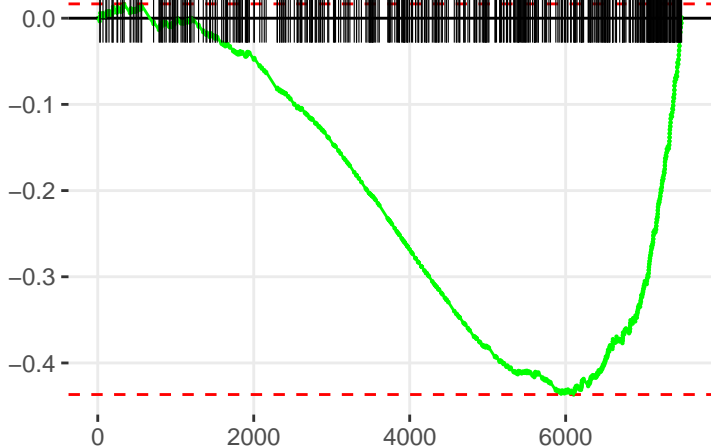


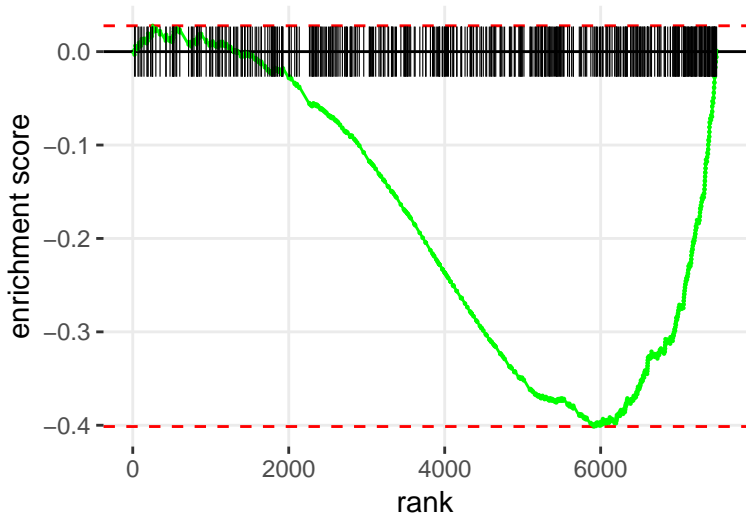
TREHALOSE DEGRADATION II (TREHALASE)

enrichment score

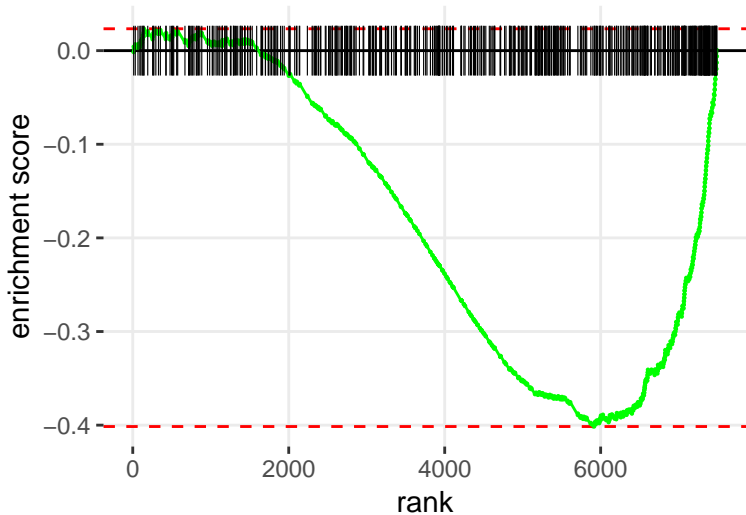
rank



RETINOATE BIOSYNTHESIS I



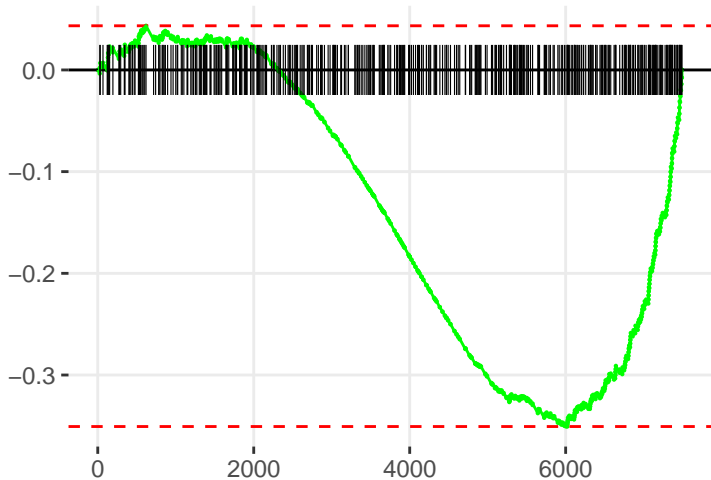
PROLINE BIOSYNTHESIS II (FROM ARGININE)



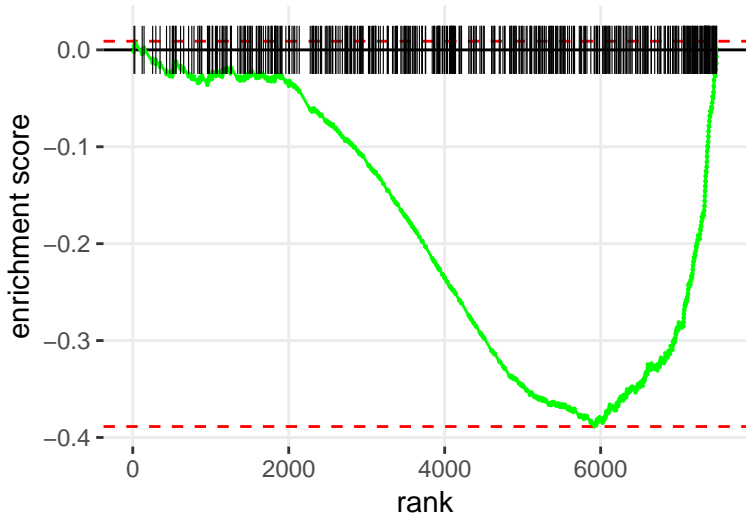
FATTY ACID &BETA;-OXIDATION I

enrichment score

rank



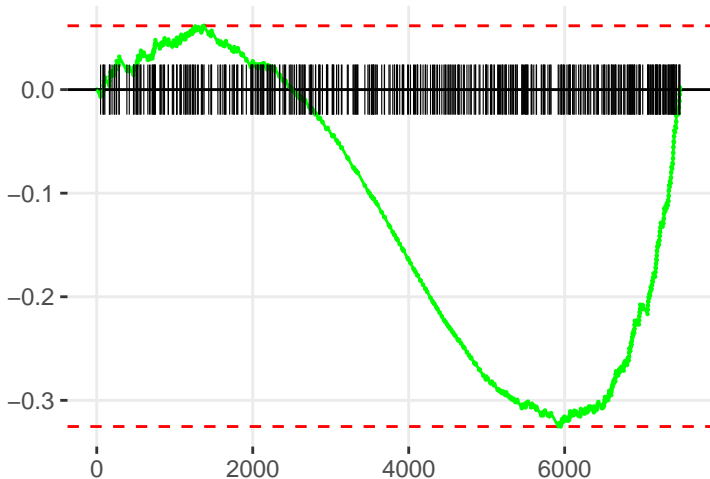
2-OXOISOVALERATE DECARBOXYLATION TO ISOBUTANOYL-COA



GLYCINE BETAINE DEGRADATION

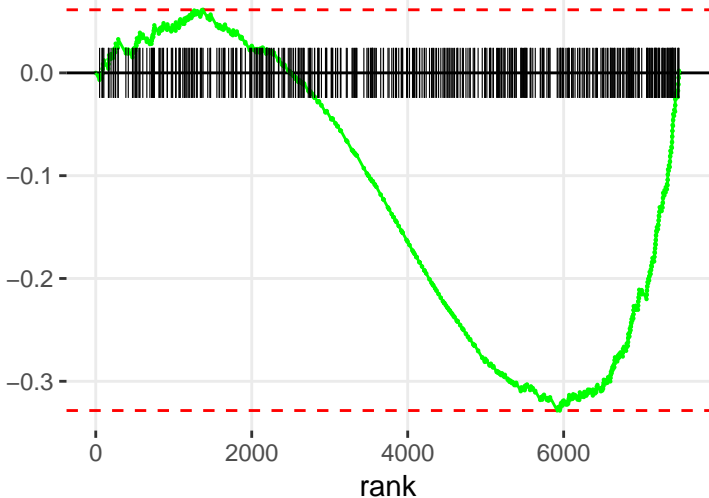
enrichment score

rank



GLYCINE BIOSYNTHESIS I

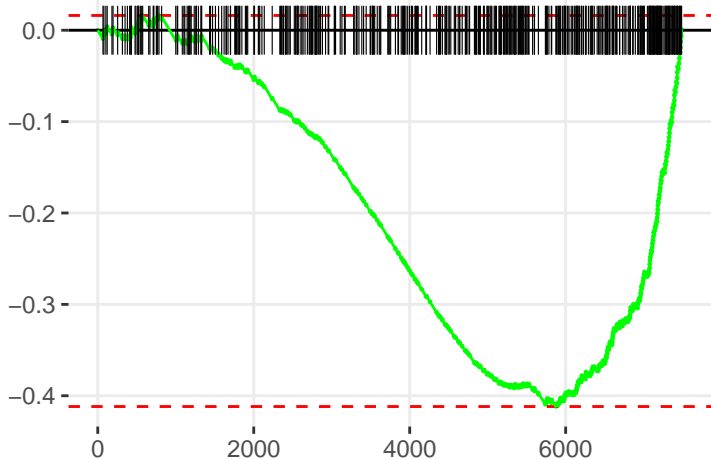
enrichment score



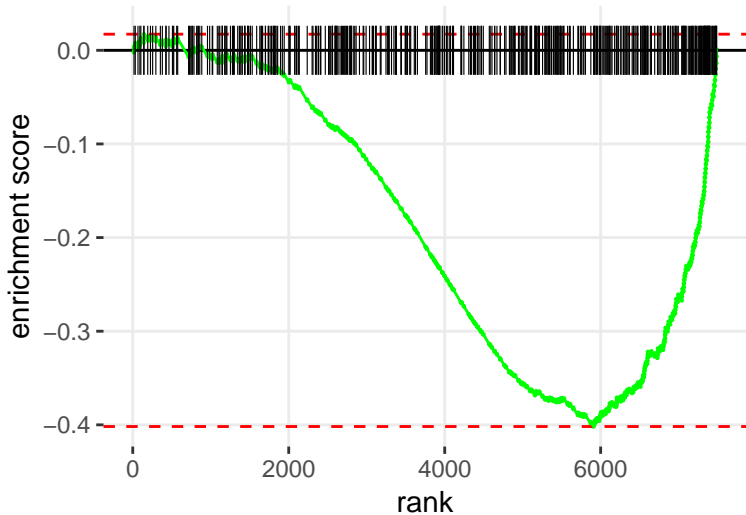
UDP-<IN</I>-ACETYL-D-GLUCOSAMINE BIOSYNTHESIS II

enrichment score

rank



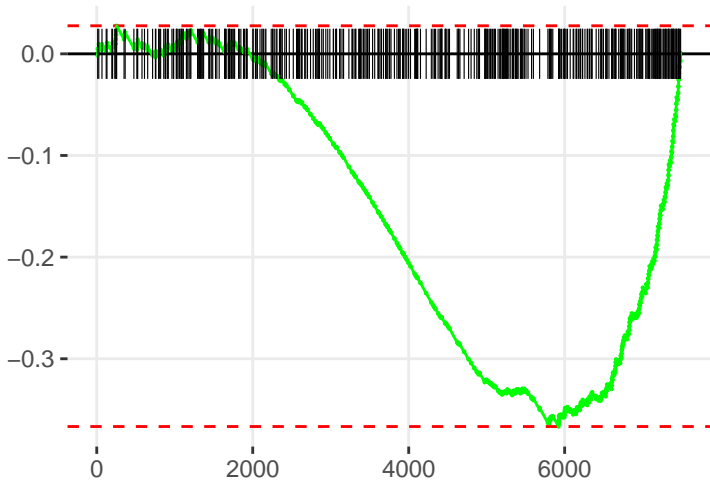
CITRULLINE BIOSYNTHESIS



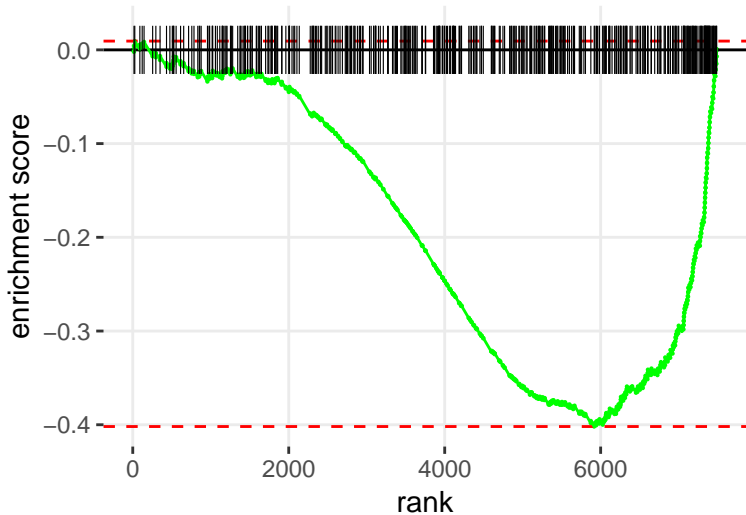
MEVALONATE PATHWAY I

enrichment score

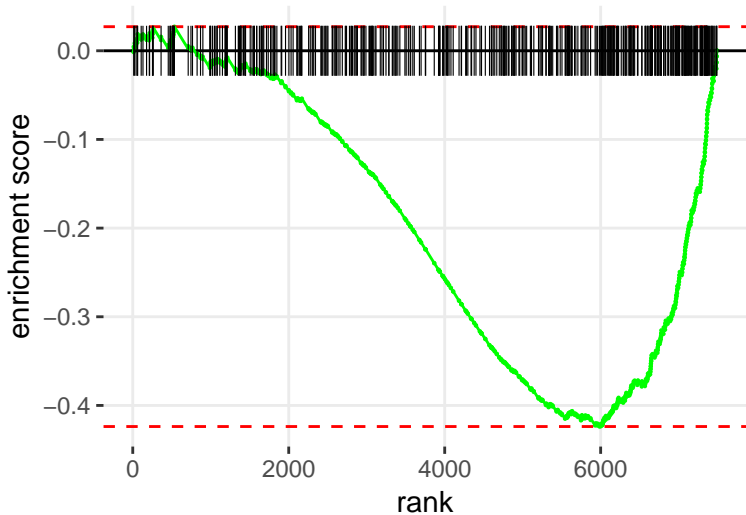
rank



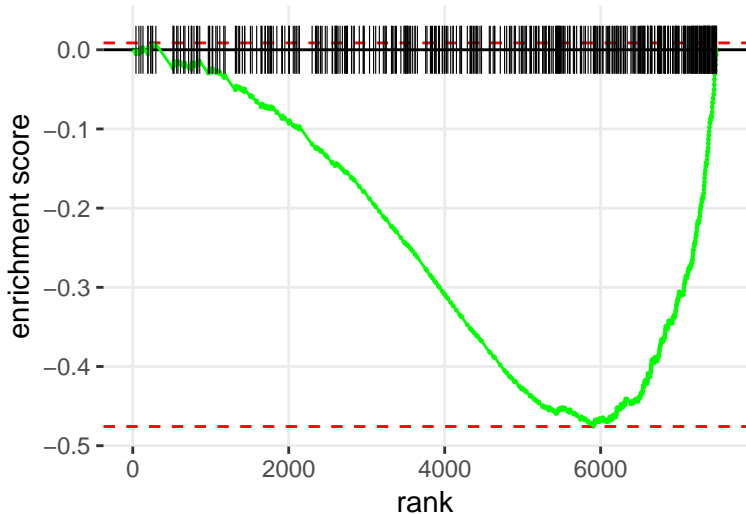
GLYCINE CLEAVAGE



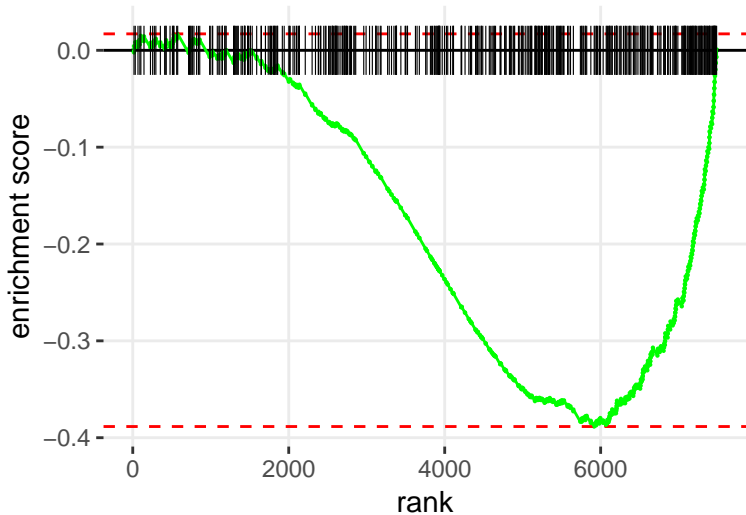
SALVAGE PATHWAYS OF PYRIMIDINE RIBONUCLEOTIDES



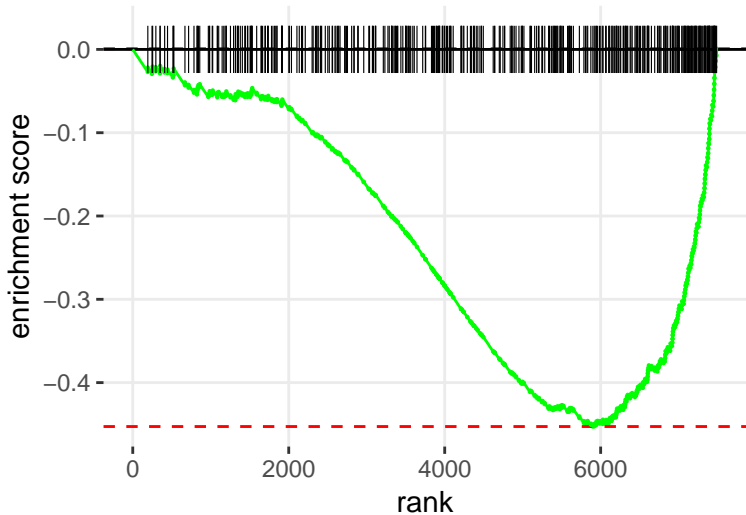
PENTOSE PHOSPHATE PATHWAY (OXIDATIVE BRANCH)



UREA CYCLE



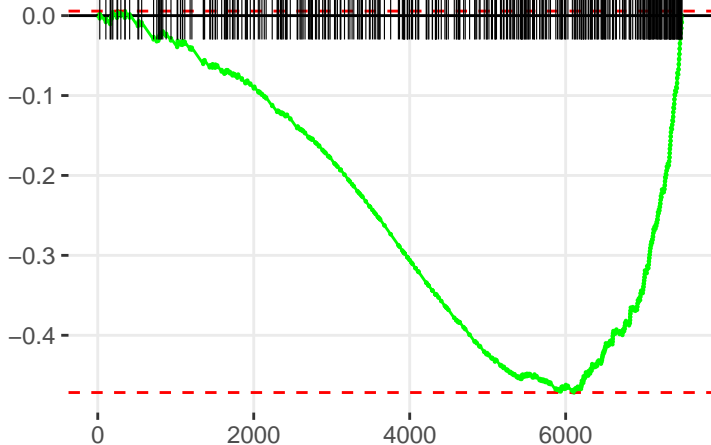
CYSTEINE BIOSYNTHESIS/HOMOCYSTEINE DEGRADATION



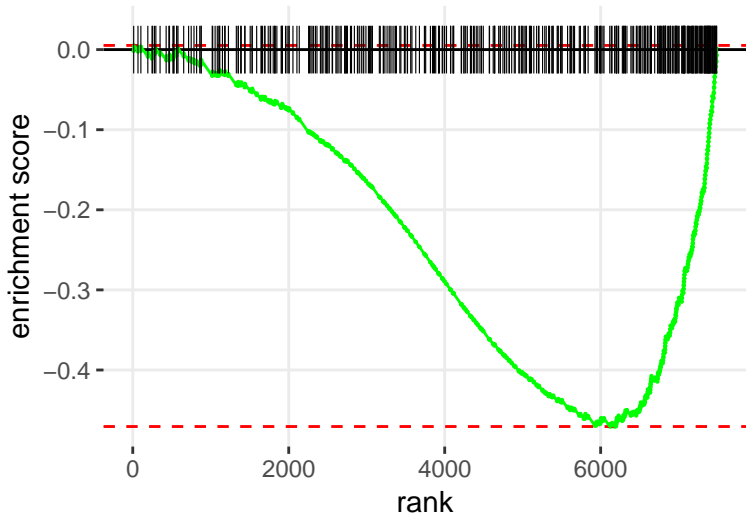
GLYCOGEN BIOSYNTHESIS II (FROM UDP-D-GLUCOSE)

enrichment score

rank



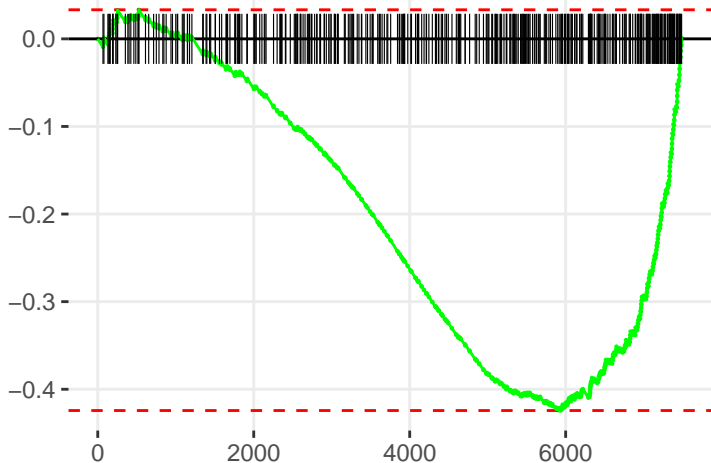
ASPARTATE DEGRADATION II



GLYCOGEN DEGRADATION II

enrichment score

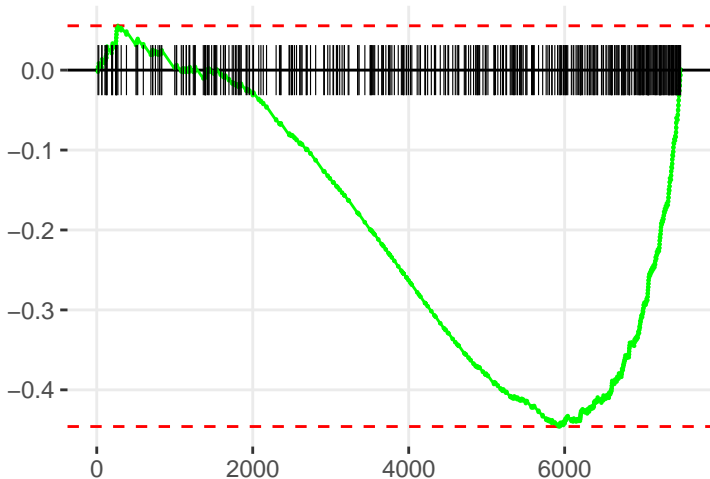
rank



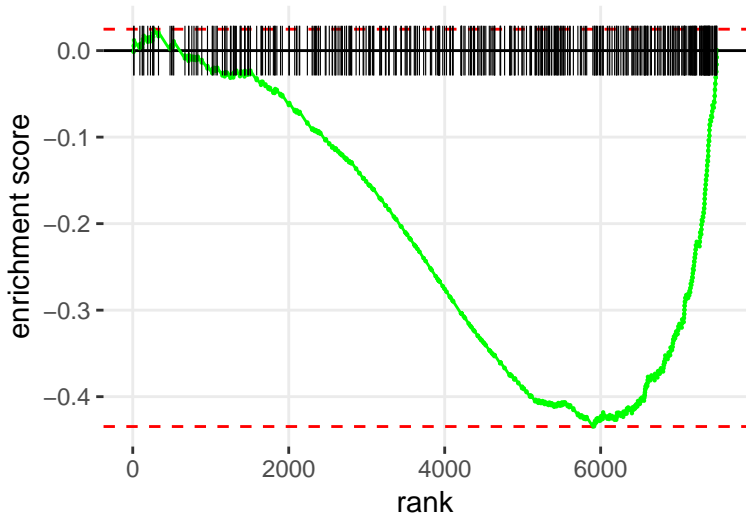
SUPEROXIDE RADICALS DEGRADATION

enrichment score

rank



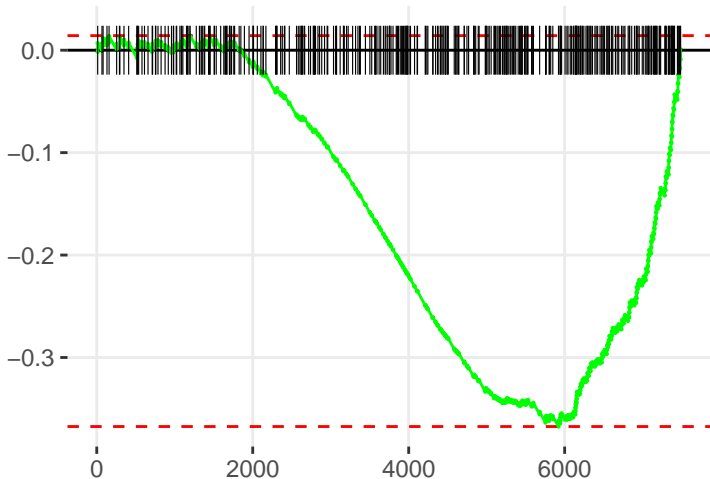
ARGININE DEGRADATION VI (ARGINASE 2 PATHWAY)



