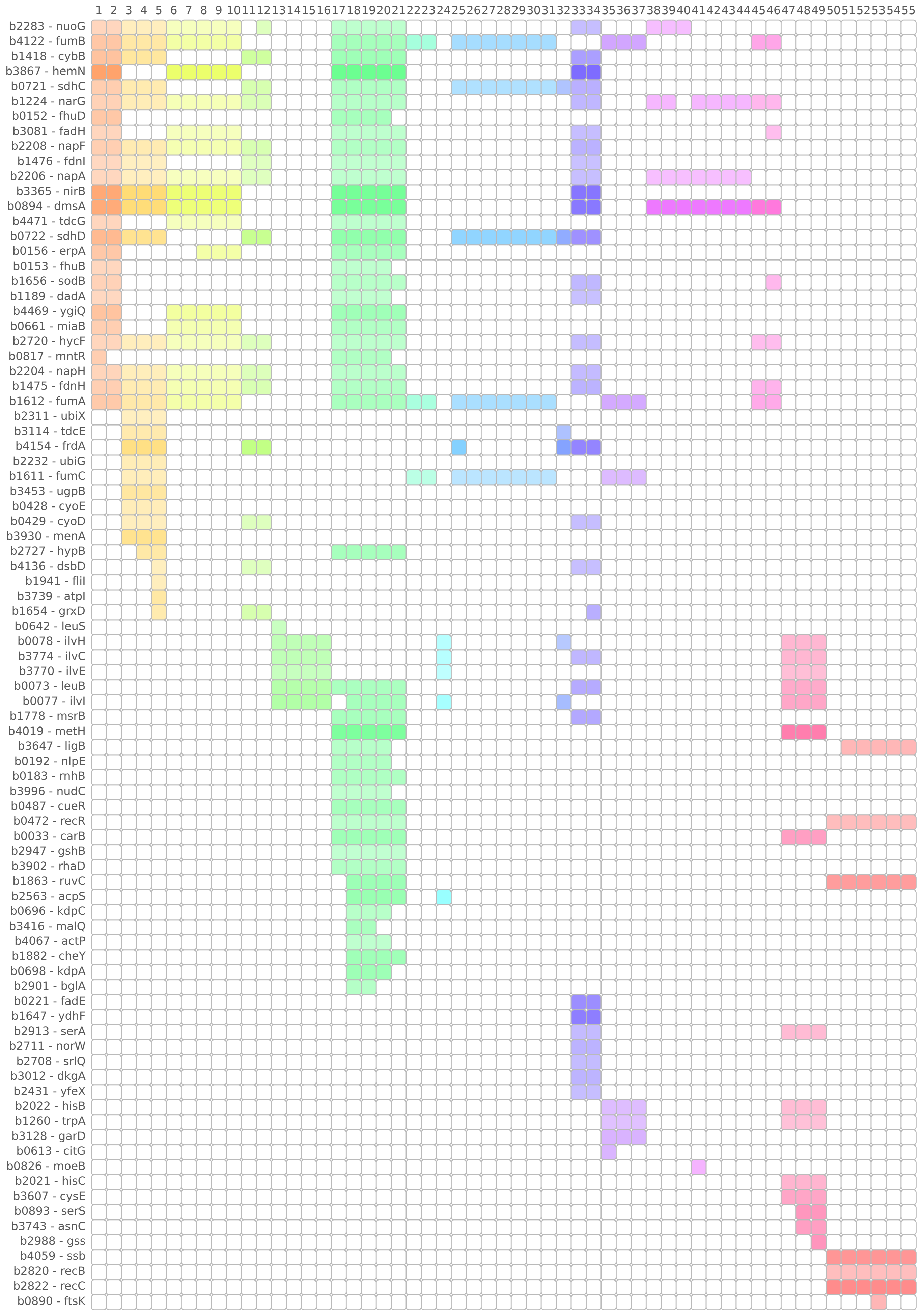

1: 2.19 GO:0005506~iron ion binding
2: 2.19 iron
3: 2.39 GO:0045333~cellular respiration
4: 2.21 GO:0015980~energy derivation by oxidation of organic compounds
5: 1.81 GO:0006091~generation of precursor metabolites and energy
6: 3.16 GO:0051539~4 iron,4 sulfur cluster binding
7: 3.17 4fe-4s
8: 2.64 iron-sulfur
9: 2.45 GO:0051536~iron-sulfur cluster binding
10: 2.45 GO:0051540~metal cluster binding
11: 2.87 electron transport
12: 2.54 GO:0022900~electron transport chain
13: 4.76 ecw00290:Valine,leucine and isoleucine biosynthesis
14: 6.21 branched-chain amino acid biosynthesis
15: 3.53 GO:0009082~branched chain family amino acid biosynthetic process
16: 3.04 GO:0009081~branched chain family amino acid metabolic process
17: 1.53 GO:0046914~transition metal ion binding
18: 1.4 GO:0043169~cation binding
19: 1.4 GO:0043167~ion binding
20: 1.37 GO:0046872~metal ion binding
21: 1.46 metal-binding
22: 18.59 GO:0004333~fumarate hydratase activity
23: 9.02 IPR000362:Fumarate lyase
24: 5.39 ecv00770:Pantothenate and CoA biosynthesis
25: 3.77 ecc00020:Citrate cycle (TCA cycle)
26: 4.05 tricarboxylic acid cycle
27: 3.39 GO:0006099~tricarboxylic acid cycle
28: 3.39 GO:0046356~acetyl-CoA catabolic process
29: 3.27 GO:0051187~cofactor catabolic process
30: 3.27 GO:0009109~coenzyme catabolic process
31: 2.85 GO:0006084~acetyl-CoA metabolic process
32: 3.62 ece00650:Butanoate metabolism
33: 1.44 oxidoreductase
34: 1.32 GO:0055114~oxidation reduction
35: 2.84 carbon-oxygen lyase
36: 3.02 hydro-lyase
37: 2.28 GO:0016836~hydro-lyase activity
38: 6.56 IPR006656:Molybdopterin oxidoreductase
39: 6.01 IPR009010:Aspartate decarboxylase-like fold
40: 10.82 IPR006963:Molybdopterin oxidoreductase Fe4S4 region
41: 4.14 Molybdenum
42: 6.01 IPR006655:Molybdopterin oxidoreductase,prokaryotic,conserved site
43: 5.41 IPR006657:Molydopterin dinucleotide-binding region
44: 2.94 GO:0030151~molybdenum ion binding
45: 3.11 iron-sulfur protein
46: 1.94 metalloprotein
47: 2.35 amino-acid biosynthesis
48: 1.3 GO:0008652~cellular amino acid biosynthetic process
49: 1.25 GO:0009309~amine biosynthetic process
50: 5.8 ecs03440:Homologous recombination
51: 1.9 DNA damage
52: 1.78 dna repair
53: 1.36 GO:0033554~cellular response to stress
54: 1.37 GO:0006281~DNA repair
55: 1.37 GO:0006974~response to DNA damage stimulus

group 1: 3.64 🟧
group 2: 3.51 🟧
group 3: 3.45 🟨
group 4: 2.91 🟩
group 5: 2.12 🟩
group 6: 2.09 🟩
group 7: 1.75 🟩
group 8: 1.60 🟦
group 9: 1.47 🟦
group 10: 1.43 🟦
group 11: 1.26 🟦
group 12: 1.25 🟪
group 13: 1.24 🟪
group 14: 1.17 🟪
group 15: 1.01 🟥
group 16: 1.01 🟥