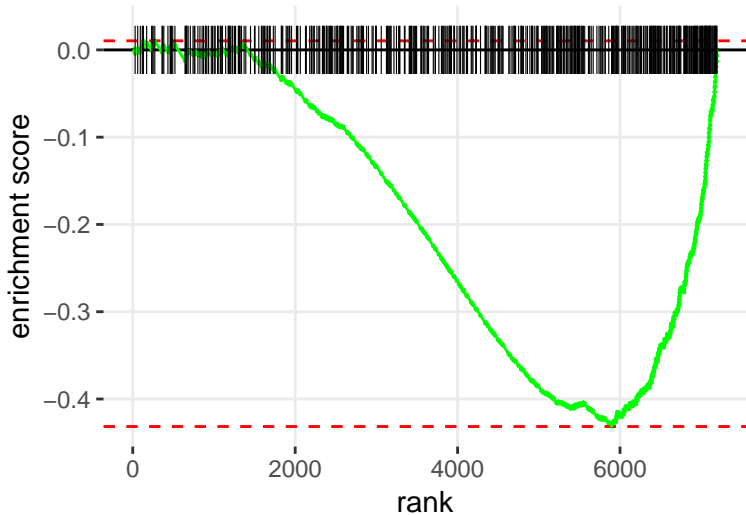


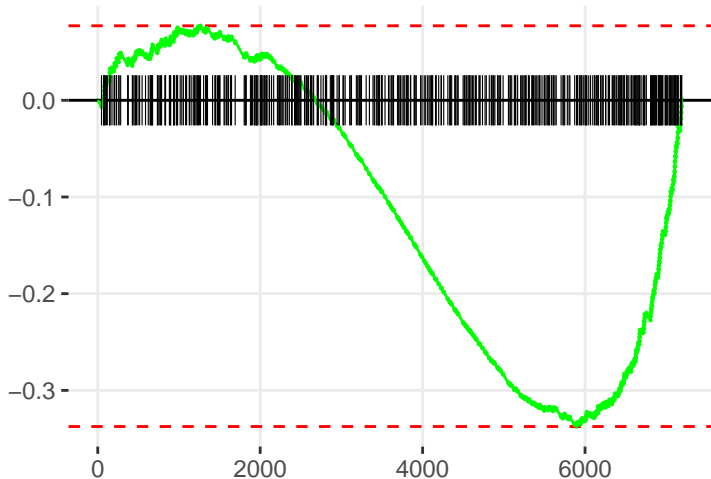
ARGININE BIOSYNTHESIS IV



FOLATE TRANSFORMATIONS I

enrichment score

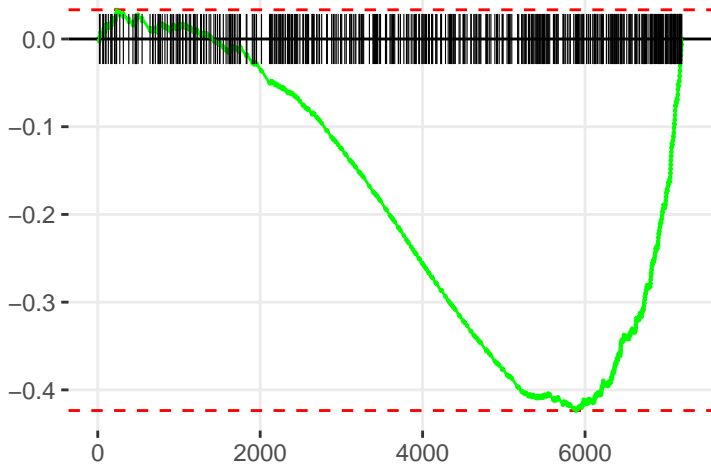
rank



RETINOATE BIOSYNTHESIS I

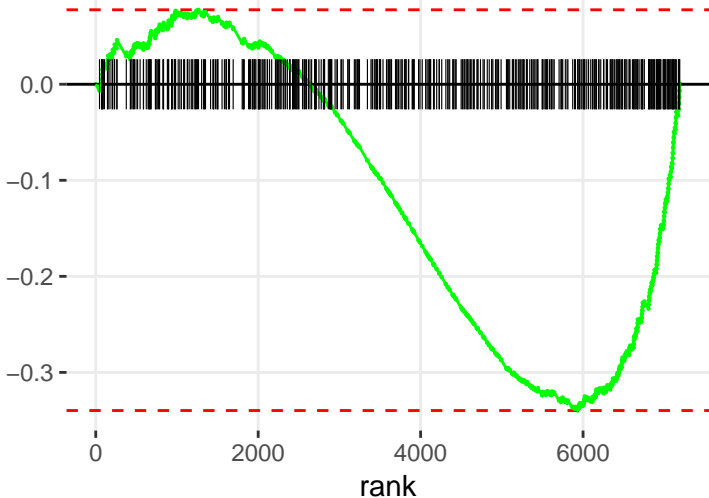
enrichment score

rank

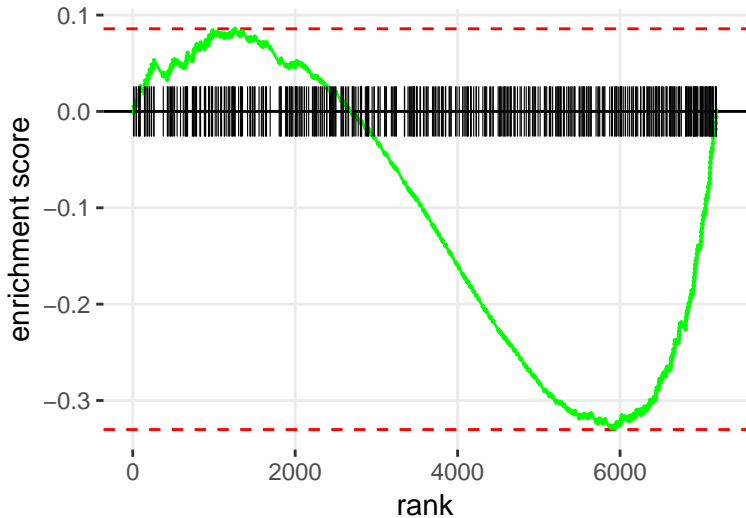


FOLATE POLYGLUTAMYLATION

enrichment score



DTMP <IDE NOVO</I> BIOSYNTHESIS



TREHALOSE DEGRADATION II (TREHALASE)

enrichment score

0.0
-0.1
-0.2
-0.3
-0.4

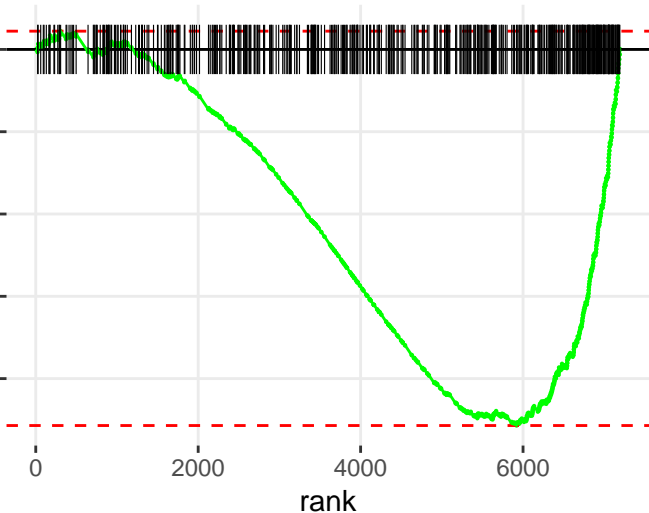
0

2000

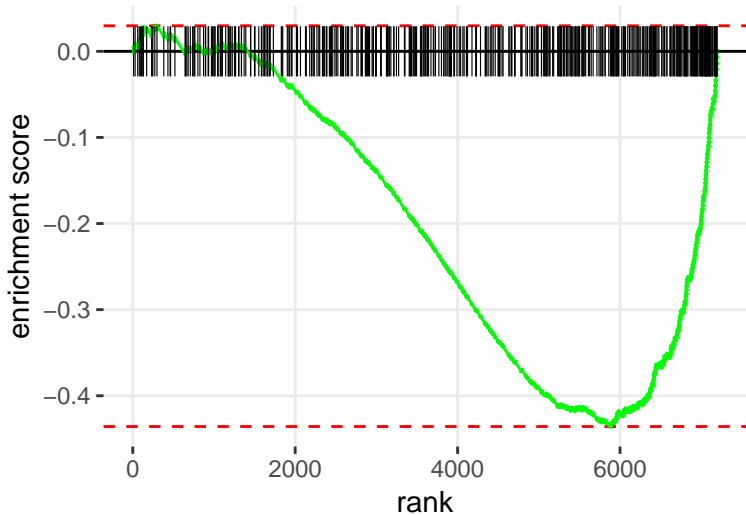
4000

6000

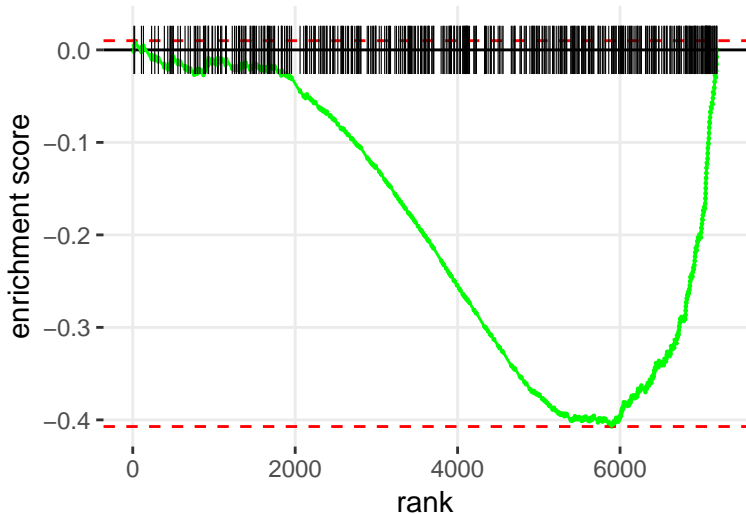
rank



PROLINE BIOSYNTHESIS II (FROM ARGinine)



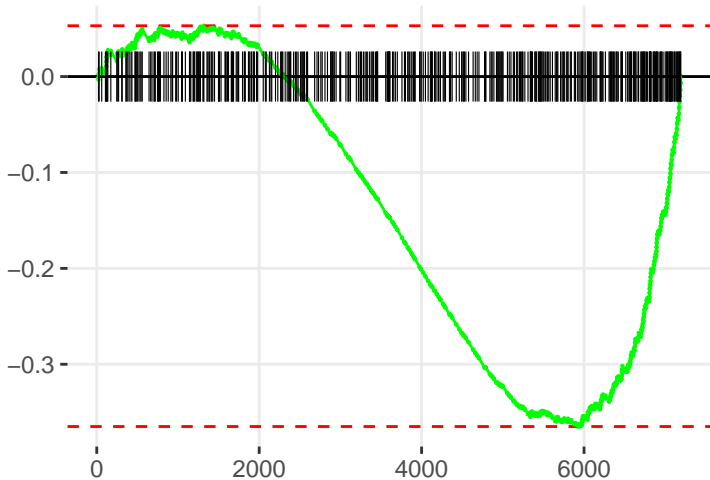
2-OXOISOVALERATE DECARBOXYLATION TO ISOBUTANOYL-COA



FATTY ACID &BETA;-OXIDATION I

enrichment score

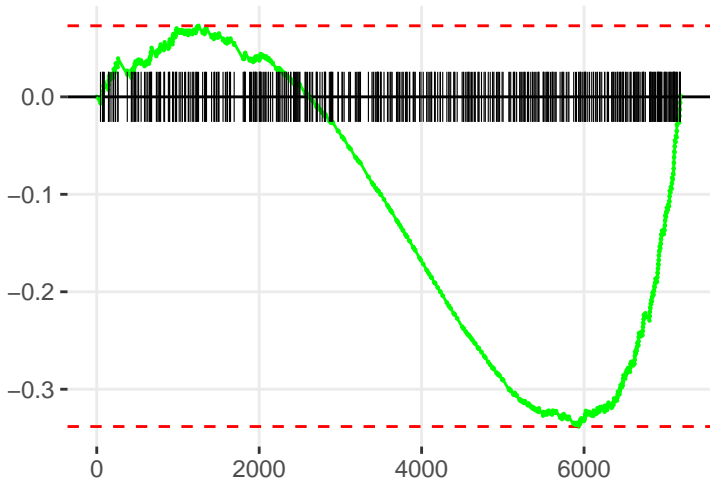
rank



GLYCINE BETAIN DEGRADATION

enrichment score

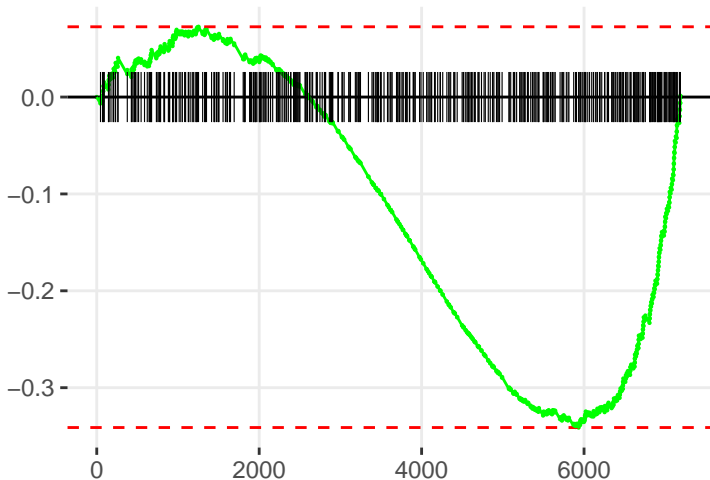
rank



GLYCINE BIOSYNTHESIS I

enrichment score

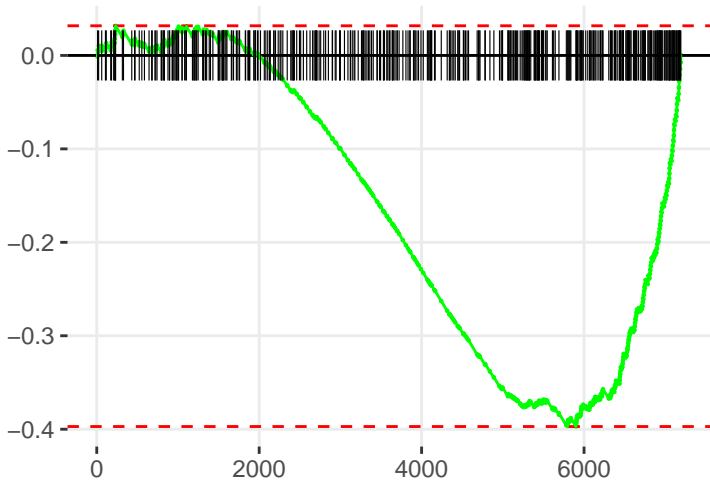
rank



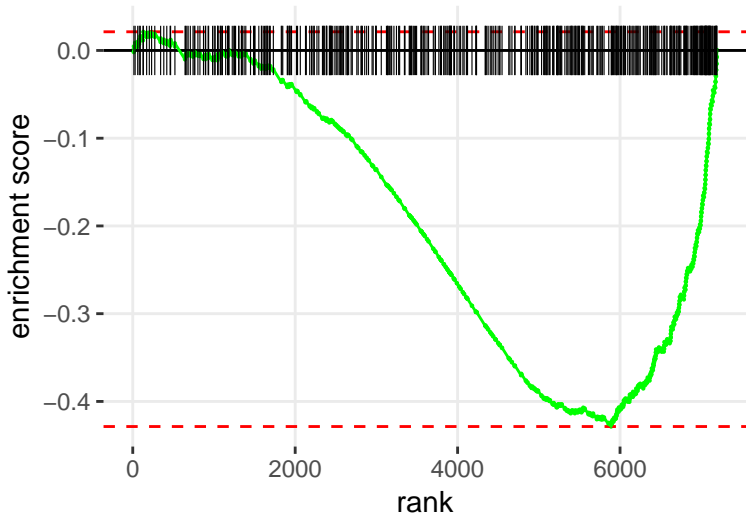
MEVALONATE PATHWAY I

enrichment score

rank



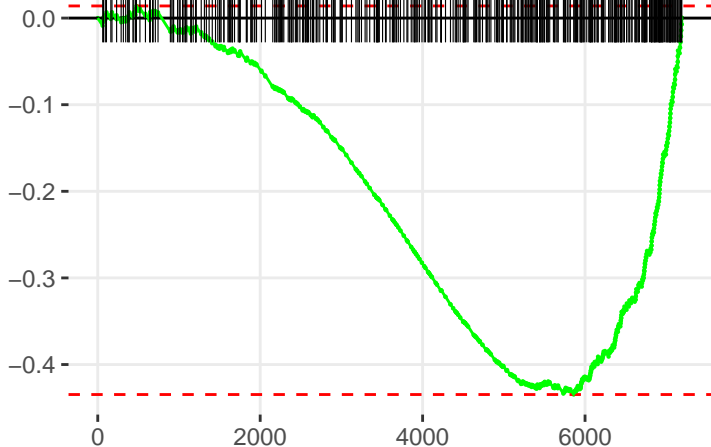
CITRULLINE BIOSYNTHESIS



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

enrichment score

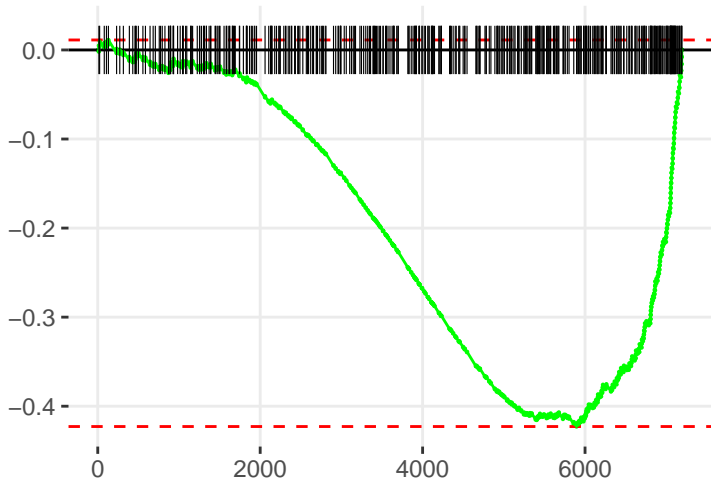
rank



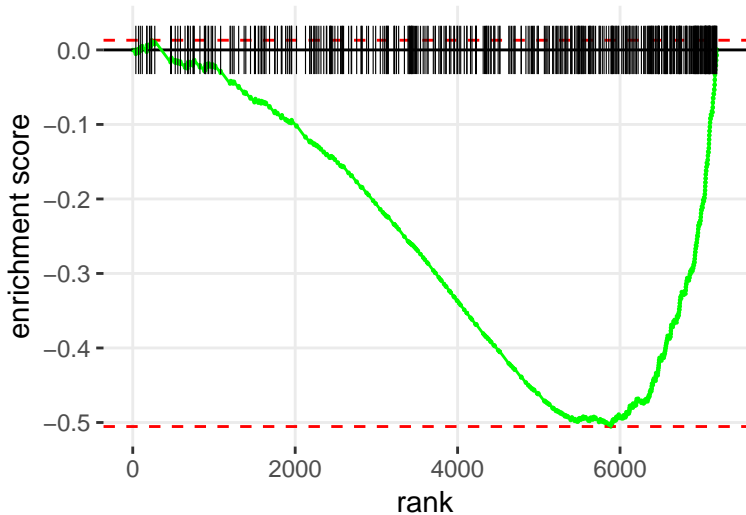
GLYCINE CLEAVAGE

enrichment score

rank



PENTOSE PHOSPHATE PATHWAY (OXIDATIVE BRANCH)



SALVAGE PATHWAYS OF PYRIMIDINE RIBONUCLEOTIDES

enrichment score

rank

0.0

-0.1

-0.2

-0.3

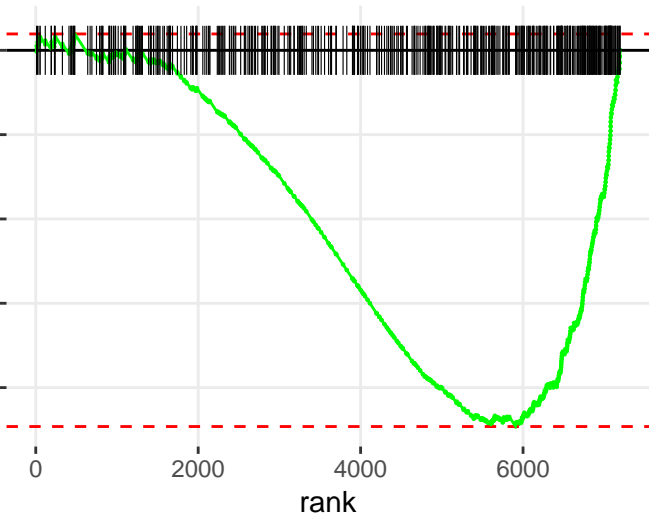
-0.4

0

2000

4000

6000



UREA CYCLE

enrichment score

rank

0.0

-0.1

-0.2

-0.3

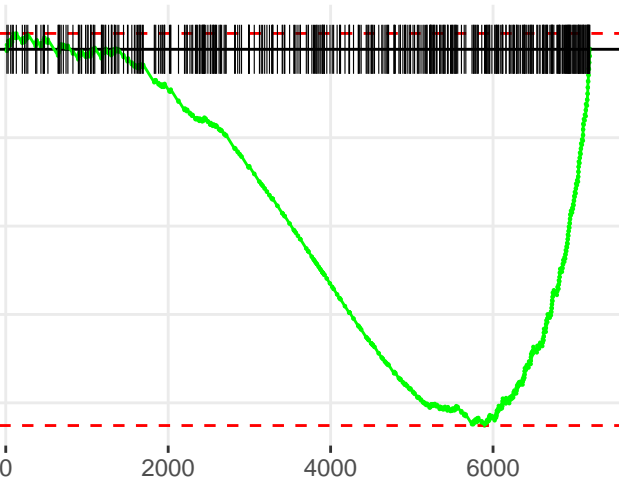
-0.4

0

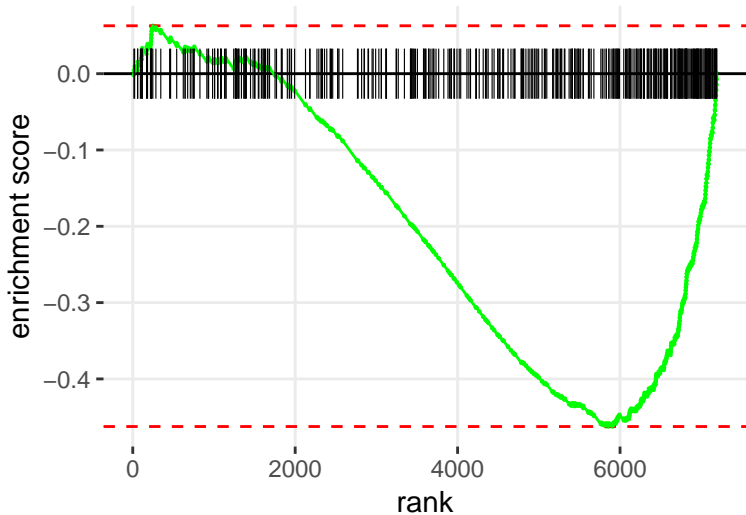
2000

4000

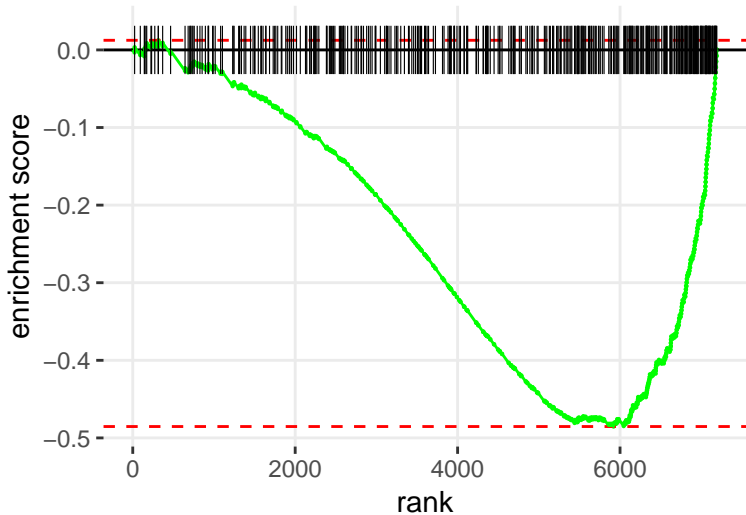
6000



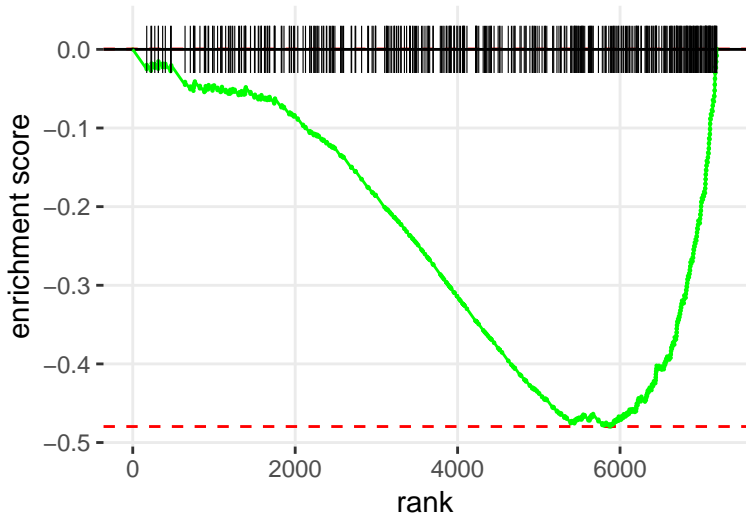
SUPEROXIDE RADICALS DEGRADATION



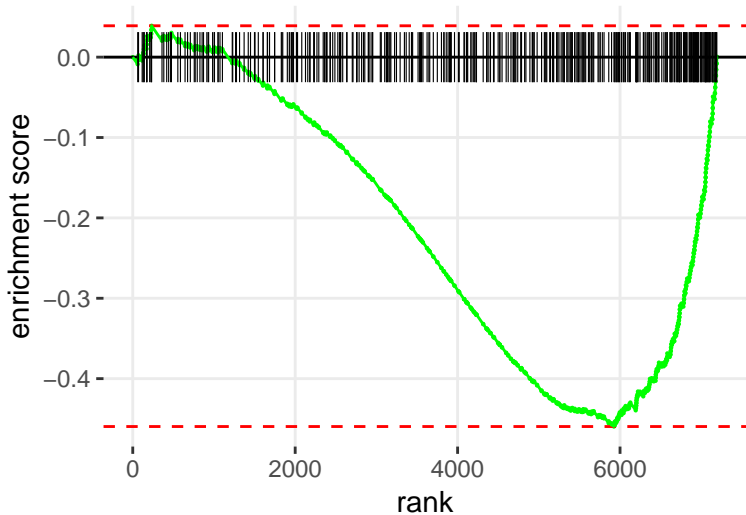
GLYCOGEN BIOSYNTHESIS II (FROM UDP-D-GLUCOSE)