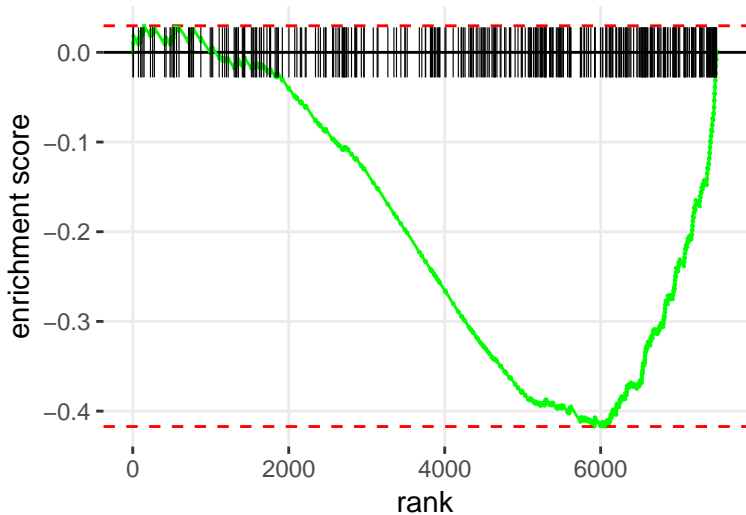
SELENOCYSTEINE BIOSYNTHESIS II (ARCHAEA AND EUKARYOTES)

enrichment score

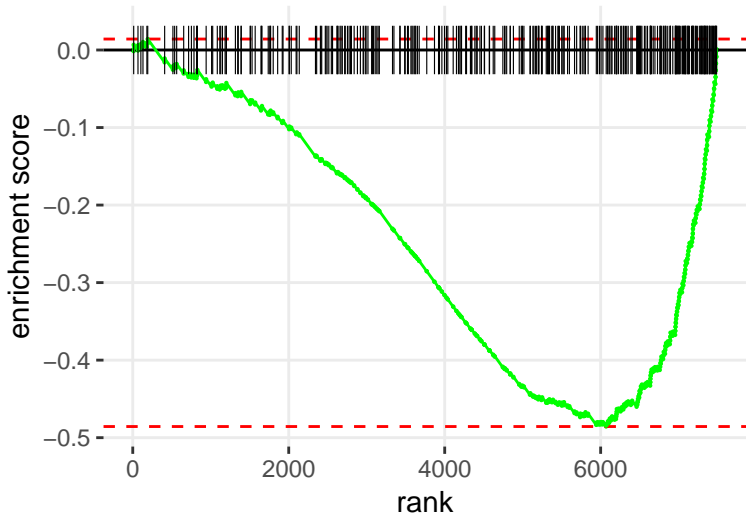
rank



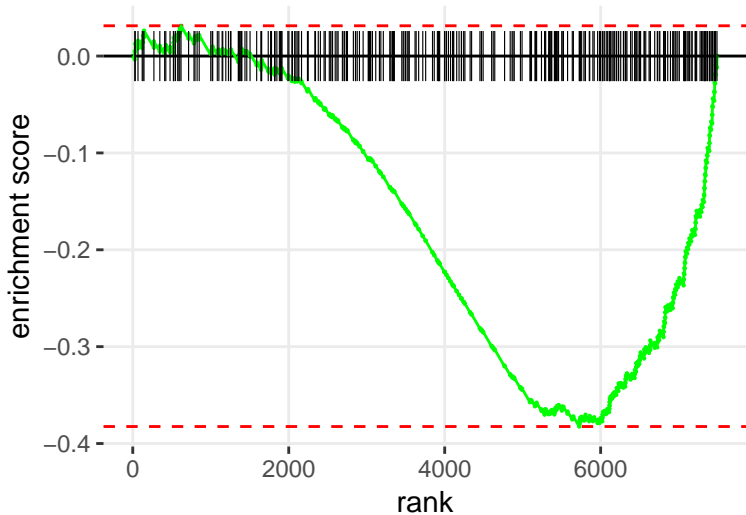
CITRULLINE-NITRIC OXIDE CYCLE



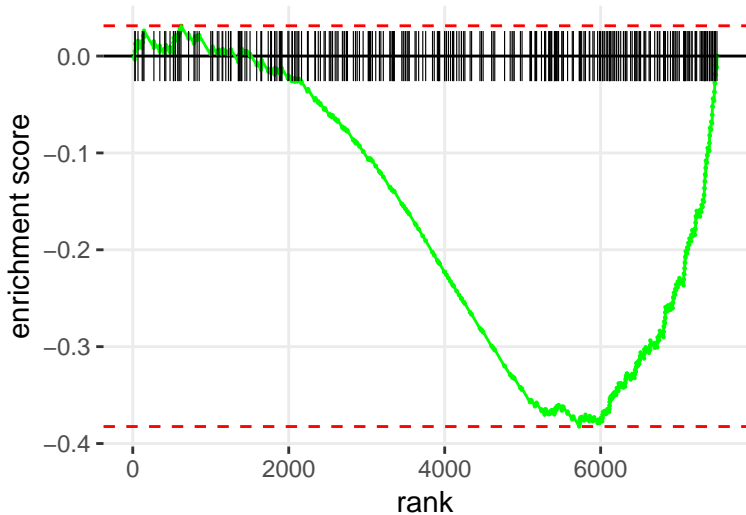
PENTOSE PHOSPHATE PATHWAY (NON-OXIDATIVE BRANCH)



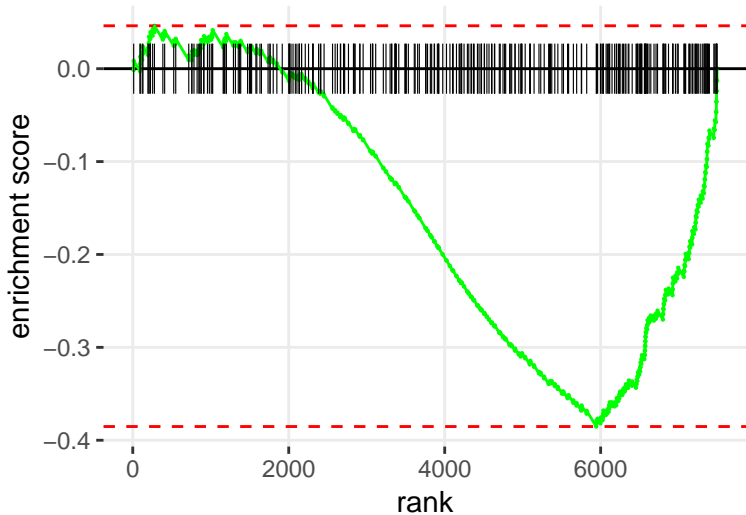
STEARATE BIOSYNTHESIS I (ANIMALS)



EICOSAPENTAENOATE BIOSYNTHESIS II (METAZOA)



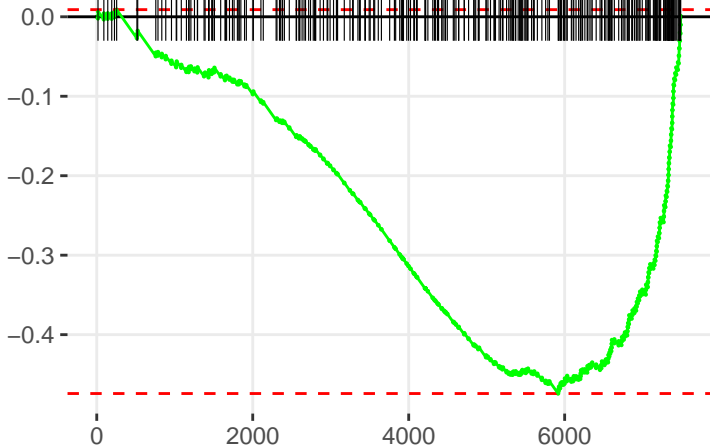
URATE BIOSYNTHESIS/INOSINE 5'-PHOSPHATE DEGRADATION



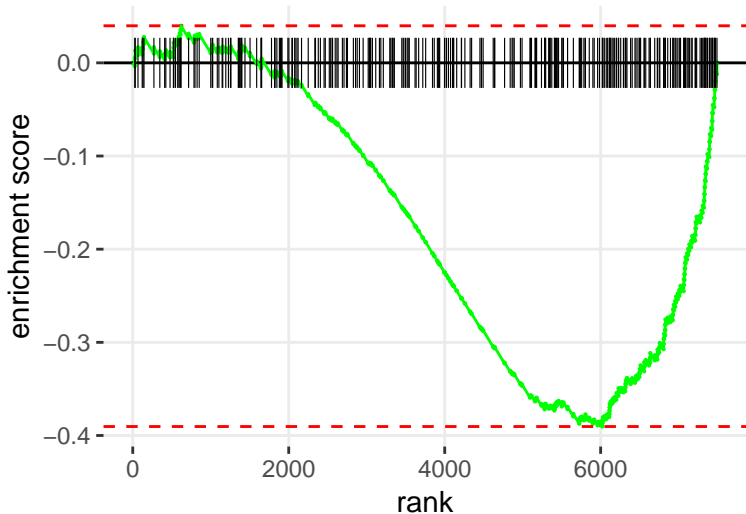
ARGININE DEGRADATION I (ARGINASE PATHWAY)

enrichment score

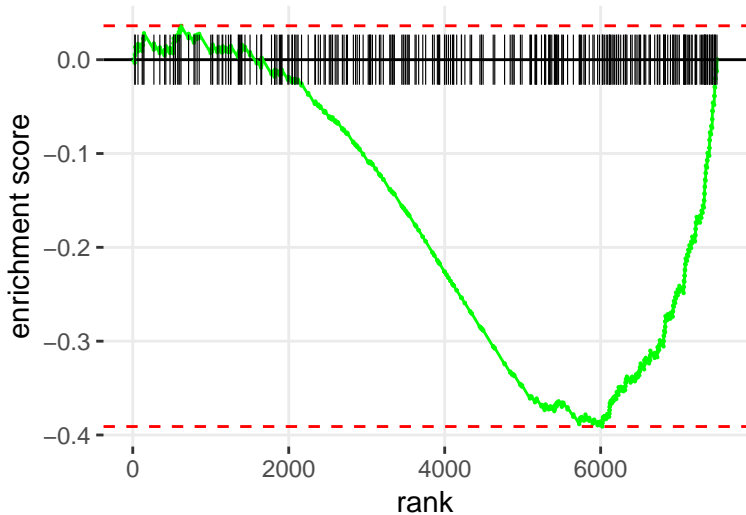
rank



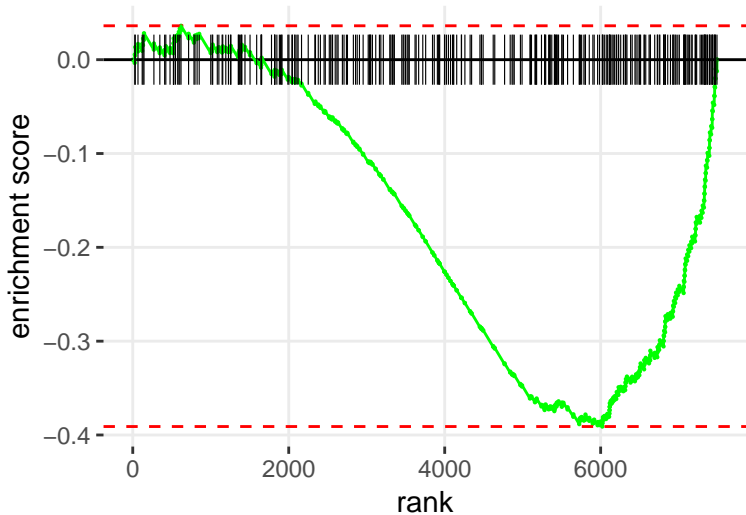
&GAMMA;-LINOLENATE BIOSYNTHESIS II (ANIMALS)



FATTY ACID ACTIVATION



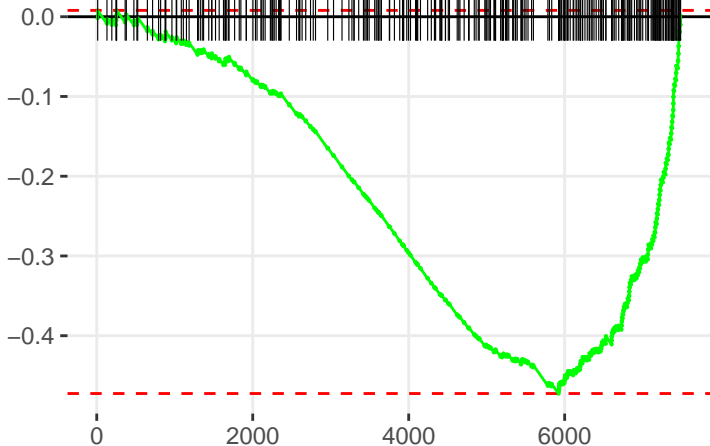
FATTY ACID &ALPHA;-OXIDATION II



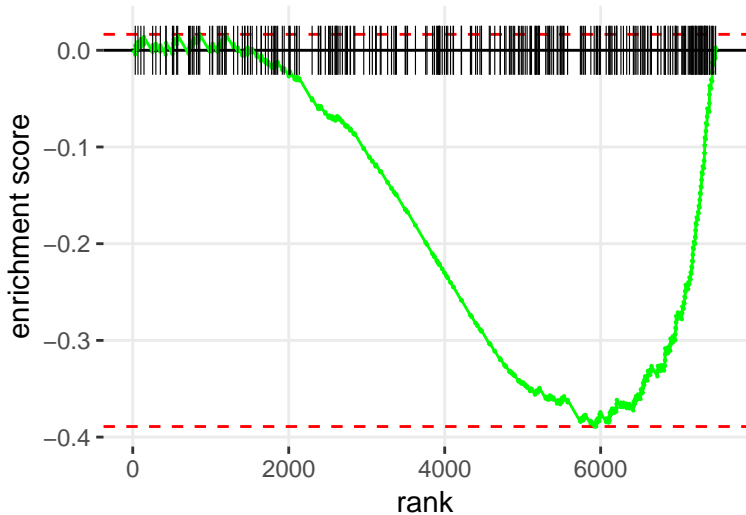
KETOGENESIS

enrichment score

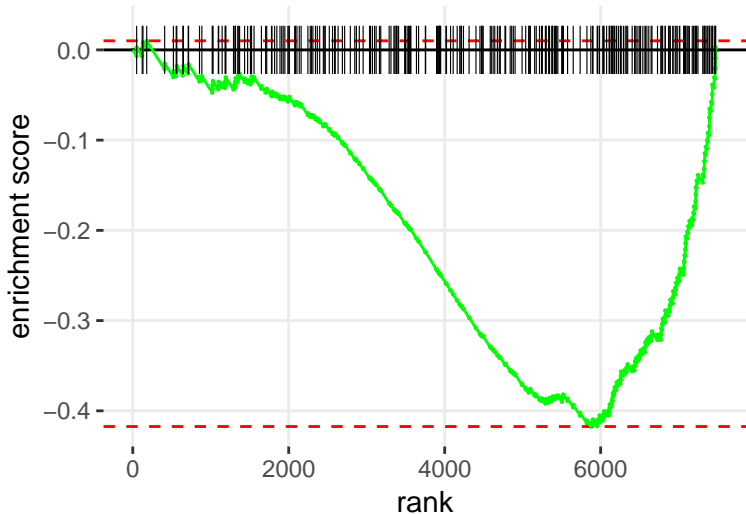
rank



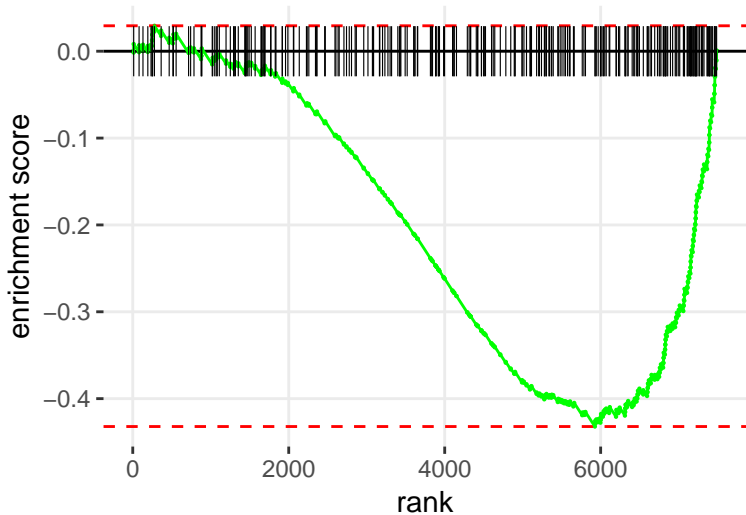
CITRULLINE DEGRADATION



TRIACYLGLYCEROL BIOSYNTHESIS



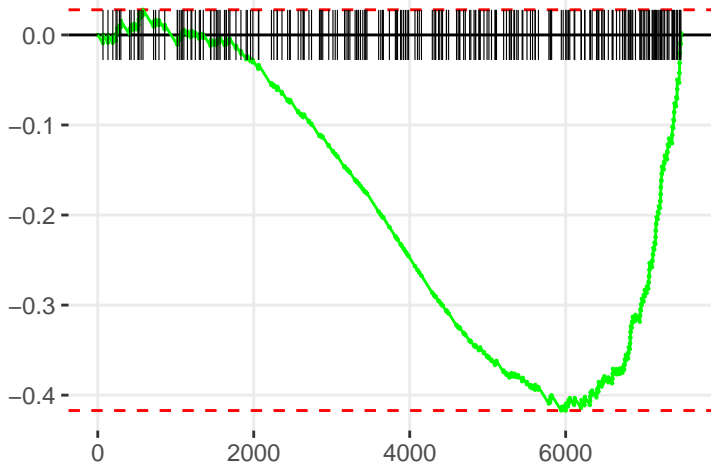
ISOLEUCINE DEGRADATION I



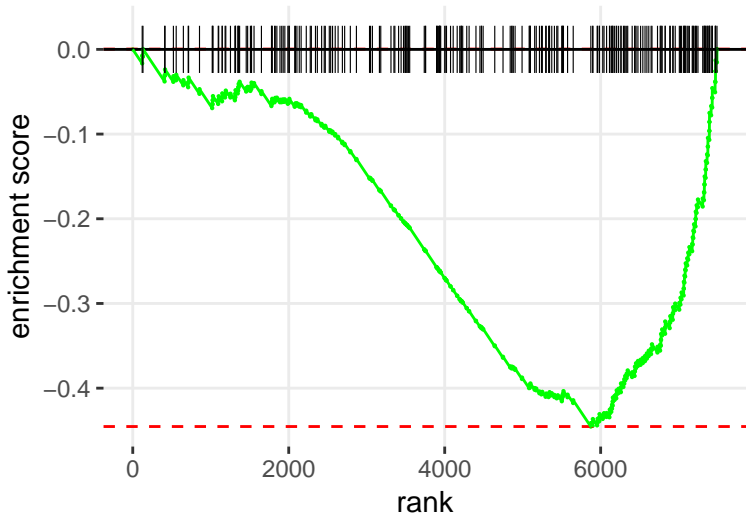
VALINE DEGRADATION I

enrichment score

rank



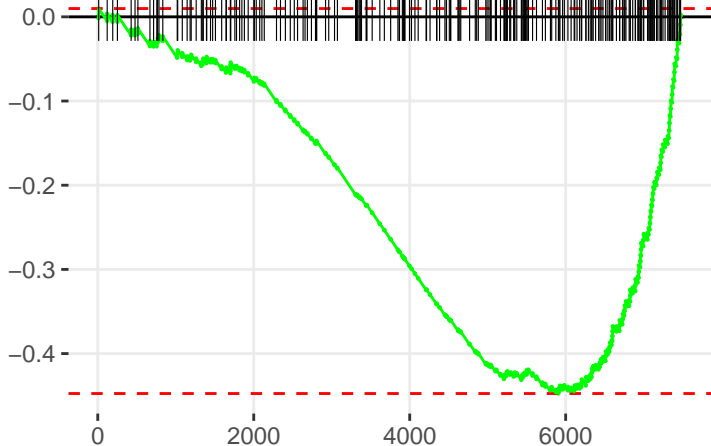
CDP-DIACYLGLYCEROL BIOSYNTHESIS I



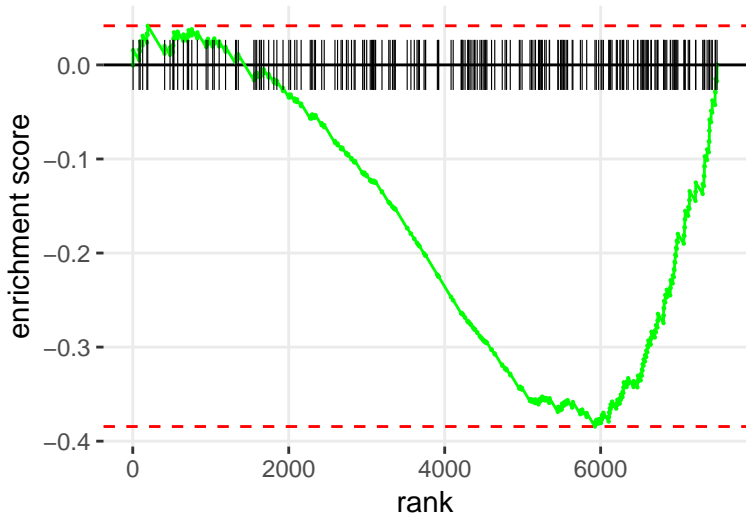
GALACTOSE DEGRADATION I (LELOIR PATHWAY)

enrichment score

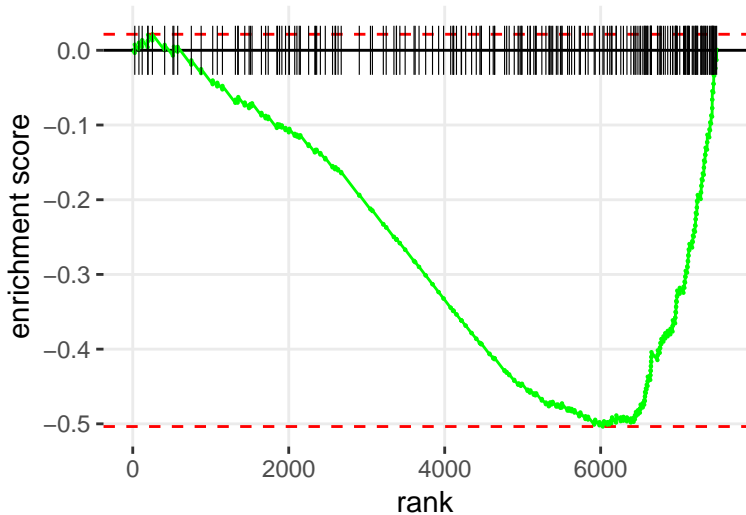
rank



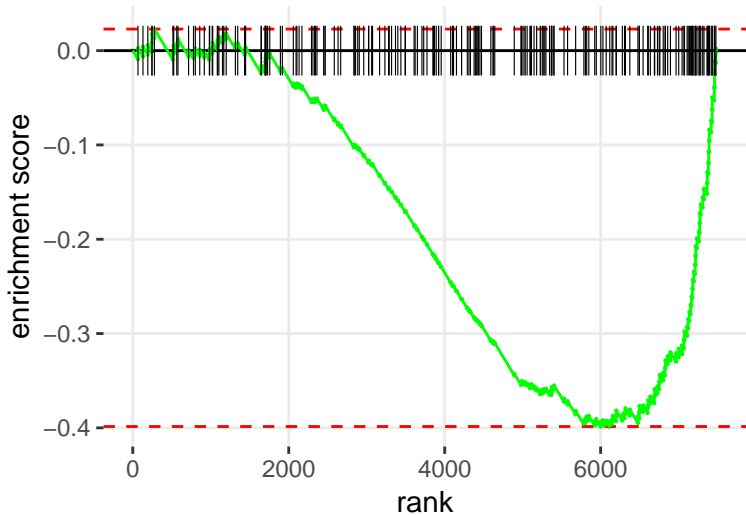
CHOLINE BIOSYNTHESIS III



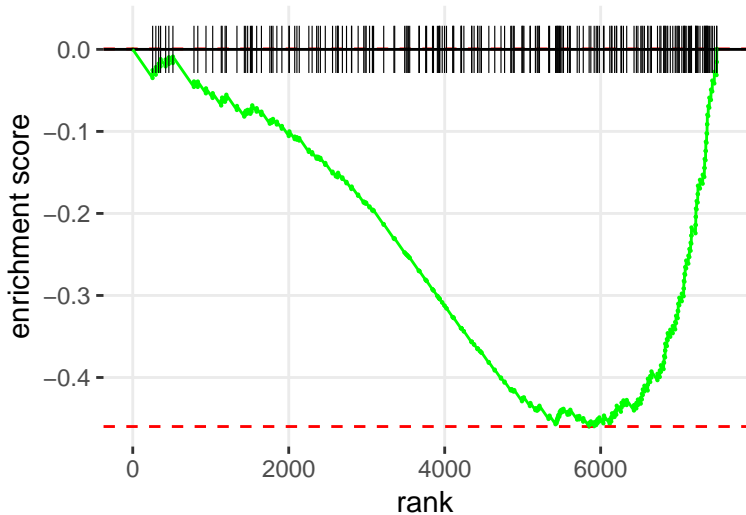
<IMYO</I>-INOSITOL BIOSYNTHESIS



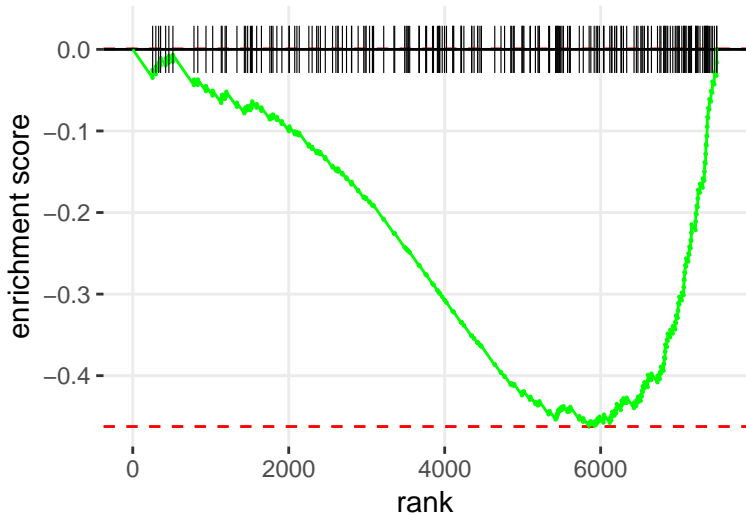
5-AMINOIMIDAZOLE RIBONUCLEOTIDE BIOSYNTHESIS I



