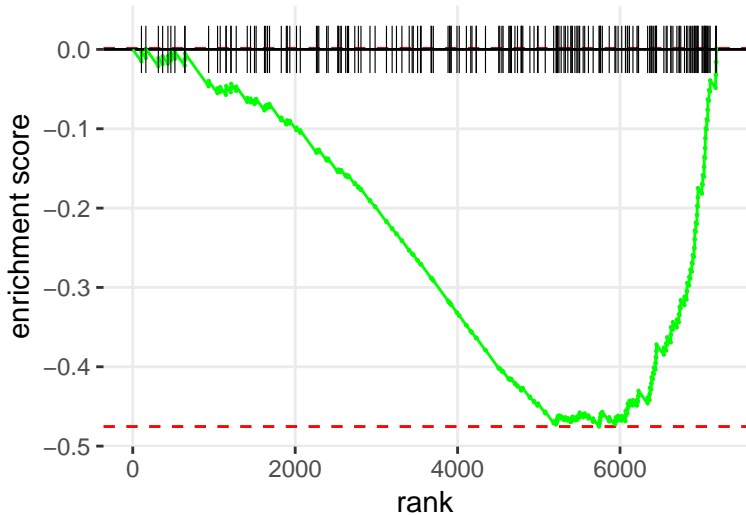


# UDP-*N*-ACETYL-D-GLUCOSAMINE BIOSYNTHESIS II



<IMYO</I>-INOSITOL BIOSYNTHESIS

enrichment score

rank

0.0

-0.2

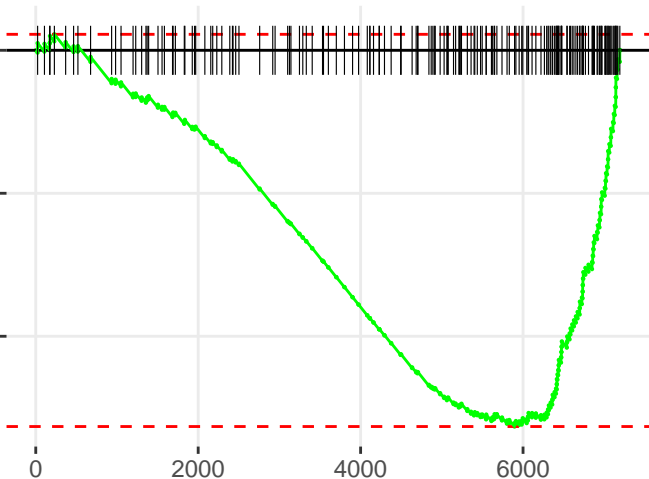
-0.4

0

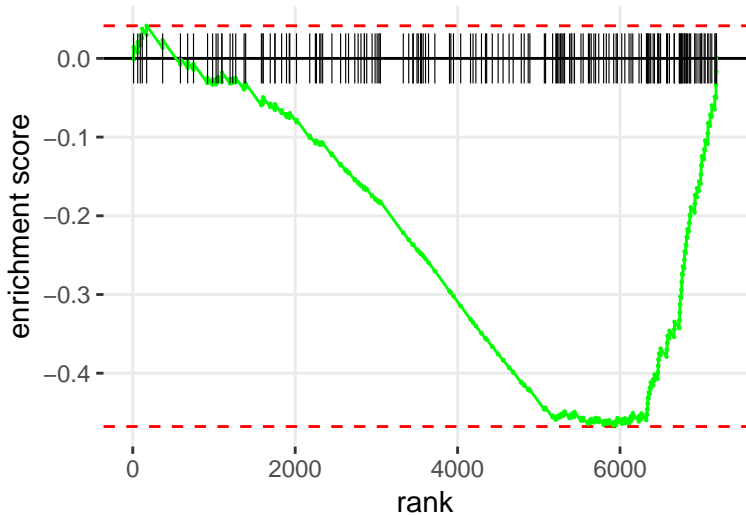
2000

4000

6000



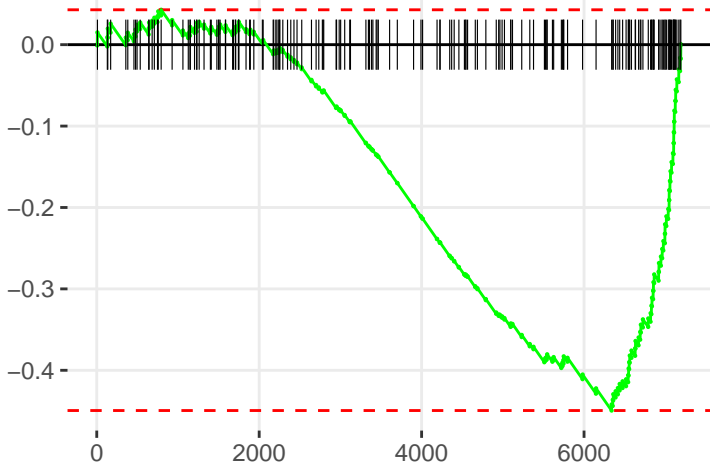
PENTOSE PHOSPHATE PATHWAY (NON-OXIDATIVE BRANCH)



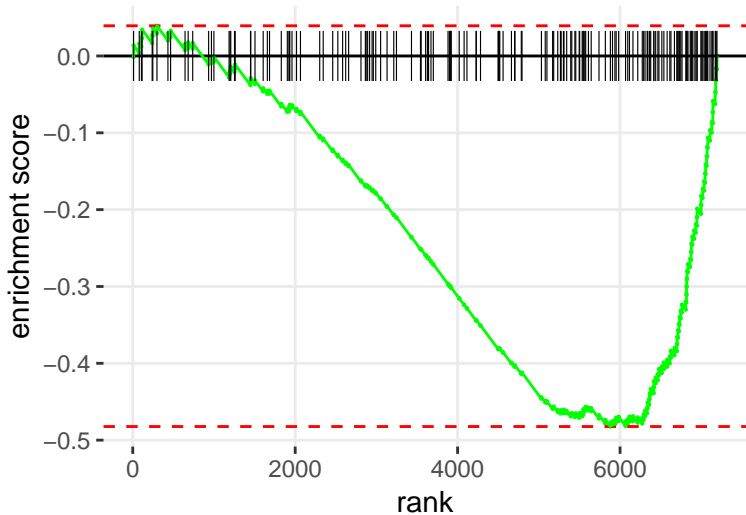
# ALANINE BIOSYNTHESIS III

enrichment score

rank



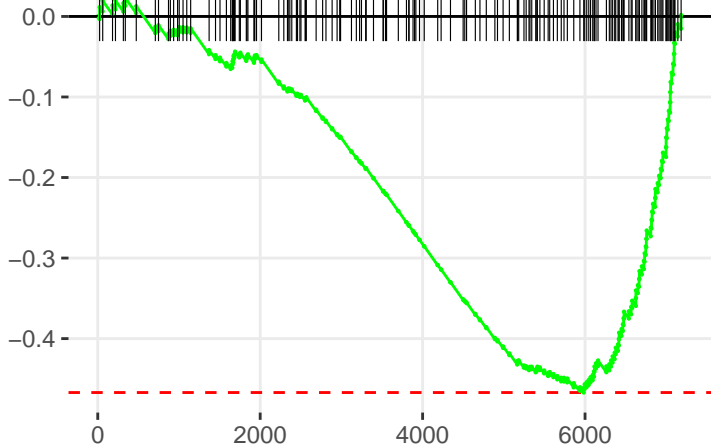
# PROLINE BIOSYNTHESIS I



# GDP-MANNOSE BIOSYNTHESIS

enrichment score

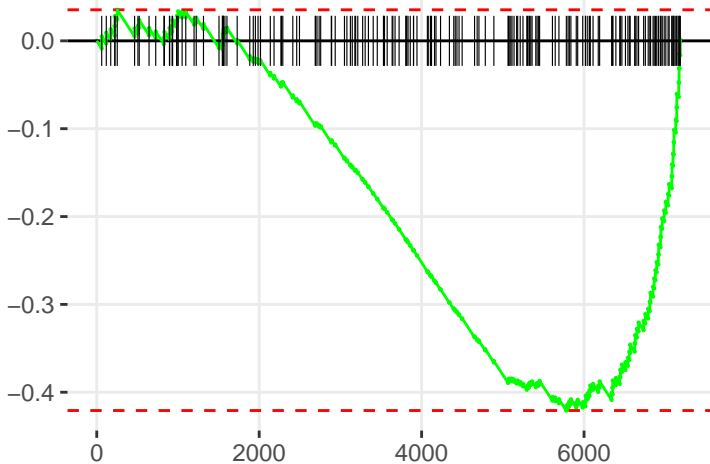
rank



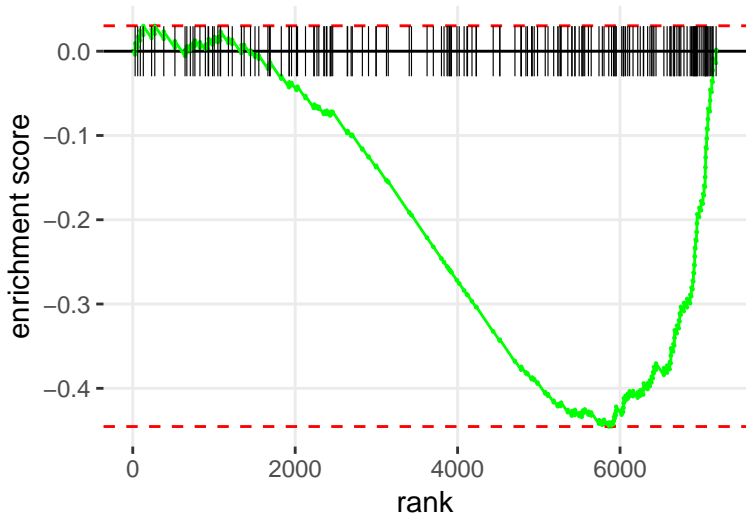
# 5-AMINOIMIDAZOLE RIBONUCLEOTIDE BIOSYNTHESIS I

enrichment score

rank

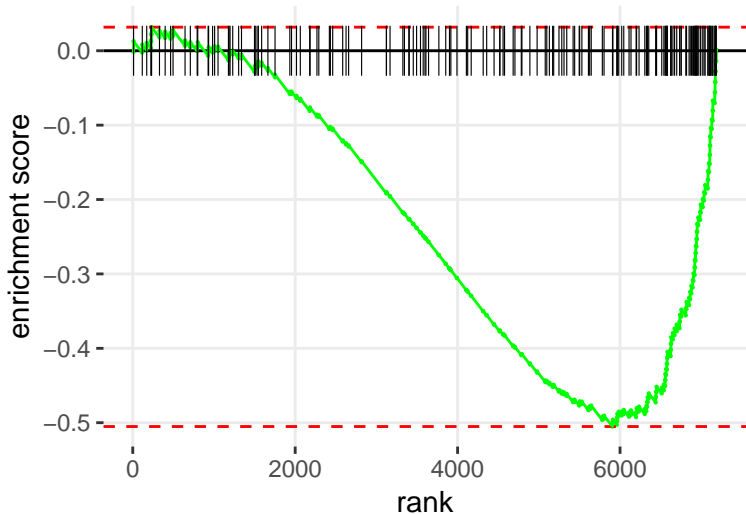


# CITRULLINE DEGRADATION





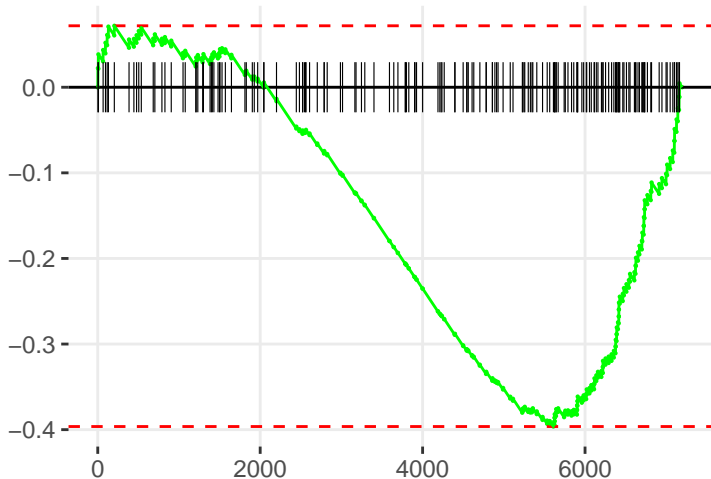
# GLUTARYL-COA DEGRADATION



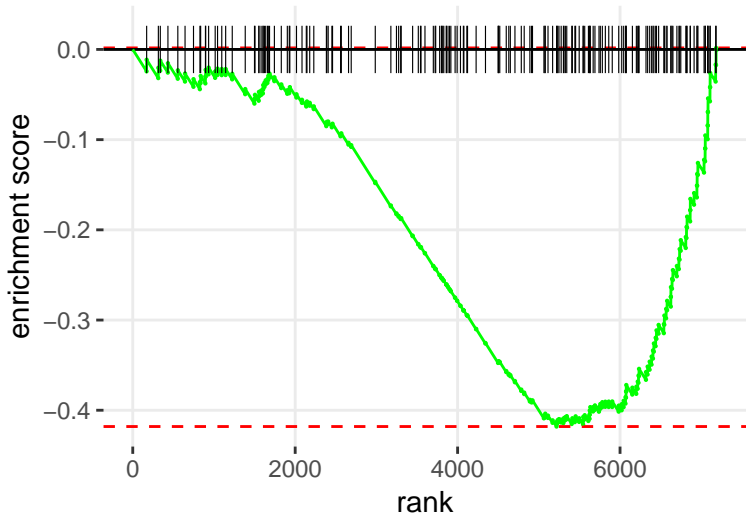
# CITRULLINE-NITRIC OXIDE CYCLE

enrichment score

rank



# S-ADENOSYL-L-METHIONINE BIOSYNTHESIS



# VALINE DEGRADATION I

enrichment score

rank

0.0

-0.1

-0.2

-0.3

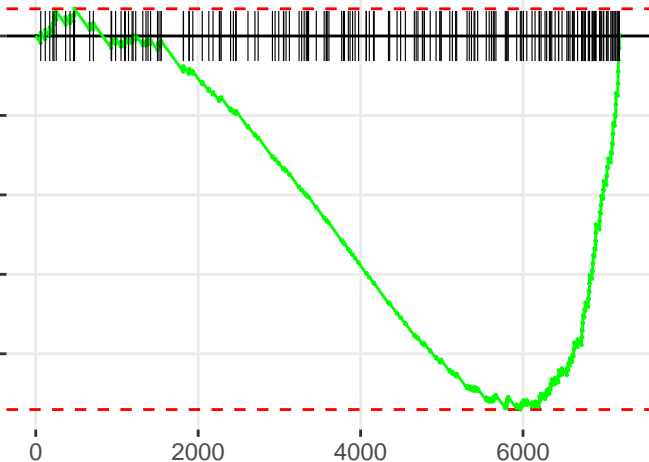
-0.4

0

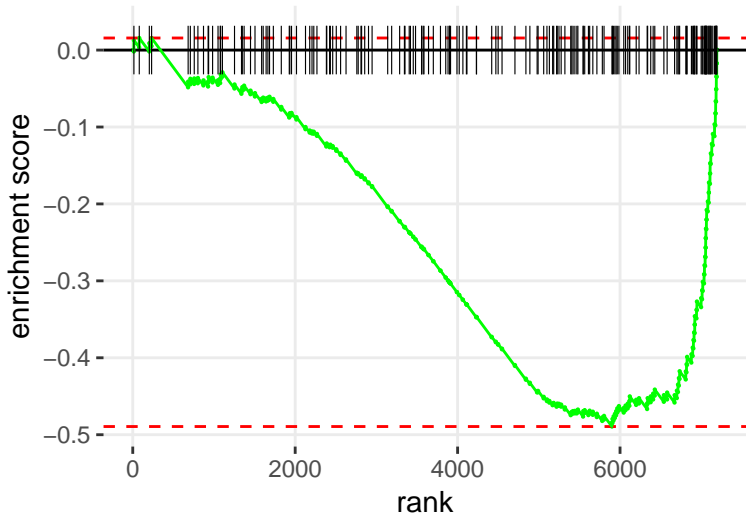
2000

4000

6000



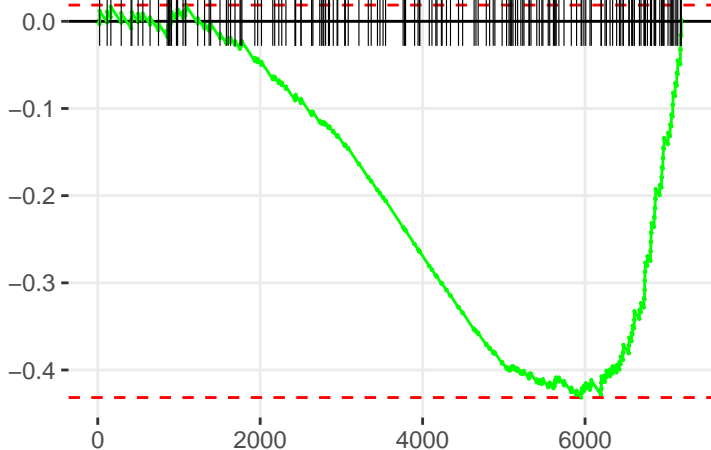
# ARGININE DEGRADATION I (ARGINASE PATHWAY)



# GLUCOSE AND GLUCOSE-1-PHOSPHATE DEGRADATION

enrichment score

rank



# CYSTEINE BIOSYNTHESIS/HOMOCYSTEINE DEGRADATION

enrichment score

0.0  
-0.1  
-0.2  
-0.3  
-0.4

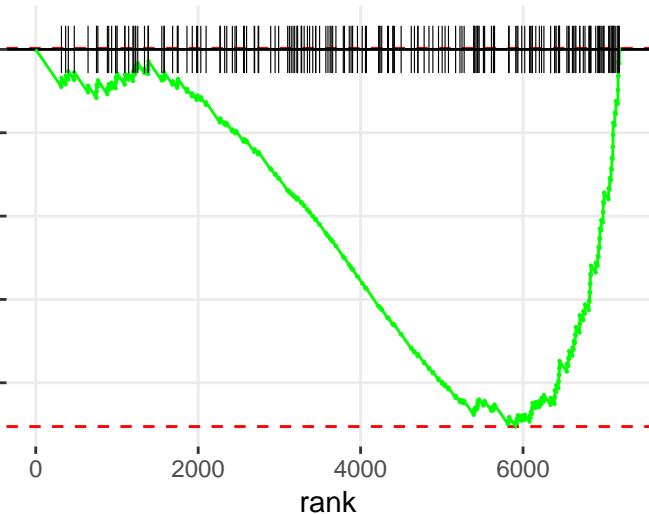
0

2000

4000

6000

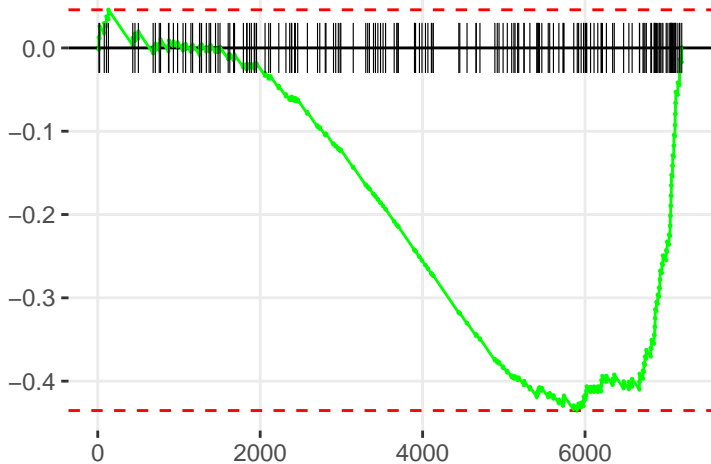
rank



# GLYCINE CLEAVAGE

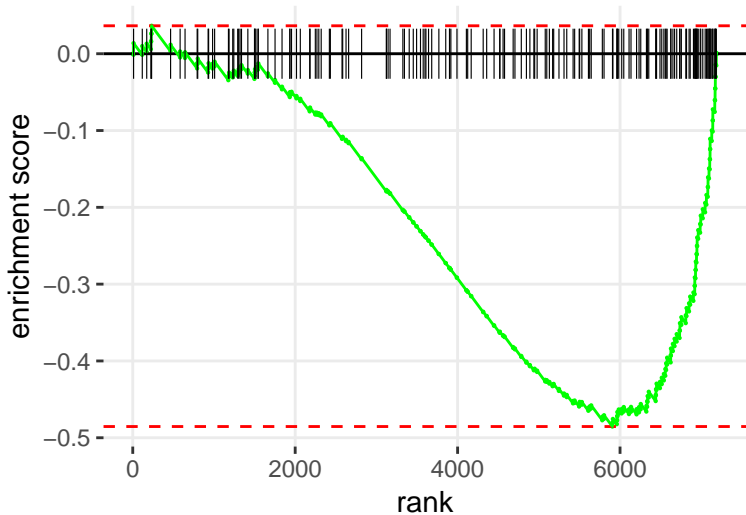
enrichment score

rank





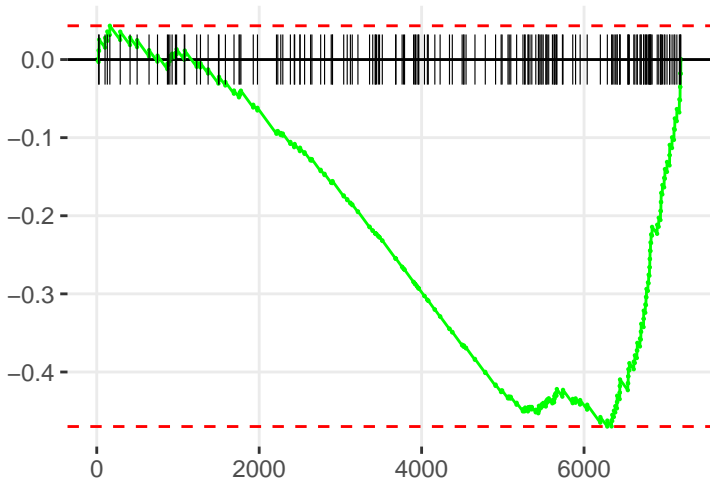
KETOLYSIS



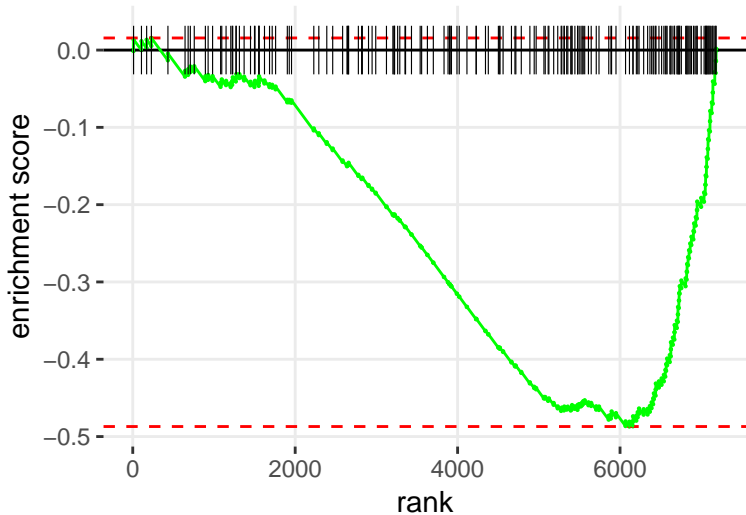
# TREHALOSE DEGRADATION II (TREHALASE)

enrichment score

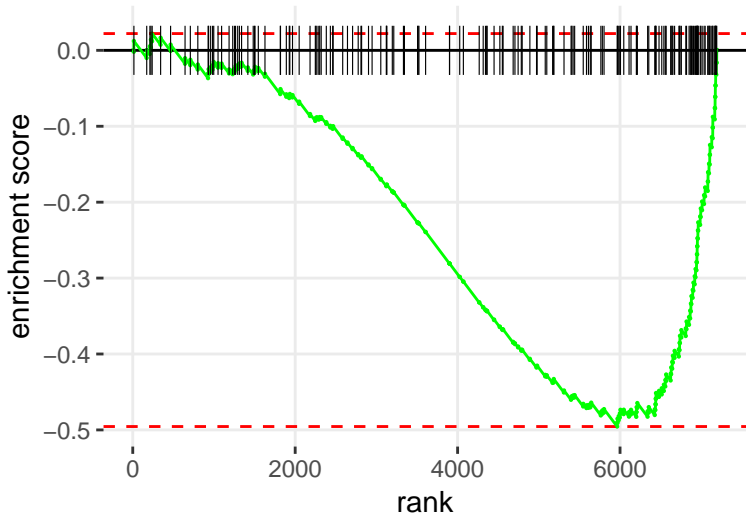
rank



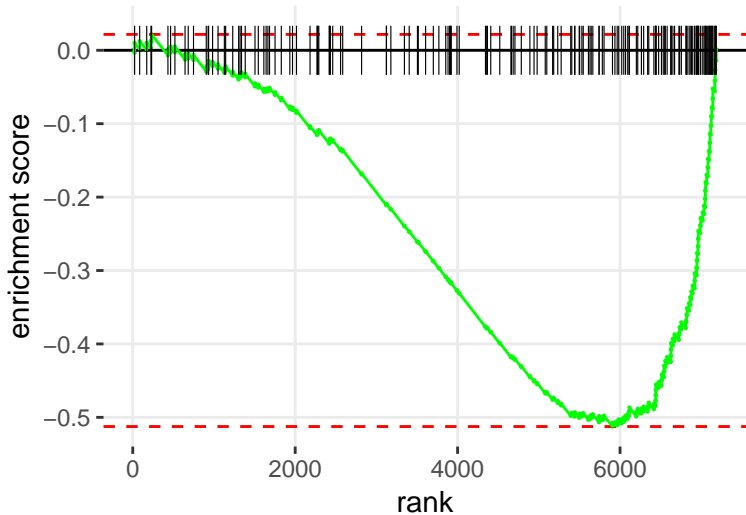
# GALACTOSE DEGRADATION I (LELOIR PATHWAY)



# LEUCINE DEGRADATION I



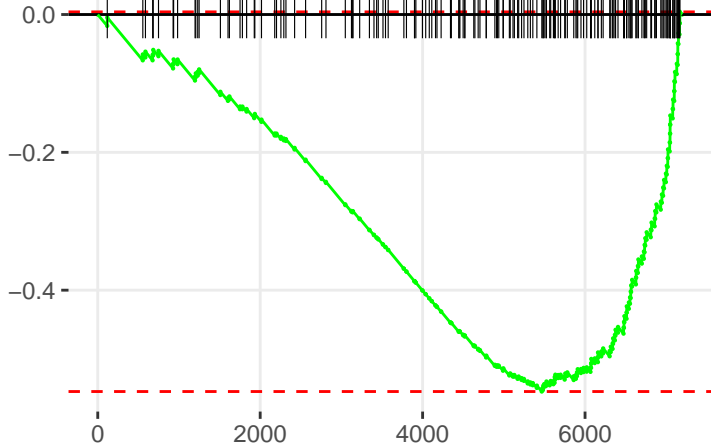
# ACETATE CONVERSION TO ACETYL-COA



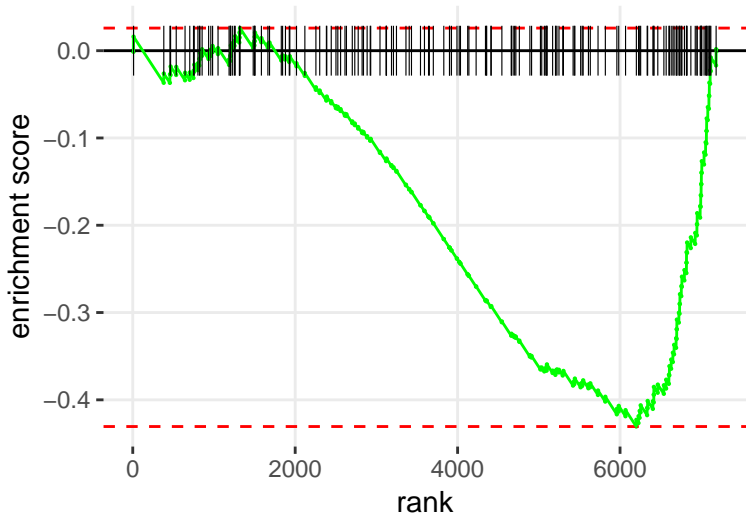
# PENTOSE PHOSPHATE PATHWAY (OXIDATIVE BRANCH)

enrichment score

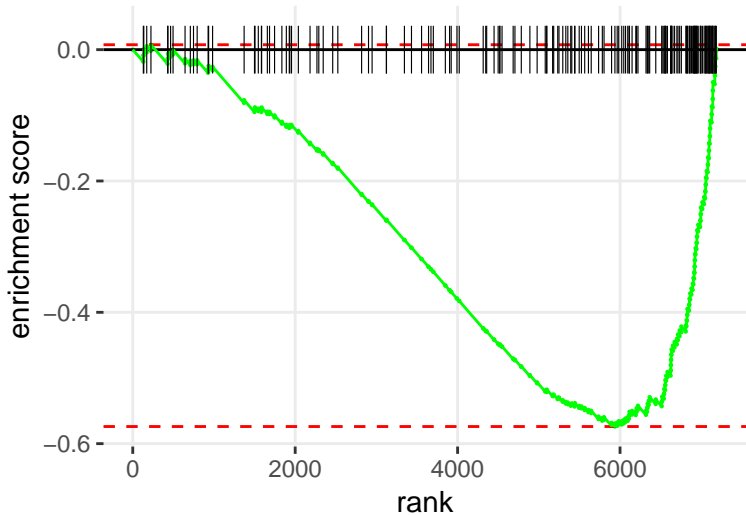
rank



TCA CYCLE II (EUKARYOTIC)



