

# CDP-DIACYLGLYCEROL BIOSYNTHESIS I

enrichment score

0.0  
-0.1  
-0.2  
-0.3  
-0.4

0

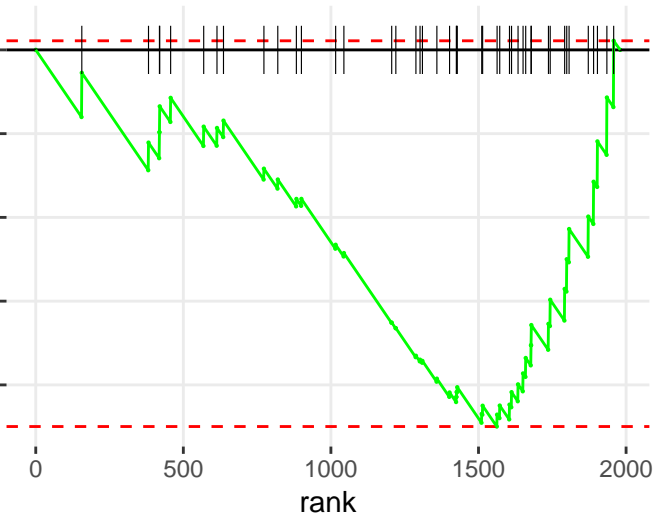
500

1000

1500

2000

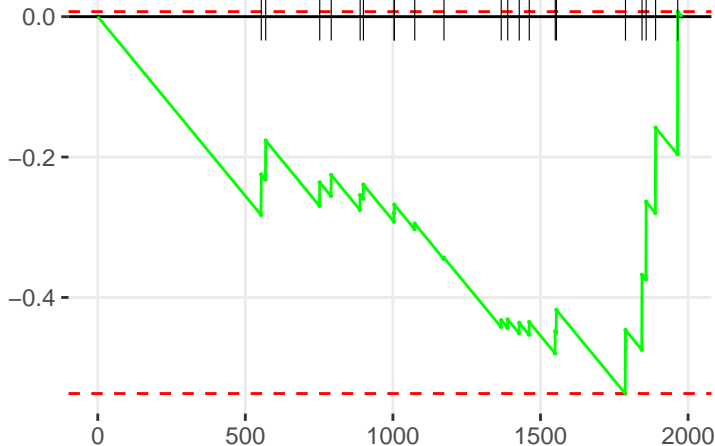
rank



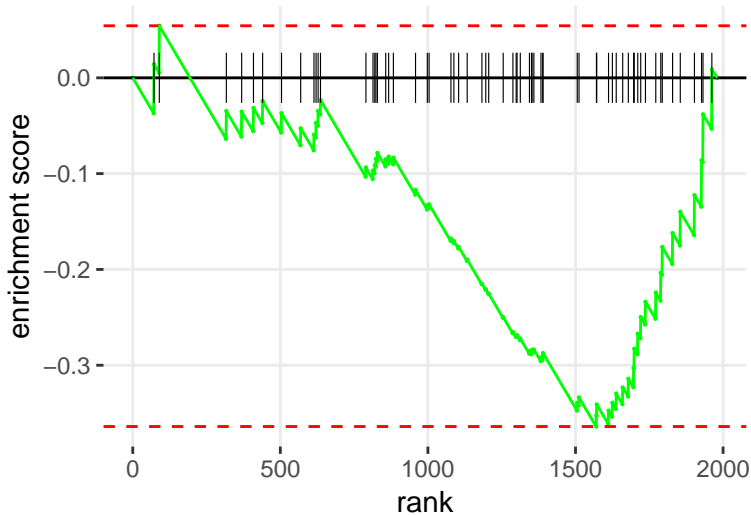
# RETINOL BIOSYNTHESIS

enrichment score

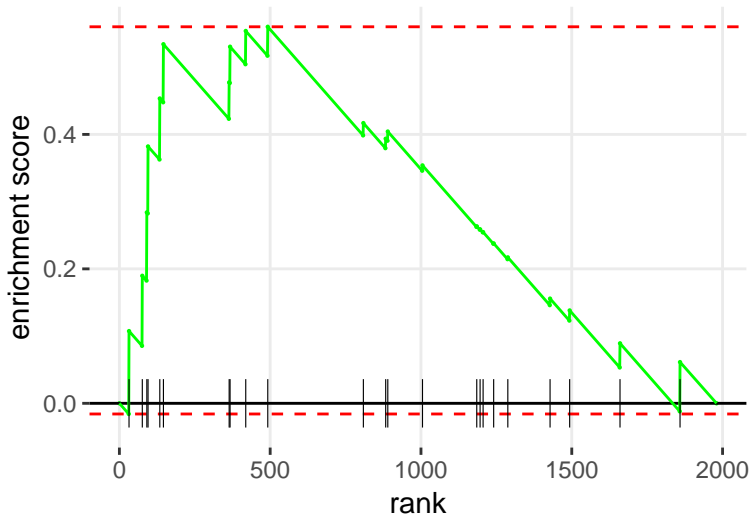
rank



# PENTOSE PHOSPHATE PATHWAY (NON-OXIDATIVE BRANCH)



# ANDROGEN BIOSYNTHESIS



# PHOSPHOLIPASES

enrichment score

0.3

0.2

0.1

0.0

0

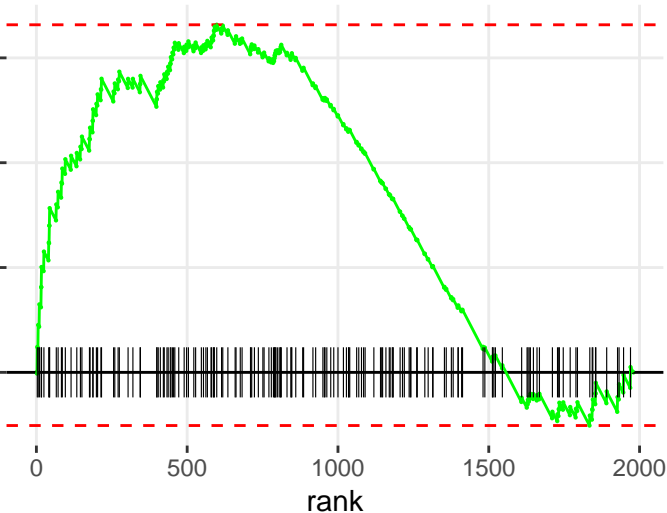
500

1000

1500

2000

rank



# D-MYO-INOSITOL-5-PHOSPHATE METABOLISM

enrichment score

0.3

0.2

0.1

0.0

0

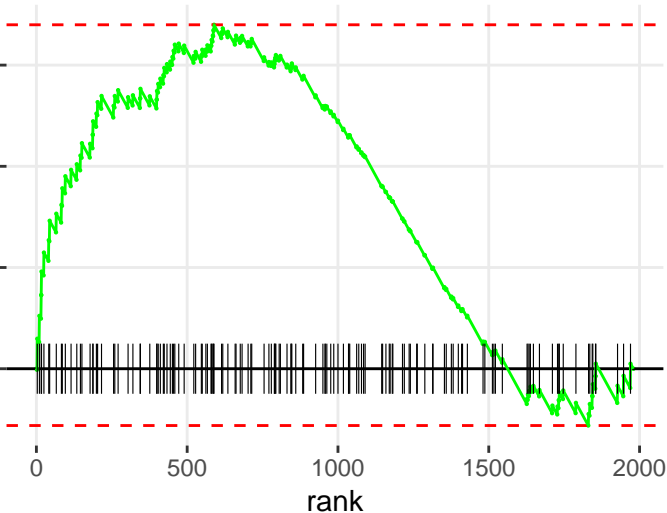
500

1000

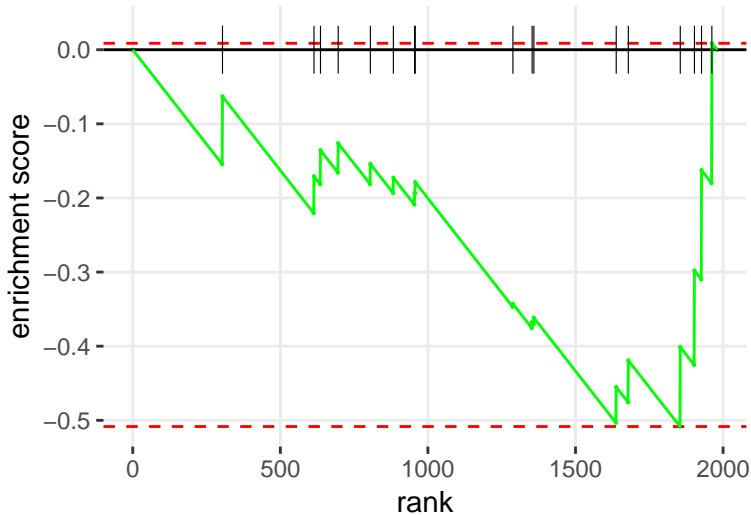
1500

2000

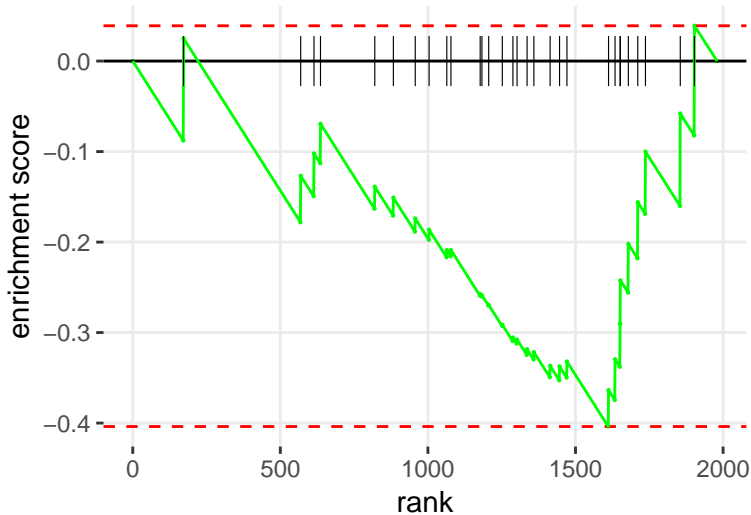
rank



## GLYCEROL-3-PHOSPHATE SHUTTLE



# HYPUSINE BIOSYNTHESIS





# GLUTARYL-COA DEGRADATION

enrichment score

0.0

-0.1

-0.2

-0.3

-0.4

0

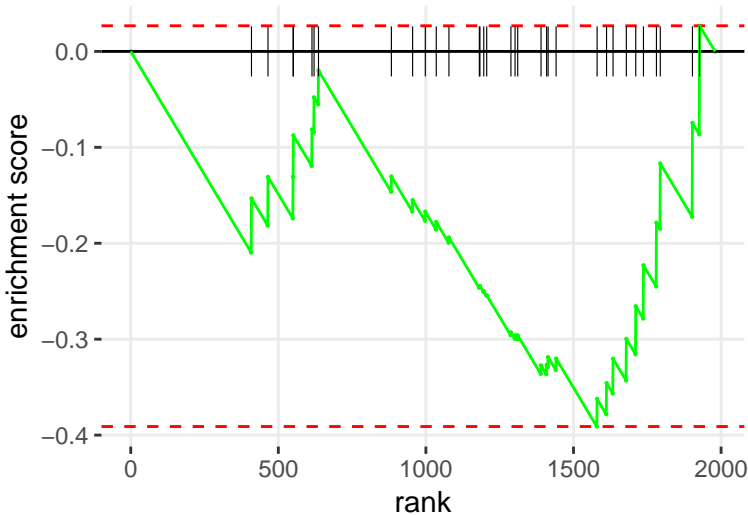
500

1000

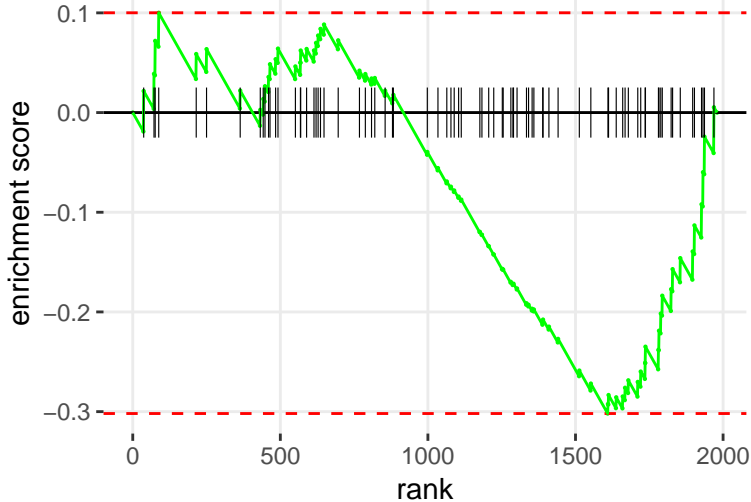
1500

2000

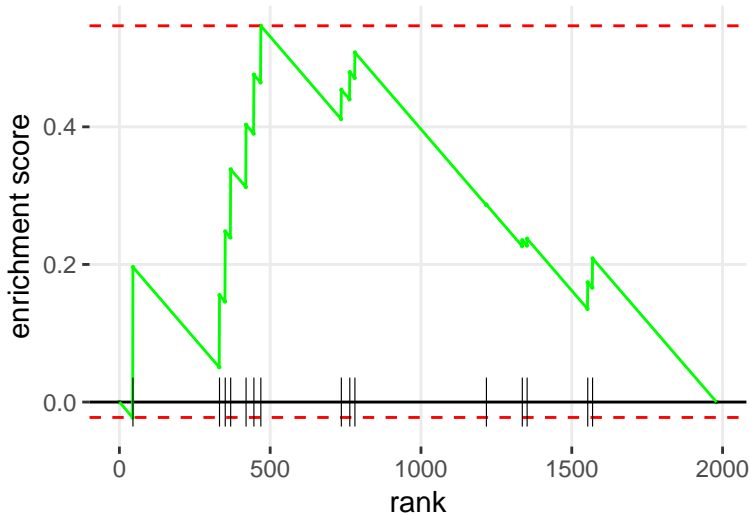
rank



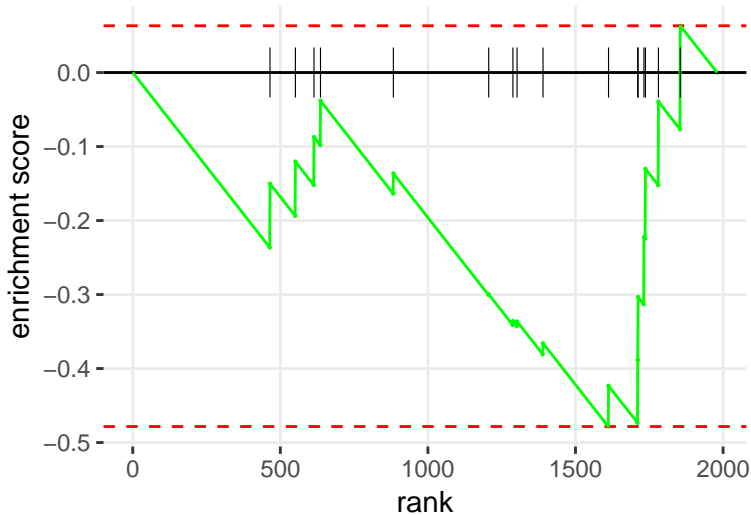
# SUPEROXIDE RADICALS DEGRADATION



## SPERMINE AND SPERMIDINE DEGRADATION I



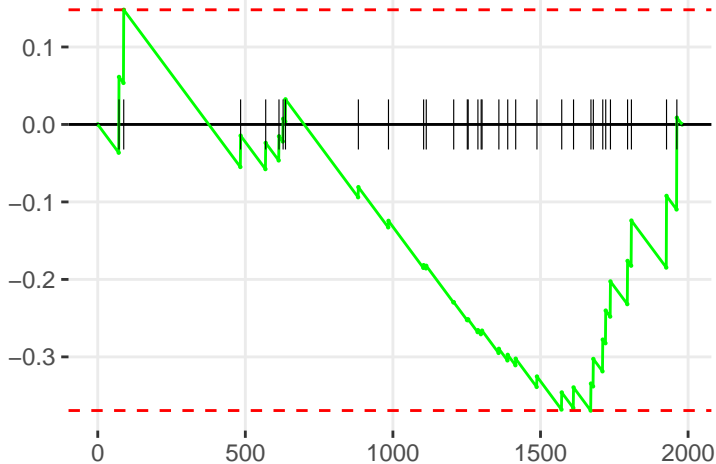
# L-CYSTEINE DEGRADATION II



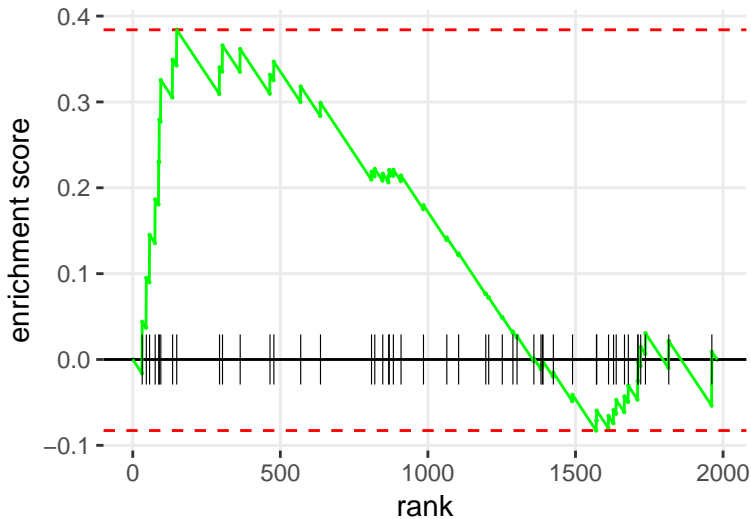
<IMYO</I>-INOSITOL BIOSYNTHESIS

enrichment score

rank

