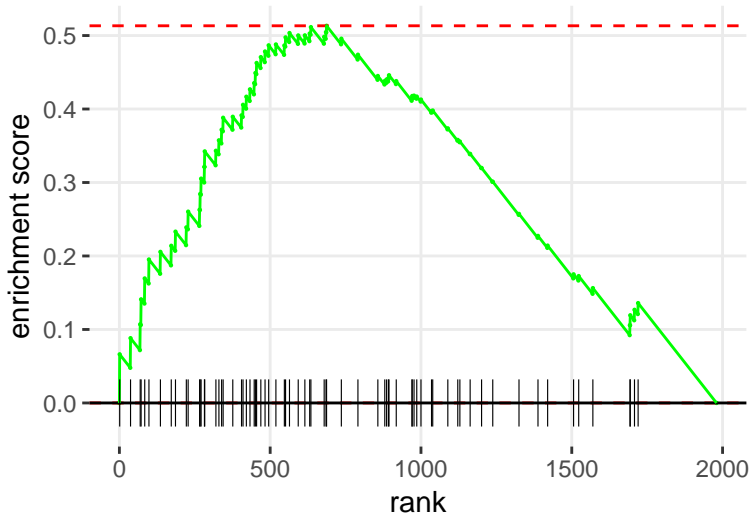
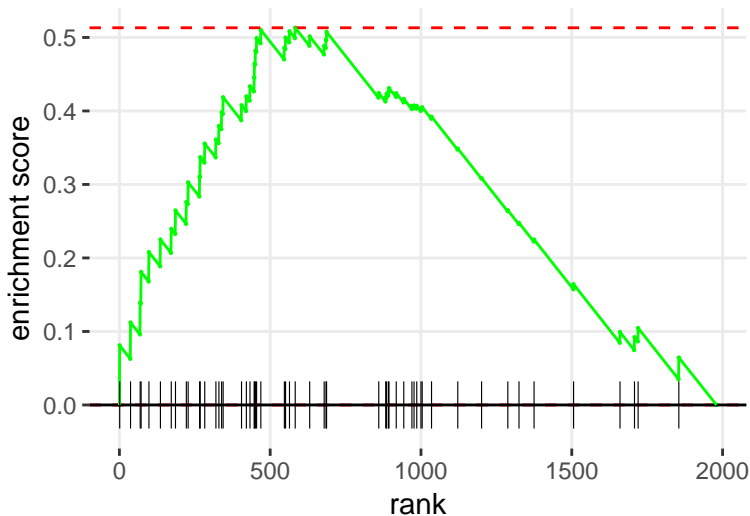


TRNA SPLICING

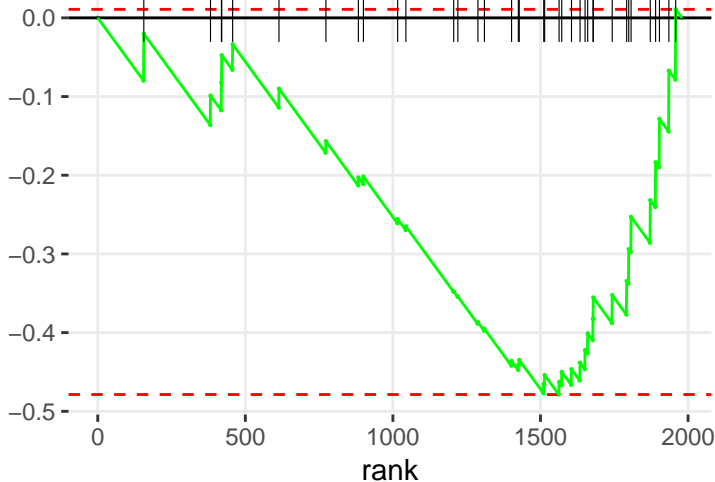


ALL-<ITRANS</I>-DECAPRENYL DIPHOSPHATE BIOSYNTHESIS

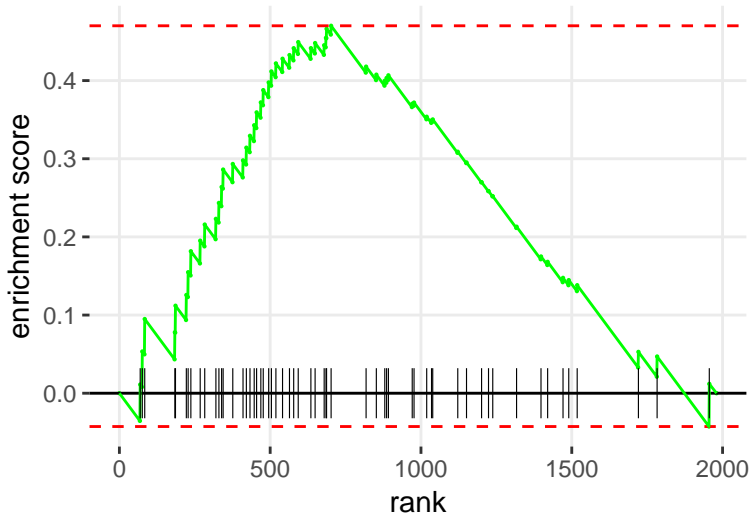


CDP-DIACYLGLYCEROL BIOSYNTHESIS I

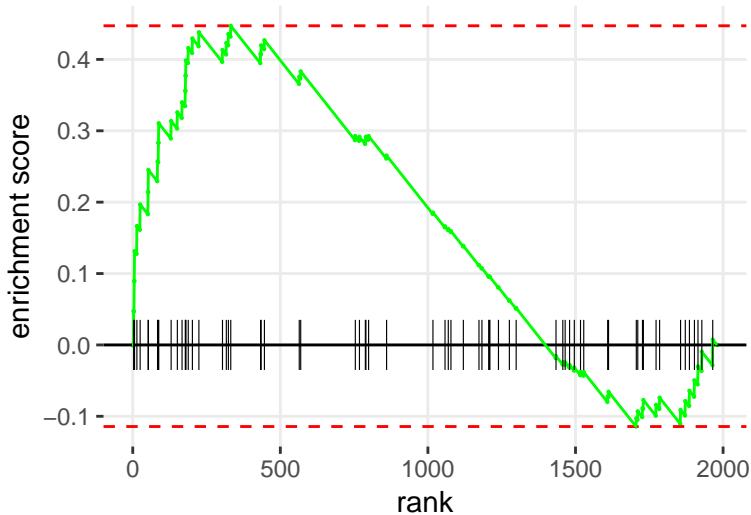
enrichment score



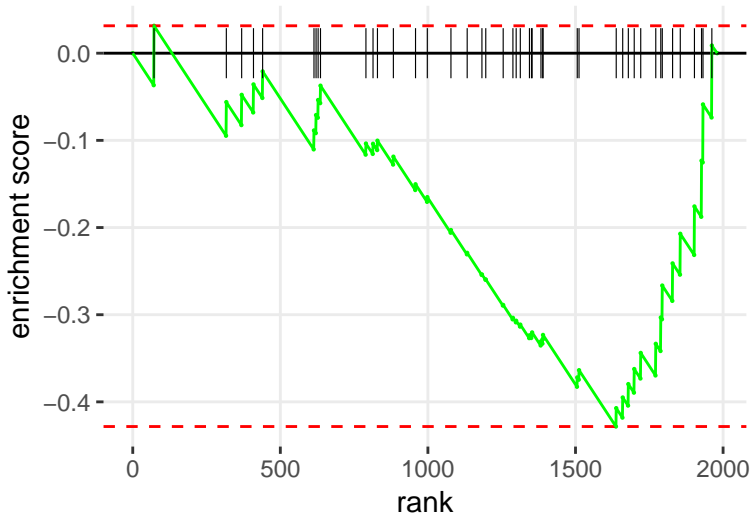
NADH REPAIR



4-HYDROXYPROLINE DEGRADATION I



PENTOSE PHOSPHATE PATHWAY (NON-OXIDATIVE BRANCH)



HISTAMINE BIOSYNTHESIS

enrichment score

rank

0.0

-0.1

-0.2

-0.3

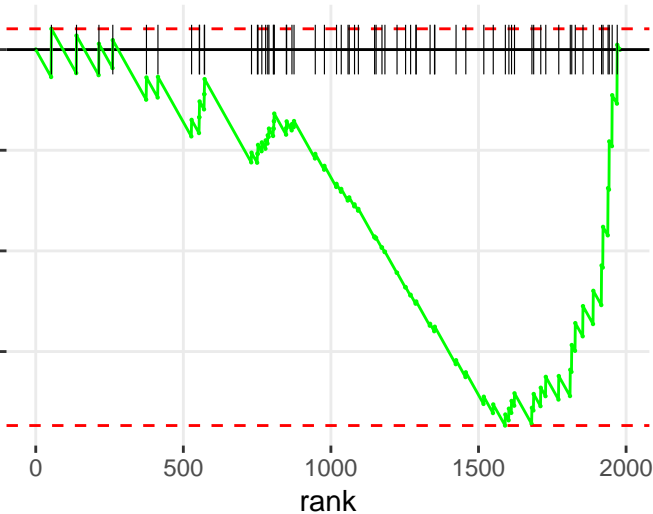
0

500

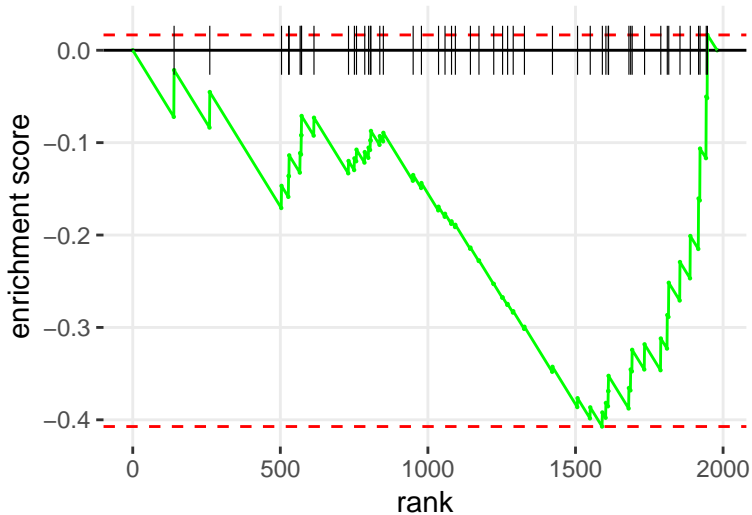
1000

1500

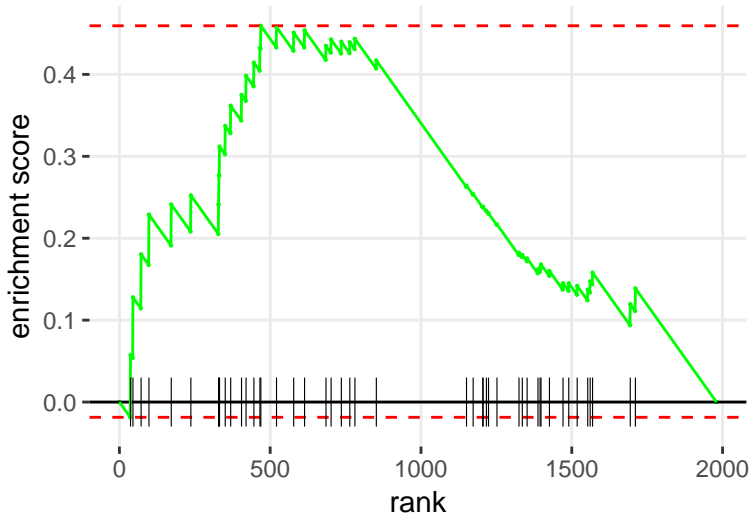
2000



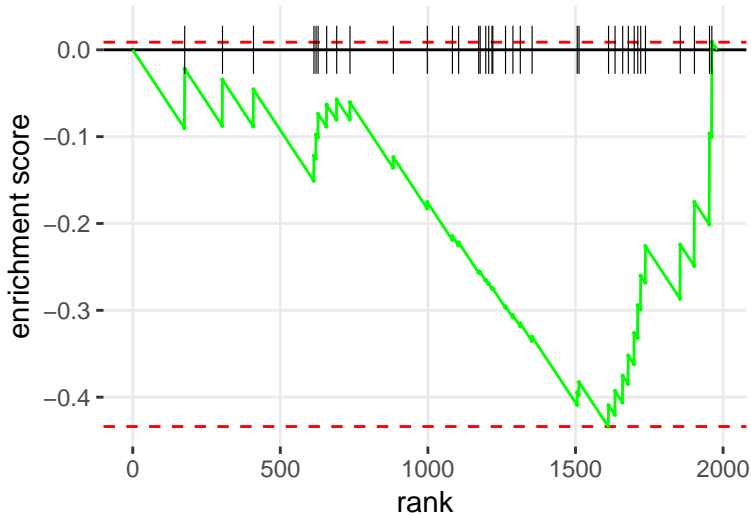
3-PHOSPHOINOSITIDE DEGRADATION



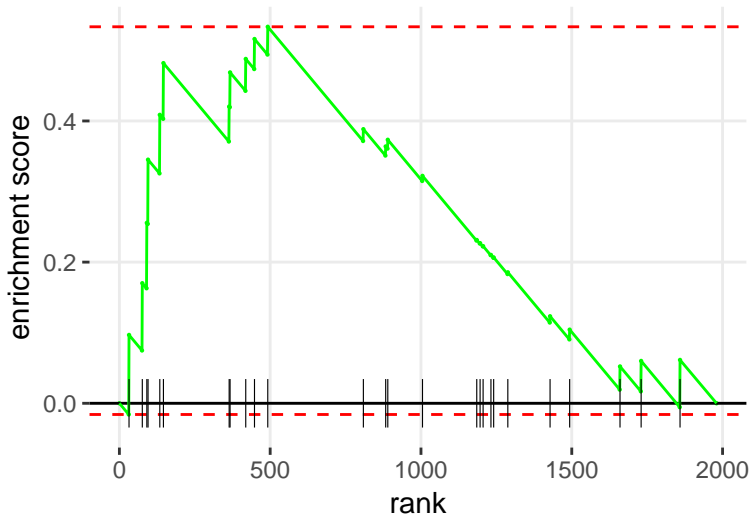
SPERMINE AND SPERMIDINE DEGRADATION I



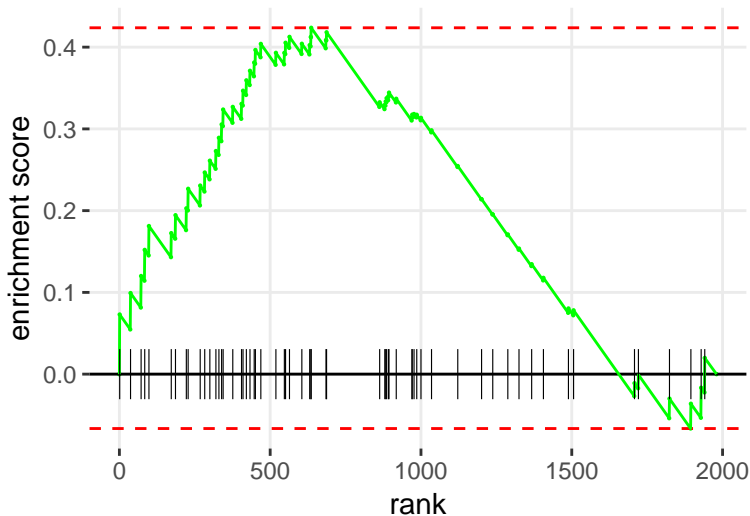
PENTOSE PHOSPHATE PATHWAY (OXIDATIVE BRANCH)



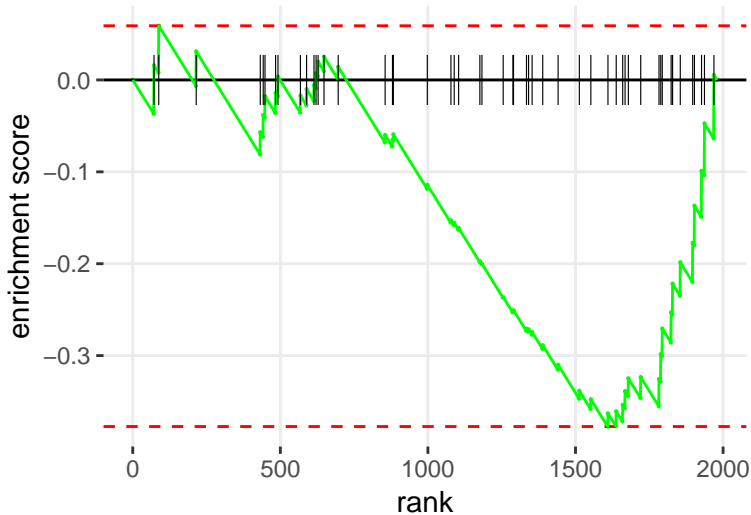
ANDROGEN BIOSYNTHESIS



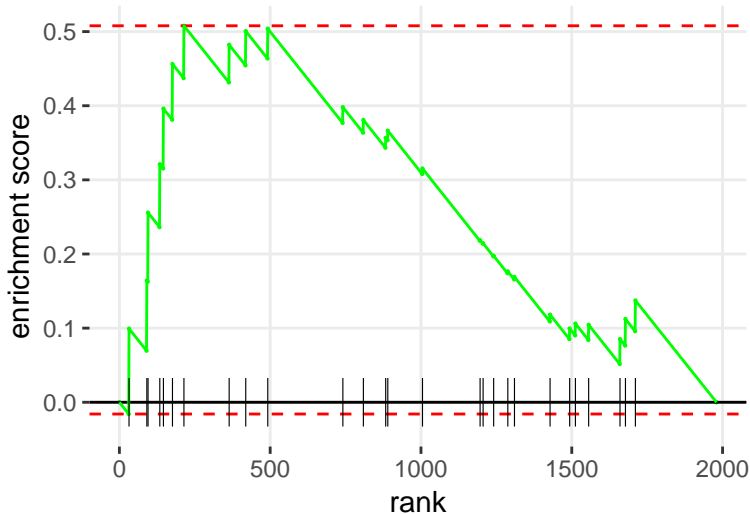
THIAMIN SALVAGE III



SUPEROXIDE RADICALS DEGRADATION



ESTROGEN BIOSYNTHESIS



GDP-MANNOSE BIOSYNTHESIS

enrichment score

0.0
-0.1
-0.2
-0.3
-0.4

0

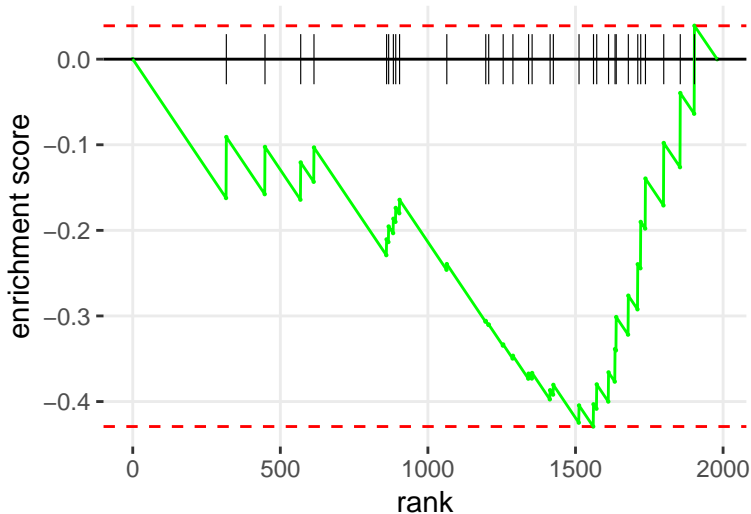
500

1000

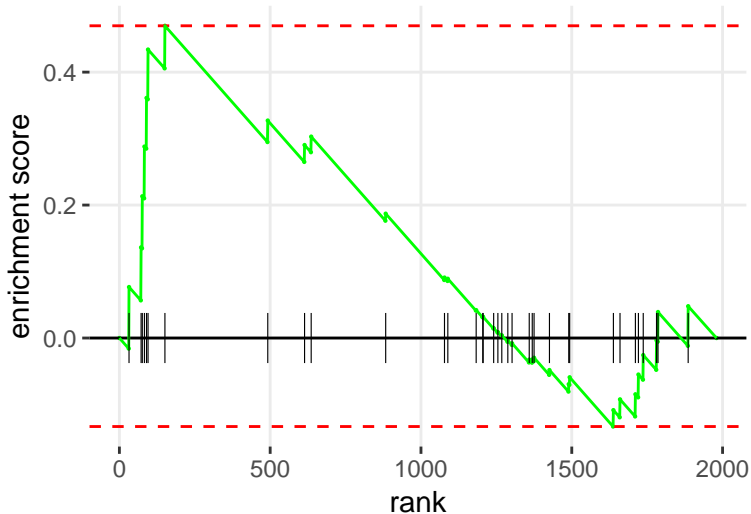
1500

2000

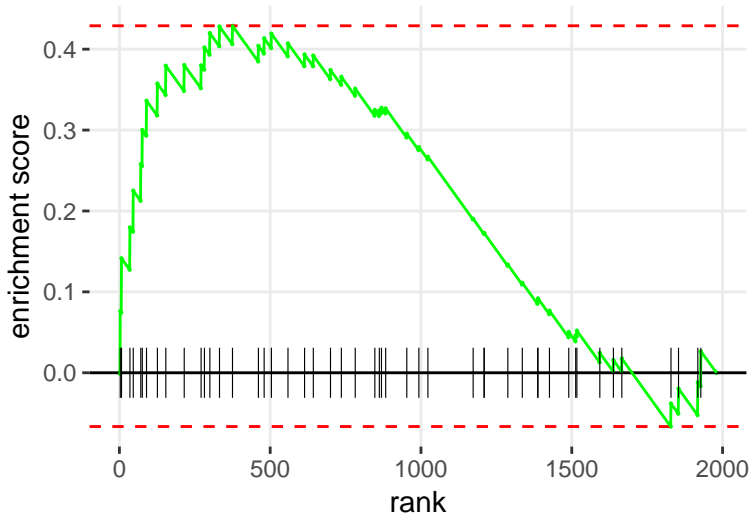
rank



THIOSULFATE DISPROPORTIONATION III (RHODANESE)



METHYLMALONYL PATHWAY



RETINOL BIOSYNTHESIS

enrichment score

0.0
-0.1
-0.2
-0.3
-0.4

0

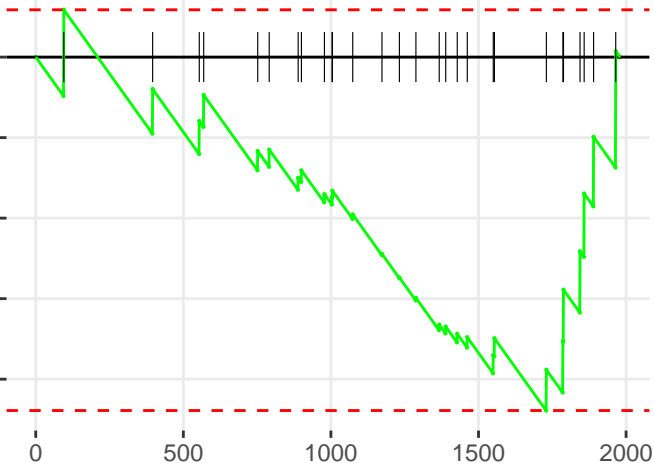
500

1000

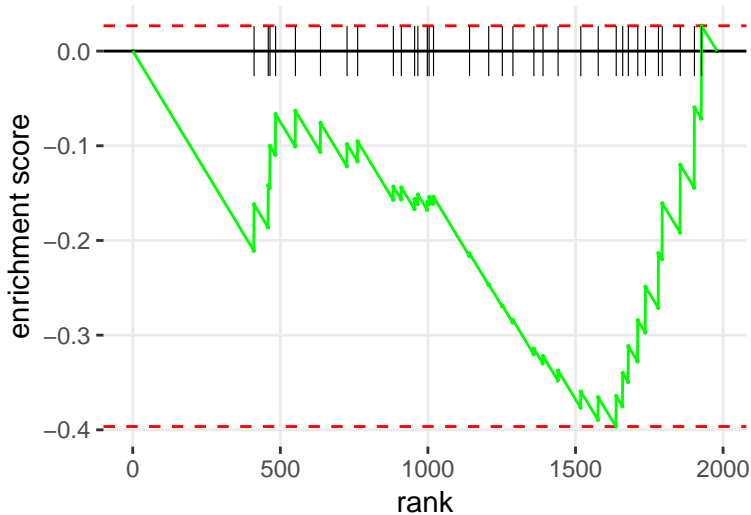
1500

2000

rank



VALINE DEGRADATION I



GLUTATHIONE-MEDIATED DETOXIFICATION I

enrichment score

0.4
0.3
0.2
0.1
0.0

0

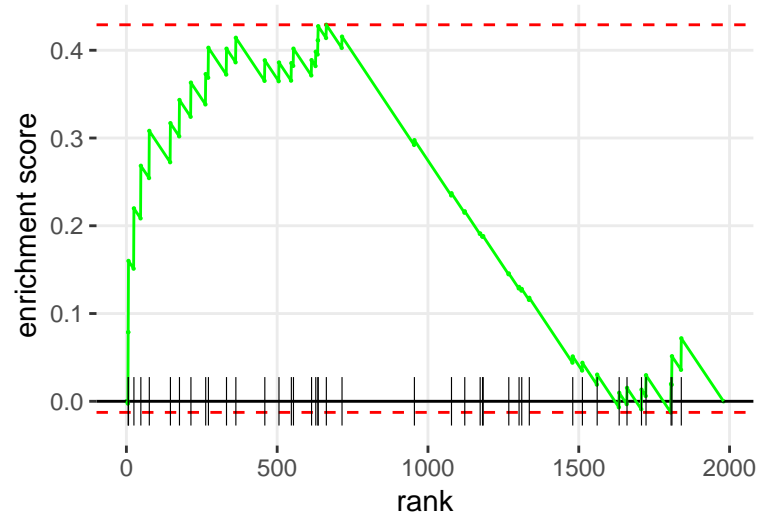
500

1000

1500

2000

rank



4-HYDROXY-2-NONENAL DETOXIFICATION

enrichment score

0.4
0.3
0.2
0.1
0.0

0

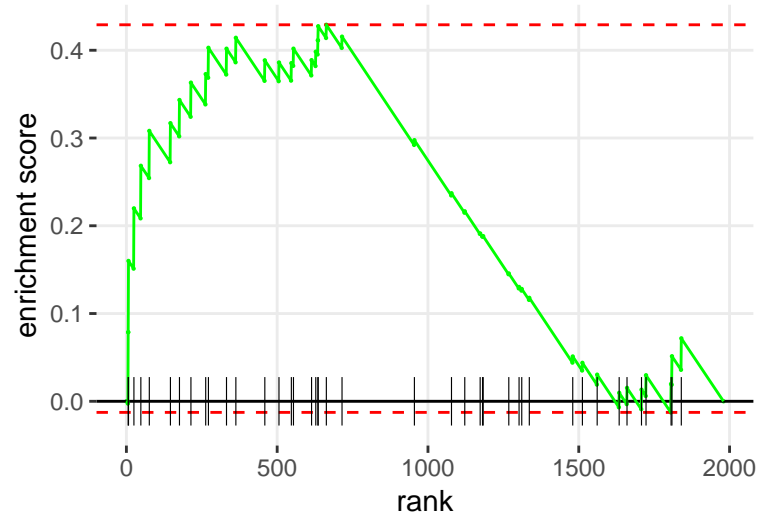
500

1000

1500

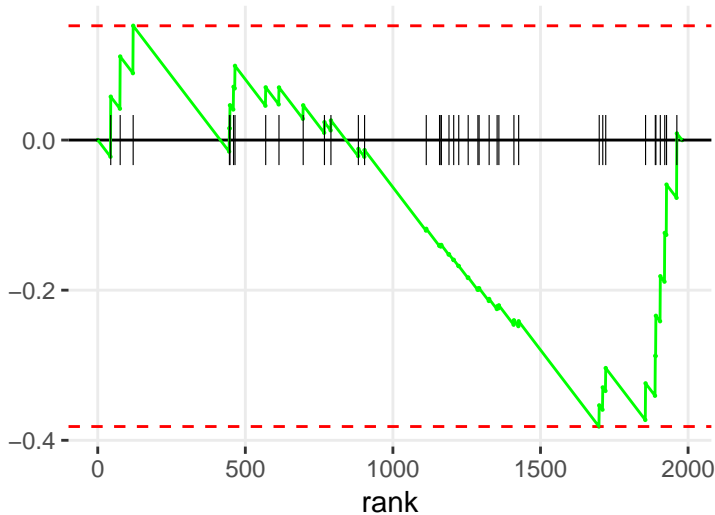
2000

rank



GLUCONEOGENESIS I

enrichment score



GLUTARYL-COA DEGRADATION

enrichment score

0.0

-0.1

-0.2

-0.3

-0.4

0

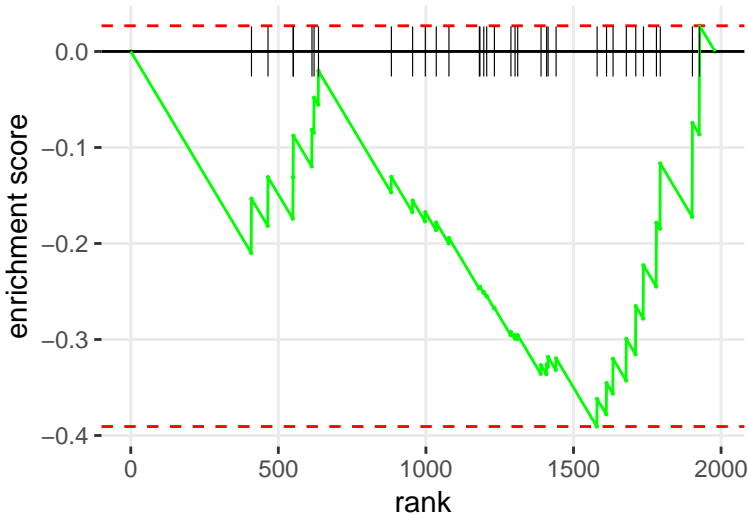
500

1000

1500

2000

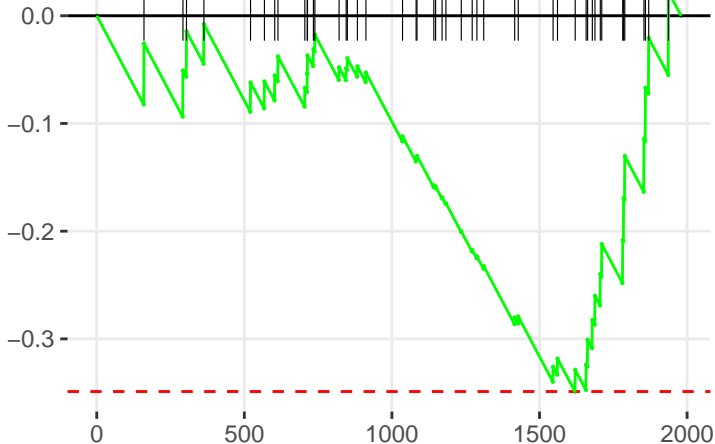
rank



FLAVIN BIOSYNTHESIS IV (MAMMALIAN)

enrichment score

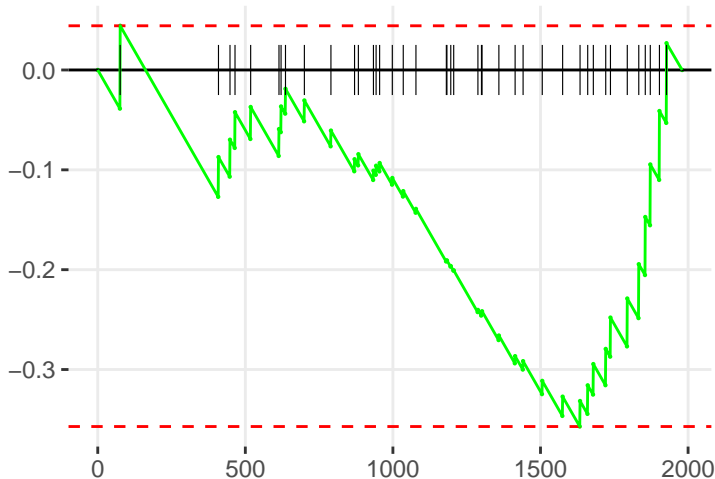
rank



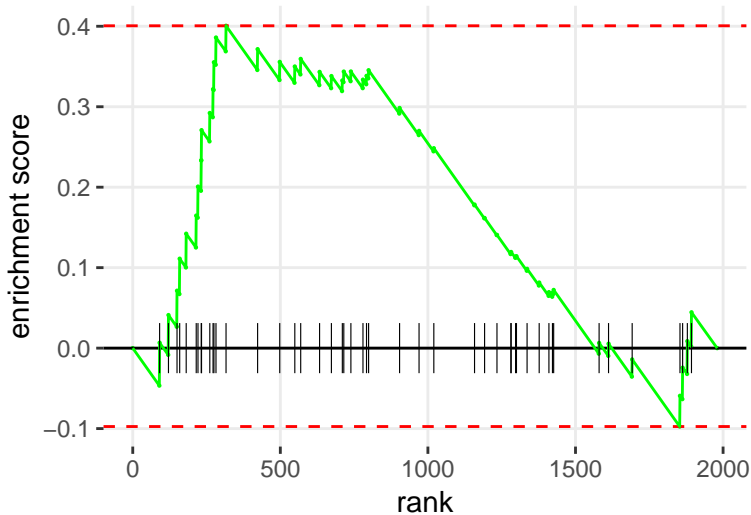
MEVALONATE PATHWAY I

enrichment score

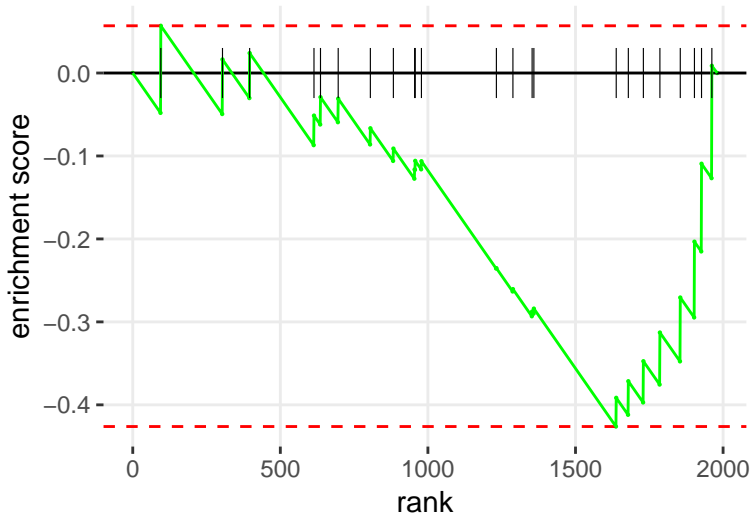
rank



EUMELANIN BIOSYNTHESIS

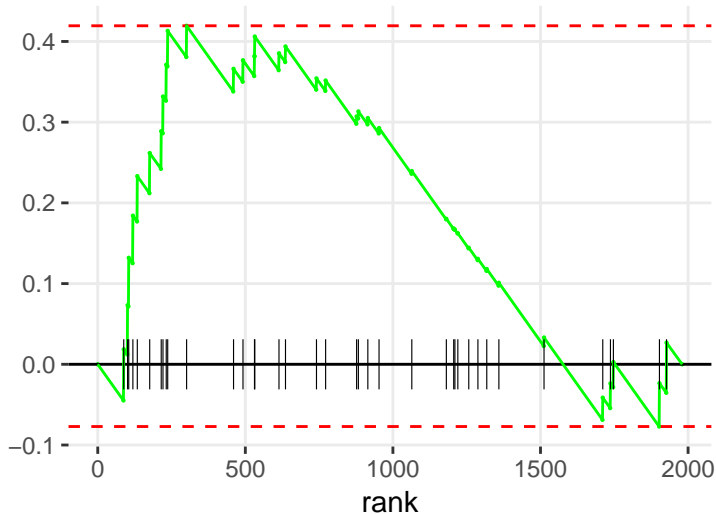


GLYCEROL-3-PHOSPHATE SHUTTLE

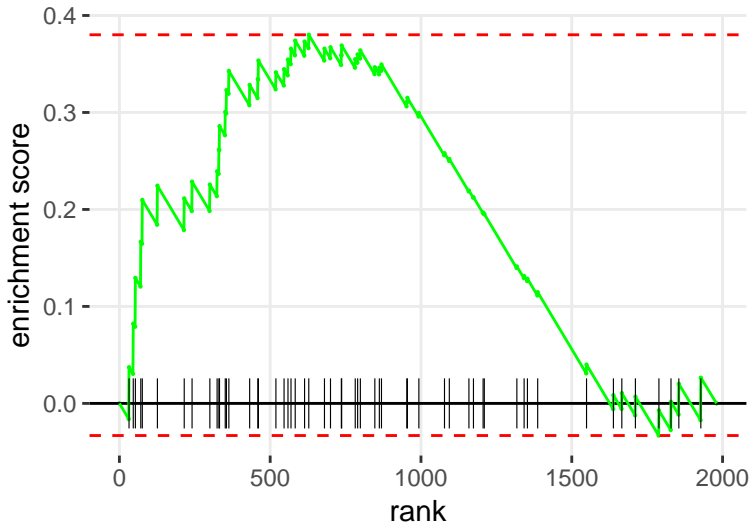


2-OXOGLUTARATE DECARBOXYLATION TO SUCCINYL-COA

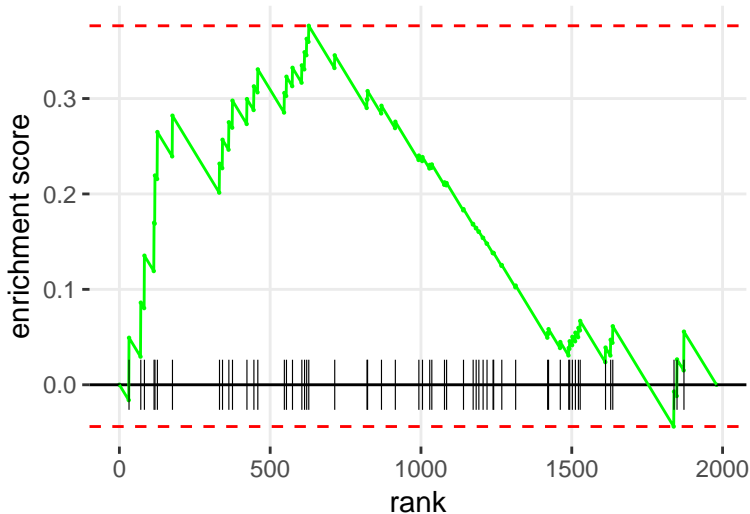
enrichment score



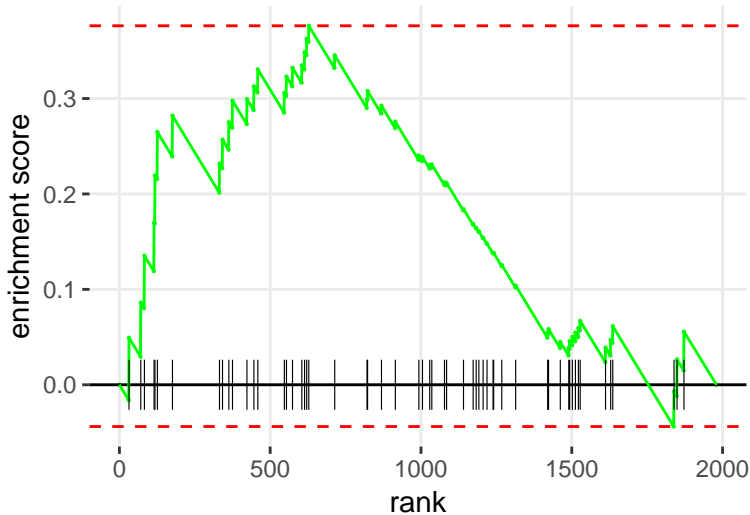
PALMITATE BIOSYNTHESIS I (ANIMALS)