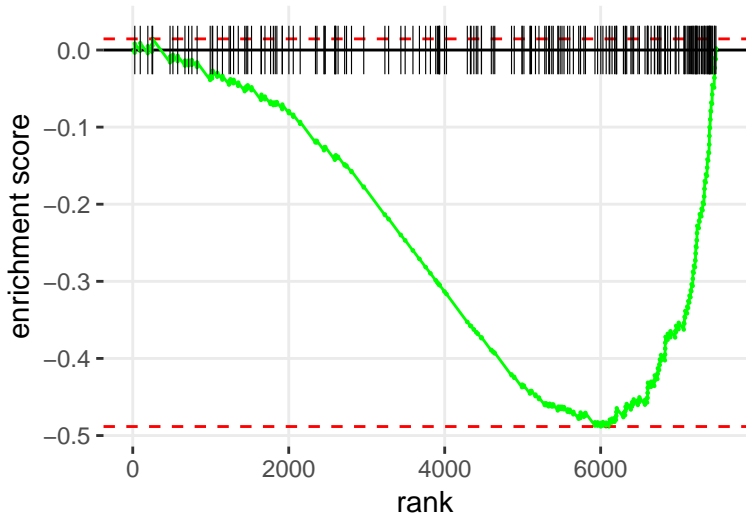
TETRAHYDROBIOPTERIN BIOSYNTHESIS I



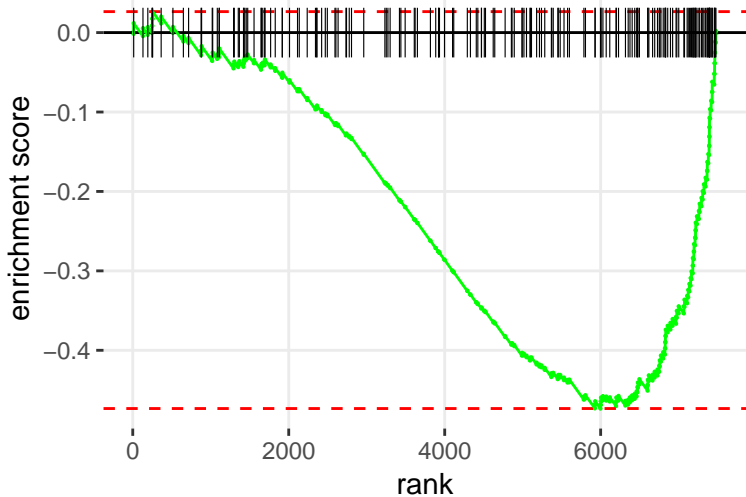
TETRAHYDROBIOPTERIN BIOSYNTHESIS II



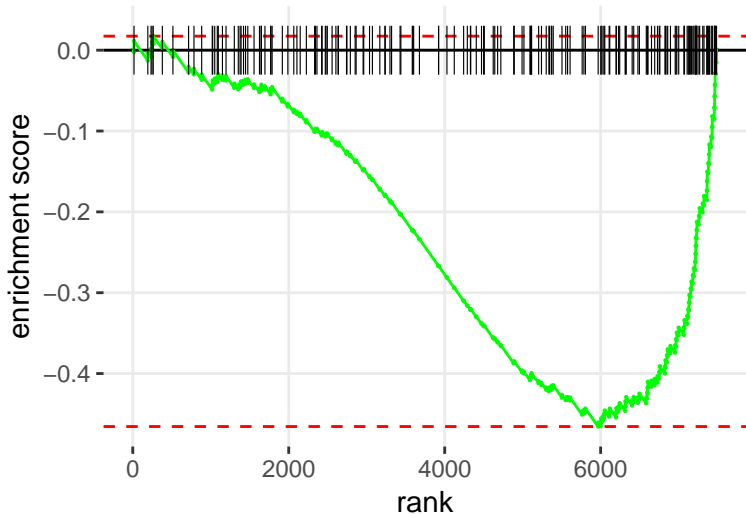
ACETATE CONVERSION TO ACETYL-COA



KETOLYSIS



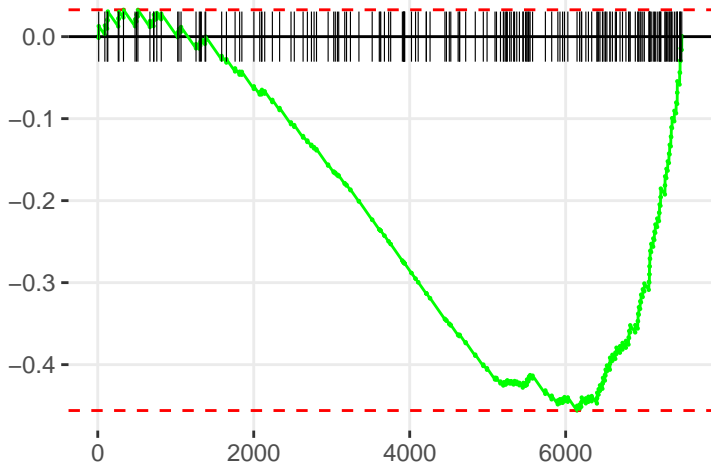
LEUCINE DEGRADATION I



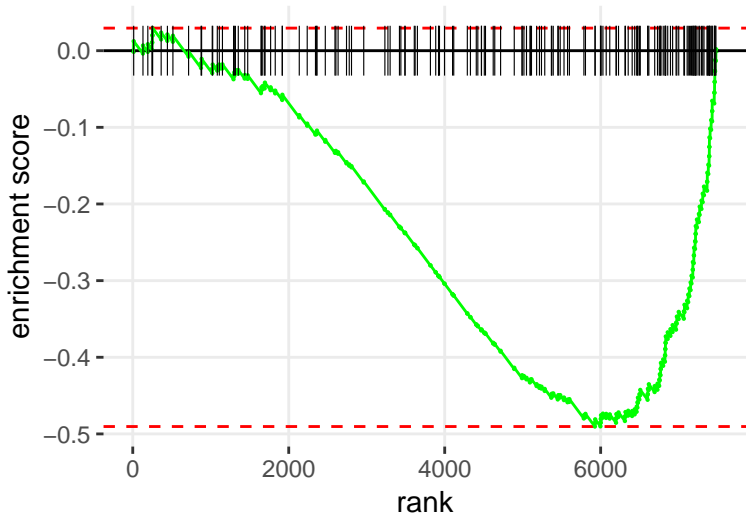
PROLINE BIOSYNTHESIS I

enrichment score

rank



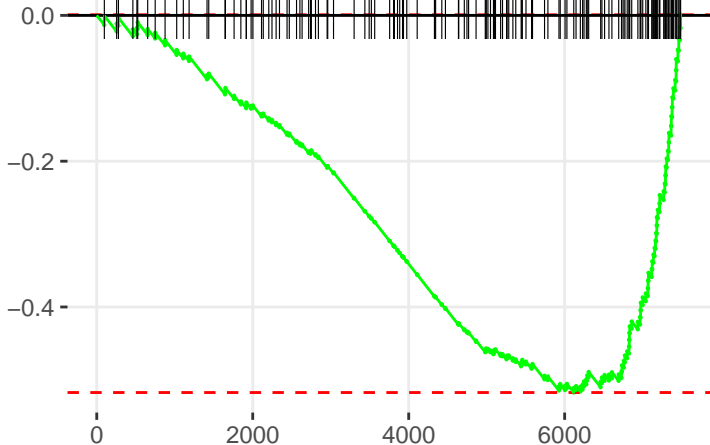
GLUTARYL-COA DEGRADATION



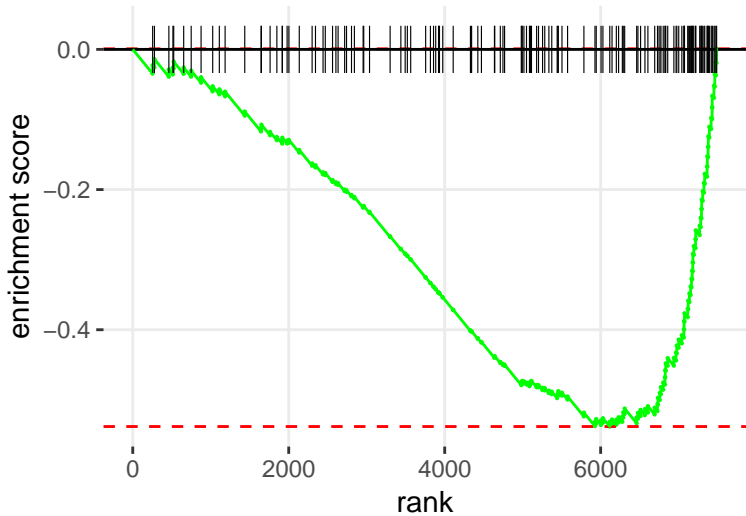
PHENYLALANINE DEGRADATION IV (MAMMALIAN, VIA SIDE CHAIN)

