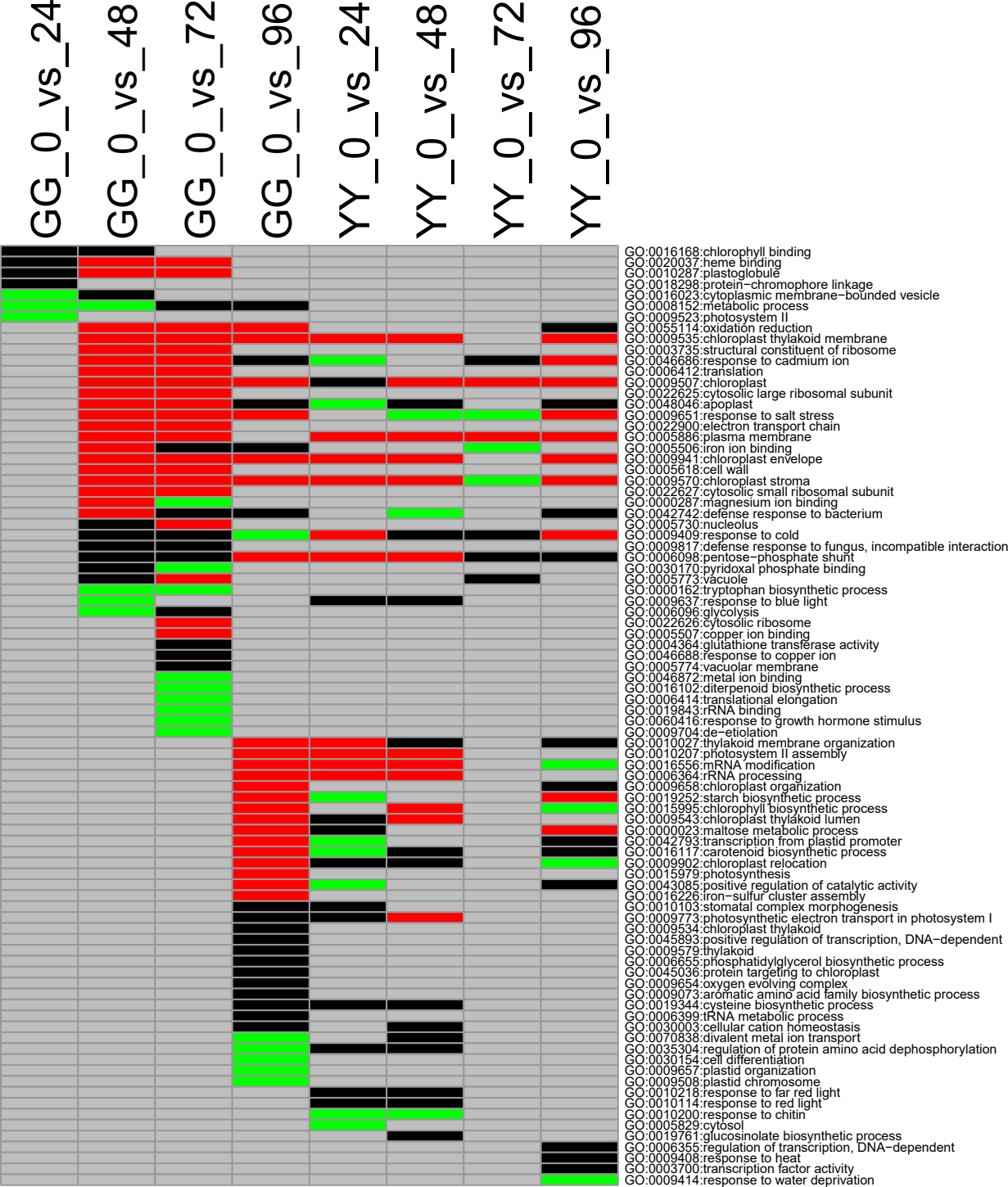
GG_0_vs_24
GG_0_vs_48
GG_0_vs_72
GG_0_vs_96
YY_0_vs_24
YY_0_vs_48
YY_0_vs_72
YY_0_vs_96
GO:0016168:chlorophyll binding
GO:0020037:heme binding
GO:0010287:plastoglobule
GO:0018298:protein−chromophore linkage
GO:0016023:cytoplasmic membrane−bounded vesicle
GO:0008152:metabolic process
GO:0009523:photosystem II
GO:0055114:oxidation reduction
GO:0009535:chloroplast thylakoid membrane
GO:0003735:structural constituent of ribosome
GO:0046686:response to cadmium ion
GO:0006412:translation
GO:0009507:chloroplast
GO:0022625:cytosolic large ribosomal subunit
GO:0048046:apoplast
GO:0009651:response to salt stress
GO:0022900:electron transport chain
GO:0005886:plasma membrane
GO:0005506:iron ion binding
GO:0009941:chloroplast envelope
GO:0005618:cell wall
GO:0009570:chloroplast stroma
GO:0022627:cytosolic small ribosomal subunit
GO:0000287:magnesium ion binding
GO:0042742:defense response to bacterium
GO:0005730:nucleolus
GO:0009409:response to cold
GO:0009817:defense response to fungus, incompatible interaction
GO:0006098:pentose−phosphate shunt
GO:0030170:pyridoxal phosphate binding
GO:0005773:vacuole
GO:0000162:tryptophan biosynthetic process
GO:0009637:response to blue light
GO:0006096:glycolysis
GO:0022626:cytosolic ribosome
GO:0005507:copper ion binding
GO:0004364:glutathione transferase activity
GO:0046688:response to copper ion
GO:0005774:vacuolar membrane
GO:0046872:metal ion binding
GO:0016102:diterpenoid biosynthetic process
GO:0006414:translational elongation
GO:0019843:rRNA binding
GO:0060416:response to growth hormone stimulus
GO:0009704:de−etiolation
GO:0010027:thylakoid membrane organization
GO:0010207:photosystem II assembly
GO:0016556:mRNA modification
GO:0006364:rRNA processing
GO:0009658:chloroplast organization
GO:0019252:starch biosynthetic process
GO:0015995:chlorophyll biosynthetic process
GO:0009543:chloroplast thylakoid lumen
GO:0000023:maltose metabolic process
GO:0042793:transcription from plastid promoter
GO:0016117:carotenoid biosynthetic process
GO:0009902:chloroplast relocation
GO:0015979:photosynthesis
GO:0043085:positive regulation of catalytic activity
GO:0016226:iron−sulfur cluster assembly
GO:0010103:stomatal complex morphogenesis
GO:0009773:photosynthetic electron transport in photosystem I
GO:0009534:chloroplast thylakoid
GO:0045893:positive regulation of transcription, DNA−dependent
GO:0009579:thylakoid
GO:0006655:phosphatidylglycerol biosynthetic process
GO:0045036:protein targeting to chloroplast
GO:0009654:oxygen evolving complex
GO:0009073:aromatic amino acid family biosynthetic process
GO:0019344:cysteine biosynthetic process
GO:0006399:tRNA metabolic process
GO:0030003:cellular cation homeostasis
GO:0070838:divalent metal ion transport
GO:0035304:regulation of protein amino acid dephosphorylation
GO:0030154:cell differentiation
GO:0009657:plastid organization
GO:0009508:plastid chromosome
GO:0010218:response to far red light
GO:0010114:response to red light
GO:0010200:response to chitin
GO:0005829:cytosol
GO:0019761:glucosinolate biosynthetic process
GO:0006355:regulation of transcription, DNA−dependent
GO:0009408:response to heat
GO:0003700:transcription factor activity
GO:0009414:response to water deprivation