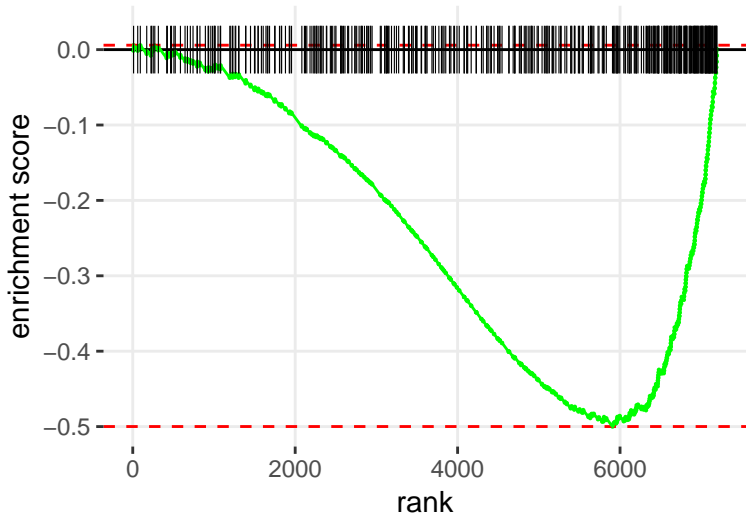
CYSTEINE BIOSYNTHESIS/HOMOCYSTEINE DEGRADATION



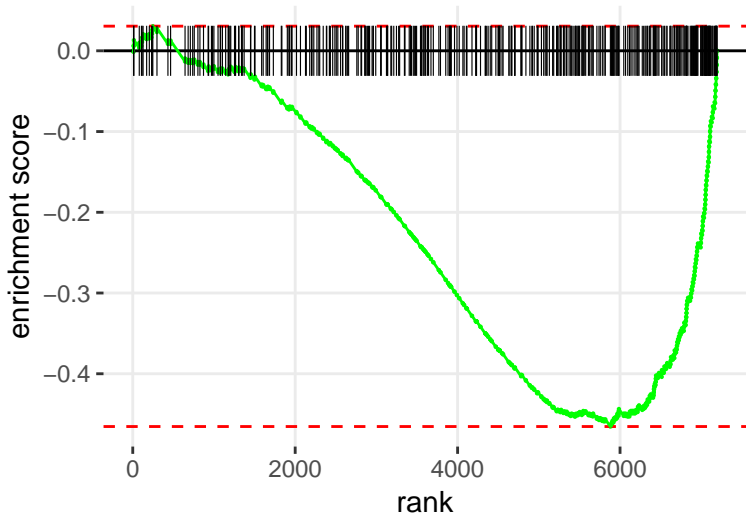
GLYCOGEN DEGRADATION II



ASPARTATE DEGRADATION II



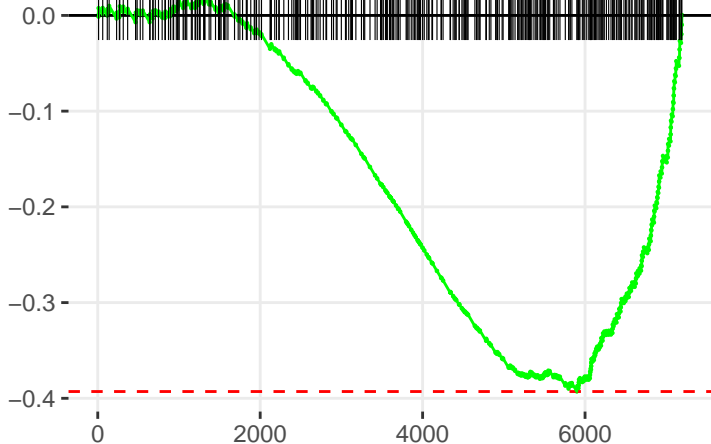
ARGININE DEGRADATION VI (ARGINASE 2 PATHWAY)



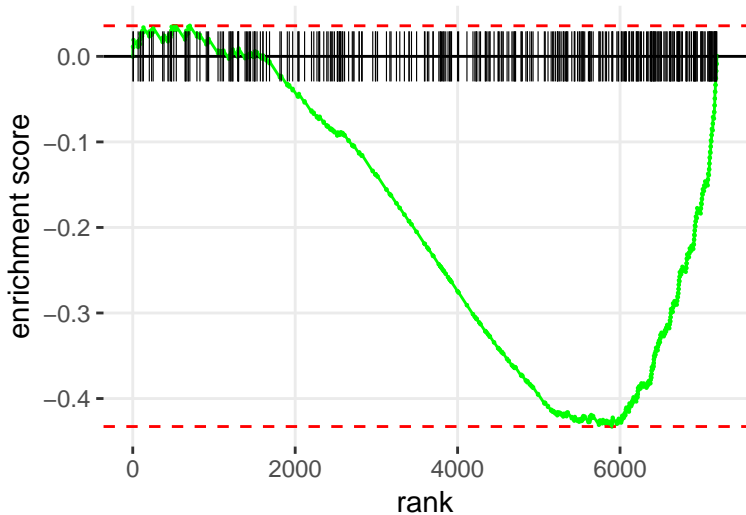
SELENOCYSTEINE BIOSYNTHESIS II (ARCHAEA AND EUKARYOTES)

enrichment score

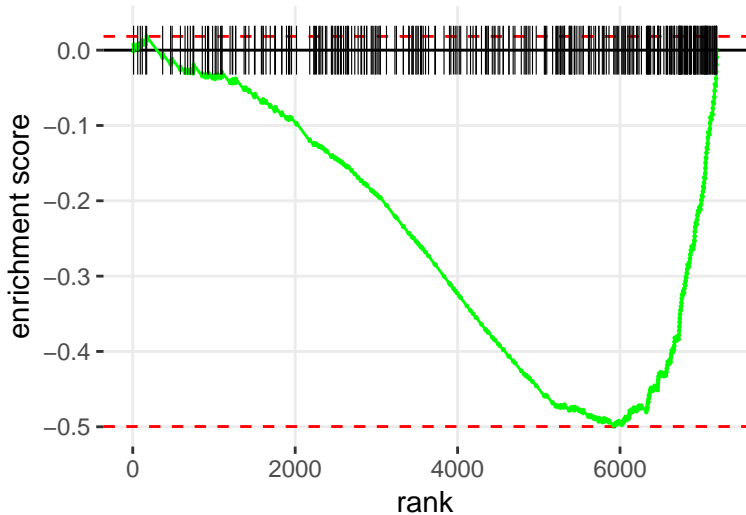
rank



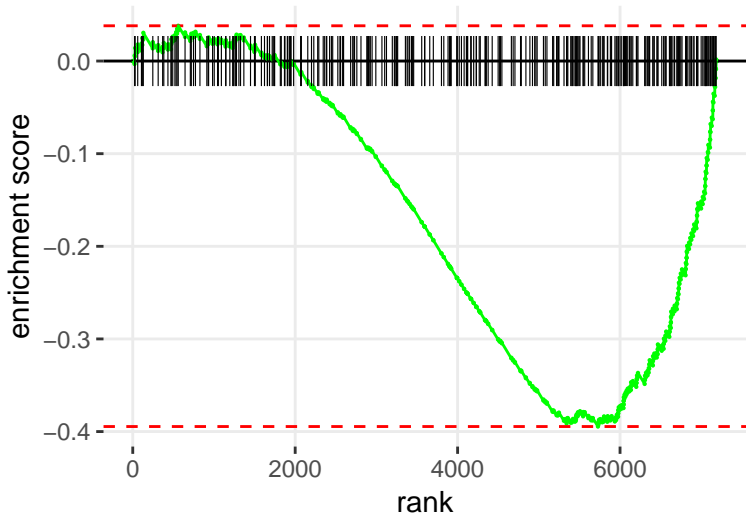
CITRULLINE-NITRIC OXIDE CYCLE



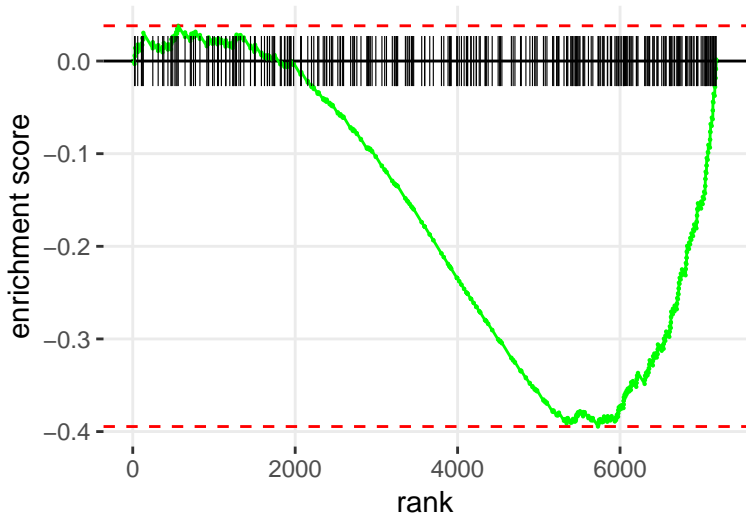
PENTOSE PHOSPHATE PATHWAY (NON-OXIDATIVE BRANCH)



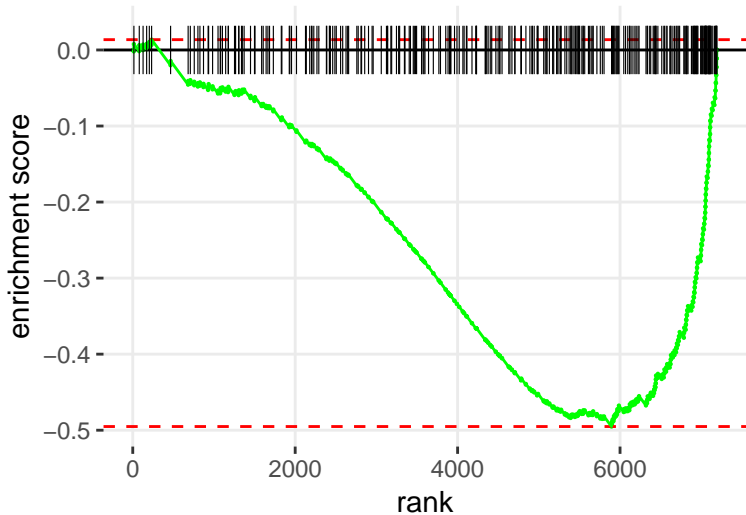
STEARATE BIOSYNTHESIS I (ANIMALS)



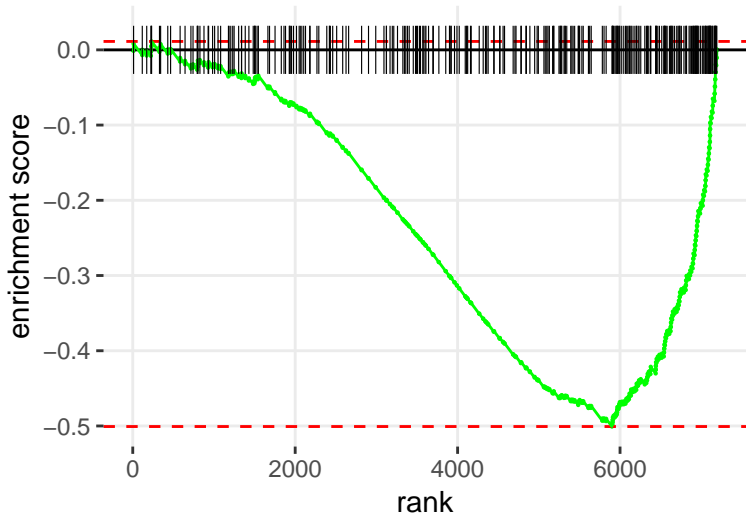
EICOSAPENTAENOATE BIOSYNTHESIS II (METAZOA)



ARGININE DEGRADATION I (ARGINASE PATHWAY)



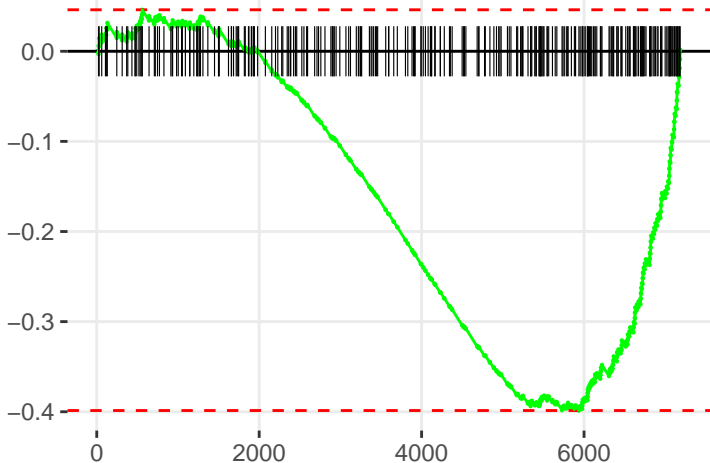
KETOGENESIS



&GAMMA;-LINOLENATE BIOSYNTHESIS II (ANIMALS)

enrichment score

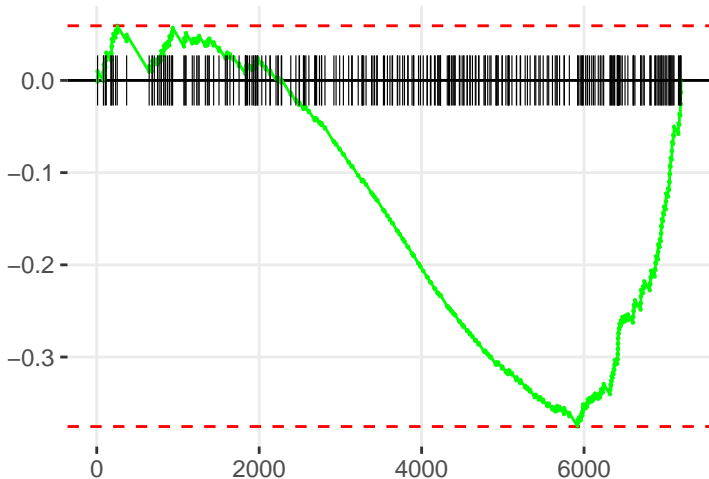
rank



URATE BIOSYNTHESIS/INOSINE 5'-PHOSPHATE DEGRADATION

enrichment score

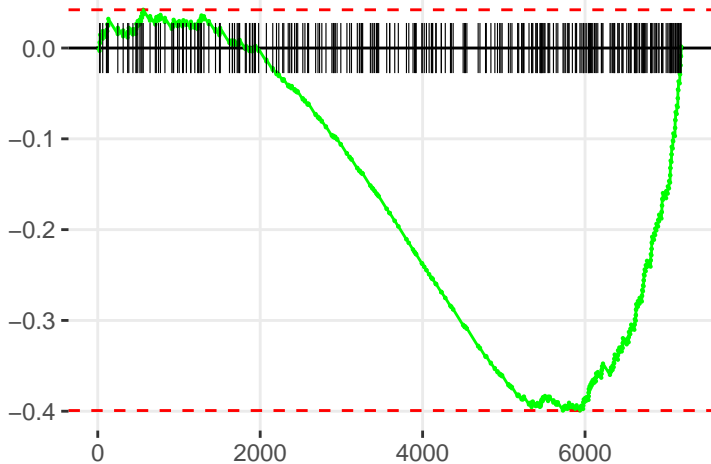
rank



FATTY ACID ACTIVATION

enrichment score

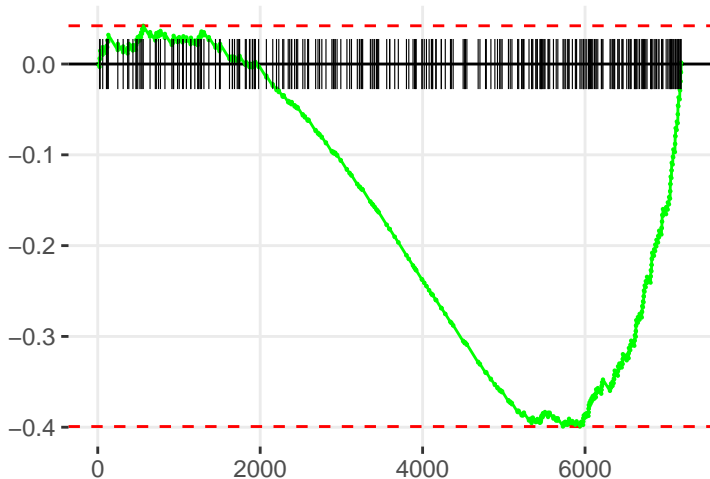
rank



FATTY ACID &ALPHA;-OXIDATION II

enrichment score

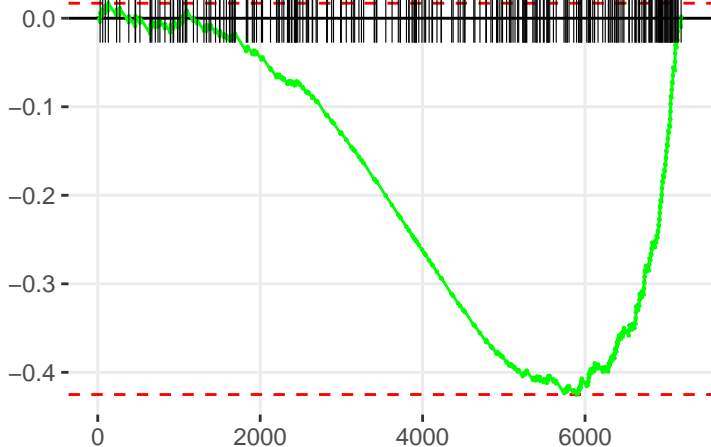
rank



CITRULLINE DEGRADATION

enrichment score

rank



ISOLEUCINE DEGRADATION I

enrichment score

0.0

-0.1

-0.2

-0.3

-0.4

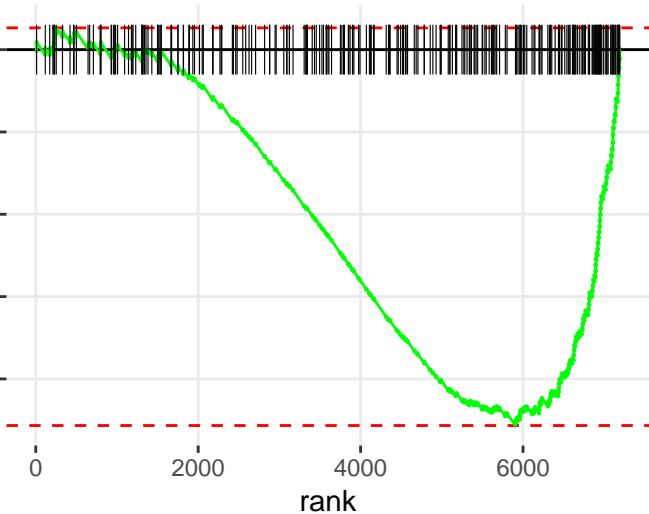
0

2000

4000

6000

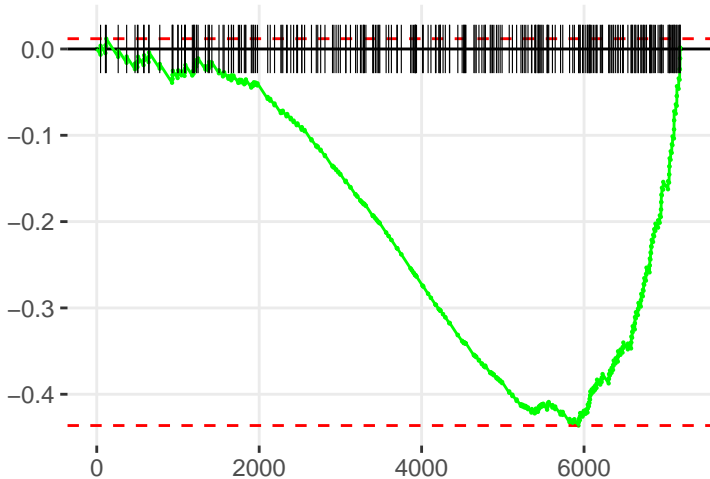
rank



TRIACYLGLYCEROL BIOSYNTHESIS

enrichment score

rank



VALINE DEGRADATION I

enrichment score

rank

0.0

-0.1

-0.2

-0.3

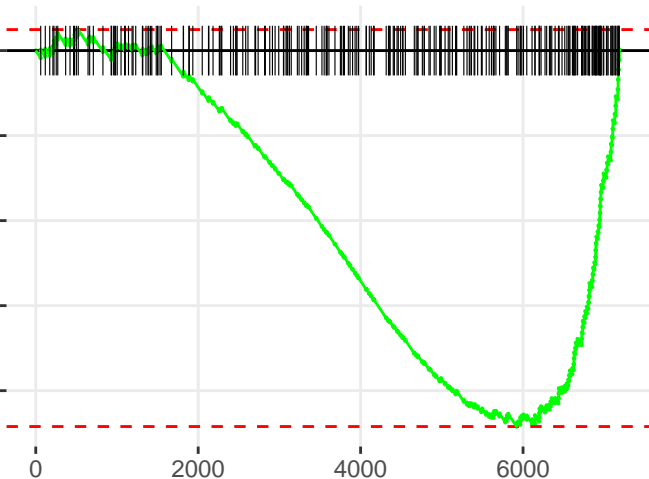
-0.4

0

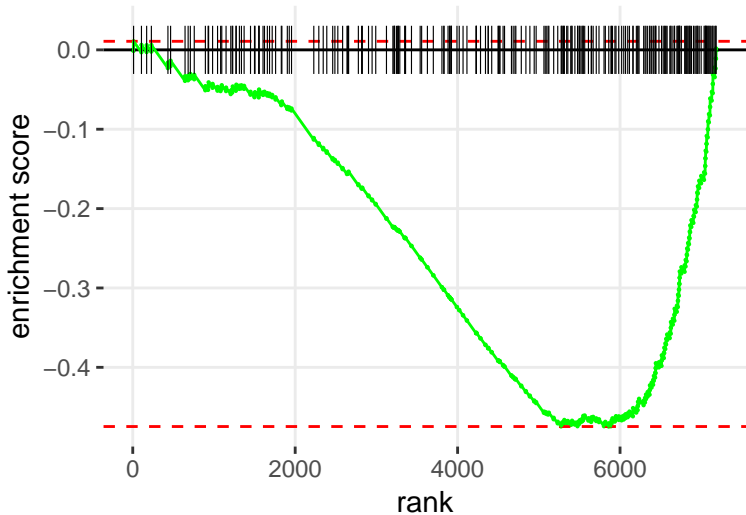
2000

4000

6000



GALACTOSE DEGRADATION I (LELOIR PATHWAY)



