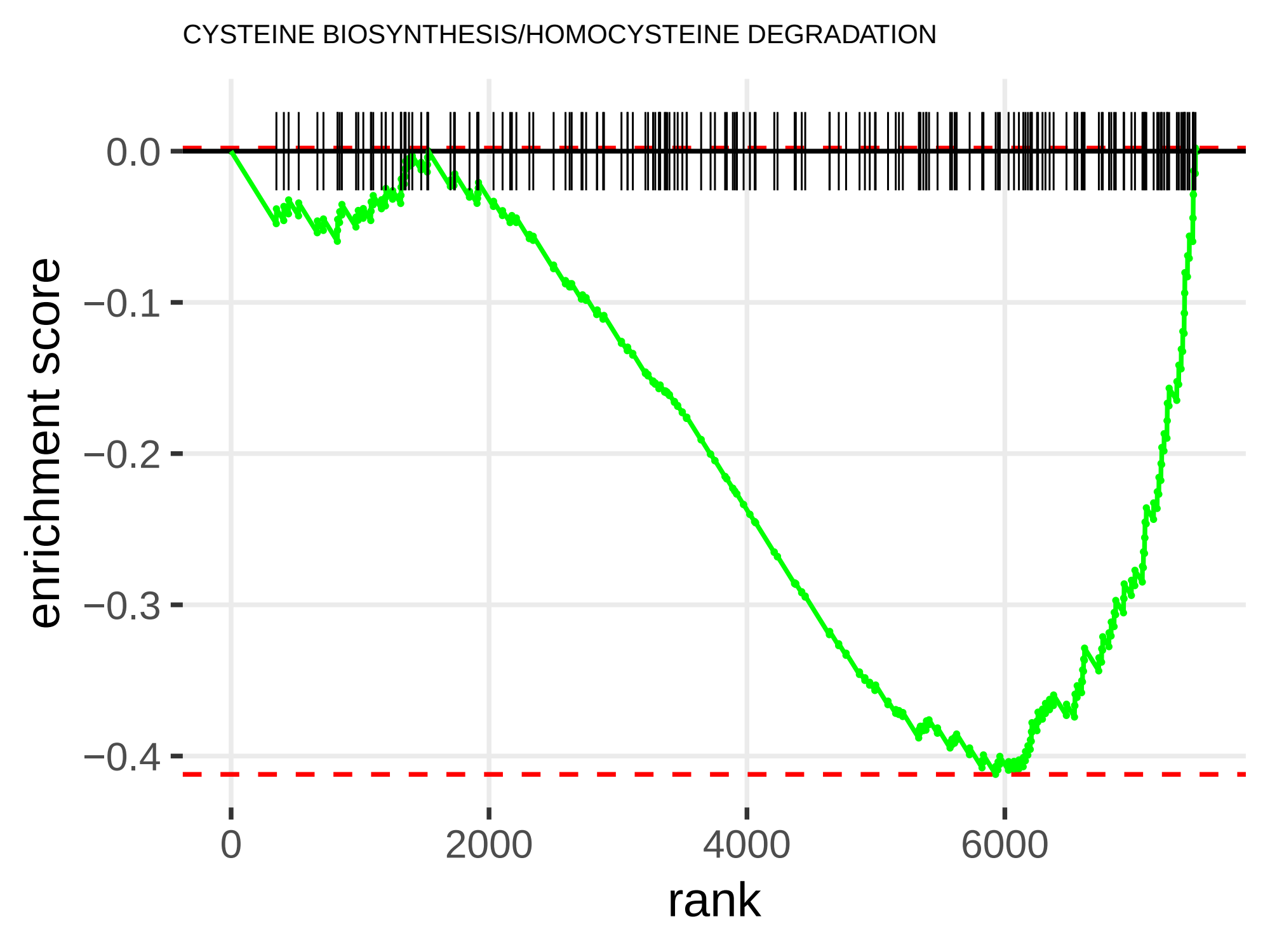
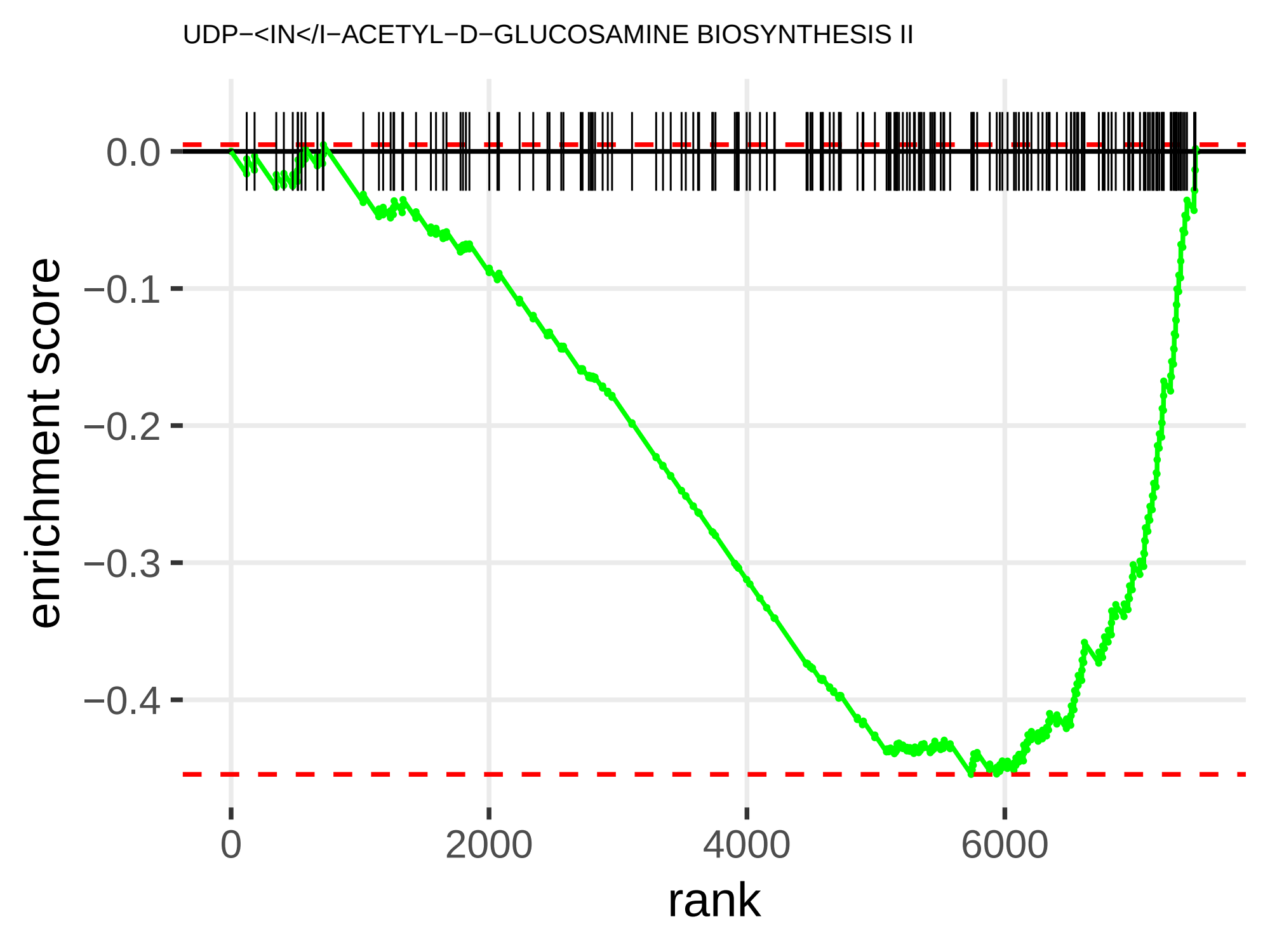
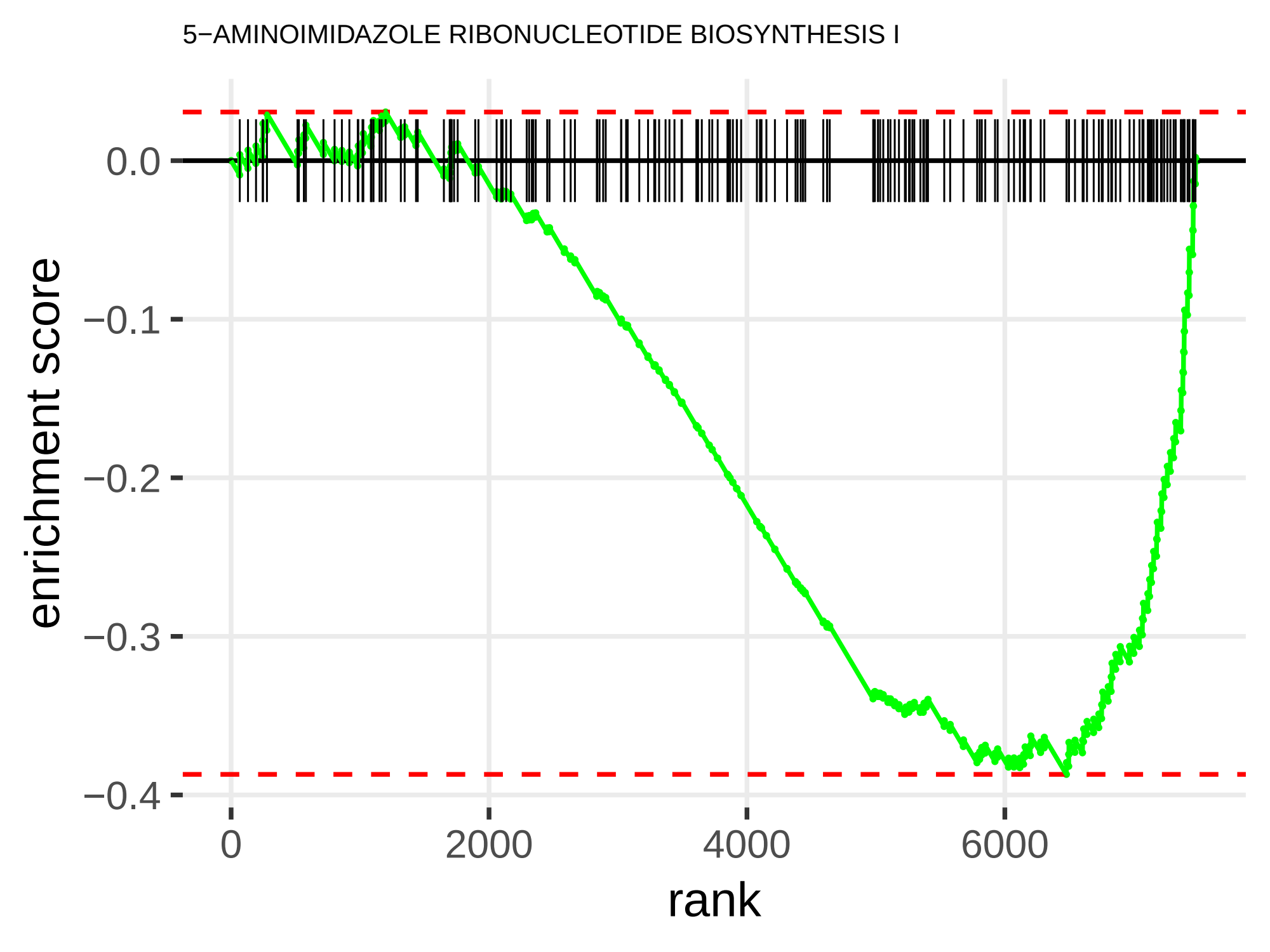
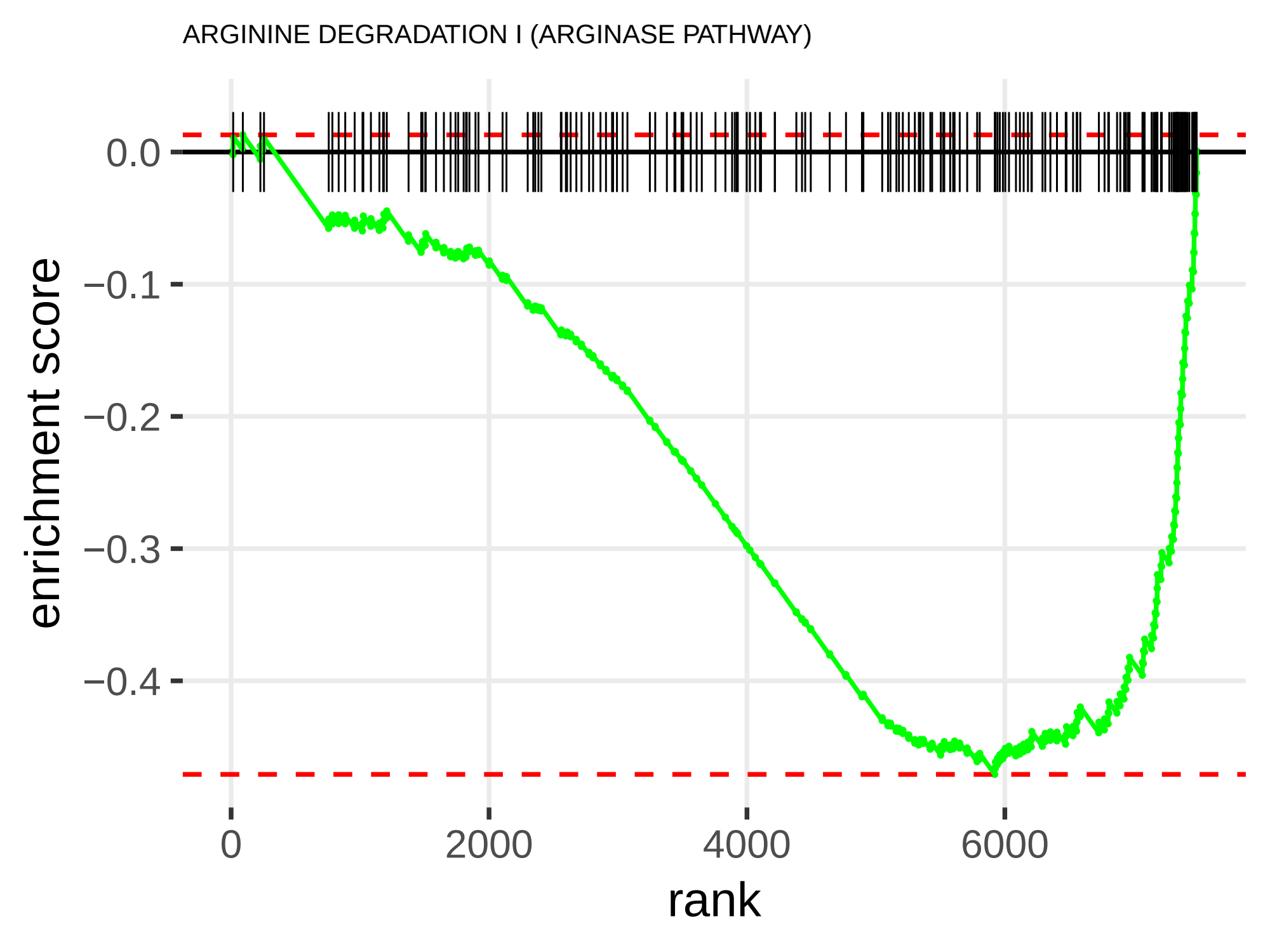
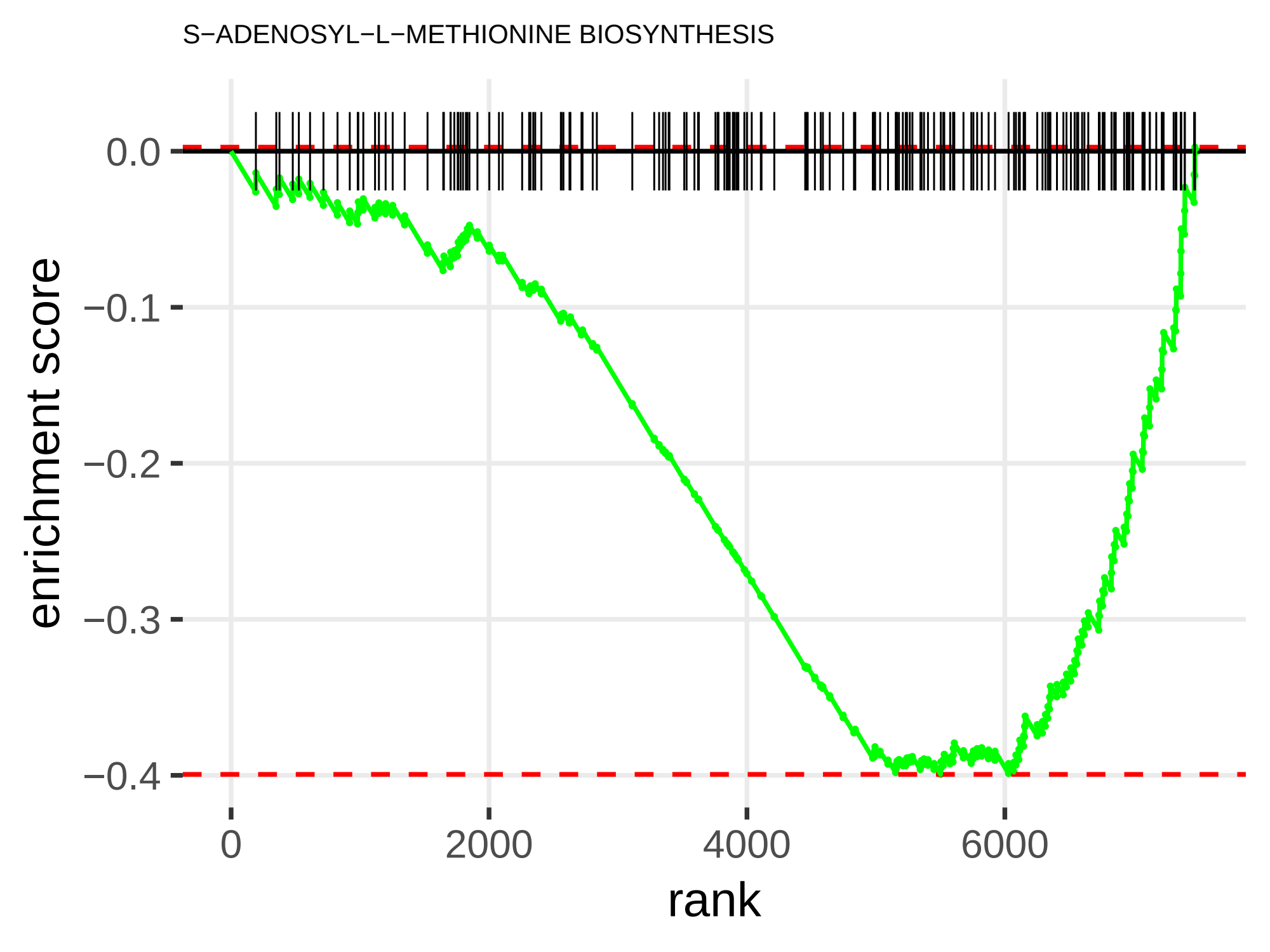
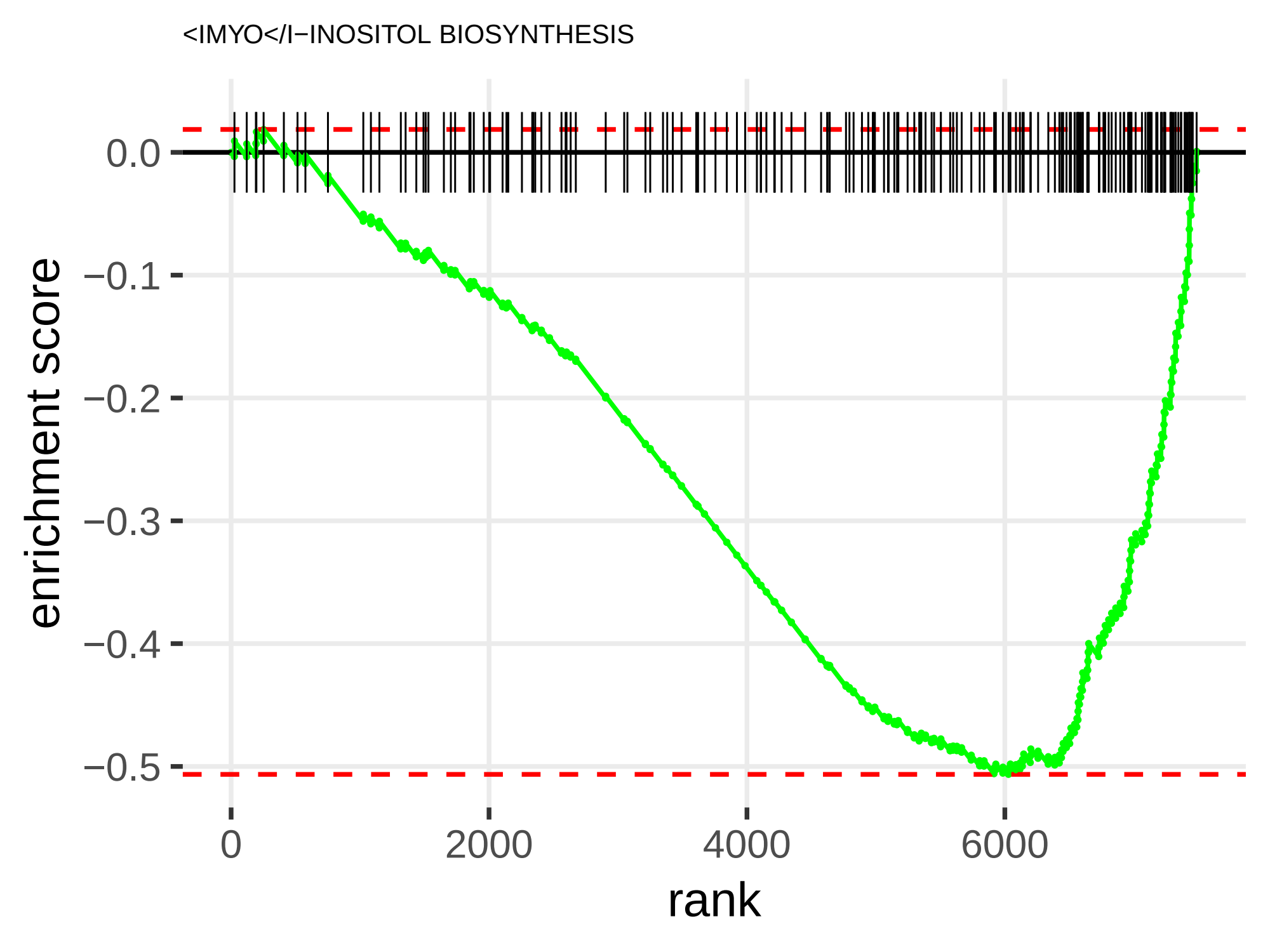

CYSTEINE BIOSYNTHESIS/HOMOCYSTEINE DEGRADATION
0.0
−0.1
−0.2
−0.3
−0.4
enrichment score
0
2000
4000
6000
rank

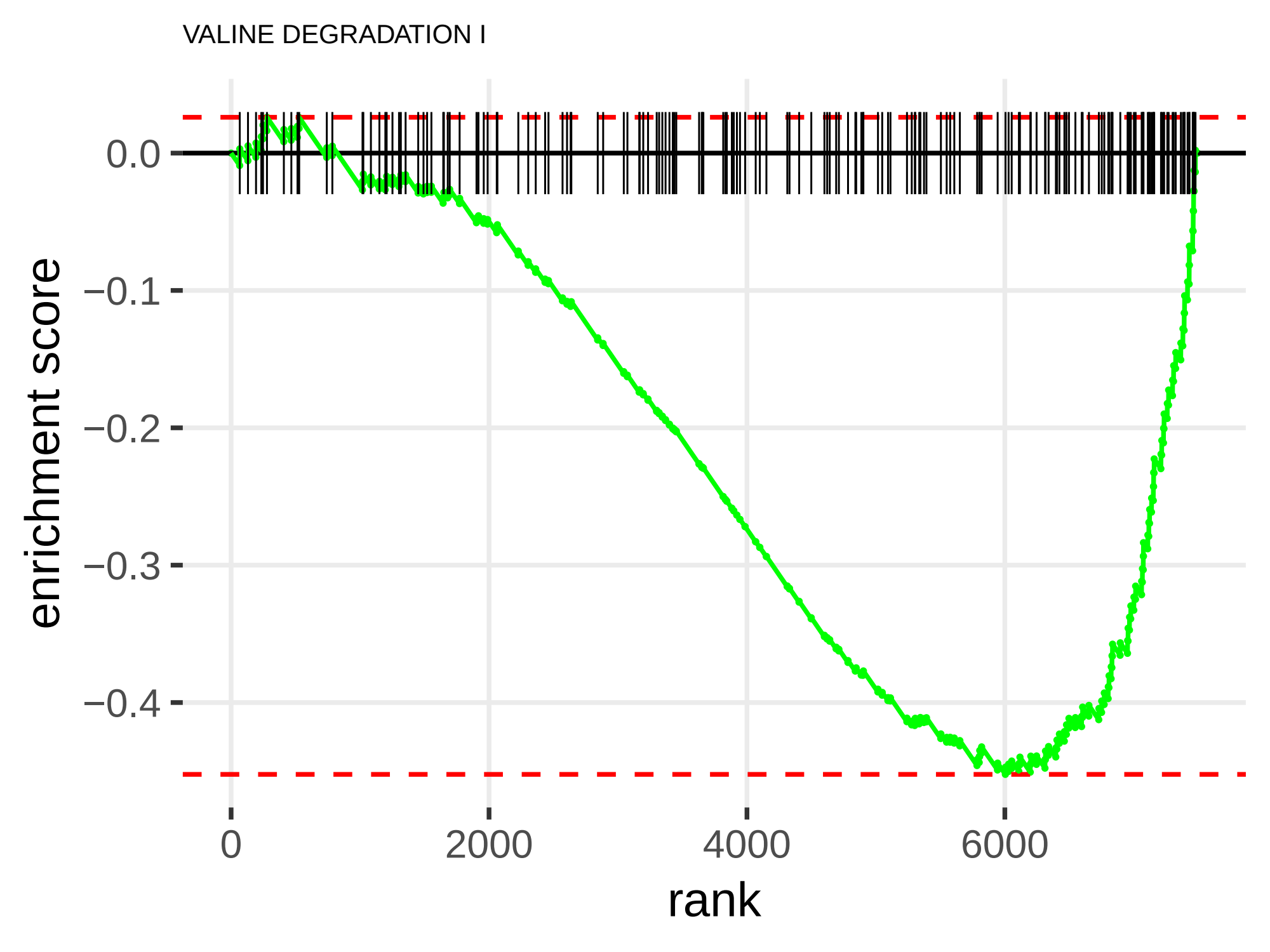

UDP−<IN</I−ACETYL−D−GLUCOSAMINE BIOSYNTHESIS II
0.0
−0.1
−0.2
−0.3
−0.4
enrichment score
0
2000
4000
6000
rank

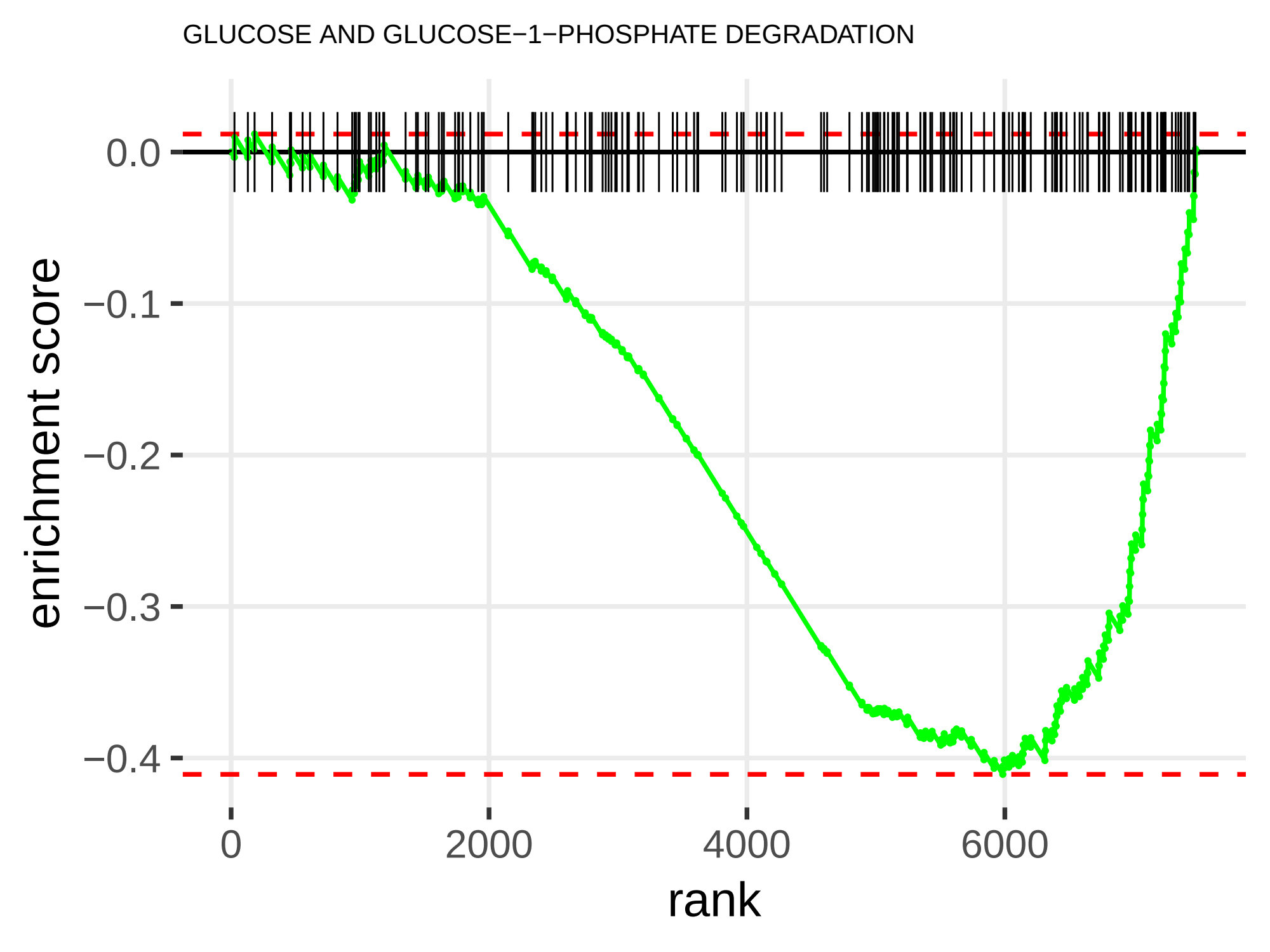

5−AMINOIMIDAZOLE RIBONUCLEOTIDE BIOSYNTHESIS I
0.0
−0.1
−0.2
−0.3
−0.4
enrichment score
0
2000
4000
6000
rank

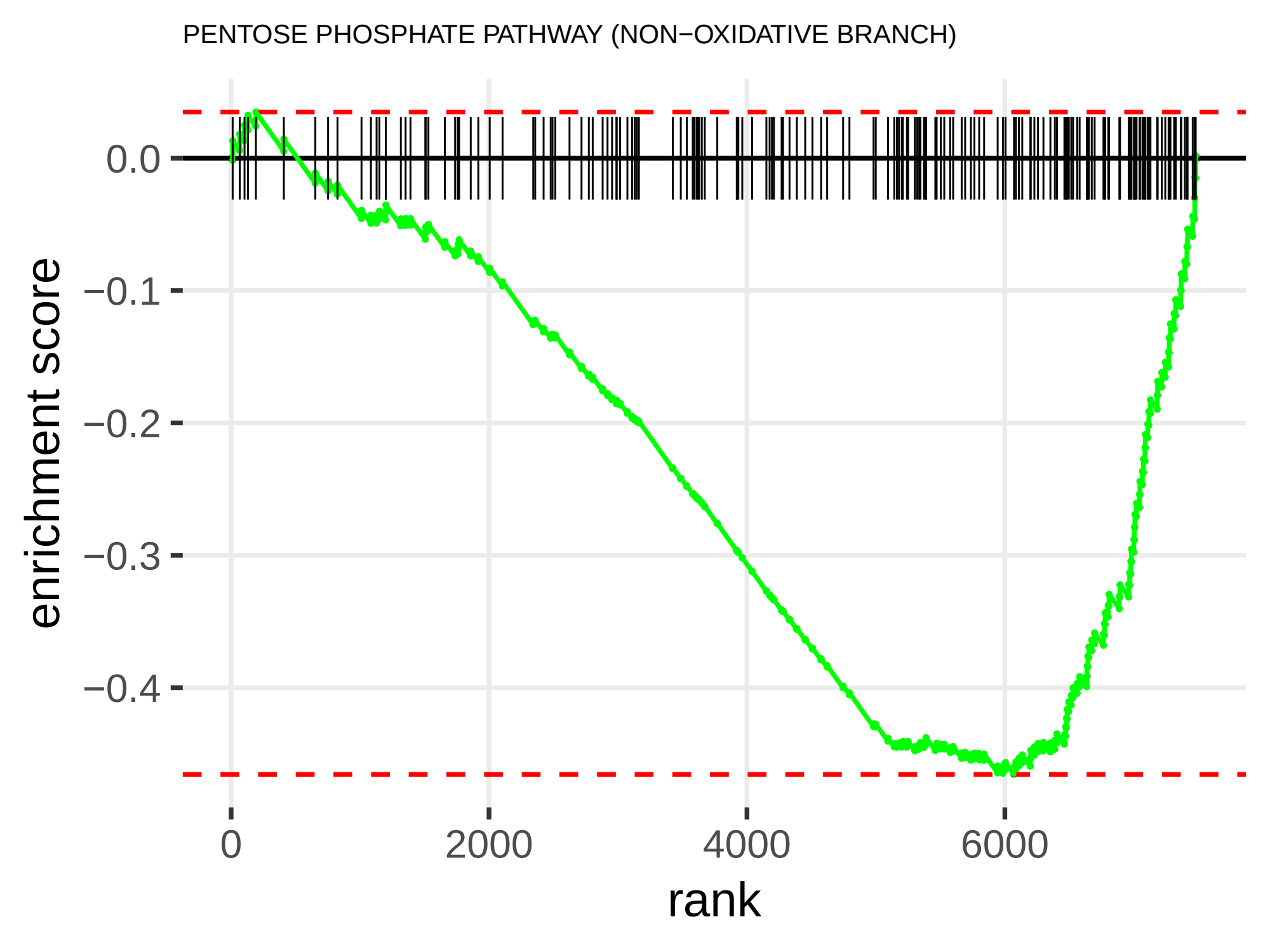

ARGININE DEGRADATION I (ARGINASE PATHWAY)
0.0
−0.1
−0.2
−0.3
−0.4
enrichment score
0
2000
4000
6000
rank

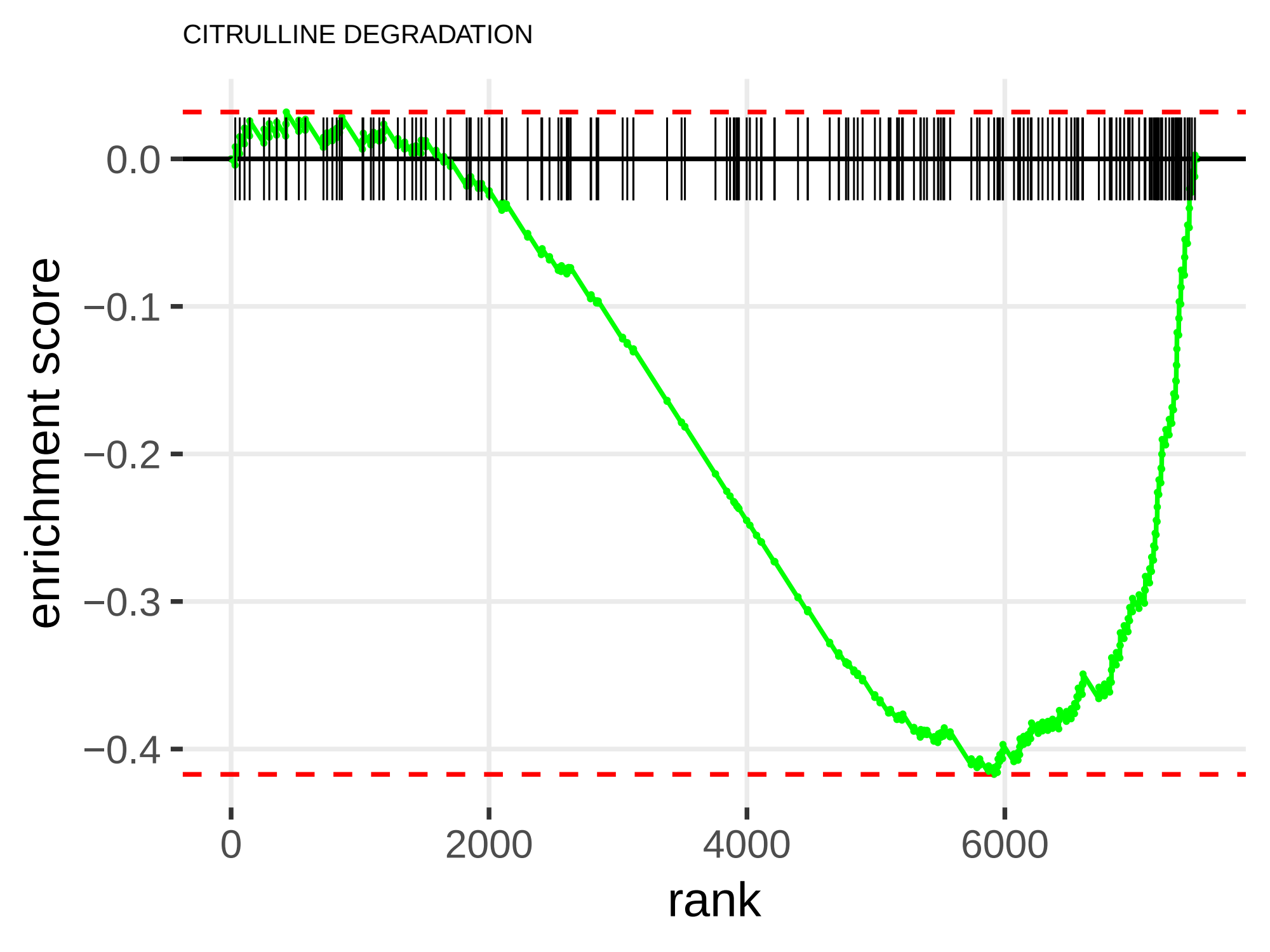

S−ADENOSYL−L−METHIONINE BIOSYNTHESIS
0.0
−0.1
−0.2
−0.3
−0.4
enrichment score
0
2000
4000
6000
rank

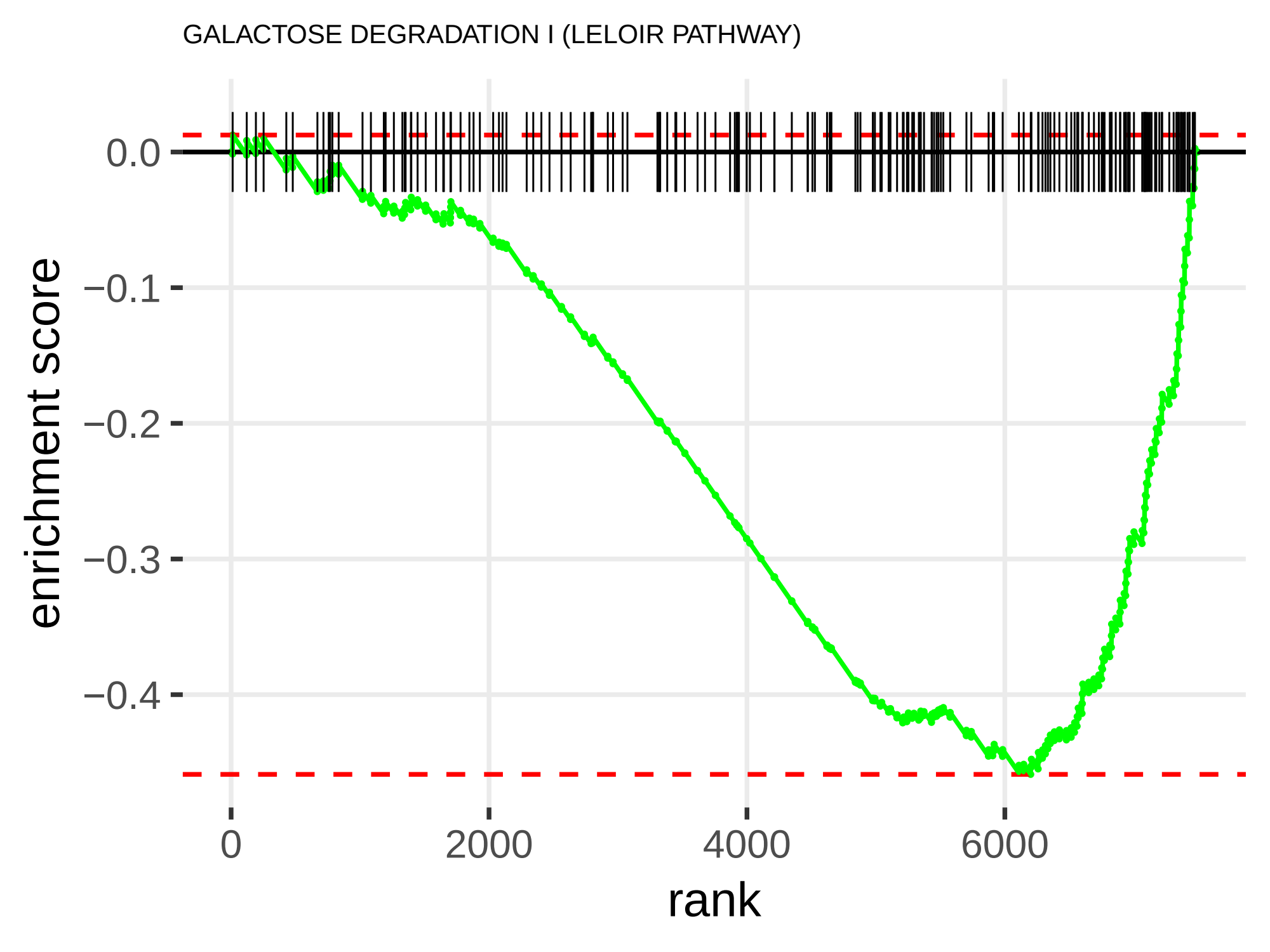

<IMYO</I−INOSITOL BIOSYNTHESIS
0.0
−0.1
−0.2
−0.3
−0.4
−0.5
enrichment score
0
2000
4000
6000
rank

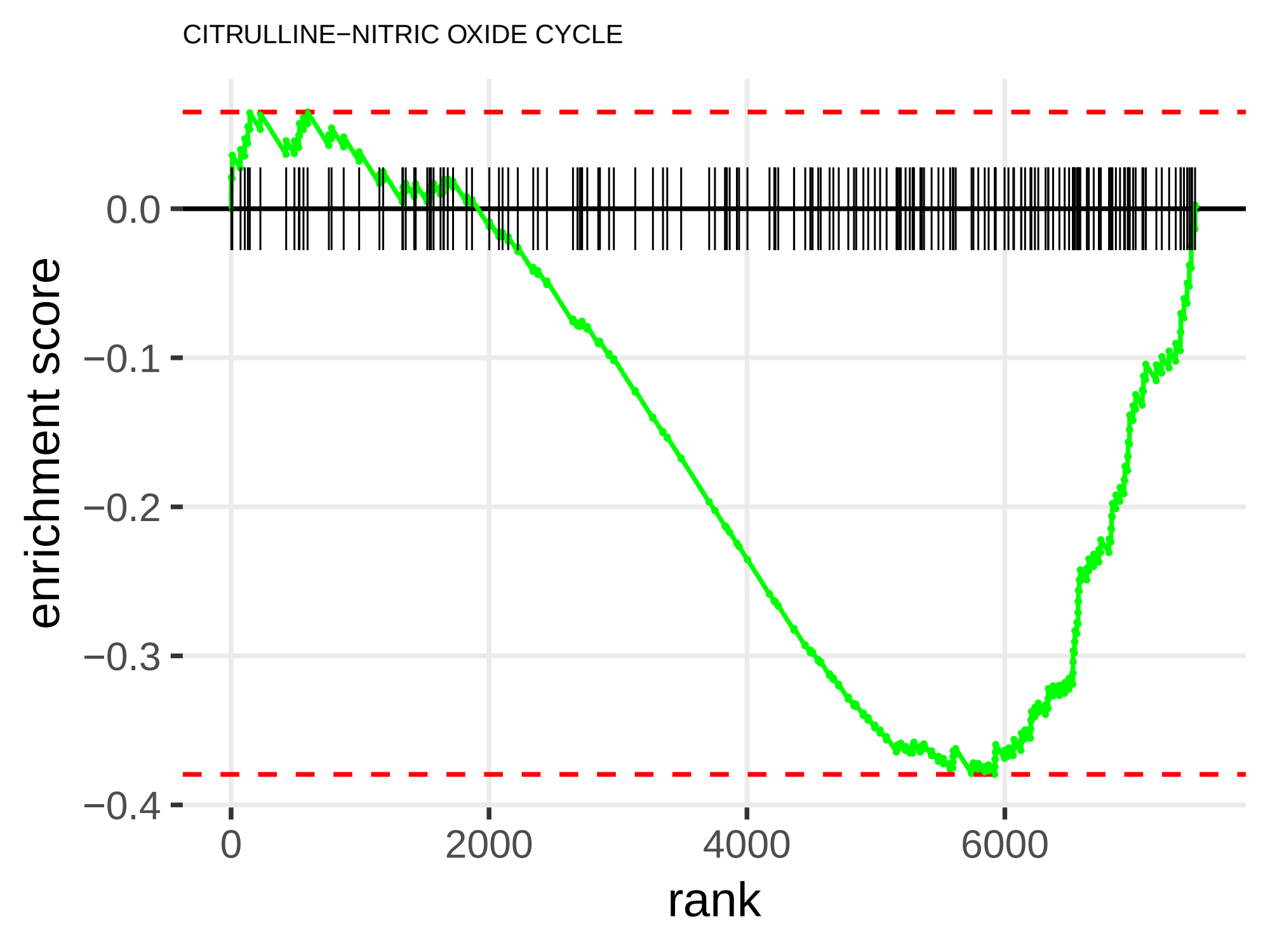

VALINE DEGRADATION I
0.0
−0.1
−0.2
−0.3
−0.4
enrichment score
0
2000
4000
6000
rank

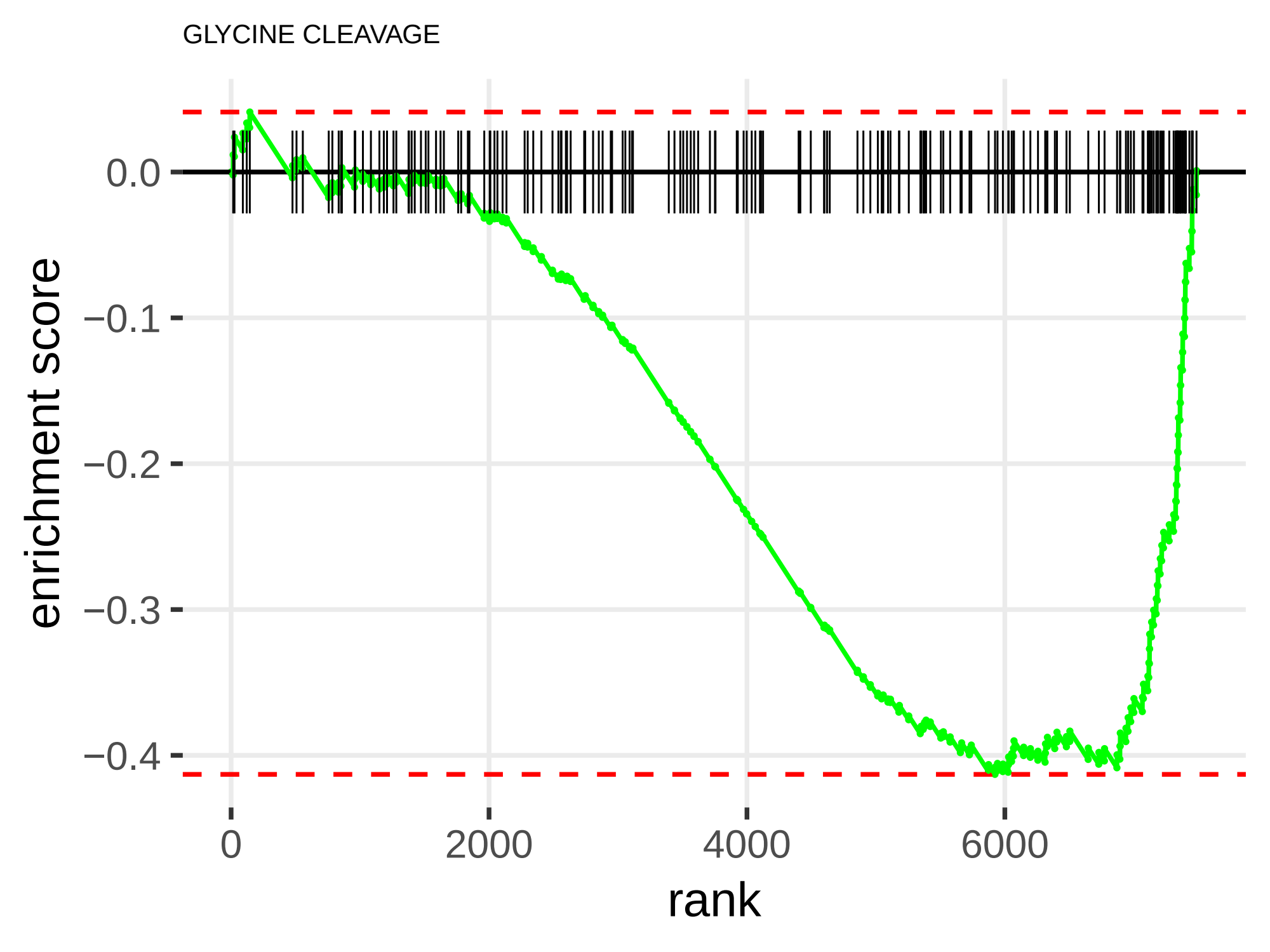

GLUCOSE AND GLUCOSE−1−PHOSPHATE DEGRADATION
enrichment score
0.0
−0.1
−0.2
−0.3
−0.4
0
2000
4000
6000
rank

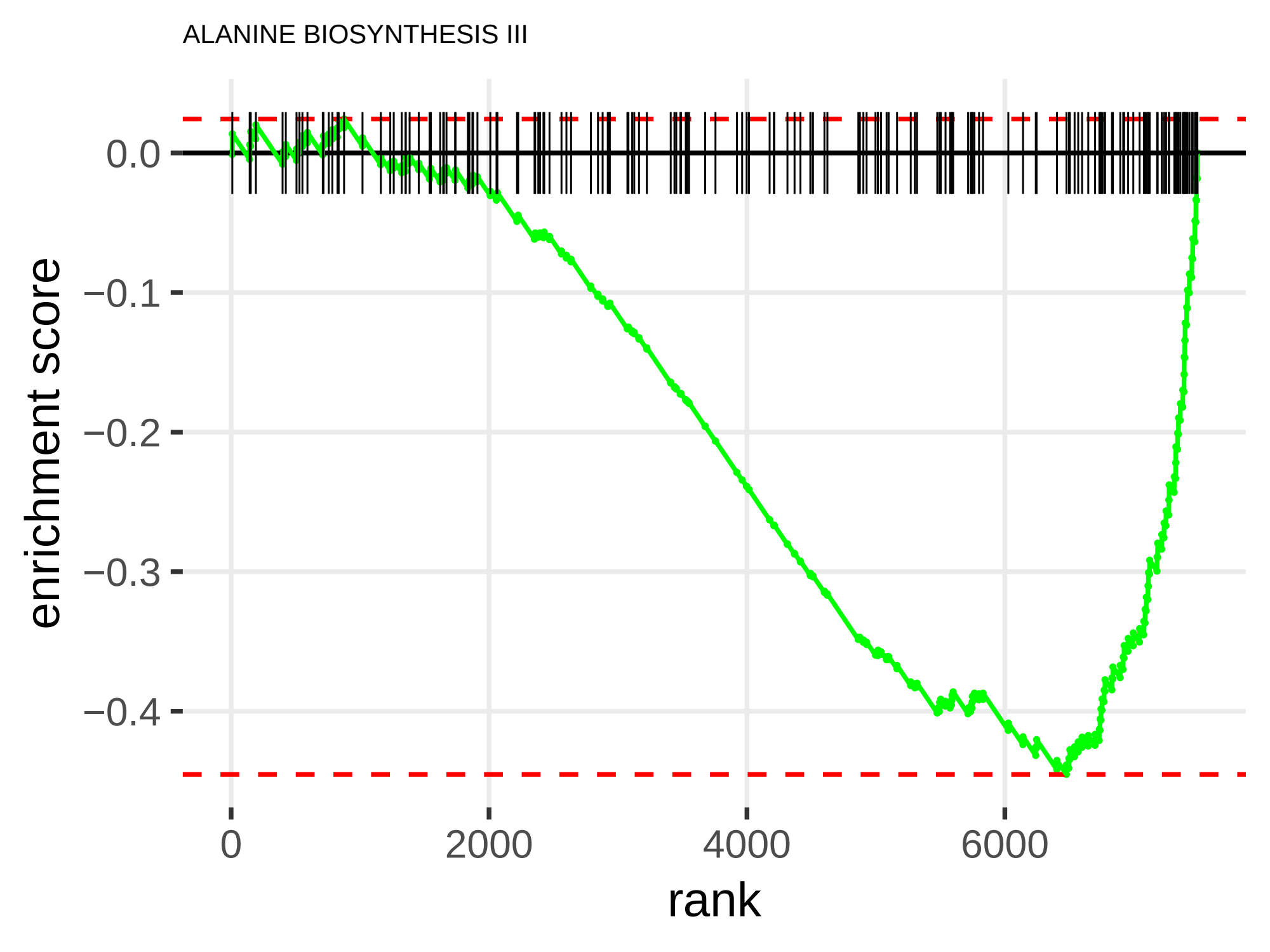

PENTOSE PHOSPHATE PATHWAY (NON−OXIDATIVE BRANCH)
0.0
−0.1
−0.2
−0.3
−0.4
enrichment score
0
2000
4000
6000
rank

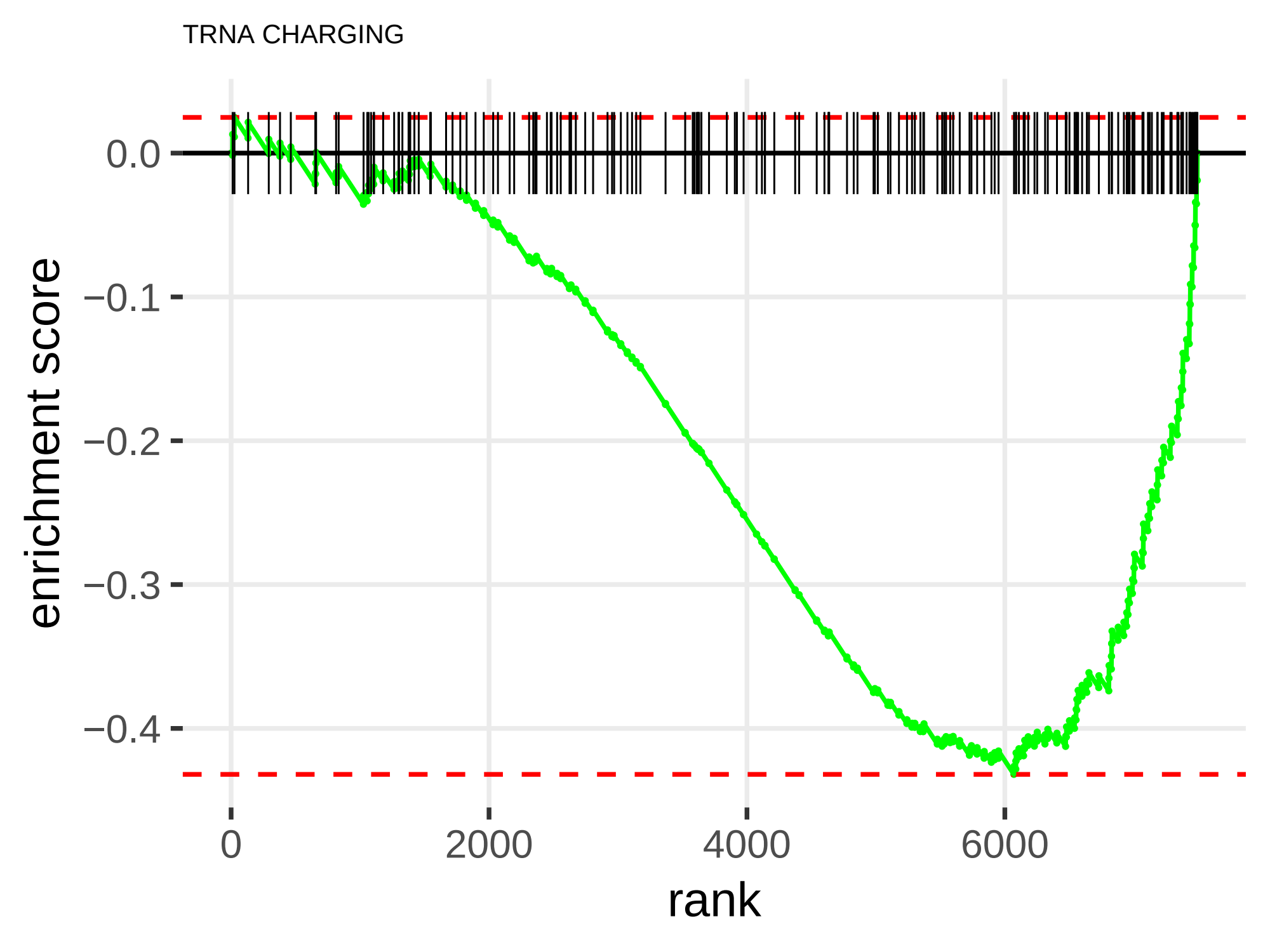

CITRULLINE DEGRADATION
0.0
−0.1
−0.2
−0.3
−0.4
enrichment score
0
2000
4000
6000
rank