HISTIDINE DEGRADATION VI



HISTIDINE DEGRADATION III



SERINE BIOSYNTHESIS

enrichment score

rank

0.1

0.0

-0.1

-0.2

-0.3

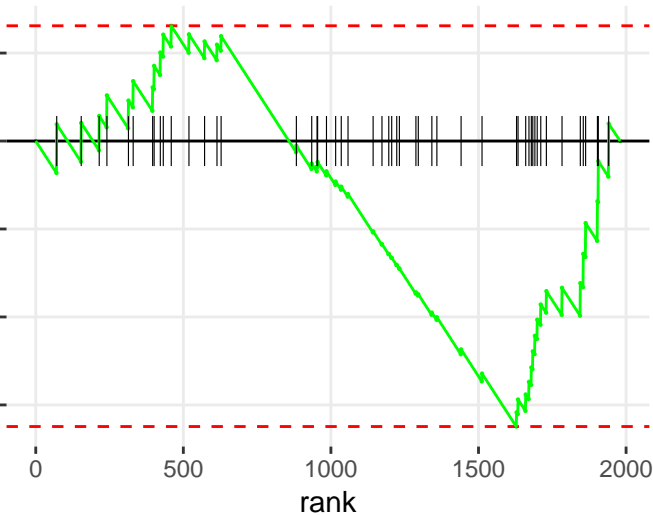
0

500

1000

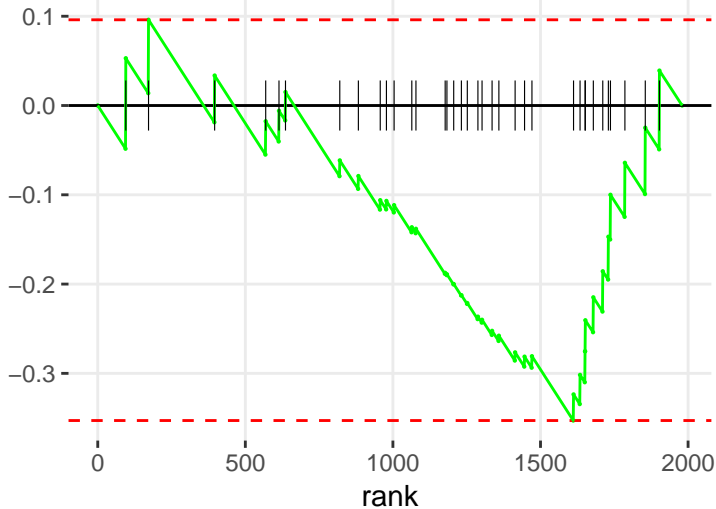
1500

2000

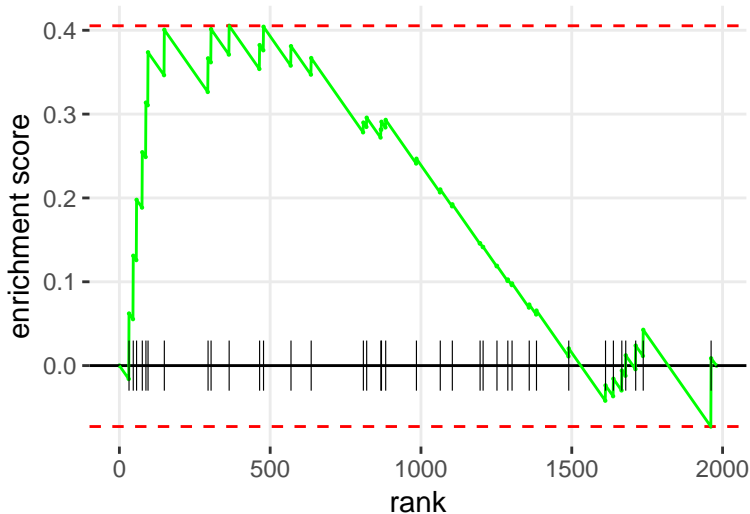


HYPUSINE BIOSYNTHESIS

enrichment score

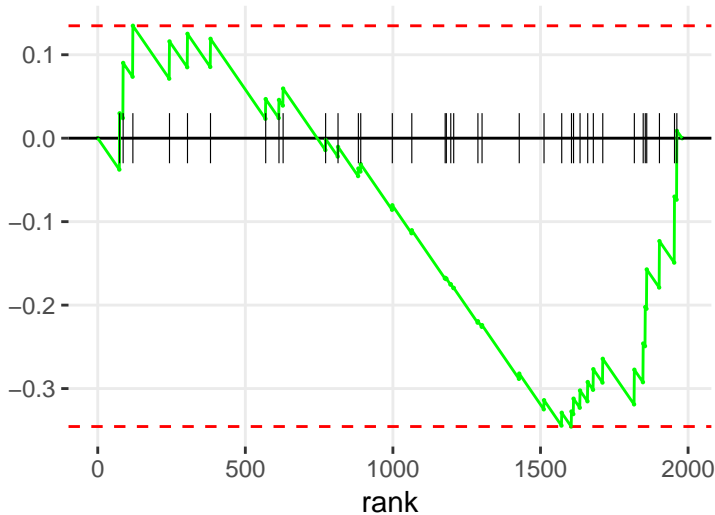


CITRULLINE DEGRADATION



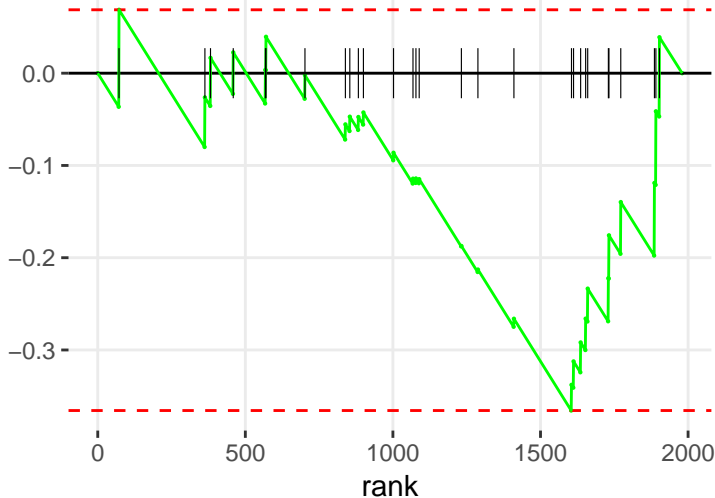
UDP-<I>l</I>-ACETYL-D-GLUCOSAMINE BIOSYNTHESIS II

enrichment score



MOLYBDENUM COFACTOR BIOSYNTHESIS

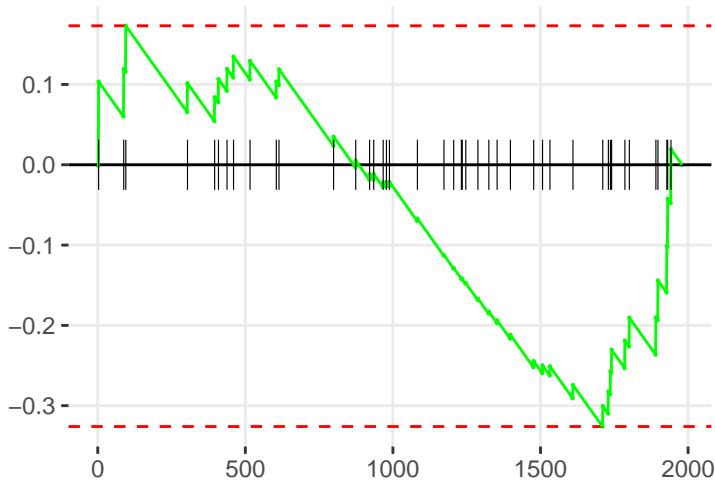
enrichment score



ACYL-COA HYDROLYSIS

enrichment score

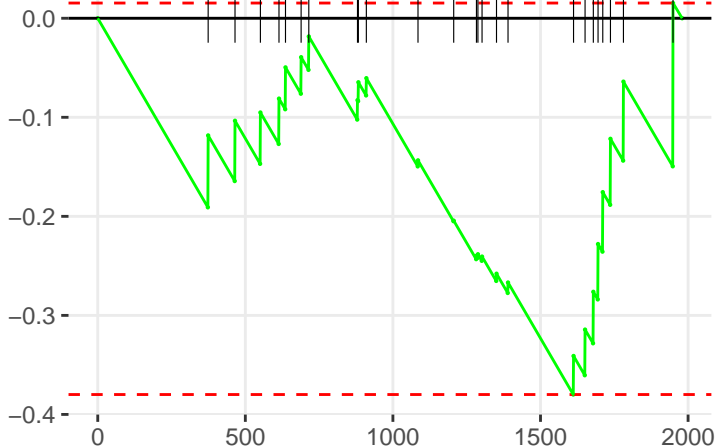
rank



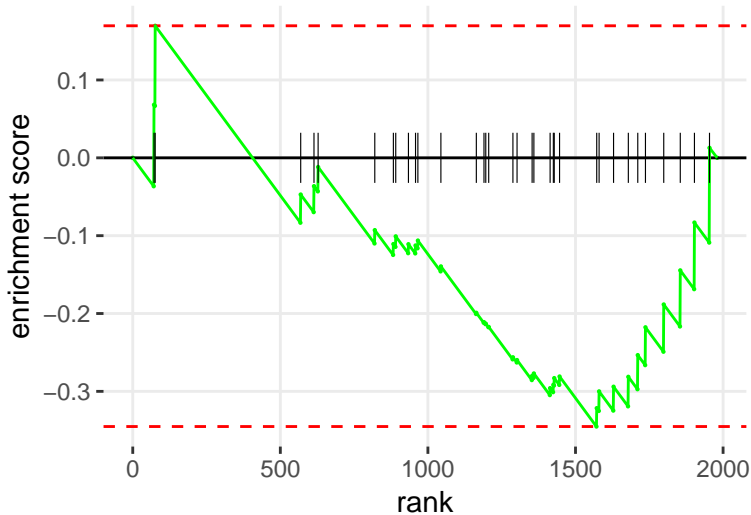
BILE ACID BIOSYNTHESIS, NEUTRAL PATHWAY

enrichment score

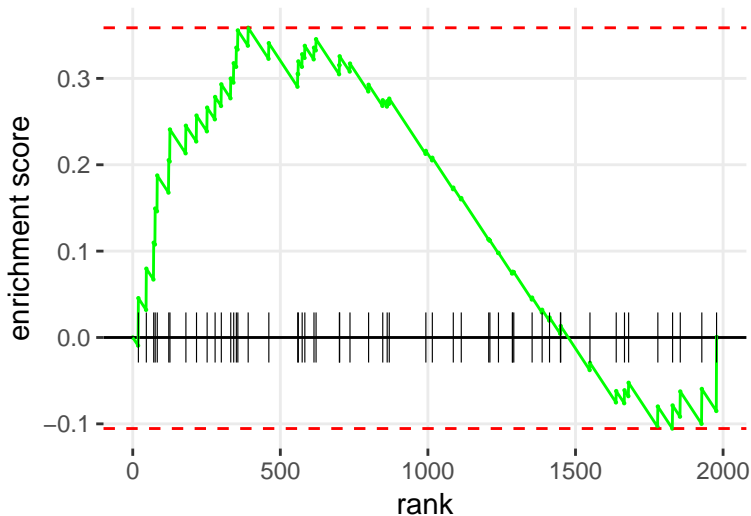
rank



S-ADENOSYL-L-METHIONINE BIOSYNTHESIS

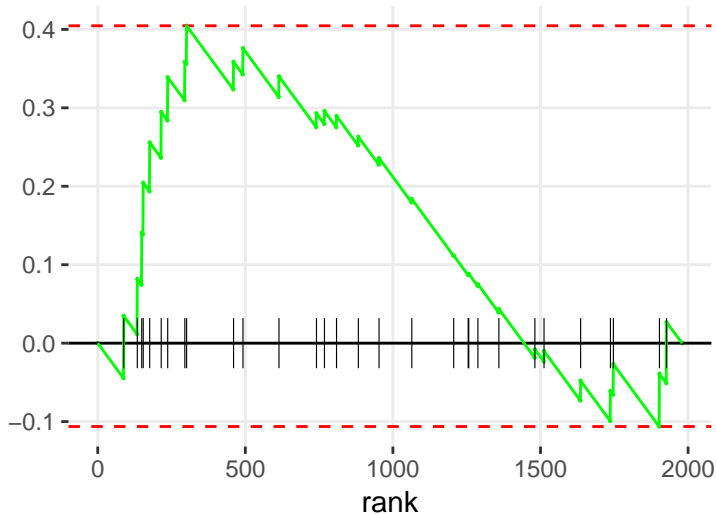


FATTY ACID BIOSYNTHESIS INITIATION II

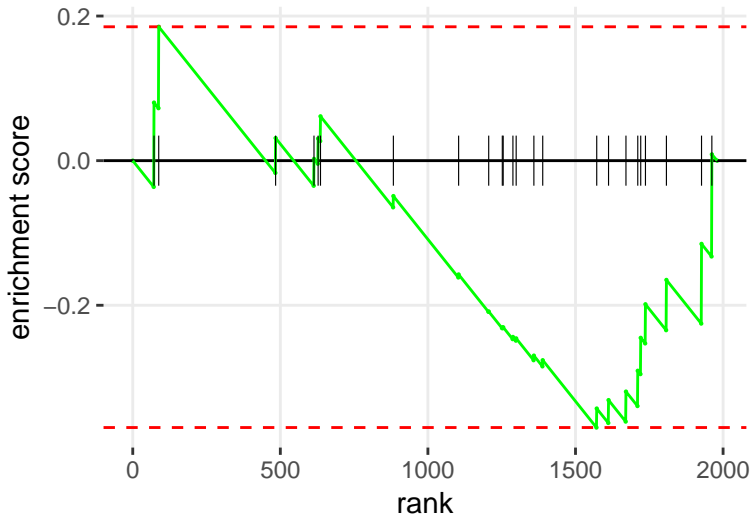


GLYCINE CLEAVAGE

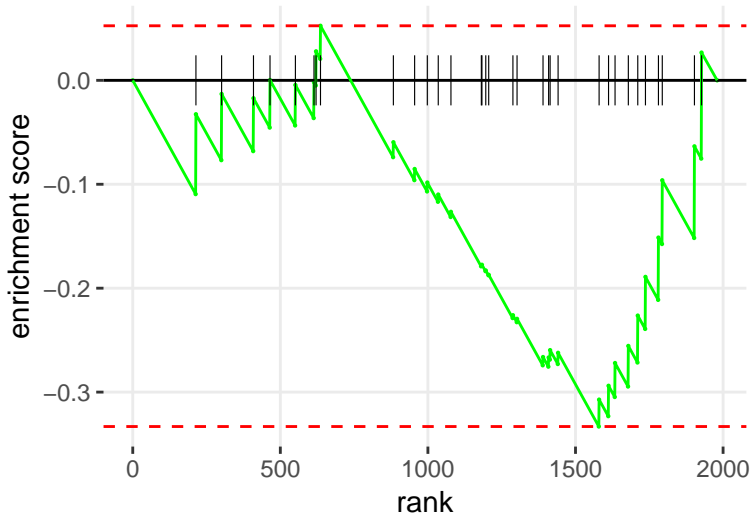
enrichment score



<IMYO</I>-INOSITOL BIOSYNTHESIS

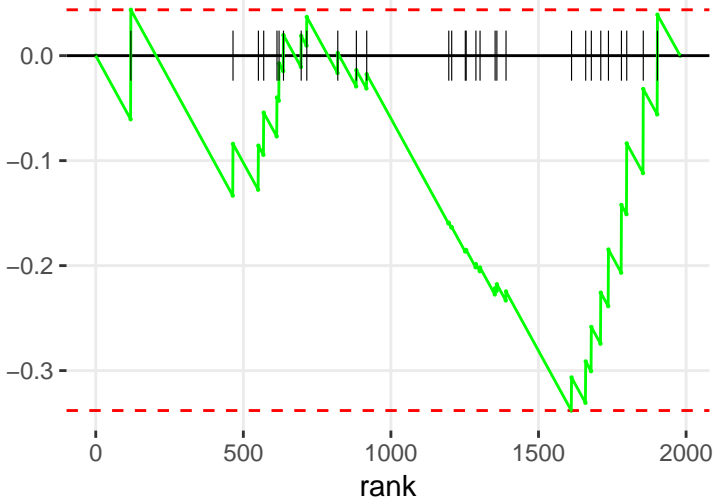


KETOLYSIS

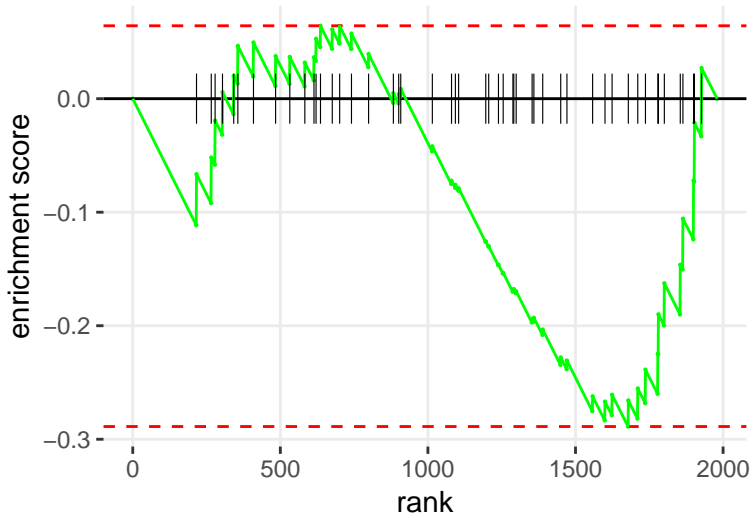


ACETATE CONVERSION TO ACETYL-COA

enrichment score

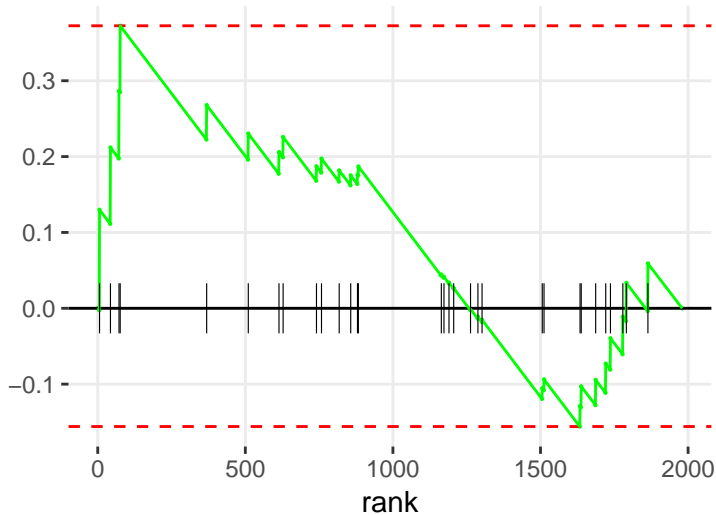


GLUCOSE AND GLUCOSE-1-PHOSPHATE DEGRADATION

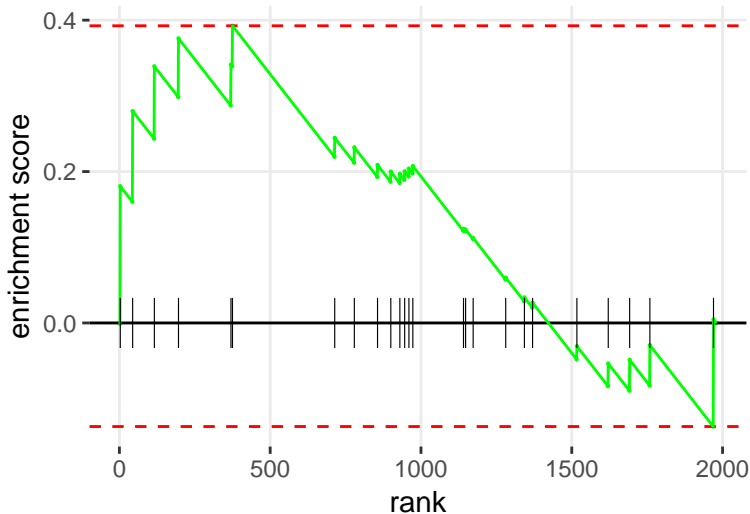


HEME BIOSYNTHESIS FROM UROPORPHYRINOGEN-III I

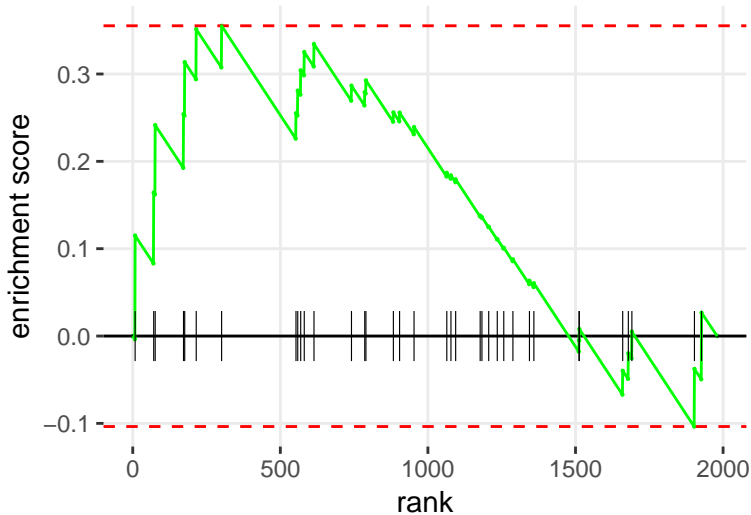
enrichment score



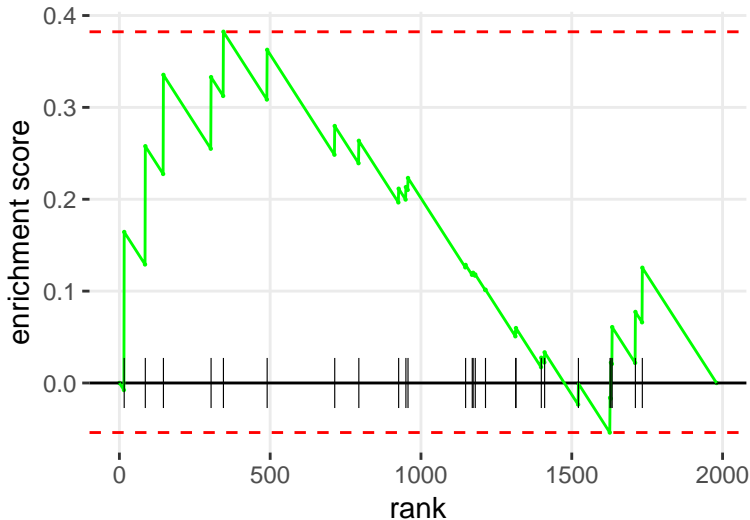
DERMATAN SULFATE BIOSYNTHESIS (LATE STAGES)



PYRUVATE DECARBOXYLATION TO ACETYL COA

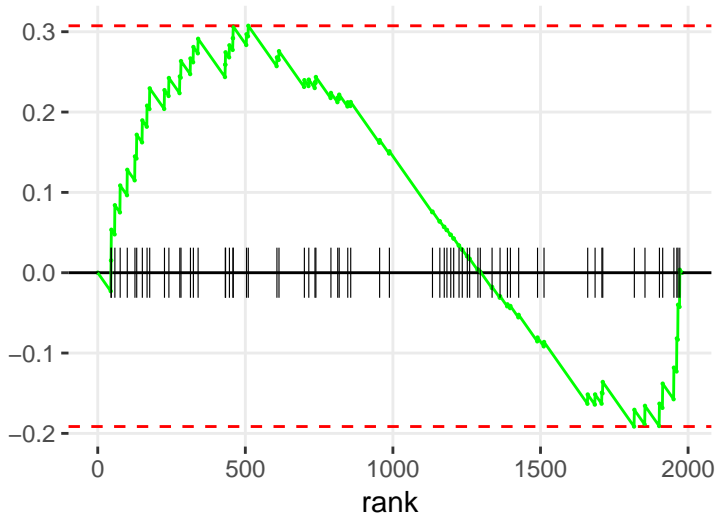


D-*IMYO*-*I*-INOSITOL-5-PHOSPHATE METABOLISM



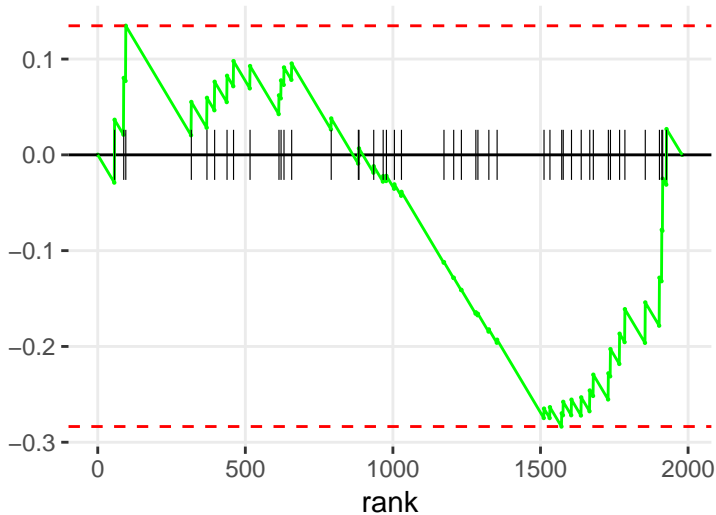
PROTEIN CITRULLINATION

enrichment score

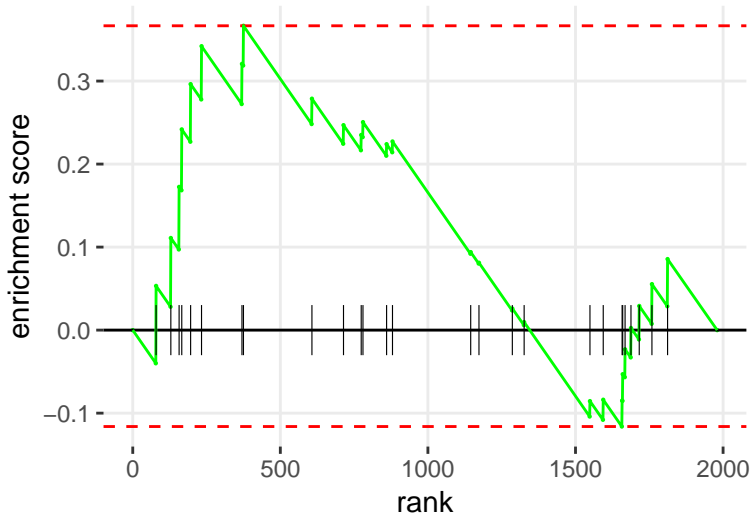


ASPARAGINE BIOSYNTHESIS I

enrichment score

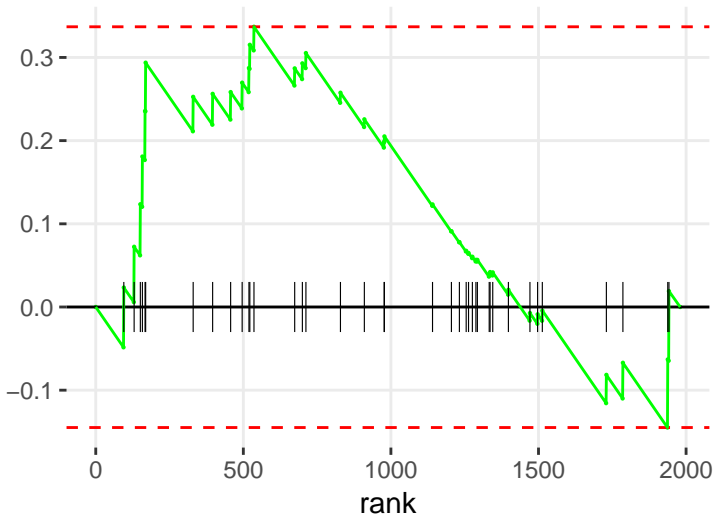


GLYCOAMINOGLYCAN-PROTEIN LINKAGE REGION BIOSYNTHESIS



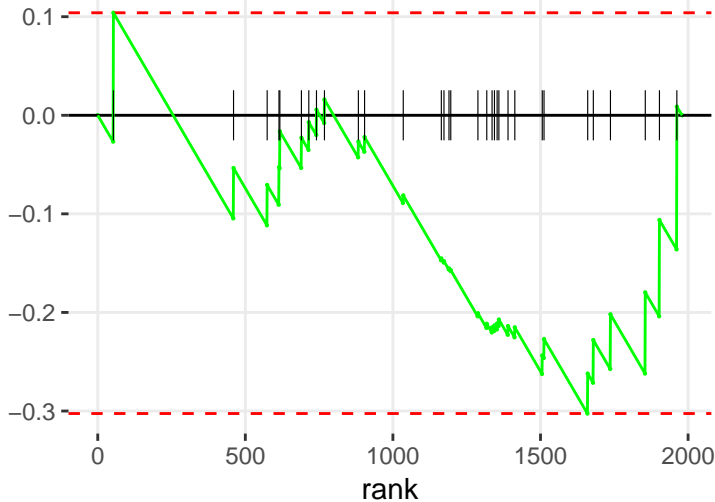
PHENYLALANINE DEGRADATION I (AEROBIC)

enrichment score



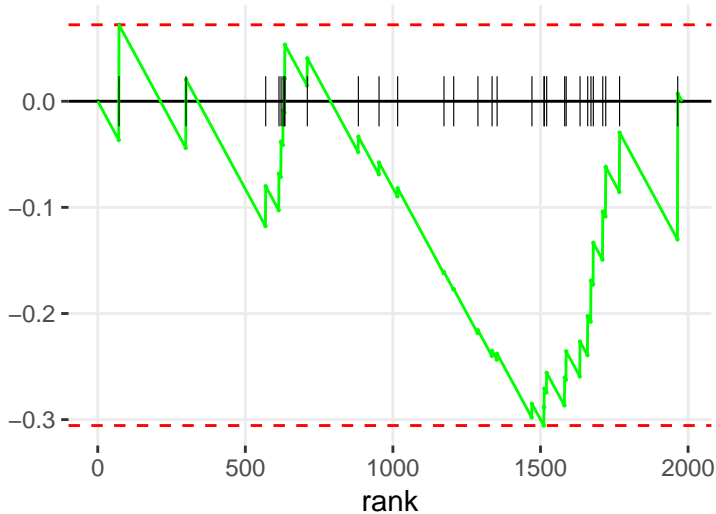
SEROTONIN DEGRADATION

enrichment score



DOLICHYL-DIPHOSPHOOLIGOSACCHARIDE BIOSYNTHESIS

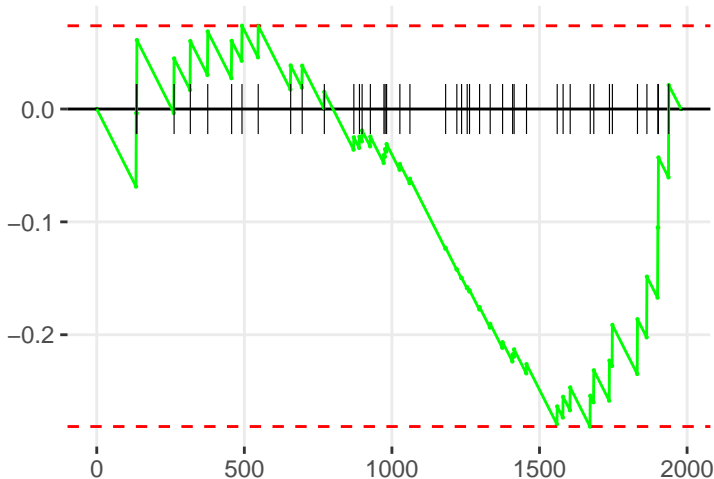
enrichment score



TYROSINE BIOSYNTHESIS IV

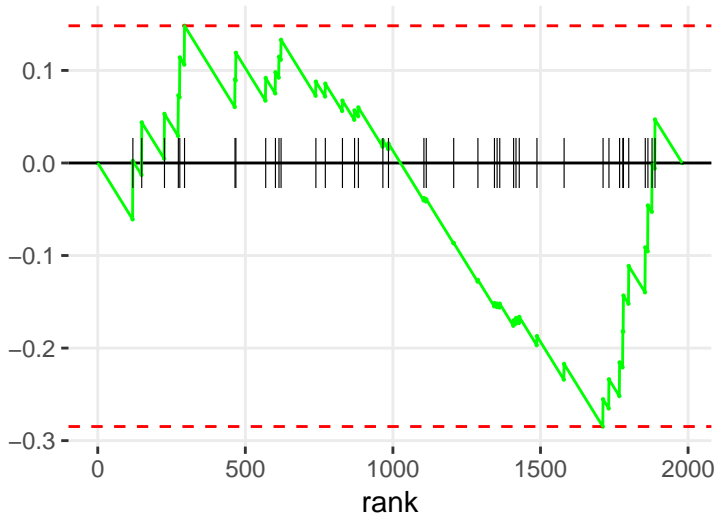
enrichment score

rank

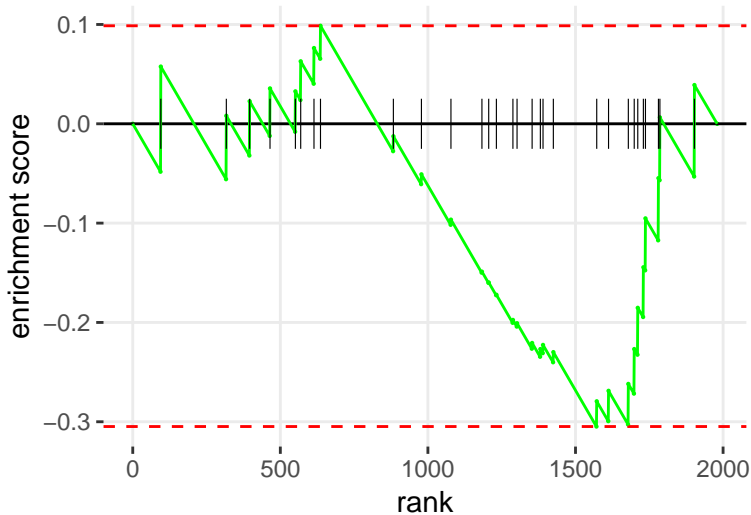


CYSTEINE BIOSYNTHESIS/HOMOCYSTEINE DEGRADATION

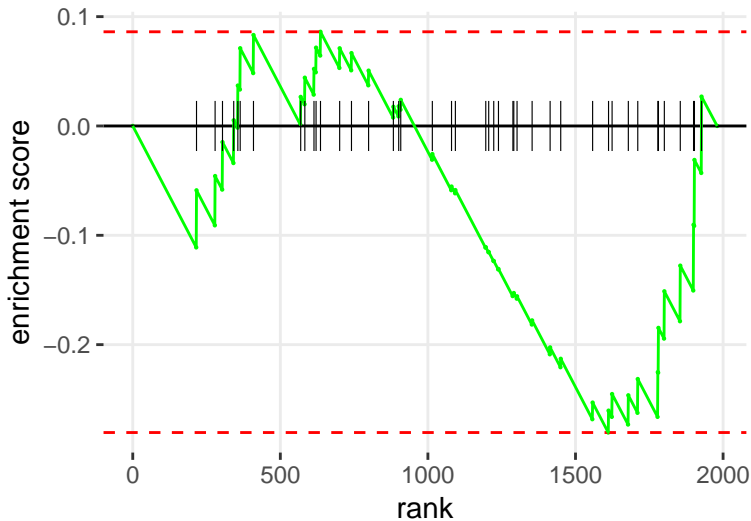
enrichment score



ADENINE AND ADENOSINE SALVAGE VI

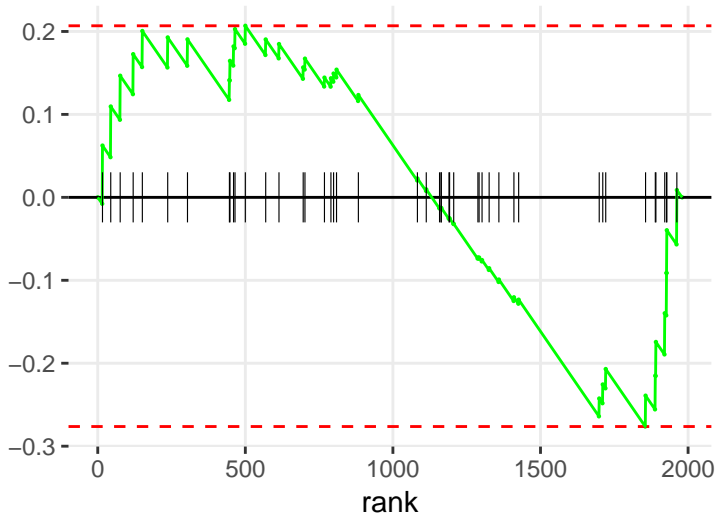


GDP-GLUCOSE BIOSYNTHESIS



GLYCOLYSIS I

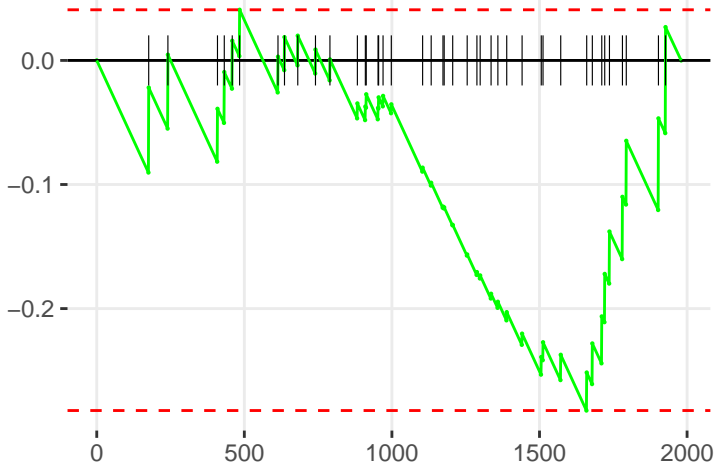
enrichment score



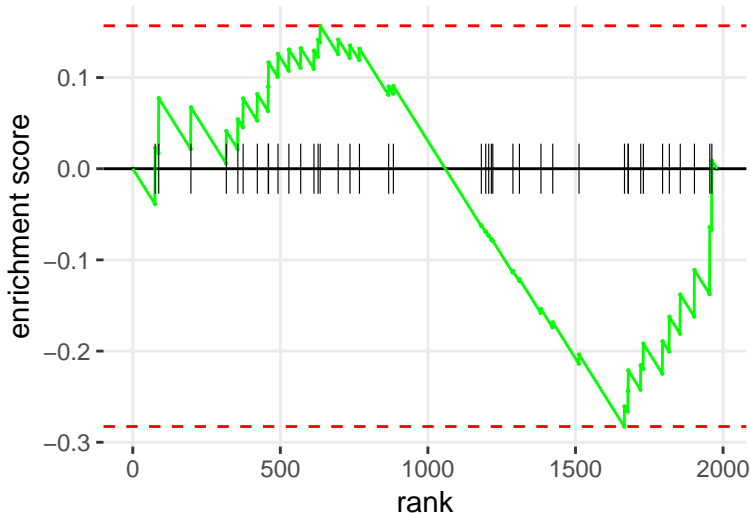
ASPARTATE DEGRADATION II

enrichment score

rank

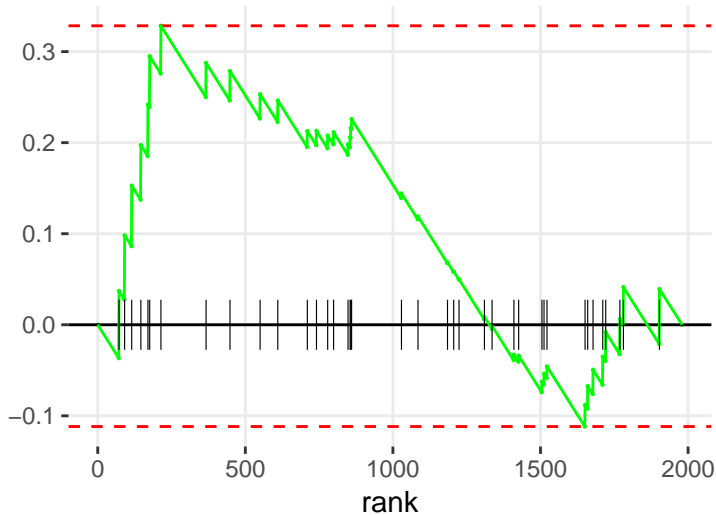


GLYCOGEN BIOSYNTHESIS II (FROM UDP-D-GLUCOSE)