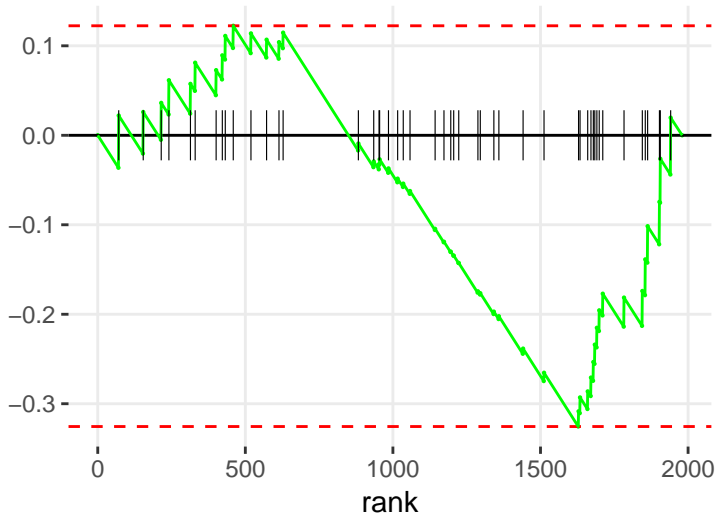


# CITRULLINE DEGRADATION

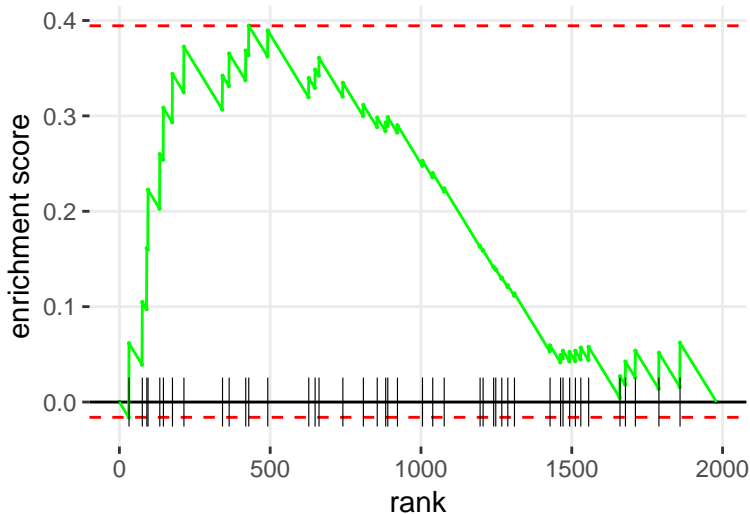


# SERINE BIOSYNTHESIS

enrichment score

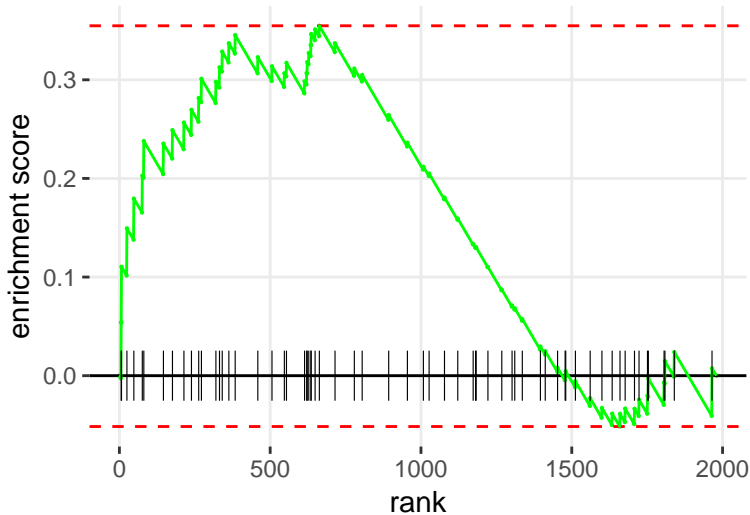


# ESTROGEN BIOSYNTHESIS

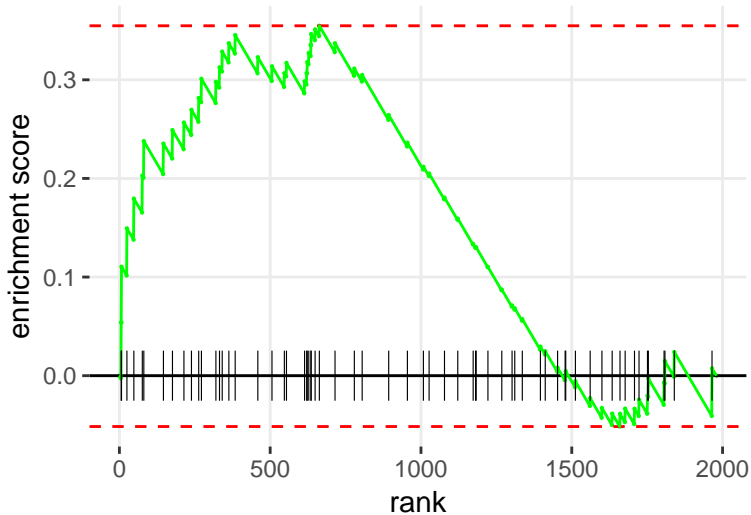




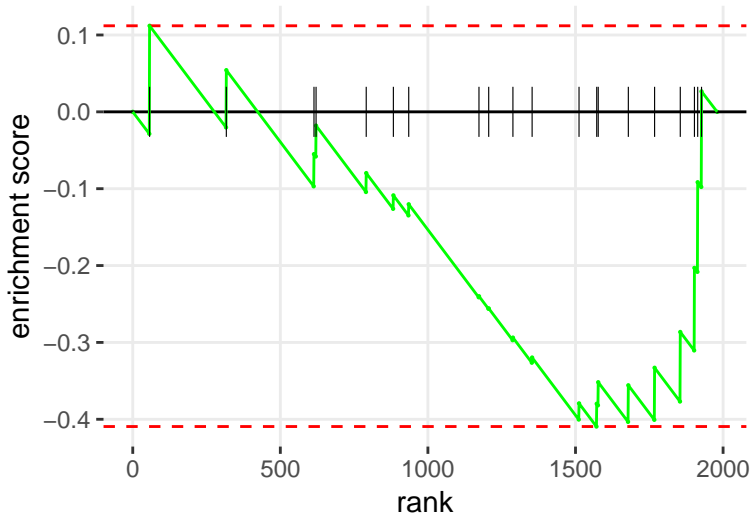
# GLUTATHIONE-MEDIATED DETOXIFICATION I



# 4-HYDROXY-2-NONENAL DETOXIFICATION

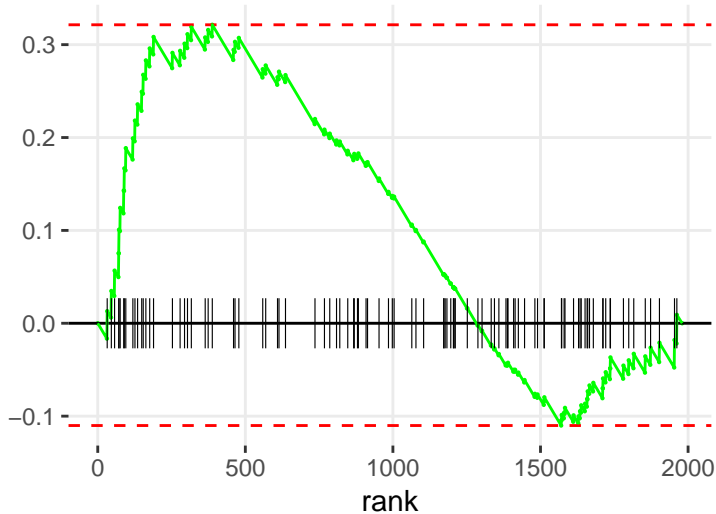


# ASPARAGINE BIOSYNTHESIS I



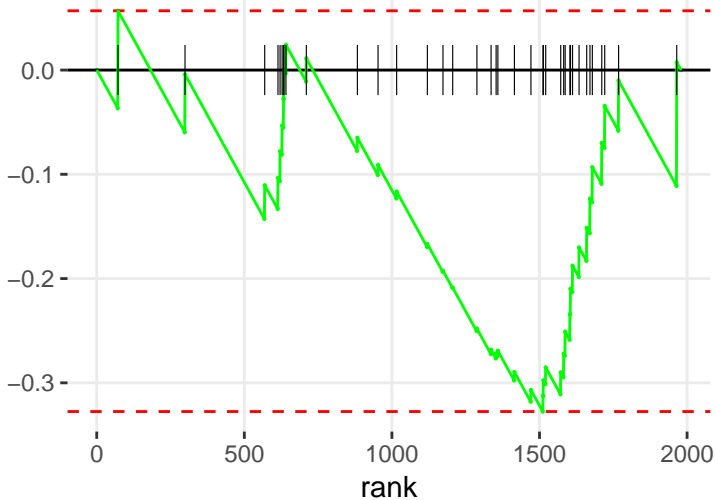
# PROLINE BIOSYNTHESIS II (FROM ARGinine)

enrichment score

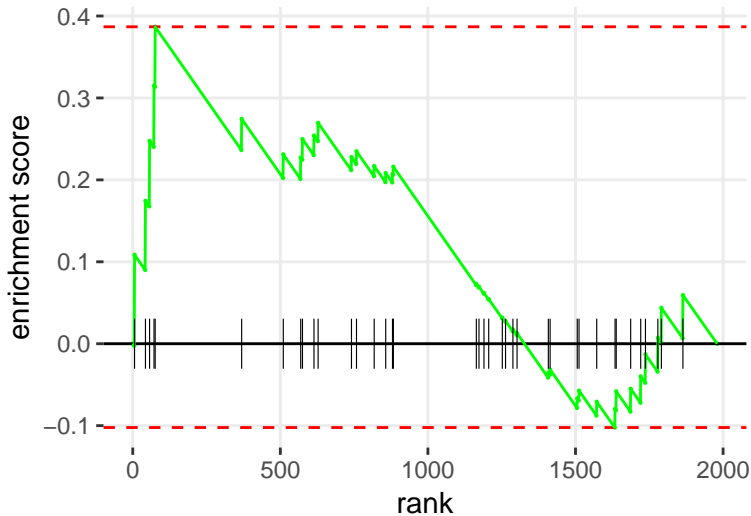


# DOLICHYL-DIPHOSPHOOLIGOSACCHARIDE BIOSYNTHESIS

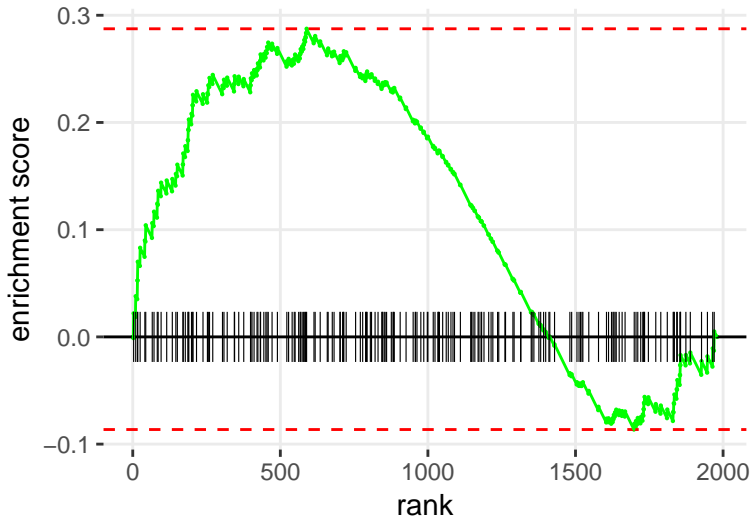
enrichment score



# HEME BIOSYNTHESIS FROM UROPORPHYRINOGEN-III I



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



# GLUTAMINE BIOSYNTHESIS I

enrichment score

0.0

-0.1

-0.2

-0.3

0

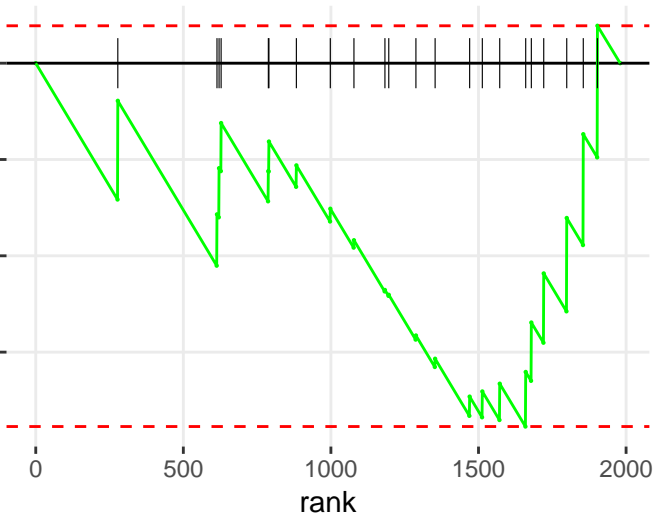
500

1000

1500

2000

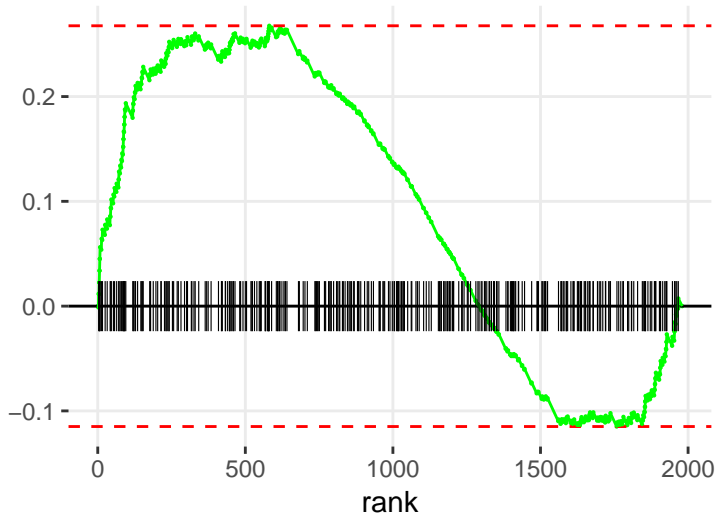
rank



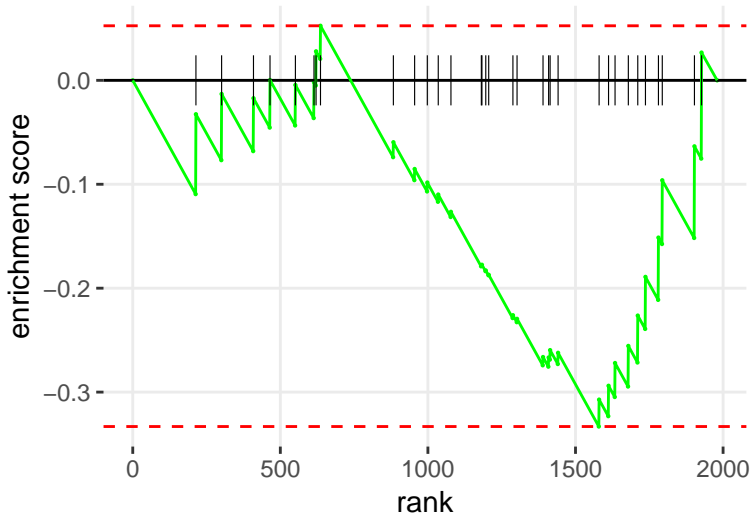


GLYCOLYSIS I

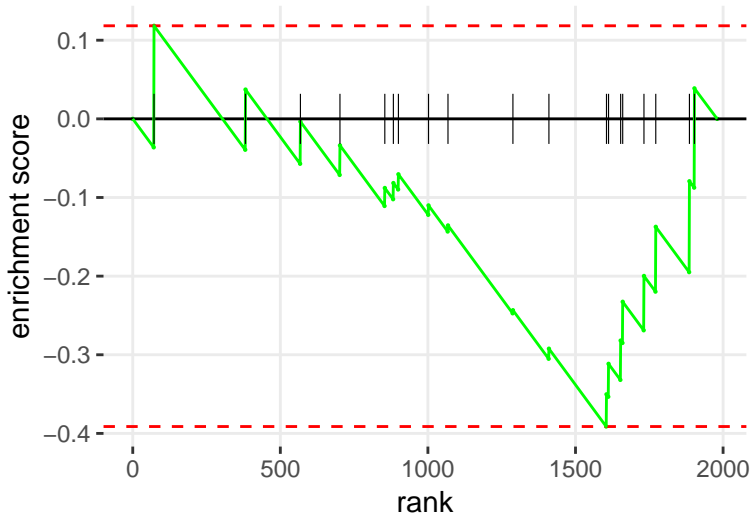
enrichment score



KETOLYSIS

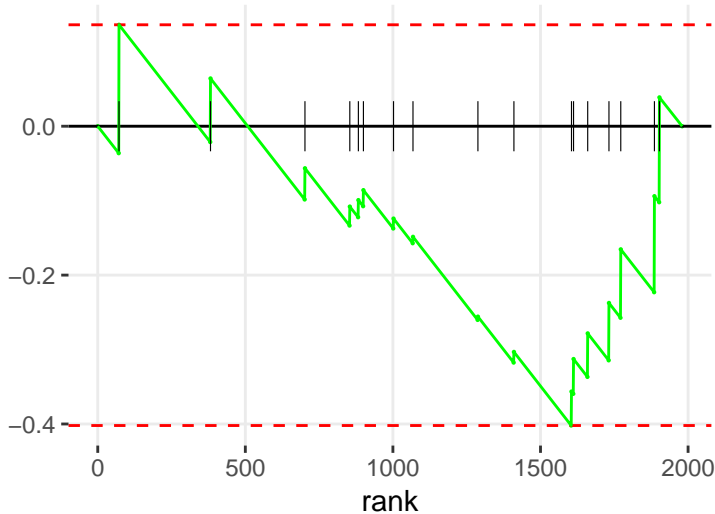


# MOLYBDENUM COFACTOR BIOSYNTHESIS



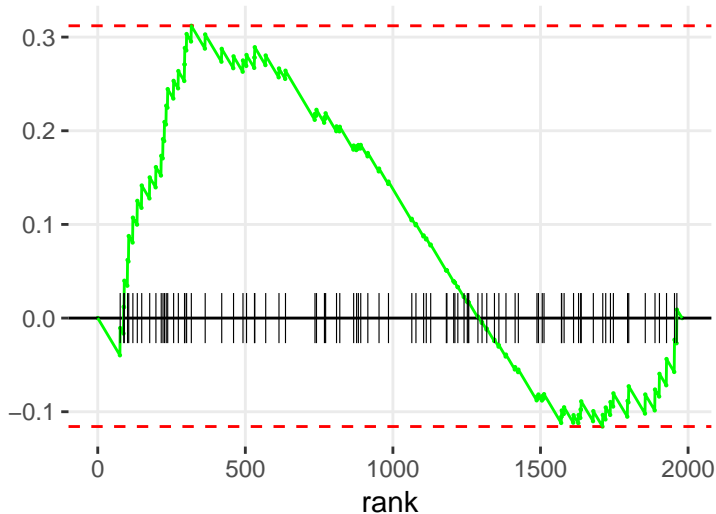
# ALANINE BIOSYNTHESIS III

enrichment score



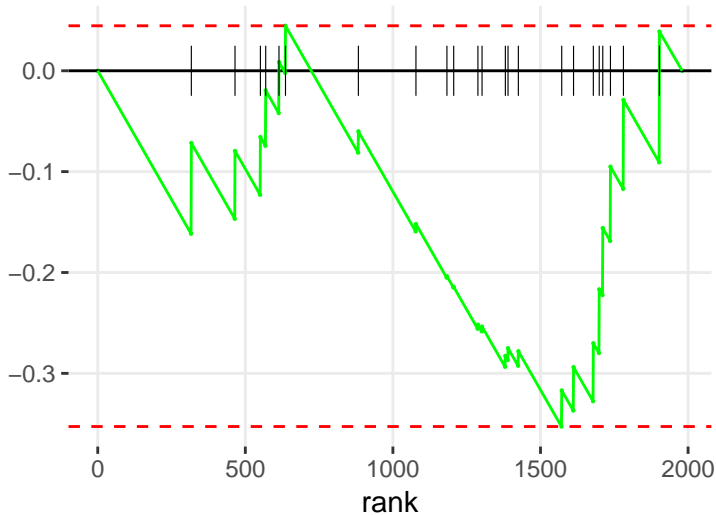
# 2-OXOGLUTARATE DECARBOXYLATION TO SUCCINYL-COA