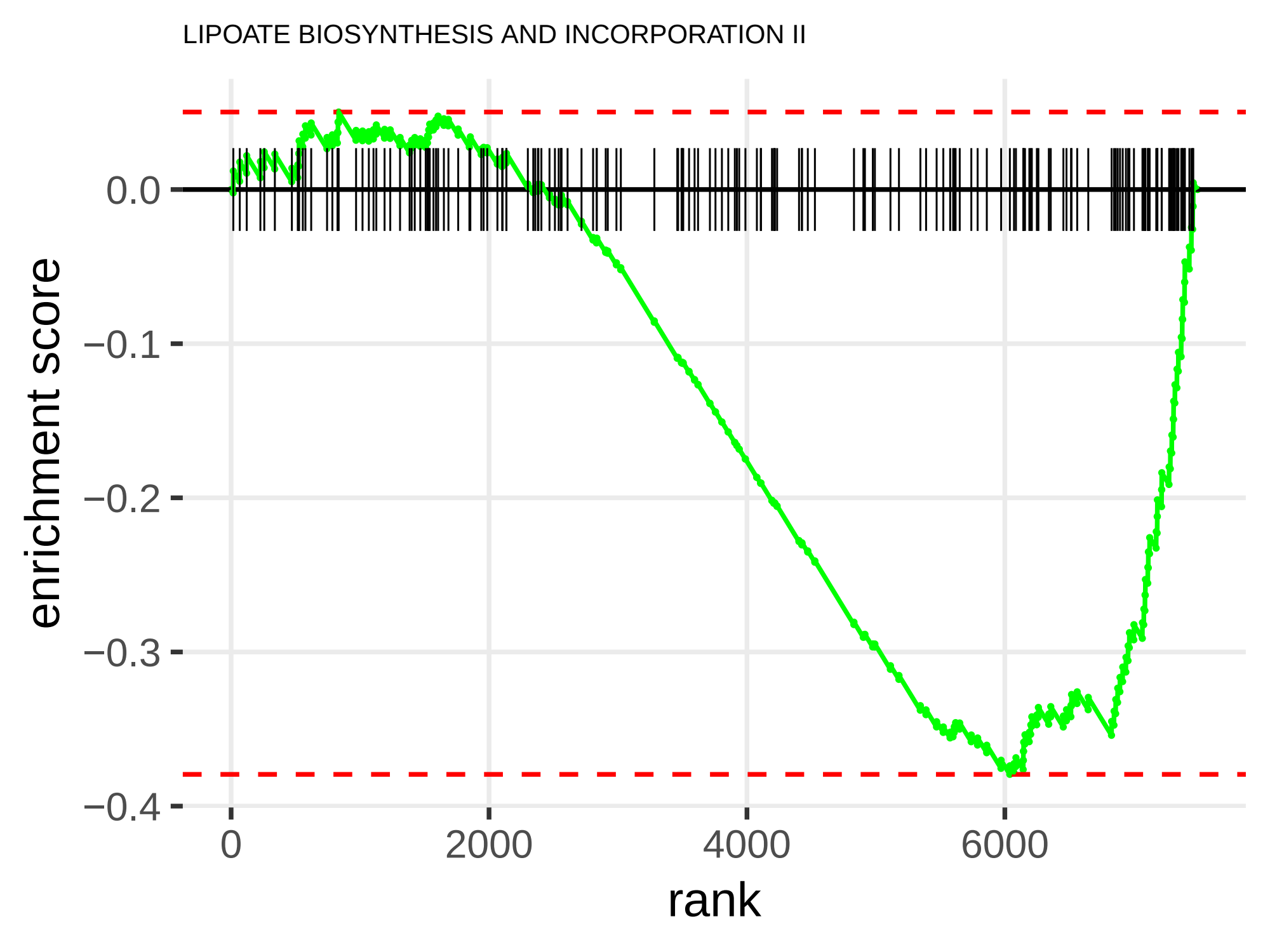

GALACTOSE DEGRADATION I (LELOIR PATHWAY)
0.0
−0.1
−0.2
−0.3
−0.4
enrichment score
0
2000
4000
6000
rank

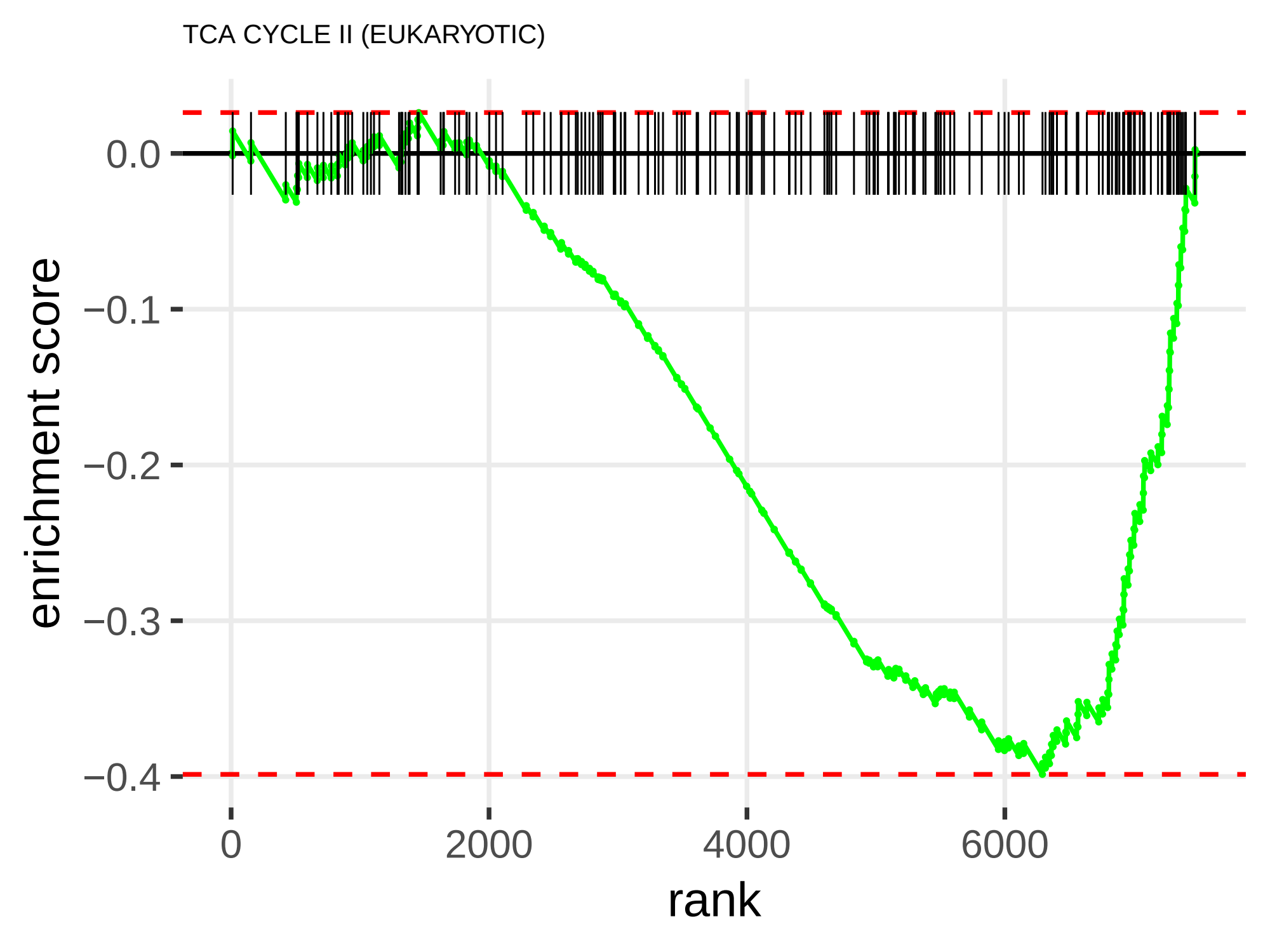

CITRULLINE−NITRIC OXIDE CYCLE
enrichment score
0.0
−0.1
−0.2
−0.3
−0.4
0
2000
4000
6000
rank

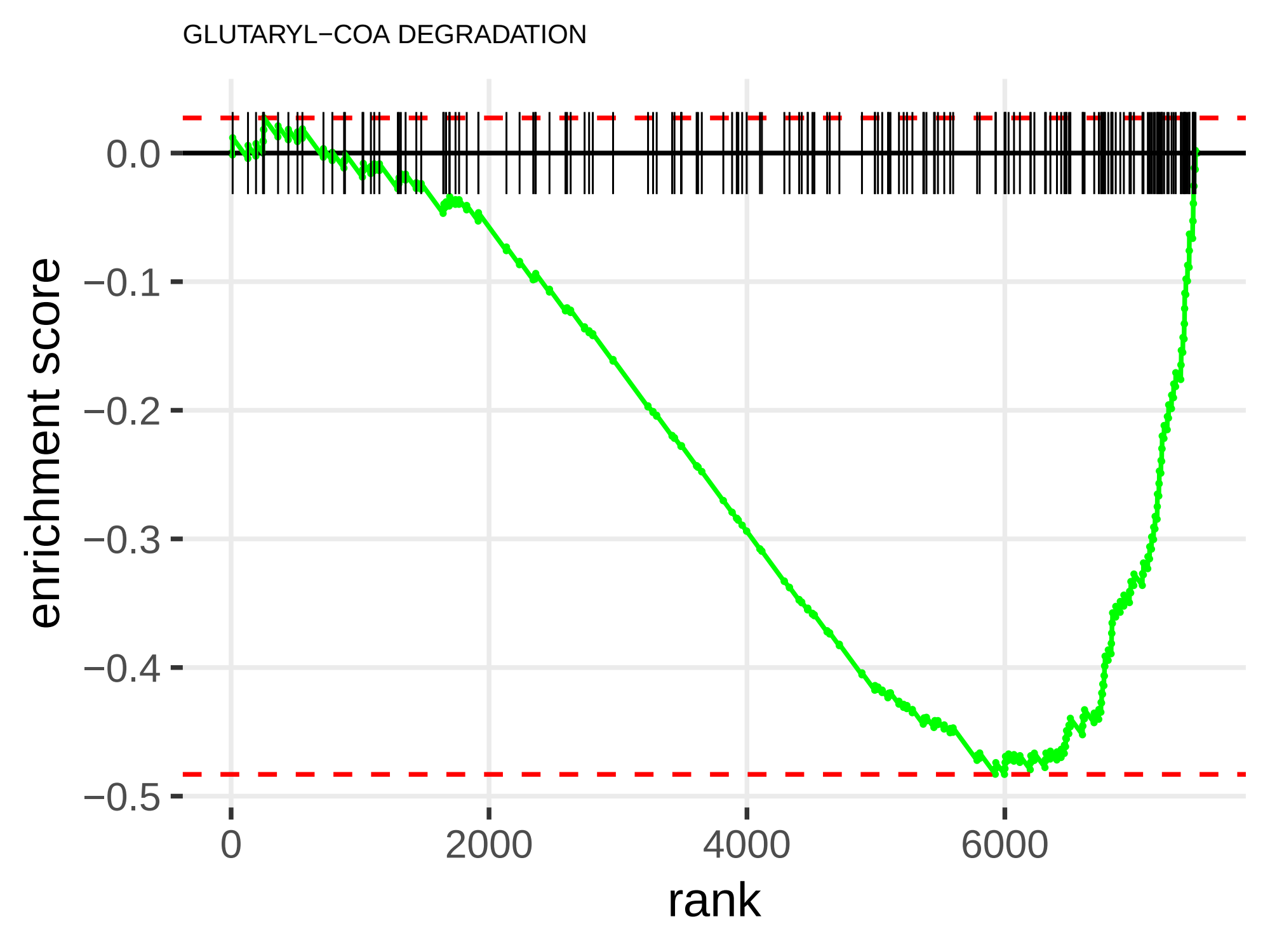

GLYCINE CLEAVAGE
0.0
−0.1
−0.2
−0.3
−0.4
enrichment score
0
2000
4000
6000
rank

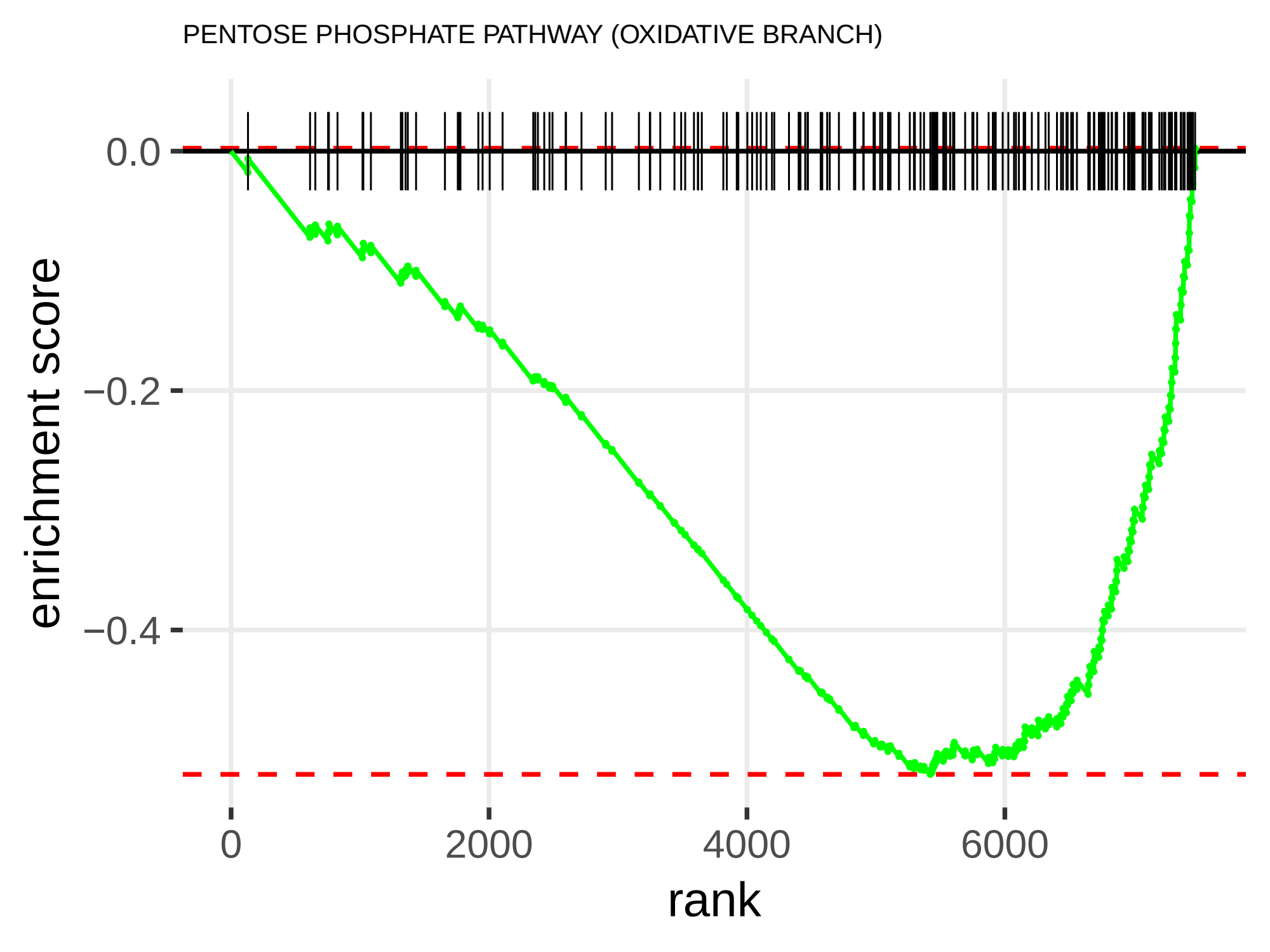

ALANINE BIOSYNTHESIS III
0.0
−0.1
−0.2
−0.3
−0.4
enrichment score
0
2000
4000
6000
rank

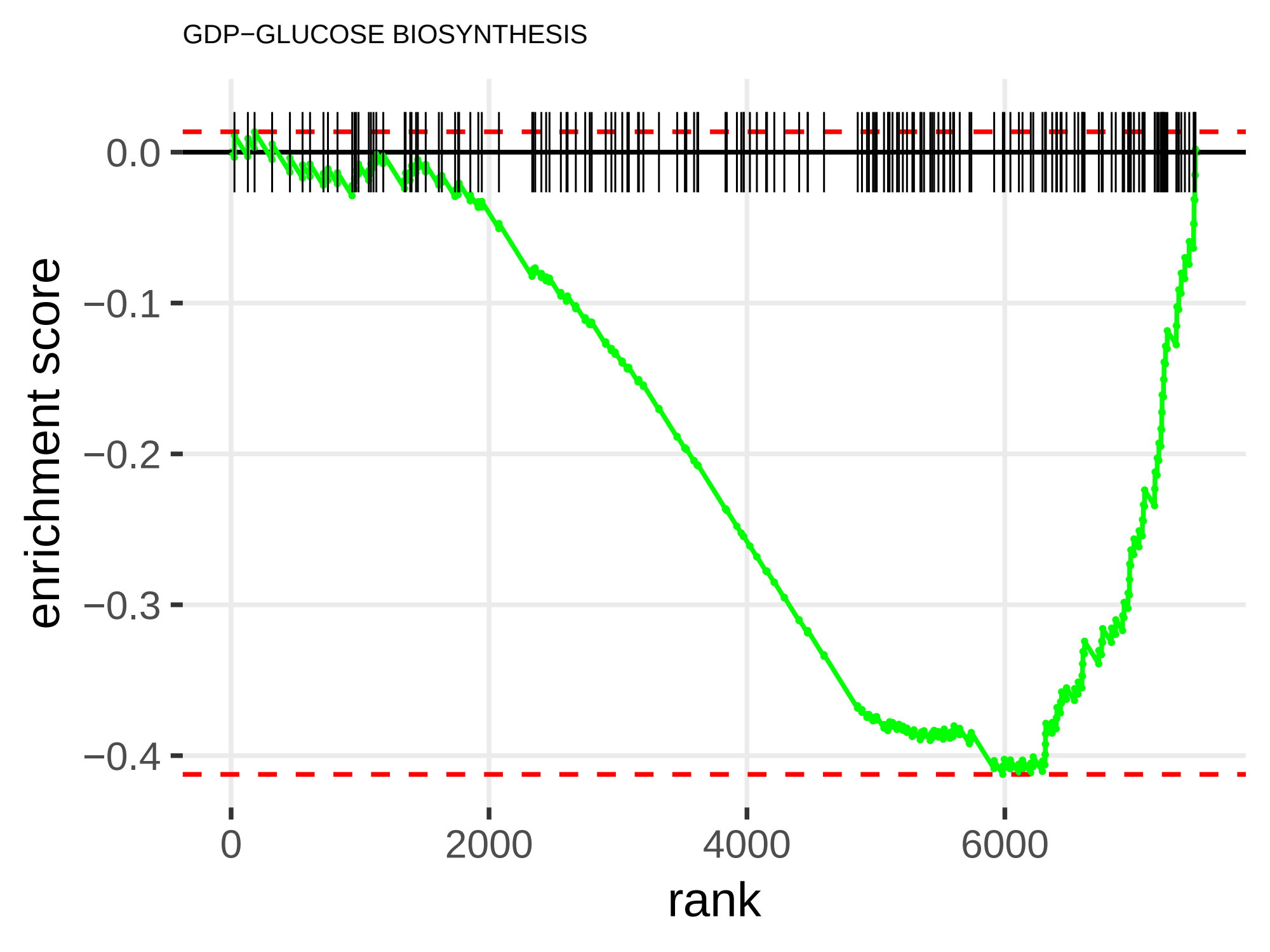

TRNA CHARGING
0.0
−0.1
−0.2
−0.3
−0.4
enrichment score
0
2000
4000
6000
rank

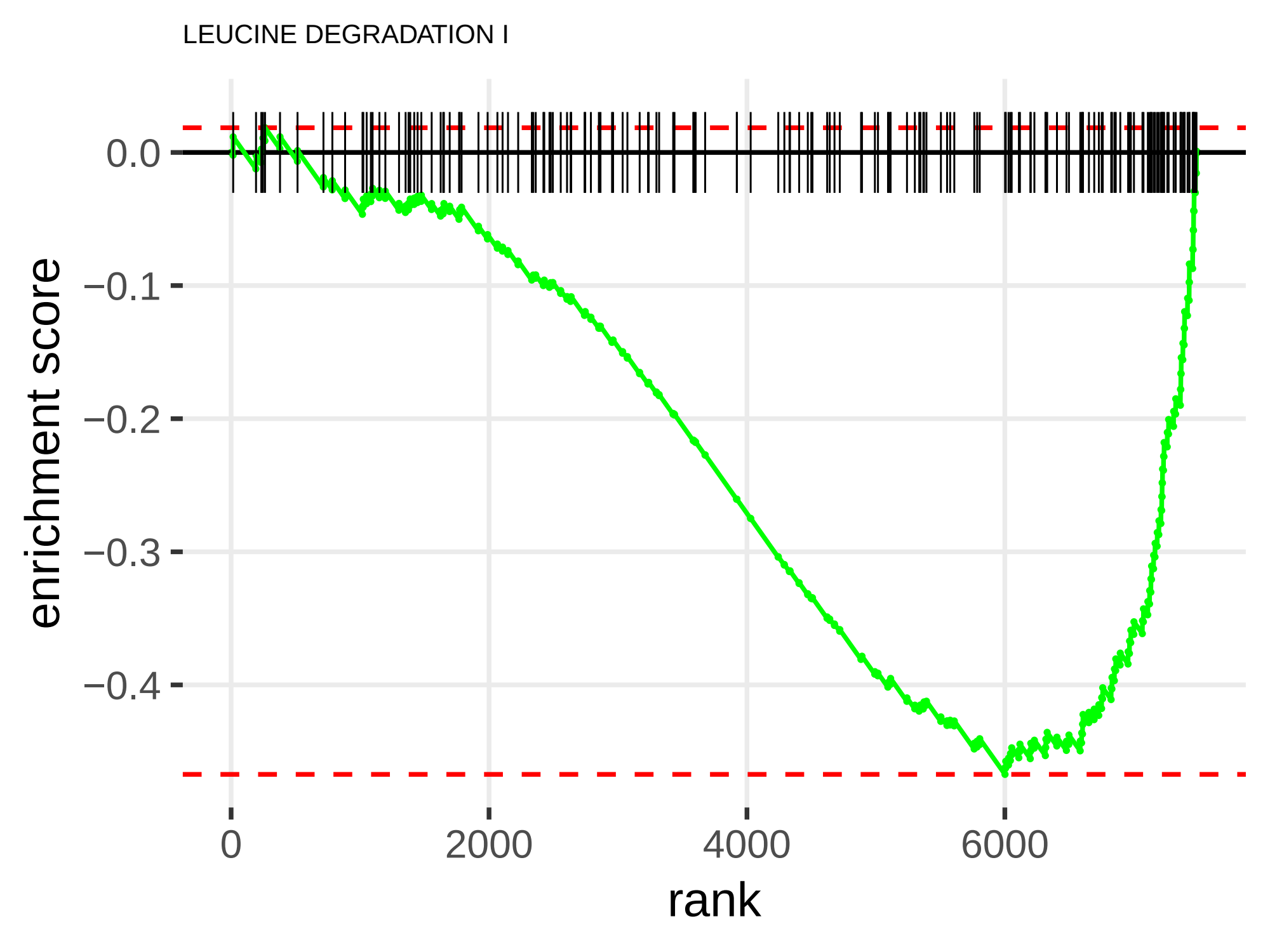

LIPOATE BIOSYNTHESIS AND INCORPORATION II
enrichment score
0.0
−0.1
−0.2
−0.3
−0.4
0
2000
4000
6000
rank

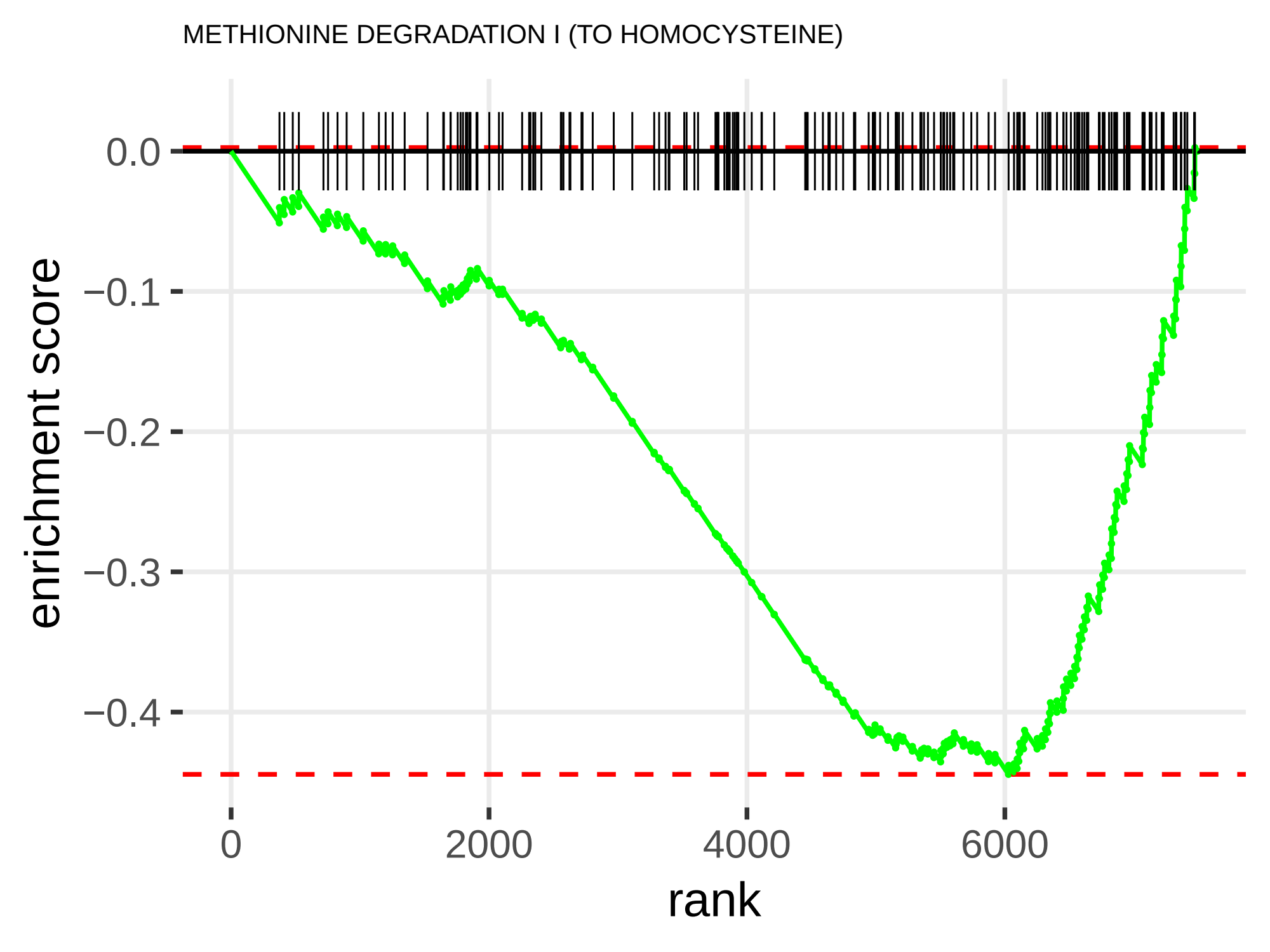

TCA CYCLE II (EUKARYOTIC)
0.0
−0.1
−0.2
−0.3
−0.4
enrichment score
0
2000
4000
6000
rank

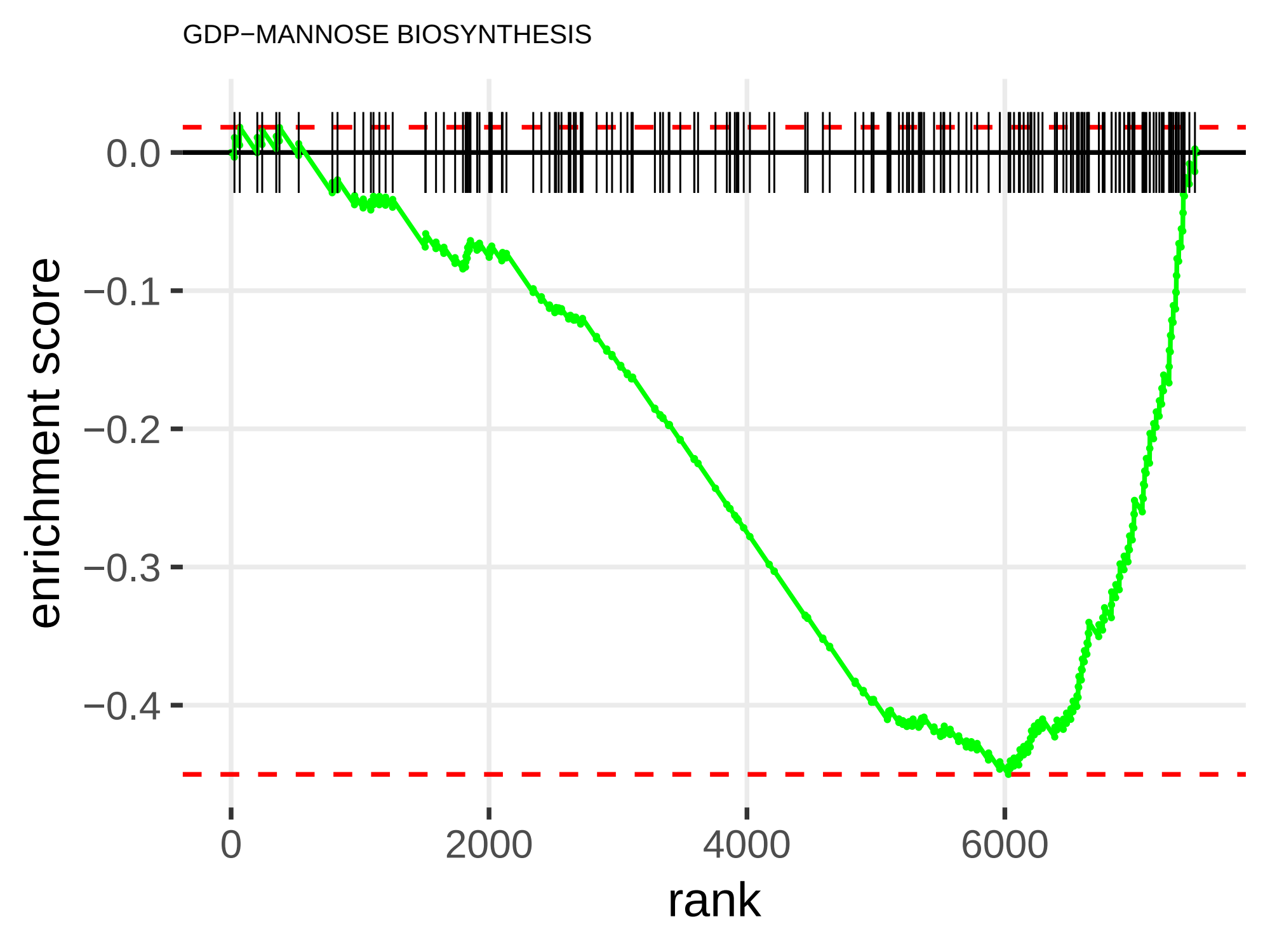

GLUTARYL−COA DEGRADATION
0.0
−0.1
−0.2
−0.3
−0.4
−0.5
enrichment score
0
2000
4000
6000
rank

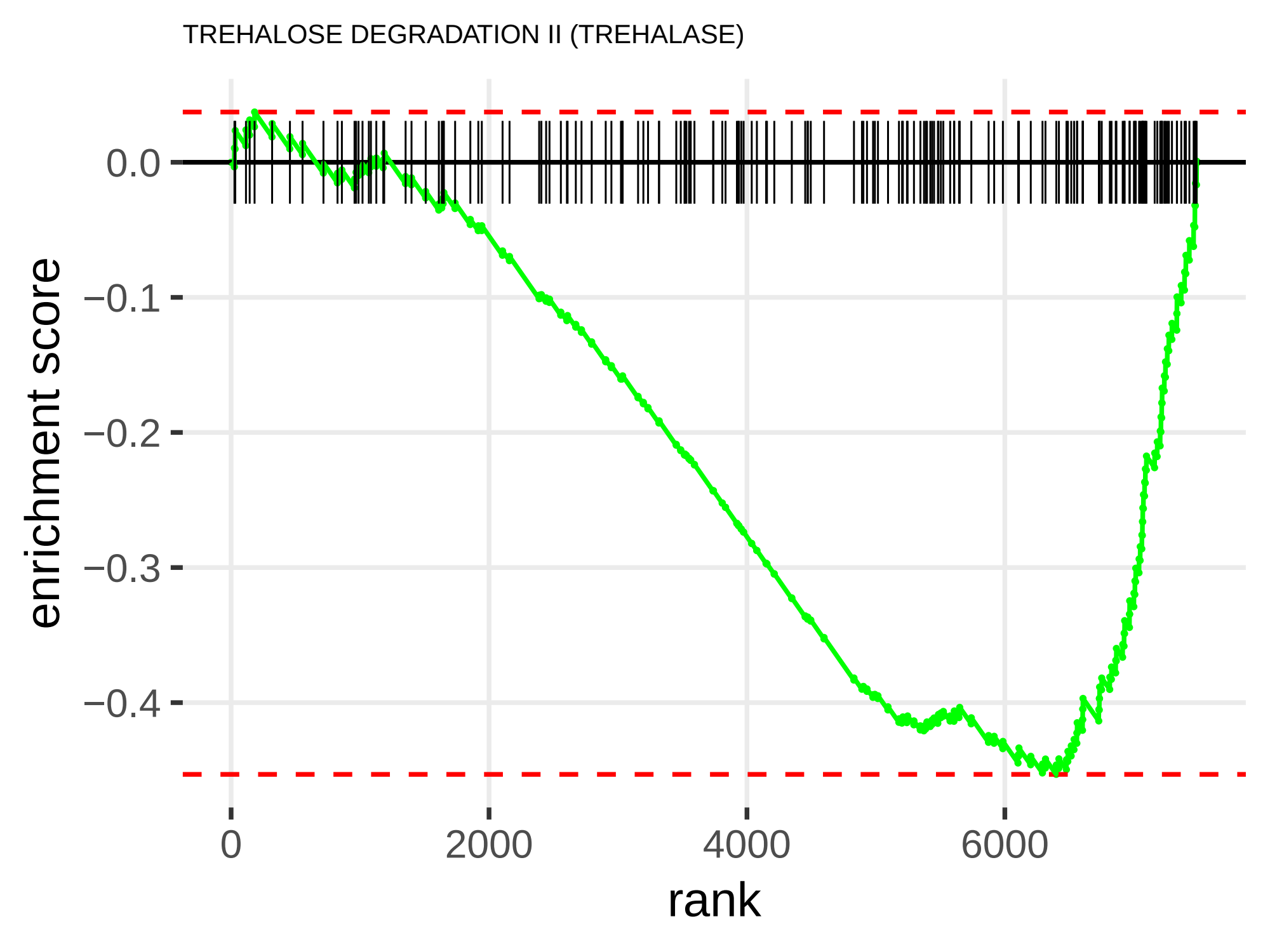

PENTOSE PHOSPHATE PATHWAY (OXIDATIVE BRANCH)
0.0
−0.2
−0.4
enrichment score
0
2000
4000
6000
rank

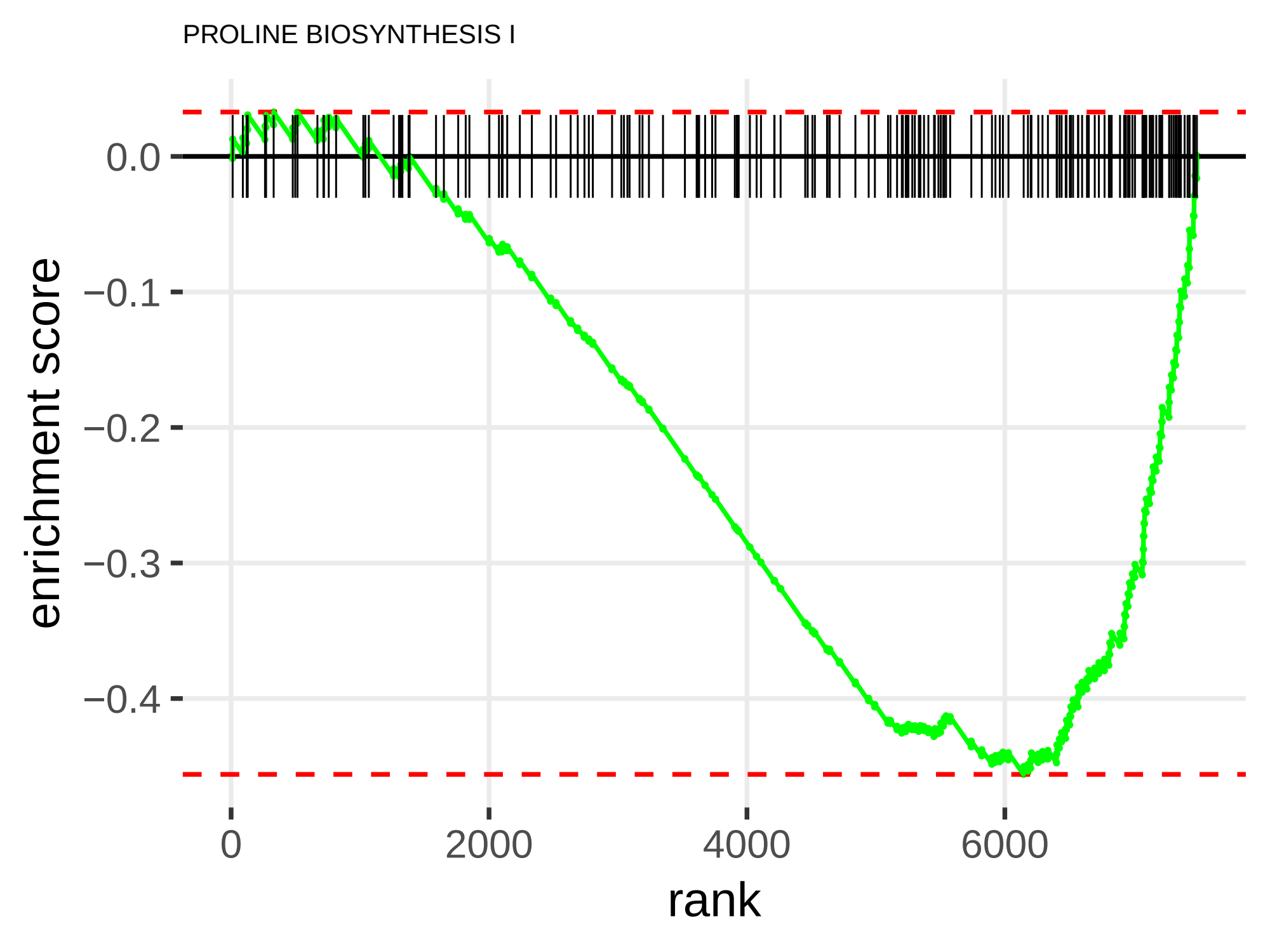

GDP−GLUCOSE BIOSYNTHESIS
0.0
−0.1
−0.2
−0.3
−0.4
enrichment score
0
2000
4000
6000
rank

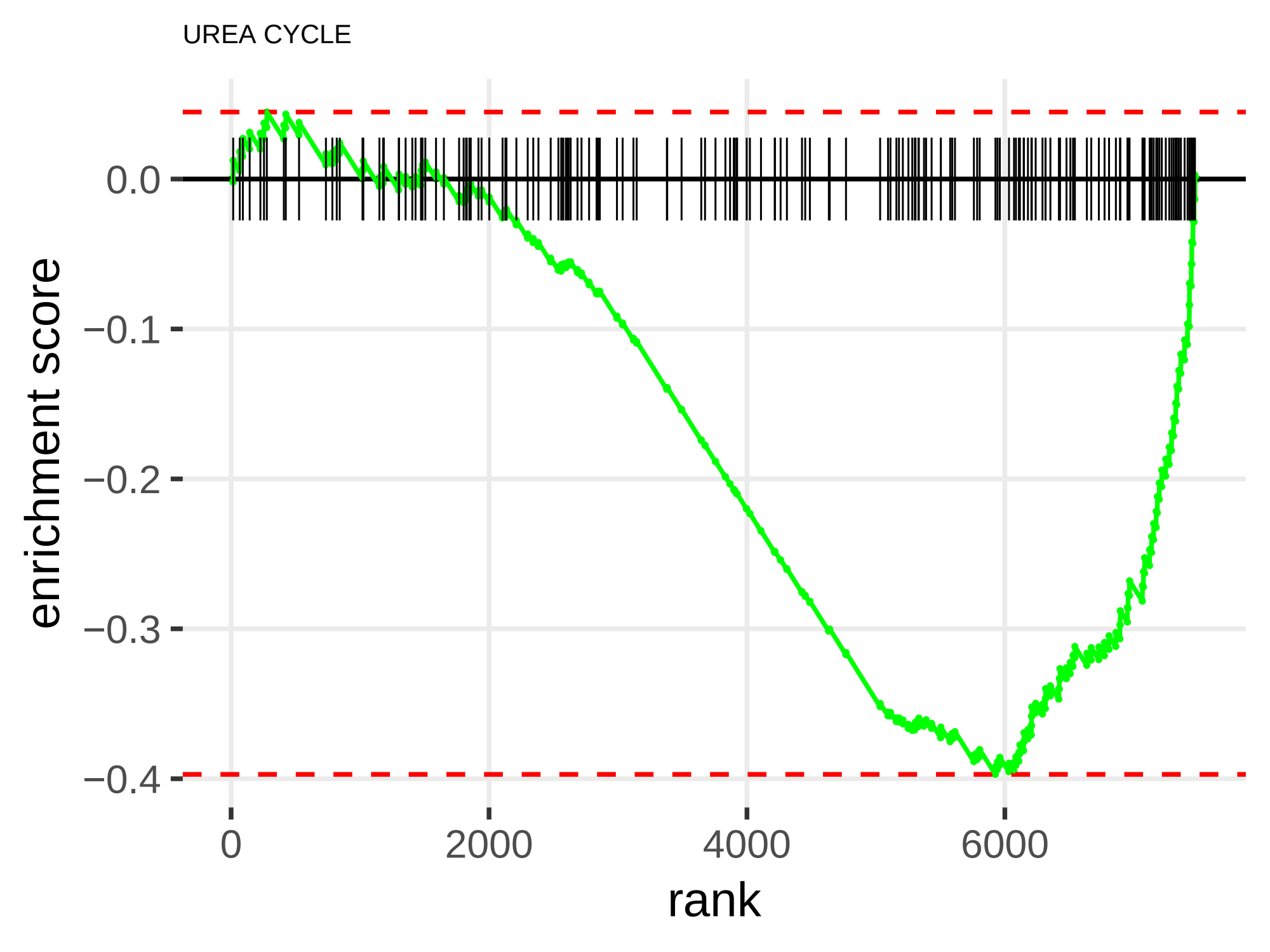

LEUCINE DEGRADATION I
0.0
−0.1
−0.2
−0.3
−0.4
enrichment score
0
2000
4000
6000
rank

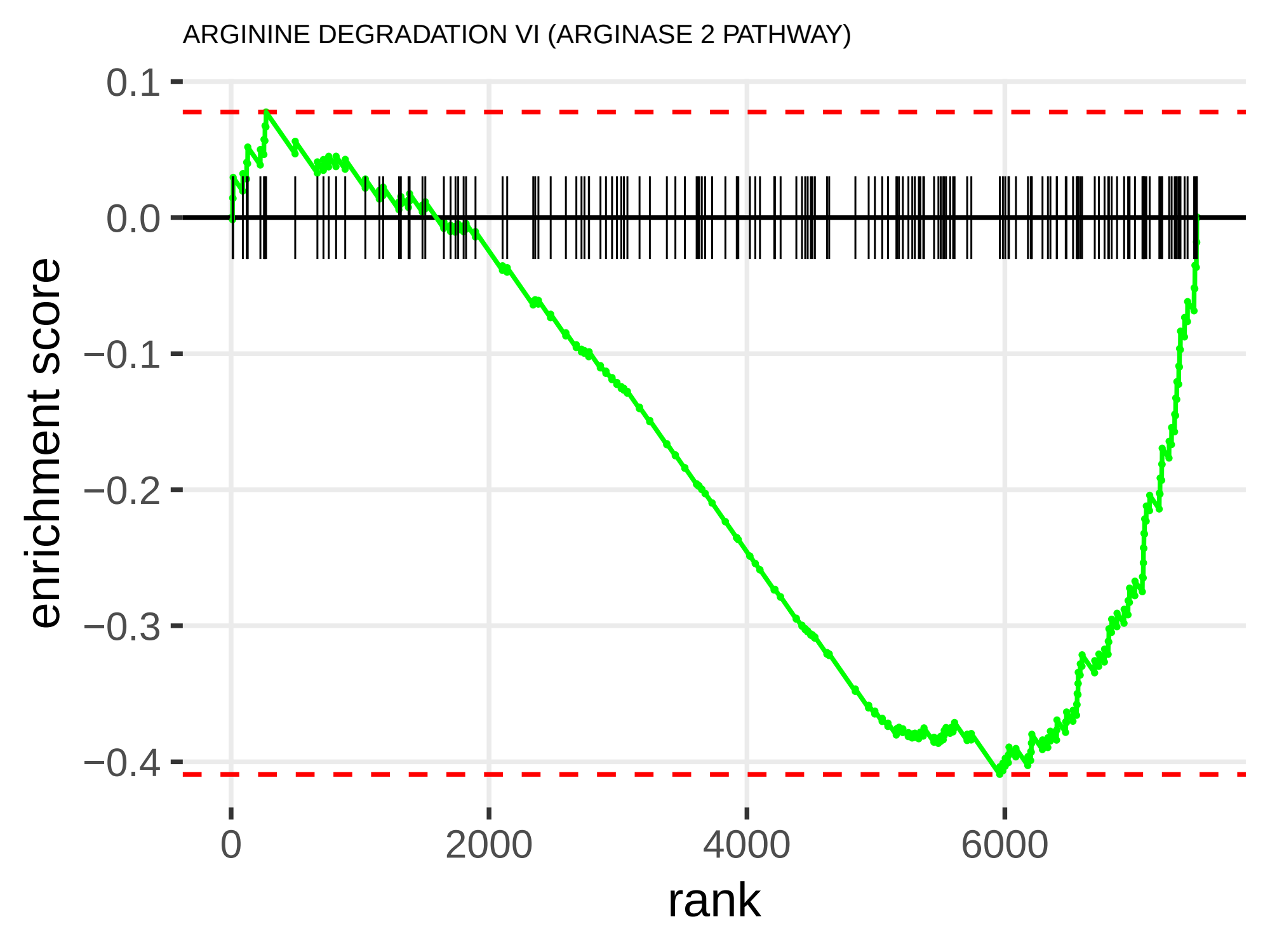

METHIONINE DEGRADATION I (TO HOMOCYSTEINE)
0.0
−0.1
−0.2
−0.3
−0.4
enrichment score
0
2000
4000
6000
rank

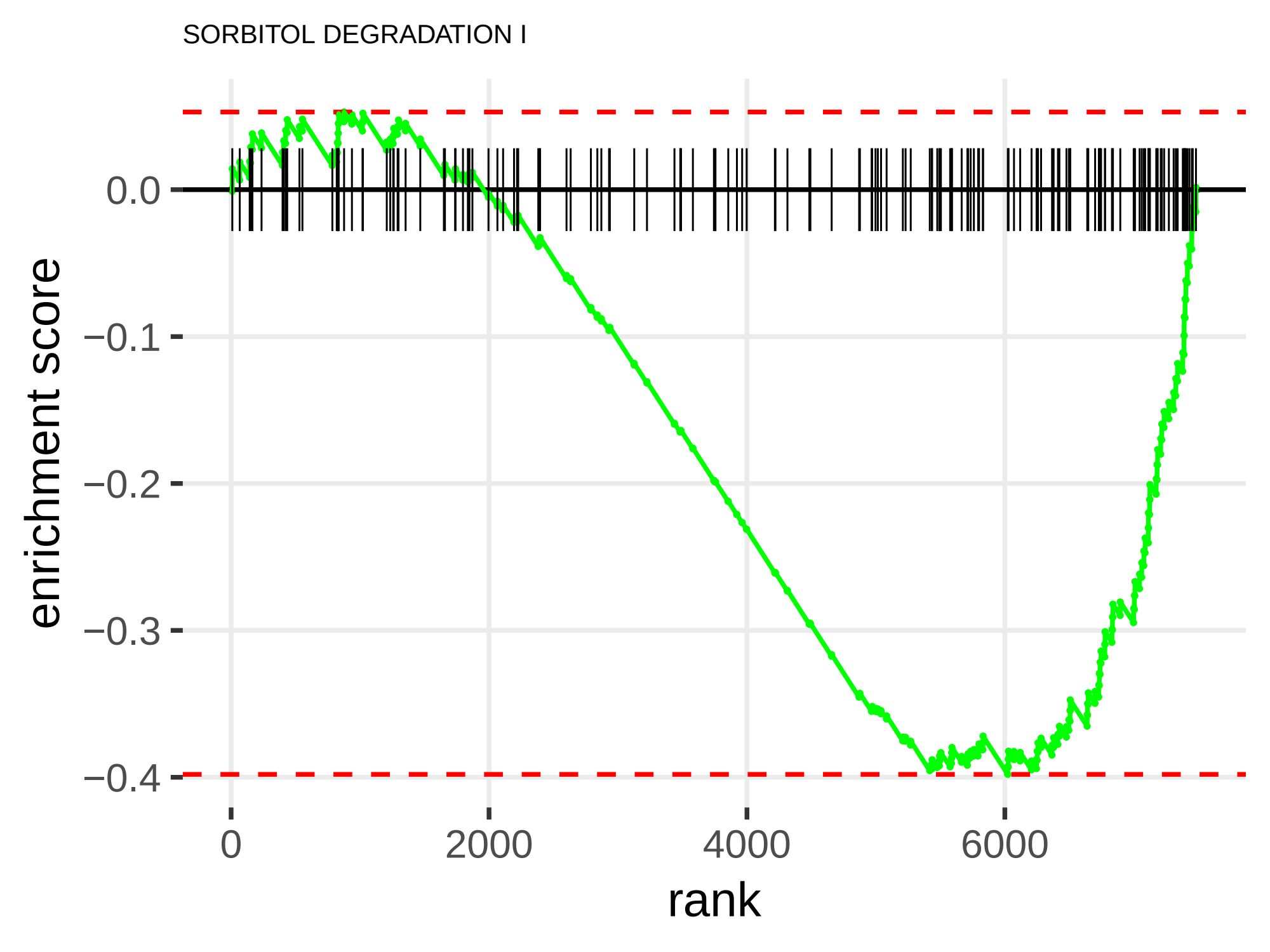

GDP−MANNOSE BIOSYNTHESIS
0.0
−0.1
−0.2
−0.3
−0.4
enrichment score
0
2000
4000
6000
rank

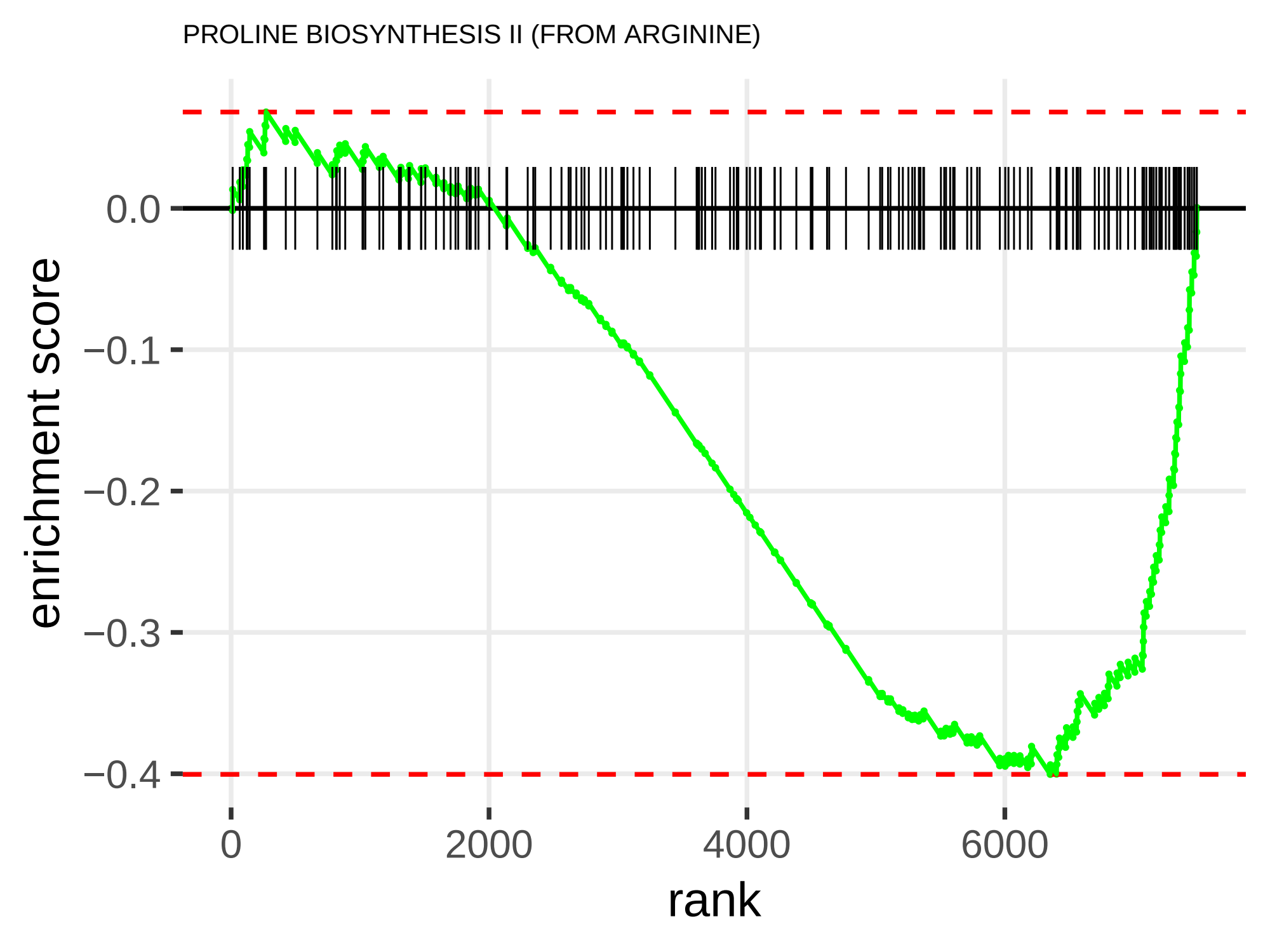

TREHALOSE DEGRADATION II (TREHALASE)
0.0
−0.1
−0.2
−0.3
−0.4
enrichment score
0
2000
4000
6000
rank

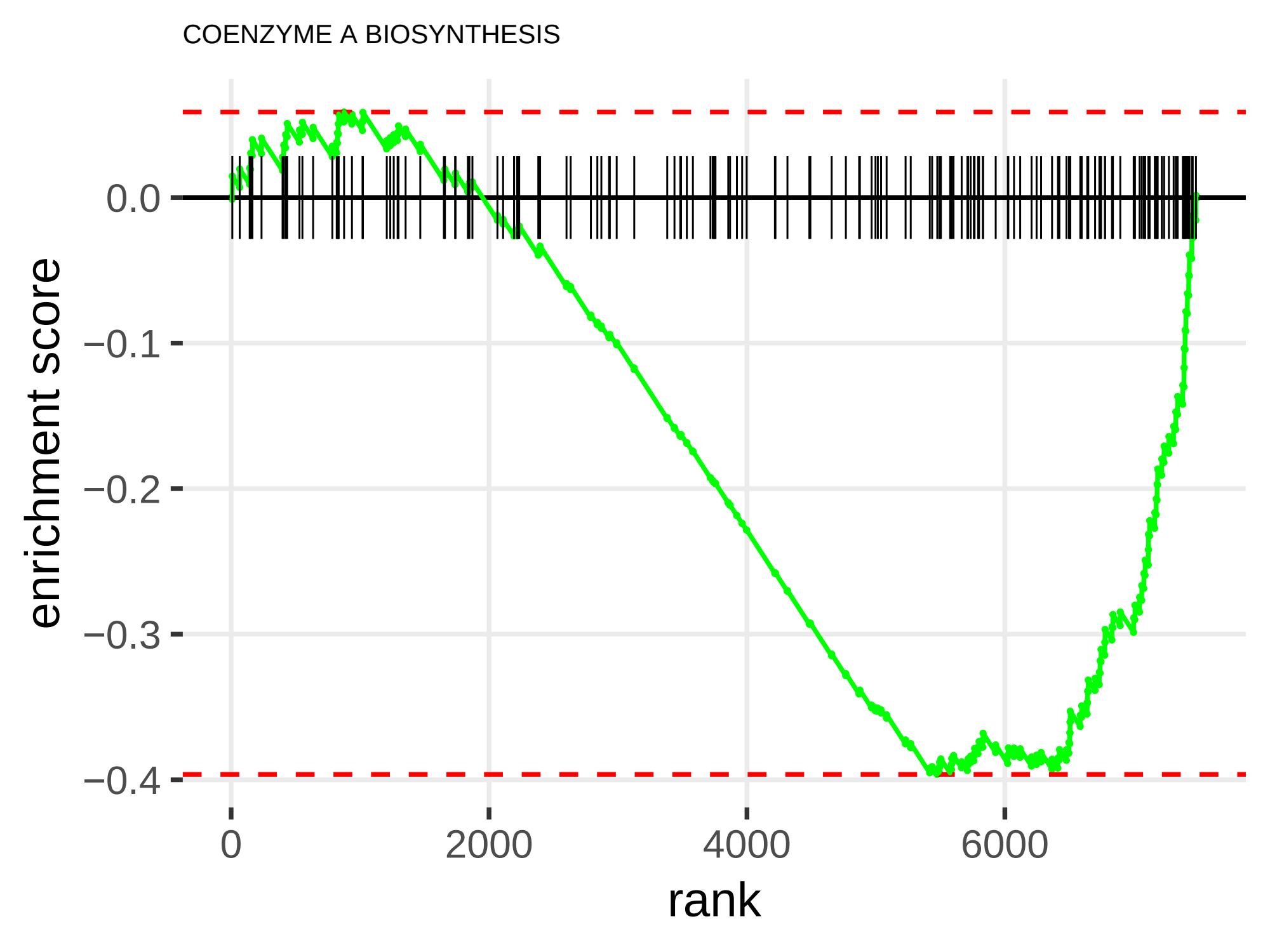

PROLINE BIOSYNTHESIS I
0.0
−0.1
−0.2
−0.3
−0.4
enrichment score
0
2000
4000
6000
rank