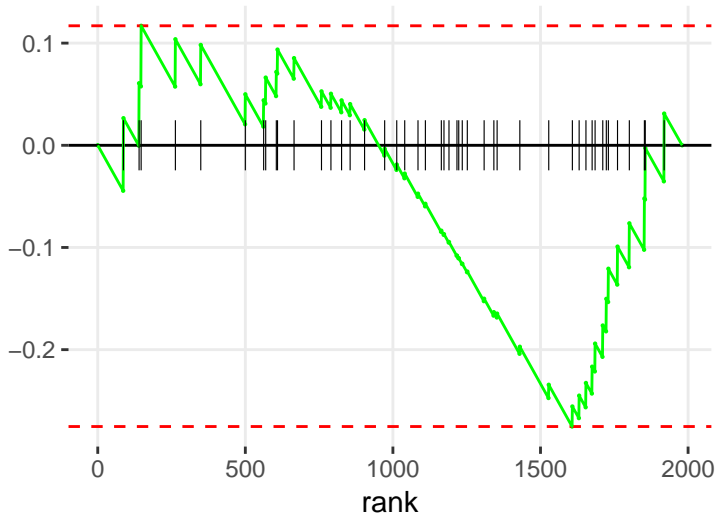
GLUCOCORTICOID BIOSYNTHESIS

enrichment score



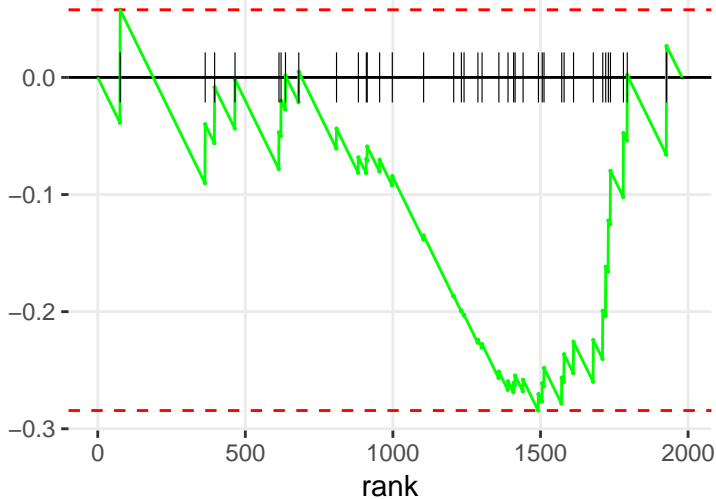
1D-<IMYO</I>-INOSITOL HEXAKISPHOSPHATE BIOSYNTHESIS II (MAMMALIAN)

enrichment score

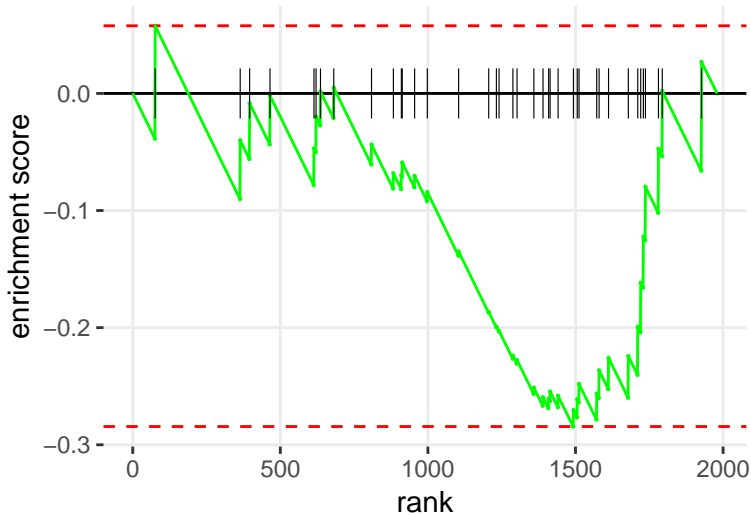


GLUTAMATE DEGRADATION II

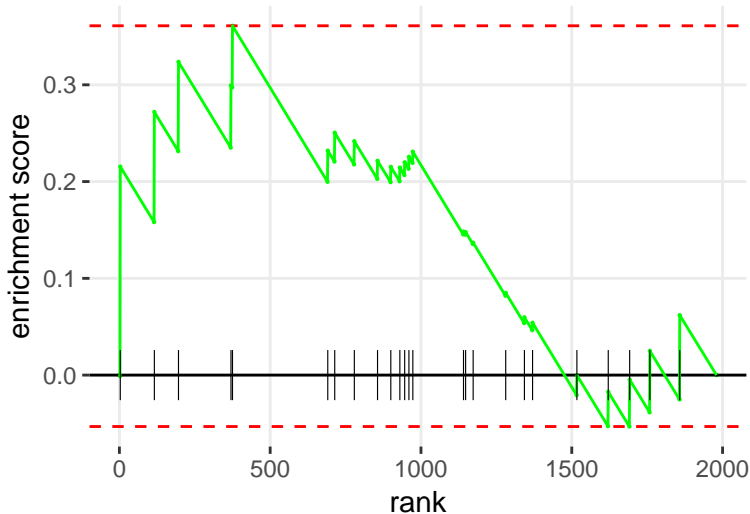
enrichment score



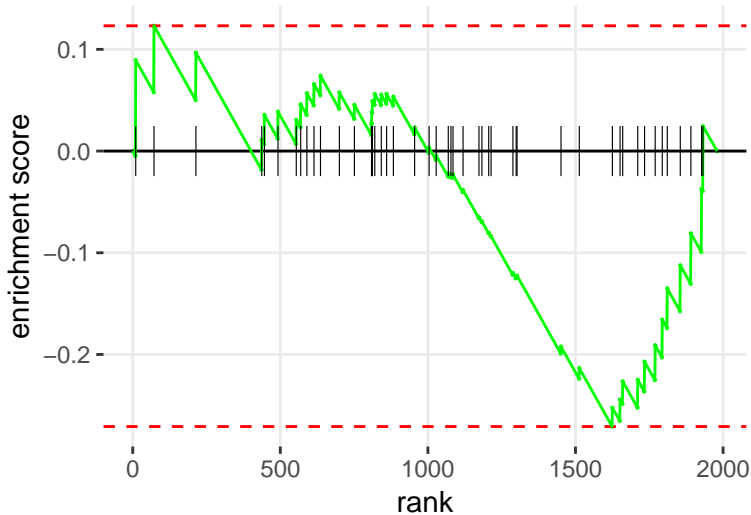
ASPARTATE BIOSYNTHESIS



CHONDROITIN SULFATE BIOSYNTHESIS (LATE STAGES)



CHOLINE BIOSYNTHESIS III



TRNA CHARGING

enrichment score

0.1
0.0
-0.1
-0.2

0

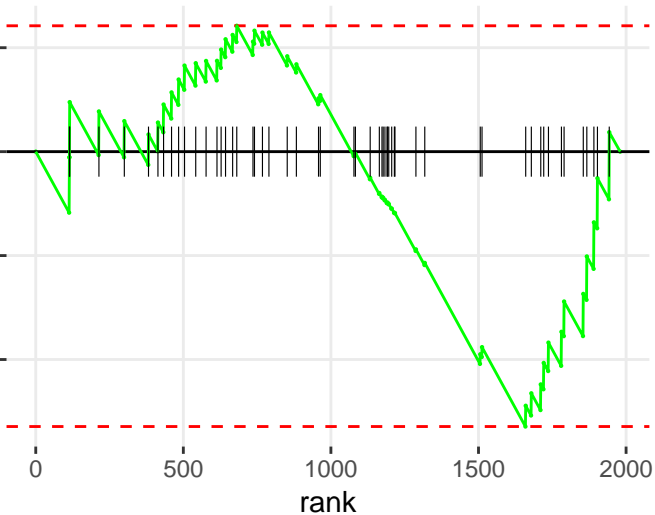
500

1000

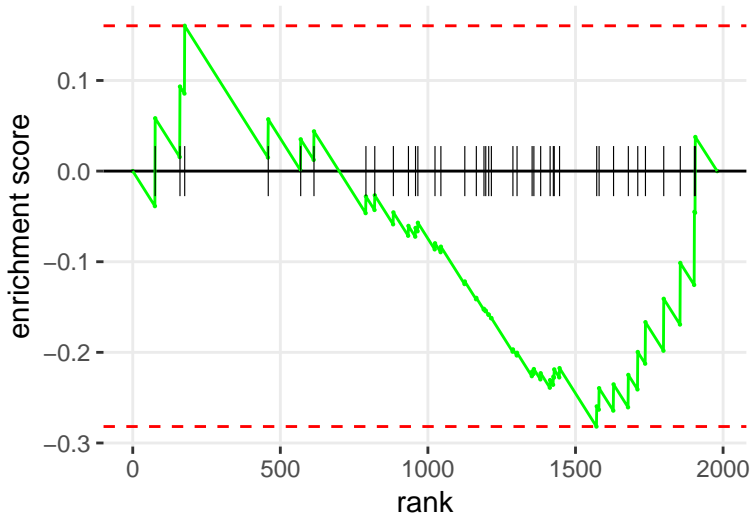
1500

2000

rank

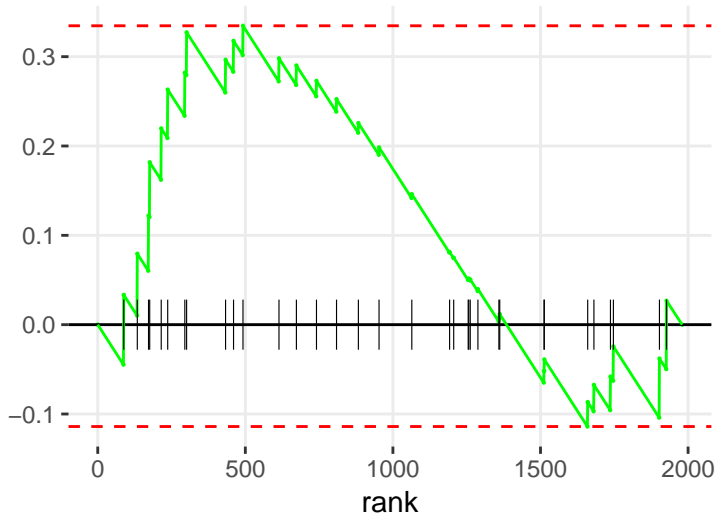


METHIONINE DEGRADATION I (TO HOMOCYSTEINE)



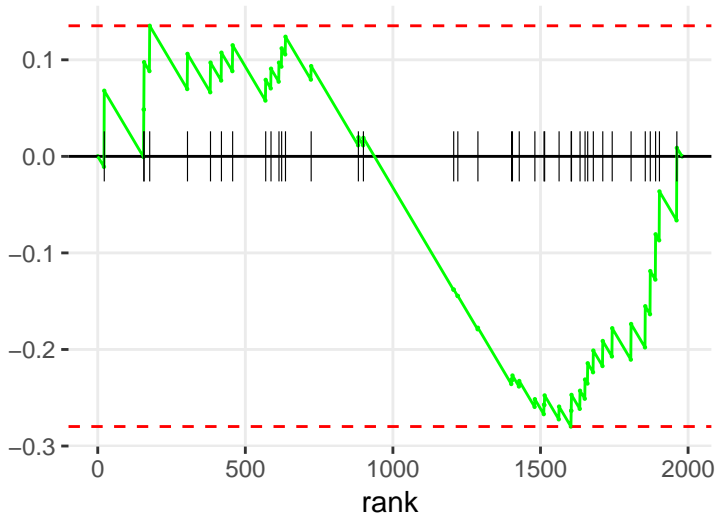
2-OXISOVALERATE DECARBOXYLATION TO ISOBUTANOYL-COA

enrichment score

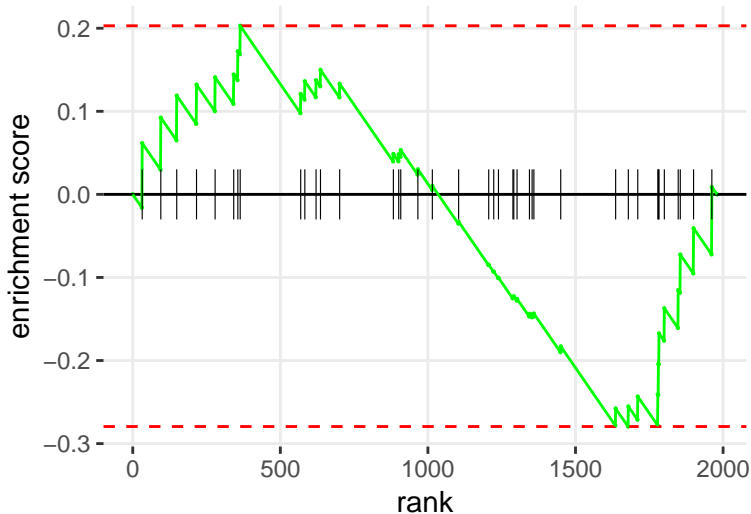


TRIACYLGLYCEROL BIOSYNTHESIS

enrichment score

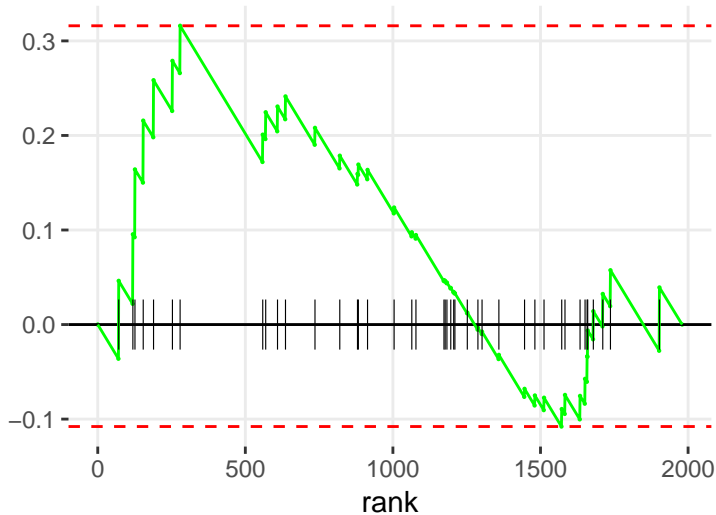


TREHALOSE DEGRADATION II (TREHALASE)

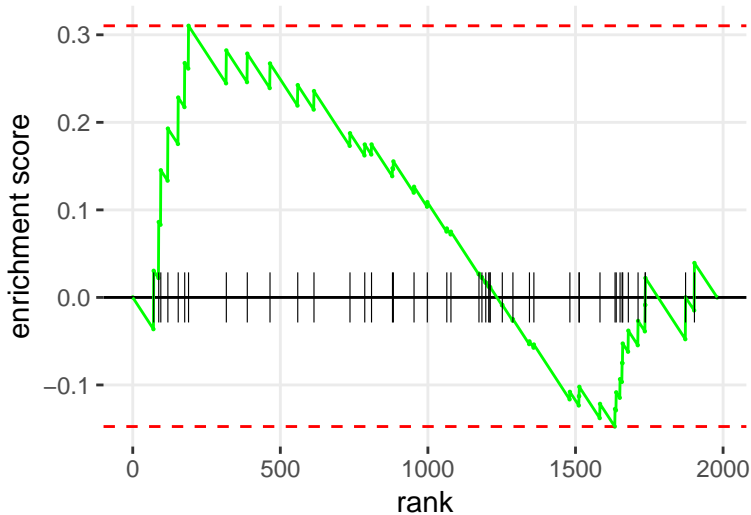


PROLINE BIOSYNTHESIS I

enrichment score

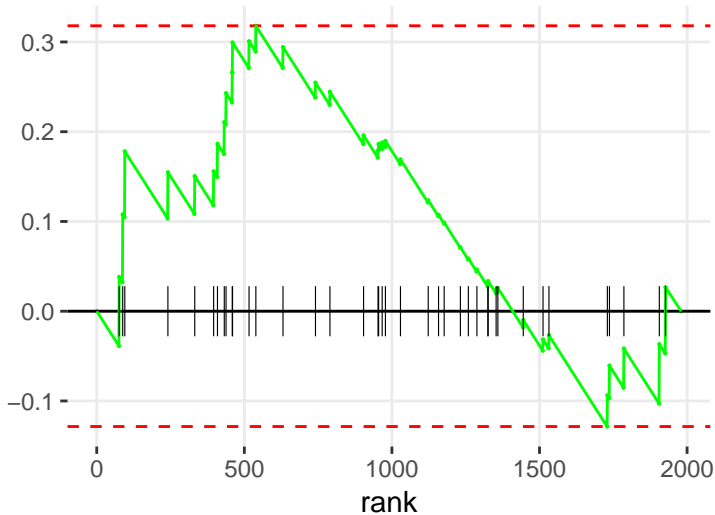


PROLINE BIOSYNTHESIS II (FROM ARGinine)

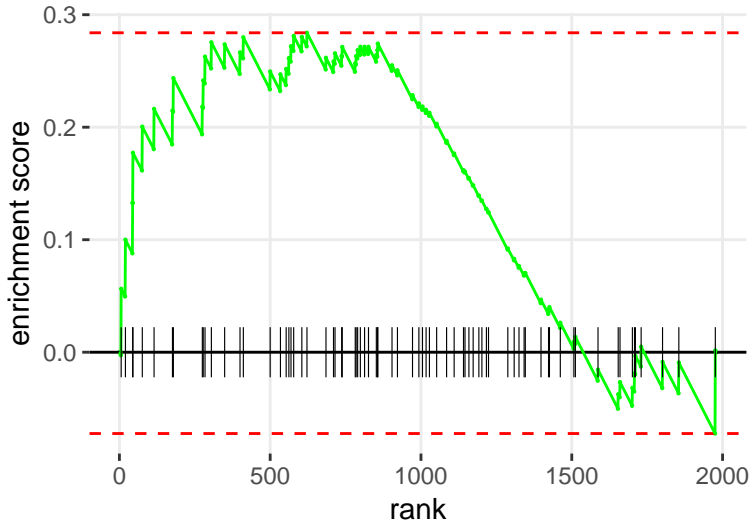


CREATINE-PHOSPHATE BIOSYNTHESIS

enrichment score



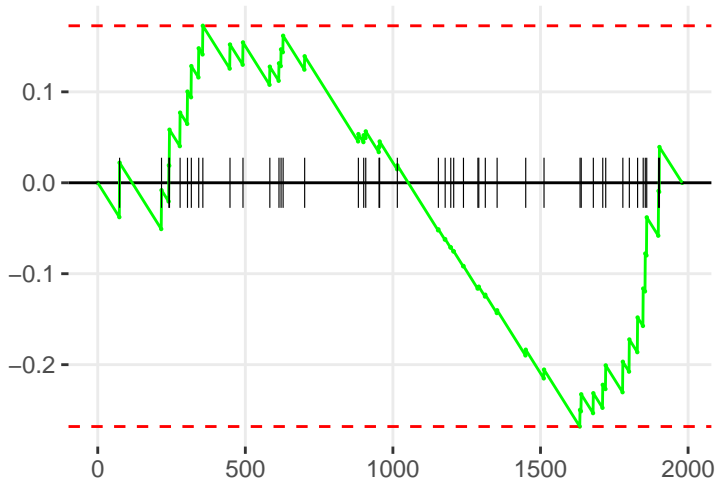
SEROTONIN AND MELATONIN BIOSYNTHESIS



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

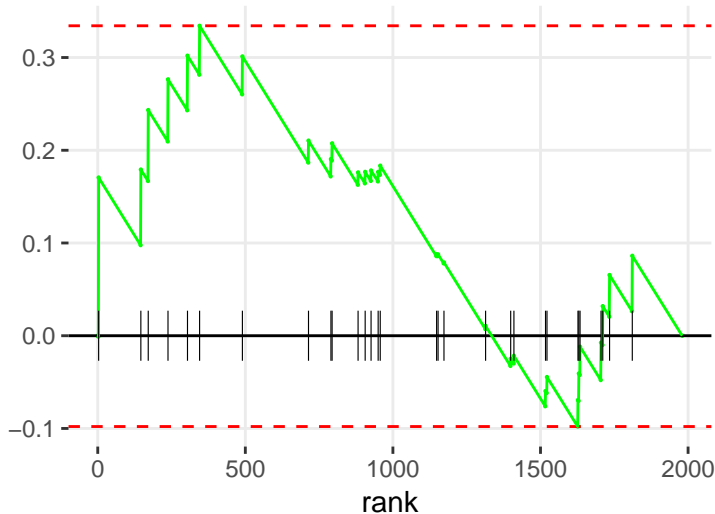
enrichment score

rank



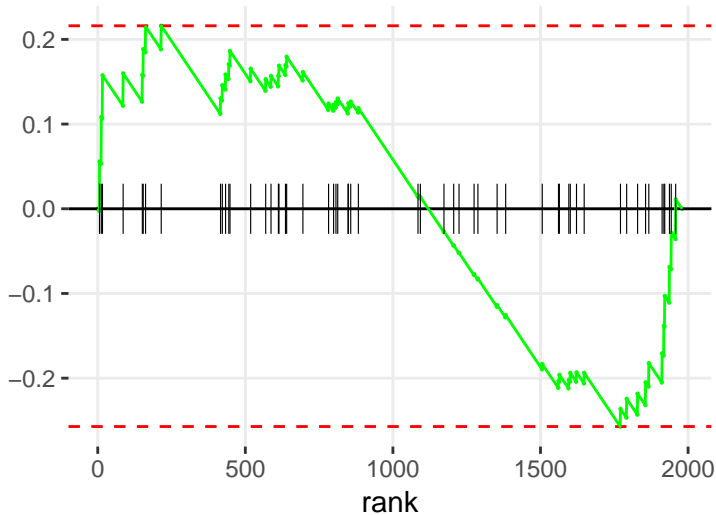
D-<IMYO</I>-INOSITOL (1,4,5)-TRISPHOSPHATE BIOSYNTHESIS

enrichment score

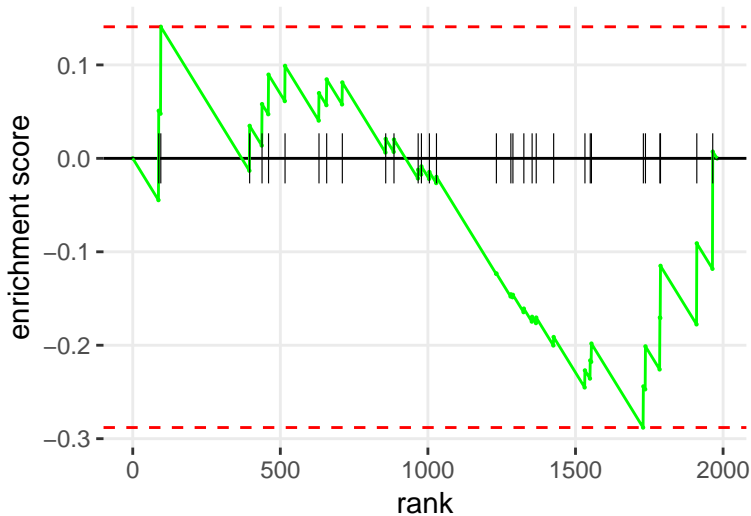


PHENYLETHYLAMINE DEGRADATION I

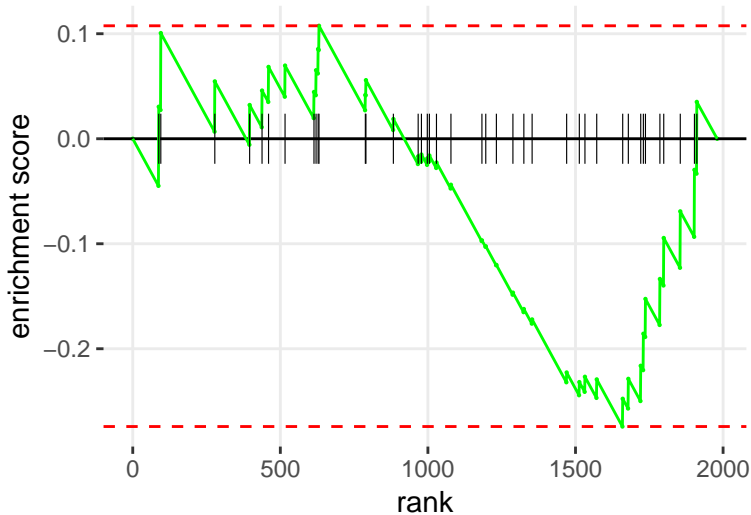
enrichment score



THE VISUAL CYCLE I (VERTEBRATES)

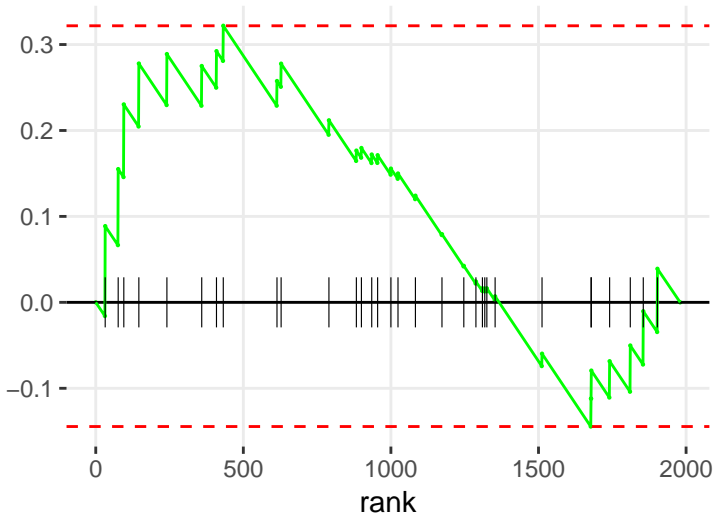


GLUTAMINE BIOSYNTHESIS I



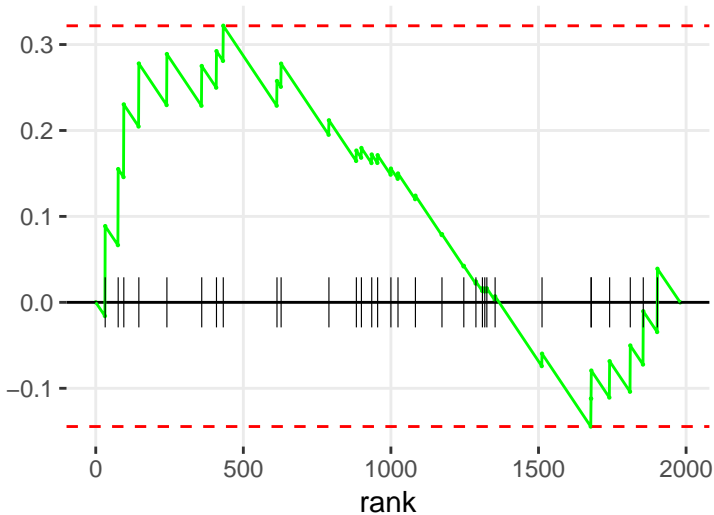
STEARATE BIOSYNTHESIS I (ANIMALS)

enrichment score

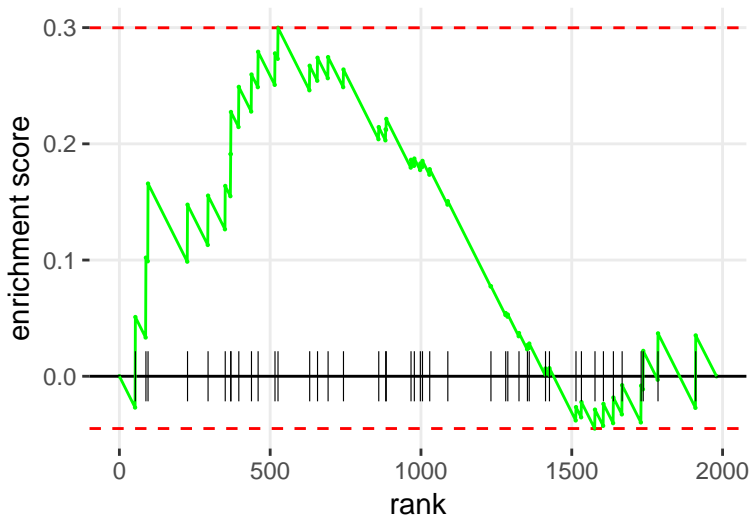


EICOSAPENTAENOATE BIOSYNTHESIS II (METAZOA)

enrichment score

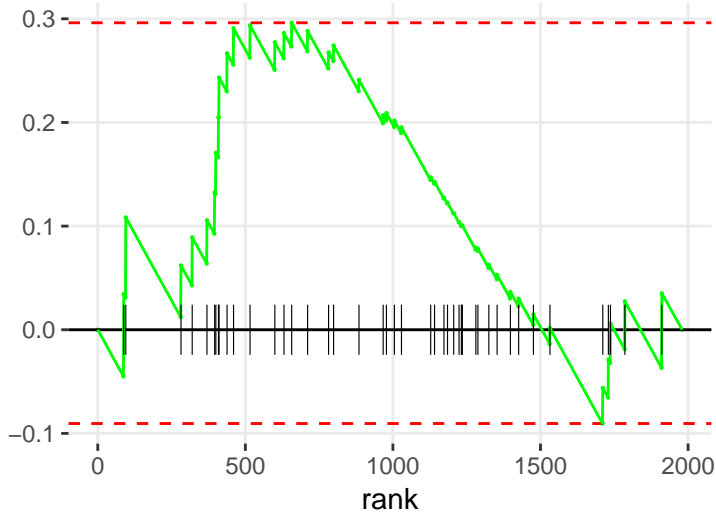


FORMALDEHYDE OXIDATION II (GLUTATHIONE-DEPENDENT)