enrichment score



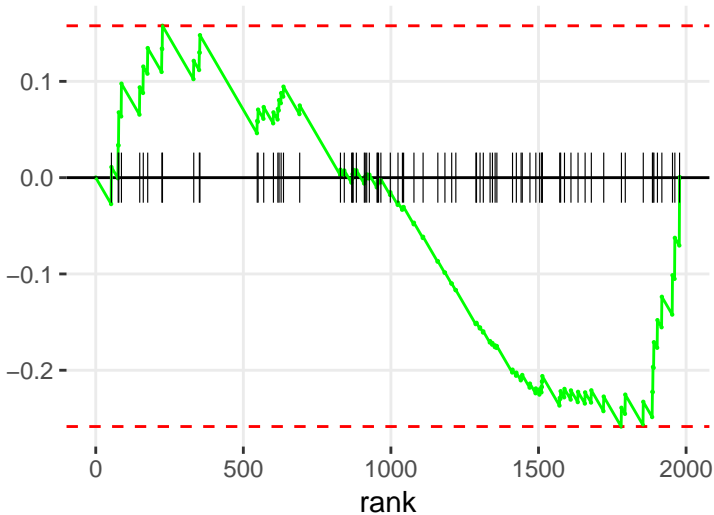
# ADENINE AND ADENOSINE SALVAGE VI

enrichment score



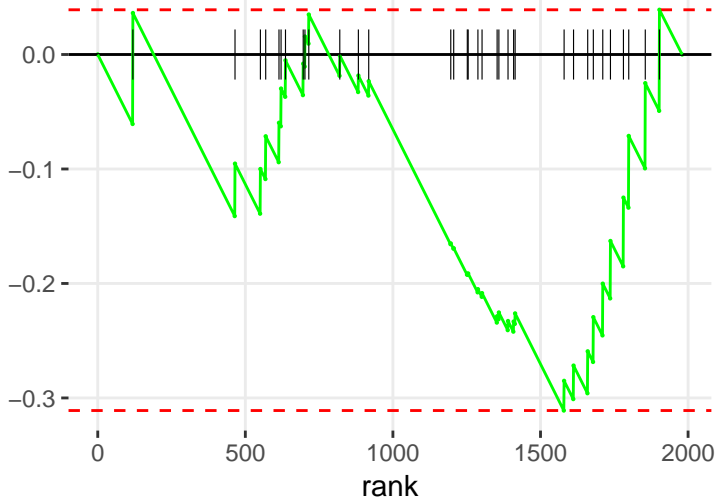
# URATE BIOSYNTHESIS/INOSINE 5'-PHOSPHATE DEGRADATION

enrichment score



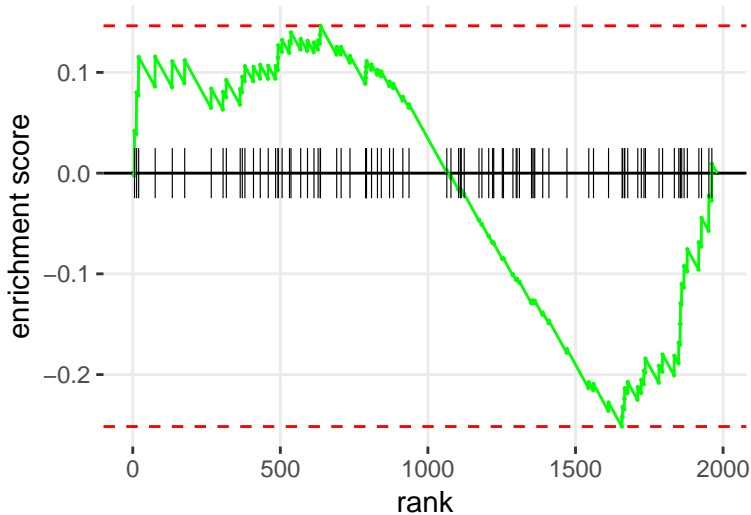
# ACETATE CONVERSION TO ACETYL-COA

enrichment score





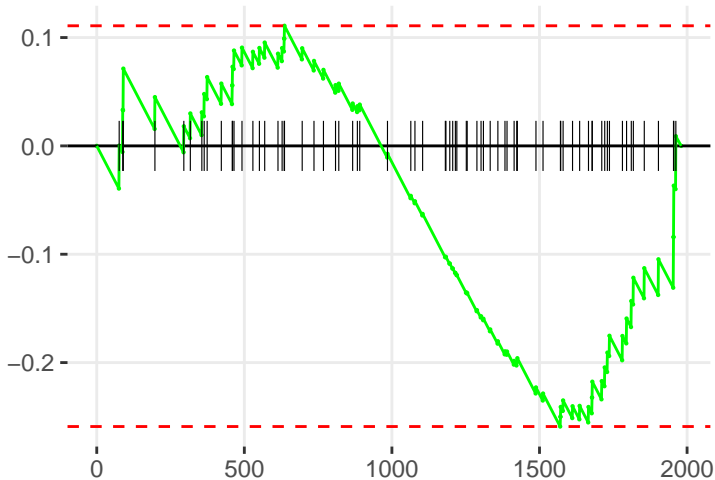
# SALVAGE PATHWAYS OF PYRIMIDINE RIBONUCLEOTIDES



# GLYCOGEN BIOSYNTHESIS II (FROM UDP-D-GLUCOSE)

enrichment score

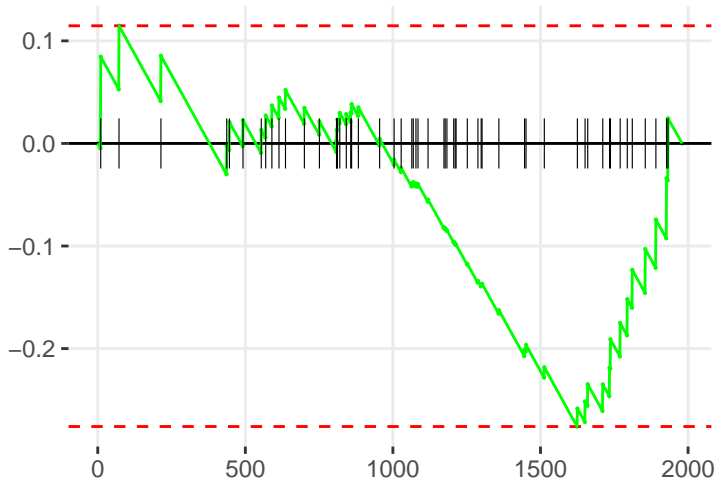
rank



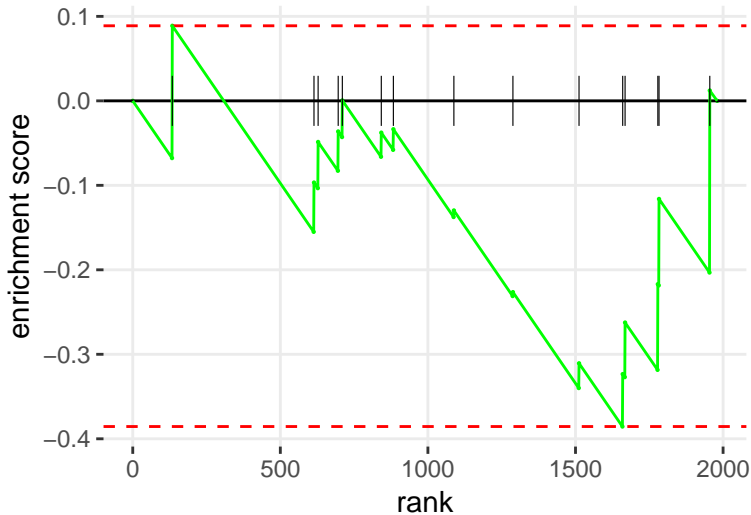
# CHOLINE BIOSYNTHESIS III

enrichment score

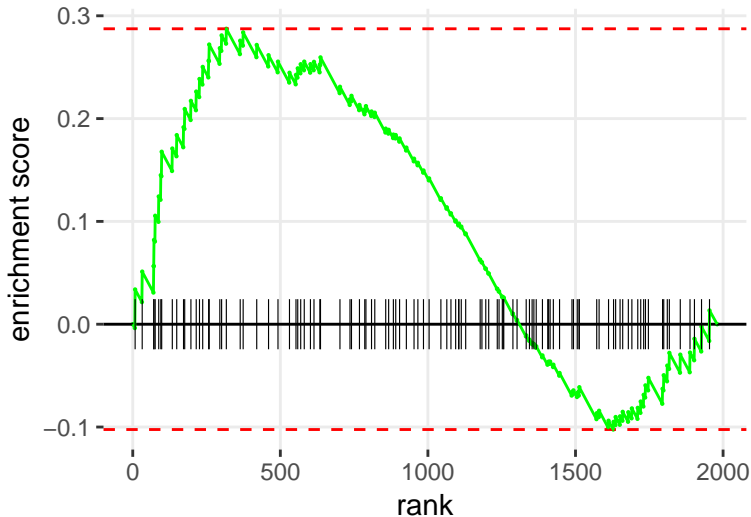
rank



# GLUTATHIONE REDOX REACTIONS I

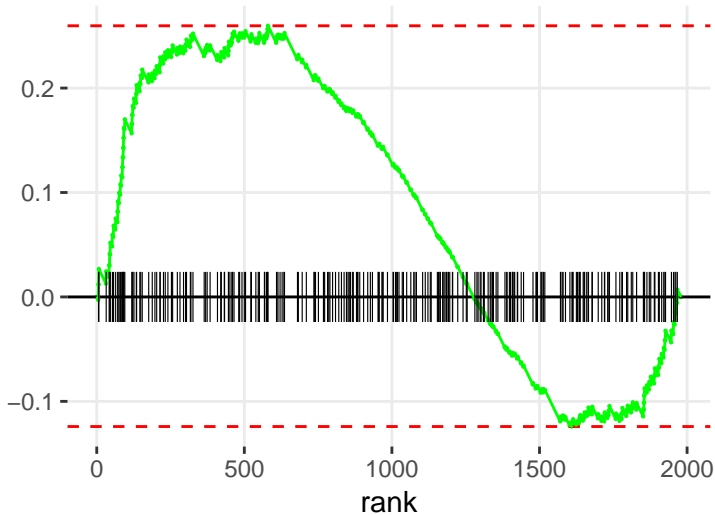


# PYRUVATE DECARBOXYLATION TO ACETYL COA

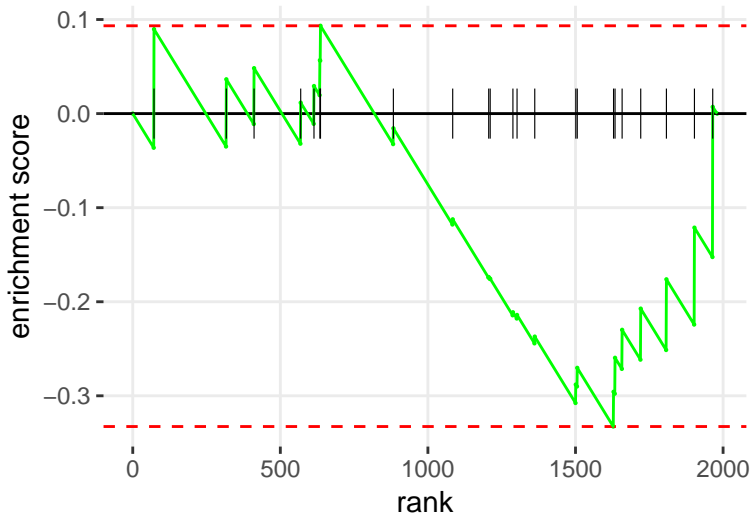


# GLUCONEOGENESIS I

enrichment score

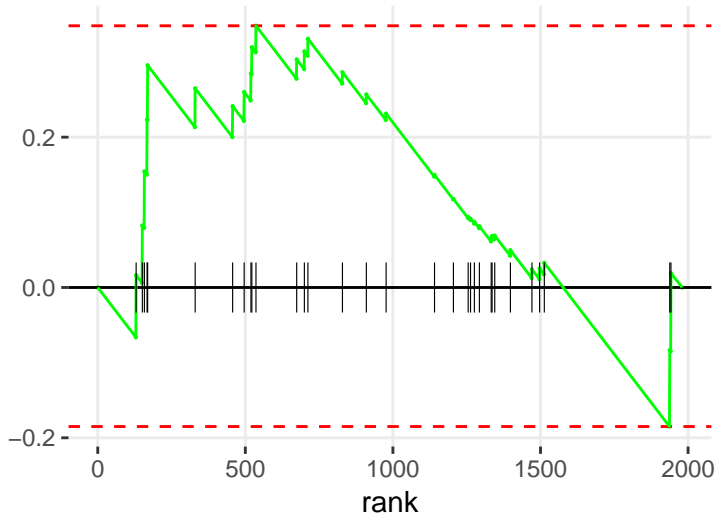


# TRYPTOPHAN DEGRADATION TO 2-AMINO-3-CARBOXYMUCONATE SEMIALDEHYDE



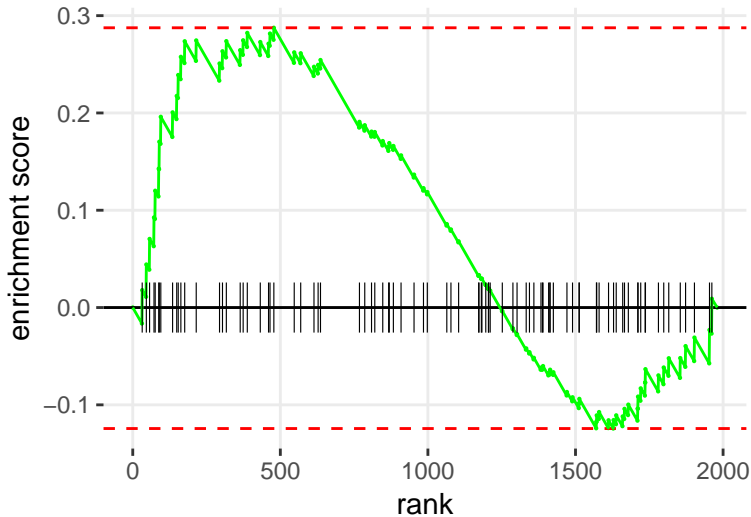
# PHENYLALANINE DEGRADATION I (AEROBIC)

enrichment score

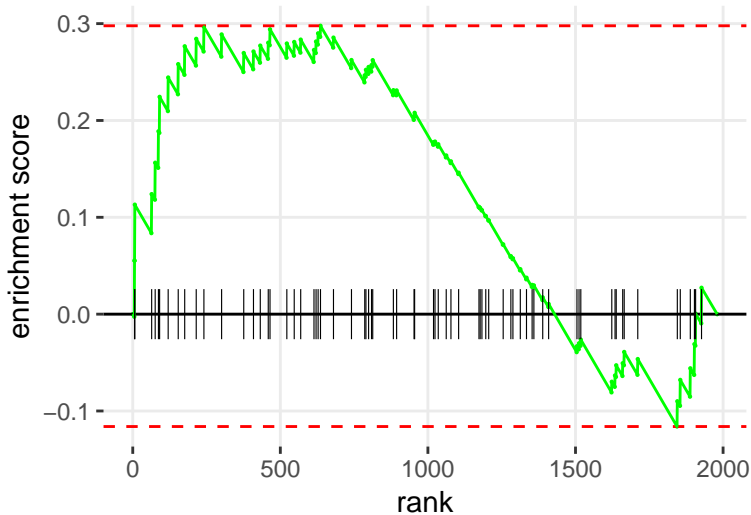




# CITRULLINE BIOSYNTHESIS

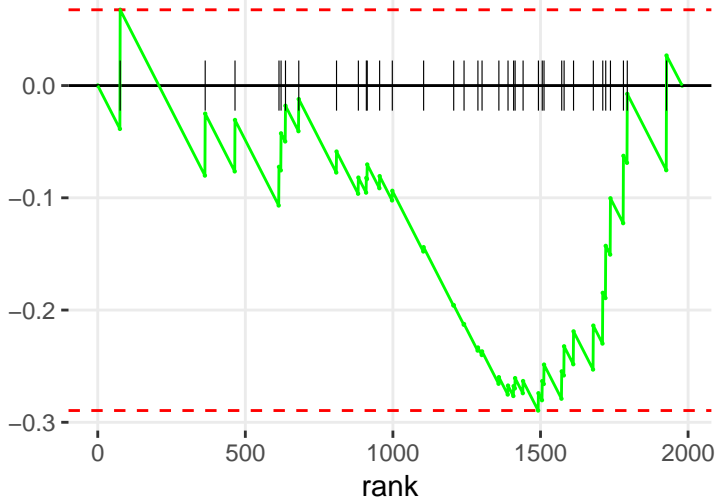


# SUCROSE DEGRADATION V (MAMMALIAN)

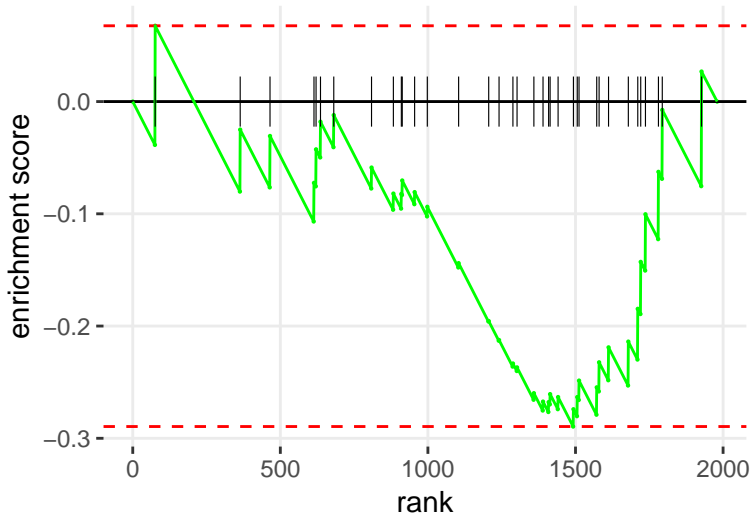


# GLUTAMATE DEGRADATION II

enrichment score

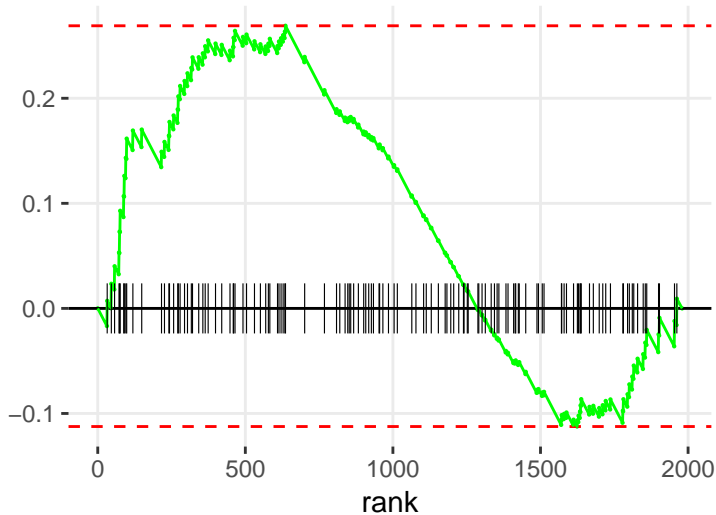


# ASPARTATE BIOSYNTHESIS



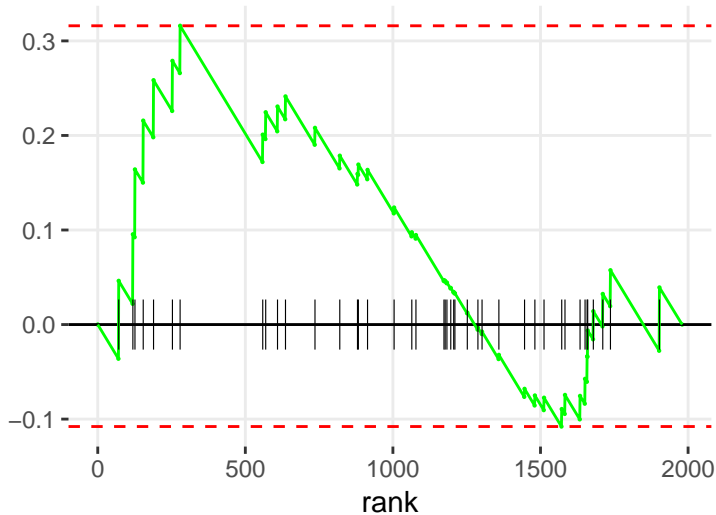
UDP-<IN</I>-ACETYL-D-GALACTOSAMINE BIOSYNTHESIS II

