

File S4

Lists of functional terms common and exclusive to each of the expression patterns shown in Figure 9

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Common and exclusive to all down regulated protective

- [1,] "GOTERM\_BP\_FAT " "energy derivation by oxidation of organic compounds "
- [2,] "GOTERM\_BP\_FAT " "cellular respiration "
- [3,] "GOTERM\_CC\_FAT " "respiratory chain "
- [4,] "GOTERM\_BP\_FAT " "electron transport chain "
- [5,] "GOTERM\_CC\_FAT " "mitochondrial respiratory chain "
- [6,] "GOTERM\_BP\_FAT " "respiratory electron transport chain "
- [7,] "GOTERM\_BP\_FAT " "ATP synthesis coupled electron transport "
- [8,] "GOTERM\_BP\_FAT " "mitochondrial ATP synthesis coupled electron transport "
- [9,] "GOTERM\_CC\_FAT " "mitochondrial membrane part "
- [10,] "GOTERM\_BP\_FAT " "mitochondrial electron transport, NADH to ubiquinone "
- [11,] "GOTERM\_CC\_FAT " "NADH dehydrogenase complex "
- [12,] "GOTERM\_CC\_FAT " "respiratory chain complex I "
- [13,] "GOTERM\_CC\_FAT " "mitochondrial respiratory chain complex I "
- [14,] "GOTERM\_MF\_FAT " "NADH dehydrogenase activity "
- [15,] "GOTERM\_MF\_FAT " "oxidoreductase activity, acting on NADH or NADPH "

- [16,] "GOTERM\_MF\_FAT " "NADH dehydrogenase (quinone) activity "
- [17,] "GOTERM\_MF\_FAT " "NADH dehydrogenase (ubiquinone) activity "
- [18,] "GOTERM\_MF\_FAT " "oxidoreductase activity, acting on NADH or NADPH, quinone or similar compound as acceptor "
- [19,] "GOTERM\_BP\_FAT " "cofactor catabolic process "
- [20,] "GOTERM\_BP\_FAT " "acetyl-CoA metabolic process "
- [21,] "GOTERM\_BP\_FAT " "tricarboxylic acid cycle "
- [22,] "GOTERM\_BP\_FAT " "acetyl-CoA catabolic process "
- [23,] "GOTERM\_BP\_FAT " "coenzyme catabolic process "
- [24,] "GOTERM\_BP\_FAT " "aerobic respiration "
- [25,] "GOTERM\_CC\_FAT " "proton-transporting ATP synthase complex "
- [26,] "GOTERM\_CC\_FAT " "mitochondrial proton-transporting ATP synthase complex "
- [27,] "GOTERM\_CC\_FAT " "proton-transporting ATP synthase complex, coupling factor F(o) "
- [28,] "GOTERM\_CC\_FAT " "mitochondrial proton-transporting ATP synthase complex, coupling factor F(o) "
- [29,] "GOTERM\_BP\_FAT " "glucose metabolic process "
- [30,] "GOTERM\_BP\_FAT " "hexose metabolic process "
- [31,] "GOTERM\_BP\_FAT " "glycolysis "
- [32,] "GOTERM\_BP\_FAT " "cellular carbohydrate catabolic process "
- [33,] "GOTERM\_BP\_FAT " "monosaccharide metabolic process "
- [34,] "GOTERM\_BP\_FAT " "carbohydrate catabolic process "
- [35,] "GOTERM\_BP\_FAT " "hexose catabolic process "
- [36,] "GOTERM\_BP\_FAT " "glucose catabolic process "

[37,] "GOTERM\_BP\_FAT " "alcohol catabolic process "

[38,] "GOTERM\_BP\_FAT " "monosaccharide catabolic process "

[39,] "GOTERM\_BP\_FAT " "regulation of cellular component size "

[40,] "GOTERM\_BP\_FAT " "cell growth "

[41,] "GOTERM\_BP\_FAT " "regulation of cell size "

[42,] "GOTERM\_BP\_FAT " "growth "

[43,] "GOTERM\_BP\_FAT " "developmental growth "

[44,] "GOTERM\_BP\_FAT " "developmental cell growth "

[45,] "GOTERM\_BP\_FAT " "protein amino acid phosphorylation "

[46,] "INTERPRO " "Protein kinase, ATP binding site "

[47,] "GOTERM\_MF\_FAT " "protein serine/threonine kinase activity "

[48,] "SMART " "S\_TKc "

[49,] "INTERPRO " "Serine/threonine protein kinase "

[50,] "SP\_PIR\_KEYWORDS " "kinase "

[51,] "SP\_PIR\_KEYWORDS " "serine/threonine-protein kinase "

