 18: omega peptidase activity | 44: 3-isopropylmalate dehydrogenase activity | 70: phosphoethanolamine N-methyltransferase activity |
| 19: oxidoreductase activity | 45: double-stranded RNA binding | 71: glutamate decarboxylase activity |
| 20: phosphatidyl-N-methylethanolamine N-methyltransferase activity | 46: peptide-methionine (S)-S-oxide reductase activity | 72: 4-hydroxy-tetrahydrodipicolinate synthase |
| 21: dolichyl-phosphate-glucose-glycolipid alpha-glucosyltransferase activity | 47: peptide-methionine (R)-S-oxide reductase activity | 73: phosphogluconate dehydrogenase (decarboxylating) activity |
| 22: transketolase activity | 48: tRNA-intron endonuclease activity | 74: glycogen (starch) synthase activity |
| 23: thiosulfate sulfurtransferase activity | 49: 3'-5'-exoribonuclease activity | 75: zinc ion binding |
| 24: GTP binding | 50: ribonuclease III activity | 76: intramolecular transferase activity |
| 25: profilin binding | 51: methyl jasmonate esterase activity | 77: nucleotidase activity |
| 26: nucleic acid binding | 52: double-stranded DNA binding | 78: methionine adenosyltransferase activity |

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F]

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|---|--|--|
| 1: transcription factor activity, sequence-specific DNA binding | 42: acetyl-CoA:L-glutamate N-acetyltransferase activity | 77: ribose-5-phosphate isomerase activity |
| 2: transcription corepressor activity | 43: RNA binding | 78: beta-ureidopropionase activity |
| 3: catalytic activity | 44: magnesium ion binding | 79: nitronate monooxygenase activity |
| 4: acid phosphatase activity | 45: NADPH-hemoprotein reductase activity | 80: ammonium transmembrane transporter activity |
| 5: phosphoprotein phosphatase activity | 46: ribonucleoside-diphosphate reductase activity, thioredoxin disulfide as acceptor | 81: NAD+ kinase activity |
| 6: protein serine/threonine phosphatase activity | 47: protochlorophyllide reductase activity | 82: histidinol-phosphatase activity |
| 7: GDP-dissociation inhibitor activity | 48: 4-hydroxy-tetrahydrodipicolinate reductase | 83: arginyltransferase activity |
| 8: transporter activity | 49: nucleic acid binding | 84: 3-methyl-2-oxobutanoate hydroxymethyltransferase activity |
| 9: binding | 50: pantothenate kinase activity | 85: nucleotide binding |
| 10: GTP binding | 51: peptide-methionine (S)-S-oxide reductase activity | 86: glutamate-ammonia ligase activity |
| 11: electron carrier activity | 52: protein dimerization activity | 87: inorganic phosphate transmembrane transporter activity |
| 12: protein heterodimerization activity | 53: double-stranded RNA binding | 88: alpha-amylase activity |
| 13: tocopherol cyclase activity | 54: alternative oxidase activity | 89: beta-amylase activity |
| 14: inositol-3-phosphate synthase activity | 55: NAD binding | 90: phosphatidylinositol phospholipase C activity |
| 15: glyoxalase III activity | 56: N,N-dimethylaniline monooxygenase activity | 91: phospholipase D activity |
| 16: threonine-tRNA ligase activity | 57: pectin acetyltransferase activity | 92: adenosylmethionine decarboxylase activity |
| 17: cytochrome-c oxidase activity | 58: transcription regulatory region sequence-specific DNA binding | 93: asparaginase activity |
| 18: O-methyltransferase activity | 59: core promoter proximal region sequence-specific DNA binding | 94: thiol oxidase activity |
| 19: oxidoreductase activity | 60: 3'-5'-exoribonuclease activity | 95: zinc ion binding |
| 20: single-stranded DNA binding | 61: ribonuclease III activity | 96: chitinase activity |
| 21: thymidylate kinase activity | 62: UDP-galactose transmembrane transporter activity | 97: metal ion binding |
| 22: AMP deaminase activity | 63: copper ion binding | 98: dihydroneopterin aldolase activity |
| 23: 1,2-alpha-L-fucosidase activity | 64: peroxidase activity | 99: UDP-glucosyltransferase activity |
| 24: 1,4-alpha-glucan branching enzyme activity | 65: catalase activity | 100: cellulose synthase (UDP-forming) activity |
| 25: acetolactate synthase activity | 66: superoxide dismutase activity | 101: enzyme inhibitor activity |
| 26: calcium ion binding | 67: 1,4-dihydroxy-2-naphthoyl-CoA synthase activity | 102: intracellular cAMP activated cation channel activity |
| 27: translation release factor activity | 68: voltage-gated chloride channel activity | 103: diacylglycerol O-acyltransferase activity |
| 28: Ran GTPase binding | 69: protein serine/threonine kinase activity | 104: histone-lysine N-methyltransferase activity |
| 29: serine-type endopeptidase activity | 70: protein kinase activity | 105: protein-L-isoaspartate (D-aspartate) O-methyltransferase activity |
| 30: serine-type carboxypeptidase activity | 71: protein transporter activity | 106: cysteine-tRNA ligase activity |
| 31: metalloendopeptidase activity | 72: galactoside 2-alpha-L-fucosyltransferase activity | 107: Rab GDP-dissociation inhibitor activity |
| 32: actin binding | 73: allantoin uptake transmembrane transporter activity | 108: glycine-tRNA ligase activity |
| 33: ubiquitin-protein transferase activity | 74: aspartate carbamoyltransferase activity | 109: proline-tRNA ligase activity |
| 34: manganese ion binding | 75: polygalacturonase activity | 110: acireductone dioxigenase [iron(II)-requiring] activity |
| 35: GTPase activity | 76: hydrolase activity, hydrolyzing O-glycosyl compounds | 111: potassium ion transmembrane transporter activity |
| 36: shikimate kinase activity | | 112: iron ion transmembrane transporter activity |
| 37: L-lactate dehydrogenase activity | | |
| 38: sarcosine oxidase activity | | |
| 39: formate dehydrogenase (NAD+) activity | | |
| 40: nitrite reductase [NAD(P)H] activity | | |
| 41: N-acetyltransferase activity | | |

Fig. S9. Network shared names of enriched biological processes (A, B and C) or molecular functions (D, E and F) GO term for genes showing convergence in expression between subgenomes in flowers (A and D), leaves (B and E) or roots tissues (C and F). C_o indicates a convergence of $C_{bp_{Cg}}$ toward $C_{bp_{Co}}$, and C_g corresponds to a convergence of $C_{bp_{Co}}$ toward $C_{bp_{Cg}}$.