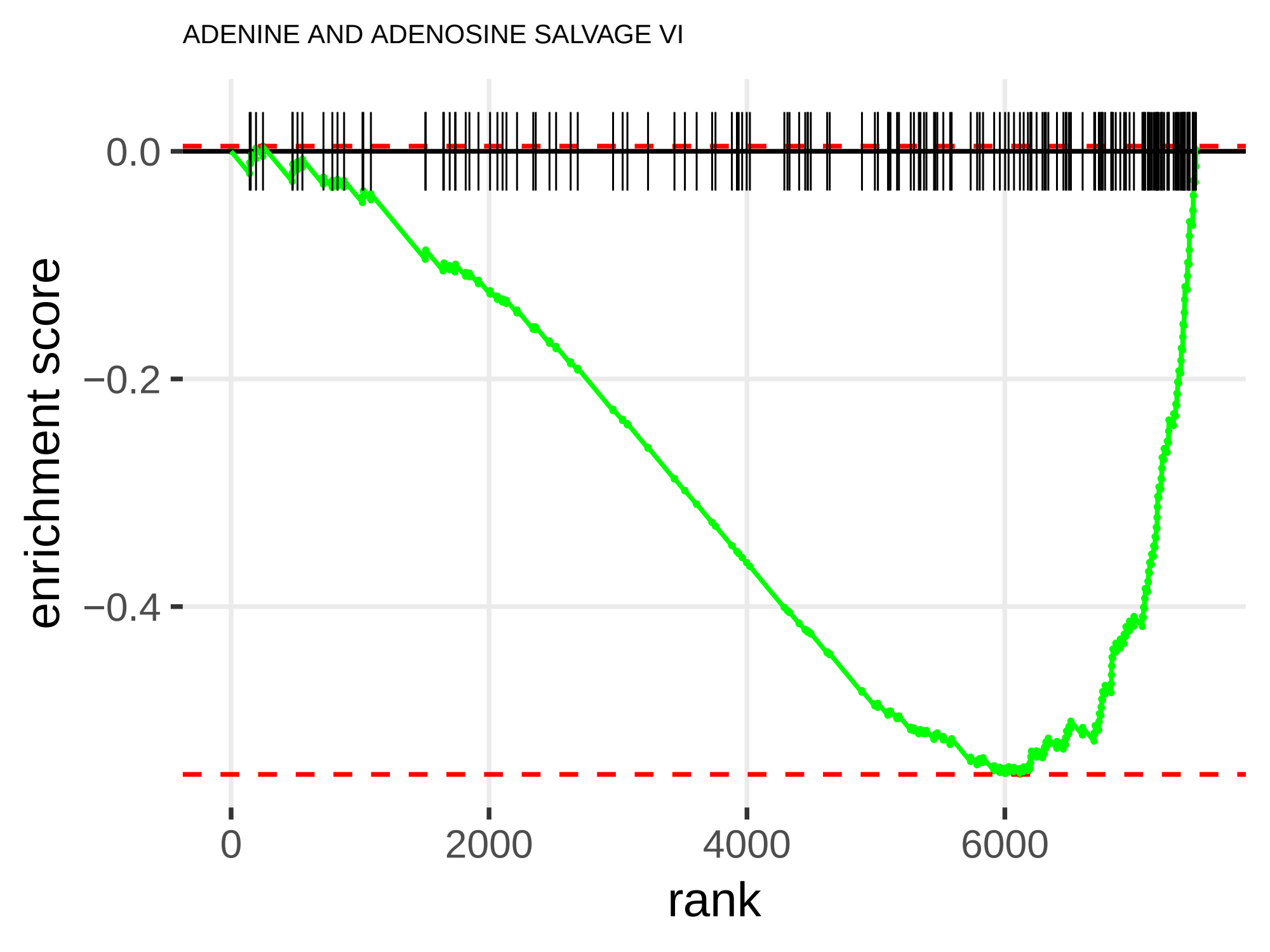

UREA CYCLE
0.0
−0.1
−0.2
−0.3
−0.4
enrichment score
0
2000
4000
6000
rank

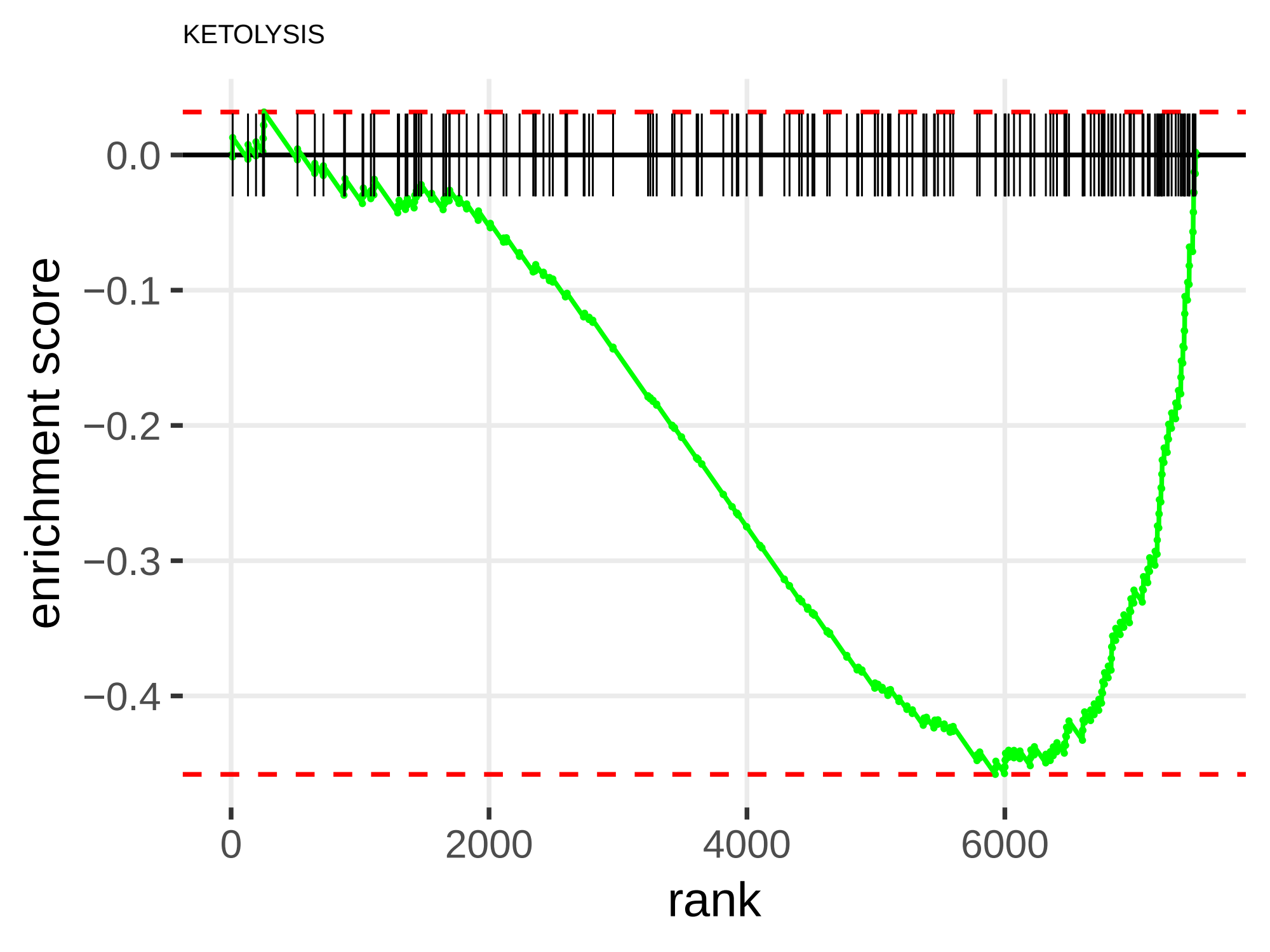

ARGININE DEGRADATION VI (ARGINASE 2 PATHWAY)
0.1
0.0
−0.1
−0.2
−0.3
−0.4
enrichment score
0
2000
4000
6000
rank

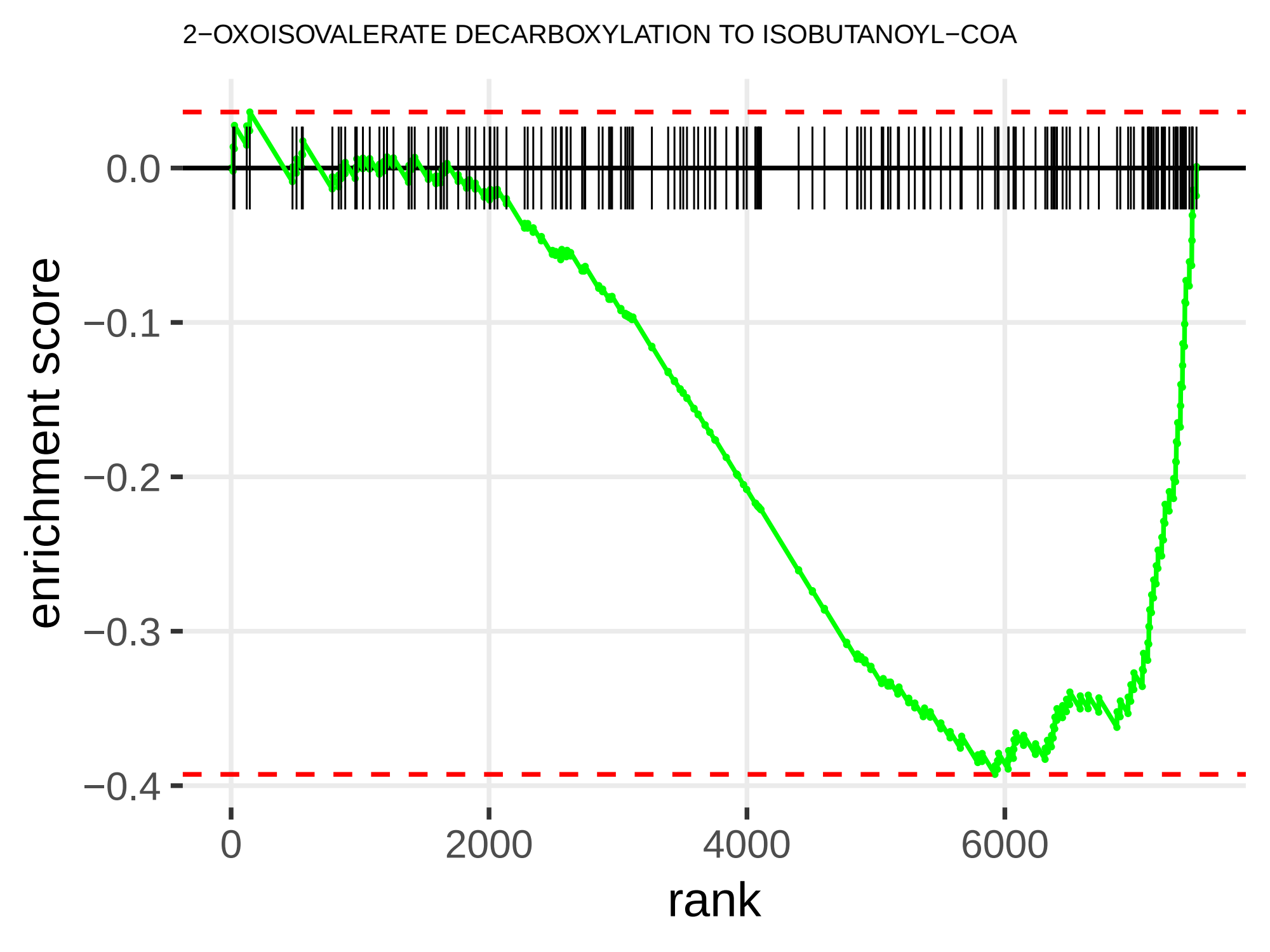

SORBITOL DEGRADATION I
enrichment score
0.0
−0.1
−0.2
−0.3
−0.4
0
2000
4000
6000
rank

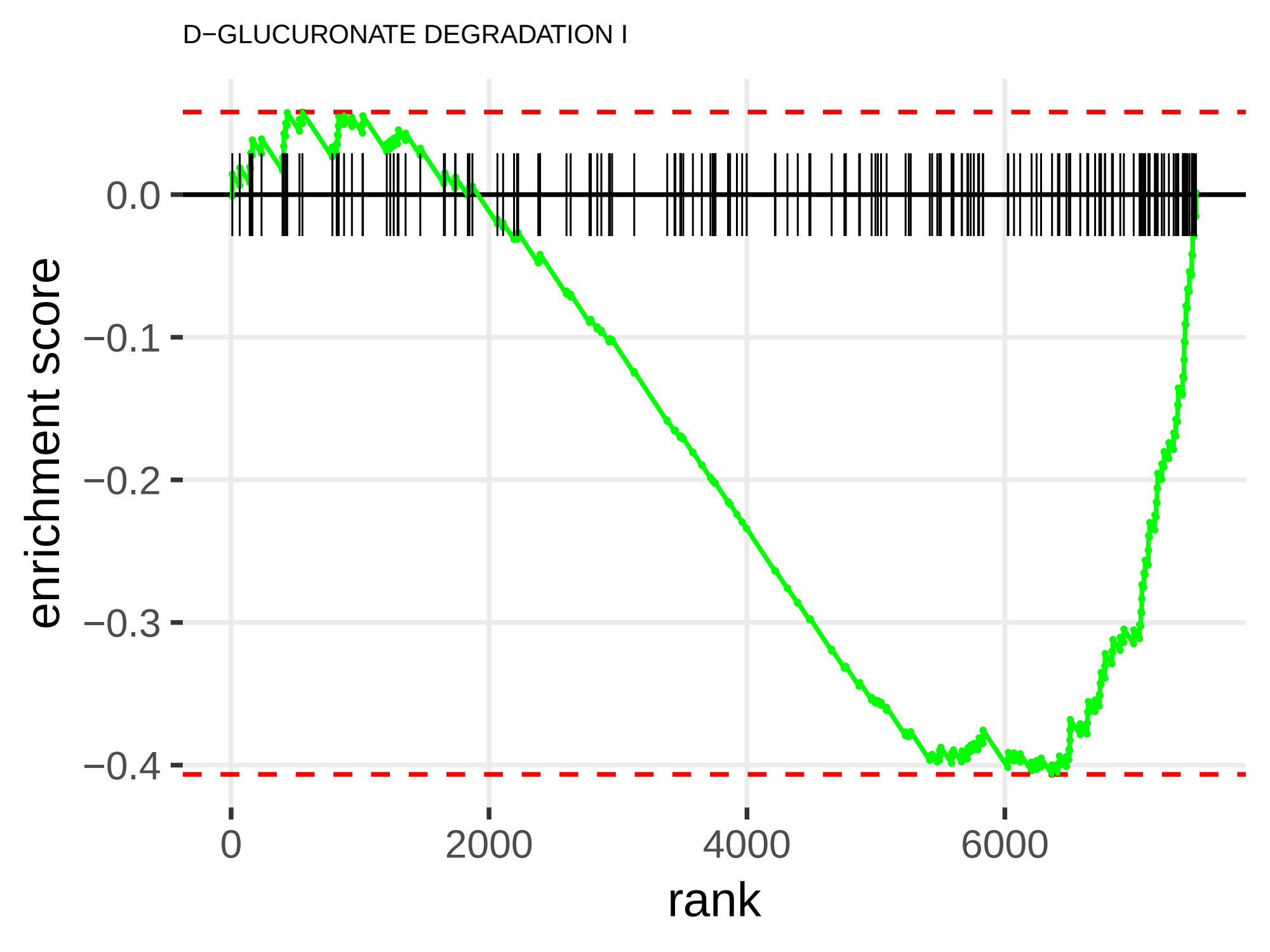

PROLINE BIOSYNTHESIS II (FROM ARGININE)
0.0
−0.1
−0.2
−0.3
−0.4
enrichment score
0
2000
4000
6000
rank

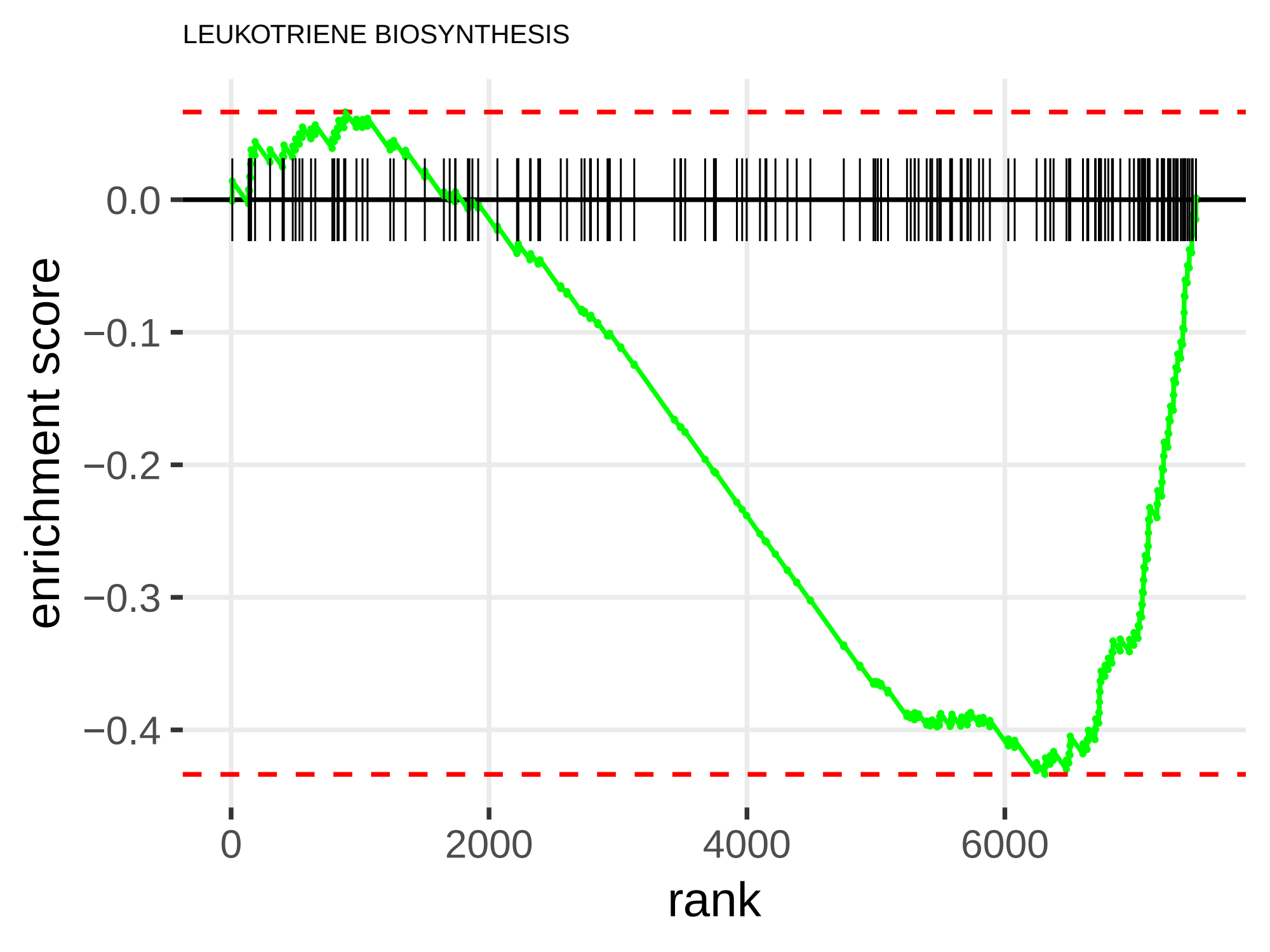

COENZYME A BIOSYNTHESIS
0.0
−0.1
−0.2
−0.3
−0.4
enrichment score
0
2000
4000
6000
rank

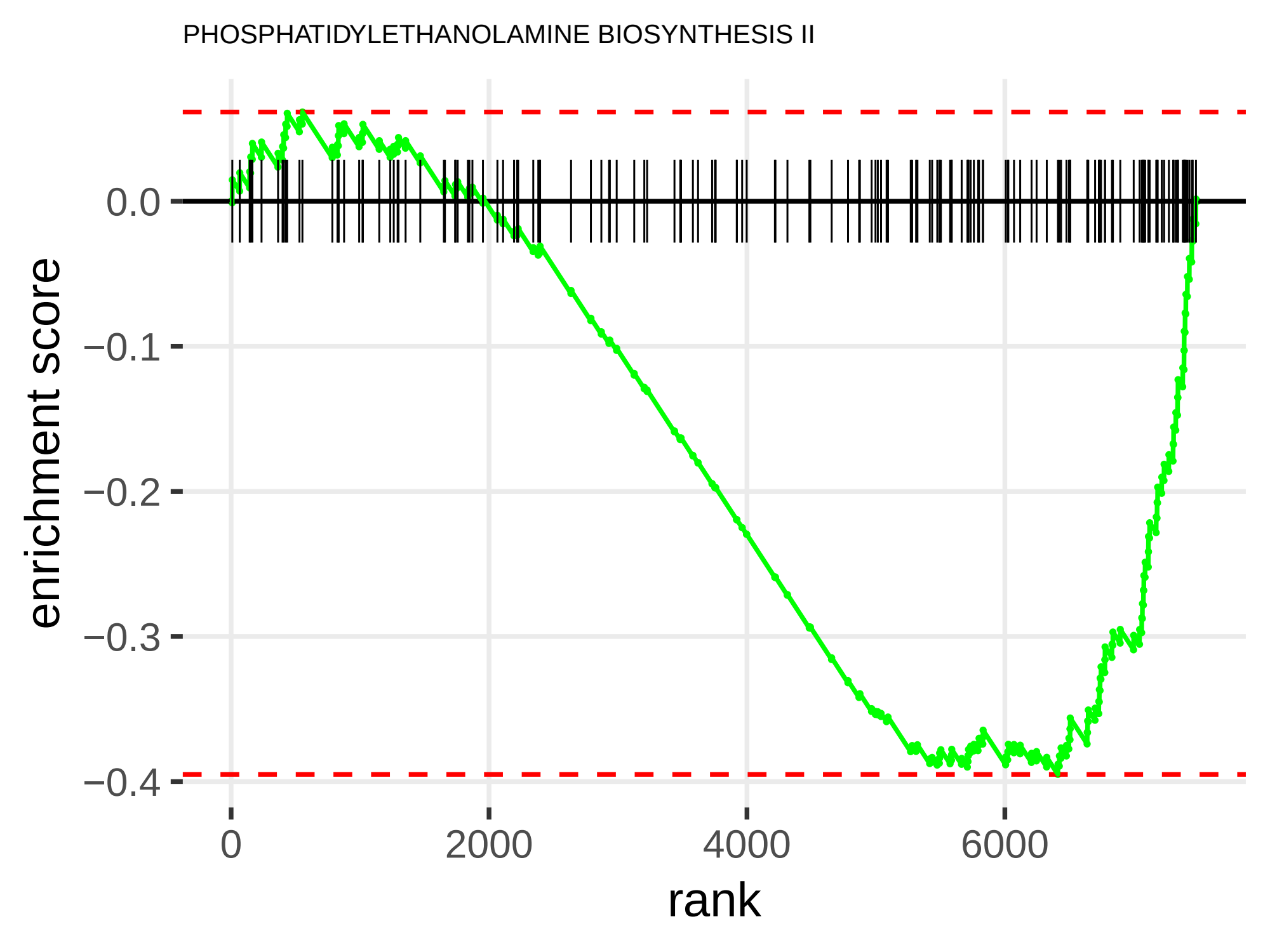

ADENINE AND ADENOSINE SALVAGE VI
0.0
−0.2
−0.4
enrichment score
0
2000
4000
6000
rank

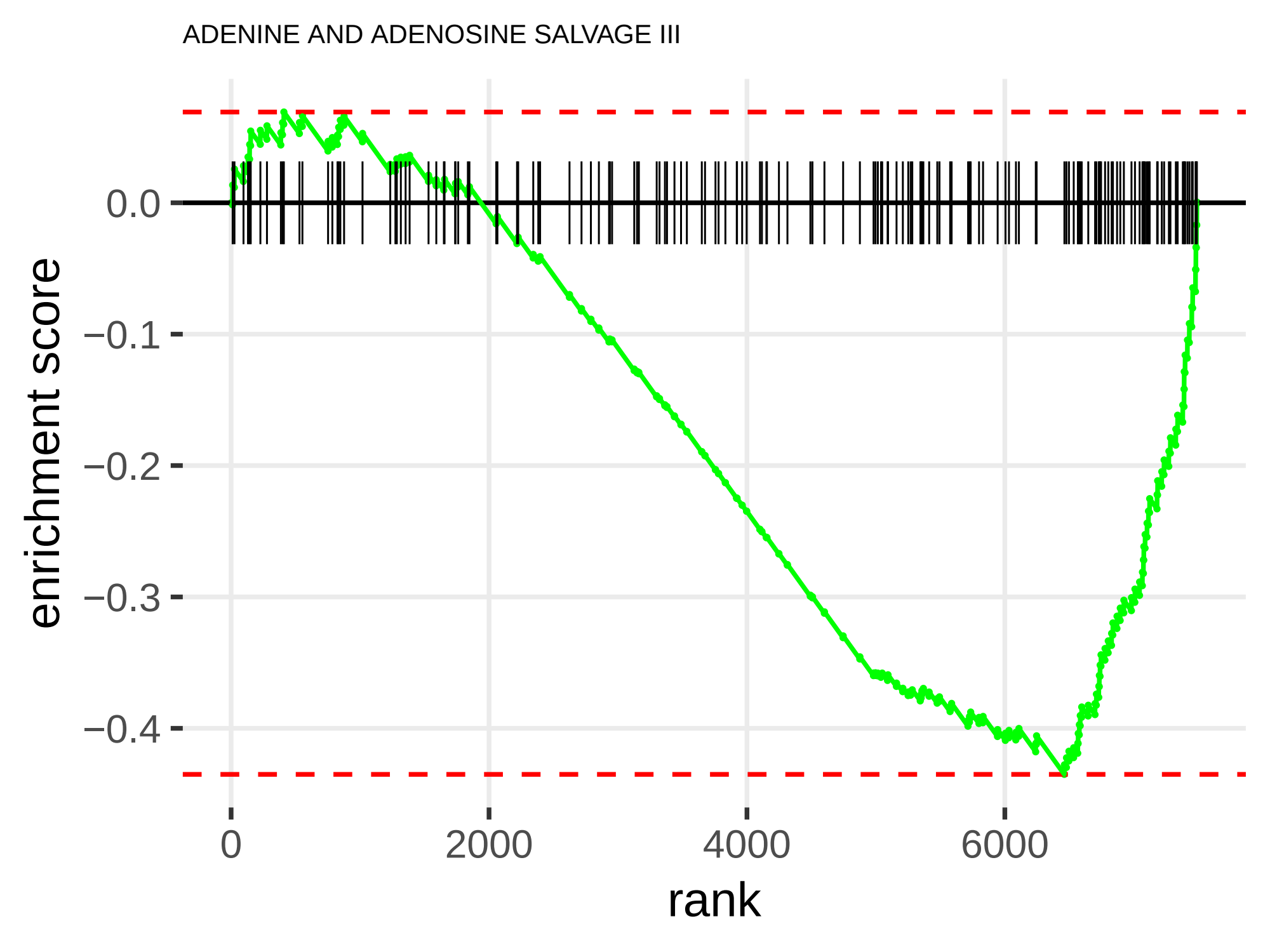

KETOLYSIS
0.0
−0.1
−0.2
−0.3
−0.4
enrichment score
0
2000
4000
6000
rank

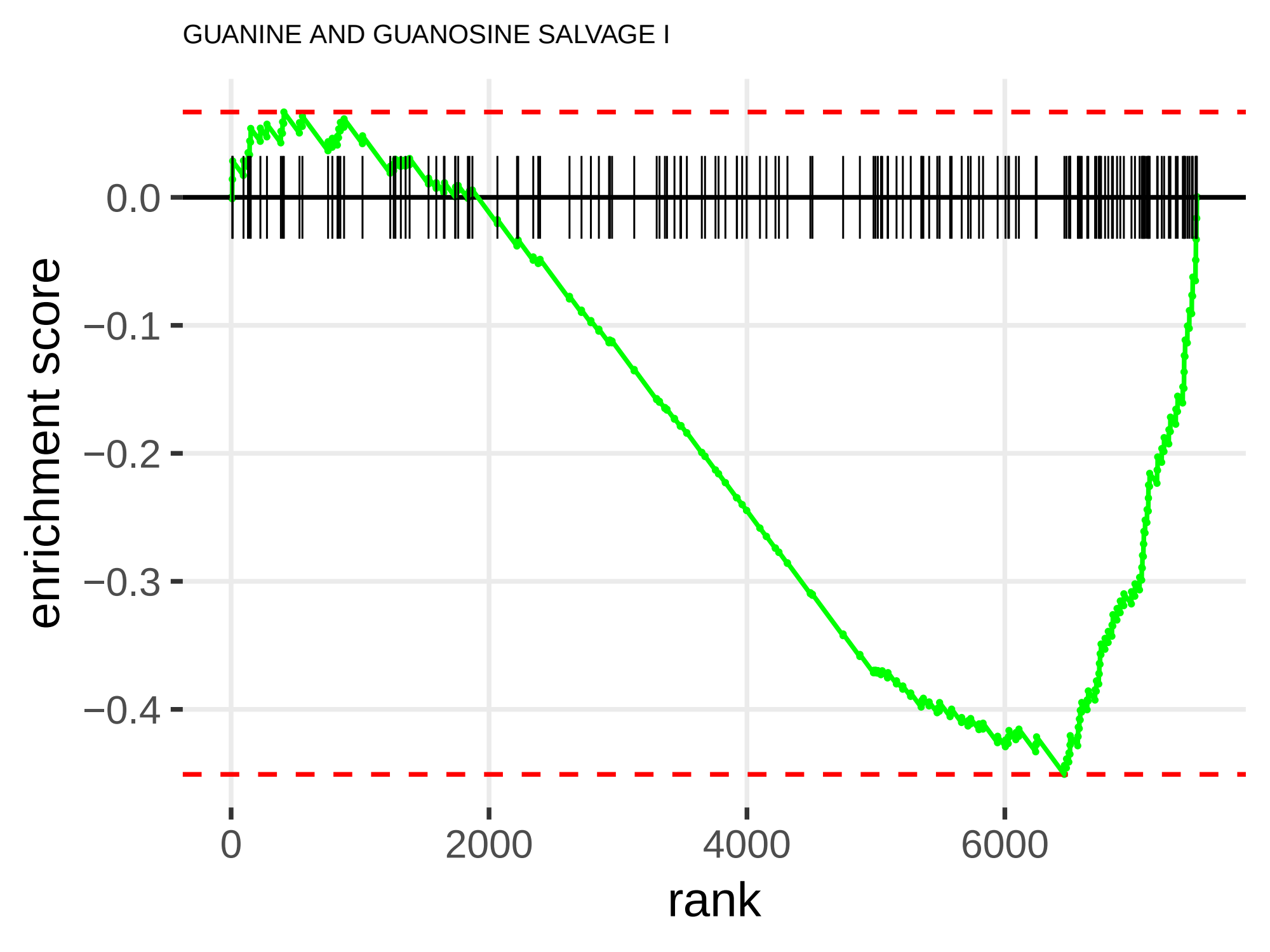

2−OXOISOVALERATE DECARBOXYLATION TO ISOBUTANOYL−COA
0.0
−0.1
−0.2
−0.3
−0.4
enrichment score
0
2000
4000
6000
rank

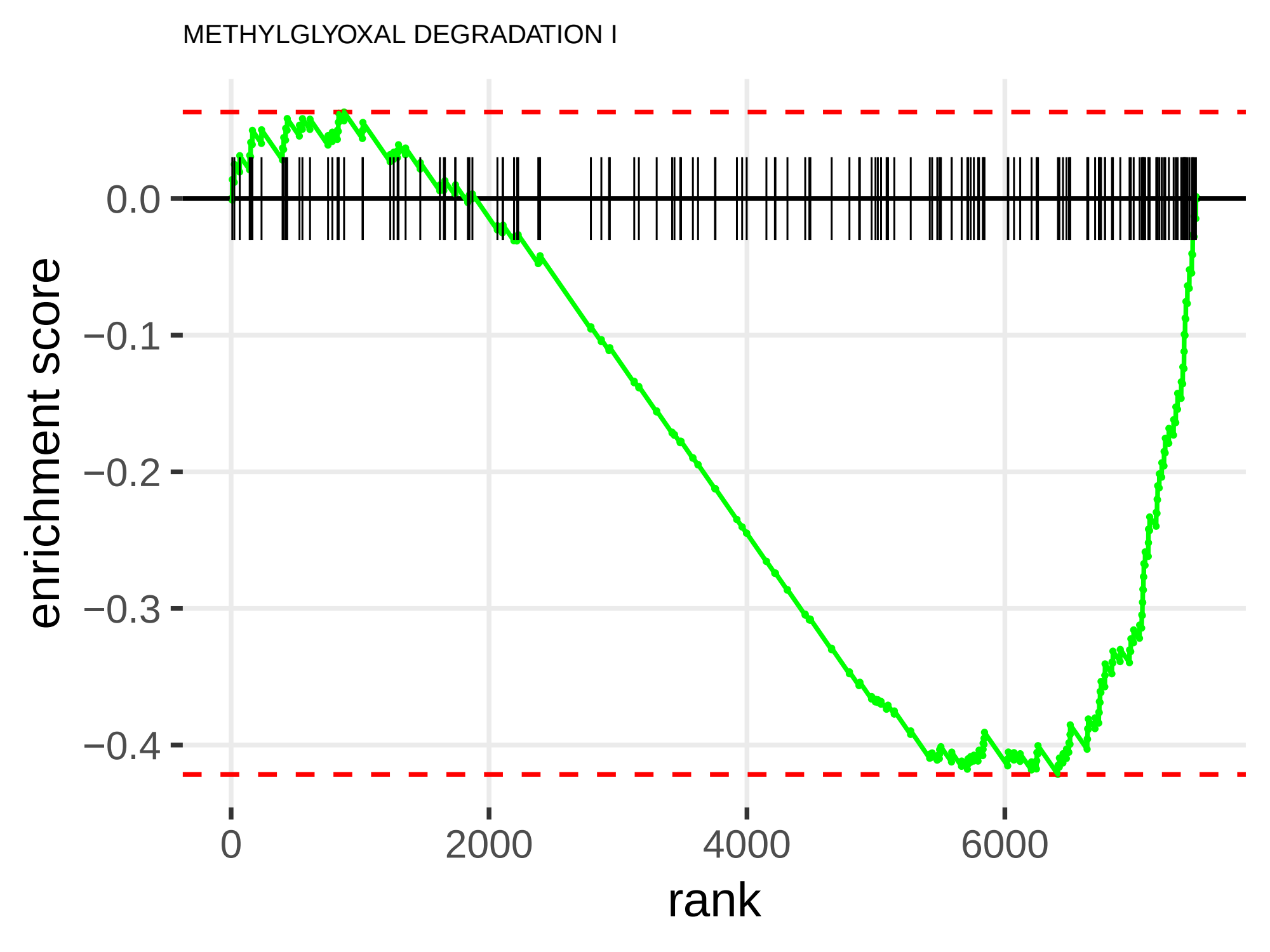

D−GLUCURONATE DEGRADATION I
0.0
−0.1
−0.2
−0.3
−0.4
enrichment score
0
2000
4000
6000
rank

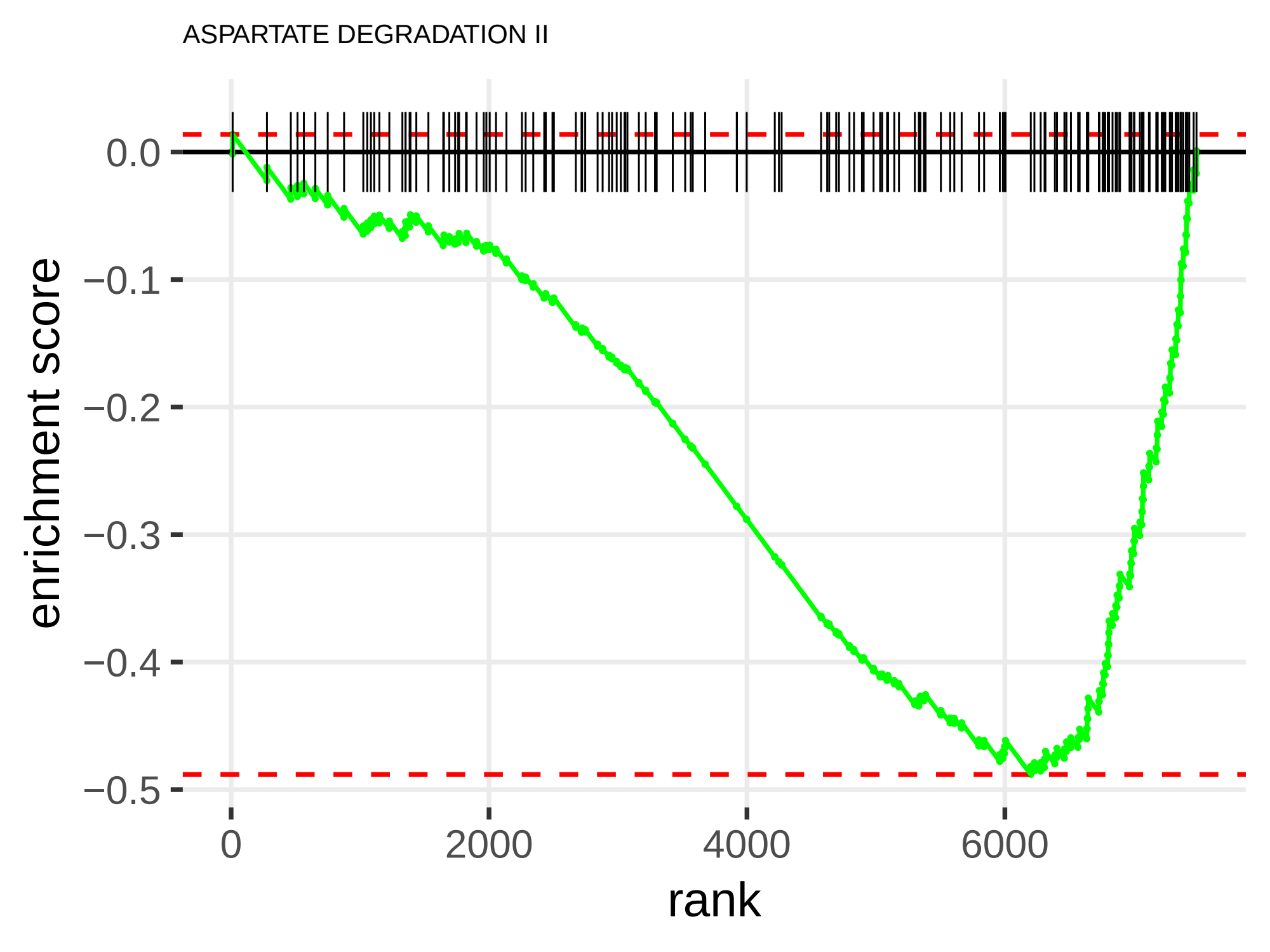

LEUKOTRIENE BIOSYNTHESIS
enrichment score
0.0
−0.1
−0.2
−0.3
−0.4
0
2000
4000
6000
rank

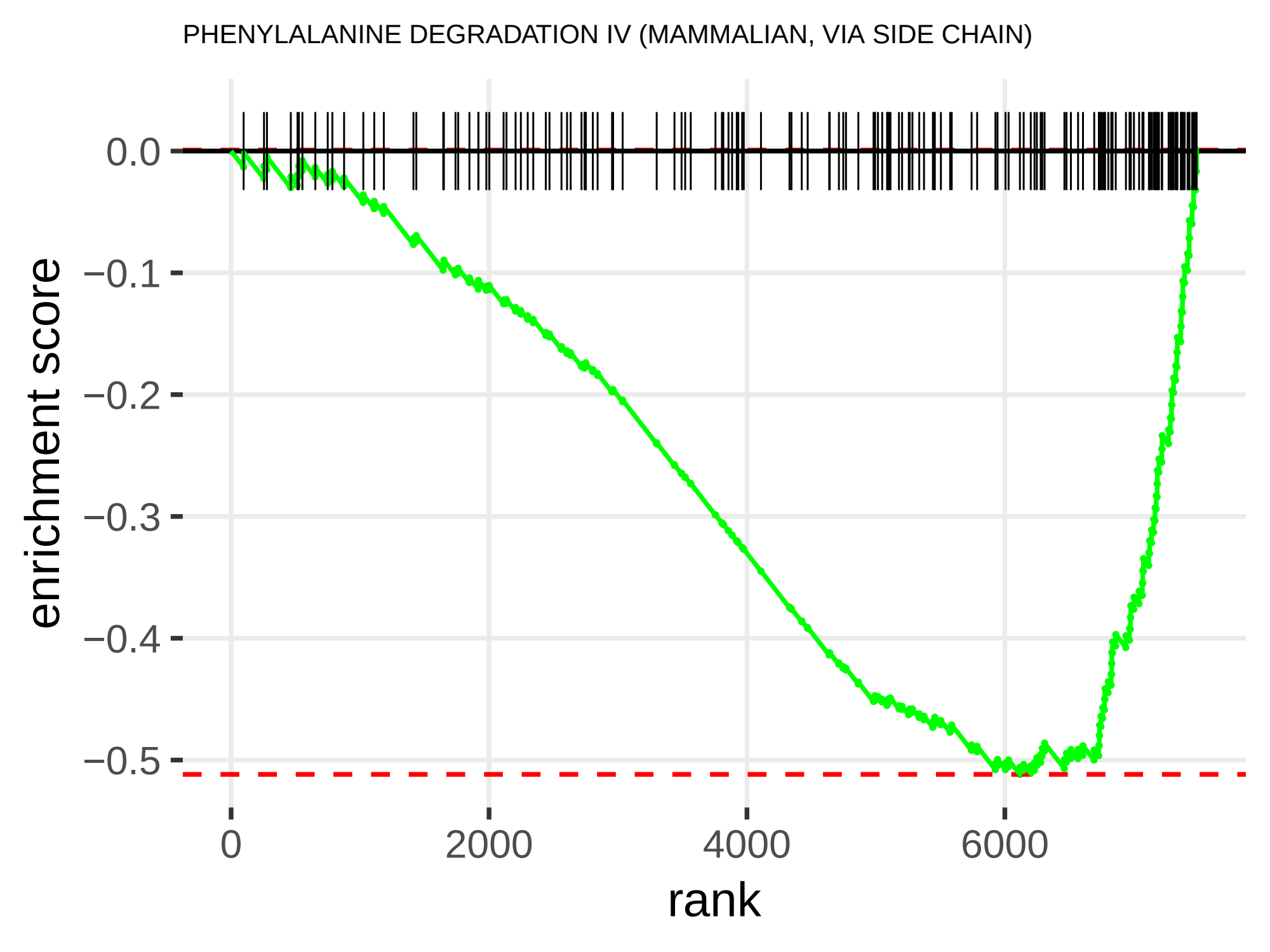

PHOSPHATIDYLETHANOLAMINE BIOSYNTHESIS II
enrichment score
0.0
−0.1
−0.2
−0.3
−0.4
0
2000
4000
6000
rank

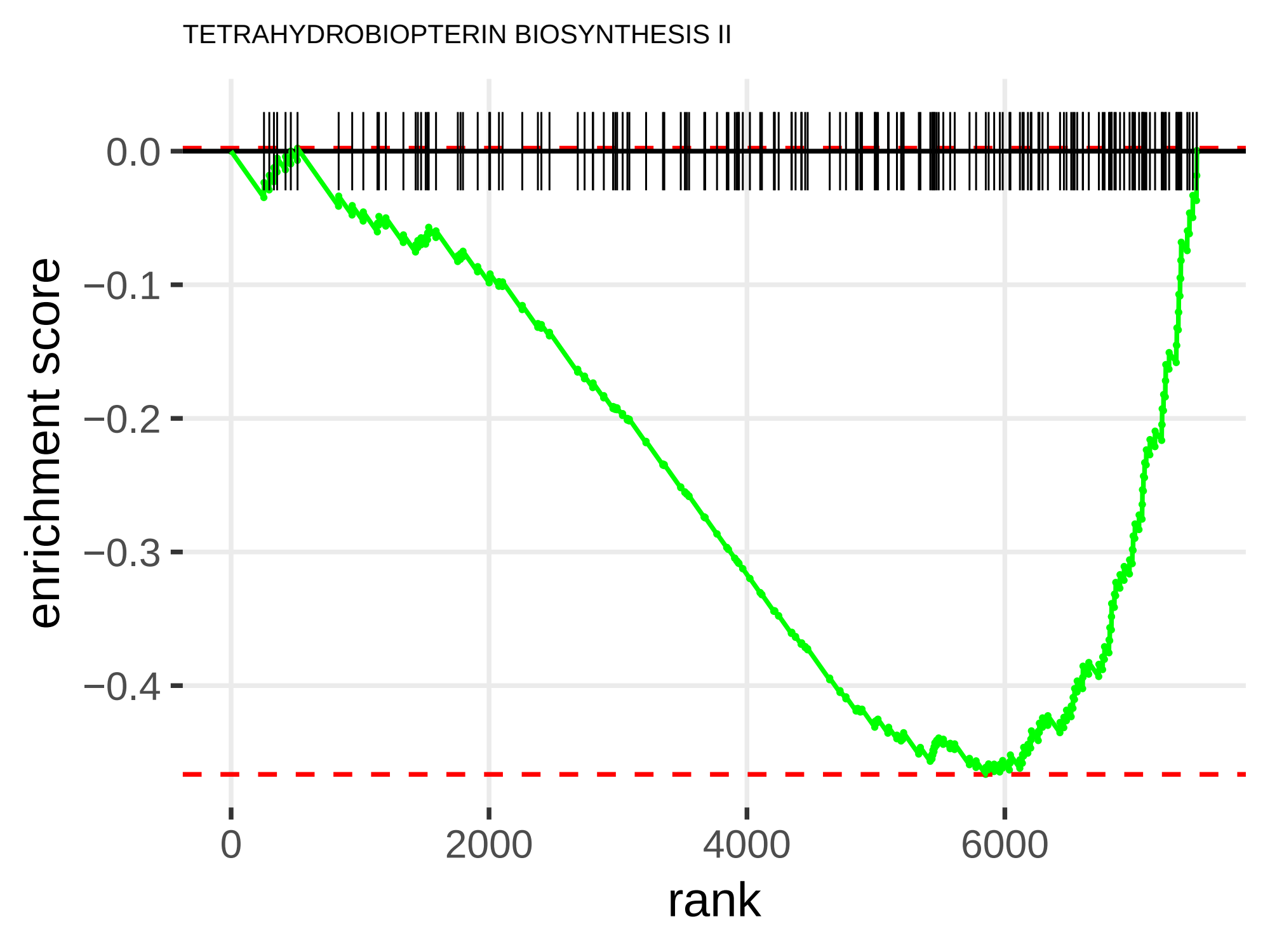

ADENINE AND ADENOSINE SALVAGE III
0.0
−0.1
−0.2
−0.3
−0.4
enrichment score
0
2000
4000
6000
rank

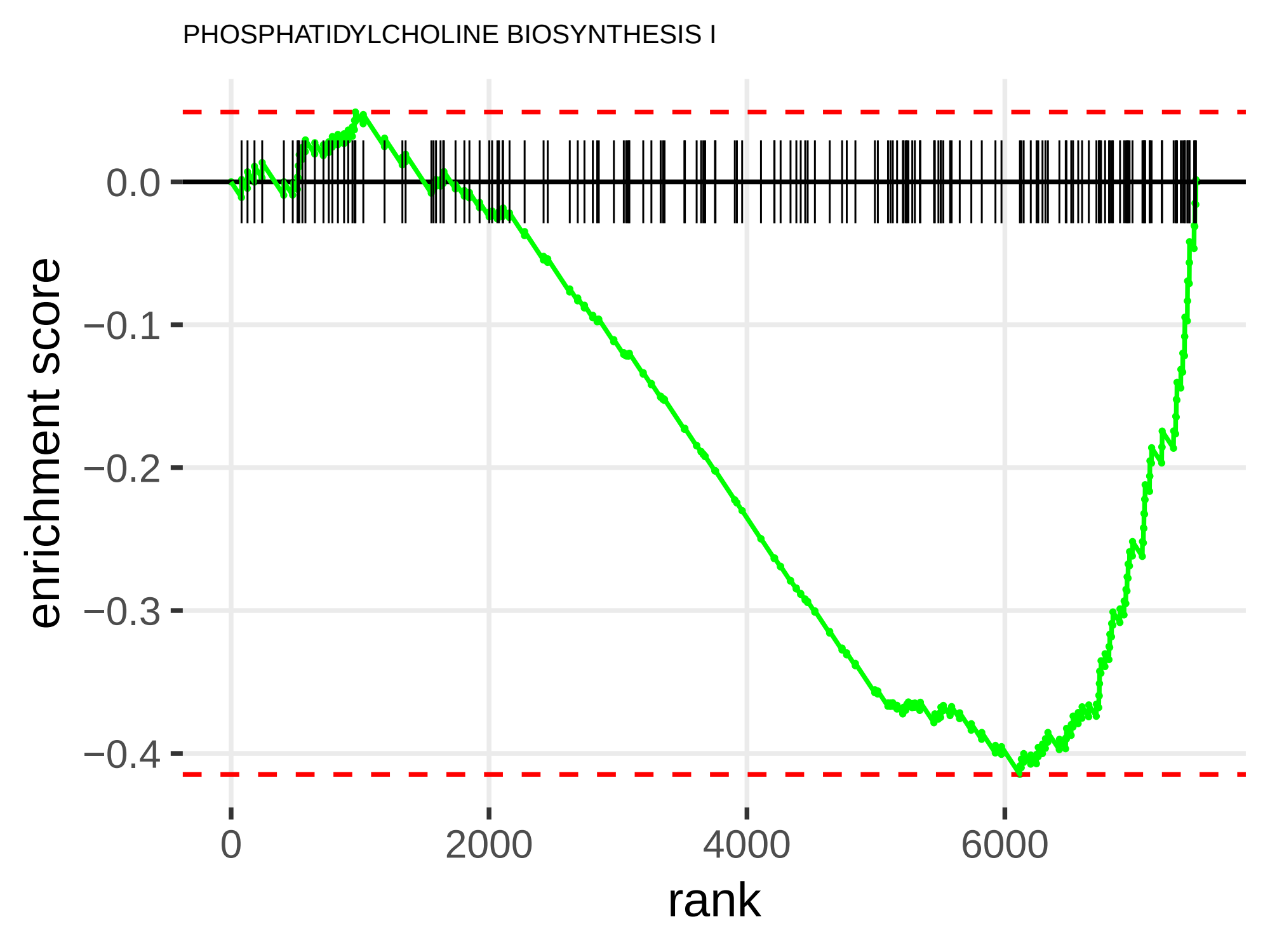

GUANINE AND GUANOSINE SALVAGE I
0.0
−0.1
−0.2
−0.3
−0.4
enrichment score
0
2000
4000
6000
rank

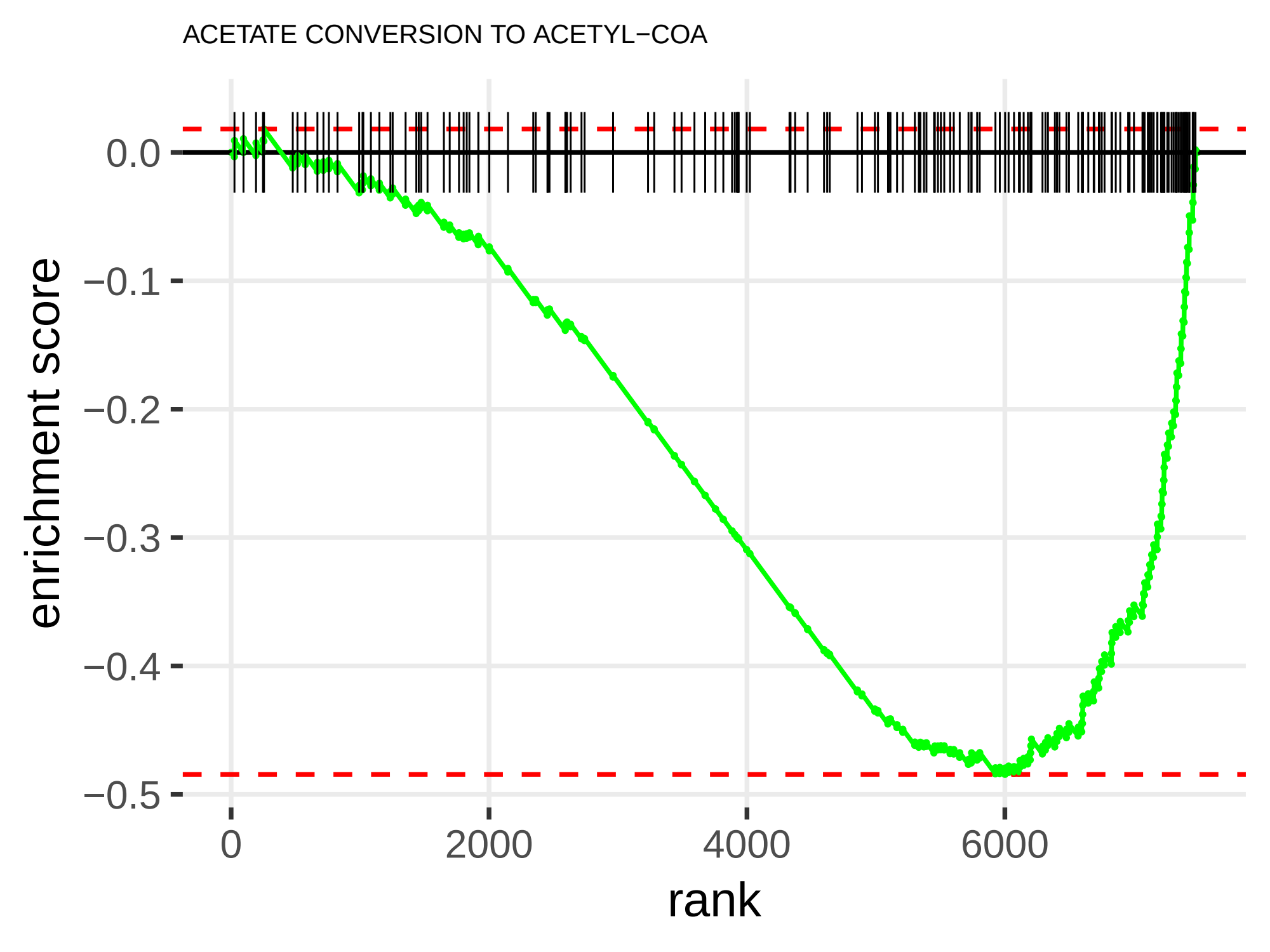

METHYLGLYOXAL DEGRADATION I
0.0
−0.1
−0.2
−0.3
−0.4
enrichment score
0
2000
4000
6000
rank

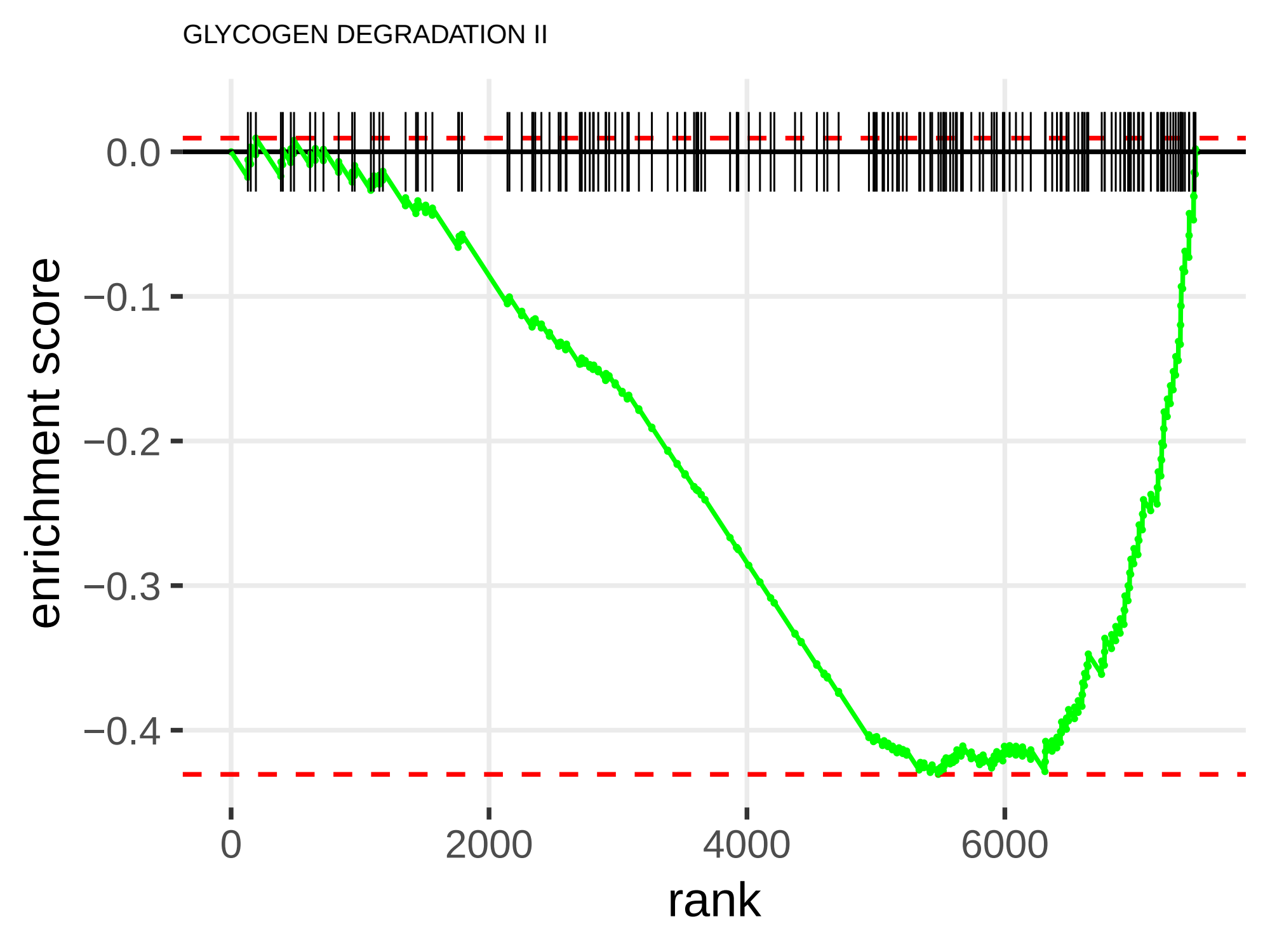

ASPARTATE DEGRADATION II
0.0
−0.1
−0.2
−0.3
−0.4
−0.5
enrichment score
0
2000
4000
6000
rank

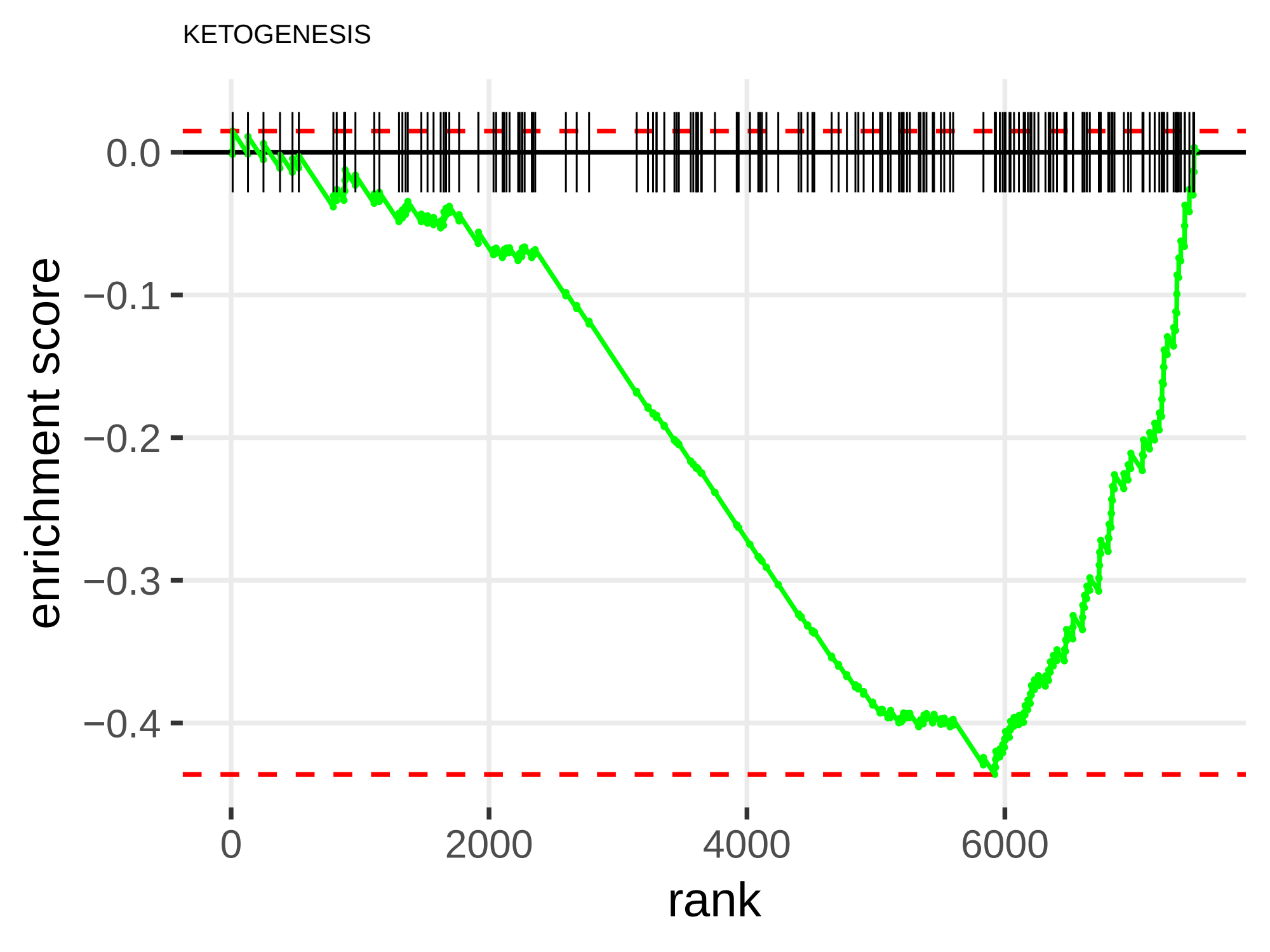

PHENYLALANINE DEGRADATION IV (MAMMALIAN, VIA SIDE CHAIN)
0.0
−0.1
−0.2
−0.3
−0.4
−0.5
enrichment score
0
2000
4000
6000
rank