[52,] "INTERPRO " "Serine/threonine protein kinase-related "

[53,] "GOTERM\_MF\_FAT " "protein kinase activity "

[54,] "INTERPRO " "Protein kinase, core "

[55,] "INTERPRO " "Serine/threonine protein kinase, active site "

[56,] "SP\_PIR\_KEYWORDS " "atp synthesis "

[57,] "GOTERM\_CC\_FAT " "mitochondrial proton-transporting ATP synthase complex, catalytic core F(1) "

[58,] "GOTERM\_CC\_FAT " "proton-transporting ATP synthase complex, catalytic core F(1) "

[59,] "SMART " "EGF "

[60,] "INTERPRO " "EGF-like "

[61,] "INTERPRO " "EGF-like, type 3 "

[62,] "SP\_PIR\_KEYWORDS " "egf-like domain "

[63,] "GOTERM\_BP\_FAT " "olfactory learning "

[64,] "GOTERM\_BP\_FAT " "learning or memory "

[65,] "GOTERM\_BP\_FAT " "chemosensory behavior "

[66,] "GOTERM\_BP\_FAT " "learning "

[67,] "GOTERM\_BP\_FAT " "olfactory behavior "

[68,] "GOTERM\_BP\_FAT " "circadian rhythm "

[69,] "GOTERM\_BP\_FAT " "rhythmic process "

[70,] "GOTERM\_BP\_FAT " "circadian behavior "

[71,] "GOTERM\_BP\_FAT " "rhythmic behavior "

[72,] "GOTERM\_BP\_FAT " "locomotor rhythm "

[73,] "GOTERM\_BP\_FAT " "epithelial tube morphogenesis "

[74,] "INTERPRO " "Pleckstrin homology-type "

[75,] "GOTERM\_BP\_FAT " "chitin-based embryonic cuticle biosynthetic process "

[76,] "GOTERM\_BP\_FAT " "cuticle development "

[77,] "GOTERM\_BP\_FAT " "chitin-based cuticle development "

[78,] "GOTERM\_BP\_FAT " "organic acid catabolic process "

[79,] "GOTERM\_BP\_FAT " "carboxylic acid catabolic process "

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Common and exclusive to all up regulated protective

[1,] "GOTERM\_MF\_FAT " "RNA polymerase activity "

[2,] "GOTERM\_MF\_FAT " "DNA-directed RNA polymerase activity "

[3,] "GOTERM\_CC\_FAT " "RNA polymerase complex "

[4,] "GOTERM\_CC\_FAT " "DNA-directed RNA polymerase complex "

[5,] "GOTERM\_CC\_FAT " "nuclear DNA-directed RNA polymerase complex "

[6,] "GOTERM\_MF\_FAT " "nucleotidyltransferase activity "

[7,] "KEGG\_PATHWAY " "RNA polymerase "

[8,] "GOTERM\_CC\_FAT " "DNA-directed RNA polymerase II, core complex "

[9,] "SP\_PIR\_KEYWORDS " "nucleotidyltransferase "

[10,] "KEGG\_PATHWAY " "Pyrimidine metabolism "

[11,] "KEGG\_PATHWAY " "Purine metabolism "

[12,] "SMART " "Sm "

[13,] "INTERPRO " "Like-Sm ribonucleoprotein, eukaryotic and archaea-type, core "

[14,] "INTERPRO " "Like-Sm ribonucleoprotein, core "

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Common and exclusive to all down regulated non-protective

None

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Common and exclusive to all up regulated non-protective

None

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Common and exclusive to all protective

None

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Common and exclusive to all non-protective

None

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Common and exclusive to all down regulated