enrichment score



# PROLINE BIOSYNTHESIS I

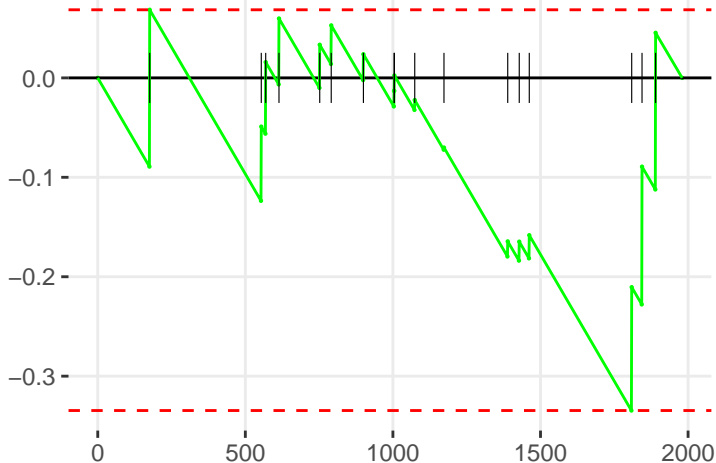
enrichment score



# TRIACYLGLYCEROL DEGRADATION

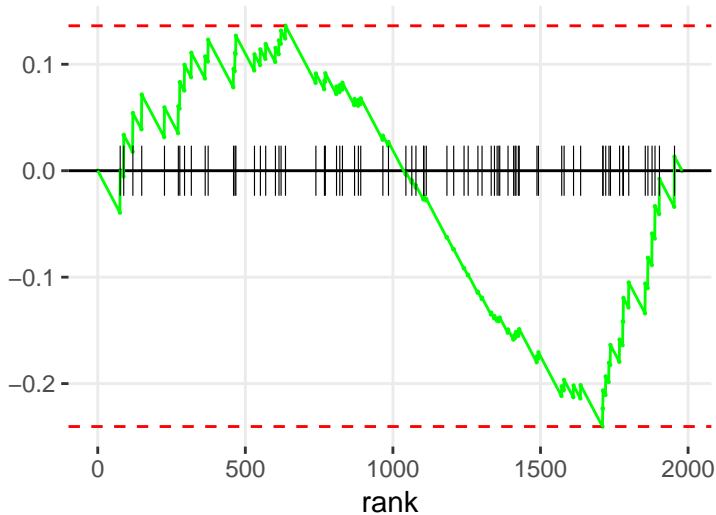
enrichment score

rank



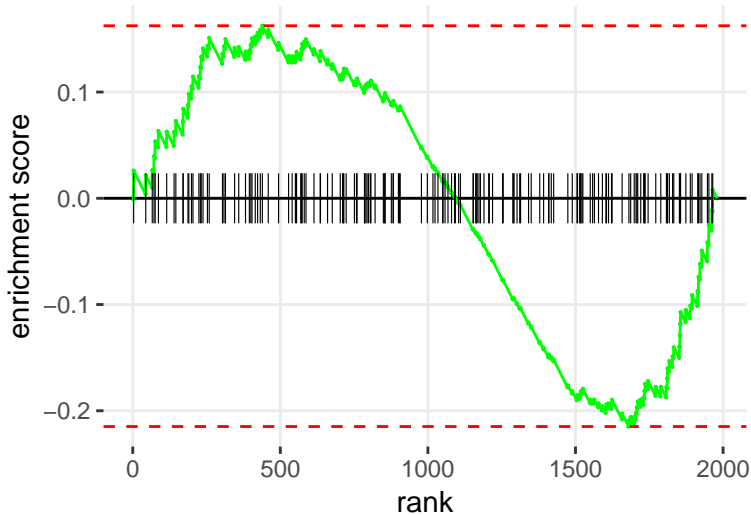
# CYSTEINE BIOSYNTHESIS/HOMOCYSTEINE DEGRADATION

enrichment score





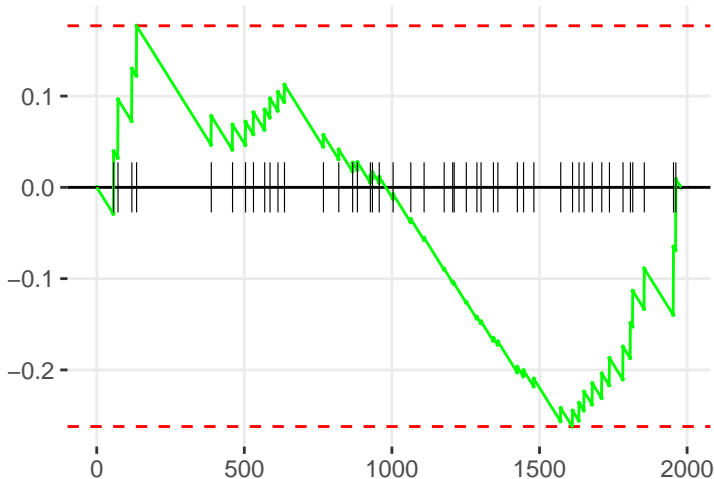
### 3-PHOSPHOINOSITIDE BIOSYNTHESIS



# GALACTOSE DEGRADATION I (LELOIR PATHWAY)

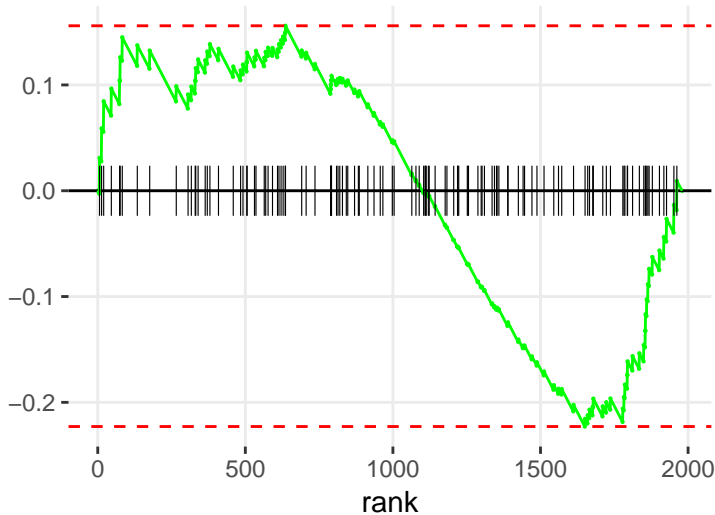
enrichment score

rank



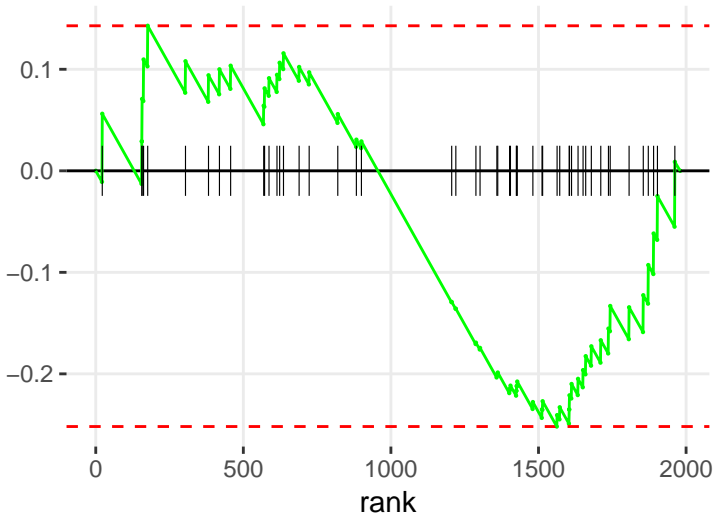
# PYRIMIDINE DEOXYRIBONUCLEOTIDES <IDE NOVO</I> BIOSYNTHESIS I

enrichment score

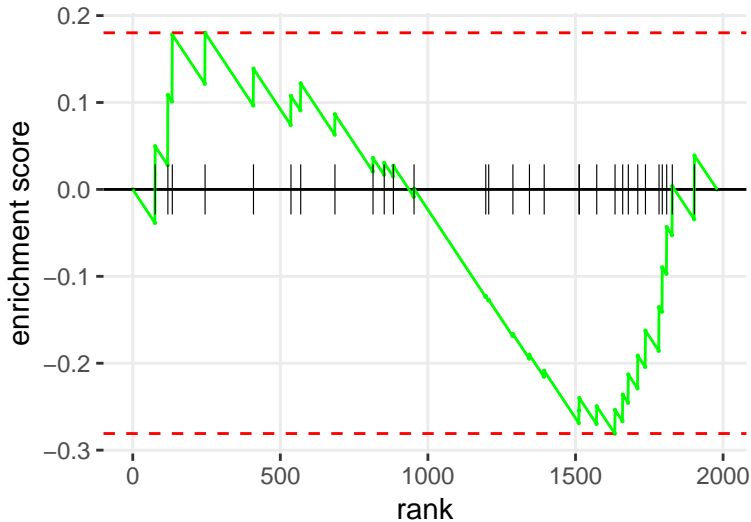


# TRIACYLGLYCEROL BIOSYNTHESIS

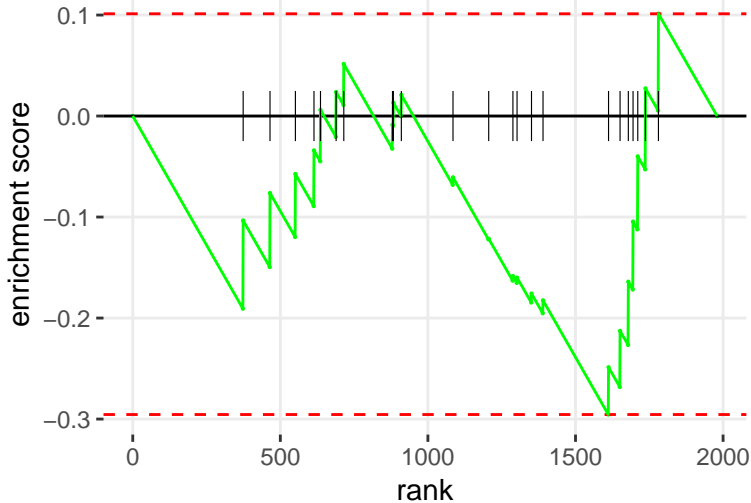
enrichment score



# PRPP BIOSYNTHESIS I

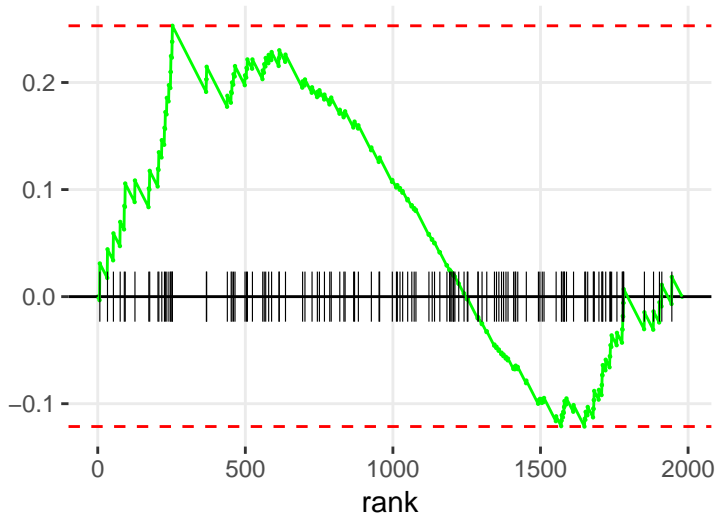


# BILE ACID BIOSYNTHESIS, NEUTRAL PATHWAY

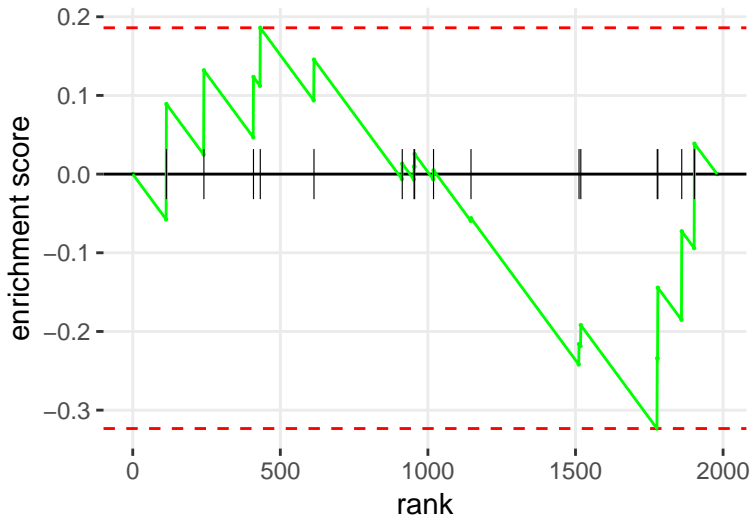


# FOLATE POLYGLUTAMYLATION

enrichment score

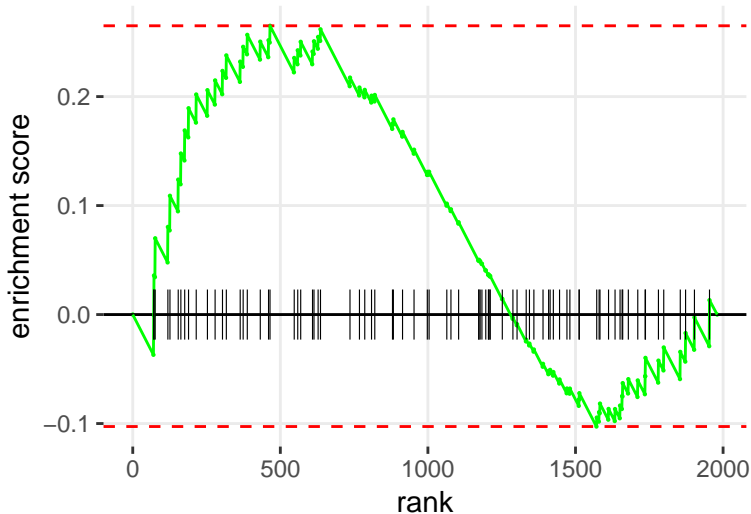


# ACETYL-COA BIOSYNTHESIS III (FROM CITRATE)

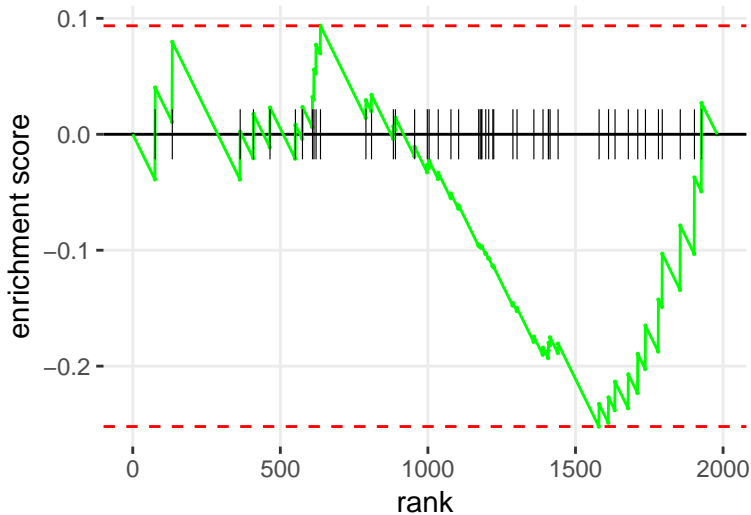




# ARGININE DEGRADATION VI (ARGINASE 2 PATHWAY)

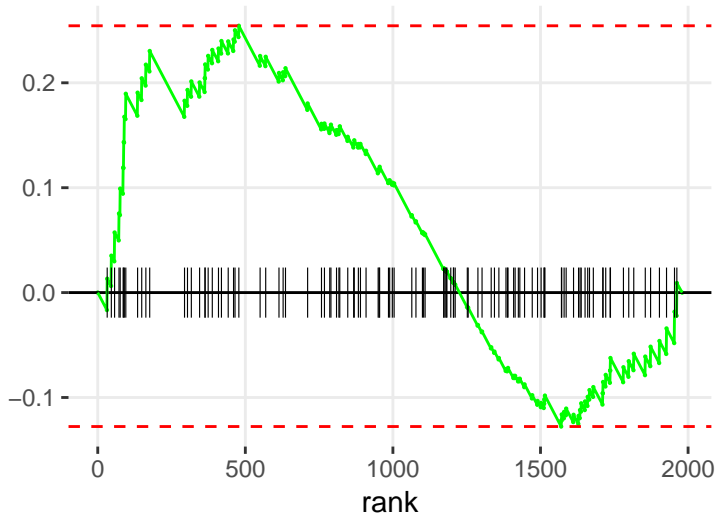


KETOGENESIS



# ARGININE BIOSYNTHESIS IV

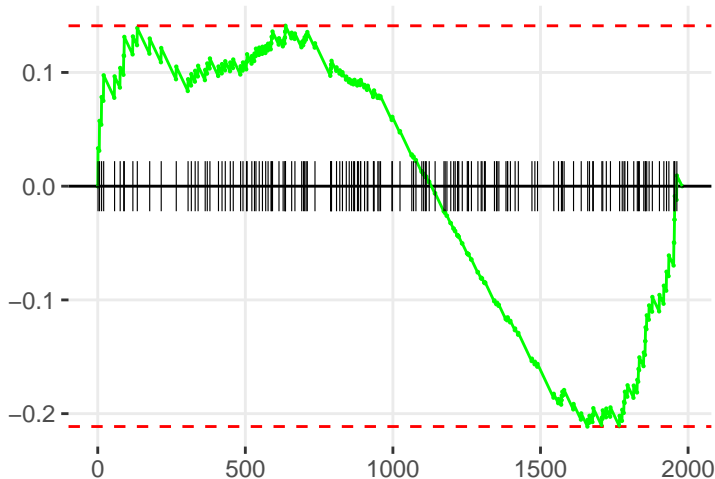
enrichment score



# PYRIMIDINE RIBONUCLEOTIDES INTERCONVERSION

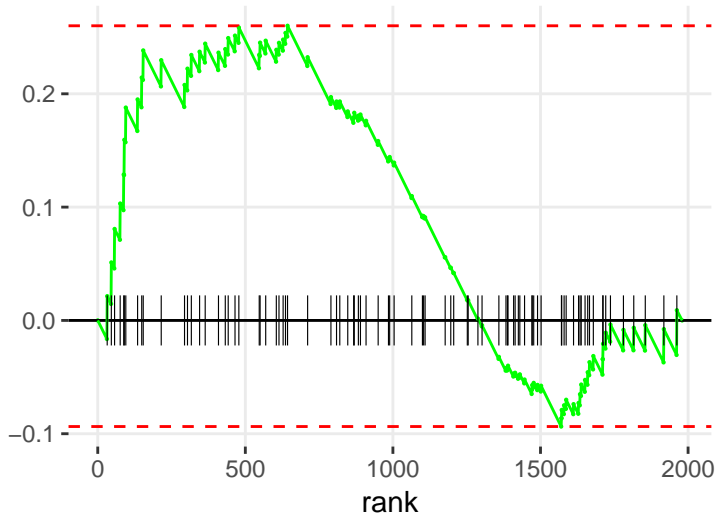
enrichment score

rank

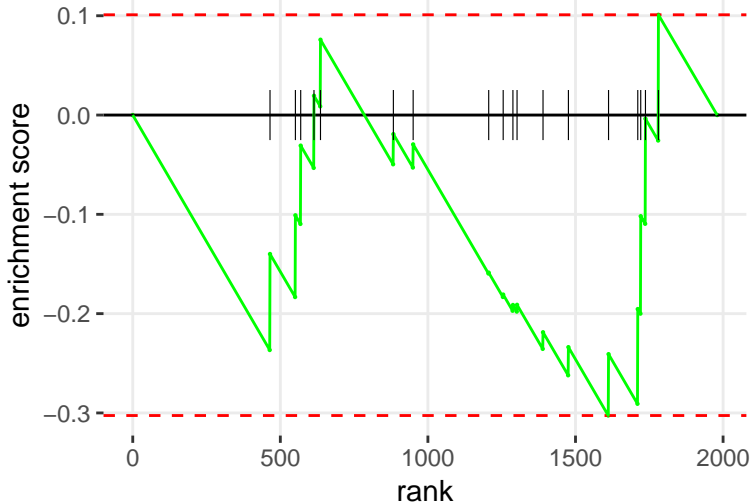


UREA CYCLE

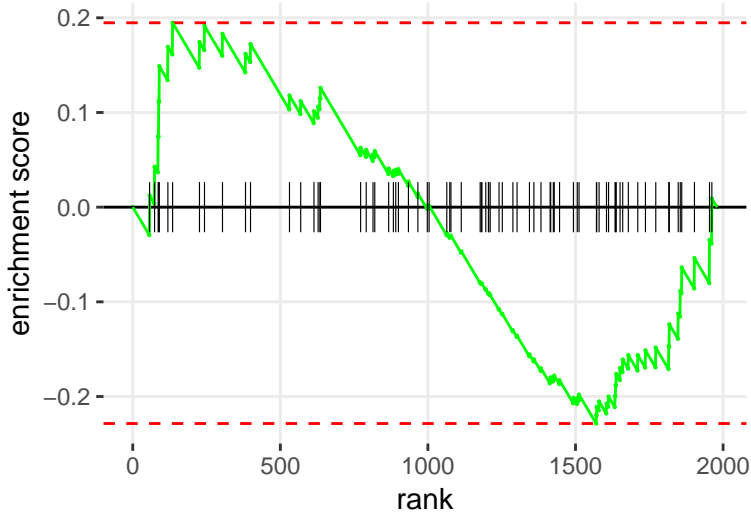
enrichment score



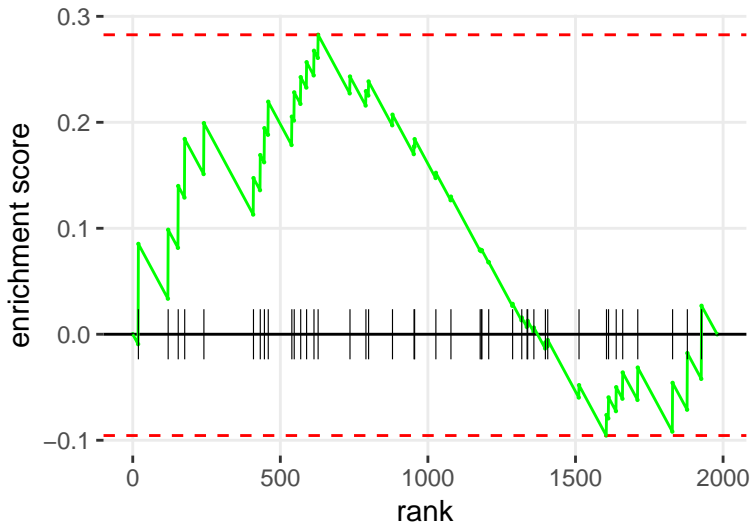
## D-MANNOSE DEGRADATION



## UDP-&lt;I&gt;l&lt;/I&gt;-ACETYL-D-GLUCOSAMINE BIOSYNTHESIS II



# PYRUVATE FERMENTATION TO LACTATE

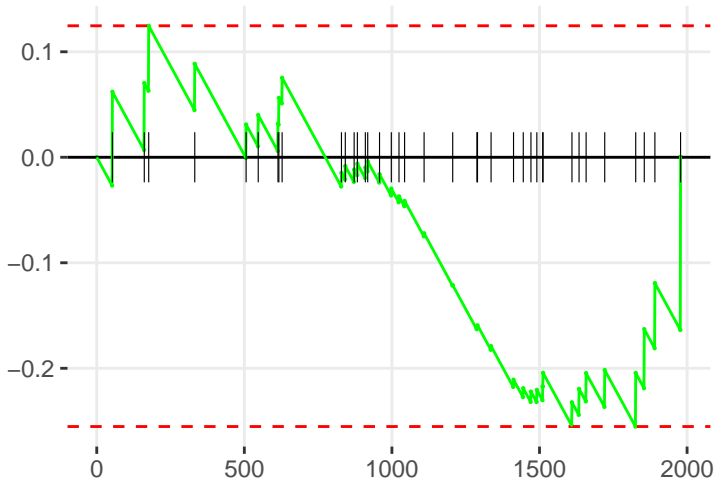




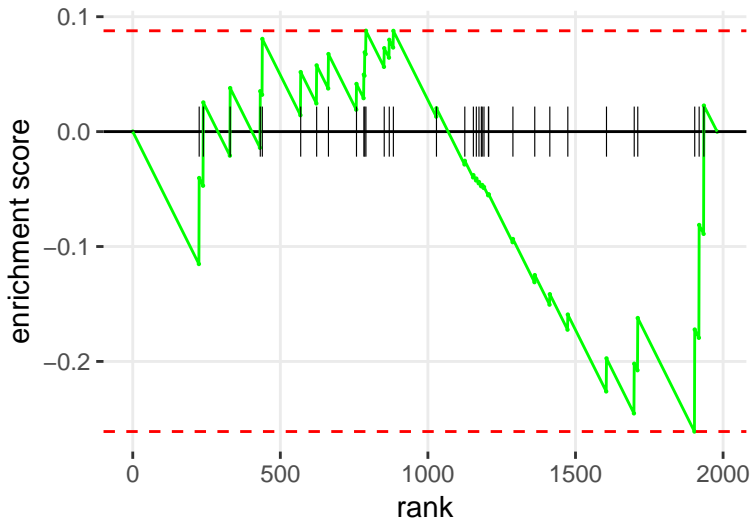
# ADENOSINE NUCLEOTIDES DEGRADATION II

enrichment score

rank



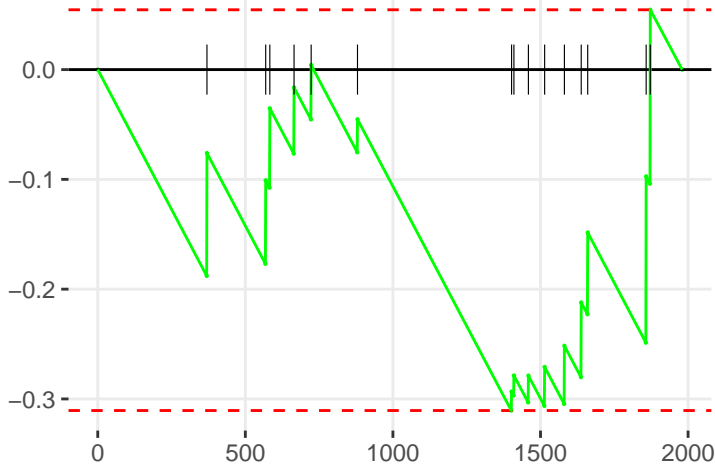
