**S4 Table. Summary of significantly enriched GO terms derived from Enrichment Maps for each comparison and tissue.** Significantly enriched GO terms are displayed by hypothesis, species and tissue in decreasing order of Normalized enrichment score (NES). Within each contrast, the numbers of significantly enriched GO terms and the direction of enrichment are indicated (enriched G1/enriched G2) together with the number of connections between GO terms in each direction produced by Cytoscape (positive/negative) and the location of the enrichment map within S2 Fig. MF, CC, BP indicate which category each enriched GO term belongs to (molecular function, cellular component, biological process) and the number after that indicates how many genes are in that set. Numbers in brackets after each GO term indicate values of (NES) and false discovery rate q-value (FDR).

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Hypothesis |  | Head | Abdomen | Immature |
| Legume vs. Other | # of enriched GO terms | 12 (7/5) | 27(10,17) | 18(0/18) |
| Enriched # of connections | 5/4 (S2 ia) | 6/20 (S2 ib) | 0/33 (S2 ic) |
| Positively enriched in G1, relative to G2: GO terms | GO\_0000786\_NUCLEOSOME: CC, 24 [2.77; 0]  GO\_0003735\_STRUCTURAL CONSTITUENT OF RIBOSOME: MF, 127 [2.58; 0]  GO\_0006412\_TRANSLATION: BP, 130 [2.51; 0]  GO\_0006334\_NUCLEOSOME ASSEMBLY: BP, 18 [2.34; 0.001]  GO\_0005840\_RIBOSOME: CC, 140 [2.25; 0.002]  GO\_0004523\_RNA-DNA HYBRID RIBONUCLEASE ACTIVITY: MF, 95 [2.10; 0.01]  GO\_0005328\_NEUROTRANSMITTER\_SODIUM SYMPORTER ACTIVITY: MF, 13 [2.10; 0.01] | GO\_0006412\_TRANSLATION: BP, 130 [2.10; 0]  GO\_0003735\_STRUCTURAL CONSTITUENT OF RIBOSOME: MF, 127 [2.10; 0]  GO\_0005840\_RIBOSOME: CC, 140 [2.04; 2.71E-04]  GO\_0005730\_NUCLEOLUS: CC, 21 [1.93; 0.003]  GO\_0006030\_CHITIN METABOLIC PROCESS: BP, 68 [1.77; 0.04]  GO\_0000786\_NUCLEOSOME: CC, 24 [1.76; 0.03]  GO\_0000166\_NUCLEOTIDE BINDING: MF, 182 [1.75; 0.03]  GO\_0000079\_REGULATION OF CYCLIN-DEPENDENT PROTEIN SERINE\_THREONINE KINASE ACTIVITY: BP, 14 [1.75; 0.03]  GO\_0008061\_CHITIN BINDING: MF, 76 [1.75; 0.03]  GO\_0015934\_LARGE RIBOSOMAL SUBUNIT: CC, 10 [1.70; 0.04] | N/A |