- [1,] "GOTERM\_MF\_FAT " "ATPase activity "
- [2,] "GOTERM\_CC\_FAT " "mitochondrial part "
- [3,] "GOTERM\_CC\_FAT " "mitochondrion "
- [4,] "GOTERM\_MF\_FAT " "ATPase activity, coupled to transmembrane movement of substances "
- [5,] "GOTERM\_MF\_FAT " "ATPase activity, coupled to movement of substances "
- [6,] "GOTERM\_MF\_FAT " "hydrolase activity, acting on acid anhydrides, catalyzing transmembrane movement of substances "
- [7,] "GOTERM\_MF\_FAT " "P-P-bond-hydrolysis-driven transmembrane transporter activity "
- [8,] "GOTERM\_MF\_FAT " "primary active transmembrane transporter activity "
- [9,] "GOTERM\_BP\_FAT " "ribonucleotide biosynthetic process "
- [10,] "GOTERM\_BP\_FAT " "purine nucleoside triphosphate biosynthetic process "
- [11,] "GOTERM\_BP\_FAT " "purine ribonucleoside triphosphate biosynthetic process "
- [12,] "GOTERM\_BP\_FAT " "ribonucleotide metabolic process "
- [13,] "GOTERM\_BP\_FAT " "purine ribonucleotide biosynthetic process "
- [14,] "GOTERM\_BP\_FAT " "nucleoside triphosphate biosynthetic process "
- [15,] "GOTERM\_BP\_FAT " "ribonucleoside triphosphate biosynthetic process "
- [16,] "GOTERM\_MF\_FAT " "ATPase activity, coupled to transmembrane movement of ions, phosphorylative mechanism "
- [17,] "GOTERM\_BP\_FAT " "cation transport "
- [18,] "GOTERM\_BP\_FAT " "purine ribonucleotide metabolic process "
- [19,] "GOTERM\_BP\_FAT " "purine nucleoside triphosphate metabolic process "
- [20,] "GOTERM\_BP\_FAT " "purine ribonucleoside triphosphate metabolic process "

- [21,] "GOTERM\_BP\_FAT " "ATP biosynthetic process "
- [22,] "SP\_PIR\_KEYWORDS " "Hydrogen ion transport "
- [23,] "GOTERM\_BP\_FAT " "ribonucleoside triphosphate metabolic process "
- [24,] "GOTERM\_BP\_FAT " "nucleoside triphosphate metabolic process "
- [25,] "GOTERM\_MF\_FAT " "ATPase activity, coupled to transmembrane movement of ions "
- [26,] "GOTERM\_BP\_FAT " "ATP metabolic process "
- [27,] "GOTERM\_BP\_FAT " "ion transport "
- [28,] "GOTERM\_BP\_FAT " "purine nucleotide biosynthetic process "
- [29,] "GOTERM\_MF\_FAT " "ATPase activity, coupled "
- [30,] "GOTERM\_BP\_FAT " "purine nucleotide metabolic process "
- [31,] "GOTERM\_MF\_FAT " "hydrogen-exporting ATPase activity, phosphorylative mechanism "
- [32,] "GOTERM\_BP\_FAT " "nucleobase, nucleoside, nucleotide and nucleic acid biosynthetic process "
- [33,] "GOTERM\_BP\_FAT " "nucleobase, nucleoside and nucleotide biosynthetic process "
- [34,] "GOTERM\_BP\_FAT " "monovalent inorganic cation transport "
- [35,] "GOTERM\_BP\_FAT " "nucleotide biosynthetic process "
- [36,] "GOTERM\_BP\_FAT " "proton transport "
- [37,] "GOTERM\_BP\_FAT " "hydrogen transport "
- [38,] "GOTERM\_BP\_FAT " "ATP synthesis coupled proton transport "
- [39,] "GOTERM\_BP\_FAT " "energy coupled proton transport, down electrochemical gradient "
- [40,] "GOTERM\_BP\_FAT " "ion transmembrane transport "
- [41,] "GOTERM\_MF\_FAT " "inorganic cation transmembrane transporter activity "



- [42,] "GOTERM\_CC\_FAT " "proton-transporting two-sector ATPase complex "
- [43,] "GOTERM\_CC\_FAT " "proton-transporting two-sector ATPase complex, catalytic domain "
- [44,] "GOTERM\_MF\_FAT " "monovalent inorganic cation transmembrane transporter activity "
- [45,] "GOTERM\_MF\_FAT " "hydrogen ion transmembrane transporter activity "
- [46,] "GOTERM\_BP\_FAT " "transmembrane transport "
- [47,] "KEGG\_PATHWAY " "Oxidative phosphorylation "
- [48,] "GOTERM\_BP\_FAT " "oxidative phosphorylation "
- [49,] "GOTERM\_CC\_FAT " "proton-transporting two-sector ATPase complex, proton-transporting domain "

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Common and exclusive to all up regulated

- [1,] "GOTERM\_CC\_FAT " "nucleoplasm part "
- [2,] "GOTERM\_BP\_FAT " "transcription from RNA polymerase II promoter "
- [3,] "GOTERM\_BP\_FAT " "transcription, DNA-dependent "
- [4,] "GOTERM\_BP\_FAT " "RNA biosynthetic process "
- [5,] "GOTERM\_CC\_FAT " "nucleoplasm "
- [6,] "GOTERM\_CC\_FAT " "DNA-directed RNA polymerase II, holoenzyme "
- [7,] "GOTERM\_BP\_FAT " "transcription "
- [8,] "GOTERM\_CC\_FAT " "nuclear lumen "