enrichment score

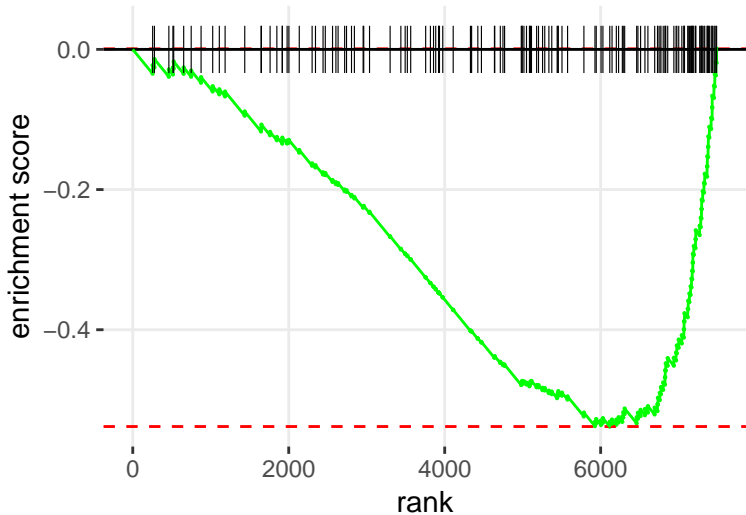
rank



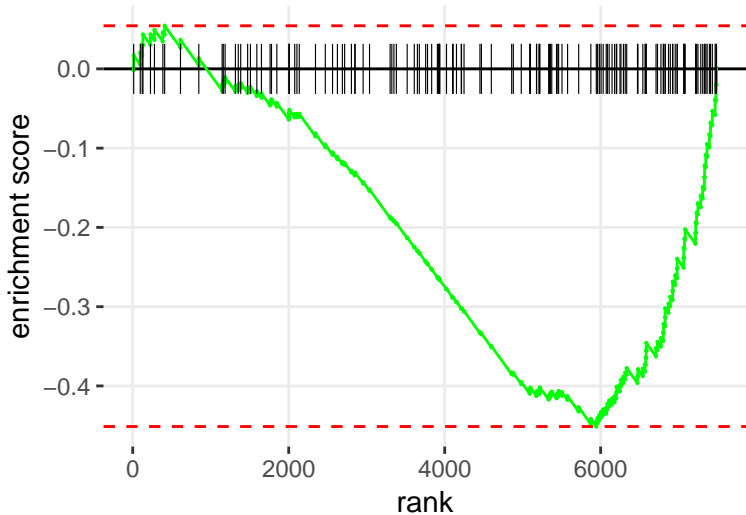
GLUTAMATE DEGRADATION II



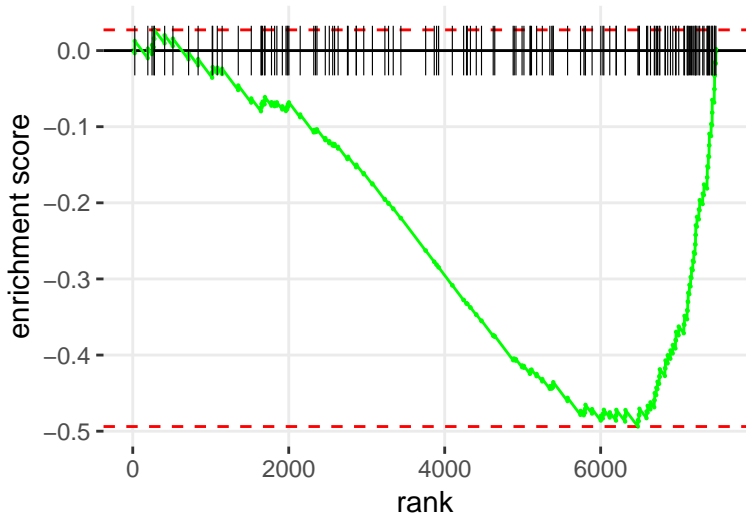
ASPARTATE BIOSYNTHESIS



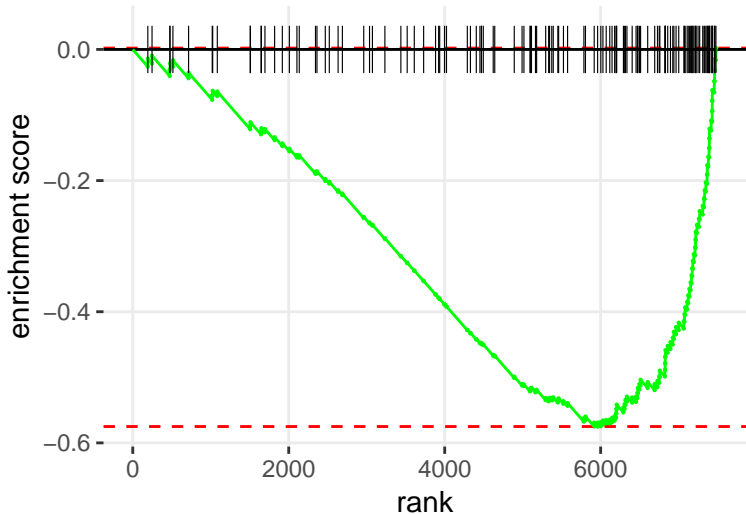
ADENINE AND ADENOSINE SALVAGE I



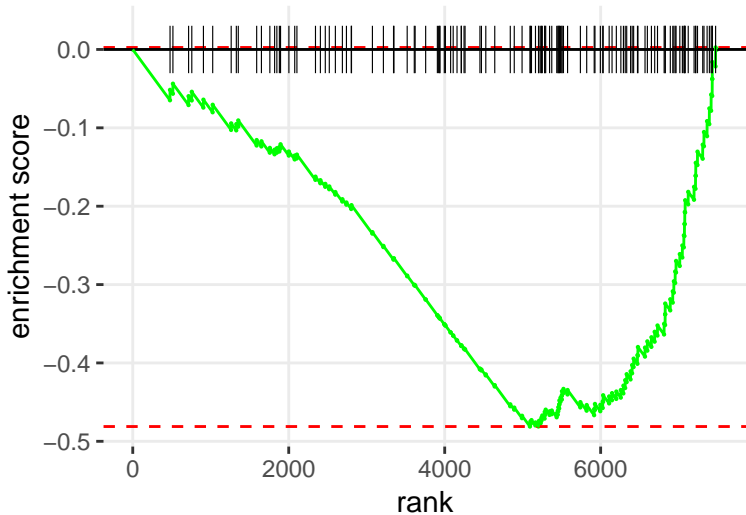
BILE ACID BIOSYNTHESIS, NEUTRAL PATHWAY



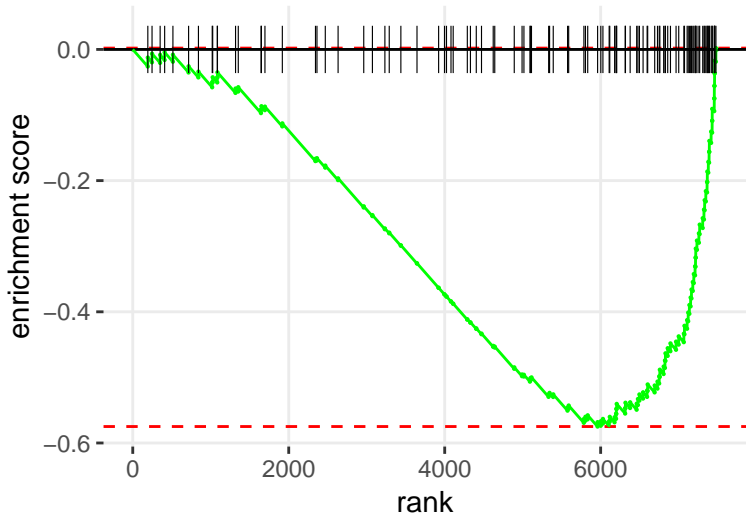
ADENINE AND ADENOSINE SALVAGE VI



HYPUSINE BIOSYNTHESIS



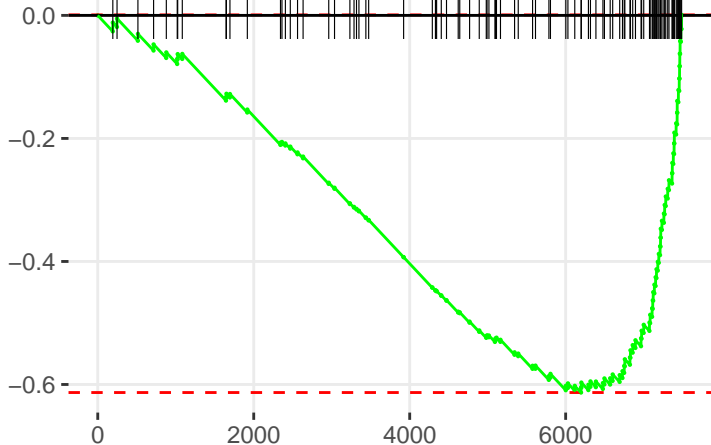
L-CYSTEINE DEGRADATION II



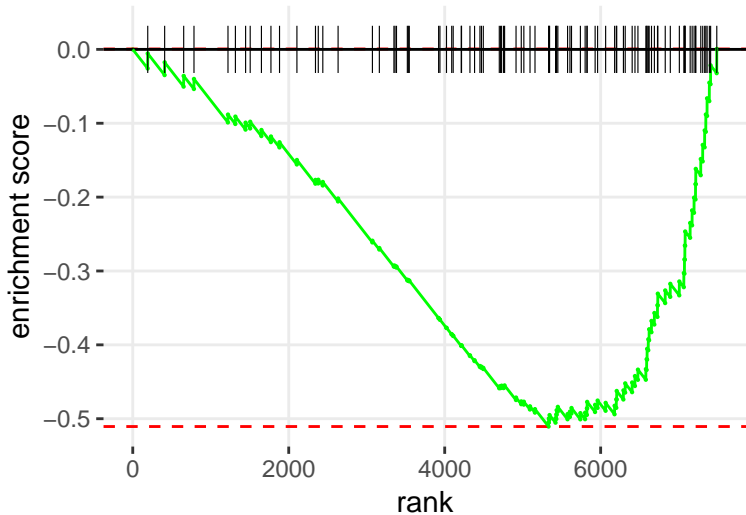
D-MANNOSE DEGRADATION

enrichment score

rank



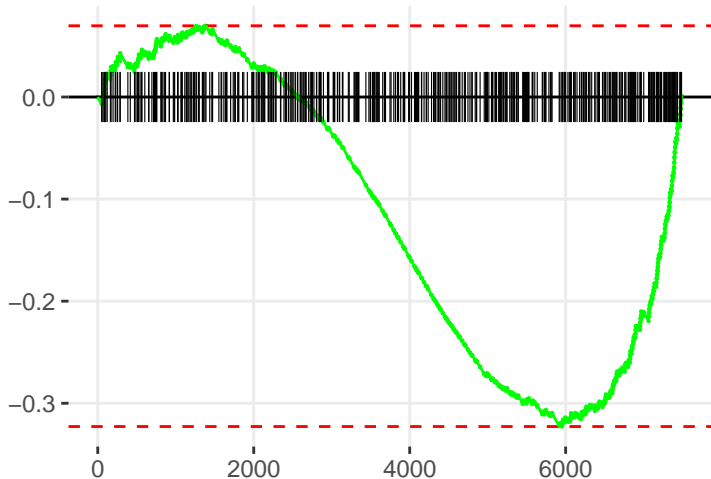
TRYPTOPHAN DEGRADATION TO 2-AMINO-3-CARBOXYMUCONATE SEMIALDEHYDE



FOLATE POLYGLUTAMYLATION

enrichment score

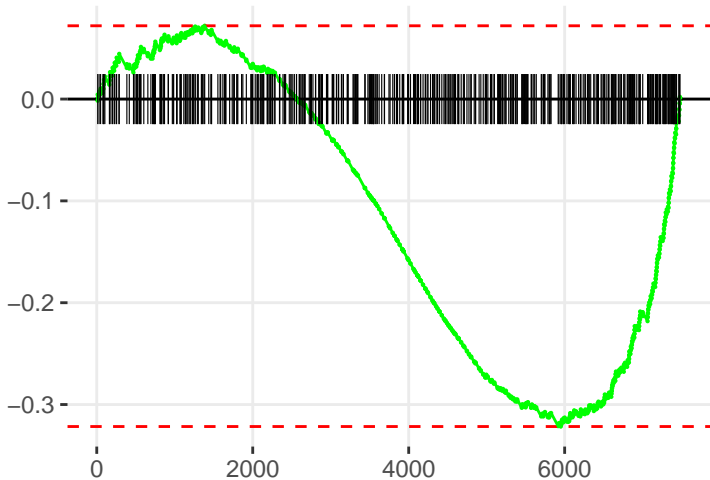
rank



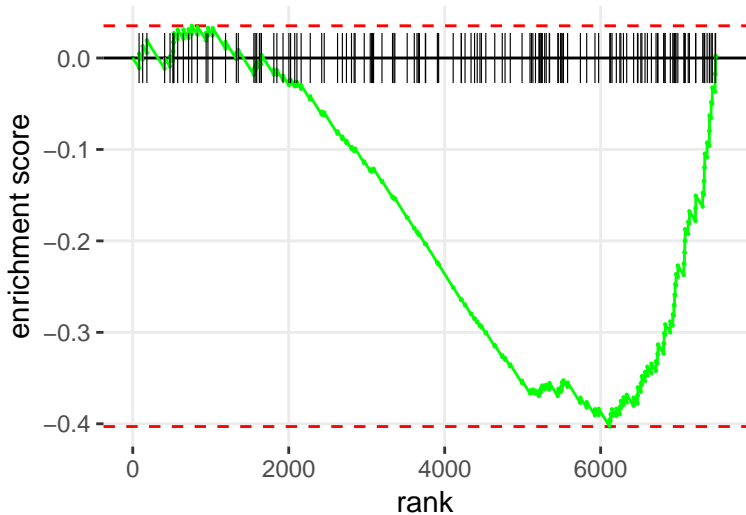
DTMP <IDE NOVO</I> BIOSYNTHESIS

enrichment score

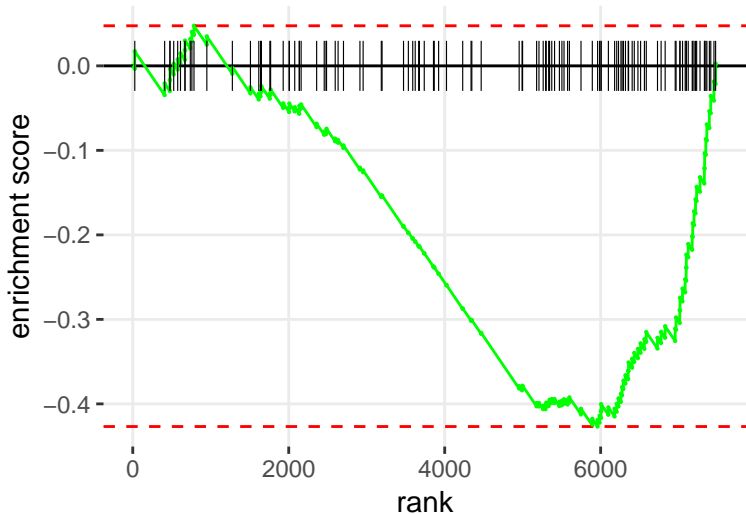
rank



PHOSPHATIDYLCHOLINE BIOSYNTHESIS I



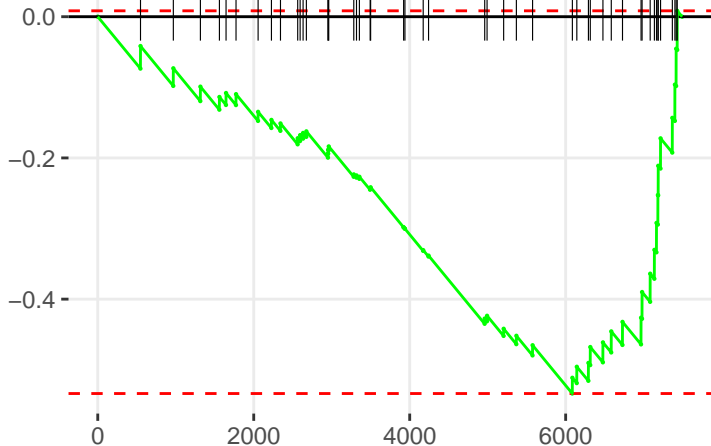
PRPP BIOSYNTHESIS I



INOSINE-5'-PHOSPHATE BIOSYNTHESIS II

enrichment score

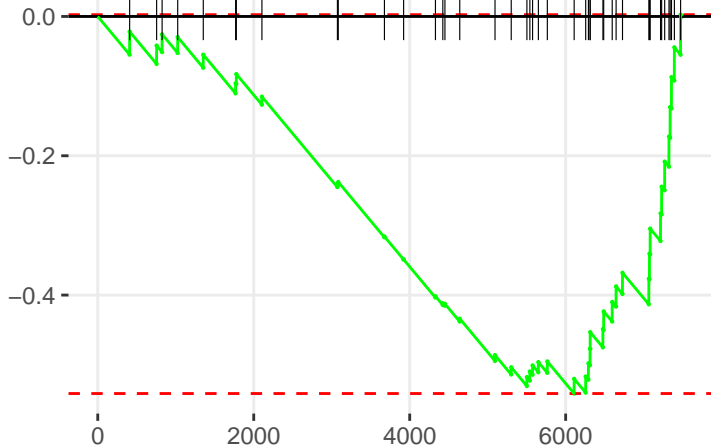
rank



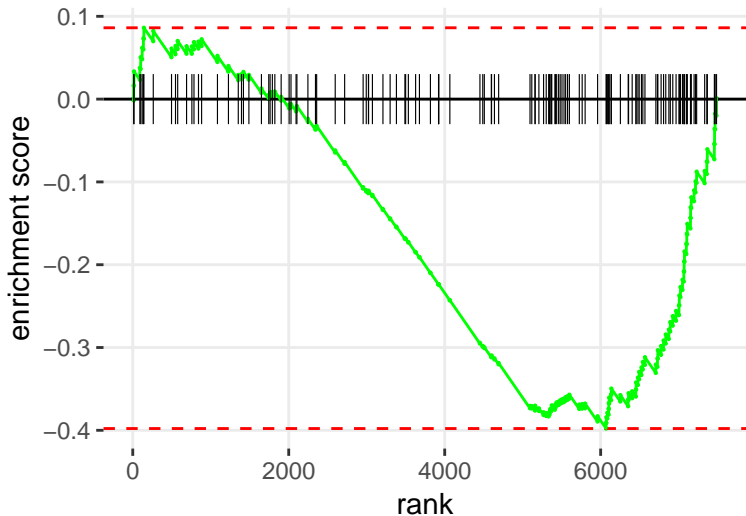
GLUTATHIONE BIOSYNTHESIS

enrichment score

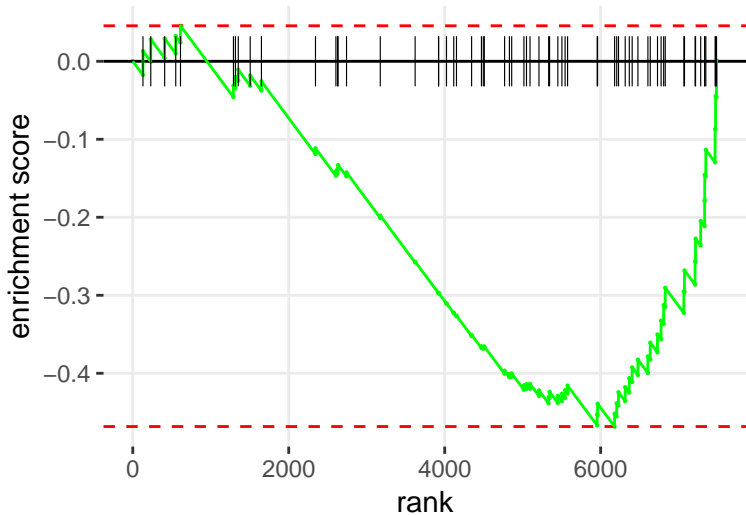
rank



SERINE BIOSYNTHESIS

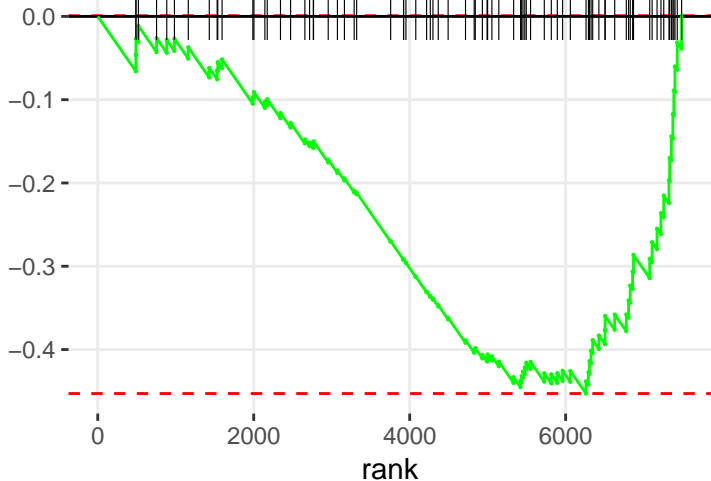


PYRIDOXAL 5'-PHOSPHATE SALVAGE PATHWAY



TRIACYLGLYCEROL DEGRADATION

enrichment score



GLUTATHIONE REDOX REACTIONS I

enrichment score

rank

0.0

-0.1

-0.2

-0.3

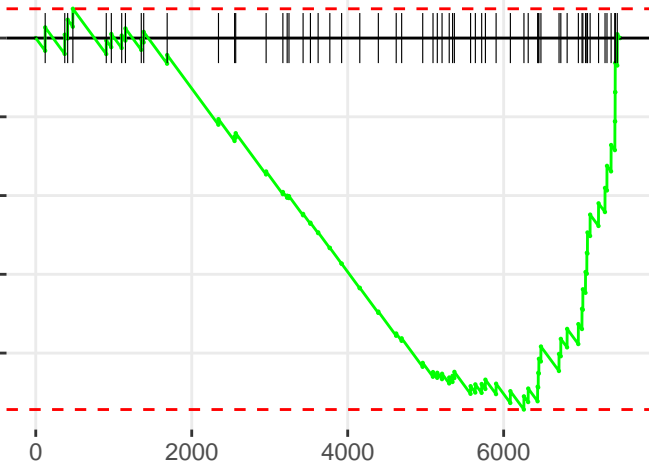
-0.4

0

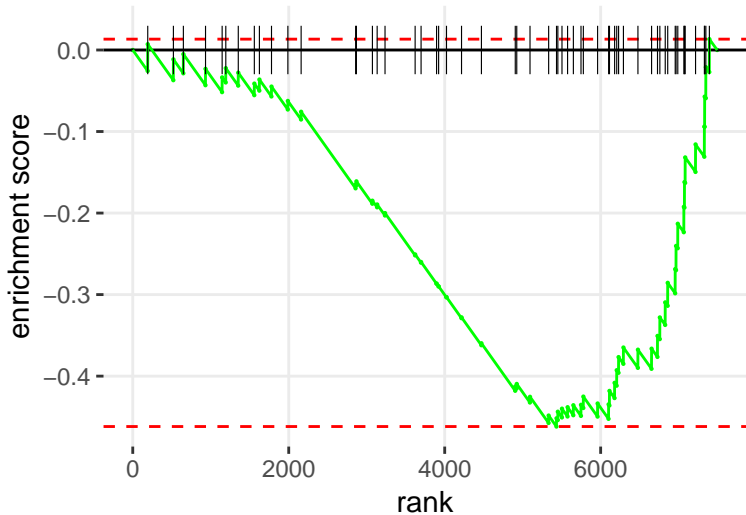
2000

4000

6000

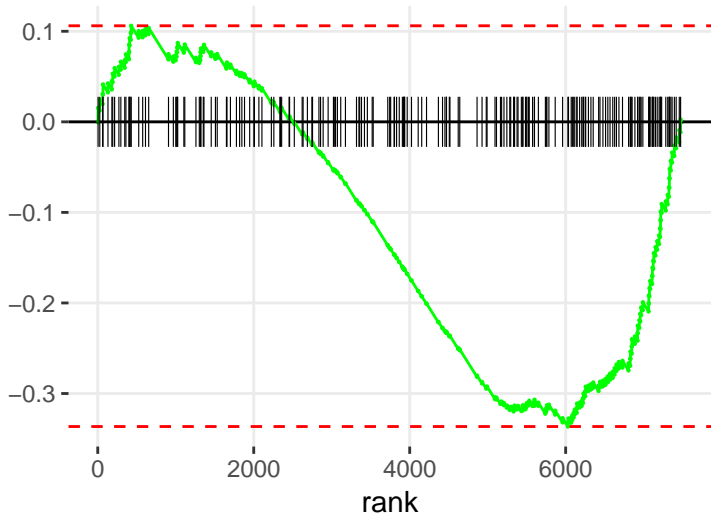


DOLICHOL AND DOLICHYL PHOSPHATE BIOSYNTHESIS

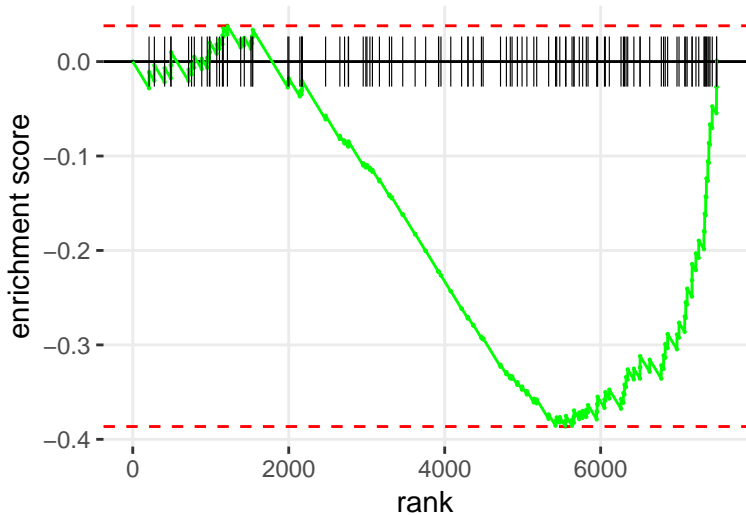


HEME BIOSYNTHESIS FROM UROPORPHYRINOGEN-III I

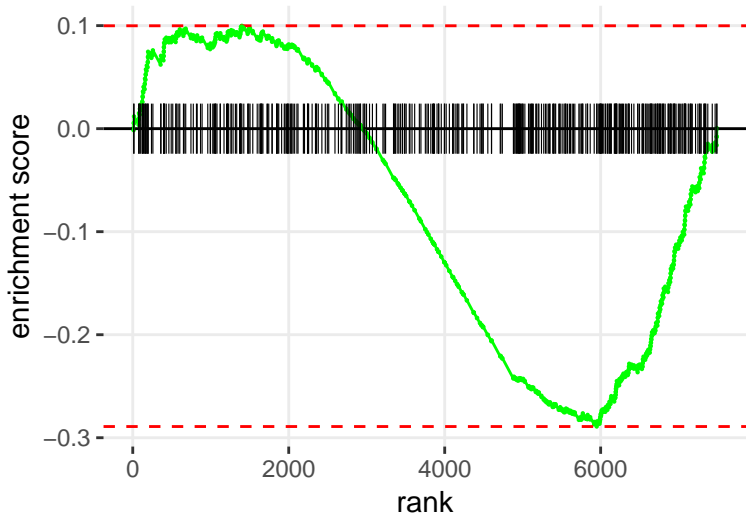
enrichment score



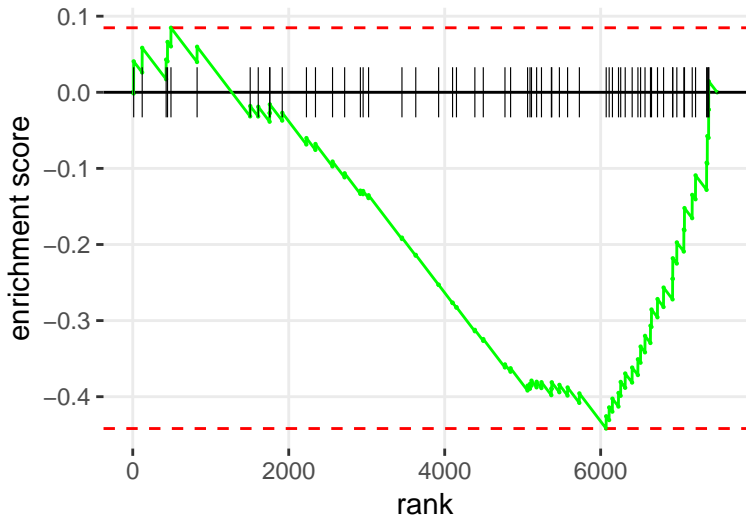
RETINOL BIOSYNTHESIS



3-PHOSPHOINOSITIDE DEGRADATION



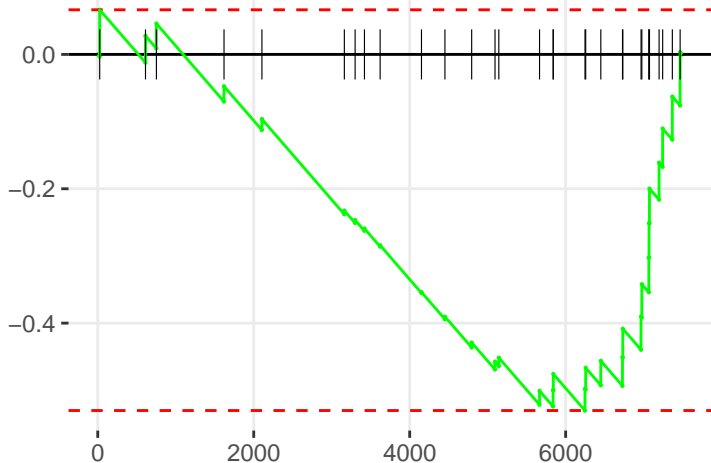
ASPARAGINE BIOSYNTHESIS I



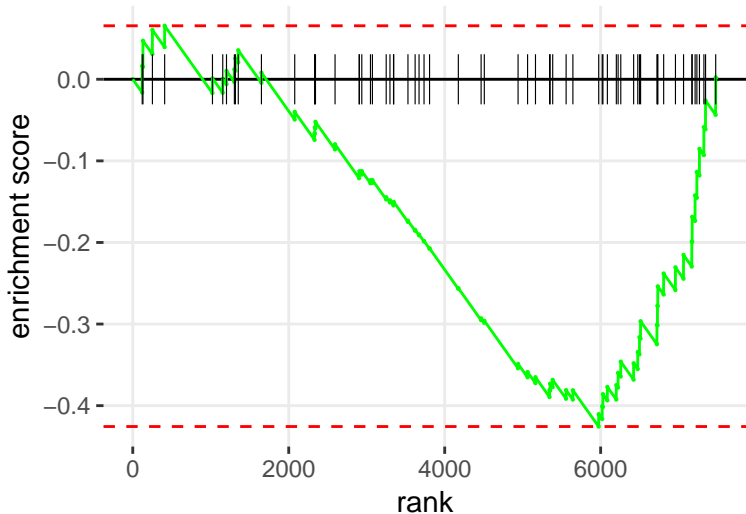
METHYLGLYOXAL DEGRADATION I

enrichment score

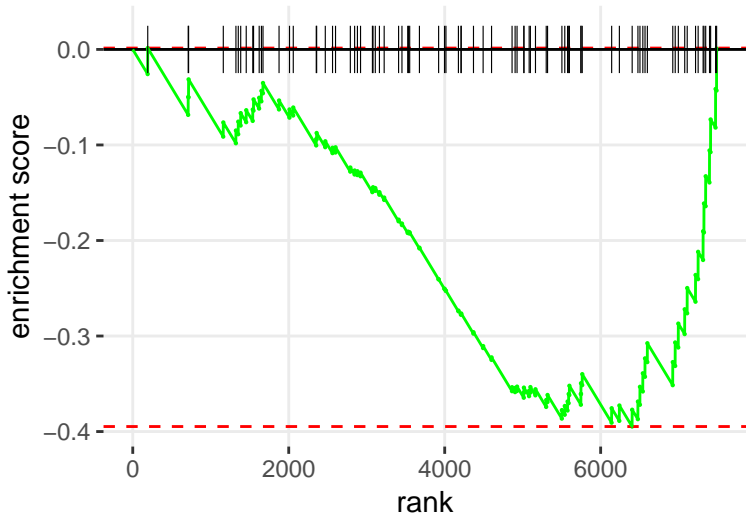
rank



D-<IMYO</I-INOSITOL (1,4,5)-TRISPHOSPHATE DEGRADATION



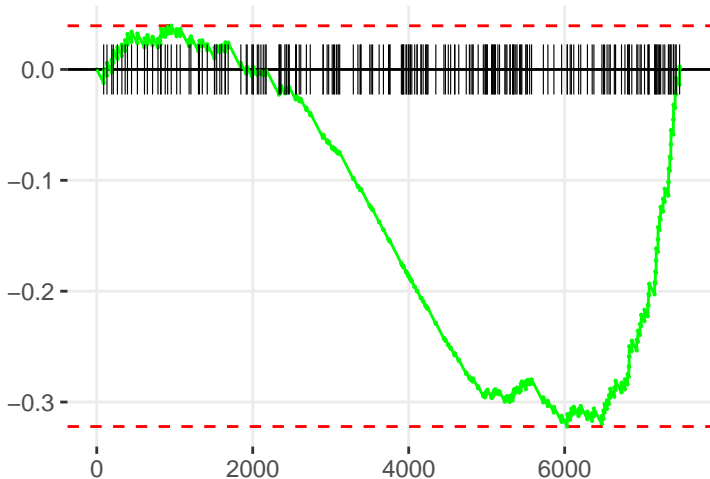
ALANINE BIOSYNTHESIS III



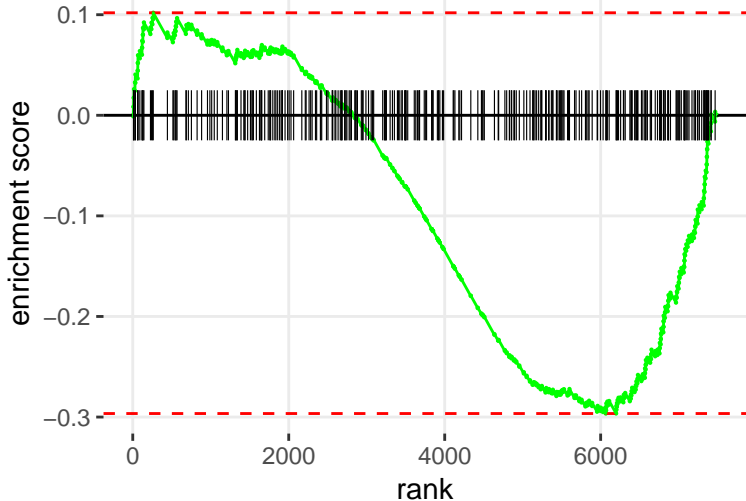
DOLICHYL-DIPHOSPHOOLIGOSACCHARIDE BIOSYNTHESIS

enrichment score

rank



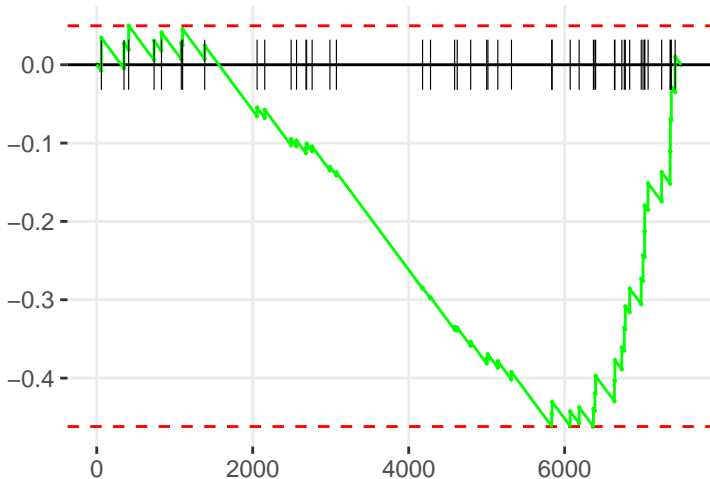
SUCROSE DEGRADATION V (MAMMALIAN)



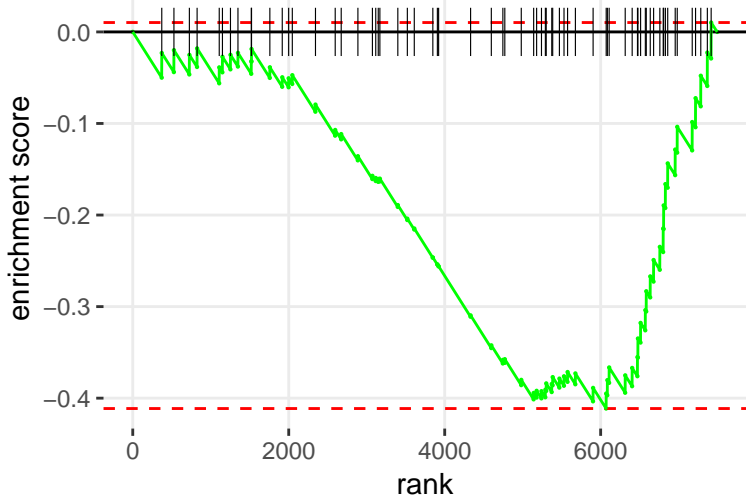
THIOREDOXIN PATHWAY

enrichment score

rank



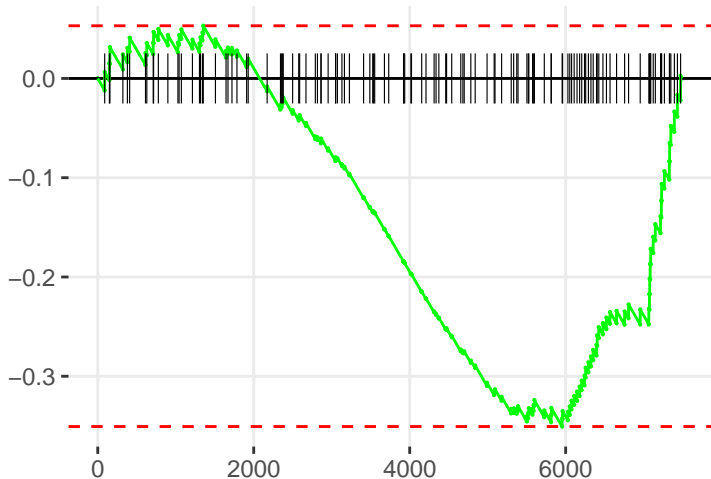
GLUTAMINE BIOSYNTHESIS I



CERAMIDE BIOSYNTHESIS

enrichment score

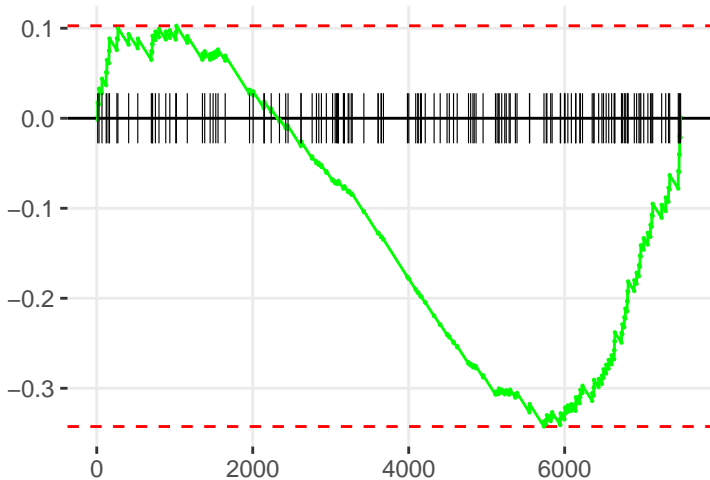
rank



PROSTANOID BIOSYNTHESIS

enrichment score

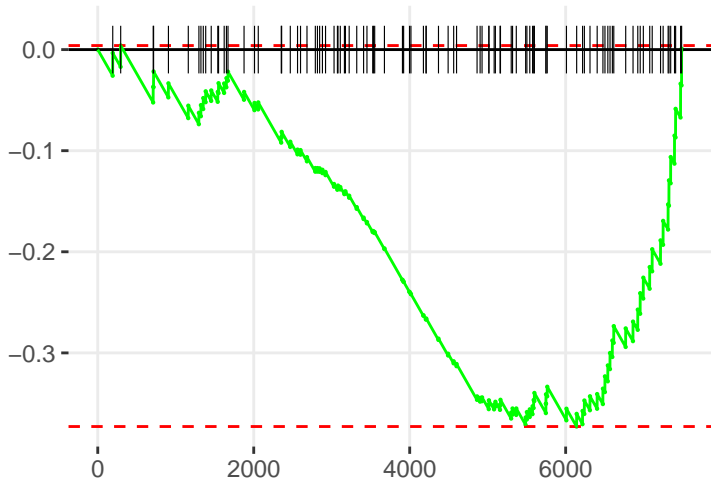
rank



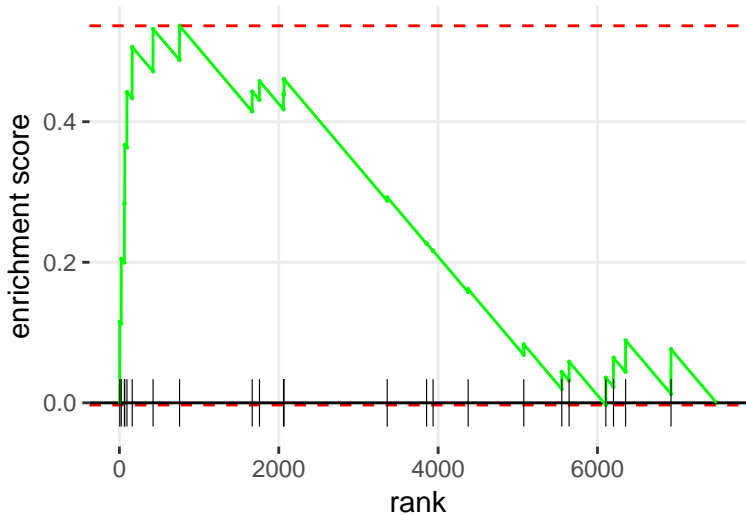
MOLYBDENUM COFACTOR BIOSYNTHESIS

enrichment score

rank



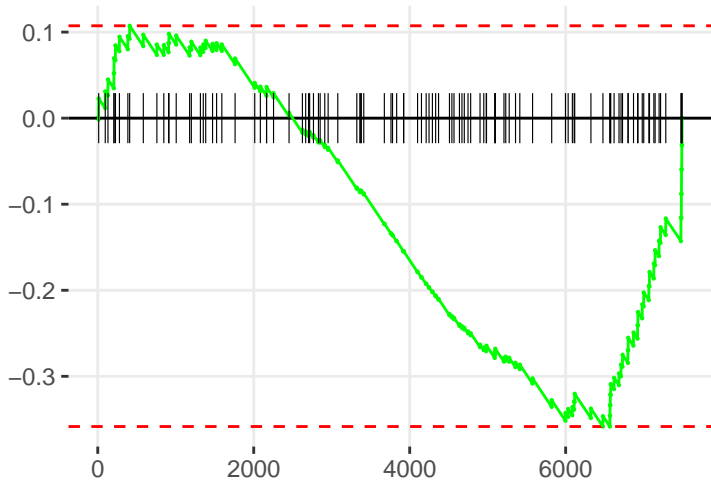
LACTOSE DEGRADATION III



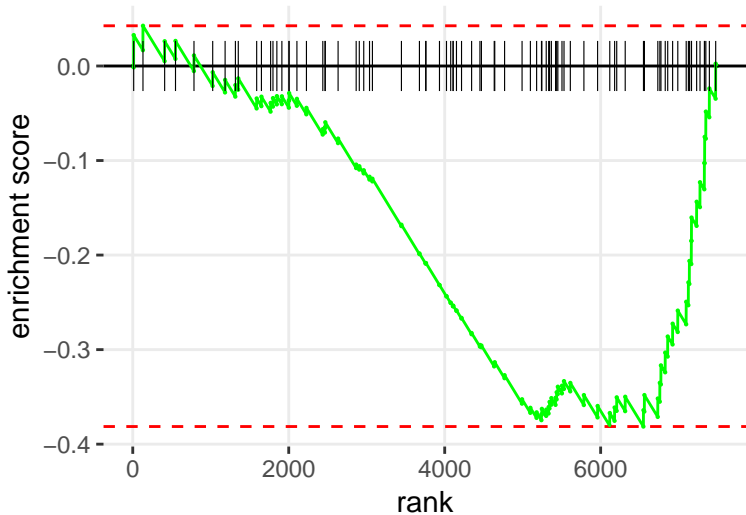
GUANOSINE NUCLEOTIDES DEGRADATION III

enrichment score

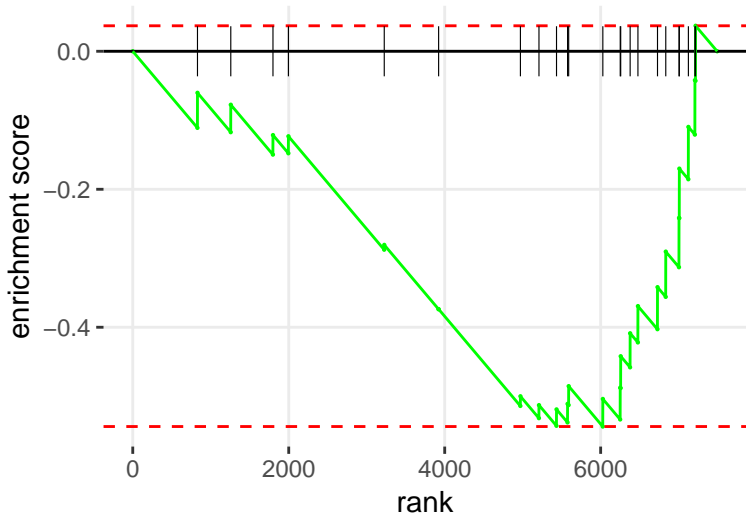
rank



SPERMIDINE BIOSYNTHESIS I



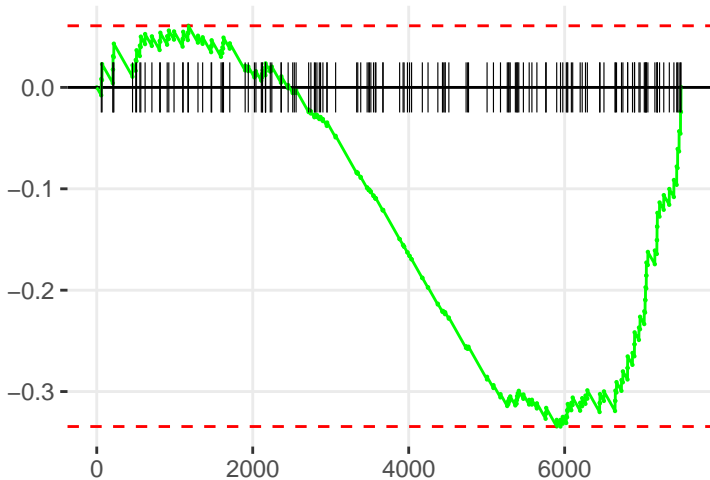
SORBITOL DEGRADATION I



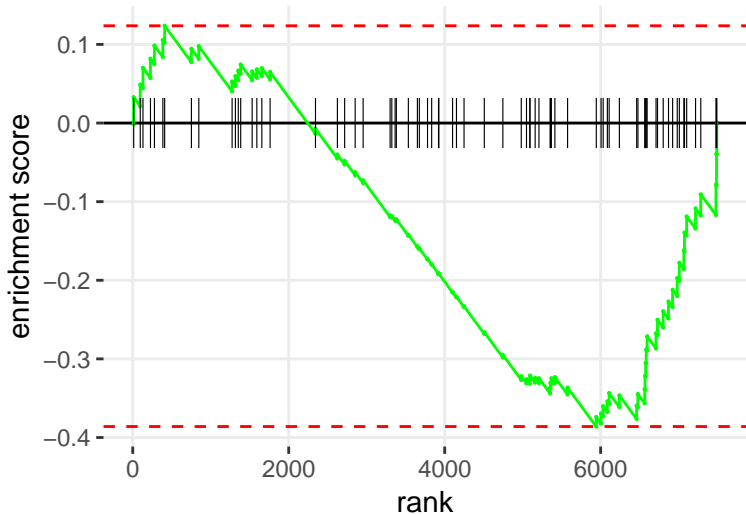
MELATONIN DEGRADATION I

enrichment score

rank



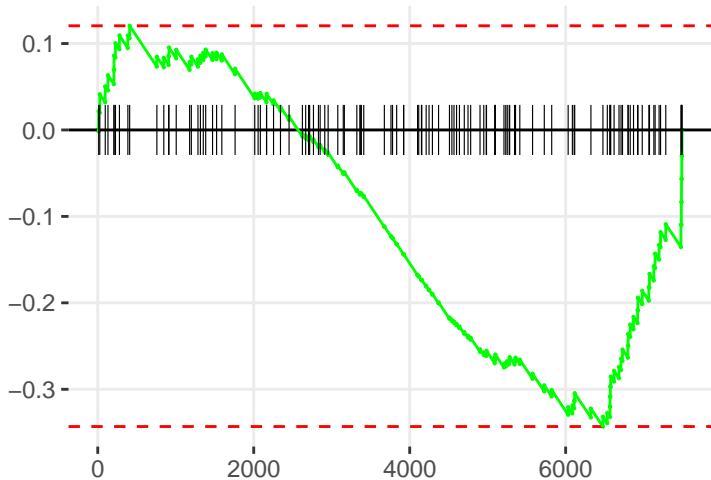
GUANINE AND GUANOSINE SALVAGE I



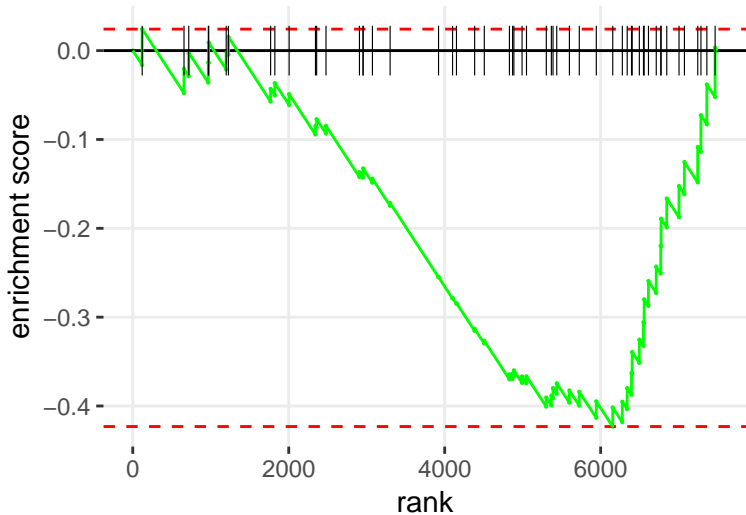
ADENOSINE NUCLEOTIDES DEGRADATION II

enrichment score

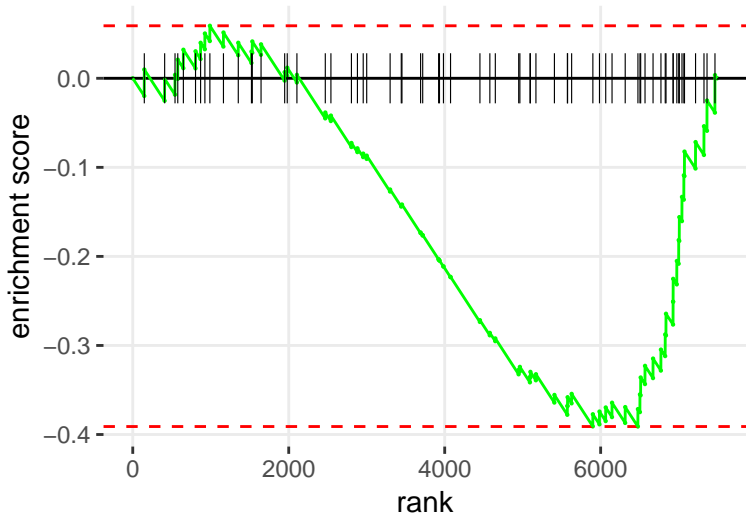
rank



ACETYL-COA BIOSYNTHESIS III (FROM CITRATE)