# CALCIUM TRANSPORT I



# CHONDROITIN SULFATE DEGRADATION (METAZOA)

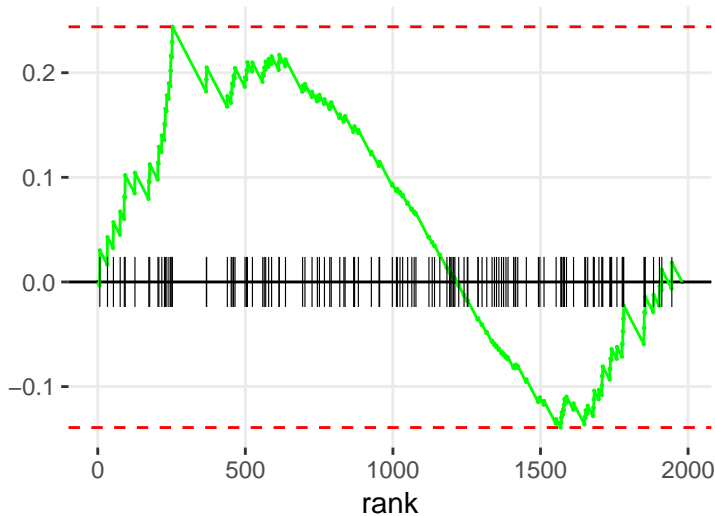
enrichment score

rank



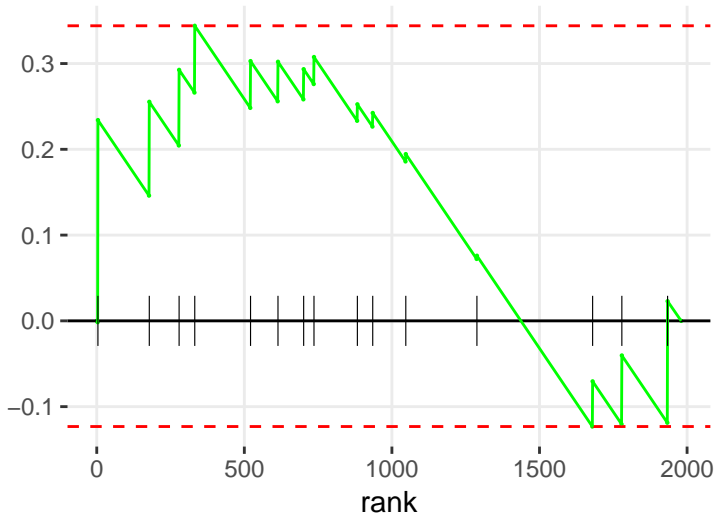
# FOLATE TRANSFORMATIONS I

enrichment score



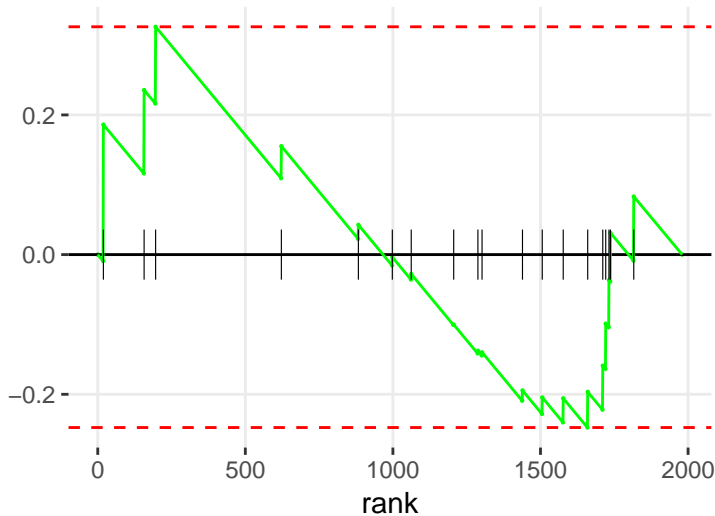
# SPHINGOMYELIN METABOLISM

enrichment score



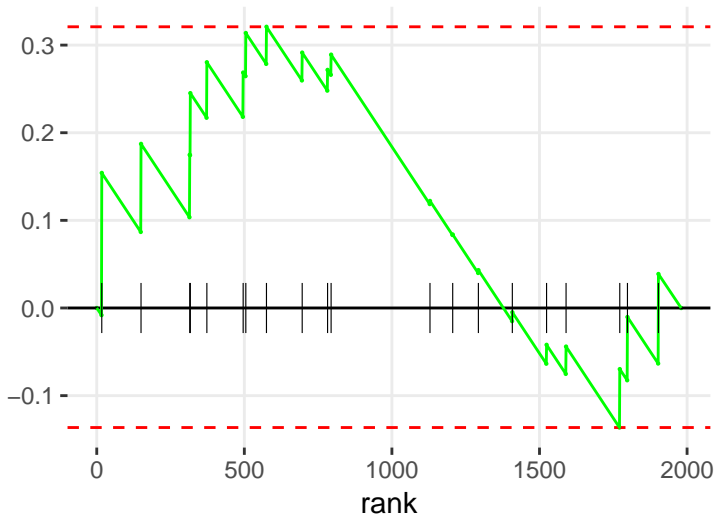
# LEUKOTRIENE BIOSYNTHESIS

enrichment score

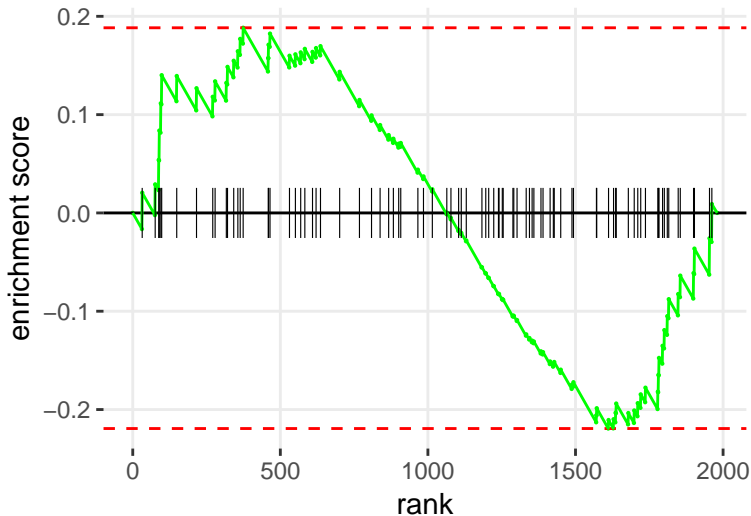


# NAD BIOSYNTHESIS FROM 2-AMINO-3-CARBOXYMUCONATE SEMIALDEHYDE

enrichment score

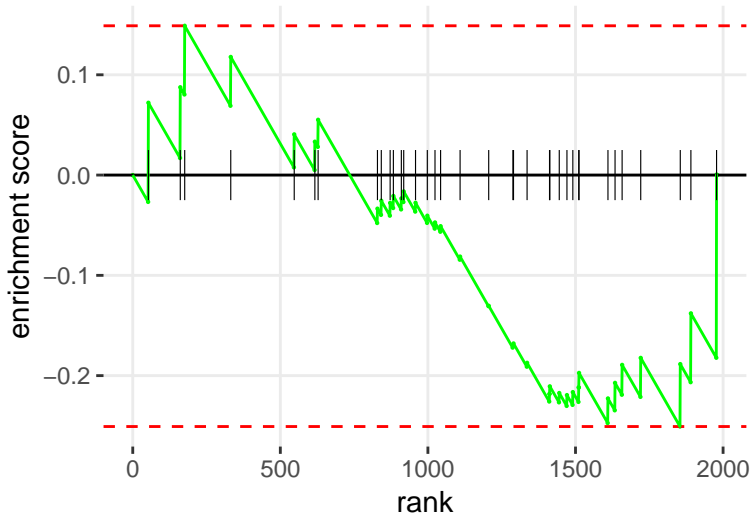


TREHALOSE DEGRADATION II (TREHALASE)



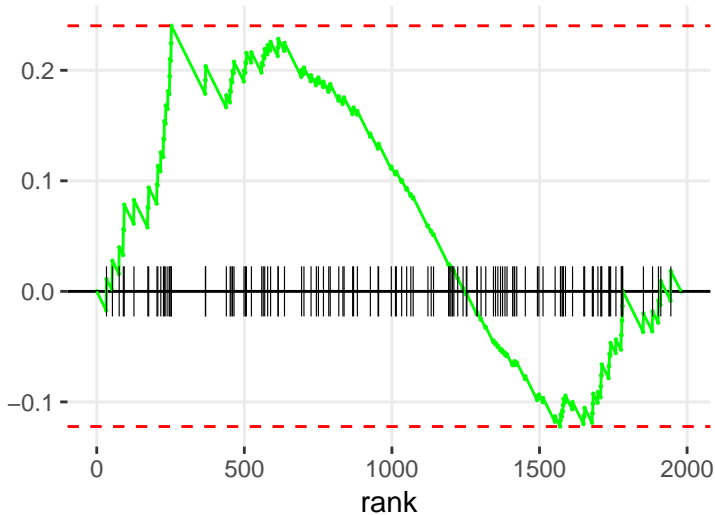


# GUANOSINE NUCLEOTIDES DEGRADATION III



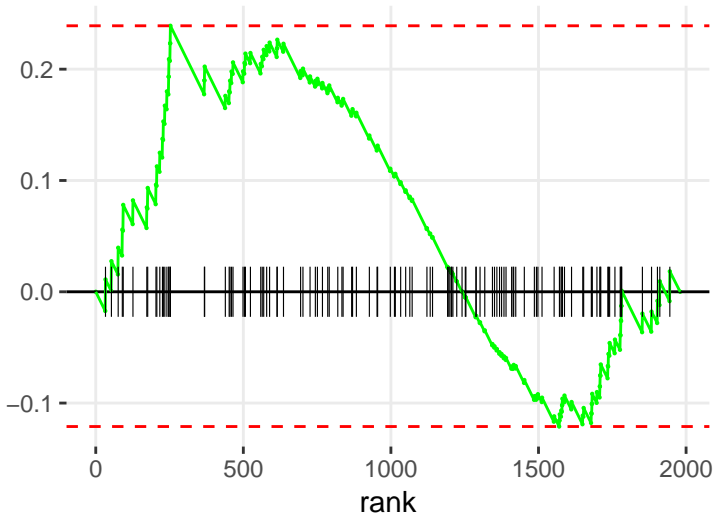
# GLYCINE BIOSYNTHESIS I

enrichment score



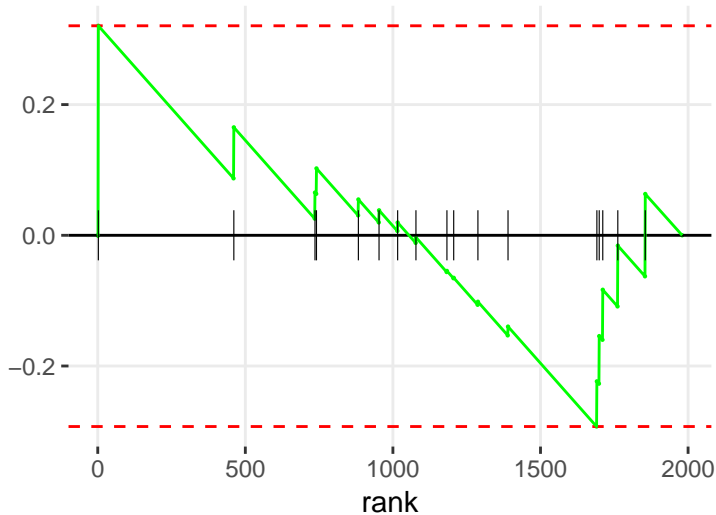
# GLYCINE BETAIN DEGRADATION

enrichment score



# MITOCHONDRIAL L-CARNITINE SHUTTLE PATHWAY

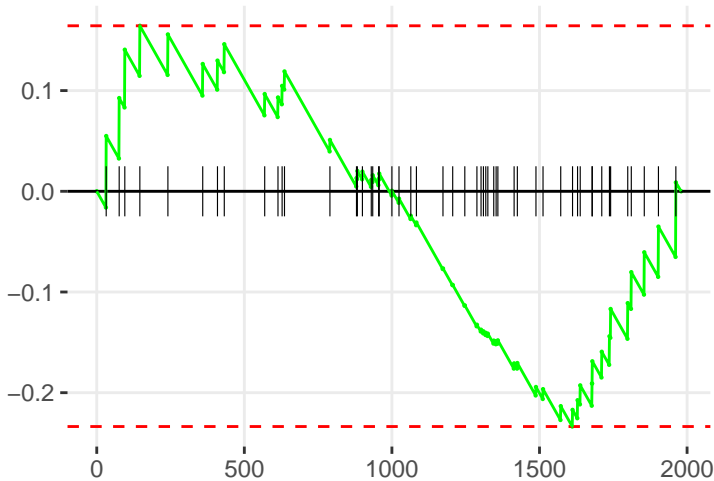
enrichment score



# STEARATE BIOSYNTHESIS I (ANIMALS)

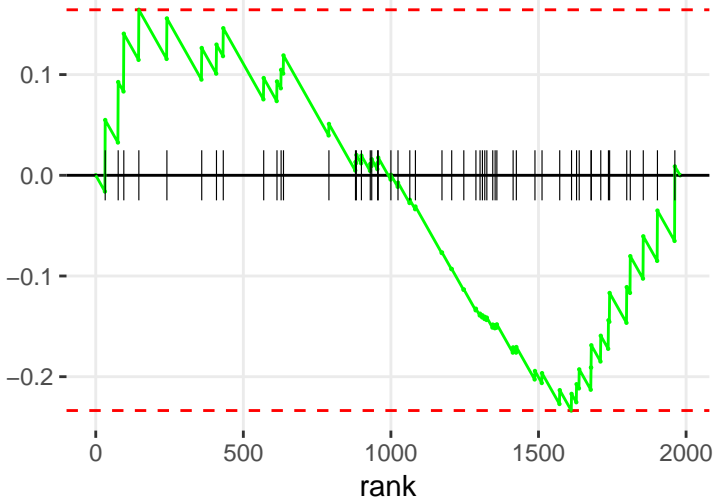
enrichment score

rank

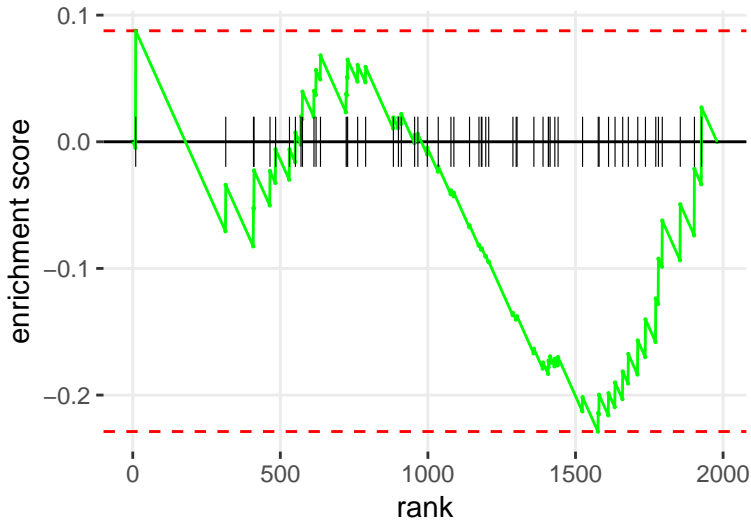


# EICOSAPENTAENOATE BIOSYNTHESIS II (METAZOA)

enrichment score

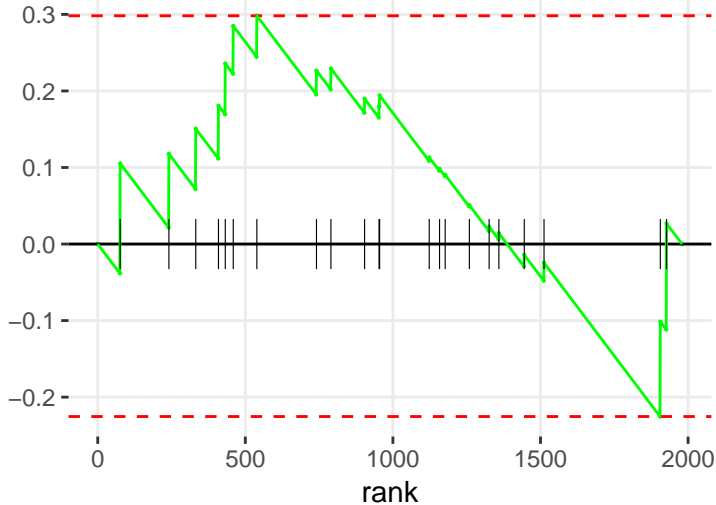


# ISOLEUCINE DEGRADATION I



# CREATINE-PHOSPHATE BIOSYNTHESIS

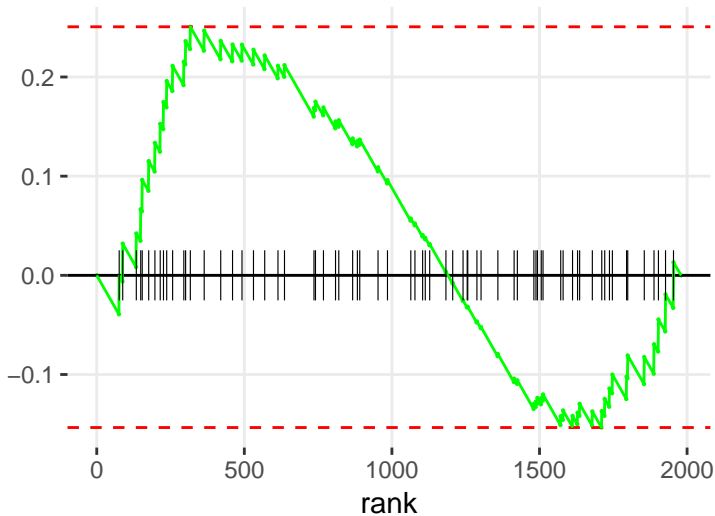
enrichment score





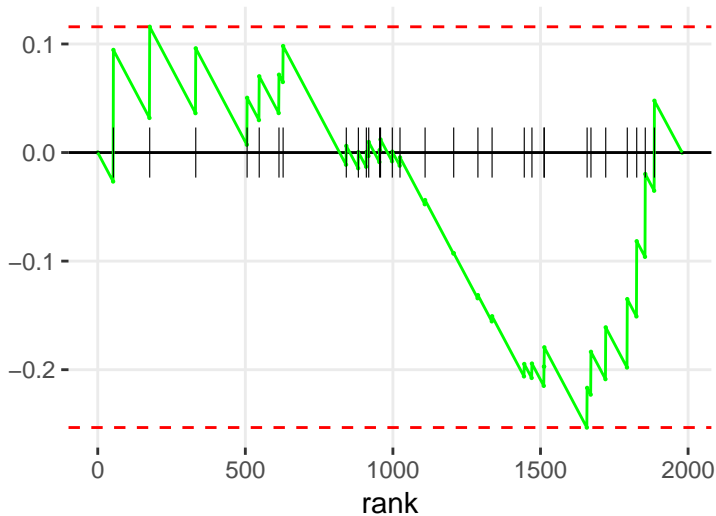
# GLYCINE CLEAVAGE

enrichment score



# ADENINE AND ADENOSINE SALVAGE III

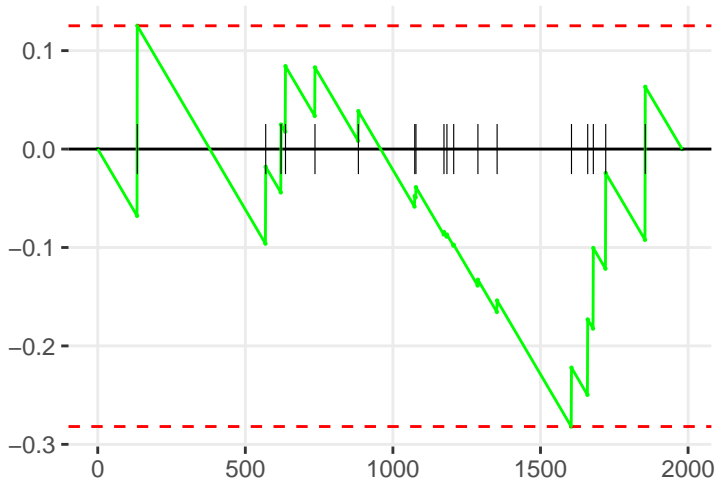
enrichment score



# OLEATE BIOSYNTHESIS II (ANIMALS)

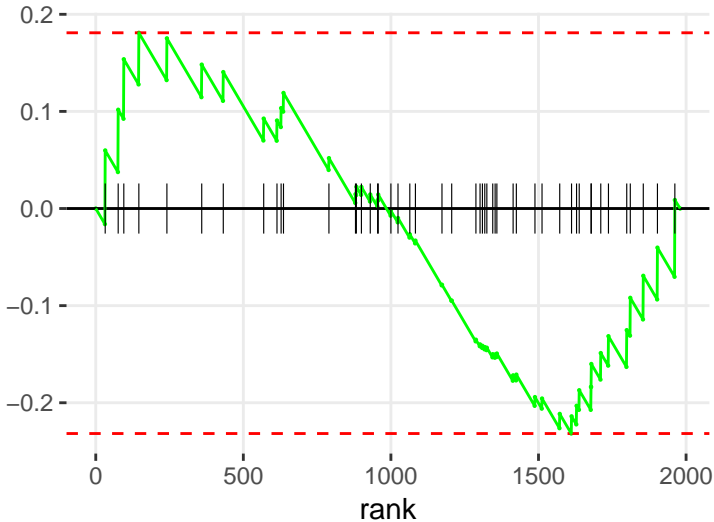
enrichment score

rank



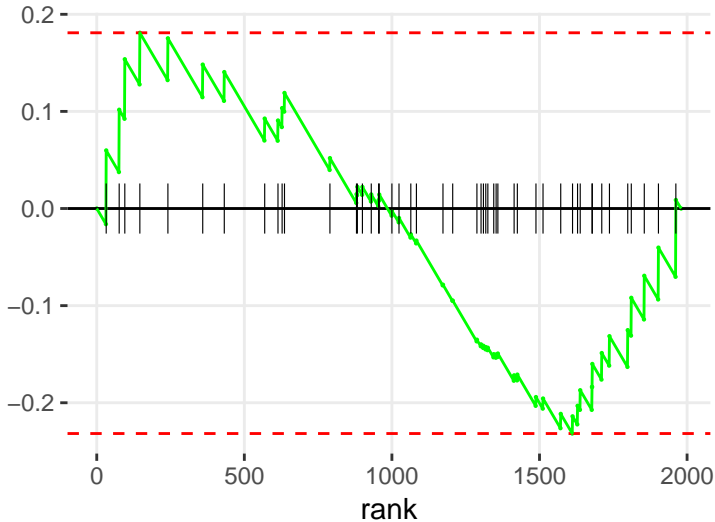
# FATTY ACID ACTIVATION

enrichment score

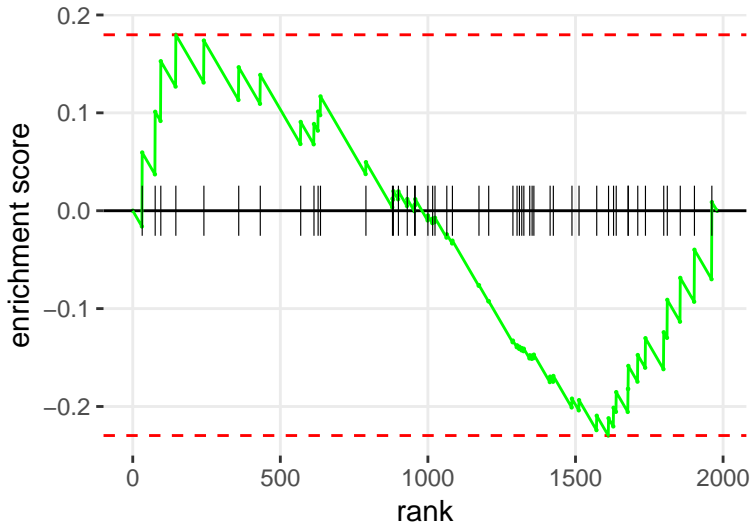


# FATTY ACID &ALPHA;-OXIDATION II

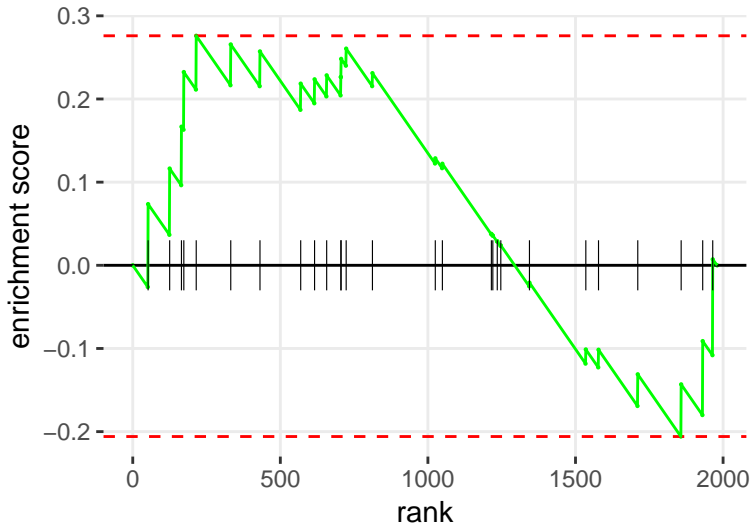
enrichment score



&GAMMA;-LINOLENATE BIOSYNTHESIS II (ANIMALS)