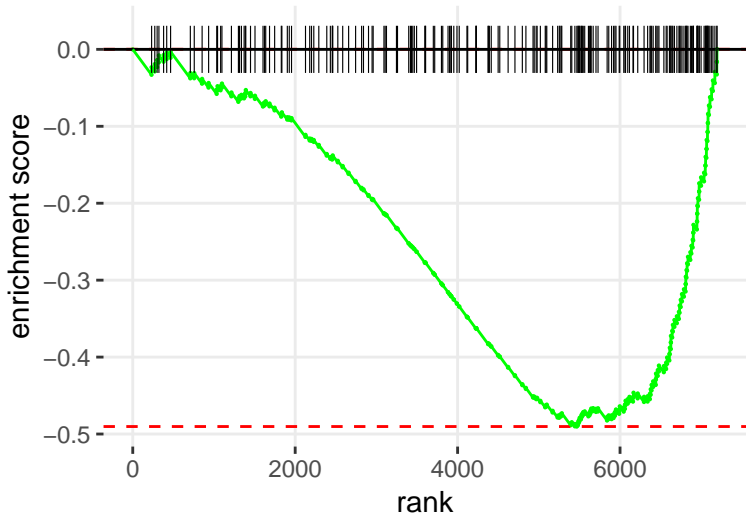
CDP-DIACYLGLYCEROL BIOSYNTHESIS I

enrichment score

rank



TETRAHYDROBIOPTERIN BIOSYNTHESIS I



<IMYO</I>-INOSITOL BIOSYNTHESIS

enrichment score

rank

0.0

-0.2

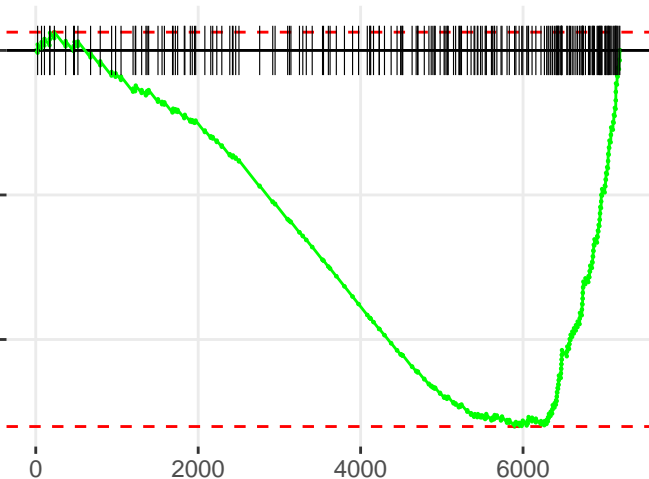
-0.4

0

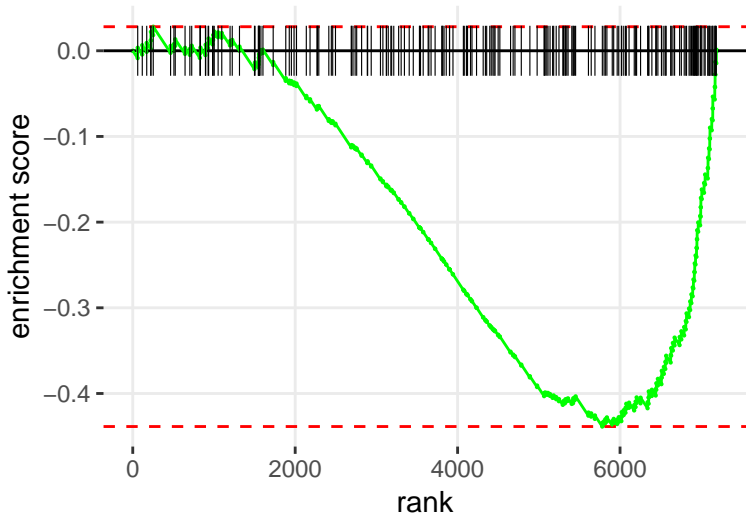
2000

4000

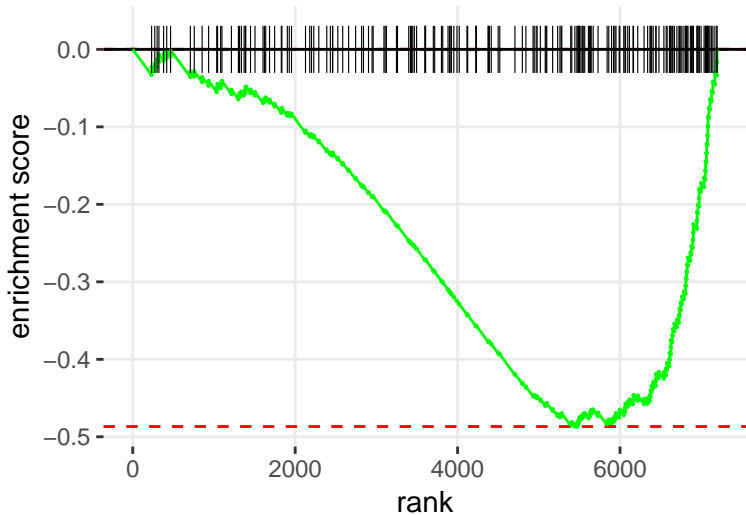
6000



5-AMINOIMIDAZOLE RIBONUCLEOTIDE BIOSYNTHESIS I



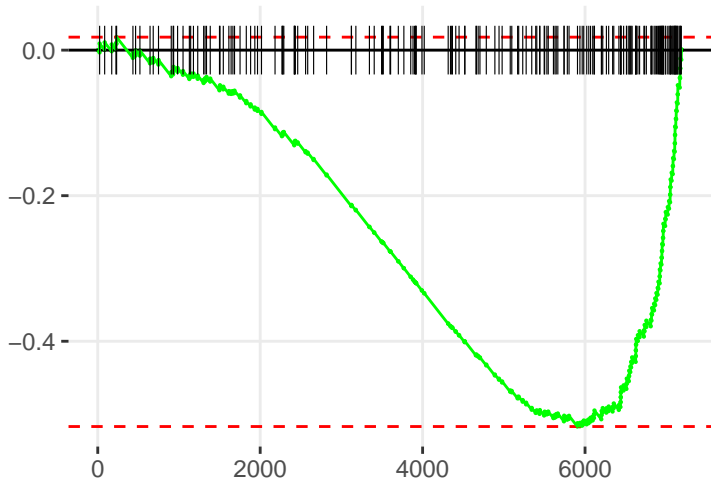
TETRAHYDROBIOPTERIN BIOSYNTHESIS II



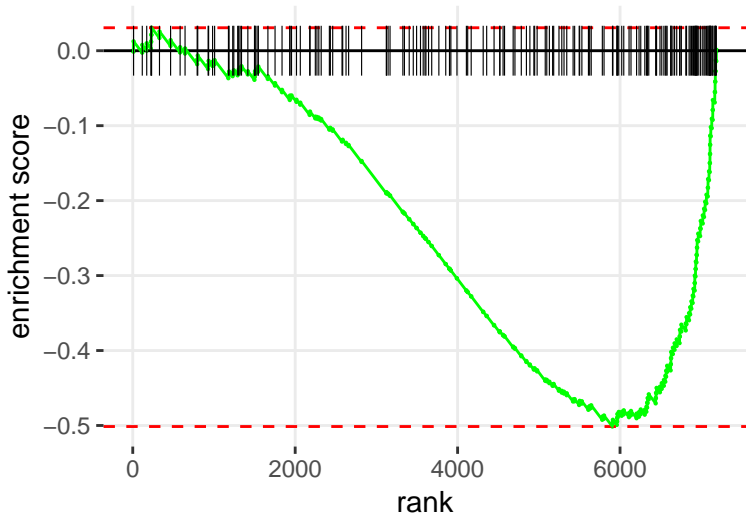
ACETATE CONVERSION TO ACETYL-COA

enrichment score

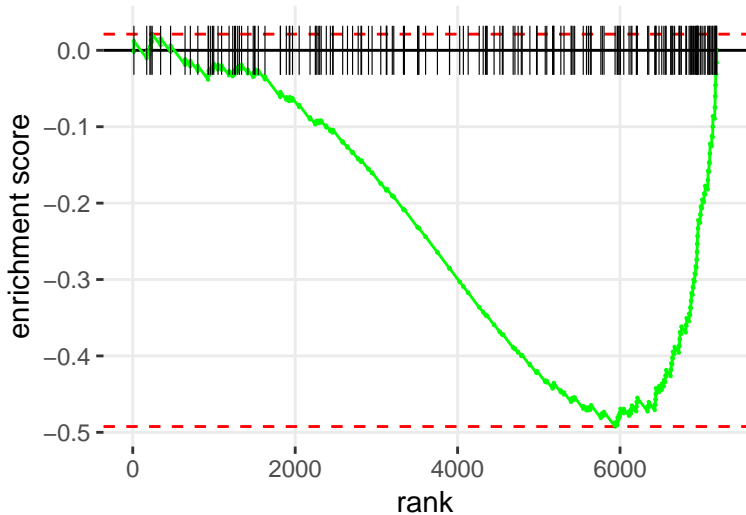
rank



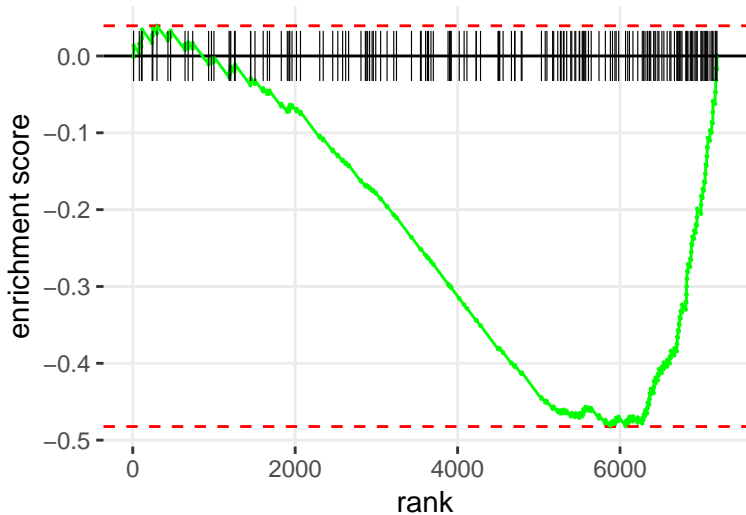
KETOLYSIS



LEUCINE DEGRADATION I



PROLINE BIOSYNTHESIS I



PHENYLALANINE DEGRADATION IV (MAMMALIAN, VIA SIDE CHAIN)

enrichment score

0.0

-0.2

-0.4

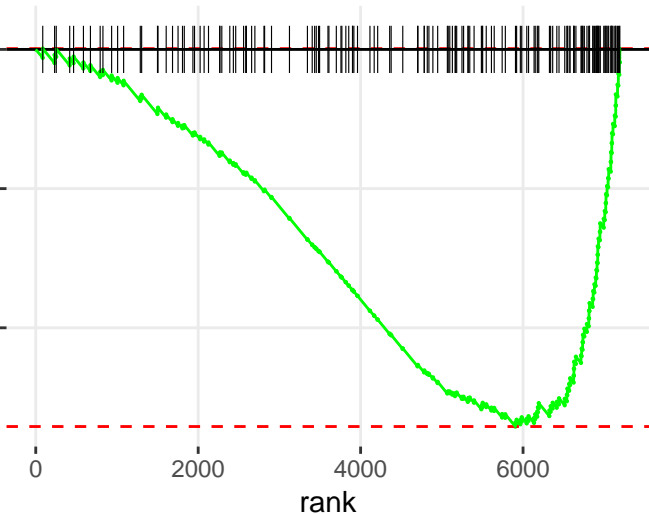
0

2000

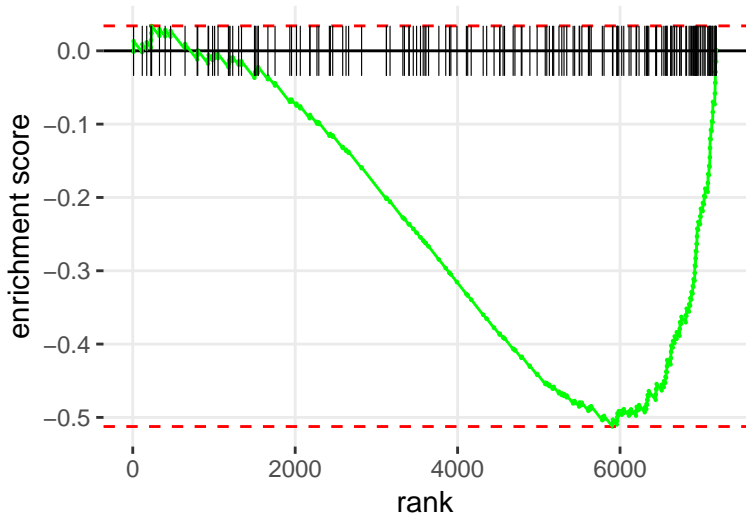
4000

6000

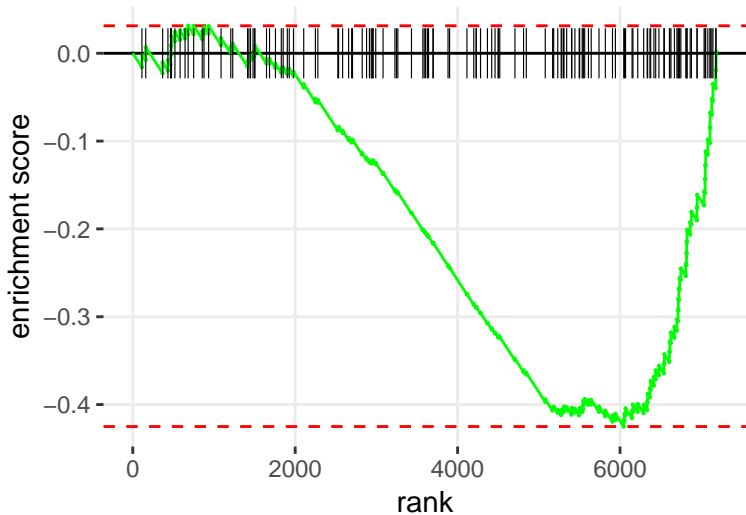
rank



GLUTARYL-COA DEGRADATION



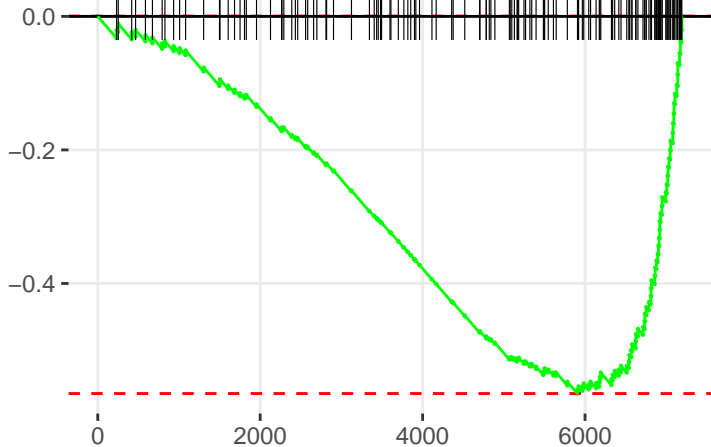
PHOSPHATIDYLCHOLINE BIOSYNTHESIS I



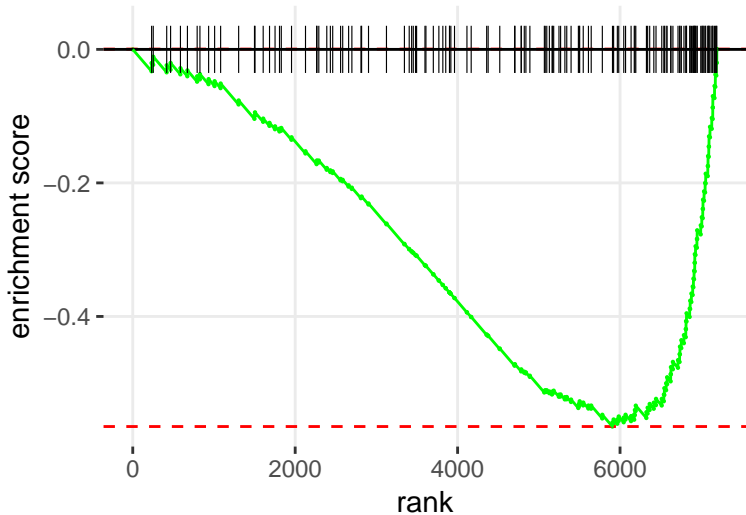
GLUTAMATE DEGRADATION II

enrichment score

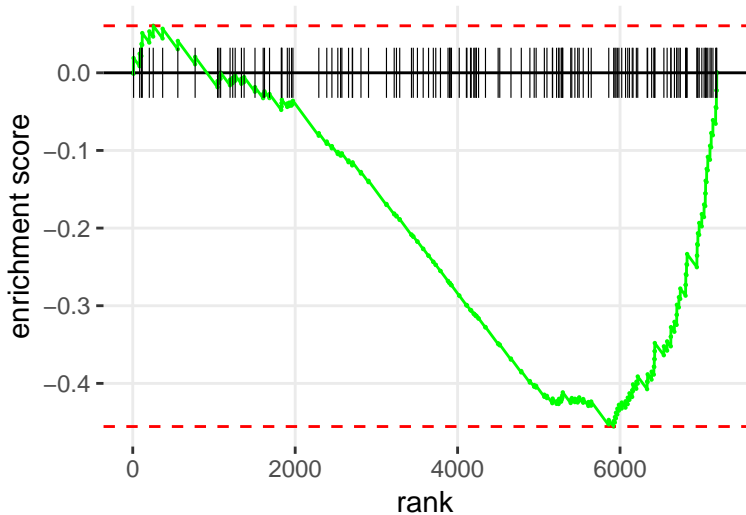
rank



ASPARTATE BIOSYNTHESIS



ADENINE AND ADENOSINE SALVAGE I



BILE ACID BIOSYNTHESIS, NEUTRAL PATHWAY

enrichment score

rank

0.0

-0.2

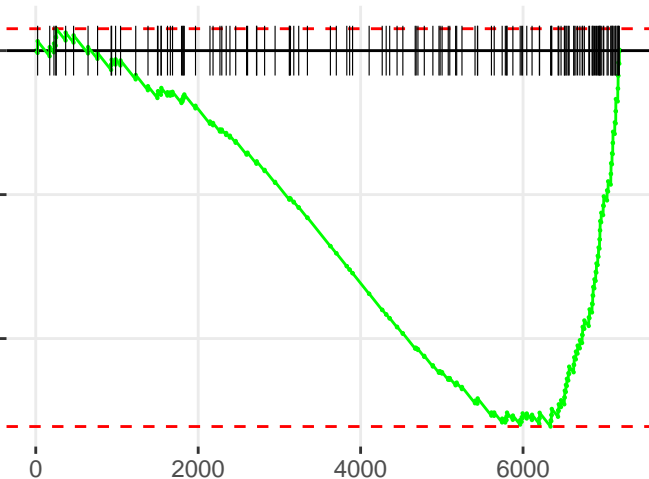
-0.4

0

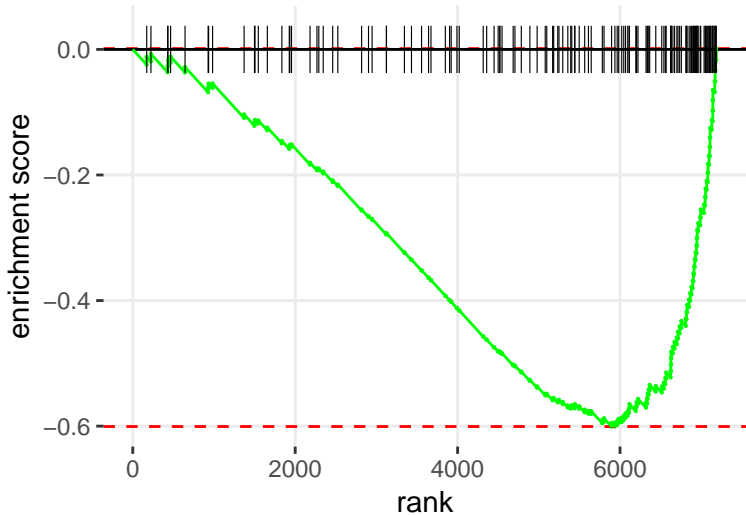
2000

4000

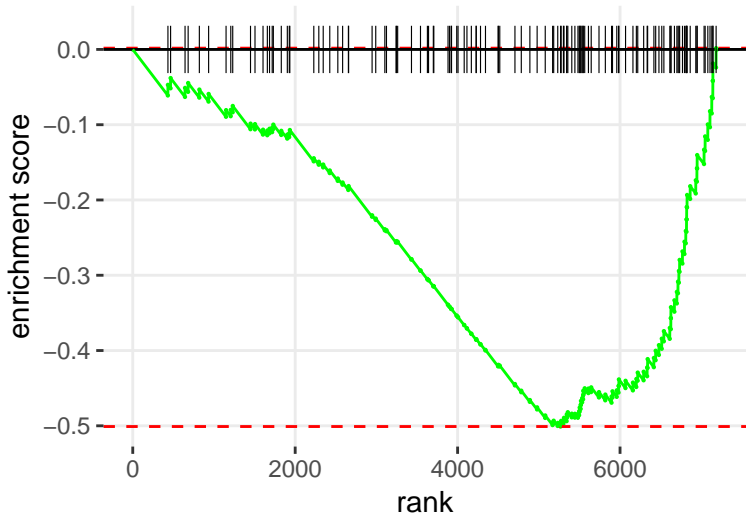
6000



ADENINE AND ADENOSINE SALVAGE VI



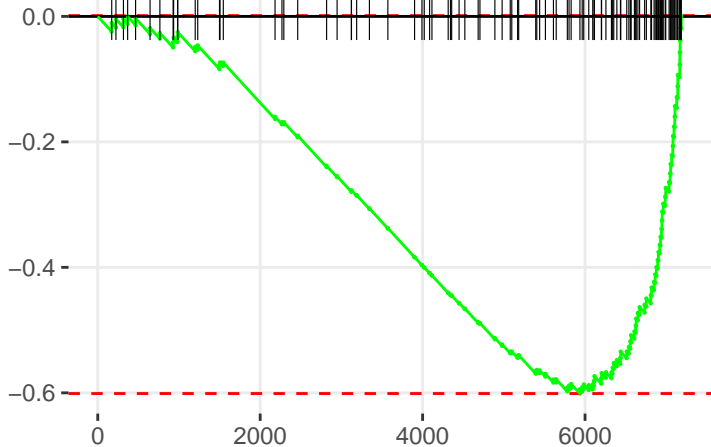
HYPUSINE BIOSYNTHESIS



L-CYSTEINE DEGRADATION II

enrichment score

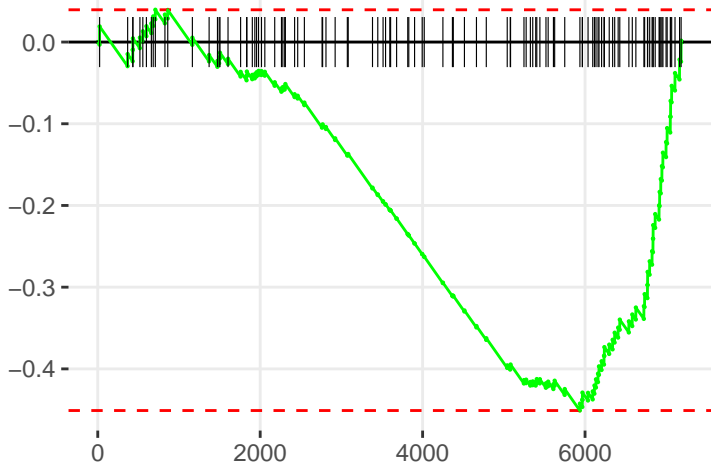
rank



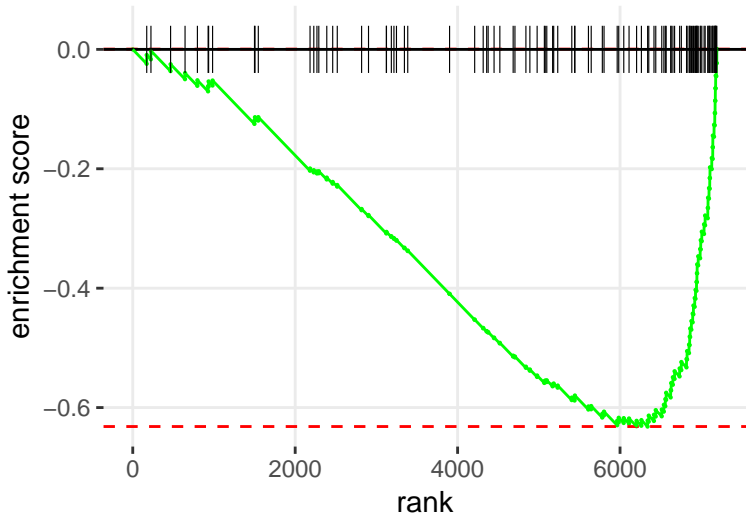
PRPP BIOSYNTHESIS I

enrichment score

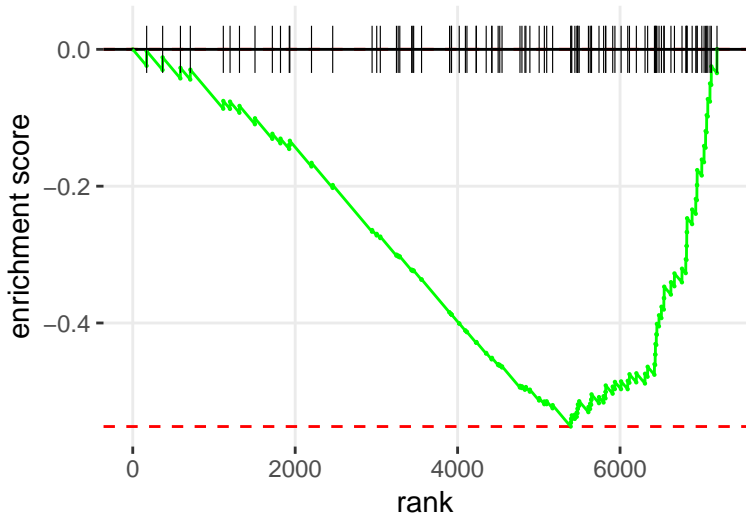
rank



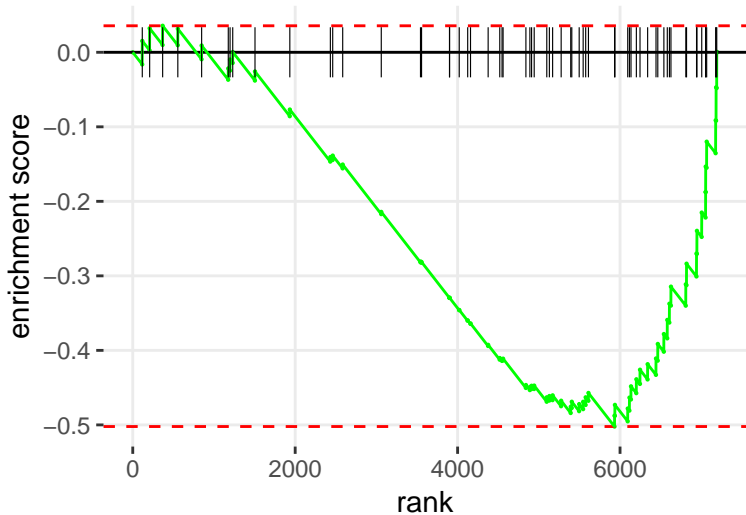
D-MANNOSE DEGRADATION



TRYPTOPHAN DEGRADATION TO 2-AMINO-3-CARBOXYMUCONATE SEMIALDEHYDE



PYRIDOXAL 5'-PHOSPHATE SALVAGE PATHWAY



INOSINE-5'-PHOSPHATE BIOSYNTHESIS II

enrichment score

0.0

-0.2

-0.4

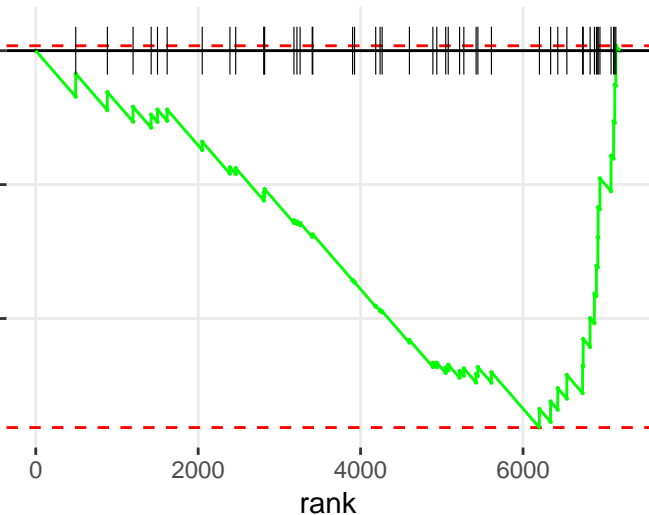
0

2000

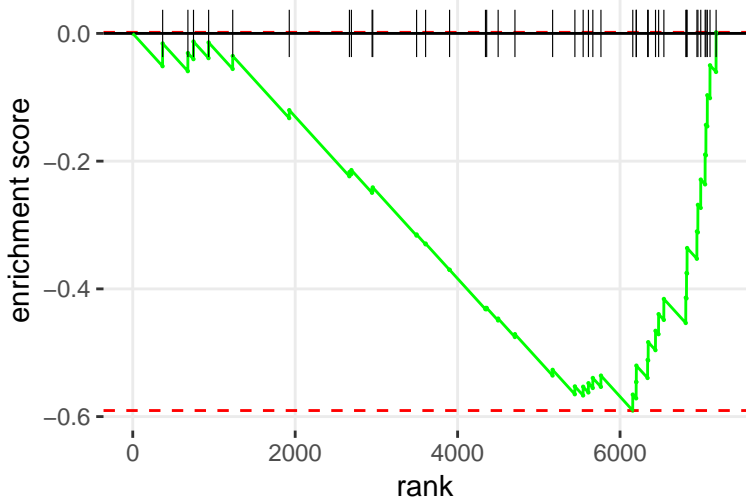
4000

6000

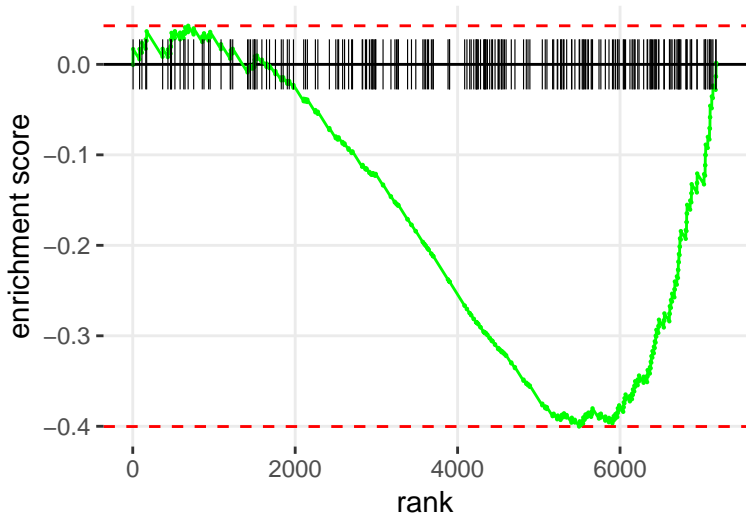
rank



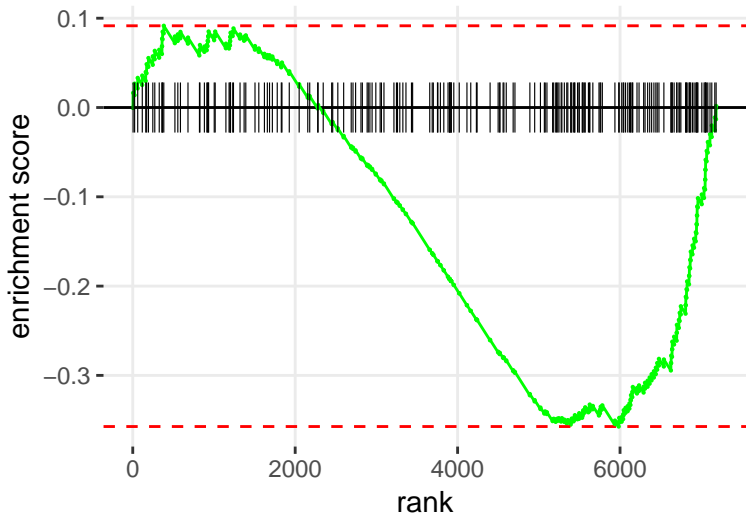
GLUTATHIONE BIOSYNTHESIS



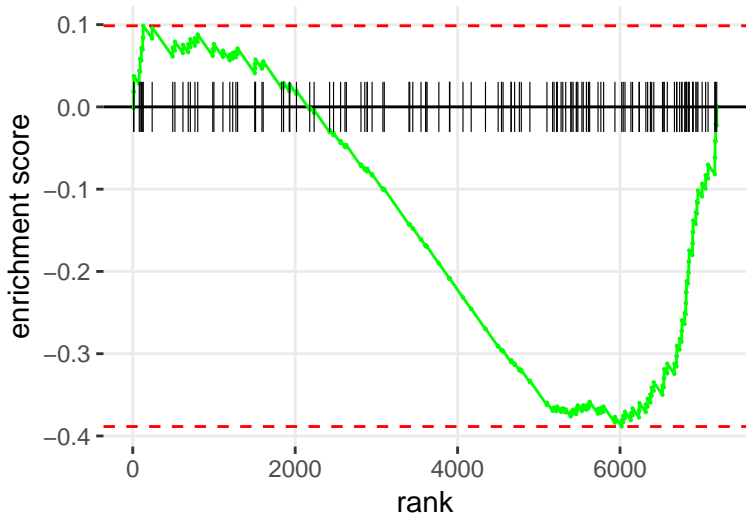
CHOLINE BIOSYNTHESIS III



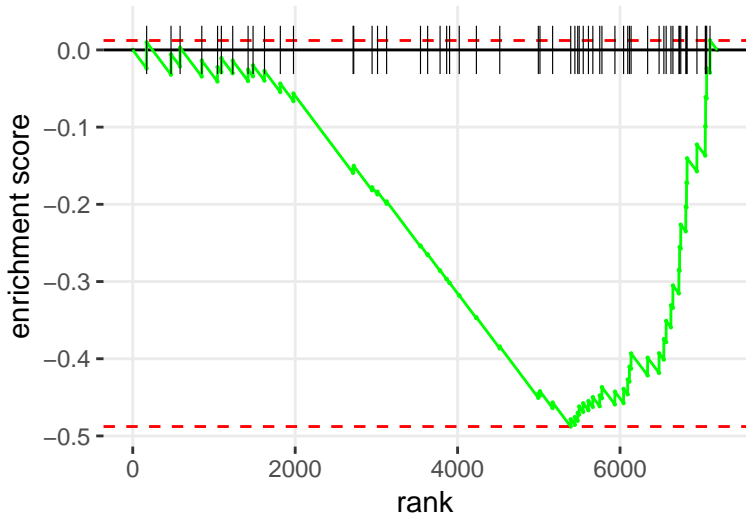
HEME BIOSYNTHESIS FROM UROPORPHYRINOGEN-III I