# ADENINE AND ADENOSINE SALVAGE VI

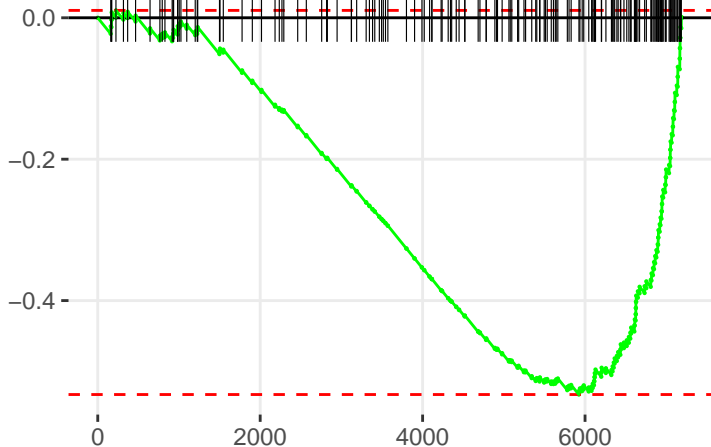




# L-CYSTEINE DEGRADATION II

enrichment score

rank



# TRNA CHARGING

enrichment score

rank

0.0

-0.1

-0.2

-0.3

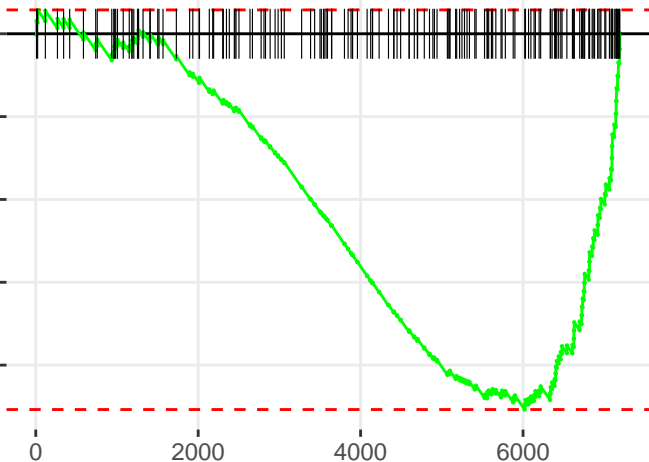
-0.4

0

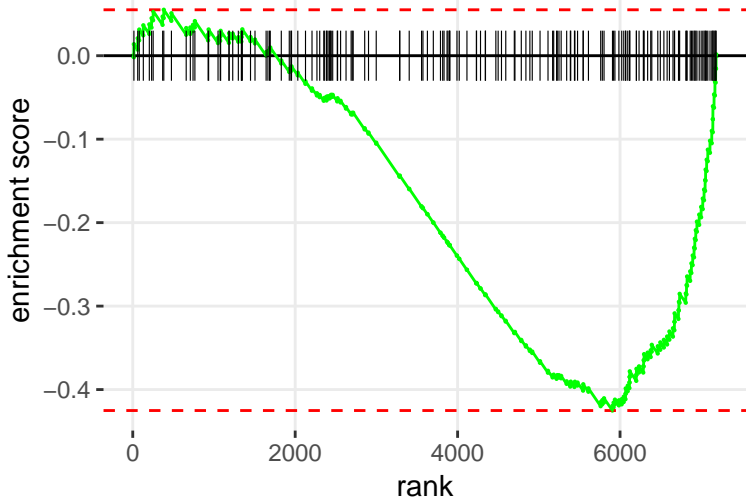
2000

4000

6000



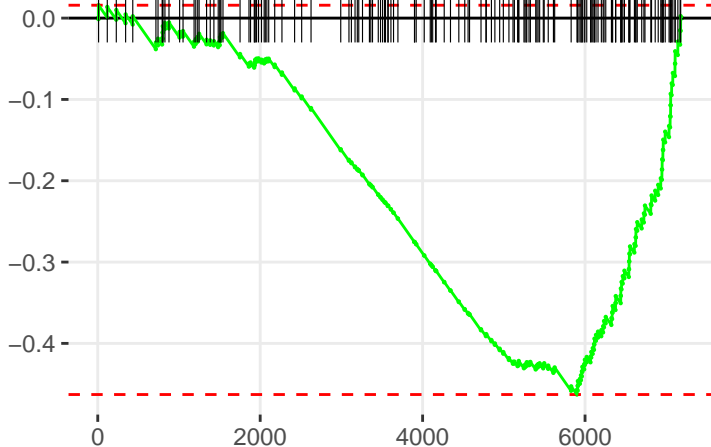
UREA CYCLE



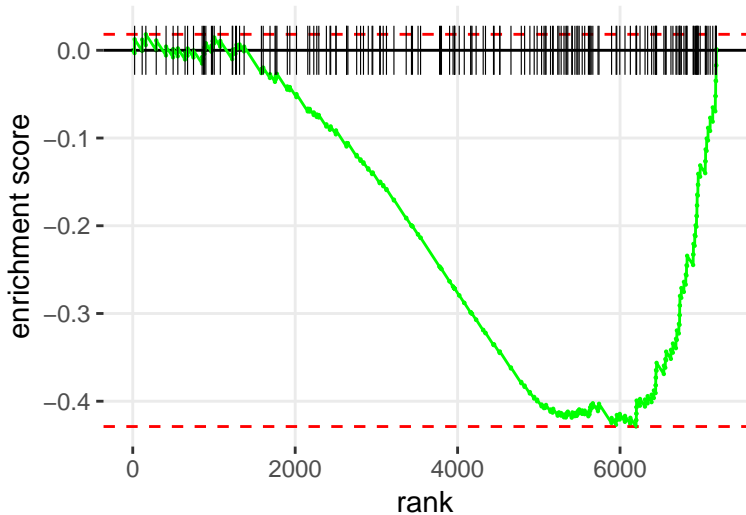
KETOGENESIS

enrichment score

rank

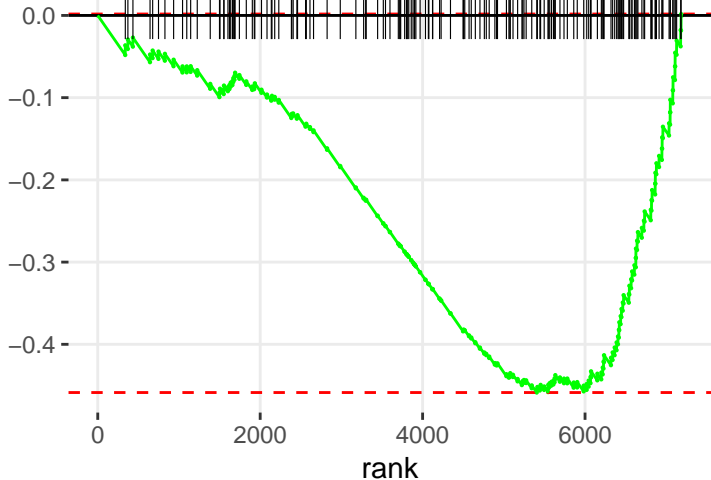


# GDP-GLUCOSE BIOSYNTHESIS

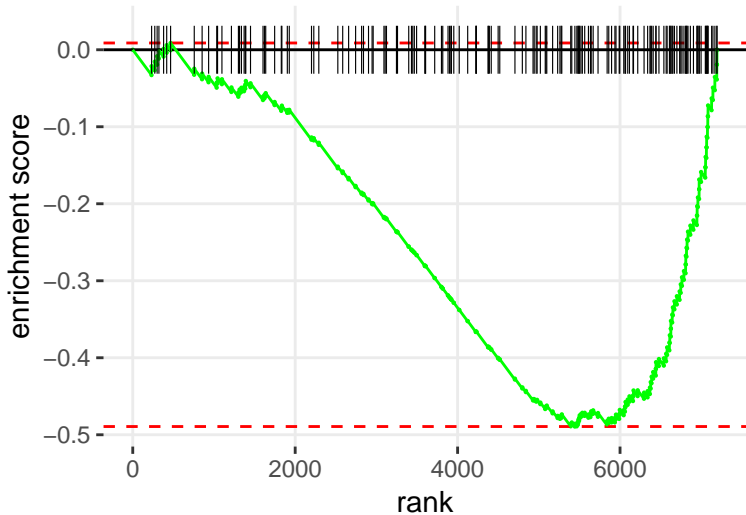


# METHIONINE DEGRADATION I (TO HOMOCYSTEINE)

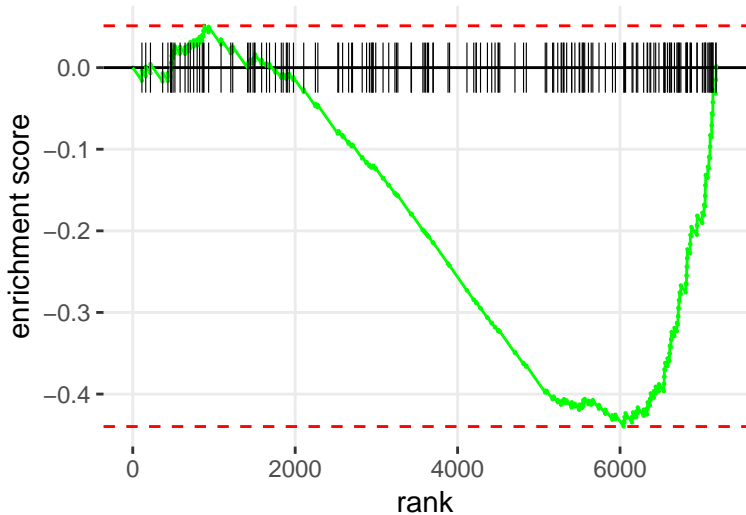
enrichment score



# TETRAHYDROBIOPTERIN BIOSYNTHESIS II

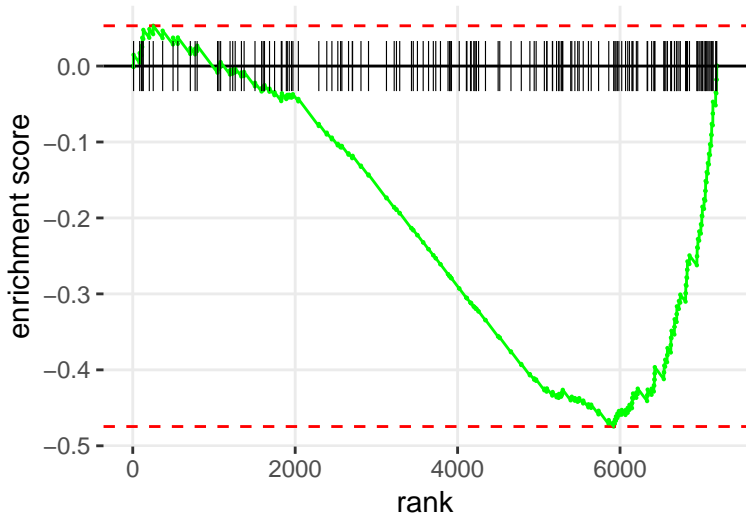


# PHOSPHATIDYLCHOLINE BIOSYNTHESIS I





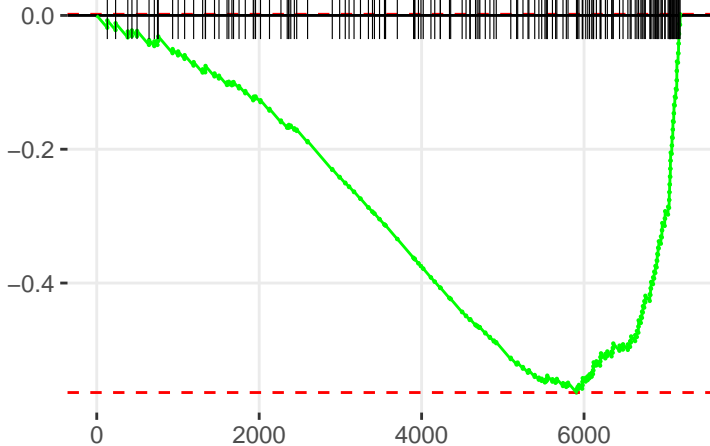
# ADENINE AND ADENOSINE SALVAGE I



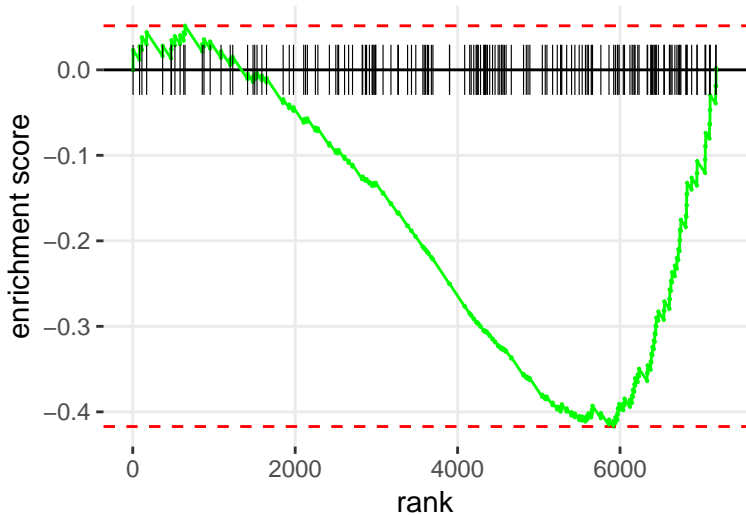
# RETINOATE BIOSYNTHESIS I

enrichment score

rank



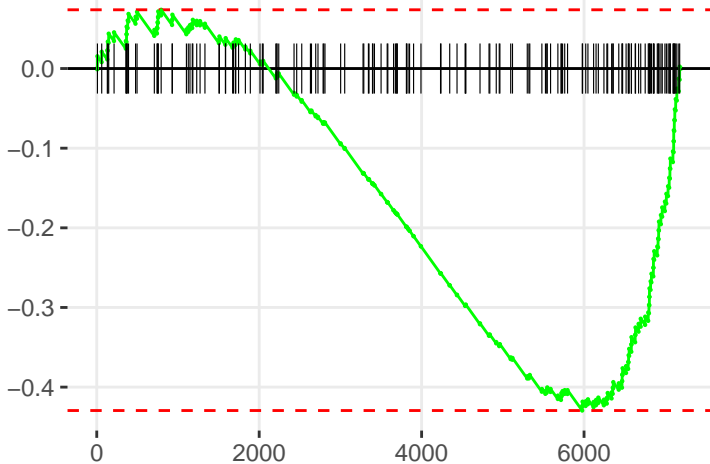
# CHOLINE BIOSYNTHESIS III



# D-GLUCURONATE DEGRADATION I

enrichment score

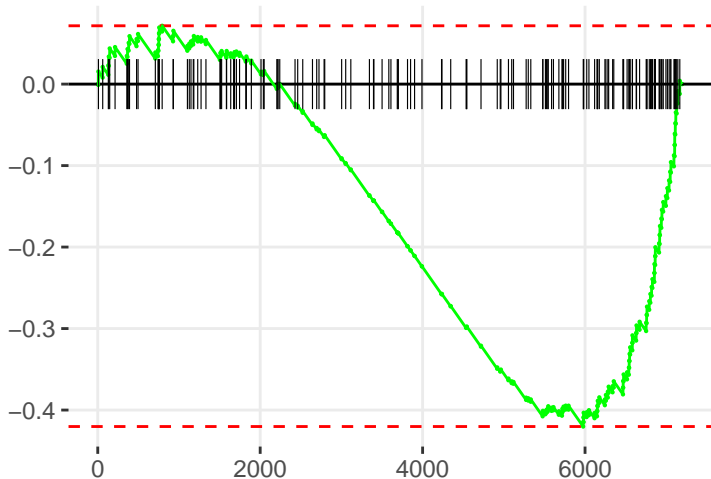
rank



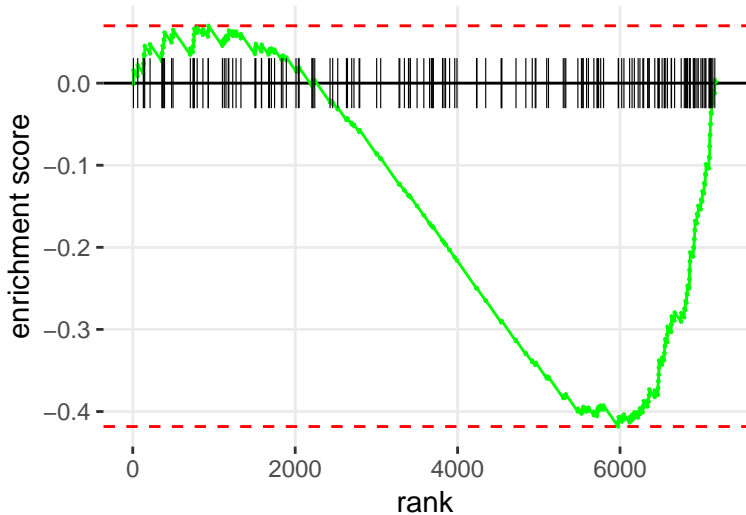
# SORBITOL DEGRADATION I

enrichment score

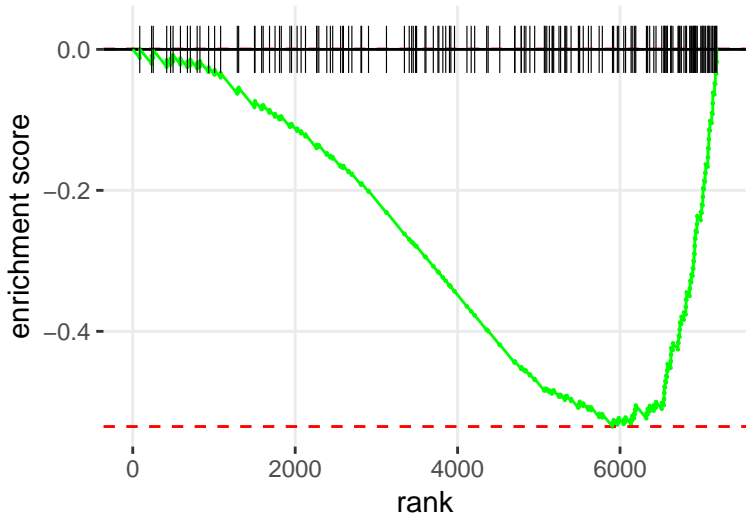
rank



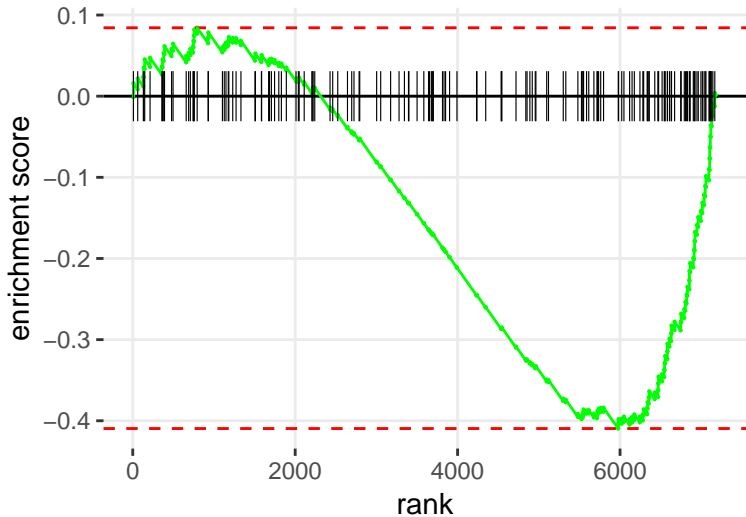
# DIPHTHAMIDE BIOSYNTHESIS



PHENYLALANINE DEGRADATION IV (MAMMALIAN, VIA SIDE CHAIN)

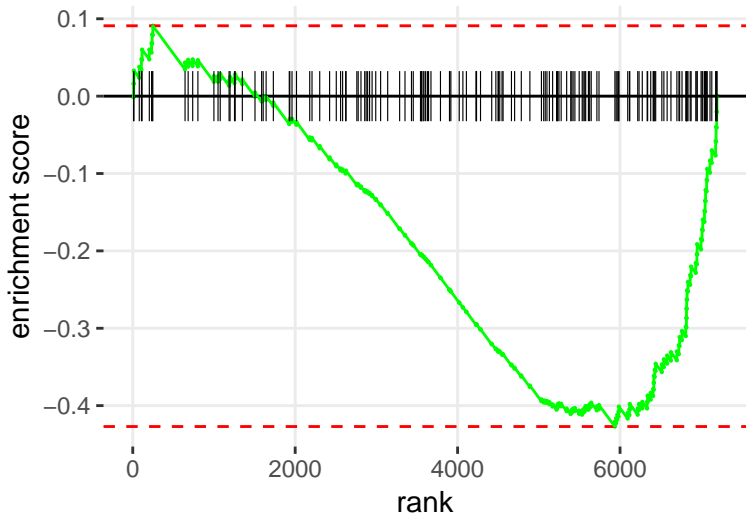


# HEME DEGRADATION





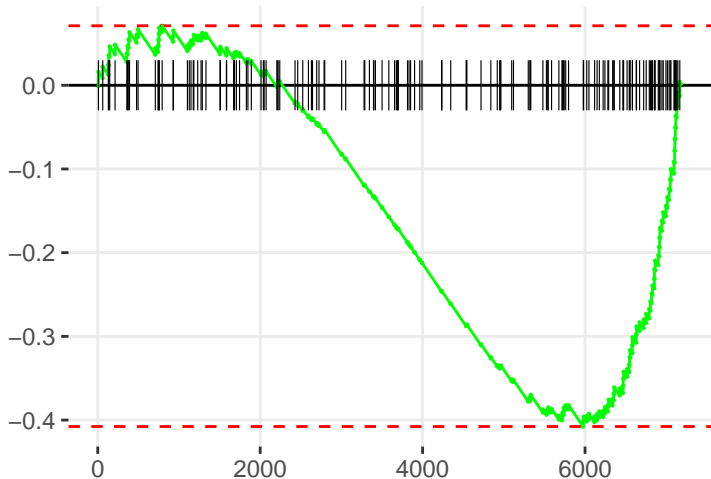
# ARGININE DEGRADATION VI (ARGINASE 2 PATHWAY)



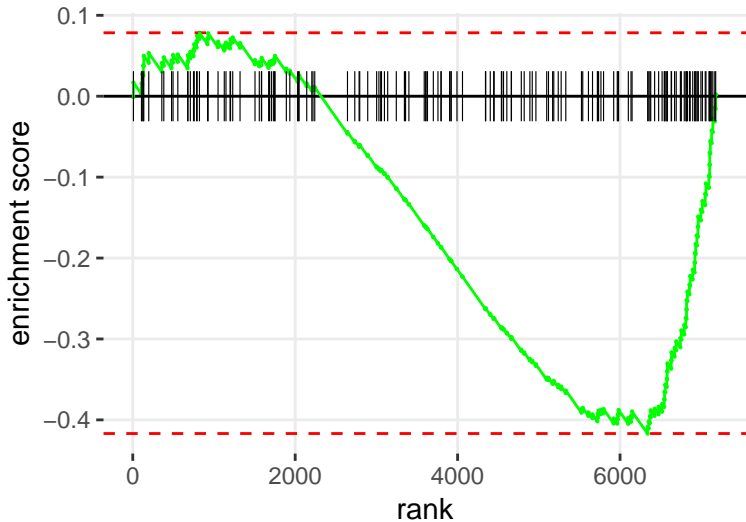
# MELATONIN DEGRADATION II

enrichment score

rank



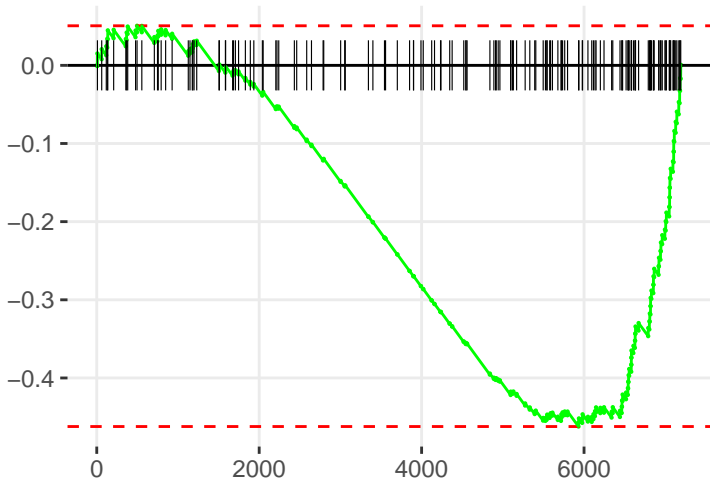
## TETRAPYRROLE BIOSYNTHESIS II



# PYRIDOXAL 5'-PHOSPHATE SALVAGE PATHWAY

enrichment score

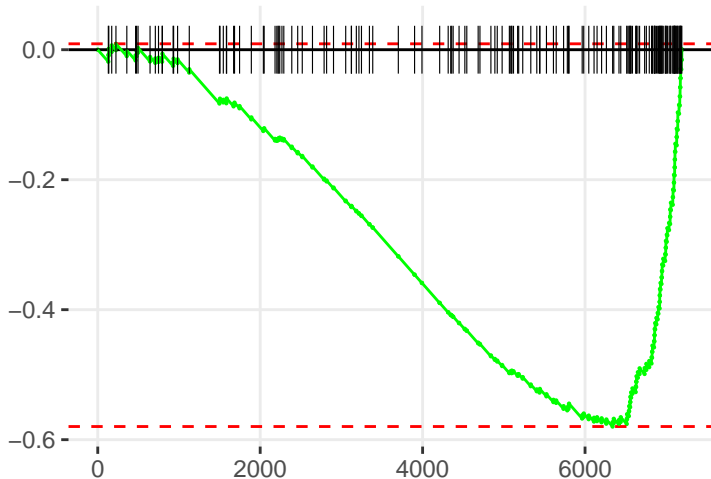
rank



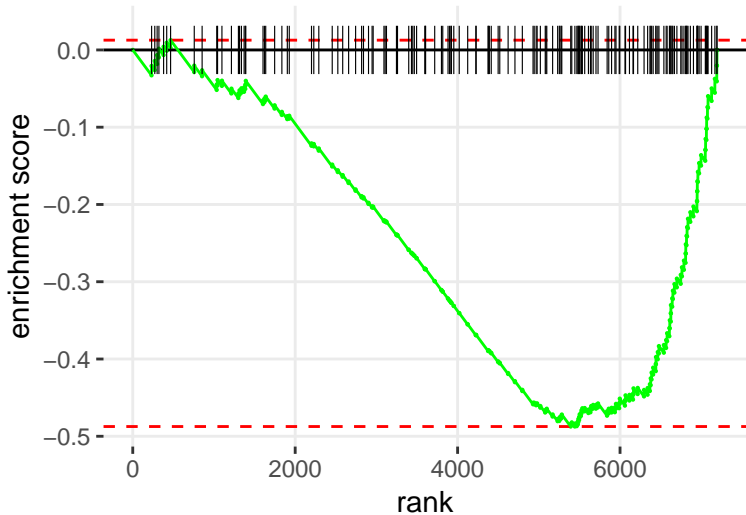
# D-MANNOSE DEGRADATION

enrichment score

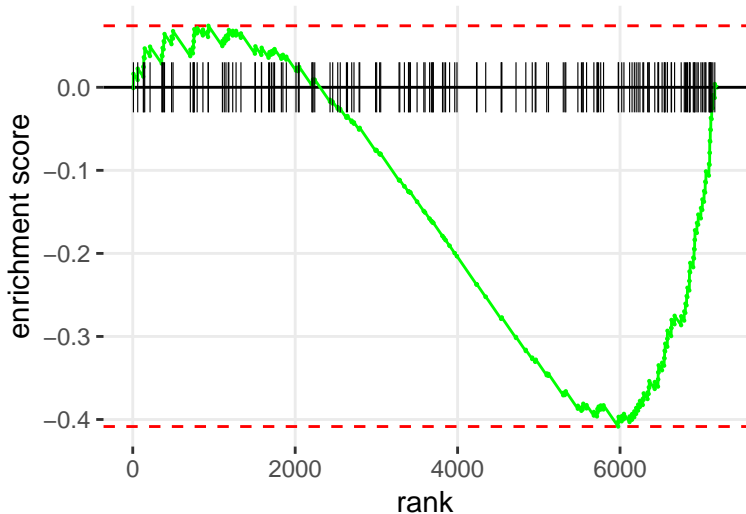
rank



# TETRAHYDROBIOPTERIN BIOSYNTHESIS I



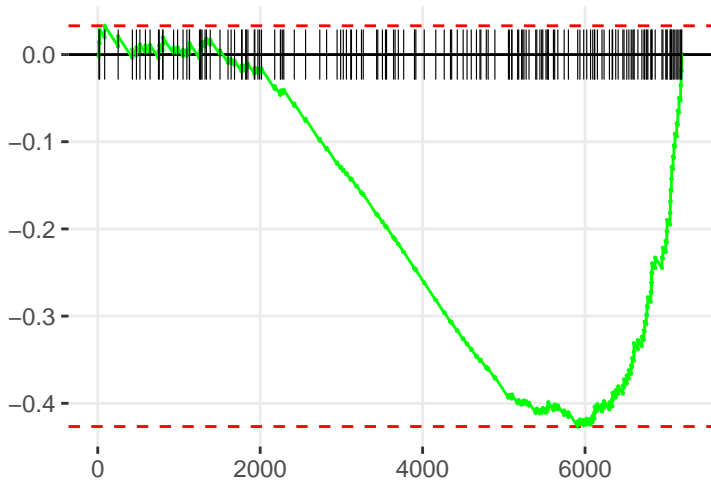
D-<IMYO</I-INOSITOL (1,4,5,6)-TETRAKISPHOSPHATE BIOSYNTHESIS



# ETHANOL DEGRADATION IV

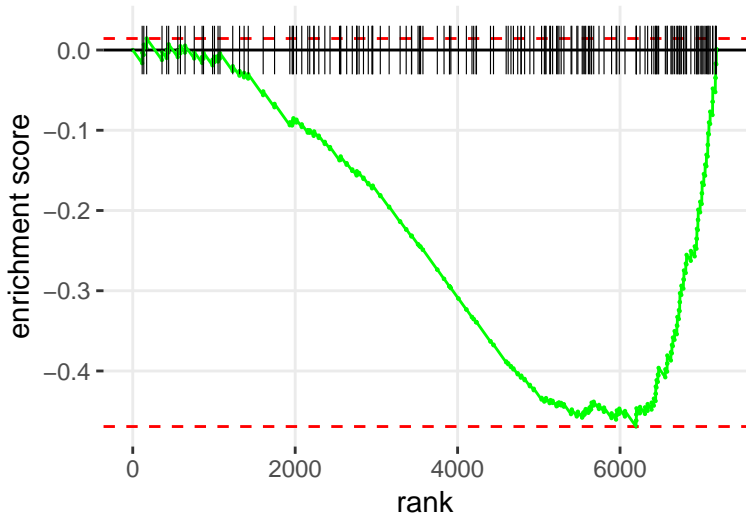
enrichment score

rank





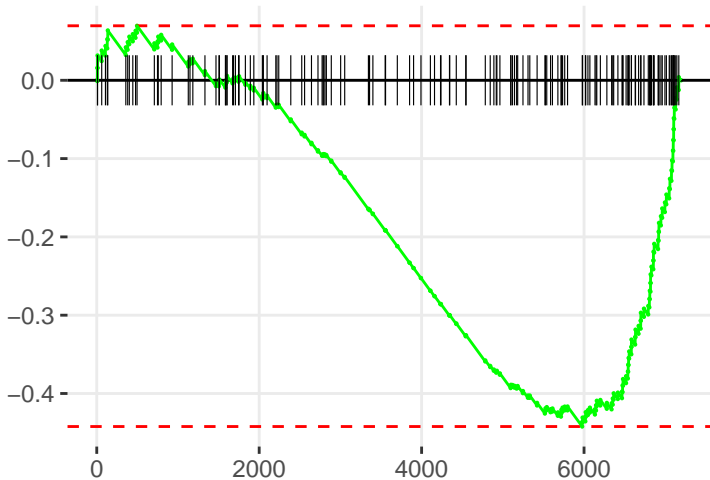
# GLYCOGEN DEGRADATION II



# ASPARAGINE BIOSYNTHESIS I

enrichment score

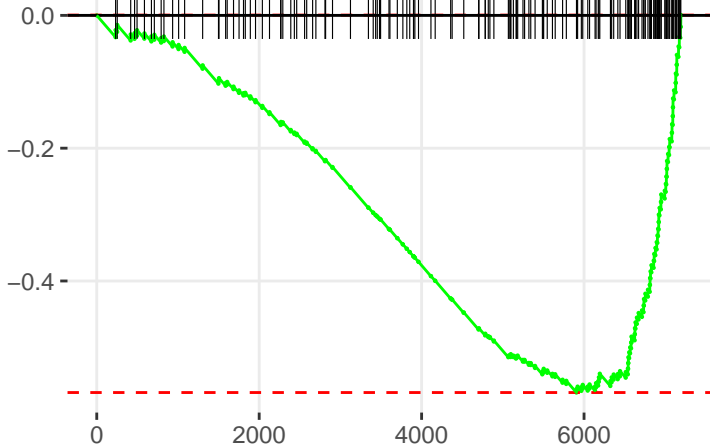
rank



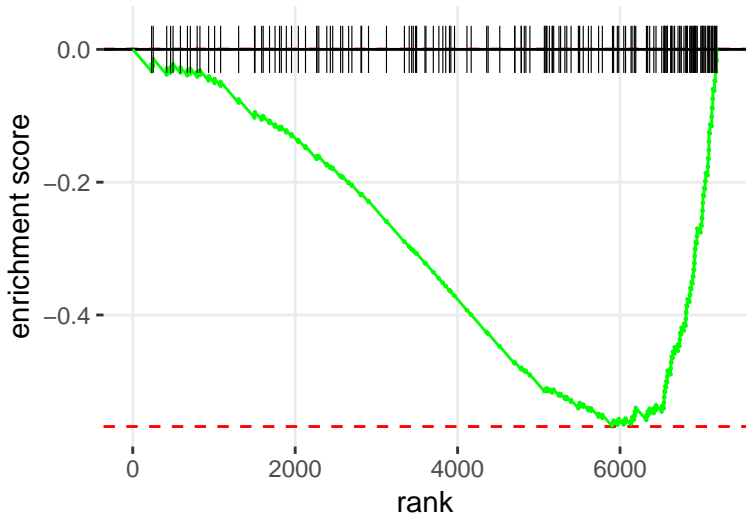
# GLUTAMATE DEGRADATION II

enrichment score

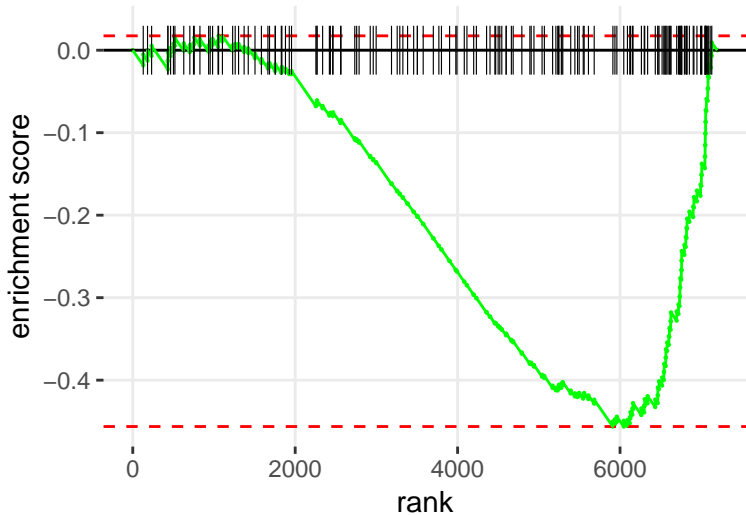
rank



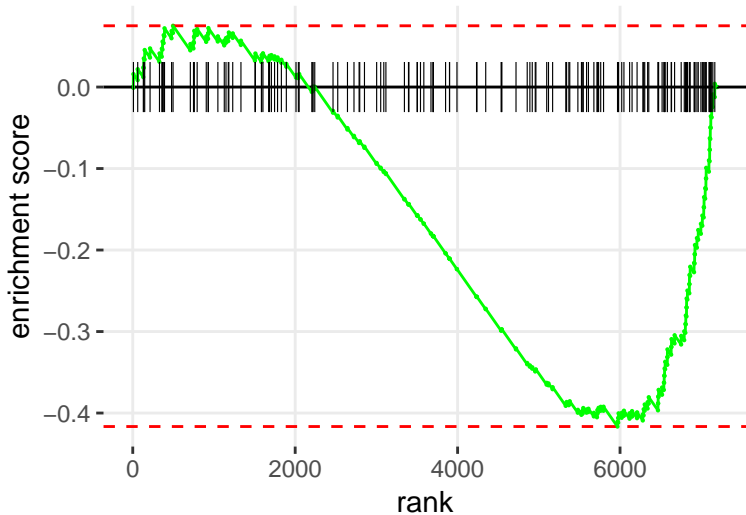
# ASPARTATE BIOSYNTHESIS



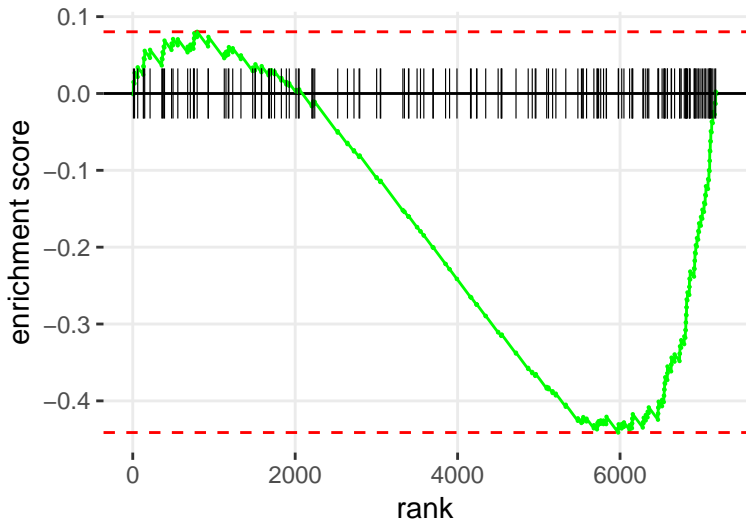
# GLUCONEOGENESIS I



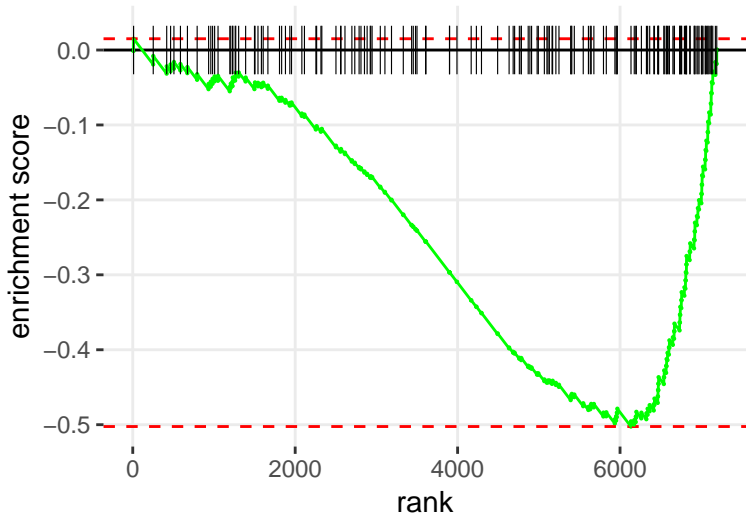
# PHOSPHATIDYLETHANOLAMINE BIOSYNTHESIS II



# METHYLGLYOXAL DEGRADATION I

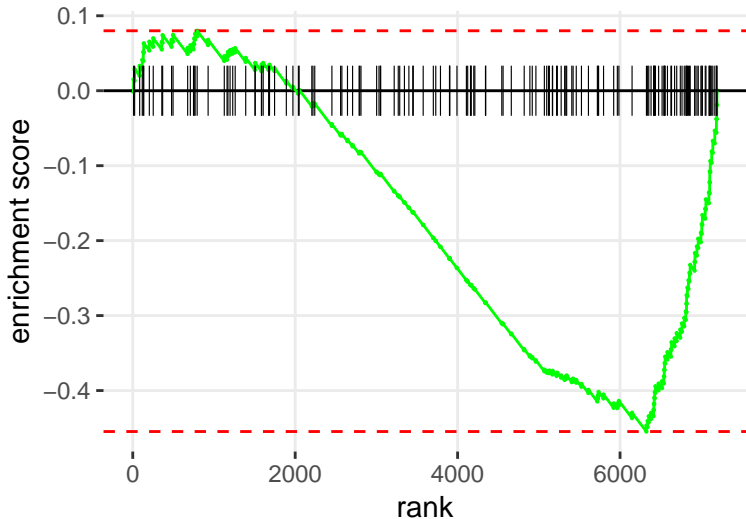


# ASPARTATE DEGRADATION II

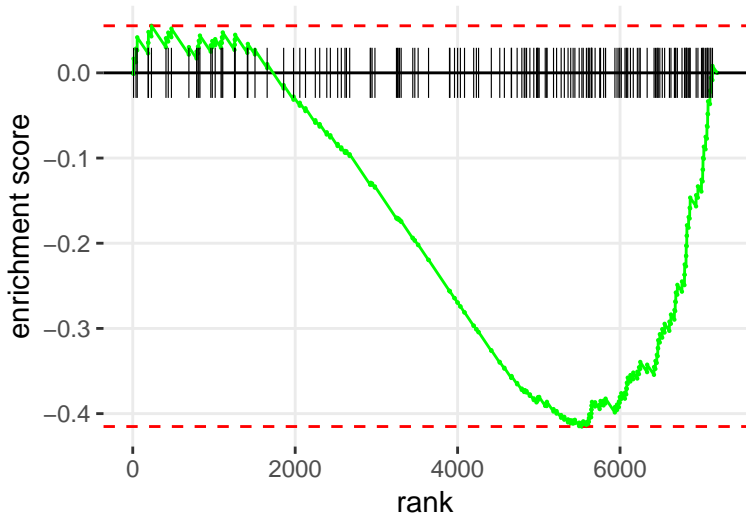




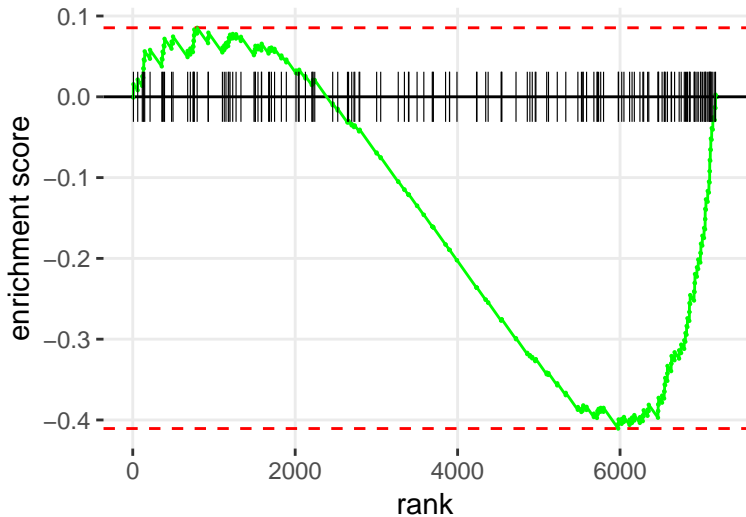
# ADENINE AND ADENOSINE SALVAGE III



# SALVAGE PATHWAYS OF PYRIMIDINE RIBONUCLEOTIDES



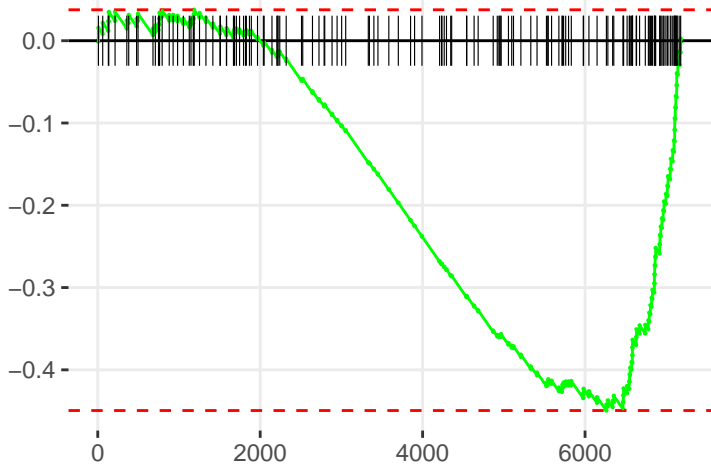
# <IN</I>-ACETYLGLUCOSAMINE DEGRADATION I