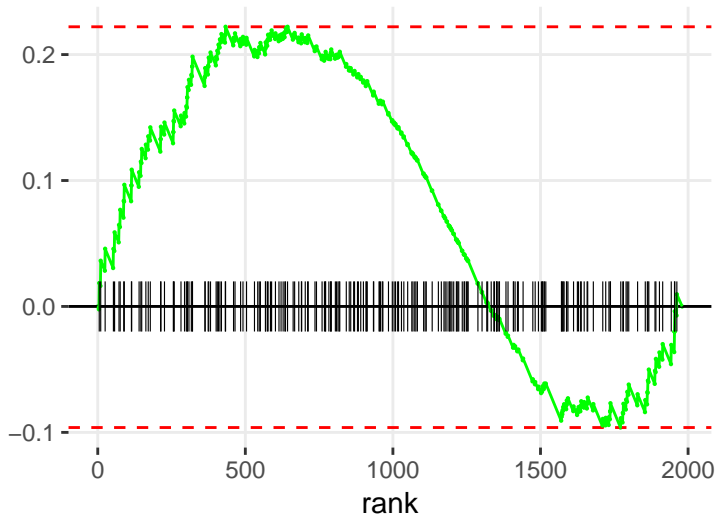


# SALVAGE PATHWAYS OF PYRIMIDINE DEOXYRIBONUCLEOTIDES



# TRNA CHARGING

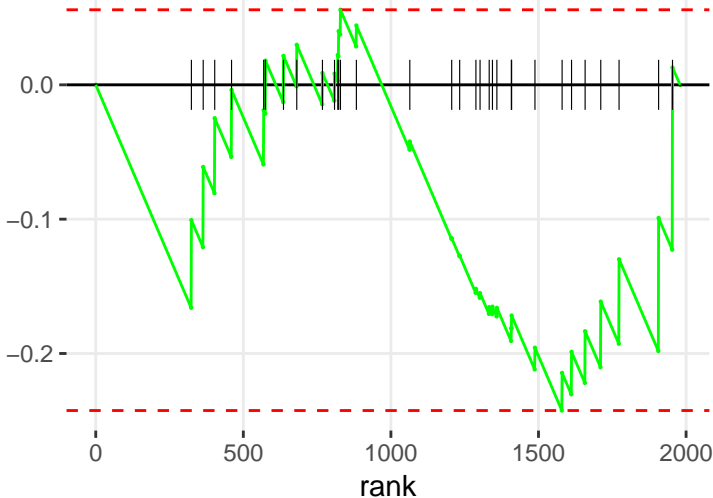
enrichment score





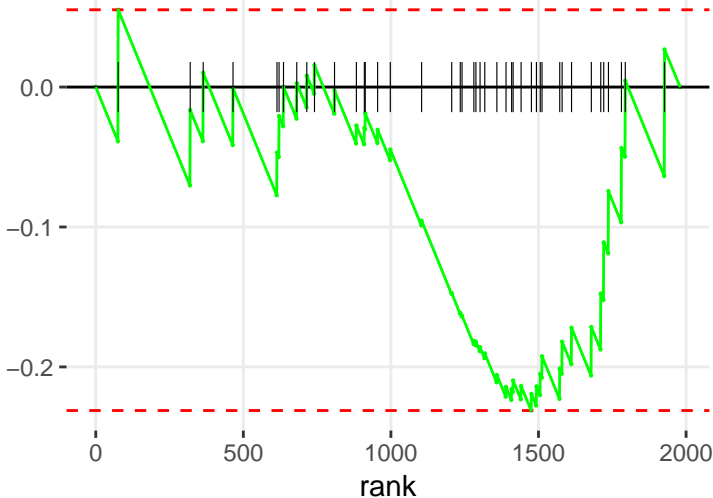
# TETRAHYDROBIOPTERIN BIOSYNTHESIS II

enrichment score

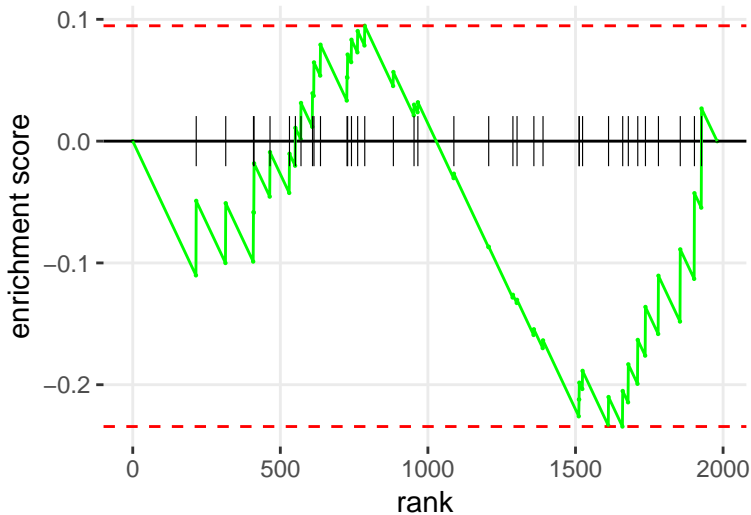


# PHENYLALANINE DEGRADATION IV (MAMMALIAN, VIA SIDE CHAIN)

enrichment score

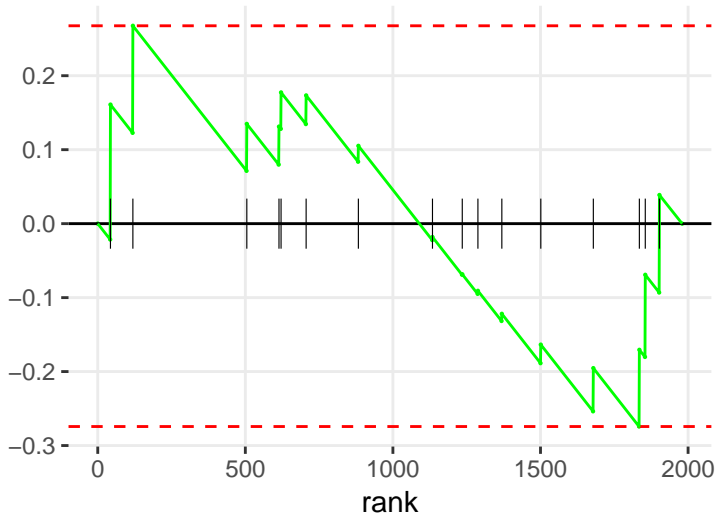


# LEUCINE DEGRADATION I

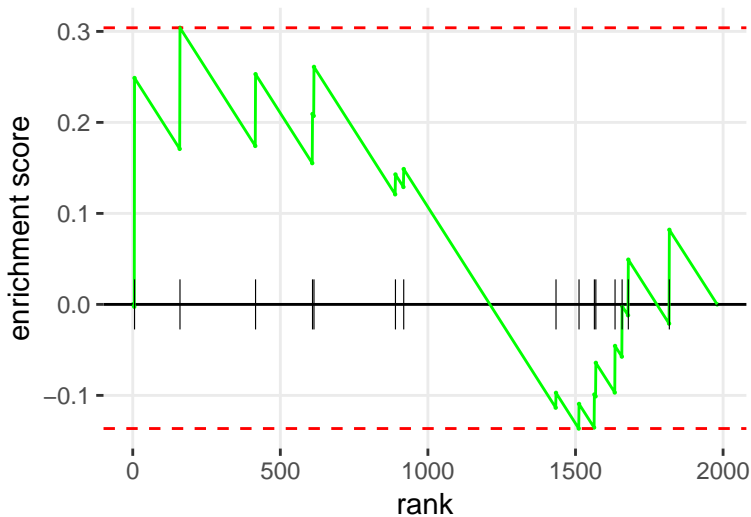


# TETRAPYRROLE BIOSYNTHESIS II

enrichment score

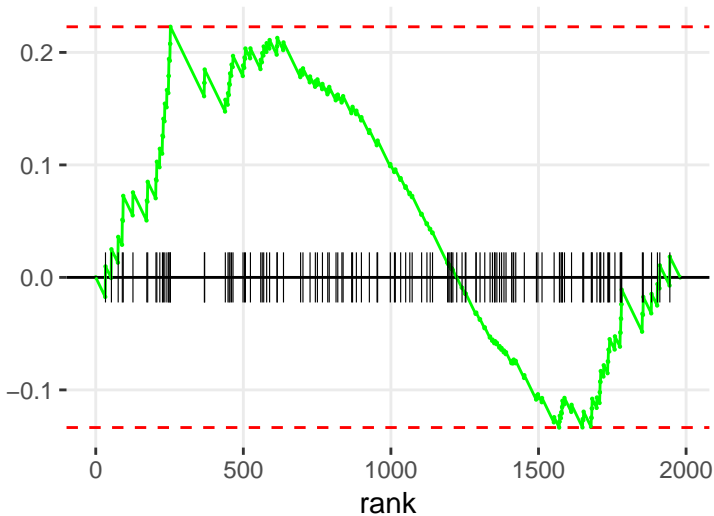


<IS</I-METHYL-5-THIO-&ALPHA;-D-RIBOSE 1-PHOSPHATE DEGRADATION



DTMP <IDE NOVO</I> BIOSYNTHESIS

enrichment score



# TETRAHYDROBIOPTERIN BIOSYNTHESIS I

enrichment score

0.0

-0.1

-0.2

0

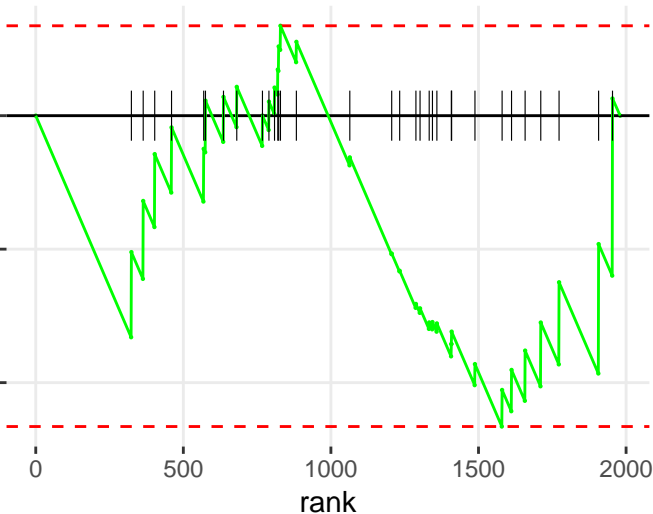
500

1000

1500

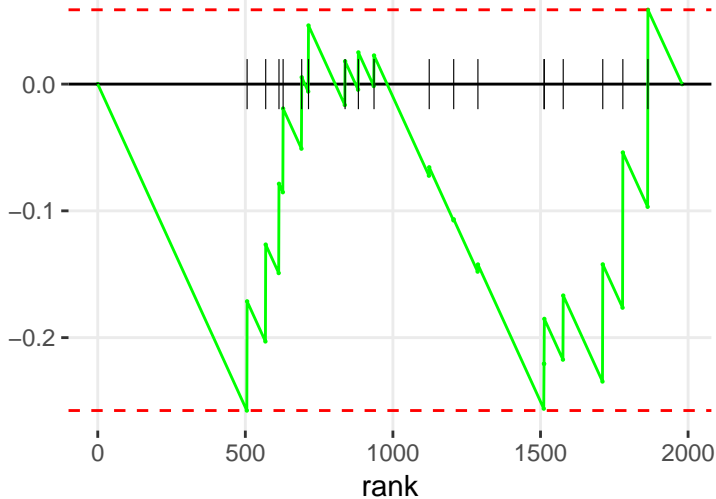
2000

rank



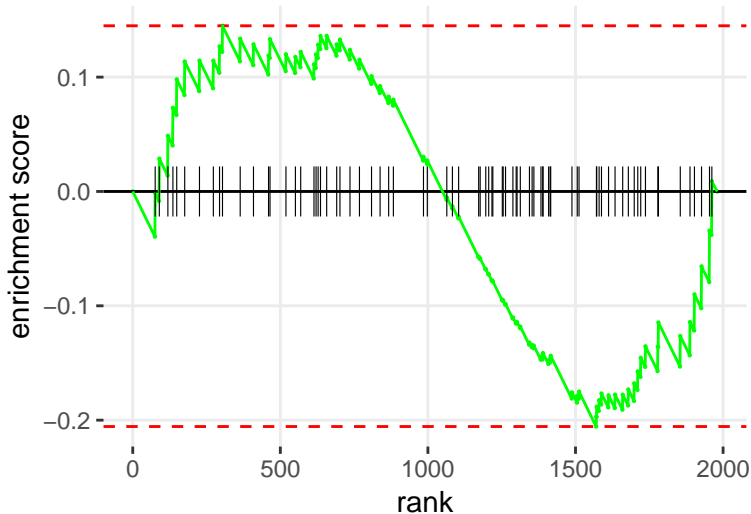
# INOSINE-5'-PHOSPHATE BIOSYNTHESIS II

enrichment score

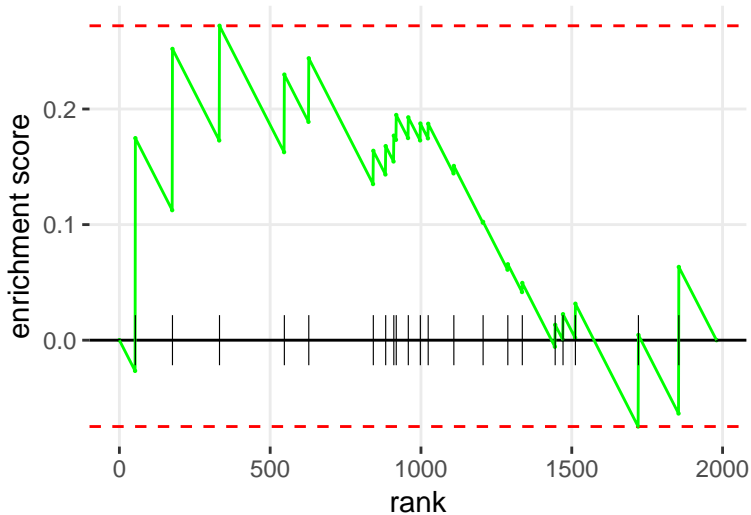




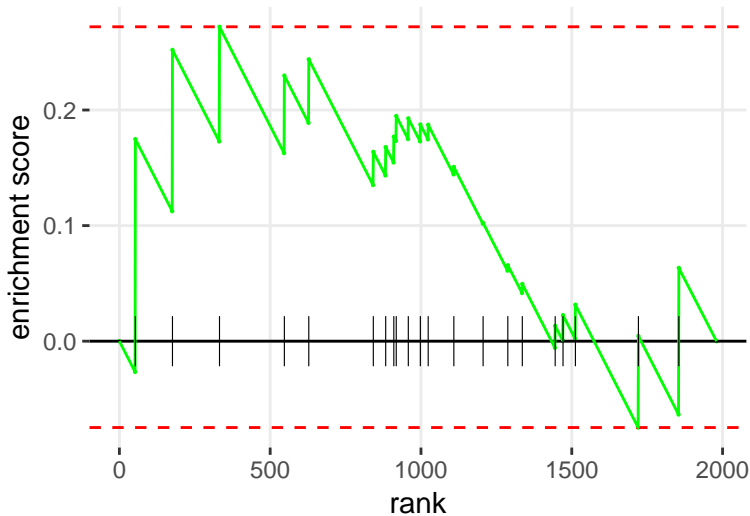
# PENTOSE PHOSPHATE PATHWAY (OXIDATIVE BRANCH)



# XANTHINE AND XANTHOSINE SALVAGE

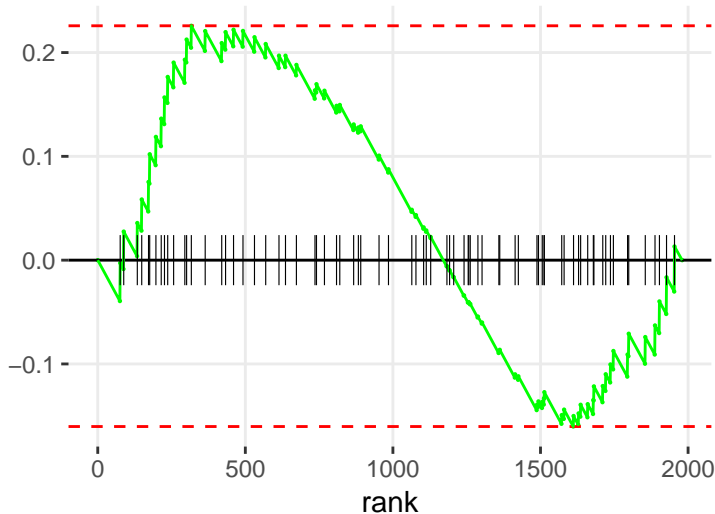


# ARSENATE DETOXIFICATION I (GLUTAREDOXIN)

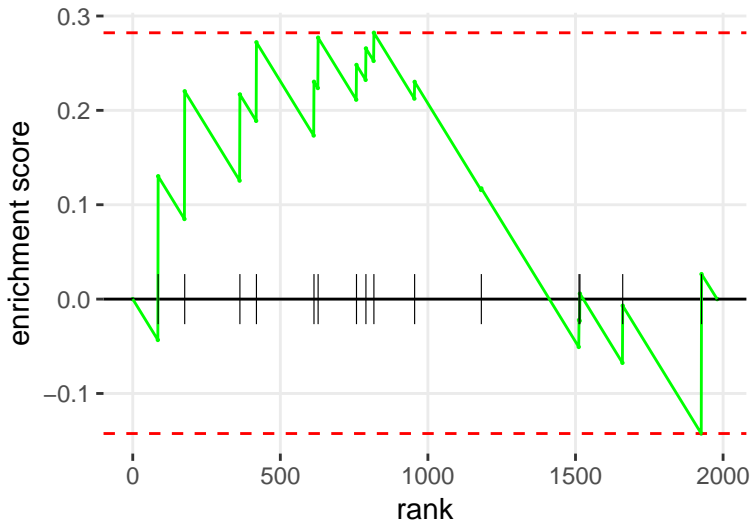


# 2-OXISOVALERATE DECARBOXYLATION TO ISOBUTANOYL-COA

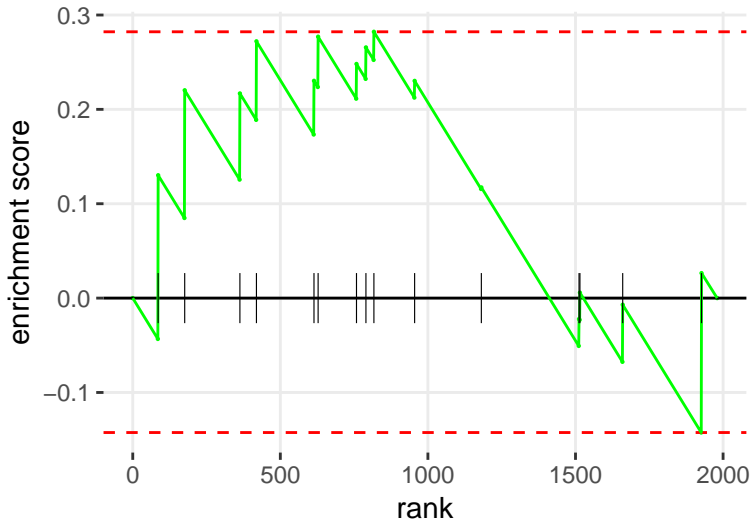
enrichment score



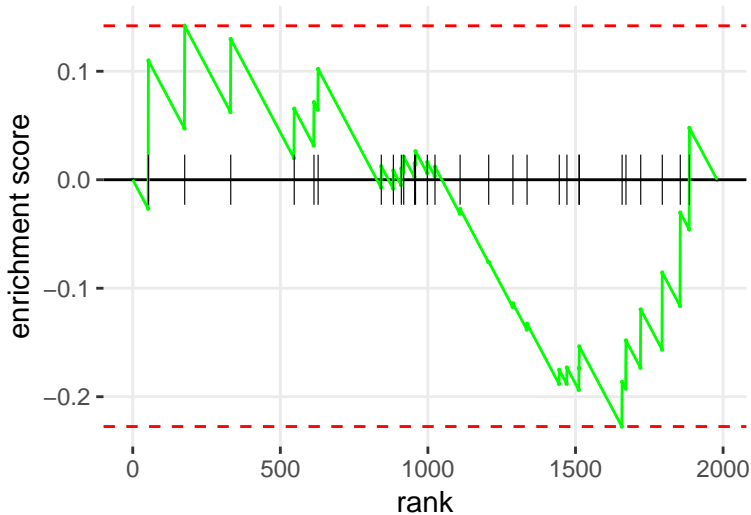
# GLUTAMATE BIOSYNTHESIS II



GLUTAMATE DEGRADATION X

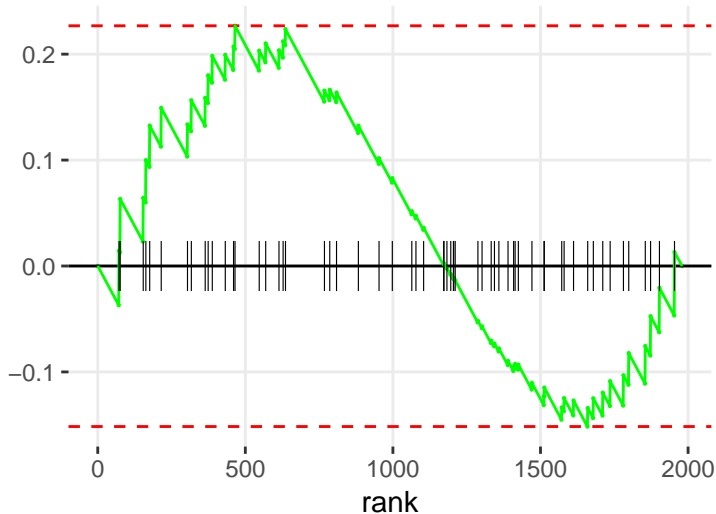


# GUANINE AND GUANOSINE SALVAGE I



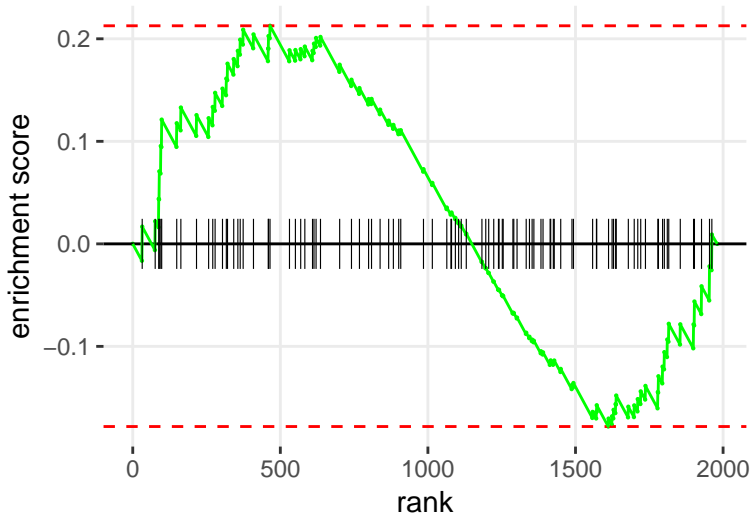
# ARGININE DEGRADATION I (ARGINASE PATHWAY)