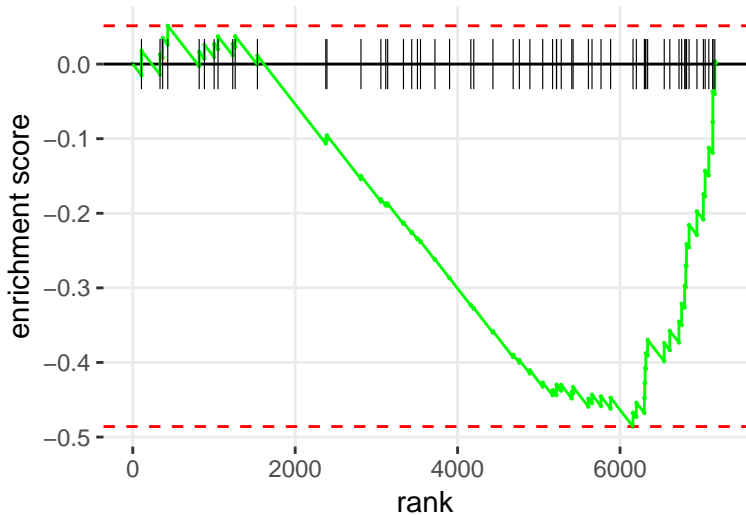
SERINE BIOSYNTHESIS



DOLICHOL AND DOLICHYL PHOSPHATE BIOSYNTHESIS



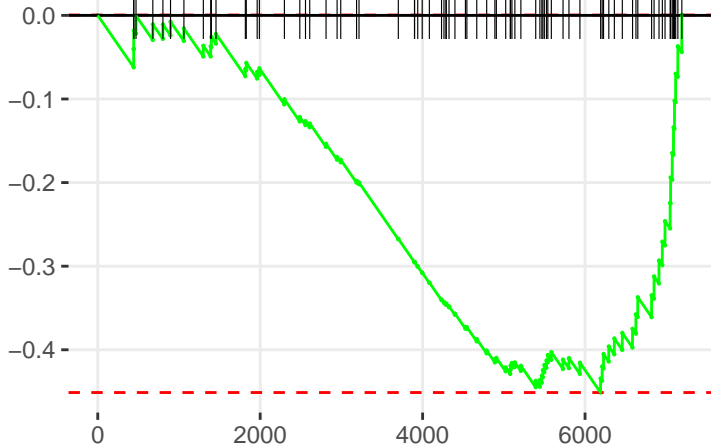
GLUTATHIONE REDOX REACTIONS I



TRIACYLGLYCEROL DEGRADATION

enrichment score

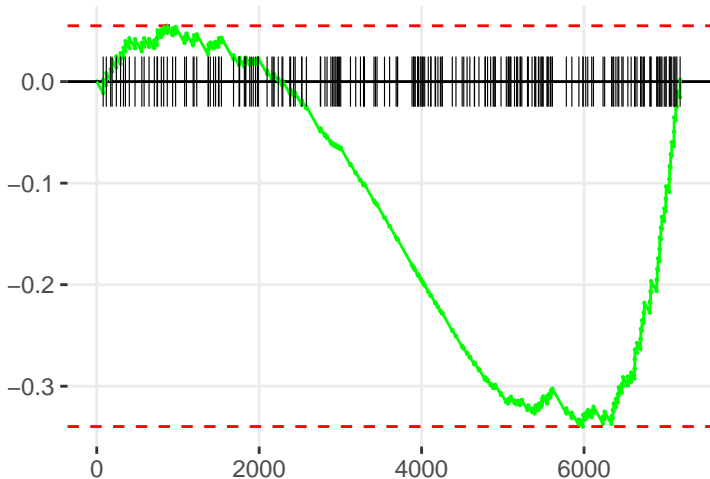
rank



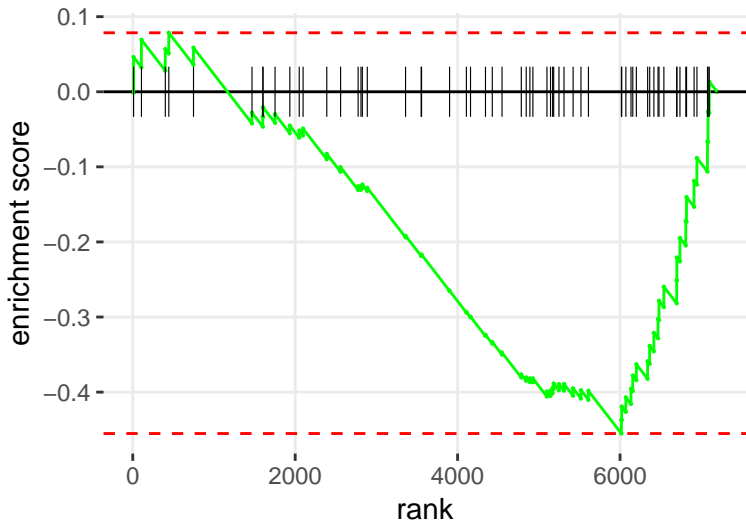
DOLICHYL-DIPHOSPHOOLIGOSACCHARIDE BIOSYNTHESIS

enrichment score

rank

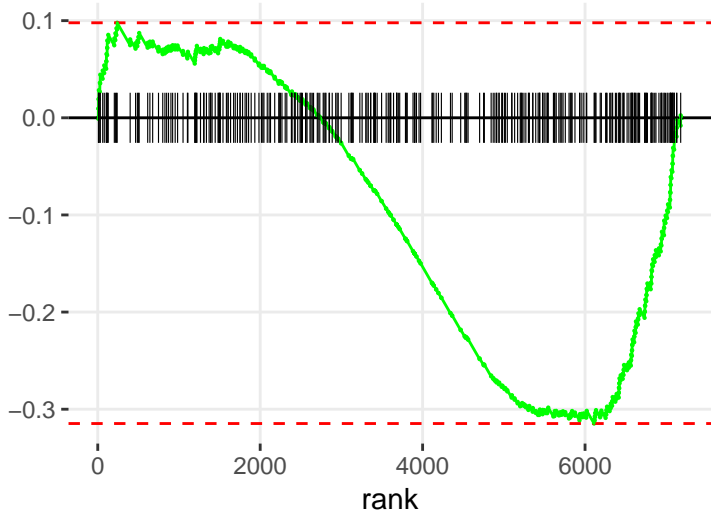


ASPARAGINE BIOSYNTHESIS I



SUCROSE DEGRADATION V (MAMMALIAN)

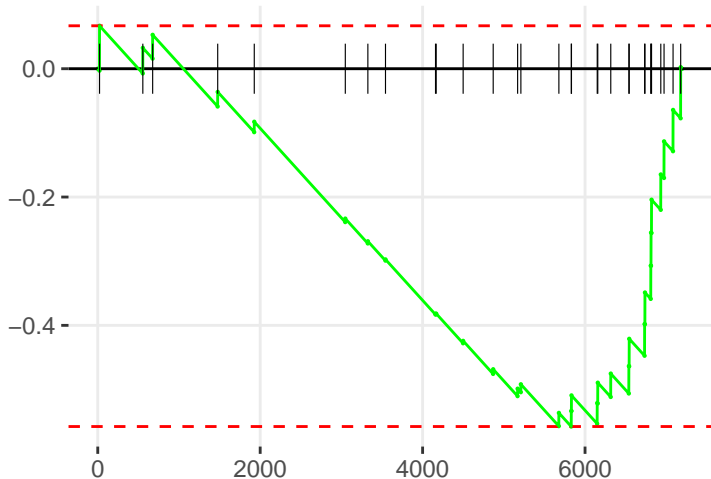
enrichment score



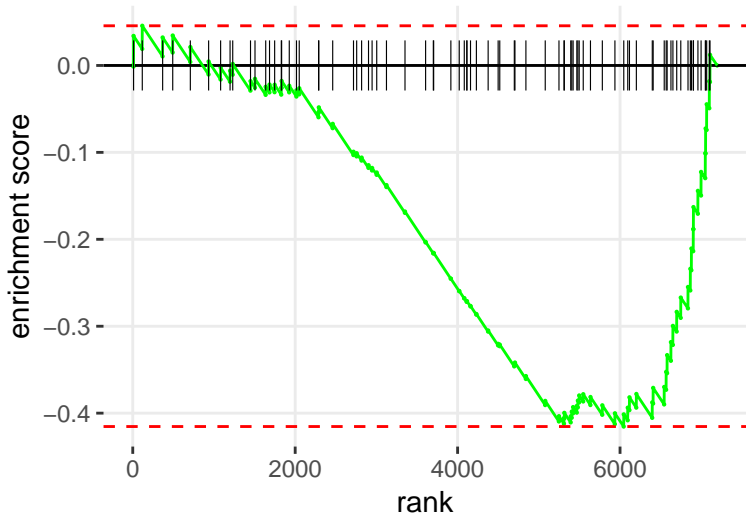
METHYLGLYOXAL DEGRADATION I

enrichment score

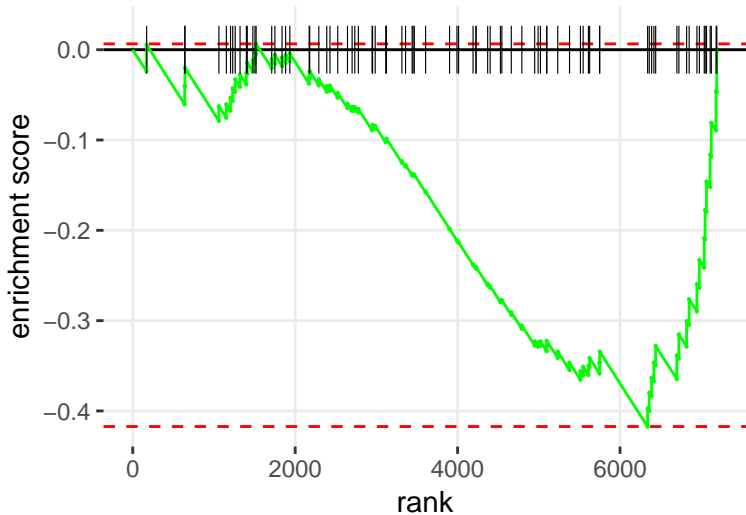
rank



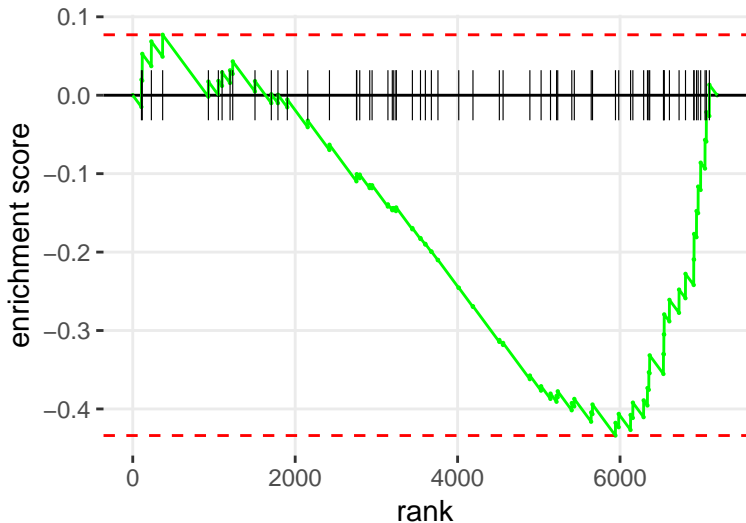
SPERMIDINE BIOSYNTHESIS I



ALANINE BIOSYNTHESIS III



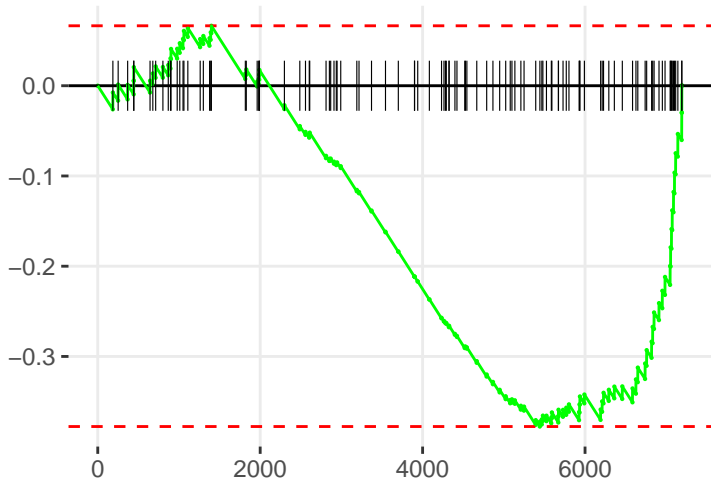
D-<IMYO</I-INOSITOL (1,4,5)-TRISPHOSPHATE DEGRADATION



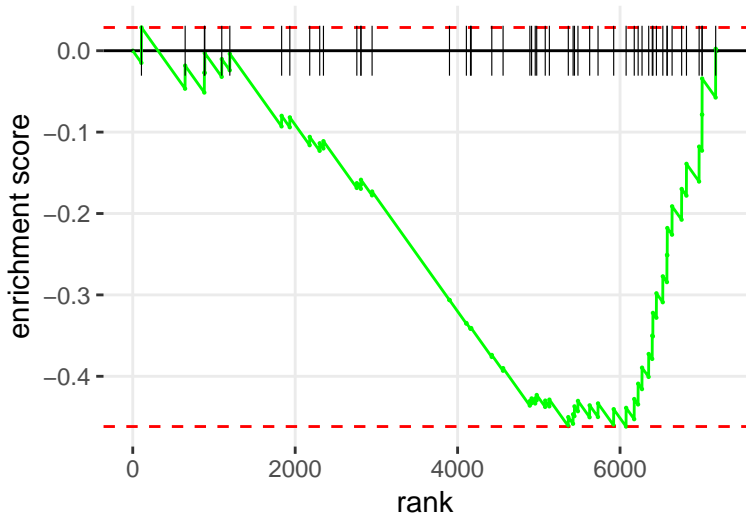
RETINOL BIOSYNTHESIS

enrichment score

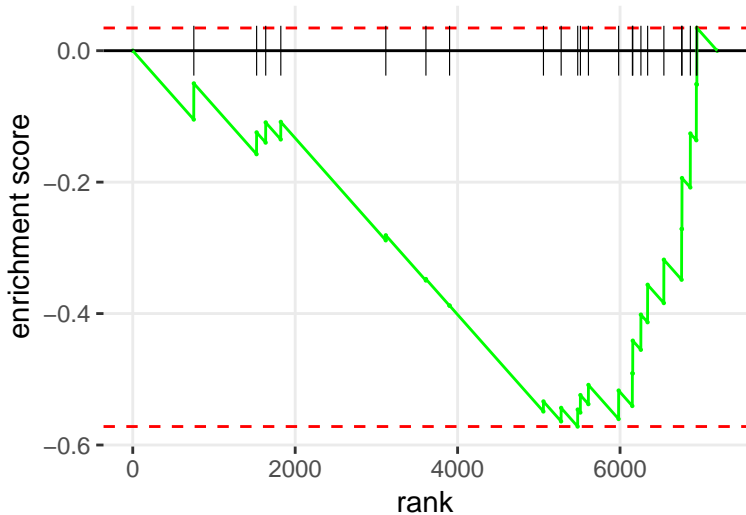
rank



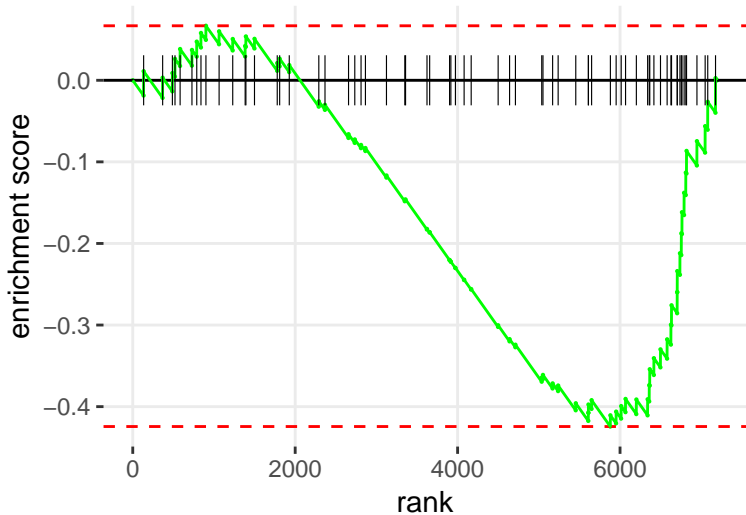
ACETYL-COA BIOSYNTHESIS III (FROM CITRATE)



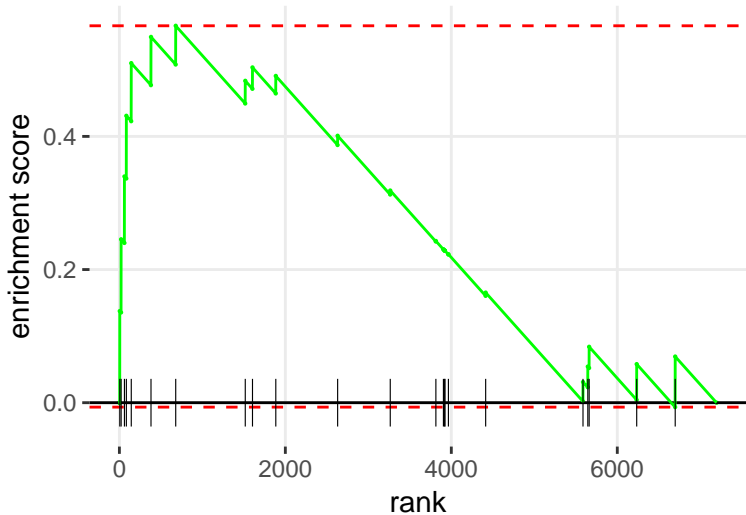
SORBITOL DEGRADATION I



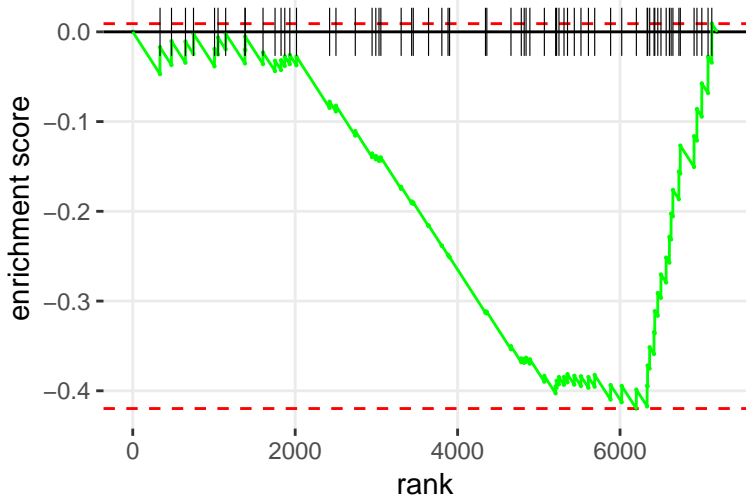
GLYCEROL DEGRADATION I



LACTOSE DEGRADATION III



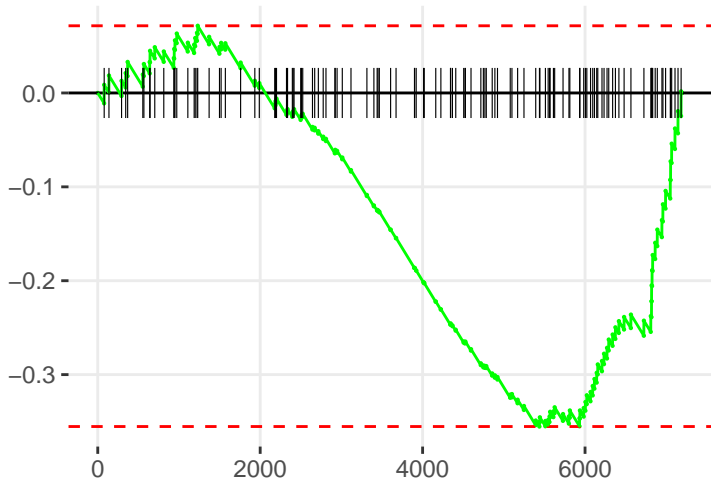
GLUTAMINE BIOSYNTHESIS I



CERAMIDE BIOSYNTHESIS

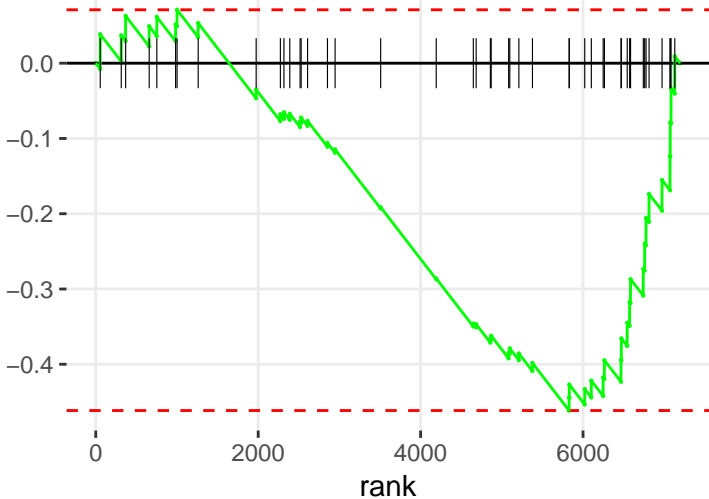
enrichment score

rank



THIOREDOXIN PATHWAY

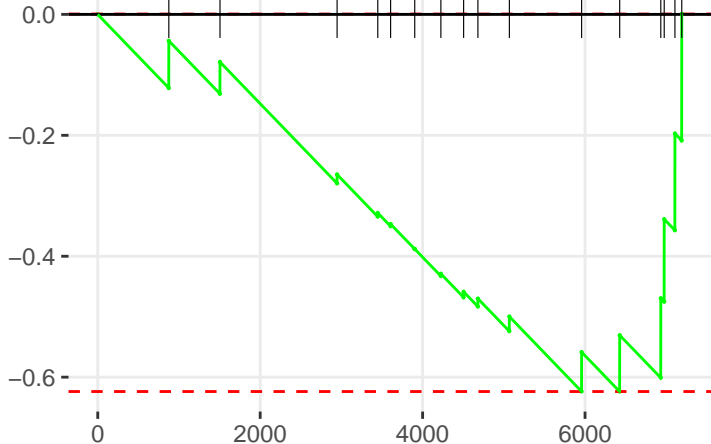
enrichment score



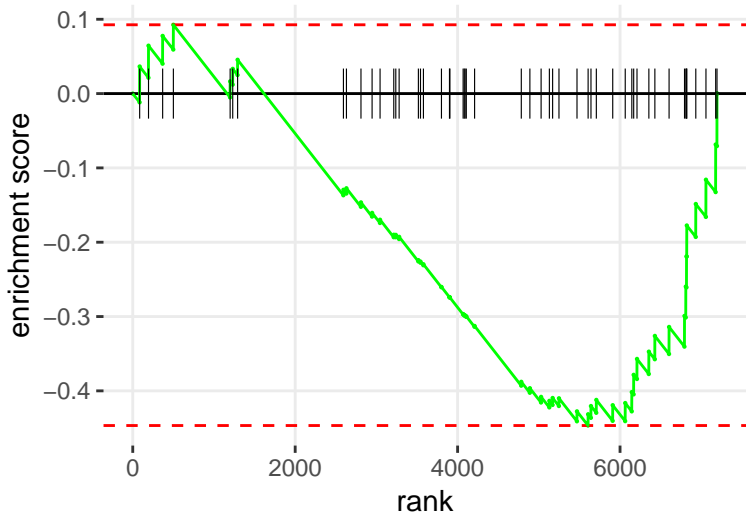
GDP-L-FUCOSE BIOSYNTHESIS I (FROM GDP-D-MANNOSE)