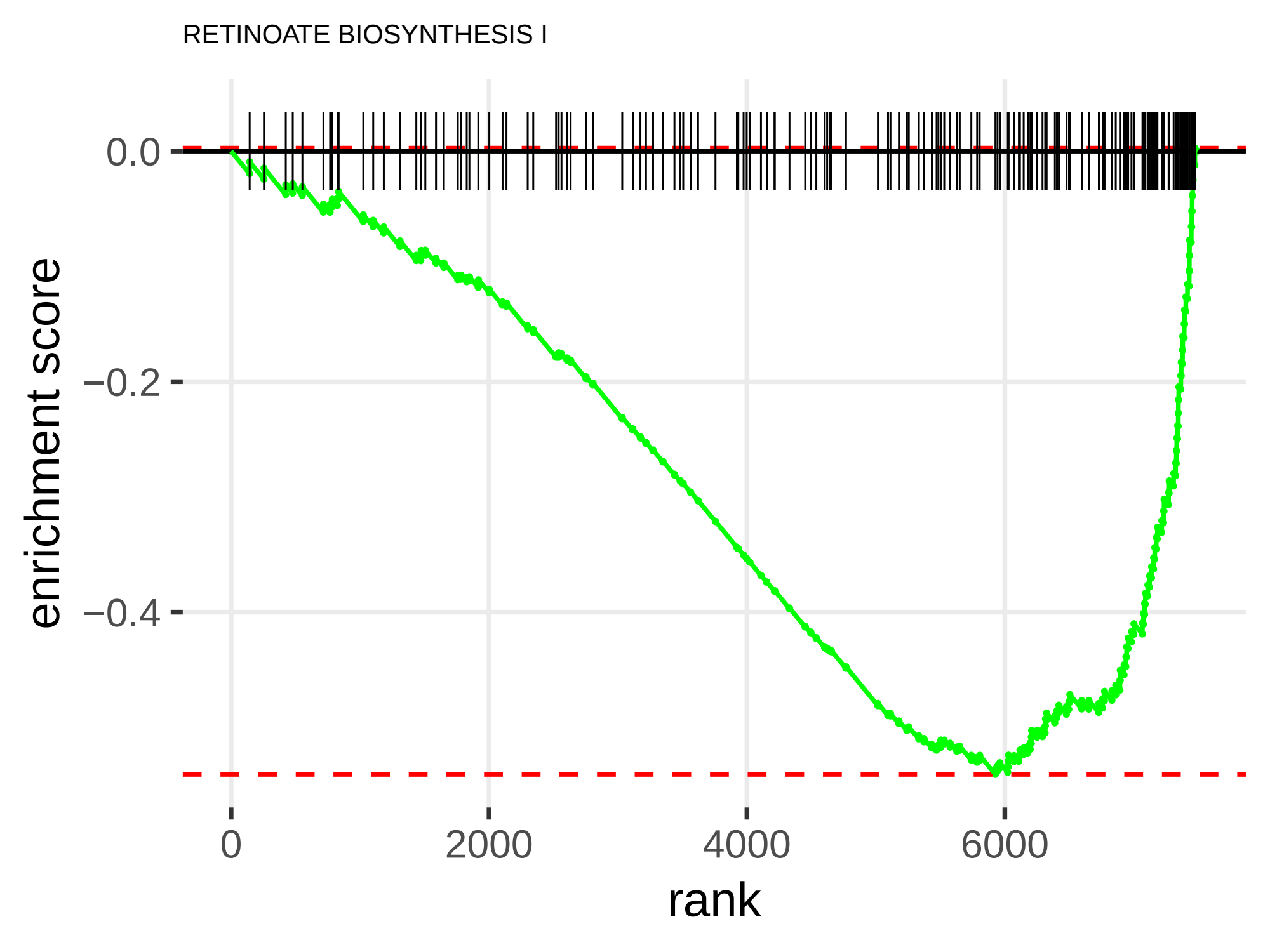

TETRAHYDROBIOPTERIN BIOSYNTHESIS II
0.0
−0.1
−0.2
−0.3
−0.4
enrichment score
0
2000
4000
6000
rank

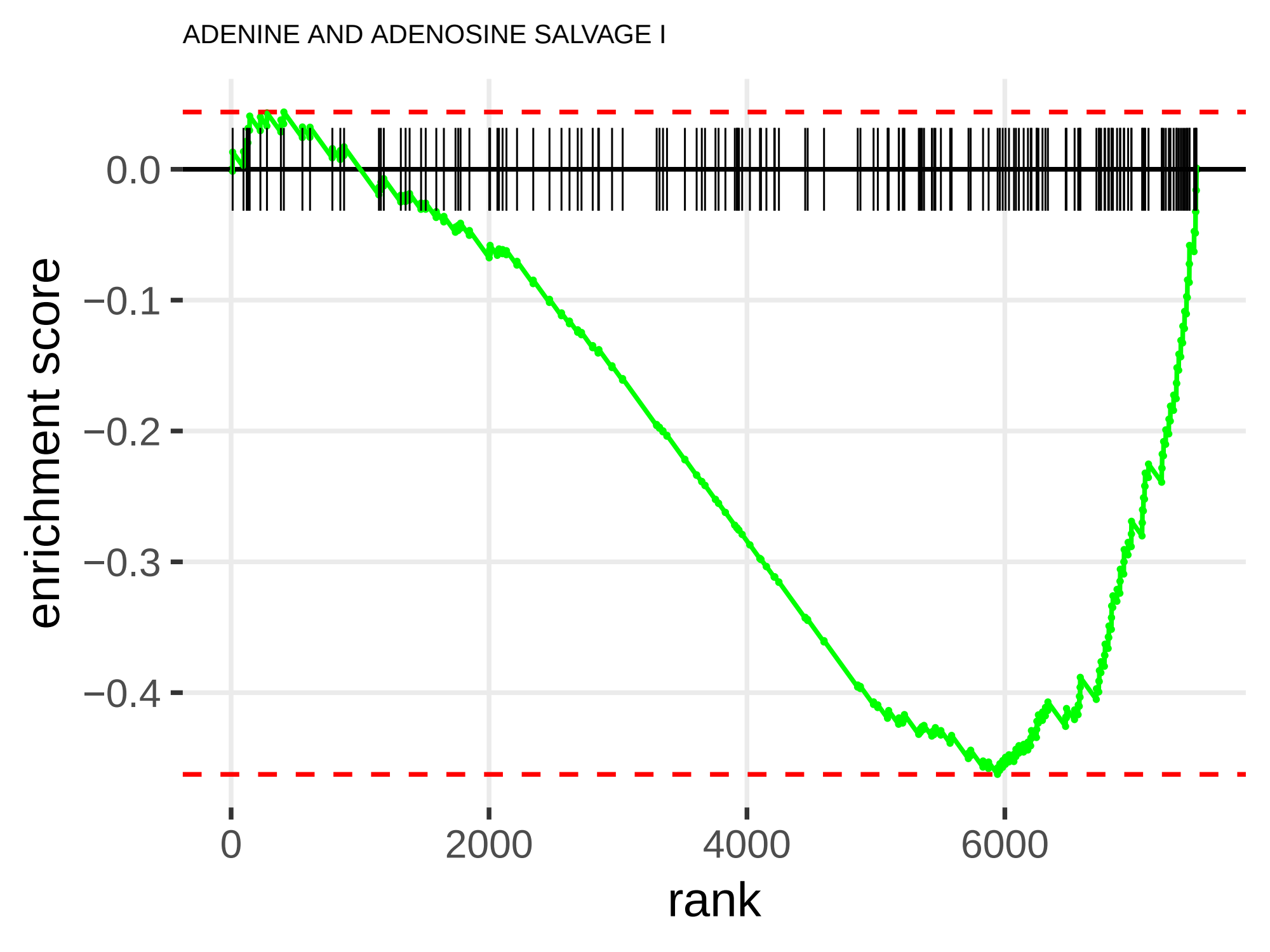

PHOSPHATIDYLCHOLINE BIOSYNTHESIS I
0.0
−0.1
−0.2
−0.3
−0.4
enrichment score
0
2000
4000
6000
rank

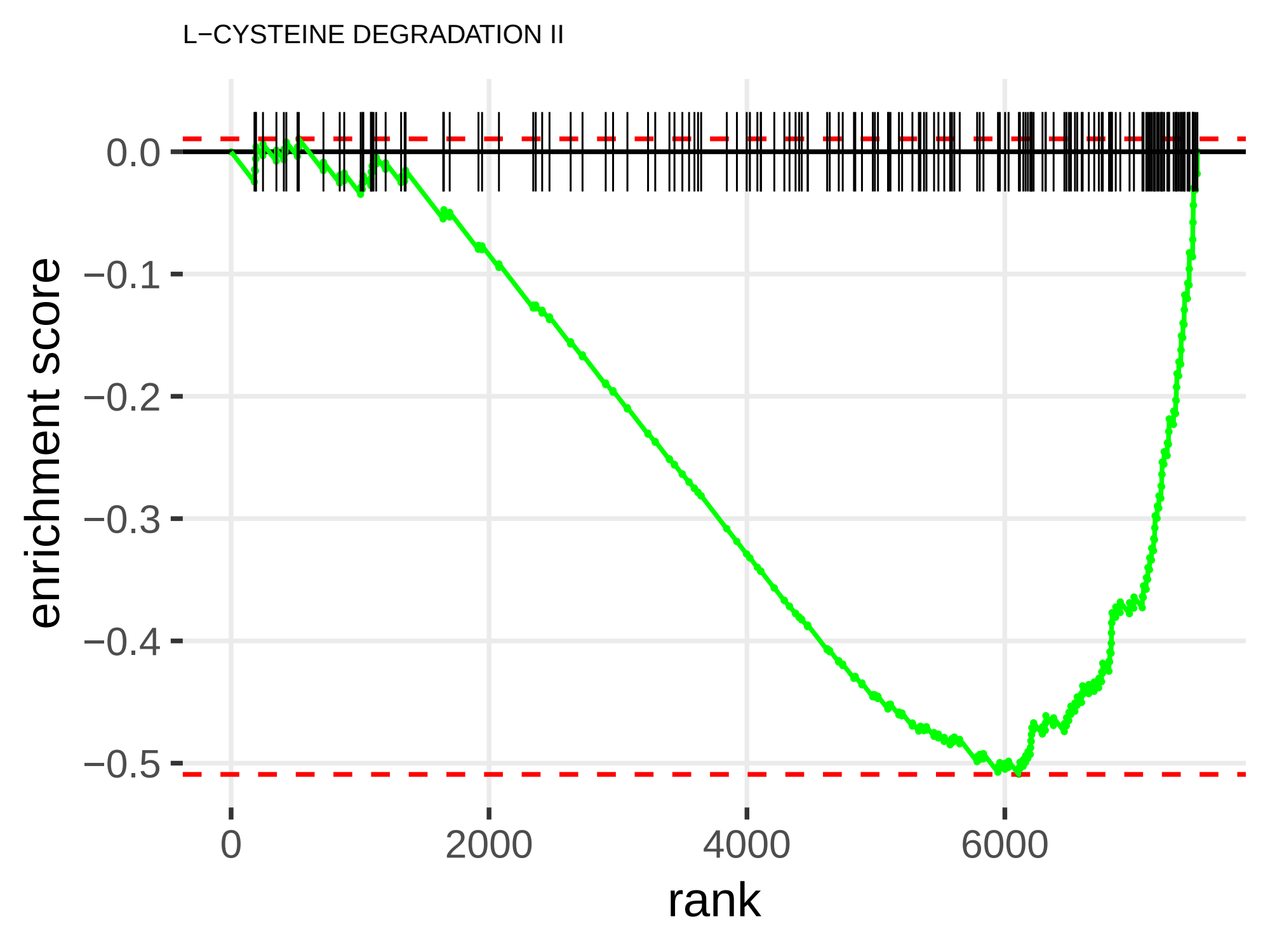

ACETATE CONVERSION TO ACETYL−COA
0.0
−0.1
−0.2
−0.3
−0.4
−0.5
enrichment score
0
2000
4000
6000
rank

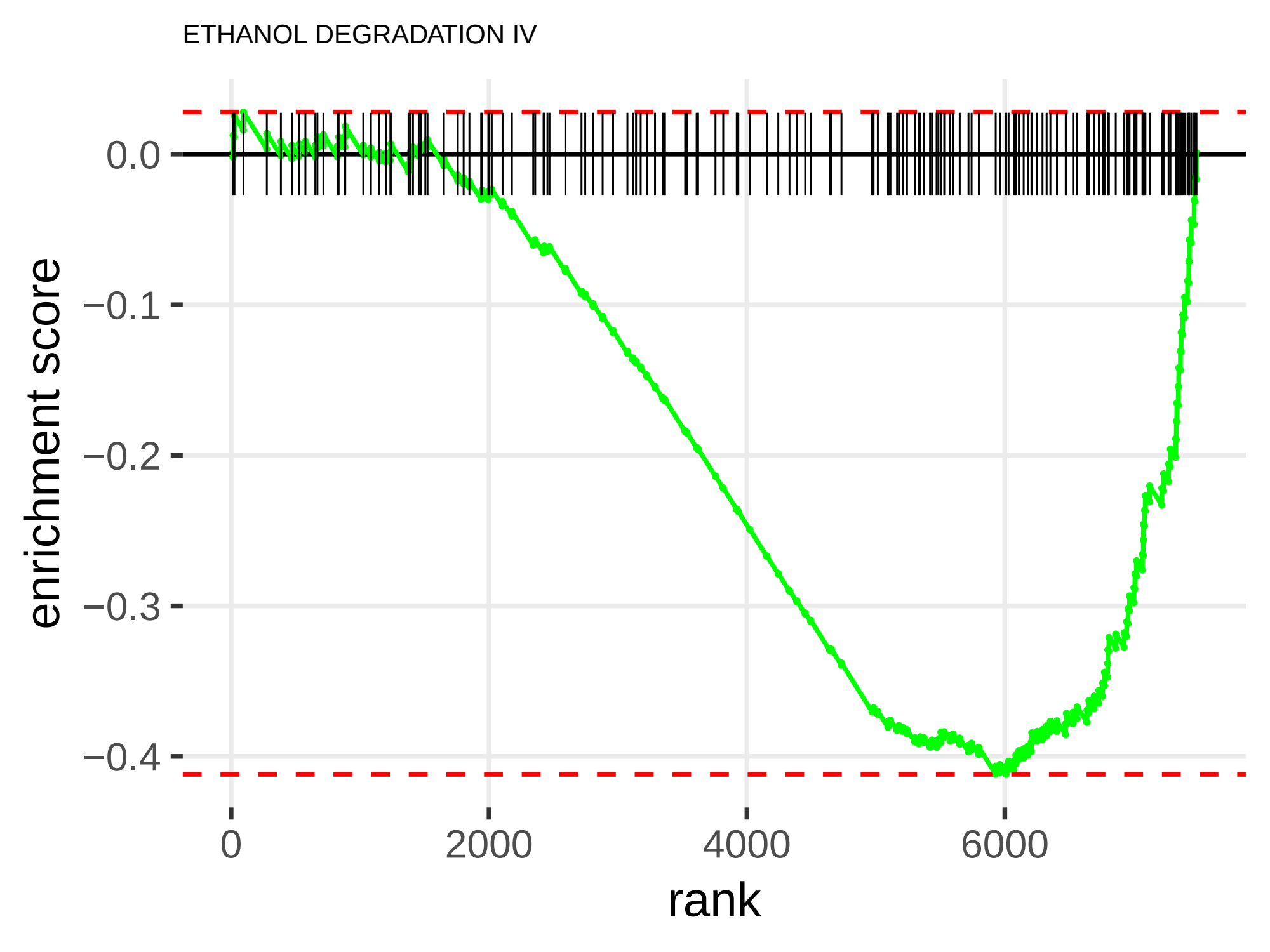

GLYCOGEN DEGRADATION II
0.0
−0.1
−0.2
−0.3
−0.4
enrichment score
0
2000
4000
6000
rank

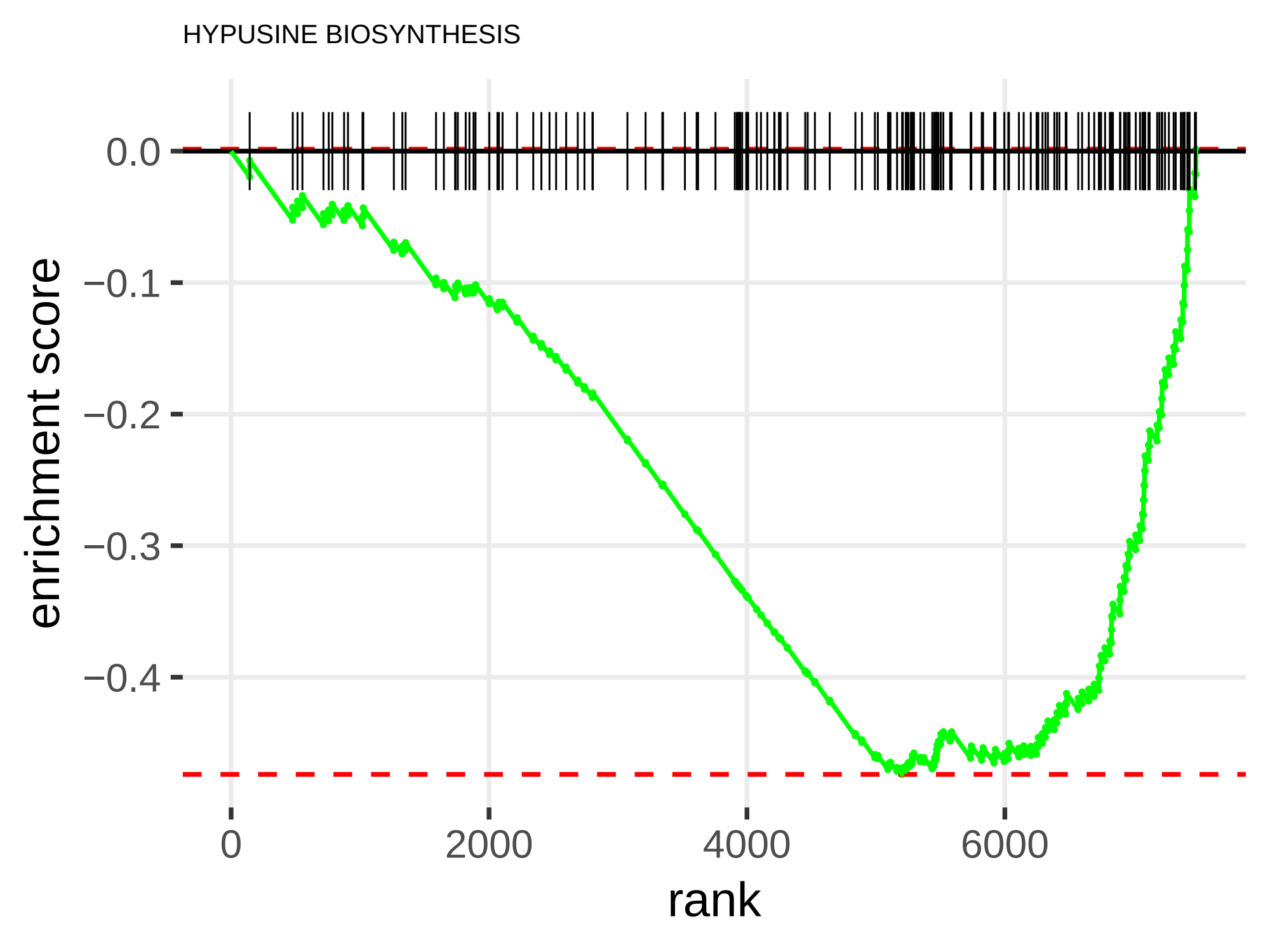

KETOGENESIS
0.0
−0.1
−0.2
−0.3
−0.4
enrichment score
0
2000
4000
6000
rank

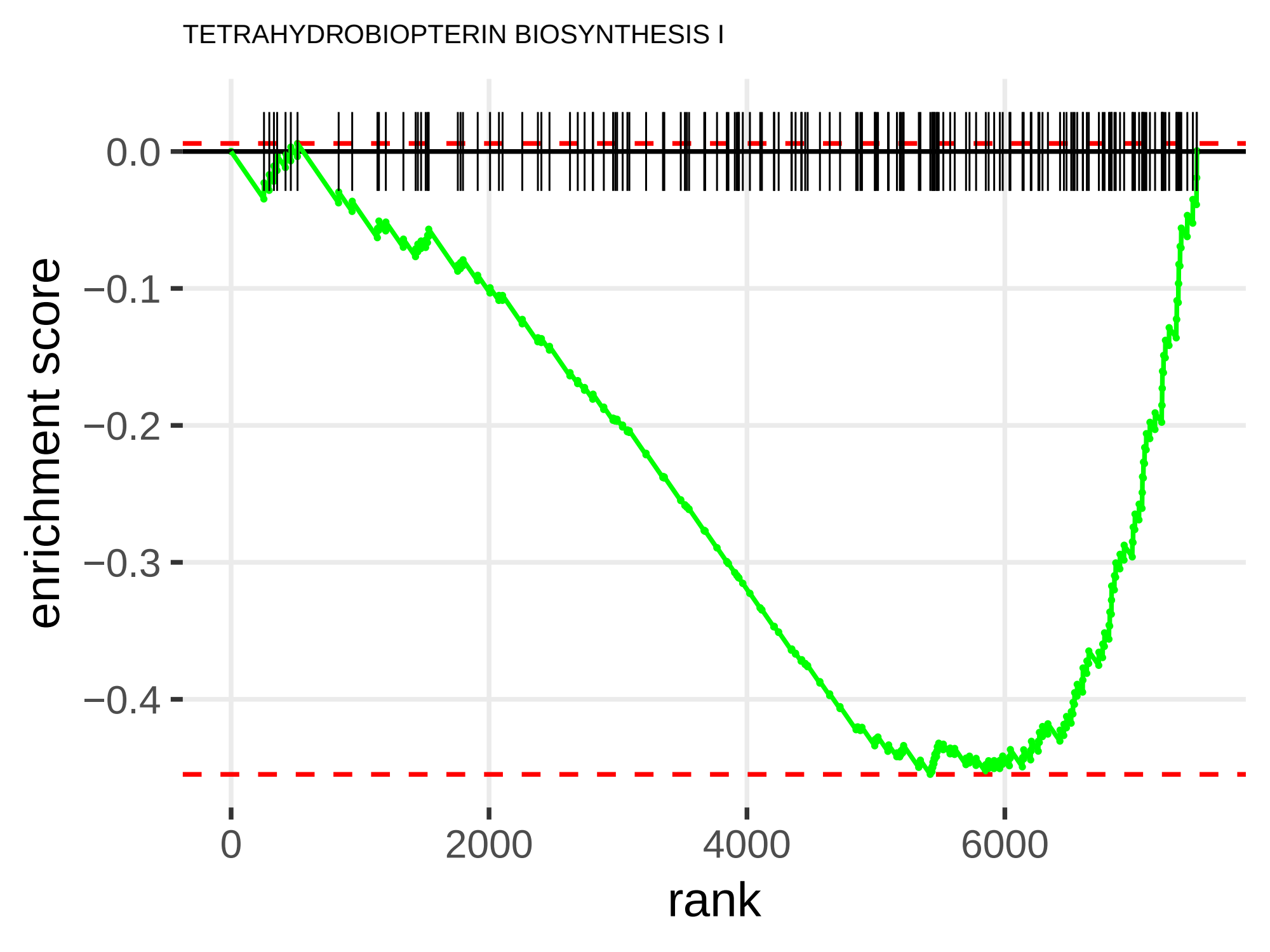

RETINOATE BIOSYNTHESIS I
0.0
−0.2
−0.4
enrichment score
0
2000
4000
6000
rank

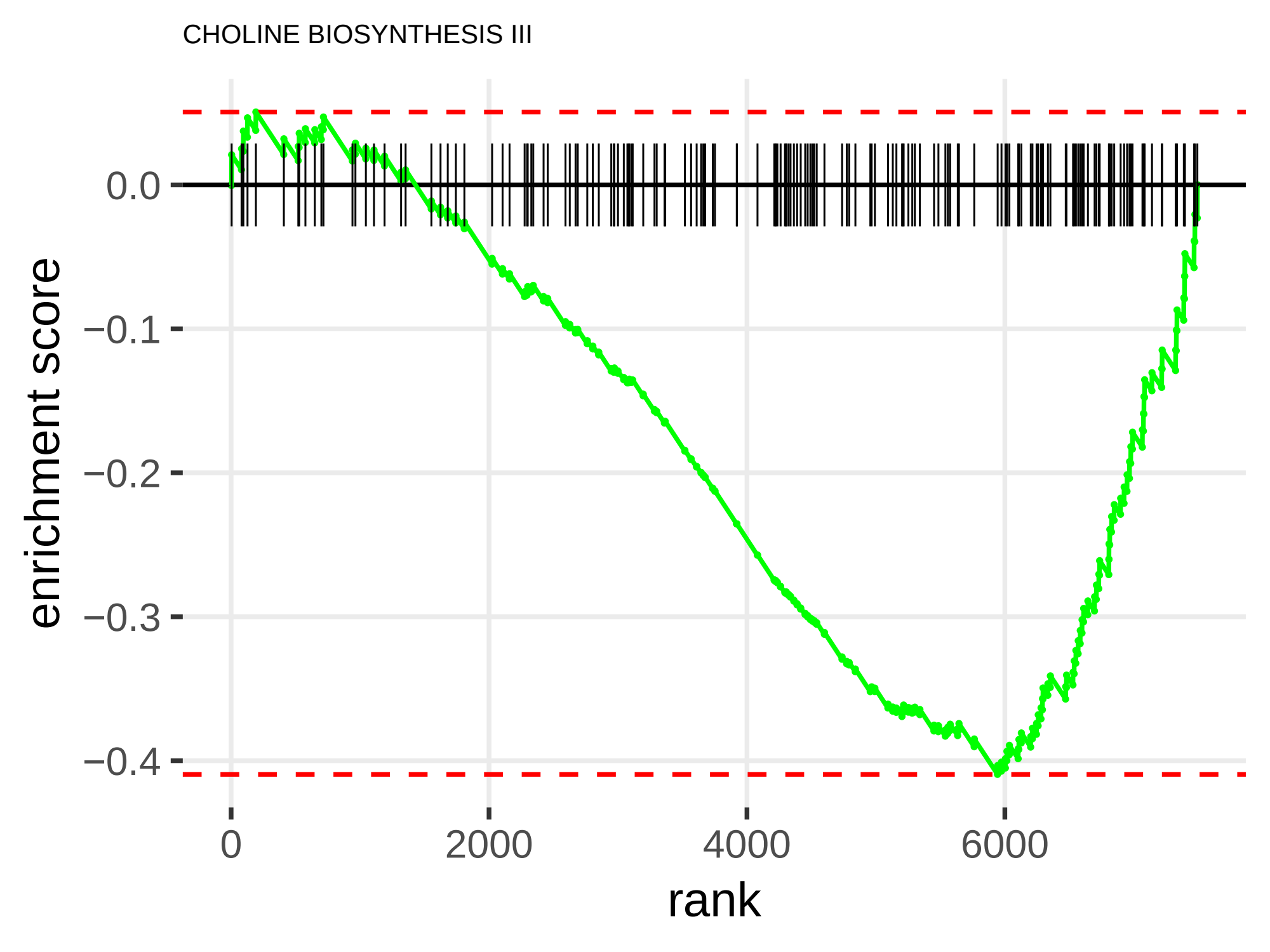

ADENINE AND ADENOSINE SALVAGE I
0.0
−0.1
−0.2
−0.3
−0.4
enrichment score
0
2000
4000
6000
rank

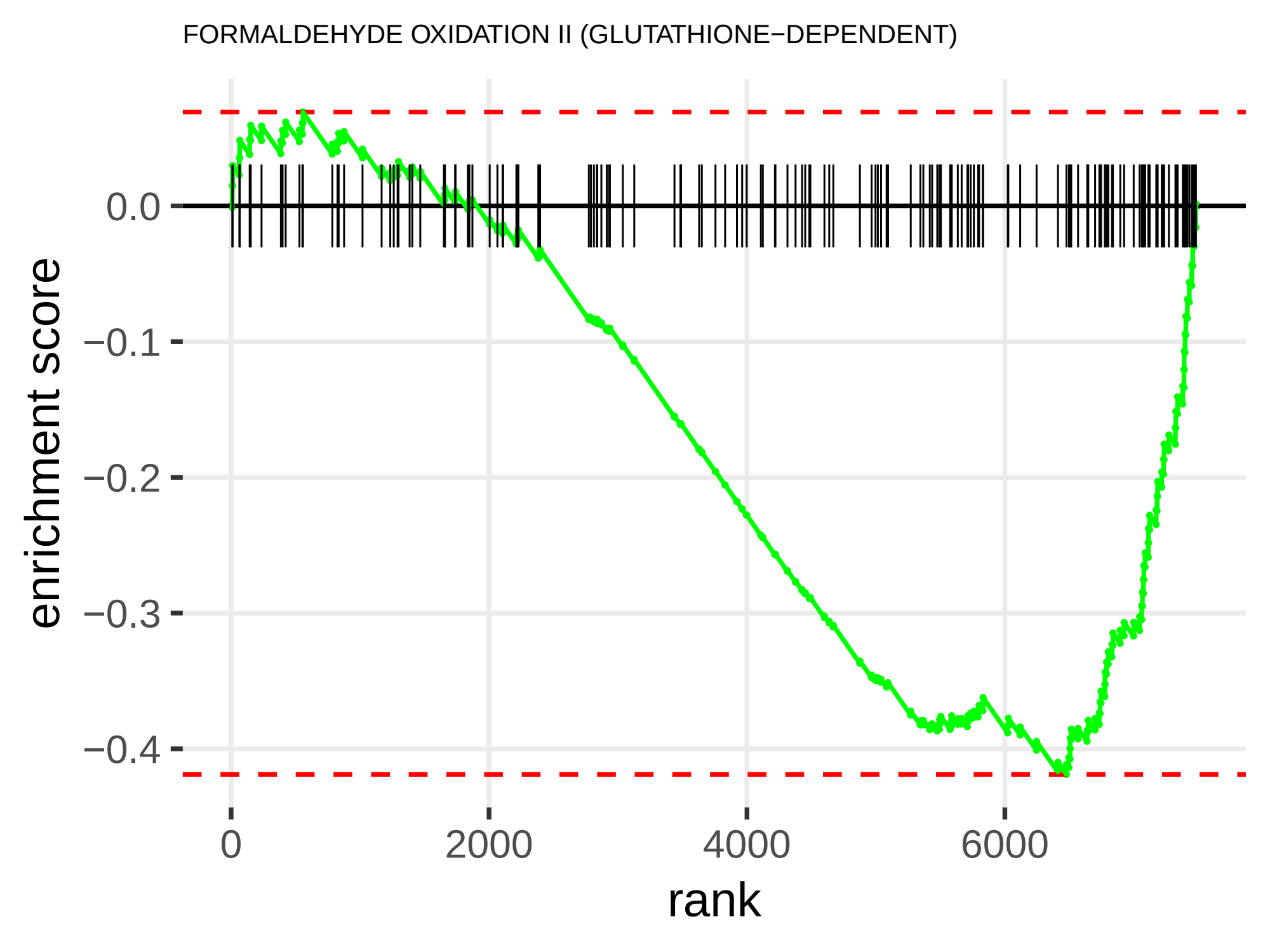

L−CYSTEINE DEGRADATION II
0.0
−0.1
−0.2
−0.3
−0.4
−0.5
enrichment score
0
2000
4000
6000
rank

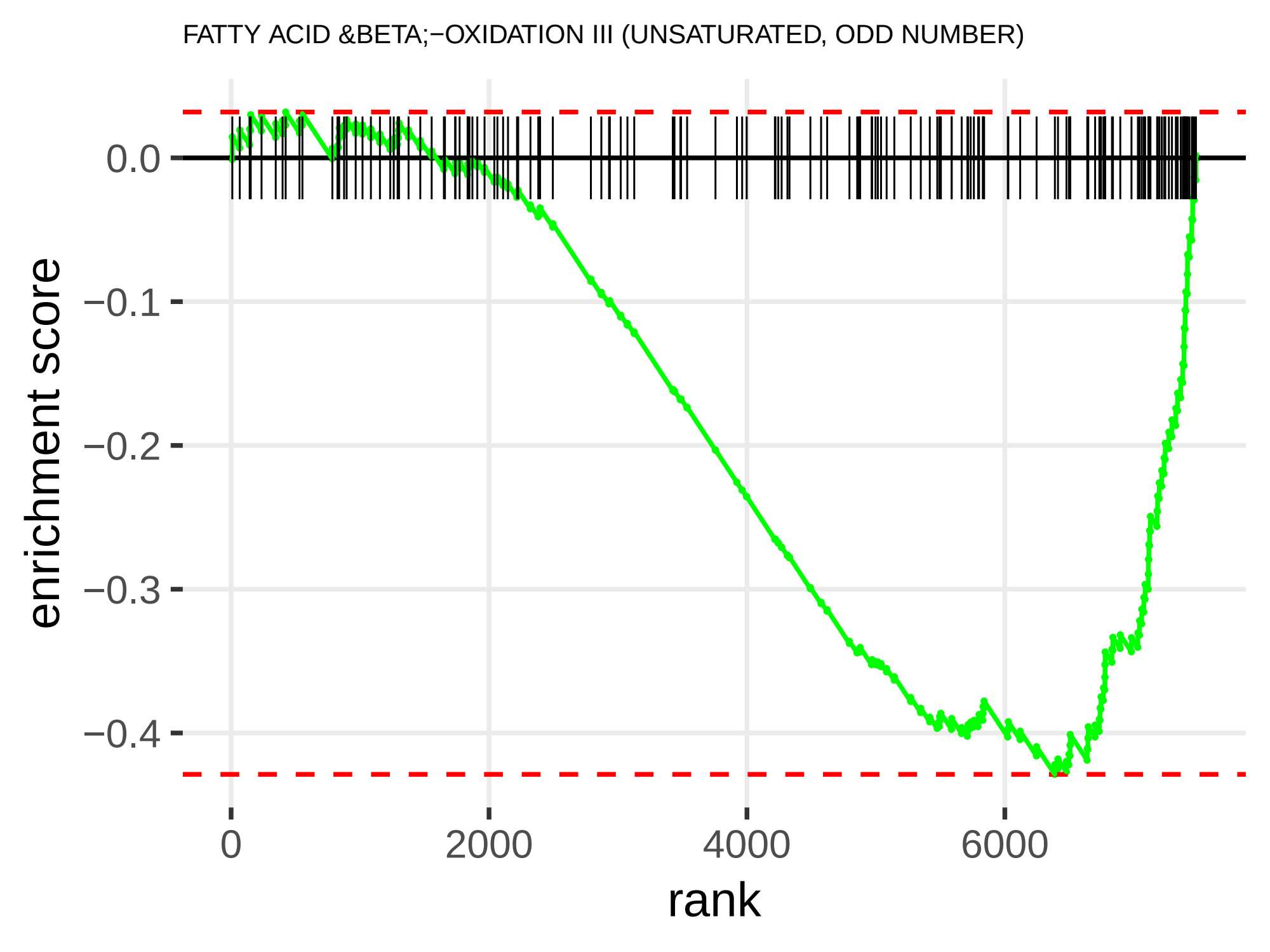

ETHANOL DEGRADATION IV
0.0
−0.1
−0.2
−0.3
−0.4
enrichment score
0
2000
4000
6000
rank

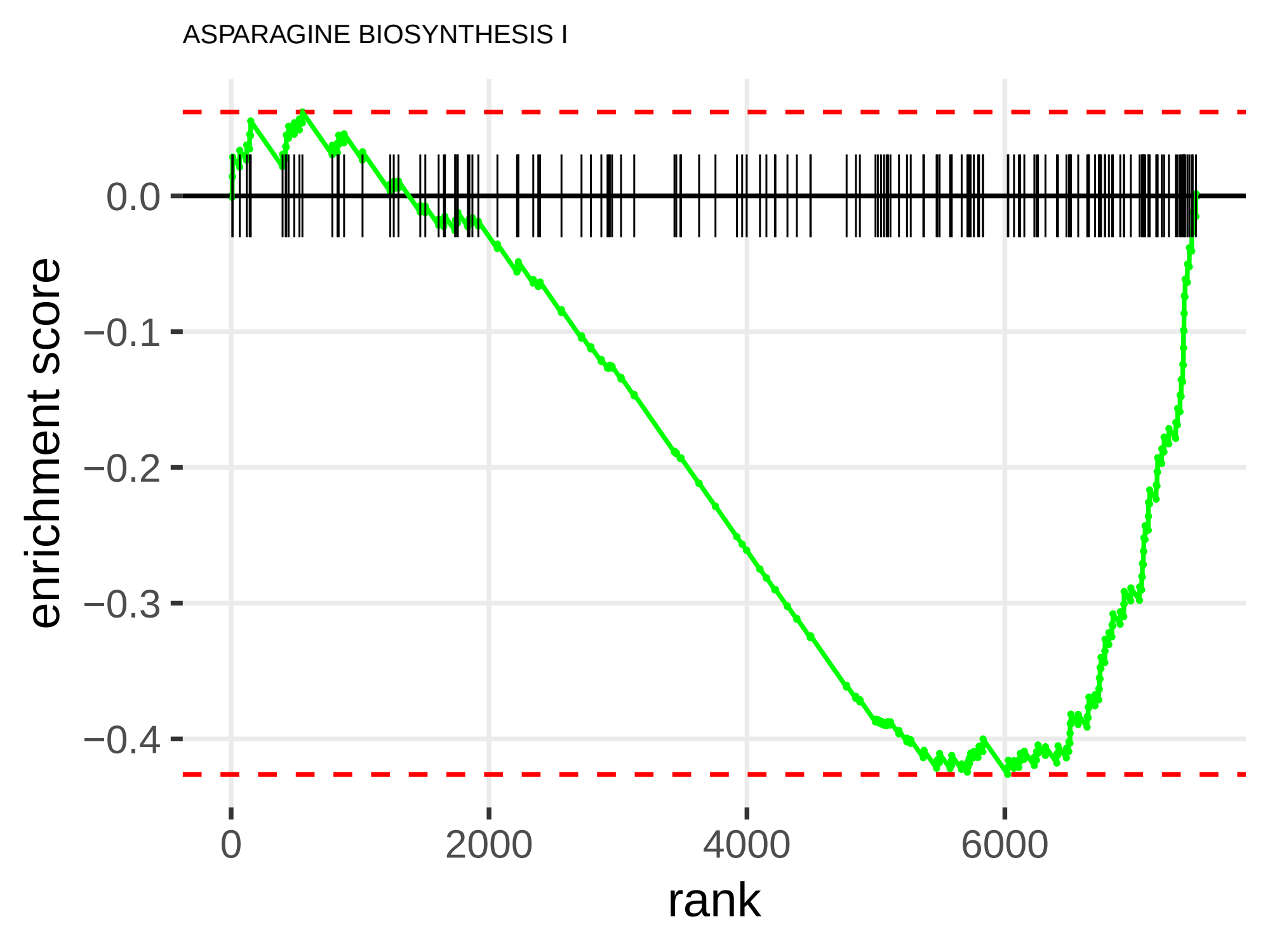

HYPUSINE BIOSYNTHESIS
0.0
−0.1
−0.2
−0.3
−0.4
enrichment score
0
2000
4000
6000
rank

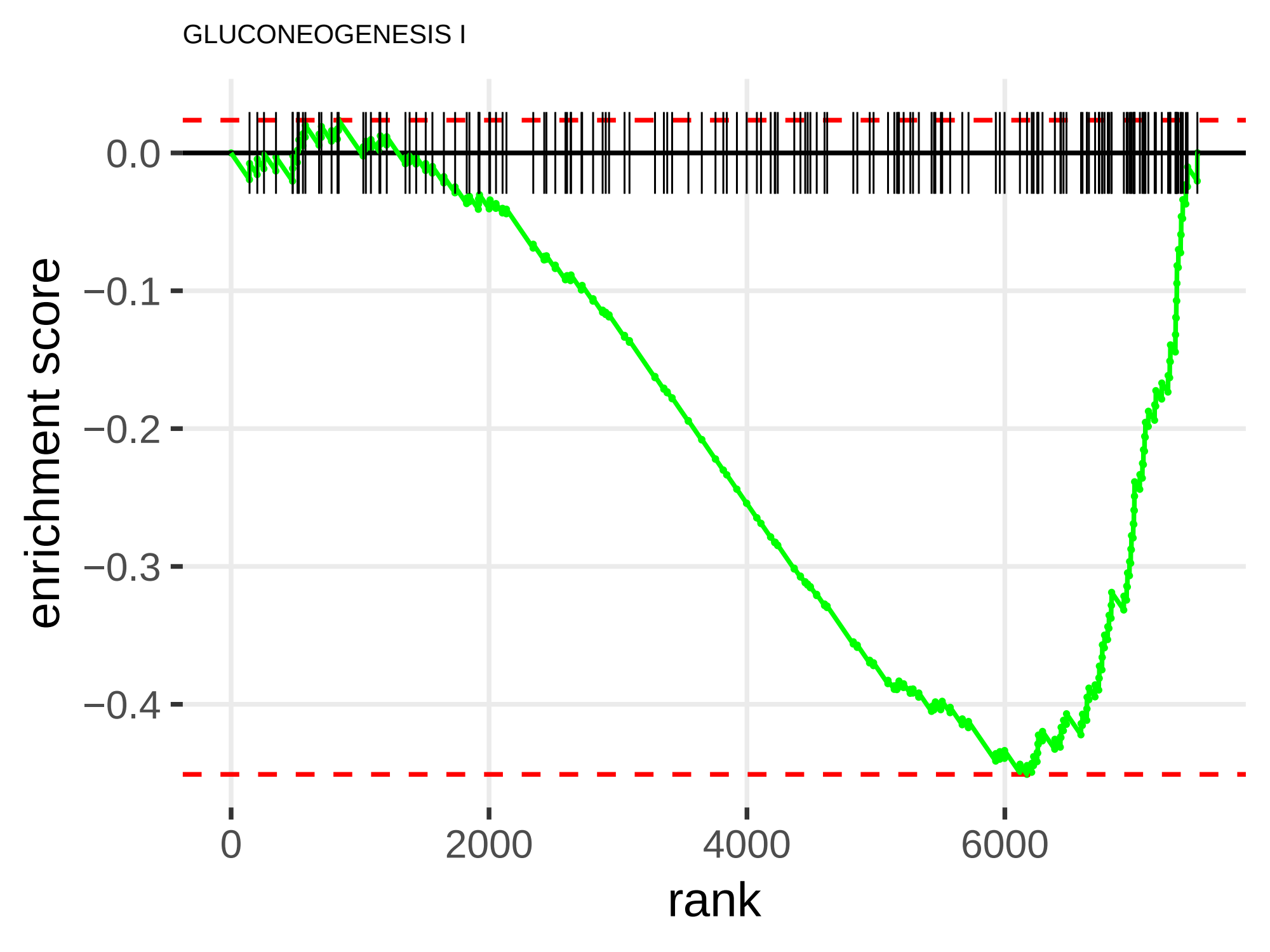

TETRAHYDROBIOPTERIN BIOSYNTHESIS I
0.0
−0.1
−0.2
−0.3
−0.4
enrichment score
0
2000
4000
6000
rank

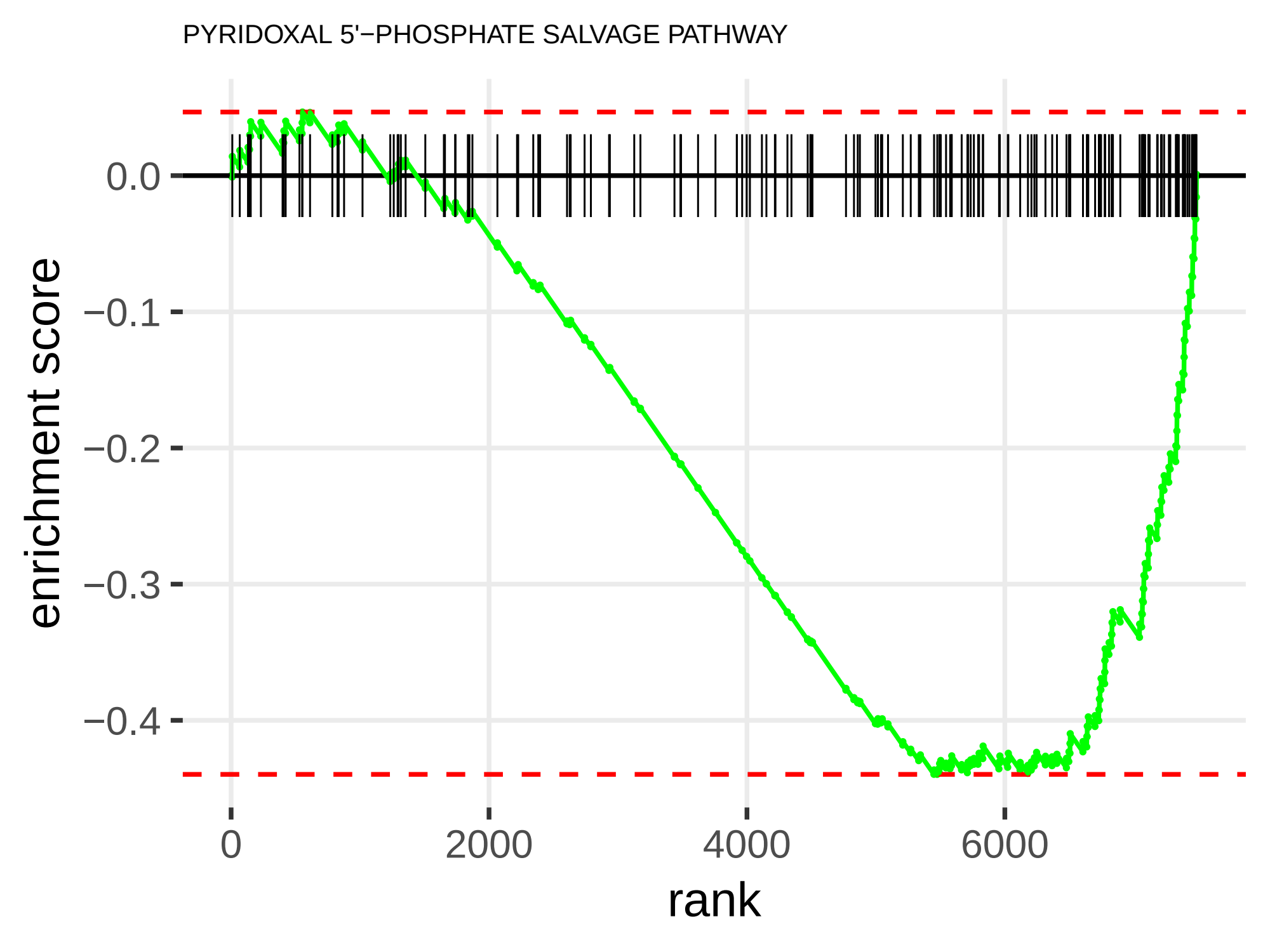

CHOLINE BIOSYNTHESIS III
0.0
−0.1
−0.2
−0.3
−0.4
enrichment score
0
2000
4000
6000
rank

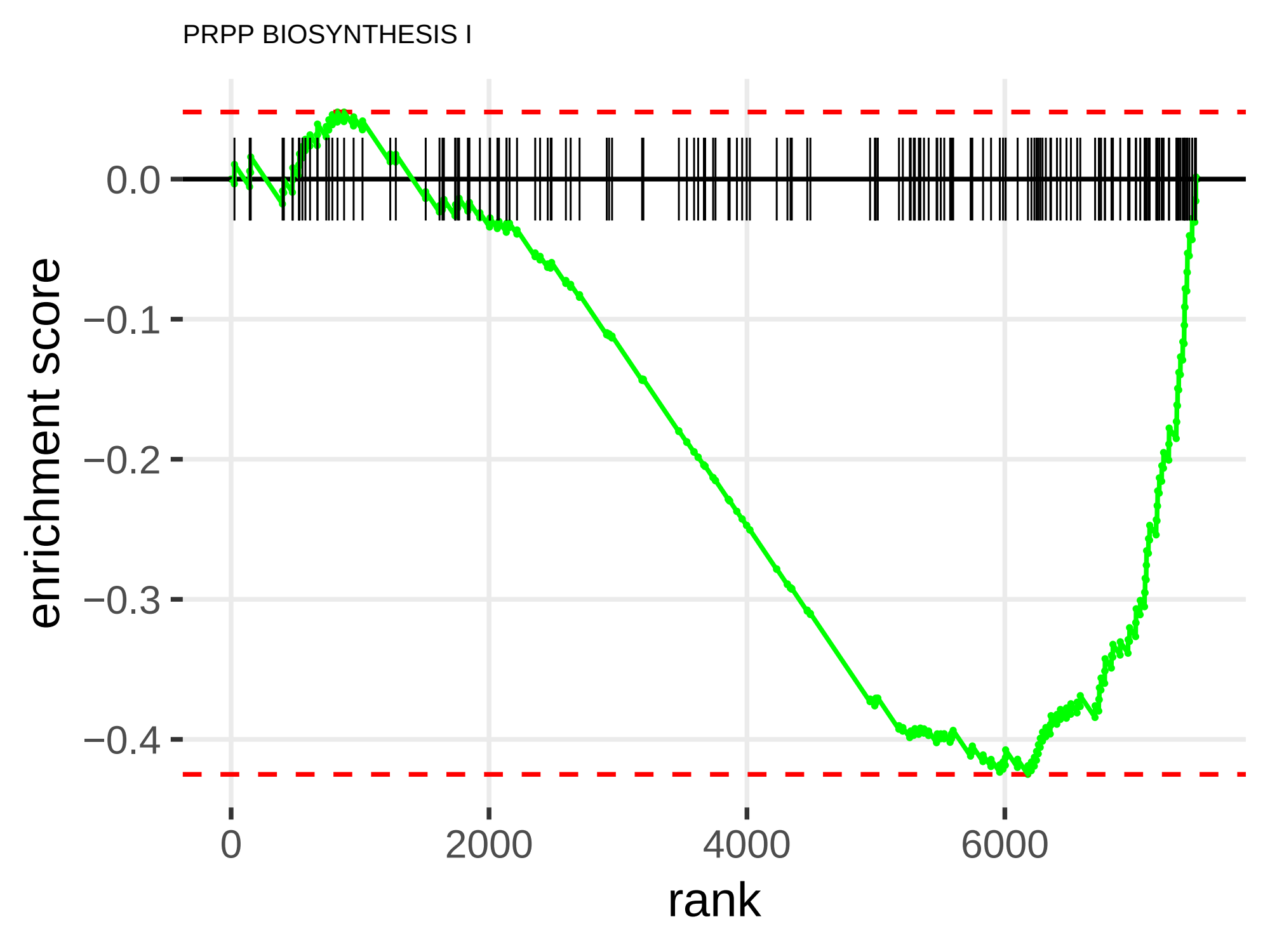

FORMALDEHYDE OXIDATION II (GLUTATHIONE−DEPENDENT)
0.0
−0.1
−0.2
−0.3
−0.4
enrichment score
0
2000
4000
6000
rank

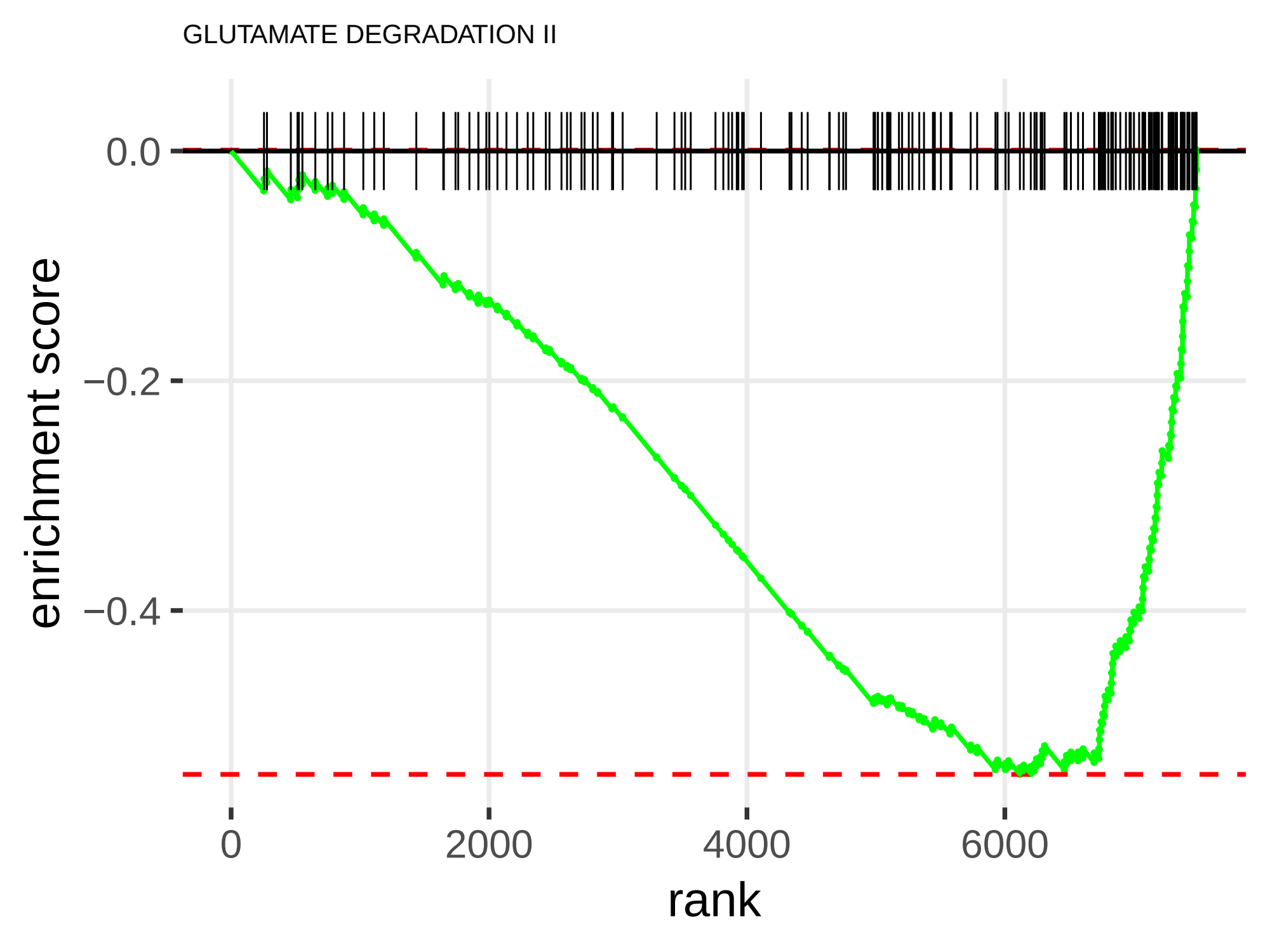

FATTY ACID &BETA;−OXIDATION III (UNSATURATED, ODD NUMBER)
0.0
−0.1
−0.2
−0.3
−0.4
enrichment score
0
2000
4000
6000
rank

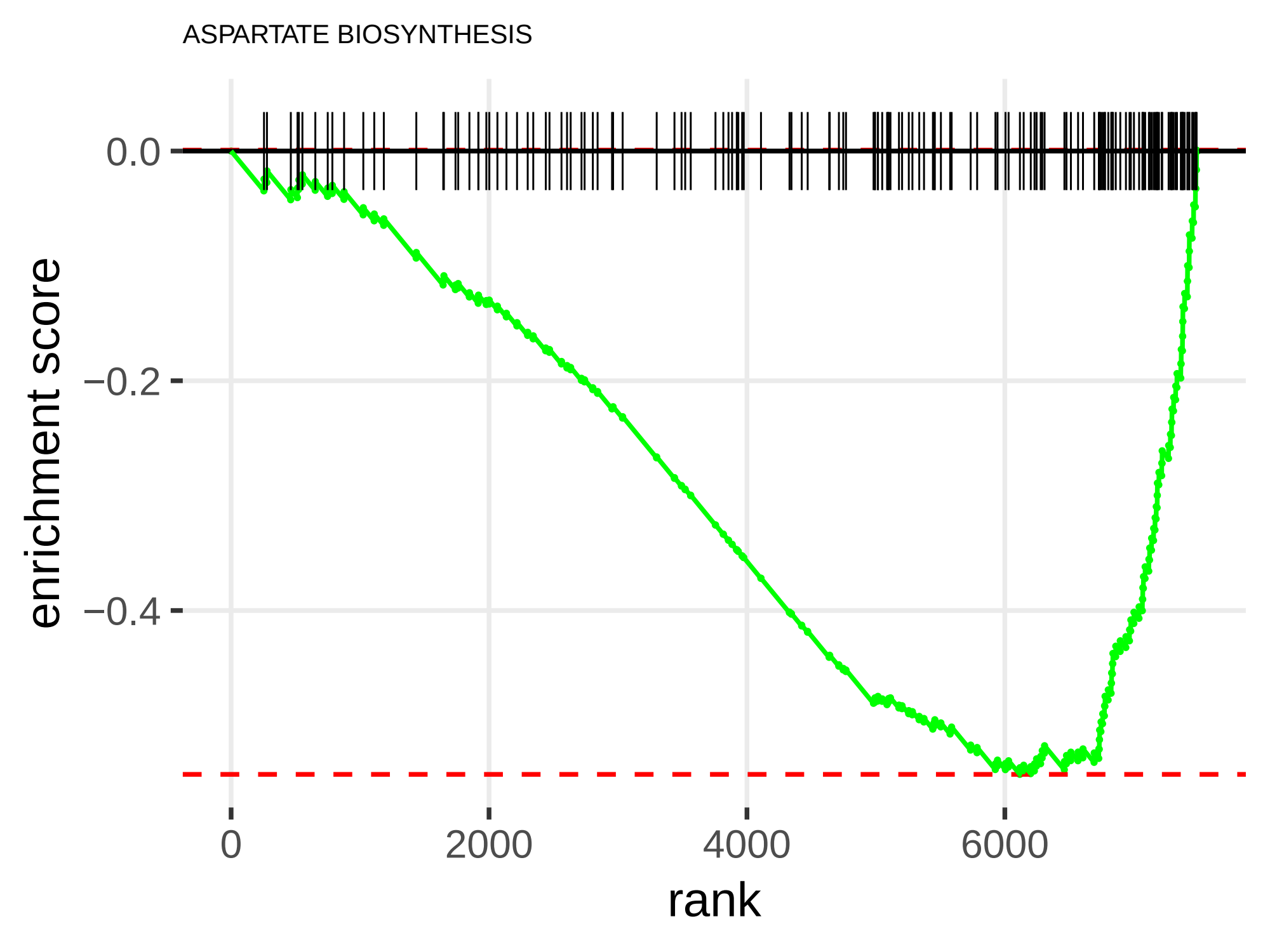

ASPARAGINE BIOSYNTHESIS I
enrichment score
0.0
−0.1
−0.2
−0.3
−0.4
0
2000
4000
6000
rank