enrichment score

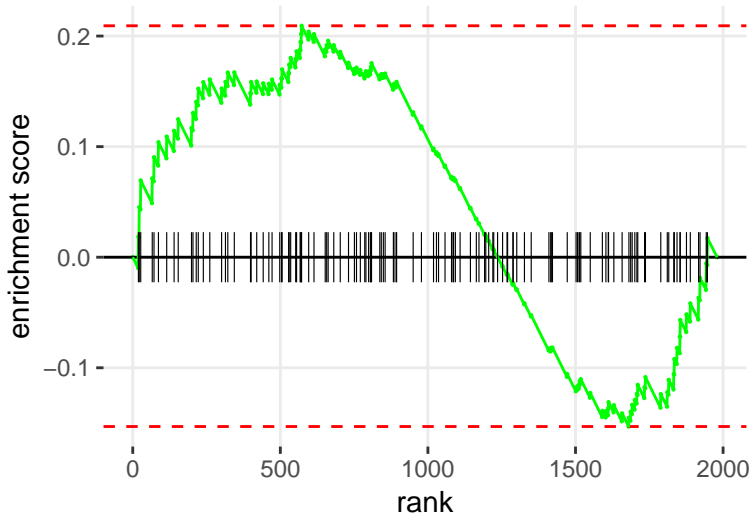




# GDP-GLUCOSE BIOSYNTHESIS

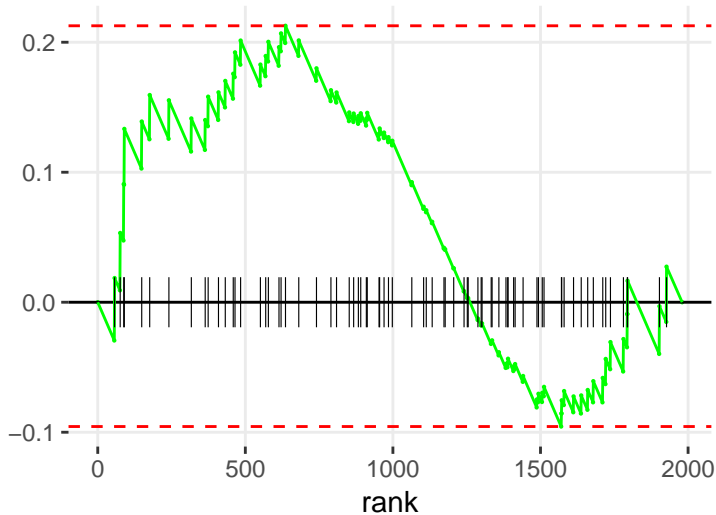


### 3-PHOSPHOINOSITIDE DEGRADATION



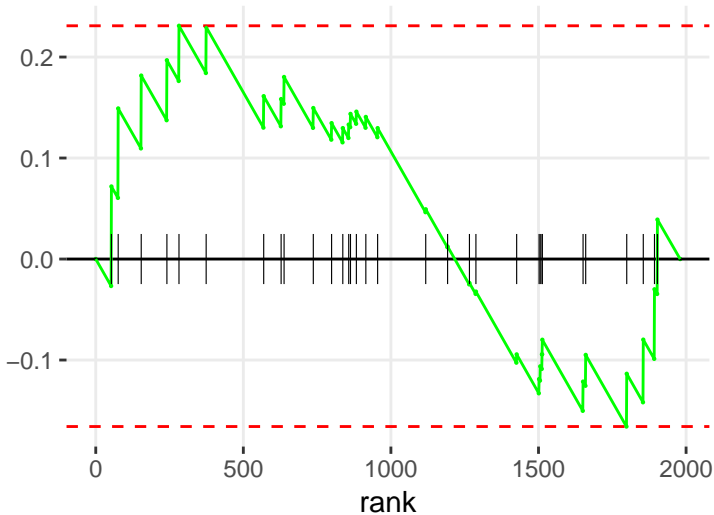
# ASPARTATE DEGRADATION II

enrichment score

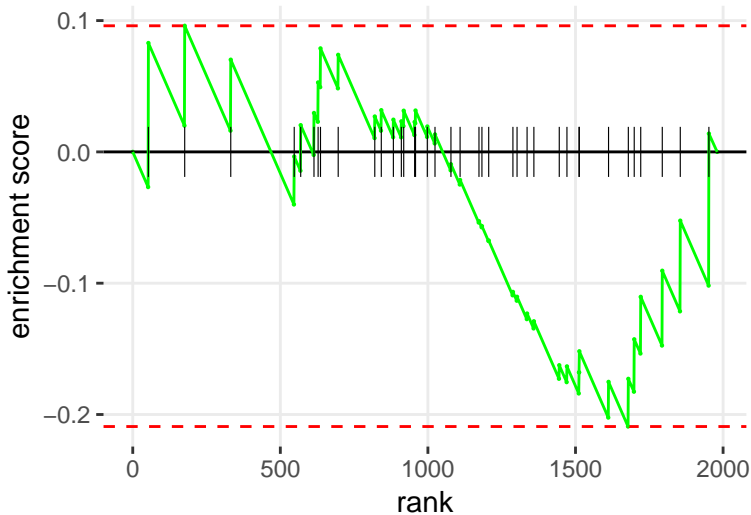


# ZYMOSTEROL BIOSYNTHESIS

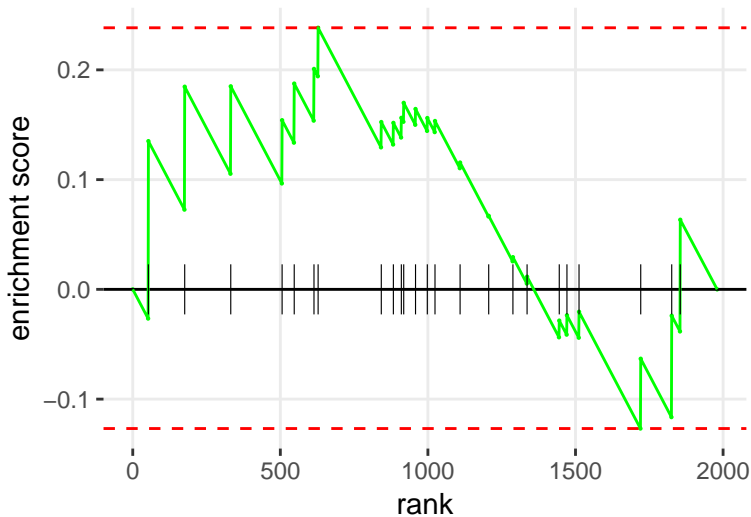
enrichment score



# ADENINE AND ADENOSINE SALVAGE I

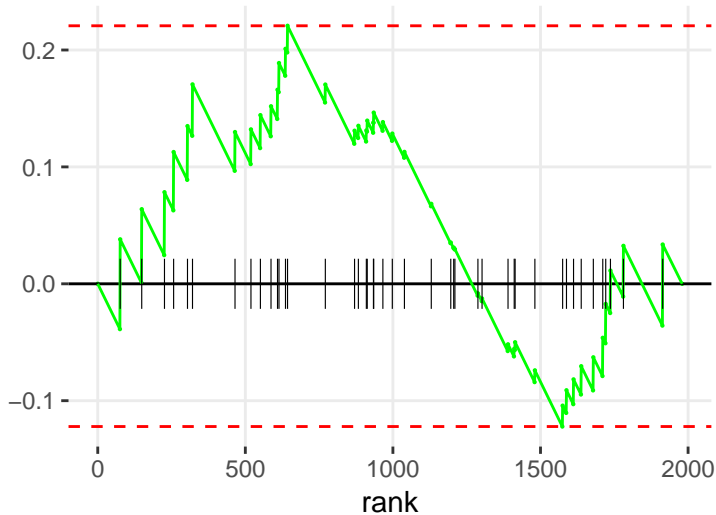


# PURINE RIBONUCLEOSIDES DEGRADATION TO RIBOSE-1-PHOSPHATE



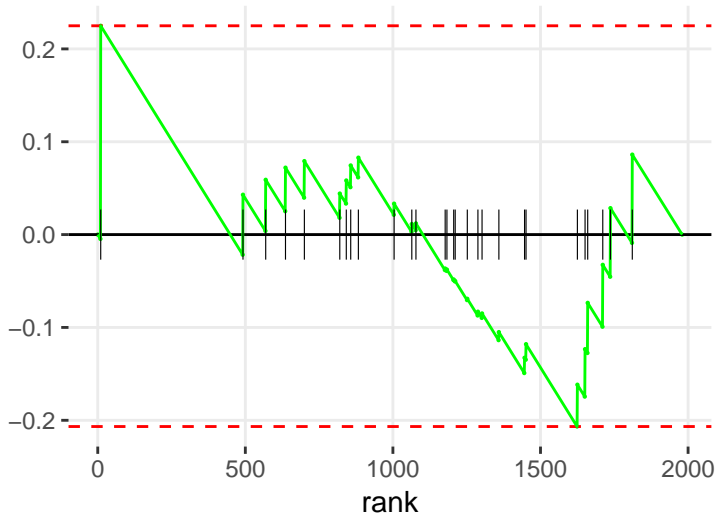
# 5-AMINOIMIDAZOLE RIBONUCLEOTIDE BIOSYNTHESIS I

enrichment score



# PHOSPHATIDYLCHOLINE BIOSYNTHESIS I

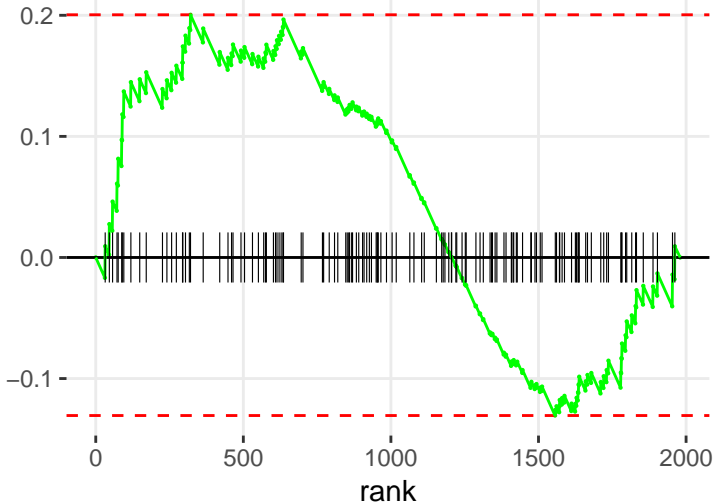
enrichment score



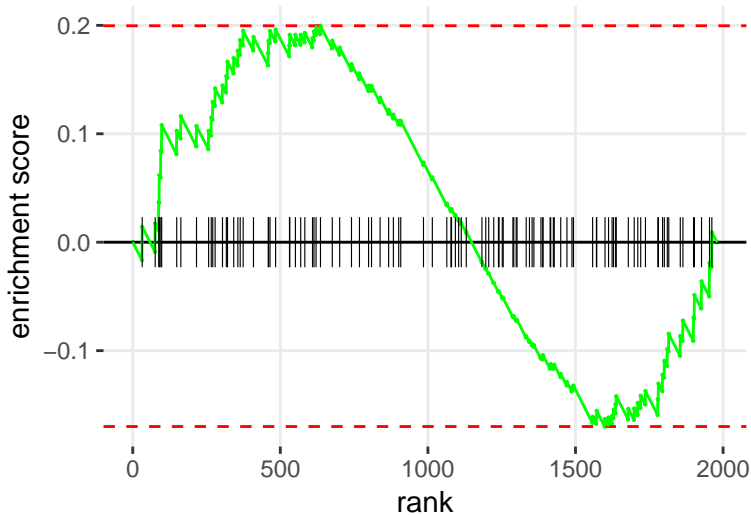


# GDP-MANNOSE BIOSYNTHESIS

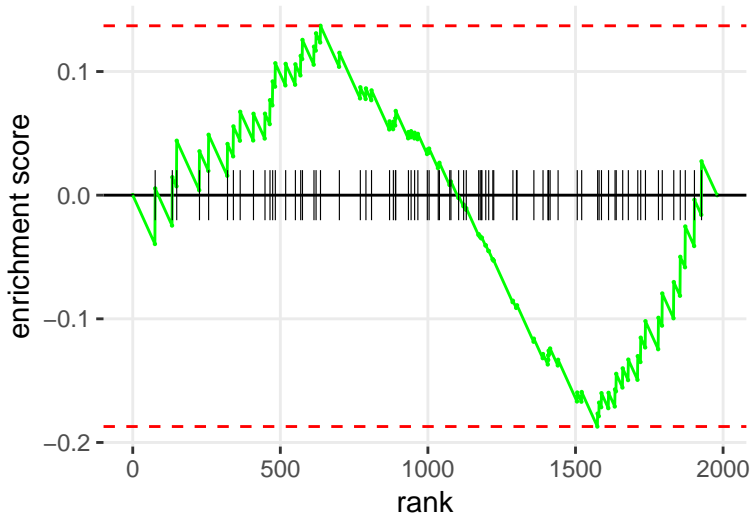
enrichment score



# GLUCOSE AND GLUCOSE-1-PHOSPHATE DEGRADATION

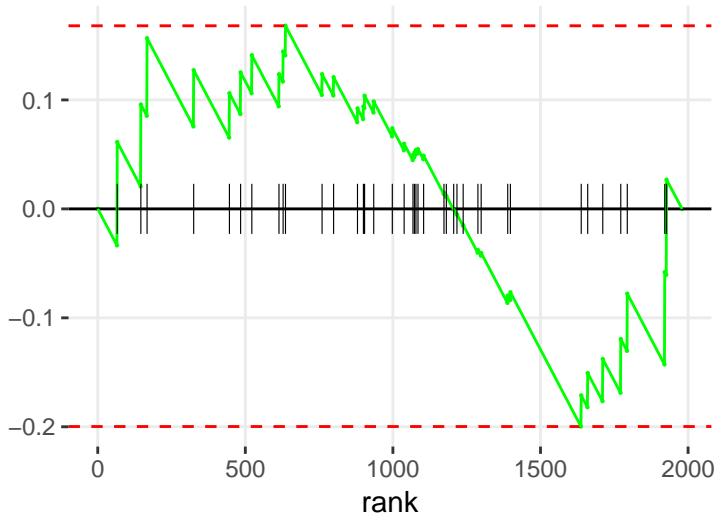


# MEVALONATE PATHWAY I

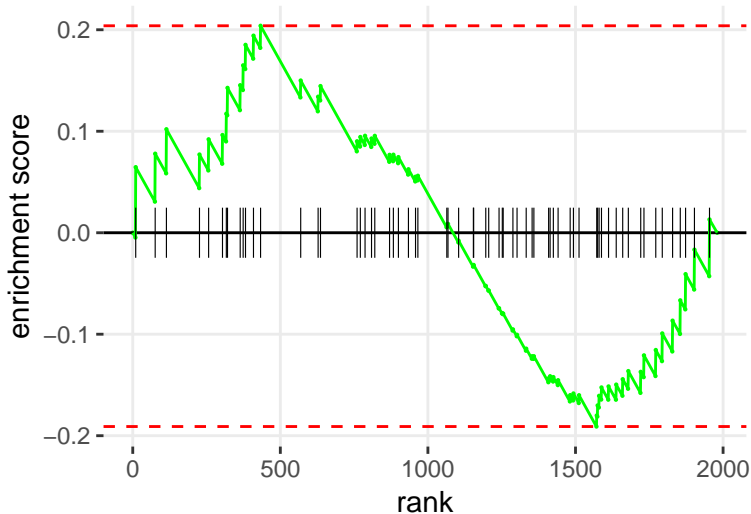


# PROSTANOID BIOSYNTHESIS

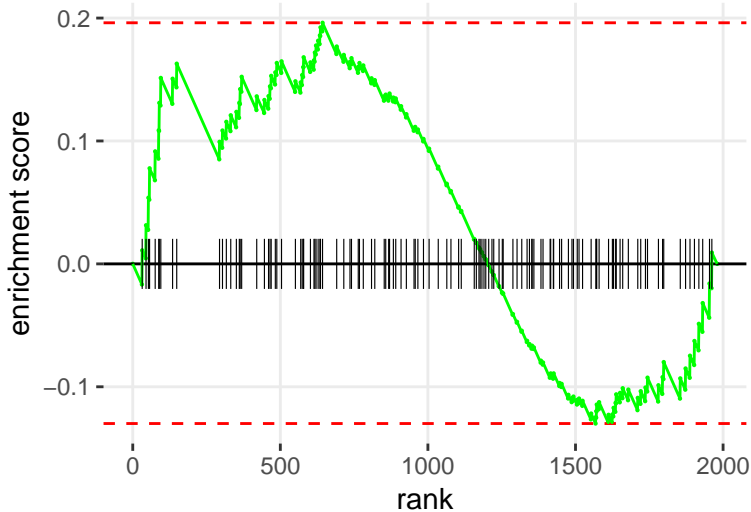
enrichment score



# SELENOCYSTEINE BIOSYNTHESIS II (ARCHAEA AND EUKARYOTES)

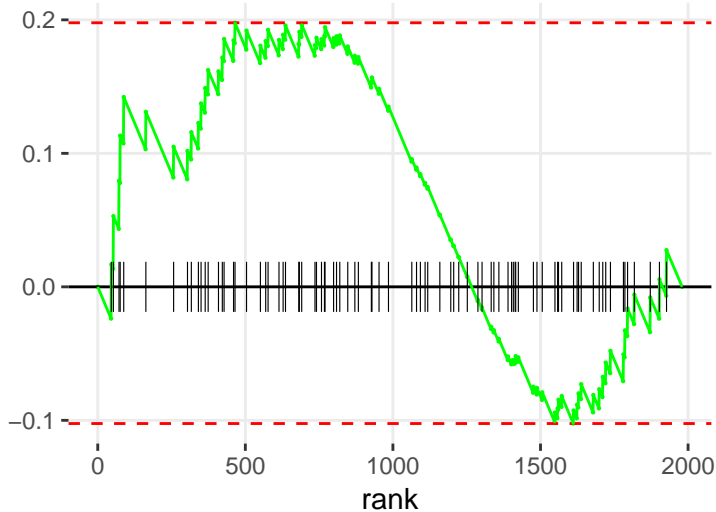


# PUTRESCINE DEGRADATION III

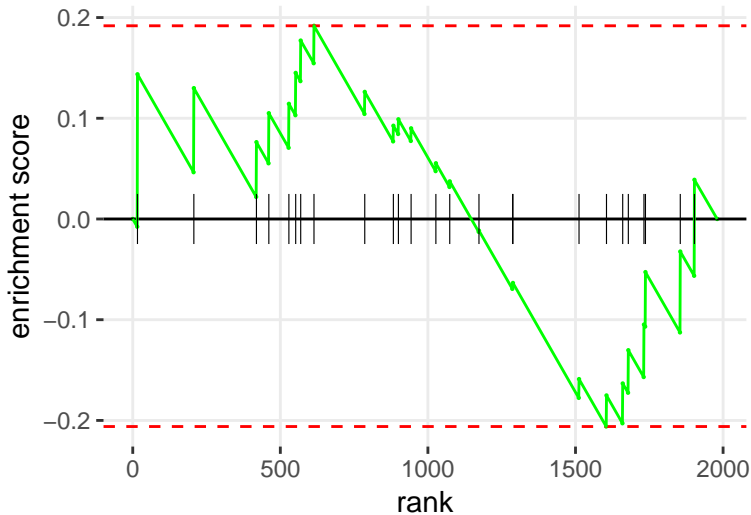


# GLYCOGEN DEGRADATION II

enrichment score

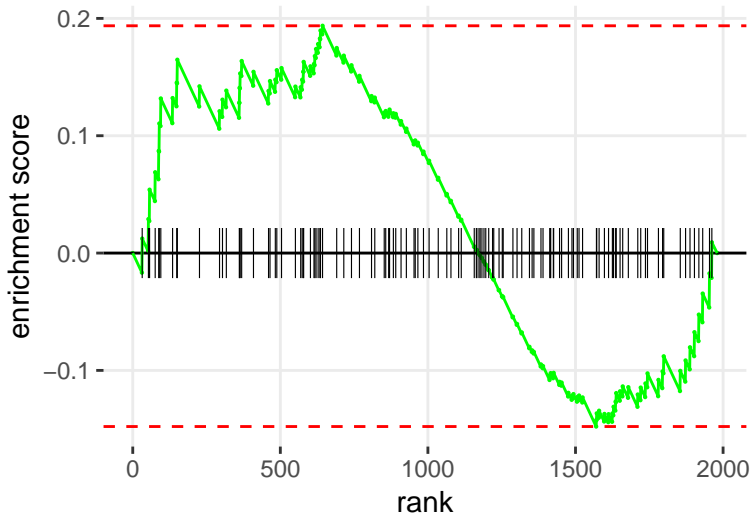


# CERAMIDE BIOSYNTHESIS

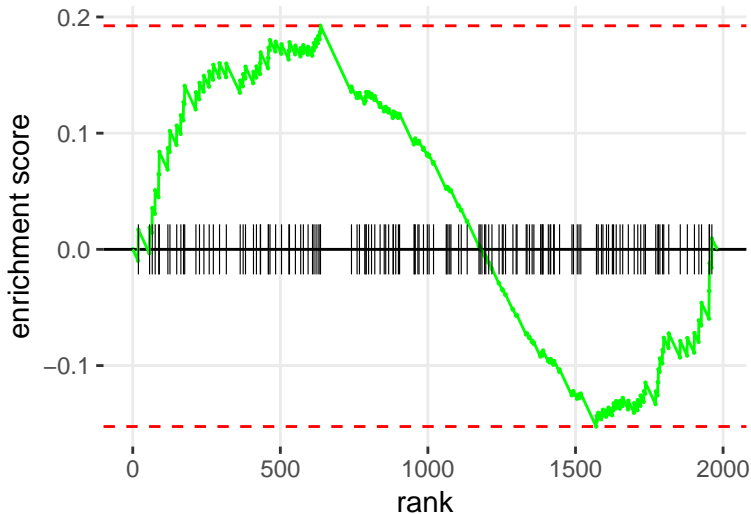




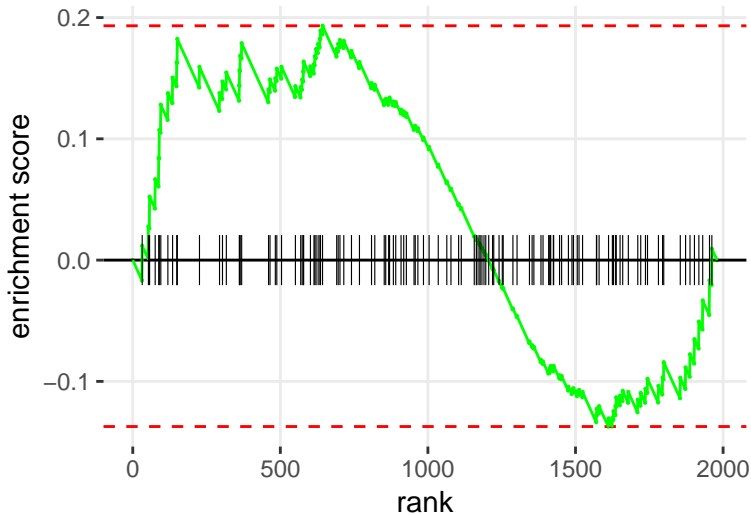
# NORADRENALINE AND ADRENALINE DEGRADATION