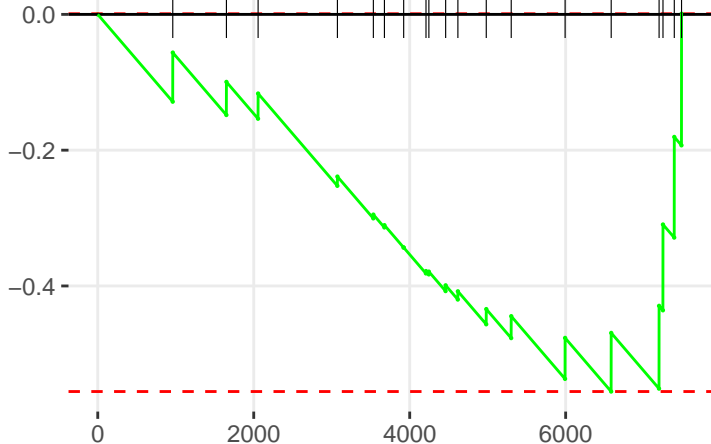
GLYCEROL DEGRADATION I



GDP-L-FUCOSE BIOSYNTHESIS I (FROM GDP-D-MANNOSE)

enrichment score

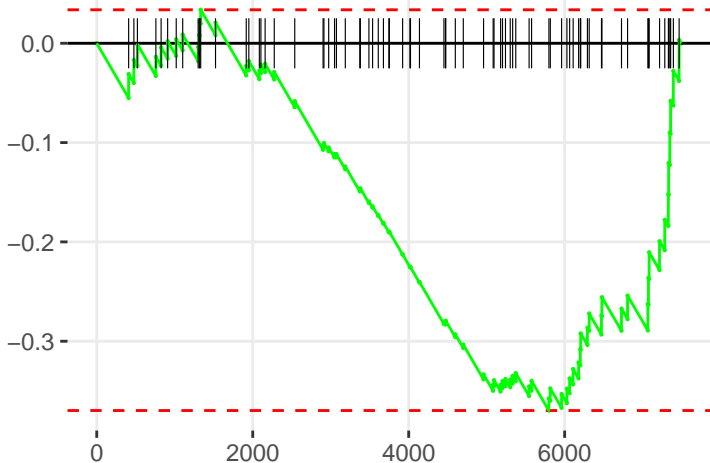
rank



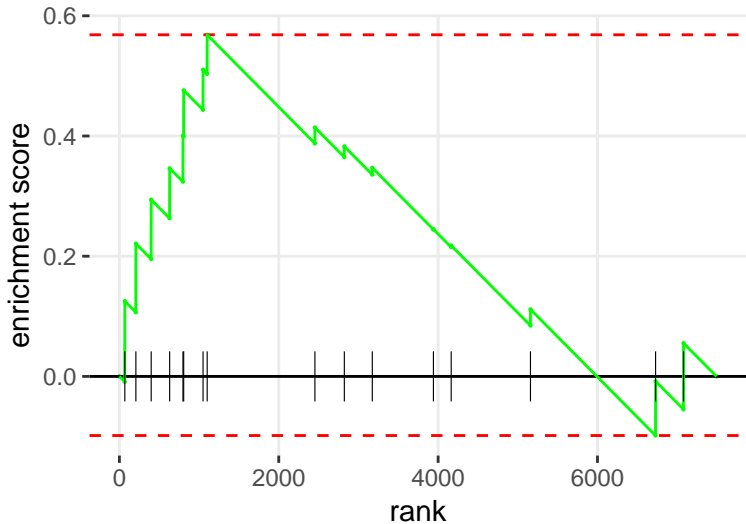
OLEATE BIOSYNTHESIS II (ANIMALS)

enrichment score

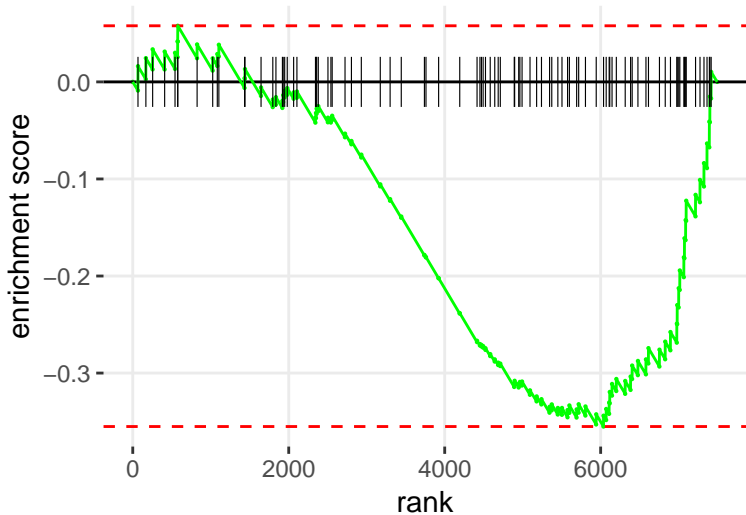
rank



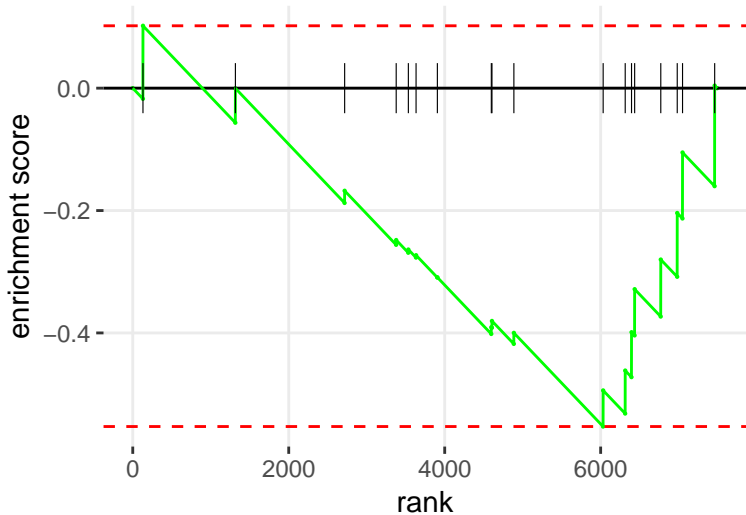
GLUCOCORTICOID BIOSYNTHESIS



GLYCEROL-3-PHOSPHATE SHUTTLE



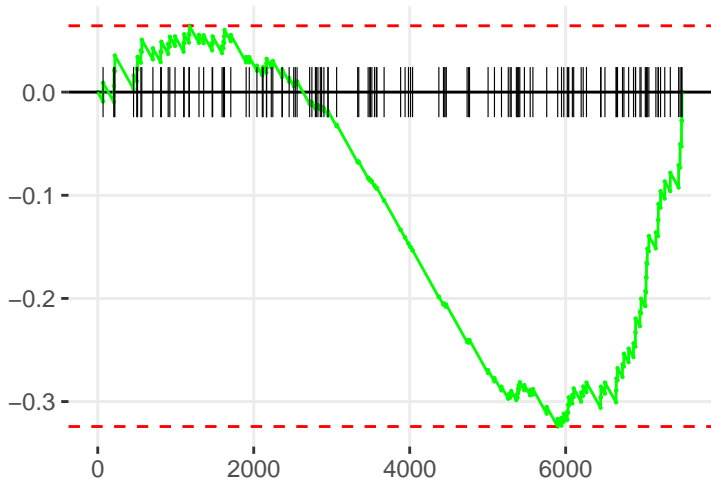
NADH REPAIR



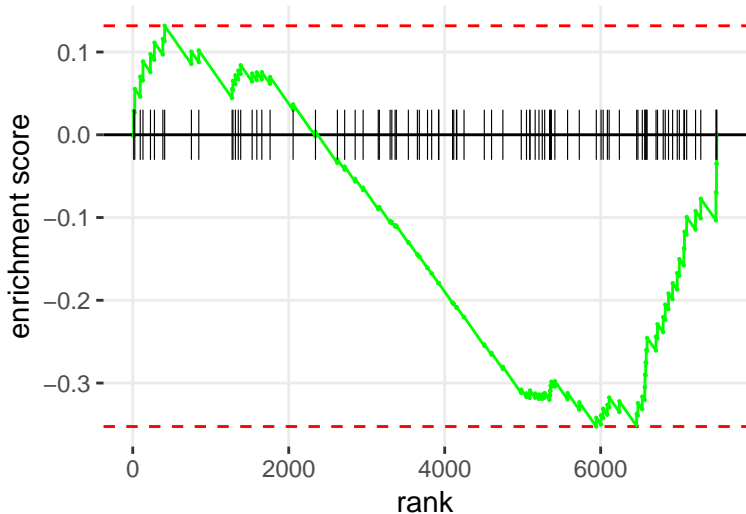
NICOTINE DEGRADATION III

enrichment score

rank



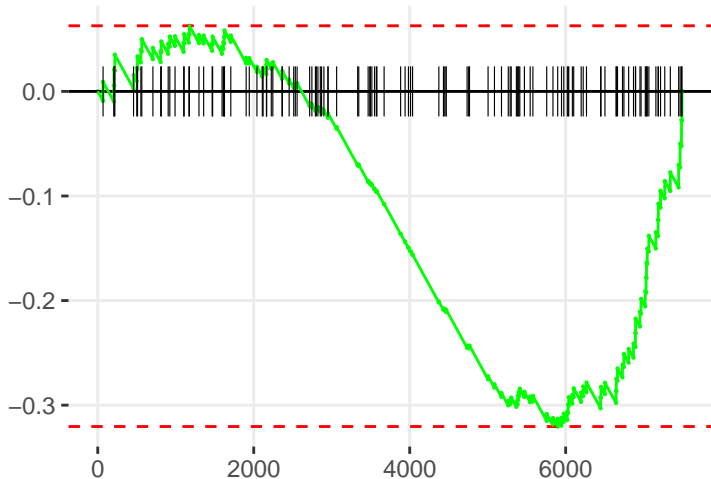
ADENINE AND ADENOSINE SALVAGE III



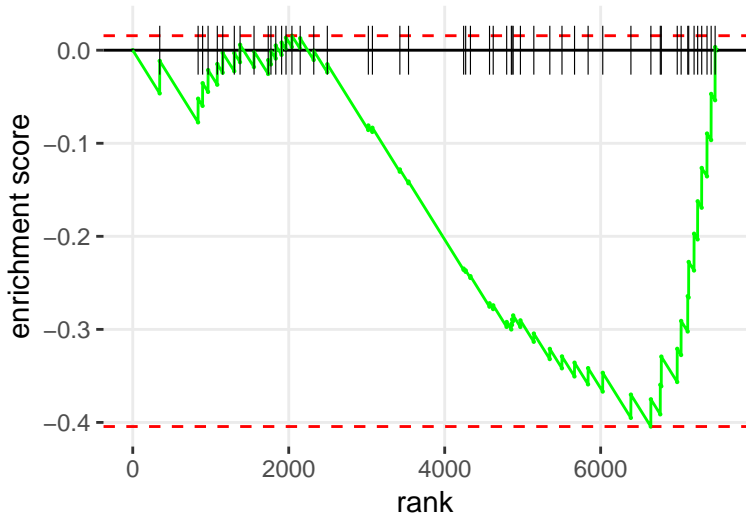
NICOTINE DEGRADATION IV

enrichment score

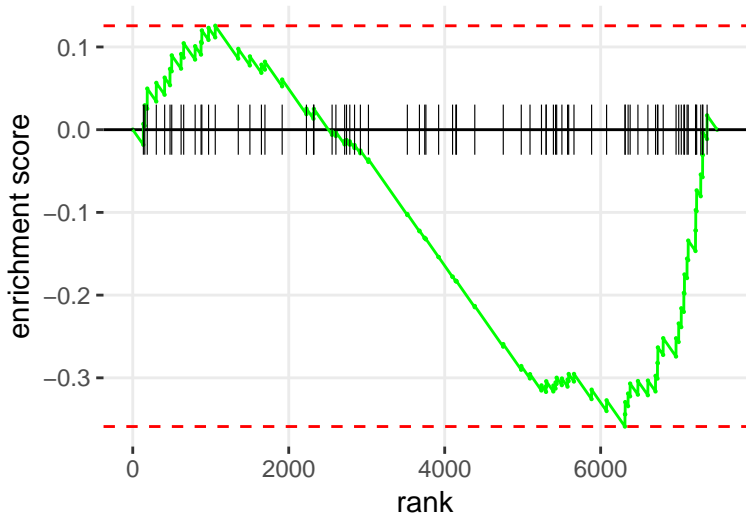
rank



FATTY ACID & BETA;-OXIDATION III (UNSATURATED, ODD NUMBER)

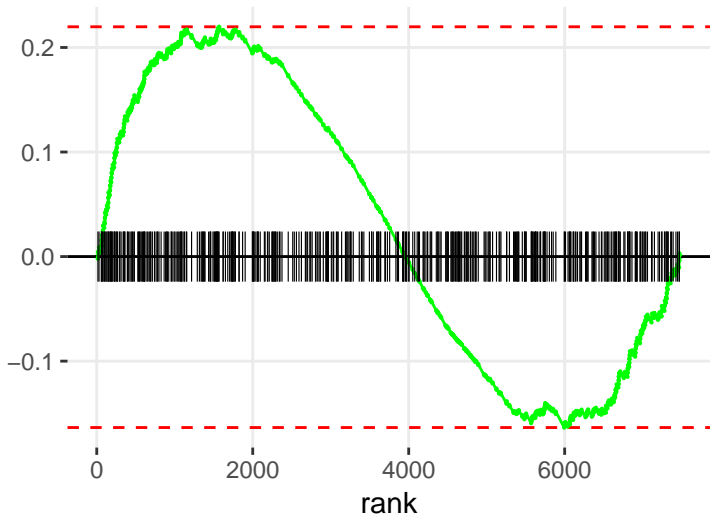


LEUKOTRIENE BIOSYNTHESIS

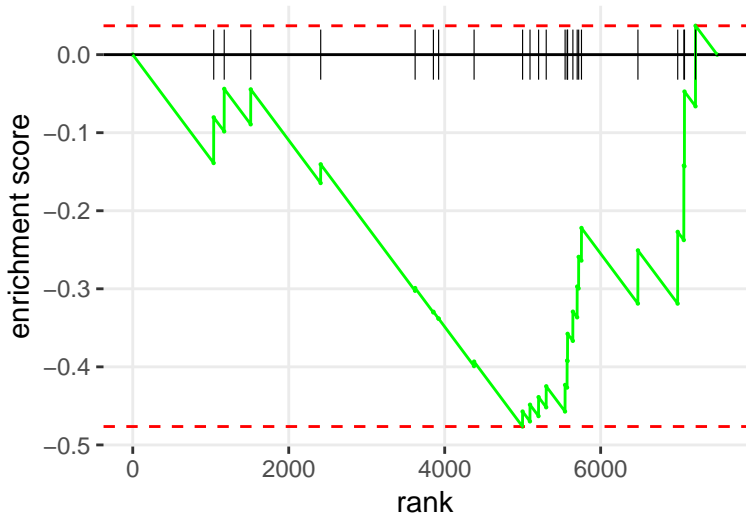


D-<IMYO</I-INOSITOL-5-PHOSPHATE METABOLISM

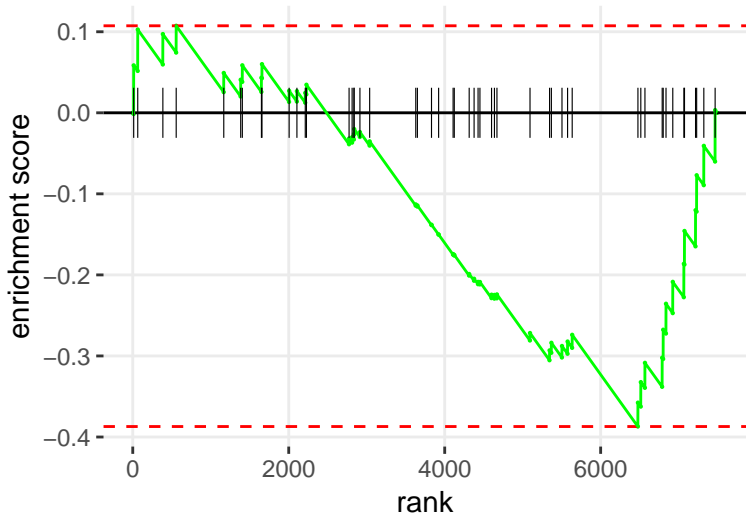
enrichment score



PUTRESCINE BIOSYNTHESIS III



FORMALDEHYDE OXIDATION II (GLUTATHIONE-DEPENDENT)



GLUTAMATE DEGRADATION III (VIA 4-AMINOBUTYRATE)

enrichment score

0.0

-0.1

-0.2

-0.3

-0.4

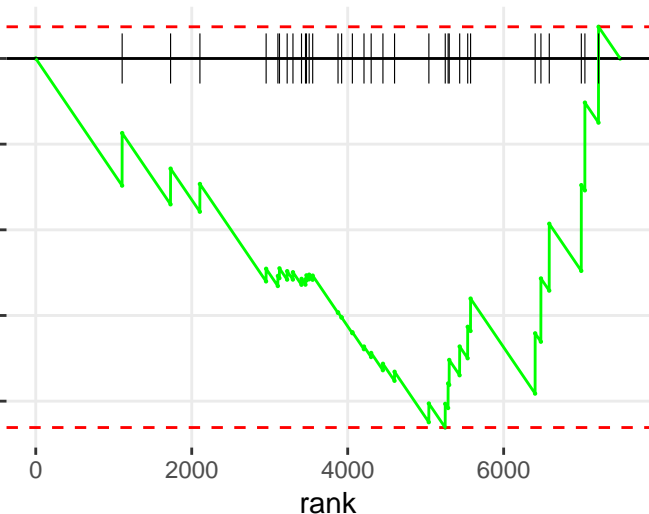
0

2000

4000

6000

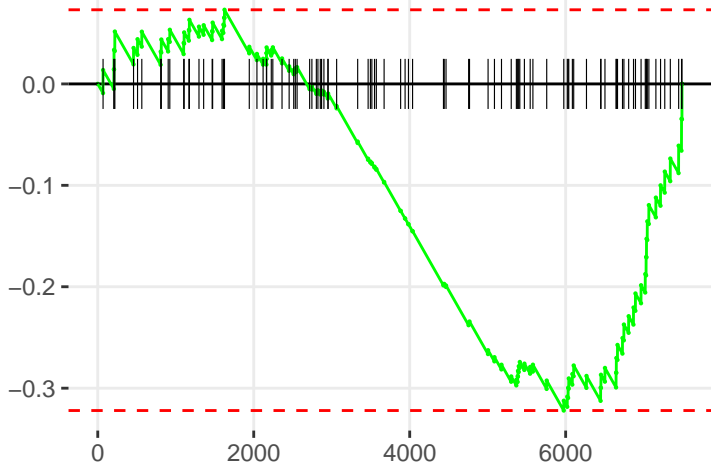
rank



ACETONE DEGRADATION I (TO METHYLGLYOXAL)