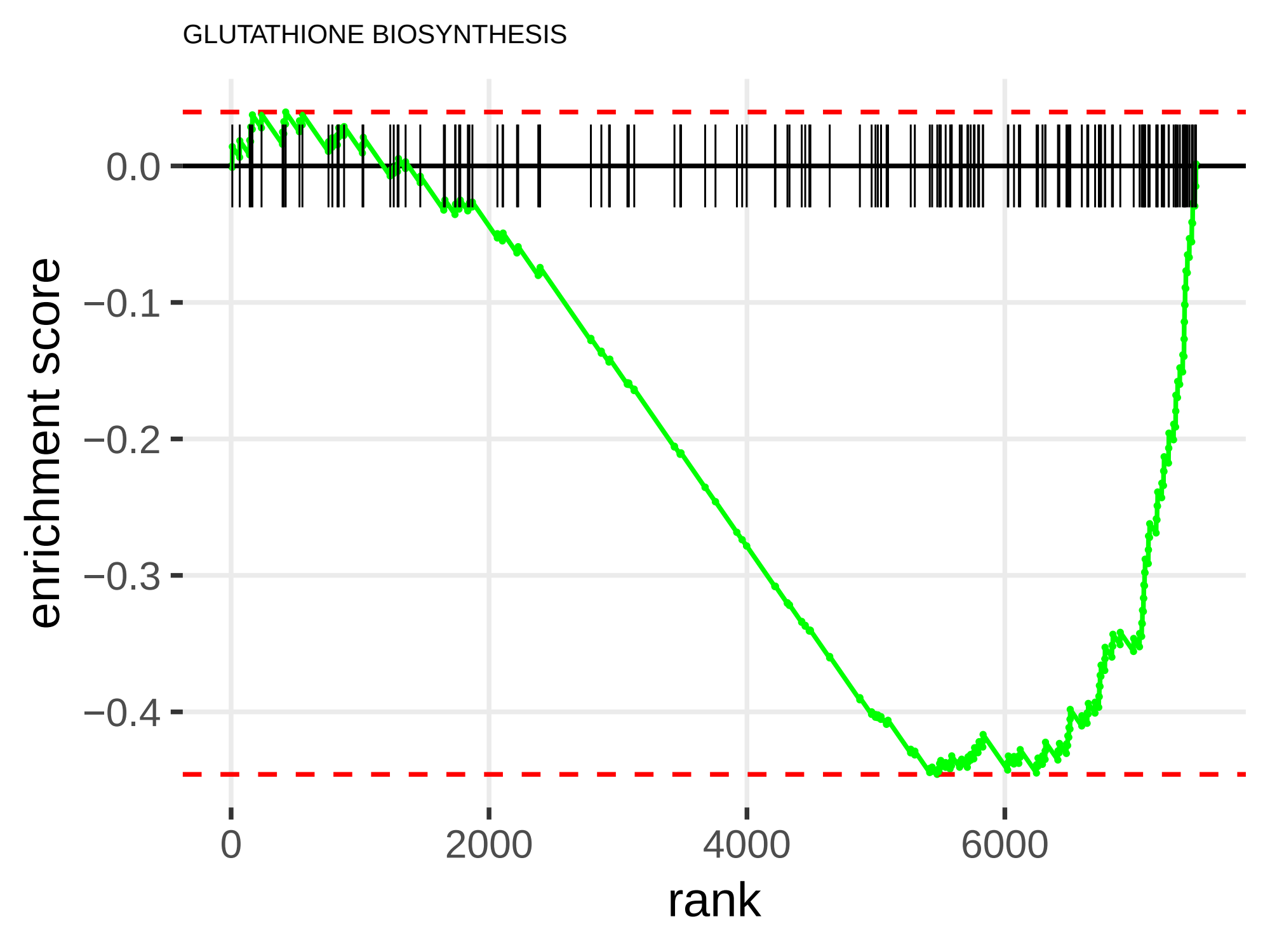

GLUCONEOGENESIS I
0.0
−0.1
−0.2
−0.3
−0.4
enrichment score
0
2000
4000
6000
rank

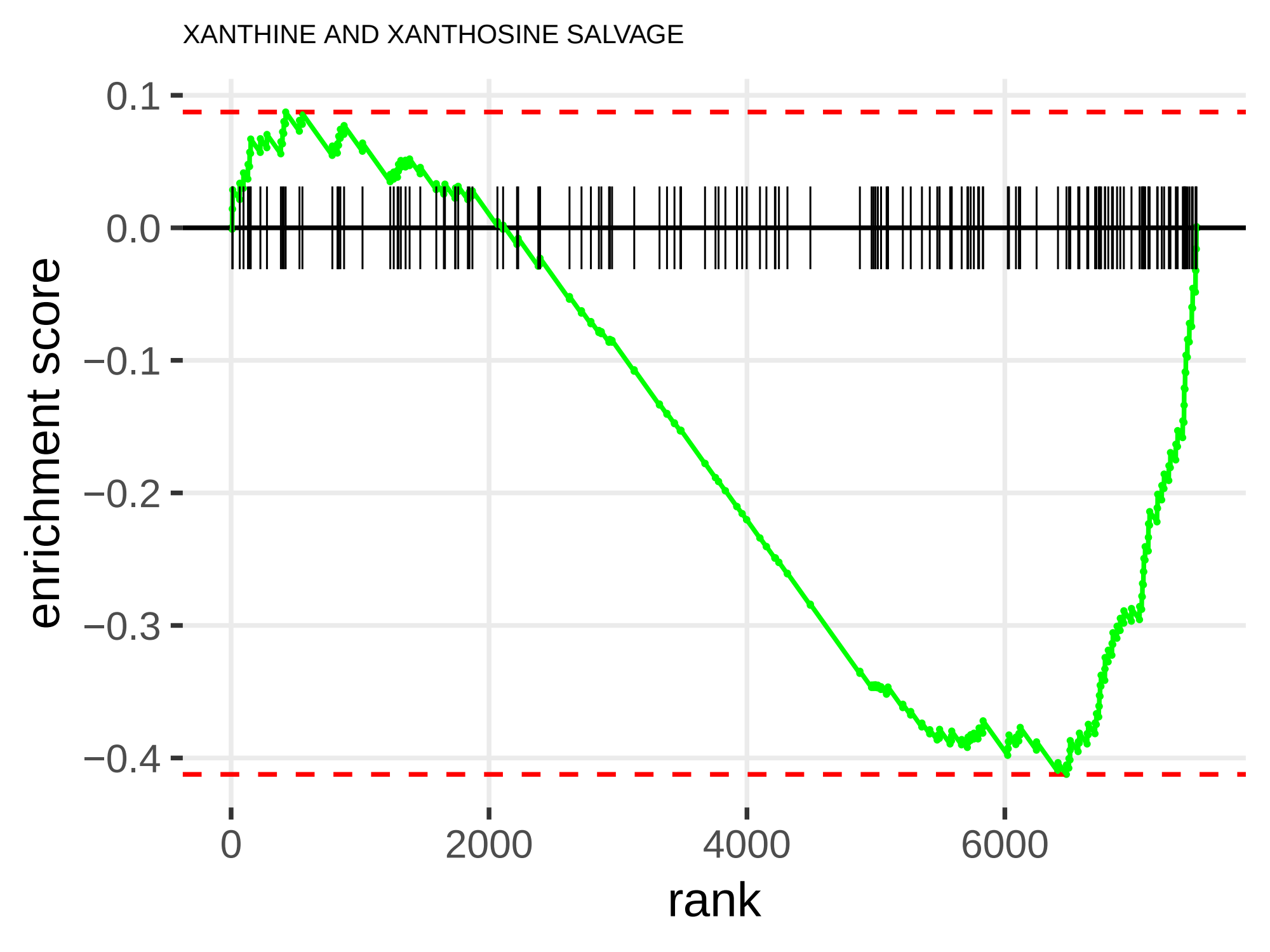

PYRIDOXAL 5'−PHOSPHATE SALVAGE PATHWAY
0.0
−0.1
−0.2
−0.3
−0.4
enrichment score
0
2000
4000
6000
rank

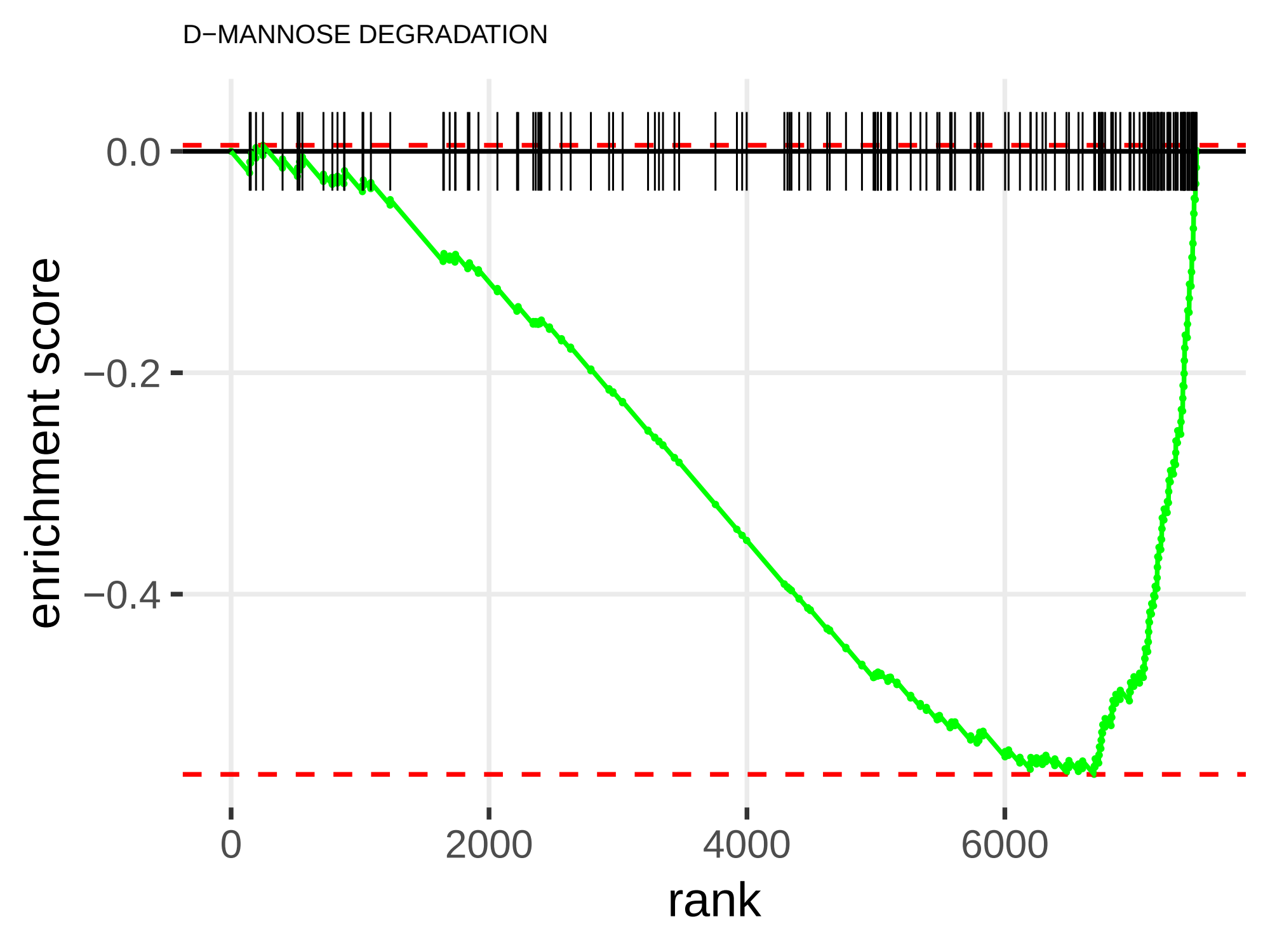

PRPP BIOSYNTHESIS I
0.0
−0.1
−0.2
−0.3
−0.4
enrichment score
0
2000
4000
6000
rank

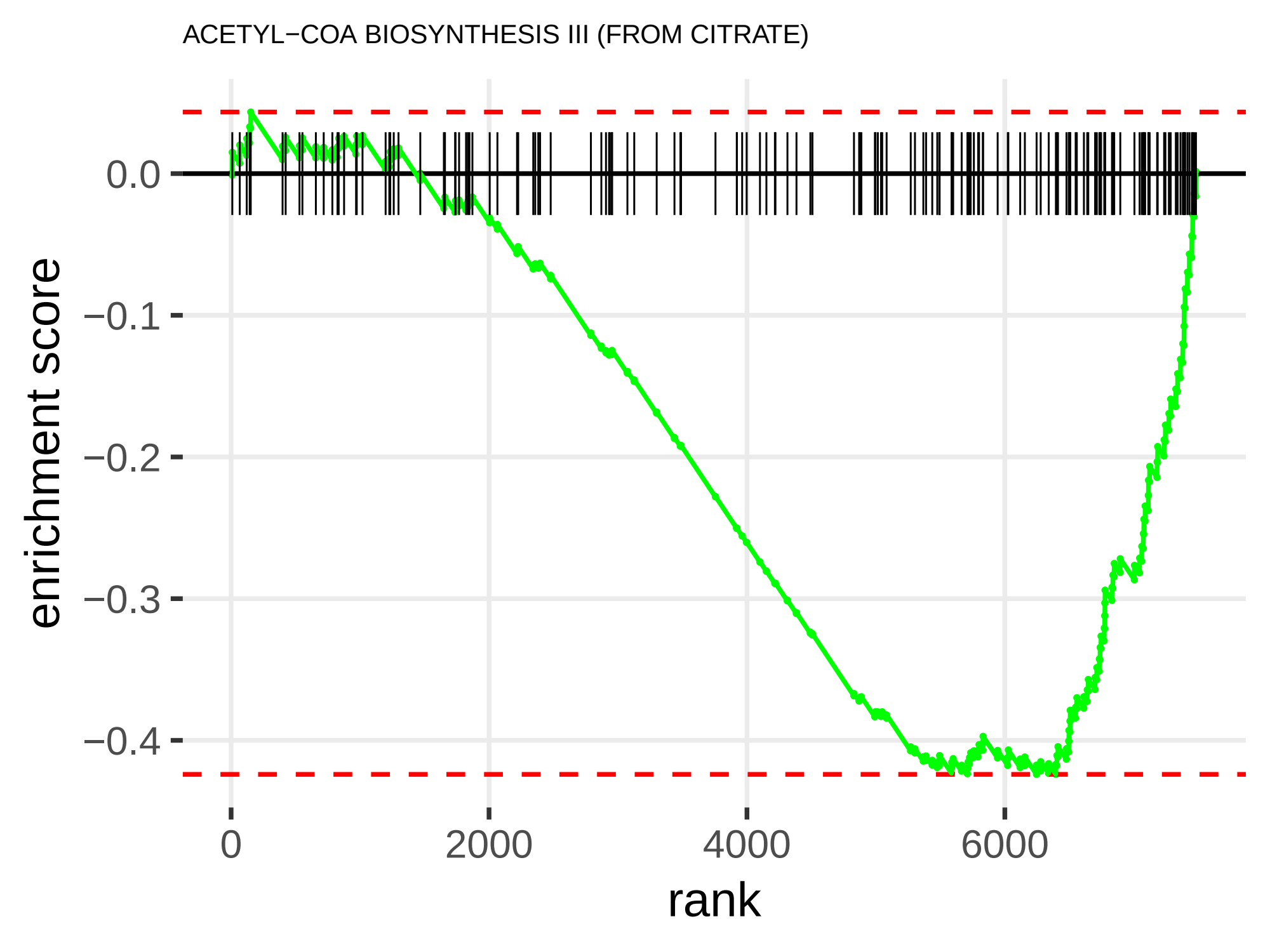

GLUTAMATE DEGRADATION II
0.0
−0.2
−0.4
enrichment score
0
2000
4000
6000
rank

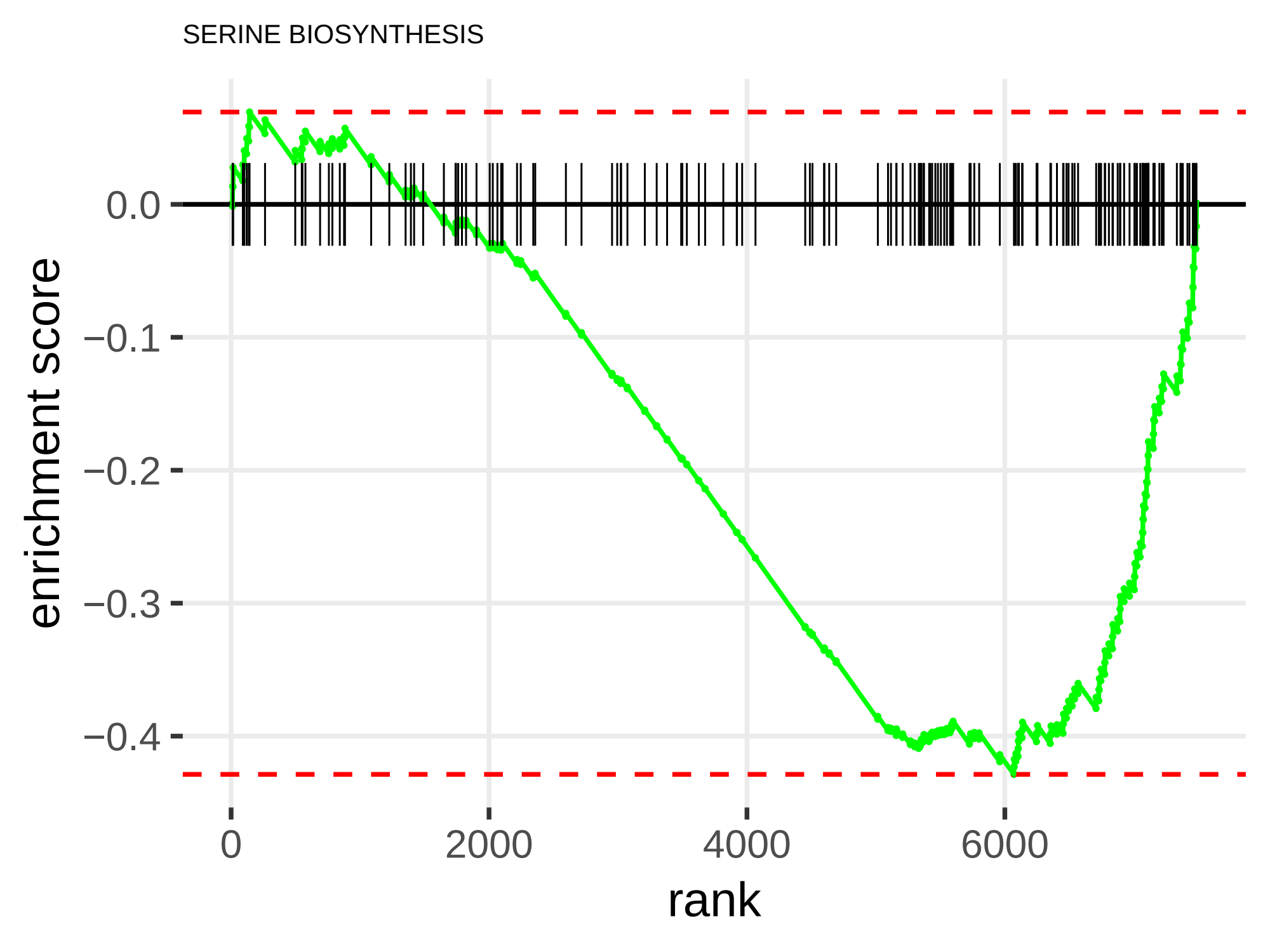

ASPARTATE BIOSYNTHESIS
0.0
−0.2
−0.4
enrichment score
0
2000
4000
6000
rank

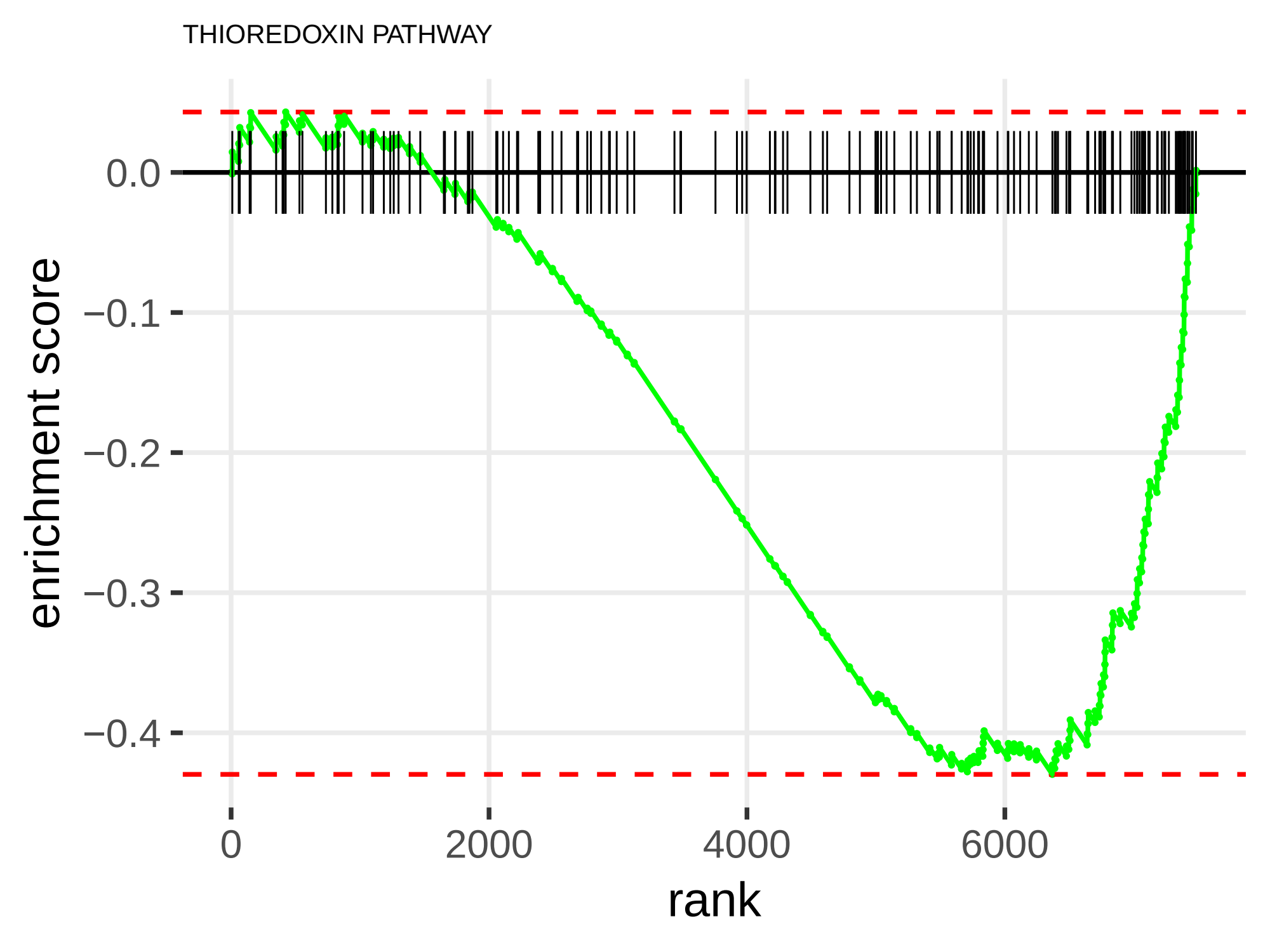

GLUTATHIONE BIOSYNTHESIS
0.0
−0.1
−0.2
−0.3
−0.4
enrichment score
0
2000
4000
6000
rank

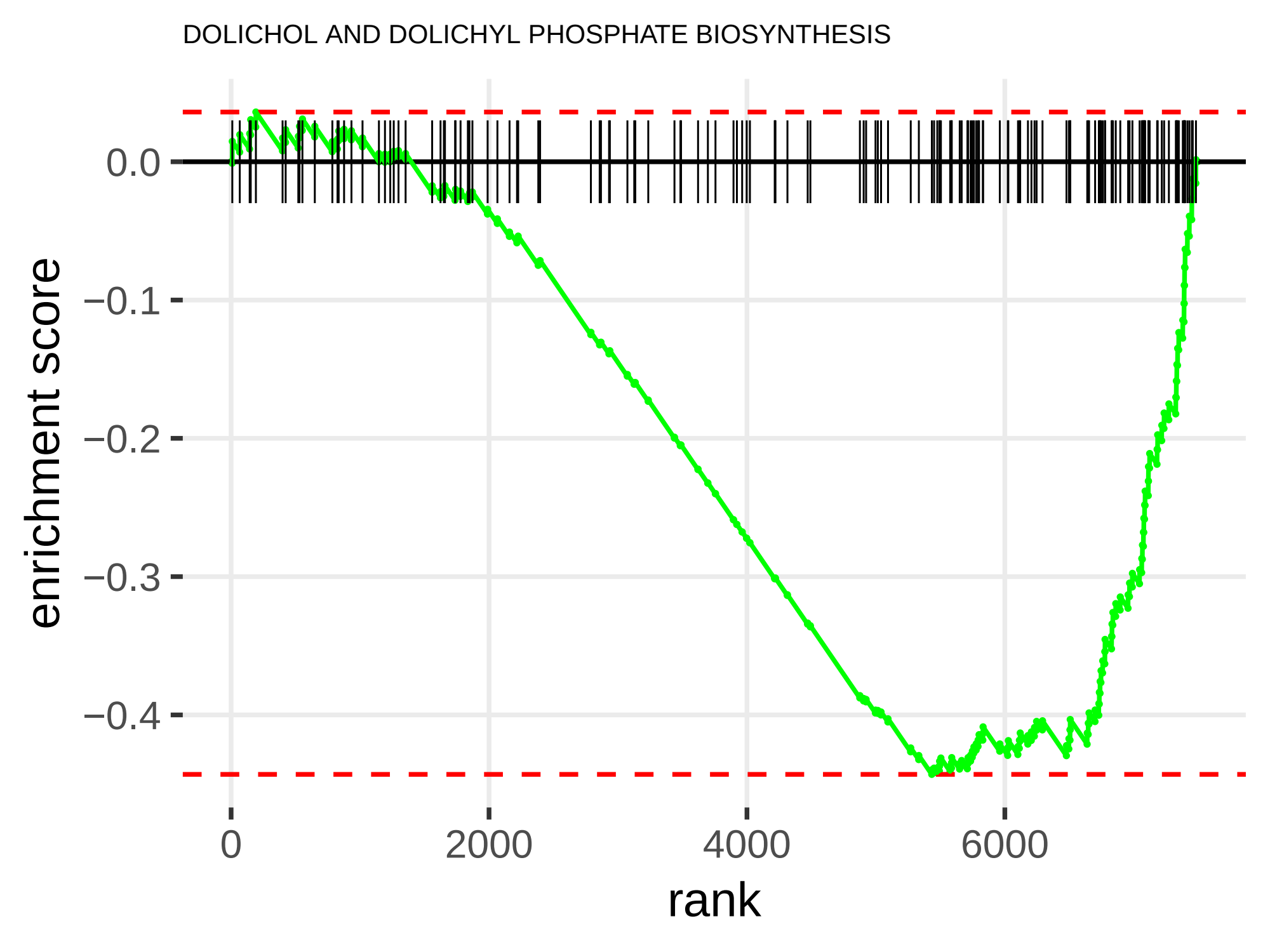

XANTHINE AND XANTHOSINE SALVAGE
0.1
0.0
−0.1
−0.2
−0.3
−0.4
enrichment score
0
2000
4000
6000
rank

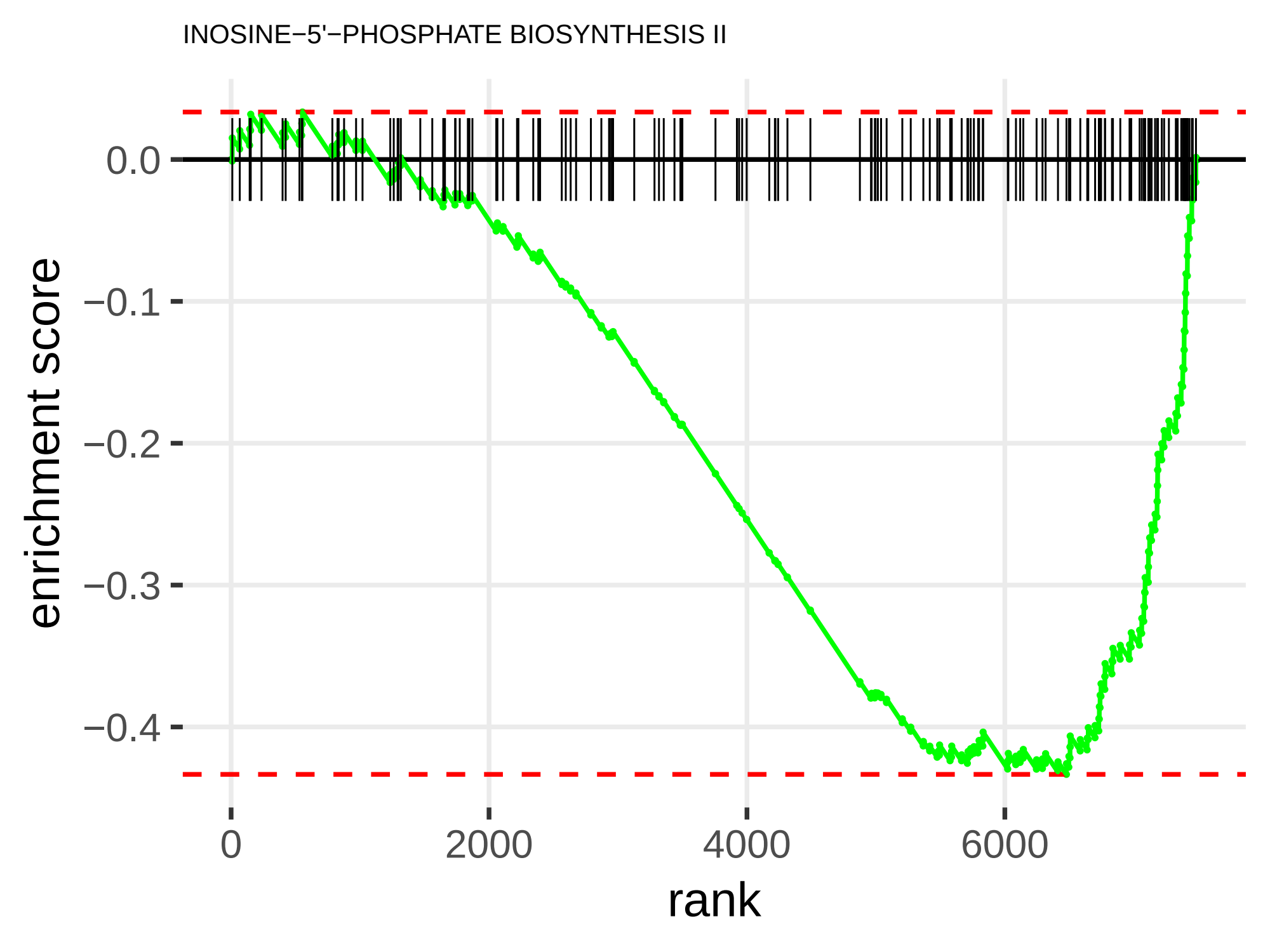

D−MANNOSE DEGRADATION
0.0
−0.2
−0.4
enrichment score
0
2000
4000
6000
rank

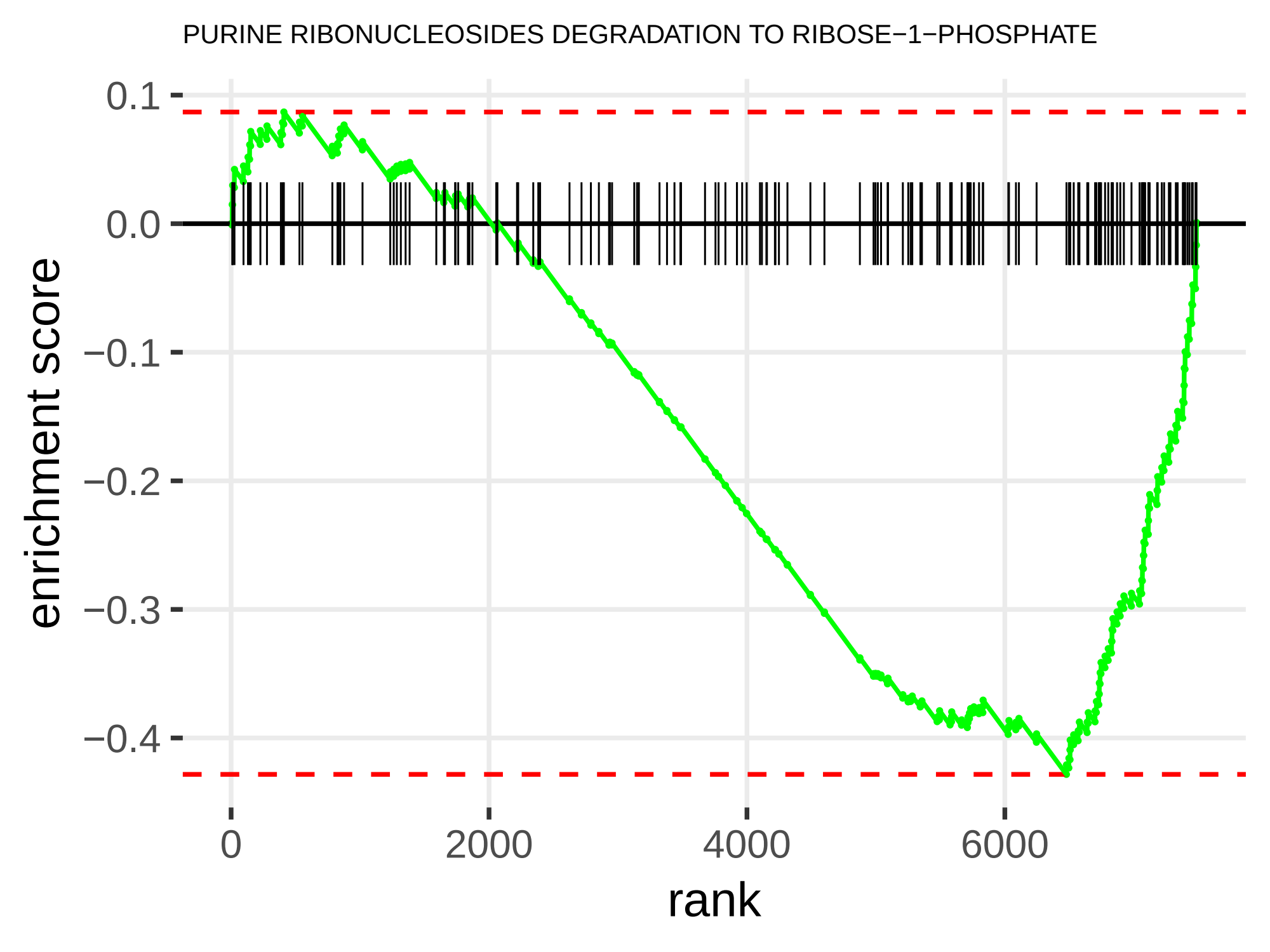

ACETYL−COA BIOSYNTHESIS III (FROM CITRATE)
0.0
−0.1
−0.2
−0.3
−0.4
enrichment score
0
2000
4000
6000
rank

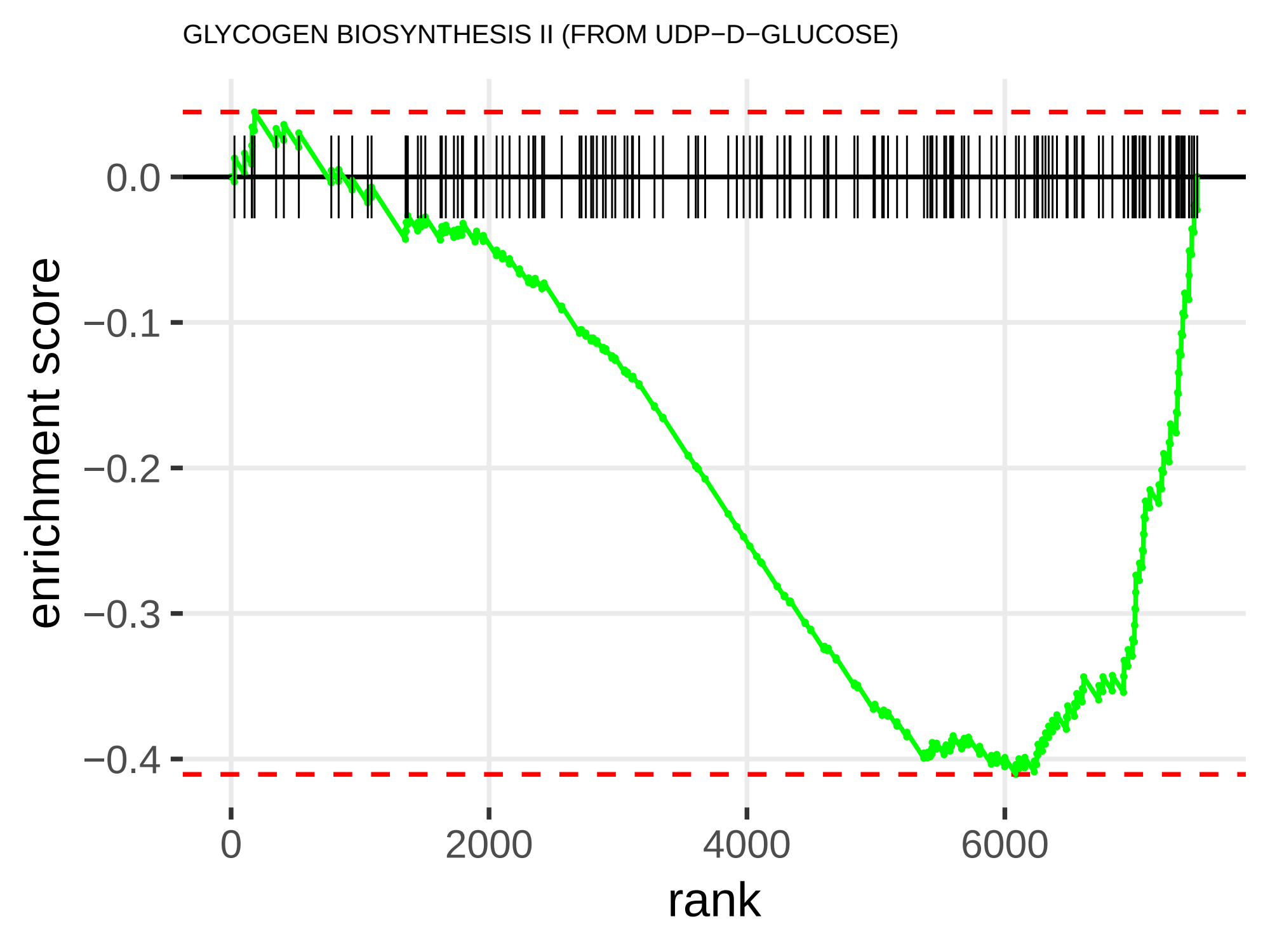

SERINE BIOSYNTHESIS
0.0
−0.1
−0.2
−0.3
−0.4
enrichment score
0
2000
4000
6000
rank

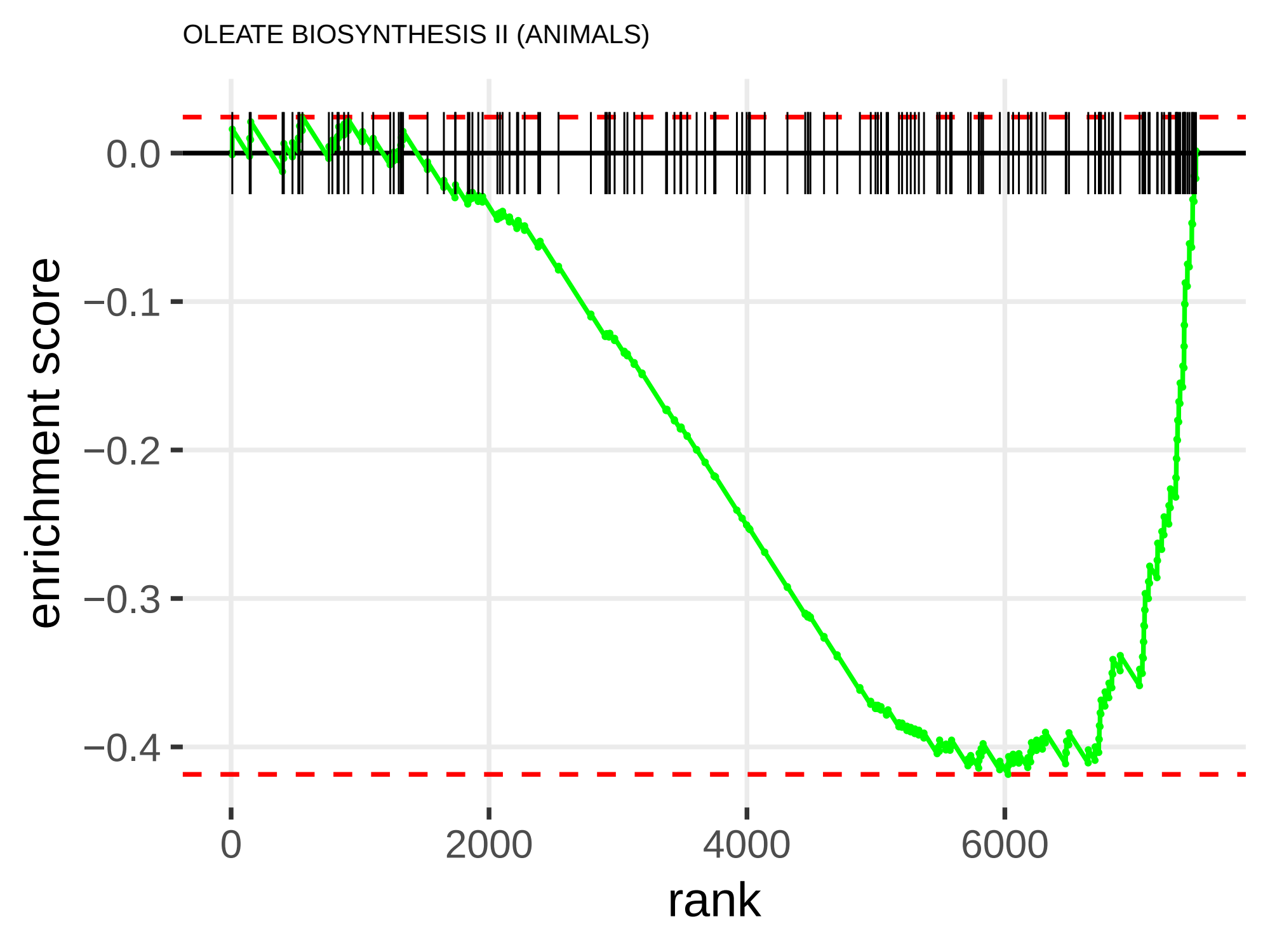

THIOREDOXIN PATHWAY
0.0
−0.1
−0.2
−0.3
−0.4
enrichment score
0
2000
4000
6000
rank

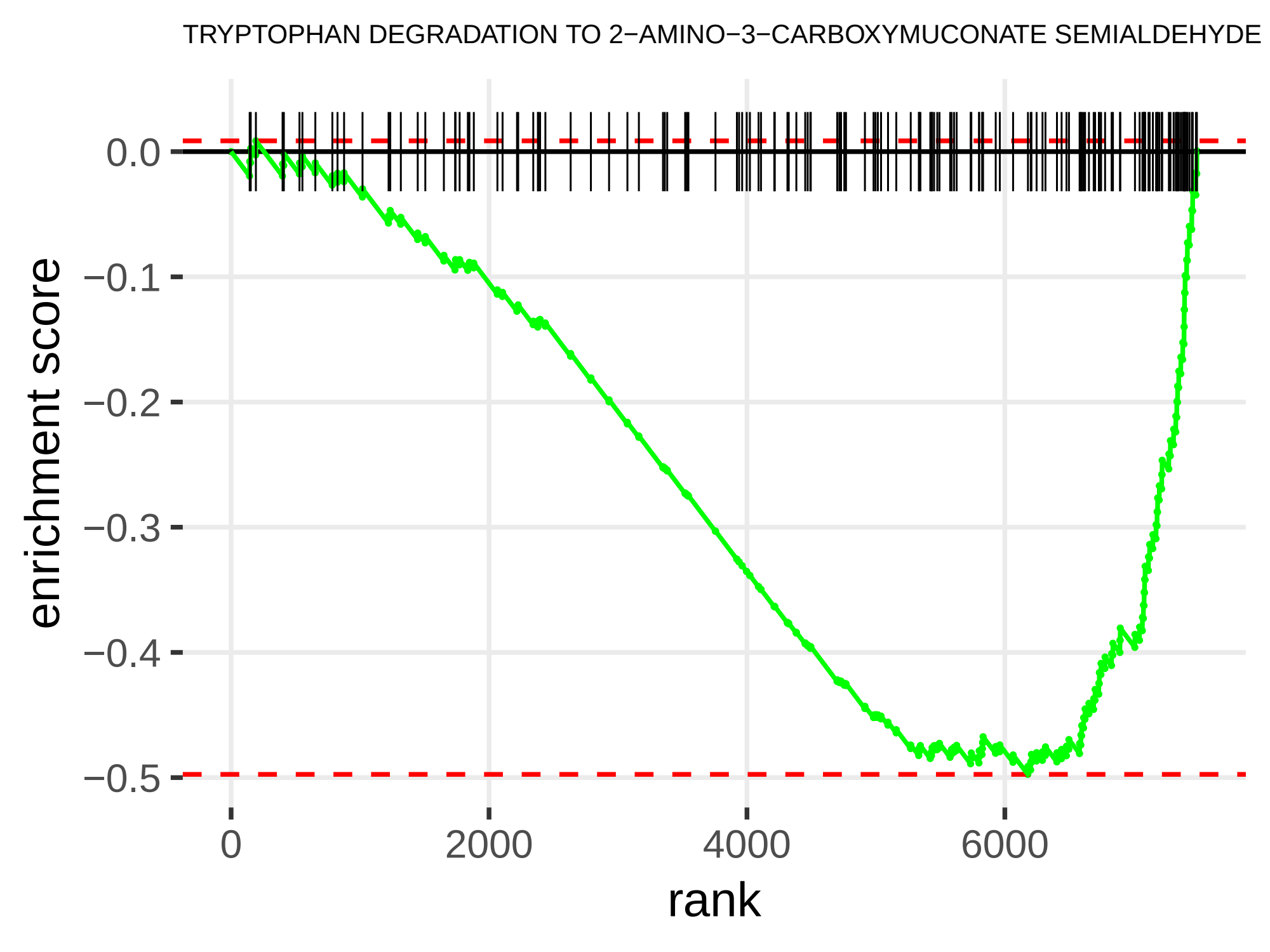

DOLICHOL AND DOLICHYL PHOSPHATE BIOSYNTHESIS
0.0
−0.1
−0.2
−0.3
−0.4
enrichment score
0
2000
4000
6000
rank

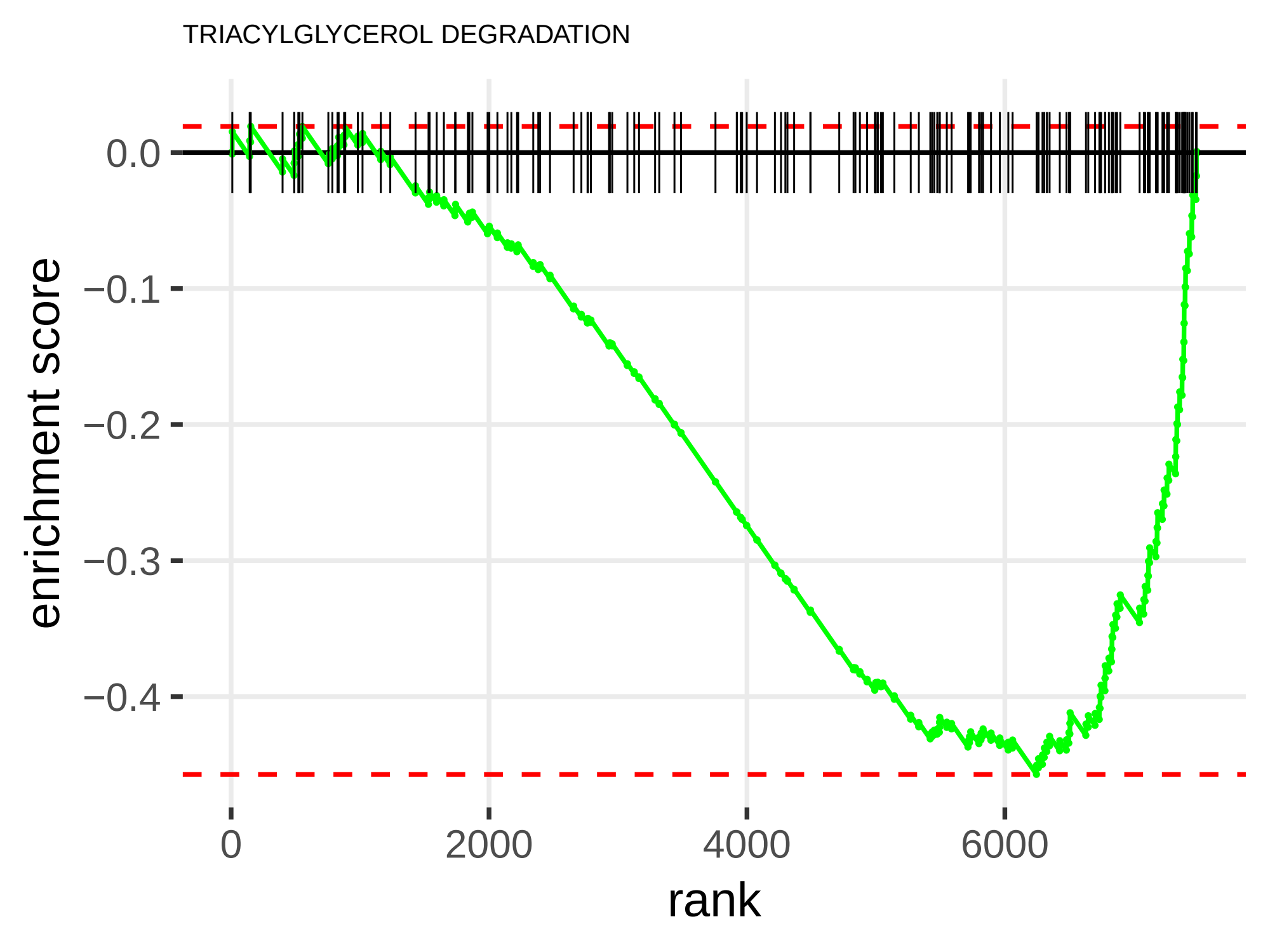

INOSINE−5'−PHOSPHATE BIOSYNTHESIS II
0.0
−0.1
−0.2
−0.3
−0.4
enrichment score
0
2000
4000
6000
rank

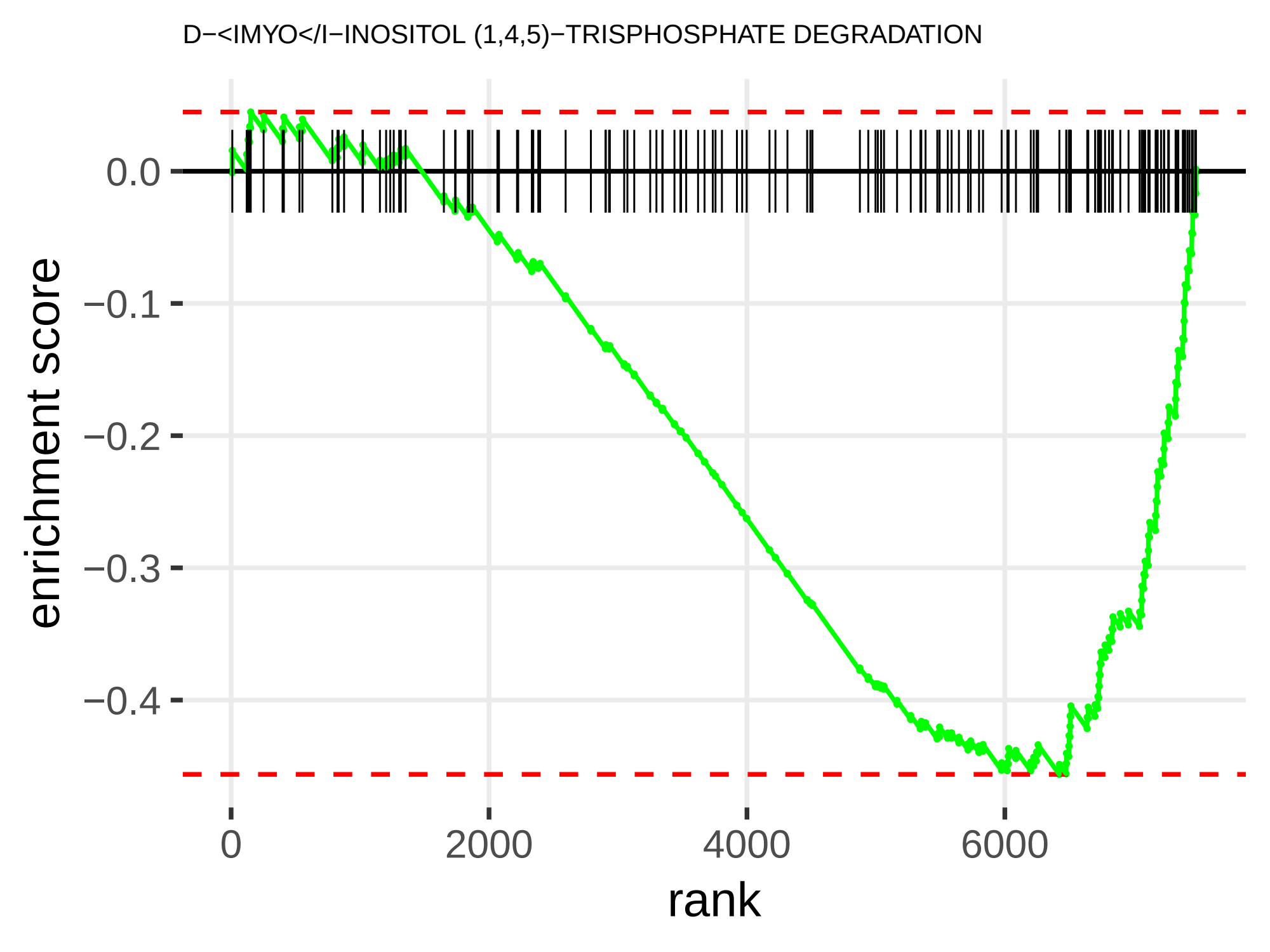

PURINE RIBONUCLEOSIDES DEGRADATION TO RIBOSE−1−PHOSPHATE
0.1
0.0
−0.1
−0.2
−0.3
−0.4
enrichment score
0
2000
4000
6000
rank

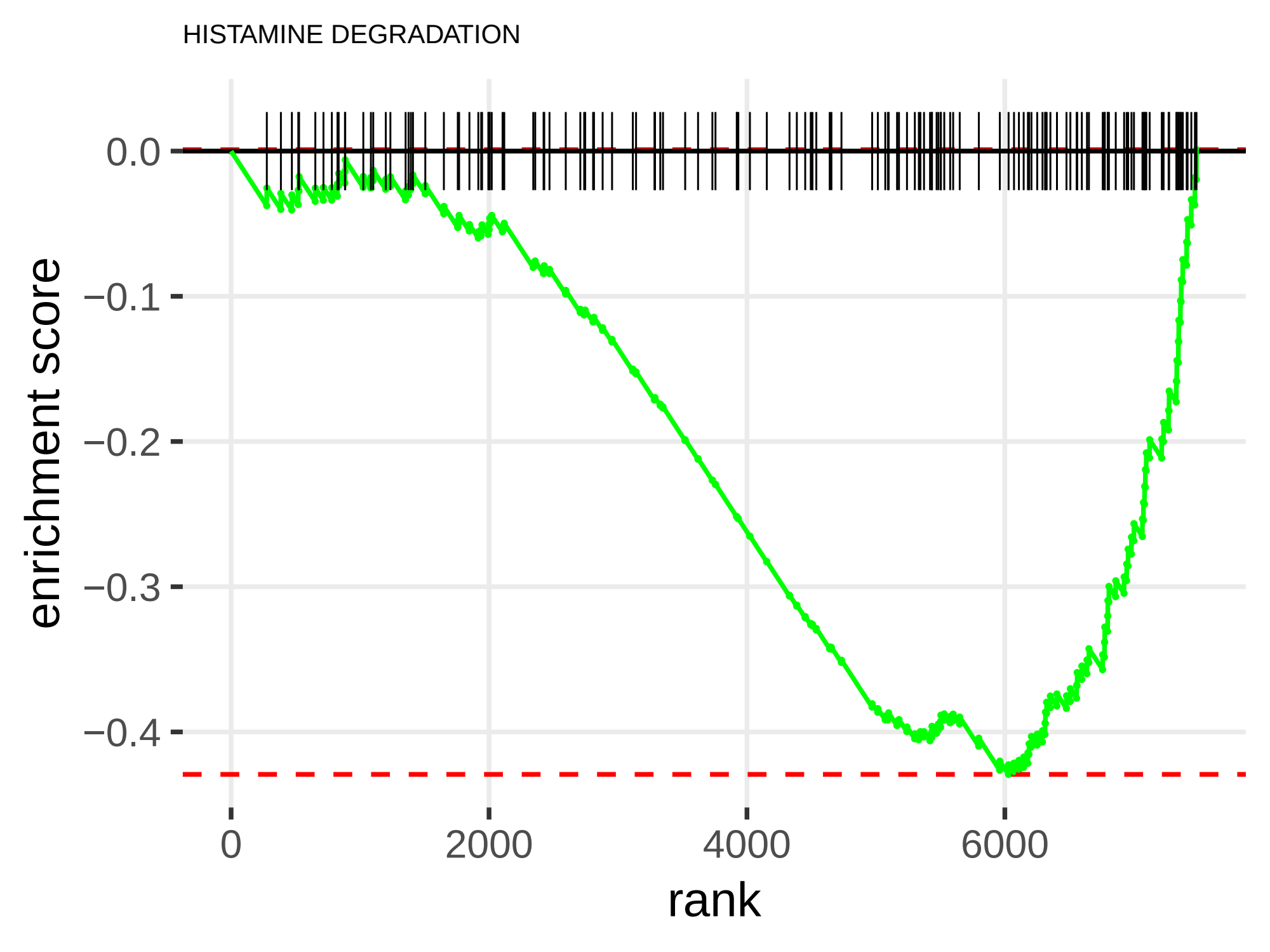

GLYCOGEN BIOSYNTHESIS II (FROM UDP−D−GLUCOSE)
0.0
−0.1
−0.2
−0.3
−0.4
enrichment score
0
2000
4000
6000
rank