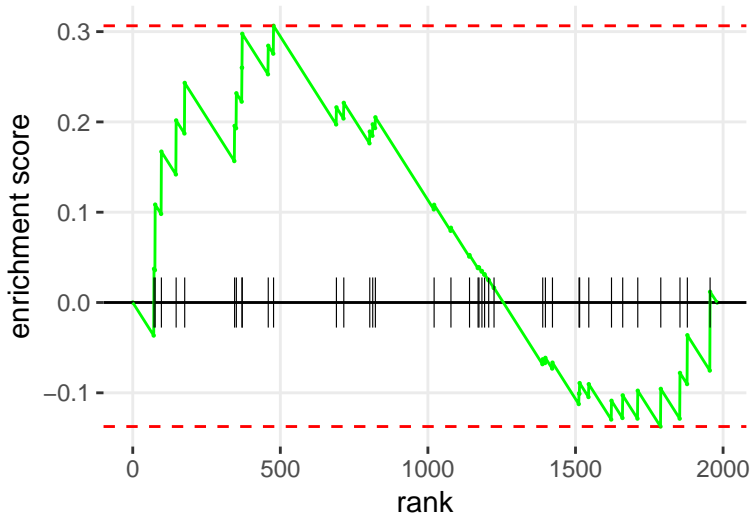


TYROSINE DEGRADATION I

enrichment score

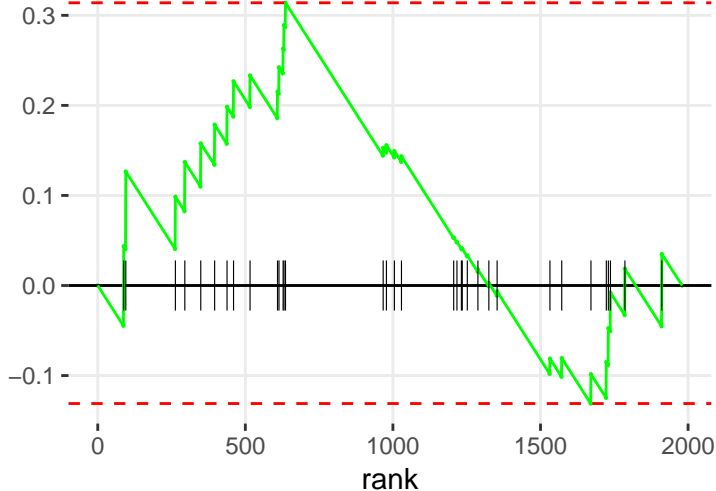


ANANDAMIDE DEGRADATION



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

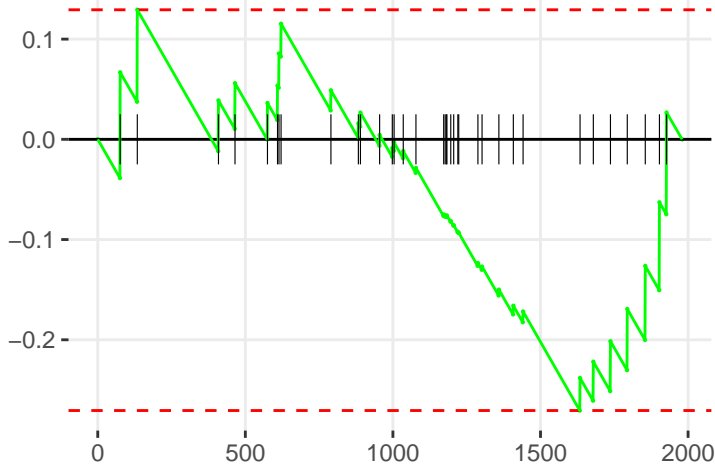
enrichment score



KETOGENESIS

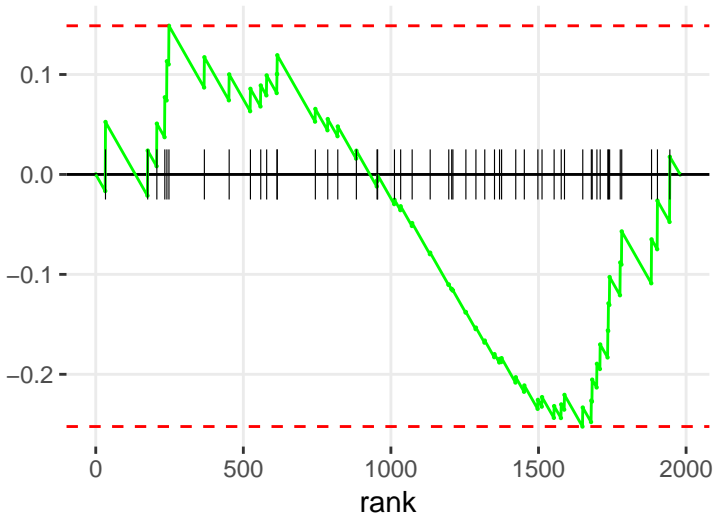
enrichment score

rank



GLYCINE BIOSYNTHESIS I

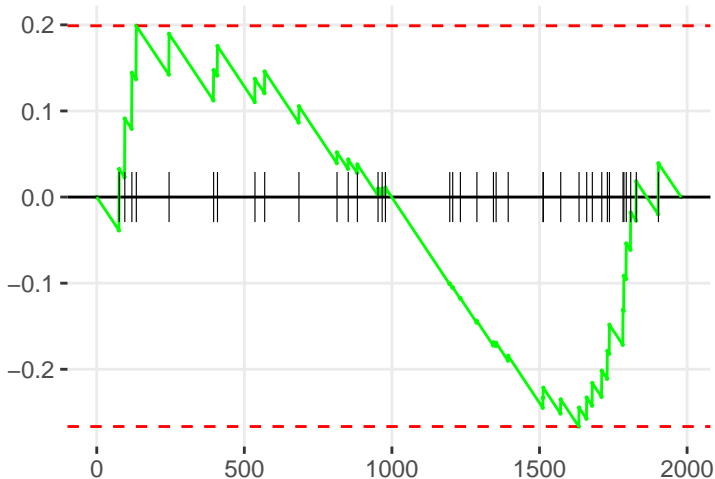
enrichment score



PRPP BIOSYNTHESIS I

enrichment score

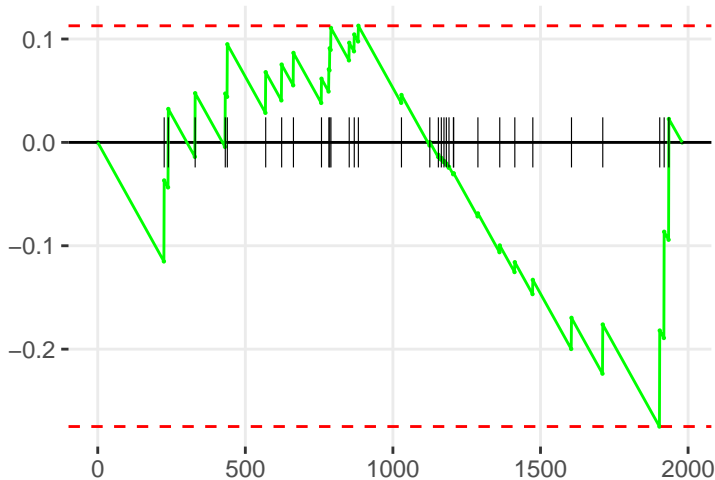
rank



CALCIUM TRANSPORT I

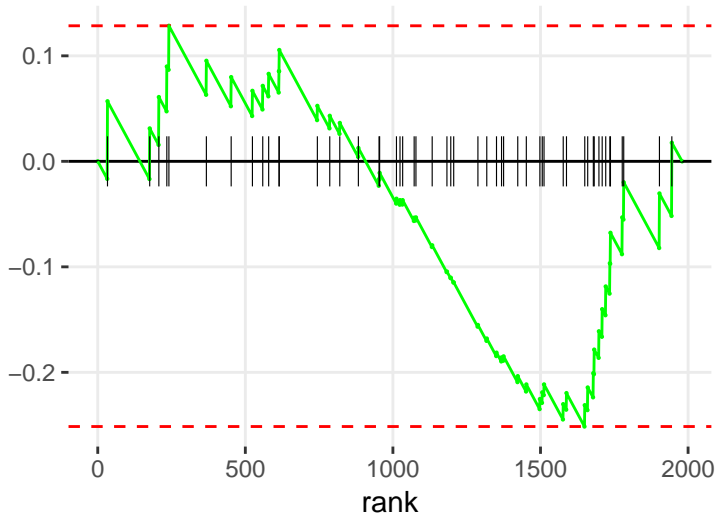
enrichment score

rank

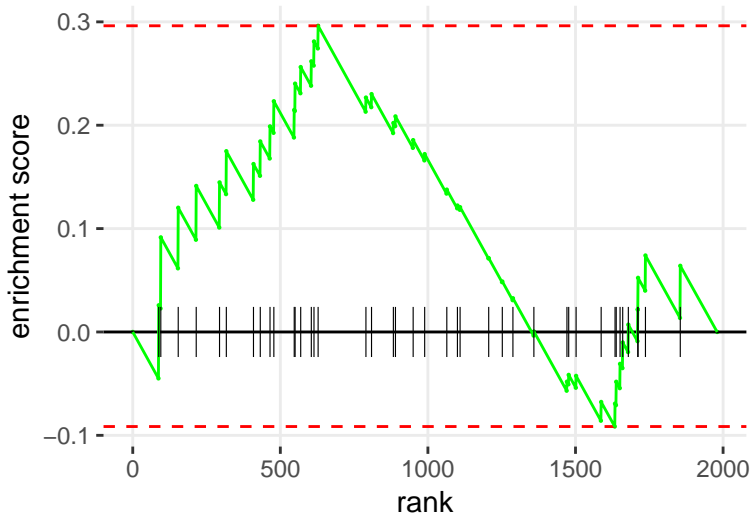


FOLATE POLYGLUTAMYLATION

enrichment score



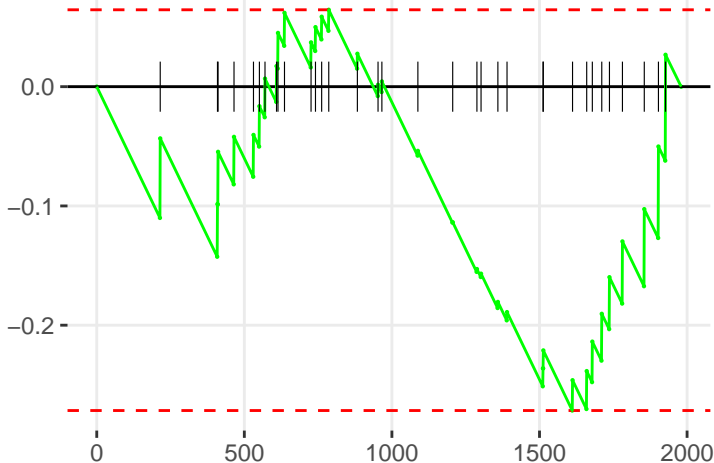
UREA CYCLE



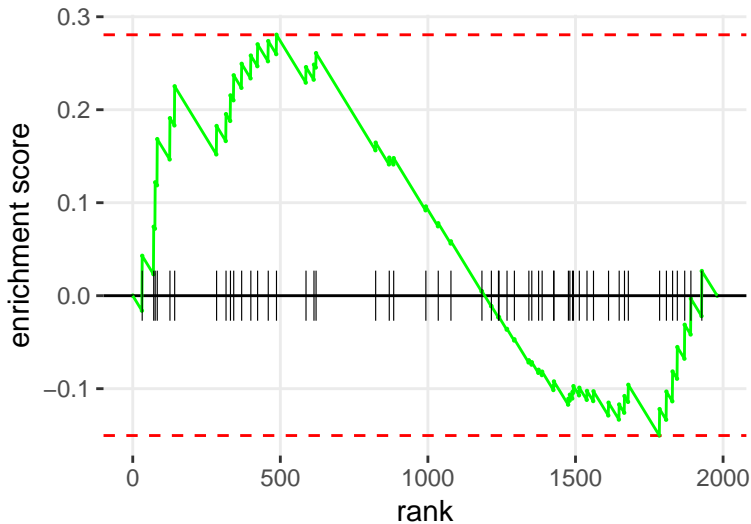
LEUCINE DEGRADATION I

enrichment score

rank

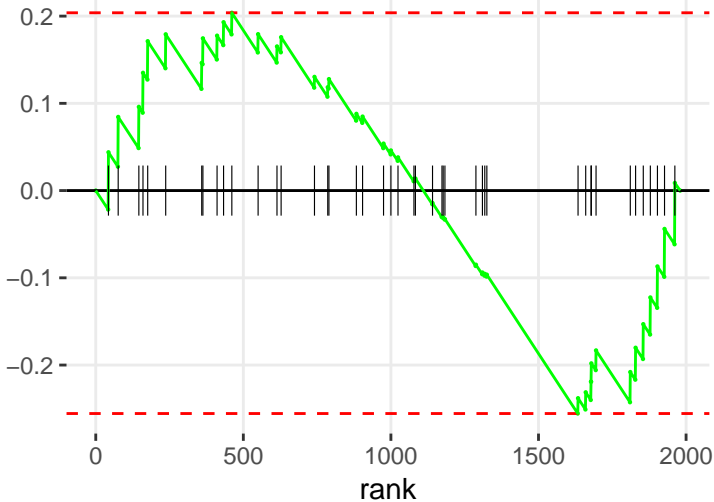


CHOLINE DEGRADATION I

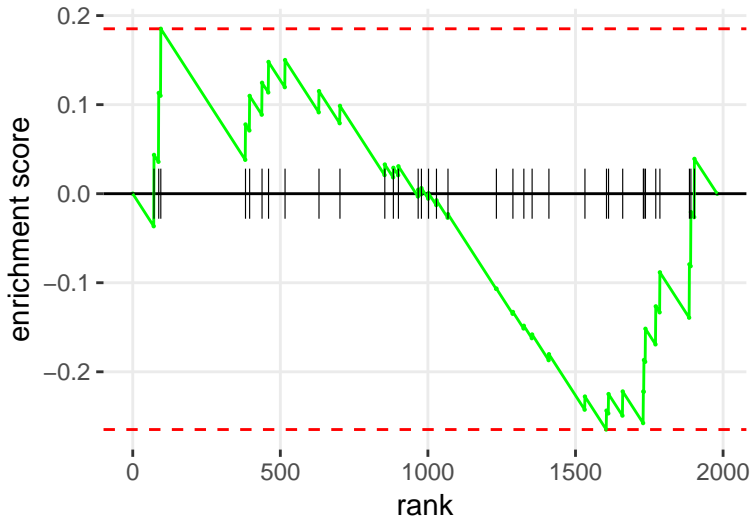


FATTY ACID &BETA;-OXIDATION I

enrichment score



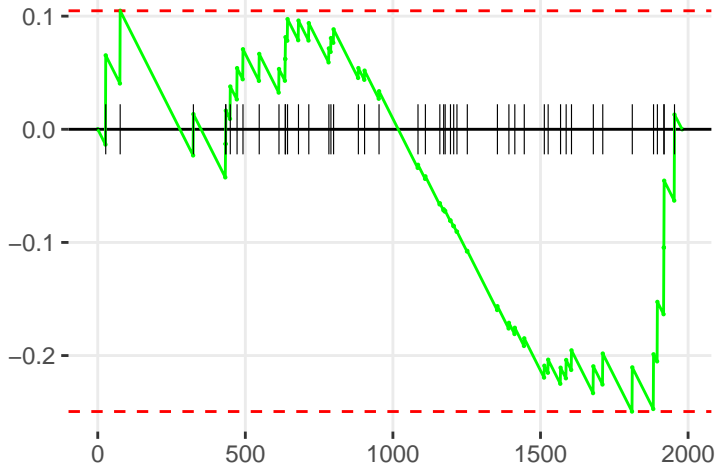
ALANINE BIOSYNTHESIS III



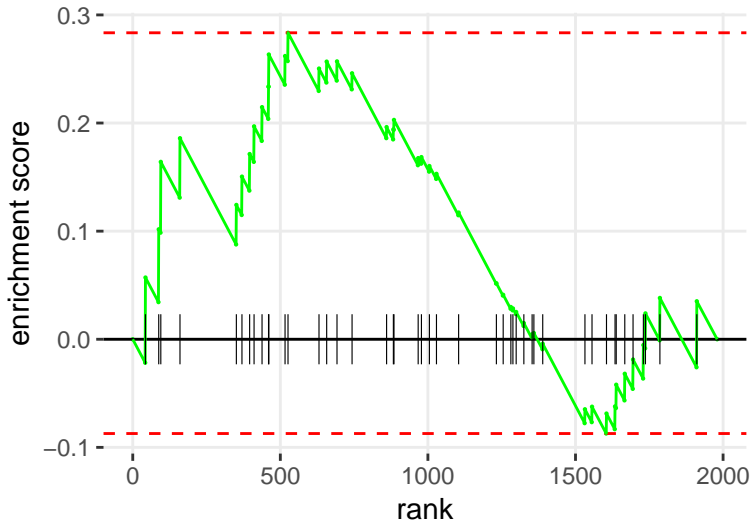
CITRULLINE-NITRIC OXIDE CYCLE

enrichment score

rank

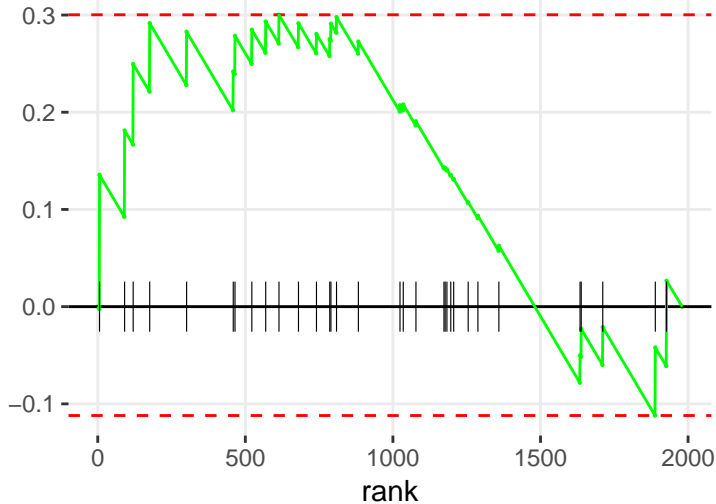


FATTY ACID &BETA;-OXIDATION III (UNSATURATED, ODD NUMBER)

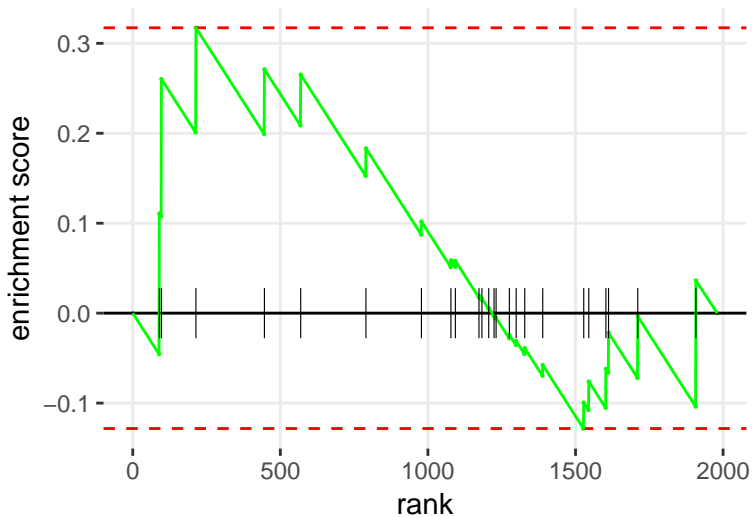


SUCROSE DEGRADATION V (MAMMALIAN)

enrichment score



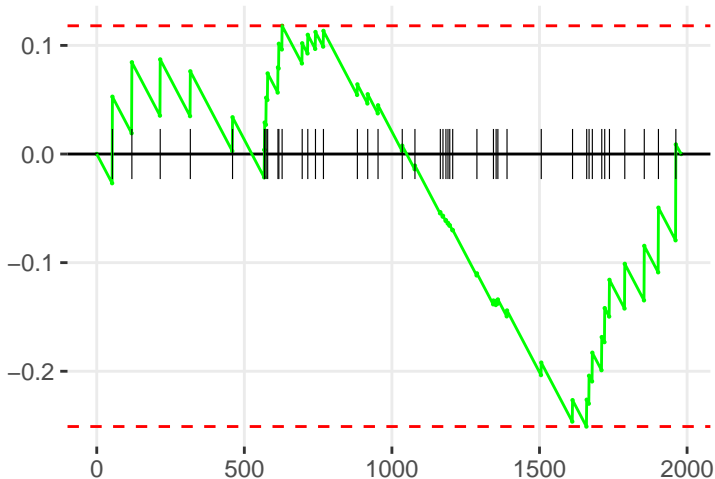
2-AMINO-3-CARBOXYMUCONATE SEMIALDEHYDE DEGRADATION TO GLUTARYL-CO



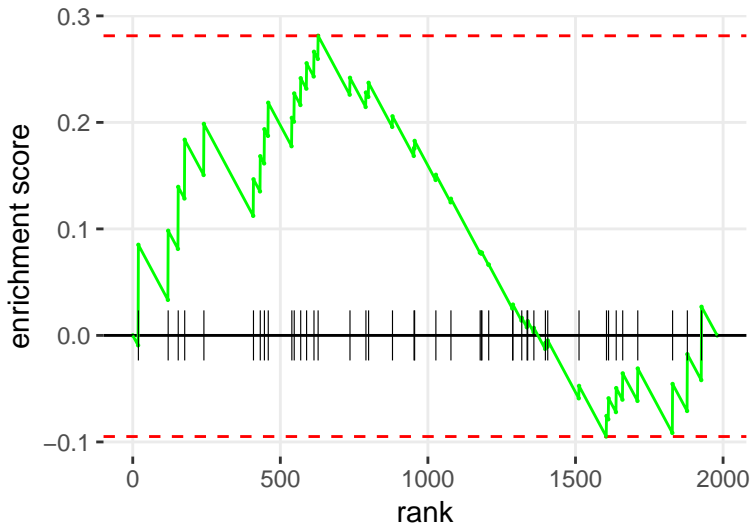
ETHANOL DEGRADATION IV

enrichment score

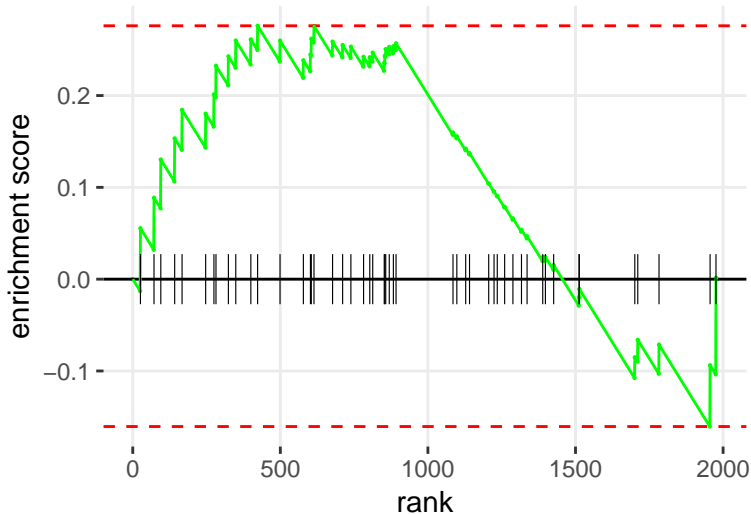
rank



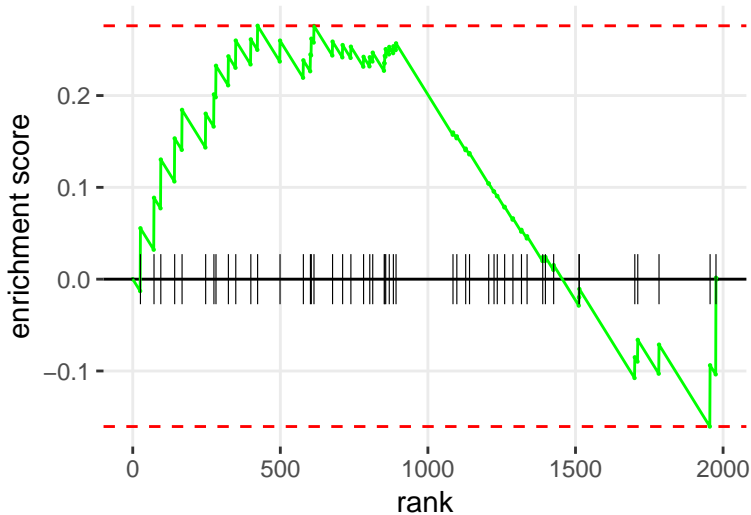
PYRUVATE FERMENTATION TO LACTATE



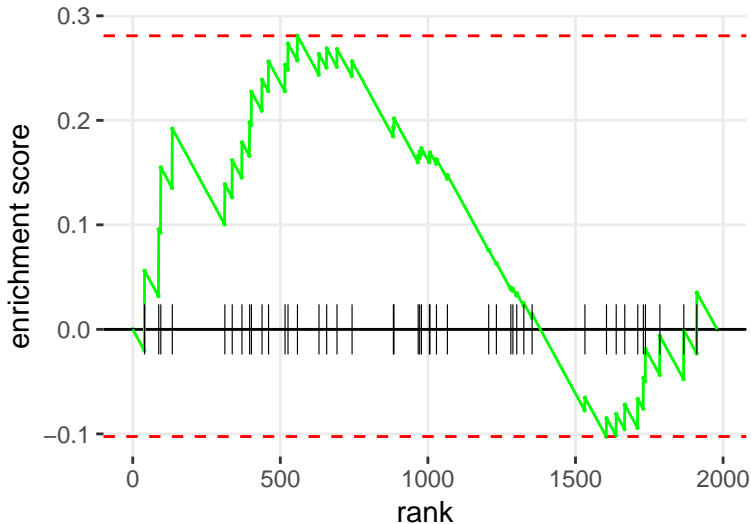
4-HYDROXYPHENYLPYRUVATE BIOSYNTHESIS



4-HYDROXYBENZOATE BIOSYNTHESIS



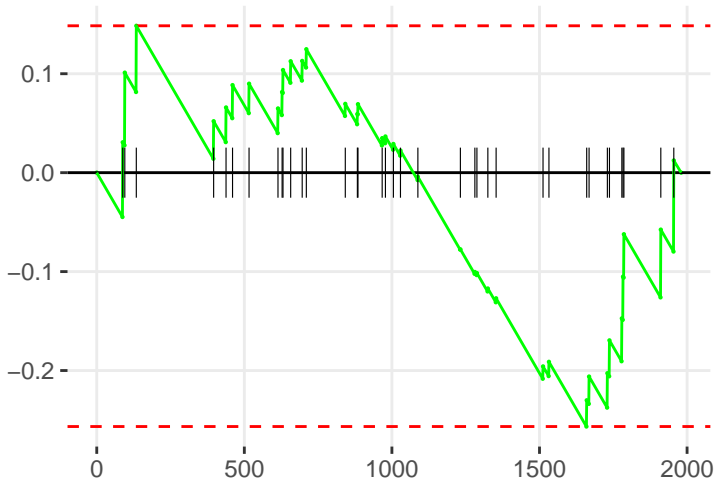
METHYLGLYOXAL DEGRADATION VI



GLUTATHIONE REDOX REACTIONS I

enrichment score

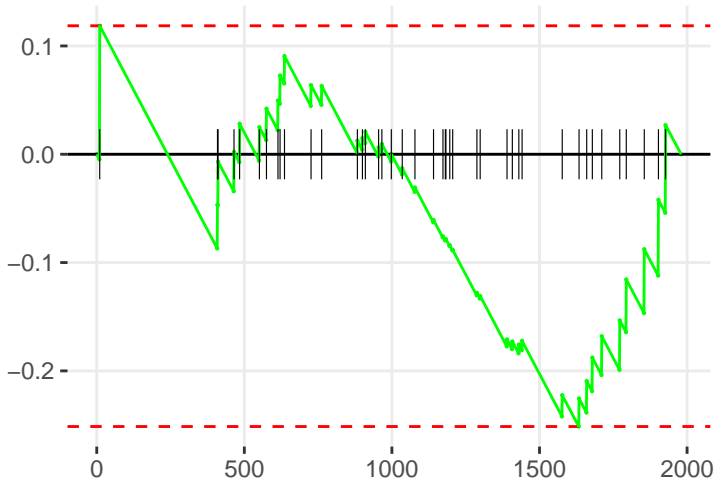
rank



ISOLEUCINE DEGRADATION I

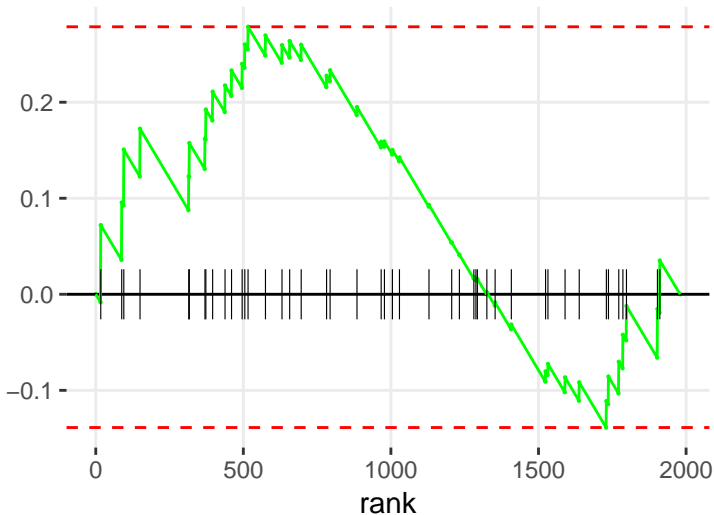
enrichment score

rank

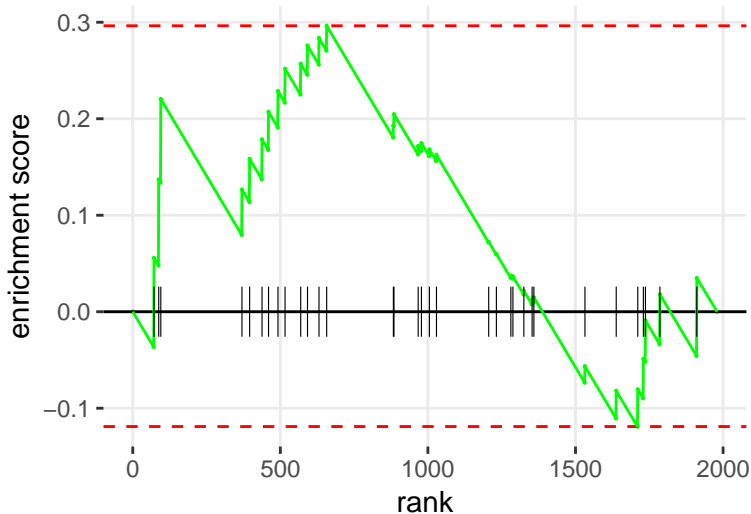


NAD BIOSYNTHESIS FROM 2-AMINO-3-CARBOXYMUCONATE SEMIALDEHYDE

enrichment score

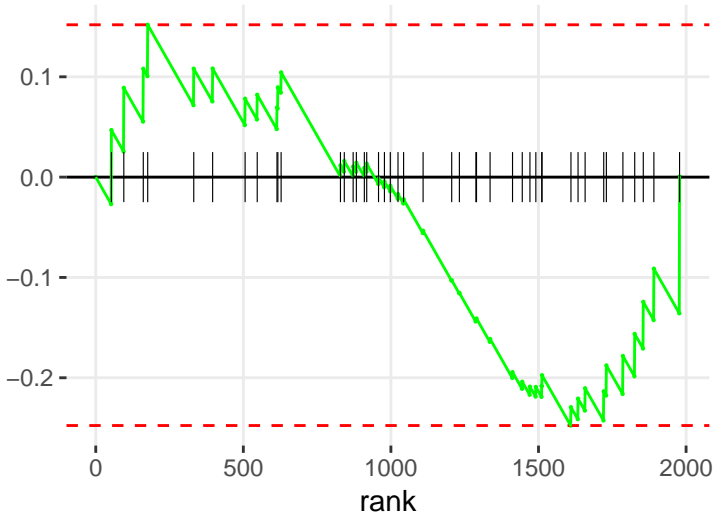


DOLICHOL AND DOLICHYL PHOSPHATE BIOSYNTHESIS

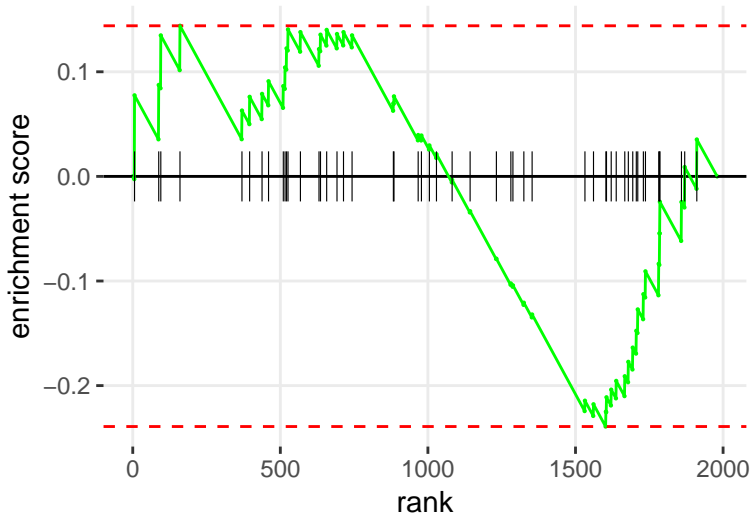


ADENOSINE NUCLEOTIDES DEGRADATION II

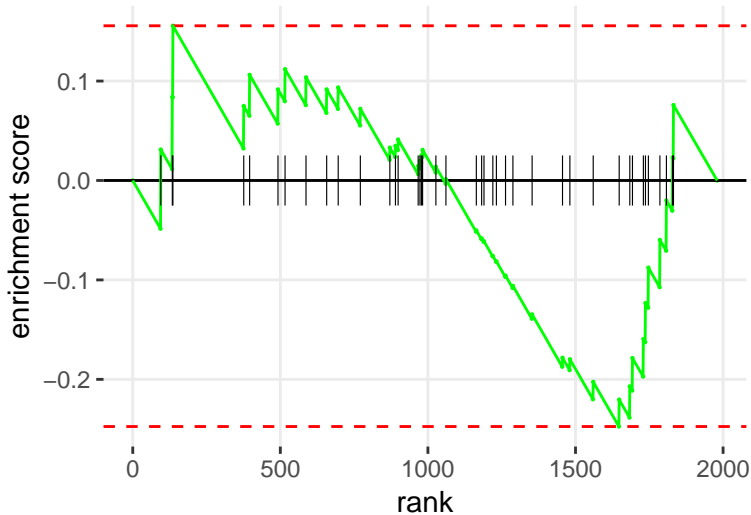
enrichment score



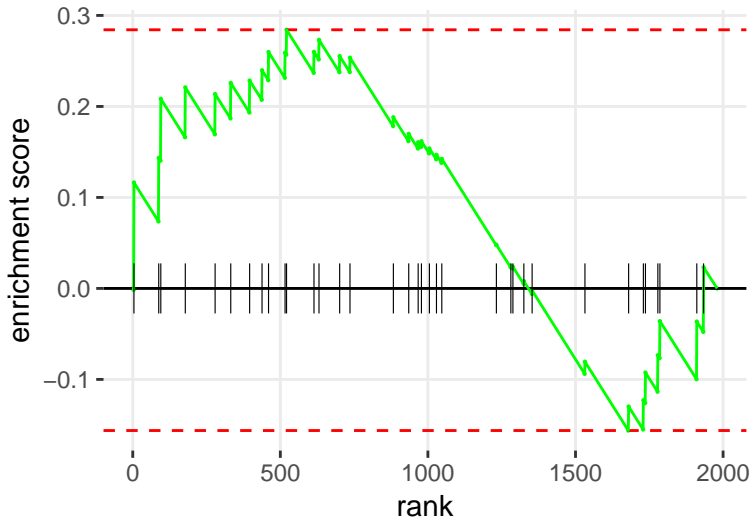
LACTOSE DEGRADATION III



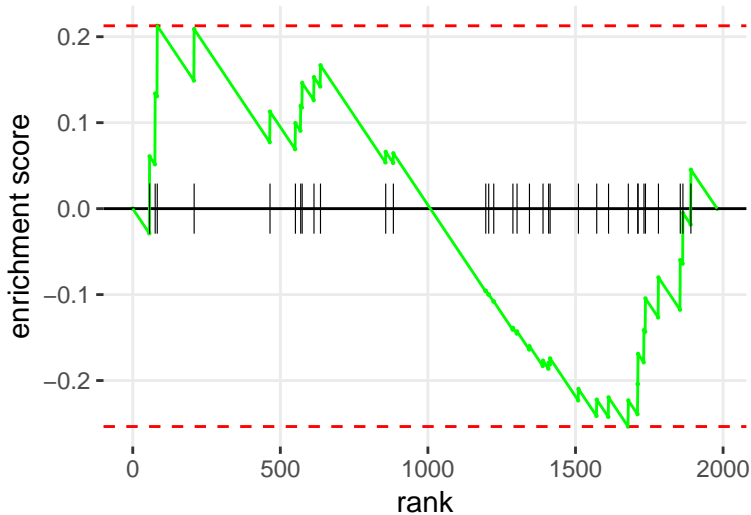
CARDIOLIPIN BIOSYNTHESIS II



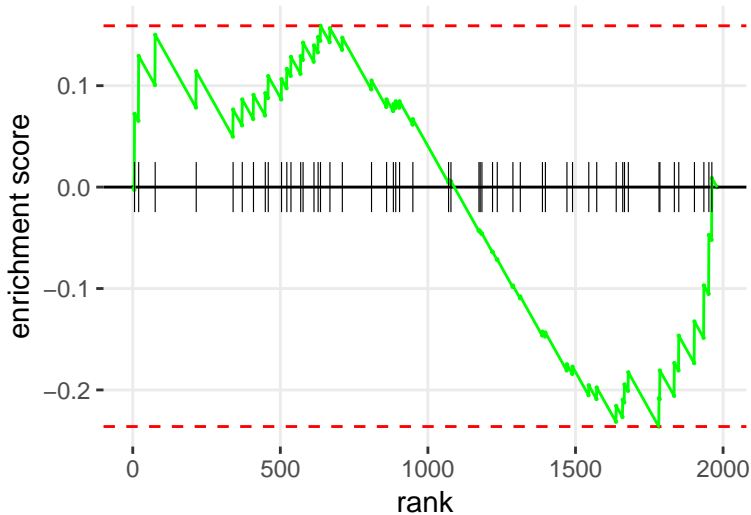
SPHINGOMYELIN METABOLISM



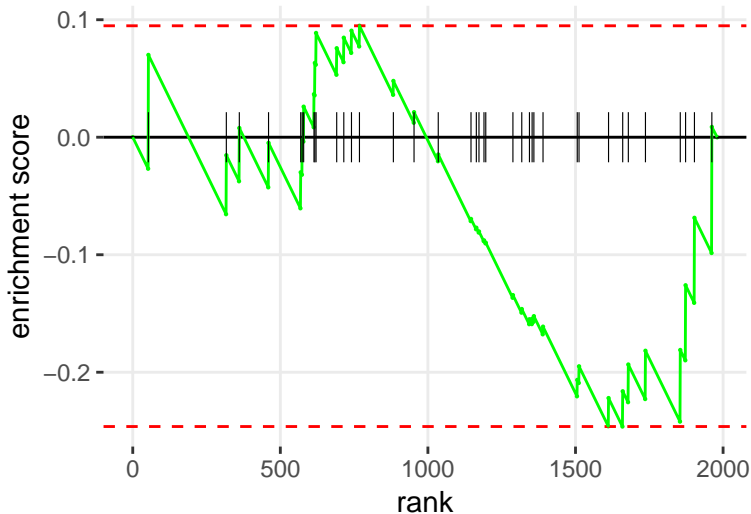
L-CYSTEINE DEGRADATION II



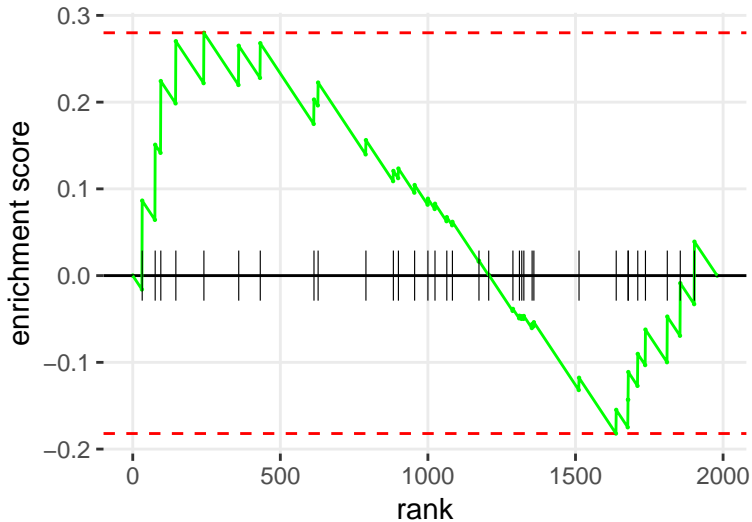
PYRIMIDINE RIBONUCLEOTIDES INTERCONVERSION