enrichment score

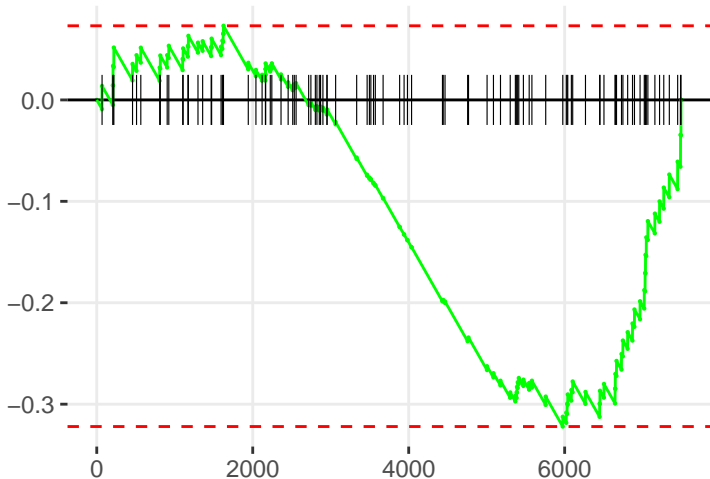
rank



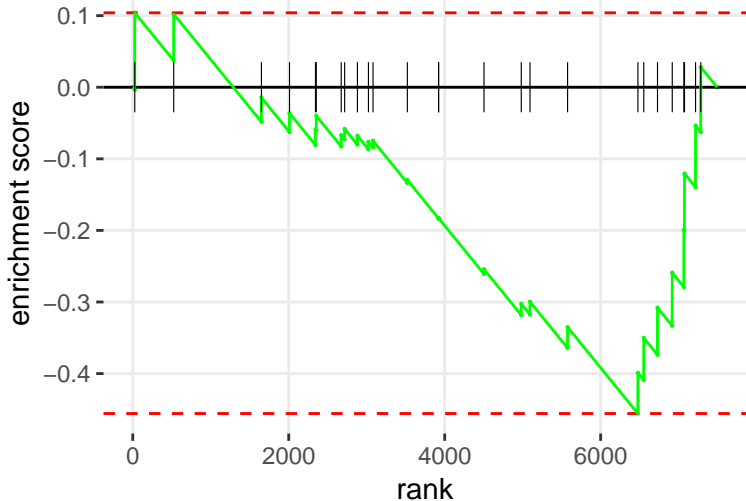
BUPROPION DEGRADATION

enrichment score

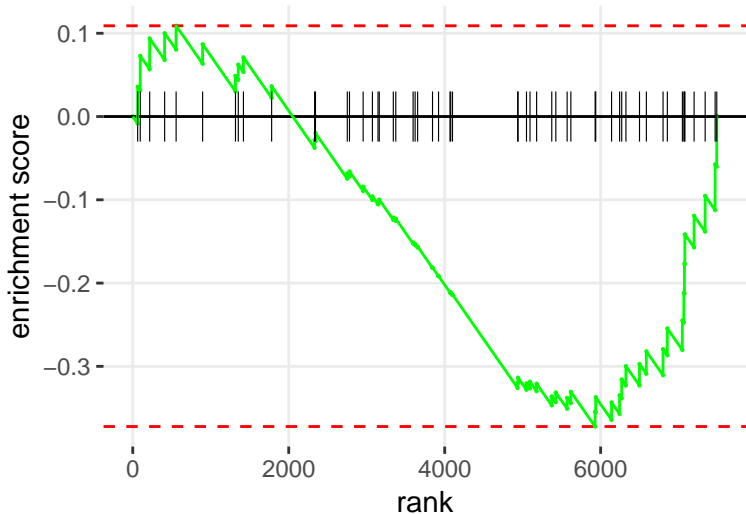
rank



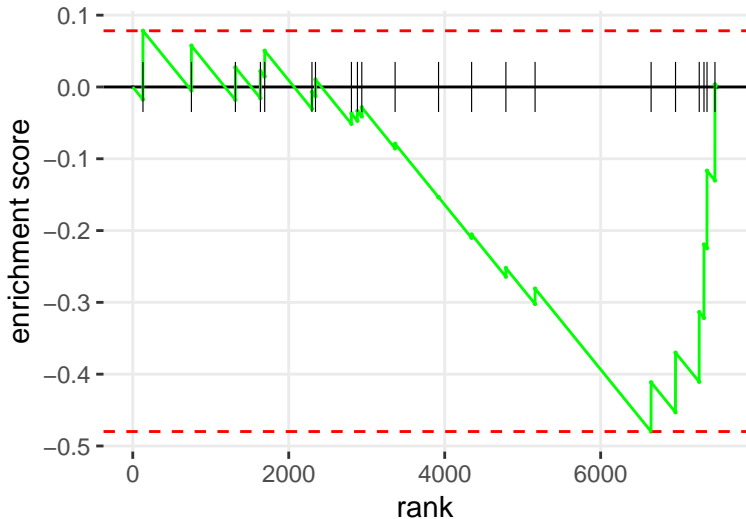
L-CYSTEINE DEGRADATION III



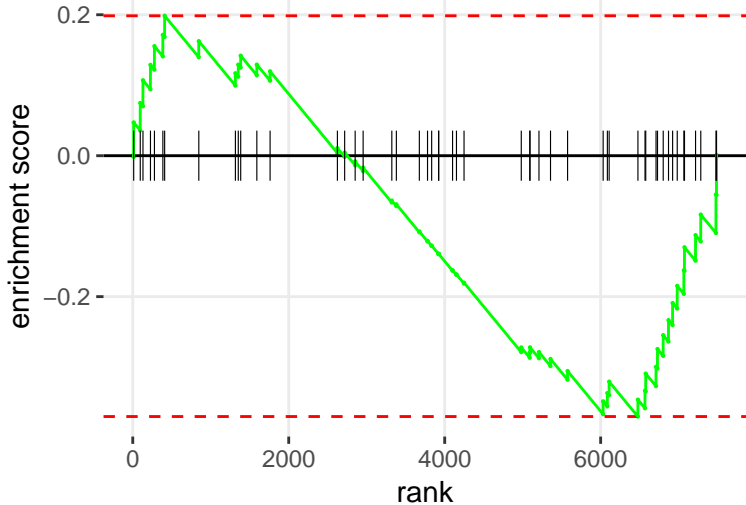
<IS</I-METHYL-5-THIO-&ALPHA;-D-RIBOSE 1-PHOSPHATE DEGRADATION



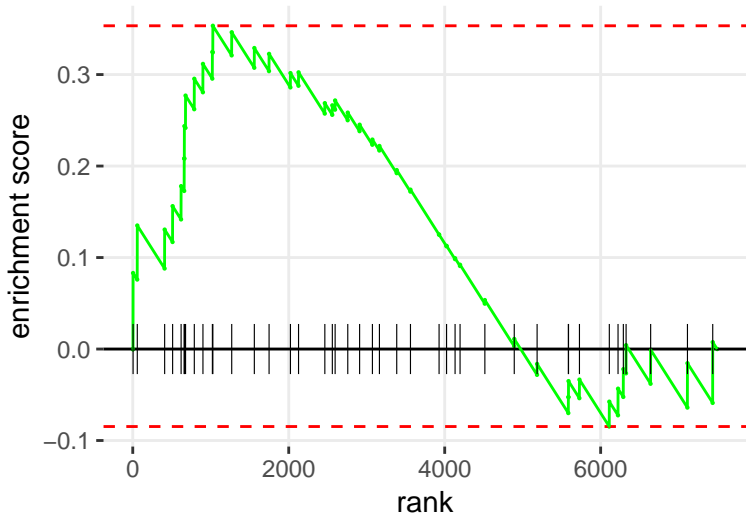
<IN</I>-ACETYLGLUCOSAMINE DEGRADATION I



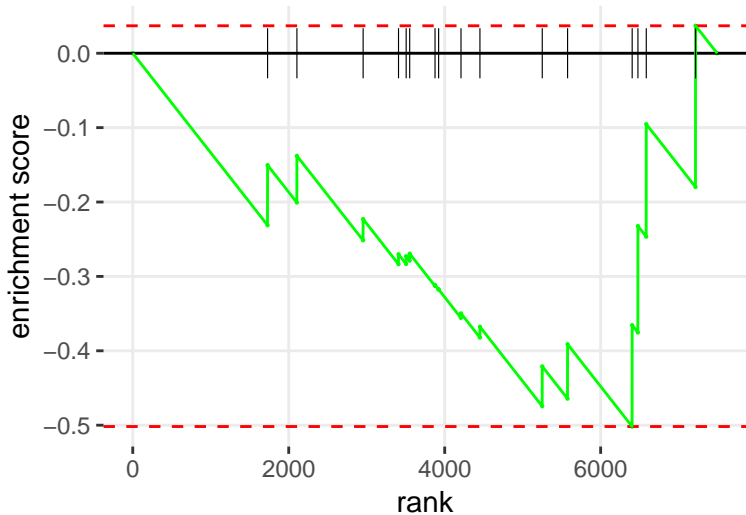
XANTHINE AND XANTHOSINE SALVAGE



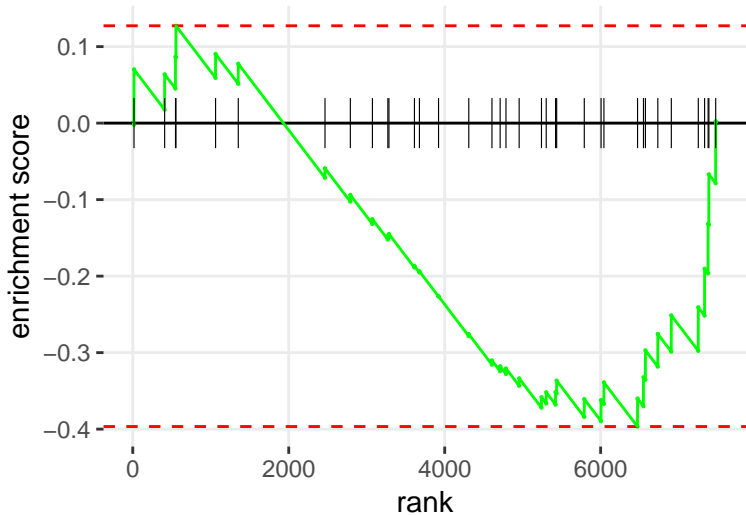
CHONDROITIN SULFATE BIOSYNTHESIS (LATE STAGES)



4-AMINOBUTYRATE DEGRADATION I

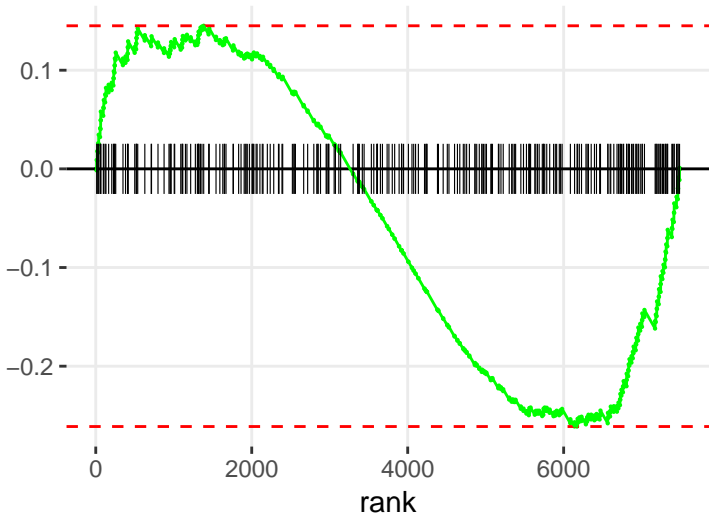


SPERMINE BIOSYNTHESIS



GLUTATHIONE-MEDIATED DETOXIFICATION I

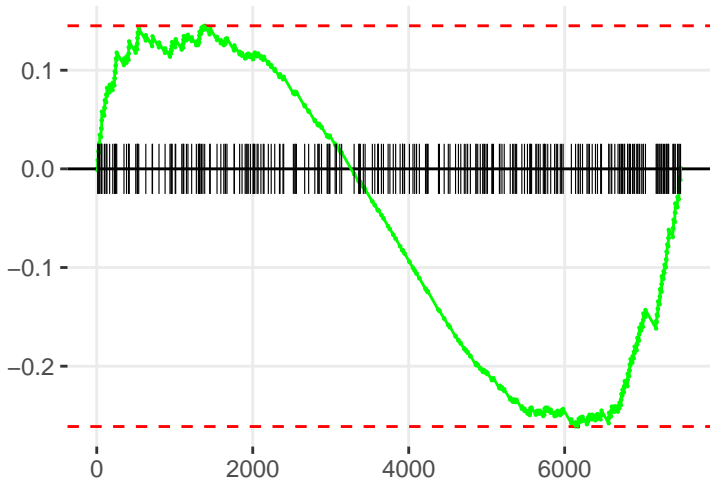
enrichment score



4-HYDROXY-2-NONENAL DETOXIFICATION

enrichment score

rank



CATECHOLAMINE BIOSYNTHESIS

enrichment score

0.0

-0.1

-0.2

-0.3

-0.4

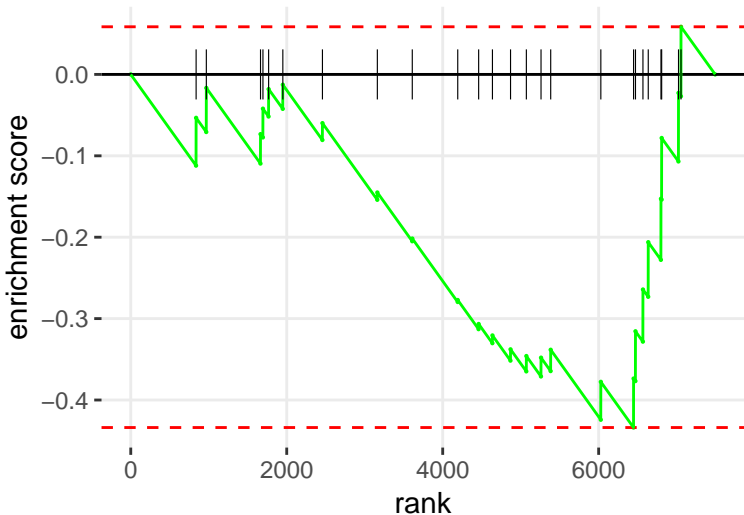
0

2000

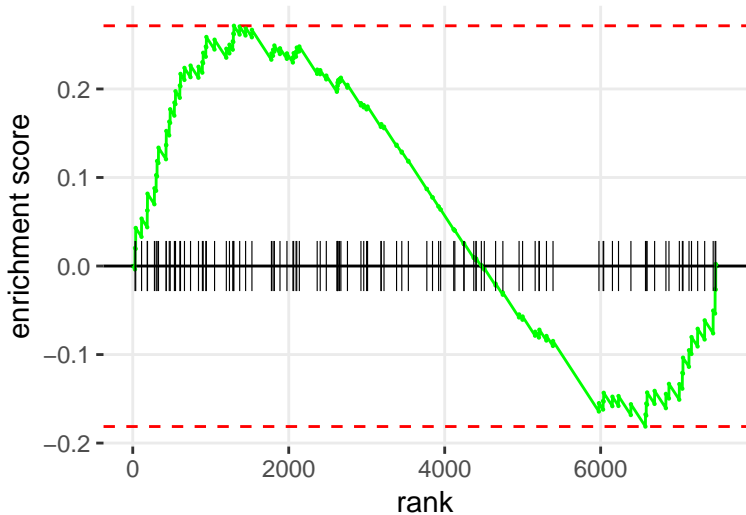
4000

6000

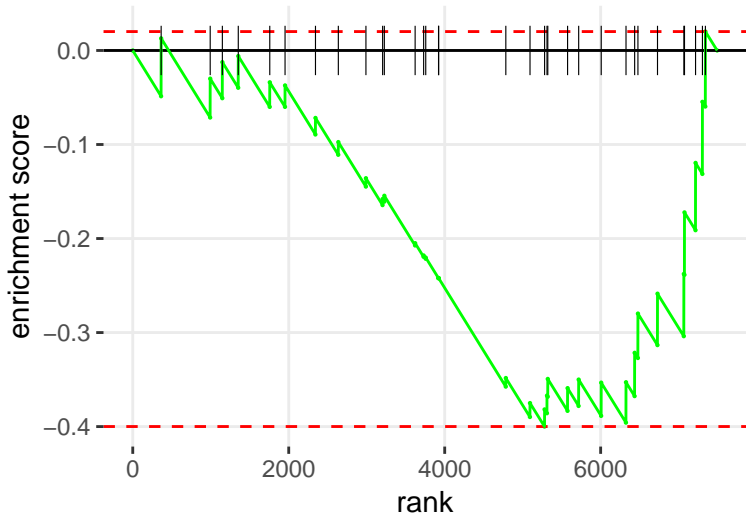
rank



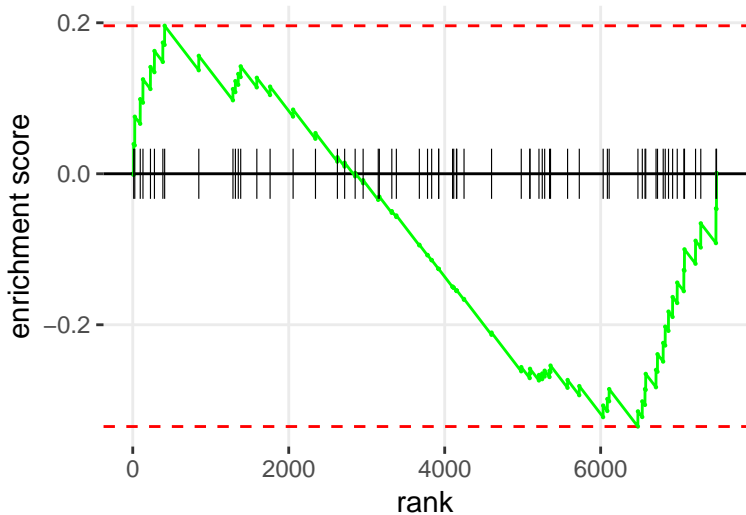
PHENYLALANINE DEGRADATION I (AEROBIC)



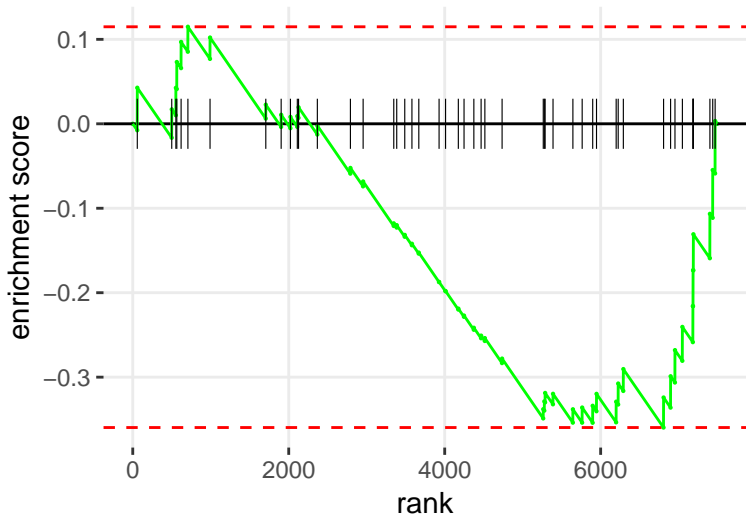
PHOSPHATIDYLETHANOLAMINE BIOSYNTHESIS II



PURINE RIBONUCLEOSIDES DEGRADATION TO RIBOSE-1-PHOSPHATE

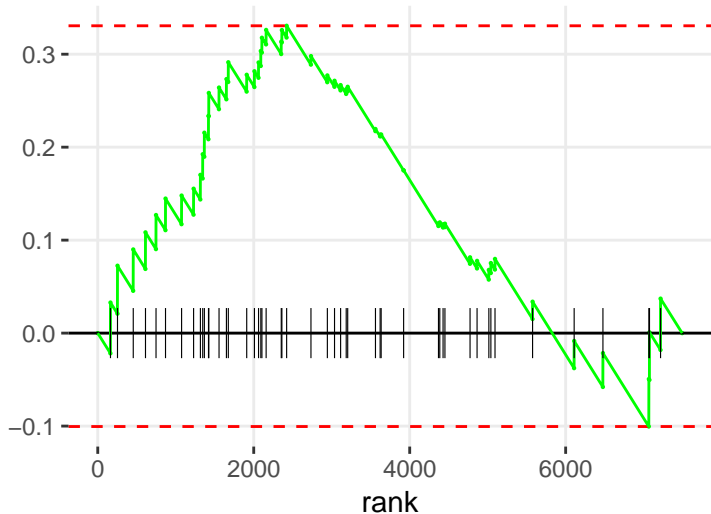


THYROID HORMONE METABOLISM II (VIA CONJUGATION AND/OR DEGRADATION)



UBIQUINOL-10 BIOSYNTHESIS (EUKARYOTIC)

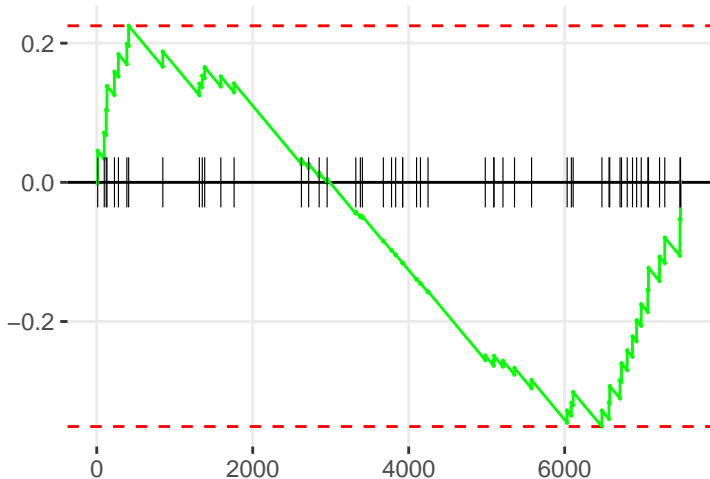
enrichment score



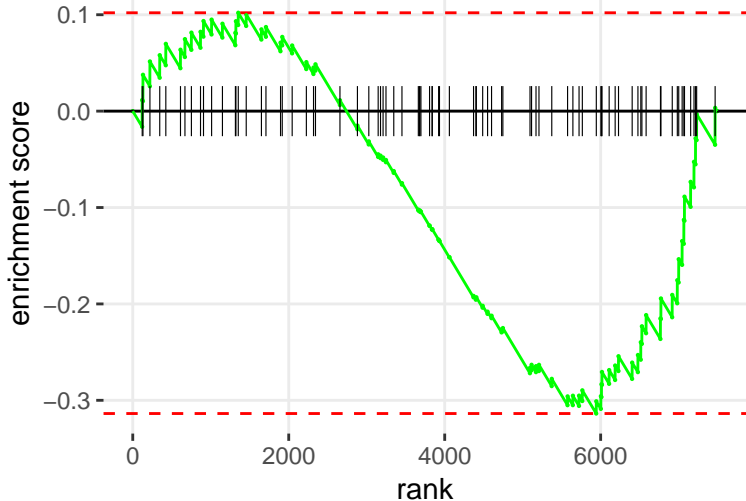
ARSENATE DETOXIFICATION I (GLUTAREDOXIN)

enrichment score

rank



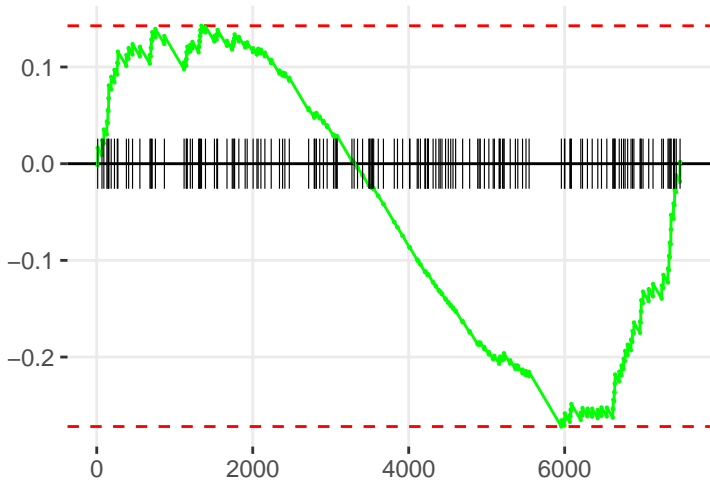
TETRAPYRROLE BIOSYNTHESIS II



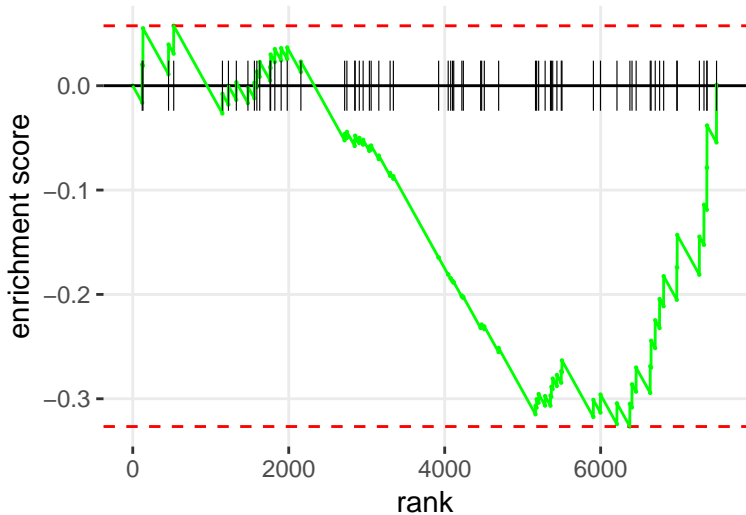
PYRUVATE FERMENTATION TO LACTATE

enrichment score

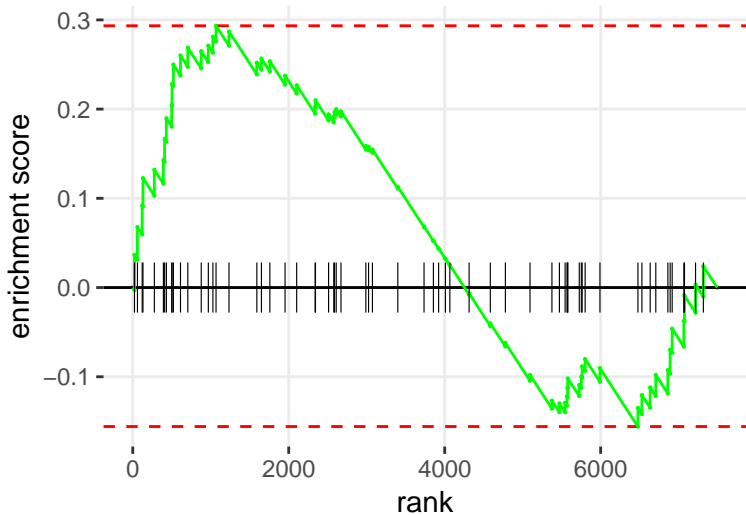
rank



CREATINE-PHOSPHATE BIOSYNTHESIS

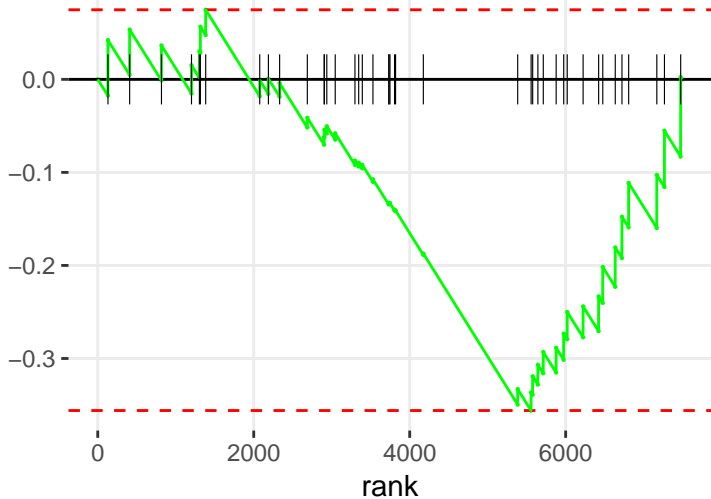


SPHINGOMYELIN METABOLISM

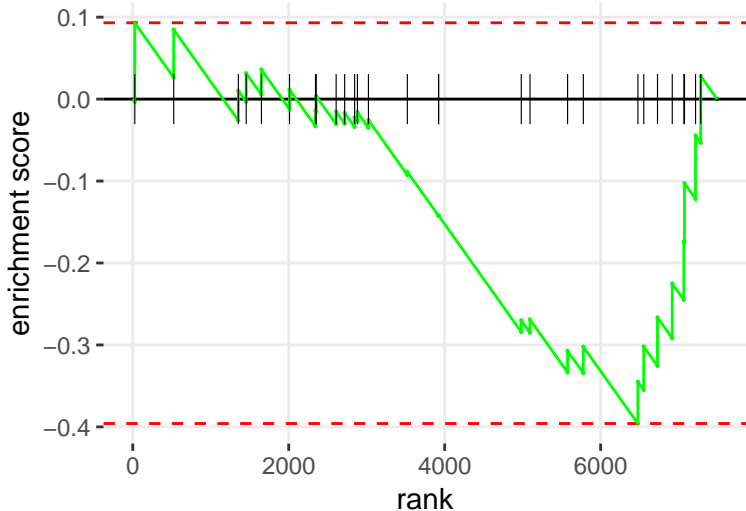


1D-<IMYO</I>-INOSITOL HEXAKISPHOSPHATE BIOSYNTHESIS II (MAMMALIAN)

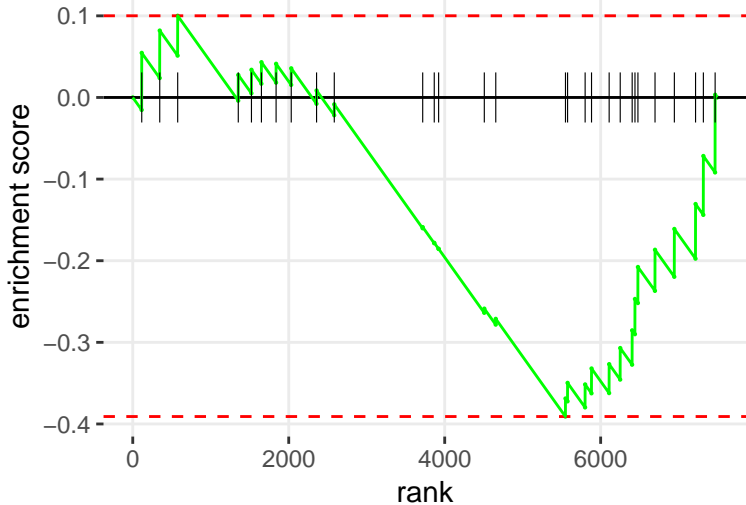
enrichment score



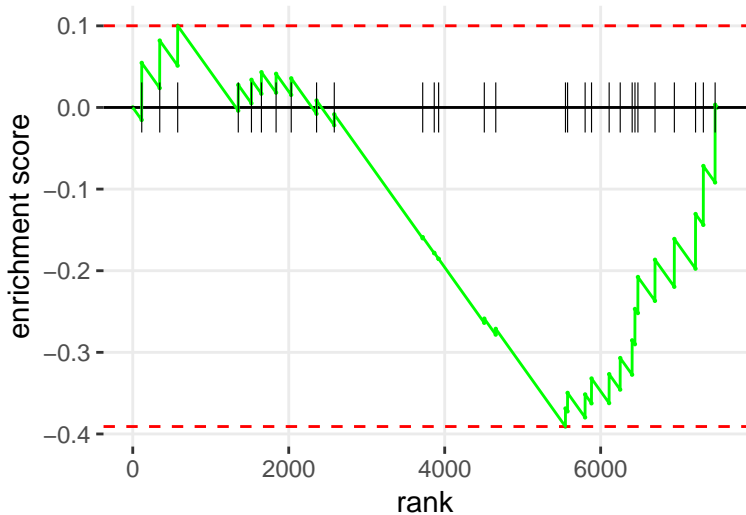
THIOSULFATE DISPROPORTIONATION III (RHODANESE)