| Negatively enriched in G1, relative to G2: GO terms | GO\_0030599\_PECTINESTERASE ACTIVITY: MF, 29 [-2.07; 0]  GO\_0045330\_ASPARTYL ESTERASE ACTIVITY: MF, 29 [-2.06; 0]  GO\_0004650\_POLYGALACTURONASE ACTIVITY: MF, 33 [-2.04; 0]  GO\_0045735\_NUTRIENT RESERVOIR ACTIVITY: MF, 18 [-1.93; 6.28 E-04]  GO\_0005319\_LIPID TRANSPORTER ACTIVITY: MF, 35 [-1.73; 0.04] | GO\_0004650\_POLYGALACTURONASE ACTIVITY: MF, 33 [-3.20; 0]  GO\_0045735\_NUTRIENT RESERVOIR ACTIVITY: MF, 18 [-2.87; 0]  GO\_0045330\_ASPARTYL ESTERASE ACTIVITY: MF, 29 [-2.79; 0]  GO\_0030599\_PECTINESTERASE ACTIVITY: MF, 29 [-2.79; 0]  GO\_0005319\_LIPID TRANSPORTER ACTIVITY: MF, 35 [-2.60; 0]  GO\_0050790\_REGULATION OF CATALYTIC ACTIVITY: BP, 39 [-2.54; 0]  GO\_0004197\_CYSTEINE-TYPE ENDOPEPTIDASE ACTIVITY: MF, 50 [-2.52; 0]  GO\_0004566\_BETA-GLUCURONIDASE ACTIVITY: BP, 23 [-2.49; 0]  GO\_0005975\_CARBOHYDRATE METABOLIC PROCESS: BP, 369 [-2.47; 0]  GO\_0004497\_MONOOXYGENASE ACTIVITY: MF, 269 [-2.40; 1.15E-04]  GO\_0020037\_HEME BINDING: MF, 309 [-2.31; 5.43E-04]  GO\_0016491\_OXIDOREDUCTASE ACTIVITY: MF, [-2.31; 5.07E-04]  GO\_0005506\_IRON ION BINDING: MF, [-2.29; 6.79E-04]  GO\_0016787\_HYDROLASE ACTIVITY: MF, [-2.40; 1.15E-04]  GO\_0016705\_OXIDOREDUCTASE ACTIVITY, ACTING ON PAIRED DONORS, WITH INCORPORATION OR REDUCTION OF MOLECULAR OXYGEN: MF, 269 [-2.31; 1.15E-04]  GO\_0005576\_EXTRACELLULAR REGION: CC, 256 [-2.01; 0.009]  GO\_0016772\_TRANSFERASE ACTIVITY, TRANSFERRING PHOSPHORUS-CONTAINING GROUPS MF, 192 [-2.17; 0.002] | GO\_0006030\_CHITIN METABOLIC PROCESS: BP, 57 [-2.28; 0]  GO\_0005975\_CARBOHYDRATE METABOLIC PROCESS: BP, 424 [-2.24; 0]  GO\_0008061\_CHITIN BINDING: MF, 87 [-2.24; 0]  GO\_0004197\_CYSTEINE-TYPE ENDOPEPTIDASE ACTIVITY: MF, 53 [-2.21; 0]  GO\_0005576\_EXTRACELLULAR REGION: CC, 287 [-2.21; 0]  GO\_0008234\_CYSTEINE-TYPE PEPTIDASE ACTIVITY: MF, 116 [-2.15; 0]  GO\_0004553\_HYDROLASE ACTIVITY, HYDROLYZING O-GLYCOSYL COMPOUNDS: MF, 129 [ -2.14; 0]  GO\_0004252\_SERINE-TYPE ENDOPEPTIDASE ACTIVITY: MF, 307 [ -2.14; 0]  GO\_0050790\_REGULATION OF CATALYTIC ACTIVITY: BP, 42 [-2.13; 0]  GO\_0008810\_CELLULASE ACTIVITY: MF, 43 [-2.04; 0]  GO\_0016491\_OXIDOREDUCTASE ACTIVITY: MF, 436 [-1.92; 8.57E-05]  GO\_0020037\_HEME BINDING: MF, 362 [-1.67; 0.009]  GO\_0005506\_IRON ION BINDING: MF, 374 [-1.65; 0.01]  GO\_0016787\_HYDROLASE ACTIVITY: MF, 323 [-2.00; 0]  GO\_0016705\_OXIDOREDUCTASE ACTIVITY, ACTING ON PAIRED DONORS, WITH INCORPORATION OR REDUCTION OF MOLECULAR OXYGEN: MF, 313 [-1.65; 0.01]  GO\_0004497\_MONOOXYGENASE ACTIVITY: MF, 314 [-1.64; 0.01]  GO\_0016772\_TRANSFERASE ACTIVITY, TRANSFERRING PHOSPHORUS-CONTAINING GROUPS: MF, 219 [-2.19; 0.002] |