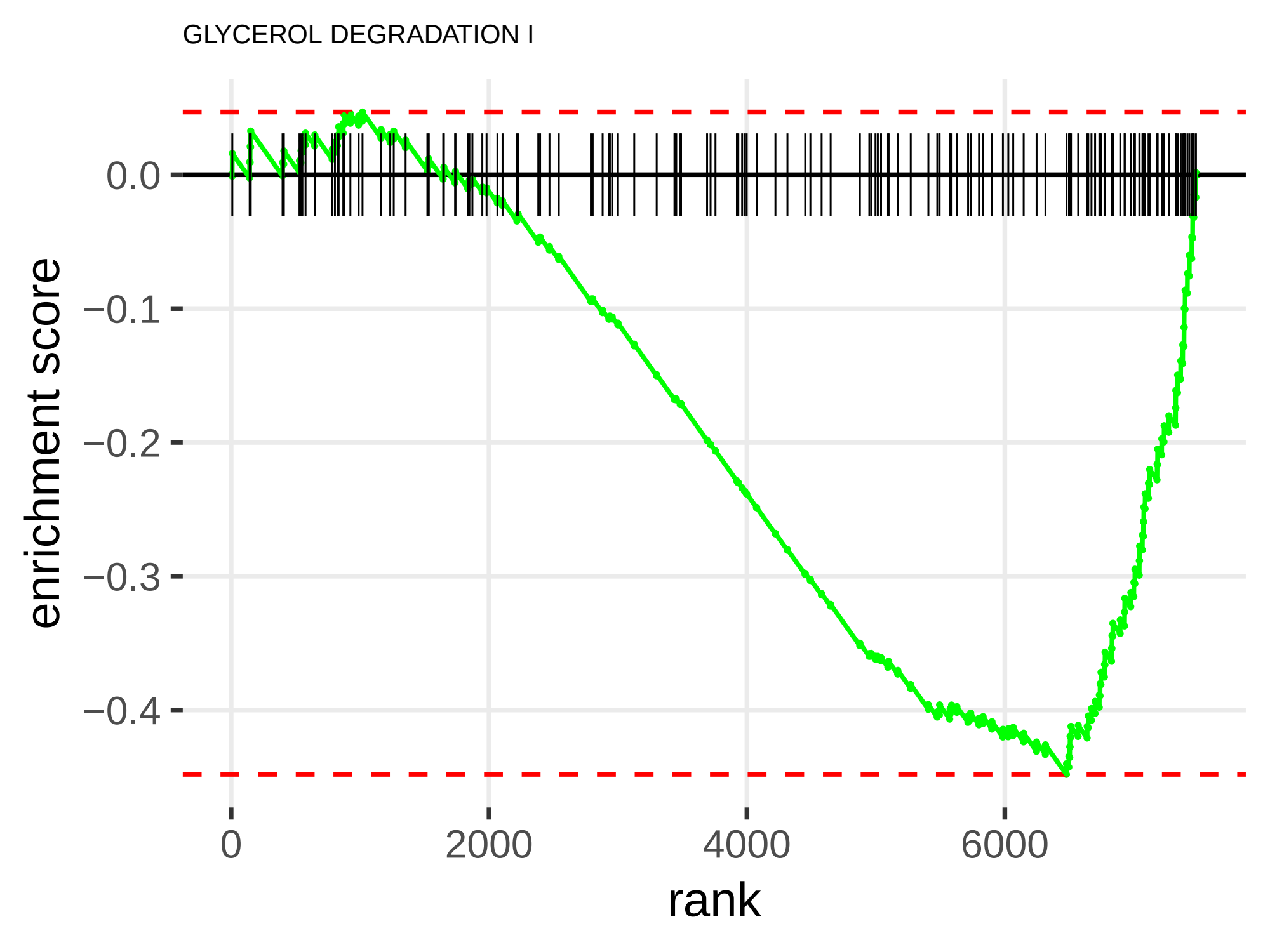

OLEATE BIOSYNTHESIS II (ANIMALS)
0.0
−0.1
−0.2
−0.3
−0.4
enrichment score
0
2000
4000
6000
rank

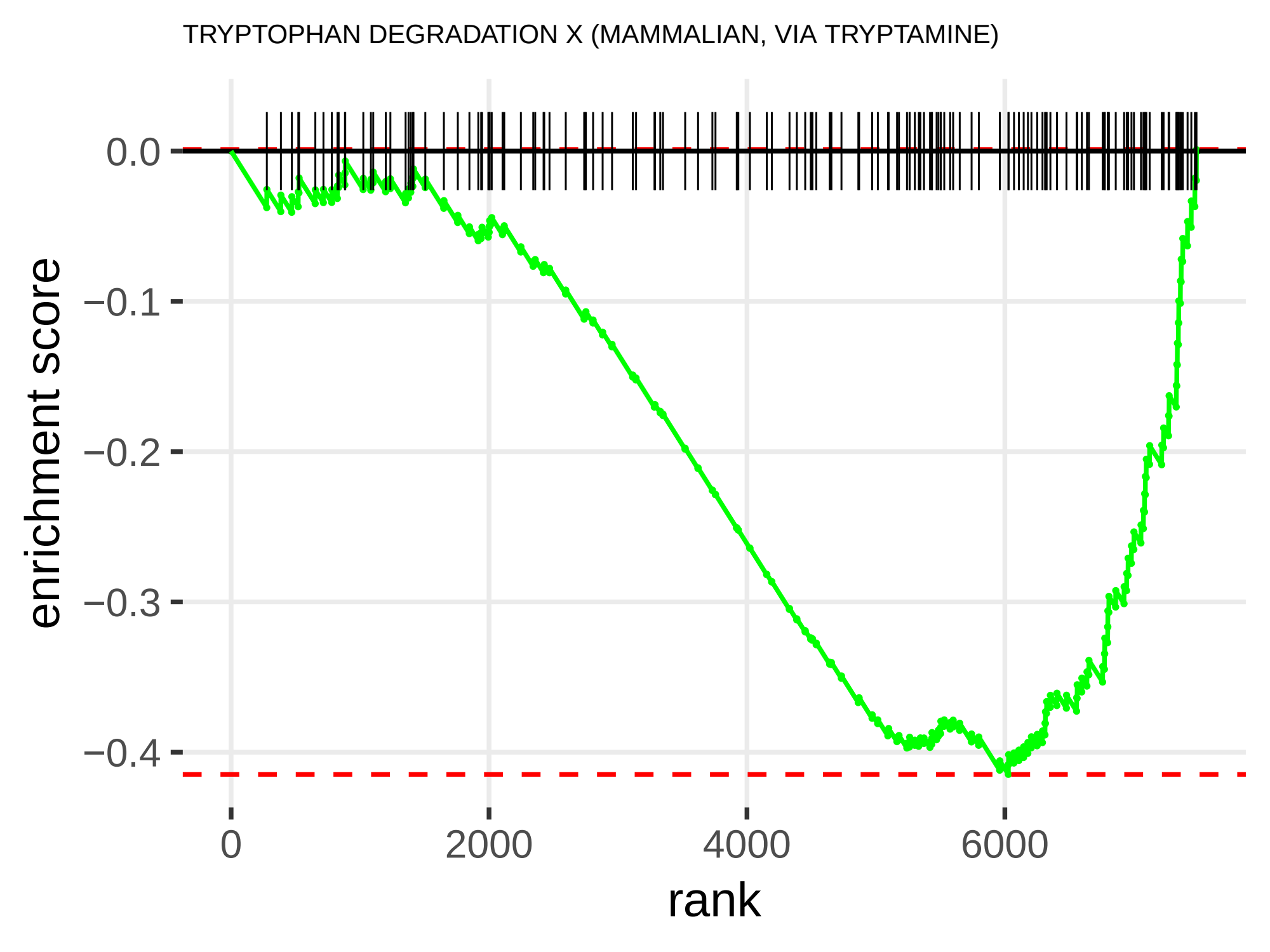

TRYPTOPHAN DEGRADATION TO 2−AMINO−3−CARBOXYMUCONATE SEMIALDEHYDE
0.0
−0.1
−0.2
−0.3
−0.4
−0.5
enrichment score
0
2000
4000
6000
rank

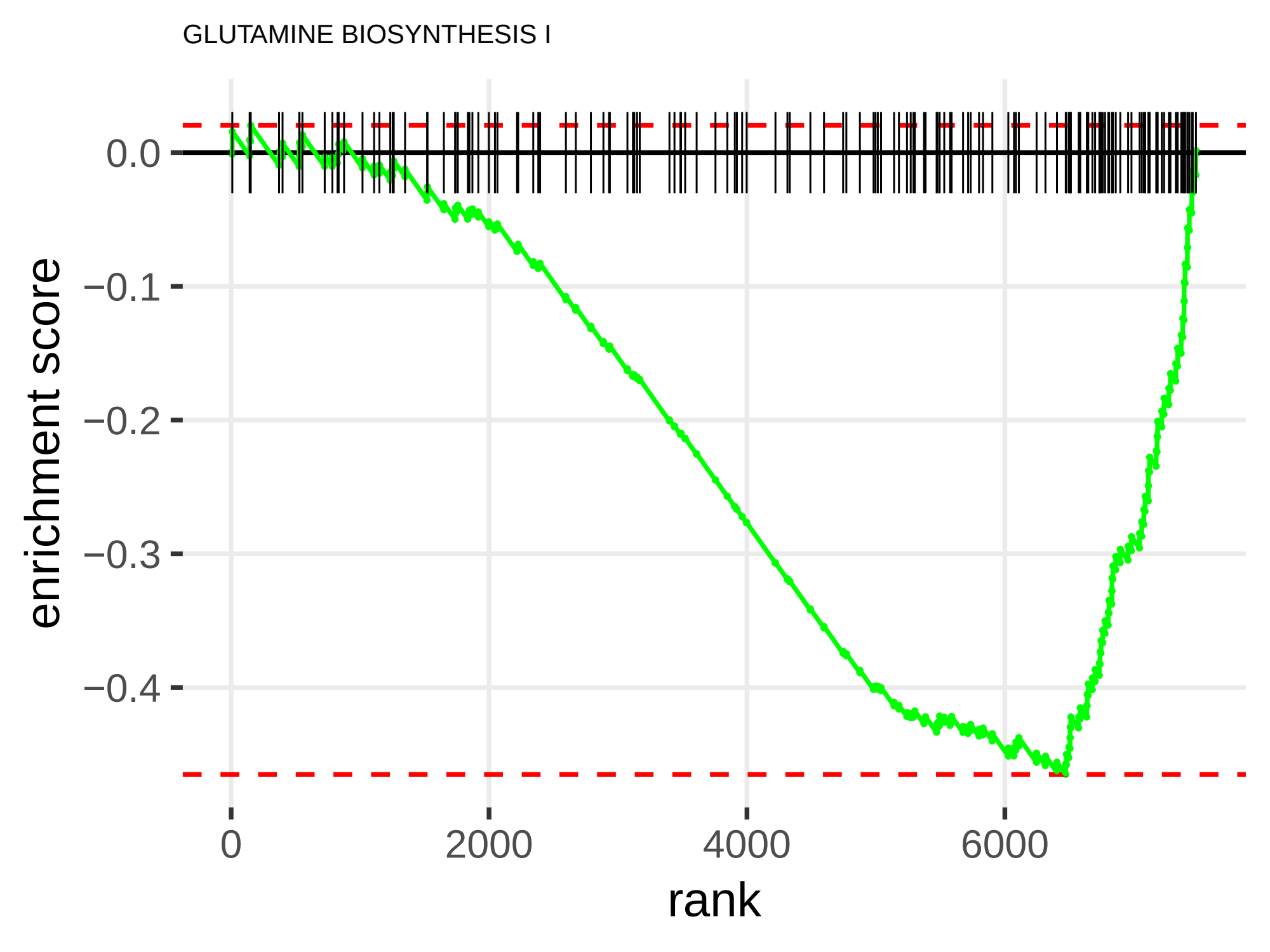

TRIACYLGLYCEROL DEGRADATION
0.0
−0.1
−0.2
−0.3
−0.4
enrichment score
0
2000
4000
6000
rank

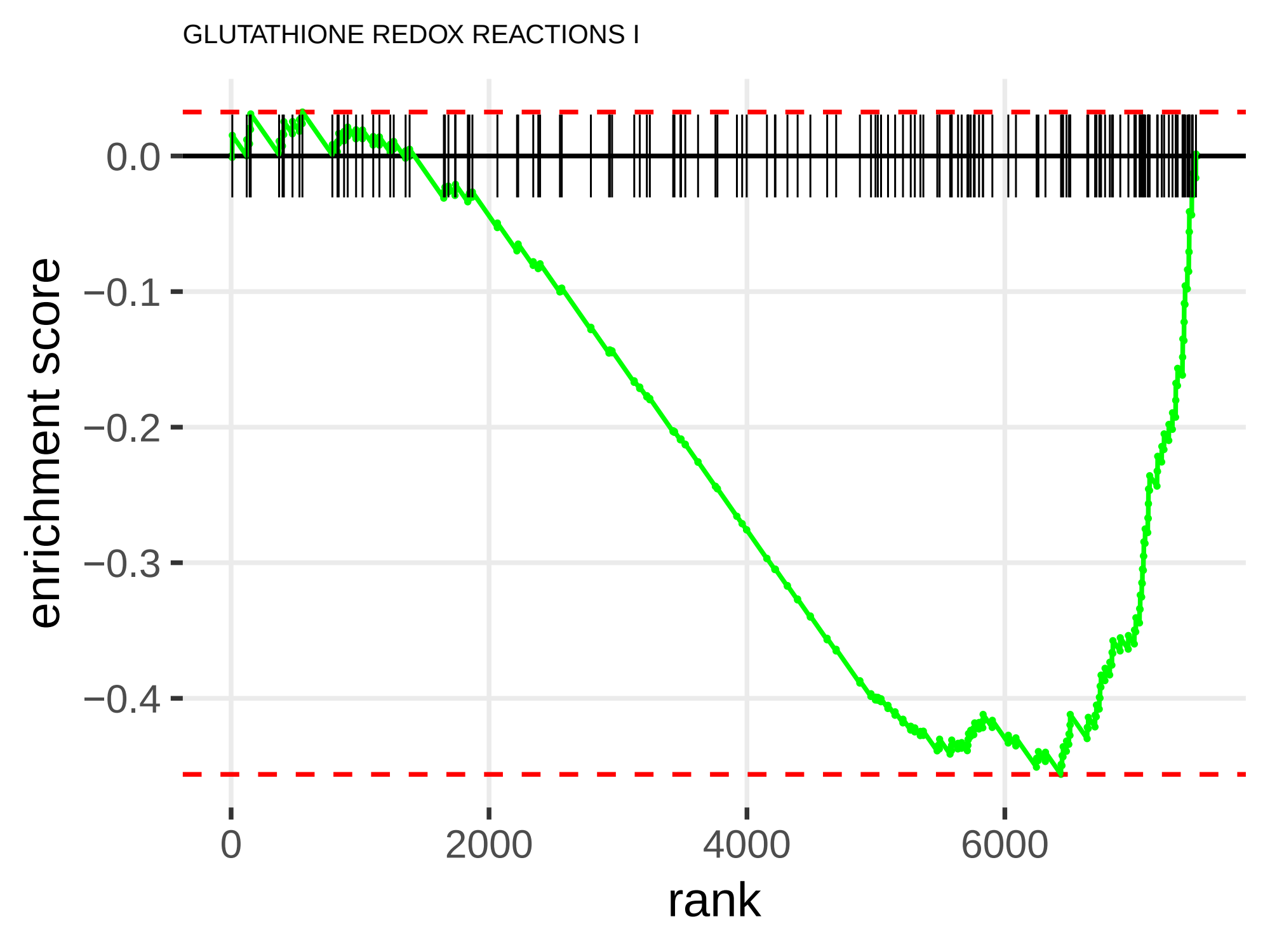

D−<IMYO</I−INOSITOL (1,4,5)−TRISPHOSPHATE DEGRADATION
enrichment score
0.0
−0.1
−0.2
−0.3
−0.4
0
2000
4000
6000
rank

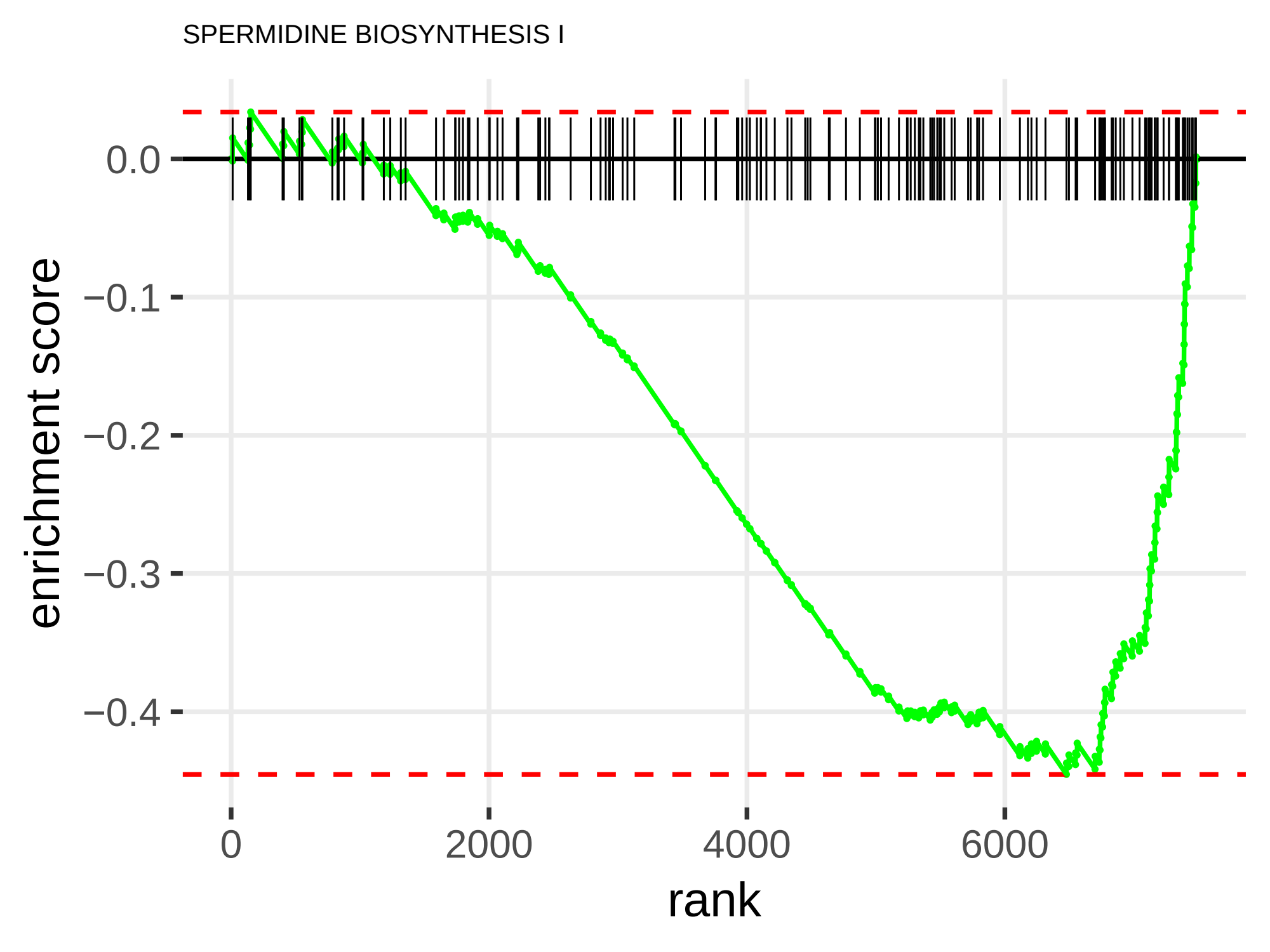

HISTAMINE DEGRADATION
0.0
−0.1
−0.2
−0.3
−0.4
enrichment score
0
2000
4000
6000
rank

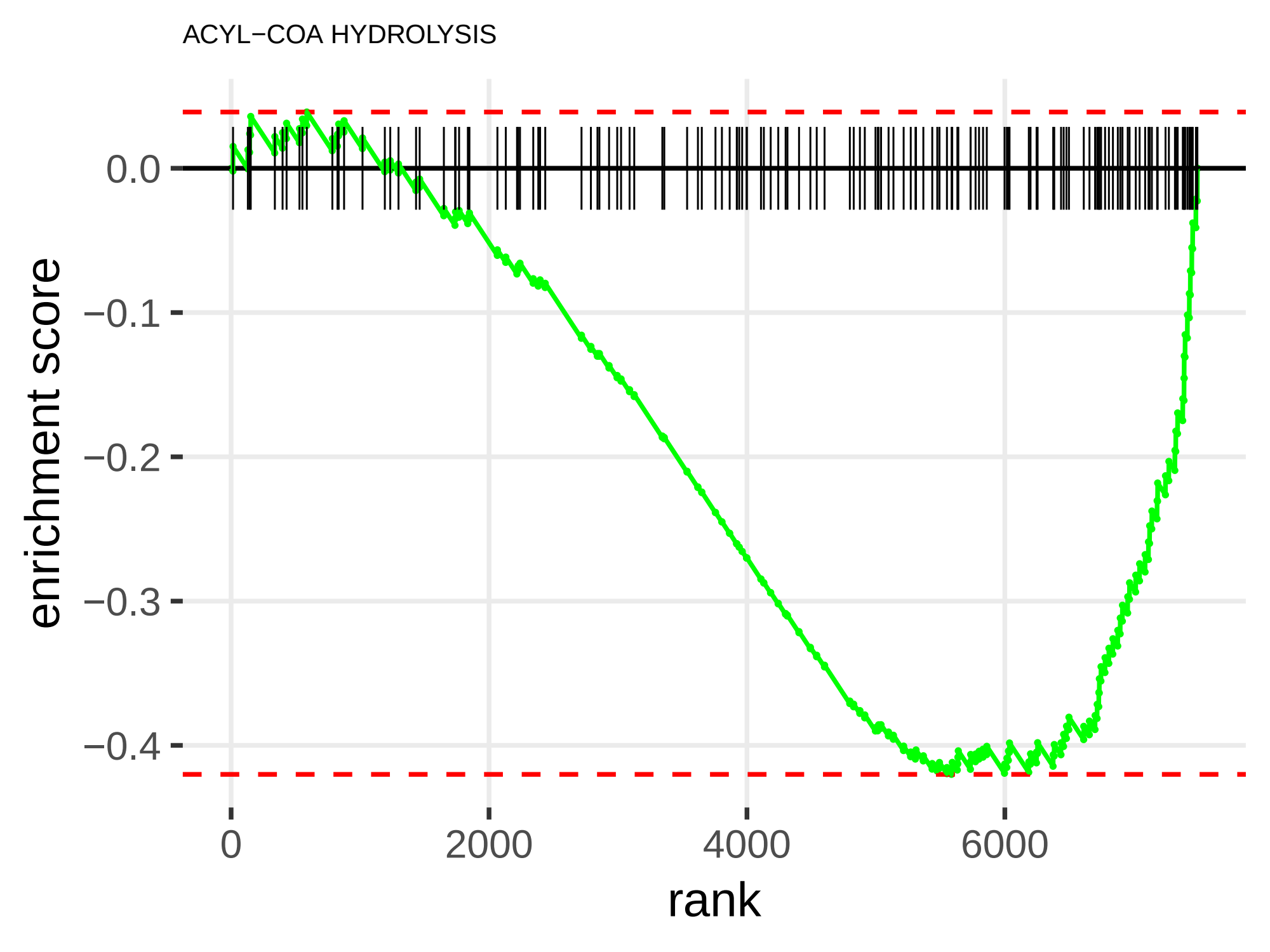

GLYCEROL DEGRADATION I
0.0
−0.1
−0.2
−0.3
−0.4
enrichment score
0
2000
4000
6000
rank

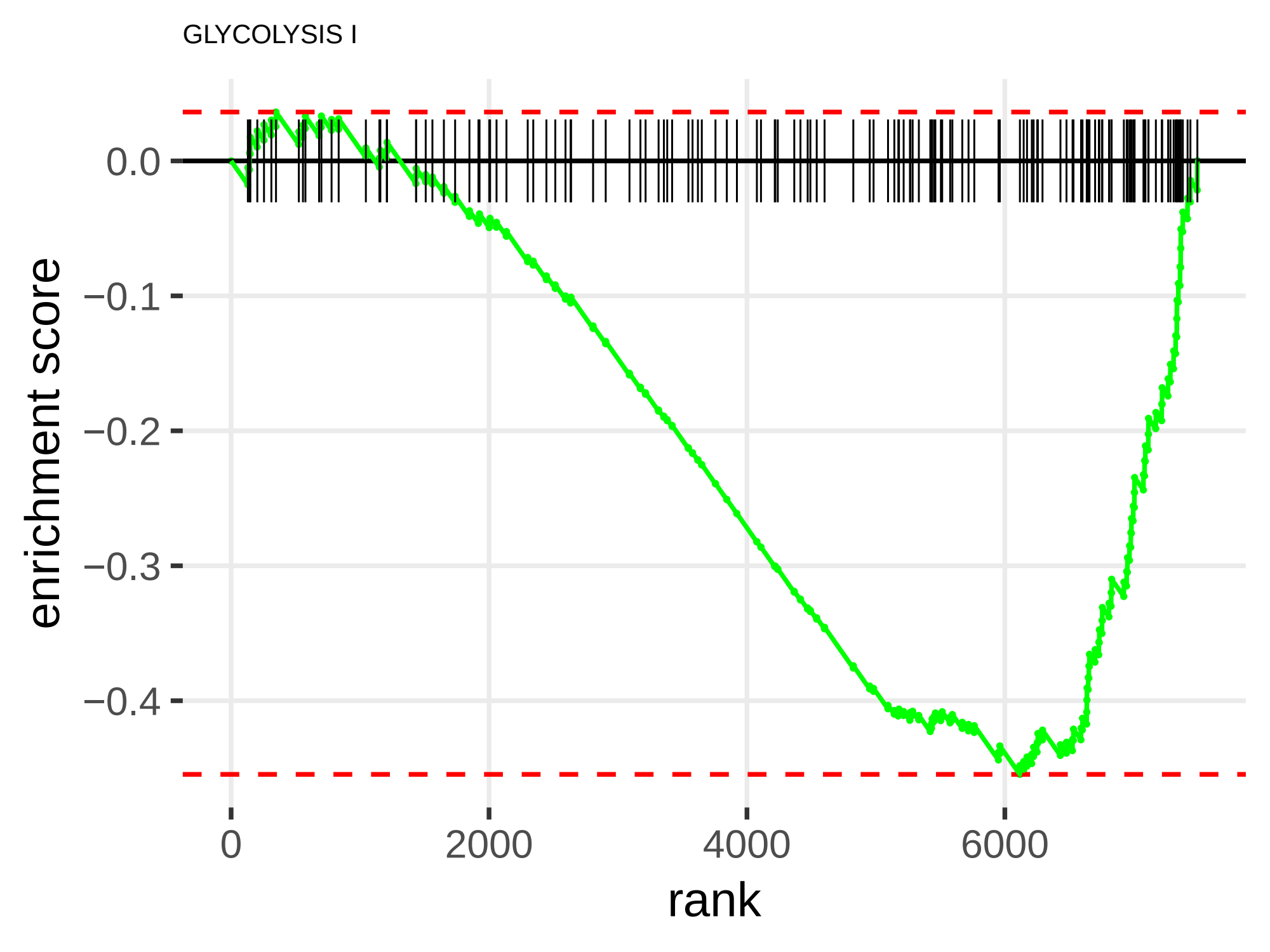

TRYPTOPHAN DEGRADATION X (MAMMALIAN, VIA TRYPTAMINE)
0.0
−0.1
−0.2
−0.3
−0.4
enrichment score
0
2000
4000
6000
rank

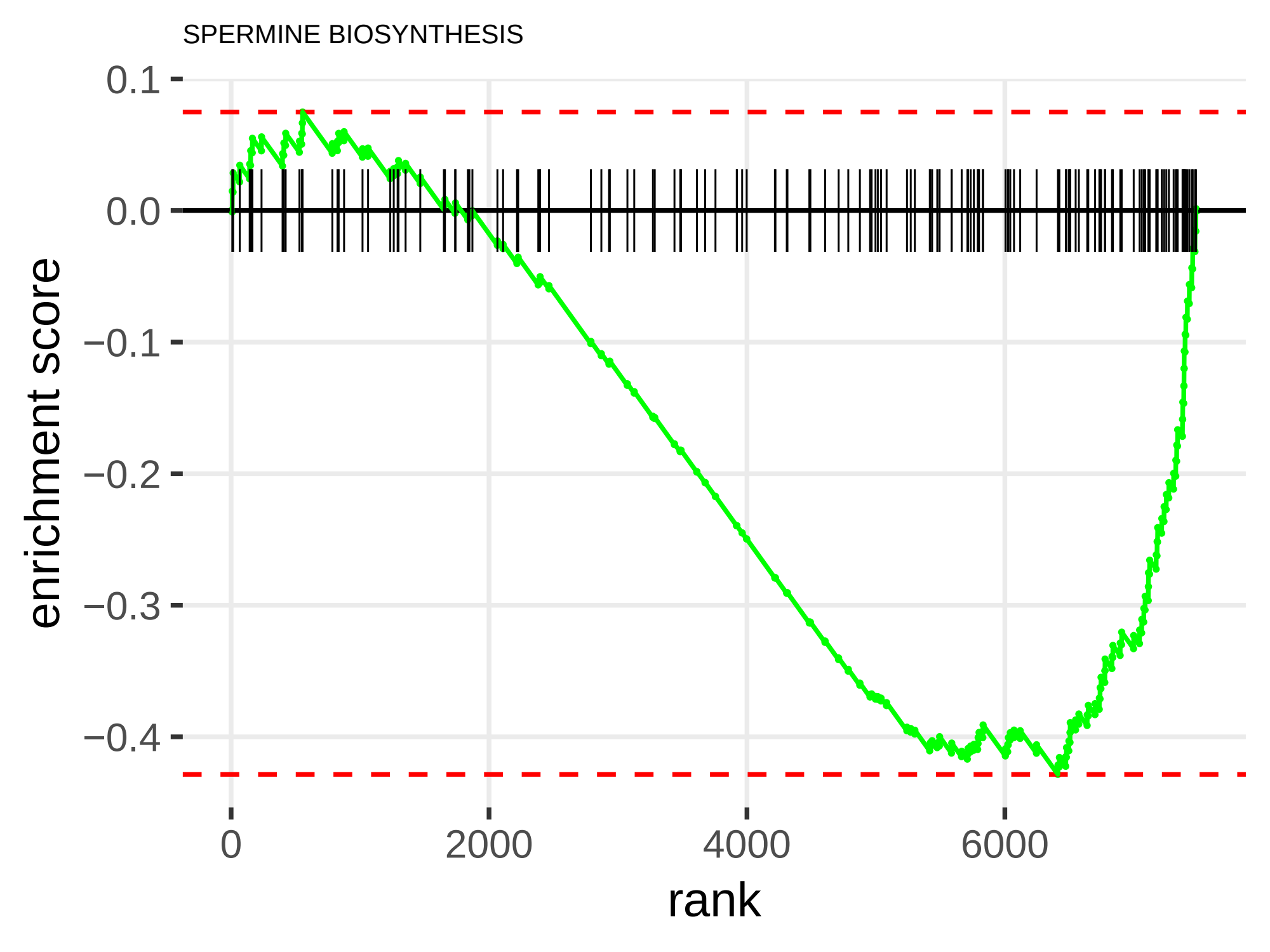

GLUTAMINE BIOSYNTHESIS I
enrichment score
0.0
−0.1
−0.2
−0.3
−0.4
0
2000
4000
6000
rank

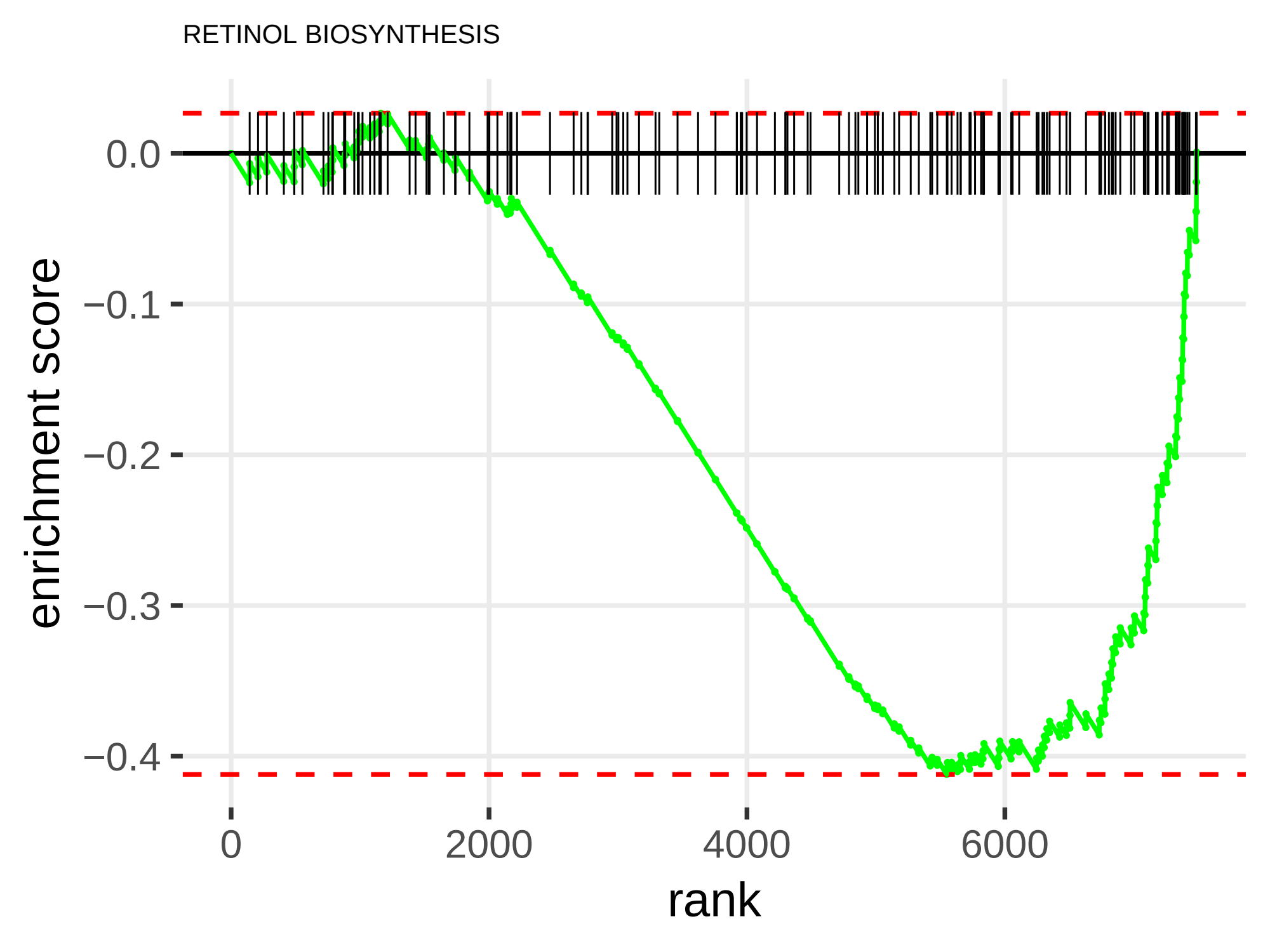

GLUTATHIONE REDOX REACTIONS I
0.0
−0.1
−0.2
−0.3
−0.4
enrichment score
0
2000
4000
6000
rank

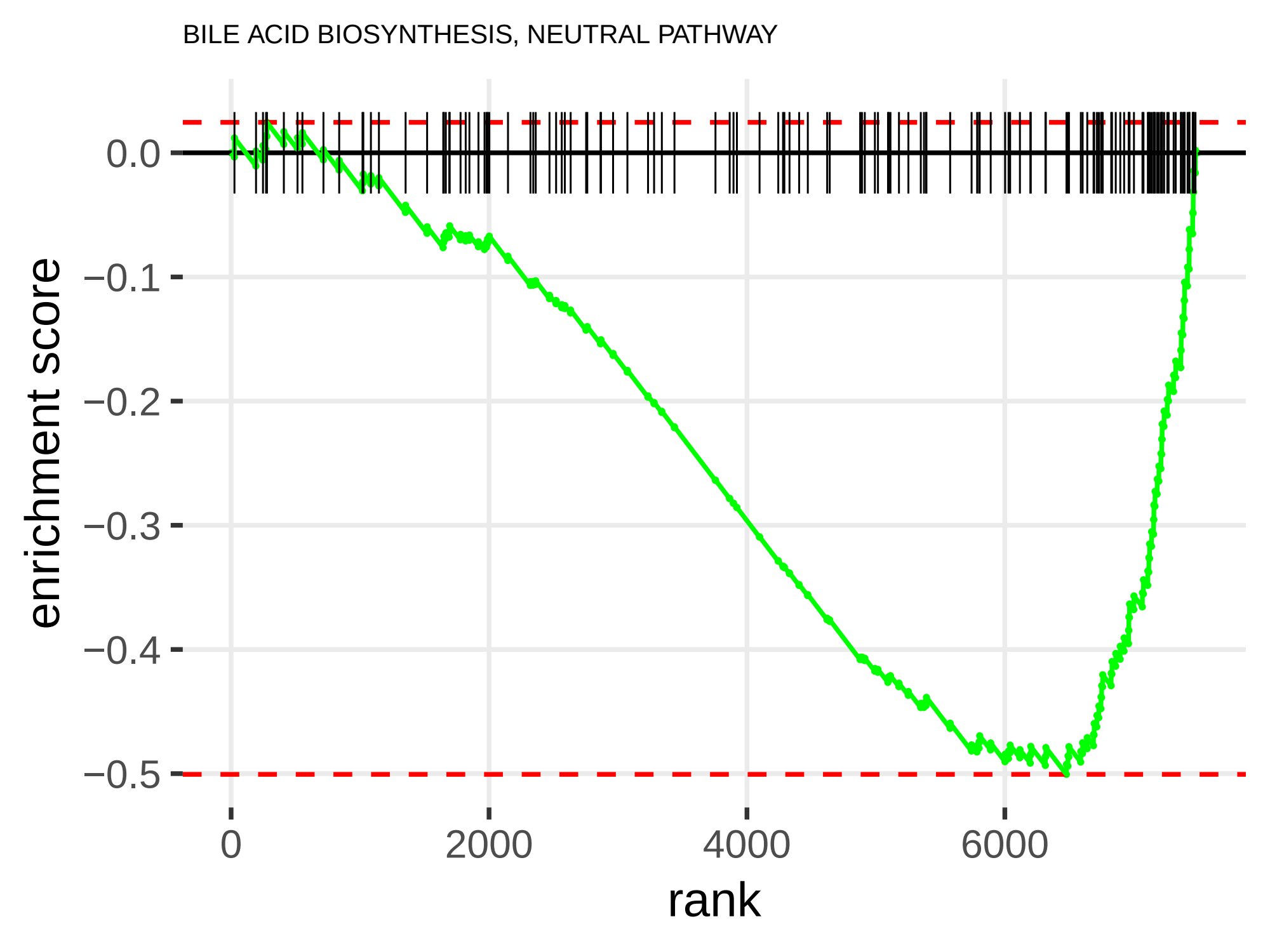

SPERMIDINE BIOSYNTHESIS I
0.0
−0.1
−0.2
−0.3
−0.4
enrichment score
0
2000
4000
6000
rank

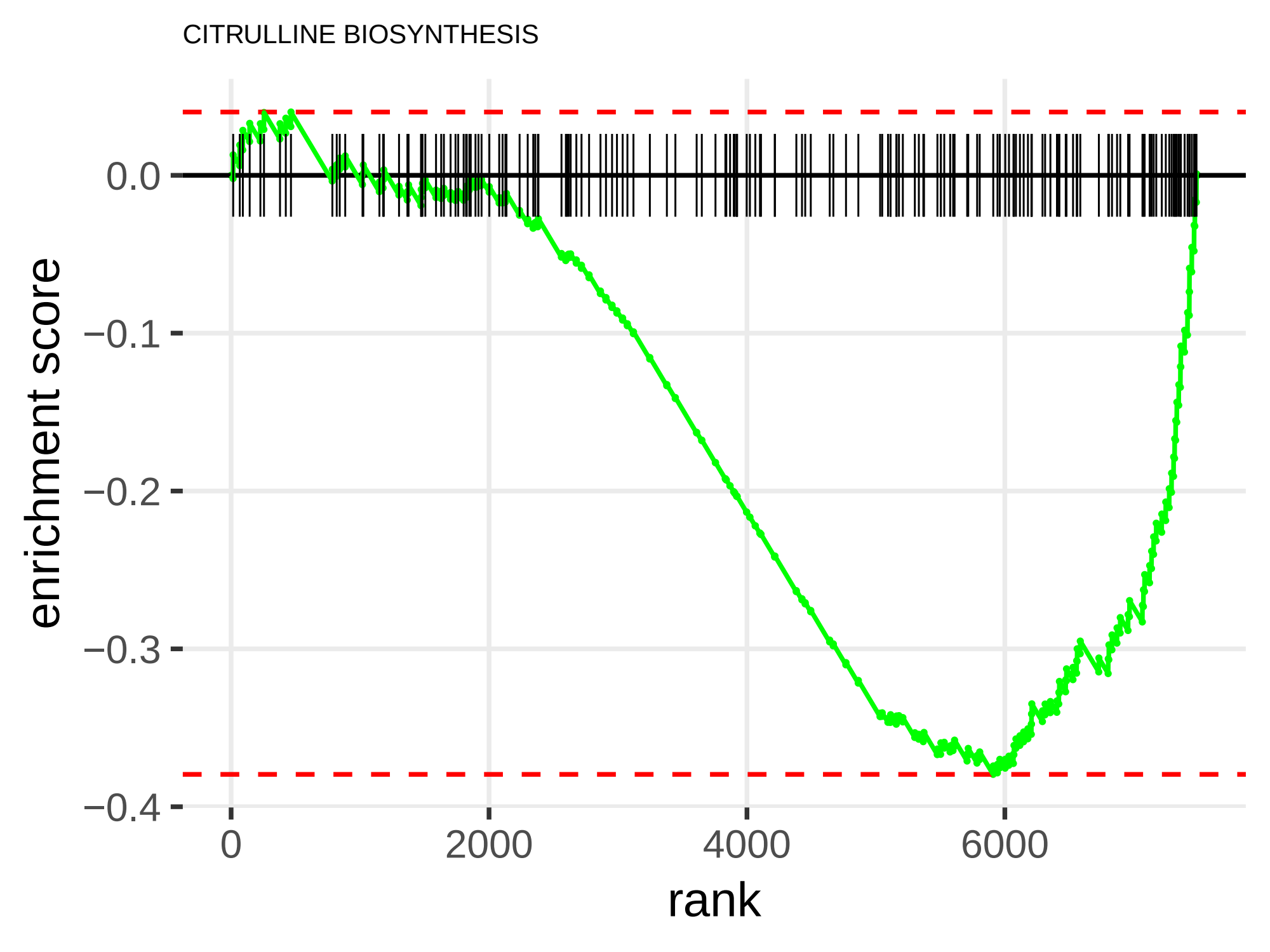

ACYL−COA HYDROLYSIS
0.0
−0.1
−0.2
−0.3
−0.4
enrichment score
0
2000
4000
6000
rank

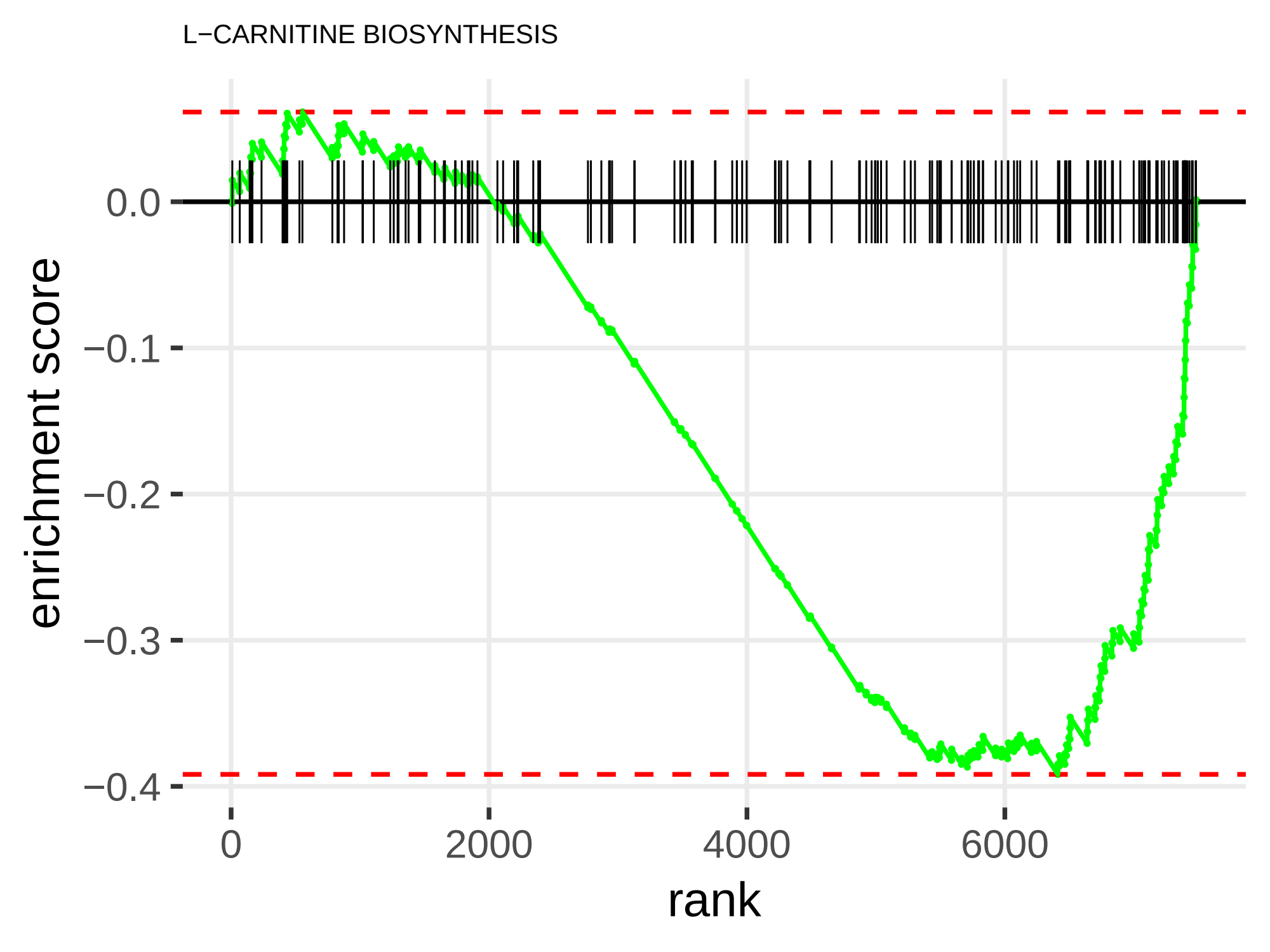

GLYCOLYSIS I
0.0
−0.1
−0.2
−0.3
−0.4
enrichment score
0
2000
4000
6000
rank

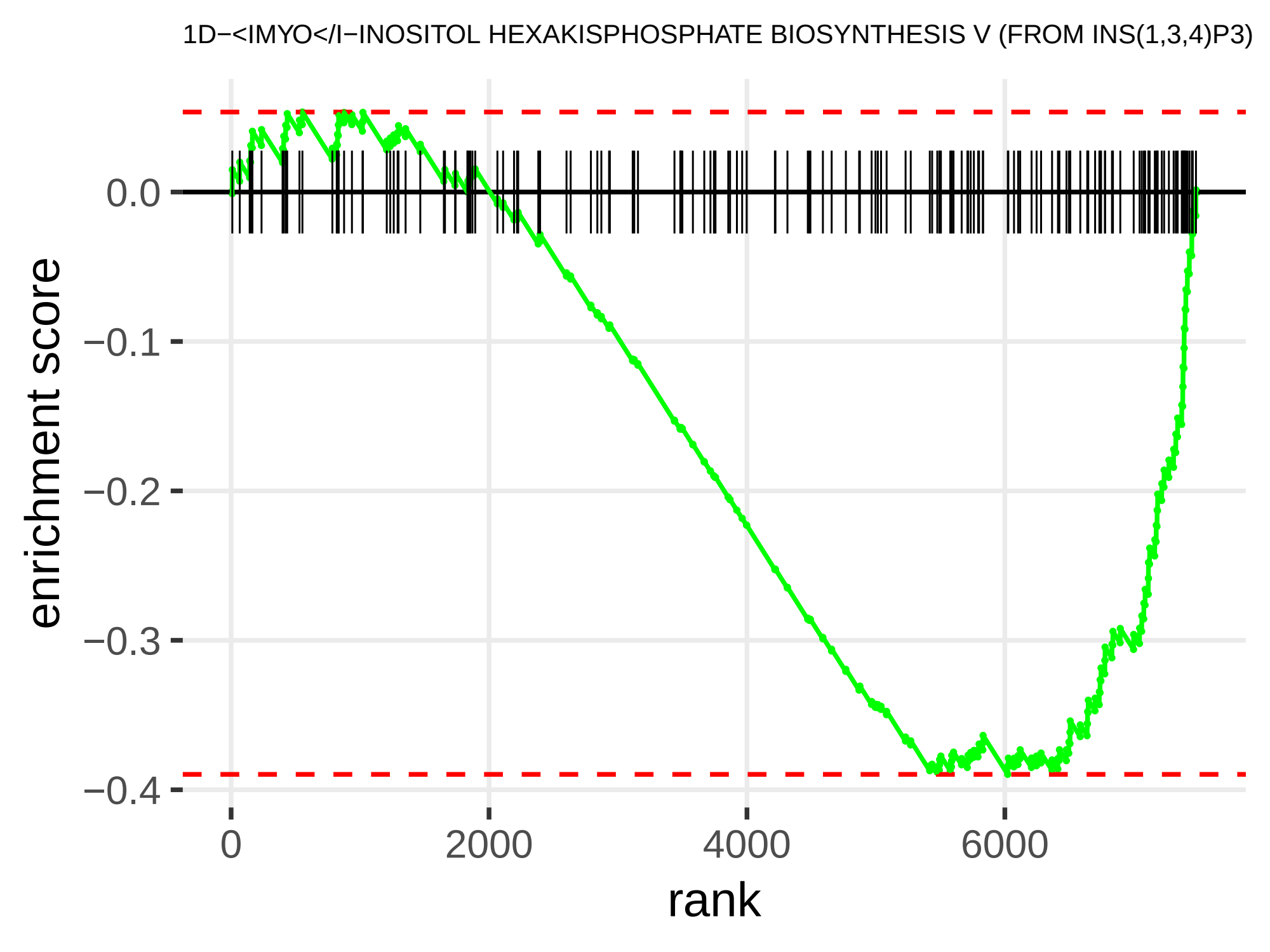

SPERMINE BIOSYNTHESIS
0.1
0.0
−0.1
−0.2
−0.3
−0.4
enrichment score
0
2000
4000
6000
rank

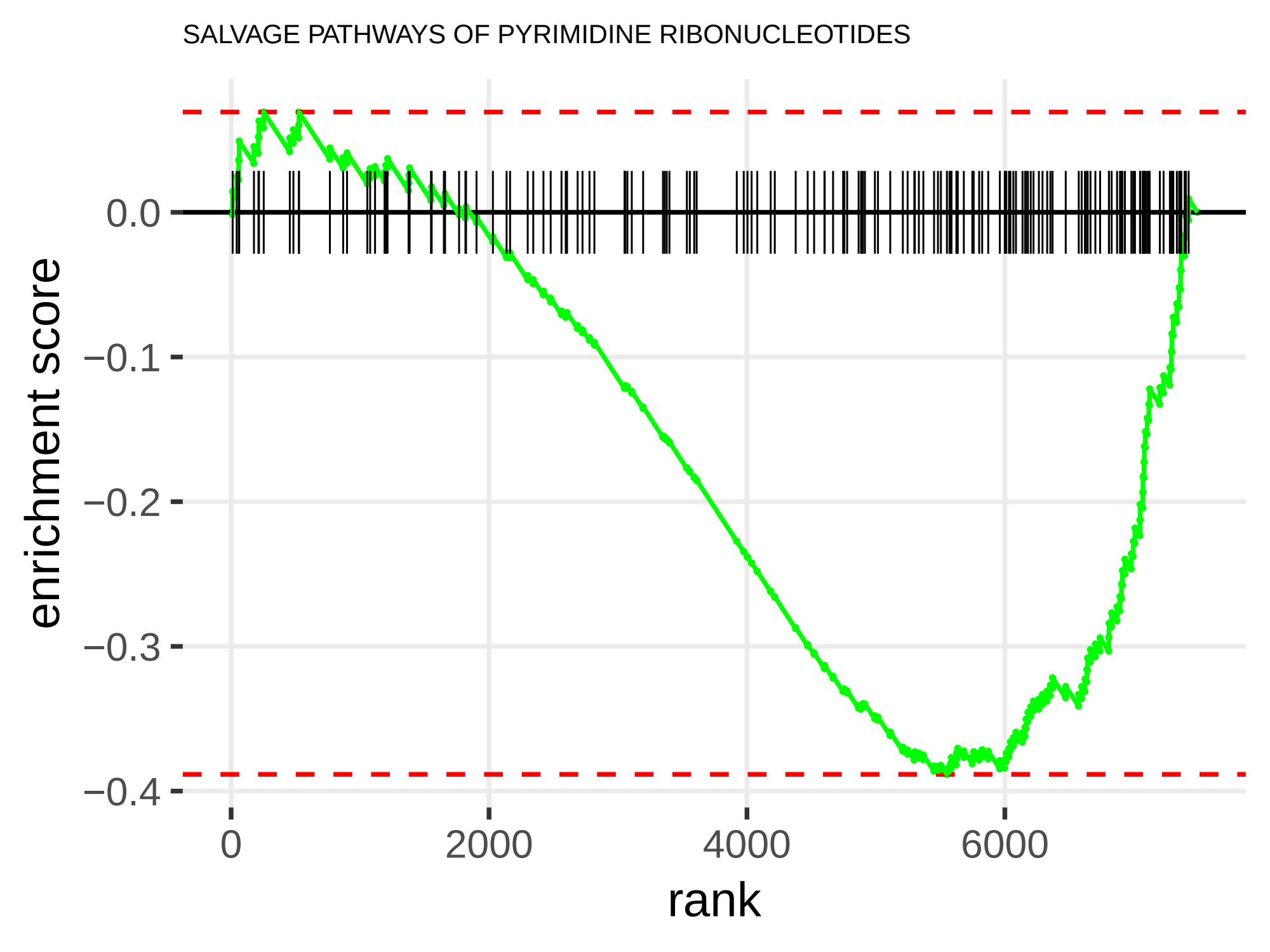

RETINOL BIOSYNTHESIS
0.0
−0.1
−0.2
−0.3
−0.4
enrichment score
0
2000
4000
6000
rank

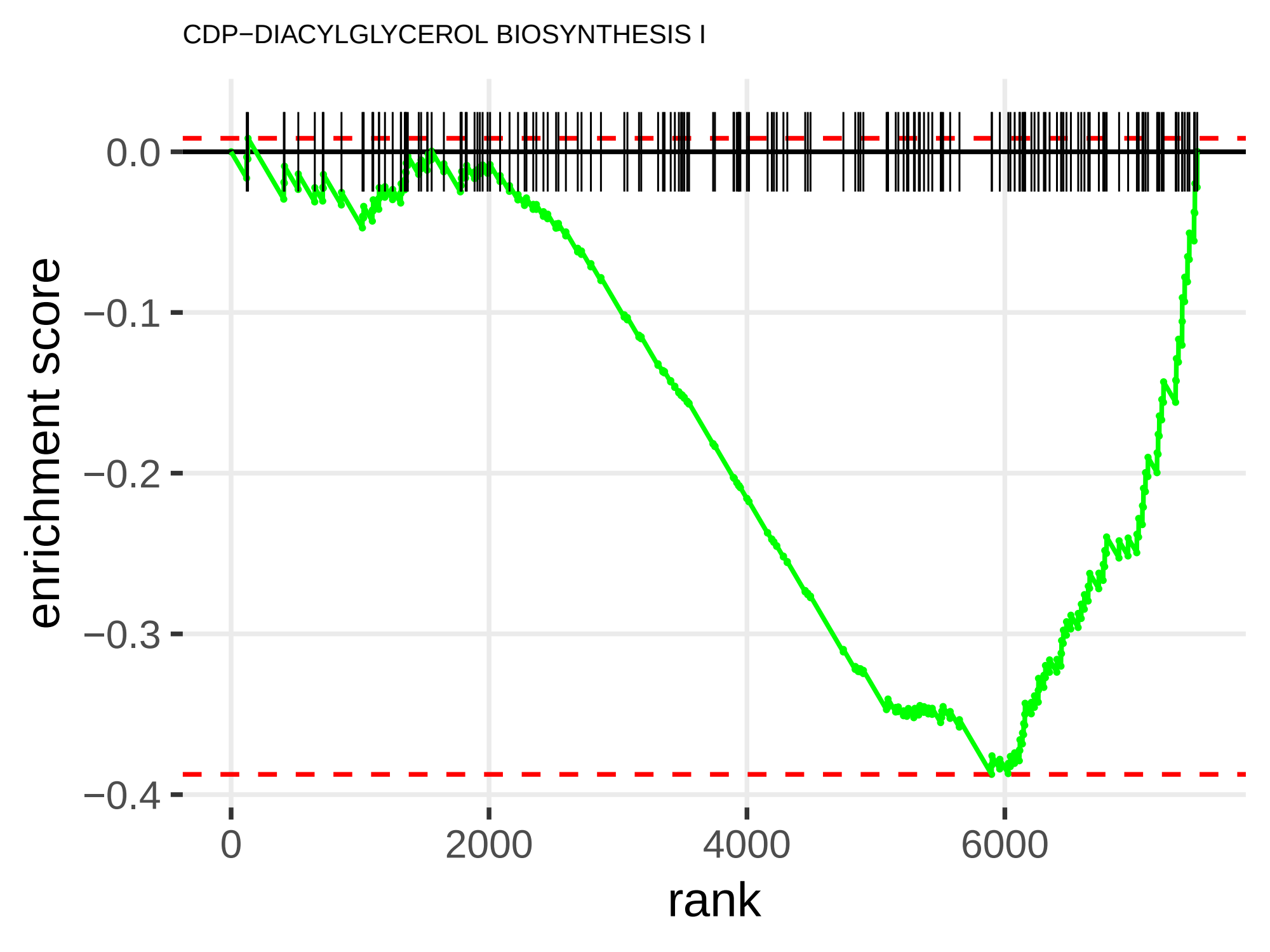

BILE ACID BIOSYNTHESIS, NEUTRAL PATHWAY
0.0
−0.1
−0.2
−0.3
−0.4
−0.5
enrichment score
0
2000
4000
6000
rank

