GO: Day 7 WGCNA MEblack transcription, DNA-templated cellular response to manganese ion heparan sulfate 6-O-sulfotransferase activity nuclear envelope organization positive regulation of isotype switching to IgG isotypes negative regulation of inward rectifier potassium channel activity cellular response to gamma radiation DNA binding establishment of epithelial cell polarity heparan sulfate proteoglycan biosynthetic process, enzymatic modification response to organonitrogen compound voltage-gated anion channel activity gene silencing by RNA isotype switching heparan sulfate proteoglycan biosynthetic process, polysaccharide chain biosynthetic process D-xylose metabolic process cyclic-GMP-AMP binding -DNA repair mismatch repair positive regulation of response to DNA damage stimulus DNA replication-dependent nucleosome assembly cyclic-di-GMP binding cytoplasmic pattern recognition receptor signaling pathway in response to virus regulation of apoptotic process heterotrimeric G-protein complex assembly positive regulation of G2/M transition of mitotic cell cycle hyaluronan synthase activity regulation of mRNA stability regulation of intrinsic apoptotic signaling pathway positive regulation of MAP kinase activity enzyme binding peptidyl-aspartic acid hydroxylation positive regulation of protein binding intrinsic apoptotic signaling pathway in response to DNA damage positive regulation of cell cycle G2/M phase transition mRNA binding positive regulation of interleukin-1 beta production ventricular cardiac muscle tissue development response to tumor necrosis factor DNA metabolic process palmitoyltransferase activity positive regulation of proteasomal protein catabolic process cellular response to leukemia inhibitory factor protein import into nucleus NAD+ binding inositol phosphorylation neural tube patterning midbody abscission glycosaminoglycan biosynthetic process metal ion binding mRNA cis splicing, via spliceosome protein targeting to membrane limb development regulation of hemocyte proliferation protein dimerization activity positive regulation of proteasomal ubiquitin-dependent protein catabolic process negative regulation of translation ribosomal small subunit assembly phosphoprotein phosphatase activity amyloid precursor protein catabolic process spliceosomal tri-snRNP complex assembly G1/S transition of mitotic cell cycle negative regulation of epithelial cell differentiation protein kinase activity protein palmitoylation eye development regulation of growth xylulose metabolic process transferase activity myeloid cell development cellular response to exogenous dsRNA positive regulation of skeletal muscle tissue growth bicarbonate transport protein-macromolecule adaptor activity regulation of gene silencing by miRNA regulation of synaptic vesicle transport negative regulation of triglyceride biosynthetic process syntaxin-1 binding regulation of pole plasm oskar mRNA localization hepatocyte apoptotic process prostaglandin secretion response to heat ion transmembrane transporter activity, phosphorylative mechanism regulation of glucose metabolic process positive regulation of protein kinase activity regulation of exocytosis negative regulation of glial cell apoptotic process U12 snRNA binding regulation of synaptic vesicle endocytosis intracellular transport of virus dTTP biosynthetic process exodeoxyribonuclease III activity -B cell proliferation positive regulation of oocyte development protein transport mitotic centrosome separation phospholipid binding regulation of meiotic nuclear division thymidine biosynthetic process positive regulation of mRNA processing hypoglossal nerve morphogenesis tubulin binding mitotic spindle assembly caveola assembly positive regulation of RNA export from nucleus tRNA (guanine(9)–N(1))–methyltransferase activity primary palate development regulation of autophagy peptidyl-serine ADP-deribosylation negative regulation of mitotic recombination 3'(2'),5'-bisphosphate nucleotidase activity meiotic spindle midzone assembly meiotic metaphase I plate congression NAD metabolic process positive regulation of histone acetylation ADP-ribosylserine hydrolase activity mitotic cytokinesis regulation of cellular response to oxidative stress T cell homeostasis protein sumoylation zinc ion binding regulation of cellular response to heat Notch receptor processing, ligand-dependent reticulophagy protein-cysteine S-palmitoyltransferase activity dormancy process piRNA metabolic process positive regulation of protein ubiquitination microtubule severing inositol-3-phosphate synthase activity positive regulation of transcription by RNA polymerase cellular response to dopamine olfactory behavior positive regulation of cell cycle G1/S phase transition acetyltransferase activity ubiquitin-independent protein catabolic process via the multivesicular body sorting pathway regulation of cilium assembly positive regulation of mitotic cell cycle O-acetyl-ADP-ribose deacetylase activity activation of innate immune response vesicle-mediated transport basement membrane organization phosphorylation aminocarboxymuconate-semialdehyde decarboxylase activity cellular response to calcium ion regulation of T cell receptor signaling pathway regulation of dendritic spine morphogenesis regulation of heart rate by cardiac conduction inositol pentakisphosphate 2-kinase activity regulation of signal transduction by p53 class mediator negative regulation of quinolinate