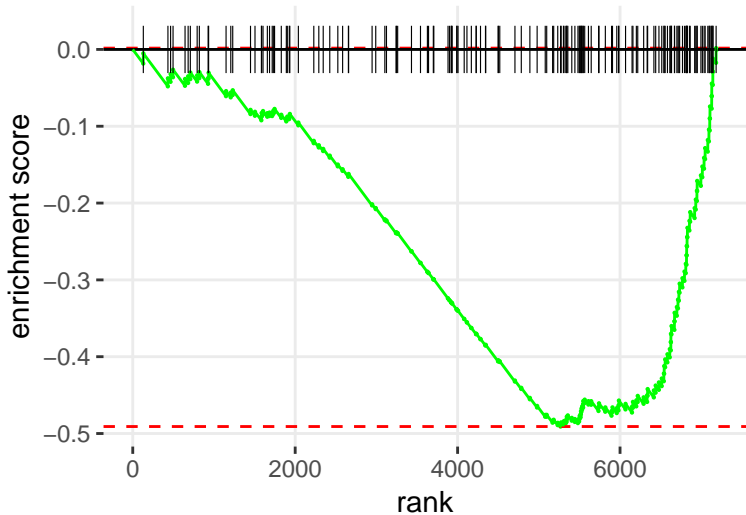
FATTY ACID & BETA;-OXIDATION III (UNSATURATED, ODD NUMBER)

enrichment score

rank



# HYPUSINE BIOSYNTHESIS



# GLUTAMINE BIOSYNTHESIS I

enrichment score

rank

0.0

-0.1

-0.2

-0.3

-0.4

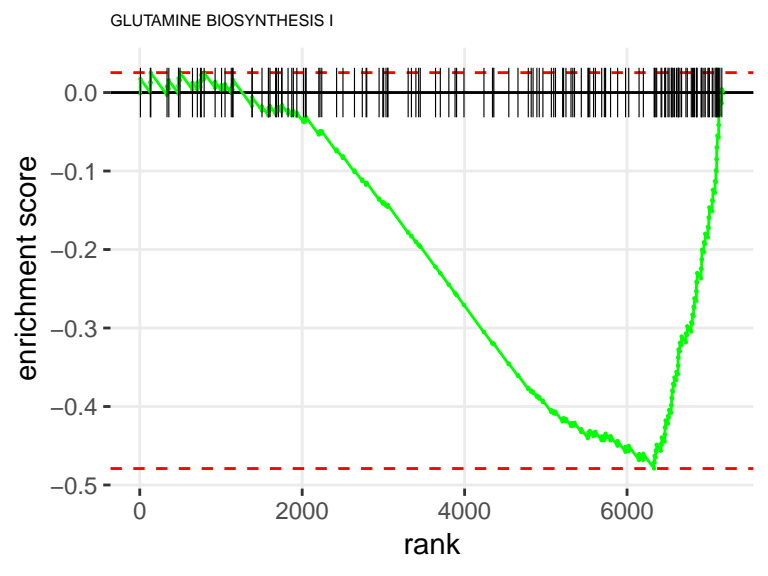
-0.5

0

2000

4000

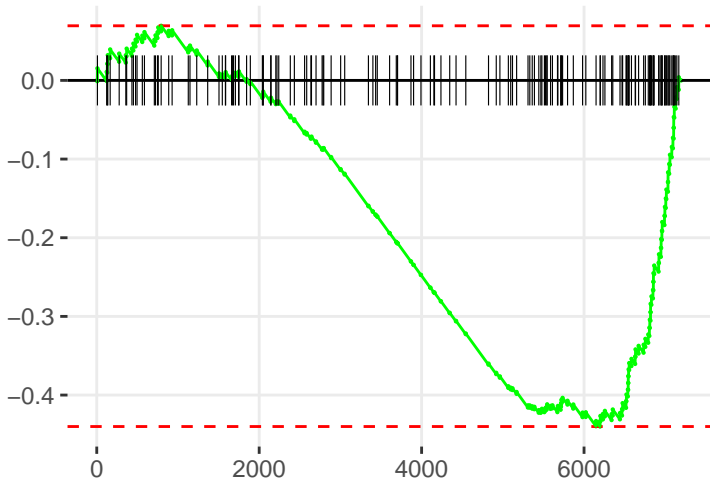
6000



# LEUKOTRIENE BIOSYNTHESIS

enrichment score

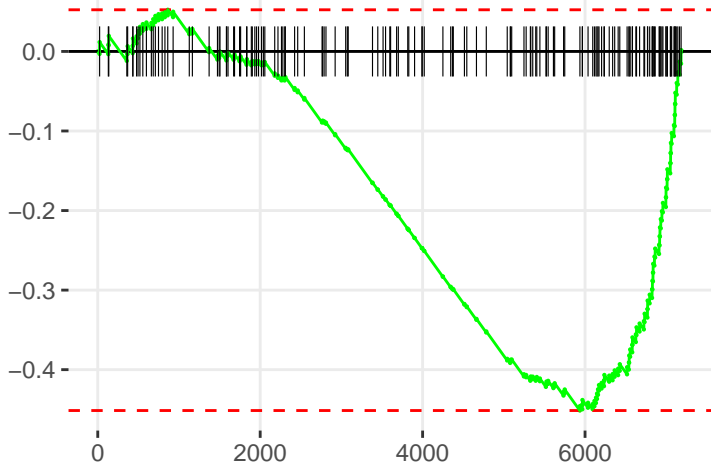
rank



# PRPP BIOSYNTHESIS I

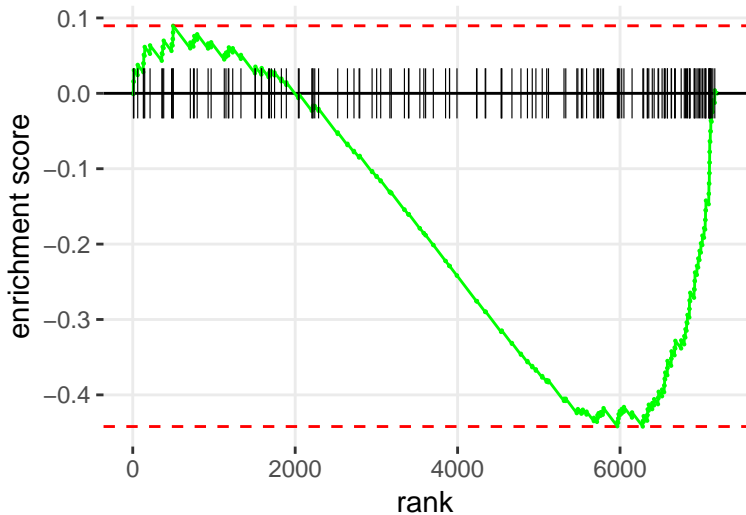
enrichment score

rank

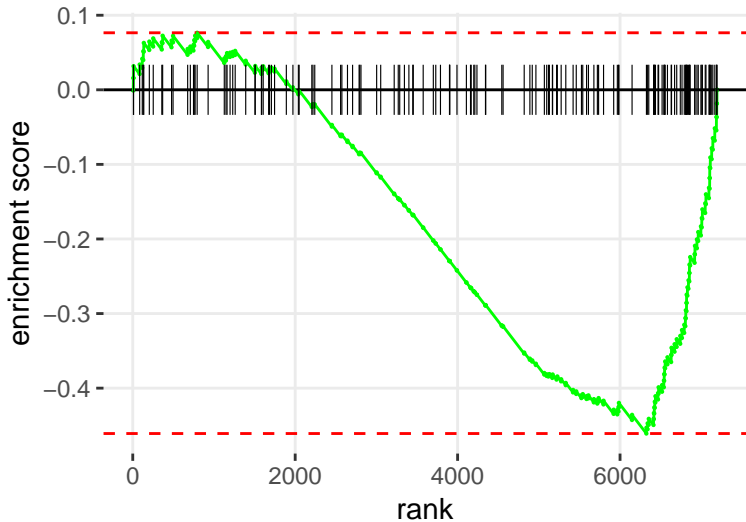




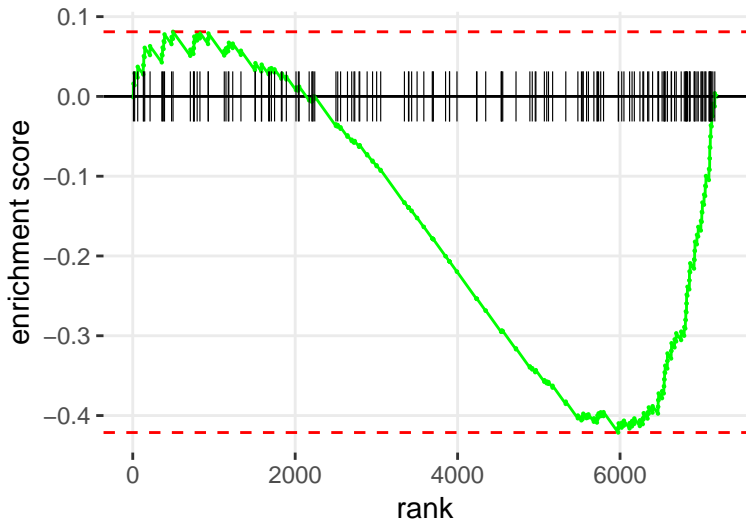
# SPERMINE BIOSYNTHESIS



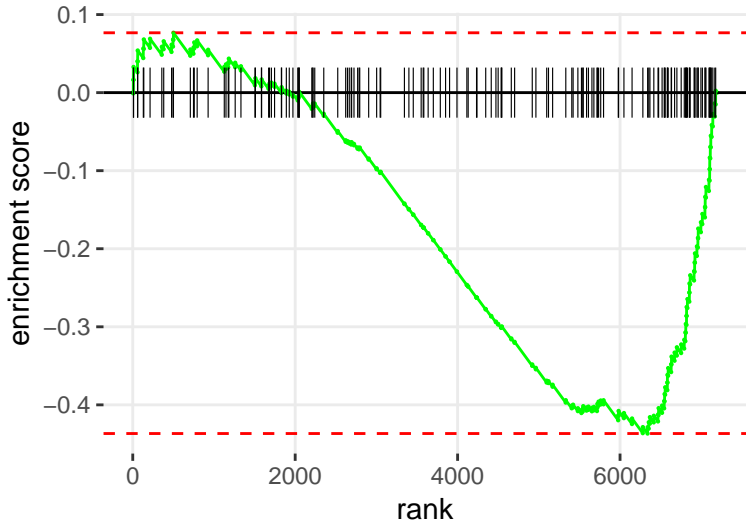
# GUANINE AND GUANOSINE SALVAGE I



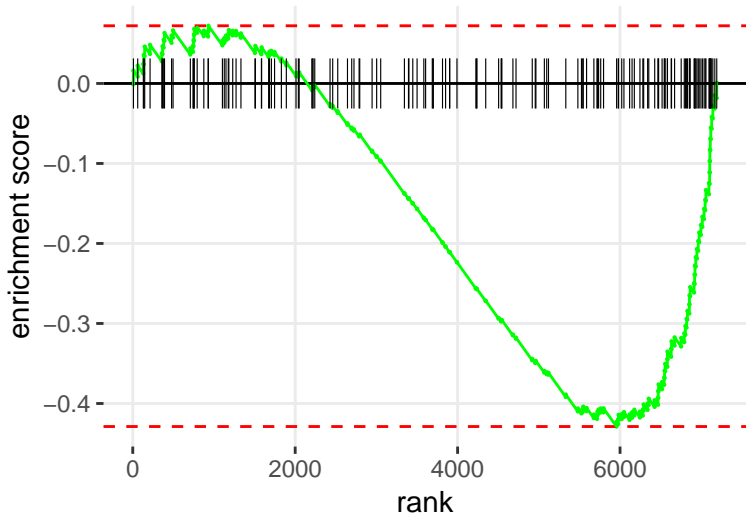
# L-CYSTEINE DEGRADATION III



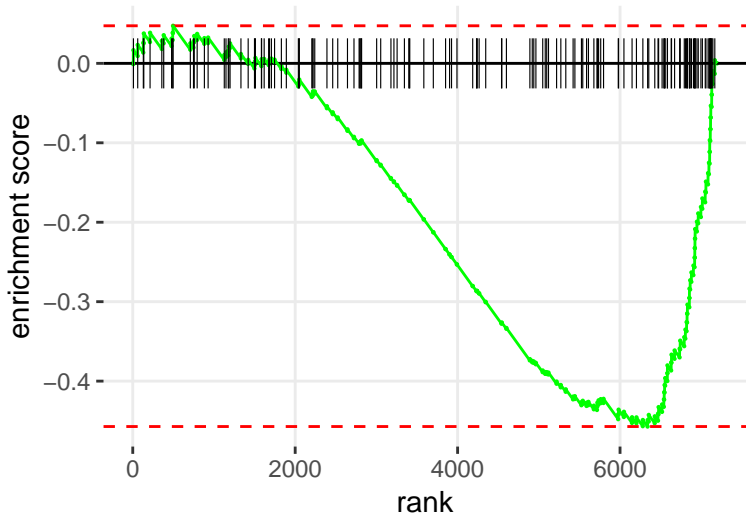
FORMALDEHYDE OXIDATION II (GLUTATHIONE-DEPENDENT)



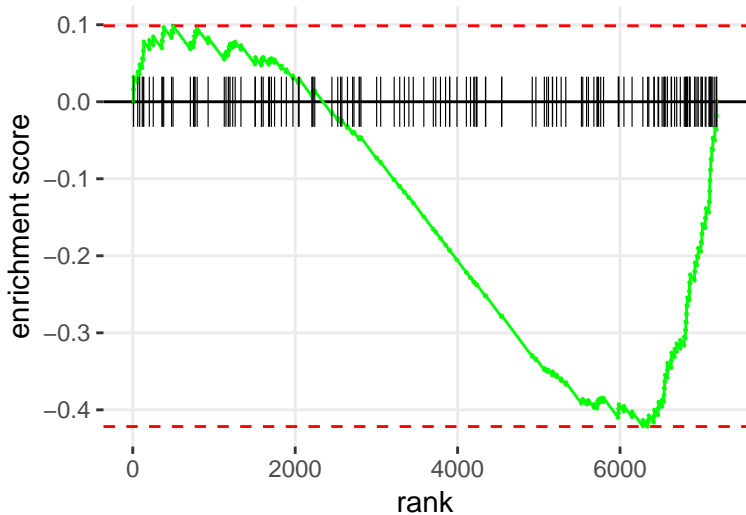
GDP-L-FUCOSE BIOSYNTHESIS I (FROM GDP-D-MANNOSE)



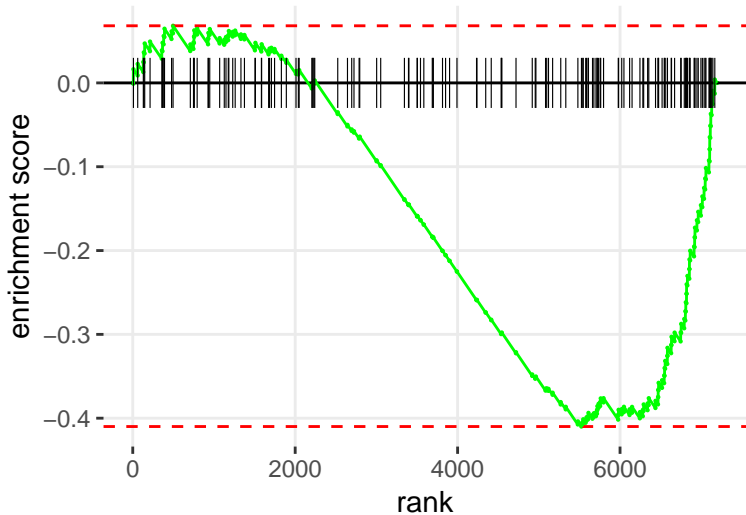
# INOSINE-5'-PHOSPHATE BIOSYNTHESIS II



# XANTHINE AND XANTHOSINE SALVAGE

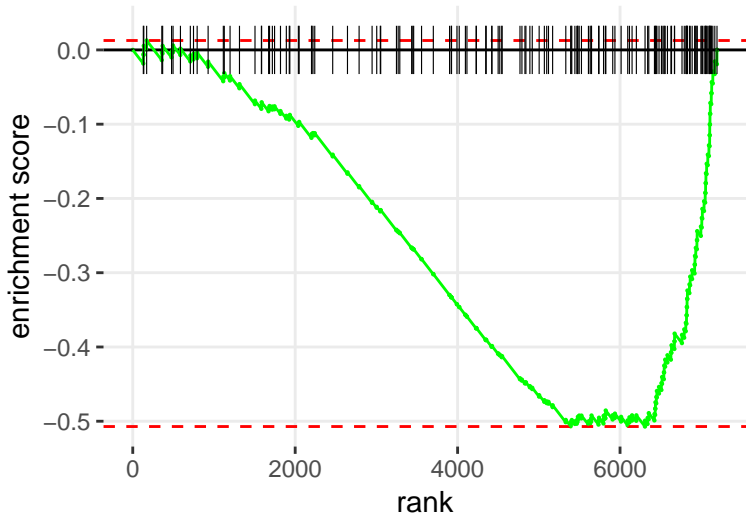


# PUTRESCINE BIOSYNTHESIS III

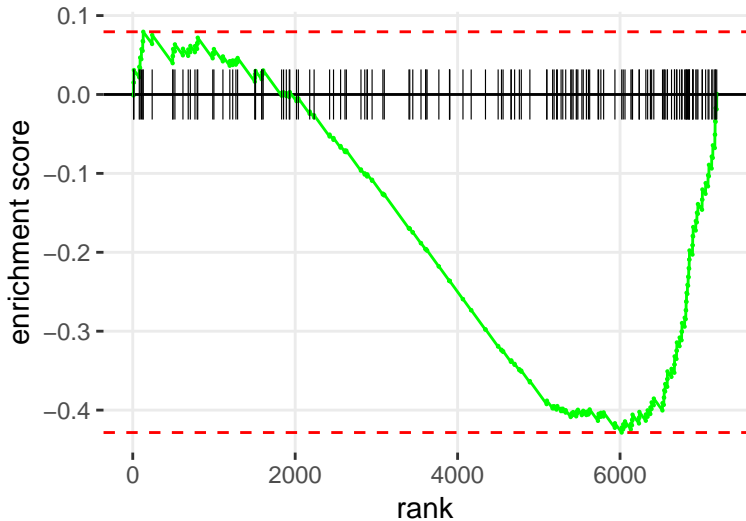




# TRYPTOPHAN DEGRADATION TO 2-AMINO-3-CARBOXYMUCONATE SEMIALDEHYDE



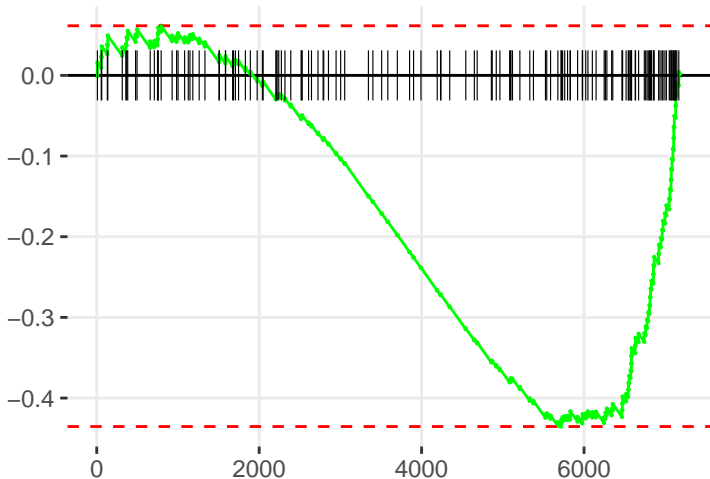
# SERINE BIOSYNTHESIS



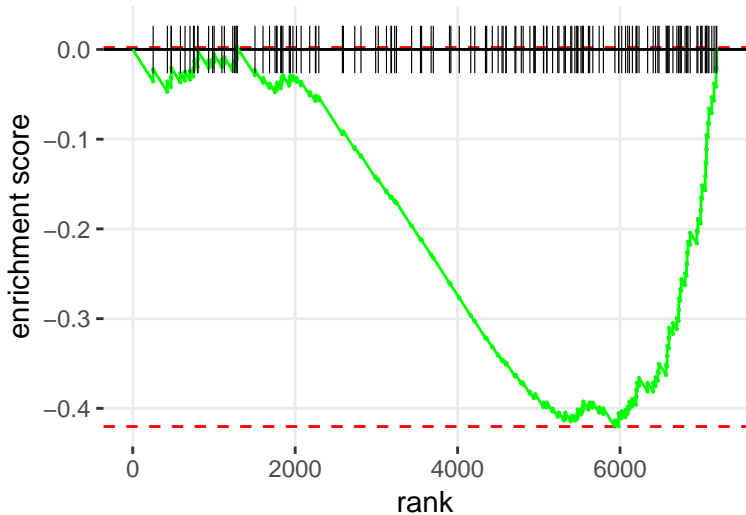
# THIOREDOXIN PATHWAY

enrichment score

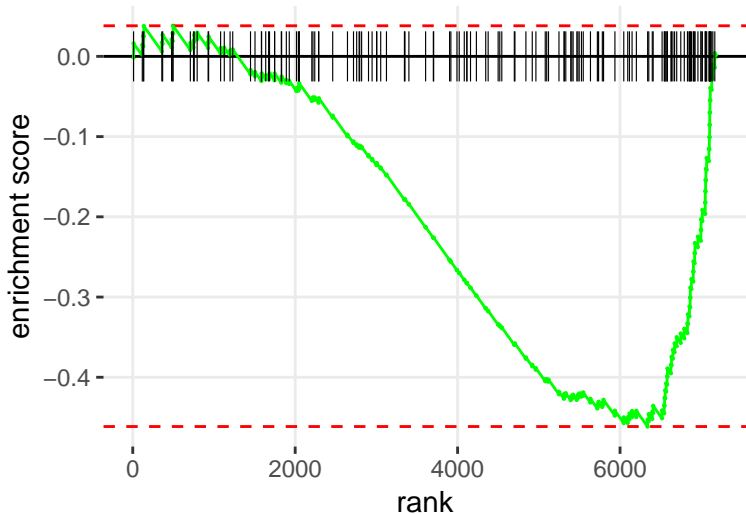
rank



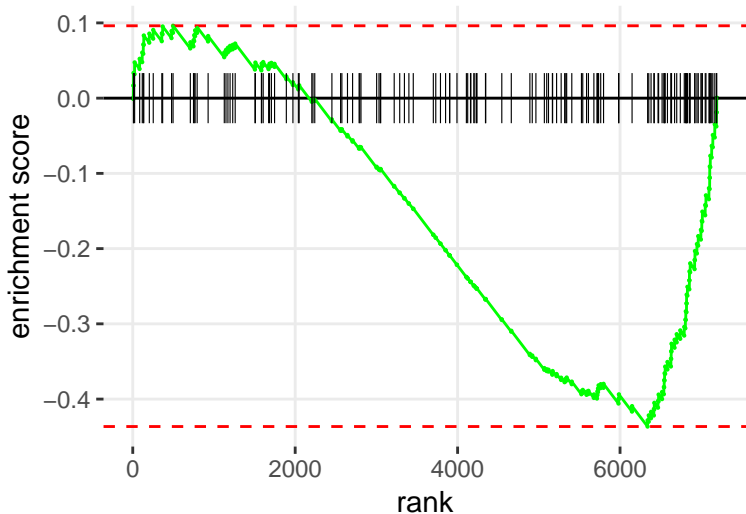
TRYPTOPHAN DEGRADATION X (MAMMALIAN, VIA TRYPTAMINE)



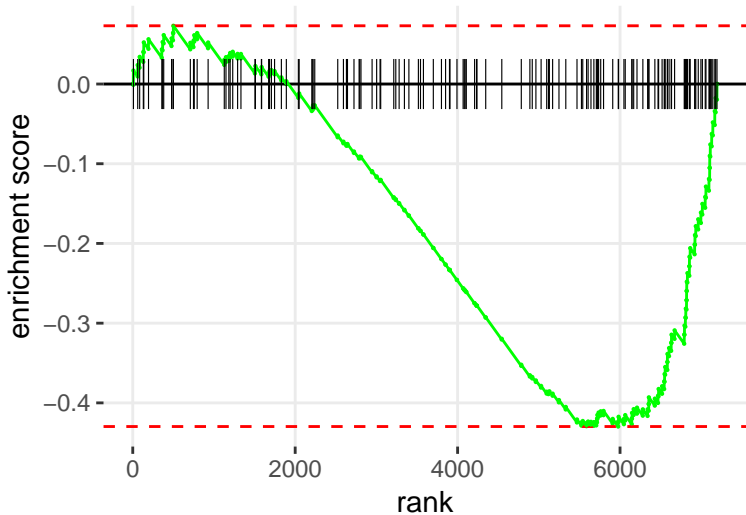
# SPERMIDINE BIOSYNTHESIS I



# PURINE RIBONUCLEOSIDES DEGRADATION TO RIBOSE-1-PHOSPHATE



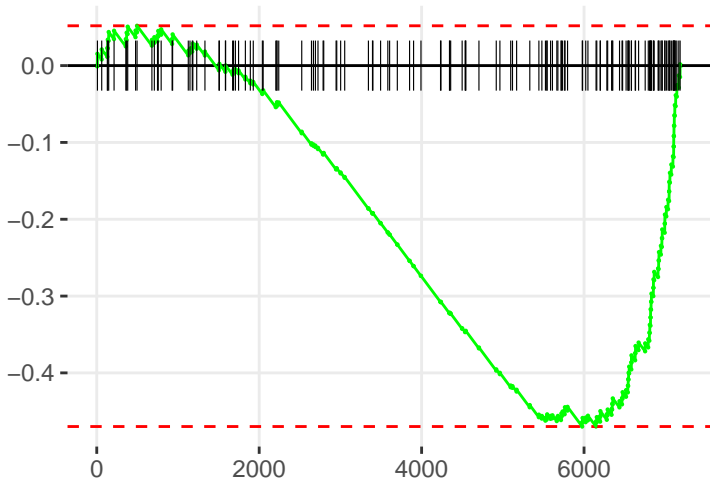
<IS</I-METHYL-5-THIO-&ALPHA;-D-RIBOSE 1-PHOSPHATE DEGRADATION



# GLUTATHIONE BIOSYNTHESIS

enrichment score

rank

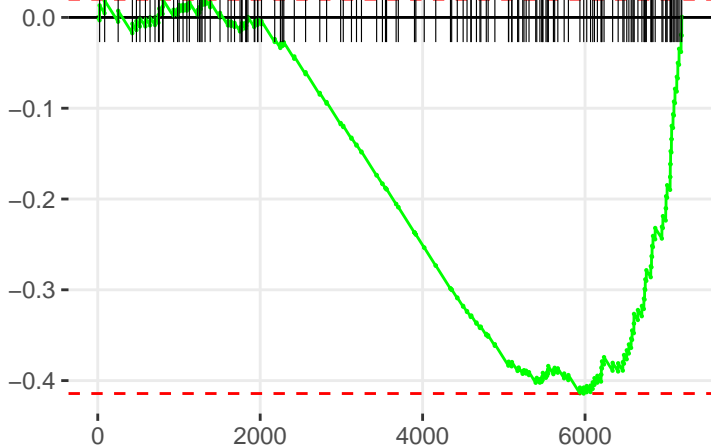




# OXIDATIVE ETHANOL DEGRADATION III

enrichment score

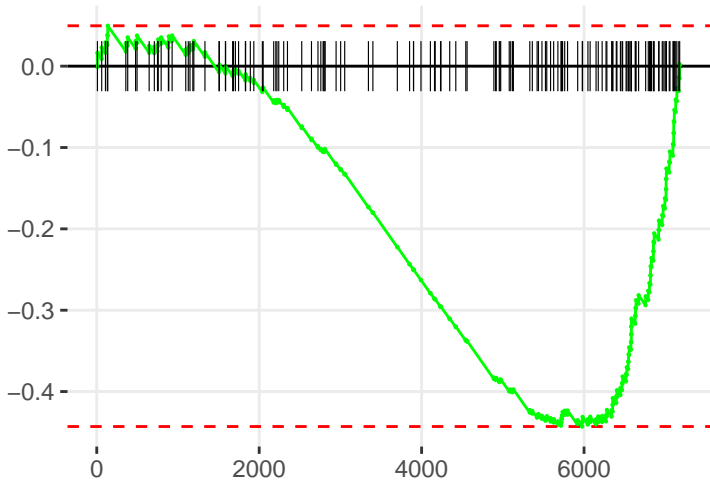
rank



# ACETYL-COA BIOSYNTHESIS III (FROM CITRATE)

enrichment score

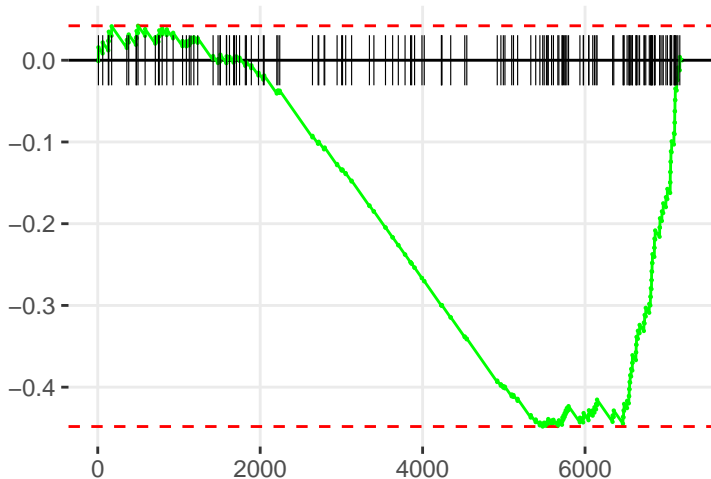
rank



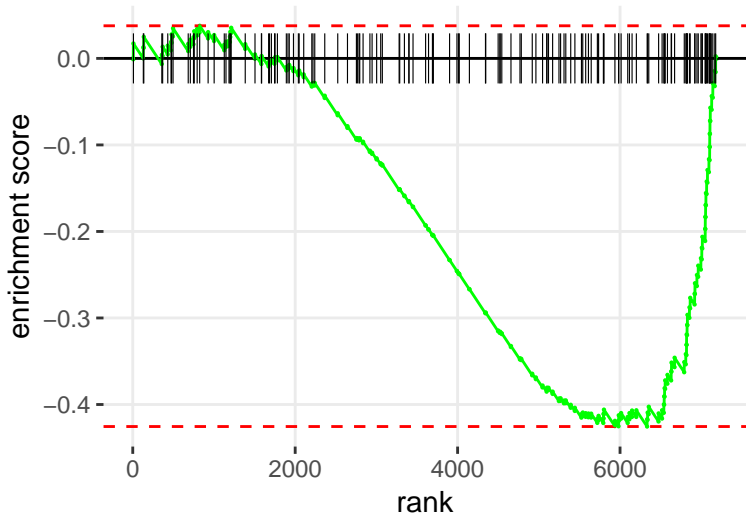
# DOLICHOL AND DOLICHYL PHOSPHATE BIOSYNTHESIS

enrichment score

rank



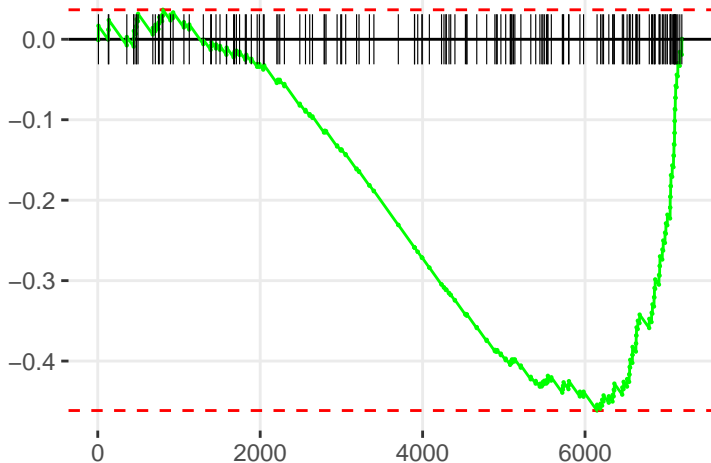
# OLEATE BIOSYNTHESIS II (ANIMALS)



# TRIACYLGLYCEROL DEGRADATION

enrichment score

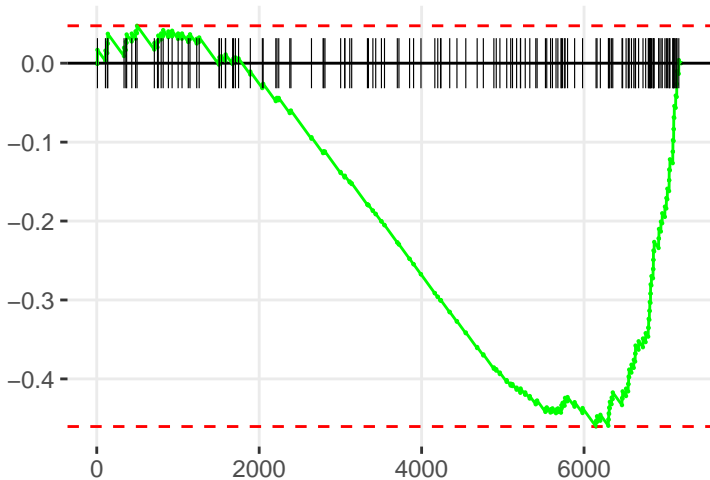
rank



# GLUTATHIONE REDOX REACTIONS I

enrichment score

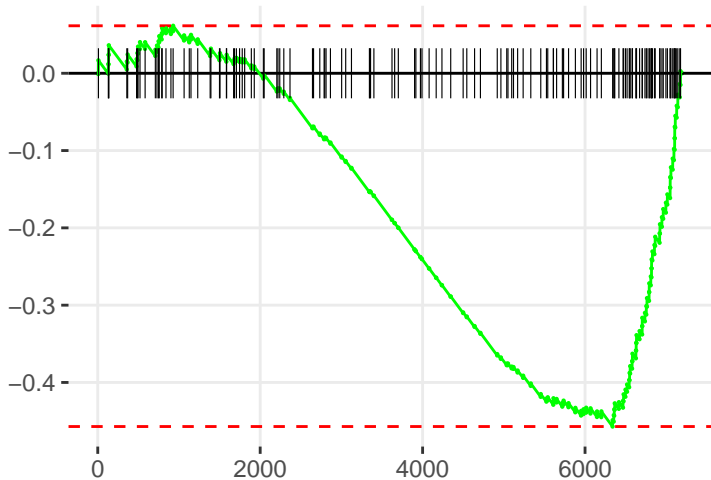
rank



# GLYCEROL DEGRADATION I

enrichment score

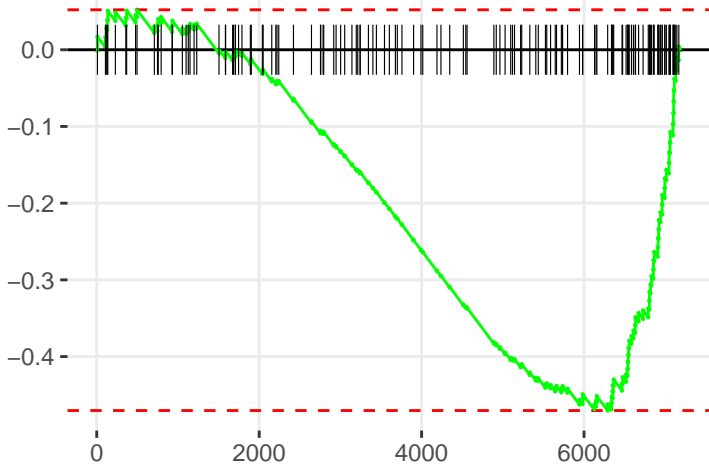
rank



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

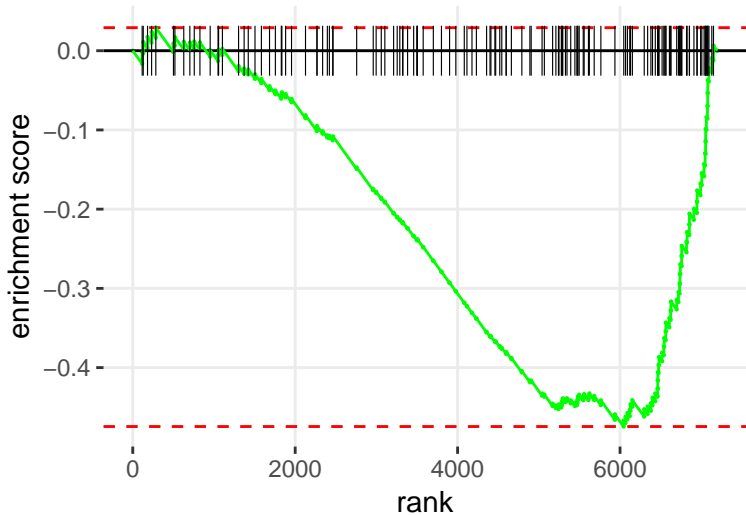
enrichment score

rank

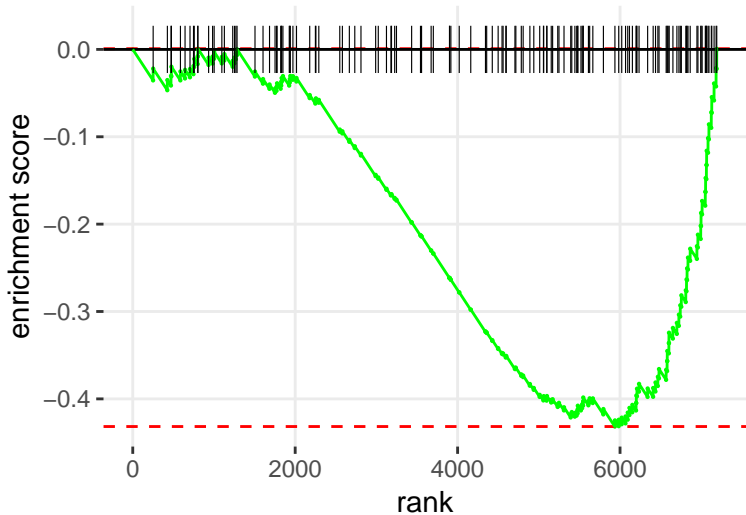




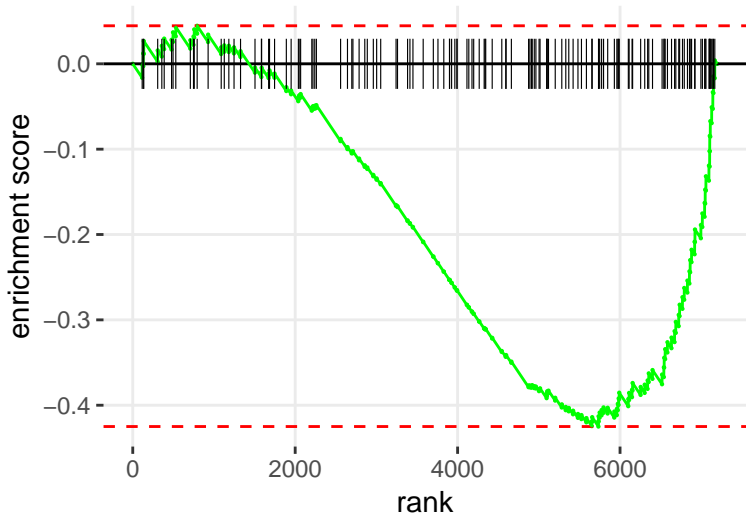
GLYCOLYSIS I



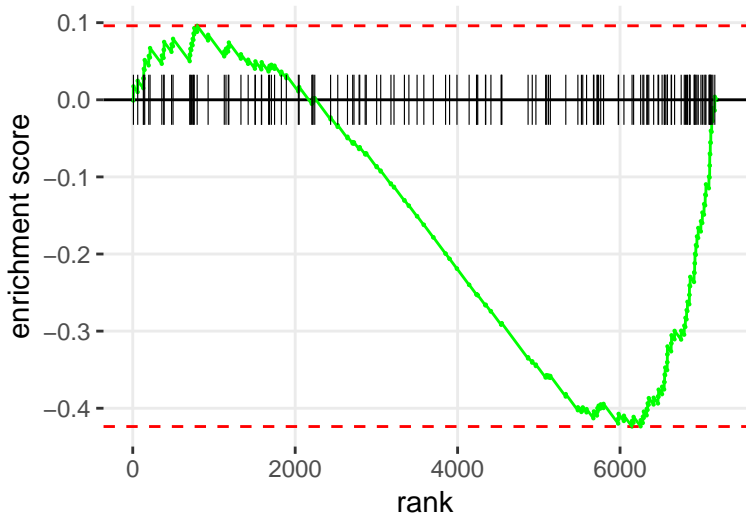
# HISTAMINE DEGRADATION



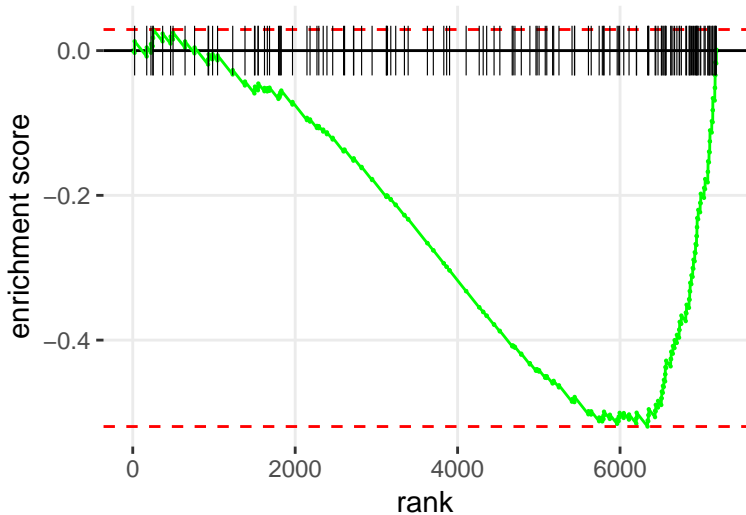
# ACYL-COA HYDROLYSIS



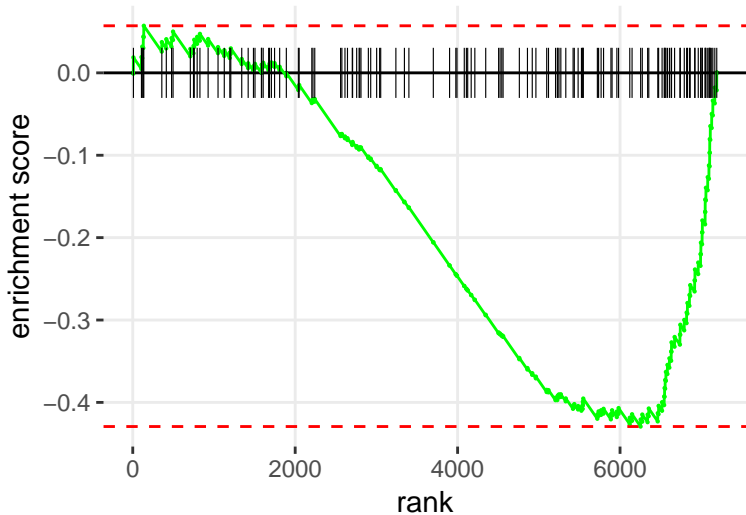
# THIO-MOLYBDENUM COFACTOR BIOSYNTHESIS



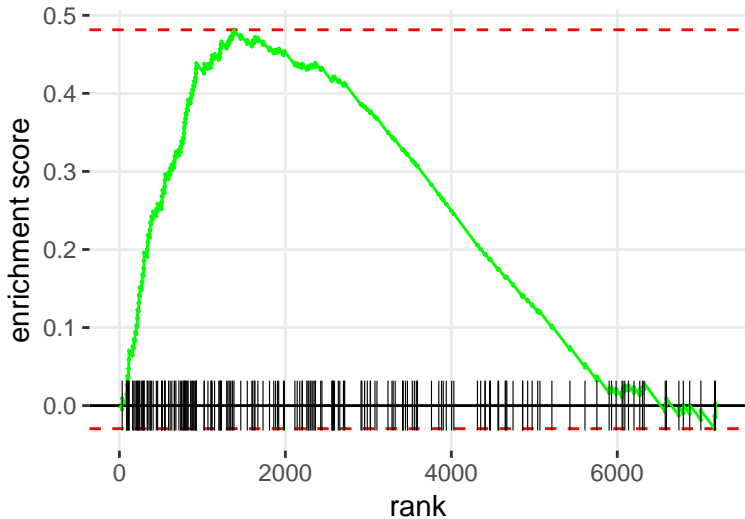
# BILE ACID BIOSYNTHESIS, NEUTRAL PATHWAY