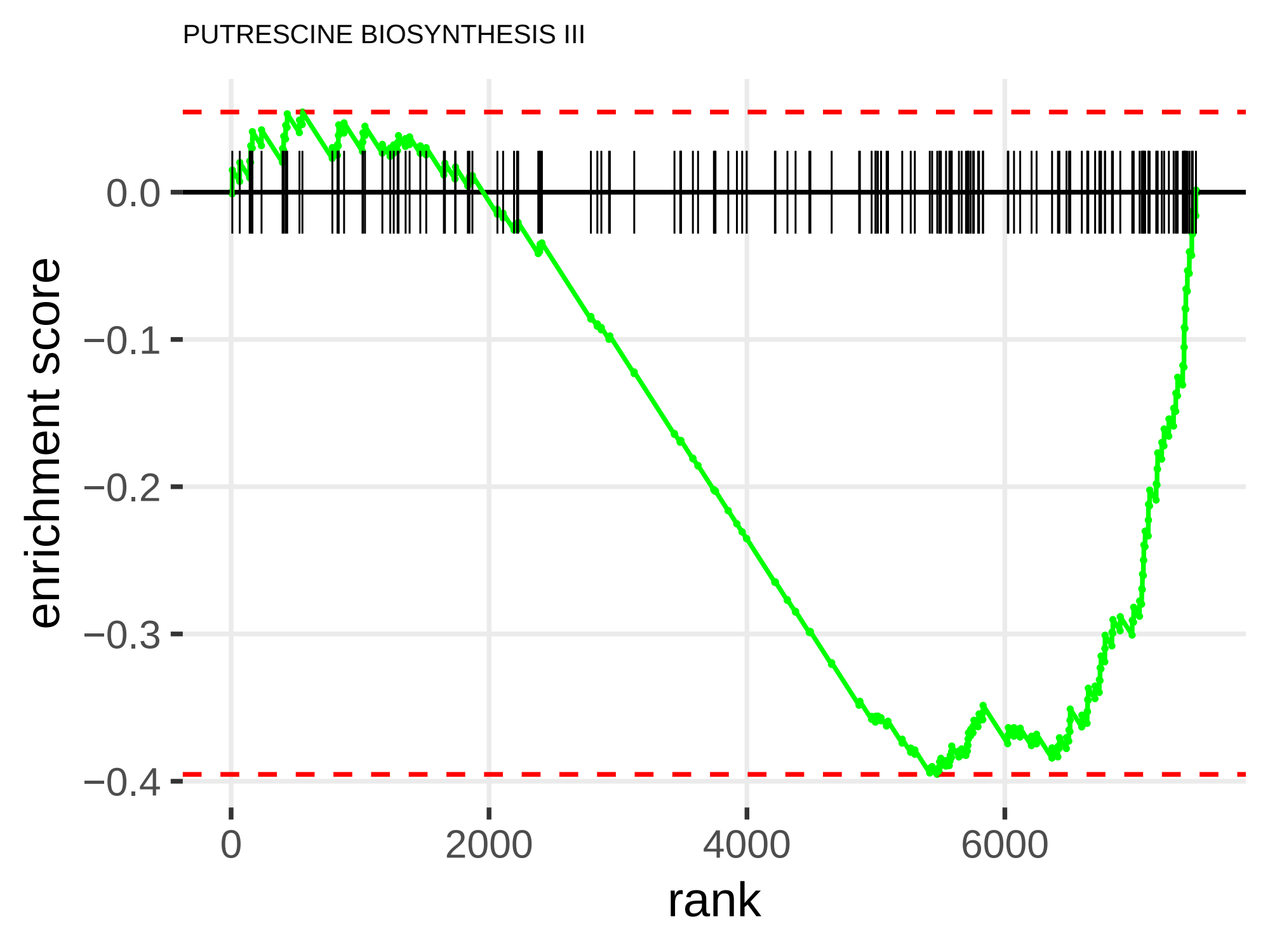

CITRULLINE BIOSYNTHESIS
0.0
−0.1
−0.2
−0.3
−0.4
enrichment score
0
2000
4000
6000
rank

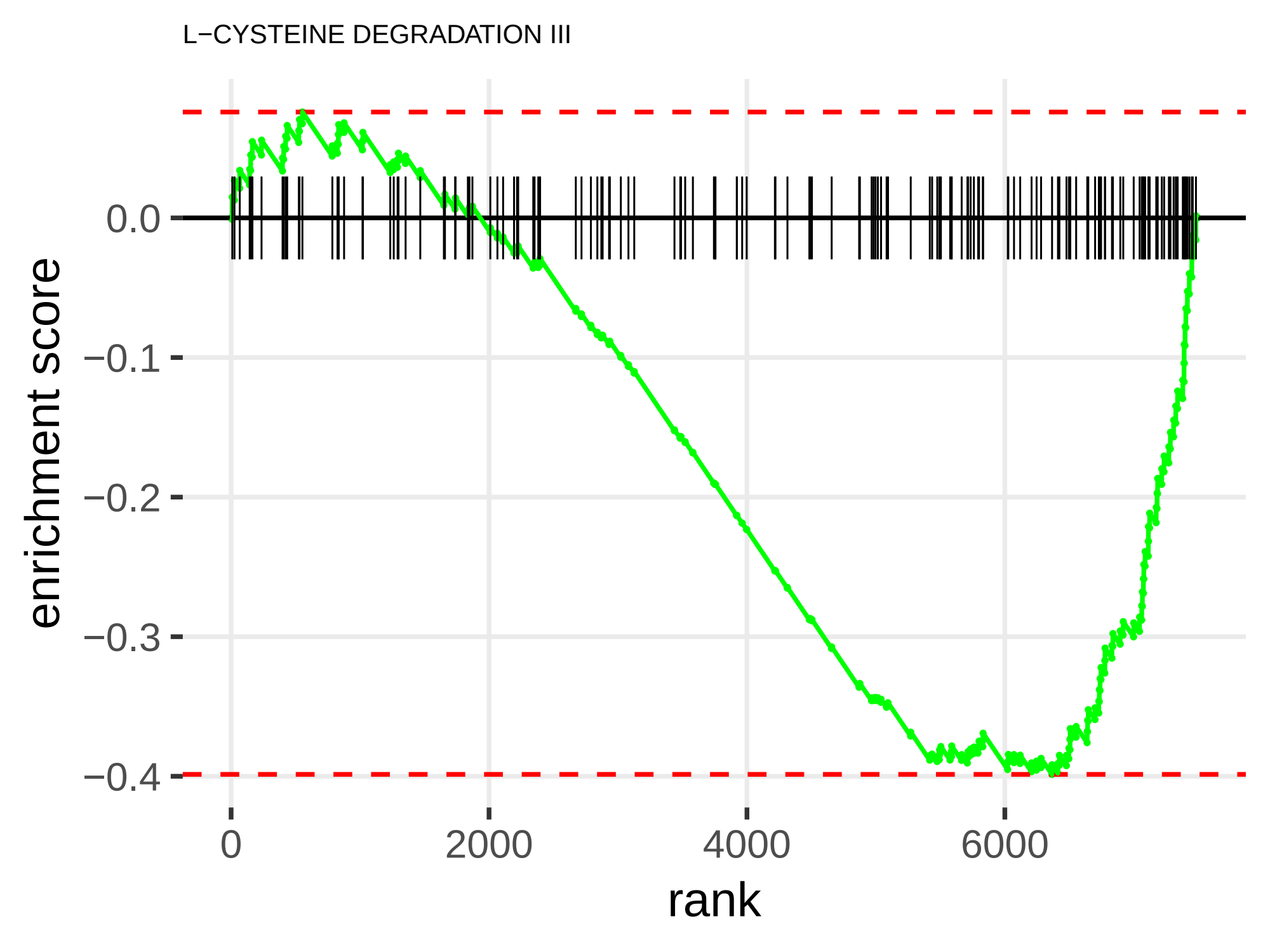

L−CARNITINE BIOSYNTHESIS
enrichment score
0.0
−0.1
−0.2
−0.3
−0.4
0
2000
4000
6000
rank

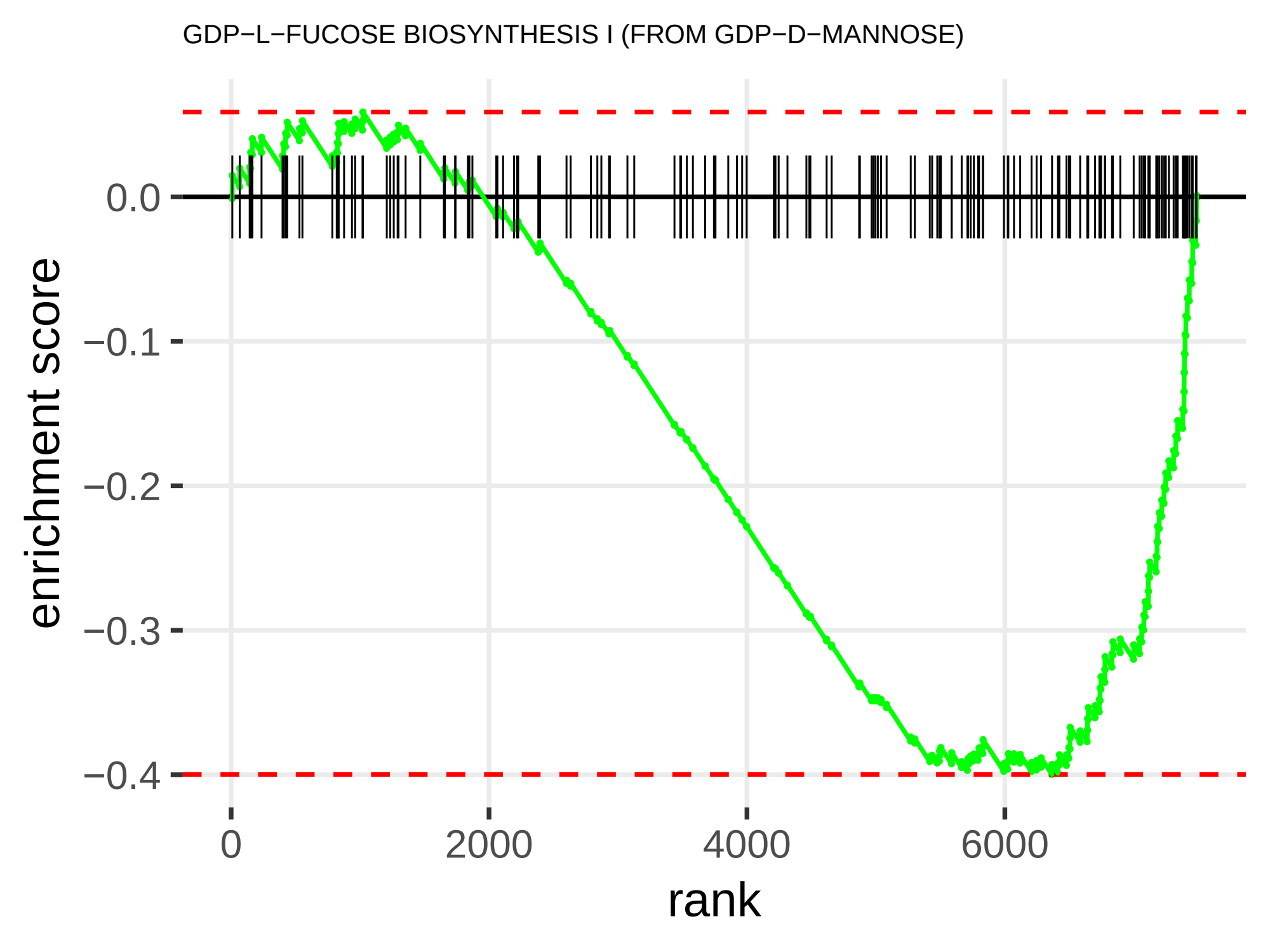

1D−<IMYO</I−INOSITOL HEXAKISPHOSPHATE BIOSYNTHESIS V (FROM INS(1,3,4)P3)
0.0
−0.1
−0.2
−0.3
−0.4
enrichment score
0
2000
4000
6000
rank

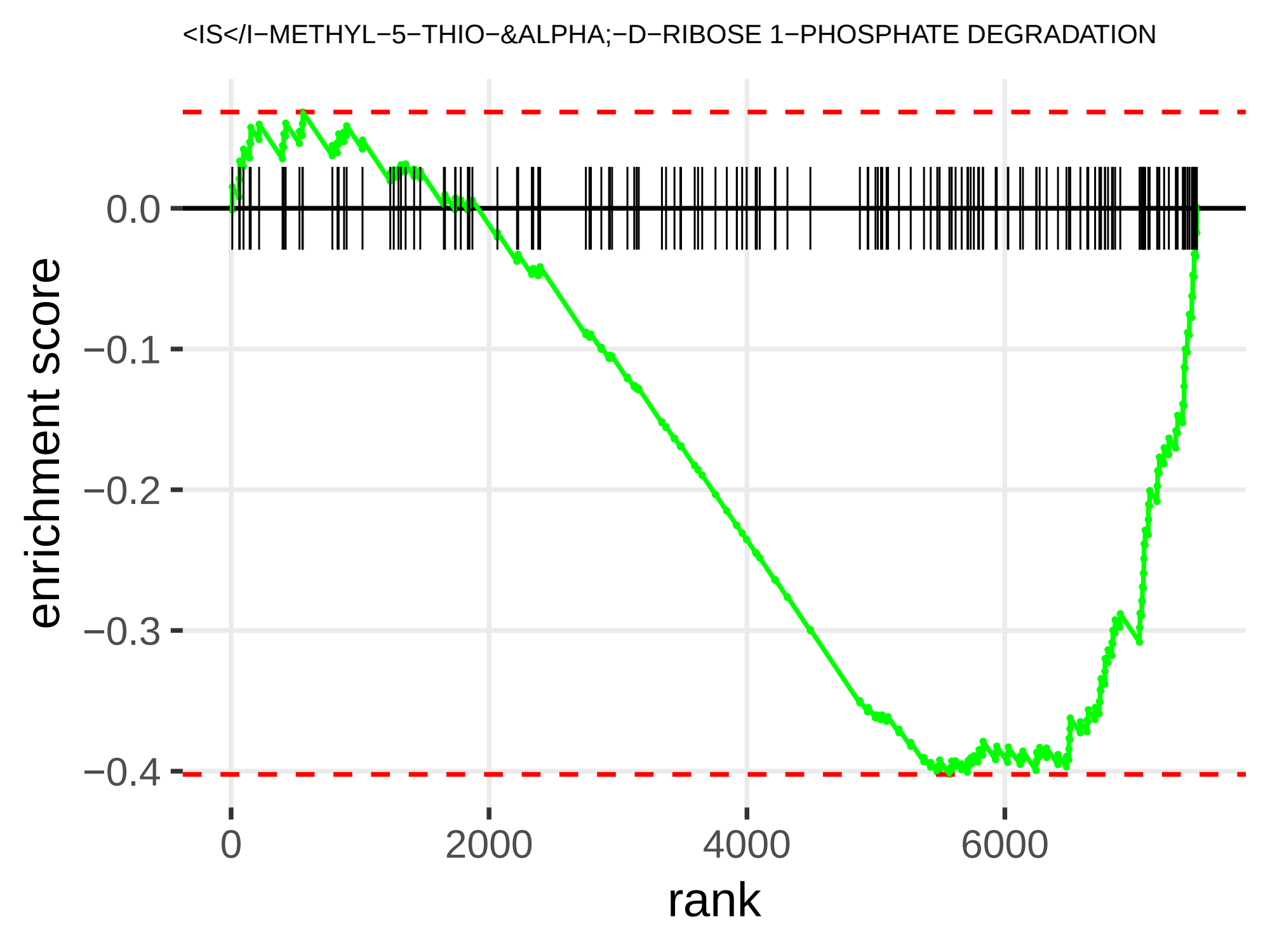

SALVAGE PATHWAYS OF PYRIMIDINE RIBONUCLEOTIDES
enrichment score
0.0
−0.1
−0.2
−0.3
−0.4
0
2000
4000
6000
rank

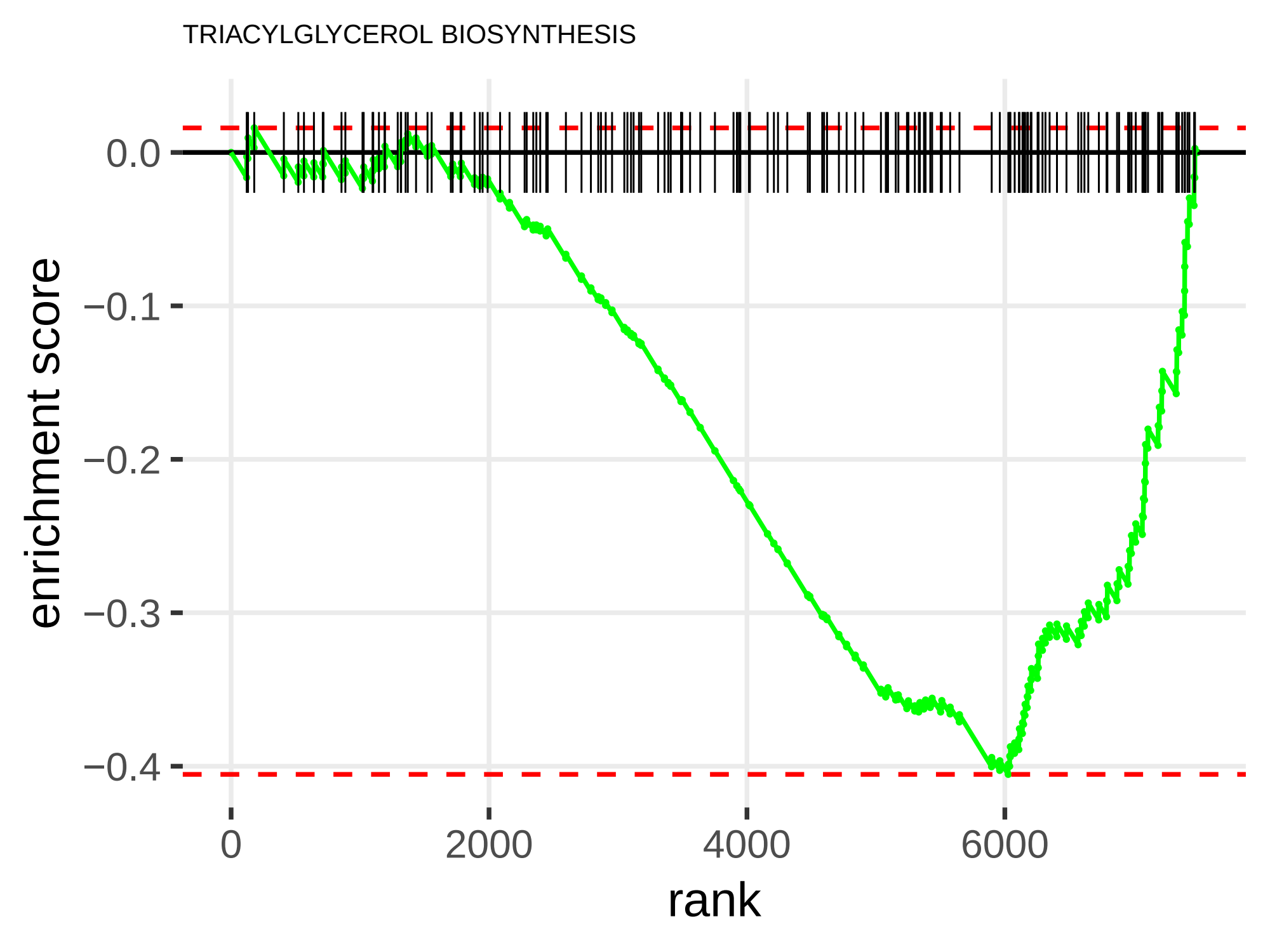

CDP−DIACYLGLYCEROL BIOSYNTHESIS I
enrichment score
0.0
−0.1
−0.2
−0.3
−0.4
0
2000
4000
6000
rank

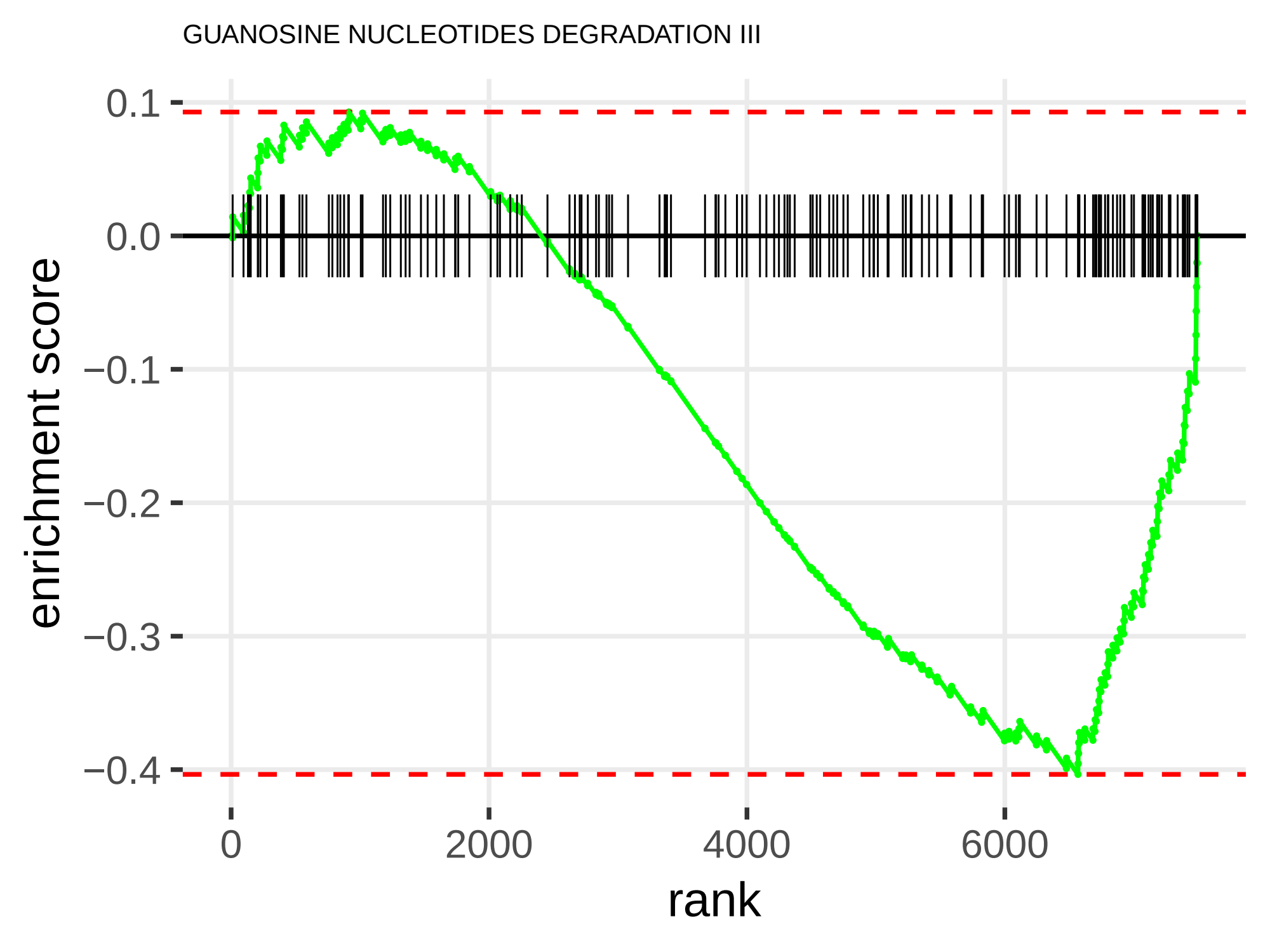

PUTRESCINE BIOSYNTHESIS III
0.0
−0.1
−0.2
−0.3
−0.4
enrichment score
0
2000
4000
6000
rank

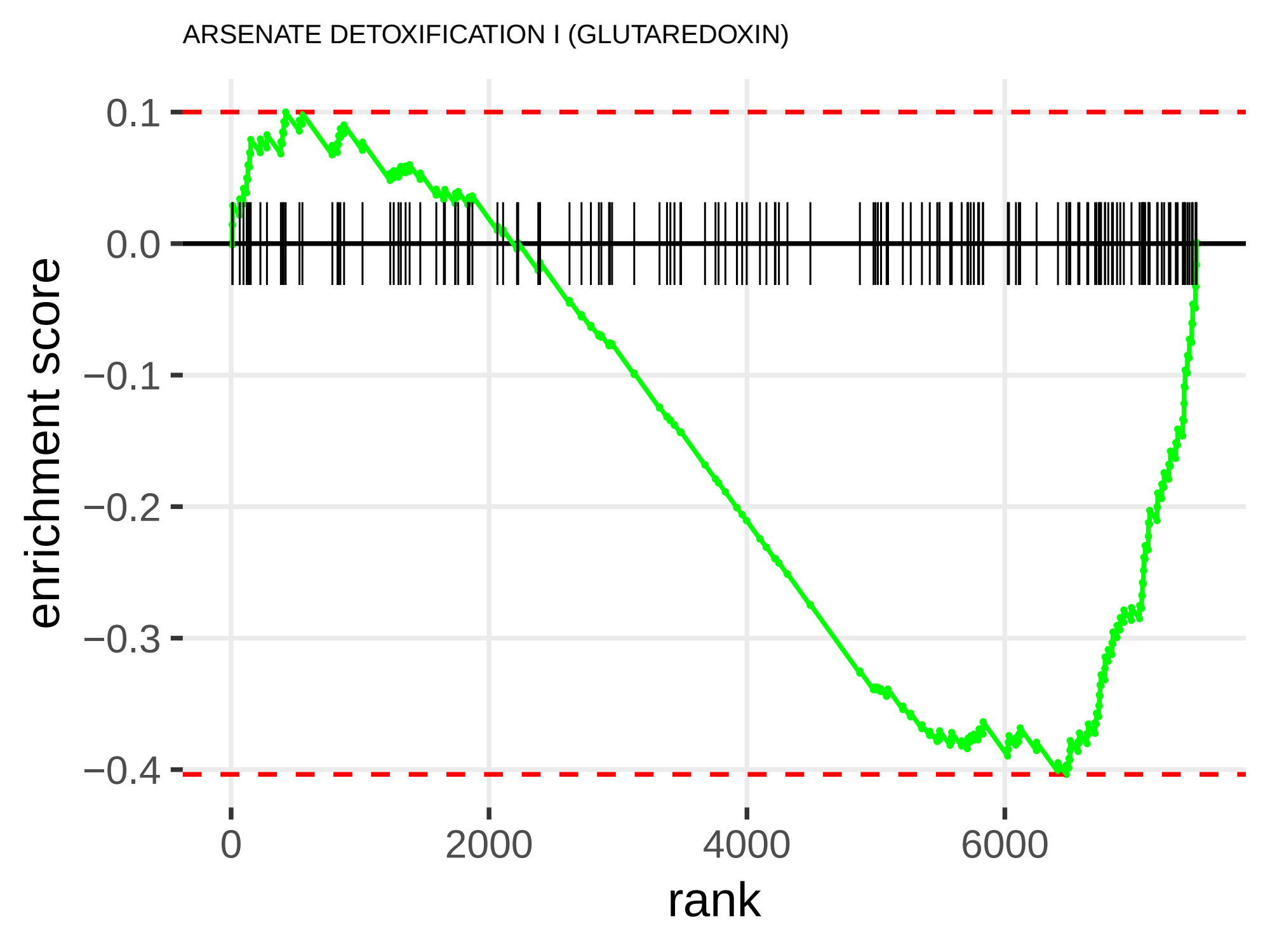

L−CYSTEINE DEGRADATION III
enrichment score
0.0
−0.1
−0.2
−0.3
−0.4
0
2000
4000
6000
rank

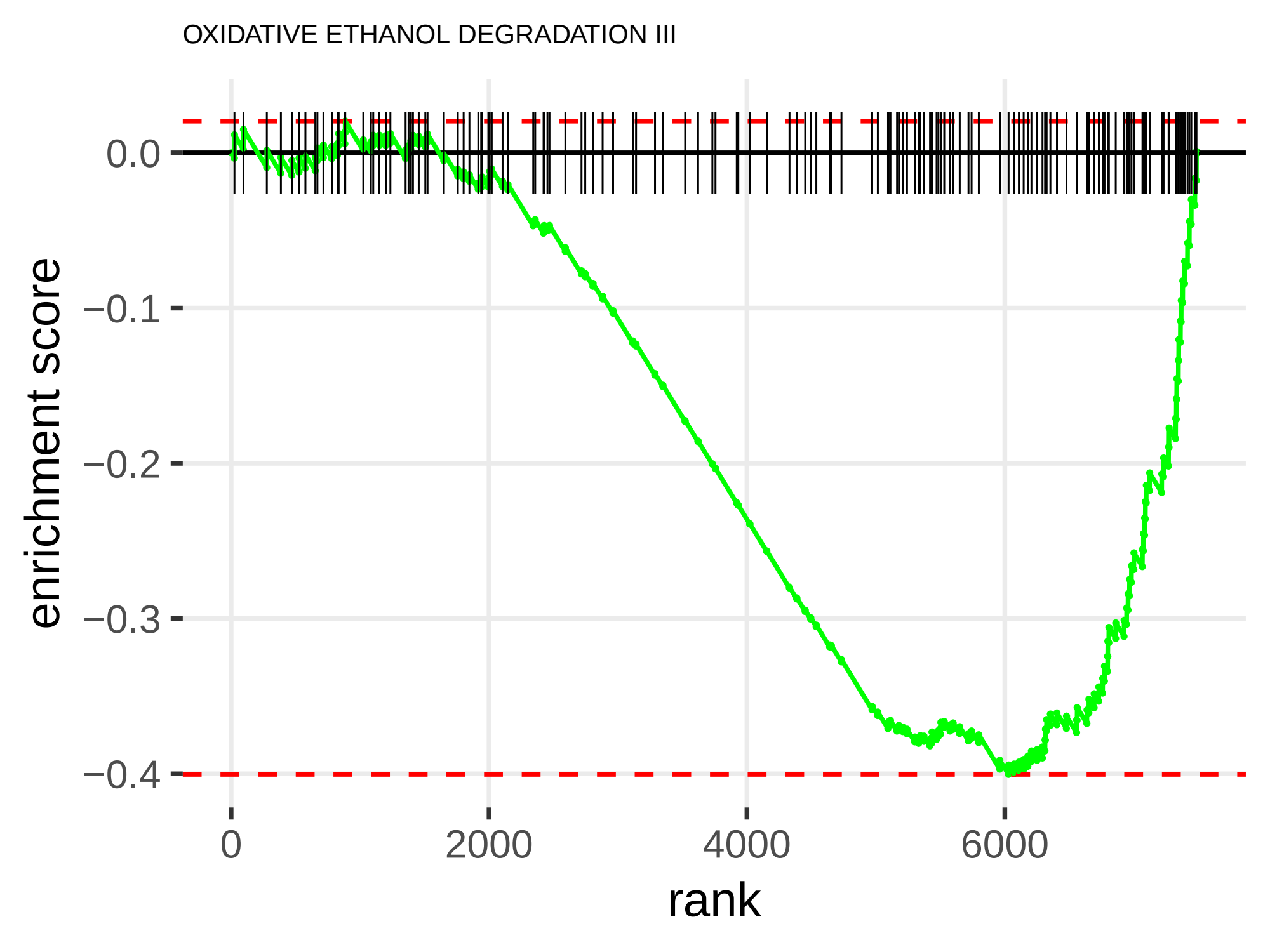

GDP−L−FUCOSE BIOSYNTHESIS I (FROM GDP−D−MANNOSE)
0.0
−0.1
−0.2
−0.3
−0.4
enrichment score
0
2000
4000
6000
rank

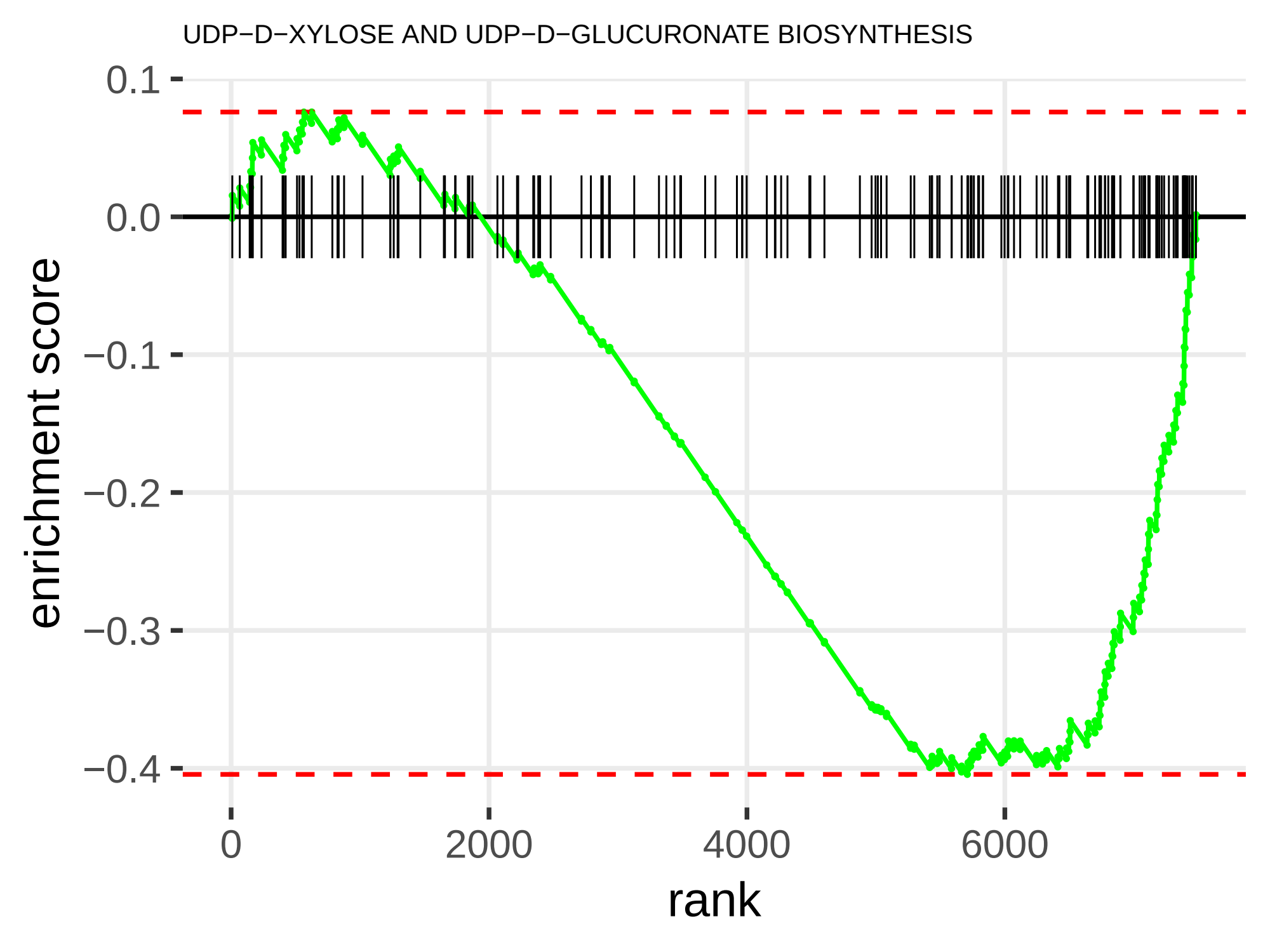

<IS</I−METHYL−5−THIO−&ALPHA;−D−RIBOSE 1−PHOSPHATE DEGRADATION
enrichment score
0.0
−0.1
−0.2
−0.3
−0.4
0
2000
4000
6000
rank

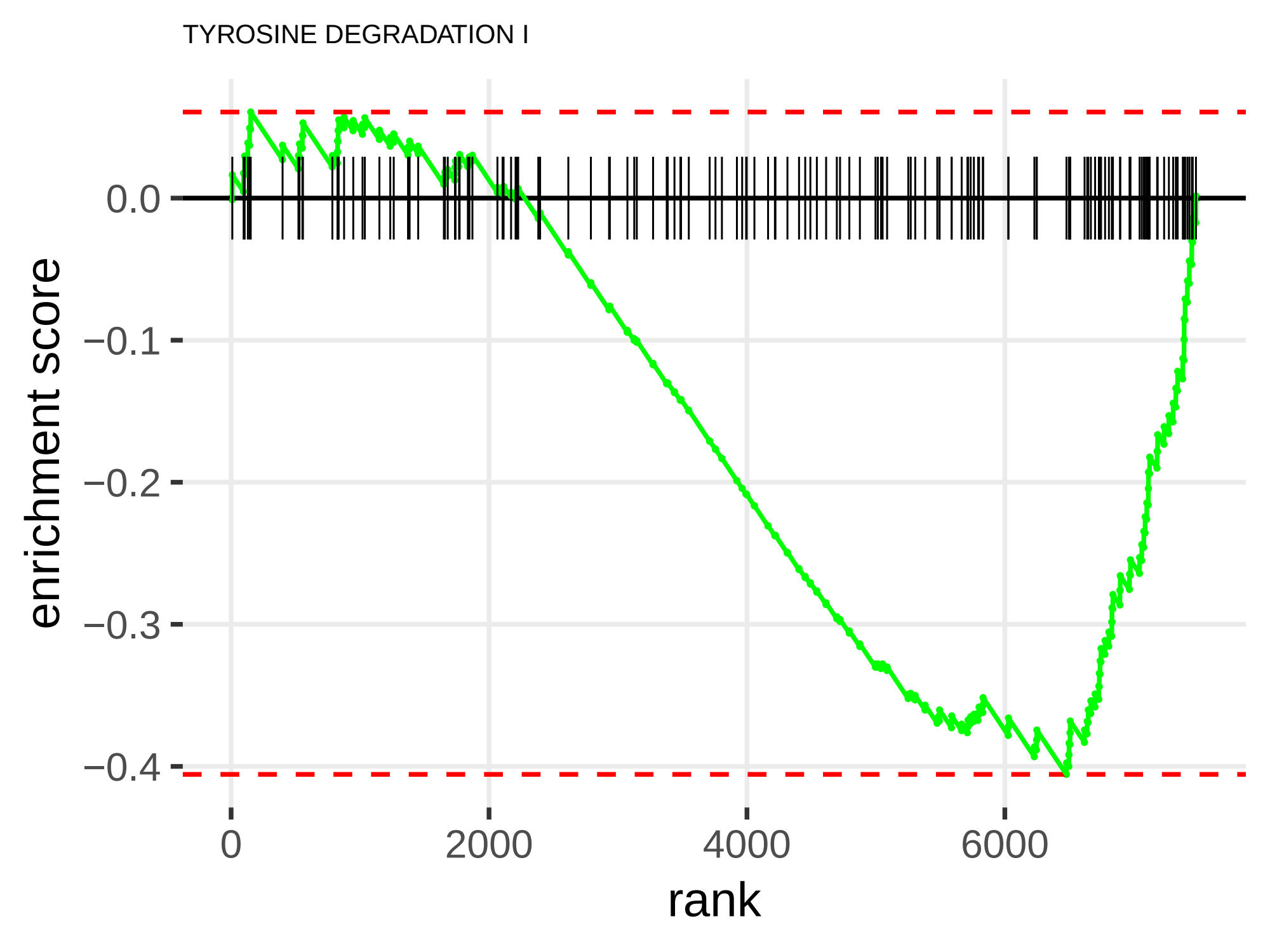

TRIACYLGLYCEROL BIOSYNTHESIS
0.0
−0.1
−0.2
−0.3
−0.4
enrichment score
0
2000
4000
6000
rank

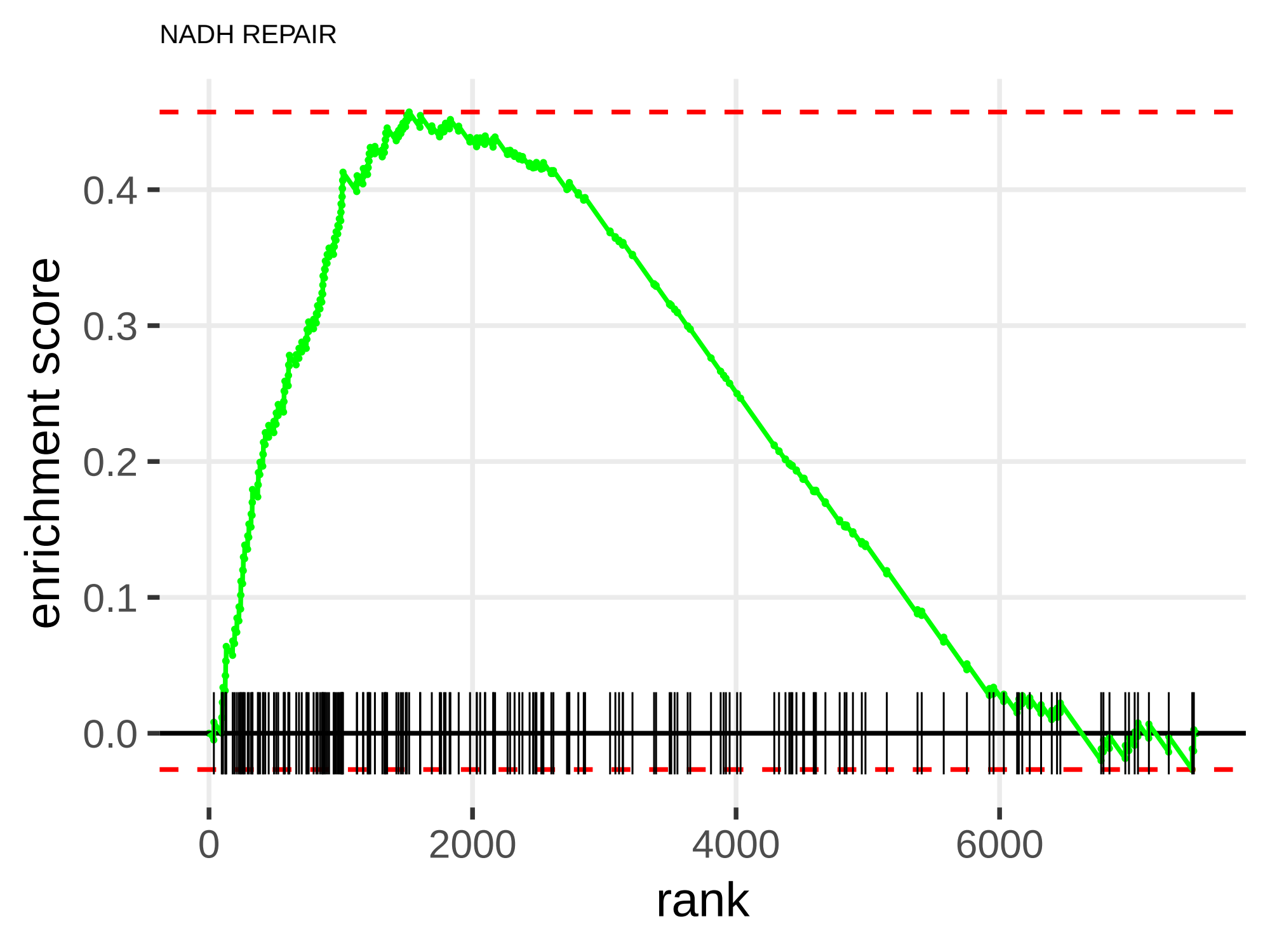

GUANOSINE NUCLEOTIDES DEGRADATION III
0.1
0.0
−0.1
−0.2
−0.3
−0.4
enrichment score
0
2000
4000
6000
rank

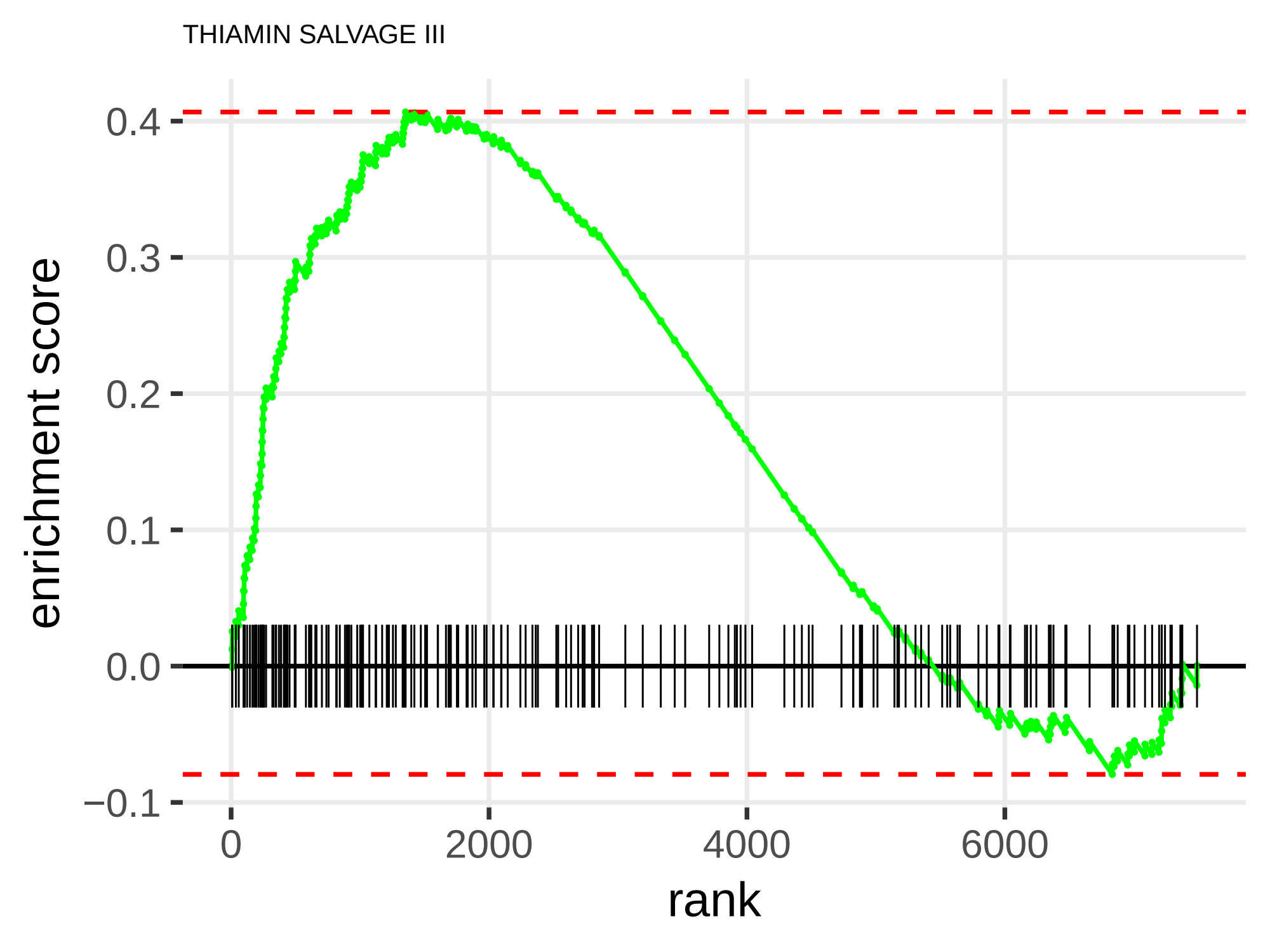

ARSENATE DETOXIFICATION I (GLUTAREDOXIN)
0.1
0.0
−0.1
−0.2
−0.3
−0.4
enrichment score
0
2000
4000
6000
rank

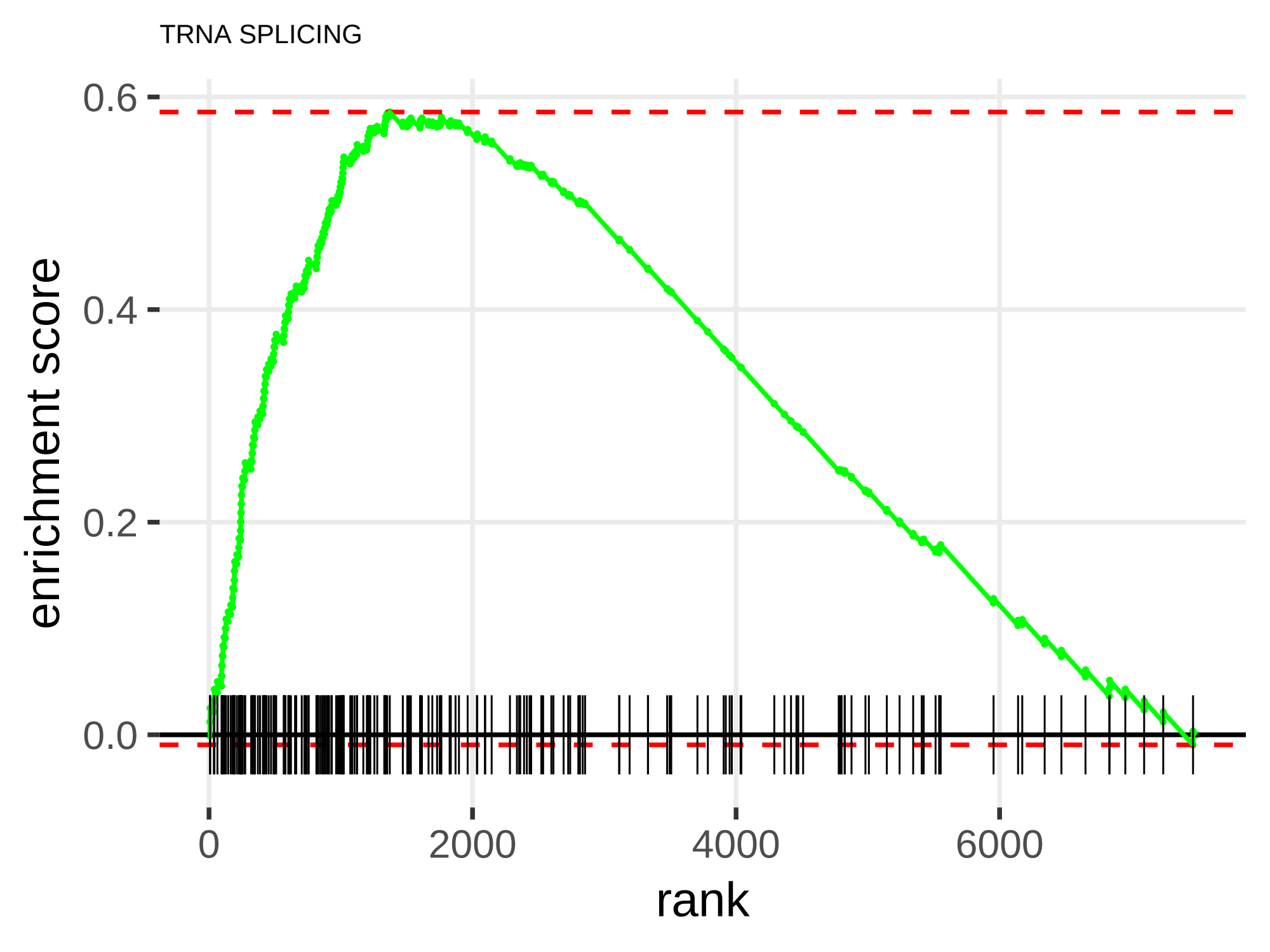

OXIDATIVE ETHANOL DEGRADATION III
0.0
−0.1
−0.2
−0.3
−0.4
enrichment score
0
2000
4000
6000
rank

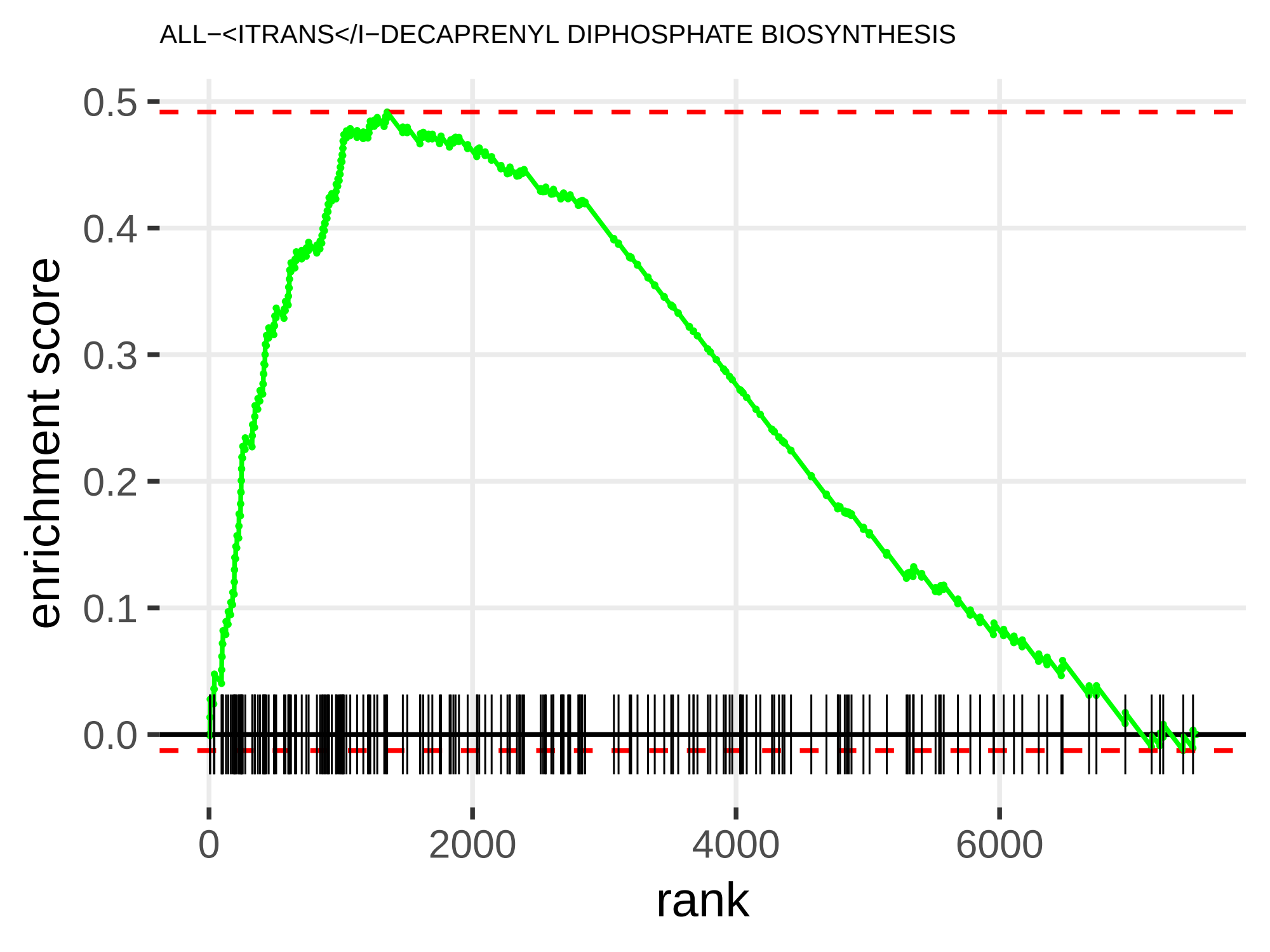

UDP−D−XYLOSE AND UDP−D−GLUCURONATE BIOSYNTHESIS
0.1
0.0
−0.1
−0.2
−0.3
−0.4
enrichment score
0
2000
4000
6000
rank

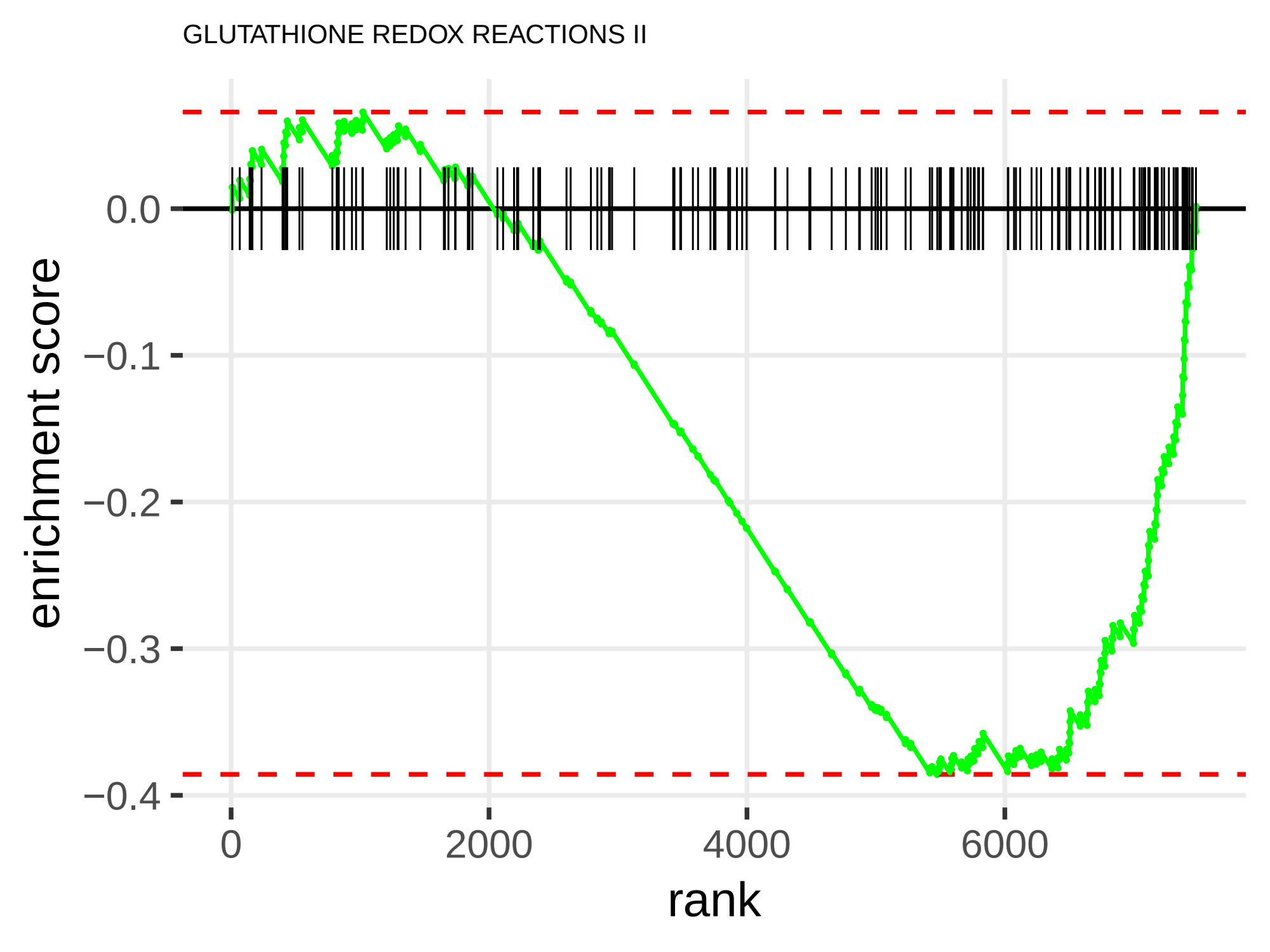

TYROSINE DEGRADATION I
0.0
−0.1
−0.2
−0.3
−0.4
enrichment score
0
2000
4000
6000
rank

