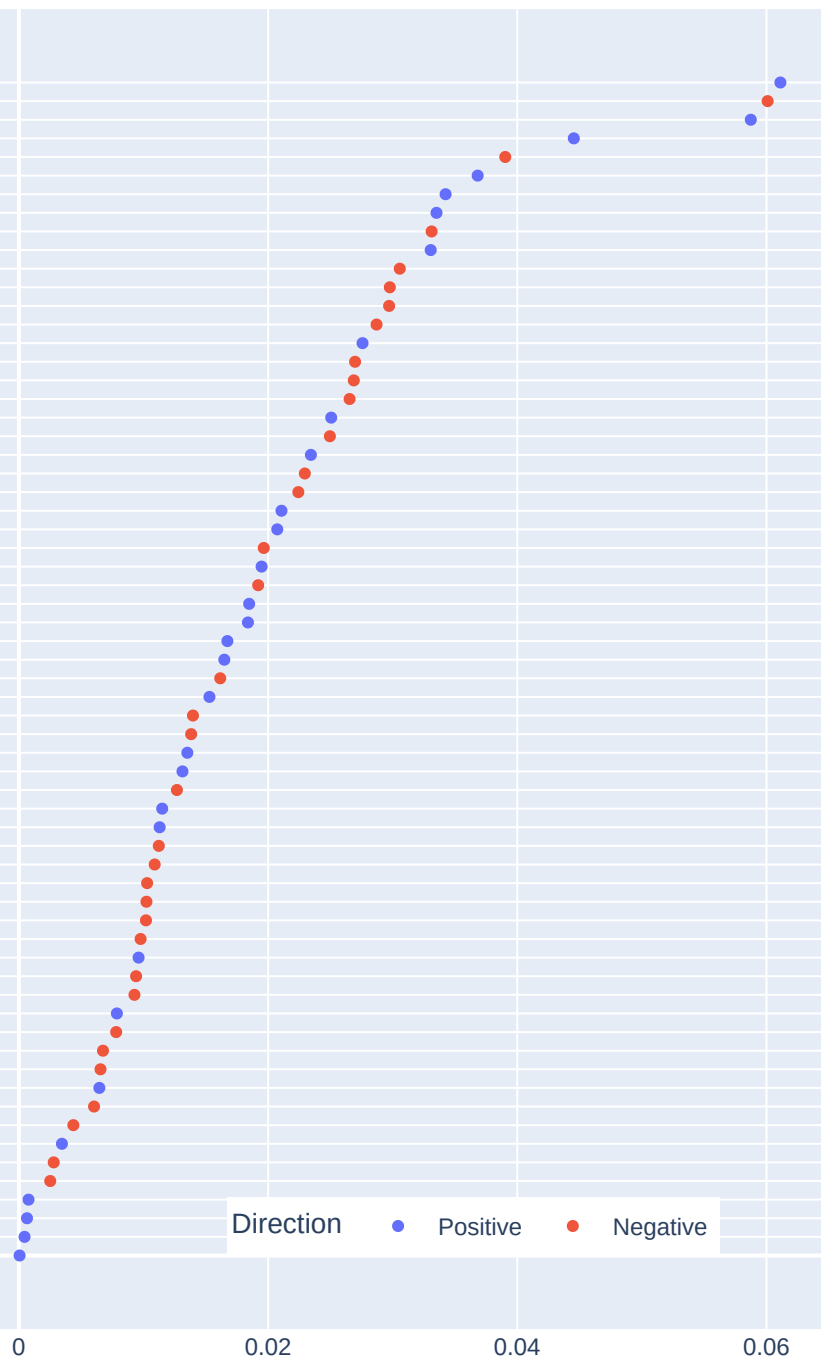


GEM: Desulfobacterota

Pathway Features

Thiamine biosynthesis
 Pantothenate/CoA biosynthesis
 Pyrimidine degradation
 Urea cycle
 Na+-translocating NADH dehydrogenase
 CRISPR-Cas system
 Na+-translocating Fd:NADH oxidoreductase
 Ribosome 30S subunit
 Translation factors
 Glycine cleavage
 Pyruvate oxidation
 Folate biosynthesis
 Cysteine biosynthesis
 Proline biosynthesis
 Pentose phosphate pathway
 Pyrimidine biosynthesis
 Phospholipid biosynthesis
 Aromatic amino acid biosynthesis
 Gluconeogenesis
 Pyrimidine salvage
 Heme biosynthesis
 Lysine biosynthesis
 FoF1-type ATP synthase
 NADH dehydrogenase
 Purine biosynthesis
 Pyridoxal phosphate biosynthesis
 Unknown
 Ribosome 50S subunit
 Glycine cleavage
 Serine biosynthesis
 Histidine biosynthesis
 Molybdopterin biosynthesis
 Glutamine biosynthesis
 Asparagine biosynthesis
 Methionine biosynthesis
 RNA polymerase
 Proline degradation
 Lysine biosynthesis
 TCA cycle
 TCA cycle
 Aminoacyl-tRNA synthetases
 Unannotated
 tRNA modification
 Isoleucine, leucine, valine biosynthesis
 NAD biosynthesis
 Ubiquinone biosynthesis
 3D
 Entner-Doudoroff pathway
 Thymidylate biosynthesis
 Purine salvage
 Lipid A biosynthesis
 16S rRNA modification
 Archaeal ribosomal proteins
 Non-phosphorylated Entner-Doudoroff pathway
 Mureine biosynthesis
 Menaquinone biosynthesis
 2Fe2S
 Arginine biosynthesis
 Isoprenoid biosynthesis
 TCA cycle, glyoxylate bypass
 Histidine biosynthesis, Purine biosynthesis
 Threonine biosynthesis
 Pyruvate oxidation
 Riboflavin/FAD biosynthesis
 Cobalamine/B12 biosynthesis
 Pyrimidine salvage
 tRNA modification



LASSO Coefficient (Absolute) Value