Table 5. Pathways coregulated with *CESA1*, *3*, and *6* and *CESA4*, *7*, and *8*.

🟥 Positively coregulated pathways

🟦 Negatively coregulated pathways

Pathways coregulated with *CESA1*, *3*, and *6*.

Pathway name	**Congruence score**
Cellulose biosynthesis	76.32
Brassinosteroid biosynthesis	19.12
Homogalacturonan degradation	15.73
Gluconeogenesis	8.933
Aerobic glycerol catabolism	8.442
Glyceraldehyde 3-phosphate catabolism	8.366
Glycolysis	8.329
Glycolysis 4	8.306
Fatty acid biosynthesis, initial steps	8.05
Lactose degradation 3	6.804
Lactose degradation 2	6.782
Serine-isocitrate lyase pathway	6.281
Galactose, galactoside and glucose catabolism	5.852
Llactose degradation 4	5.649
Lipases pathway	4.958
Phytoalexin biosynthesis	4.717
Llignin biosynthesis	3.562
Ethylene biosynthesis from methionine	3.385
Sulfur assimilation	3.354
Methionine biosynthesis from homoserine	3.317
Epicuticular wax biosynthesis	2.856
Formation from methanol	2.603
Suberin biosynthesis	2.446
Carbon monoxide dehydrogenase pathway	2.343
Jasmonic acid biosynthesis	2.28
Lipoxygenase pathway	2.145
Flavonoid biosynthesis	1.861
Phytoalexin biosynthesis	1.64
Tryptophan biosynthesis	1.543
Starch biosynthesis	1.533
Arginine spermine degradation	1.529
Ornithine spermine biosynthesis	1.527
Carnitine metabolism, coa-linked	1.479
Glutamate degradation I	1.245
Calvin cycle	1.215
Biosynthesis of chlorophyll	1.112
Starch degradation	-1.027
Lysine degradation 1	-1.047
Galactose metabolism	-1.15
Oxidative branch of the pentose phosphate pathway	-1.191
Sucrose biosynthesis	-1.269
Nucleotide metabolism	-1.332
Protocatechuate ortho-cleavage	-1.353
Catechol 'ortho'-cleavage	-1.355
Cyanate catabolism	-1.409
Glutamine biosynthesis I	-1.438
Fatty acid oxidation pathway	-1.465
Xylulose-monophosphate cycle	-1.507
Glyoxylate cycle	-1.527
Pyrimidine ribonucleotide/ribonucleoside metabolism	-1.628
Ammonium assimilation	-2.068
Anthocyanin biosynthesis	-2.491
TCA cycle, aerobic respiration	-2.548
Deoxypyrimidine nucleotide/side metabolism	-3.064
Valine degradation I	-3.091
Vitamin E biosynthesis	-3.281
Tyrosine degradation 1	-3.44
L-serine degradation	-4.283
Pantothenate and coenzyme A biosynthesis	-8.064

Pathways coregulated with *CESA4*, *7*, and *8*.

Pathway name	**Congruence score**
Cellulose biosynthesis	41.9
Homogalacturonan degradation	37.292
Flavonoid biosynthesis	16.341
Suberin biosynthesis	14.271
Lignin biosynthesis	13.774
Lactose degradation 4	11.414
Phytoalexin biosynthesis	11.182
Galactose, galactoside and glucose catabolism	11.033
Lactose degradation 3	10.68
Lactose degradation 2	10.648
Phenylpropanoid pathway, initial reactions	10.458
Methionine biosynthesis from homoserine	9.847
Dtdp-rhamnose biosynthesis	9.258
Oxidative branch of the pentose phosphate pathway	8.973
Nucleotide metabolism	8.137
Salicylic acid biosynthesis	7.892
Gluconeogenesis	7.411
Glycolysis	7.36
Glycolysis 4	7.324
Arginine spermine degradation	7.217
Ornithine spermine biosynthesis	7.207
Aerobic glycerol catabolism	6.779
Glyceraldehyde 3-phosphate catabolism	6.732
Photorespiration	6.644
Triacylglycerol degradation	5.591
Serine-isocitrate lyase pathway	5.465
Anthocyanin biosynthesis	5.449
Trna charging pathway	4.968
Ammonium assimilation	4.114
Brassinosteroid biosynthesis	3.35
Biotin biosynthesis I	3.025
Biosynthesis of Arabidopsis flavonoids	3.019
Glucosinolate biosynthesis from tryptophan	3.004
Gibberellin biosynthesis	2.762
Methionine degradation 1	2.679
Phosphatidic acid synthesis	2.643
Triacylglycerol biosynthesis	2.639
Ethylene biosynthesis from methionine	2.541
Nitrate assimilation pathway	2.33
Sucrose degradation	2.145
Phospholipid desaturation pathway	1.891
Aspartate biosynthesis and degradation	1.766
Mevalonate pathway	1.766
Asparagine degradation 1	1.761
CO2 formation from methanol	1.543
Carbon monoxide dehydrogenase pathway	1.536
Lysine degradation 1	1.461
Lysine degradation III	1.456
Tryptophan degradation III	1.451
Degradation of short-chain fatty acids	1.446
Non-oxidative branch of the pentose phosphate pathway	1.37
Sucrose biosynthesis	1.252
Trehalose biosynthesis	1.226
Sinapoyl ester biosynthesis	1.135
Pyrimidine ribonucleotide/ribonucleoside metabolism	1.121
Cysteine biosynthesis I	-1.058
Xylulose-monophosphate cycle	-1.107
Starch degradation	-1.193
TCA cycle, aerobic respiration	-1.437
Maltose catabolism	-1.573
Chorismate biosynthesis	-1.805
Leucine biosynthesis	-1.948
Glutamate degradationviii	-2.175
Arginine biosynthesis II	-2.18
Tryptophan biosynthesis	-3.11
Phenylalanine biosynthesis, Bacillus subtilis	-4.471
Tyrosine degradation 1	-5.394
Glycosylglyceride biosynthesis	-5.666
Pyridoxal 5'-phosphate salvage pathway	-6.305
Auxin biosynthesis	-8.122

Score indicates congruency (i.e., the extent of coexpression between *CESA1*, *3*, and *6* or *CESA4*, *7*, and *8* complexes and the genes in the specified pathway). The sign of the score indicates positive or negative coregulation. Pathways with scores <1 were excluded from the table.