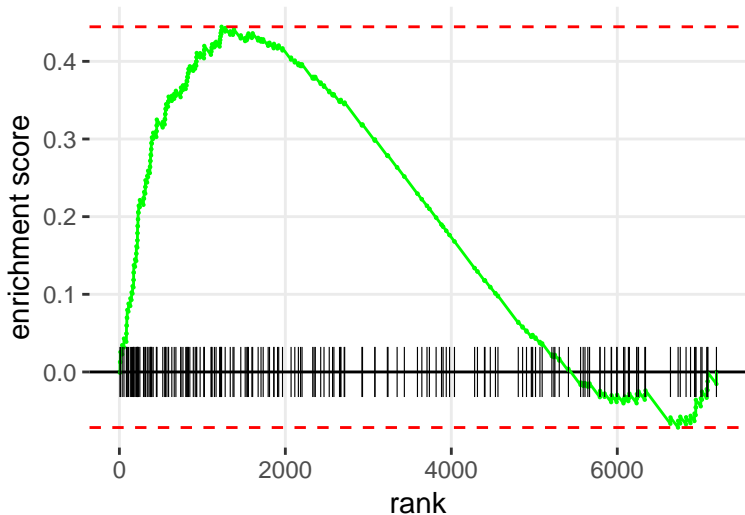
# CREATINE-PHOSPHATE BIOSYNTHESIS



NADH REPAIR



# THIAMIN SALVAGE III





TRNA SPLICING

enrichment score

0.6

0.4

0.2

0.0

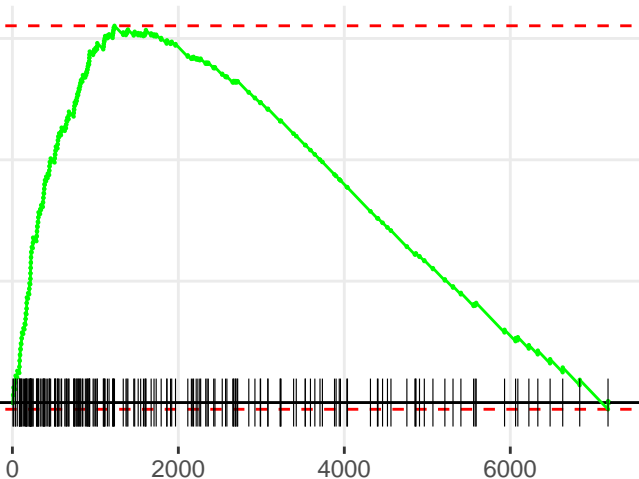
0

2000

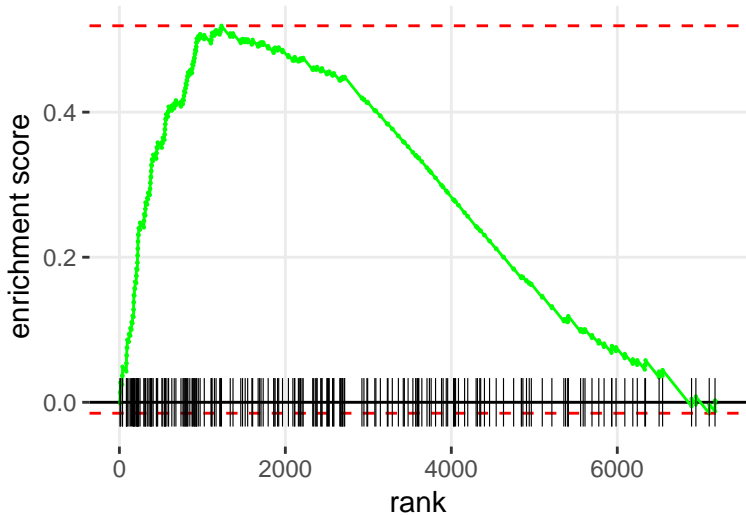
4000

6000

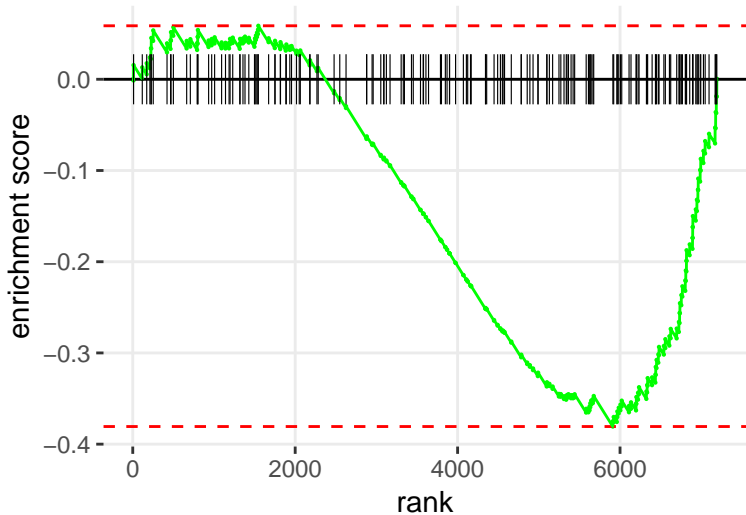
rank



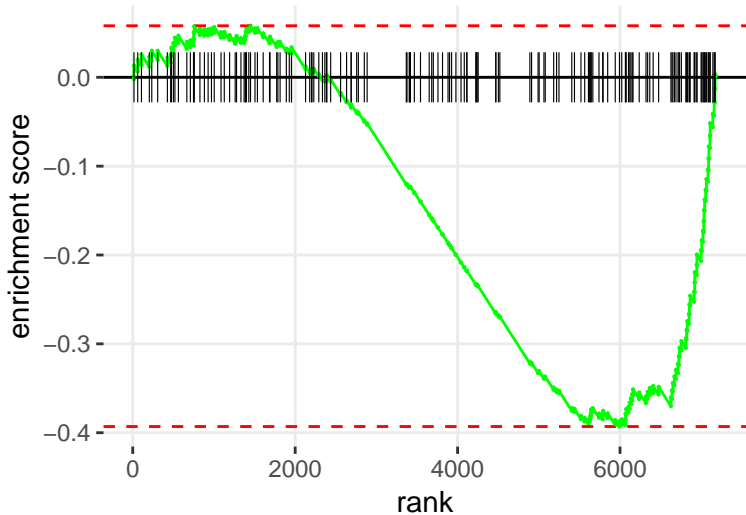
ALL-<ITRANS</I>-DECAPRENYL DIPHOSPHATE BIOSYNTHESIS



# ISOLEUCINE DEGRADATION I



# LIPOATE BIOSYNTHESIS AND INCORPORATION II



# 2-OXISOVALERATE DECARBOXYLATION TO ISOBUTANOYL-COA

enrichment score

0.0  
-0.1  
-0.2  
-0.3  
-0.4

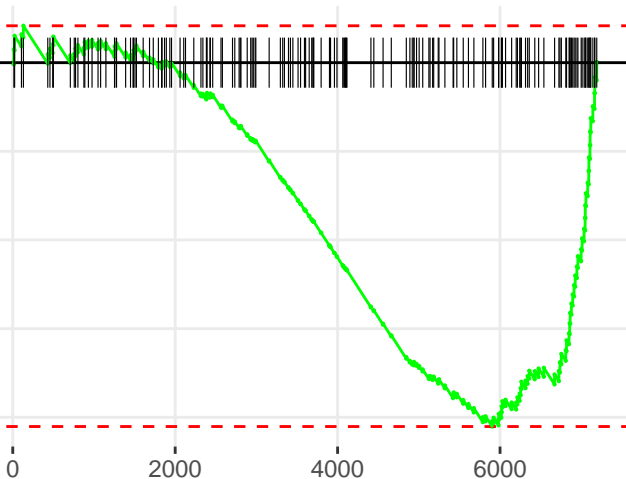
0

2000

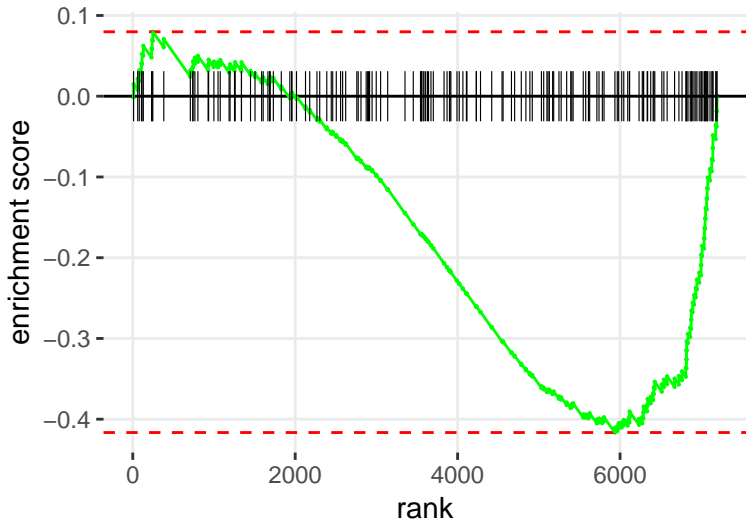
4000

6000

rank



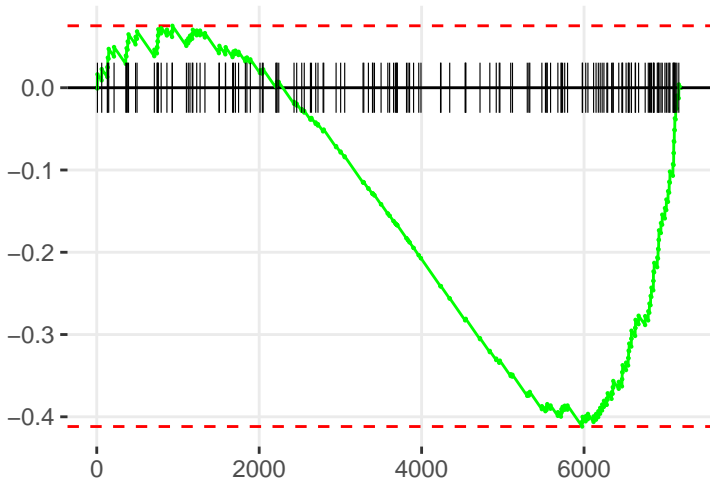
# PROLINE BIOSYNTHESIS II (FROM ARGinine)



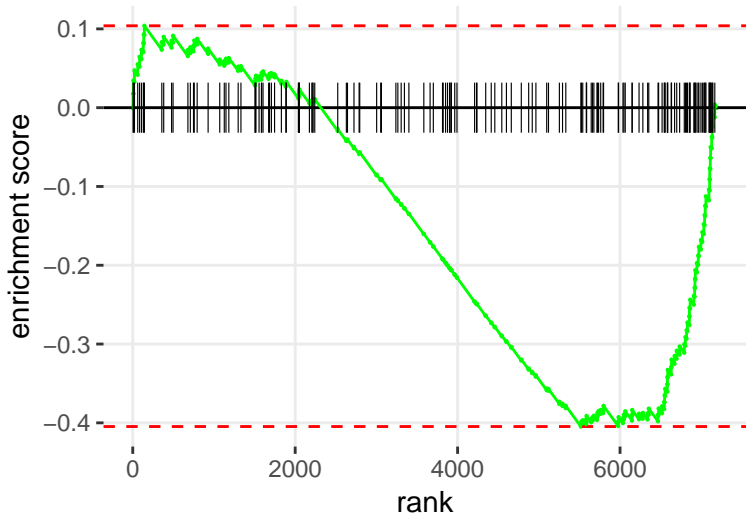
# GDP-L-FUCOSE BIOSYNTHESIS II (FROM L-FUCOSE)

enrichment score

rank

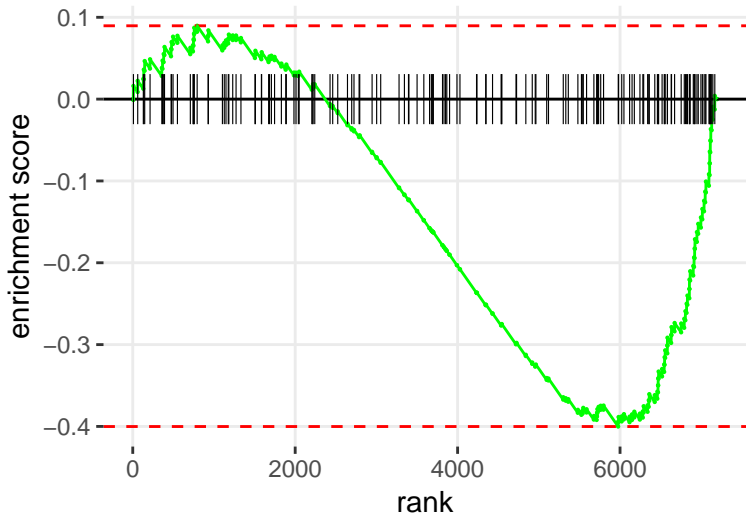


# LACTOSE DEGRADATION III

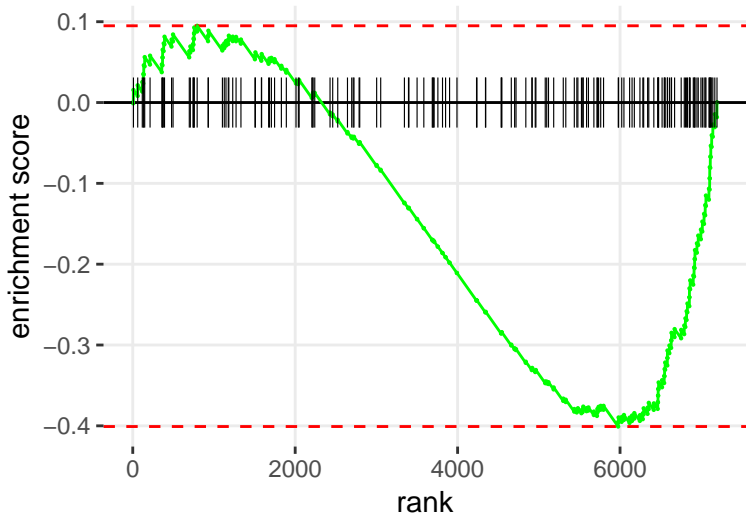




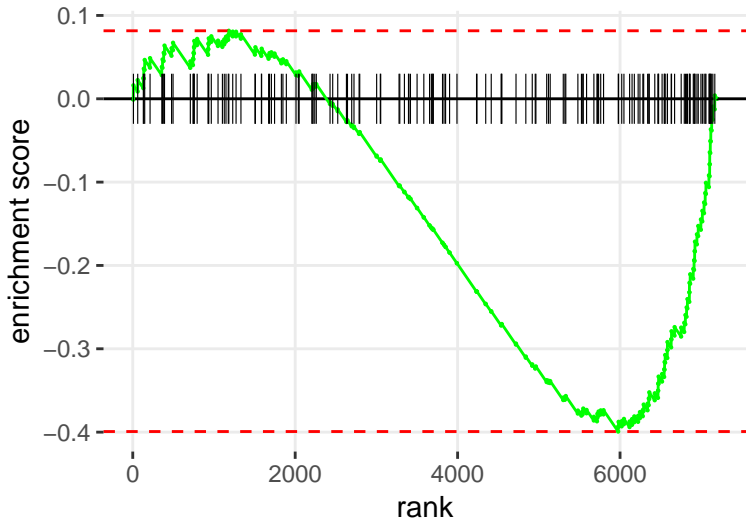
# URACIL DEGRADATION II (REDUCTIVE)



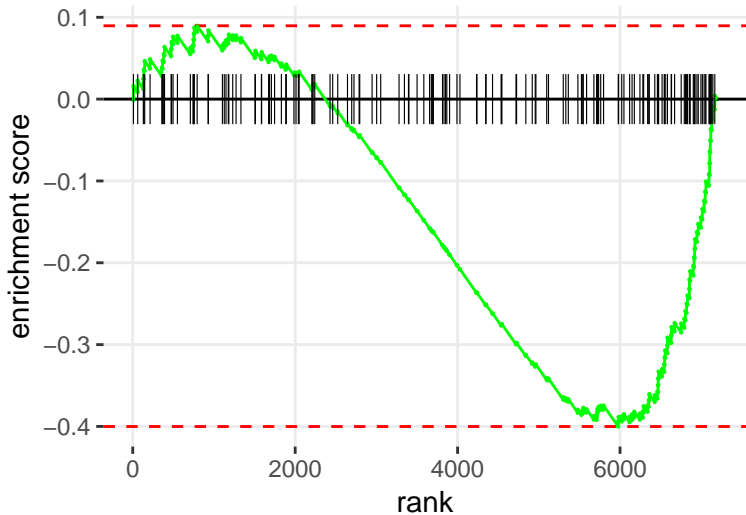
# NAD PHOSPHORYLATION AND DEPHOSPHORYLATION



# GLYCINE DEGRADATION (CREATINE BIOSYNTHESIS)



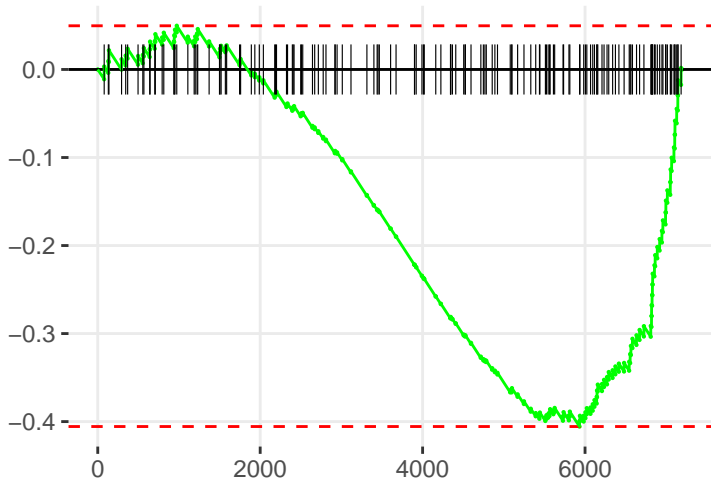
# THYMINE DEGRADATION



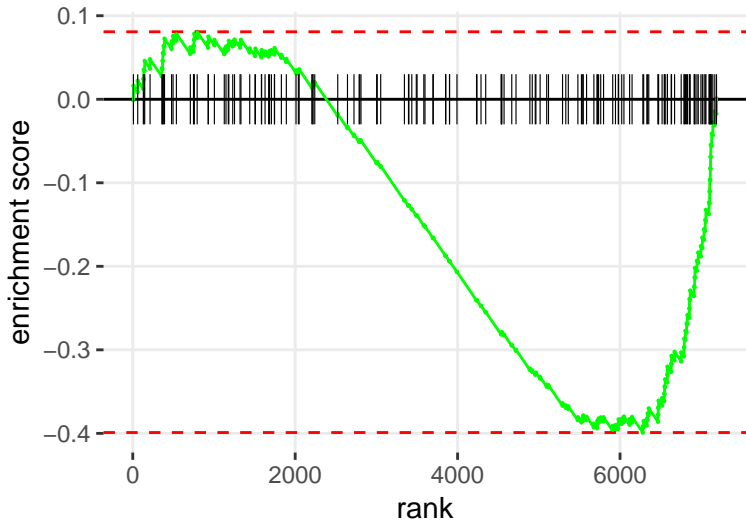
# CERAMIDE BIOSYNTHESIS

enrichment score

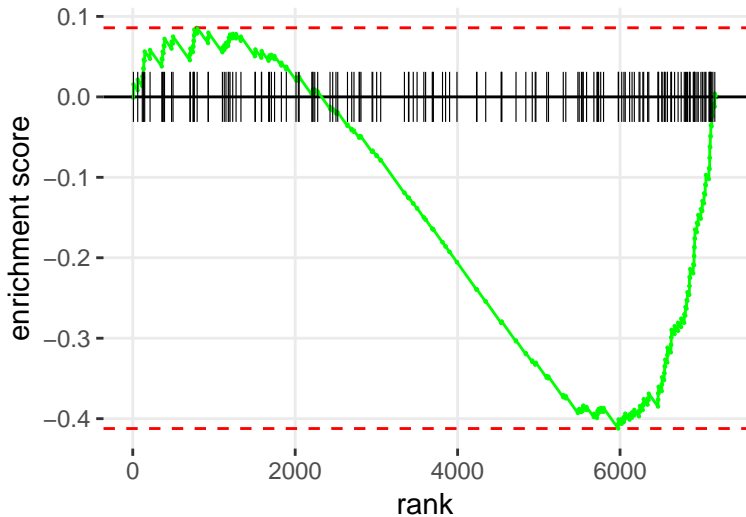
rank



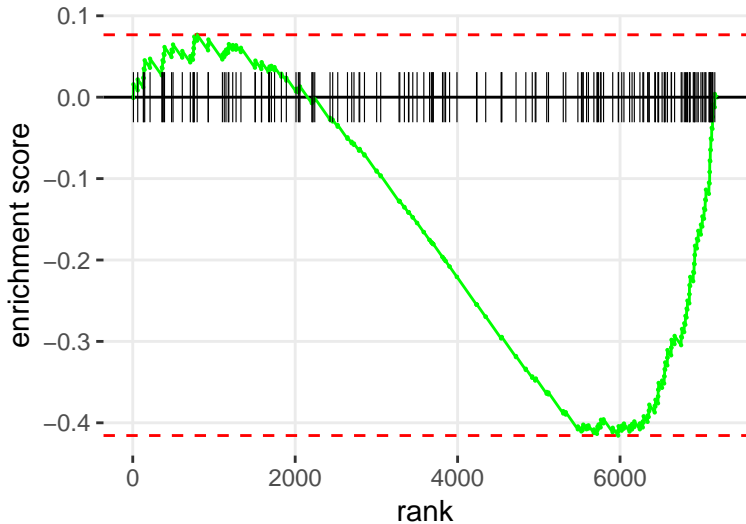
# L-CARNITINE BIOSYNTHESIS



# ACYL CARRIER PROTEIN METABOLISM

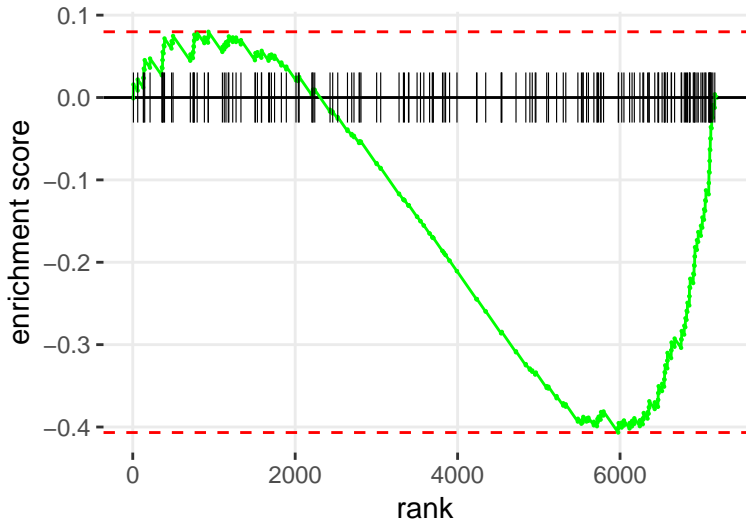


# COENZYME A BIOSYNTHESIS

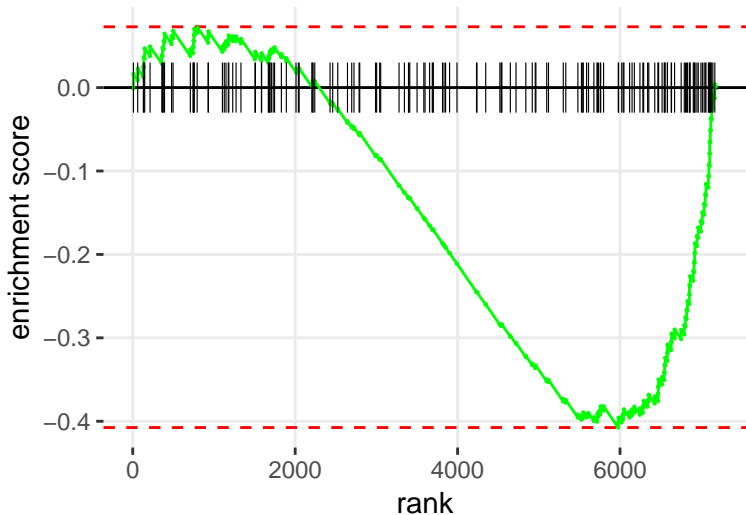




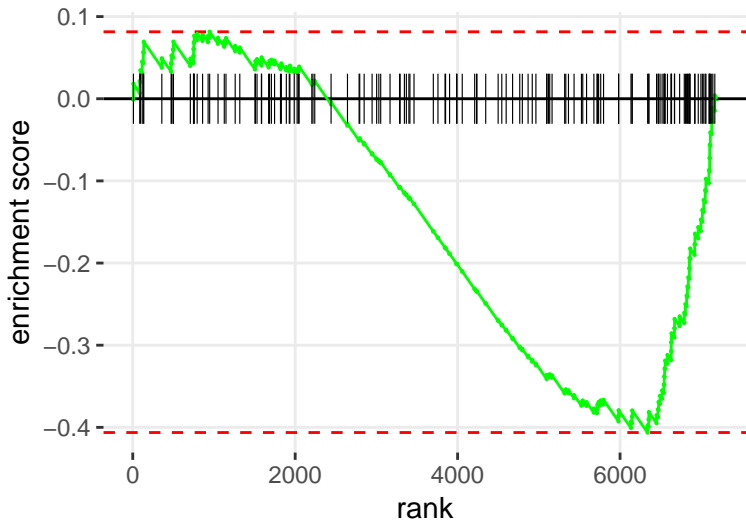
# GLUTATHIONE REDOX REACTIONS II



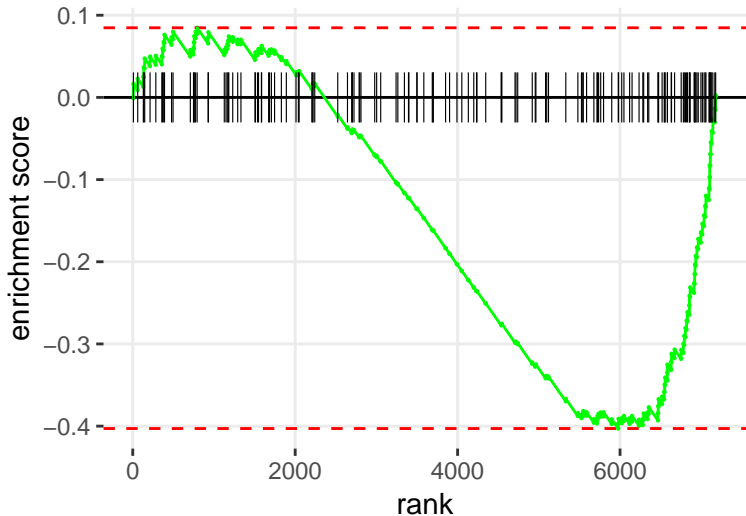
1D-<IMYO</I>-INOSITOL HEXAKISPHOSPHATE BIOSYNTHESIS V (FROM INS(1,3,4)P3)