enrichment score

rank



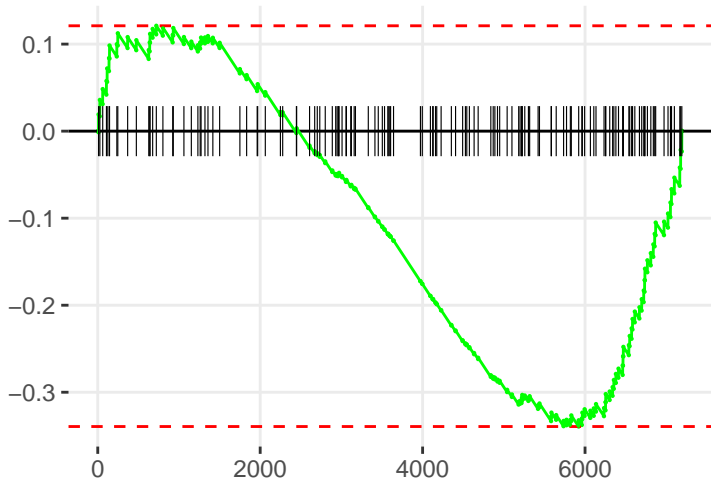
<IS</I-METHYL-5-THIO-&ALPHA;-D-RIBOSE 1-PHOSPHATE DEGRADATION



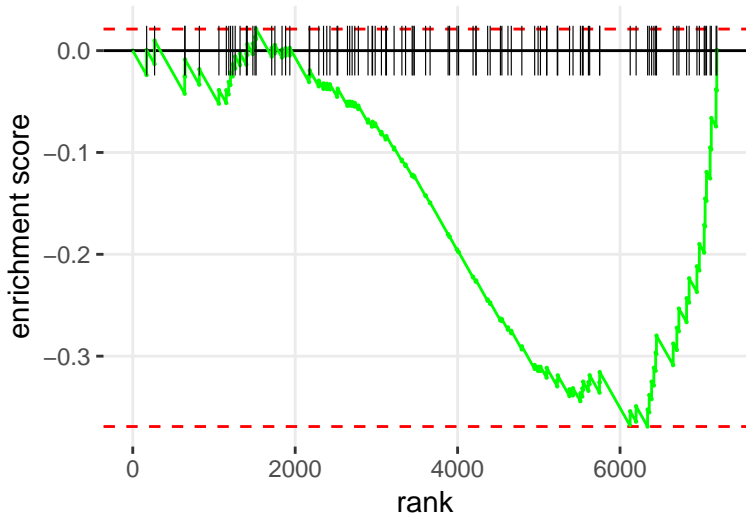
PROSTANOID BIOSYNTHESIS

enrichment score

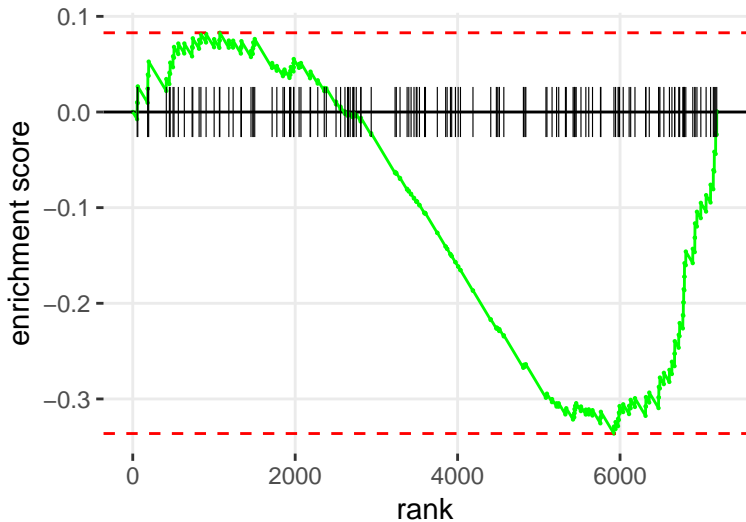
rank



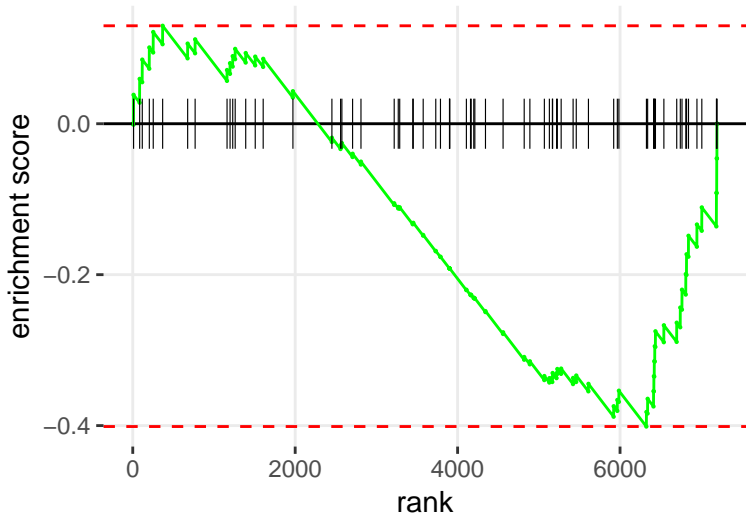
MOLYBDENUM COFACTOR BIOSYNTHESIS



MELATONIN DEGRADATION I

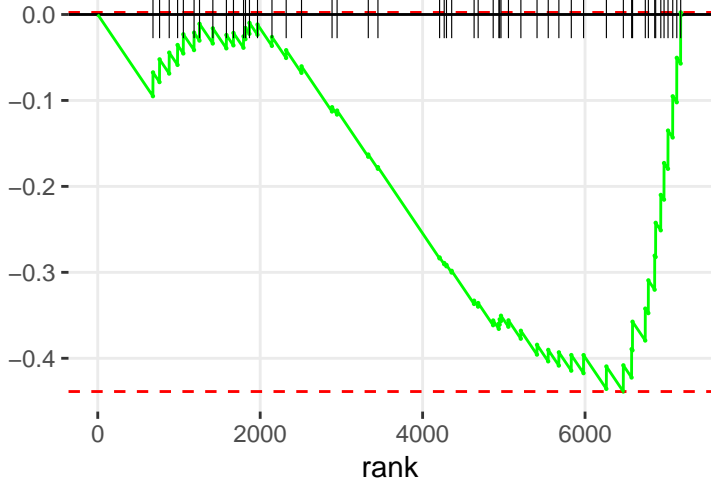


GUANINE AND GUANOSINE SALVAGE I

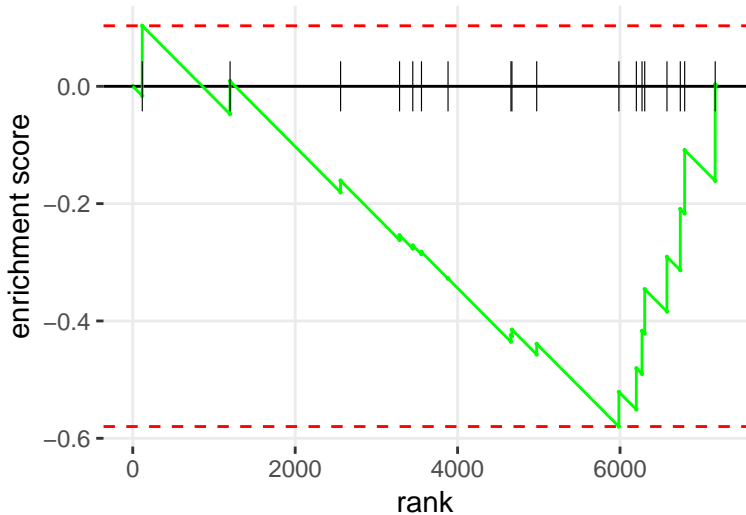


FATTY ACID &BETA;-OXIDATION III (UNSATURATED, ODD NUMBER)

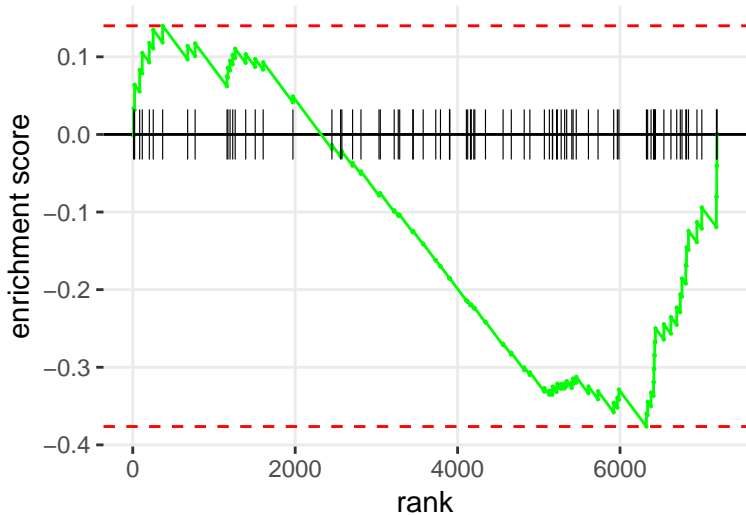
enrichment score



NADH REPAIR



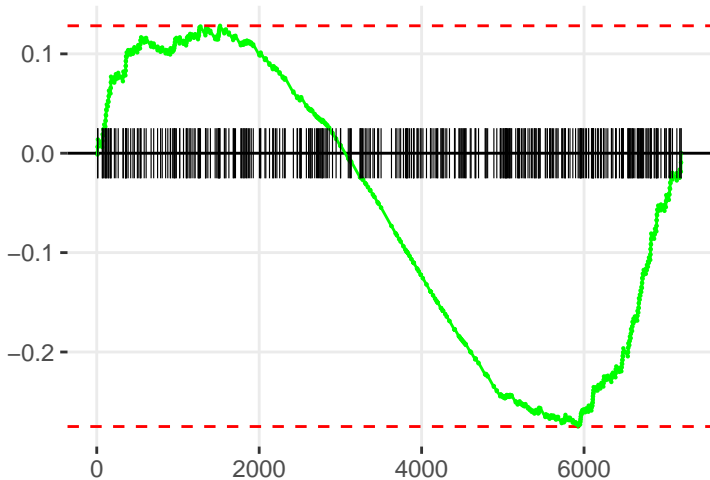
ADENINE AND ADENOSINE SALVAGE III



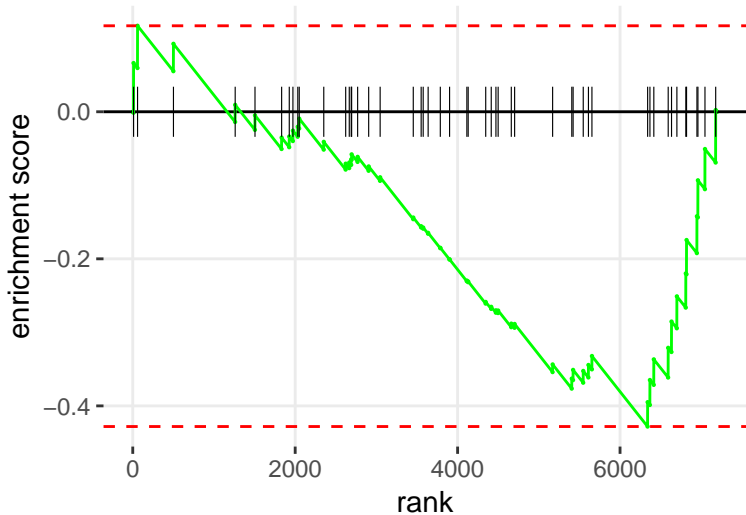
3-PHOSPHOINOSITIDE DEGRADATION

enrichment score

rank

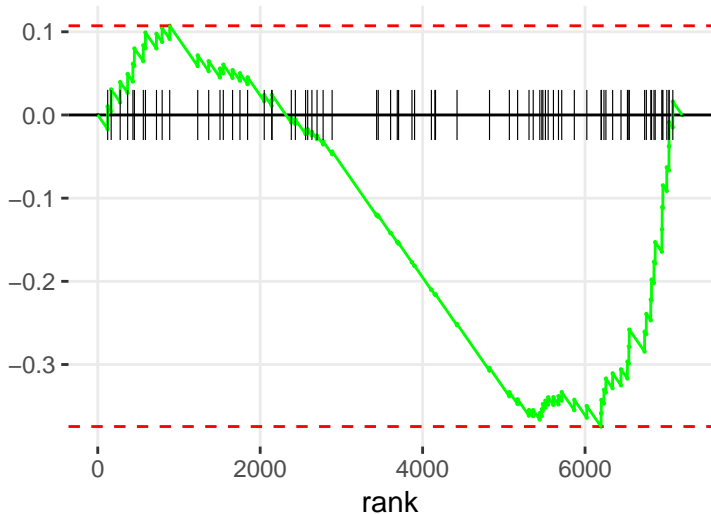


FORMALDEHYDE OXIDATION II (GLUTATHIONE-DEPENDENT)

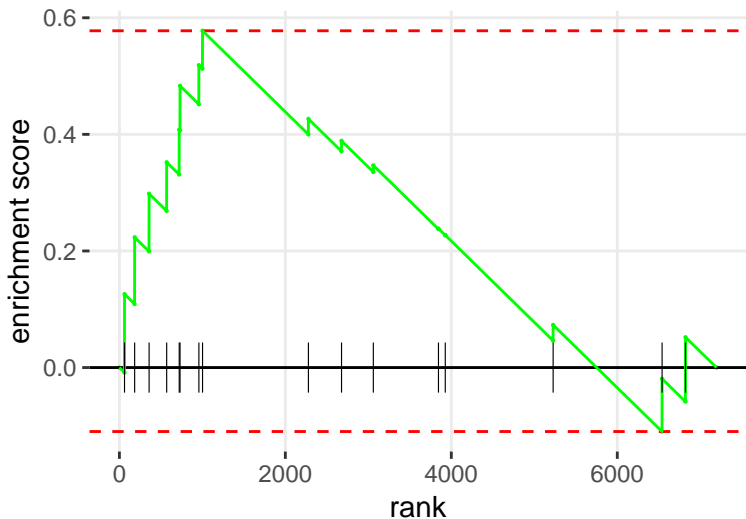


LEUKOTRIENE BIOSYNTHESIS

enrichment score

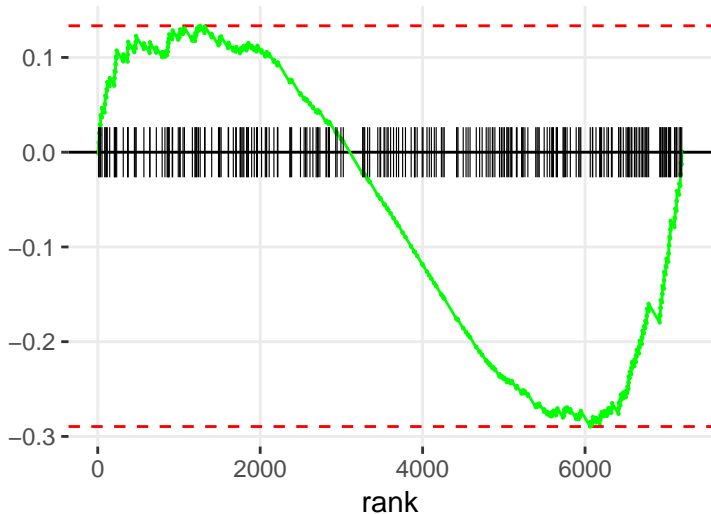


GLUCOCORTICOID BIOSYNTHESIS



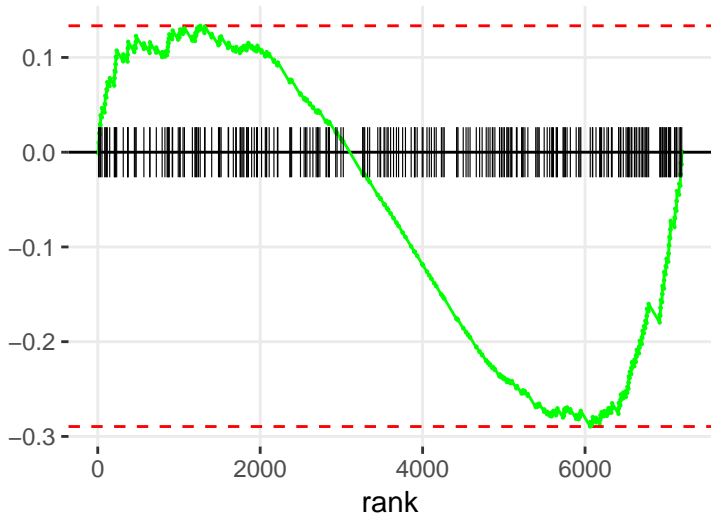
GLUTATHIONE-MEDIATED DETOXIFICATION I

enrichment score

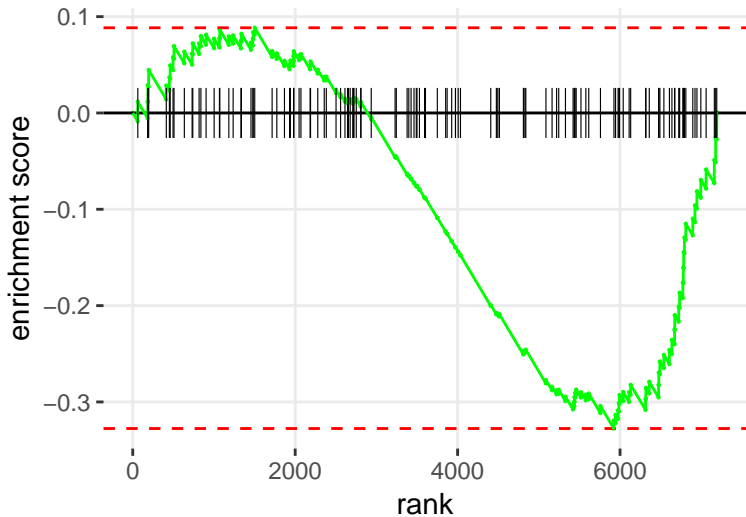


4-HYDROXY-2-NONENAL DETOXIFICATION

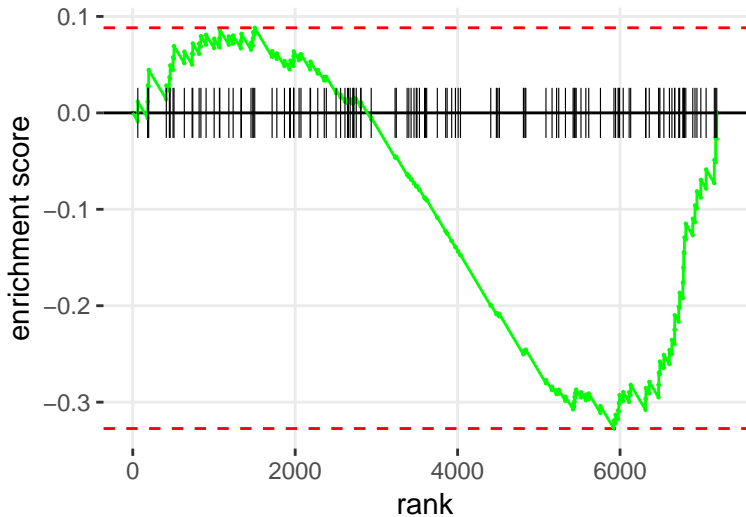
enrichment score



NICOTINE DEGRADATION III



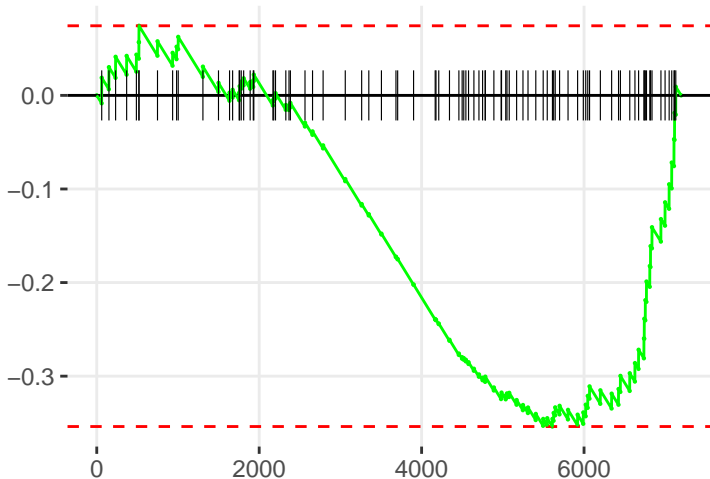
NICOTINE DEGRADATION IV



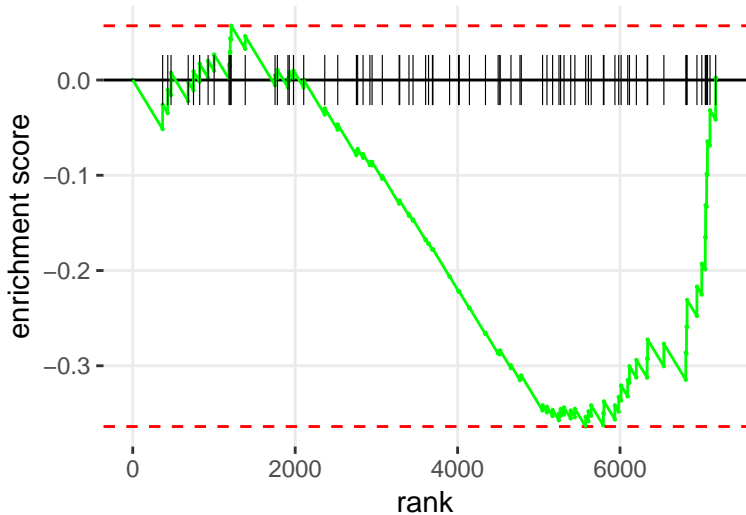
GLYCEROL-3-PHOSPHATE SHUTTLE

enrichment score

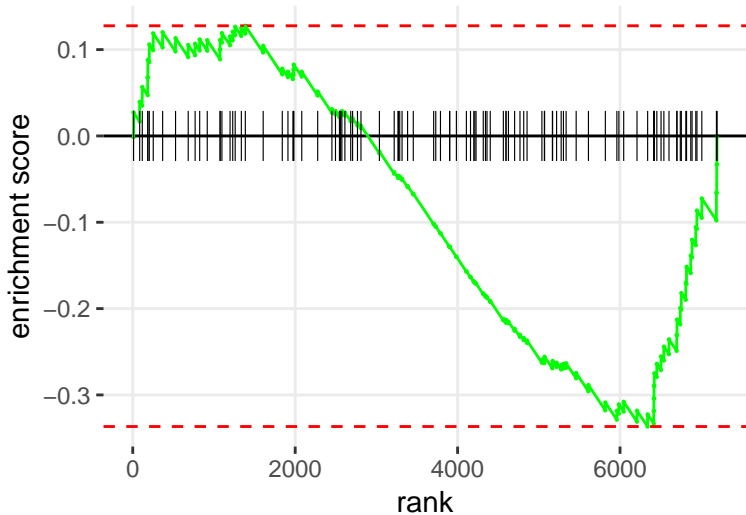
rank



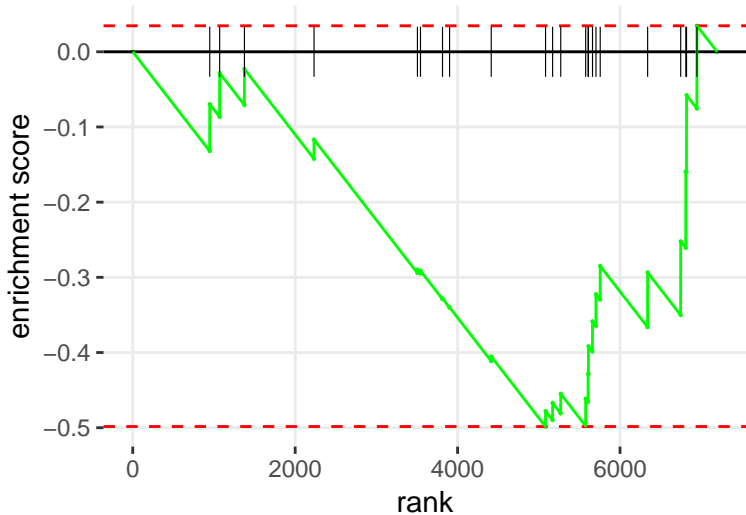
OLEATE BIOSYNTHESIS II (ANIMALS)



