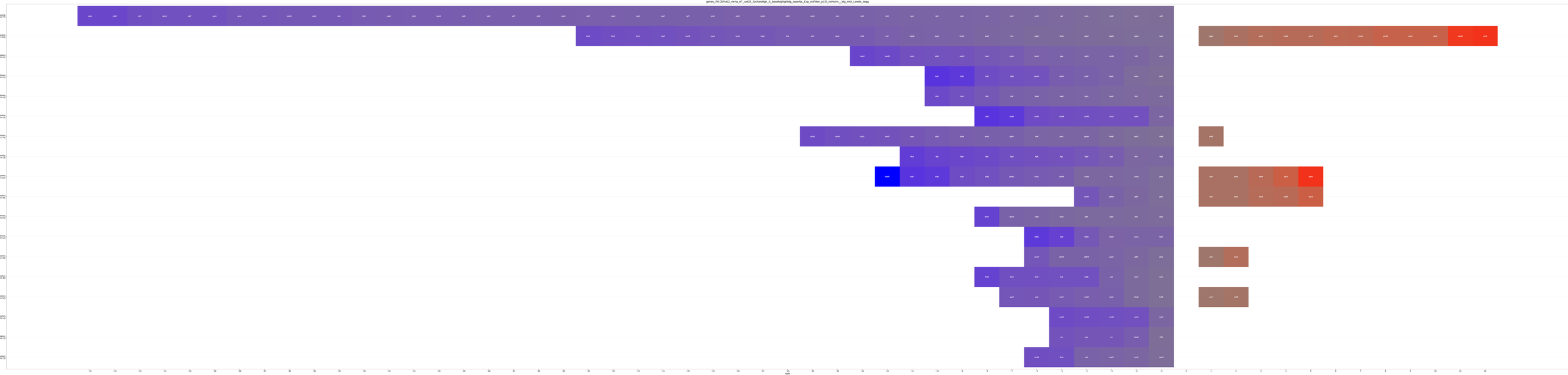
genes_PD.05FIA02_mrna_bT_sel02_StcNaslAlgh_5_baseAlgHighMAg_baseAsa_Enp_noFilter_p1Sf_noNorm__Mg_mM_Levels_kegg
Ribosome
pvk5 0.00000 %, +Inf +2 (7)
RNA transport, pvk5 0.00000 %, +Inf +2 (13)
Oxidative phosphorylation, pvk5 0.00000 %, +Inf +2 (4)
Phenylalanine, tyrosine and tryptophan biosynthesis, pvk5 0.00000 %, +Inf +2 (1)
Valine, leucine and isoleucine biosynthesis, pvk5 0.00000 %, +Inf +2 (3)
Sulfur metabolism, pvk5 0.00000 %, +Inf +2 (3)
Purine metabolism, pvk5 0.00000 %, +Inf +2 (74)
Flagellar assembly, pvk5 0.00001 %, +Inf +2 (2)
Two-component system, pvk5 0.00000 %, +Inf +2 (172)
Nitrogen metabolism, pvk5 0.00000 %, +Inf +2 (5)
Aminoacyl-tRNA biosynthesis, pvk5 0.00001 %, +Inf +2 (2)
Fatty acid biosynthesis, pvk5 0.00000 %, +Inf +2 (1)
Alanine, aspartate and glutamate metabolism, pvk5 0.00000 %, +Inf +2 (3)
Glycine, serine and threonine metabolism, pvk5 0.00179 %, +Inf +2 (6)
Pyrimidine metabolism, pvk5 0.00840 %, +Inf +2 (12)
Selenocompound metabolism, pvk5 0.01940 %, +Inf +2 (4)
RNA degradation, pvk5 0.02004 %, +Inf +2 (3)
Cysteine and methionine metabolism, pvk5 0.04481 %, +Inf +2 (2)
-49 -48 -47 -46 -45 -44 -43 -42 -41 -40 -39 -38 -37 -36 -35 -34 -33 -32 -31 -30 -29 -28 -27 -26 -25 -24 -23 -22 -21 -20 -19 -18 -17 -16 -15 -14 -13 -12 -11 -10 -9 -8 -7 -6 -5 -4 -3 -2 -1 0 1 2 3 4 5 6 7 8 9 10 11 12
rank
-signlog10(FP_log10)
-8 -6 -4 -2