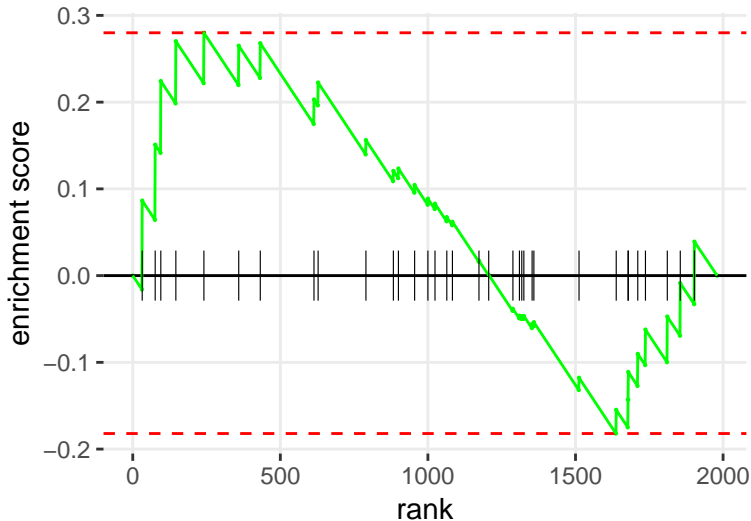
TRYPTOPHAN DEGRADATION X (MAMMALIAN, VIA TRYPTAMINE)



FATTY ACID ACTIVATION

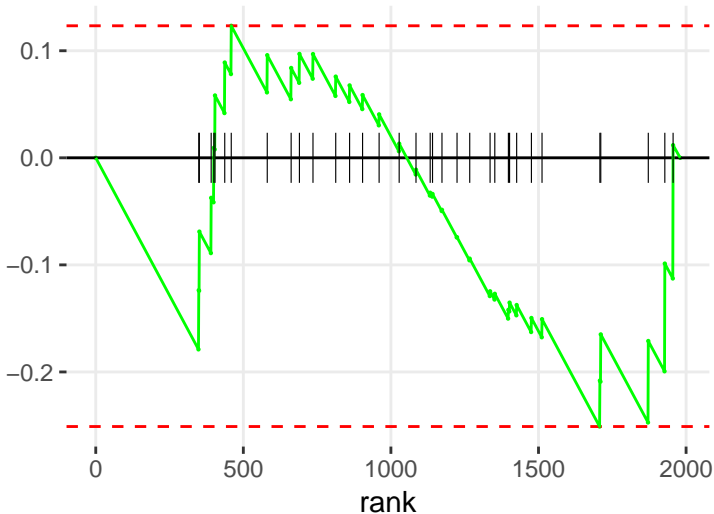


FATTY ACID &ALPHA;-OXIDATION II

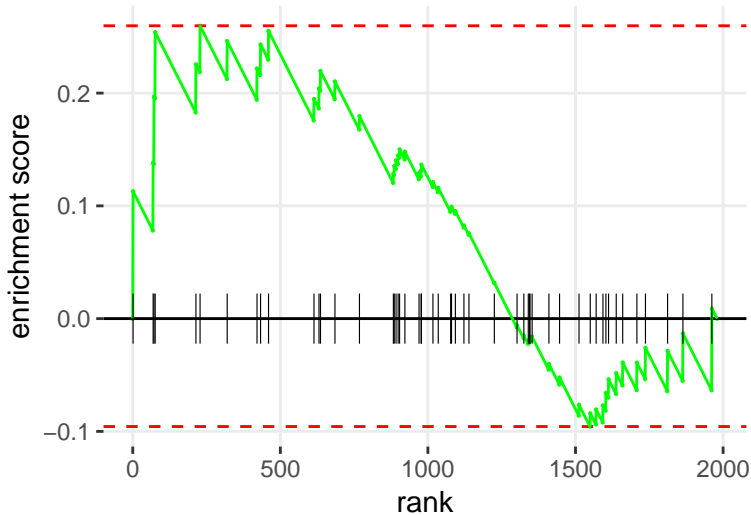


THYROID HORMONE METABOLISM II (VIA CONJUGATION AND/OR DEGRADATION)

enrichment score



GLUTAMATE DEPENDENT ACID RESISTANCE



METHYLGLYOXAL DEGRADATION I

enrichment score

0.1
0.0
-0.1
-0.2

0

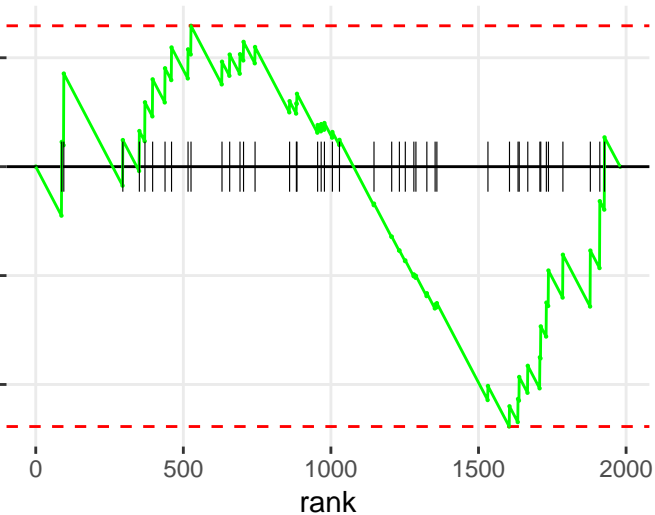
500

1000

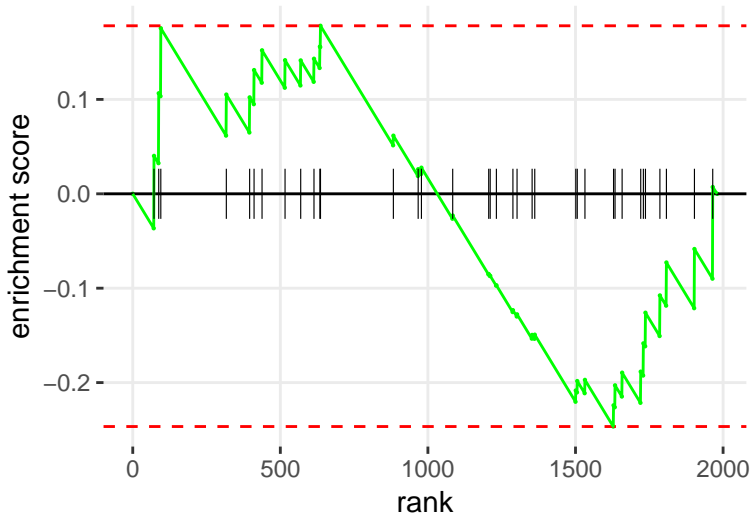
1500

2000

rank



TRYPTOPHAN DEGRADATION TO 2-AMINO-3-CARBOXYMUCONATE SEMIALDEHYDE



TETRAHYDROBIOPTERIN BIOSYNTHESIS II

enrichment score

0.0

-0.1

-0.2

0

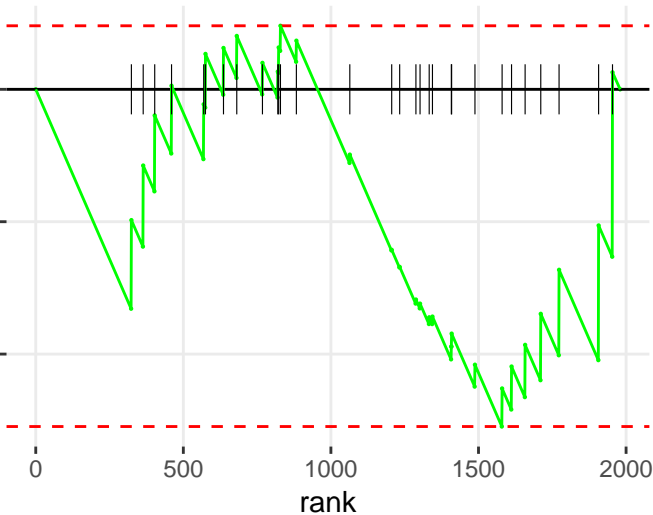
500

1000

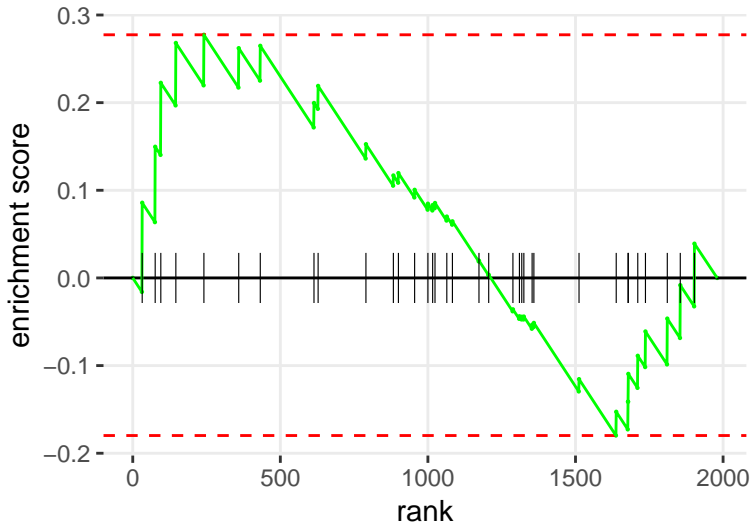
1500

2000

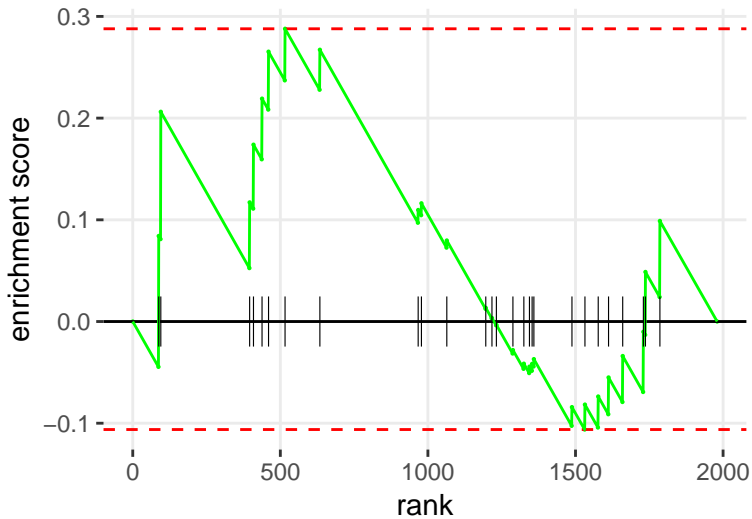
rank



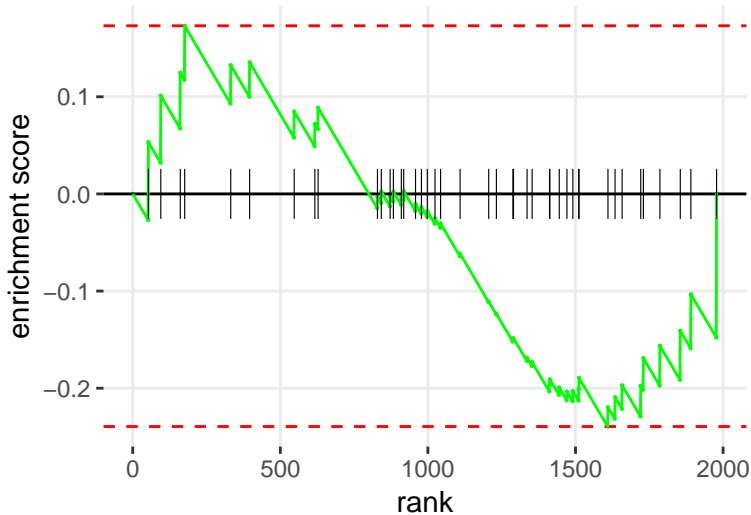
&GAMMA;-LINOLENATE BIOSYNTHESIS II (ANIMALS)



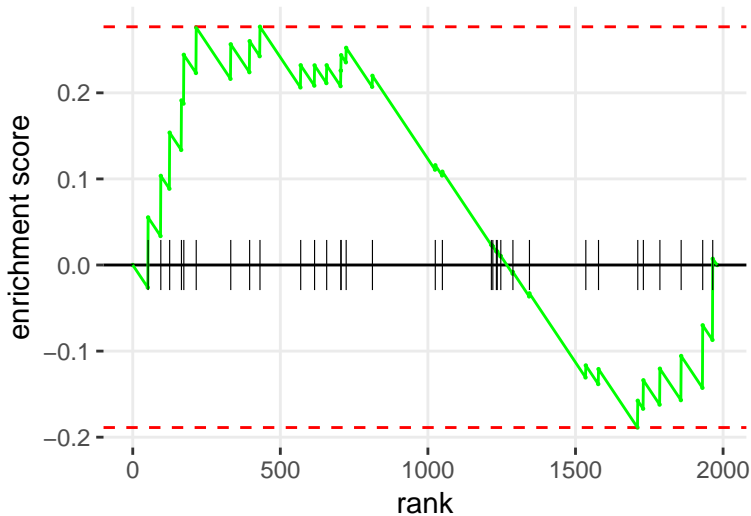
SPERMIDINE BIOSYNTHESIS I



GUANOSINE NUCLEOTIDES DEGRADATION III

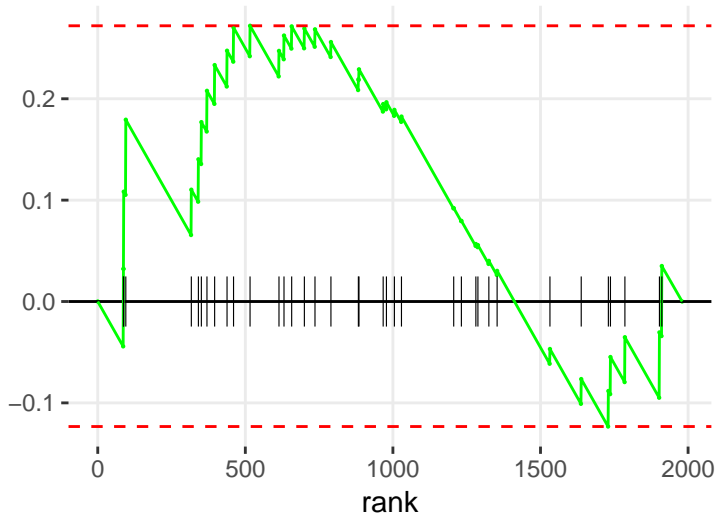


SALVAGE PATHWAYS OF PYRIMIDINE DEOXYRIBONUCLEOTIDES

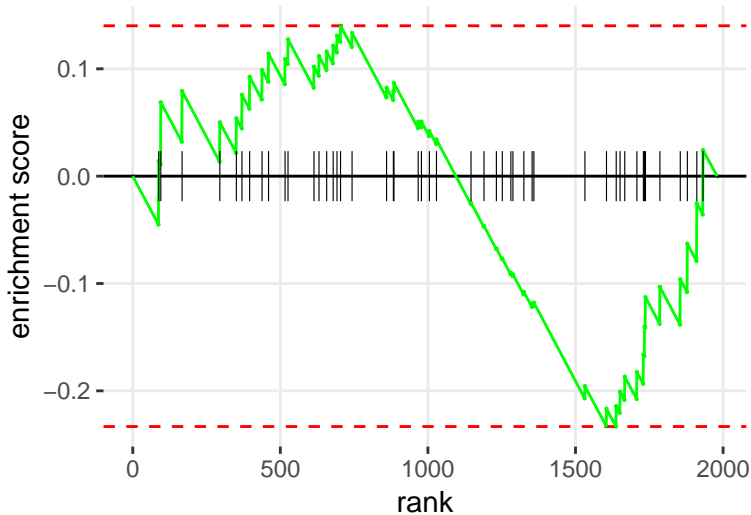


PYRIDOXAL 5'-PHOSPHATE SALVAGE PATHWAY

enrichment score

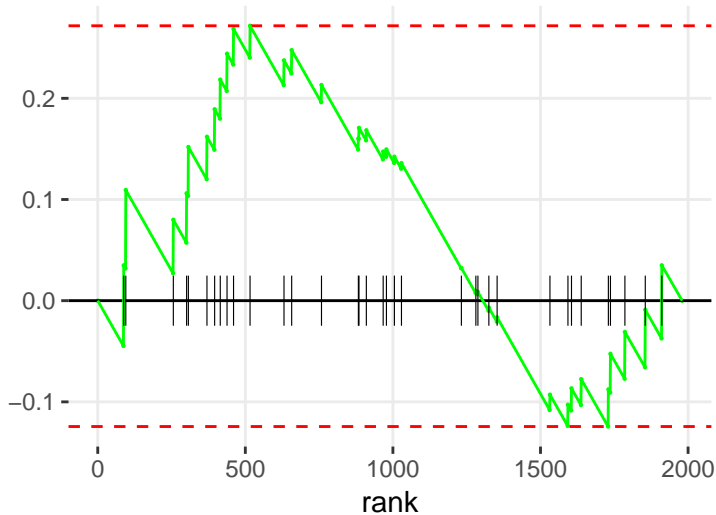


LANOSTEROL BIOSYNTHESIS



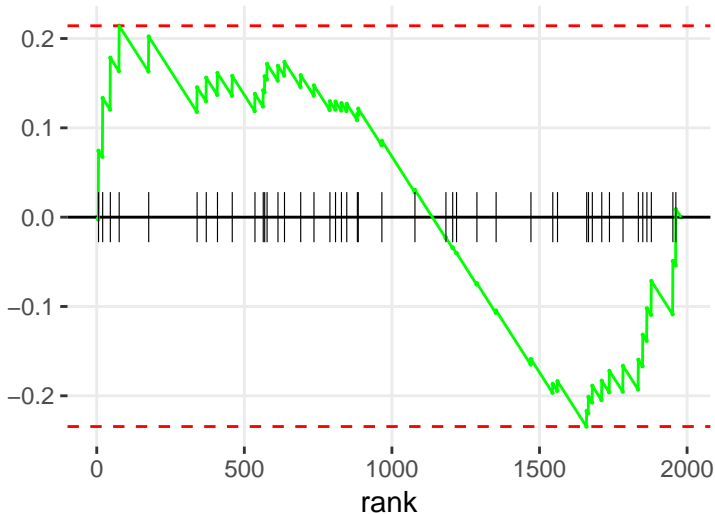
UBIQUINOL-10 BIOSYNTHESIS (EUKARYOTIC)

enrichment score

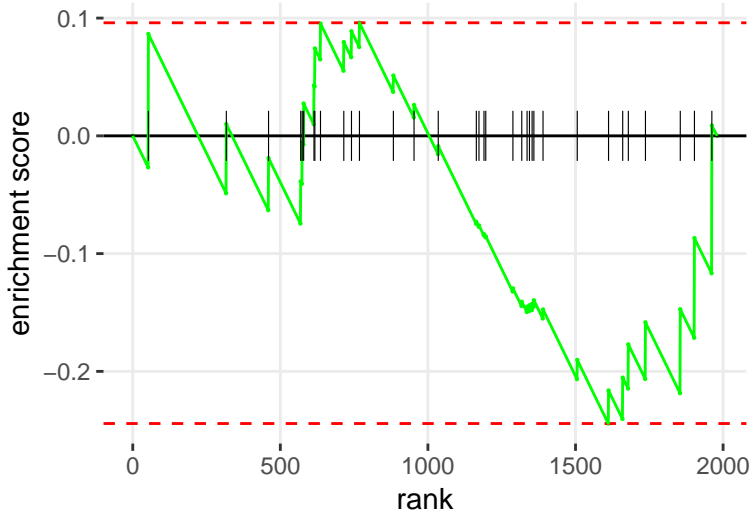


PYRIMIDINE DEOXYRIBONUCLEOTIDES <IDE NOVO</I> BIOSYNTHESIS I

enrichment score



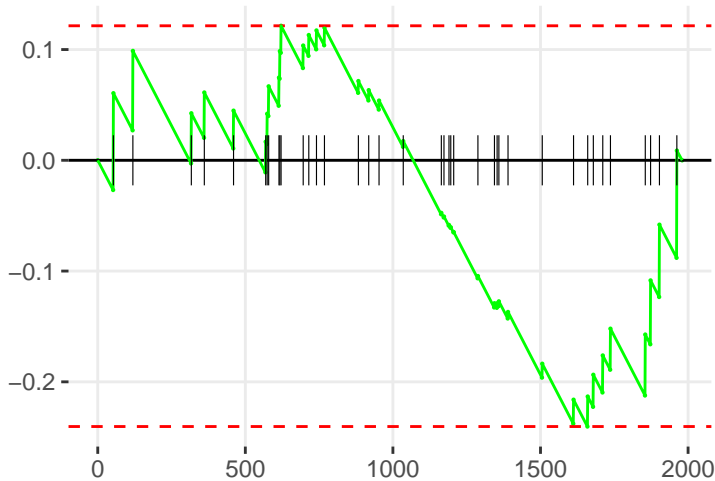
DOPAMINE DEGRADATION



OXIDATIVE ETHANOL DEGRADATION III

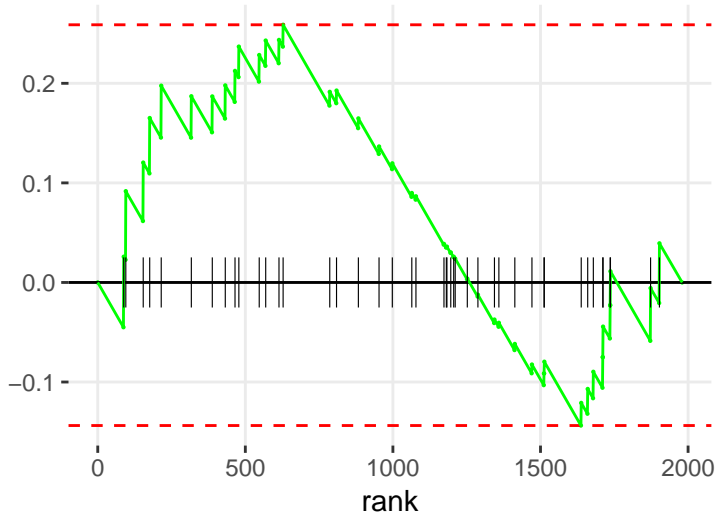
enrichment score

rank



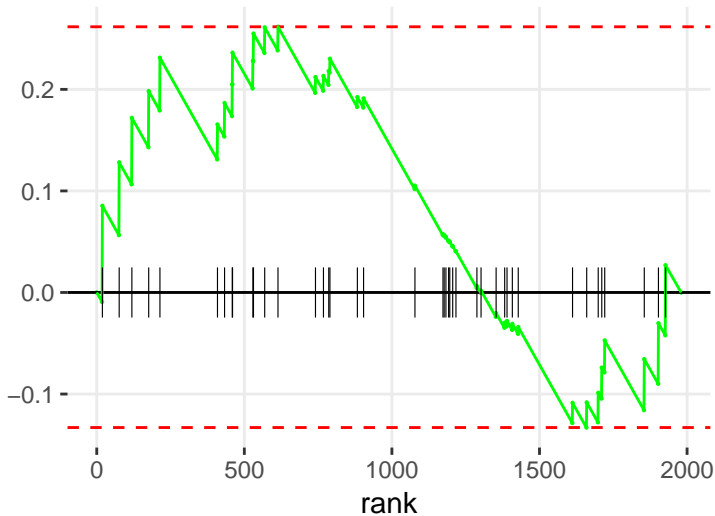
CITRULLINE BIOSYNTHESIS

enrichment score

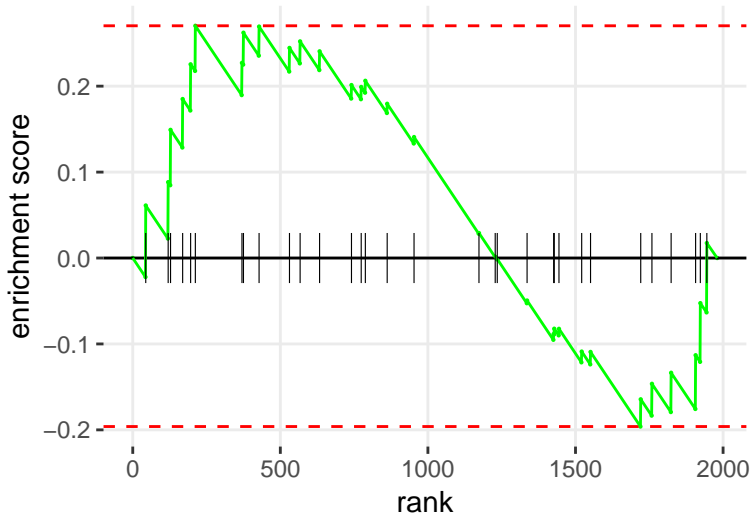


TCA CYCLE II (EUKARYOTIC)

enrichment score

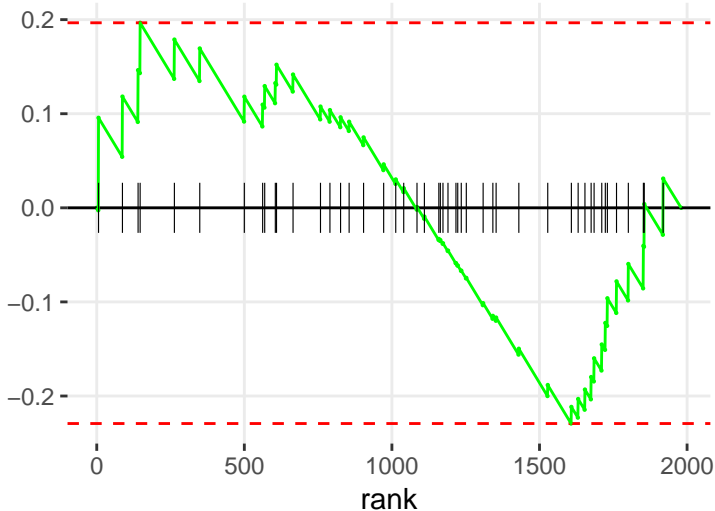


CHONDROITIN AND DERMATAN BIOSYNTHESIS

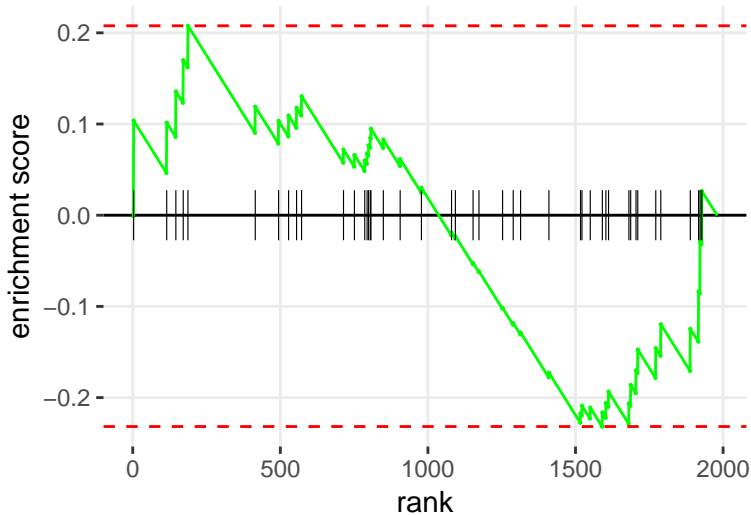


D-<IMYO</I>-INOSITOL (1,3,4)-TRISPHOSPHATE BIOSYNTHESIS

enrichment score

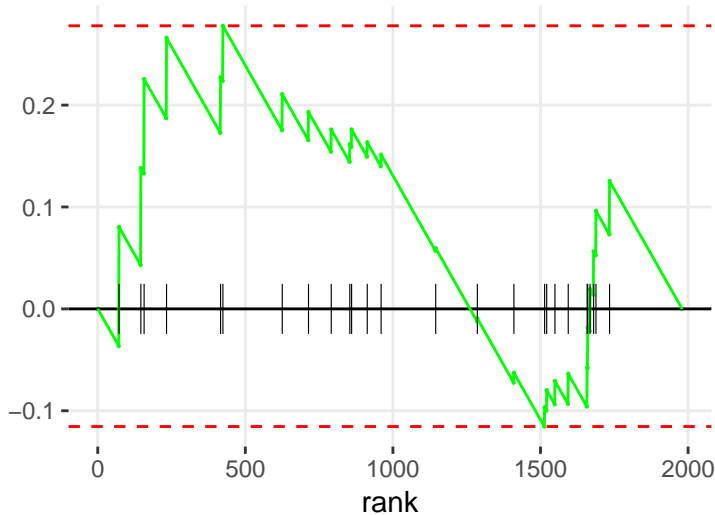


3-PHOSPHOINOSITIDE BIOSYNTHESIS

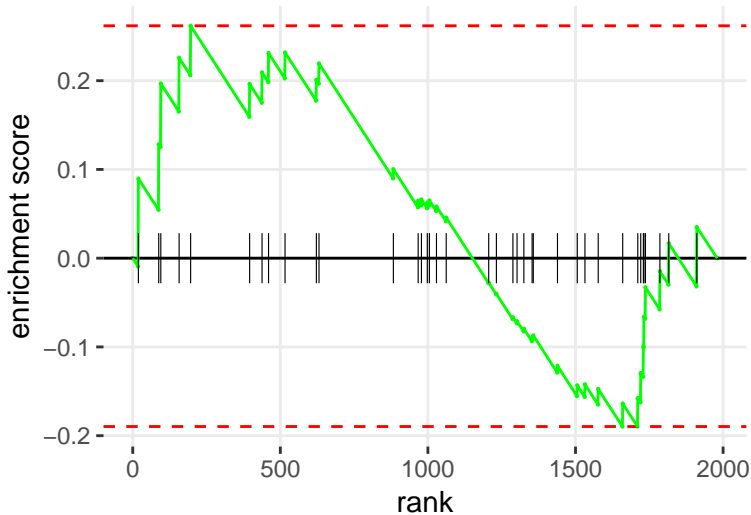


HEPARAN SULFATE BIOSYNTHESIS (LATE STAGES)

enrichment score

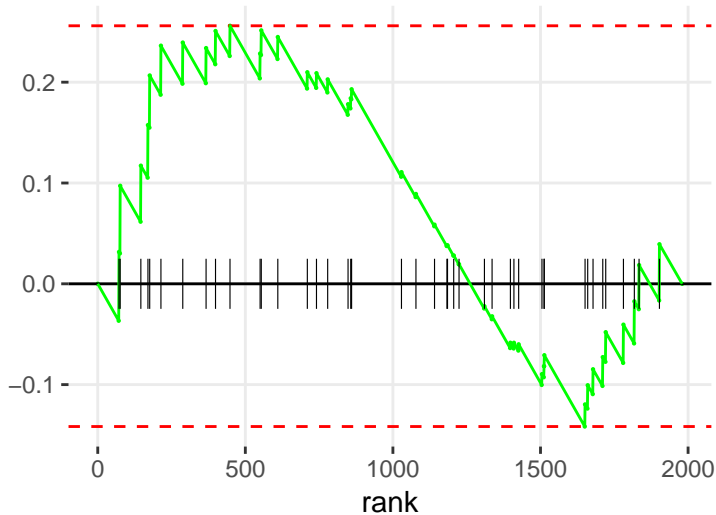


LEUKOTRIENE BIOSYNTHESIS



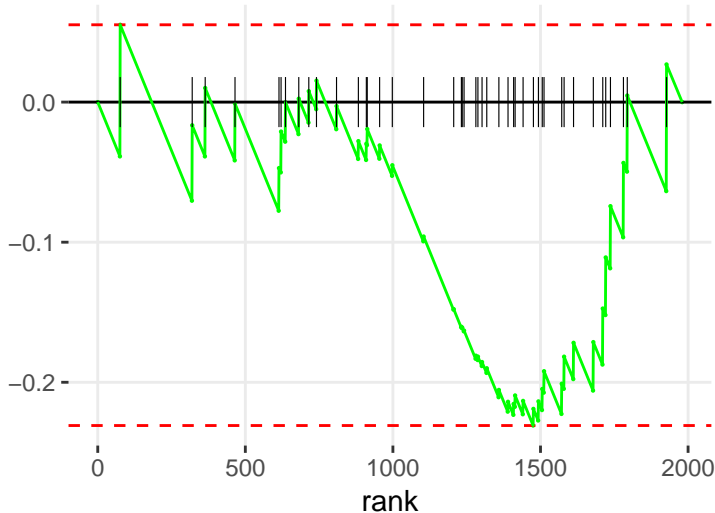
PREGNENOLONE BIOSYNTHESIS

enrichment score



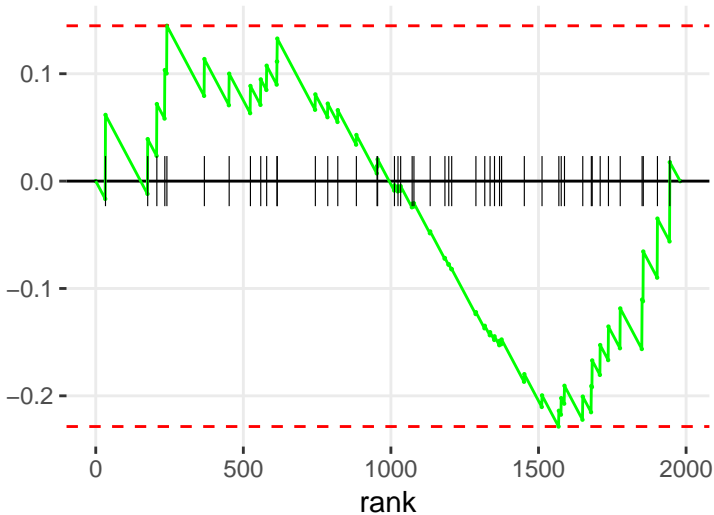
PHENYLALANINE DEGRADATION IV (MAMMALIAN, VIA SIDE CHAIN)

enrichment score



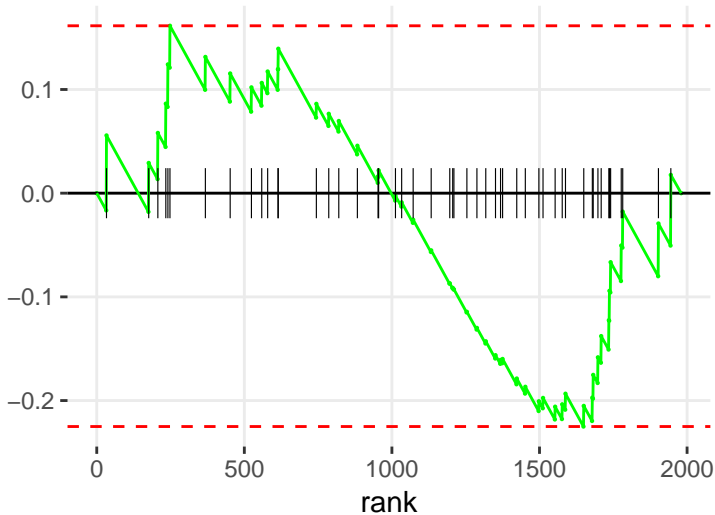
FOLATE TRANSFORMATIONS I

enrichment score

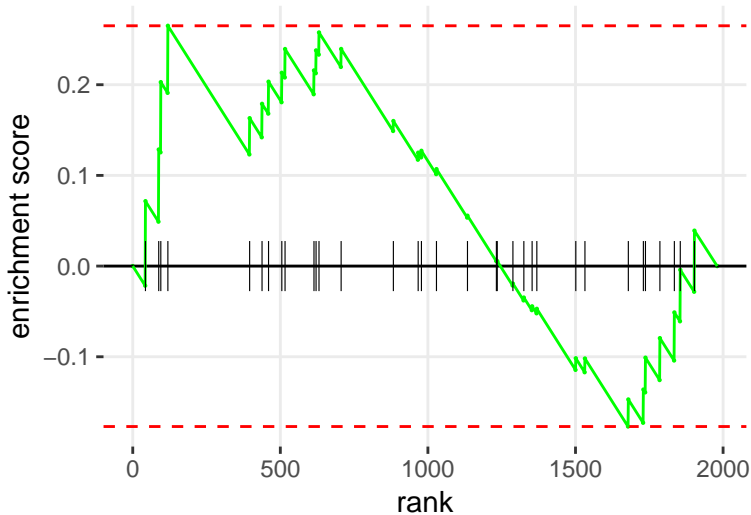


GLYCINE BETAIN DEGRADATION

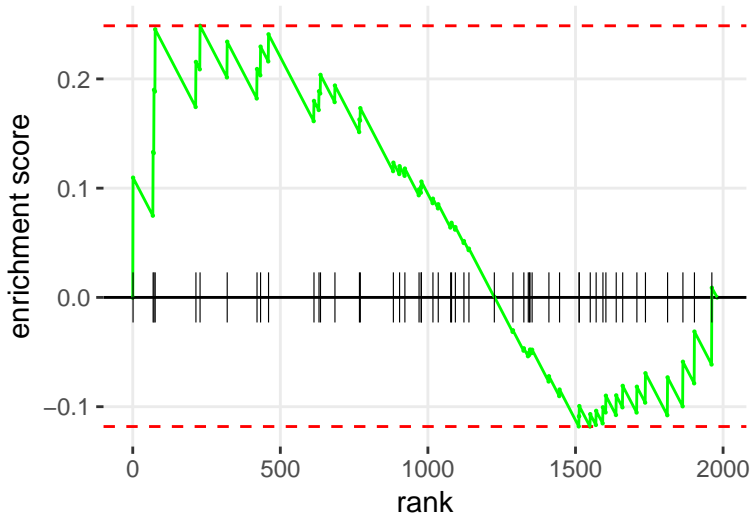
enrichment score



TETRAPYRROLE BIOSYNTHESIS II

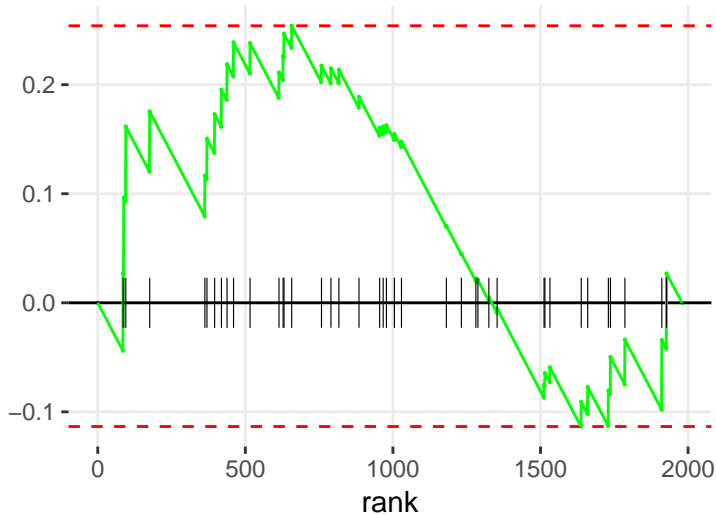


GLUTAMATE DEGRADATION III (VIA 4-AMINOBUTYRATE)