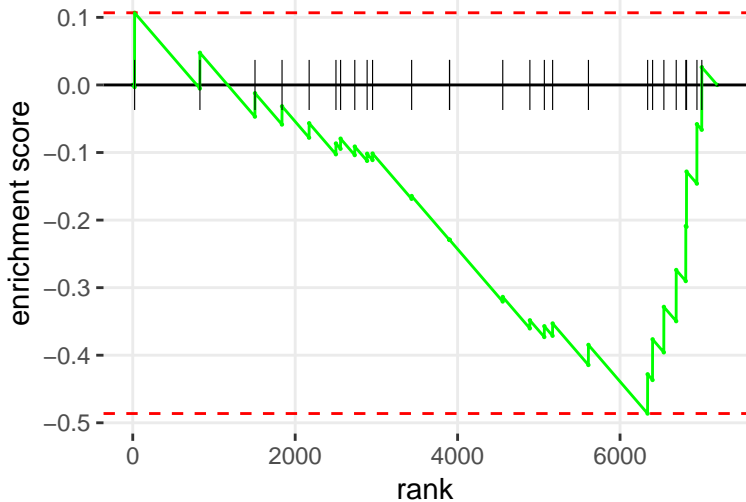
GUANOSINE NUCLEOTIDES DEGRADATION III



PUTRESCINE BIOSYNTHESIS III

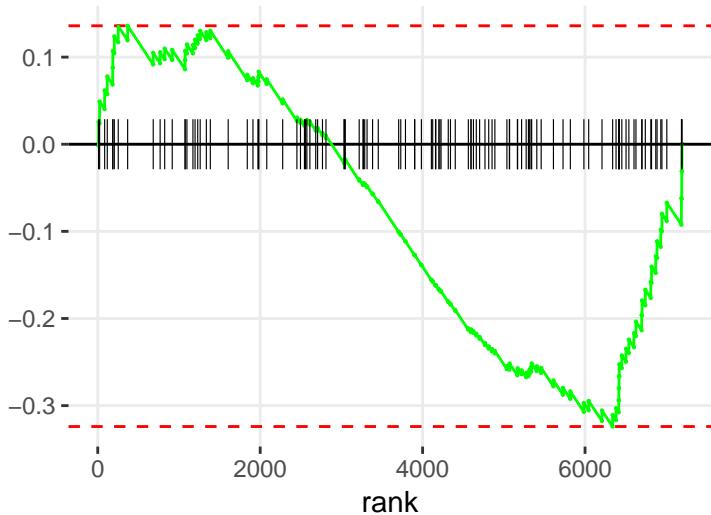


L-CYSTEINE DEGRADATION III

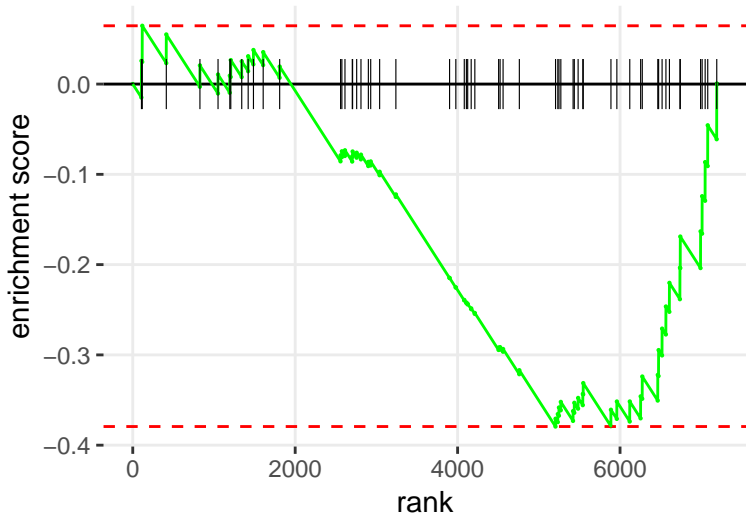


ADENOSINE NUCLEOTIDES DEGRADATION II

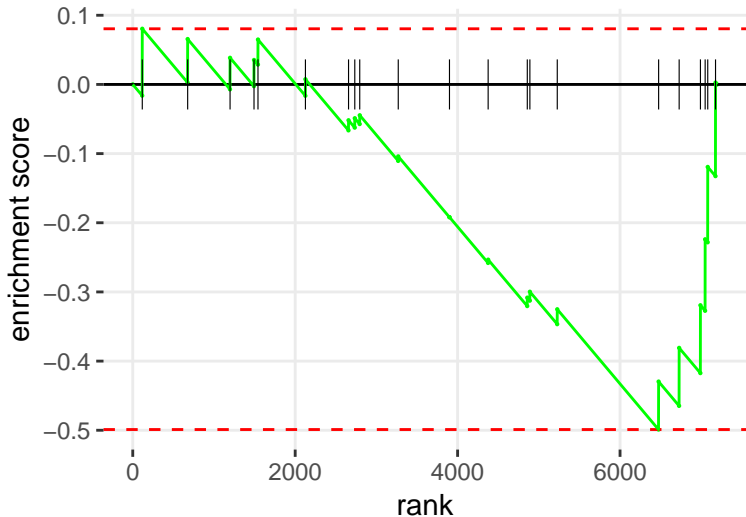
enrichment score



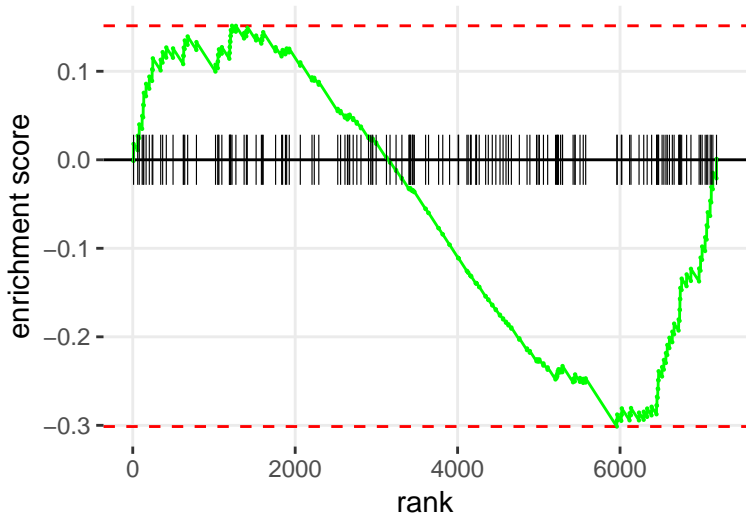
CREATINE-PHOSPHATE BIOSYNTHESIS



<IN</I>-ACETYLGLUCOSAMINE DEGRADATION I



PYRUVATE FERMENTATION TO LACTATE



PHOSPHATIDYLETHANOLAMINE BIOSYNTHESIS II

enrichment score

0.0

-0.1

-0.2

-0.3

-0.4

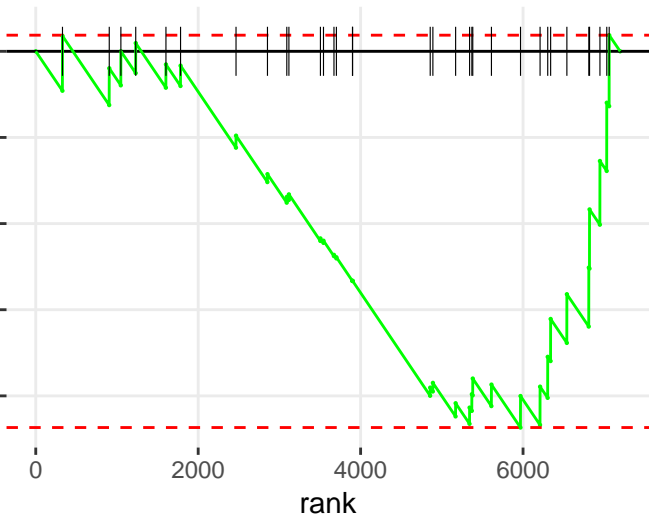
0

2000

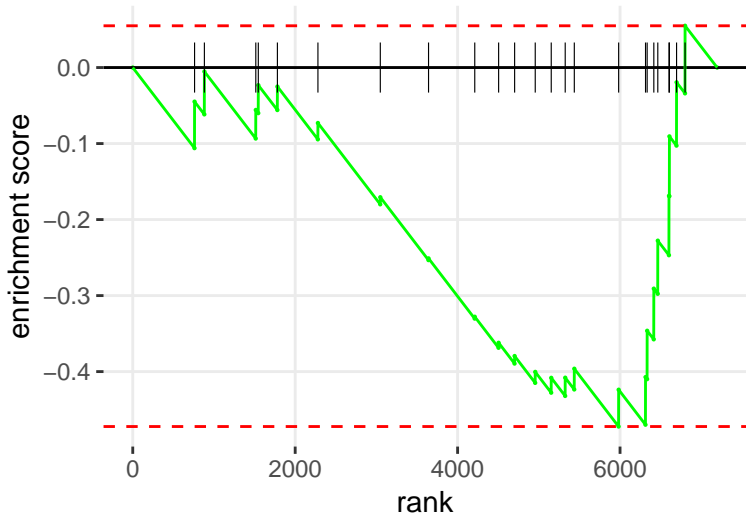
4000

6000

rank

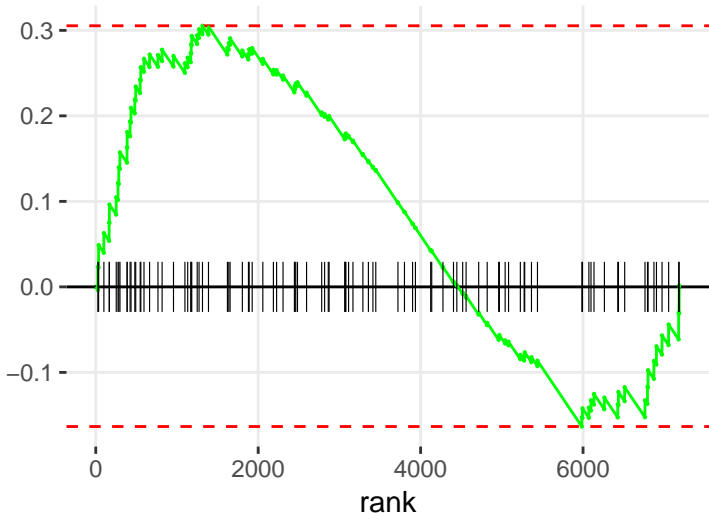


CATECHOLAMINE BIOSYNTHESIS

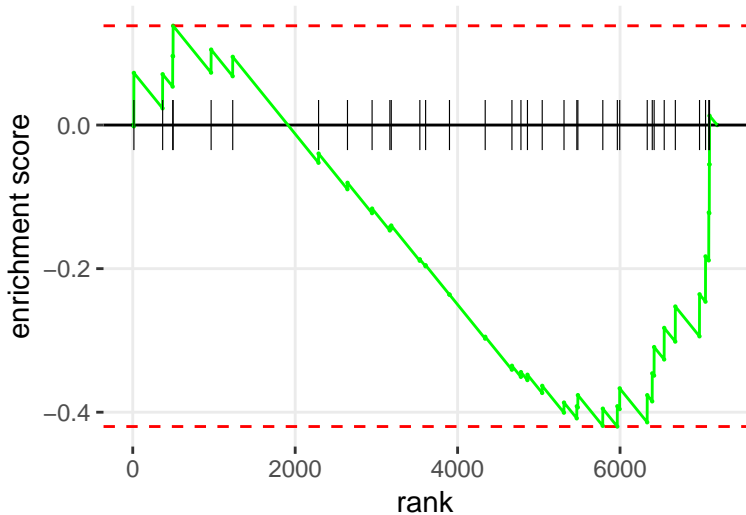


PHENYLALANINE DEGRADATION I (AEROBIC)

enrichment score

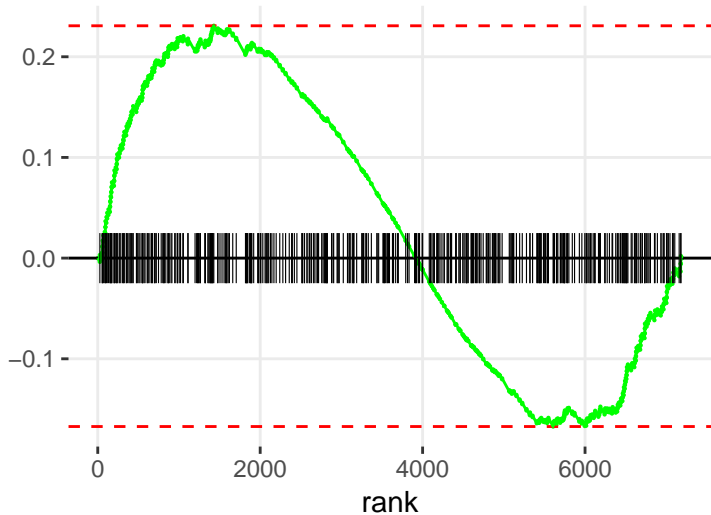


SPERMINE BIOSYNTHESIS



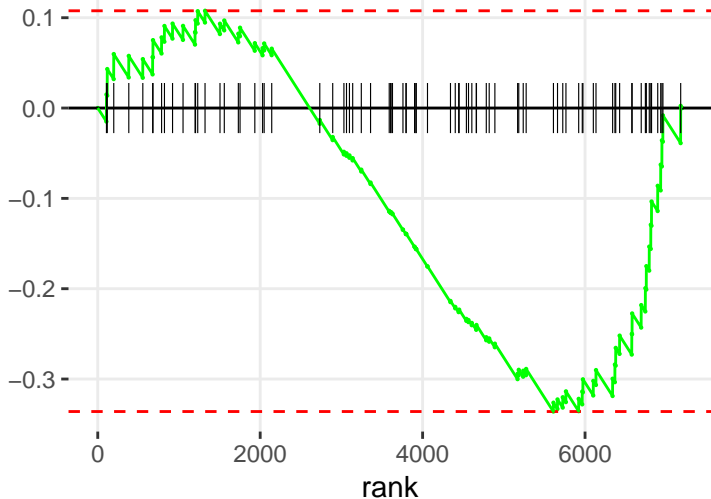
D-<IMYO</I-INOSITOL-5-PHOSPHATE METABOLISM

enrichment score

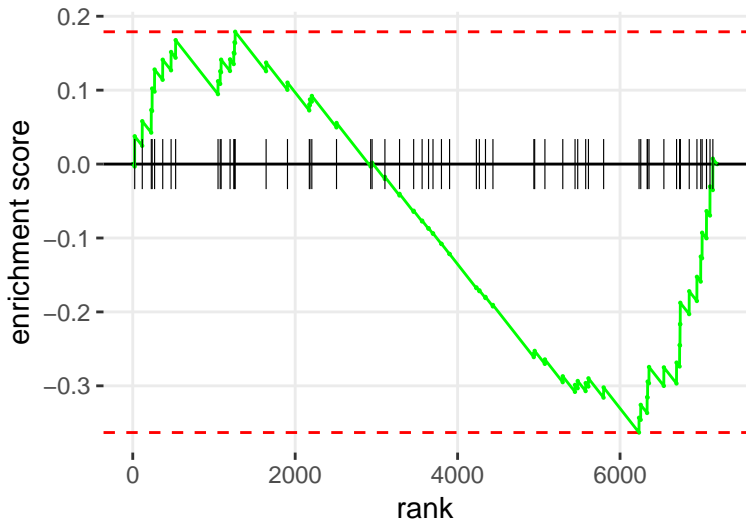


TETRAPYRROLE BIOSYNTHESIS II

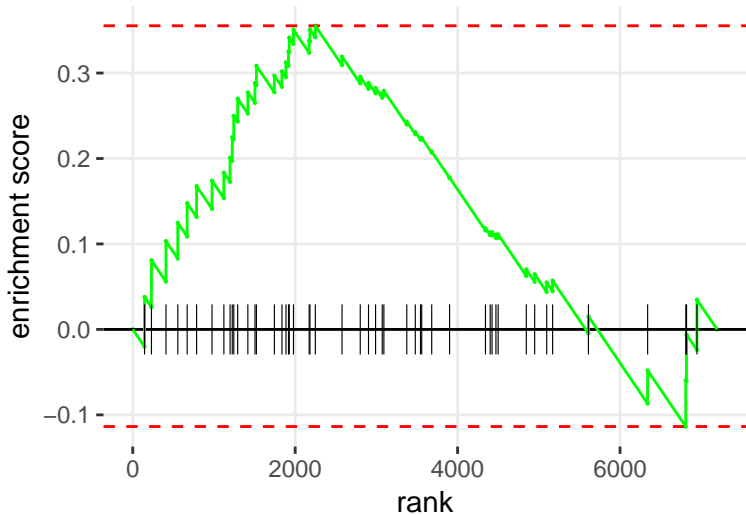
enrichment score



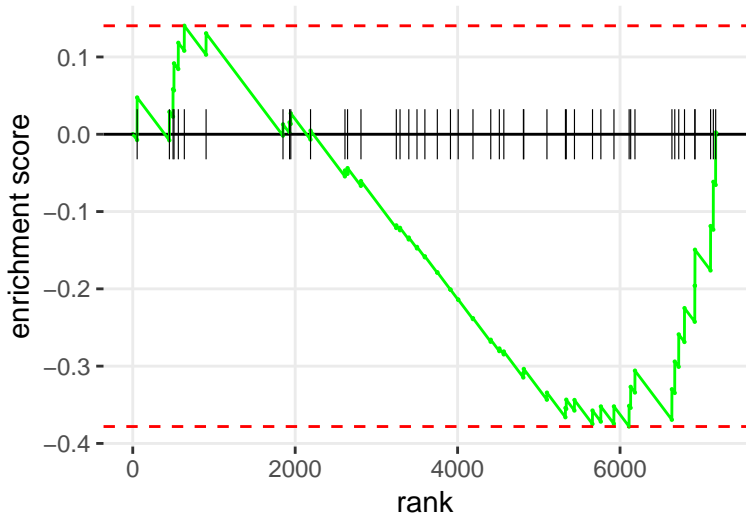
MITOCHONDRIAL L-CARNITINE SHUTTLE PATHWAY



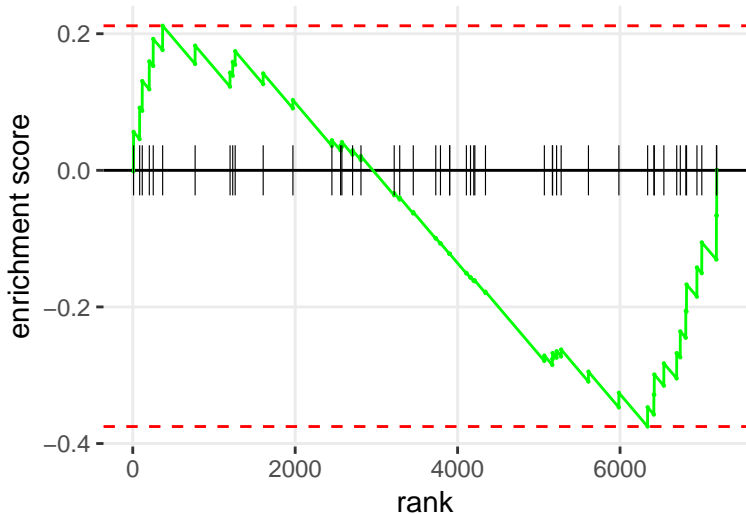
UBIQUINOL-10 BIOSYNTHESIS (EUKARYOTIC)



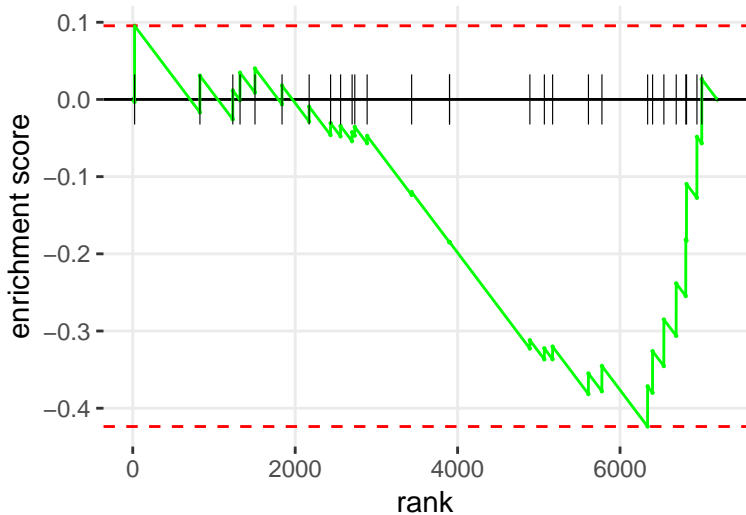
THYROID HORMONE METABOLISM II (VIA CONJUGATION AND/OR DEGRADATION)



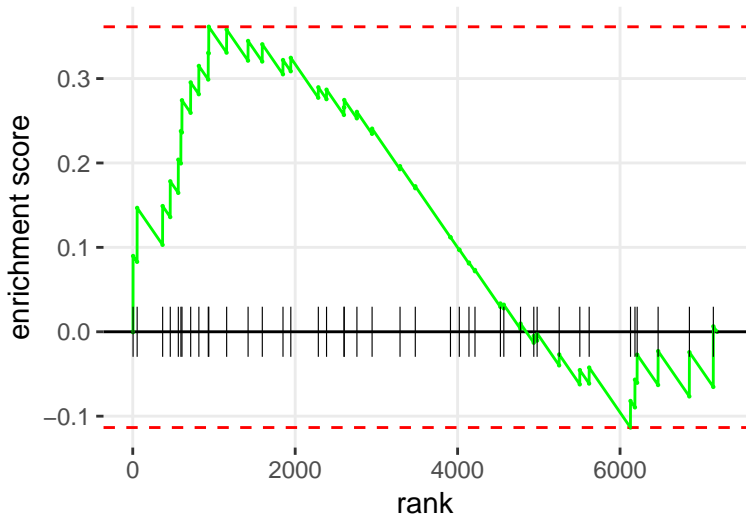
XANTHINE AND XANTHOSINE SALVAGE



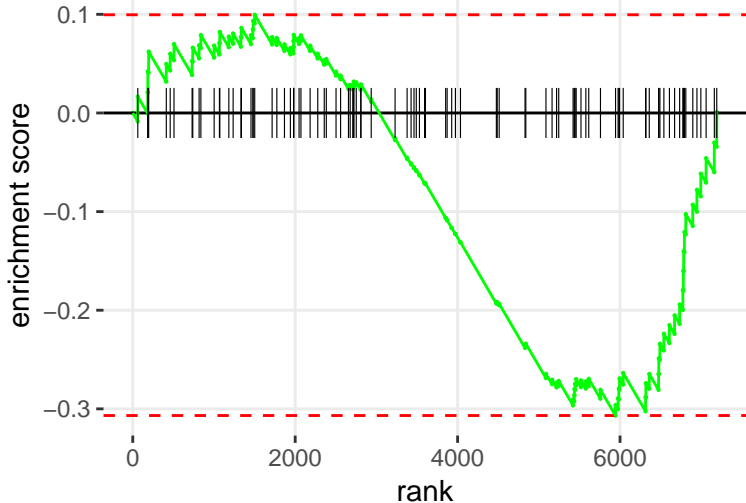
THIOSULFATE DISPROPORTIONATION III (RHODANESE)



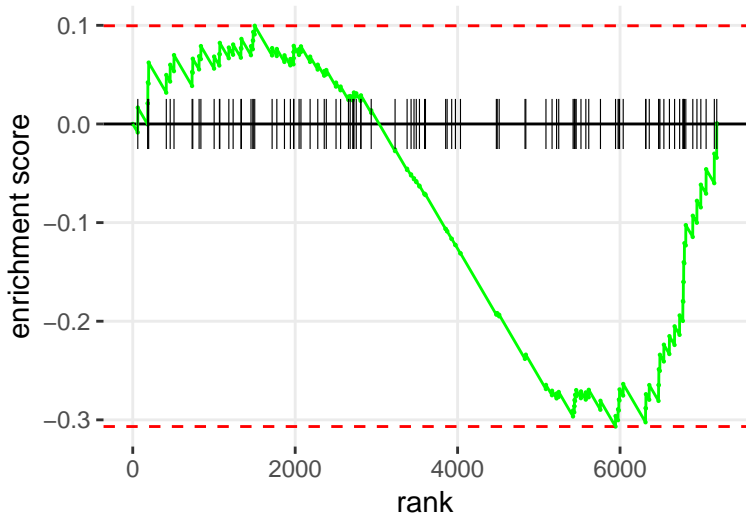
CHONDROITIN SULFATE BIOSYNTHESIS (LATE STAGES)



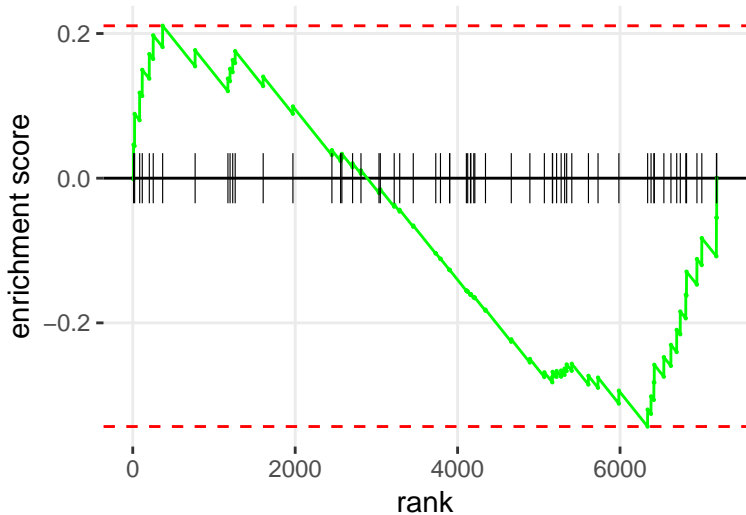
ACETONE DEGRADATION I (TO METHYLGLYOXAL)



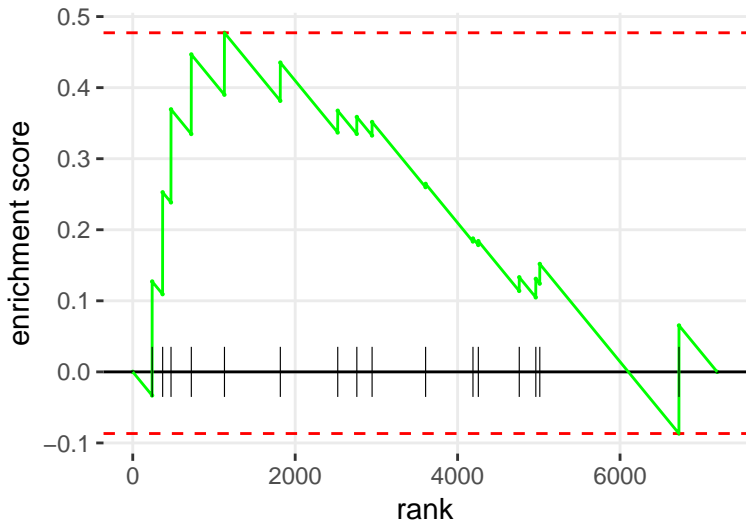
BUPROPION DEGRADATION



PURINE RIBONUCLEOSIDES DEGRADATION TO RIBOSE-1-PHOSPHATE



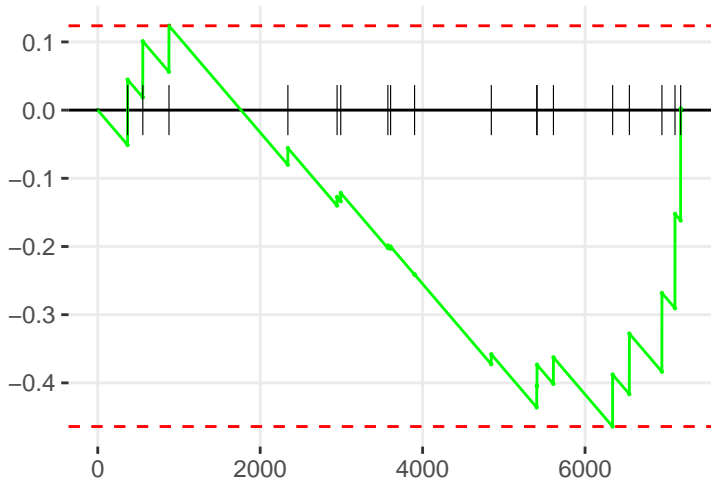
PHOSPHATIDYLETHANOLAMINE BIOSYNTHESIS III



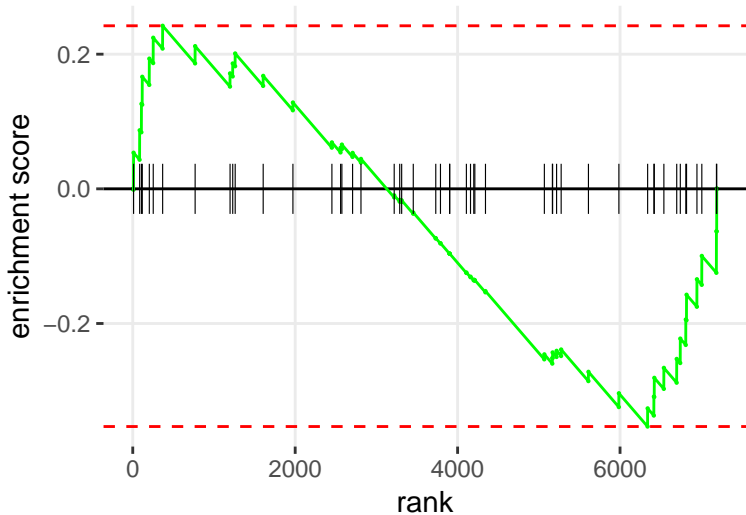
ALL-<I>TRANS</I>-DECAPRENYL DIPHOSPHATE BIOSYNTHESIS

enrichment score

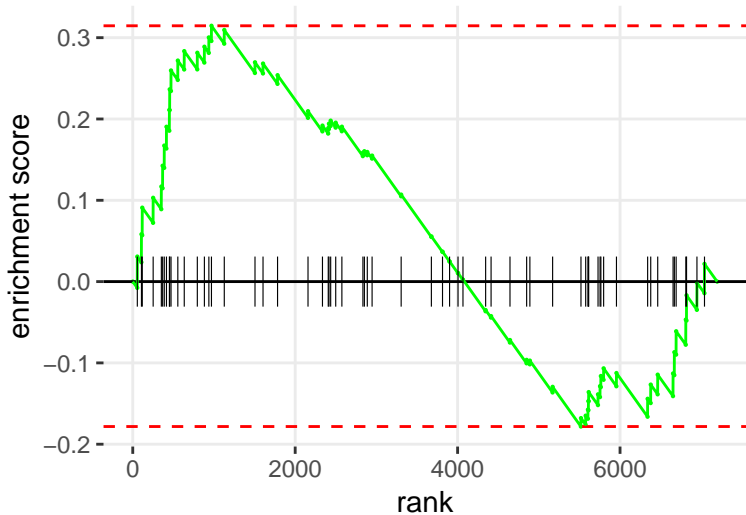
rank



ARSENATE DETOXIFICATION I (GLUTAREDOXIN)