| Legume vs. Citrus | # of enriched GO terms | 13 (5/8) | 6 (6/0) | 12 (10/2) |
| Enriched # of connections | 3/4 (S2 iia) | 2/0 (S2 iib) | 7/0 (S2 iic) |
| Positively enriched in G1, relative to G2: GO terms | GO\_0003735\_STRUCTURAL CONSTITUENT OF RIBOSOME: MF, 118 [0.52; 2.13; 0.001]  GO\_0006412\_TRANSLATION: BP, 121 [2.10; 0.002]  GO\_0005840\_RIBOSOME: CC, 127 [1.99; 0.01]  GO\_0008234\_CYSTEINE-TYPE PEPTIDASE ACTIVITY: MF, 58 [1.93; 0.02]  GO\_0004129\_CYTOCHROME-C OXIDASE ACTIVITY: MF, 25 [1.91; 0.02] | GO\_0004650\_POLYGALACTURONASE ACTIVITY: MF, 29 [2.06; 0]  GO\_0008234\_CYSTEINE-TYPE PEPTIDASE ACTIVITY: MF, 32 [2.05; 0]  GO\_0050790\_REGULATION OF CATALYTIC ACTIVITY: BP, 77 [2.03; 0]  GO\_0004185\_SERINE-TYPE CARBOXYPEPTIDASE ACTIVITY: MF, 37 [1.79; 0.01]  GO\_0004197\_CYSTEINE-TYPE ENDOPEPTIDASE ACTIVITY: MF, 23 [1.79; 0.01]  GO\_0004252\_SERINE-TYPE ENDOPEPTIDASE ACTIVITY: MF, 43 [1.76; 0.02] | GO\_0006412\_TRANSLATION: BP, 144 [1.84; 0.001]  GO\_0003735\_STRUCTURAL CONSTITUENT OF RIBOSOME: MF, 141 [1.83; 0.001]  GO\_0005840\_RIBOSOME: CC, 153 [1.82; 9.15E-04]  GO\_0008061\_CHITIN BINDING: MF, 87 [1.81; 9.19E-04]  GO\_0006030\_CHITIN METABOLIC PROCESS: BP, 77 [1.76; 0.004]  GO\_0008810\_CELLULASE ACTIVITY: MF, 43 [0.69; 1.72; 0.01]  GO\_0009253\_PEPTIDOGLYCAN CATABOLIC PROCESS: BP, 23 [0.76; 1.70; 0.01]  GO\_0030245\_CELLULOSE CATABOLIC PROCESS: BP, 20 [1.68; 0.02]  GO\_0008271\_SECONDARY ACTIVE SULFATE TRANSMEMBRANE TRANSPORTER ACTIVITY: MF, 17 [1.65; 0.03]  GO\_0004348\_GLUCOSYLCERAMIDASE ACTIVITY: MF, 12 [1.63; 0.04] |
| Negatively enriched in G1, relative to G2: GO terms | GO\_0005975\_CARBOHYDRATE METABOLIC PROCESS: BP, 214 [-1.99; 0.006]  GO\_0004553\_HYDROLASE ACTIVITY, HYDROLYZING O-GLYCOSYL COMPOUNDS: MF, 64 [-1.97; 0.005]  GO\_0016829\_LYASE ACTIVITY: MF, 28 [-1.96; 0.004]  GO\_0043169\_CATION BINDING: MF, 17 [-1.82; 0.04]  GO\_0005319\_LIPID TRANSPORTER ACTIVITY: MF, 21 [-1.80; 0.04]  GO\_0016787\_HYDROLASE ACTIVITY: MF, 156 [-1.80; 0.03]  GO\_0004565\_BETA-GALACTOSIDASE ACTIVITY: MF, 14 [-1.80; 0.03]GO\_0000786\_NUCLEOSOME: CC, 16 [-1.78; 0.03] | N/A | GO\_0042302\_STRUCTURAL CONSTITUENT OF CUTICLE: MF, 68 [-2.11; 0.005]  GO\_0034993\_LINC COMPLEX: CC, 12 [-1.97; 0.02] |