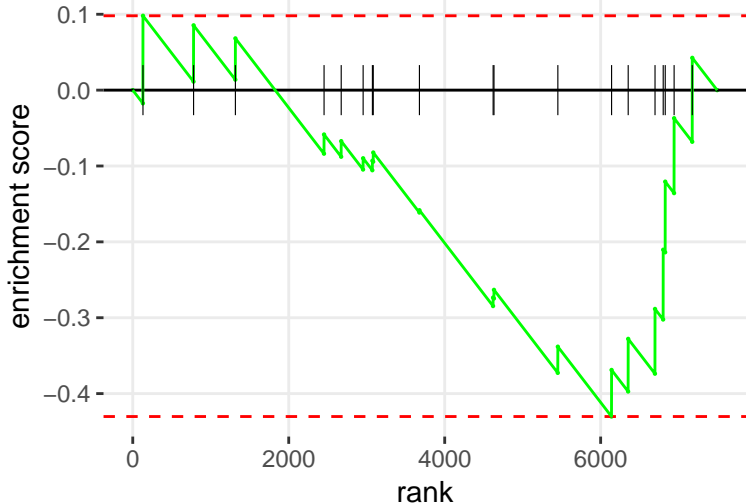
ALANINE BIOSYNTHESIS II

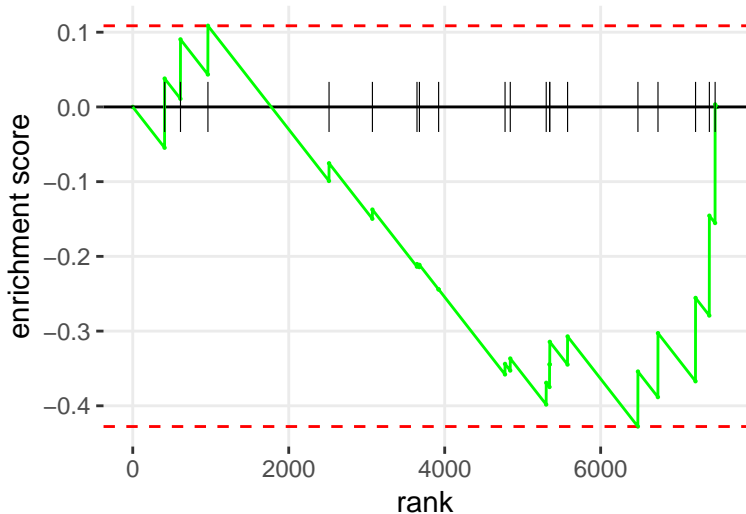


ALANINE DEGRADATION III

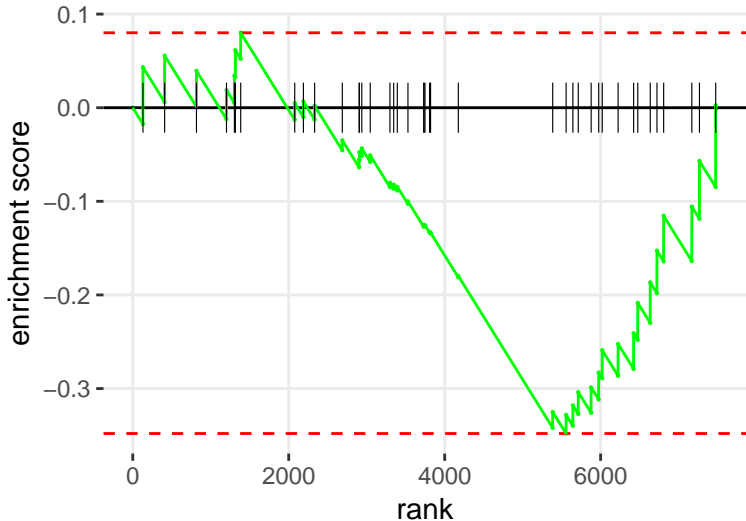


ACYL CARRIER PROTEIN METABOLISM



ALL-*l*-TRANSL-DECAPRENYL DIPHOSPHATE BIOSYNTHESIS

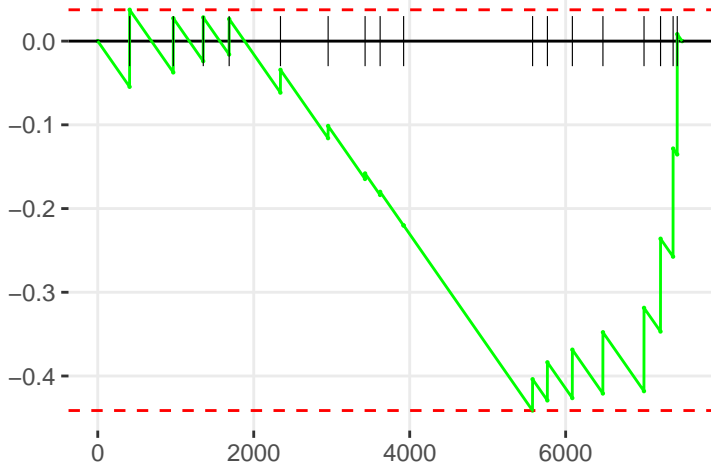
D-<IMYO</I>-INOSITOL (1,3,4)-TRISPHOSPHATE BIOSYNTHESIS



GLUTATHIONE REDOX REACTIONS II

enrichment score

rank



PHOSPHATIDYLETHANOLAMINE BIOSYNTHESIS III

enrichment score

0.4
0.3
0.2
0.1
0.0

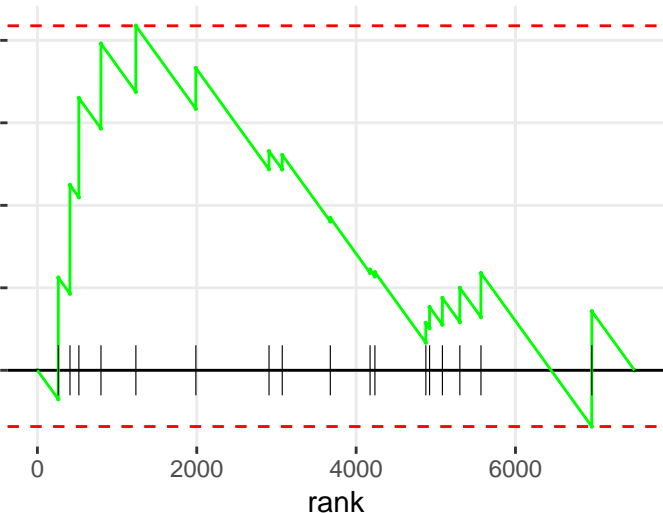
0

2000

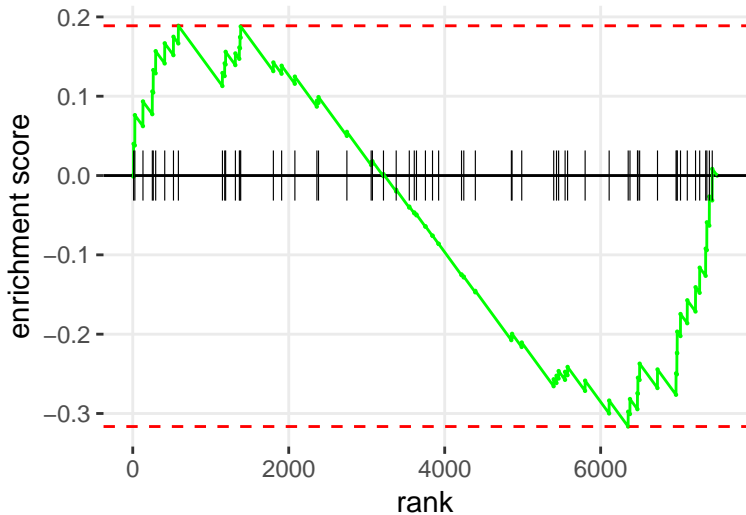
4000

6000

rank

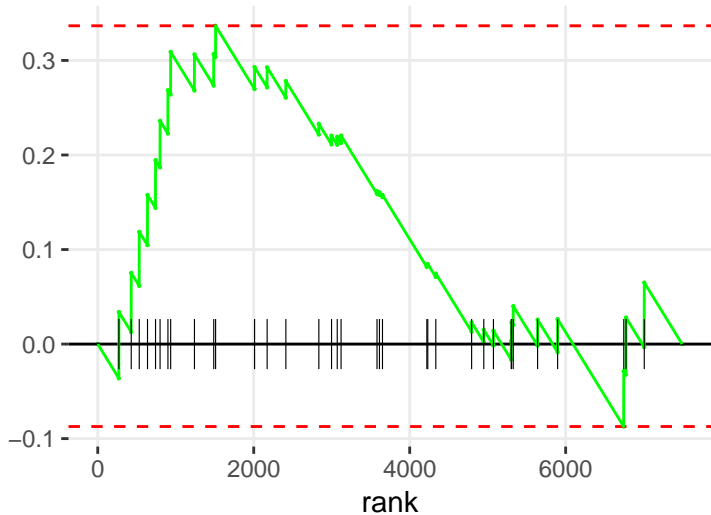


MITOCHONDRIAL L-CARNITINE SHUTTLE PATHWAY

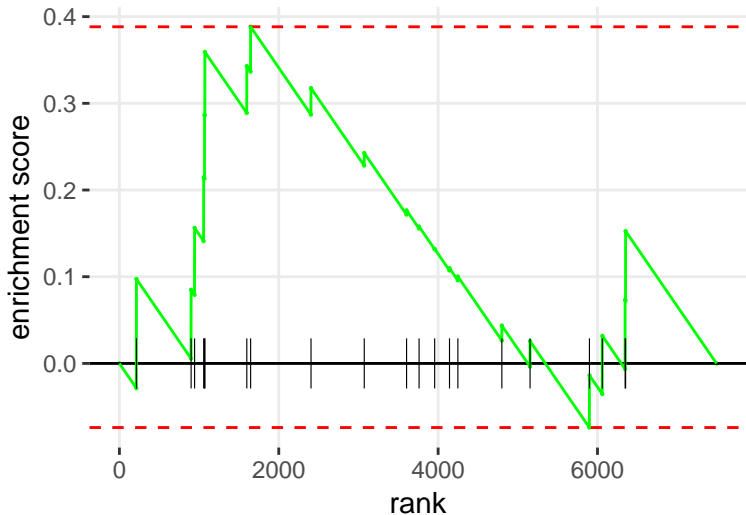


GLYCOAMINOGLYCAN-PROTEIN LINKAGE REGION BIOSYNTHESIS

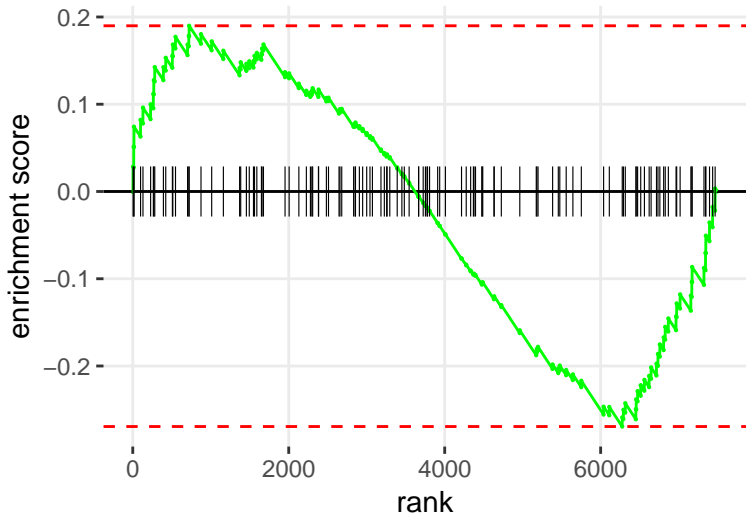
enrichment score



CHONDROITIN AND DERMATAN BIOSYNTHESIS



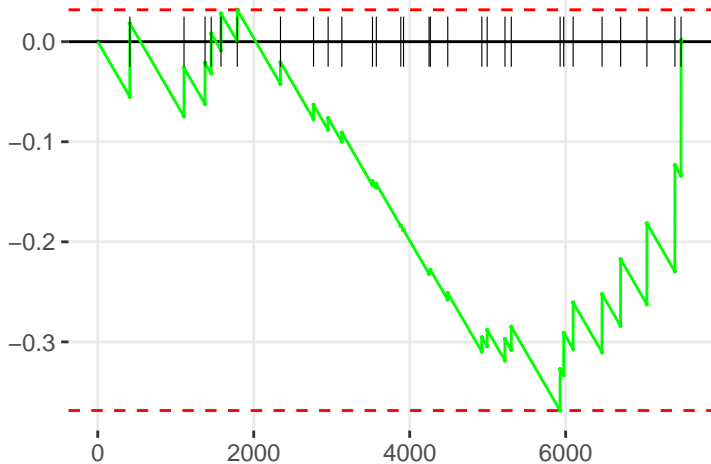
SALVAGE PATHWAYS OF PYRIMIDINE DEOXYRIBONUCLEOTIDES



L-CARNITINE BIOSYNTHESIS

enrichment score

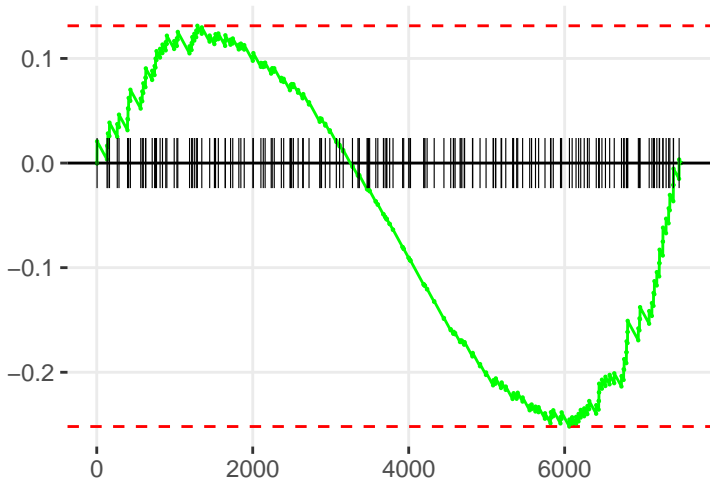
rank



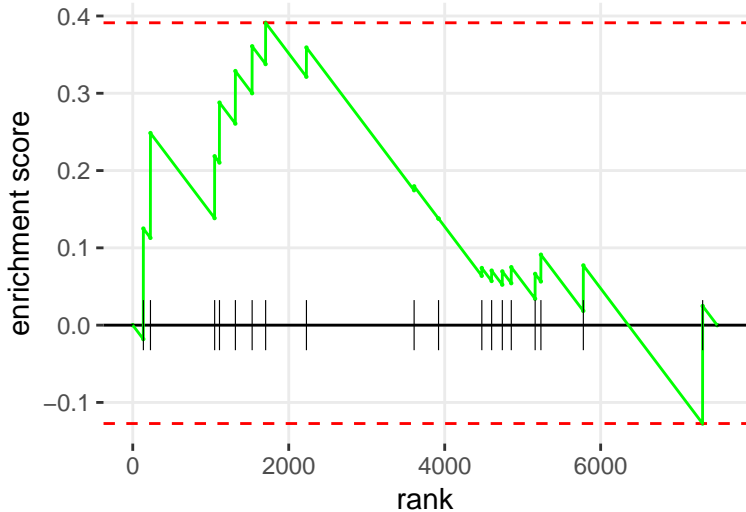
CALCIUM TRANSPORT I

enrichment score

rank

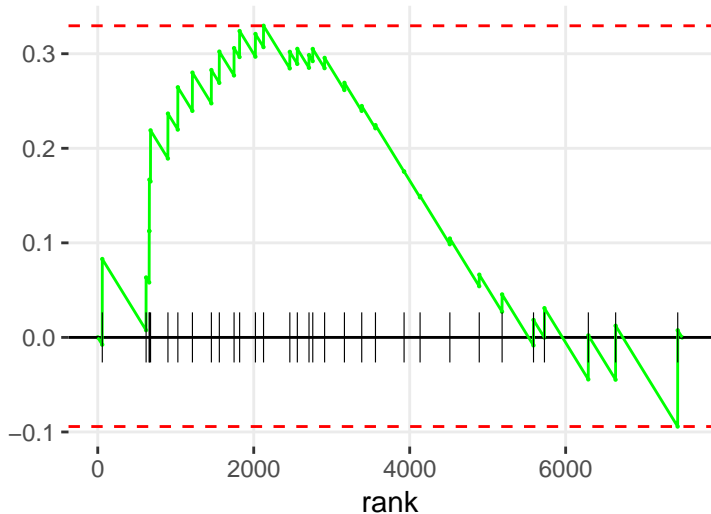


NAD BIOSYNTHESIS III



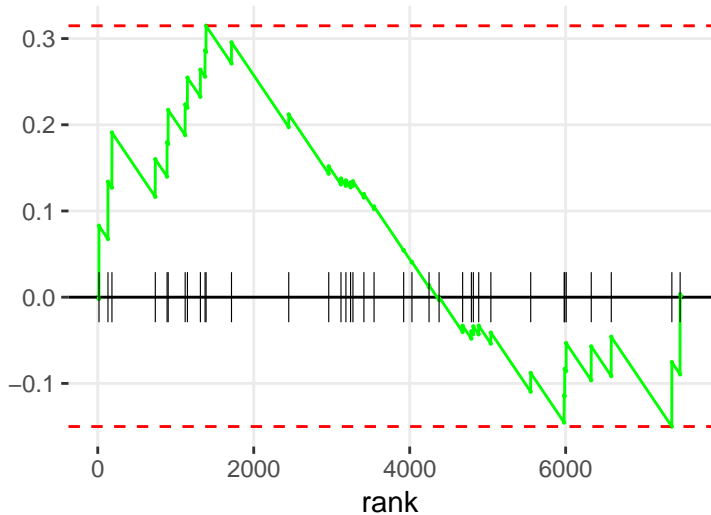
DERMATAN SULFATE BIOSYNTHESIS (LATE STAGES)

enrichment score



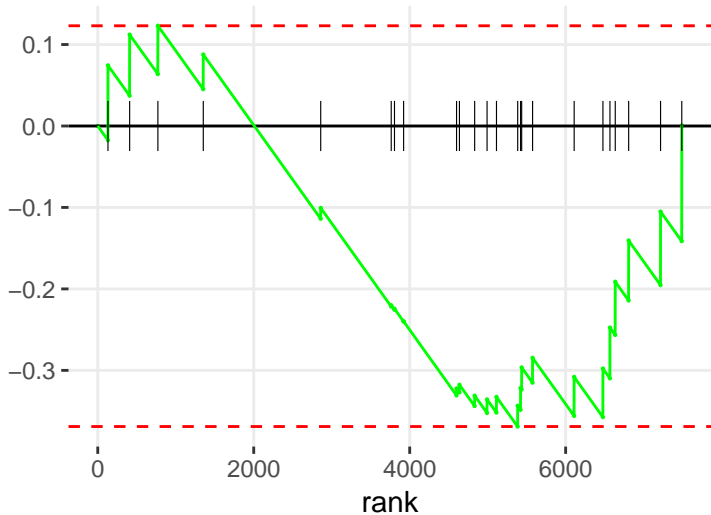
METHYLMALONYL PATHWAY

enrichment score

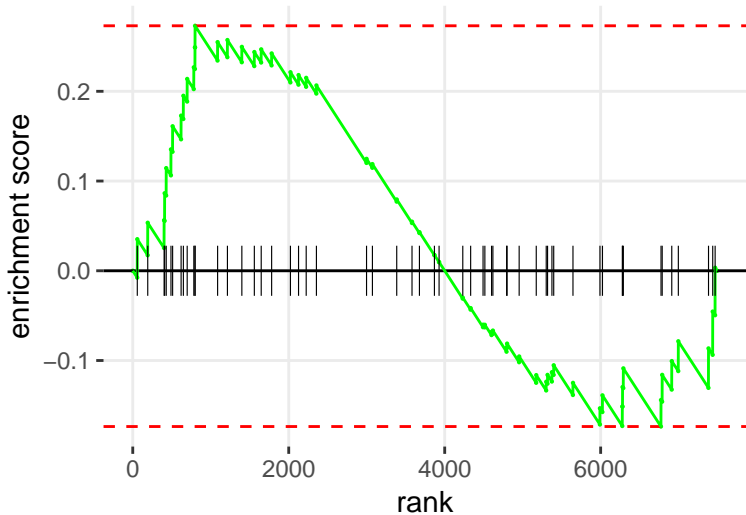


NAD PHOSPHORYLATION AND DEPHOSPHORYLATION

enrichment score



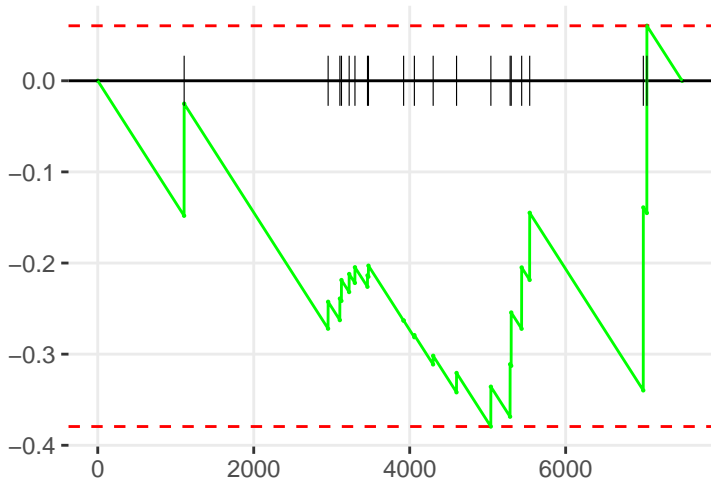
HEPARAN SULFATE BIOSYNTHESIS (LATE STAGES)



GLUTAMATE DEPENDENT ACID RESISTANCE

enrichment score

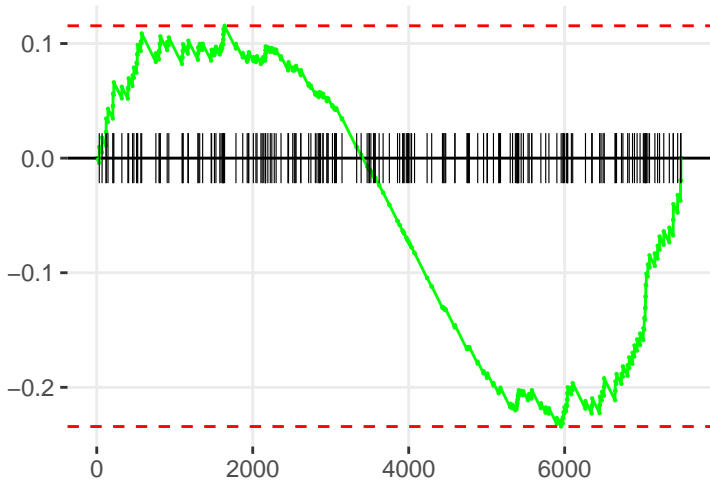
rank



ESTROGEN BIOSYNTHESIS

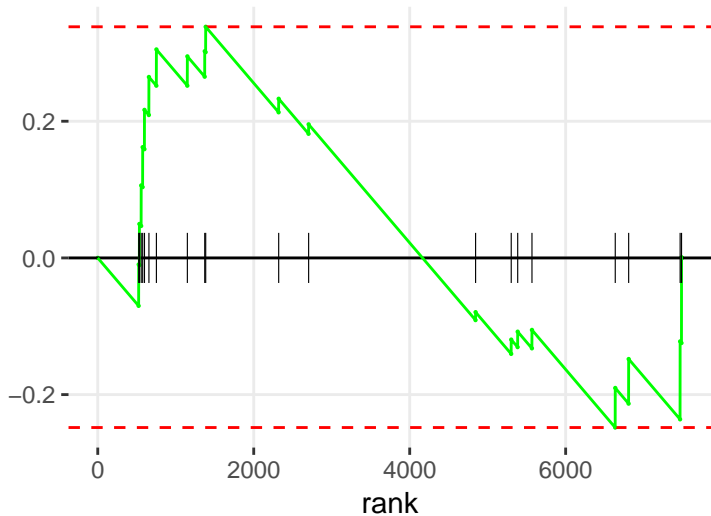
enrichment score

rank



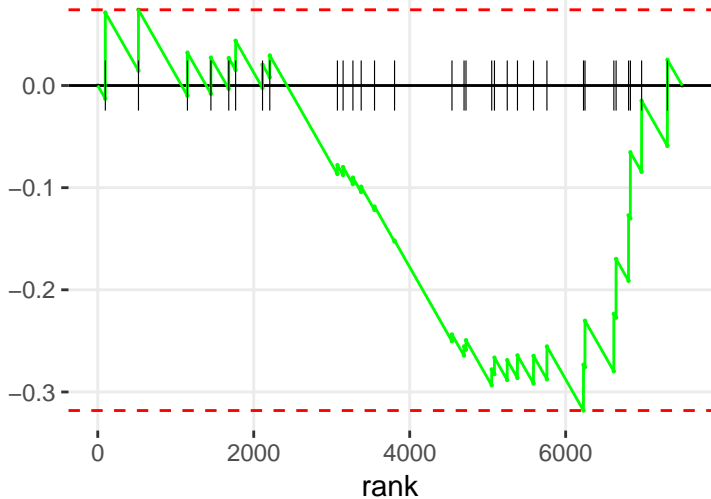
PROTEIN CITRULLINATION

enrichment score

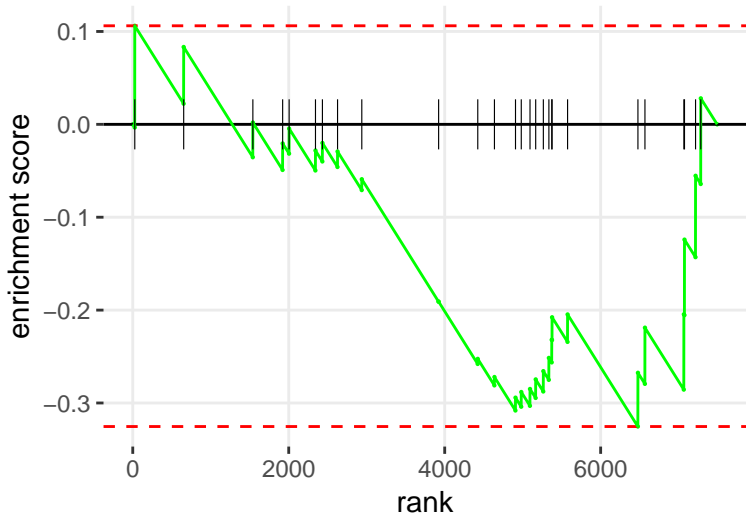


TYROSINE DEGRADATION I

enrichment score



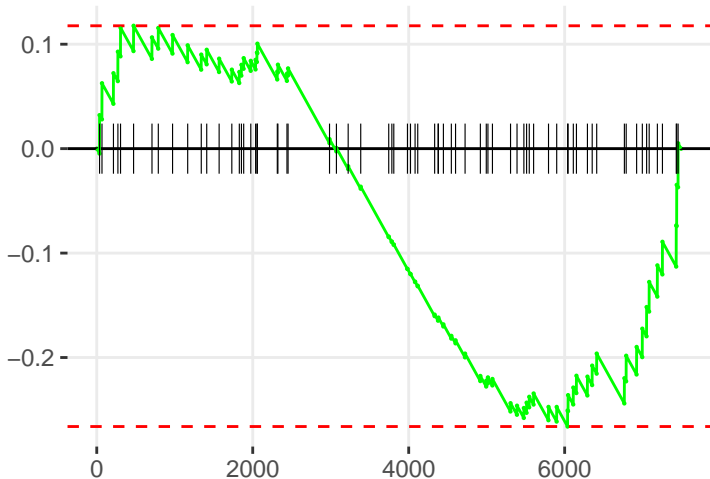
<ITRANS, TRANS</I>-FARNESYL DIPHOSPHATE BIOSYNTHESIS