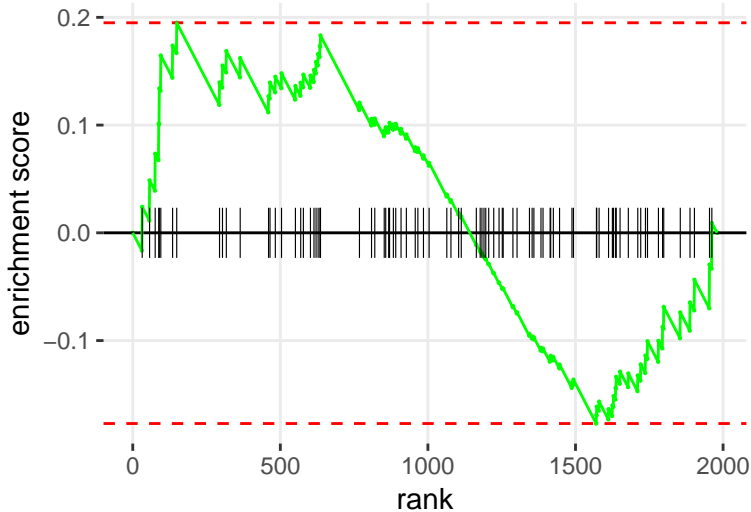
# TCA CYCLE II (EUKARYOTIC)



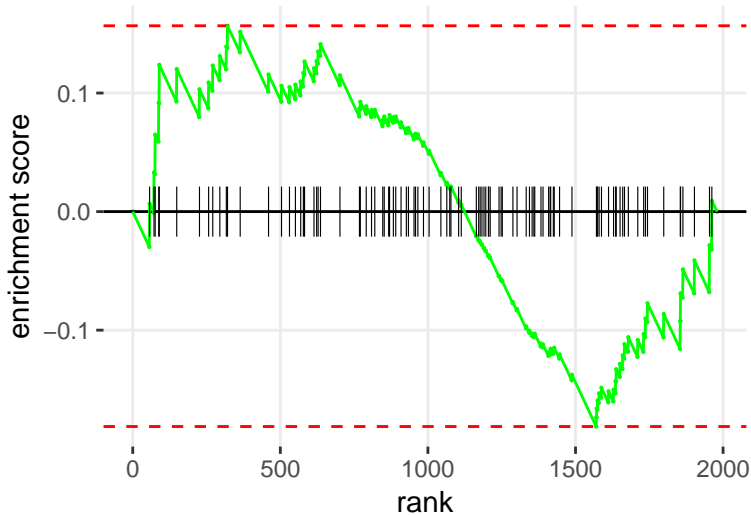
# ETHANOL DEGRADATION II



# RETINOATE BIOSYNTHESIS I

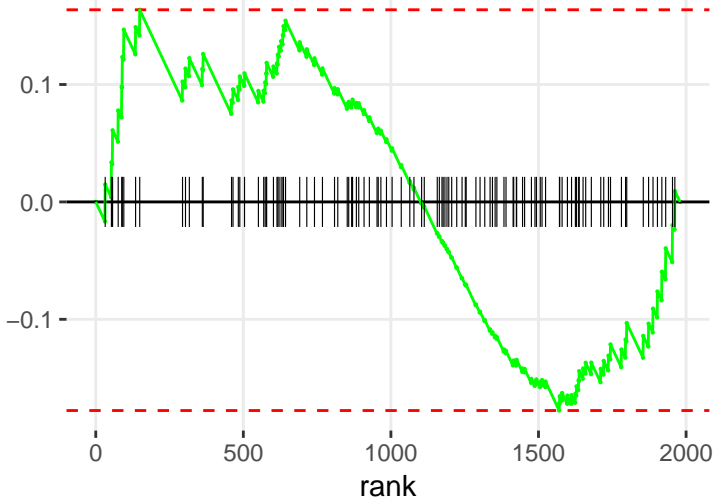


# S-ADENOSYL-L-METHIONINE BIOSYNTHESIS

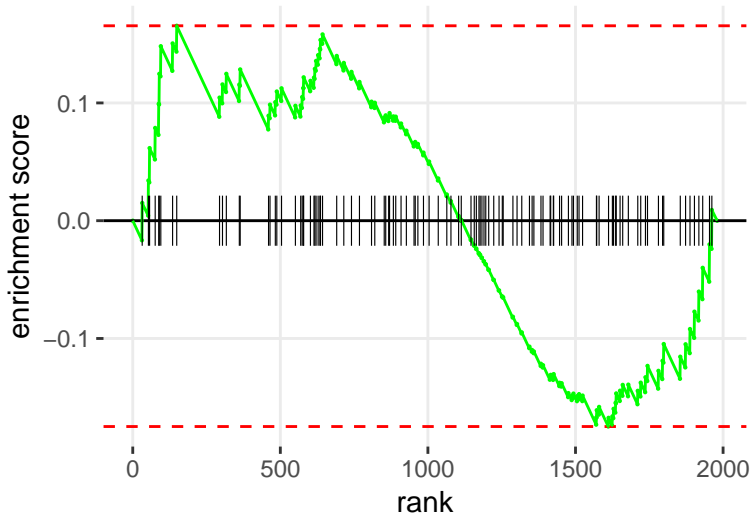


# DOPAMINE DEGRADATION

enrichment score



TRYPTOPHAN DEGRADATION X (MAMMALIAN, VIA TRYPTAMINE)



# CITRULLINE-NITRIC OXIDE CYCLE

enrichment score

0.1

0.0

-0.1

0

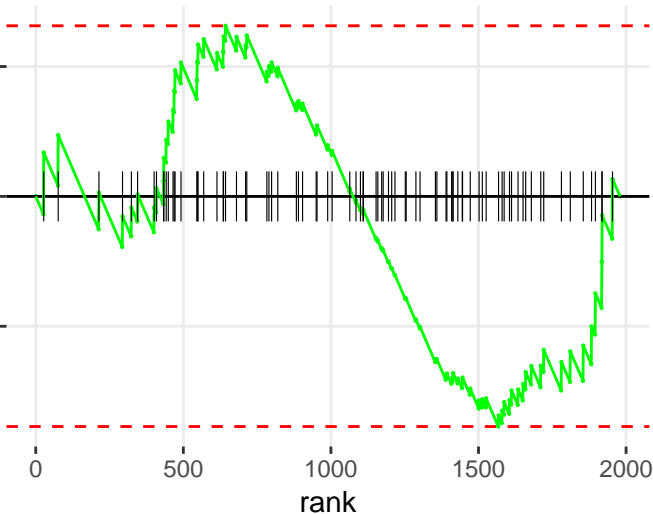
500

1000

1500

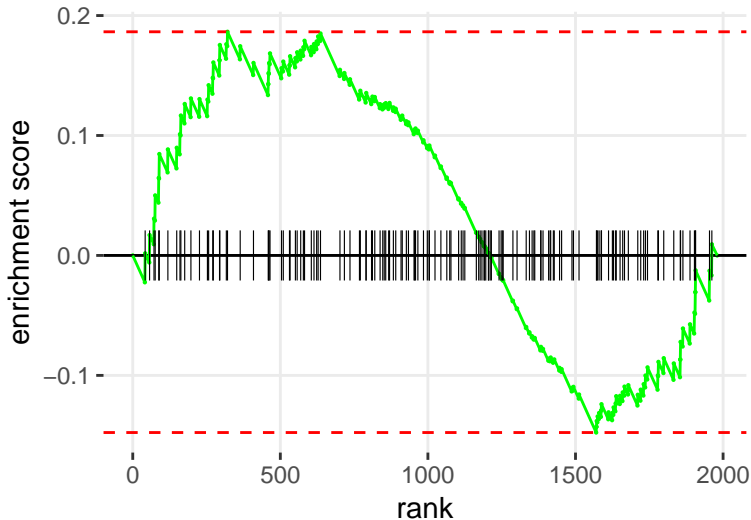
2000

rank

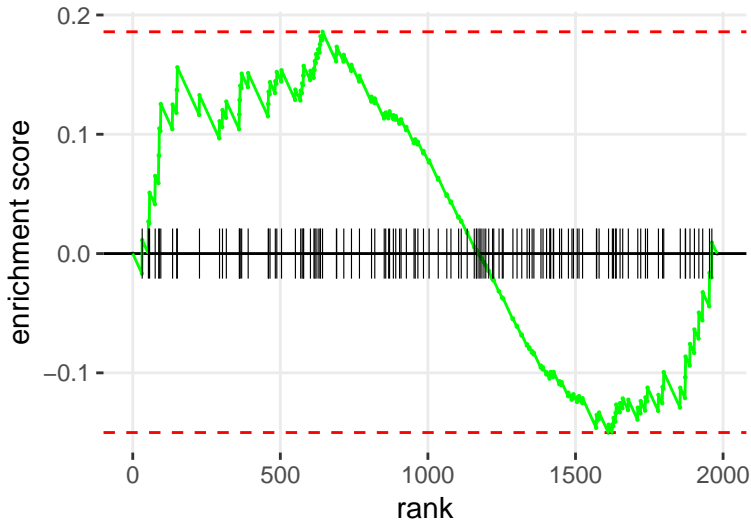




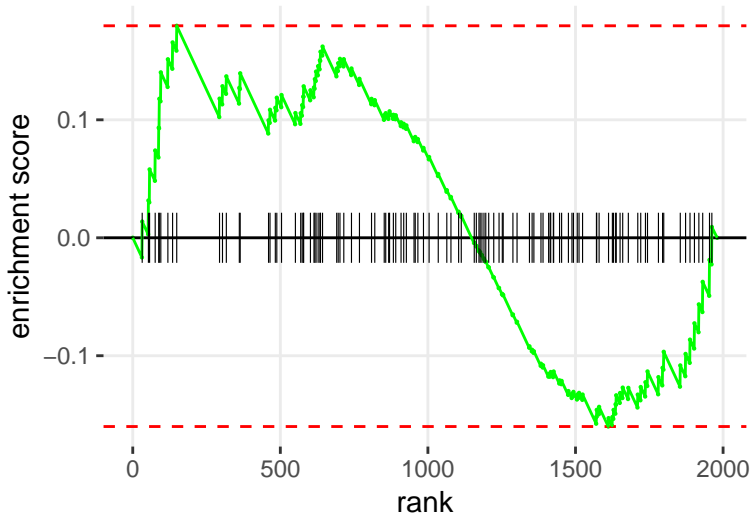
METHIONINE DEGRADATION I (TO HOMOCYSTEINE)



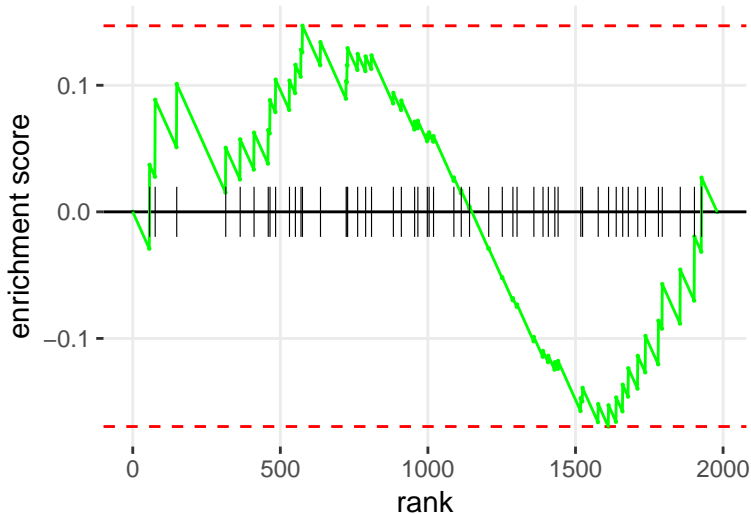
# SEROTONIN DEGRADATION



# OXIDATIVE ETHANOL DEGRADATION III

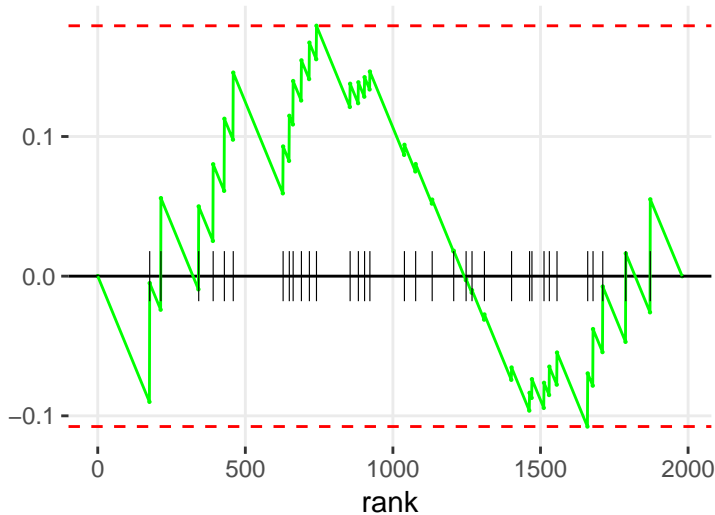


# VALINE DEGRADATION I



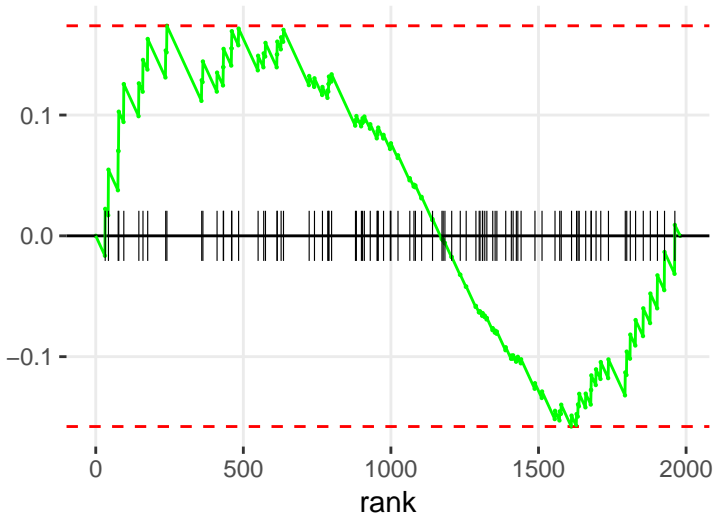
# NICOTINE DEGRADATION IV

enrichment score



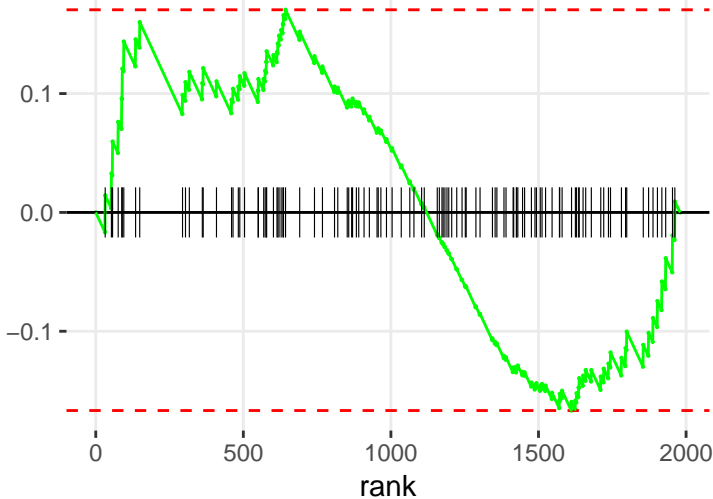
# FATTY ACID & BETA;-OXIDATION I

enrichment score



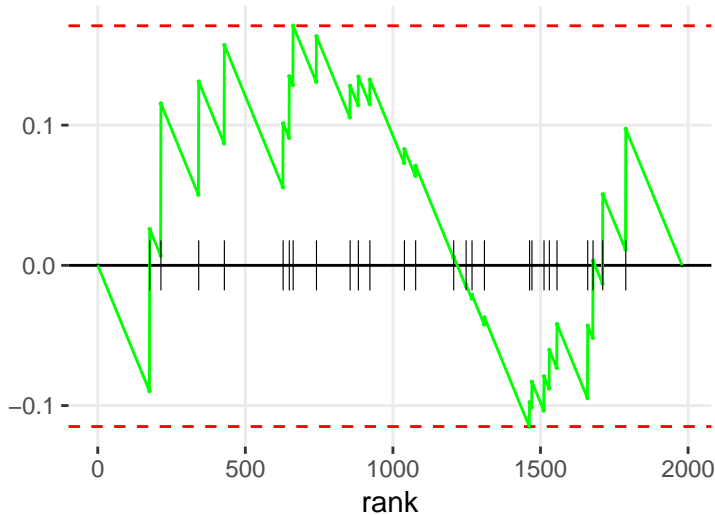
# HISTAMINE DEGRADATION

enrichment score



# ACETONE DEGRADATION I (TO METHYLGLYOXAL)

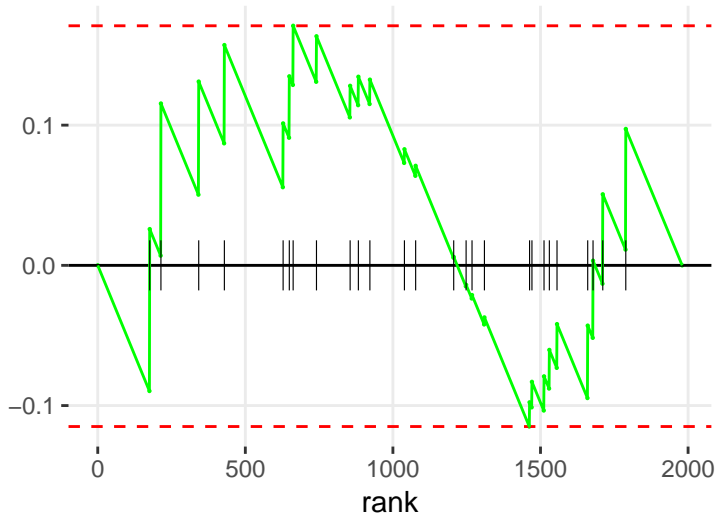
enrichment score





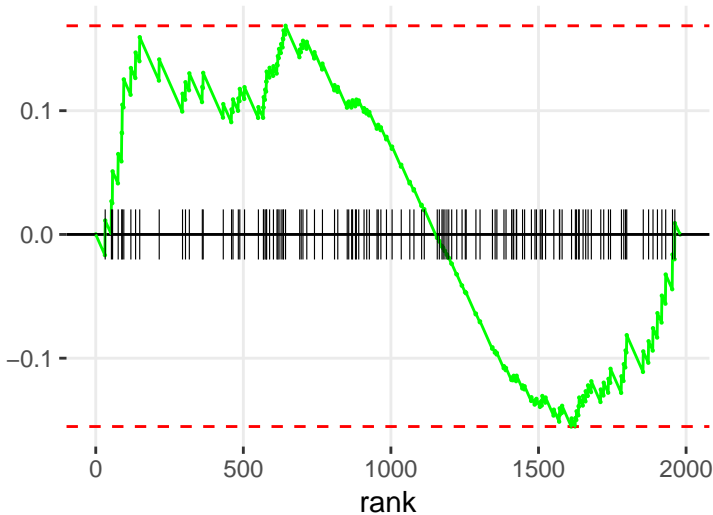
# BUPROPION DEGRADATION

enrichment score



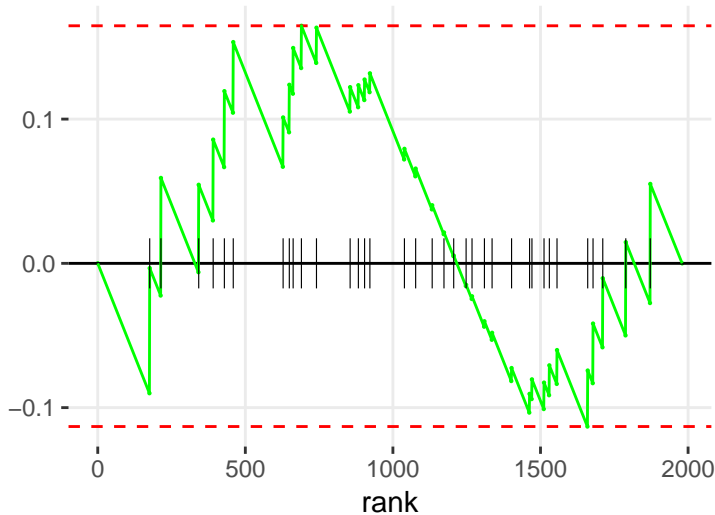
# ETHANOL DEGRADATION IV

enrichment score



# MELATONIN DEGRADATION I

enrichment score



# NICOTINE DEGRADATION III

enrichment score