| Conventional vs. Organic | # of enriched GO terms | 11 (0/11) | 18(1/17) | 2 (1/1) |
| Enriched # of connections | 0/10 (S2 iiia) | 0/19 (S2 iiib) | 0/0 (S2 iiic) |
| Positively enriched in G1, relative to G2: GO terms | N/A | GO\_0004181\_METALLOCARBOXYPEPTIDASE ACTIVITY: MF, 20 [1.87; 0.02] | GO\_0034993\_LINC COMPLEX: CC, 12 [2.02; 0.04] |
| Negatively enriched in G1, relative to G2: GO terms | GO\_0005549\_ODORANT BINDING: MF, 103 [-1.99; 0.002]  GO\_0004313\_[ACYL-CARRIER-PROTEIN] S-ACETYLTRANSFERASE ACTIVITY: MF, 25 [-1.85; 0.02]  GO\_0004316\_3-OXOACYL-[ACYL-CARRIER-PROTEIN] REDUCTASE (NADPH) ACTIVITY: MF, 25 [-1.84; 0.01]  GO\_0006412\_TRANSLATION: BP, 144 [-1.84; 0.01]  GO\_0004319\_ENOYL-[ACYL-CARRIER-PROTEIN] REDUCTASE (NADPH, B-SPECIFIC) ACTIVITY: MF, 25 [-1.83; 0.01]  GO\_0016296\_PALMITOYL-[ACYL-CARRIER-PROTEIN] HYDROLASE ACTIVITY: MF, 25 [-1.83; 0.01]  GO\_0003735\_STRUCTURAL CONSTITUENT OF RIBOSOME: MF, 141 [-1.83; 0.01]  GO\_0004317\_3-HYDROXYPALMITOYL-[ACYL-CARRIER-PROTEIN] DEHYDRATASE ACTIVITY: MF, 25 [-1.82; 0.01]  GO\_0016295\_MYRISTOYL-[ACYL-CARRIER-PROTEIN] HYDROLASE ACTIVITY: MF, 25 [-1.82; 0.01]  GO\_0004320\_OLEOYL-[ACYL-CARRIER-PROTEIN] HYDROLASE ACTIVITY: MF, 25 [-1.82; 0.009]  GO\_0005840\_RIBOSOME: CC, 153 [-1.80; 0.01] | GO\_0016491\_OXIDOREDUCTASE ACTIVITY: MF, 436 [-2.38; 0]  GO\_0008234\_CYSTEINE-TYPE PEPTIDASE ACTIVITY: MF, 116 [-2.36; 0]  GO\_0050790\_REGULATION OF CATALYTIC ACTIVITY: BP, 42 [-2.36; 0]  GO\_0004197\_CYSTEINE-TYPE ENDOPEPTIDASE ACTIVITY: MF, 53 [-2.34; 0]  GO\_0016705\_OXIDOREDUCTASE ACTIVITY, ACTING ON PAIRED DONORS, WITH INCORPORATION OR REDUCTION OF MOLECULAR OXYGEN: MF, 313 [-2.29; 0]  GO\_0004497\_MONOOXYGENASE ACTIVITY: MF, 314 [-2.26; 0]  GO\_0016772\_TRANSFERASE ACTIVITY, TRANSFERRING PHOSPHORUS-CONTAINING GROUPS: MF, 219 [-2.23; 0]  GO\_0005975\_CARBOHYDRATE METABOLIC PROCESS: BP, 424 [-2.23; 0]  GO\_0008810\_CELLULASE ACTIVITY: MF, 43 [-2.22; 0]  GO\_0005506\_IRON ION BINDING: MF, 374 [-2.19; 0]  GO\_0020037\_HEME BINDING: MF, 362 [-2.17; 0]  GO\_0004252\_SERINE-TYPE ENDOPEPTIDASE ACTIVITY: MF, 307 [-1.62; 0.03]  GO\_0042626\_ATPASE ACTIVITY, COUPLED TO TRANSMEMBRANE MOVEMENT OF SUBSTANCES: MF, 189 [-1.81; 0.002]  GO\_0016758\_TRANSFERASE ACTIVITY, TRANSFERRING HEXOSYL GROUPS: MF, 144 [-1.96; 1.63E-04]  GO\_0030246\_CARBOHYDRATE BINDING: MF, 145 [-2.06; 0]  GO\_0004553\_HYDROLASE ACTIVITY, HYDROLYZING O-GLYCOSYL COMPOUNDS: MF, 129 [-2.17; 0]  GO\_0008234\_CYSTEINE-TYPE PEPTIDASE ACTIVITY: MF, 116 [-2.36; 0] | GO\_0030245\_CELLULOSE CATABOLIC PROCESS: BP, 20 [-1.68; 0.048] |