# TYROSINE DEGRADATION I

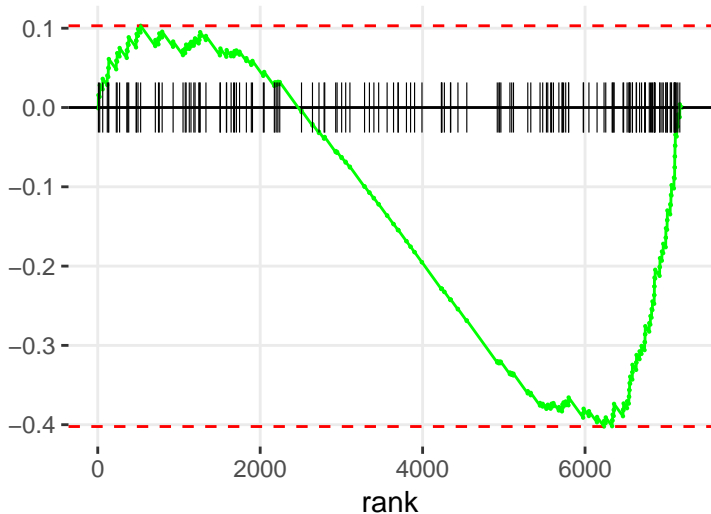


# CMP-<IN</I>-ACETYLNEURAMINATE BIOSYNTHESIS I (EUKARYOTES)

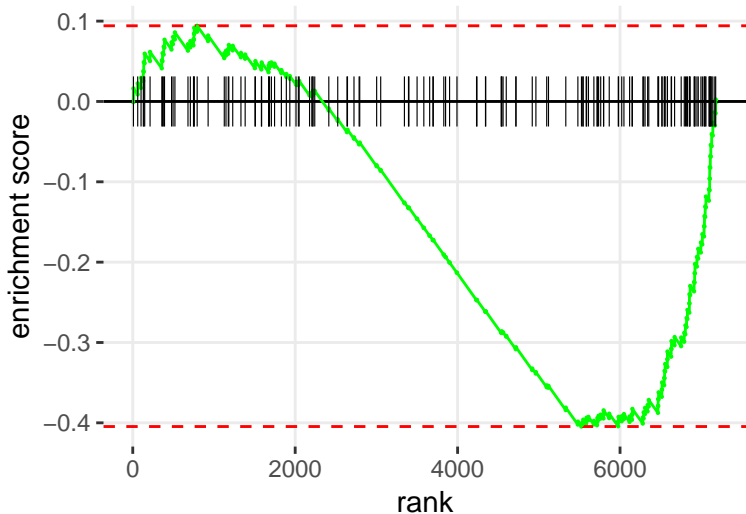


# MITOCHONDRIAL L-CARNITINE SHUTTLE PATHWAY

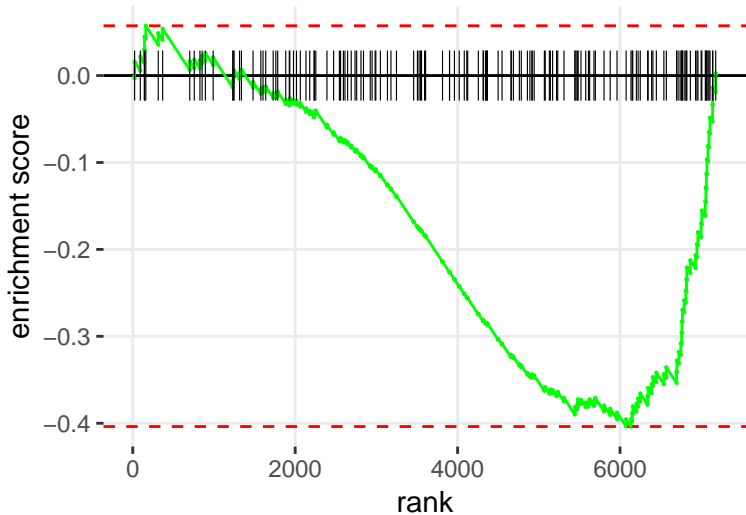
enrichment score



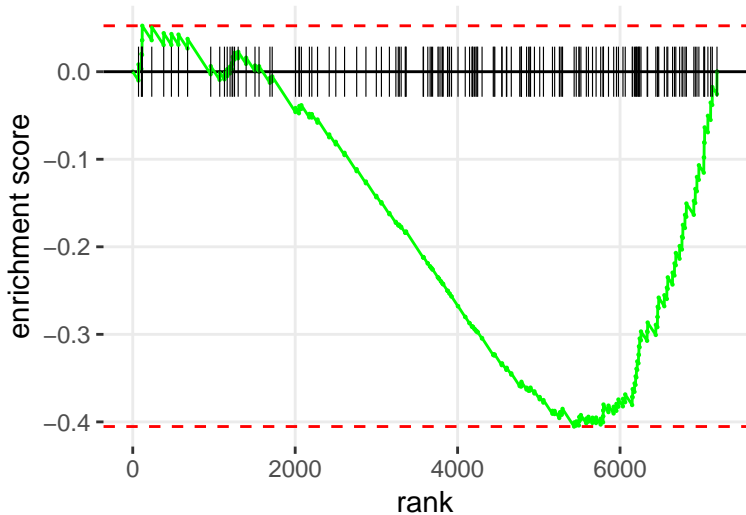
# ALANINE BIOSYNTHESIS II



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

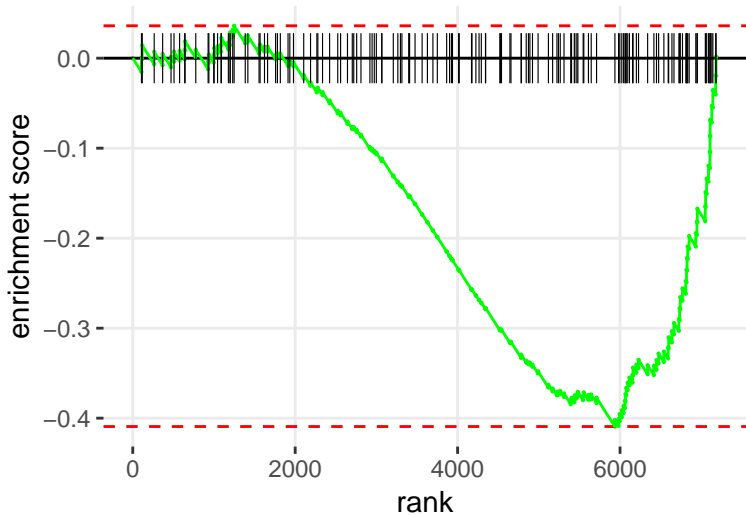


# FLAVIN BIOSYNTHESIS IV (MAMMALIAN)

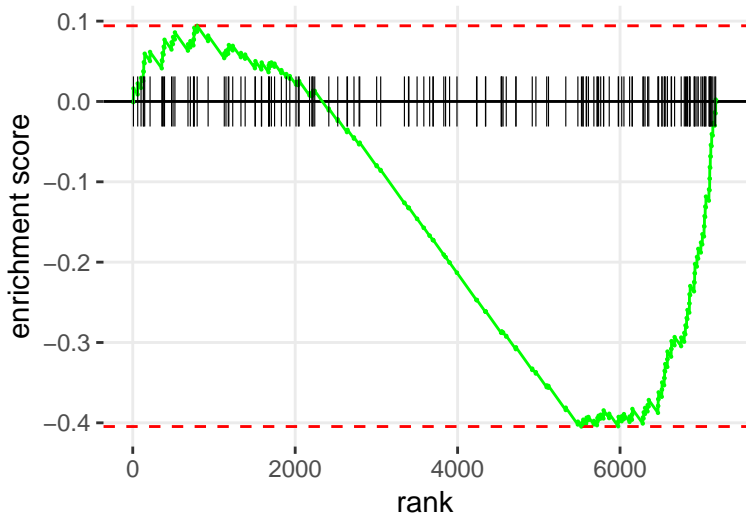




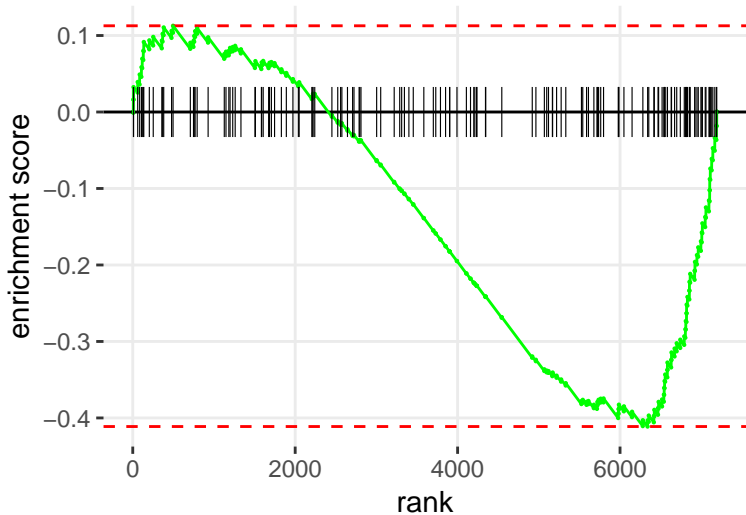
# TRIACYLGLYCEROL BIOSYNTHESIS



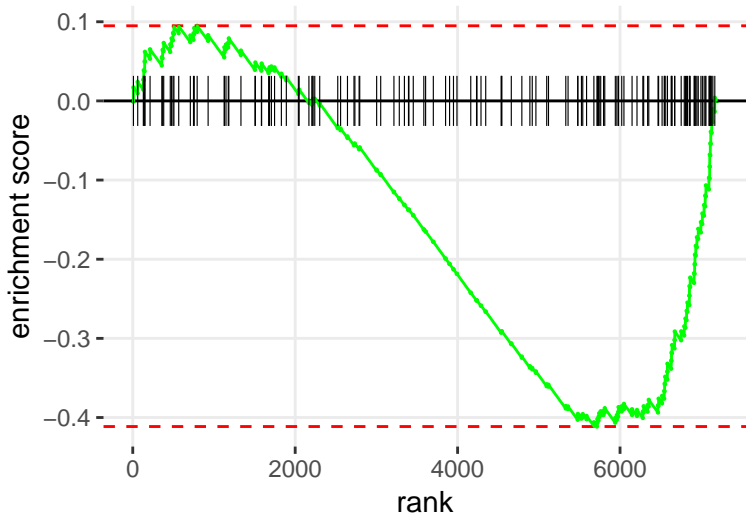
# ALANINE DEGRADATION III



# ARSENATE DETOXIFICATION I (GLUTAREDOXIN)



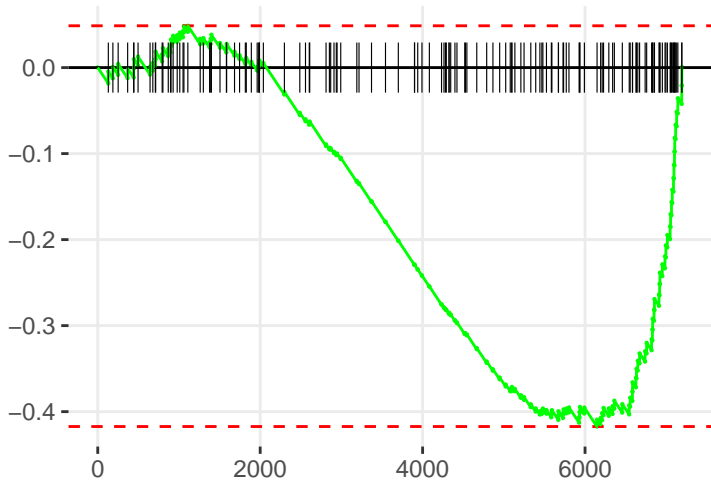
# UDP-D-XYLOSE AND UDP-D-GLUCURONATE BIOSYNTHESIS



# RETINOL BIOSYNTHESIS

enrichment score

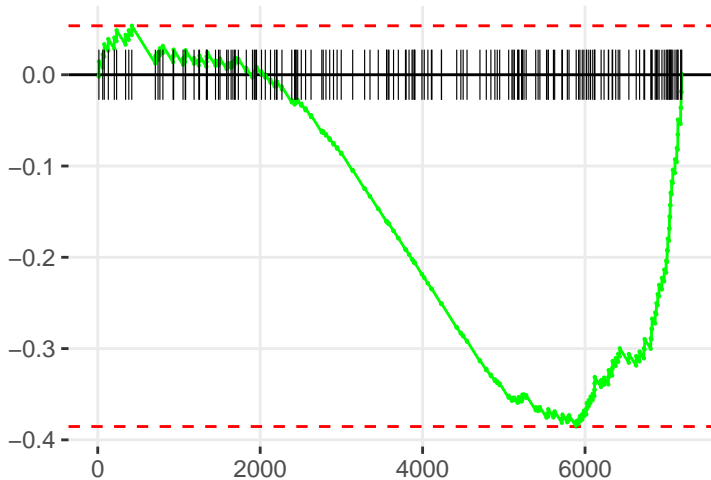
rank



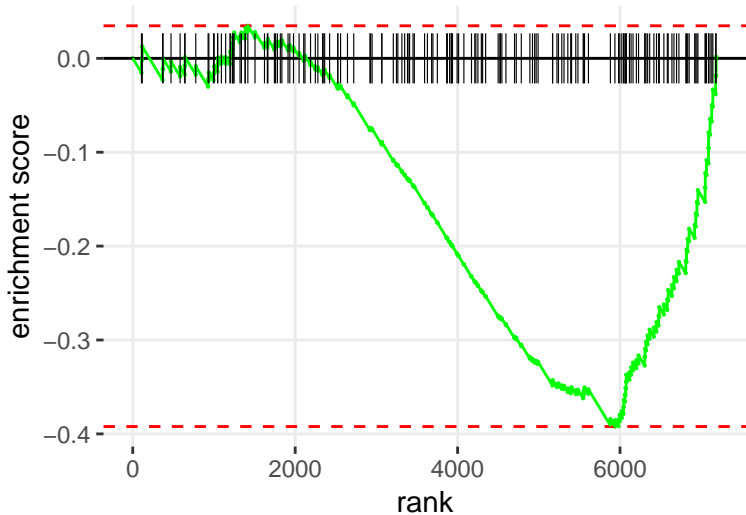
# CITRULLINE BIOSYNTHESIS

enrichment score

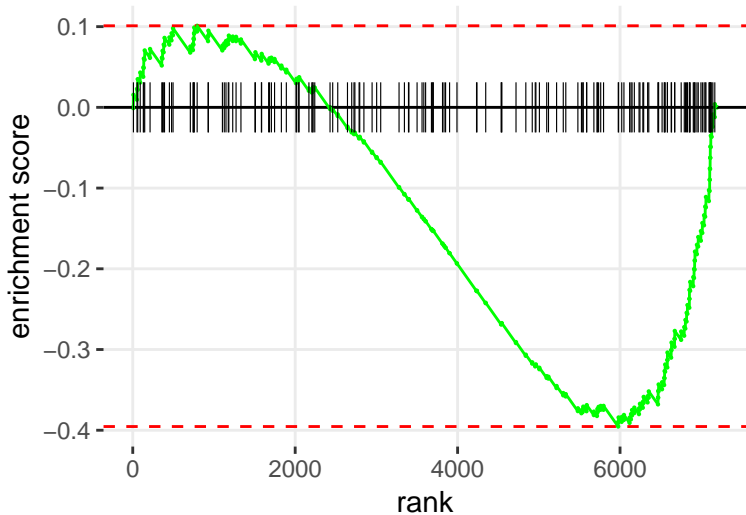
rank



# CDP-DIACYLGLYCEROL BIOSYNTHESIS I

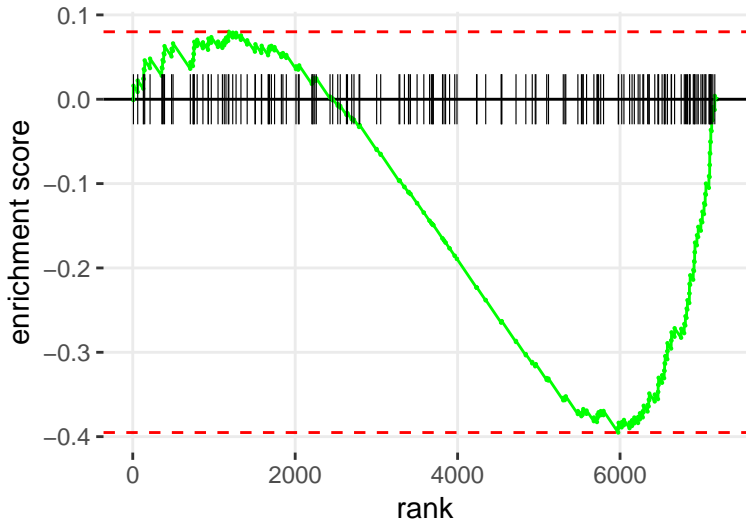


# GLUTAMATE REMOVAL FROM FOLATES



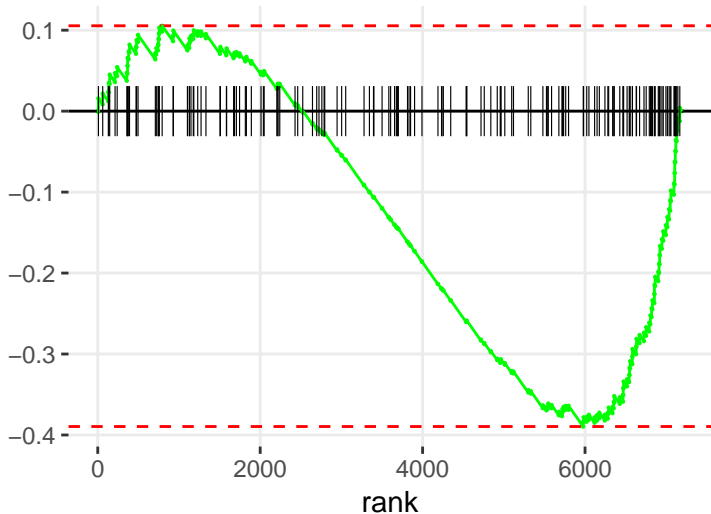


# SULFITE OXIDATION IV

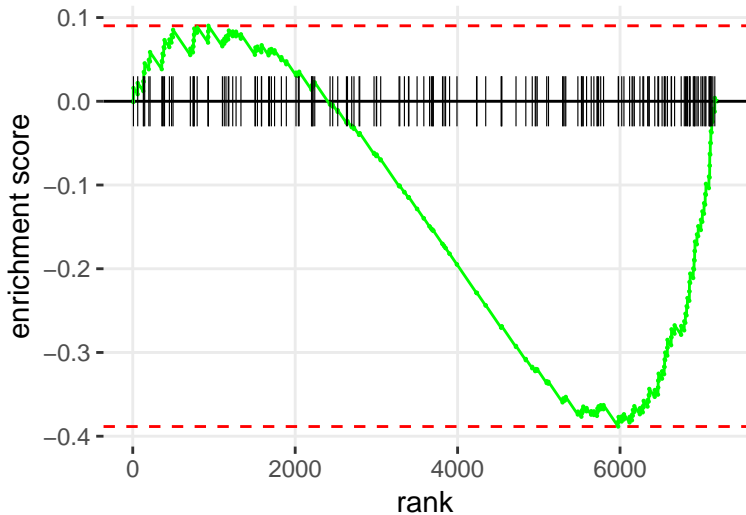


# PHOSPHATIDYLETHANOLAMINE BIOSYNTHESIS III

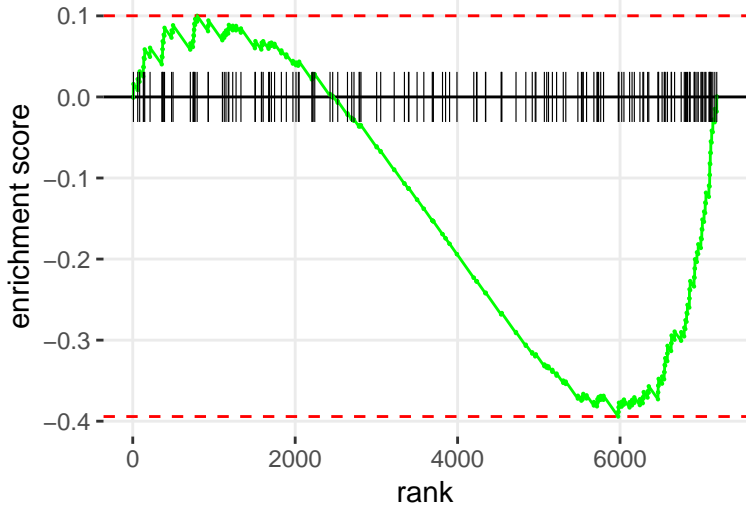
enrichment score



# L-DOPACHROME BIOSYNTHESIS

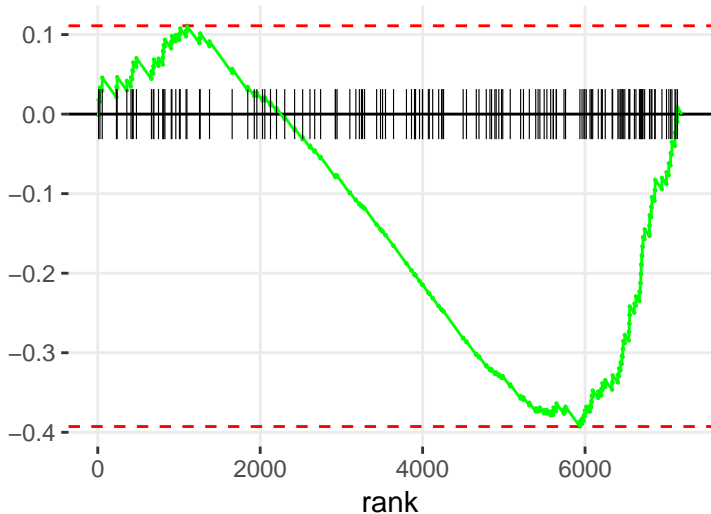


<IS>/I-METHYL-5'-THIOADENOSINE DEGRADATION II

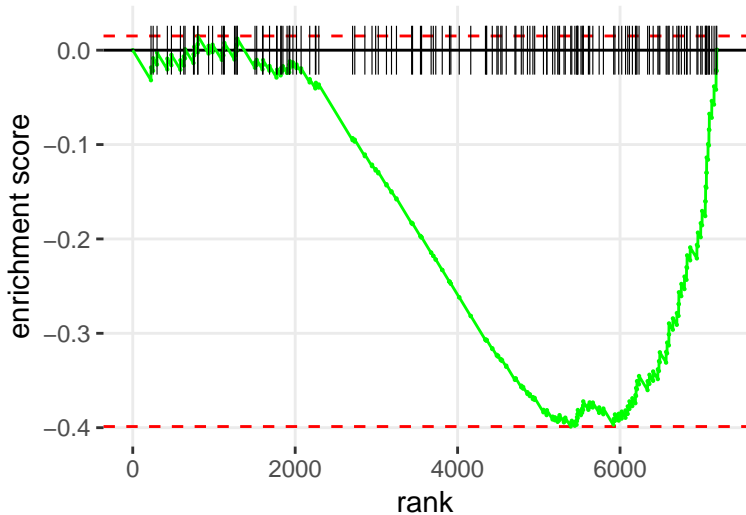


# PYRIMIDINE DEOXYRIBONUCLEOTIDES <IDE NOVO</I> BIOSYNTHESIS I

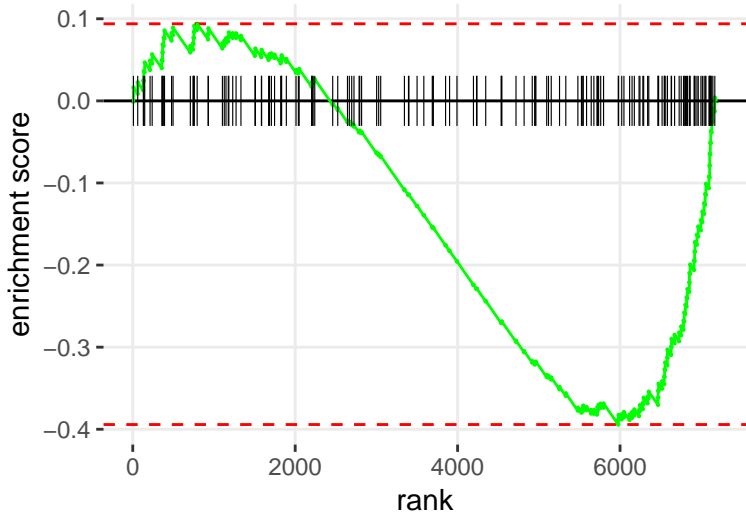
enrichment score



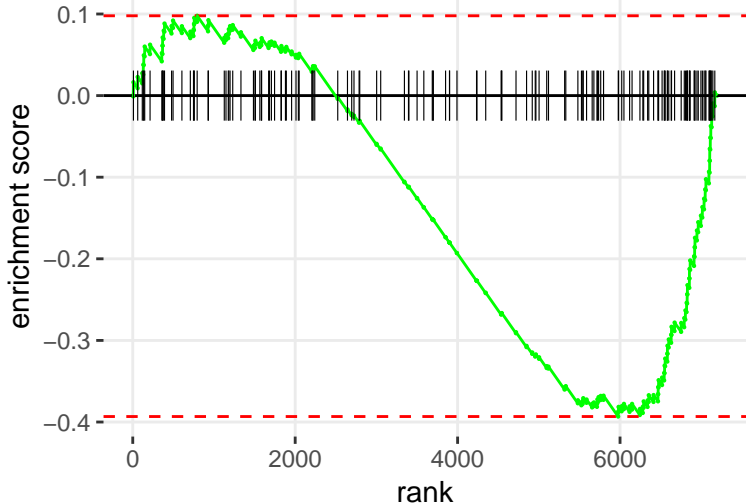
# PUTRESCINE DEGRADATION III



# L-DOPA DEGRADATION

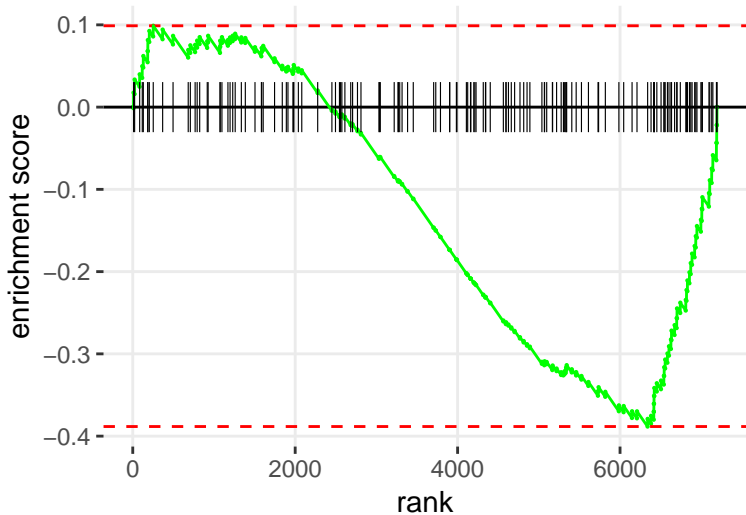


METHIONINE SALVAGE II (MAMMALIA)

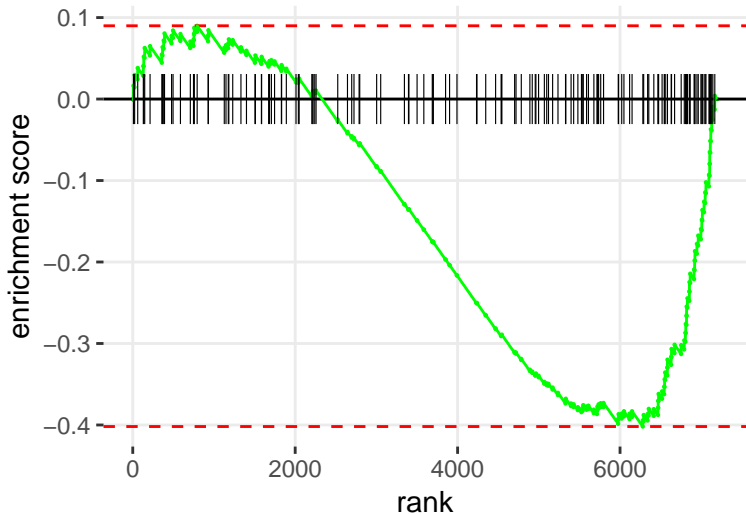




# ADENOSINE NUCLEOTIDES DEGRADATION II



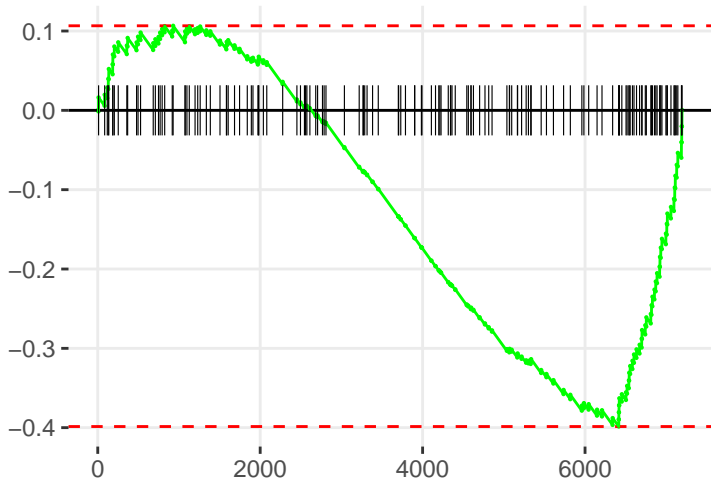
<ITRANS, TRANS</I>-FARNESYL DIPHOSPHATE BIOSYNTHESIS



# GUANOSINE NUCLEOTIDES DEGRADATION III

enrichment score

rank



# DOPAMINE DEGRADATION

enrichment score

rank

0.0

-0.1

-0.2

-0.3

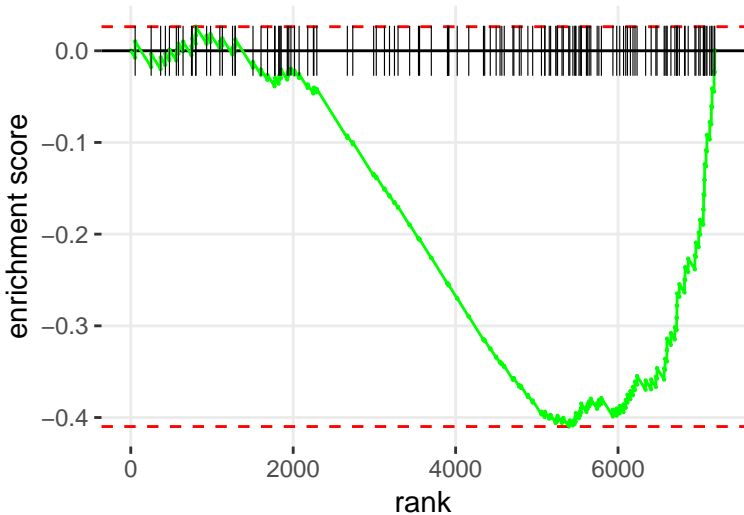
-0.4

0

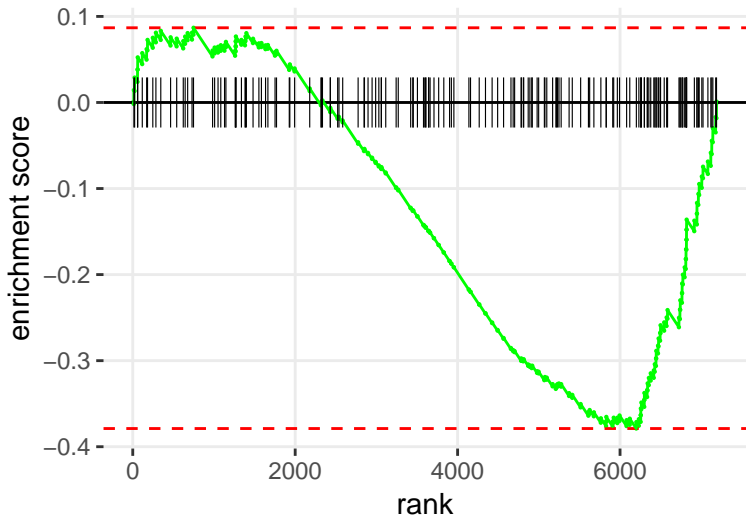
2000

4000

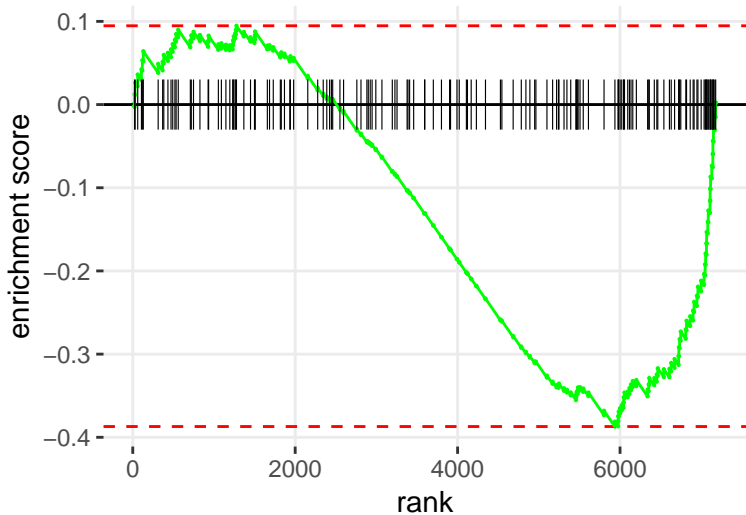
6000



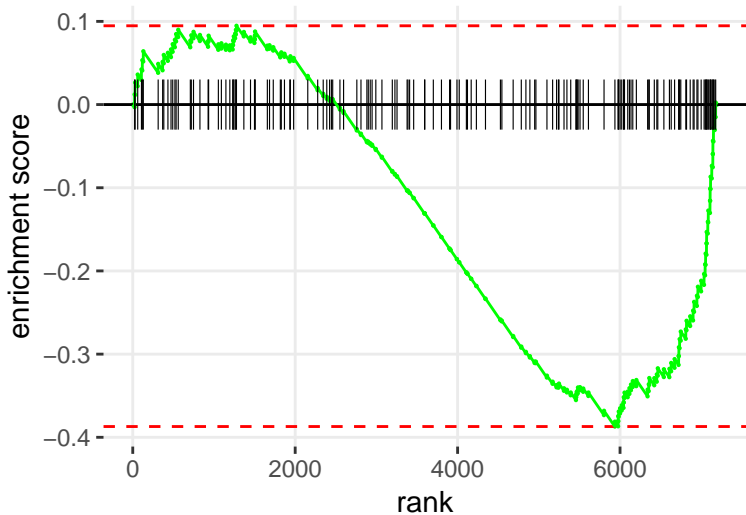
# SUPEROXIDE RADICALS DEGRADATION



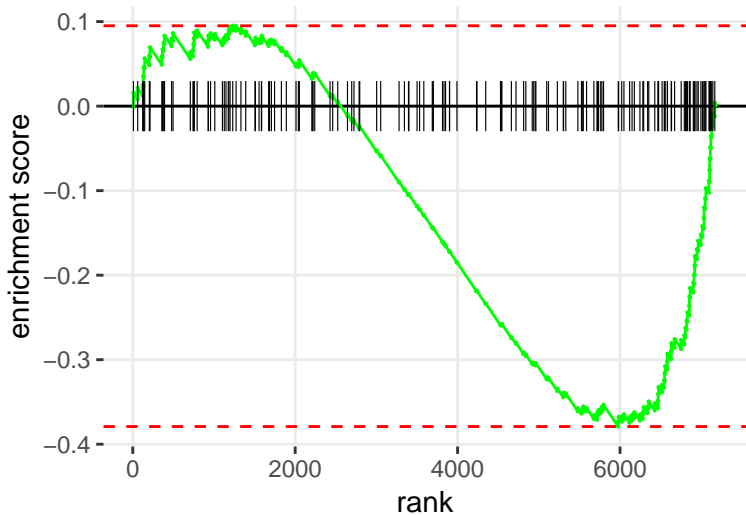
# FATTY ACID ACTIVATION



# FATTY ACID &ALPHA;-OXIDATION II

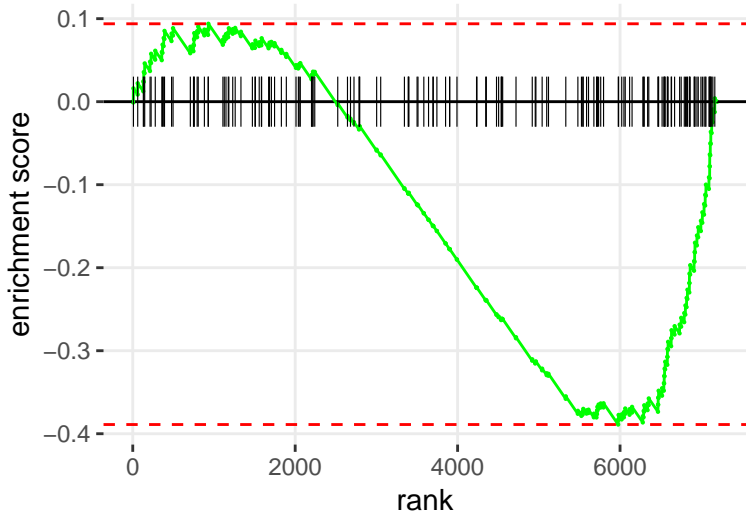


# NAD BIOSYNTHESIS III

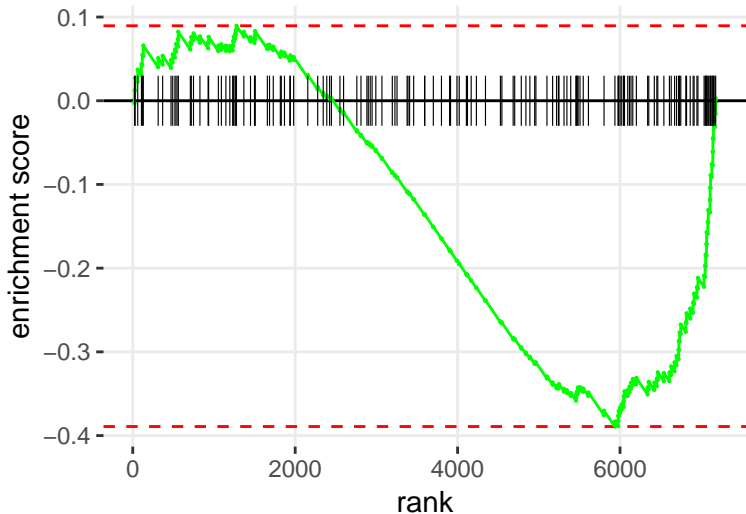




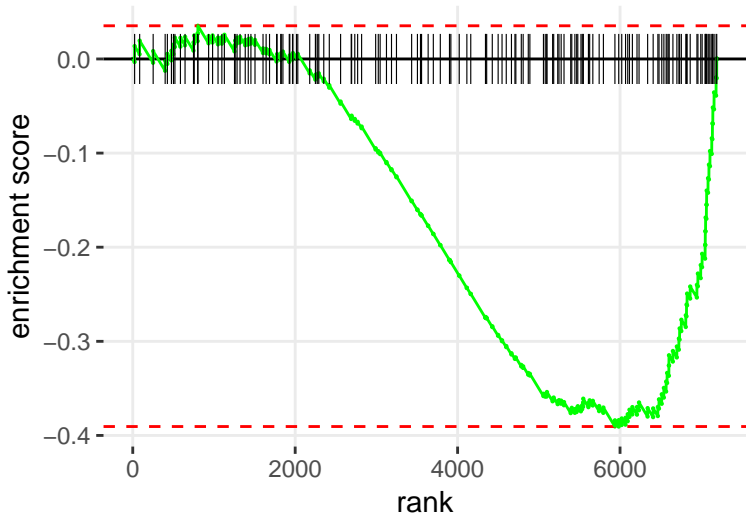
# INOSITOL PYROPHOSPHATES BIOSYNTHESIS



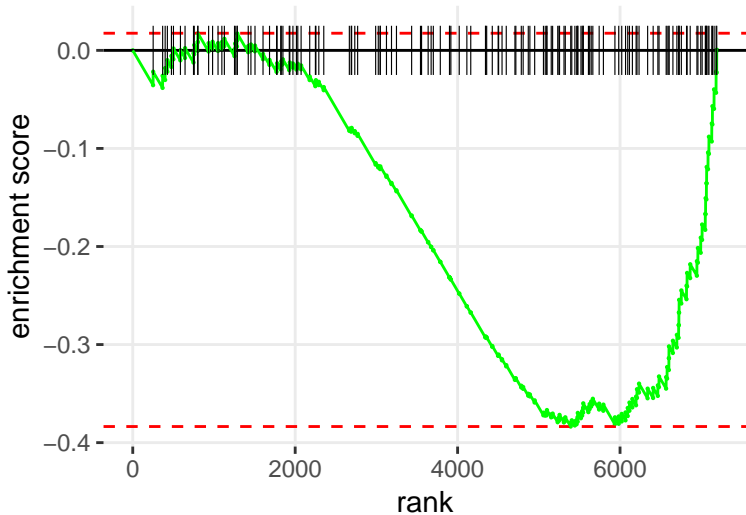
&GAMMA;-LINOLENATE BIOSYNTHESIS II (ANIMALS)



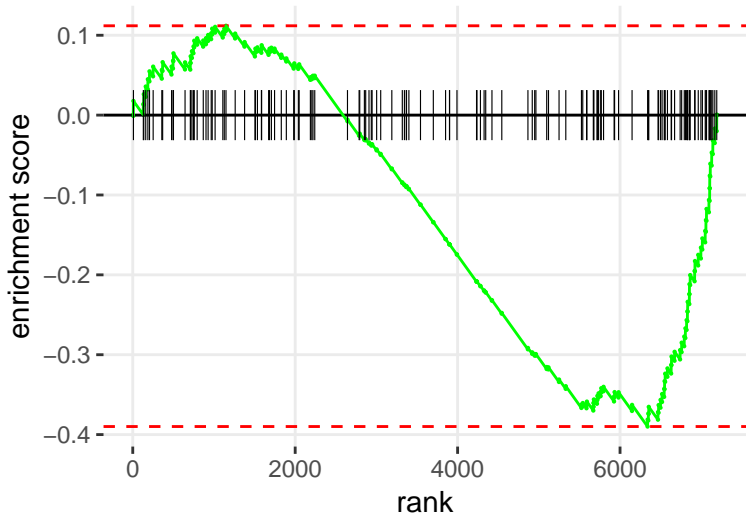
# ETHANOL DEGRADATION II



# NORADRENALINE AND ADRENALINE DEGRADATION



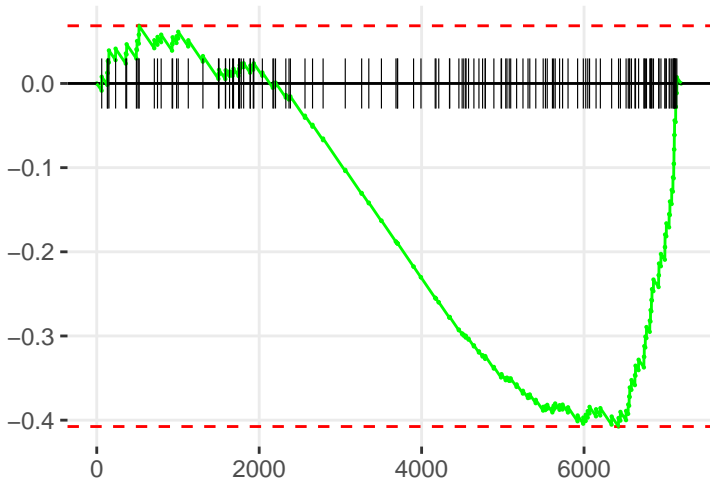
THE VISUAL CYCLE I (VERTEBRATES)