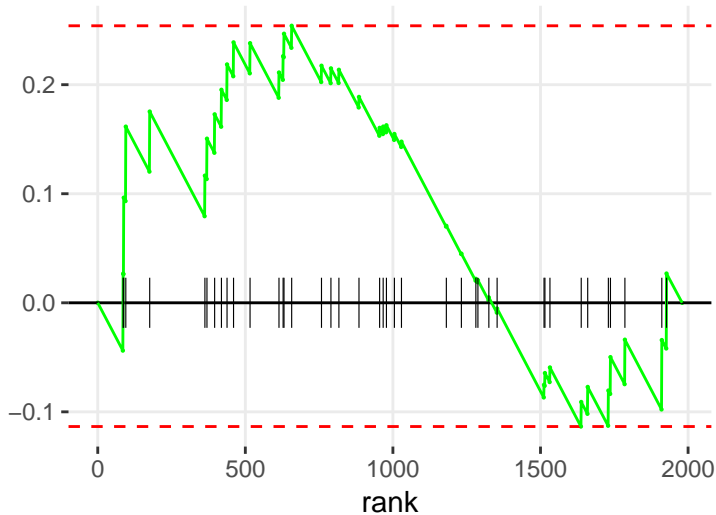
GLUTAMATE BIOSYNTHESIS II

enrichment score

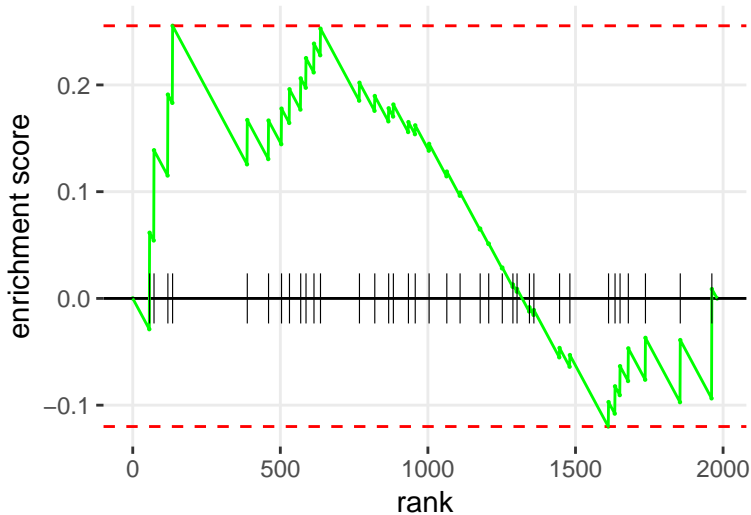


GLUTAMATE DEGRADATION X

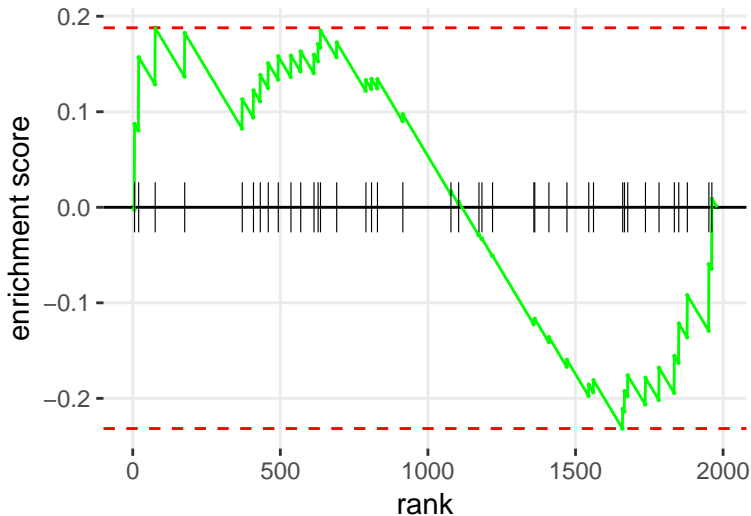
enrichment score



GALACTOSE DEGRADATION I (LELOIR PATHWAY)

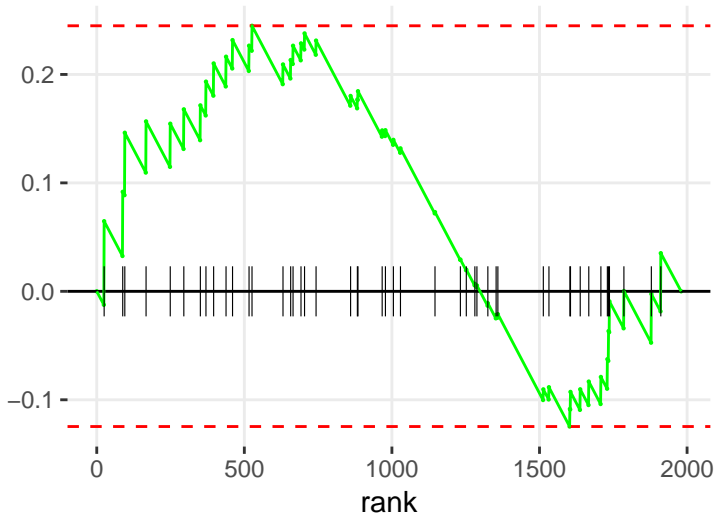


SALVAGE PATHWAYS OF PYRIMIDINE RIBONUCLEOTIDES

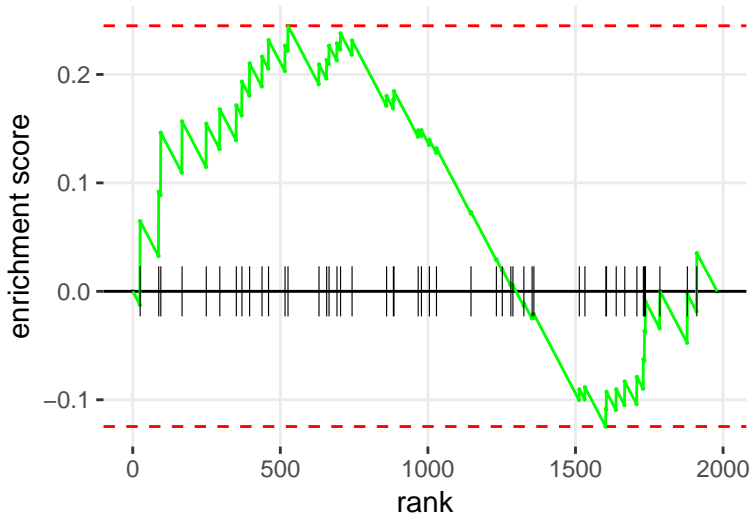


GDP-L-FUCOSE BIOSYNTHESIS II (FROM L-FUCOSE)

enrichment score

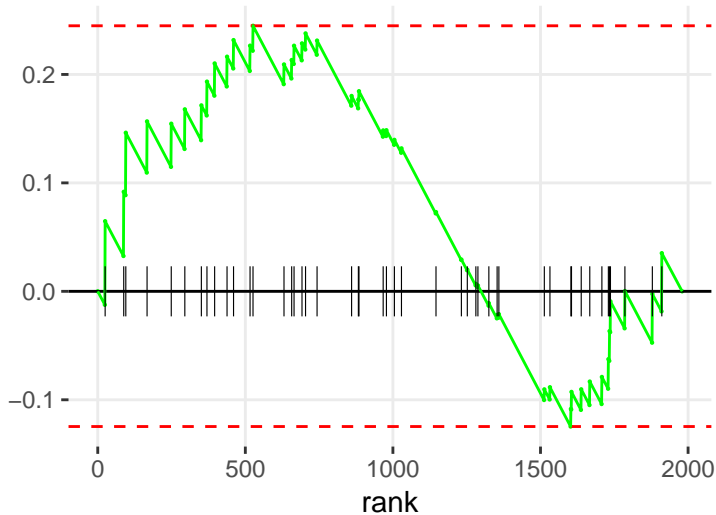


D-<IMYO</I-INOSITOL (1,4,5,6)-TETRAKISPHOSPHATE BIOSYNTHESIS

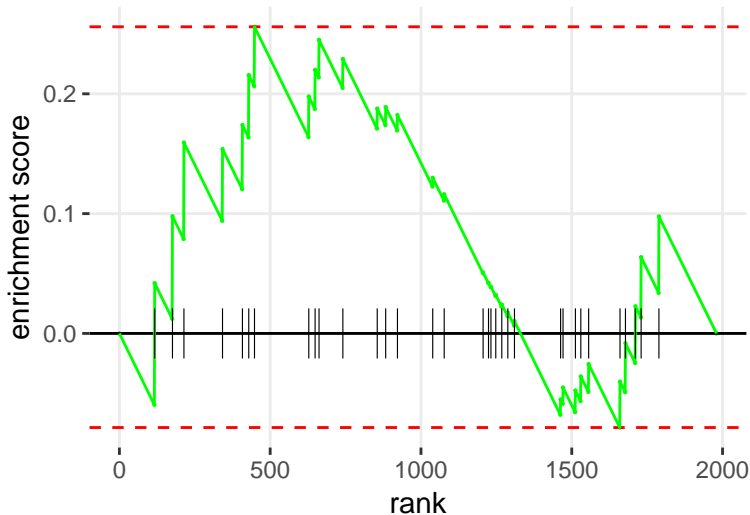


SULFITE OXIDATION IV

enrichment score



ACETONE DEGRADATION I (TO METHYLGLYOXAL)



BUPROPION DEGRADATION

enrichment score

0.2

0.1

0.0

0

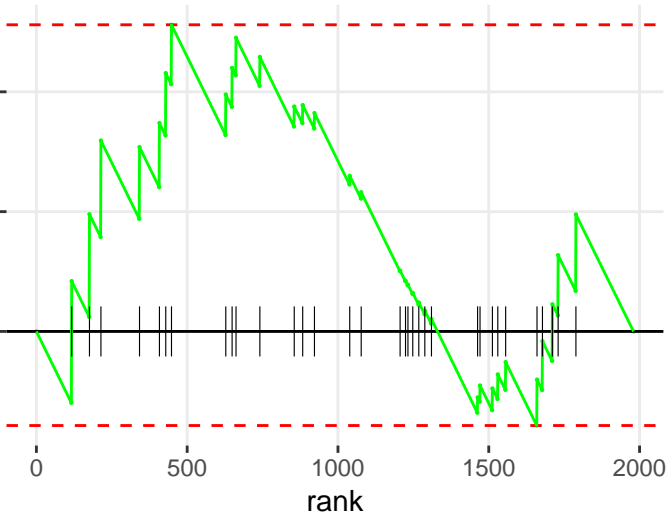
500

1000

1500

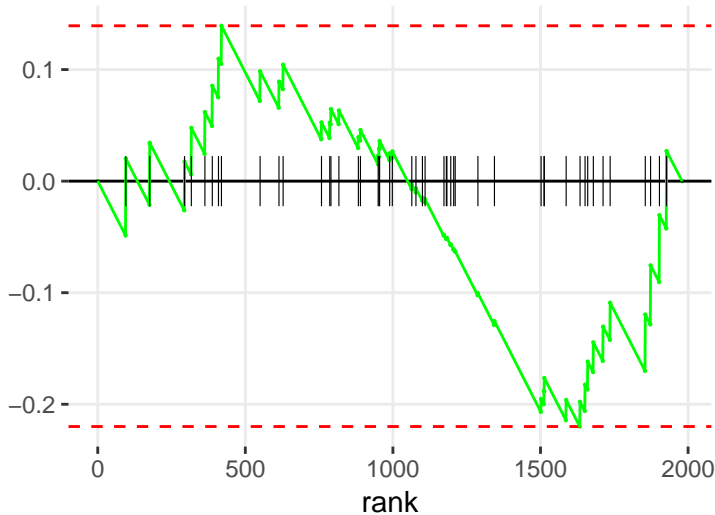
2000

rank

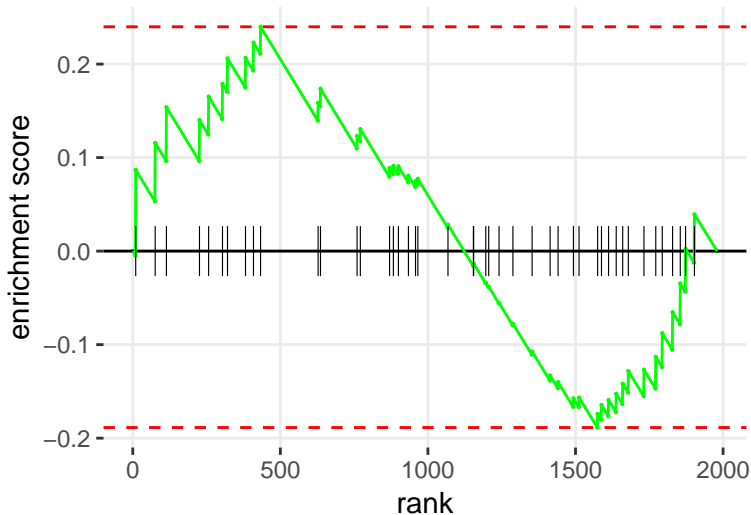


ARGININE BIOSYNTHESIS IV

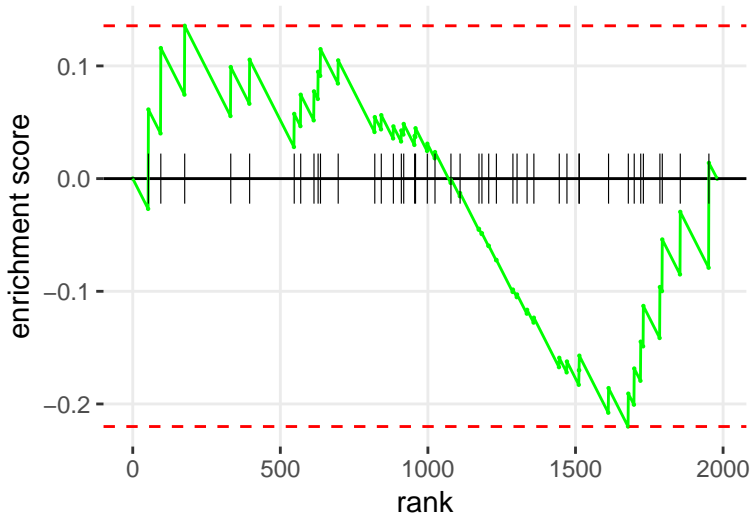
enrichment score



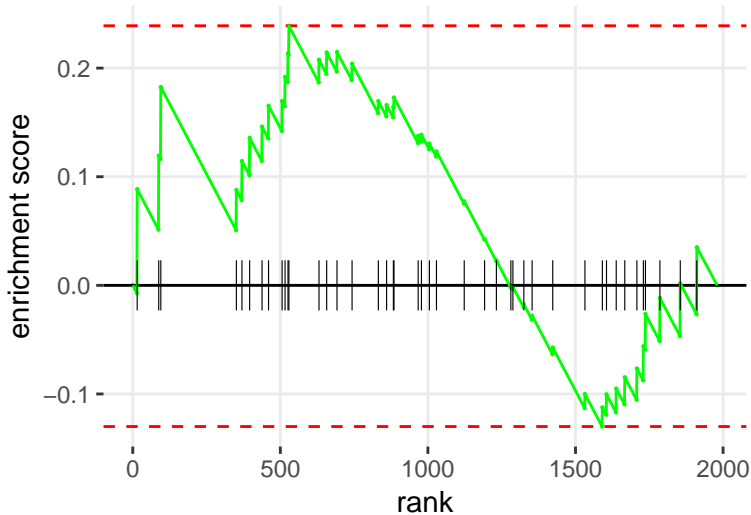
SELENOCYSTEINE BIOSYNTHESIS II (ARCHAEA AND EUKARYOTES)



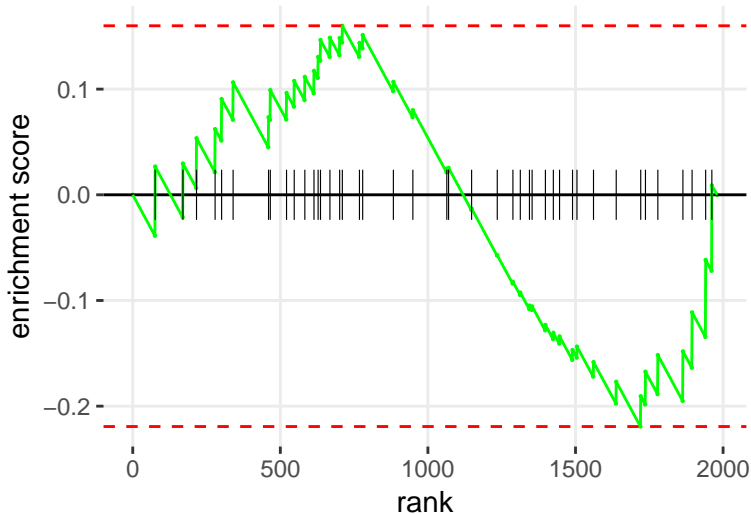
ADENINE AND ADENOSINE SALVAGE I



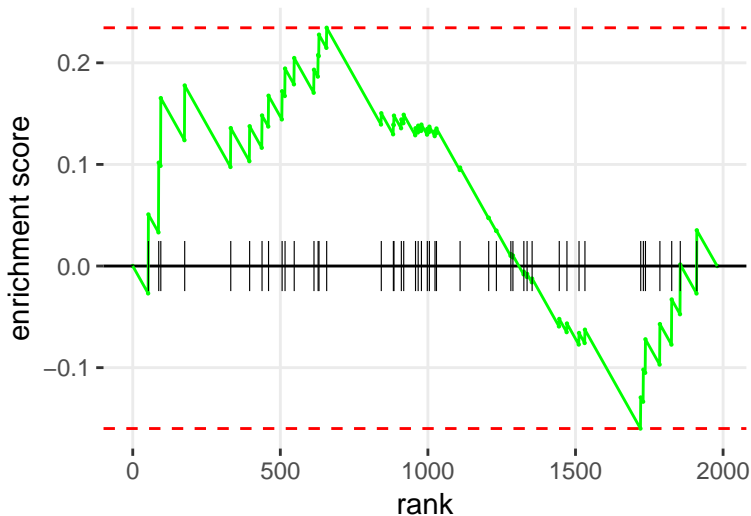
THIO-MOLYBDENUM COFACTOR BIOSYNTHESIS



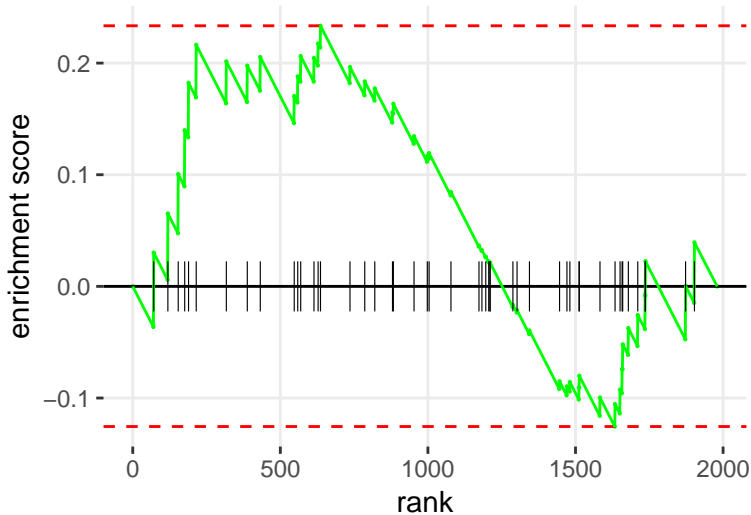
LIPOATE BIOSYNTHESIS AND INCORPORATION II



PURINE RIBONUCLEOSIDES DEGRADATION TO RIBOSE-1-PHOSPHATE



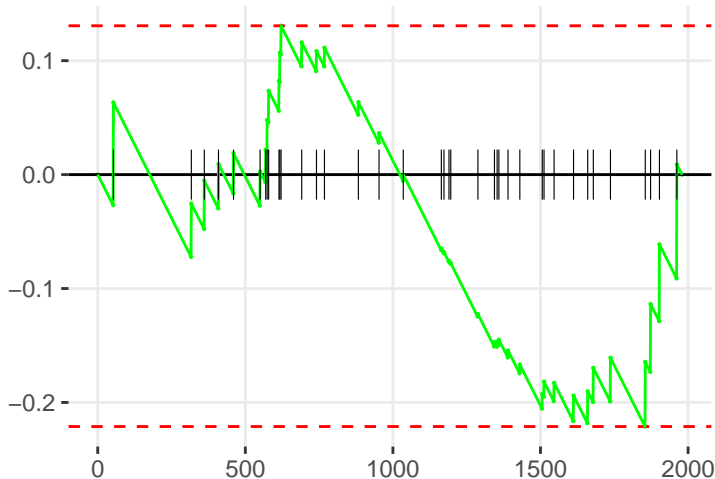
ARGININE DEGRADATION VI (ARGINASE 2 PATHWAY)



HISTAMINE DEGRADATION

enrichment score

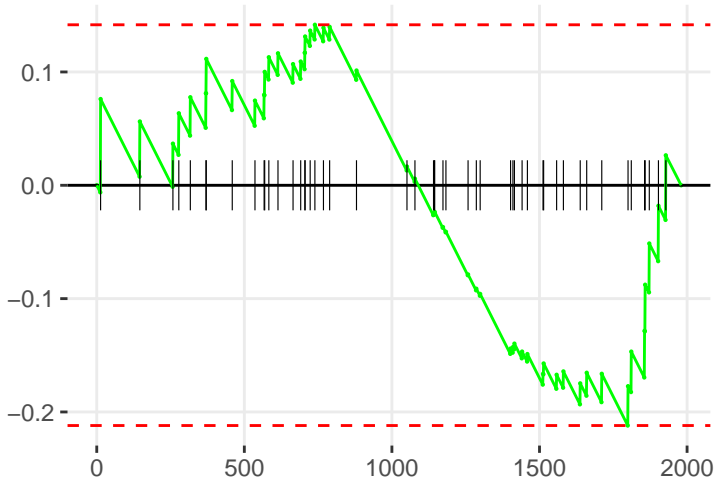
rank



CHONDROITIN SULFATE DEGRADATION (METAZOA)

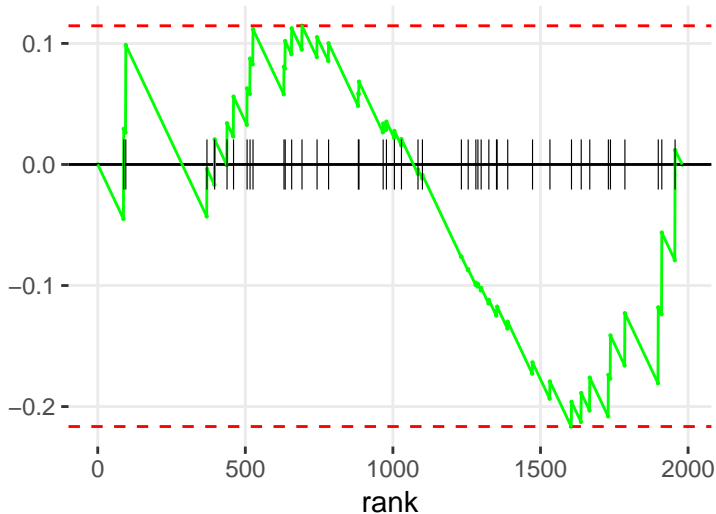
enrichment score

rank



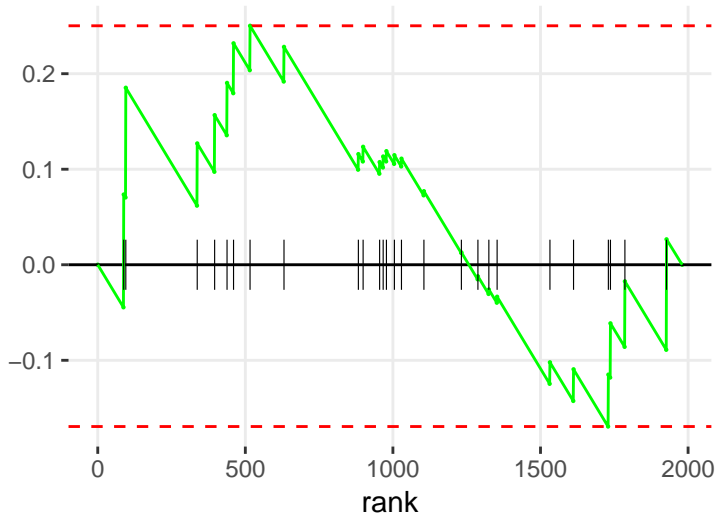
THIOREDOXIN PATHWAY

enrichment score



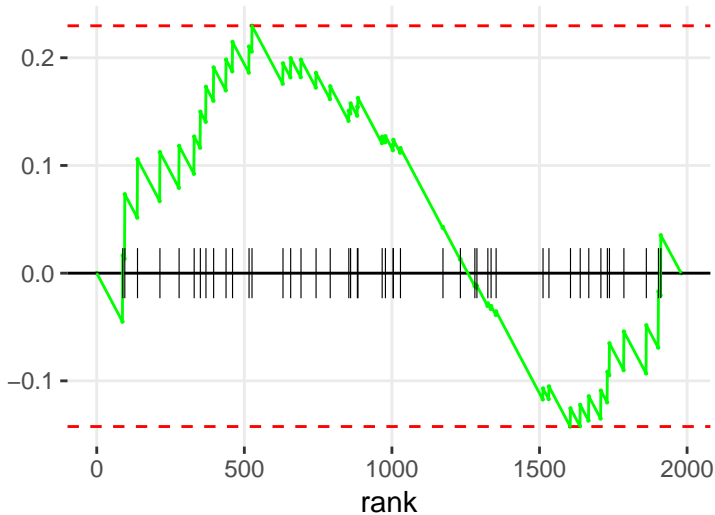
GLYCEROL DEGRADATION I

enrichment score



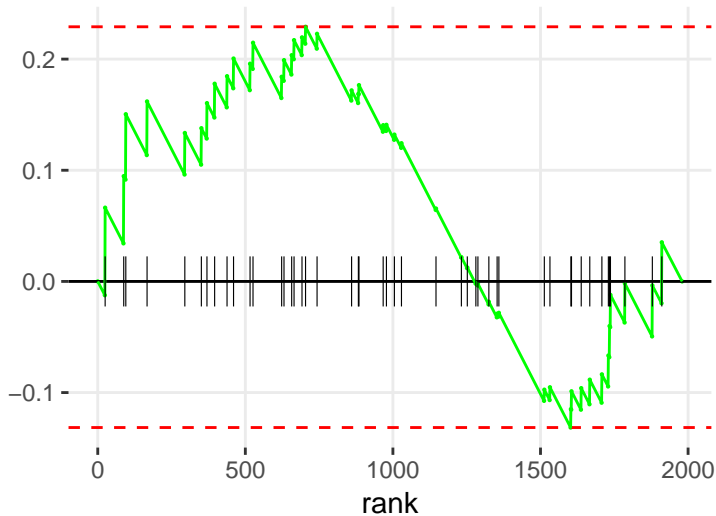
URIDINE-5'-PHOSPHATE BIOSYNTHESIS

enrichment score

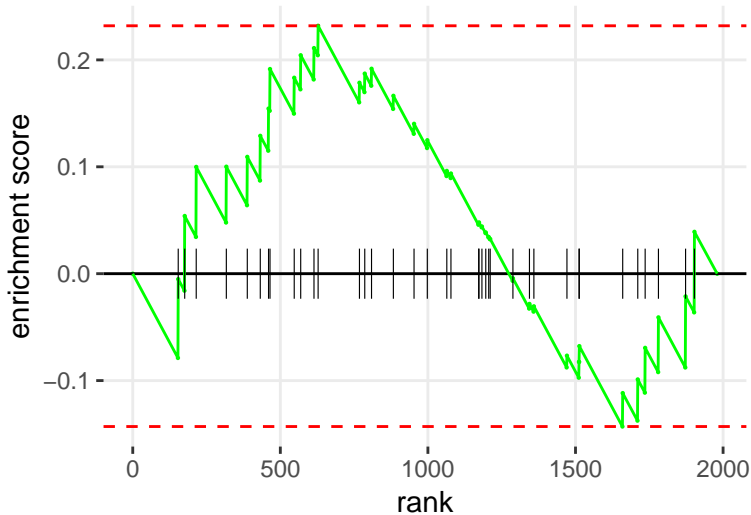


DIPHTHAMIDE BIOSYNTHESIS

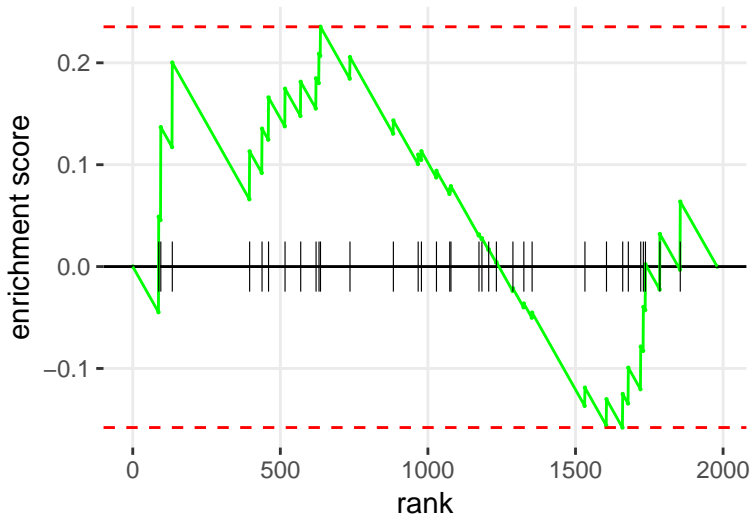
enrichment score



ARGININE DEGRADATION I (ARGINASE PATHWAY)

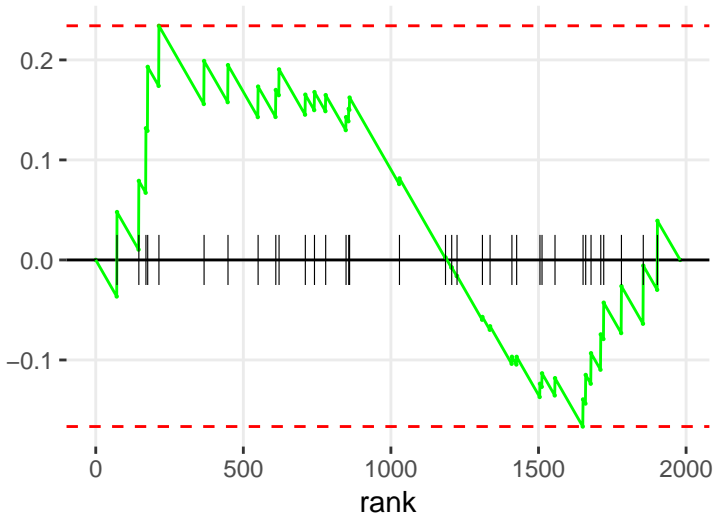


OLEATE BIOSYNTHESIS II (ANIMALS)

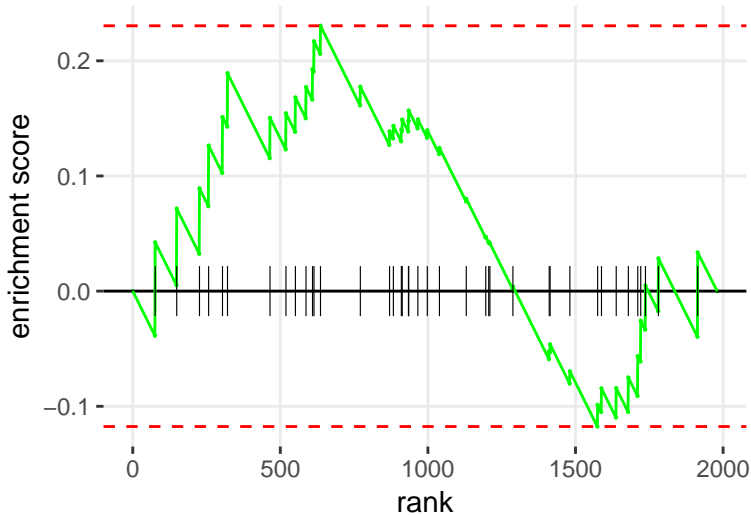


MINERALOCORTICOID BIOSYNTHESIS

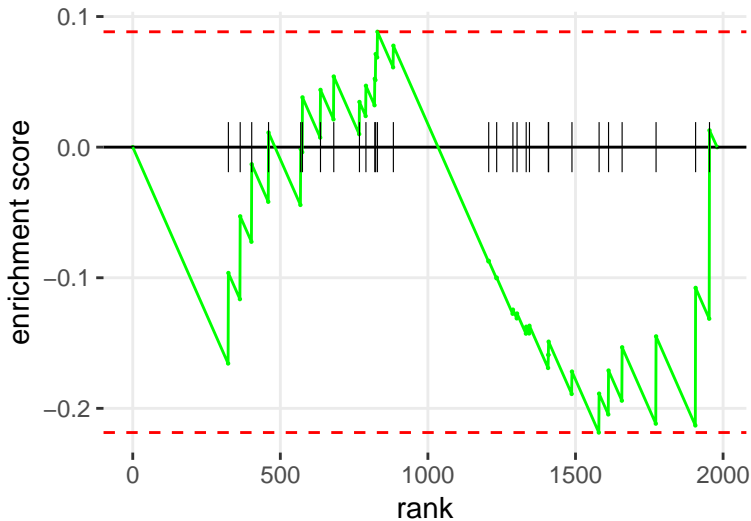
enrichment score



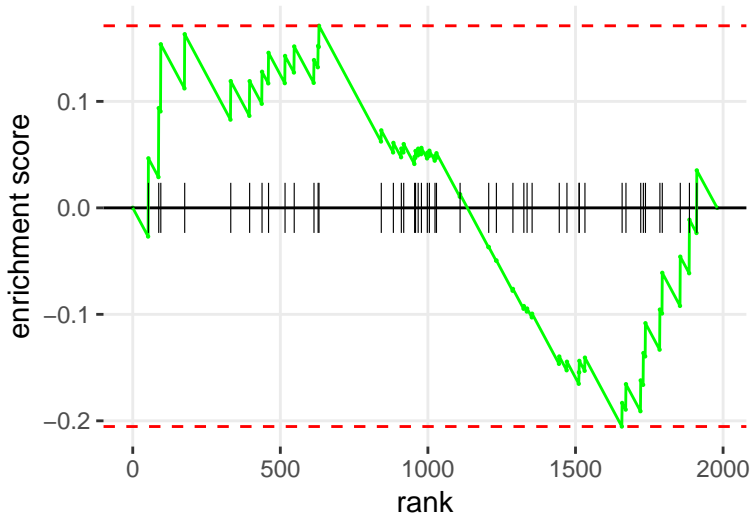
5-AMINOIMIDAZOLE RIBONUCLEOTIDE BIOSYNTHESIS I



TETRAHYDROBIOPTERIN BIOSYNTHESIS I

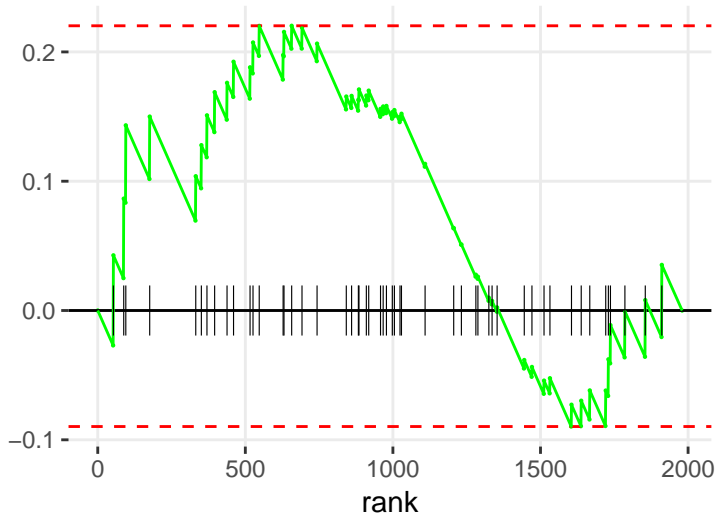


GUANINE AND GUANOSINE SALVAGE I

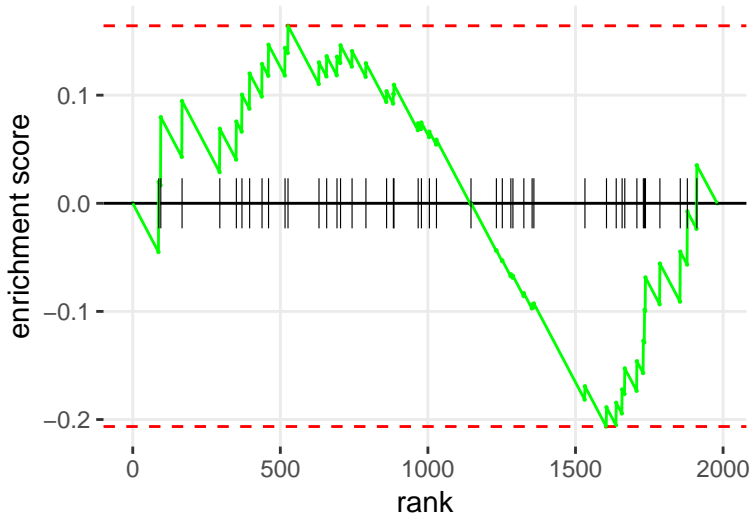


XANTHINE AND XANTHOSINE SALVAGE

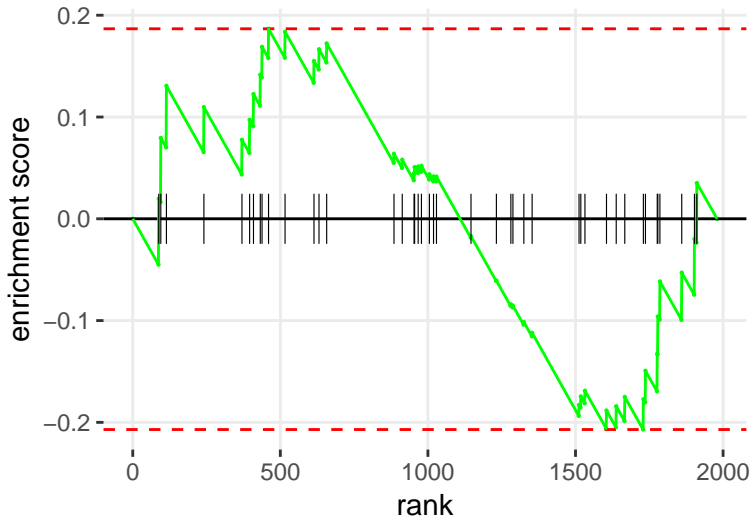
enrichment score



NAD PHOSPHORYLATION AND DEPHOSPHORYLATION

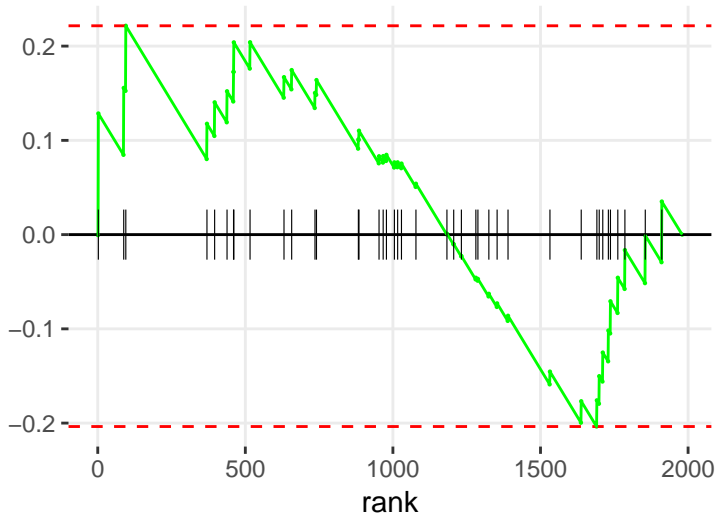


ACETYL-COA BIOSYNTHESIS III (FROM CITRATE)