| Switch vs. Maintain | # of enriched GO terms | 4 (4/0) | 25(15/10) | N/A |
| Enriched # of connections | 2/0 | 15/6 | N/A |
| Positively enriched in G1, relative to G2: GO terms | GO\_0004650\_POLYGALACTURONASE ACTIVITY: MF, 39 [1.97; 0]  GO\_0030599\_PECTINESTERASE ACTIVITY: MF, 30 [1.94; 0]  GO\_0045330\_ASPARTYL ESTERASE ACTIVITY: MF, 30 [1.90; 0]  GO\_0044822\_POLY(A) RNA BINDING: MF, 17 [1.62; 0.02] | GO\_0004650\_POLYGALACTURONASE ACTIVITY: MF, 39 [2.49; 0]  GO\_0008234\_CYSTEINE-TYPE PEPTIDASE ACTIVITY: MF, 116 [2.41; 0]  GO\_0004197\_CYSTEINE-TYPE ENDOPEPTIDASE ACTIVITY: MF, 53 [2.32; 0]GO\_0005975\_CARBOHYDRATE METABOLIC PROCESS: BP, 424 [2.31; 0]  GO\_0050790\_REGULATION OF CATALYTIC ACTIVITY: BP, 42 [2.29; 0]  GO\_0030599\_PECTINESTERASE ACTIVITY: MF, 30 [2.23; 0]  GO\_0045330\_ASPARTYL ESTERASE ACTIVITY: MF, 30 [2.21; 0]  GO\_0016829\_LYASE ACTIVITY: MF, 47 [2.15; 0]  GO\_0008810\_CELLULASE ACTIVITY: MF, 43 [2.09; 0]  GO\_0016787\_HYDROLASE ACTIVITY: MF, 323 [2.01; 0]  GO\_0016491\_OXIDOREDUCTASE ACTIVITY: MF, 436 [1.93; 1.50E-04]  GO\_0005576\_EXTRACELLULAR REGION: CC, 287 [1.65; 0.03]  GO\_0030246\_CARBOHYDRATE BINDING: MF, 145 [1.87; 7.85E-04]  GO\_0008643\_CARBOHYDRATE TRANSPORT: BP, 72 [1.61; 0.046]  GO\_0022891\_SUBSTRATE-SPECIFIC TRANSMEMBRANE TRANSPORTER ACTIVITY: MF, 69 [1.73; 0.01] | N/A |
| Negatively enriched in G1, relative to G2: GO terms | N/A | GO\_0008061\_CHITIN BINDING: MF, 87 [-2.24; 0]  GO\_0004181\_METALLOCARBOXYPEPTIDASE ACTIVITY: MF, 20 [-2.12; 7.32E-04]  GO\_0006030\_CHITIN METABOLIC PROCESS: BP, 77 [-2.10; 4.88E-04]  GO\_0005319\_LIPID TRANSPORTER ACTIVITY: MF, 38 [-1.94; 0.007]  GO\_0003993\_ACID PHOSPHATASE ACTIVITY: MF, 44 [-1.87; 0.02]  GO\_0006357\_REGULATION OF TRANSCRIPTION FROM RNA POLYMERASE II PROMOTER: BP, 22 [-1.85; 0.02]  GO\_0045735\_NUTRIENT RESERVOIR ACTIVITY: MF, 19 [-1.86; 0.03]  GO\_0004177\_AMINOPEPTIDASE ACTIVITY: MF, 65 [-1.82; 0.03]  GO\_0004697\_PROTEIN KINASE C ACTIVITY: MF, 17 [-1.80; 0.04]  GO\_0008237\_METALLOPEPTIDASE ACTIVITY: MF, 73 [-1.79; 0.04] | N/A |