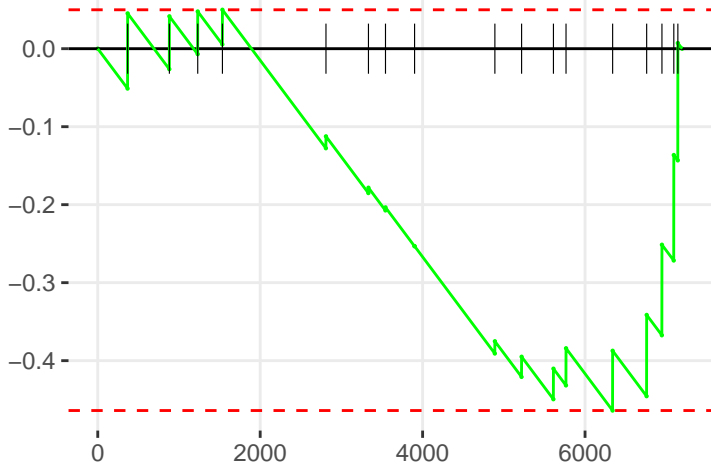
SPHINGOMYELIN METABOLISM



GLUTATHIONE REDOX REACTIONS II

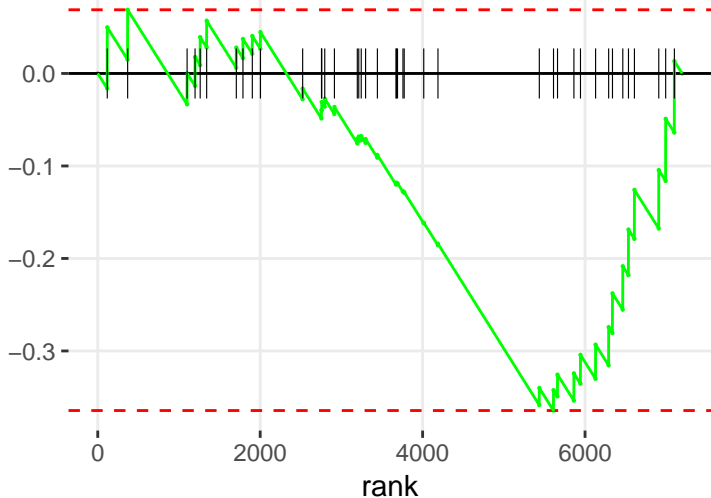
enrichment score

rank



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

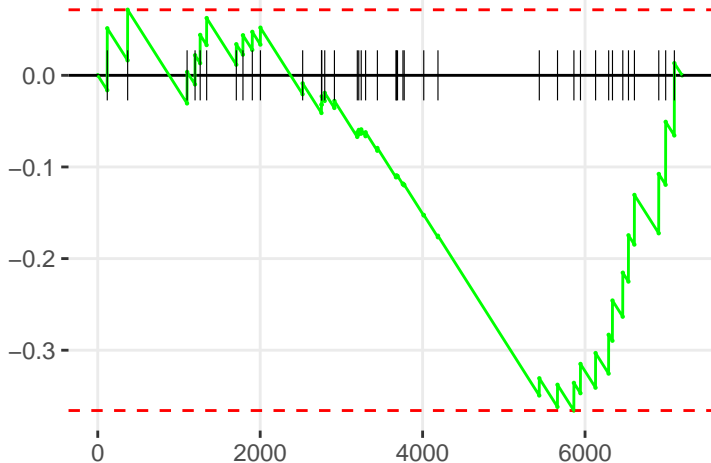
enrichment score



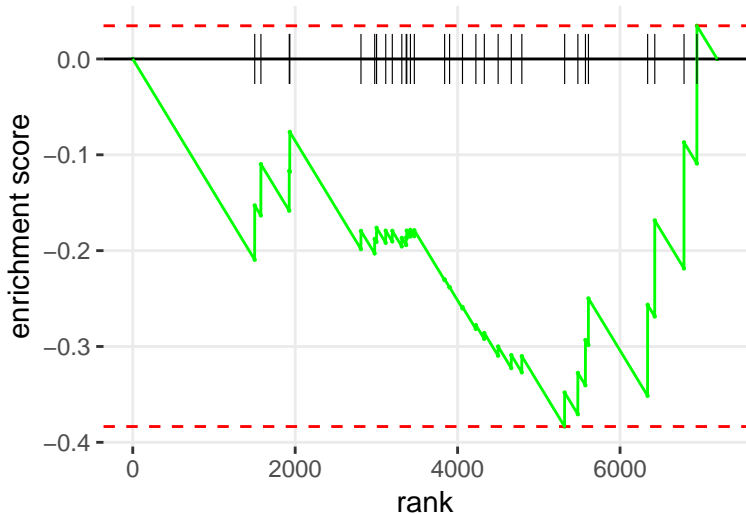
D-*MYO*-INOSITOL (1,3,4)-TRISPHOSPHATE BIOSYNTHESIS

enrichment score

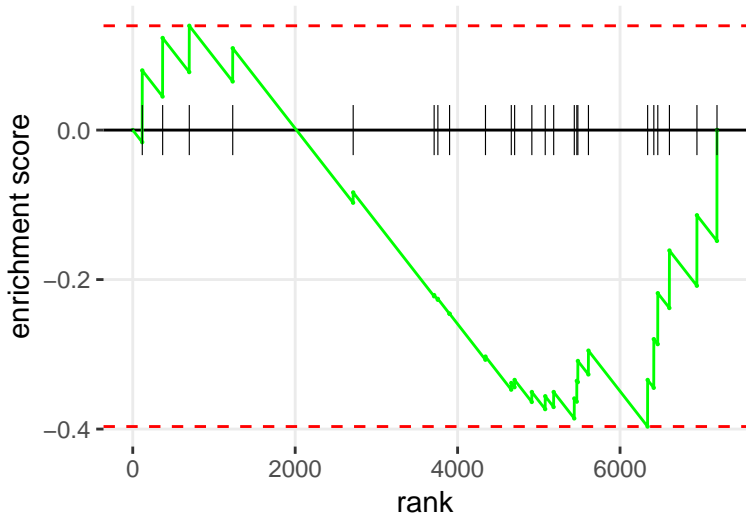
rank



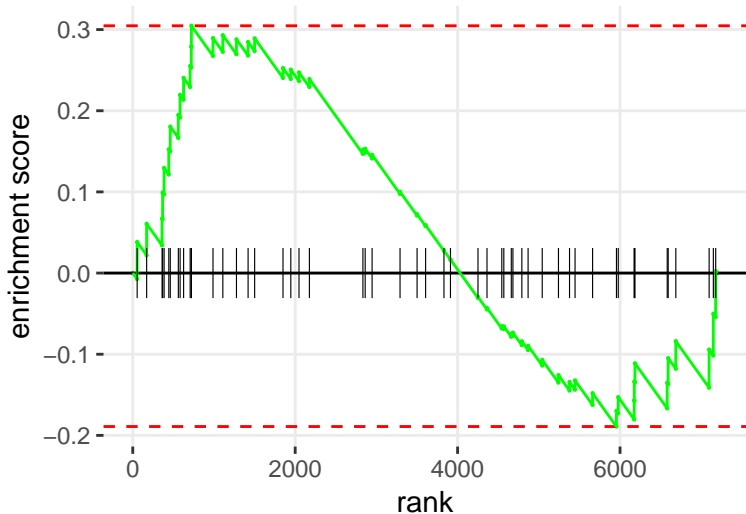
GLUTAMATE DEGRADATION III (VIA 4-AMINOBUTYRATE)



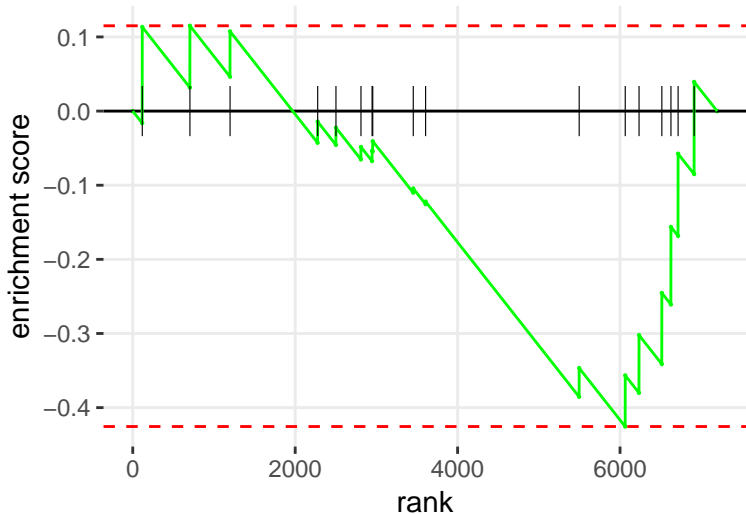
NAD PHOSPHORYLATION AND DEPHOSPHORYLATION



HEPARAN SULFATE BIOSYNTHESIS (LATE STAGES)



ACYL CARRIER PROTEIN METABOLISM



4-AMINOBUTYRATE DEGRADATION I

enrichment score

0.0

-0.1

-0.2

-0.3

-0.4

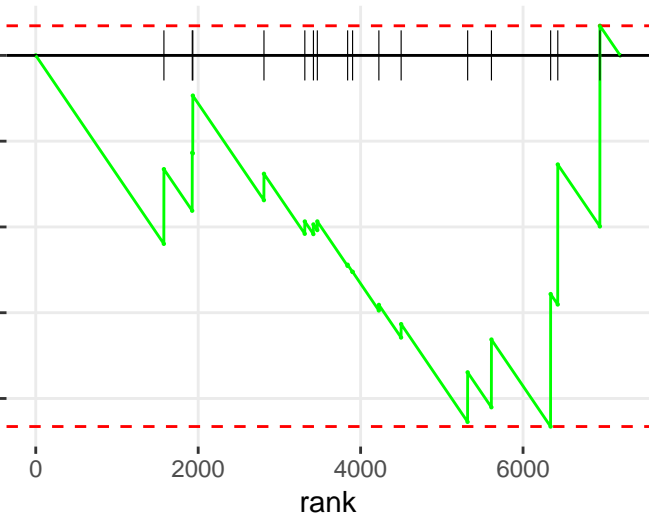
0

2000

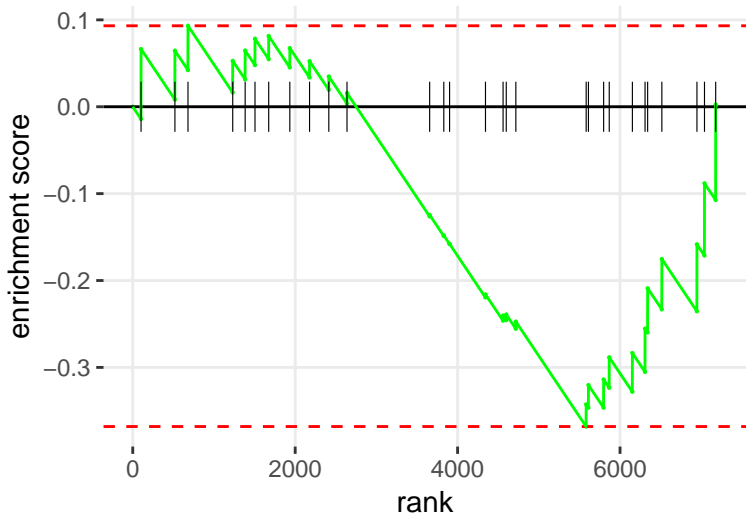
4000

6000

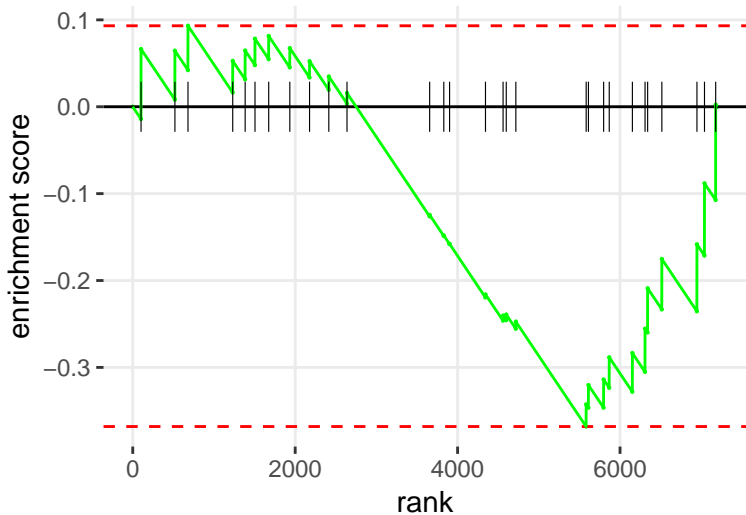
rank



ALANINE BIOSYNTHESIS II

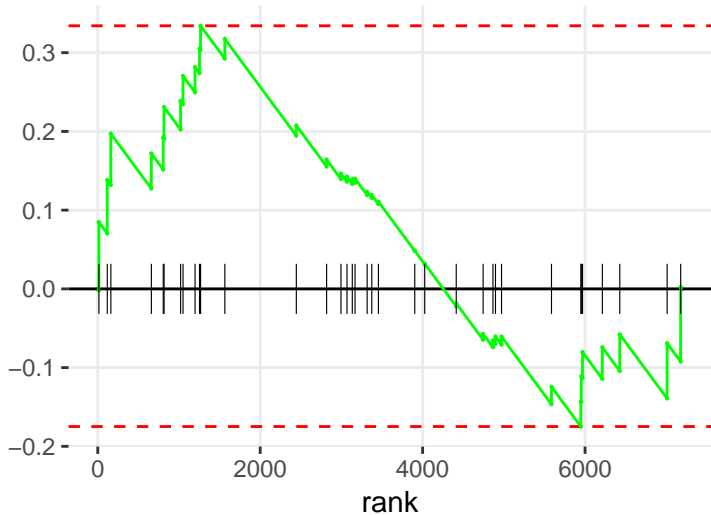


ALANINE DEGRADATION III



METHYLMALONYL PATHWAY

enrichment score



NAD BIOSYNTHESIS III

enrichment score

0.4

0.2

0.0

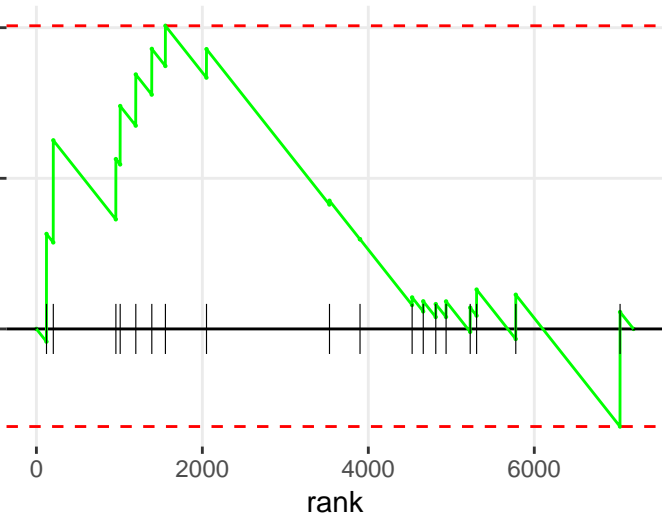
0

2000

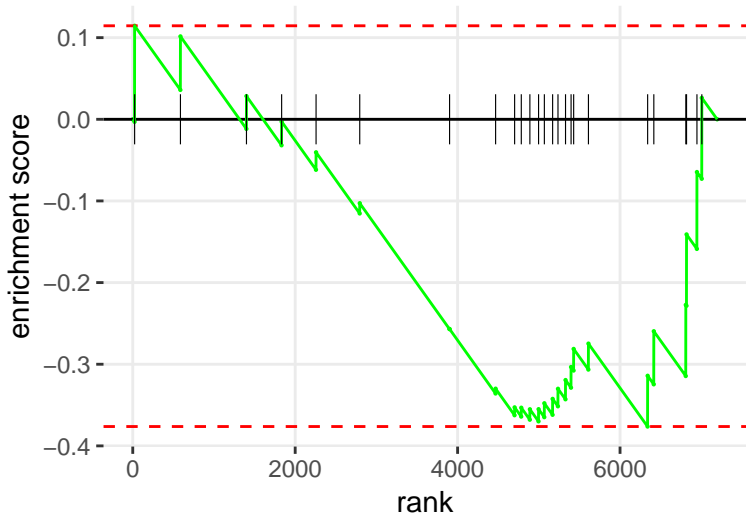
4000

6000

rank

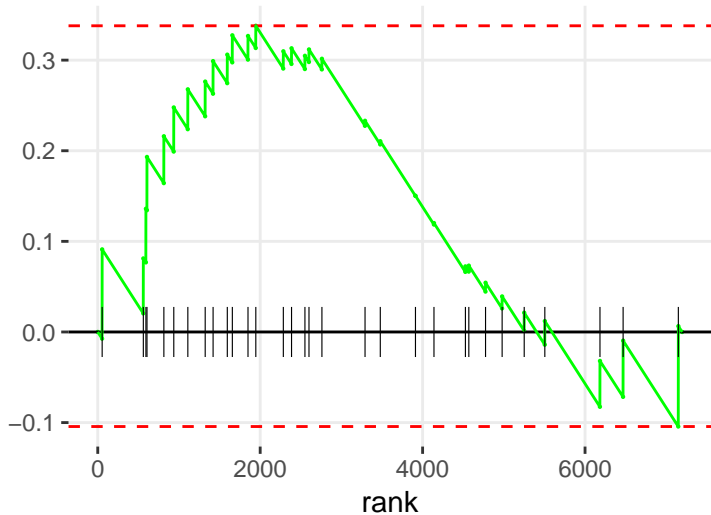


<ITRANS, TRANS</I-FARNESYL DIPHOSPHATE BIOSYNTHESIS

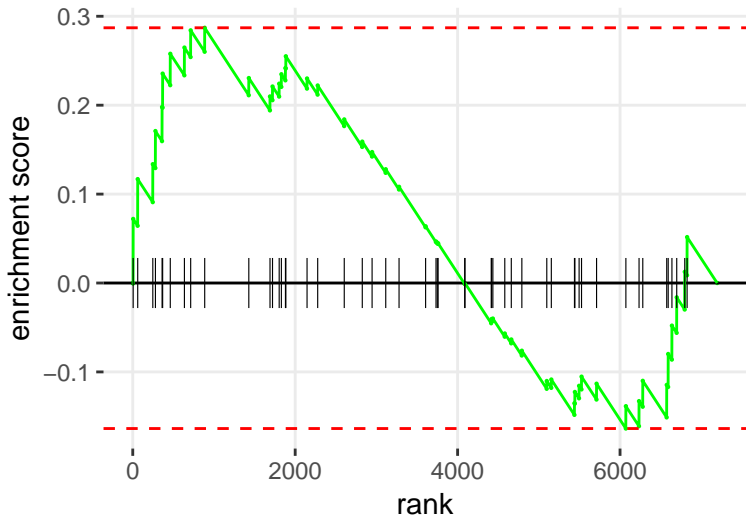


DERMATAN SULFATE BIOSYNTHESIS (LATE STAGES)

enrichment score

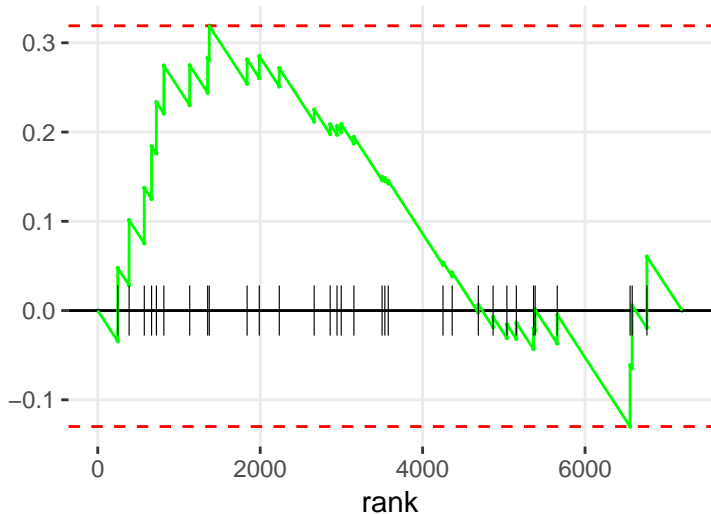


CHONDROITIN SULFATE DEGRADATION (METAZOA)



GLYCOAMINOGLYCAN-PROTEIN LINKAGE REGION BIOSYNTHESIS

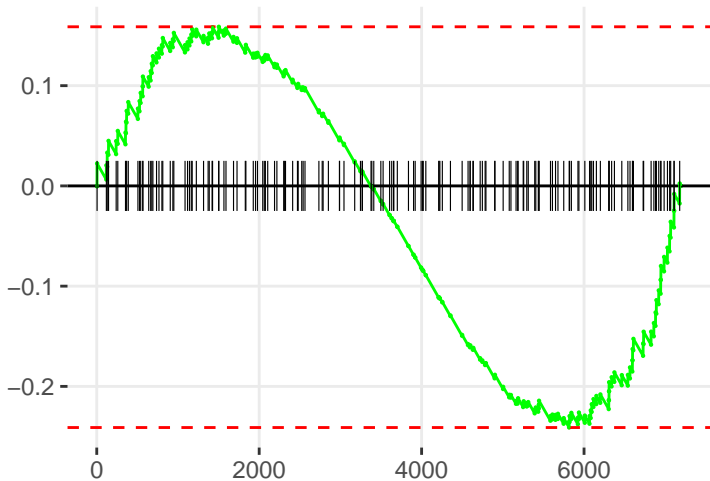
enrichment score



CALCIUM TRANSPORT I

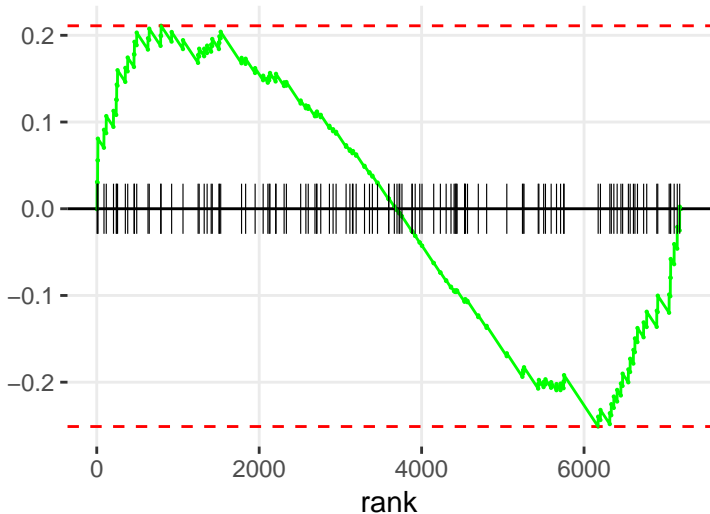
enrichment score

rank

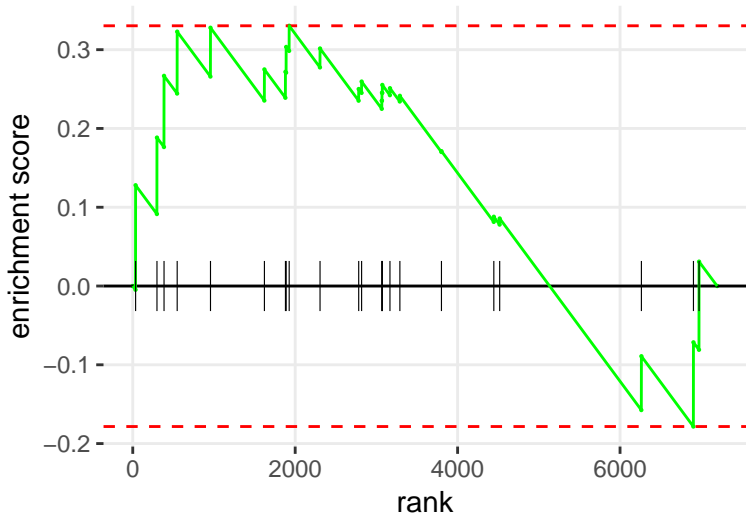


SALVAGE PATHWAYS OF PYRIMIDINE DEOXYRIBONUCLEOTIDES

enrichment score



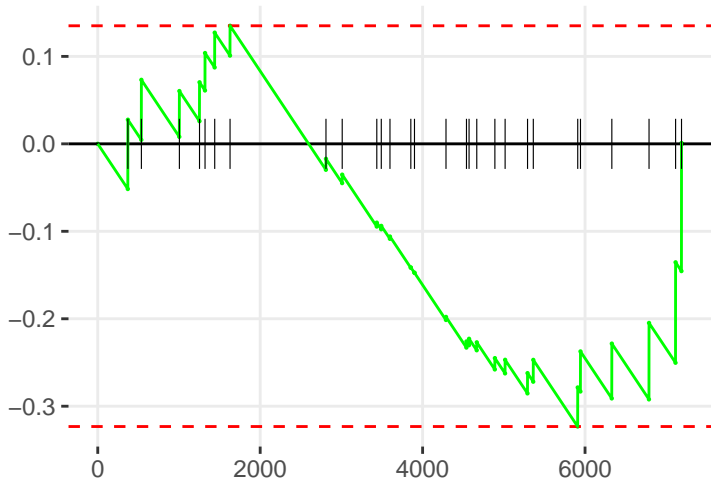
TYROSINE BIOSYNTHESIS IV



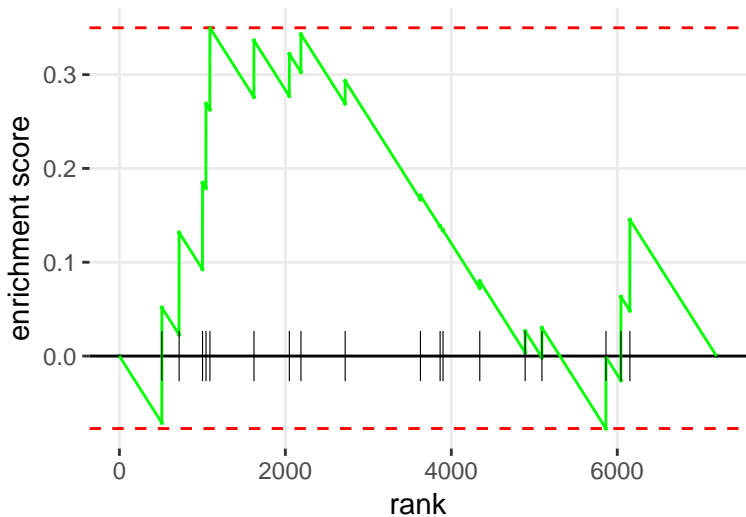
L-CARNITINE BIOSYNTHESIS

enrichment score

rank



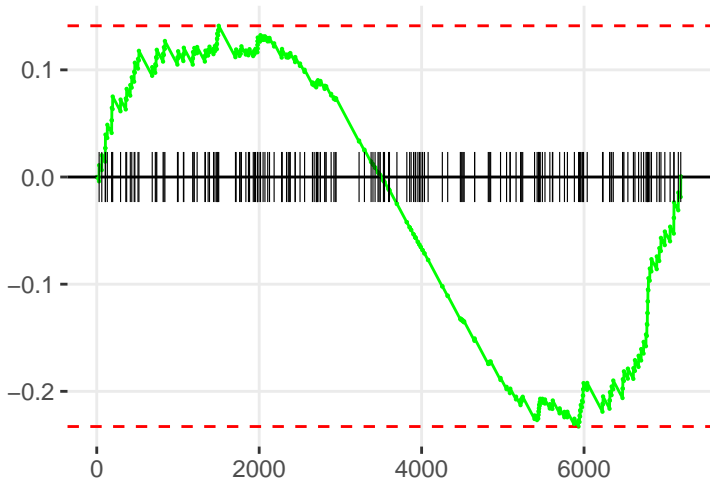
LANOSTEROL BIOSYNTHESIS



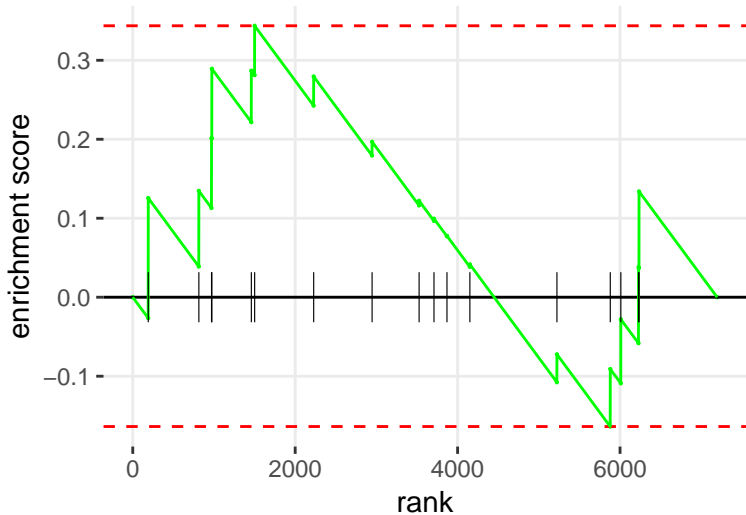
ESTROGEN BIOSYNTHESIS

enrichment score

rank

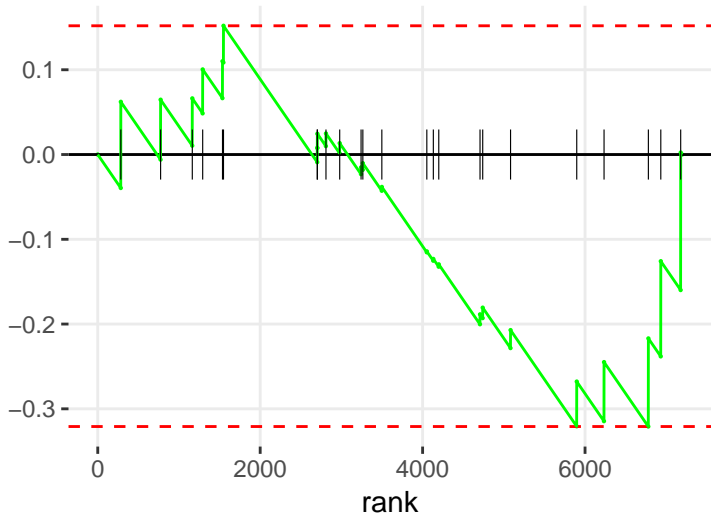


CHONDROITIN AND DERMATAN BIOSYNTHESIS



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

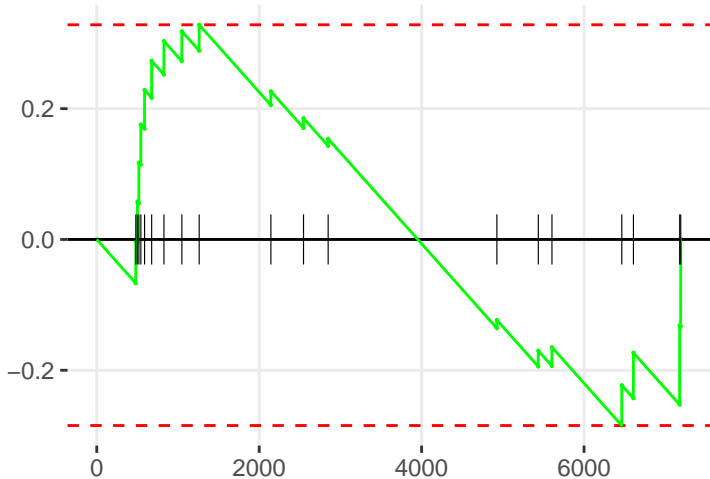
enrichment score



PROTEIN CITRULLINATION

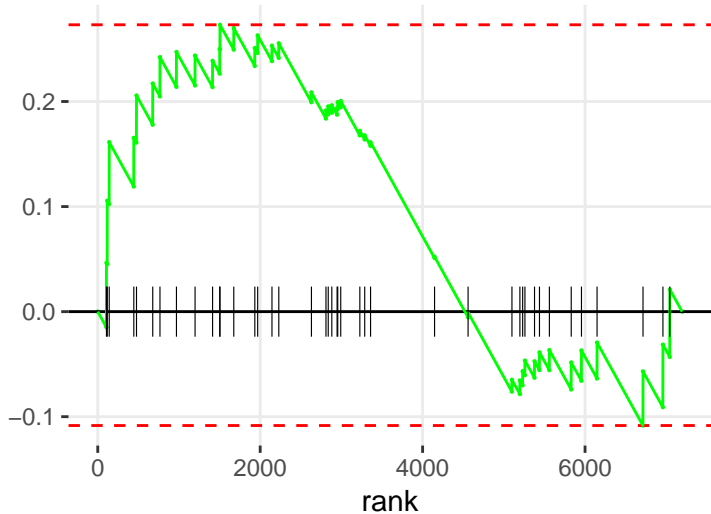
enrichment score

rank



URIDINE-5'-PHOSPHATE BIOSYNTHESIS

enrichment score



DERMATAN SULFATE DEGRADATION (METAZOA)