biosynthetic process neural precursor cell proliferation response to peptide metalloendopeptidase activity urogenital system development positive regulation of AMPA glutamate receptor clustering endosome to plasma membrane protein transport Ran GTPase binding -T cell proliferation cation transport negative regulation of myeloid cell differentiation negative regulation of Ras protein signal transduction protein phosphatase 2A binding tRNA export from nucleus lamellipodium assembly cellular response to X-ray regulation of microglial cell activation dioxygenase activity blastocyst hatching regulation of dendritic spine development nucleosome mobilization allantoinase activity reactive oxygen species metabolic process positive regulation of DNA-binding transcription factor activity cellular response to nitrosative stress non-motile cilium assembly guanine/thymine mispair binding maturation of SSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA) histone phosphorylation sphinganine biosynthetic process carnitine shuttle cullin family protein binding protein K6-linked ubiquitination lysine catabolic process bradykinin catabolic process signaling receptor complex adaptor activity viral entry into host cell positive regulation of sprouting angiogenesis negative regulation of transcription by RNA polymerase I cellular response to interleukin-1 phosphatidylinositol-3,4,5-trisphosphate 3-phosphatase activity positive regulation of keratinocyte migration myeloid cell apoptotic process syncytial blastoderm mitotic cell cycle one-carbon metabolic process death receptor binding regulation of mitochondrion organization roof of mouth development regulation of tumor necrosis factor-mediated signaling pathway peptidyl-amino acid modification G/U mismatch-specific uracil-DNA glycosylase activity positive regulation of GTPase activity protein localization to endoplasmic reticulum negative regulation of endoplasmic reticulum stress-induced intrinsic apoptotic signaling pathway DNA-dependent ATPase activity -N-glycan processing positive regulation of synapse maturation double-strand break repair via break-induced replication cellular response to heat peptidyl-histidine dioxygenase activity positive regulation of stress fiber assembly protein-DNA covalent cross-linking viral budding via host ESCRT complex cellular response to ionizing radiation peptidyl-asparagine 3-dioxygenase activity meiotic telomere clustering glycine import across plasma membrane negative regulation of Golgi to plasma membrane protein transport hypoxia-inducible factor-asparagine oxygenase activity calcineurin-NFAT signaling cascade motor neuron apoptotic process germ cell development regulation of ruffle assembly ankyrin repeat binding regulation of inner ear auditory receptor cell fate specification protein K48-linked ubiquitination fatty acid biosynthetic process peptidyl-L-cysteine S-palmitoylation cysteine-type carboxypeptidase activity regulation of DNA N-glycosylase activity mitotic spindle assembly checkpoint sphingomyelin biosynthetic process phosphatidic acid binding peptidyl-histidine hydroxylation peptidyl-asparagine hydroxylation striated muscle tissue development molting cycle, collagen and cuticulin-based cuticle translation repressor activity activation of cysteine-type endopeptidase activity involved in apoptotic process regulation of grooming behavior membrane depolarization during action potential positive regulation of JNK cascade nuclease activity adult behavior positive regulation of rRNA processing negative regulation of canonical Wnt signaling pathway ubiquitin-dependent protein binding ubiquitin-dependent protein catabolic process regulation of cellular senescence cheating during chimeric sorocarp development nuclear envelope reassembly inward rectifier potassium channel inhibitor activity protein destabilization positive regulation of cellular protein localization ATP synthesis coupled electron transport regulation of the force of heart contraction by chemical signal pyruvyltransferase activity regulation of membrane repolarization during action potential regulation of blood coagulation receptor-mediated endocytosis of virus by host cell positive regulation of gap junction assembly glycine:sodium symporter activity nitric oxide homeostasis negative regulation of peptidyl-tyrosine autophosphorylation angiotensin-activated signaling pathway involved in heart process tRNA (guanine–N1–)-methyltransferase activity maintenance of epithelial cell apical/basal polarity positive regulation of isotype switching to IgA isotypes 4,6-pyruvylated galactose residue biosynthetic process glial cell proliferation DNA-dependent protein kinase activity amyloid-beta formation positive regulation of intrinsic apoptotic signaling pathway positive regulation of heparan sulfate proteoglycan biosynthetic process male meiosis chromosome segregation ion channel binding female meiosis chromosome segregation NADP biosynthetic process defense response ATP binding regulation of fibroblast migration myelination in peripheral nervous system regulation of ecdysteroid metabolic process molting cycle, chitin-based cuticle transcription regulatory region sequence-specific DNA binding regulation of lipid storage regulation of protein stability endothelial cell-matrix adhesion DNA methylation involved in gamete generation xylose isomerase activity protein folding regulation of transcription, DNA-templated MF BP ontology ontology