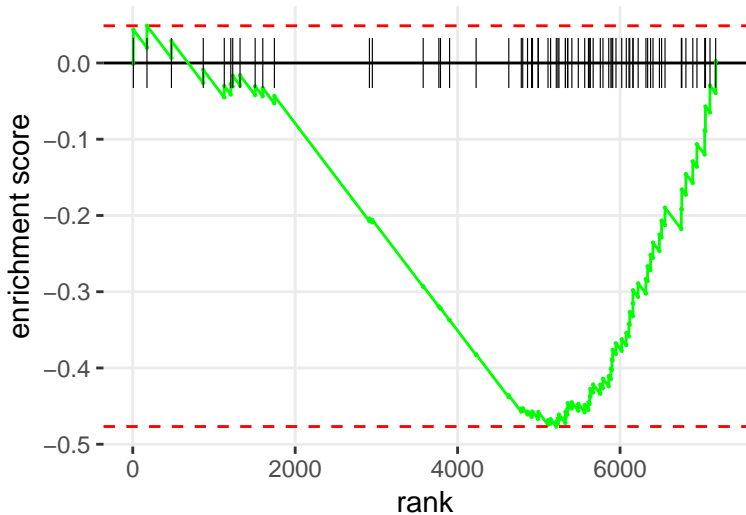
# GLYCEROL-3-PHOSPHATE SHUTTLE

enrichment score

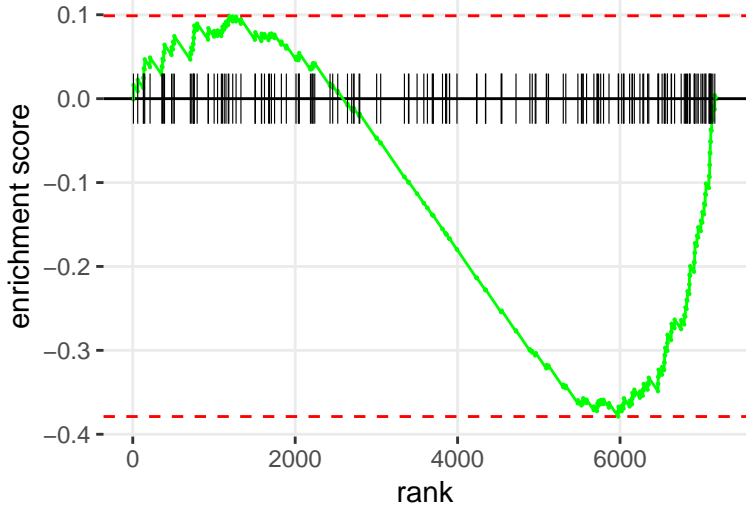
rank



# L-GLUTAMINE BIOSYNTHESIS II (TRNA-DEPENDENT)



# LANOSTEROL BIOSYNTHESIS

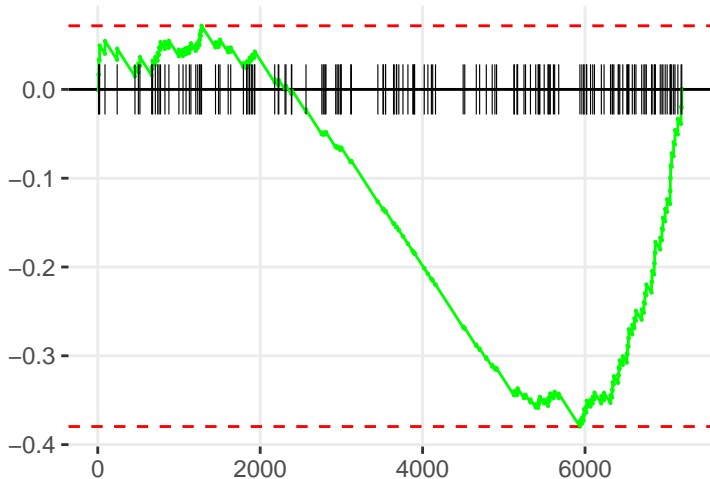




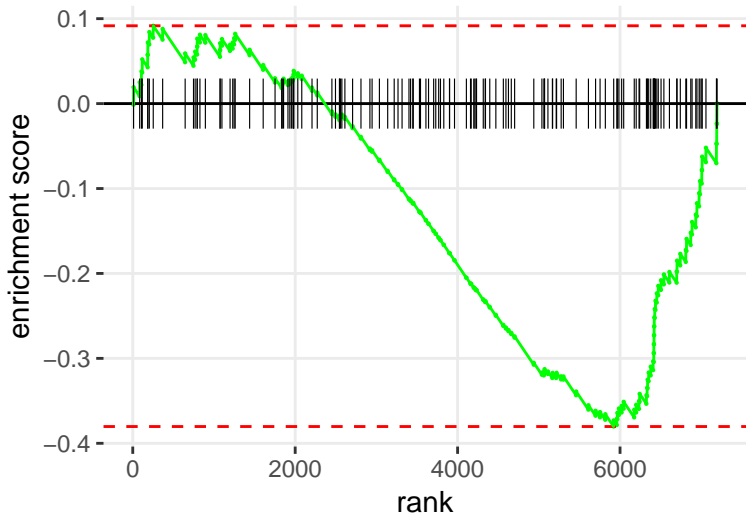
# PYRUVATE DECARBOXYLATION TO ACETYL COA

enrichment score

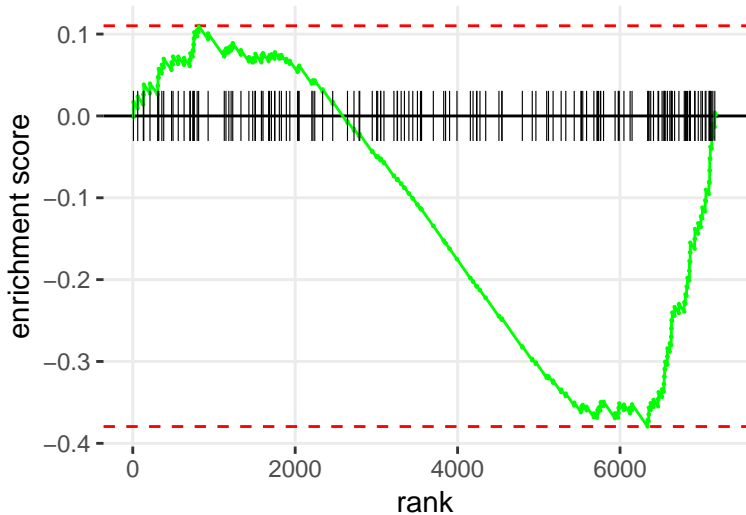
rank



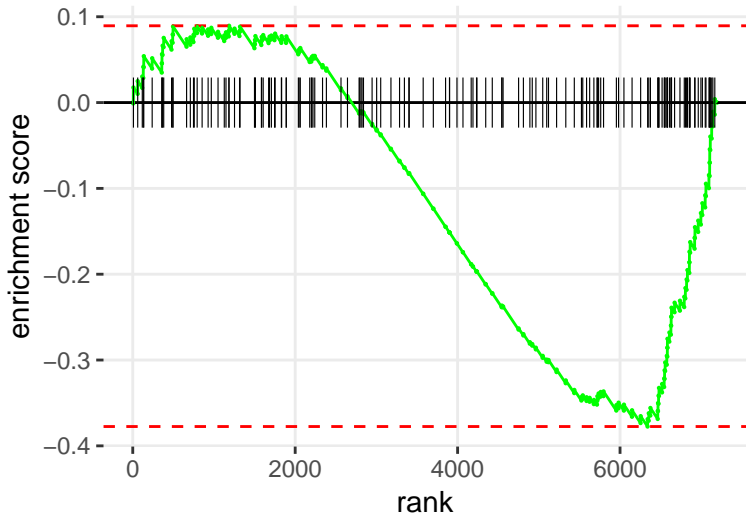
URATE BIOSYNTHESIS/INOSINE 5'-PHOSPHATE DEGRADATION



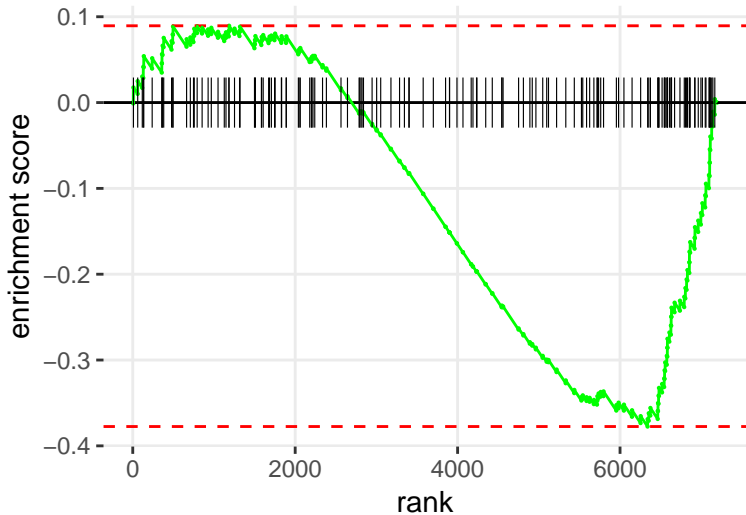
# NAD BIOSYNTHESIS FROM 2-AMINO-3-CARBOXYMUCONATE SEMIALDEHYDE



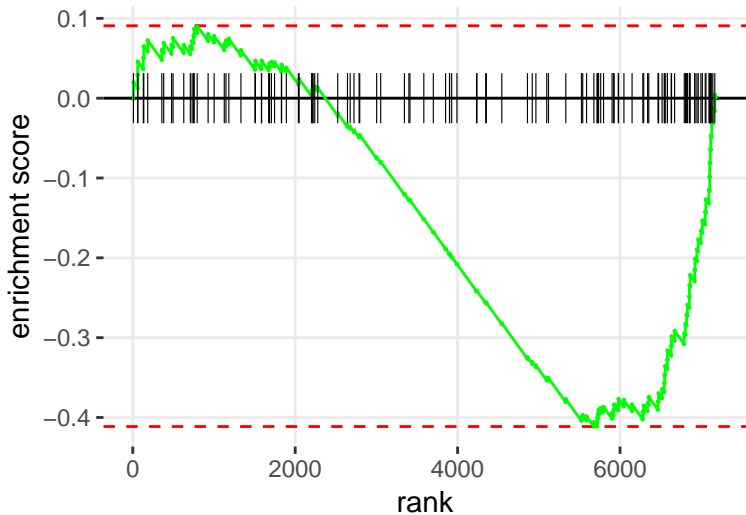
# GLUTAMATE BIOSYNTHESIS II



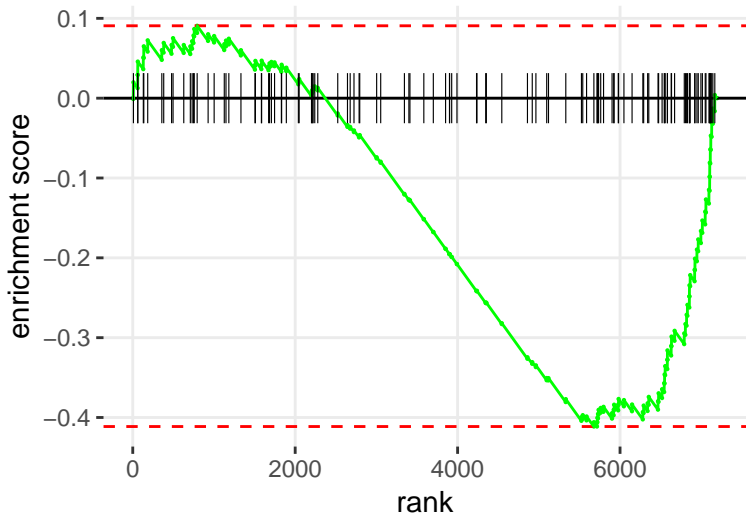
# GLUTAMATE DEGRADATION X



# TAURINE BIOSYNTHESIS



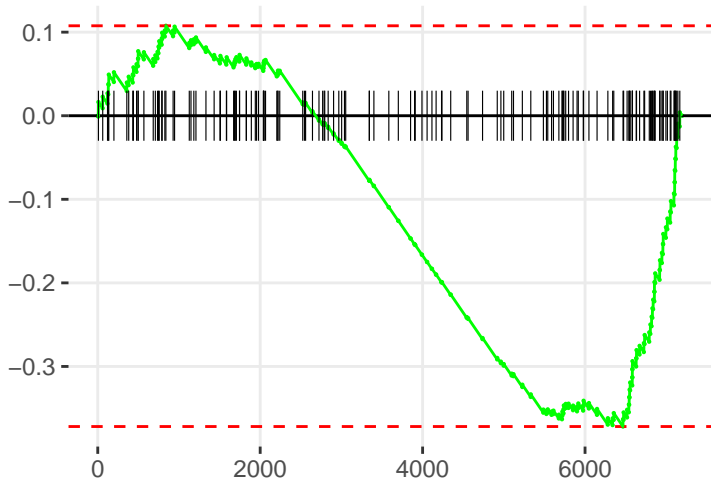
# L-CYSTEINE DEGRADATION I



# METHYLGLYOXAL DEGRADATION VI

enrichment score

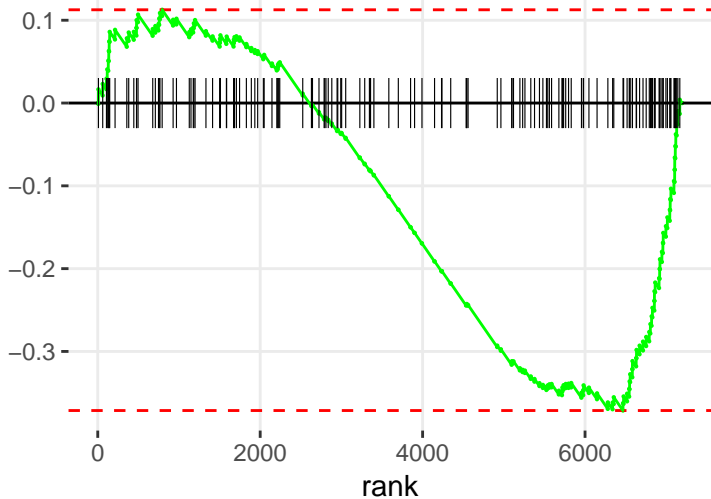
rank





# URIDINE-5'-PHOSPHATE BIOSYNTHESIS

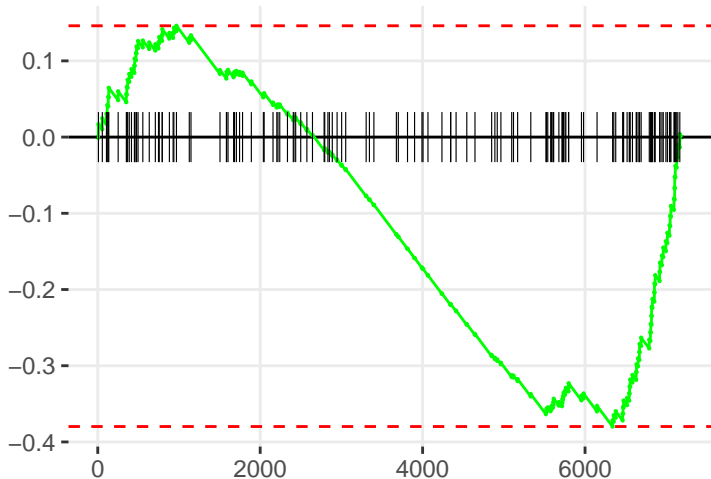
enrichment score



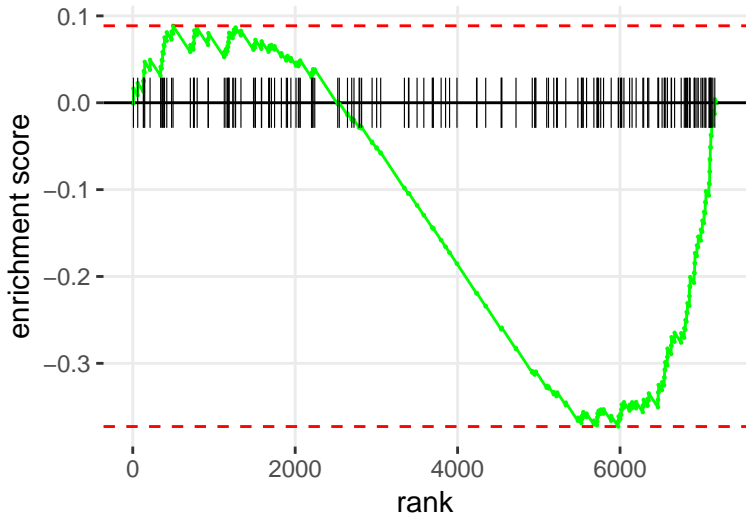
# SPHINGOMYELIN METABOLISM

enrichment score

rank



# GLUTAMINE DEGRADATION I



# SEROTONIN DEGRADATION

enrichment score

rank

0.0

-0.1

-0.2

-0.3

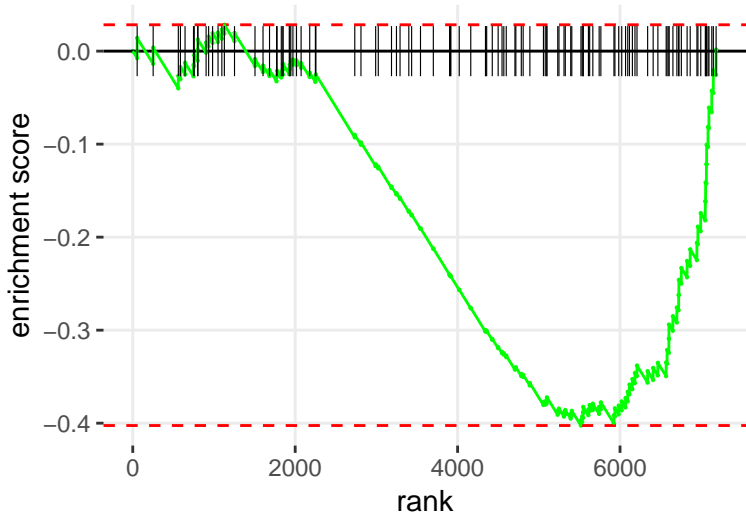
-0.4

0

2000

4000

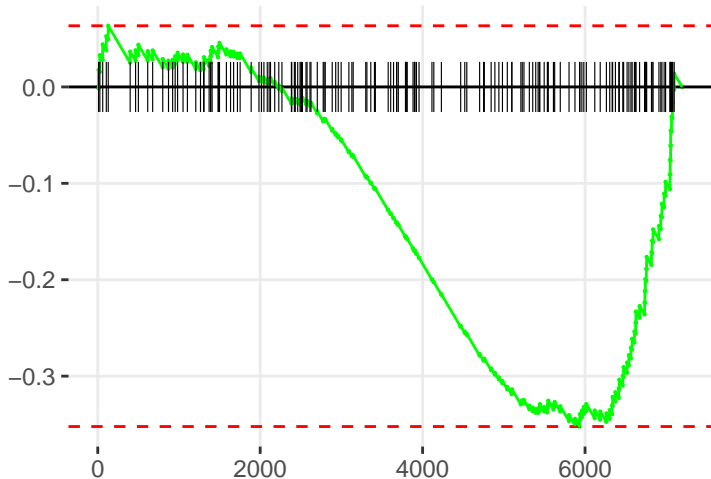
6000



# SUCROSE DEGRADATION V (MAMMALIAN)

enrichment score

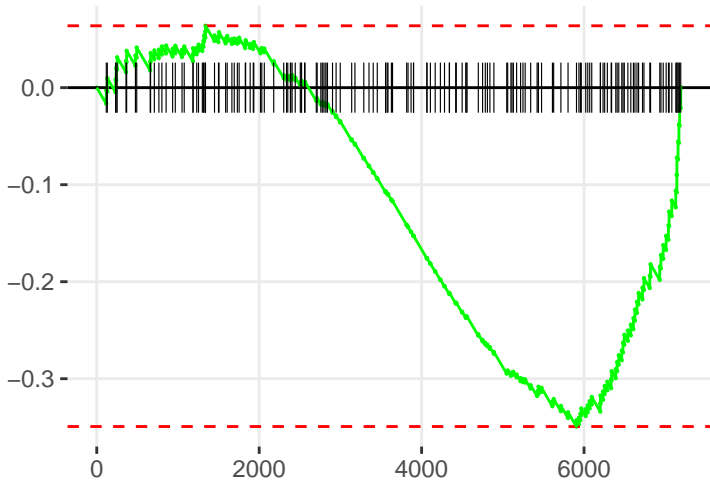
rank



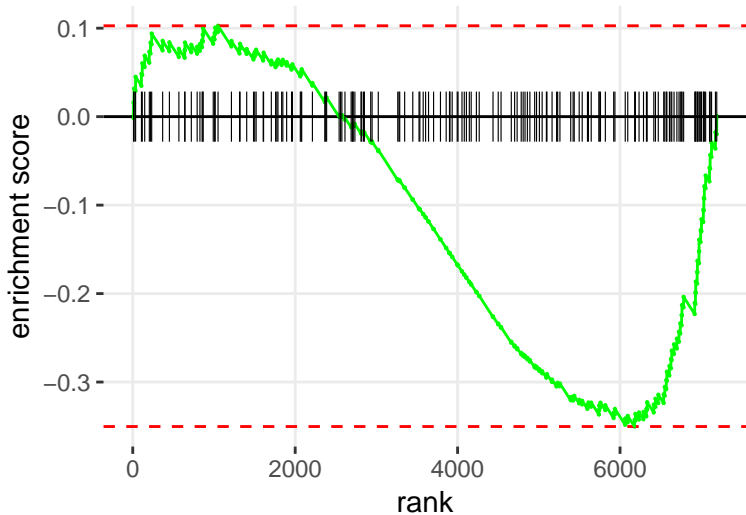
# ARGININE BIOSYNTHESIS IV

enrichment score

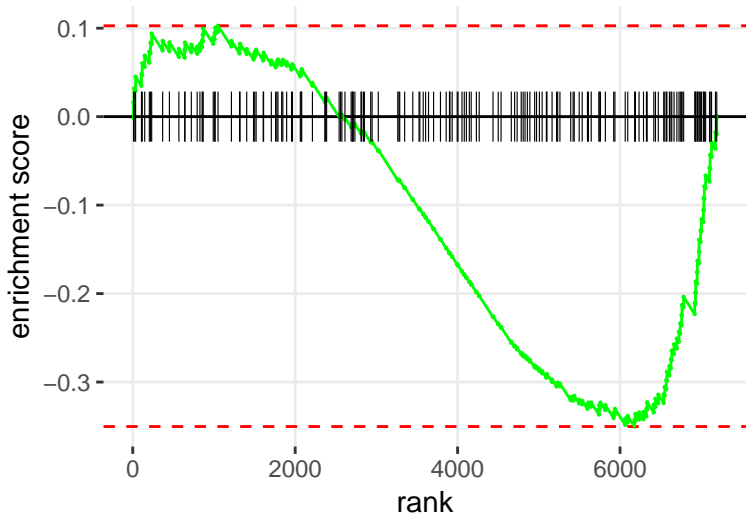
rank



# GLUTATHIONE-MEDIATED DETOXIFICATION I

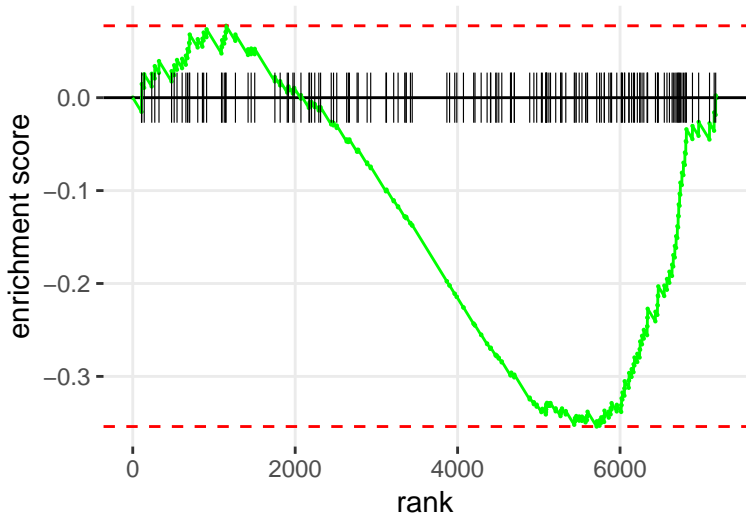


# 4-HYDROXY-2-NONENAL DETOXIFICATION





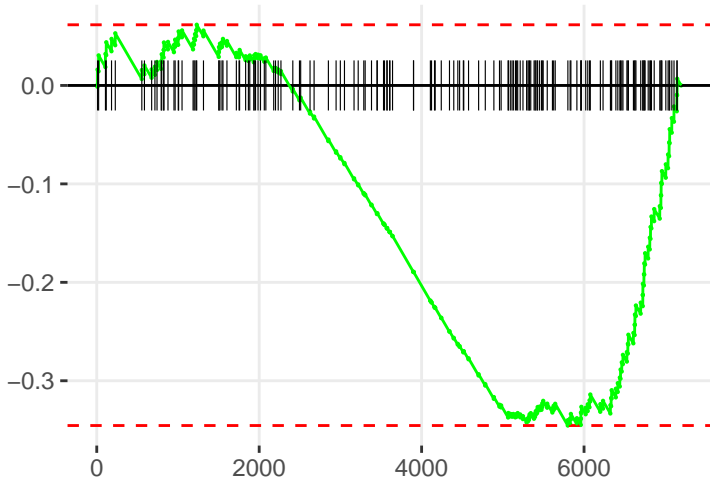
# HISTAMINE BIOSYNTHESIS



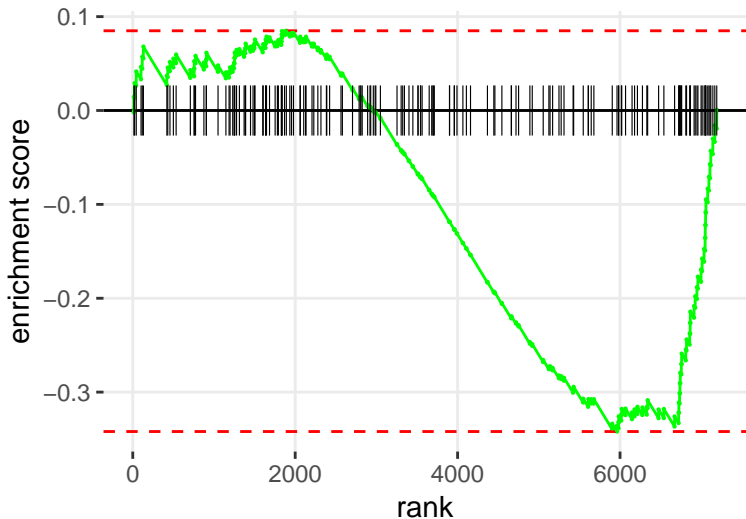
# MEVALONATE PATHWAY I

enrichment score

rank



# 2-OXOGLUTARATE DECARBOXYLATION TO SUCCINYL-COA



# 4-AMINOBTYRATE DEGRADATION I

enrichment score

0.3

0.2

0.1

0.0

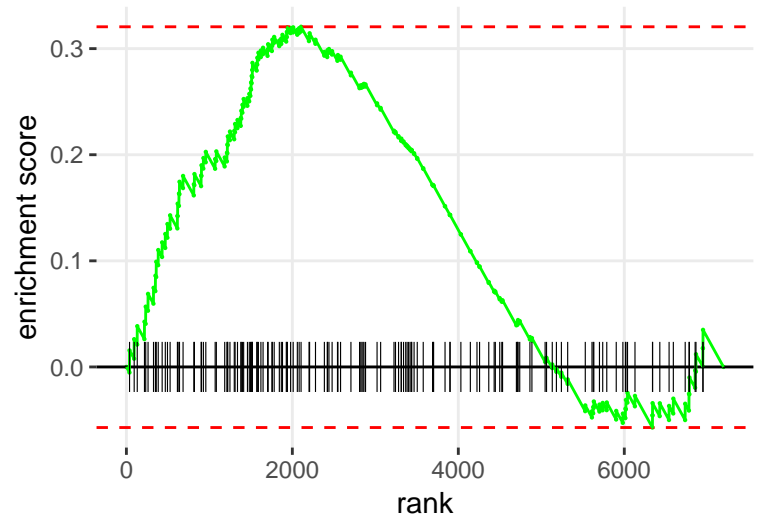
0

2000

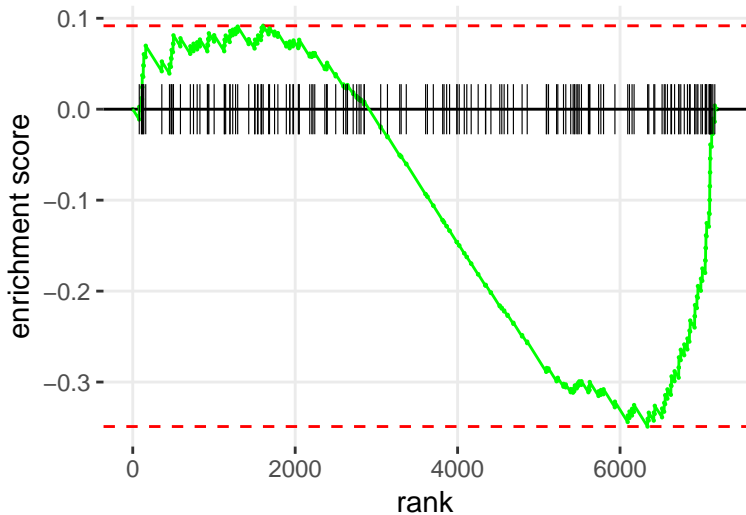
4000

6000

rank



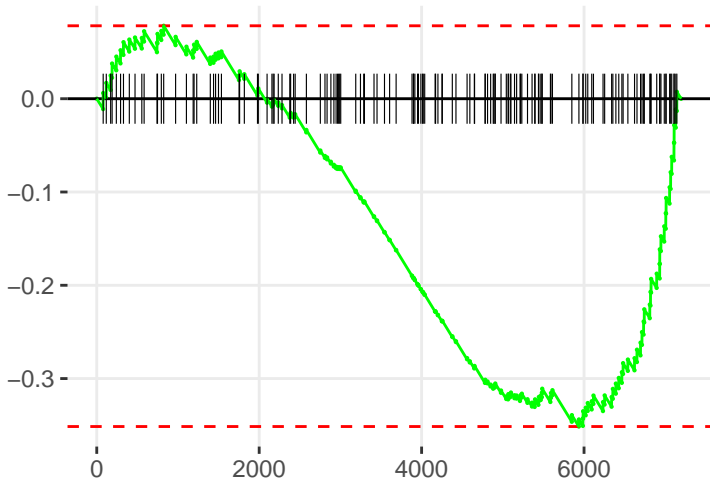
# ZYMOSTEROL BIOSYNTHESIS



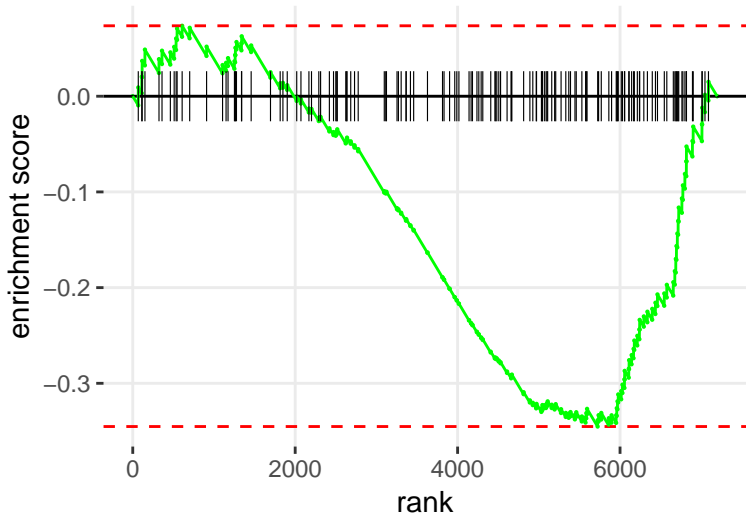
# DOLICHYL-DIPHOSPHOOLIGOSACCHARIDE BIOSYNTHESIS

enrichment score

rank



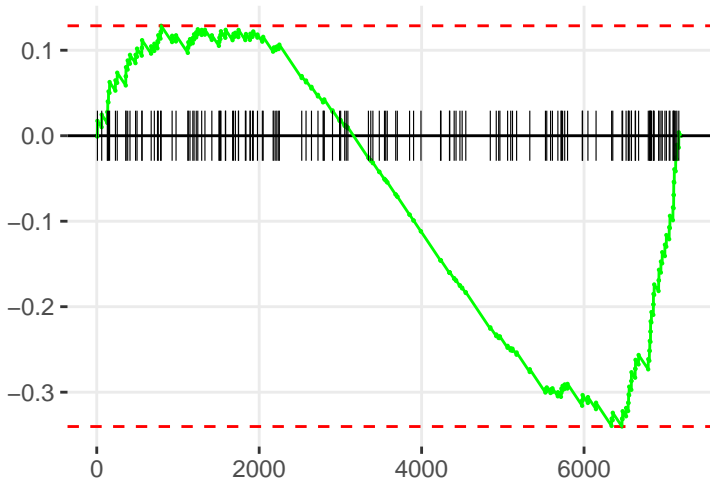
### 3-PHOSPHOINOSITIDE DEGRADATION



# UBIQUINOL-10 BIOSYNTHESIS (EUKARYOTIC)

enrichment score

rank

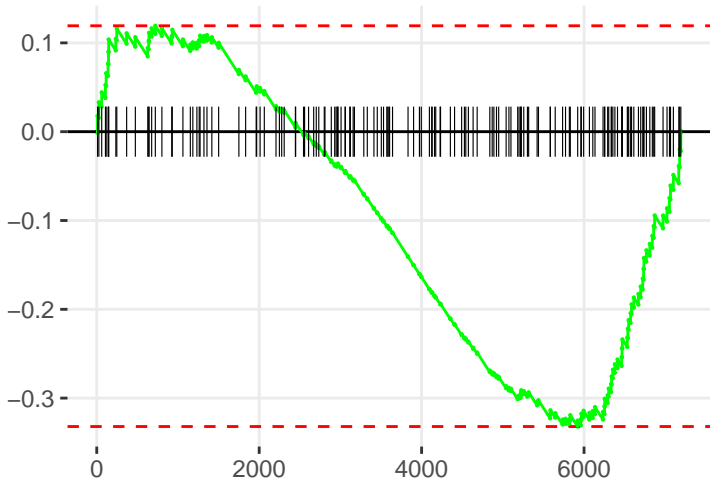




# PROSTANOID BIOSYNTHESIS

enrichment score

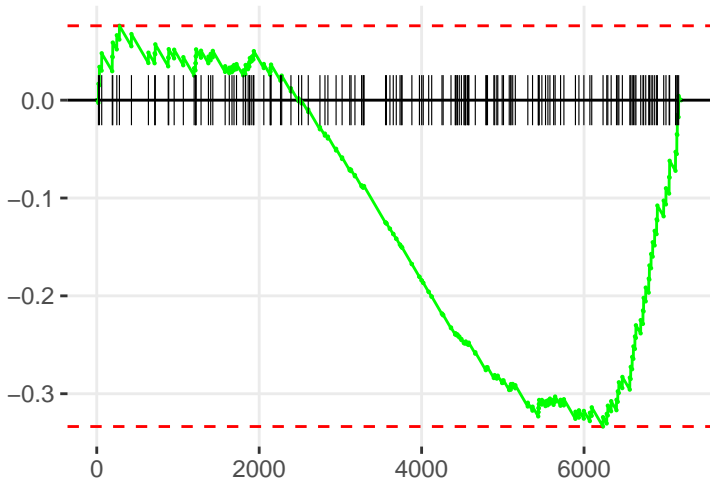
rank



# DERMATAN SULFATE DEGRADATION (METAZOA)

enrichment score

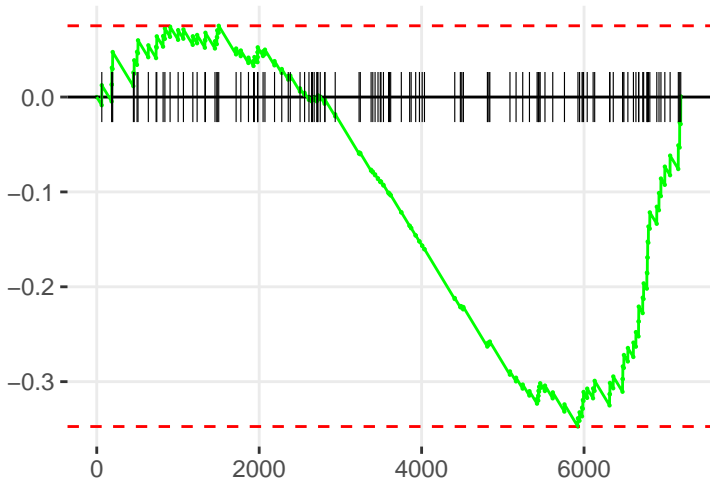
rank



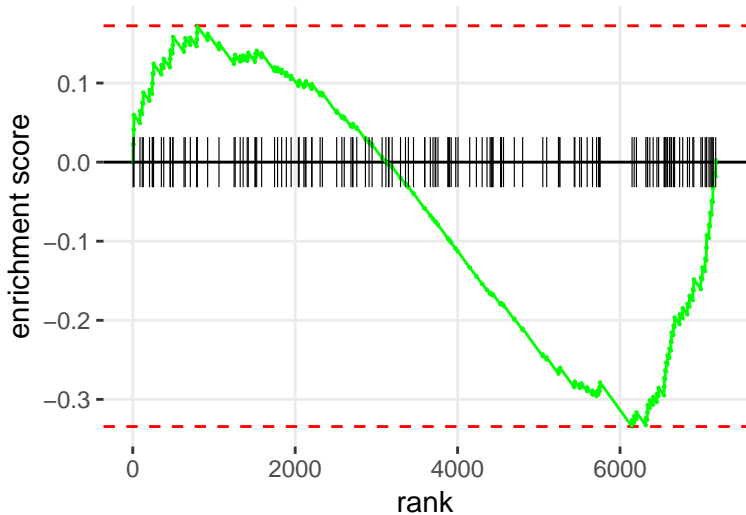
# NICOTINE DEGRADATION IV

enrichment score

rank



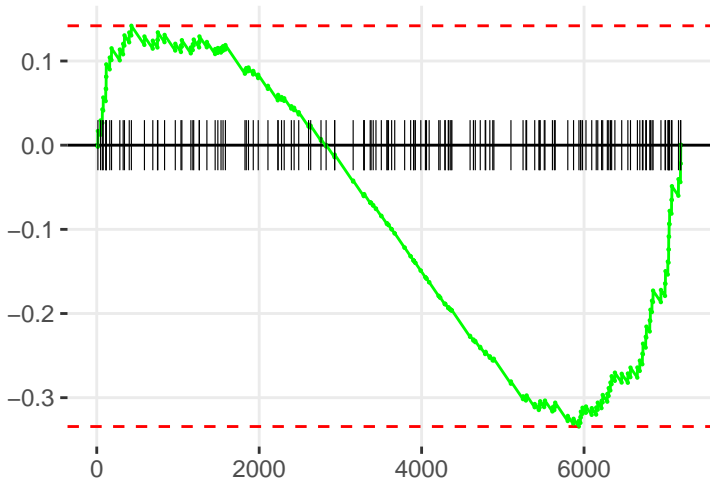
# SALVAGE PATHWAYS OF PYRIMIDINE DEOXYRIBONUCLEOTIDES



# PHENYLETHYLAMINE DEGRADATION I

enrichment score

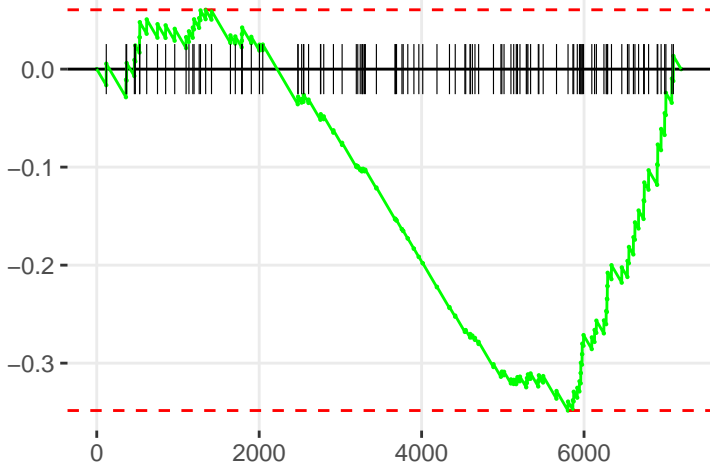
rank



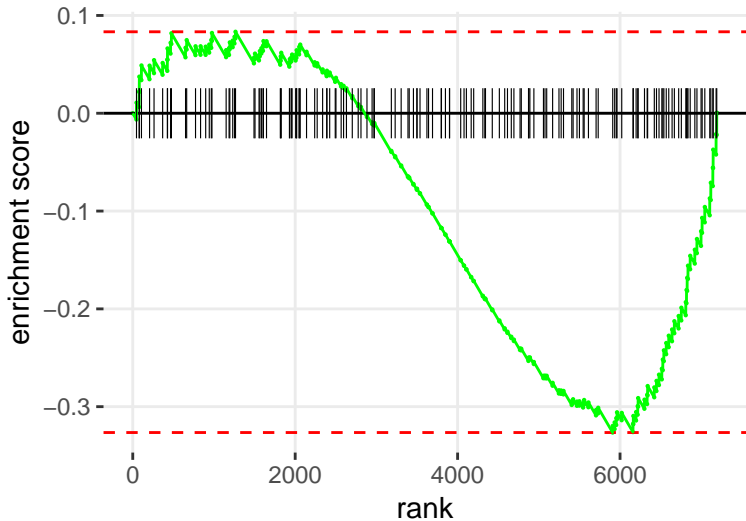
D-<IMYO</I-INOSITOL (1,3,4)-TRISPHOSPHATE BIOSYNTHESIS