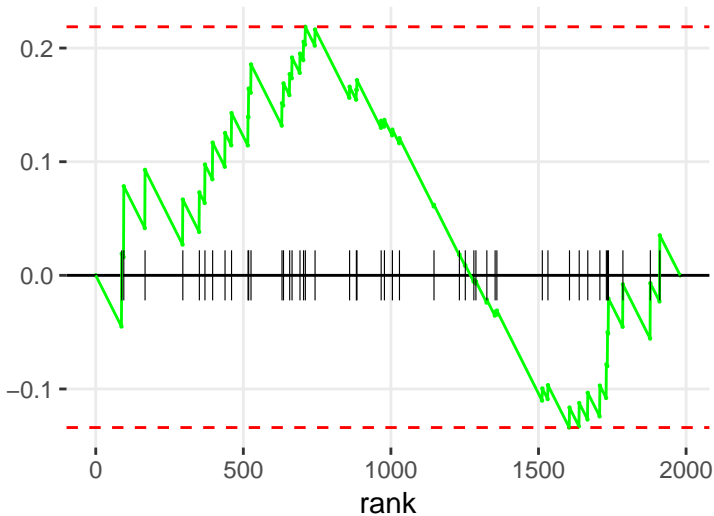
MITOCHONDRIAL L-CARNITINE SHUTTLE PATHWAY

enrichment score



L-DOPACHROME BIOSYNTHESIS

enrichment score



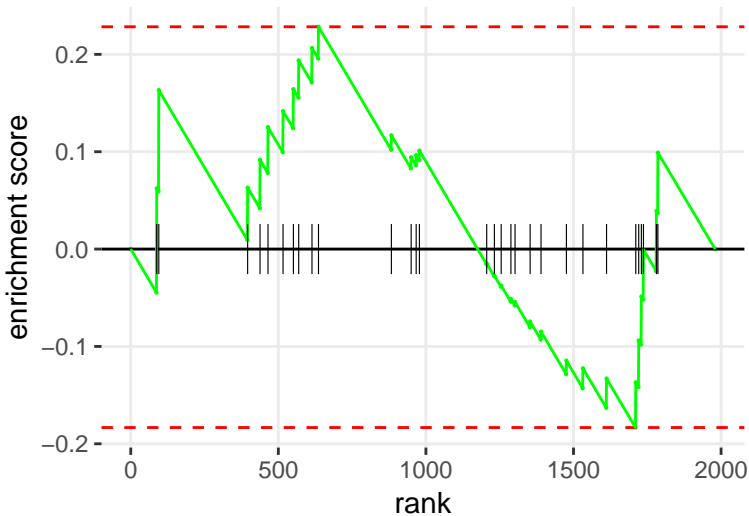
D-MANNOSE DEGRADATION

enrichment score

0.2
0.1
0.0
-0.1
-0.2

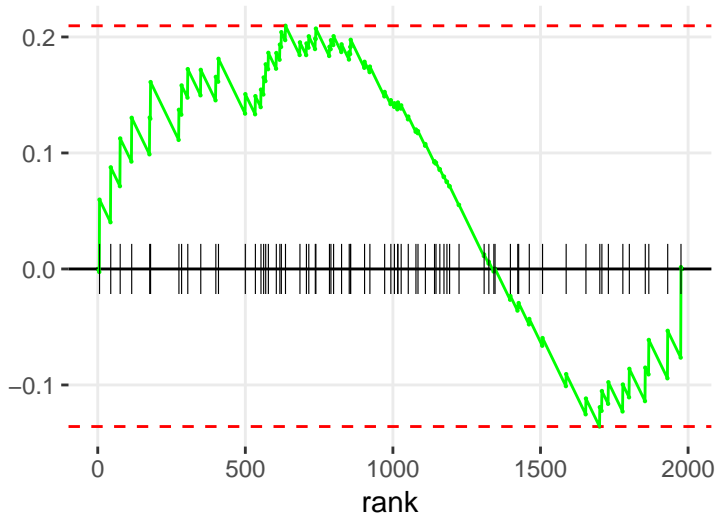
rank

0 500 1000 1500 2000



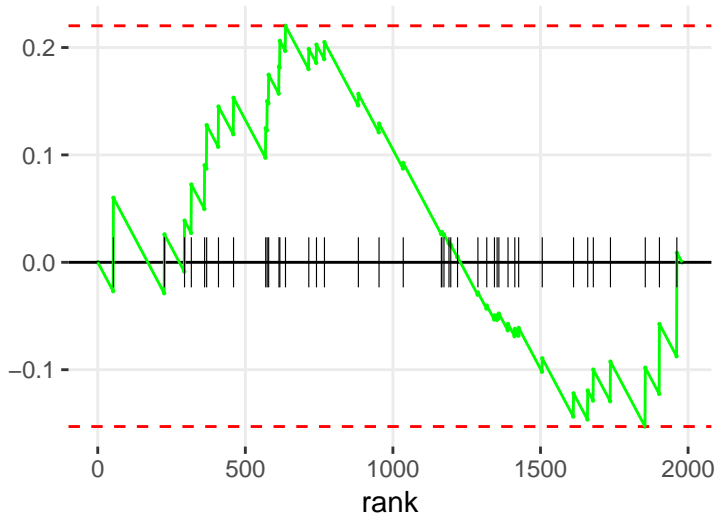
CATECHOLAMINE BIOSYNTHESIS

enrichment score



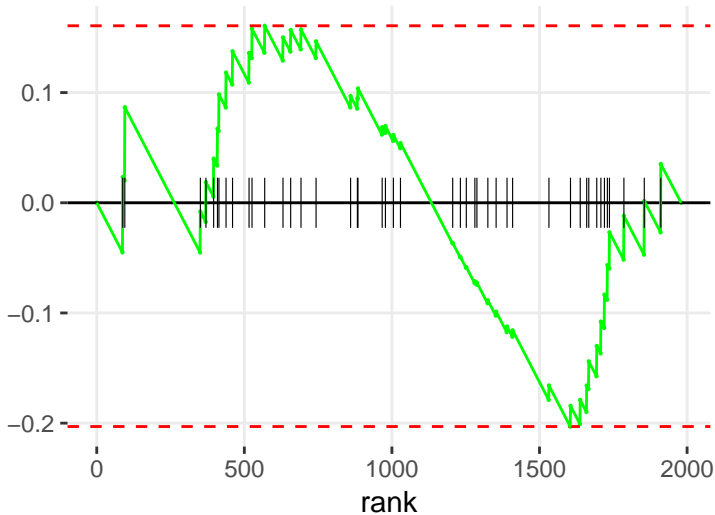
NORADRENALINE AND ADRENALINE DEGRADATION

enrichment score



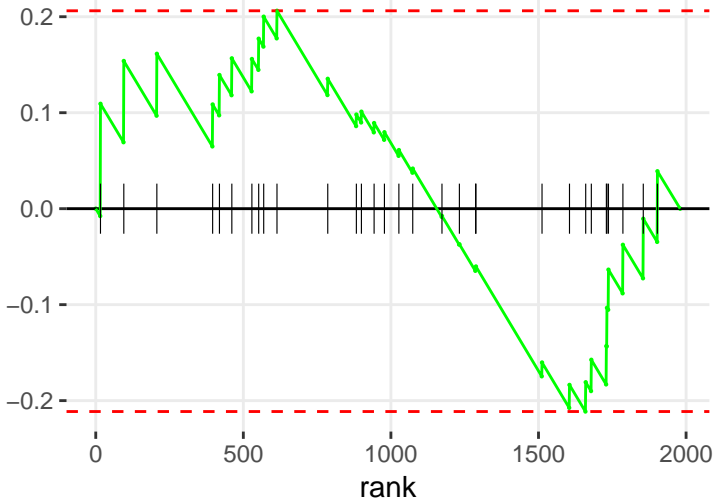
GLUTATHIONE BIOSYNTHESIS

enrichment score



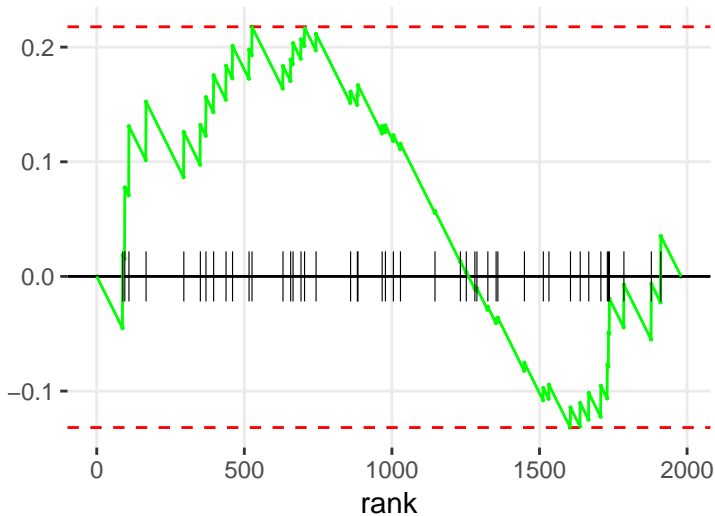
CERAMIDE BIOSYNTHESIS

enrichment score



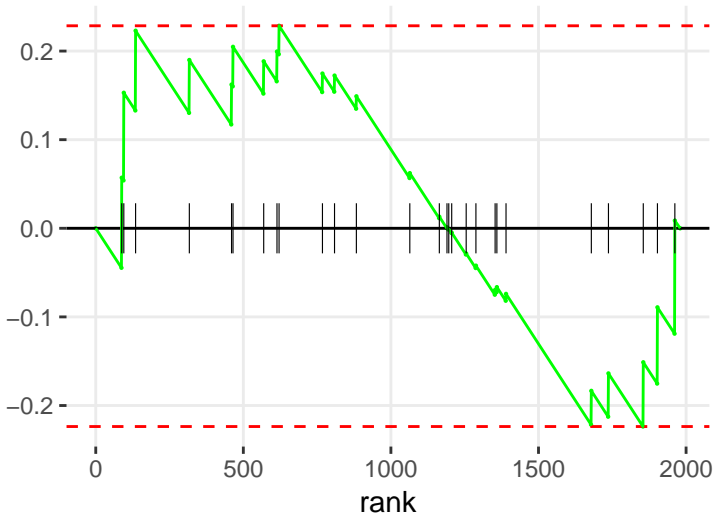
COENZYME A BIOSYNTHESIS

enrichment score



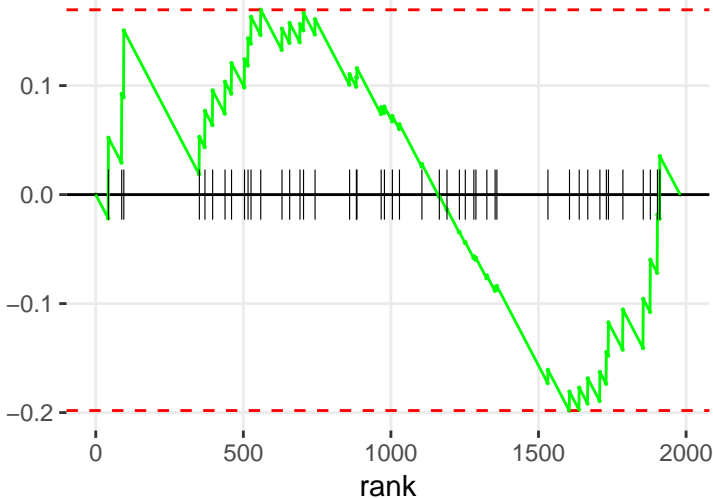
RETINOATE BIOSYNTHESIS I

enrichment score



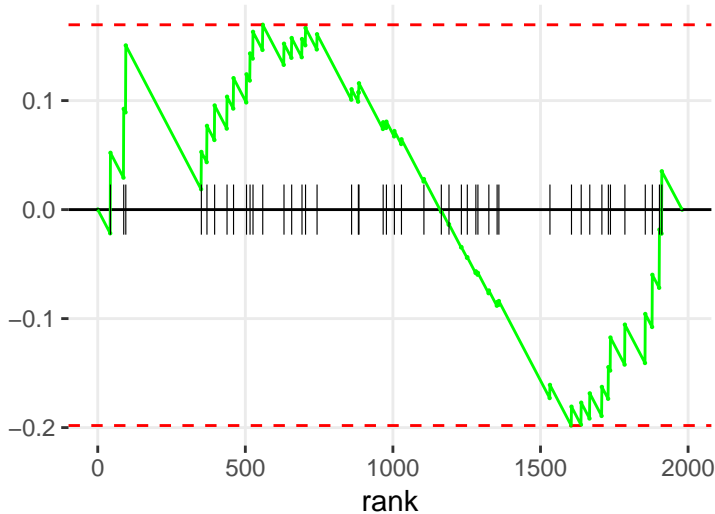
ALANINE BIOSYNTHESIS II

enrichment score



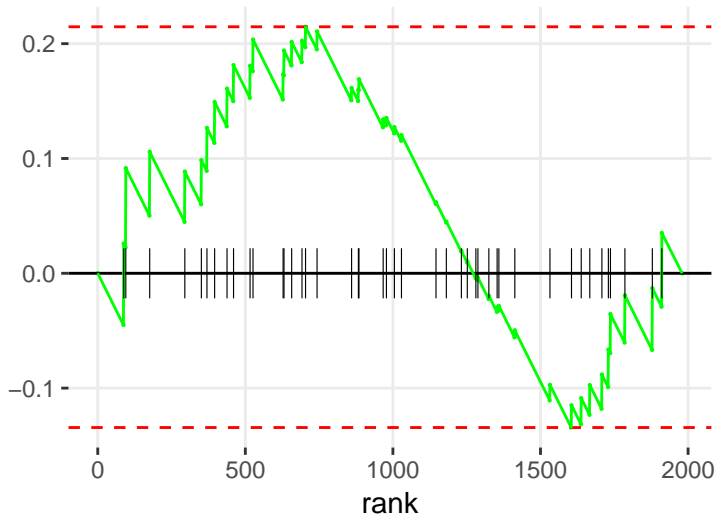
ALANINE DEGRADATION III

enrichment score



GLUTAMINE DEGRADATION I

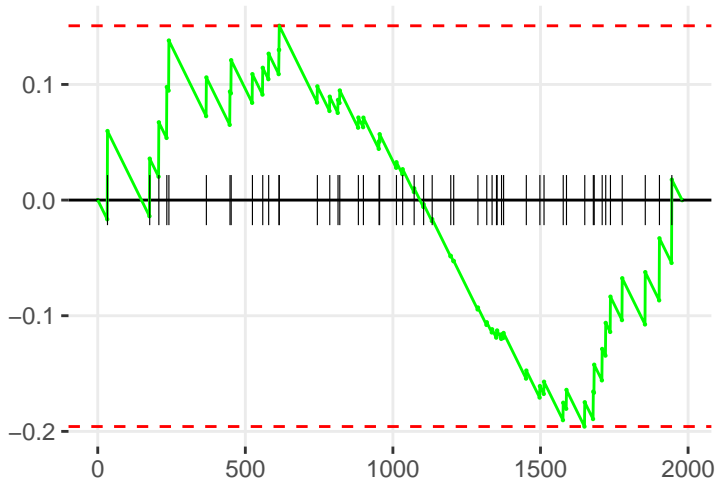
enrichment score



DTMP <IDE NOVO</I> BIOSYNTHESIS

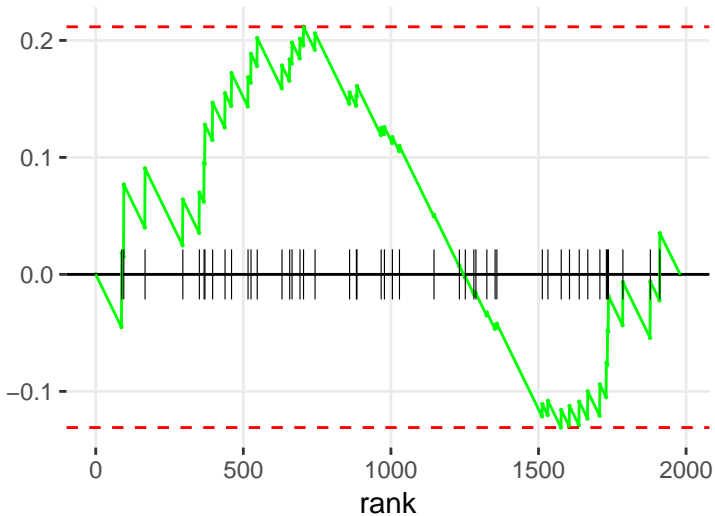
enrichment score

rank



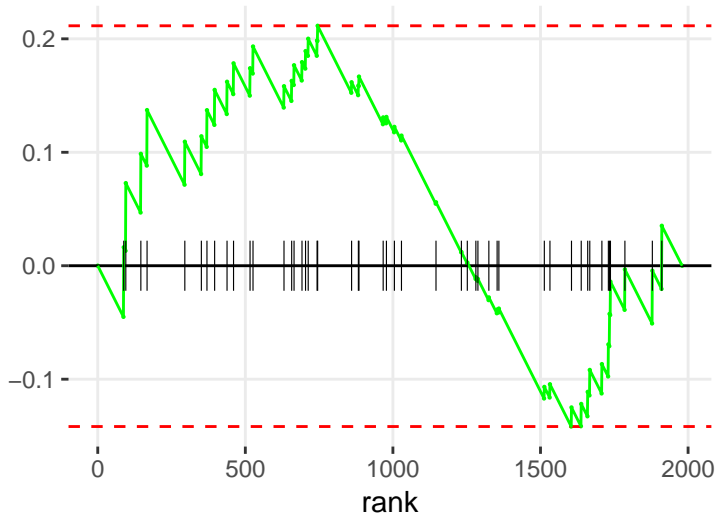
NAD BIOSYNTHESIS III

enrichment score

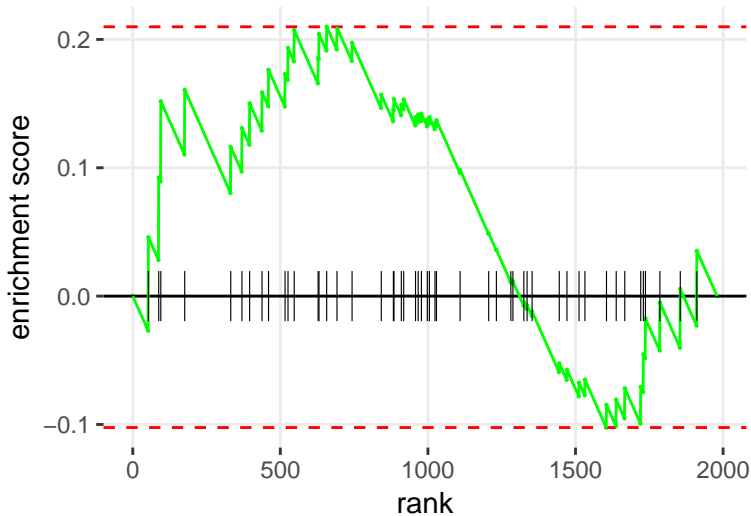


PHOSPHATIDYLETHANOLAMINE BIOSYNTHESIS III

enrichment score

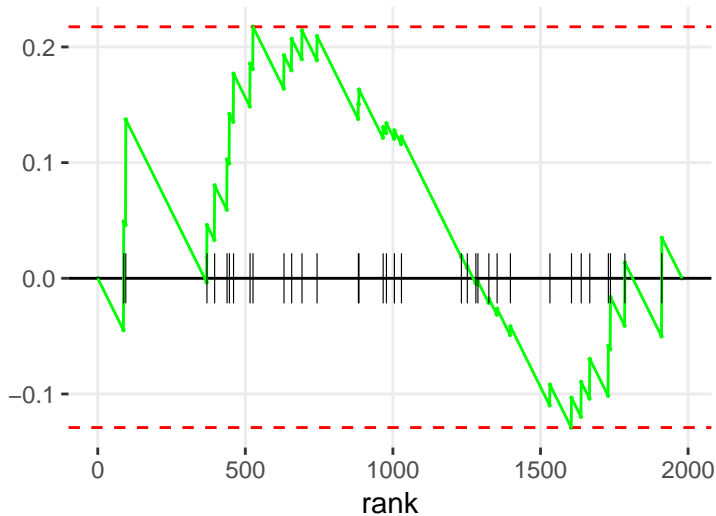


ARSENATE DETOXIFICATION I (GLUTAREDOXIN)



TAURINE BIOSYNTHESIS

enrichment score



L-CYSTEINE DEGRADATION I

enrichment score

0.2
0.1
0.0
-0.1

0

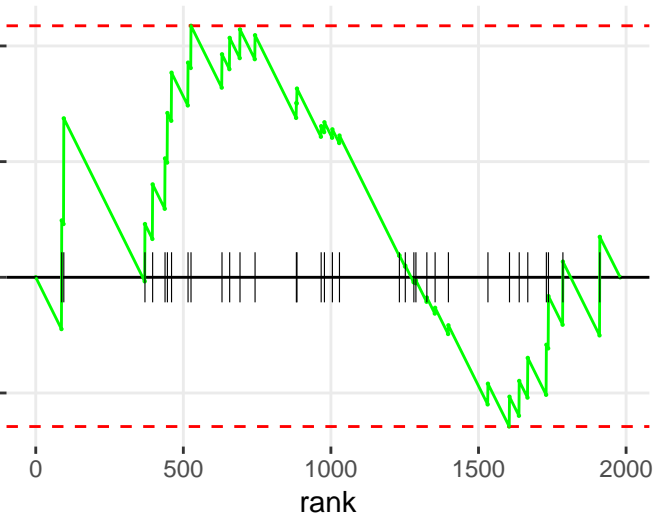
500

1000

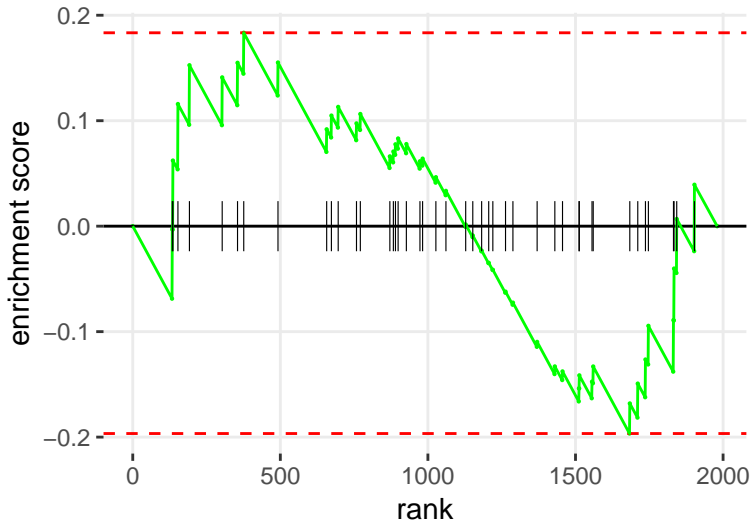
1500

2000

rank

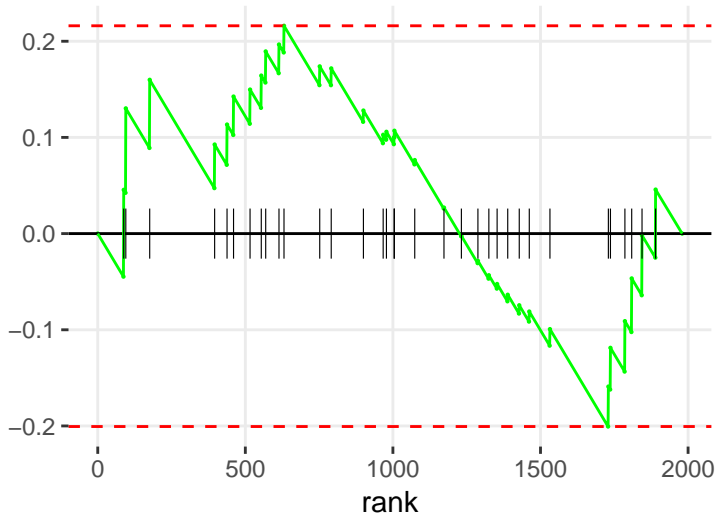


4-AMINOBUTYRATE DEGRADATION I

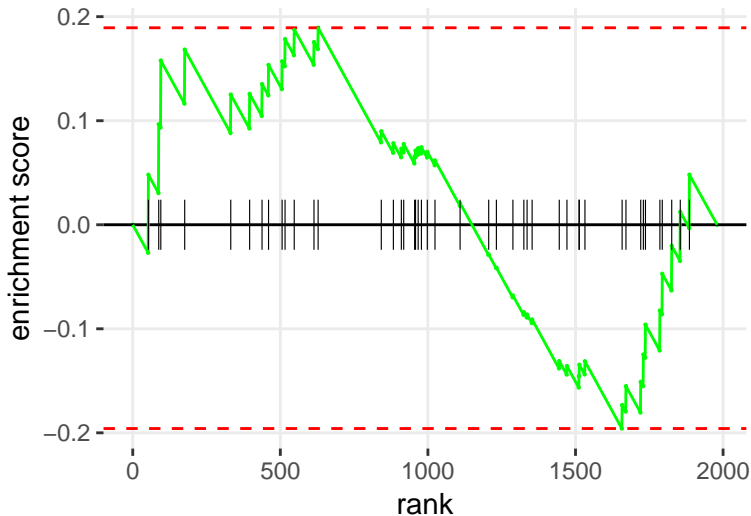


TRIACYLGLYCEROL DEGRADATION

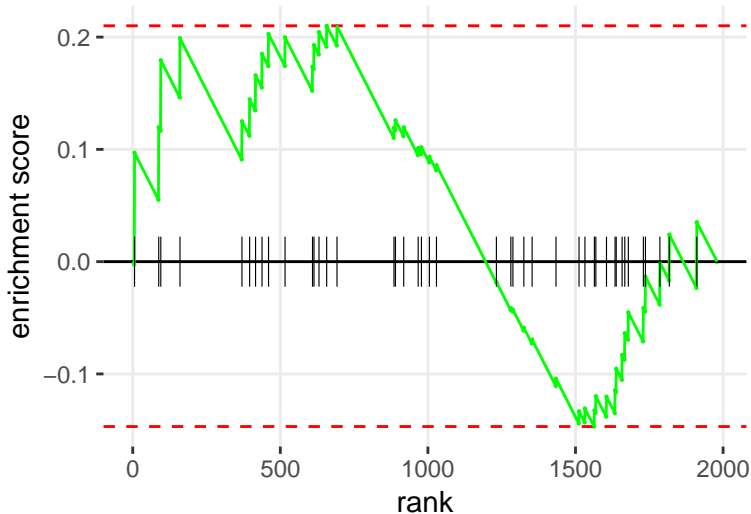
enrichment score



ADENINE AND ADENOSINE SALVAGE III

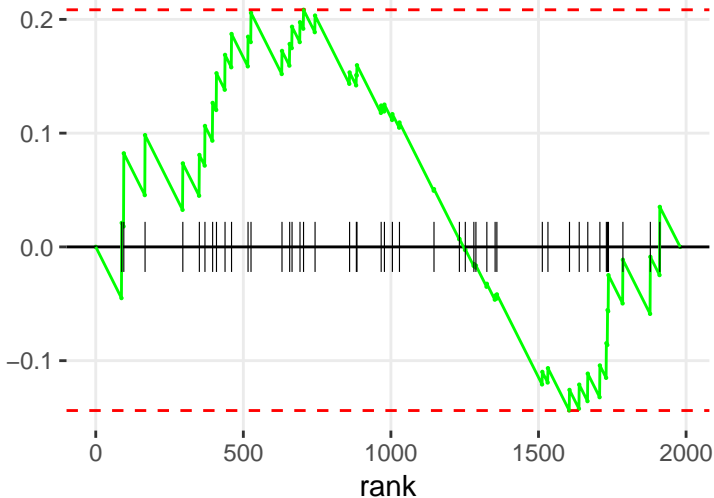


<IS</I-METHYL-5-THIO-&ALPHA;-D-RIBOSE 1-PHOSPHATE DEGRADATION

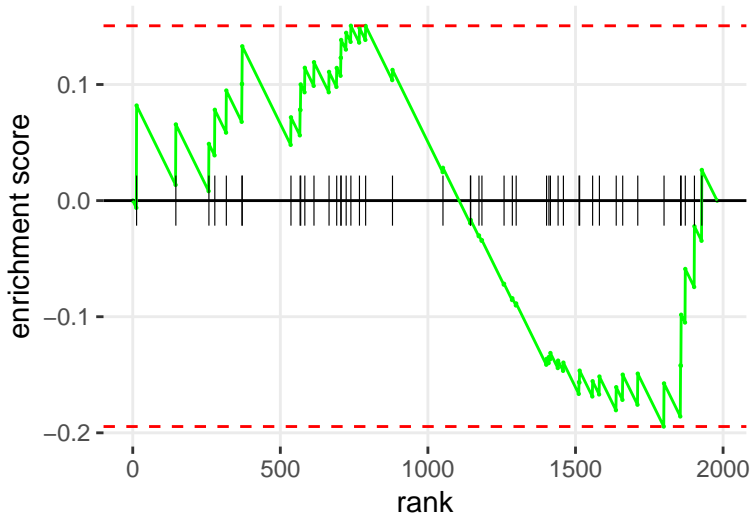


GLYCINE DEGRADATION (CREATINE BIOSYNTHESIS)

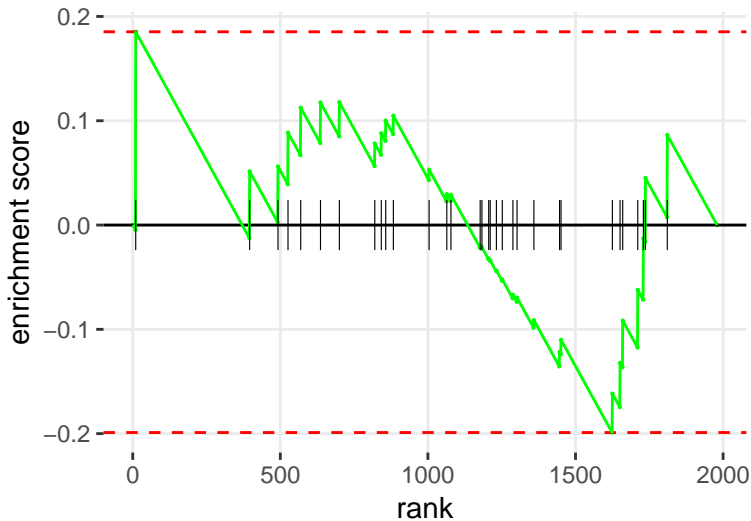
enrichment score



DERMATAN SULFATE DEGRADATION (METAZOA)



PHOSPHATIDYLCHOLINE BIOSYNTHESIS I



PHOSPHOLIPASES

enrichment score

0.2
0.1
0.0
-0.1

0

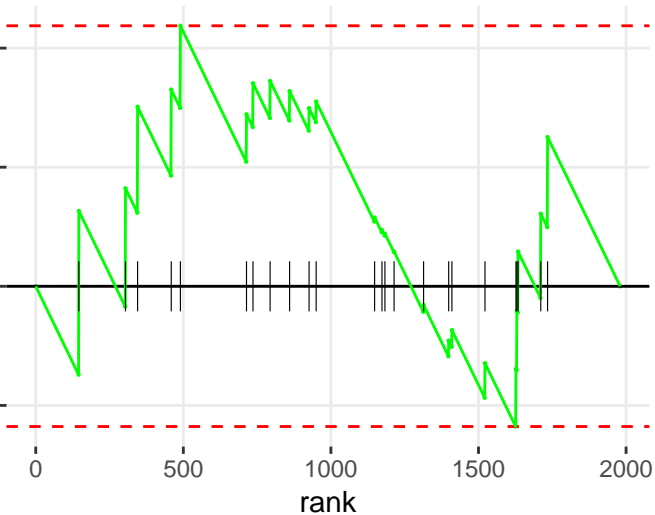
500

1000

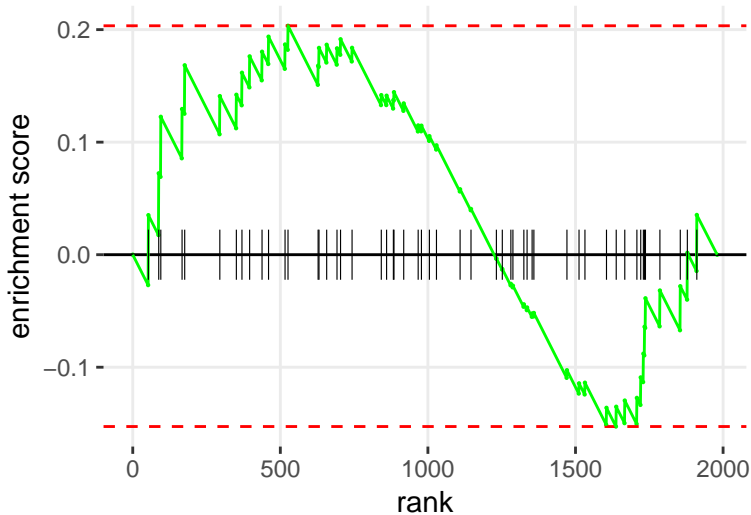
1500

2000

rank

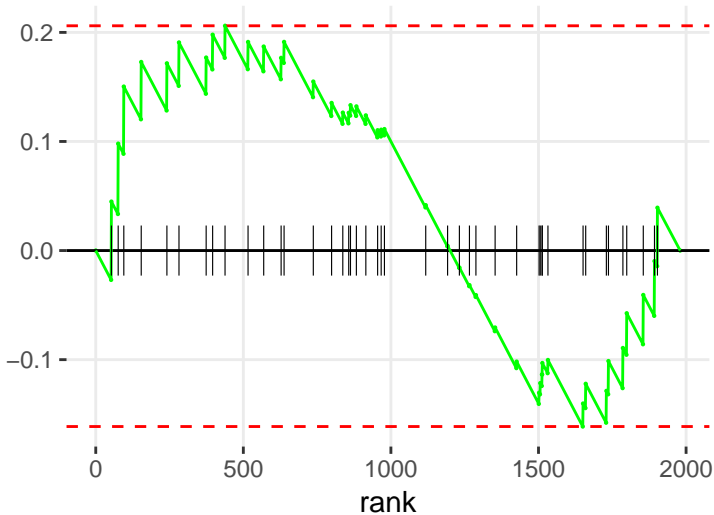


<IS</I-METHYL-5'-THIOADENOSINE DEGRADATION II

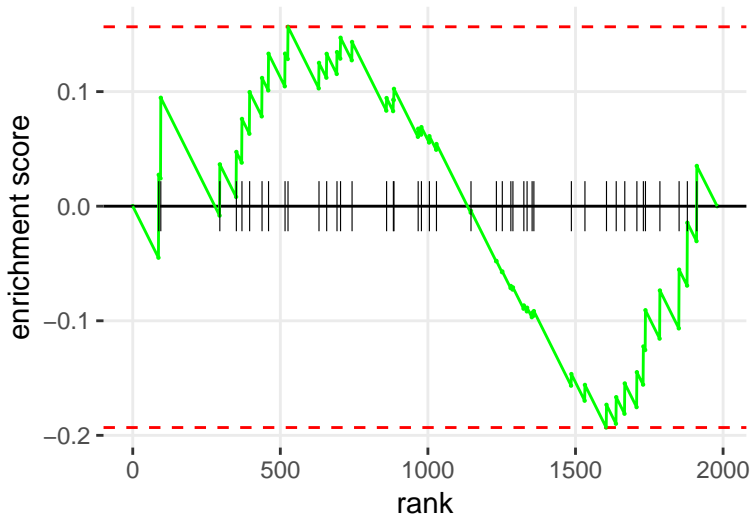


ZYMOSTEROL BIOSYNTHESIS

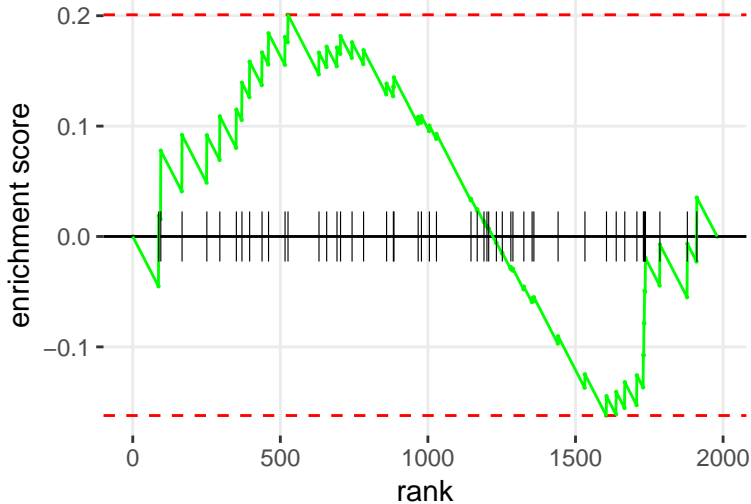
enrichment score



METHIONINE SALVAGE II (MAMMALIA)