enrichment score

0.1
0.0
-0.1
-0.2

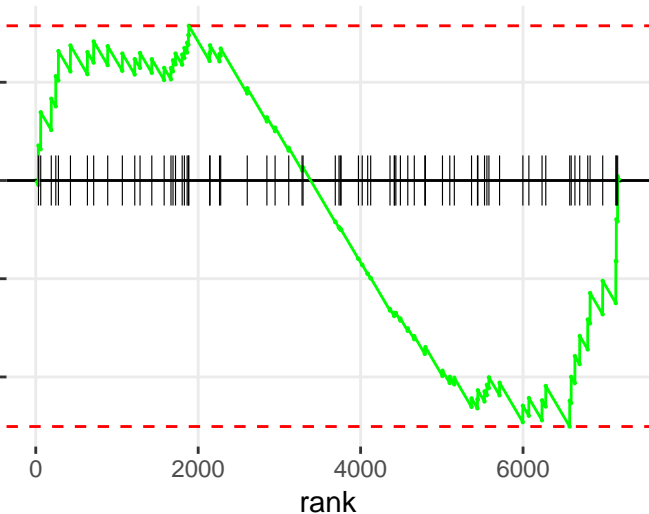
0

2000

4000

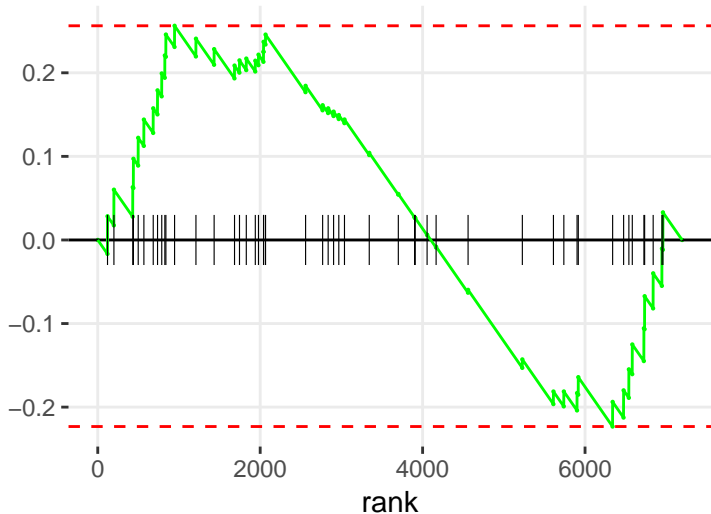
6000

rank



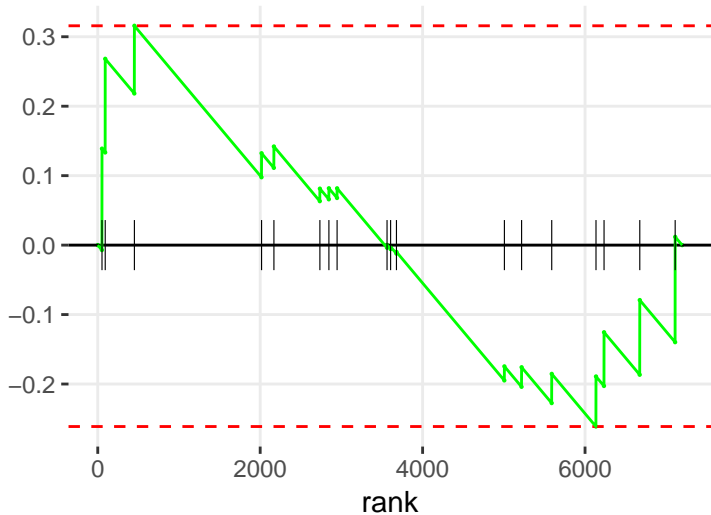
METHYLGLYOXAL DEGRADATION VI

enrichment score



GLUTAMATE REMOVAL FROM FOLATES

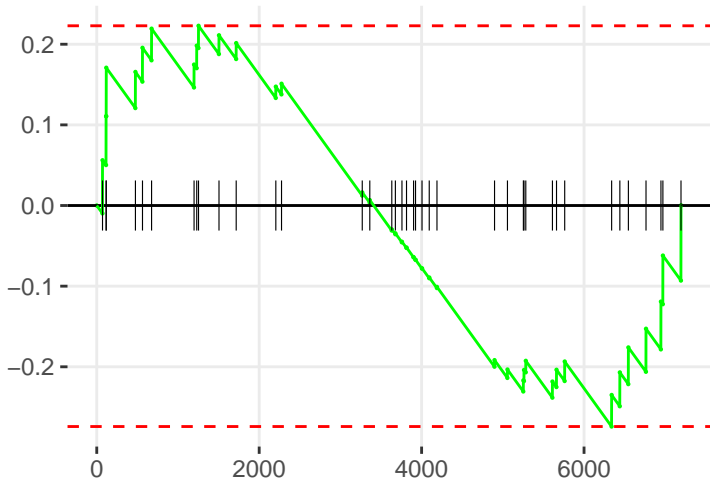
enrichment score



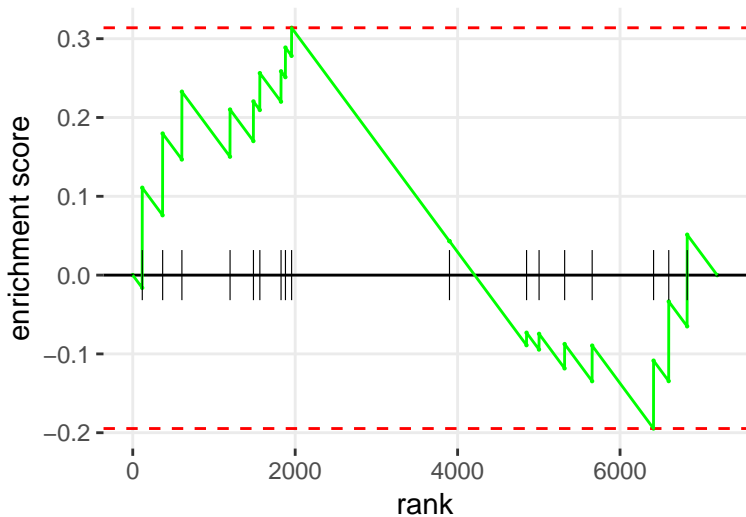
FLAVIN BIOSYNTHESIS IV (MAMMALIAN)

enrichment score

rank

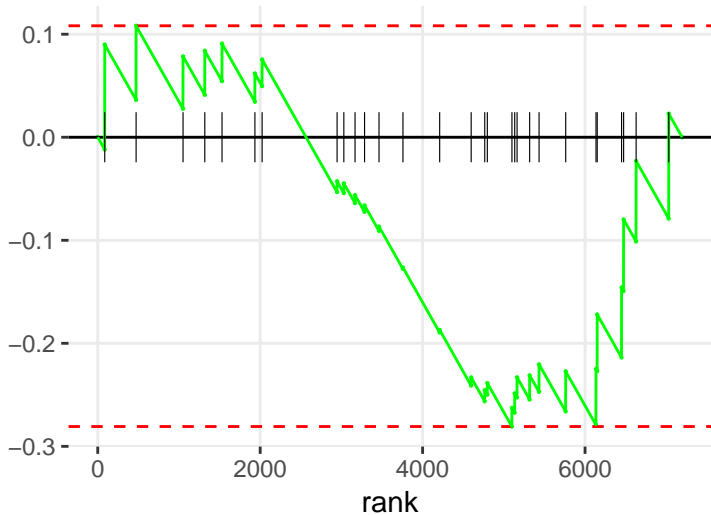


METHIONINE SALVAGE II (MAMMALIA)

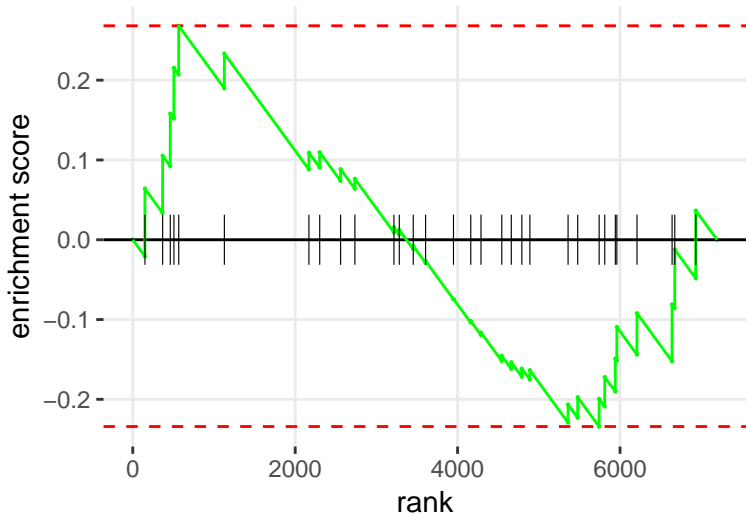


TYROSINE DEGRADATION I

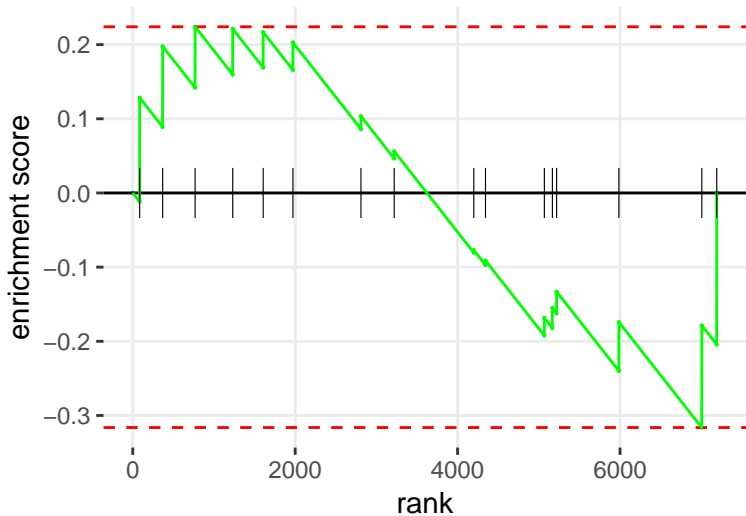
enrichment score



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



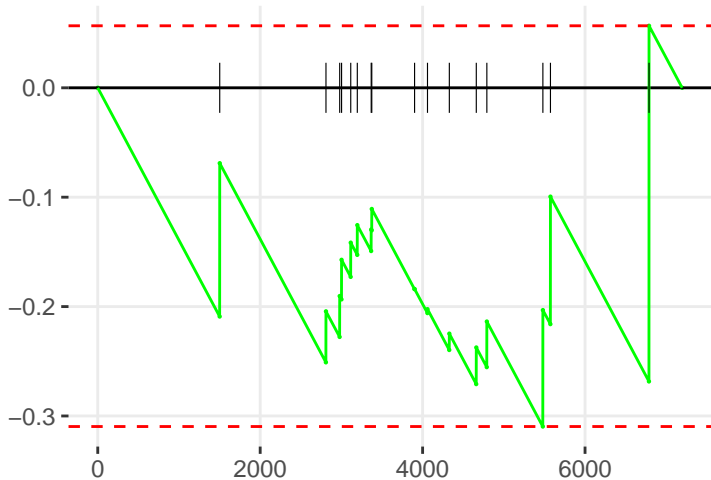
<IS</I-METHYL-5'-THIOADENOSINE DEGRADATION II



GLUTAMATE DEPENDENT ACID RESISTANCE

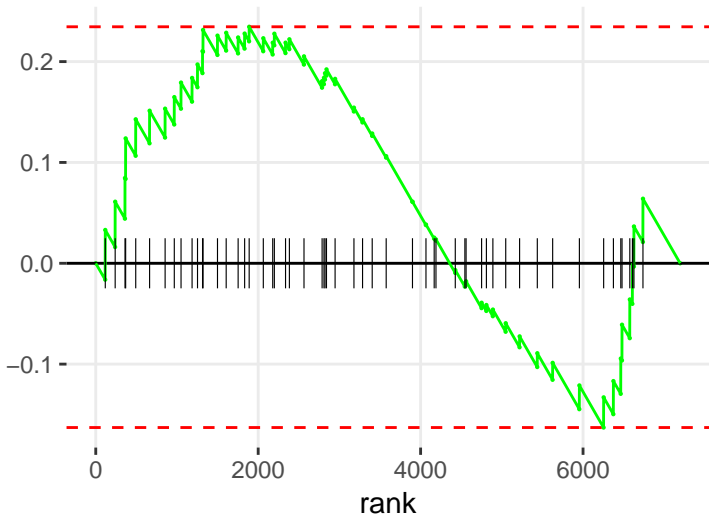
enrichment score

rank



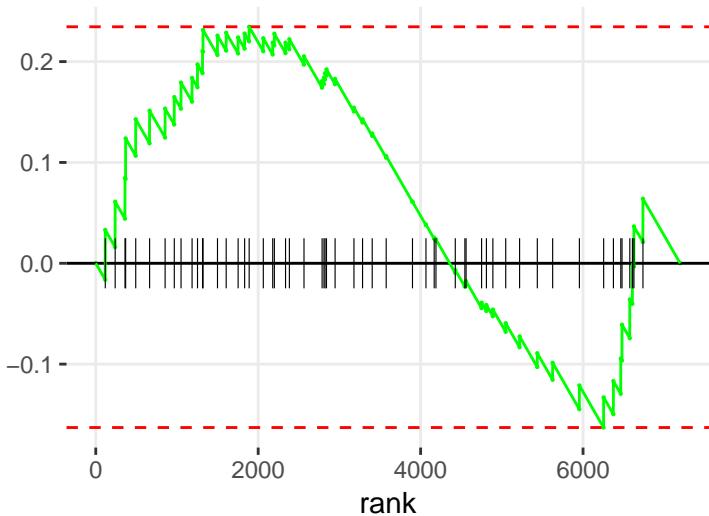
GLUTAMATE BIOSYNTHESIS II

enrichment score

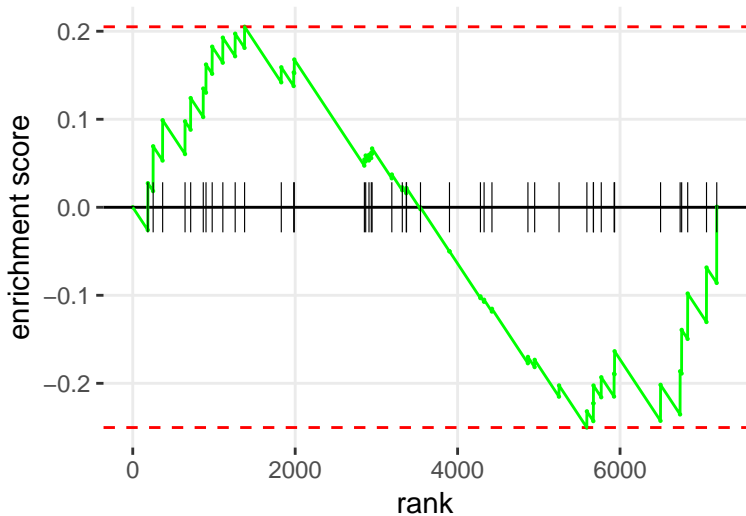


GLUTAMATE DEGRADATION X

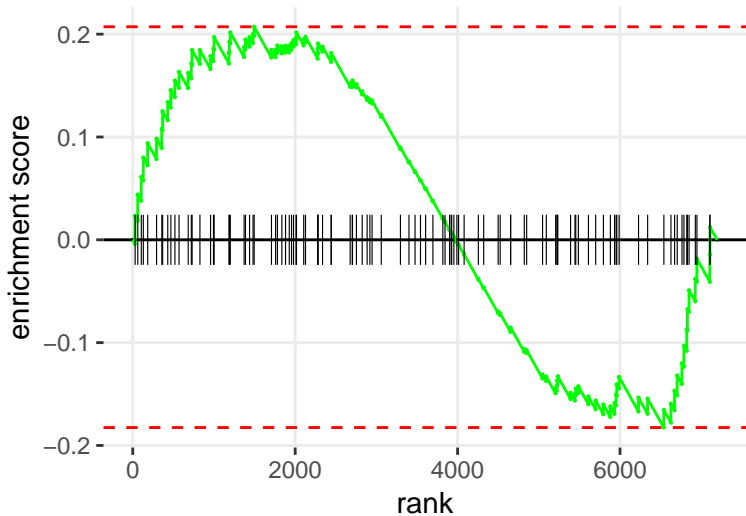
enrichment score



THE VISUAL CYCLE I (VERTEBRATES)



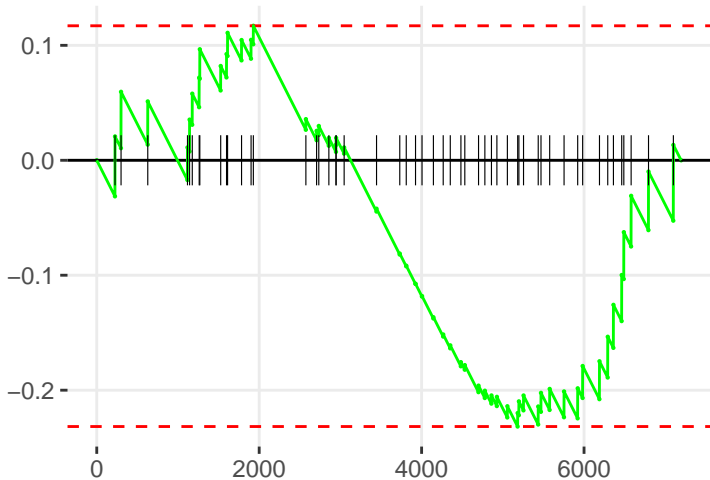
ANDROGEN BIOSYNTHESIS



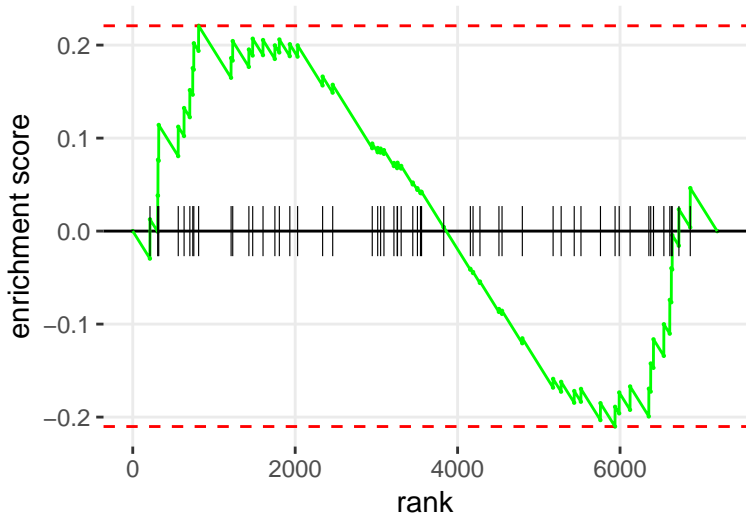
SPERMINE AND SPERMIDINE DEGRADATION I

enrichment score

rank

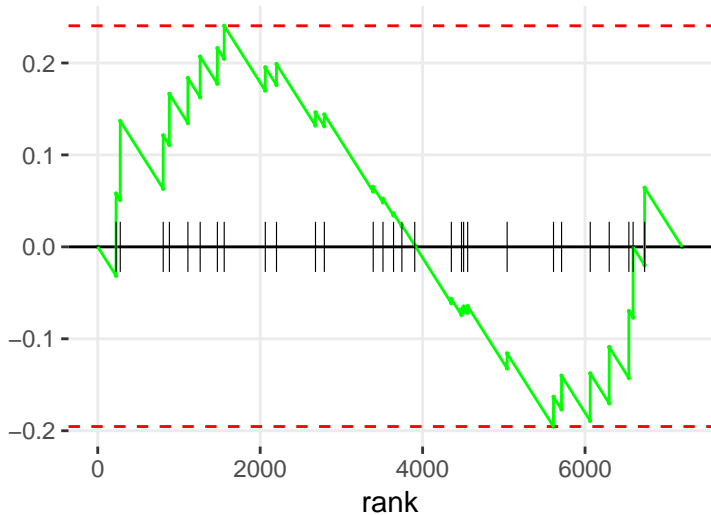


NAD BIOSYNTHESIS FROM 2-AMINO-3-CARBOXYMUCONATE SEMIALDEHYDE



INOSITOL PYROPHOSPHATES BIOSYNTHESIS

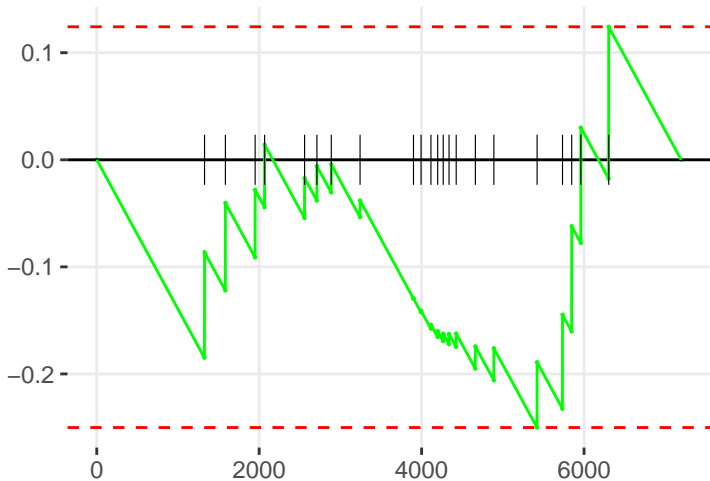
enrichment score



ACYL-COA HYDROLYSIS

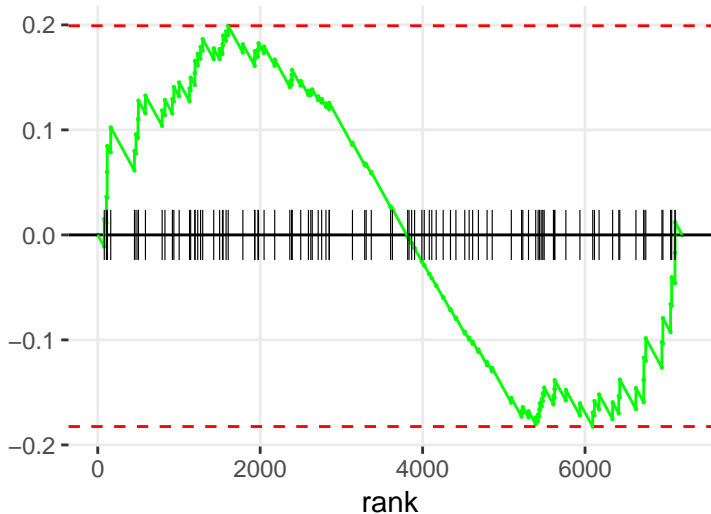
enrichment score

rank



ZYMOSTEROL BIOSYNTHESIS

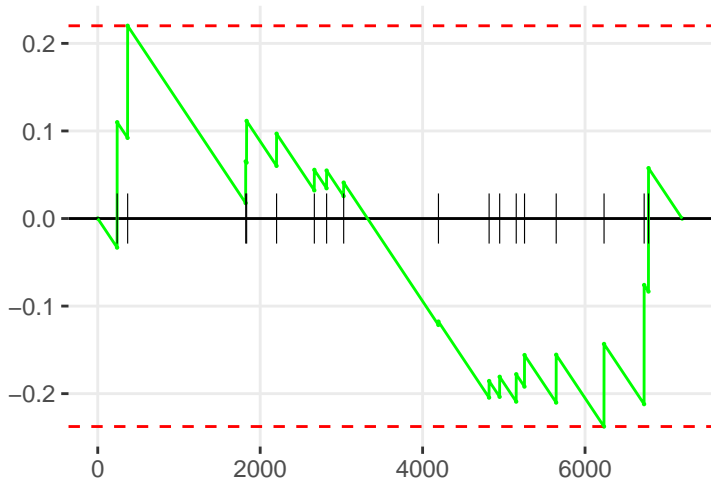
enrichment score



L-DOPA DEGRADATION

enrichment score

rank



GLUTAMINE DEGRADATION I