enrichment score

rank

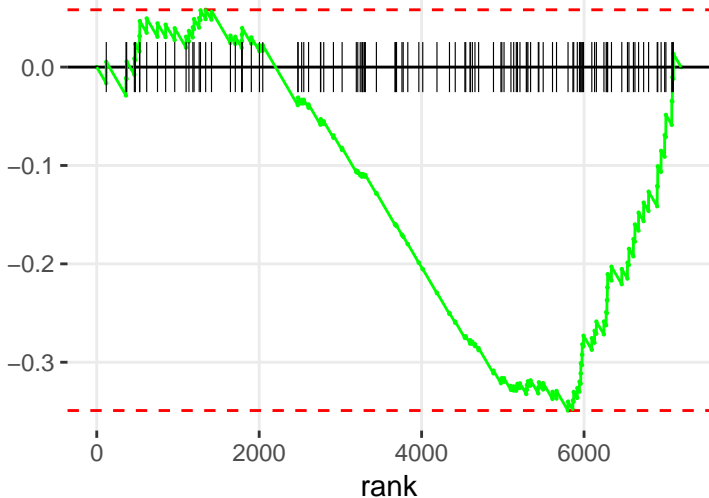


# FOLATE TRANSFORMATIONS I



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

enrichment score

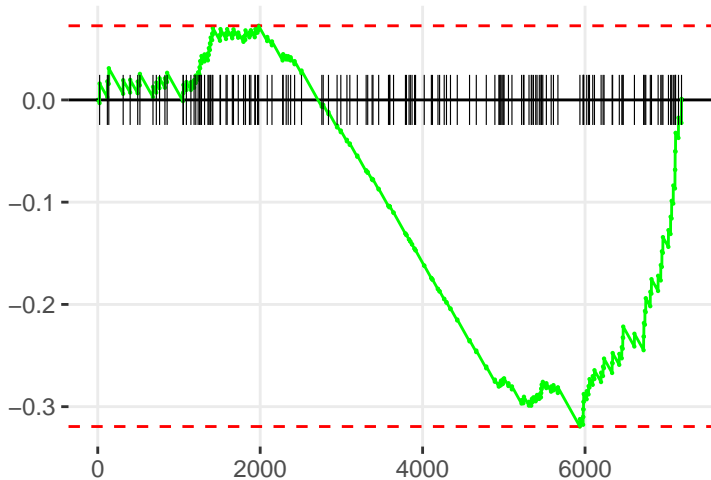




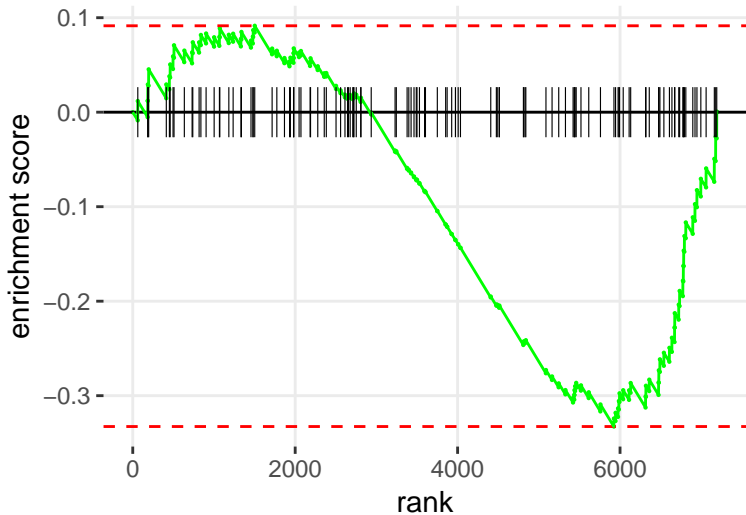
FATTY ACID & BETA;-OXIDATION I

enrichment score

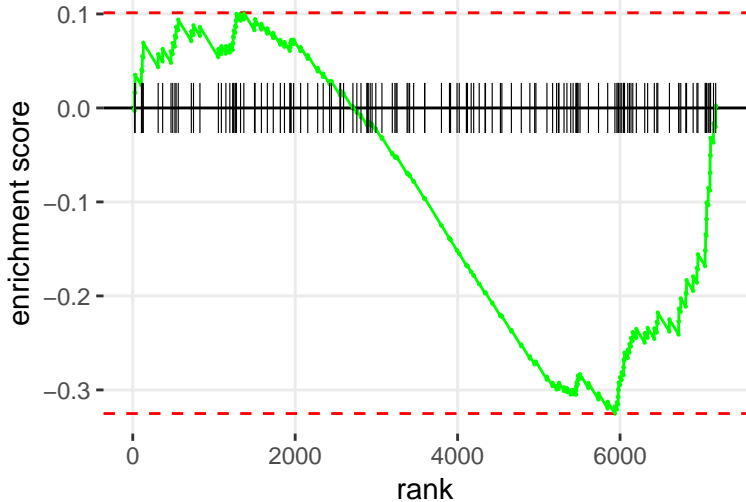
rank



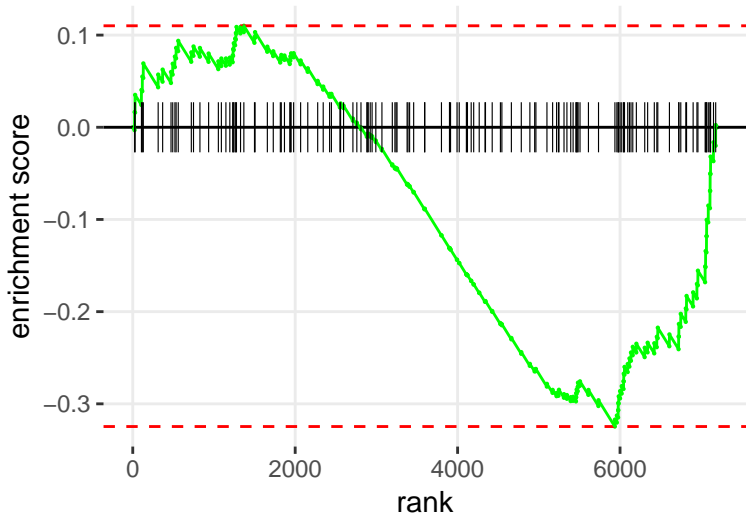
# NICOTINE DEGRADATION III



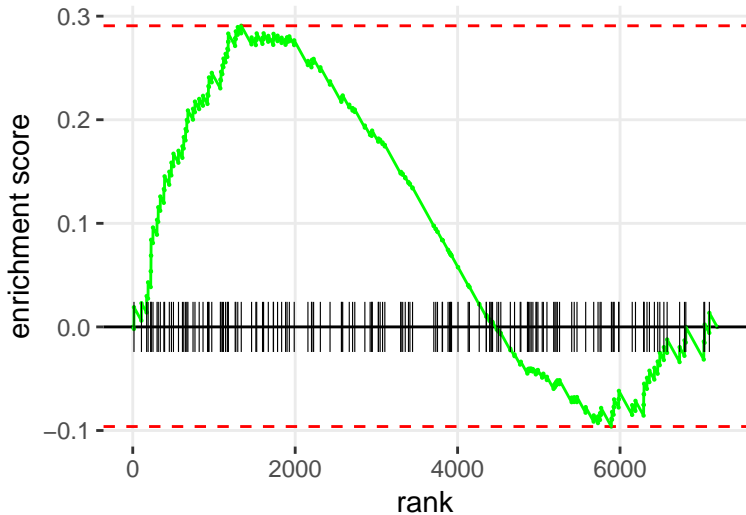
# EICOSAPENTAENOATE BIOSYNTHESIS II (METAZOA)



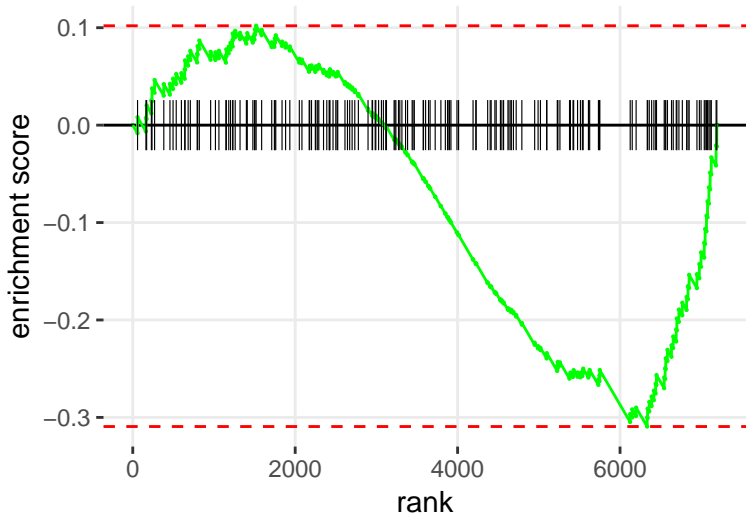
# STEARATE BIOSYNTHESIS I (ANIMALS)



# SPERMINE AND SPERMIDINE DEGRADATION I



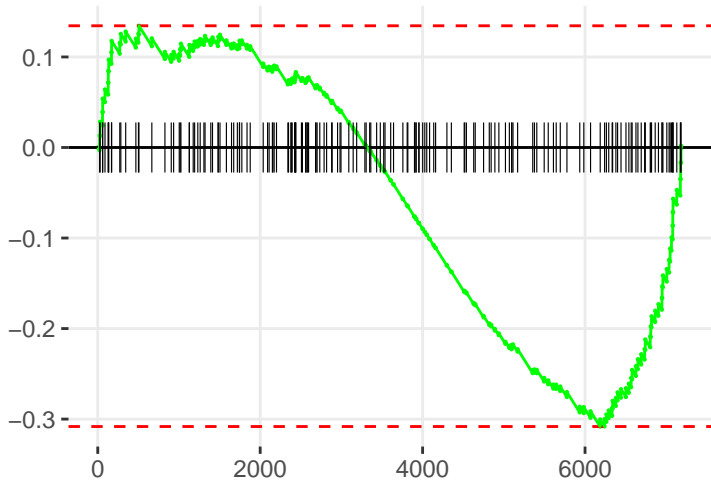
# MOLYBDENUM COFACTOR BIOSYNTHESIS



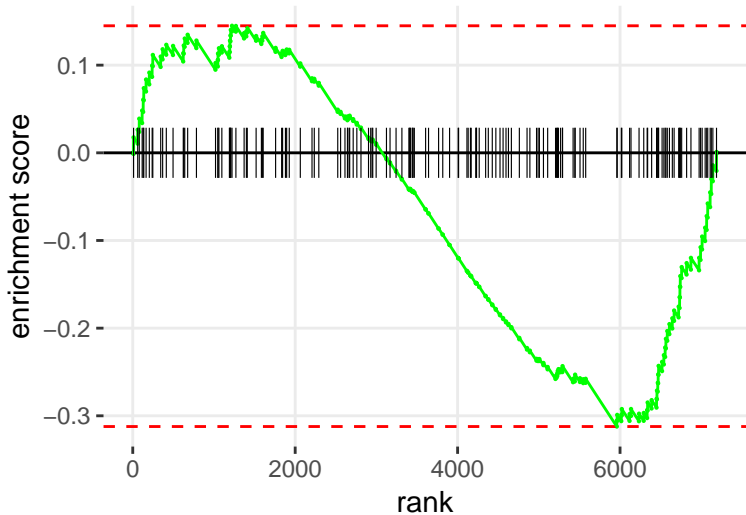
# THIOSULFATE DISPROPORTIONATION III (RHODANESE)

enrichment score

rank



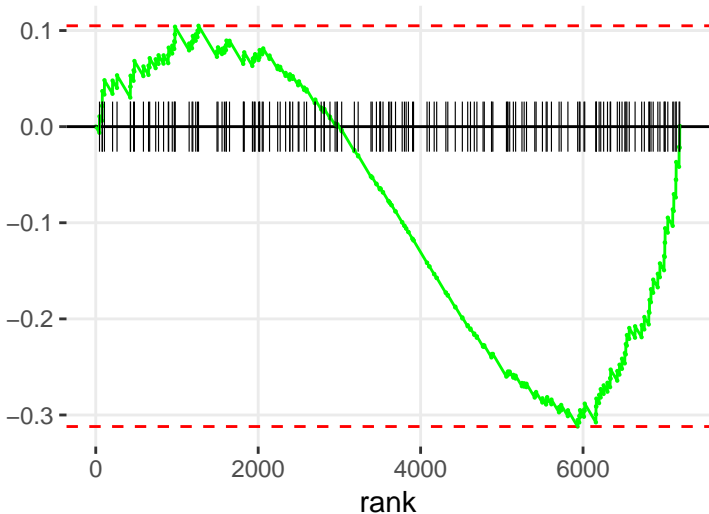
# PYRUVATE FERMENTATION TO LACTATE





# FOLATE POLYGLUTAMYLATION

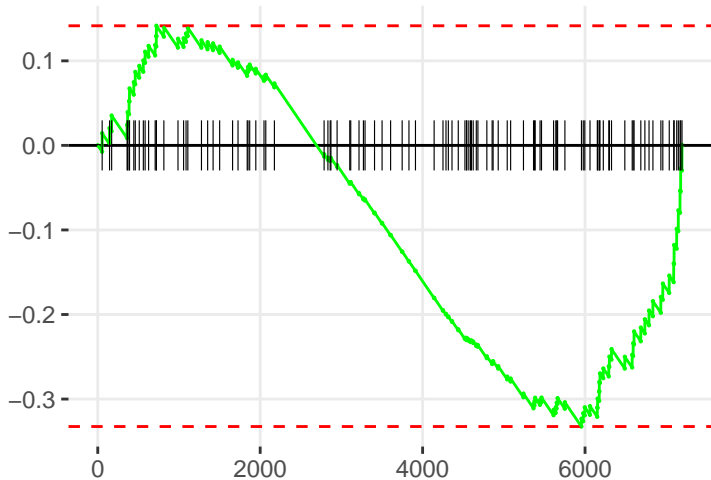
enrichment score



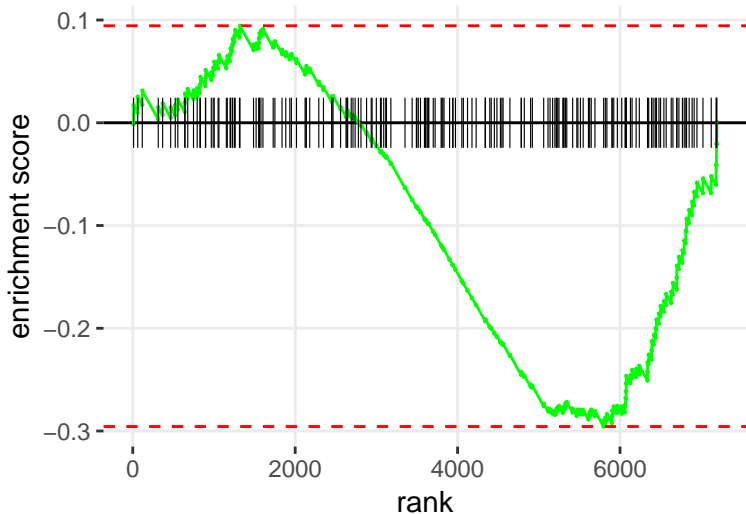
# HEPARAN SULFATE BIOSYNTHESIS (LATE STAGES)

enrichment score

rank



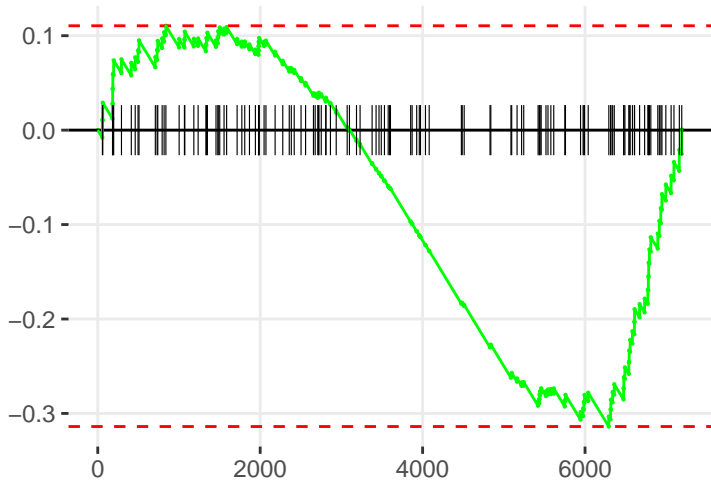
# SELENOCYSTEINE BIOSYNTHESIS II (ARCHAEA AND EUKARYOTES)



# ACETONE DEGRADATION I (TO METHYLGLYOXAL)

enrichment score

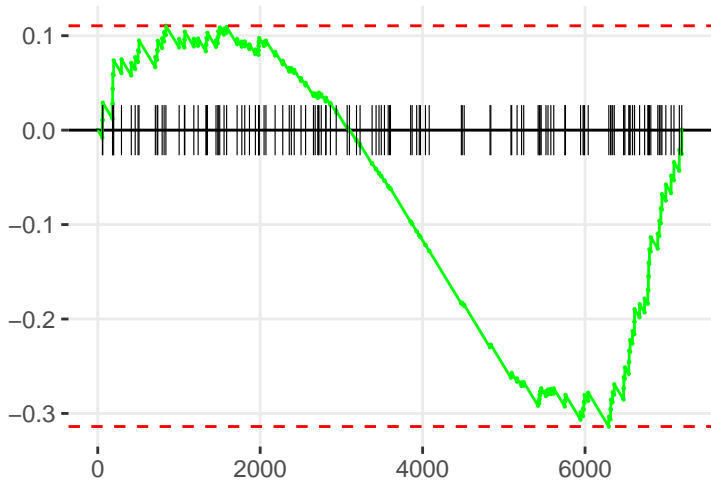
rank



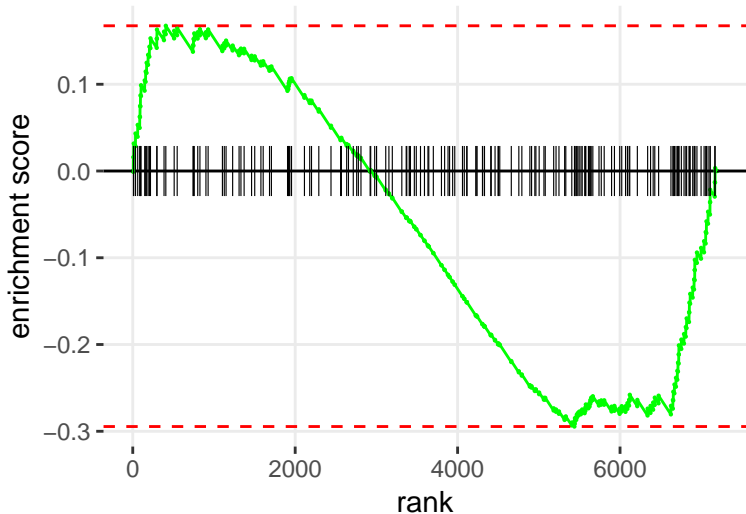
# BUPROPION DEGRADATION

enrichment score

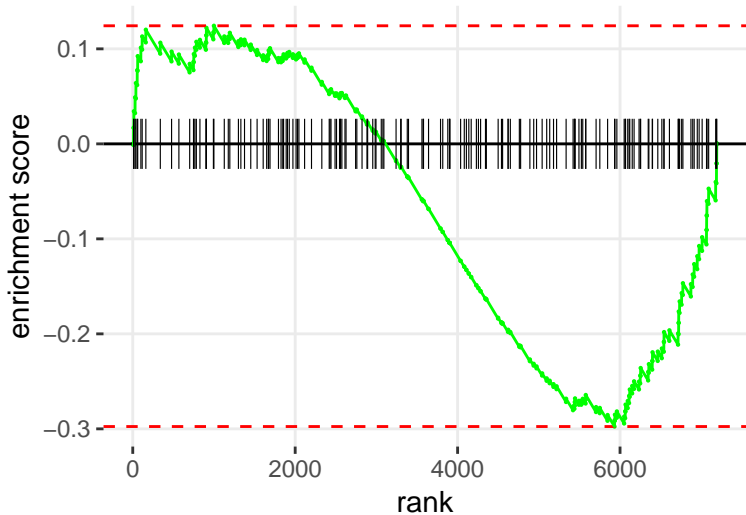
rank



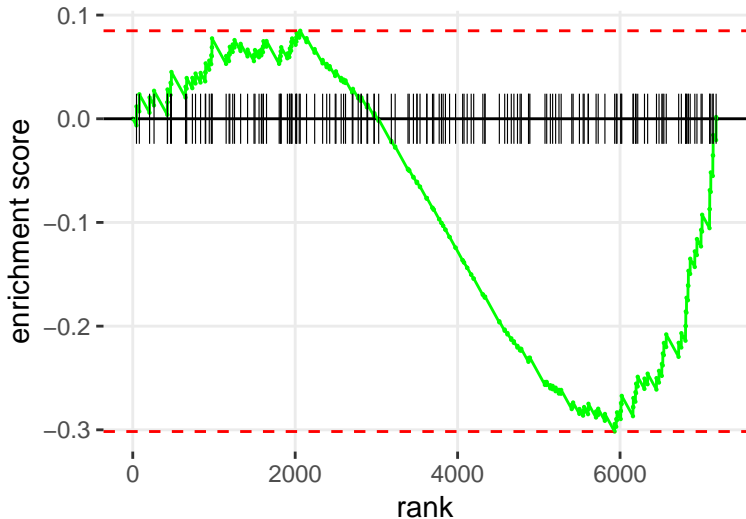
# GLUTAMATE DEGRADATION III (VIA 4-AMINOBUTYRATE)



PALMITATE BIOSYNTHESIS I (ANIMALS)

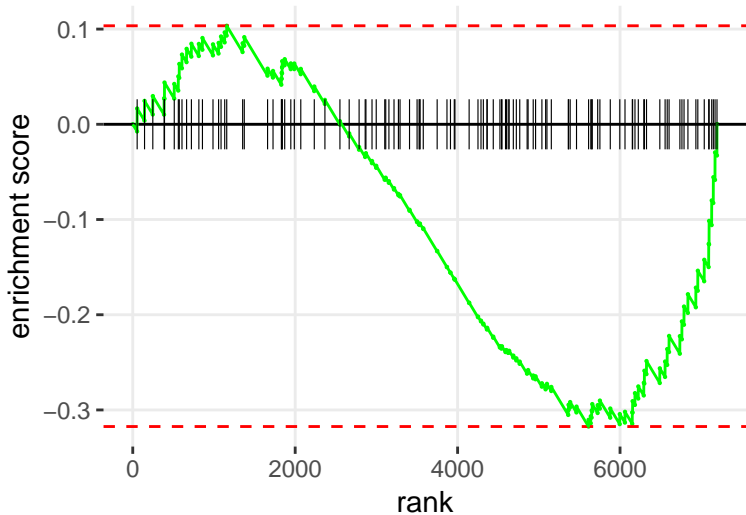


# GLYCINE BIOSYNTHESIS I

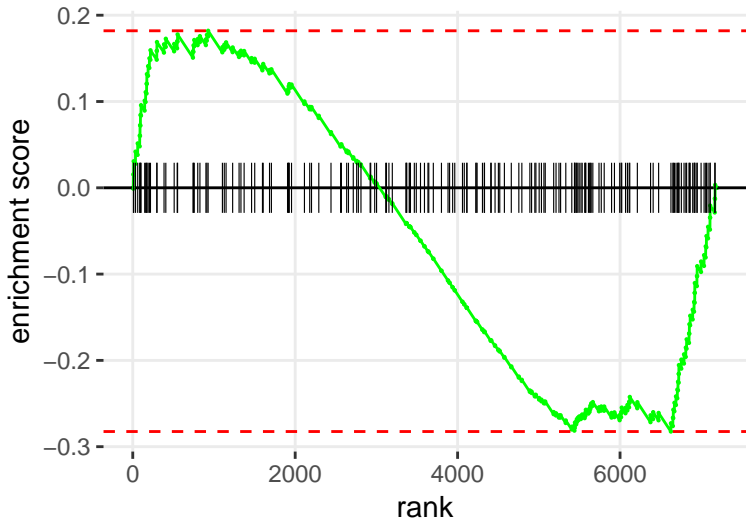




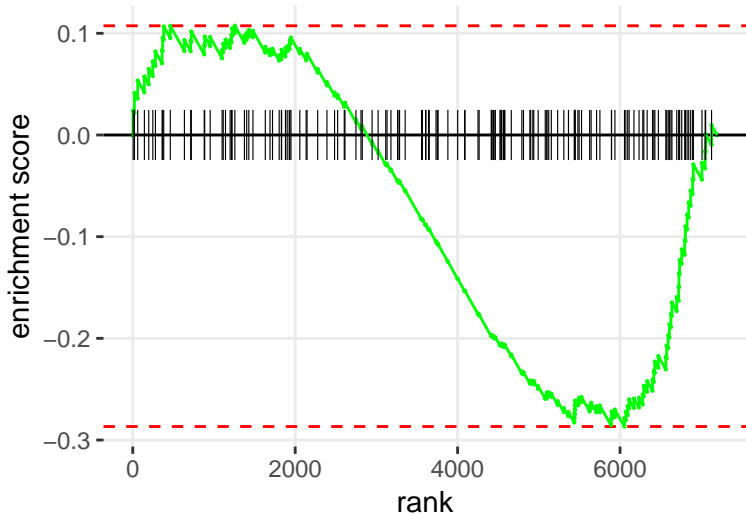
# GLYCOAMINOGLYCAN-PROTEIN LINKAGE REGION BIOSYNTHESIS



# GLUTAMATE DEPENDENT ACID RESISTANCE



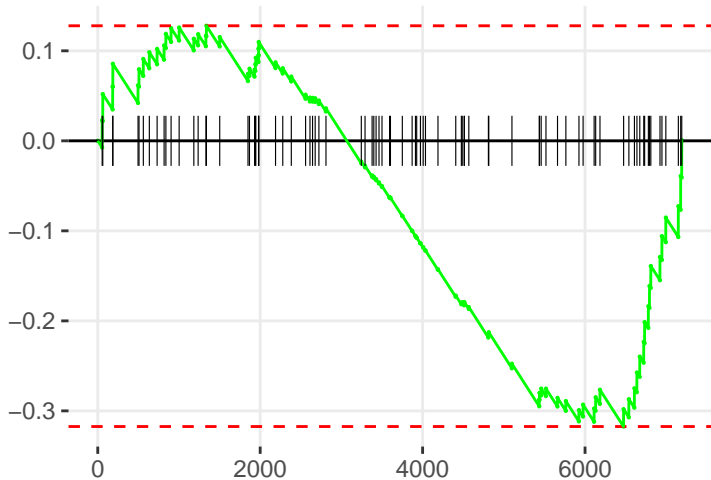
# CHONDROITIN SULFATE DEGRADATION (METAZOA)



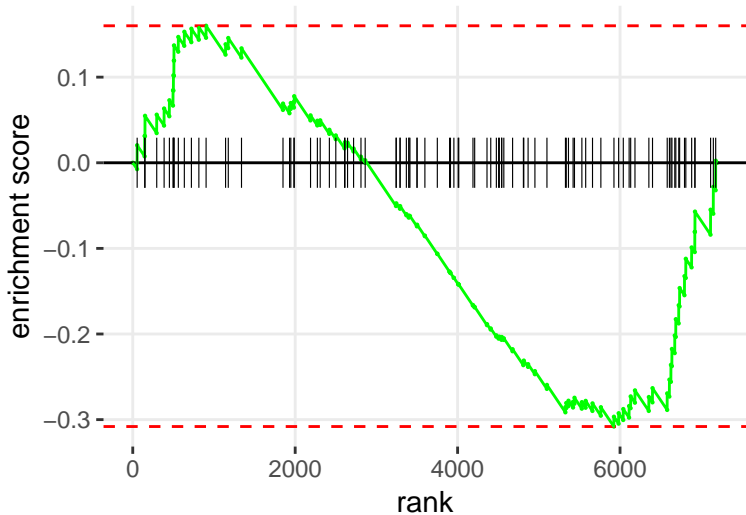
# MELATONIN DEGRADATION I

enrichment score

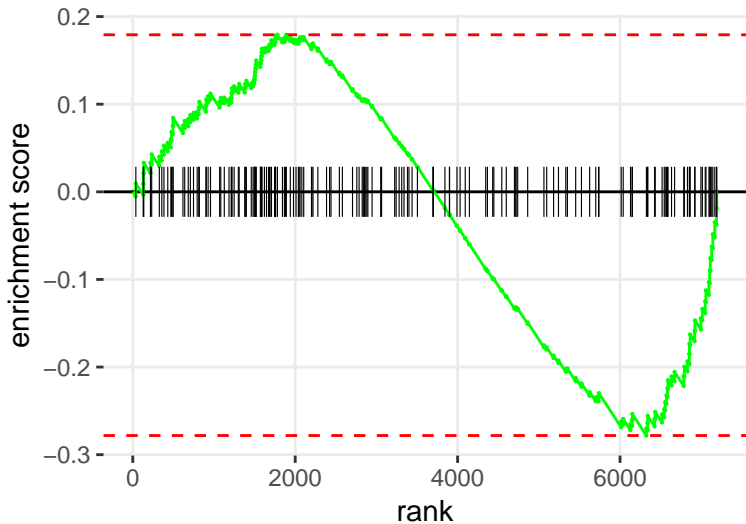
rank



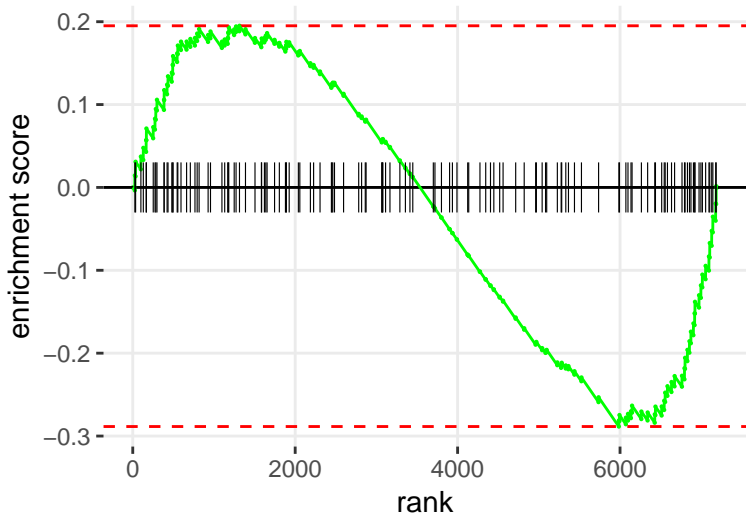
# THYROID HORMONE METABOLISM II (VIA CONJUGATION AND/OR DEGRADATION)