DERMATAN SULFATE DEGRADATION (METAZOA)

enrichment score

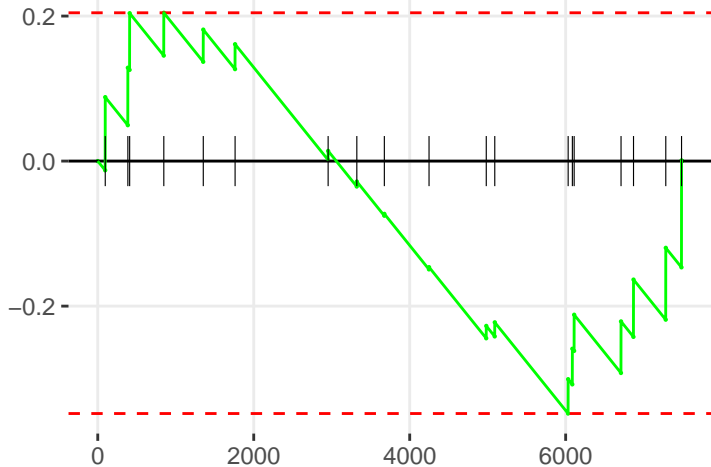
rank



<IS</I-METHYL-5'-THIOADENOSINE DEGRADATION II

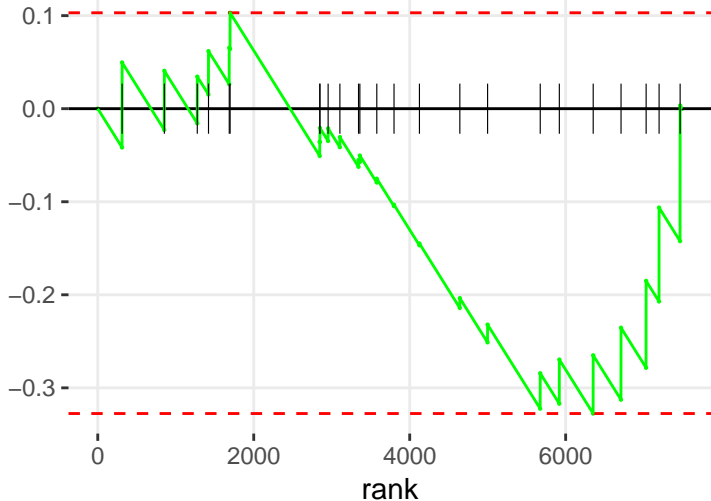
enrichment score

rank



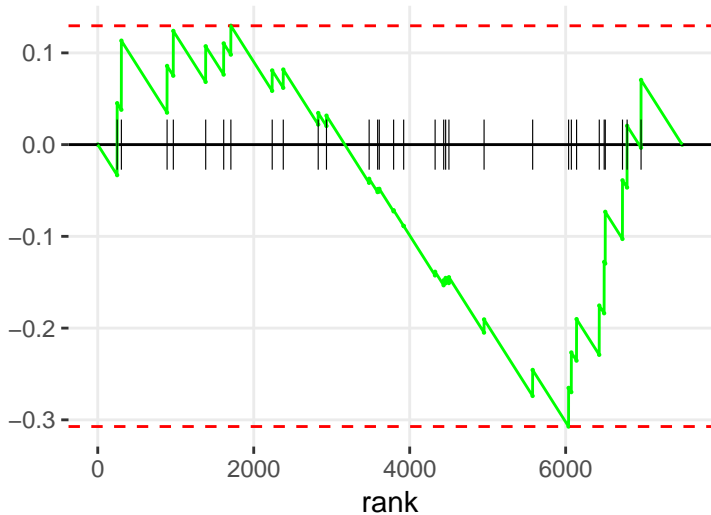
CMP-<IN</I>-ACETYLNEURAMINATE BIOSYNTHESIS I (EUKARYOTES)

enrichment score

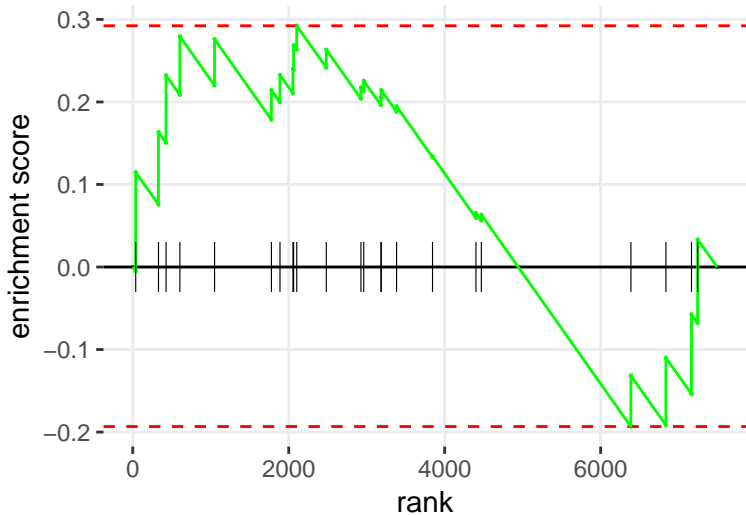


INOSITOL PYROPHOSPHATES BIOSYNTHESIS

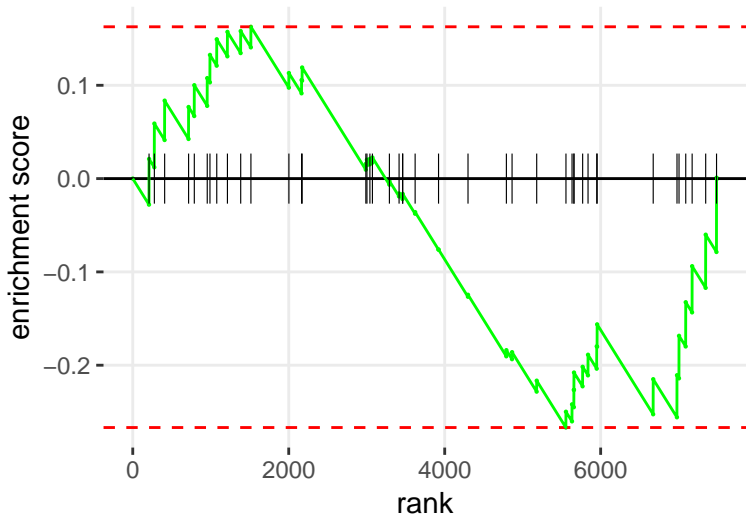
enrichment score



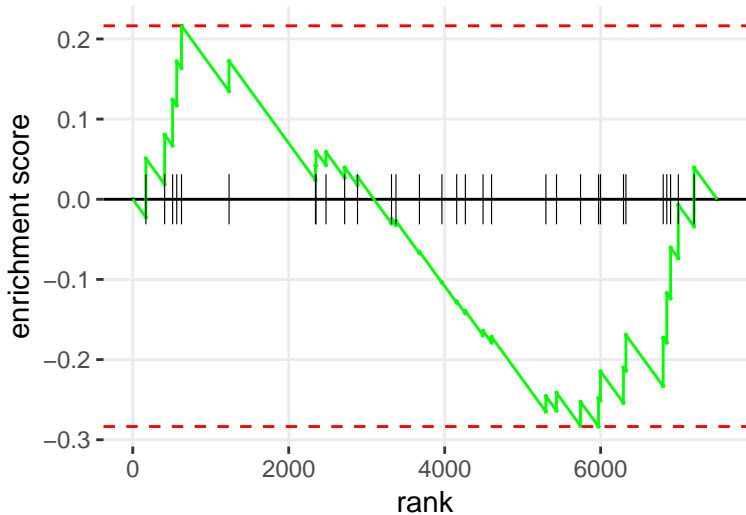
TYROSINE BIOSYNTHESIS IV



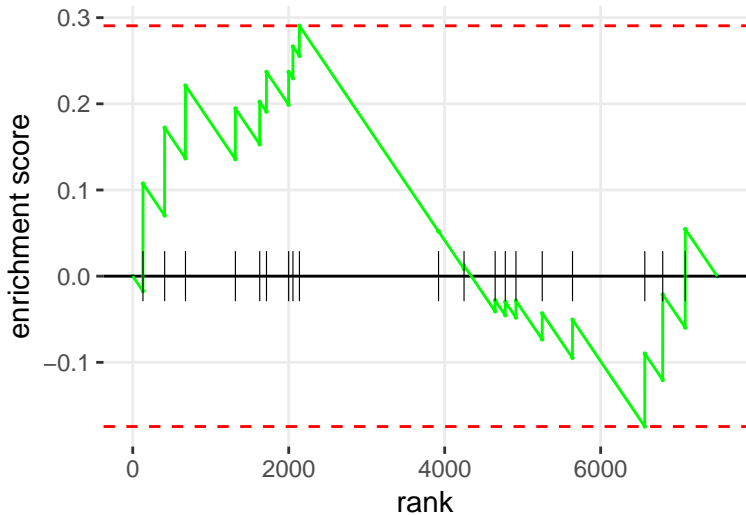
THE VISUAL CYCLE I (VERTEBRATES)



UDP-D-XYLOSE AND UDP-D-GLUCURONATE BIOSYNTHESIS



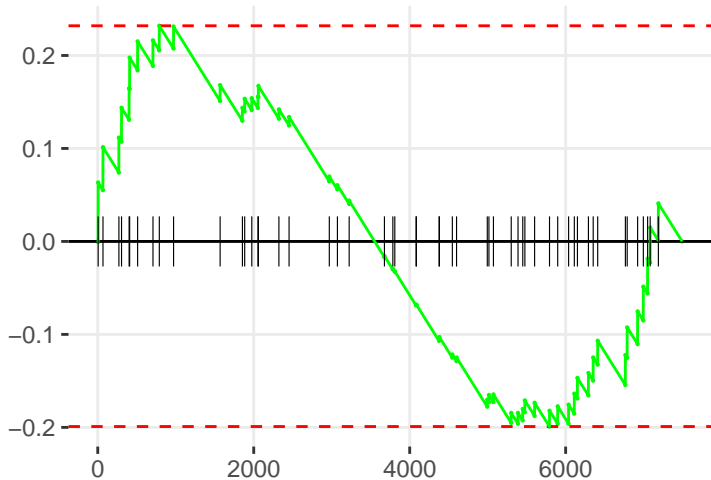
METHIONINE SALVAGE II (MAMMALIA)



CHONDROITIN SULFATE DEGRADATION (METAZOA)

enrichment score

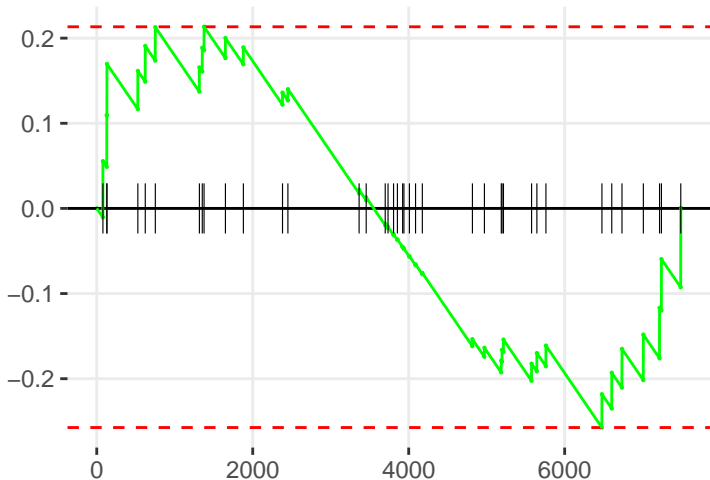
rank



FLAVIN BIOSYNTHESIS IV (MAMMALIAN)

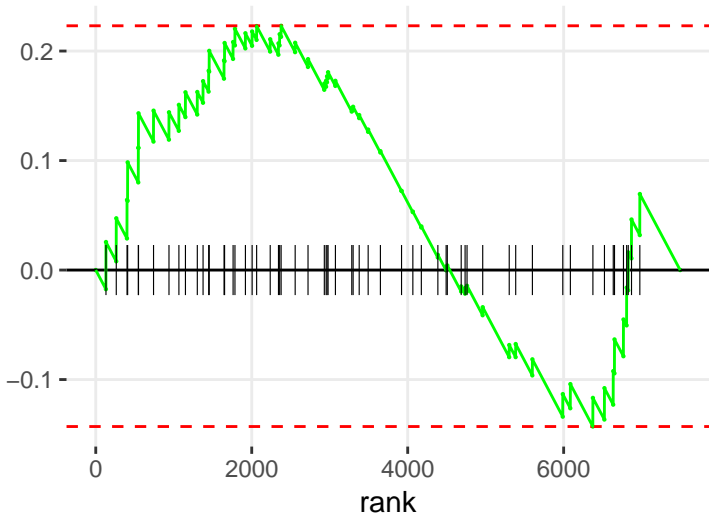
enrichment score

rank



GLUTAMATE BIOSYNTHESIS II

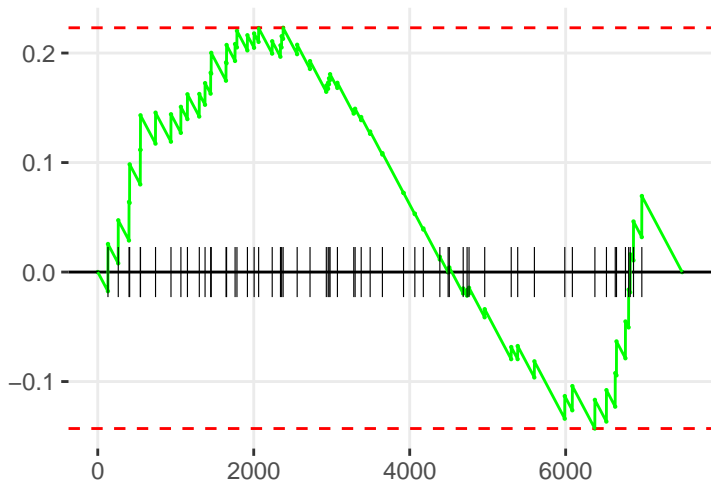
enrichment score



GLUTAMATE DEGRADATION X

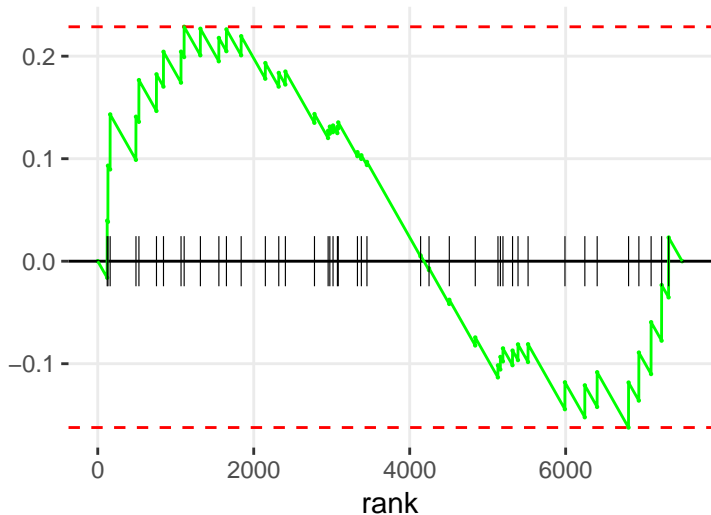
enrichment score

rank



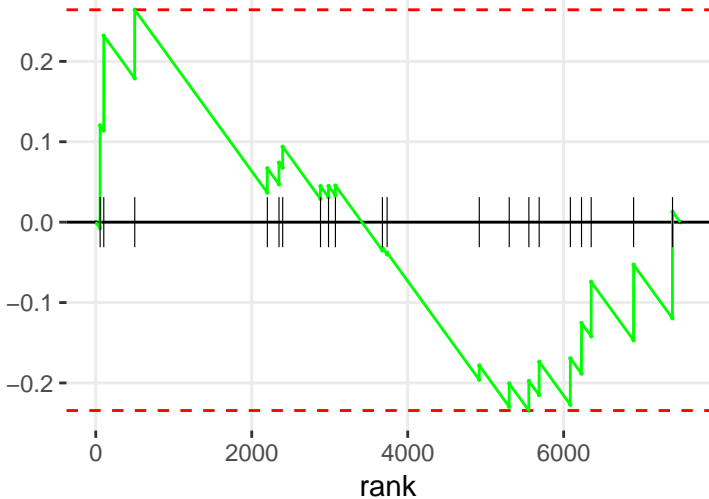
URIDINE-5'-PHOSPHATE BIOSYNTHESIS

enrichment score

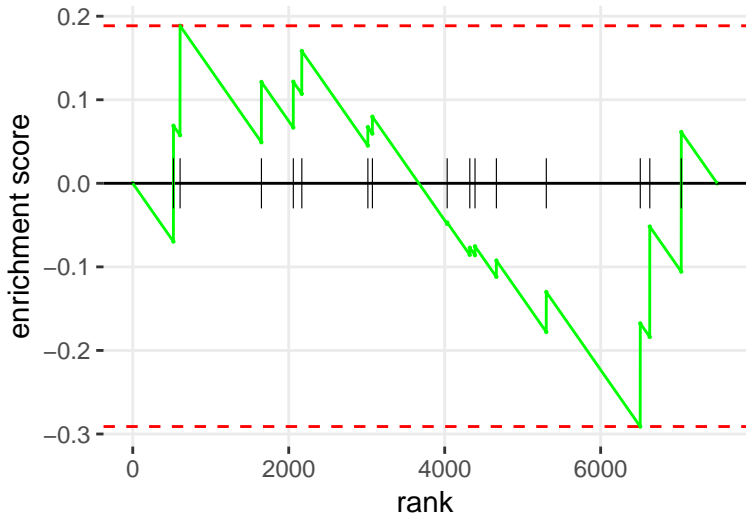


GLUTAMATE REMOVAL FROM FOLATES

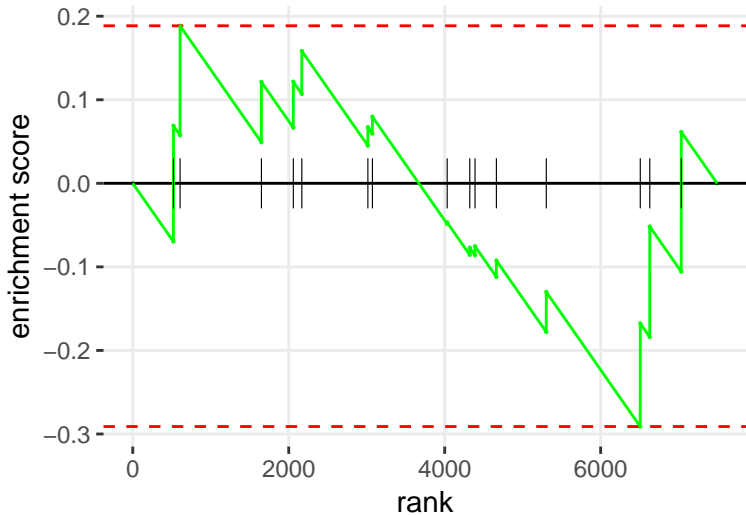
enrichment score



URACIL DEGRADATION II (REDUCTIVE)



THYMINE DEGRADATION



ACYL-COA HYDROLYSIS

enrichment score

0.1
0.0
-0.1
-0.2

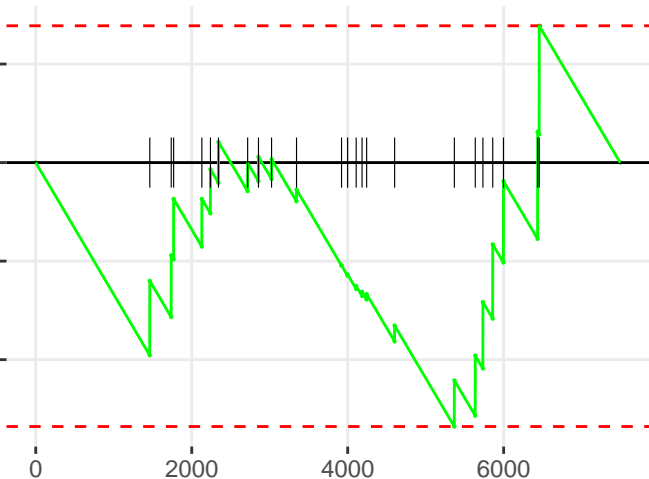
0

2000

4000

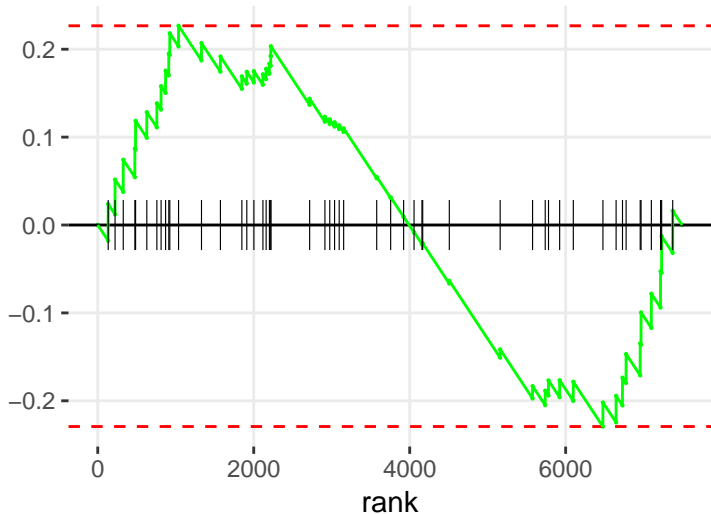
6000

rank



METHYLGLYOXAL DEGRADATION VI

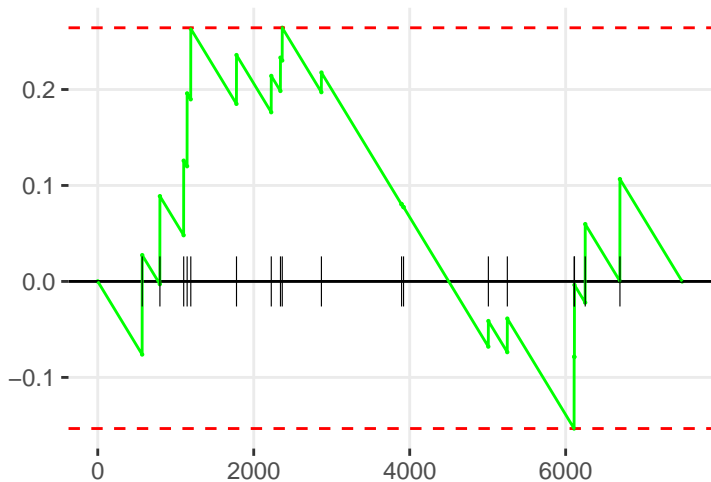
enrichment score



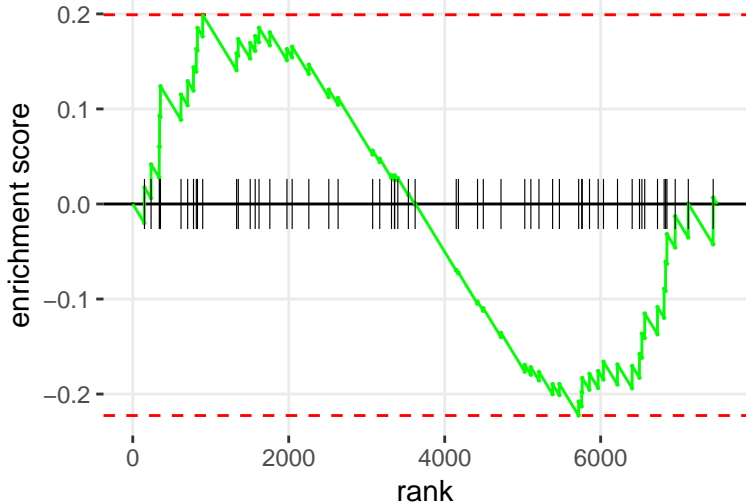
LANOSTEROL BIOSYNTHESIS

enrichment score

rank



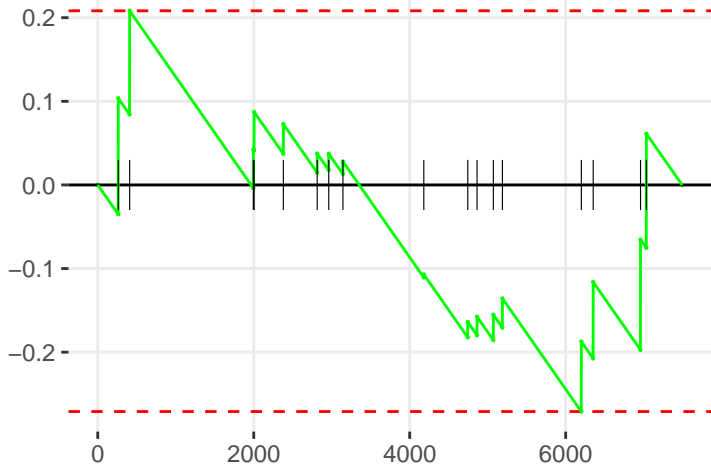
NAD BIOSYNTHESIS FROM 2-AMINO-3-CARBOXYMUCONATE SEMIALDEHYDE



L-DOPA DEGRADATION

enrichment score

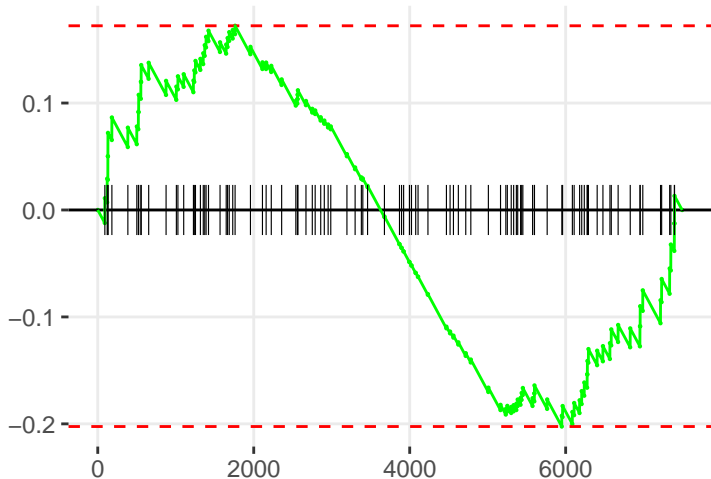
rank



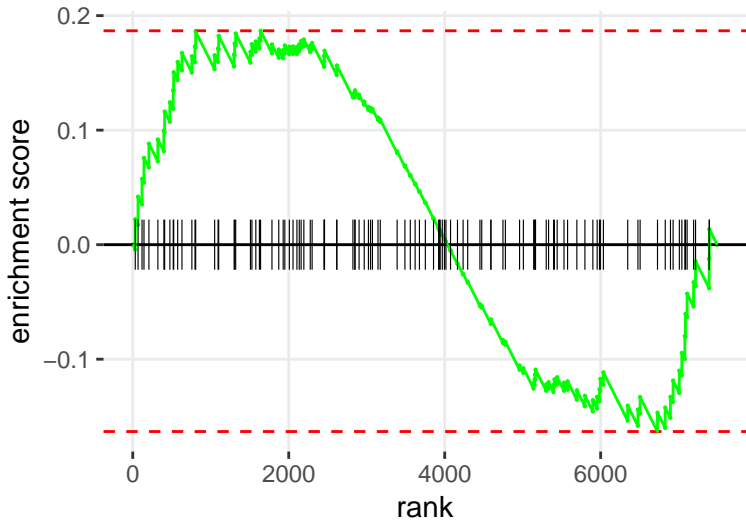
ZYMOSTEROL BIOSYNTHESIS

enrichment score

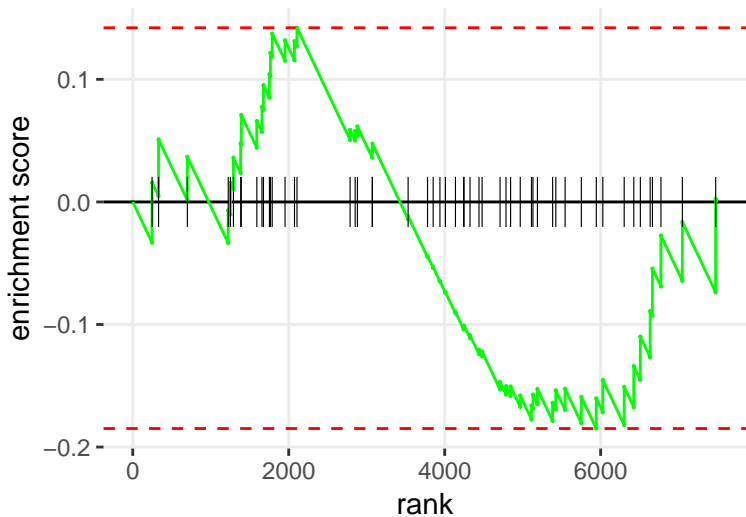
rank



ANDROGEN BIOSYNTHESIS



SPERMINE AND SPERMIDINE DEGRADATION I



GLUTAMINE DEGRADATION I

enrichment score

rank