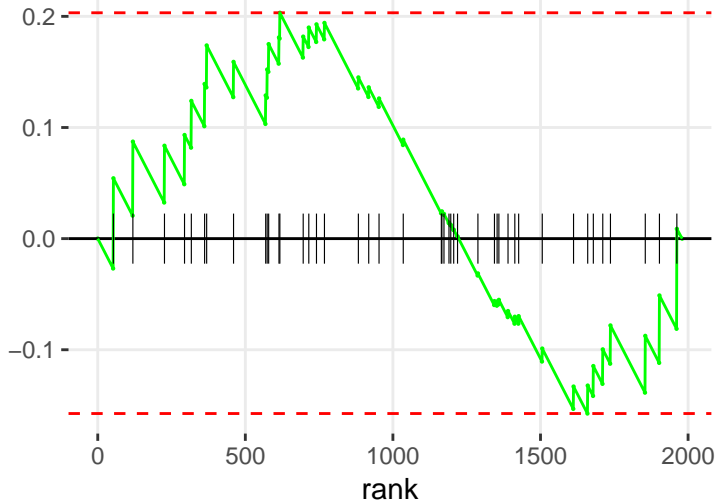


SORBITOL DEGRADATION I

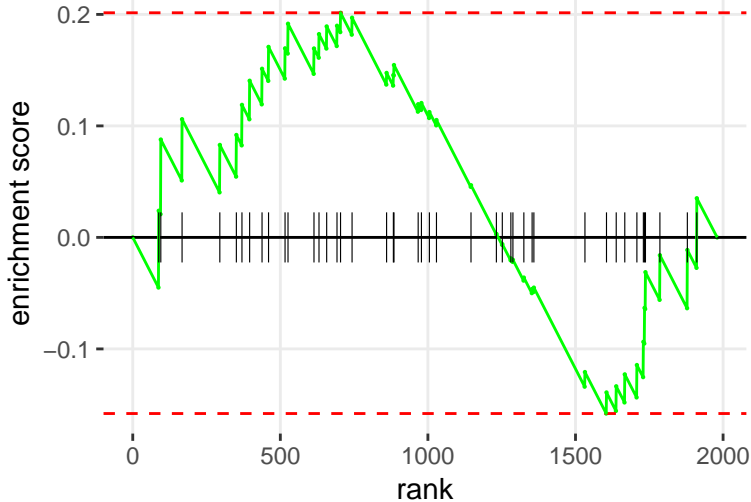


ETHANOL DEGRADATION II

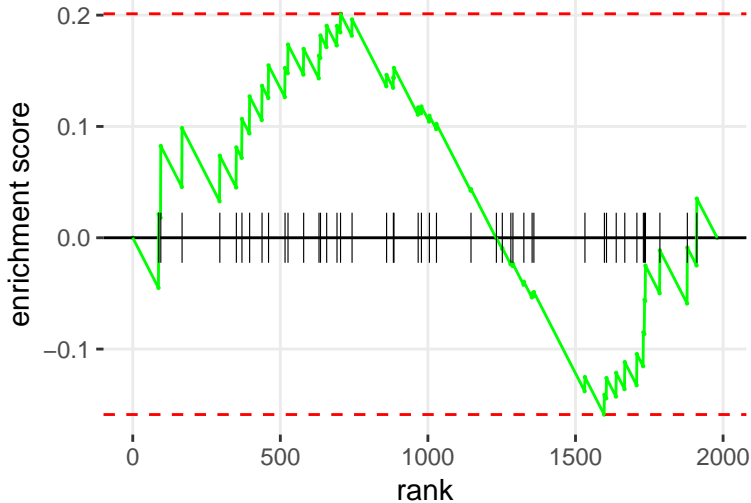
enrichment score



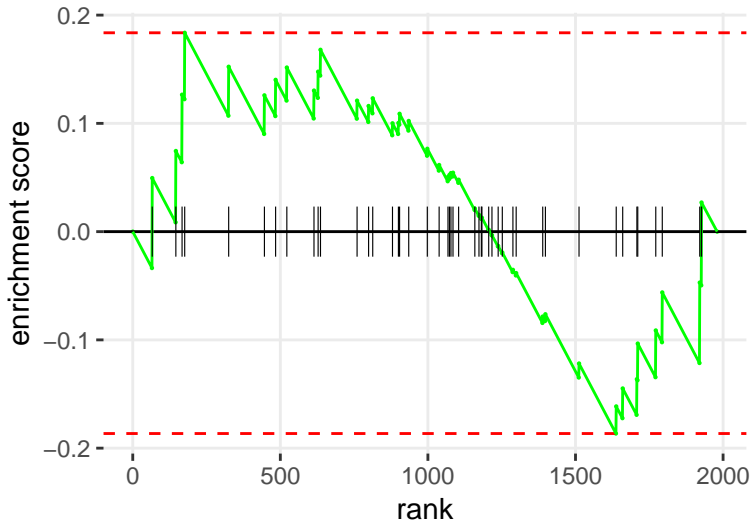
<IN</I>-ACETYLGLUCOSAMINE DEGRADATION I



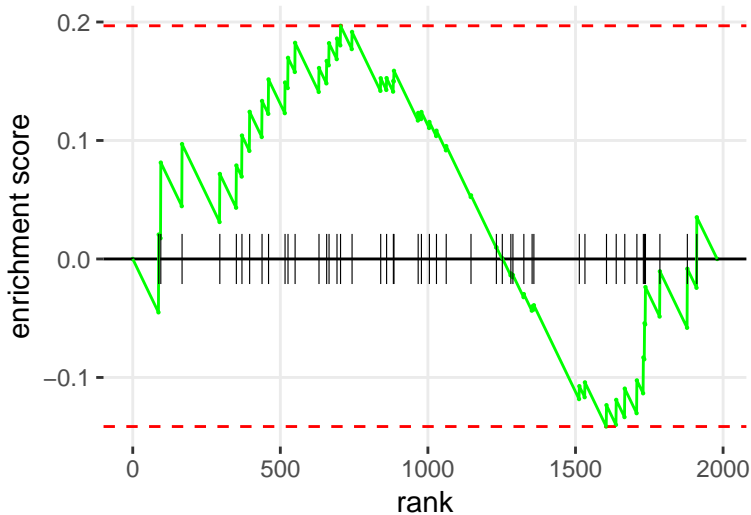
L-DOPA DEGRADATION



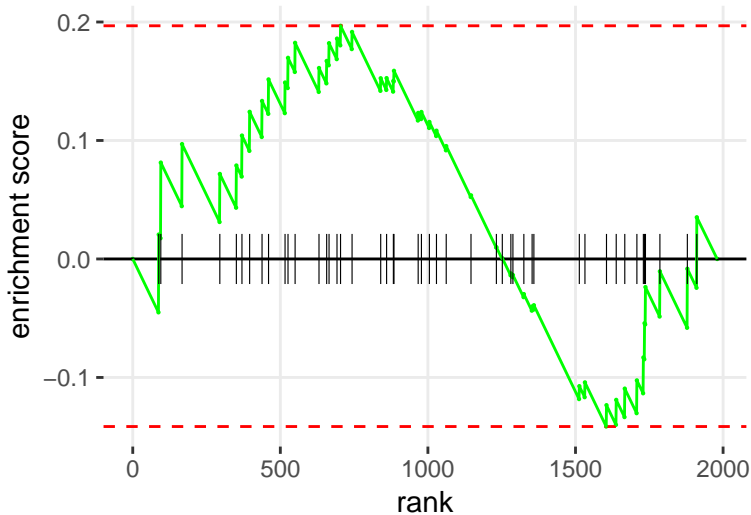
PROSTANOID BIOSYNTHESIS



URACIL DEGRADATION II (REDUCTIVE)

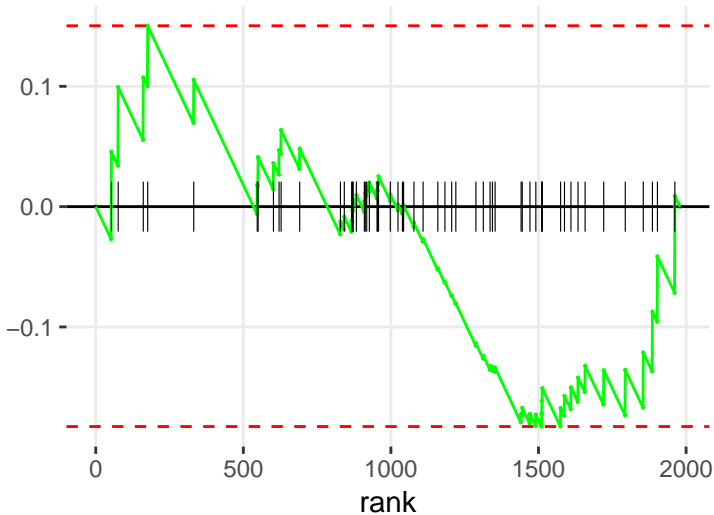


THYMINE DEGRADATION

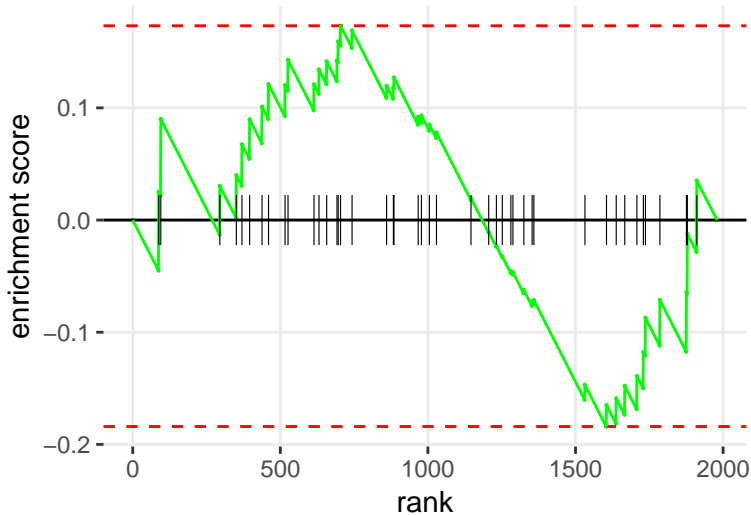


URATE BIOSYNTHESIS/INOSINE 5'-PHOSPHATE DEGRADATION

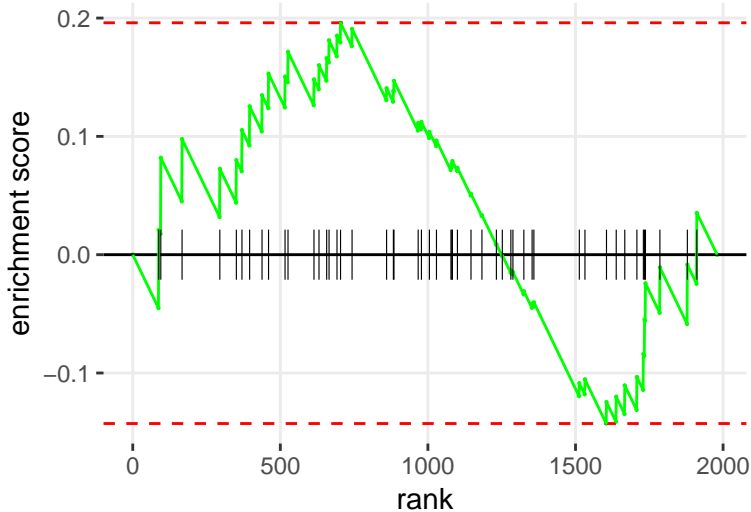
enrichment score



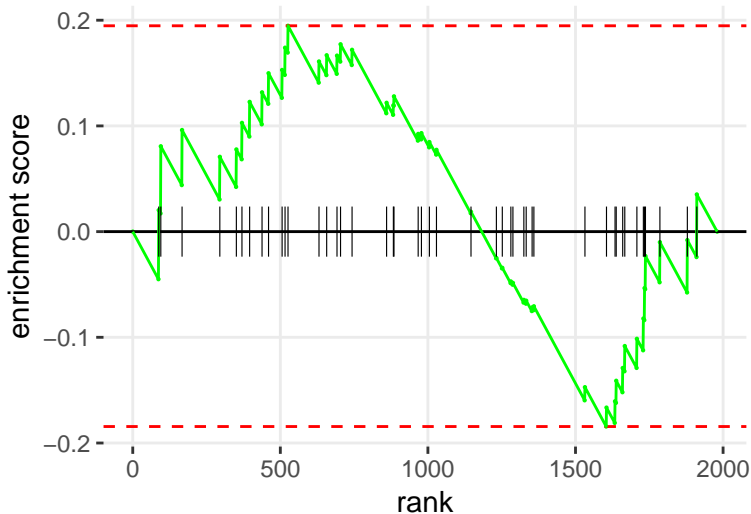
PHOSPHATIDYLETHANOLAMINE BIOSYNTHESIS II



HEME DEGRADATION



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



1D-<IMYO</I>-INOSITOL HEXAKISPHOSPHATE BIOSYNTHESIS V (FROM INS(1,3,4)P3)

enrichment score

0.1
0.0
-0.1

0

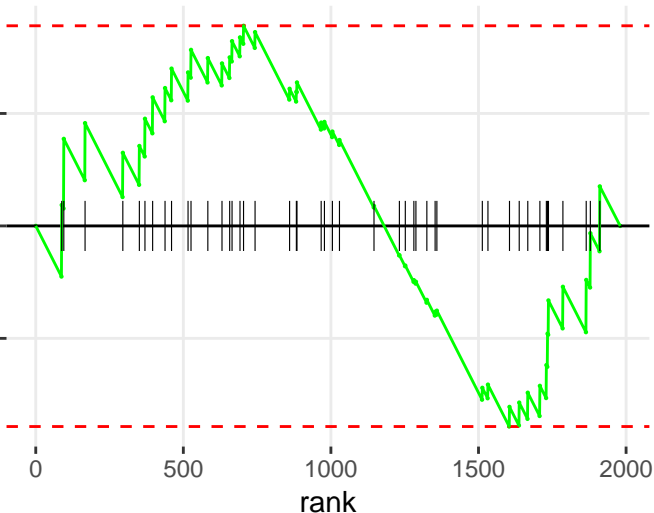
500

1000

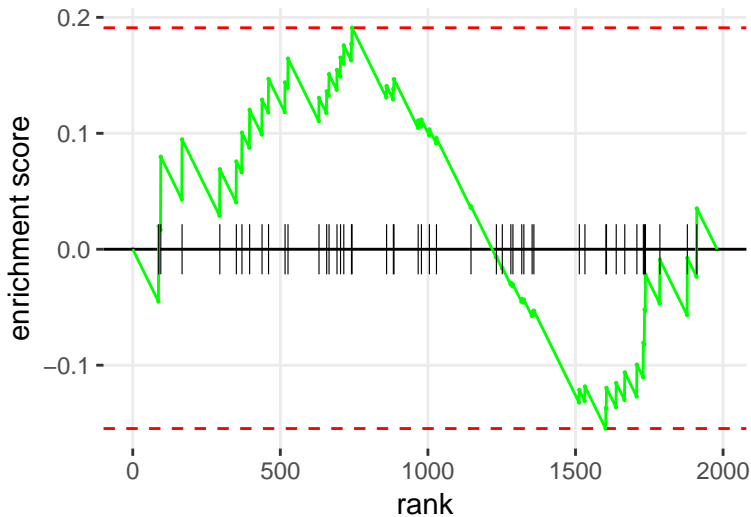
1500

2000

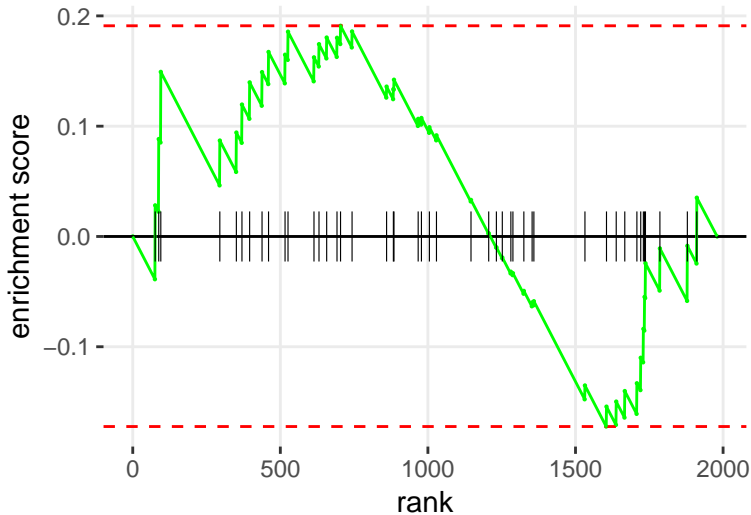
rank



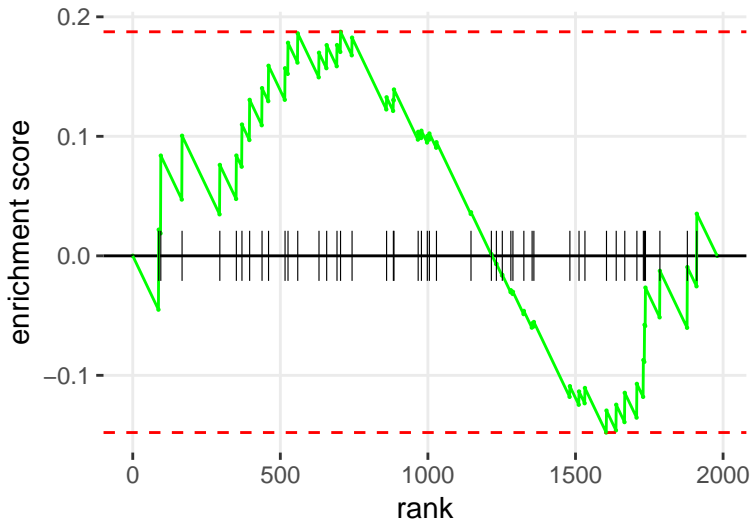
MELATONIN DEGRADATION II



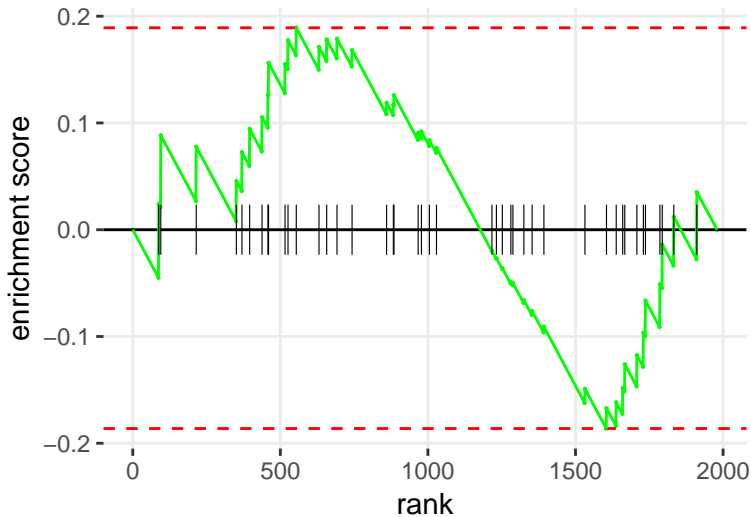
L-CYSTEINE DEGRADATION III



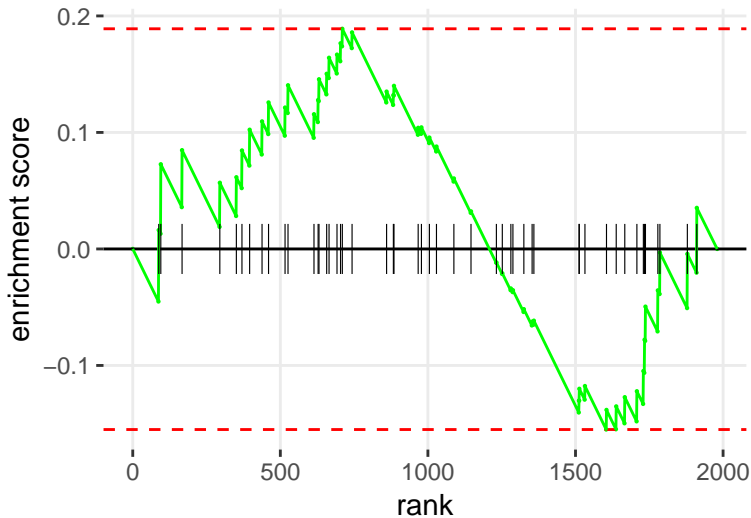
ACYL CARRIER PROTEIN METABOLISM



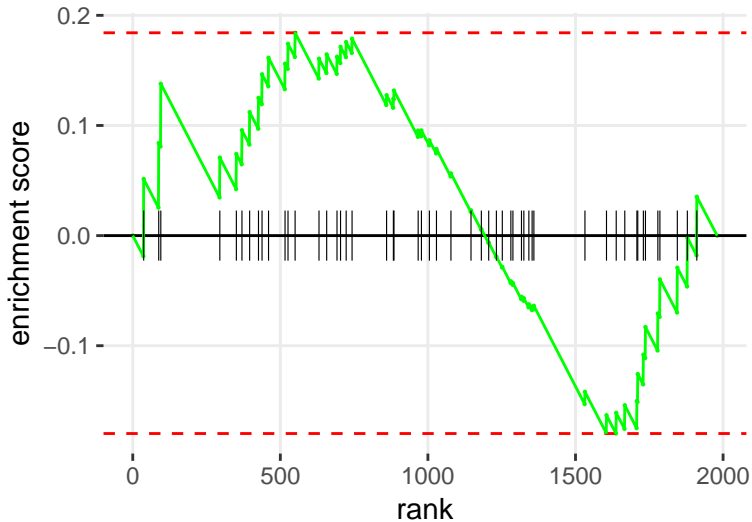
SPERMINE BIOSYNTHESIS



GLUTATHIONE REDOX REACTIONS II



INOSITOL PYROPHOSPHATES BIOSYNTHESIS



D-GLUCURONATE DEGRADATION I

enrichment score

0.1
0.0
-0.1

0

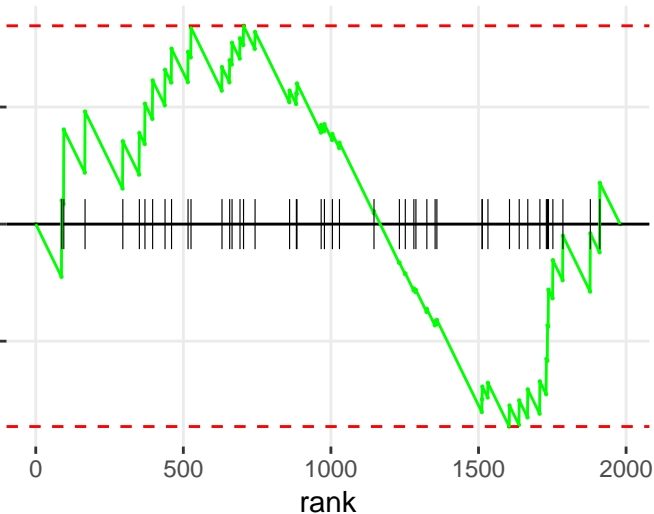
500

1000

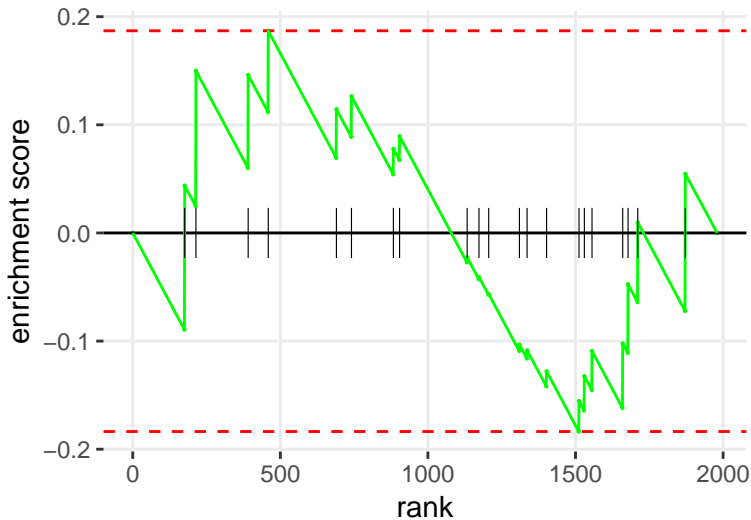
1500

2000

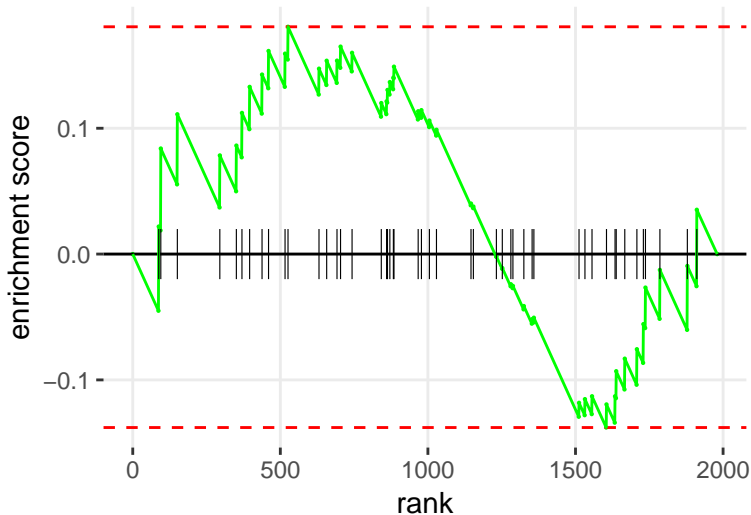
rank



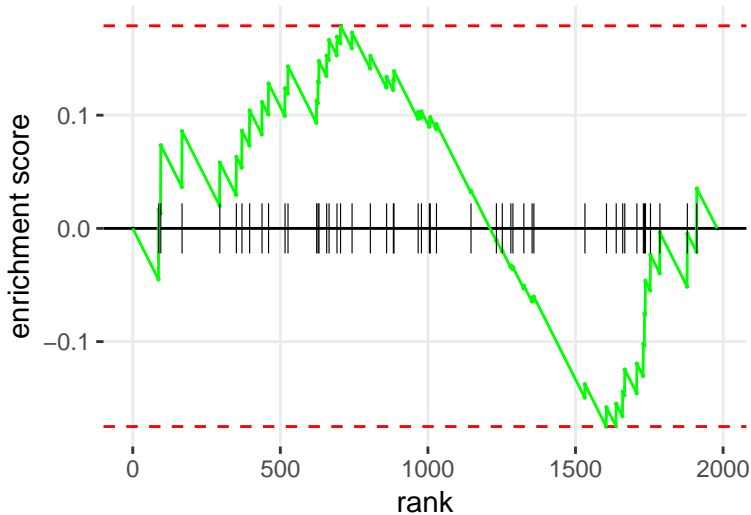
MELATONIN DEGRADATION I



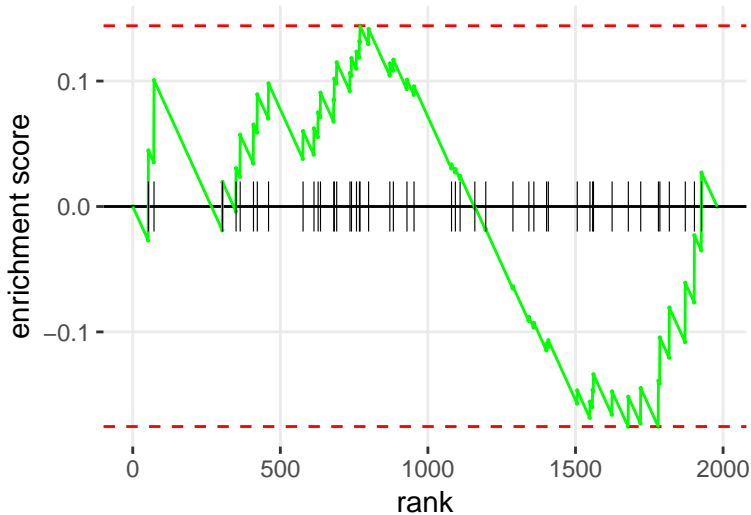
CMP-<IN</I>-ACETYLNEURAMINATE BIOSYNTHESIS I (EUKARYOTES)



GLUTAMATE REMOVAL FROM FOLATES



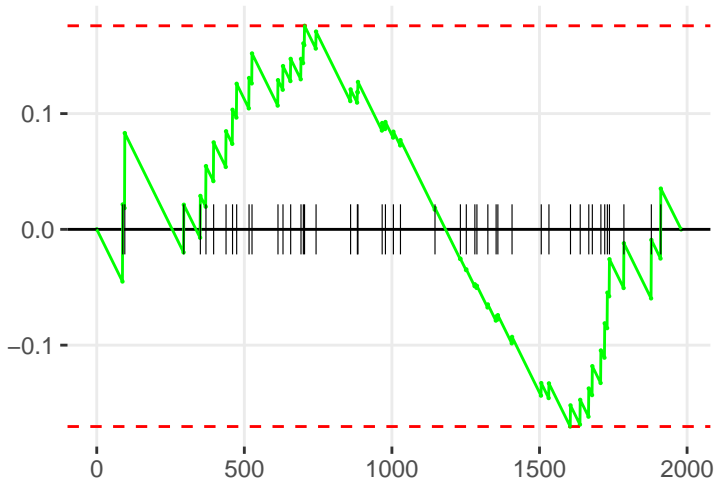
GLYCOGEN DEGRADATION II



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

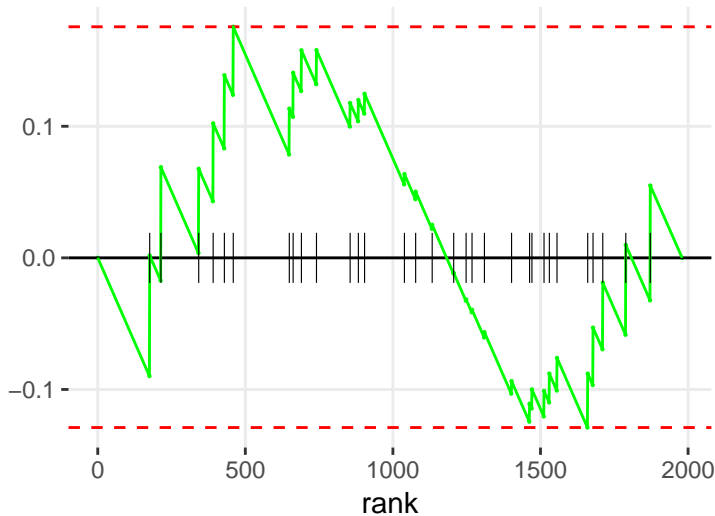
enrichment score

rank



NICOTINE DEGRADATION III

enrichment score



PUTRESCINE BIOSYNTHESIS III

enrichment score

0.1
0.0
-0.1

0

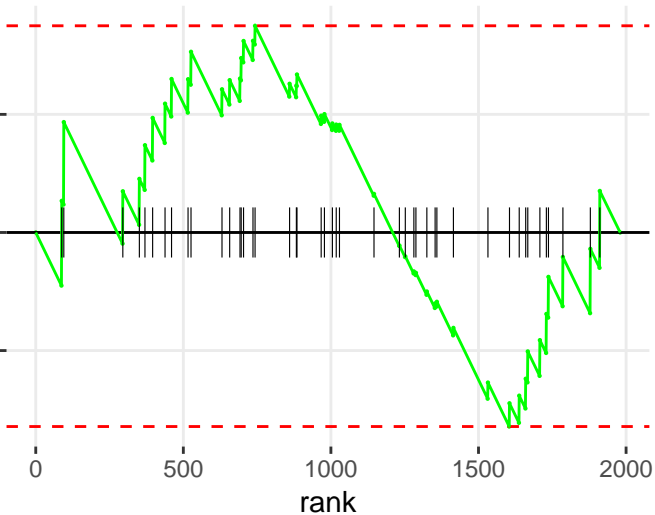
500

1000

1500

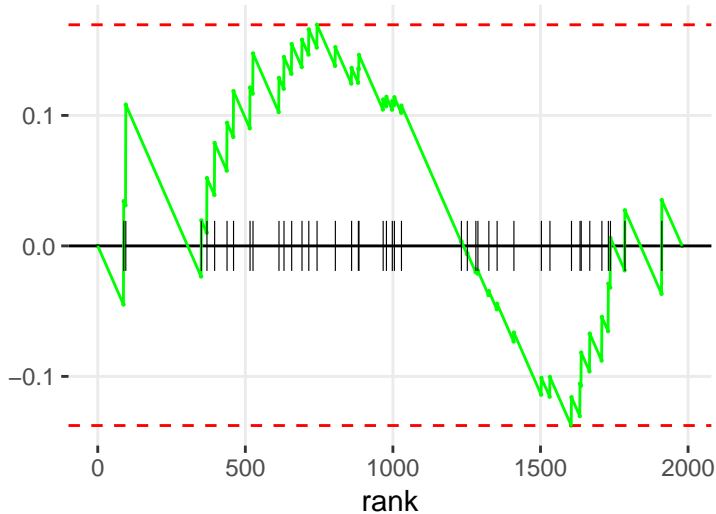
2000

rank



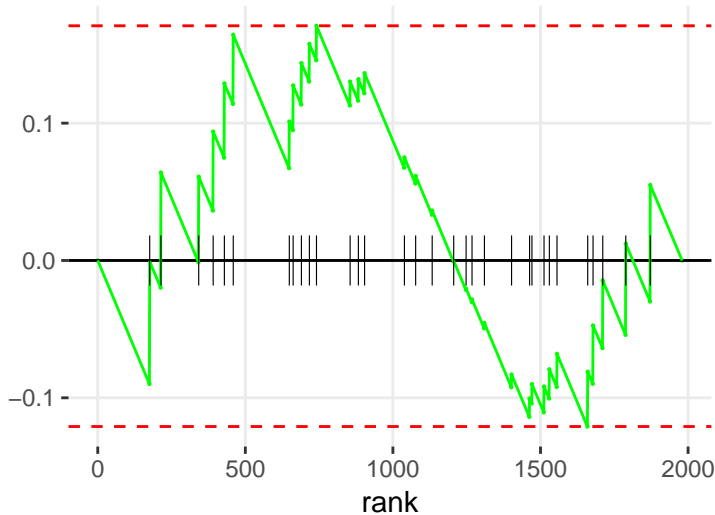
UDP-D-XYLOSE AND UDP-D-GLUCURONATE BIOSYNTHESIS

enrichment score



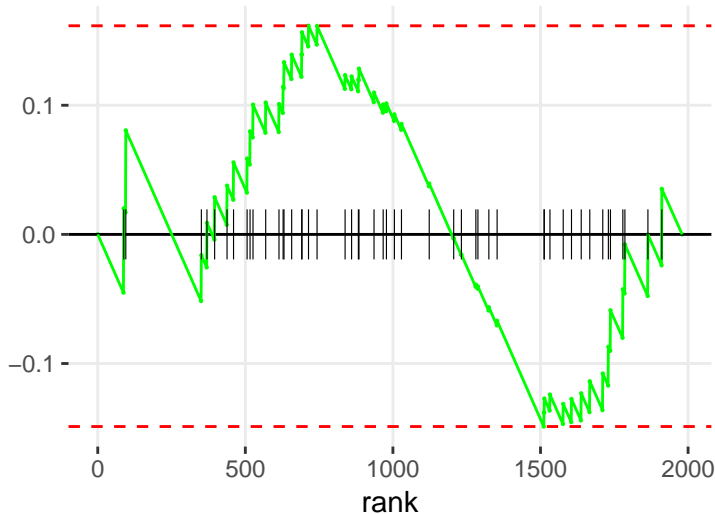
NICOTINE DEGRADATION IV

enrichment score

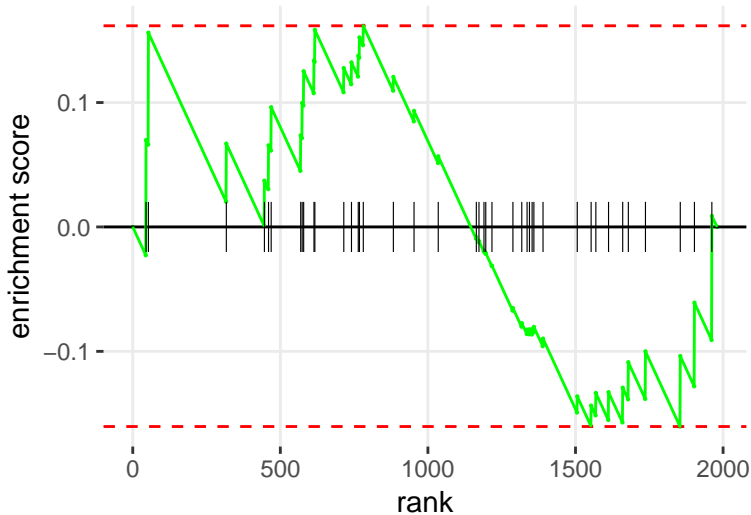


INOSINE-5'-PHOSPHATE BIOSYNTHESIS II

enrichment score



PUTRESCINE DEGRADATION III



L-CARNITINE BIOSYNTHESIS

enrichment score