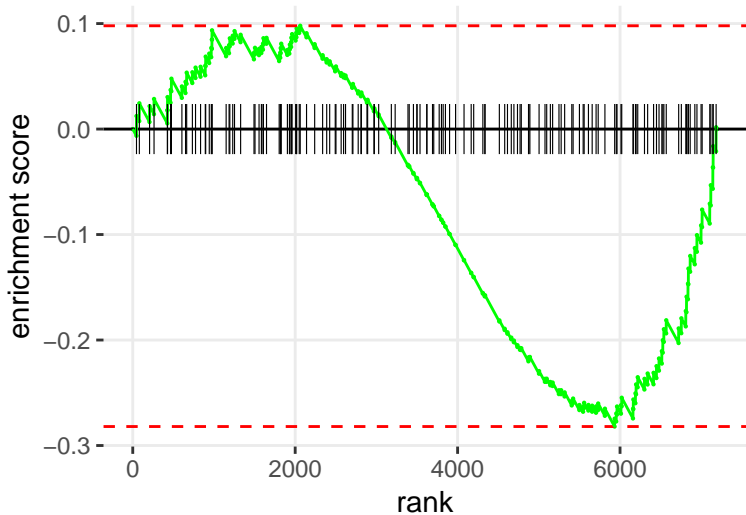
# CARDIOLIPIN BIOSYNTHESIS II



# PHENYLALANINE DEGRADATION I (AEROBIC)



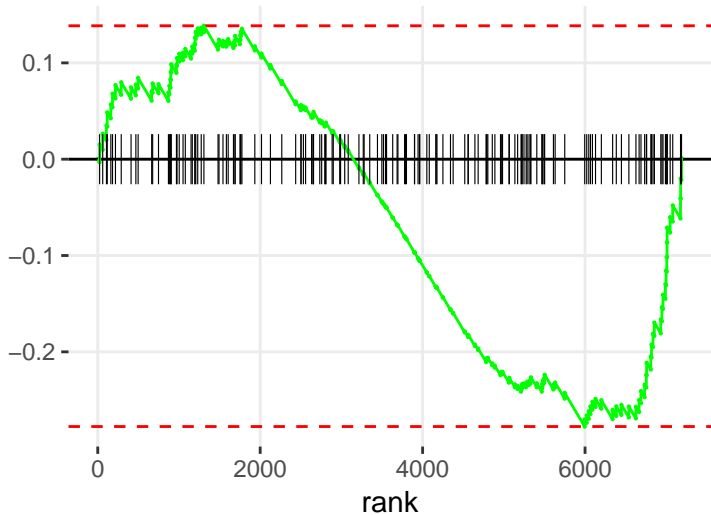
# GLYCINE BETAIN DEGRADATION





# UDP-<I>/l</I>-ACETYL-D-GALACTOSAMINE BIOSYNTHESIS II

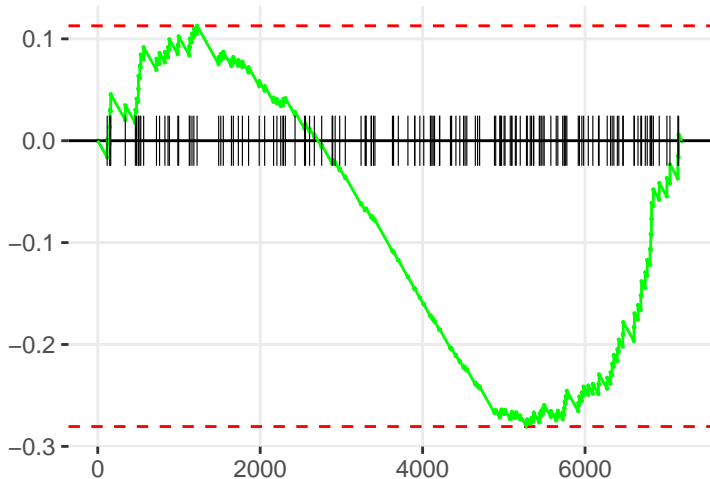
enrichment score



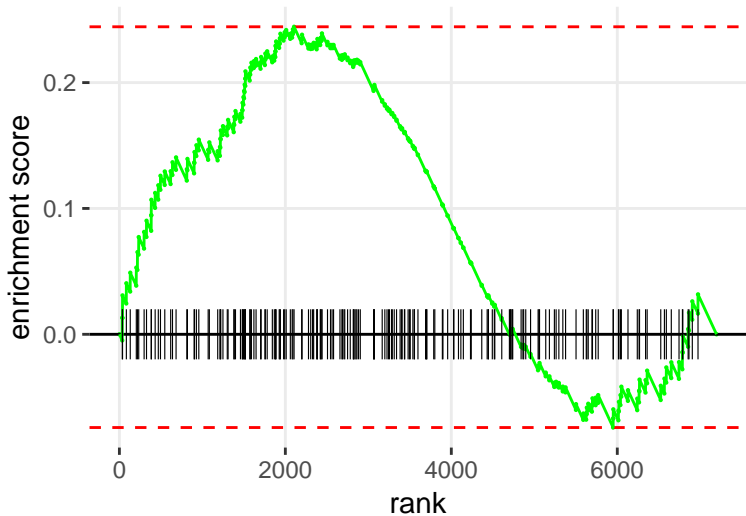
# CATECHOLAMINE BIOSYNTHESIS

enrichment score

rank



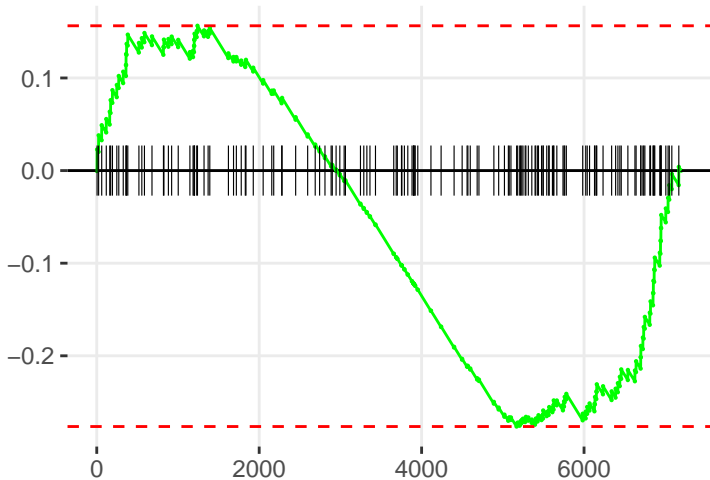
# TYROSINE BIOSYNTHESIS IV



# HEME BIOSYNTHESIS FROM UROPORPHYRINOGEN-III I

enrichment score

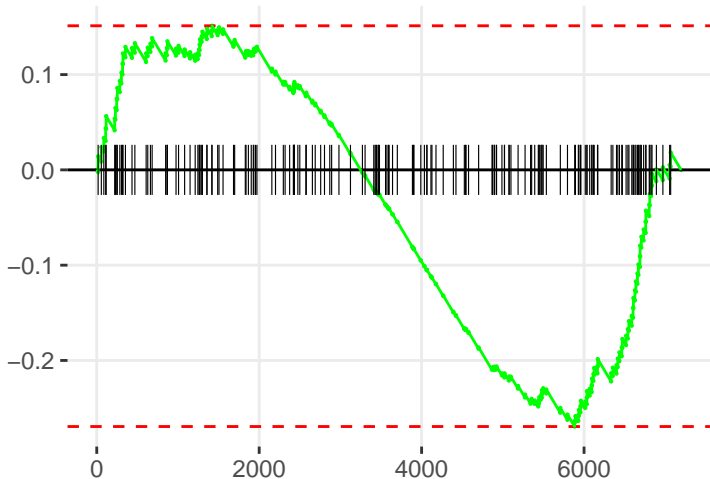
rank



# 4-HYDROXYPROLINE DEGRADATION I

enrichment score

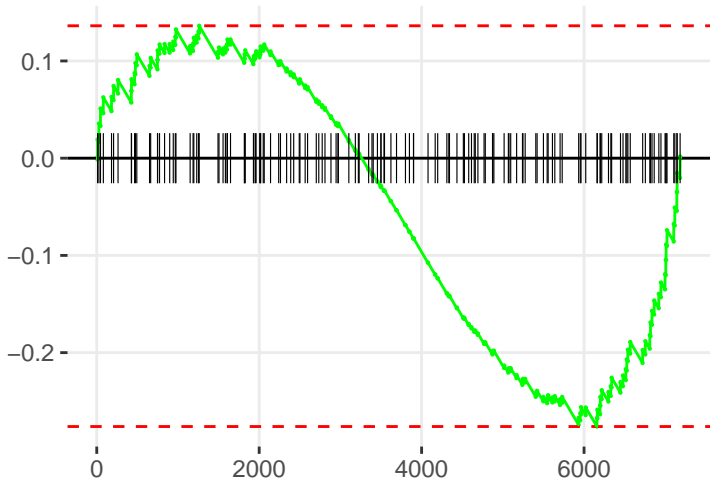
rank



DTMP <IDE NOVO</I> BIOSYNTHESIS

enrichment score

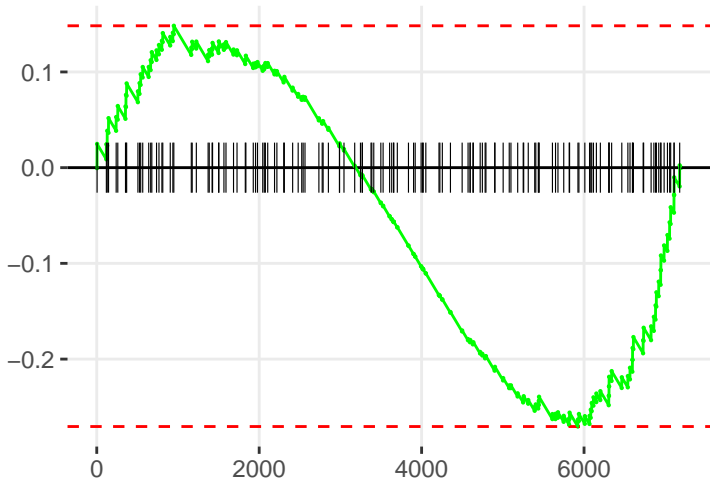
rank



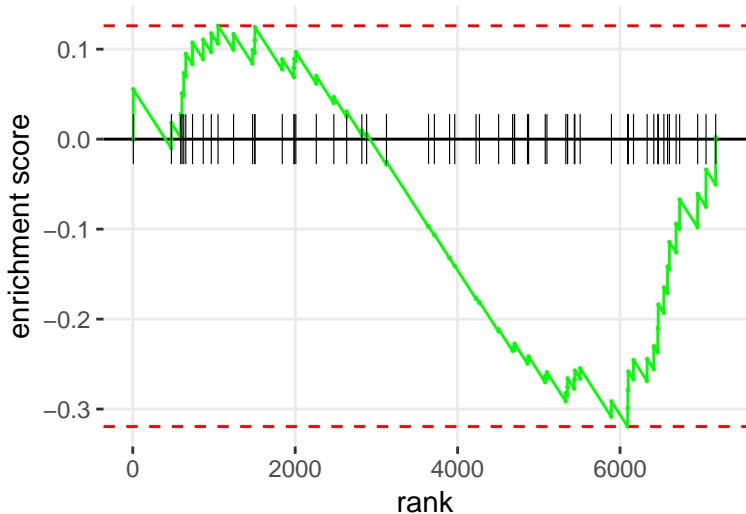
# CALCIUM TRANSPORT I

enrichment score

rank



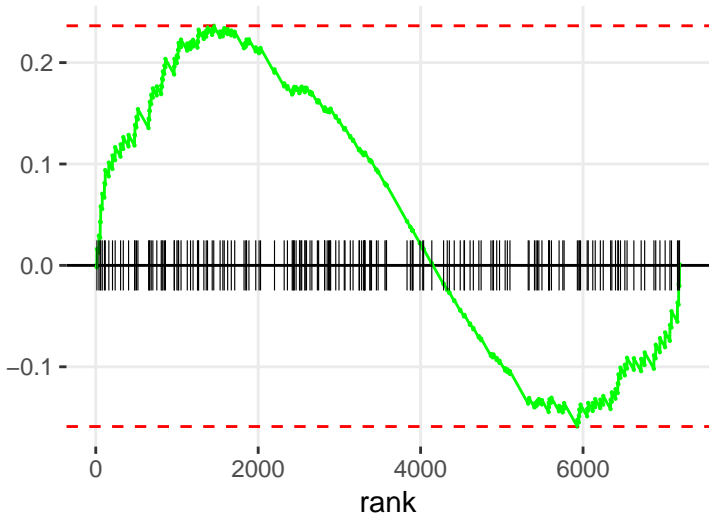
## 2-AMINO-3-CARBOXYMUCONATE SEMIALDEHYDE DEGRADATION TO GLUTARYL-CO





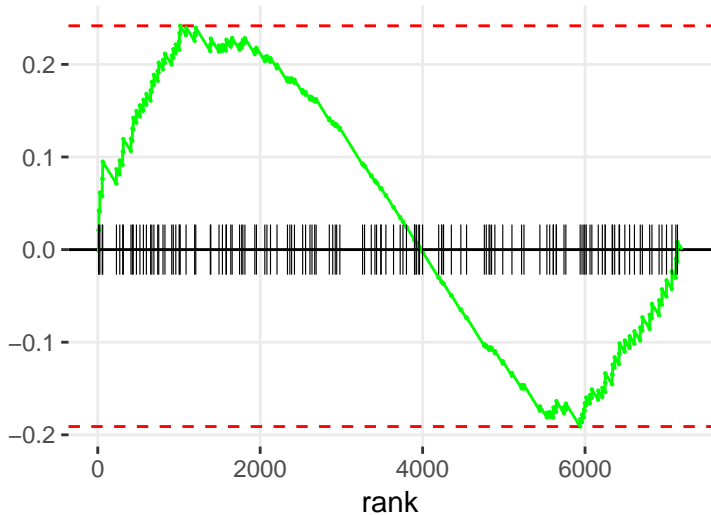
# METHYLMALONYL PATHWAY

enrichment score

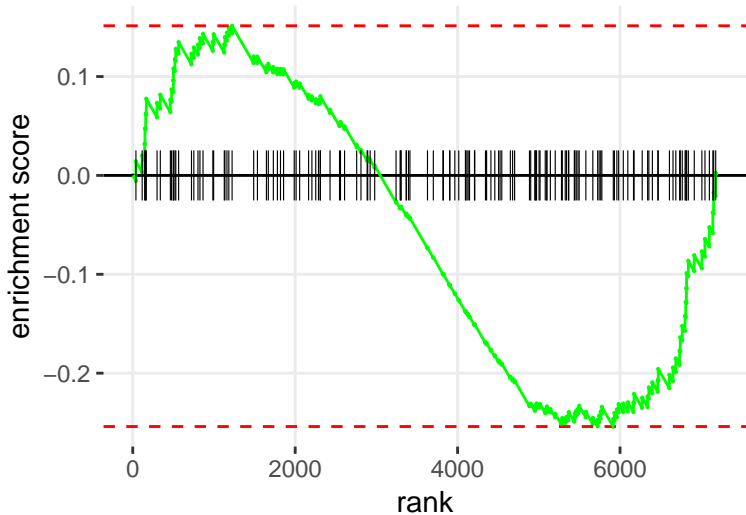


# PYRIMIDINE RIBONUCLEOTIDES INTERCONVERSION

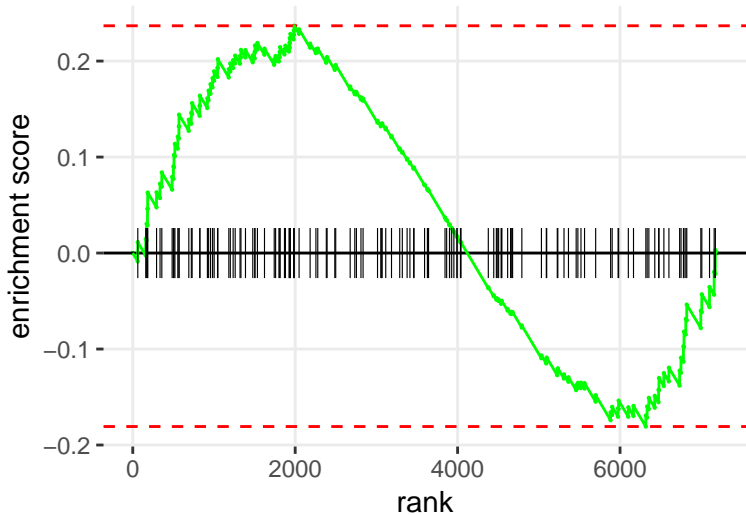
enrichment score



# SEROTONIN AND MELATONIN BIOSYNTHESIS



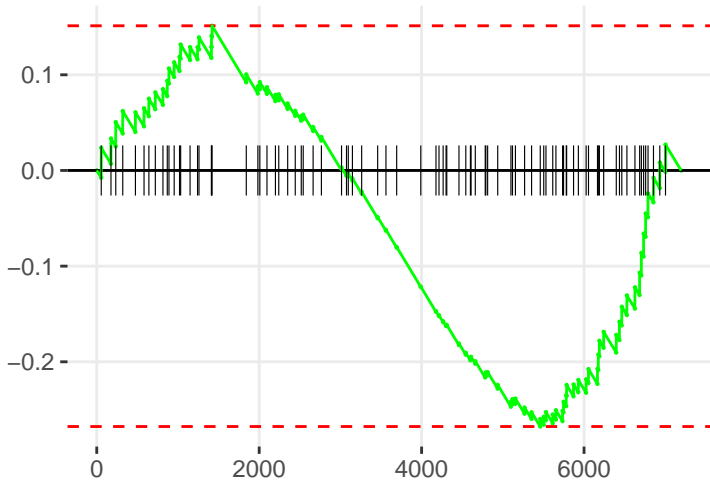
# PREGNENOLONE BIOSYNTHESIS



D-l-MYO-l-INOSITOL (1,4,5)-TRISPHOSPHATE BIOSYNTHESIS

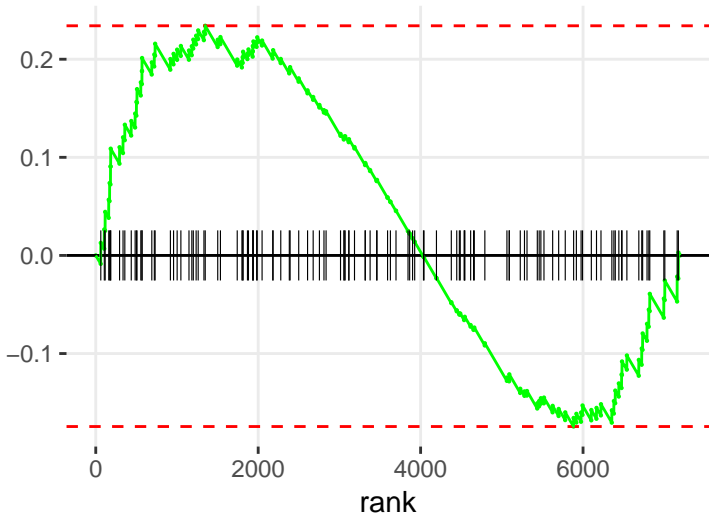
enrichment score

rank



# GLUCOCORTICOID BIOSYNTHESIS

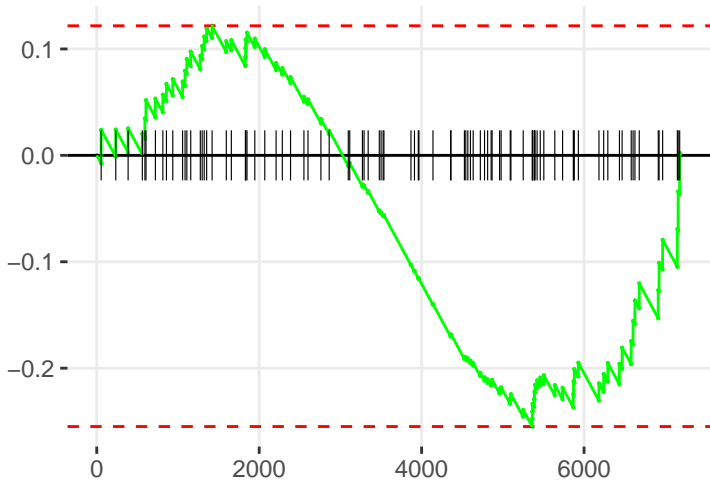
enrichment score



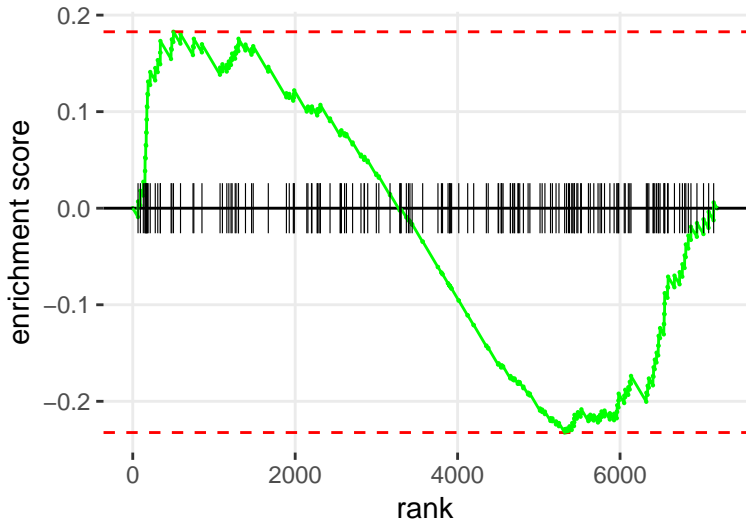
# DERMATAN SULFATE BIOSYNTHESIS (LATE STAGES)

enrichment score

rank

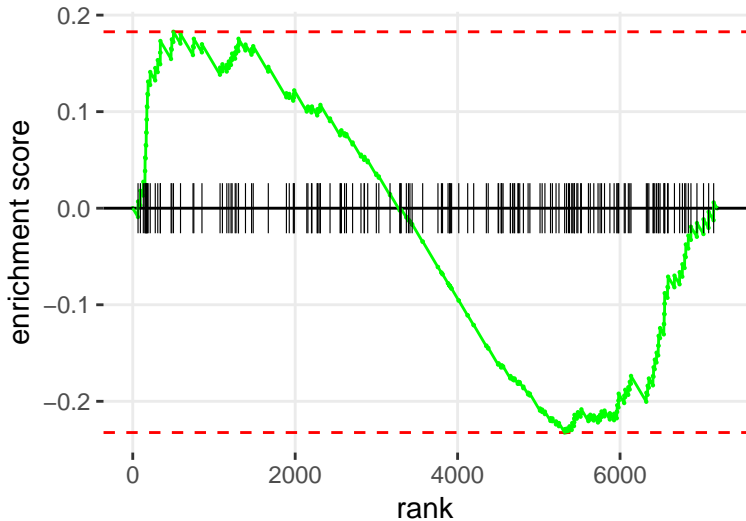


# 4-HYDROXYPHENYLPYRUVATE BIOSYNTHESIS



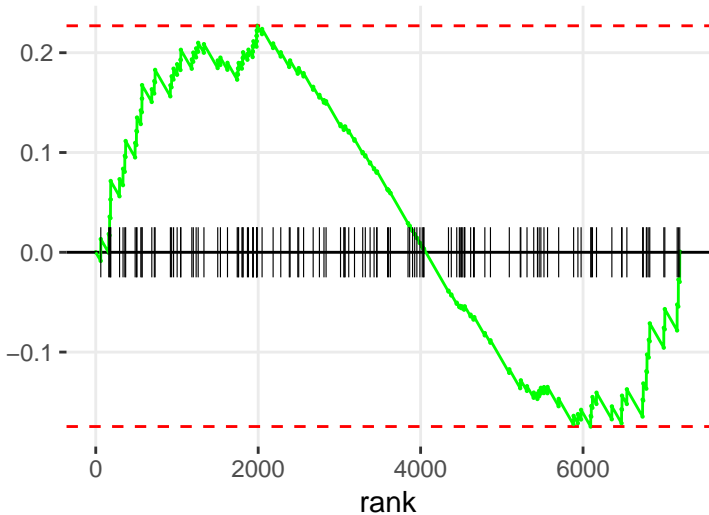


# 4-HYDROXYBENZOATE BIOSYNTHESIS



# MINERALOCORTICOID BIOSYNTHESIS

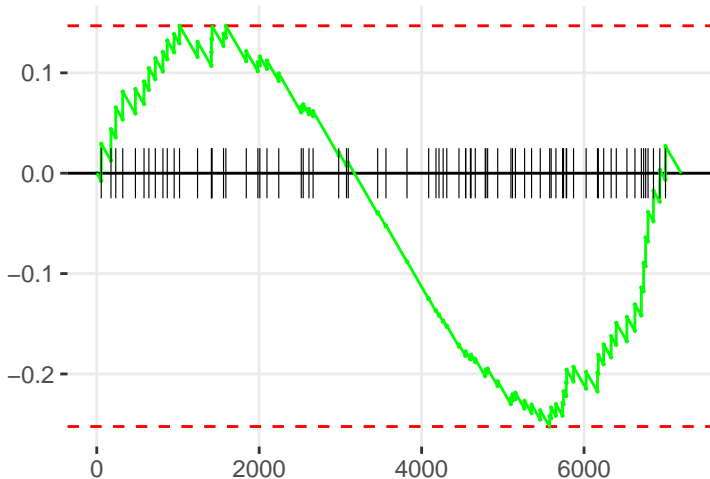
enrichment score



# PHOSPHOLIPASES

enrichment score

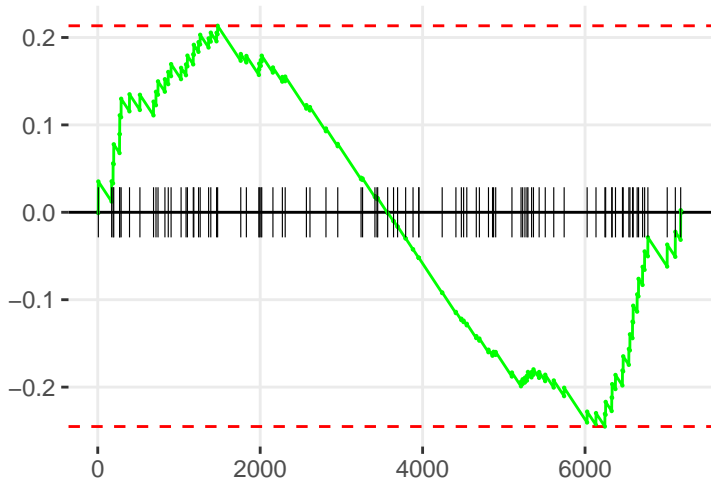
rank



# ANANDAMIDE DEGRADATION

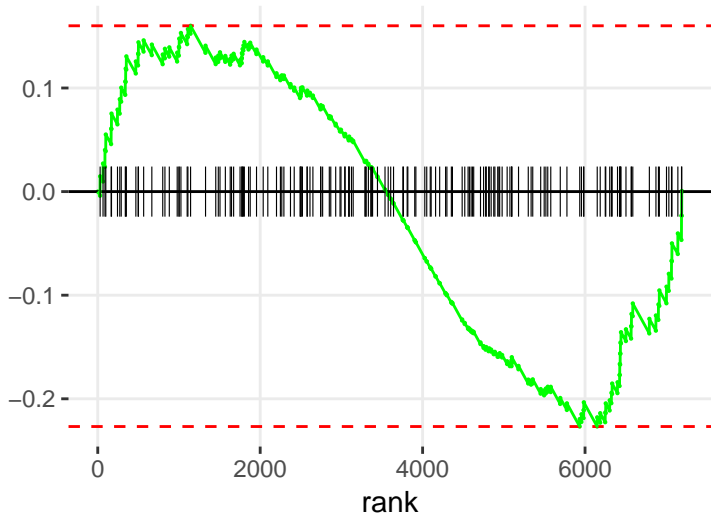
enrichment score

rank



# CHOLINE DEGRADATION I

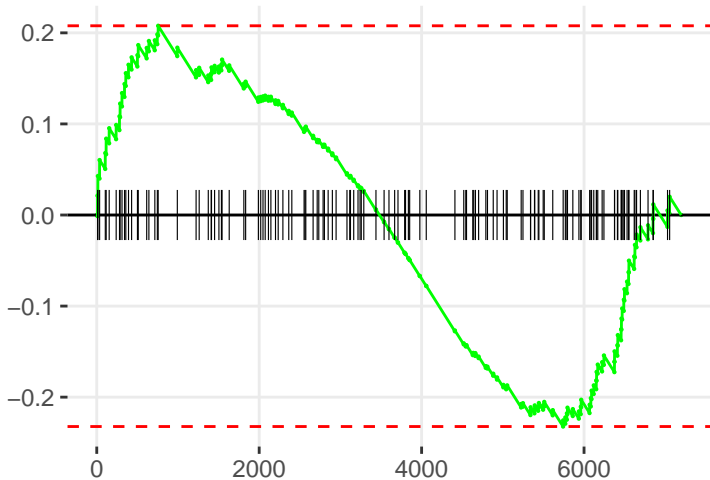
enrichment score



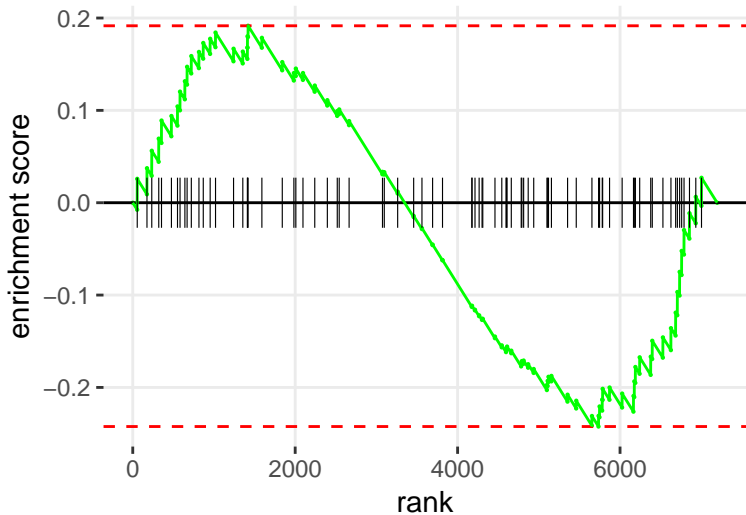
# EUMELANIN BIOSYNTHESIS

enrichment score

rank



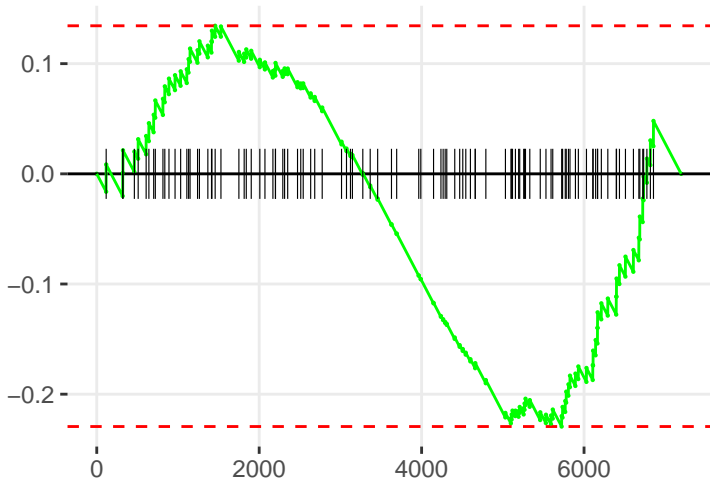
D-<IMYO</I-INOSITOL-5-PHOSPHATE METABOLISM



### 3-PHOSPHOINOSITIDE BIOSYNTHESIS

enrichment score

rank

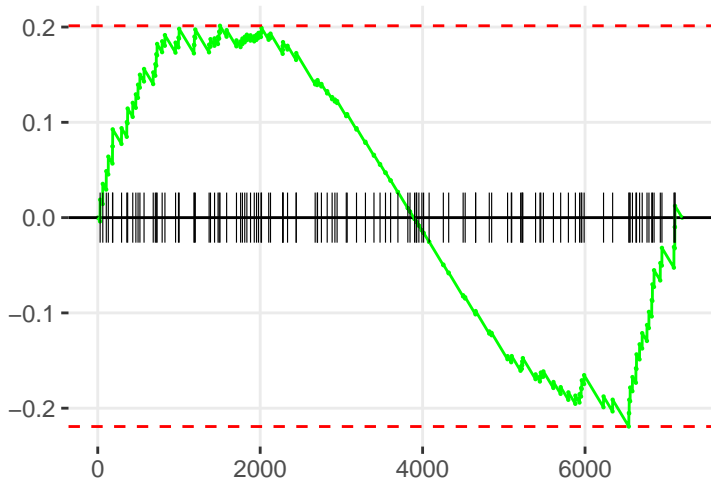




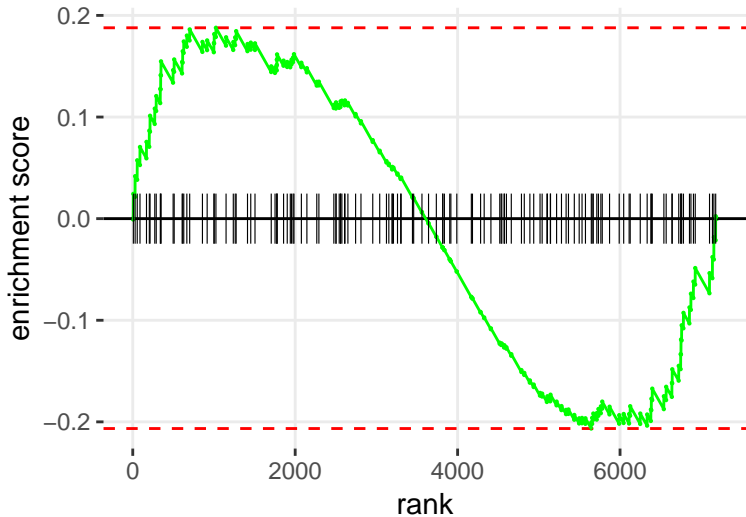
# ANDROGEN BIOSYNTHESIS

enrichment score

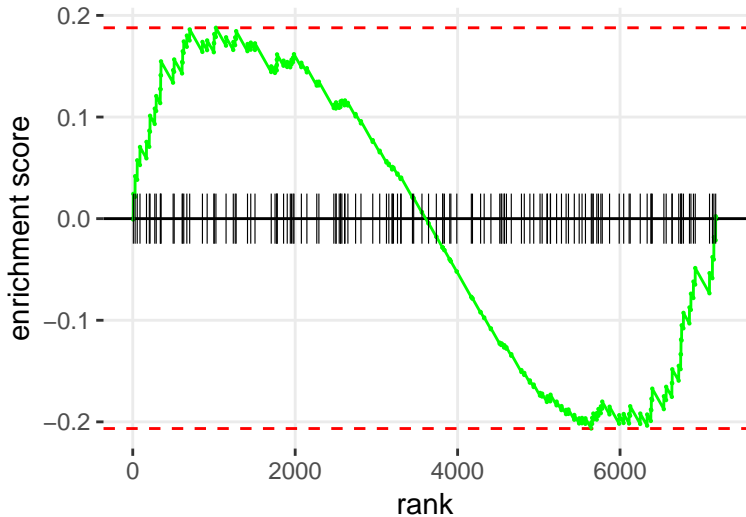
rank



# HISTIDINE DEGRADATION VI



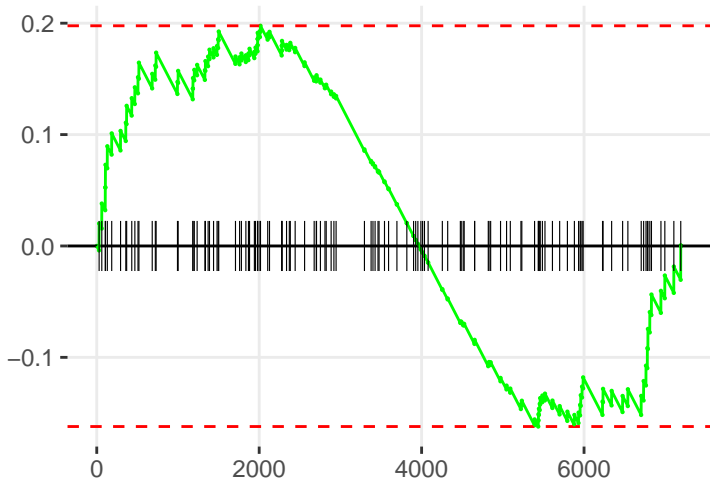
# HISTIDINE DEGRADATION III



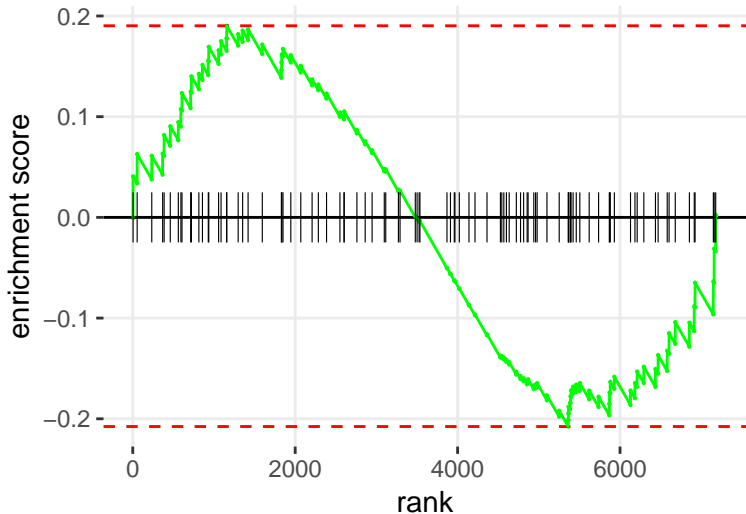
# ESTROGEN BIOSYNTHESIS

enrichment score

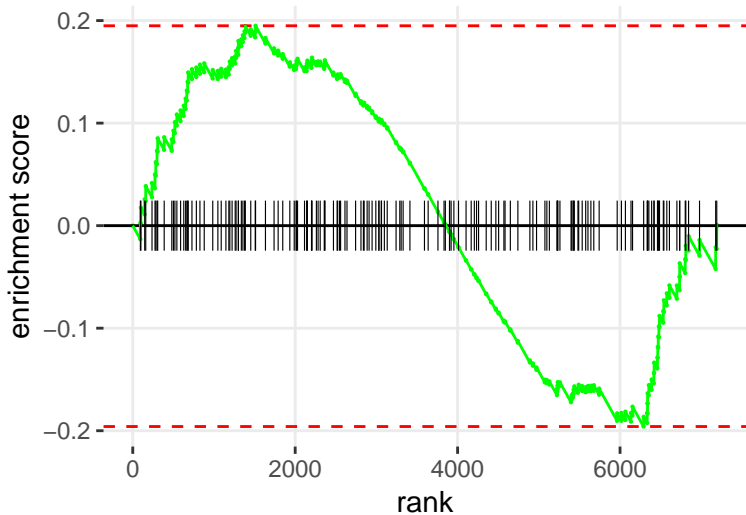
rank



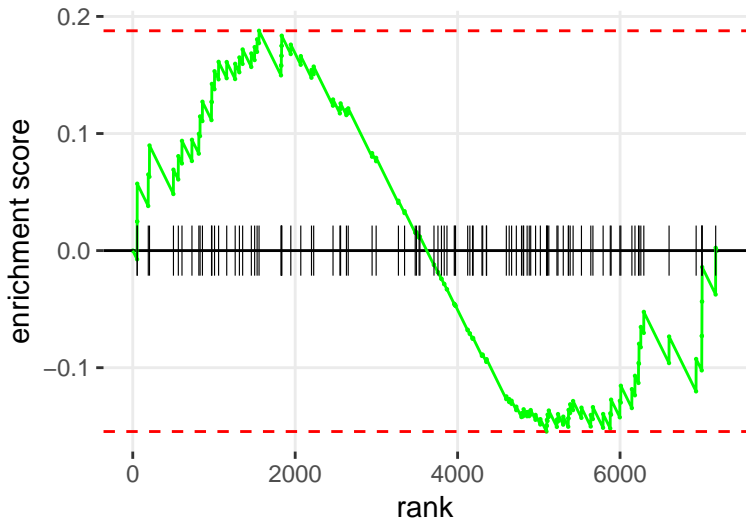
# CHONDROITIN SULFATE BIOSYNTHESIS (LATE STAGES)



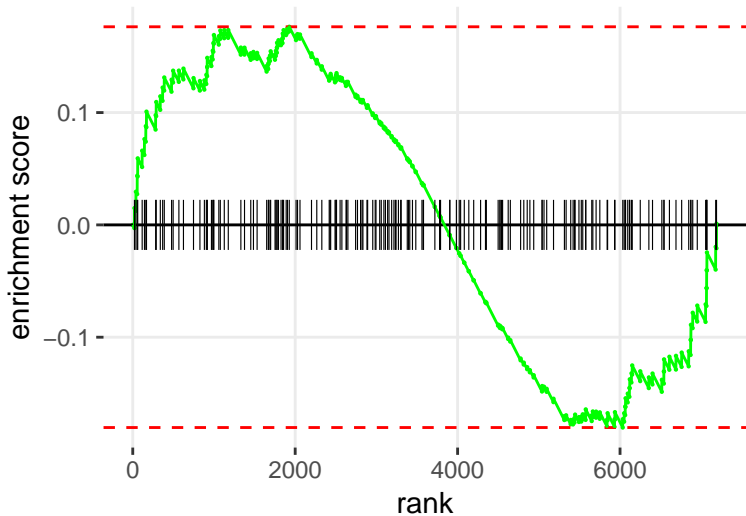
# PROTEIN CITRULLINATION



# CHONDROITIN AND DERMATAN BIOSYNTHESIS



# FATTY ACID BIOSYNTHESIS INITIATION II





# THREONINE DEGRADATION II

enrichment score