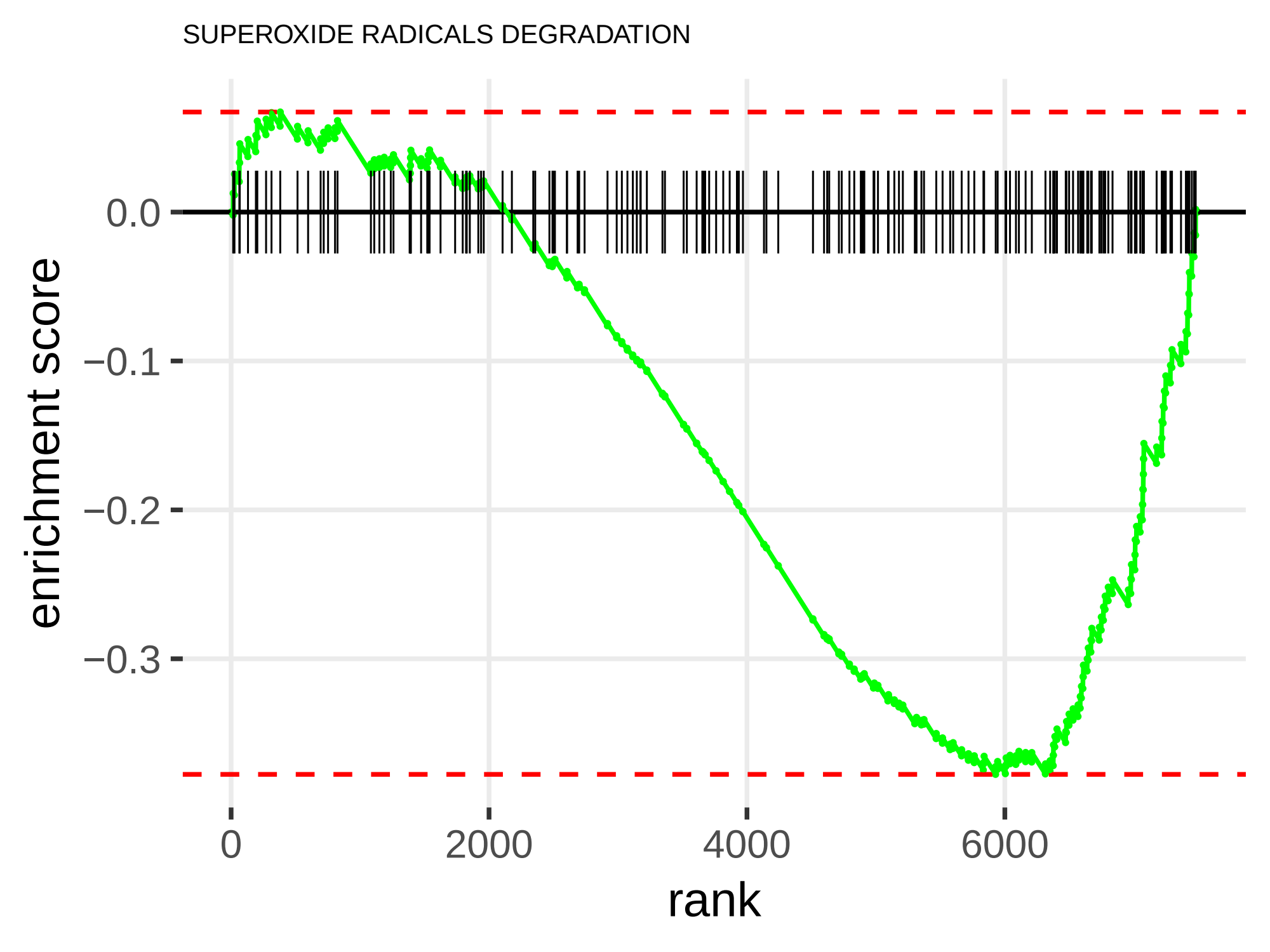

NADH REPAIR
enrichment score
0.4
0.3
0.2
0.1
0.0
0
2000
4000
6000
rank

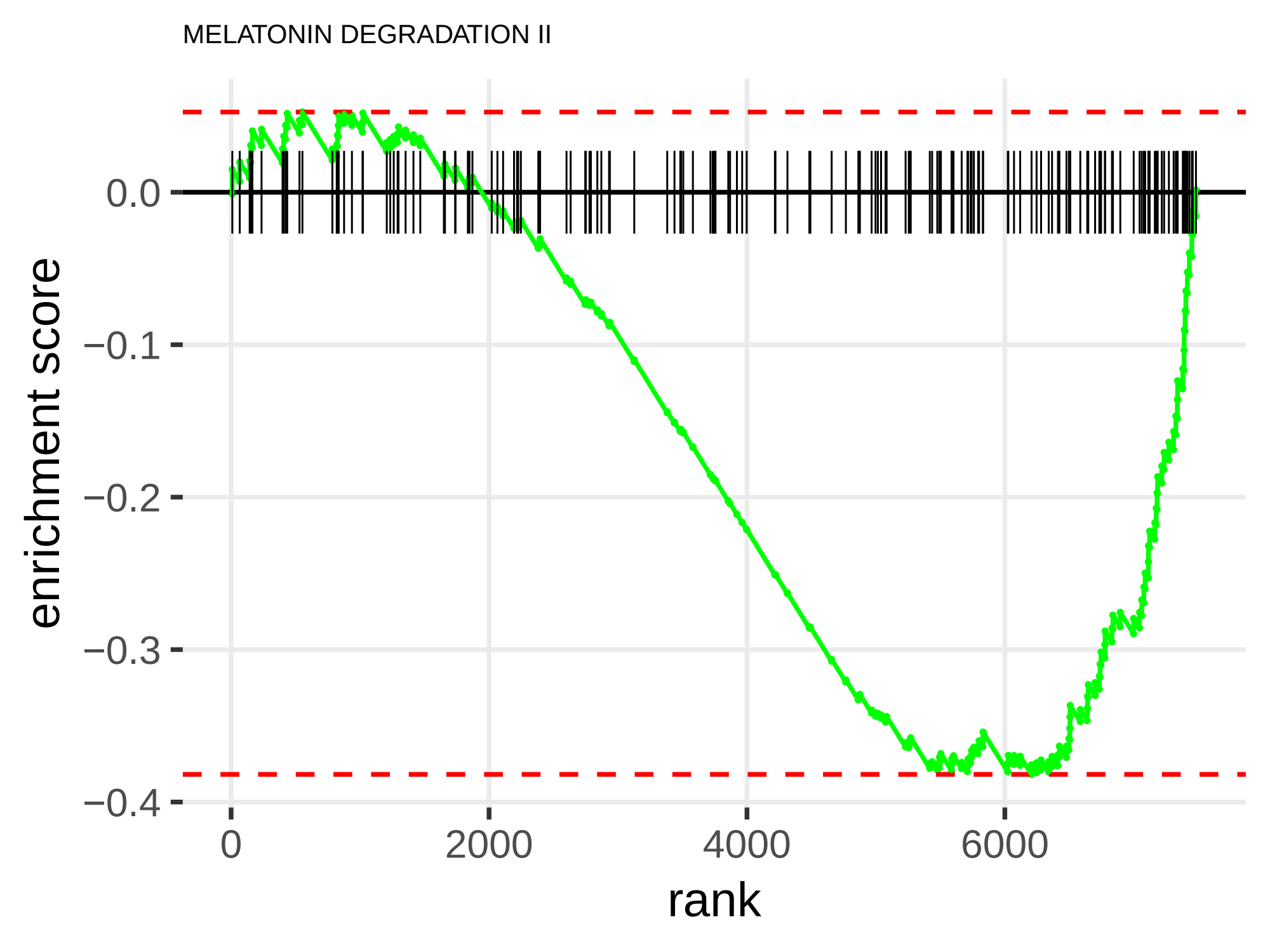

THIAMIN SALVAGE III
enrichment score
0.4
0.3
0.2
0.1
0.0
−0.1
0
2000
4000
6000
rank

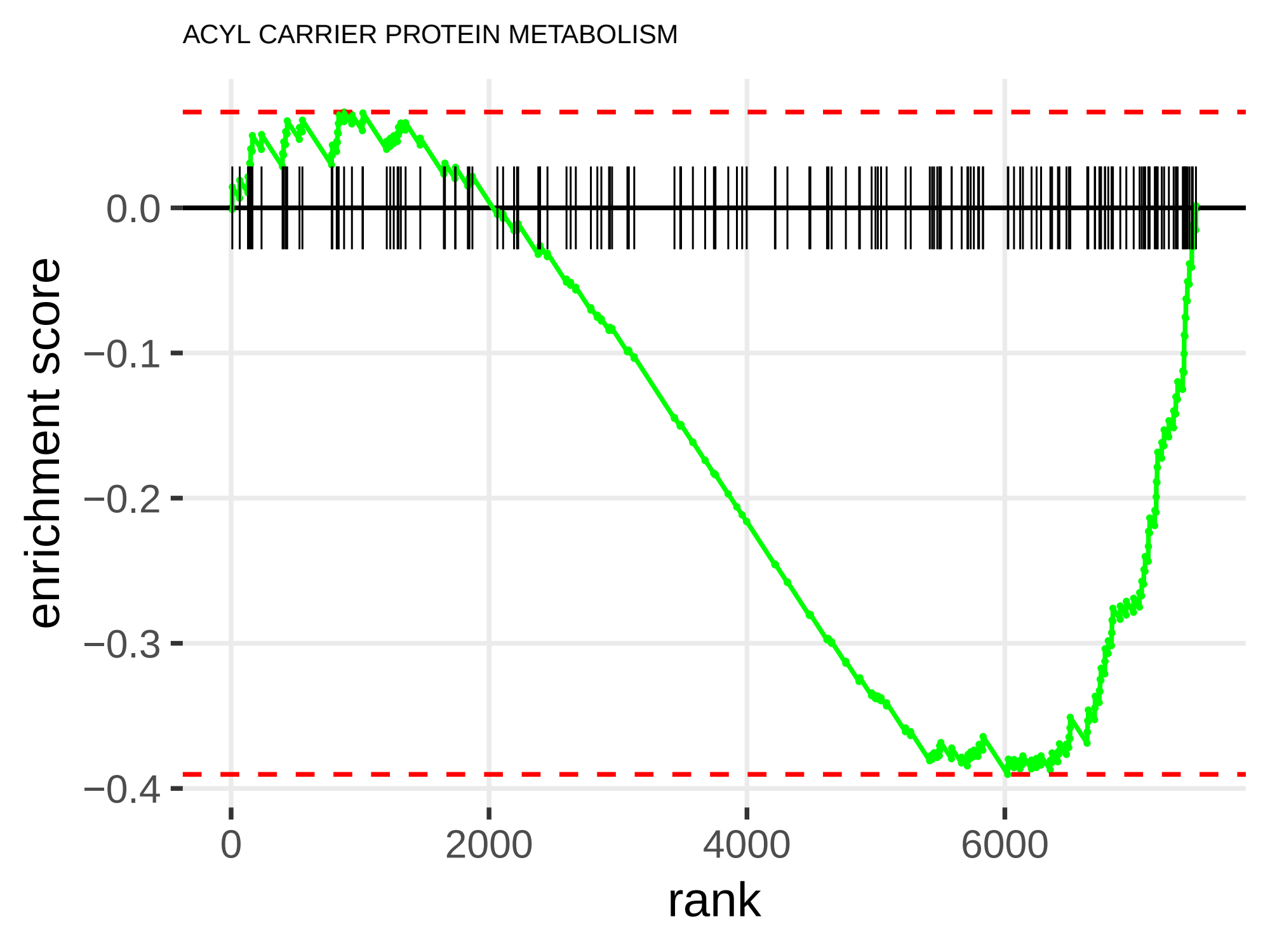

TRNA SPLICING
0.6
0.4
0.2
0.0
enrichment score
0
2000
4000
6000
rank

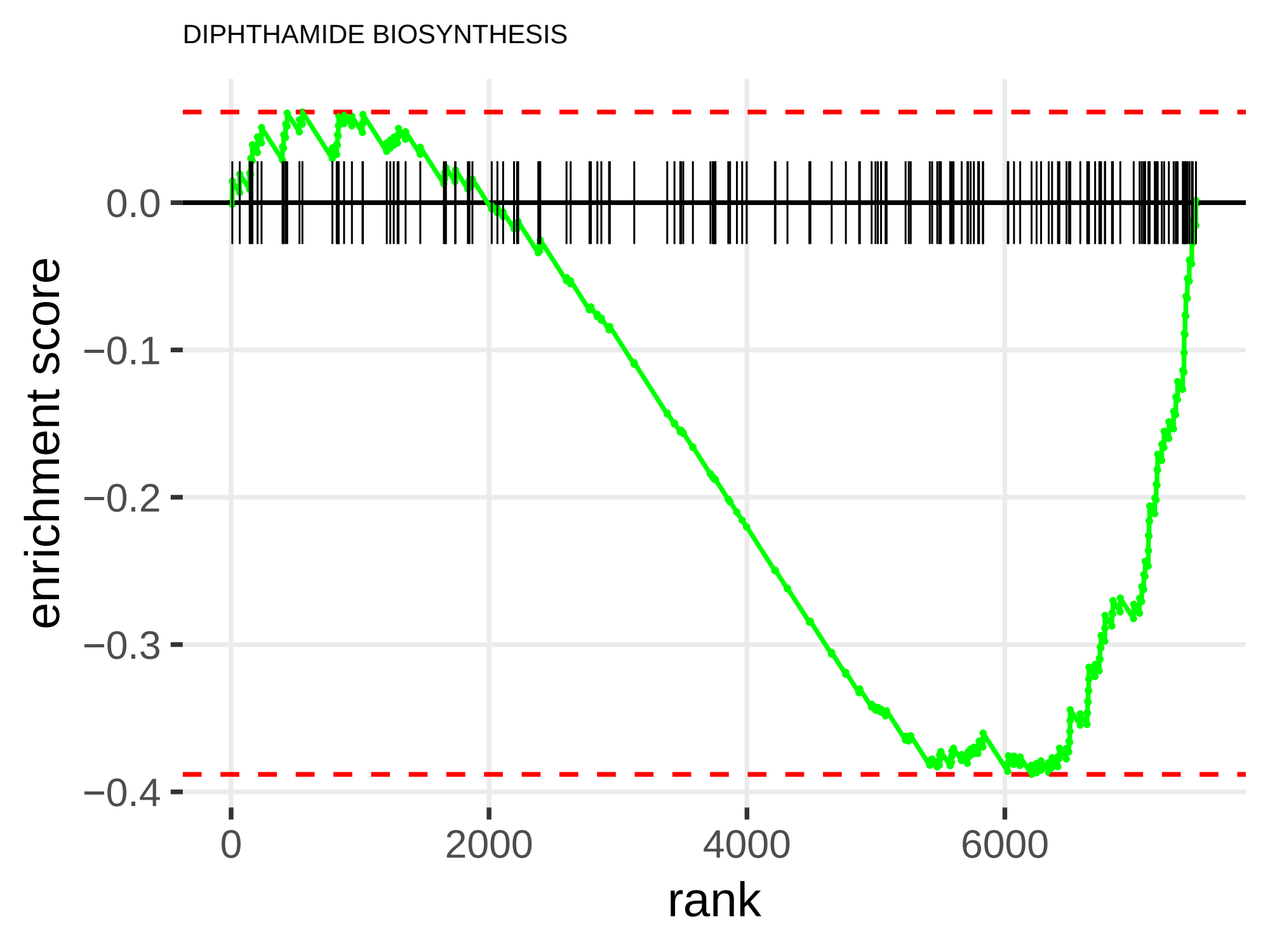

ALL−<ITRANS</I−DECAPRENYL DIPHOSPHATE BIOSYNTHESIS
0.5
0.4
0.3
0.2
0.1
0.0
enrichment score
0
2000
4000
6000
rank

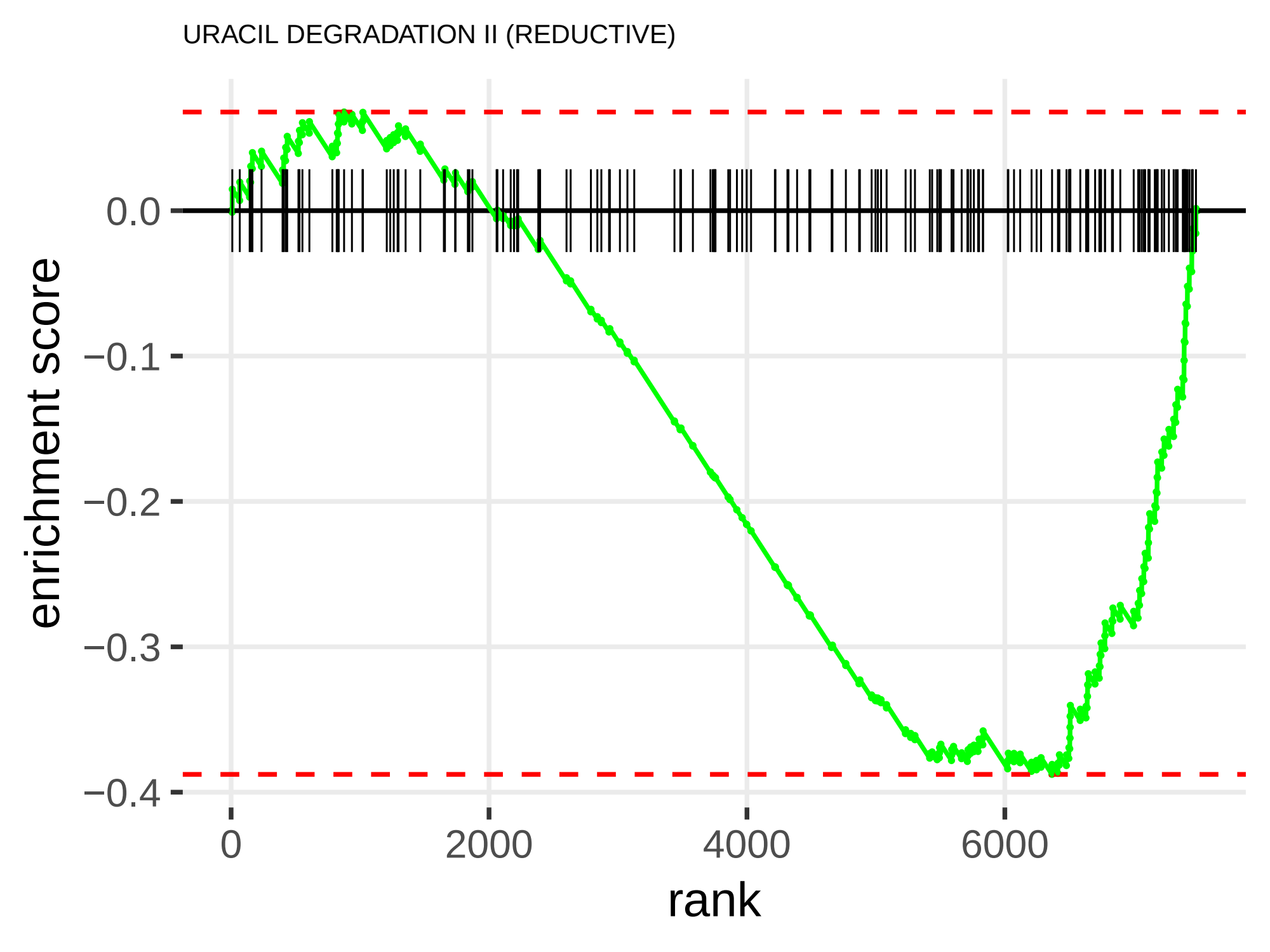

GLUTATHIONE REDOX REACTIONS II
0.0
−0.1
−0.2
−0.3
−0.4
enrichment score
0
2000
4000
6000
rank

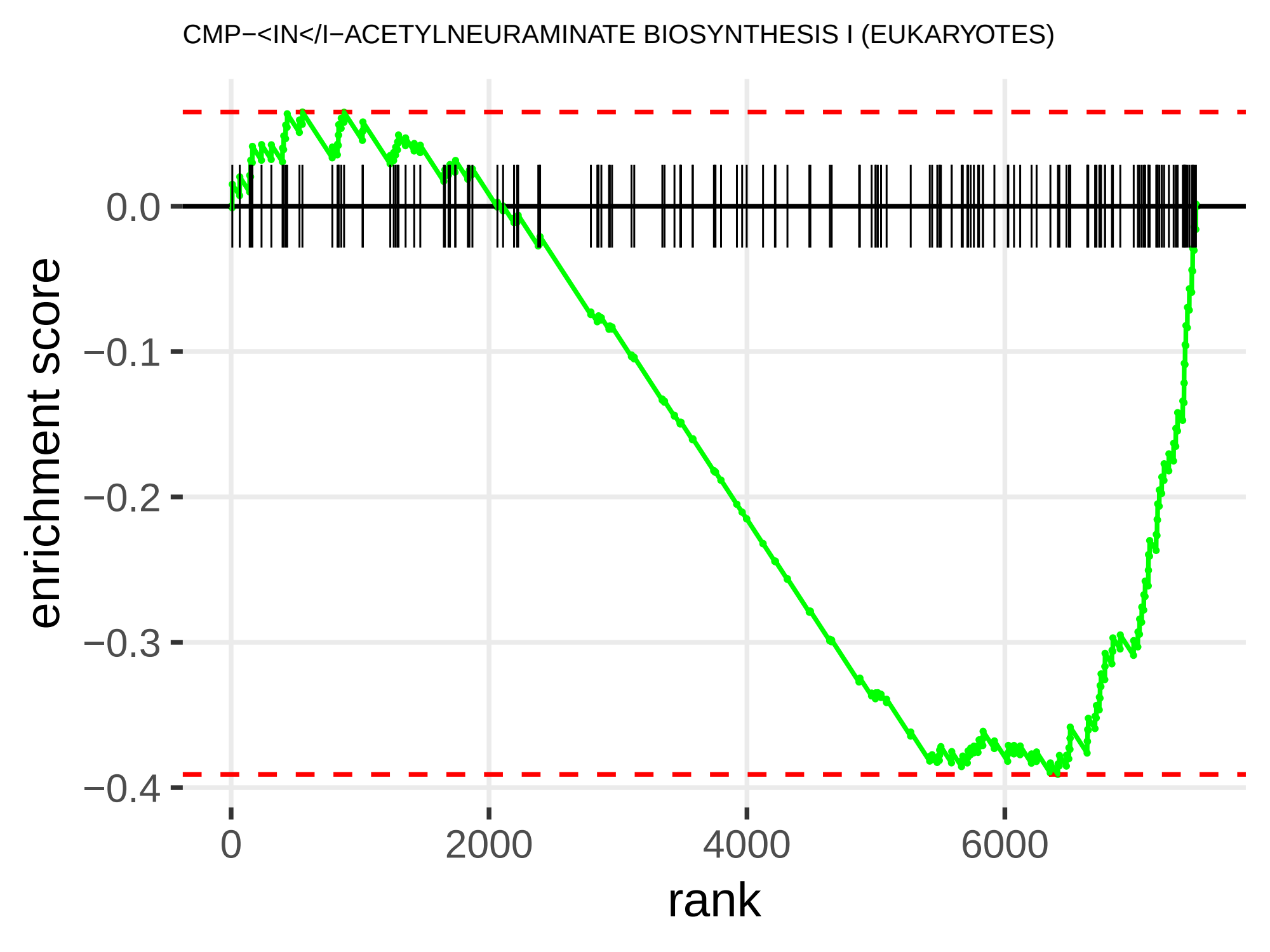

SUPEROXIDE RADICALS DEGRADATION
0.0
−0.1
−0.2
−0.3
enrichment score
0
2000
4000
6000
rank

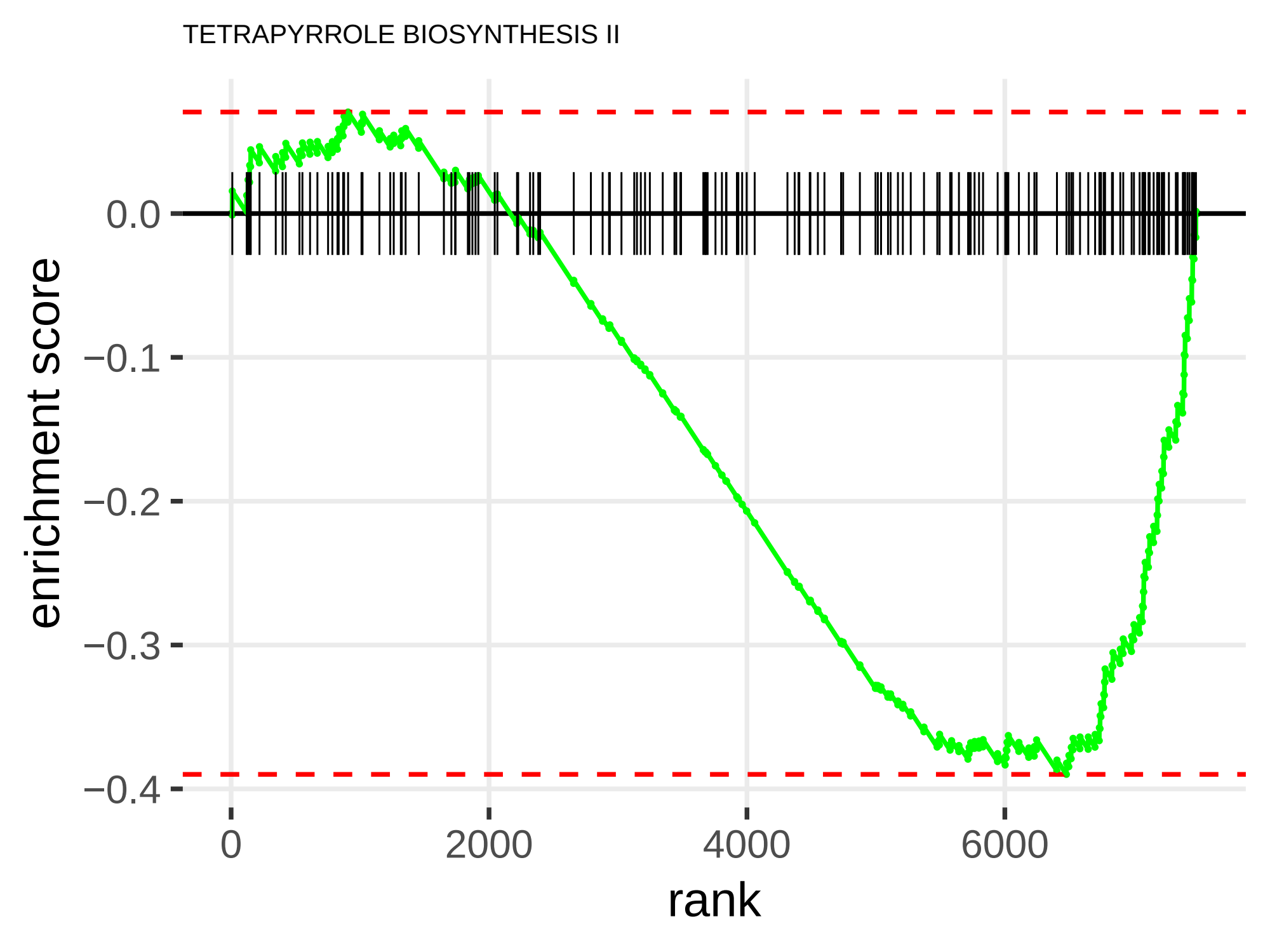

MELATONIN DEGRADATION II
0.0
−0.1
−0.2
−0.3
−0.4
enrichment score
0
2000
4000
6000
rank

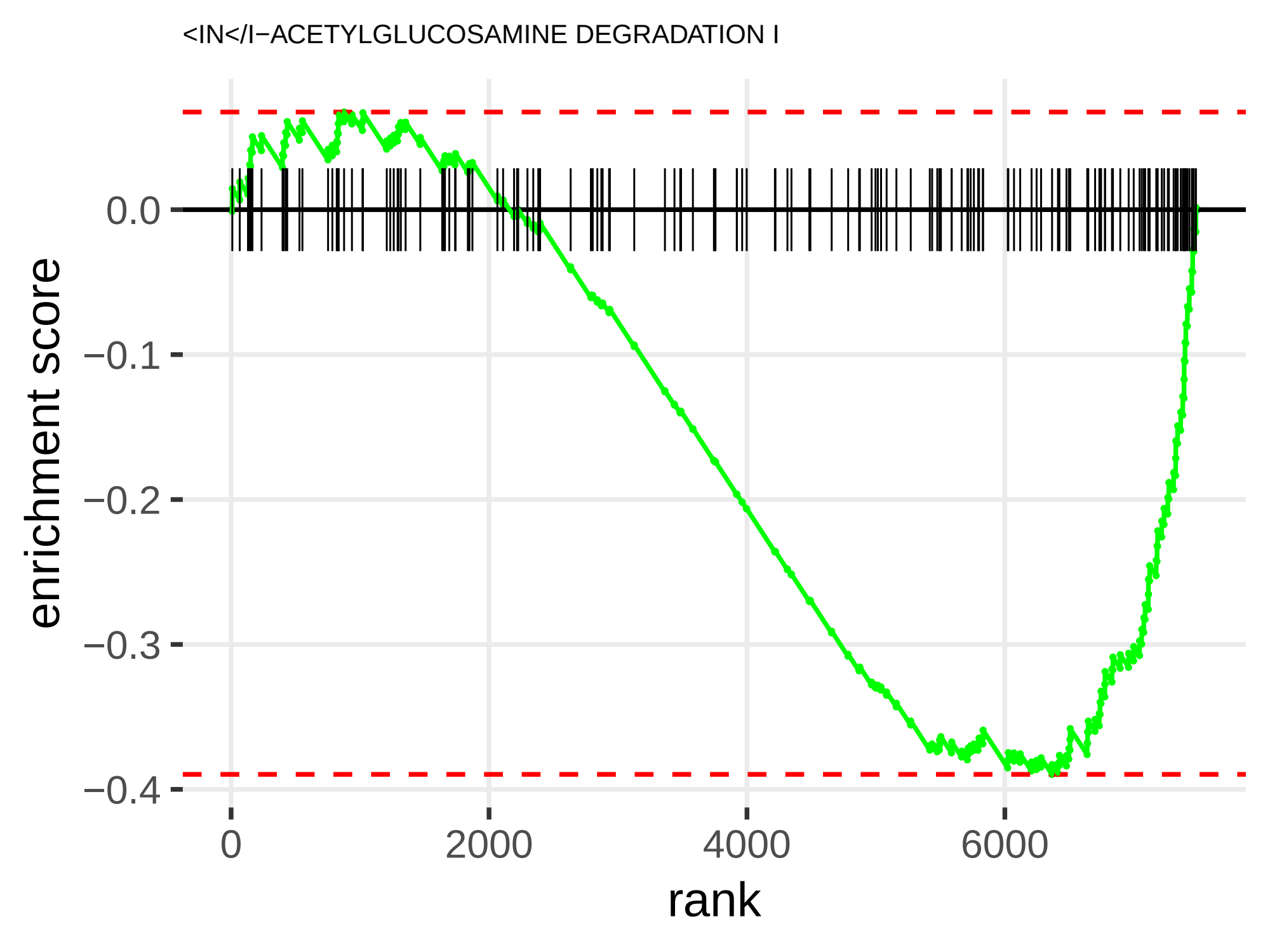

ACYL CARRIER PROTEIN METABOLISM
0.0
−0.1
−0.2
−0.3
−0.4
enrichment score
0
2000
4000
6000
rank

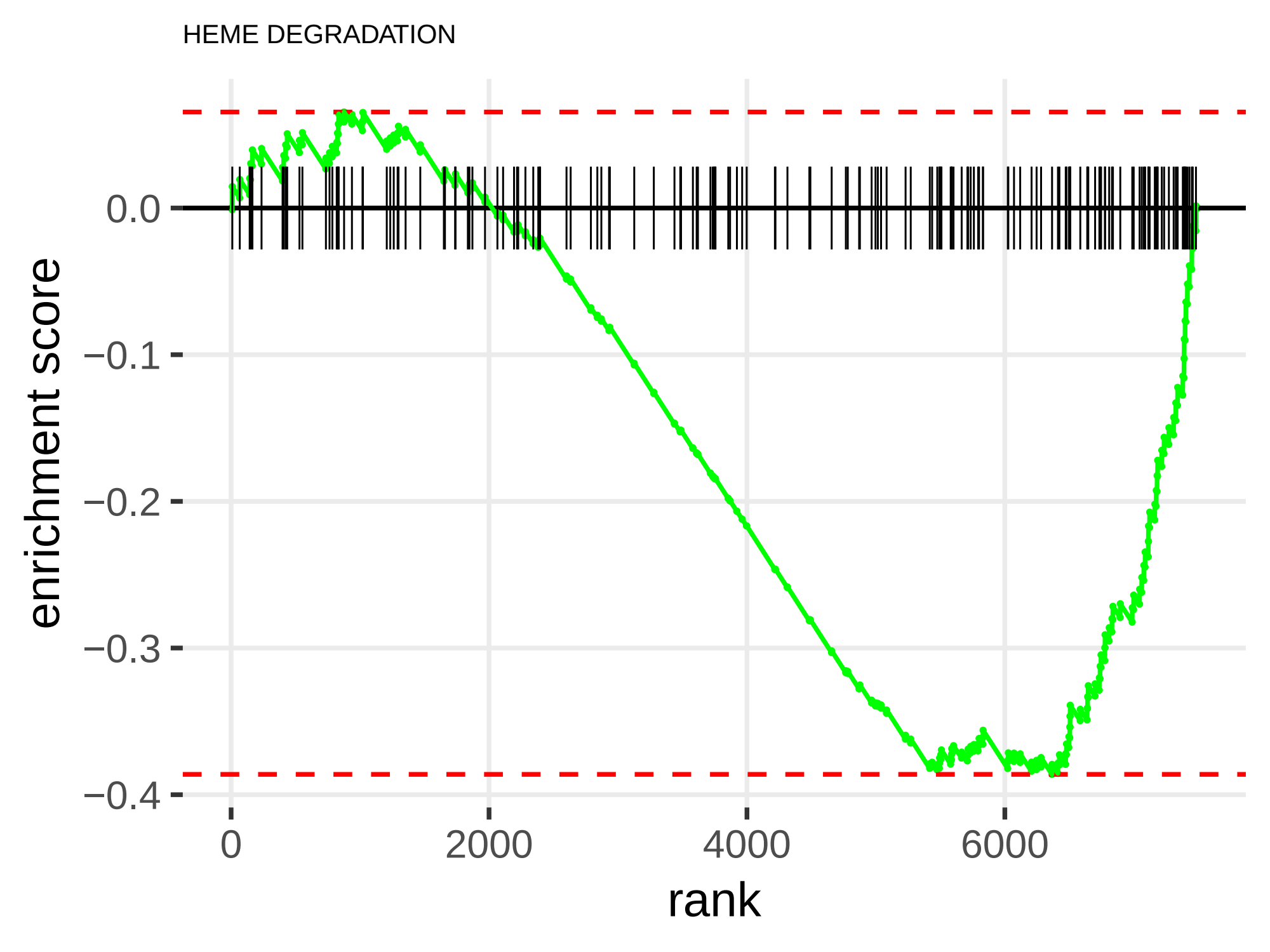

DIPHTHAMIDE BIOSYNTHESIS
0.0
−0.1
−0.2
−0.3
−0.4
enrichment score
0
2000
4000
6000
rank

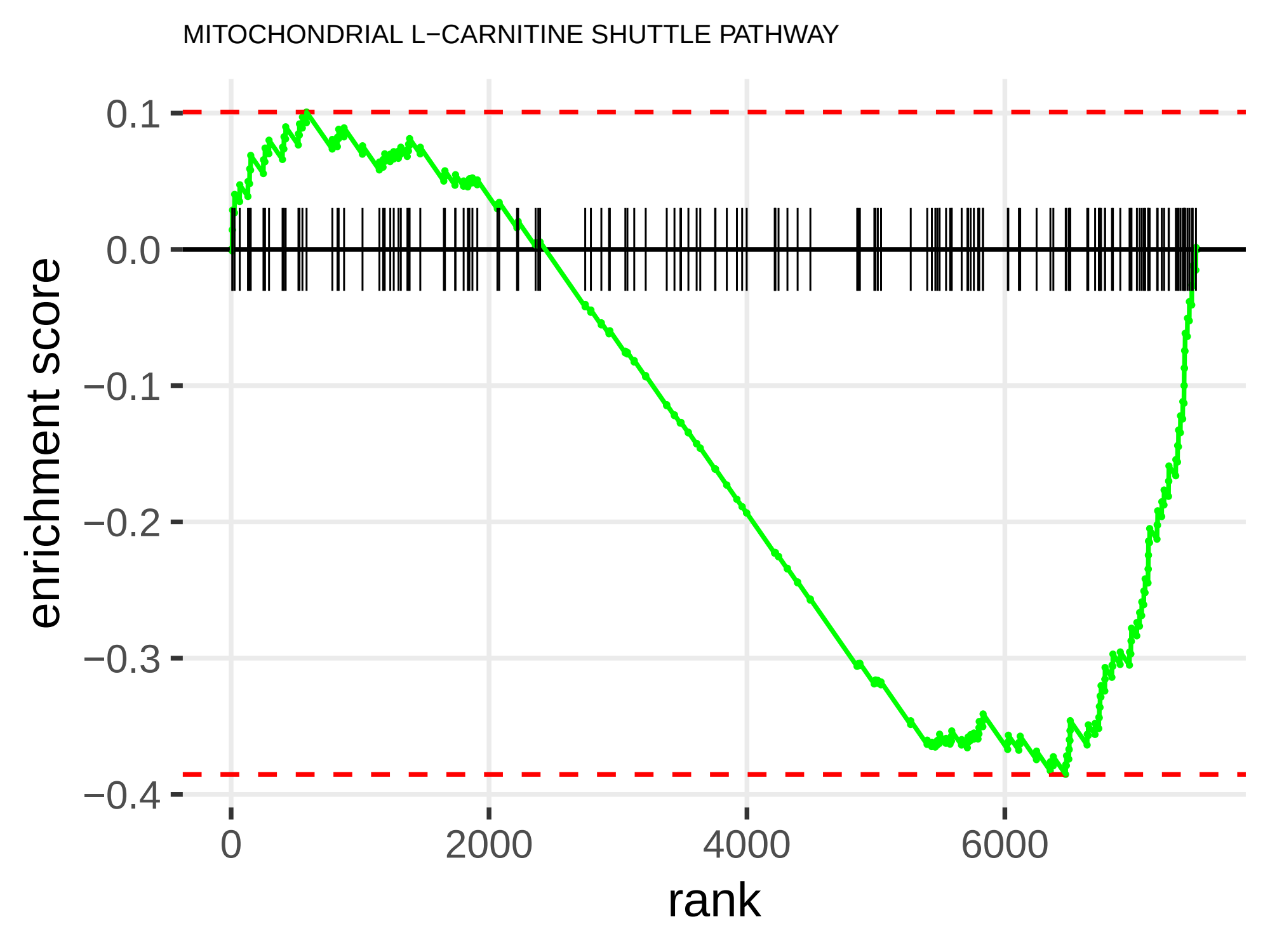

URACIL DEGRADATION II (REDUCTIVE)
enrichment score
0.0
−0.1
−0.2
−0.3
−0.4
0
2000
4000
6000
rank

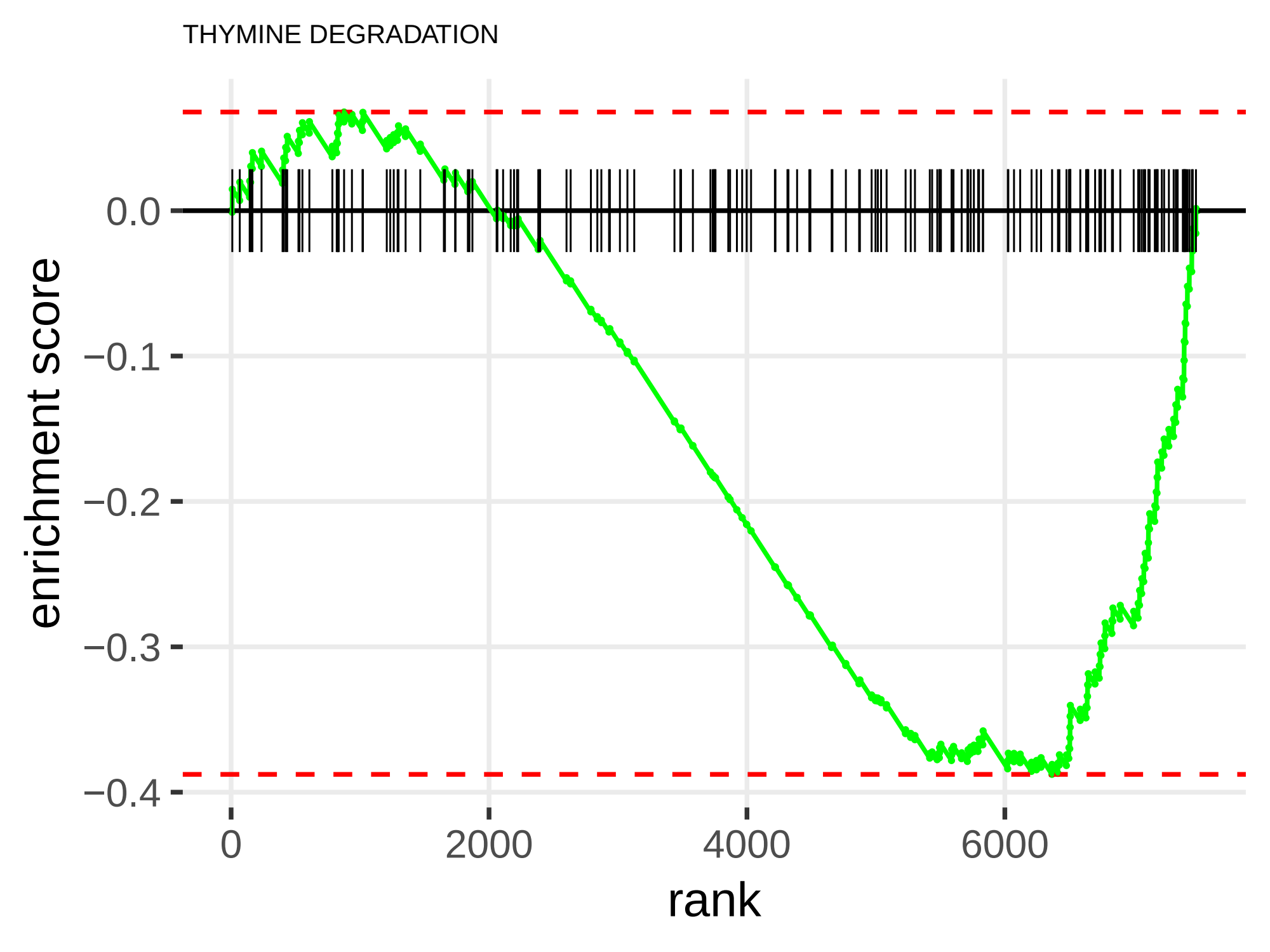

CMP−<IN</I−ACETYLNEURAMINATE BIOSYNTHESIS I (EUKARYOTES)
enrichment score
0.0
−0.1
−0.2
−0.3
−0.4
0
2000
4000
6000
rank

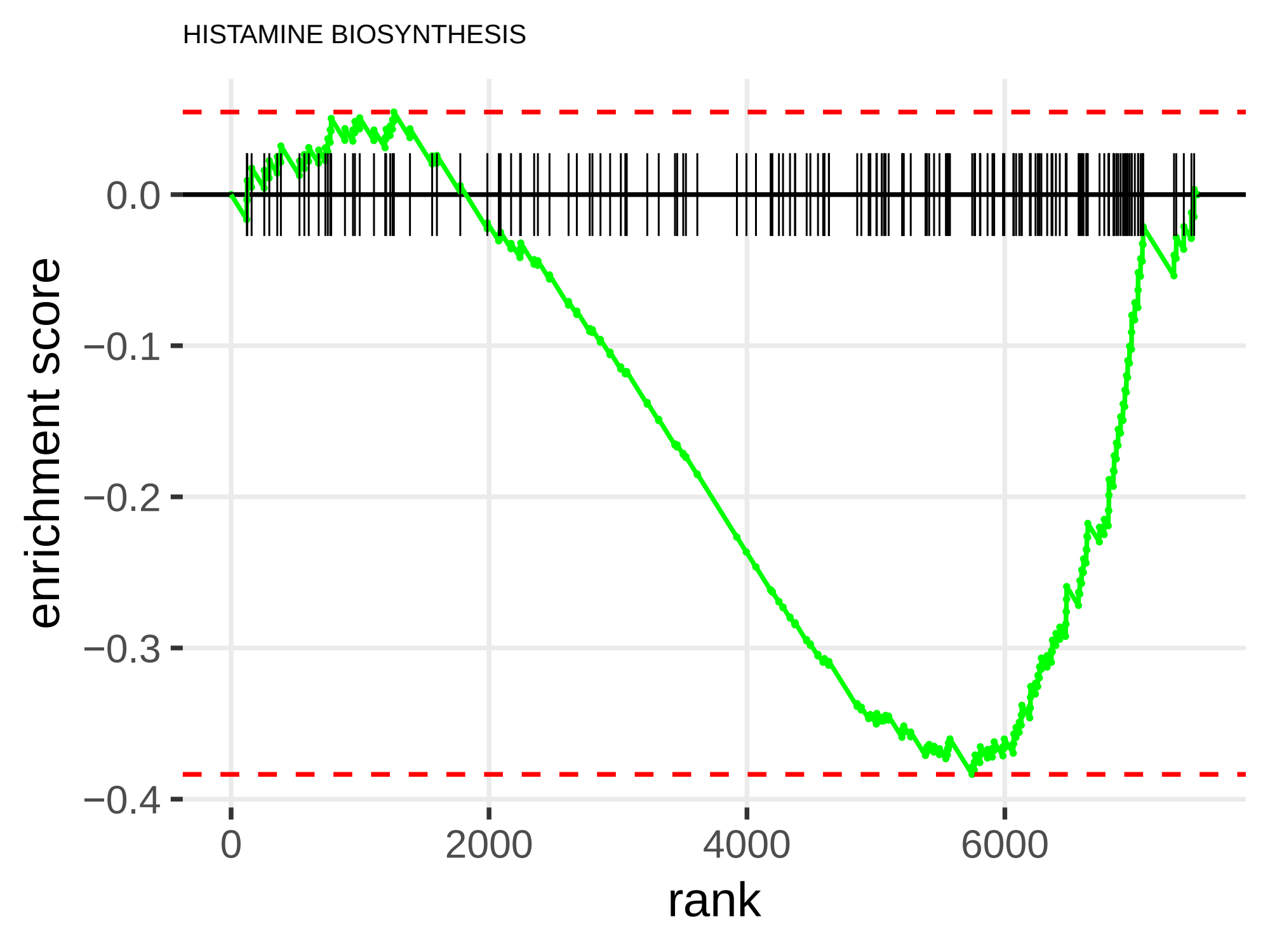

TETRAPYRROLE BIOSYNTHESIS II
0.0
−0.1
−0.2
−0.3
−0.4
enrichment score
0
2000
4000
6000
rank

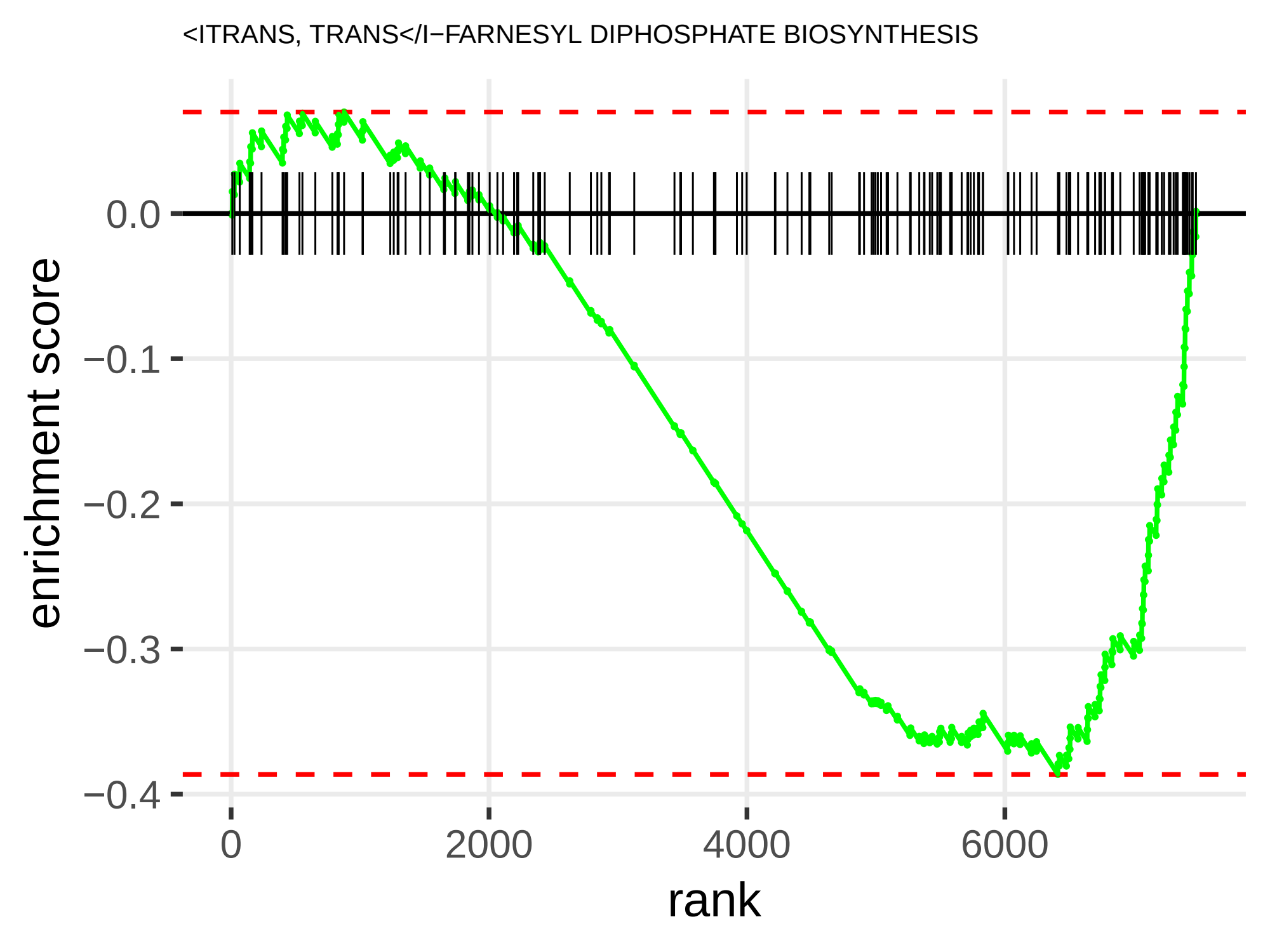

<IN</I−ACETYLGLUCOSAMINE DEGRADATION I
0.0
−0.1
−0.2
−0.3
−0.4
enrichment score
0
2000
4000
6000
rank

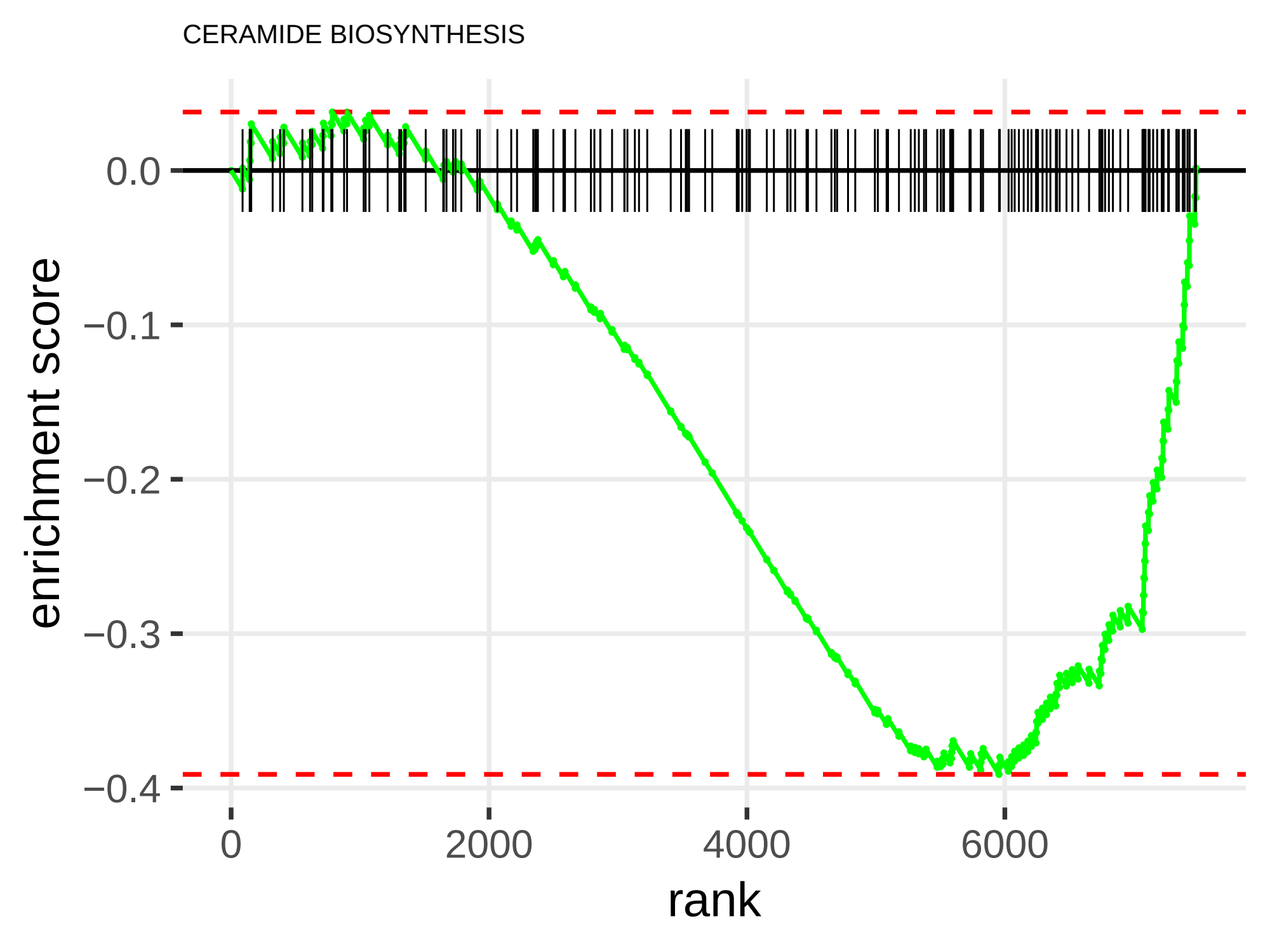

HEME DEGRADATION
0.0
−0.1
−0.2
−0.3
−0.4
enrichment score
0
2000
4000
6000
rank

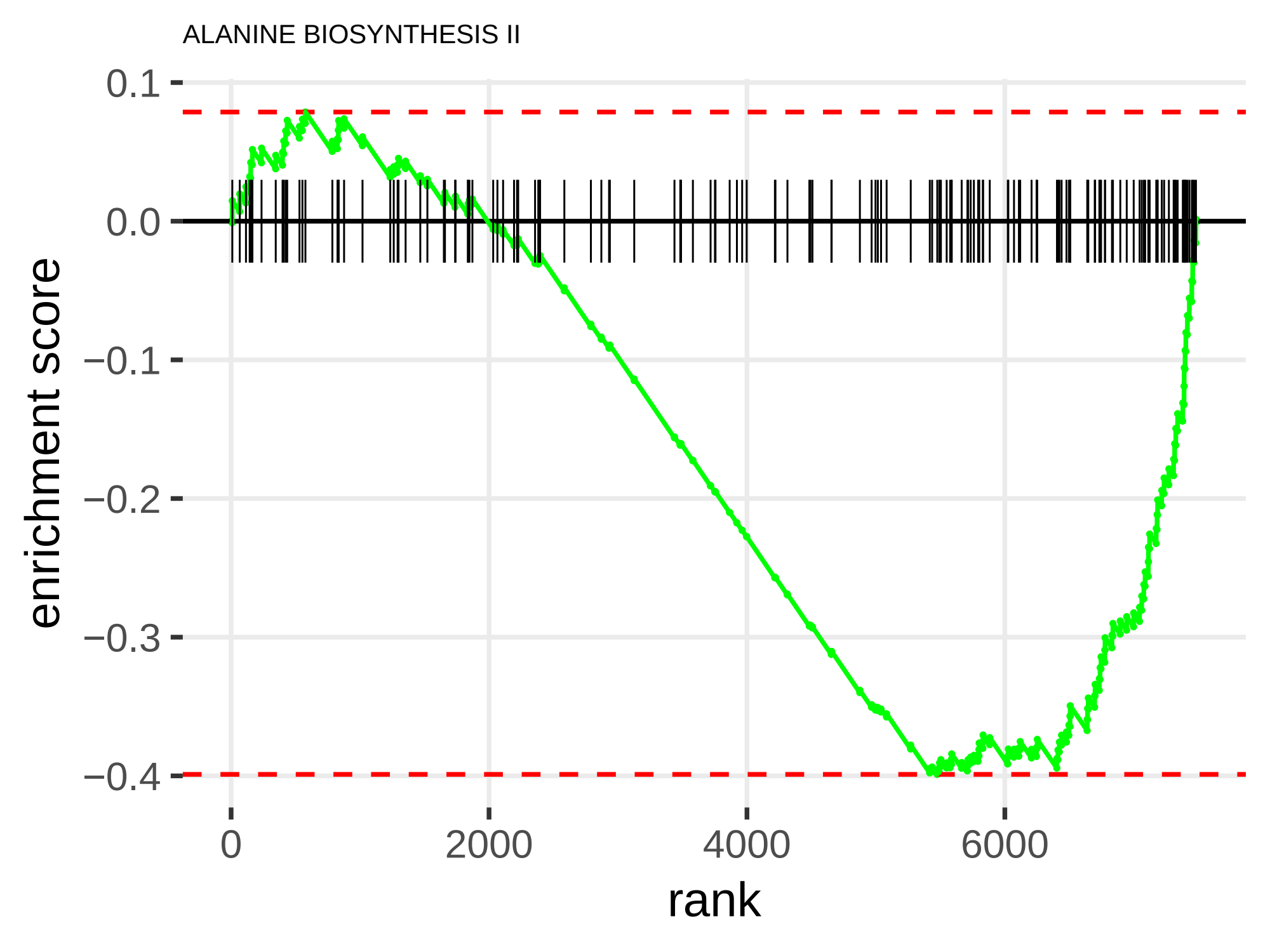

MITOCHONDRIAL L−CARNITINE SHUTTLE PATHWAY
enrichment score
0.1
0.0
−0.1
−0.2
−0.3
−0.4
0
2000
4000
6000
rank

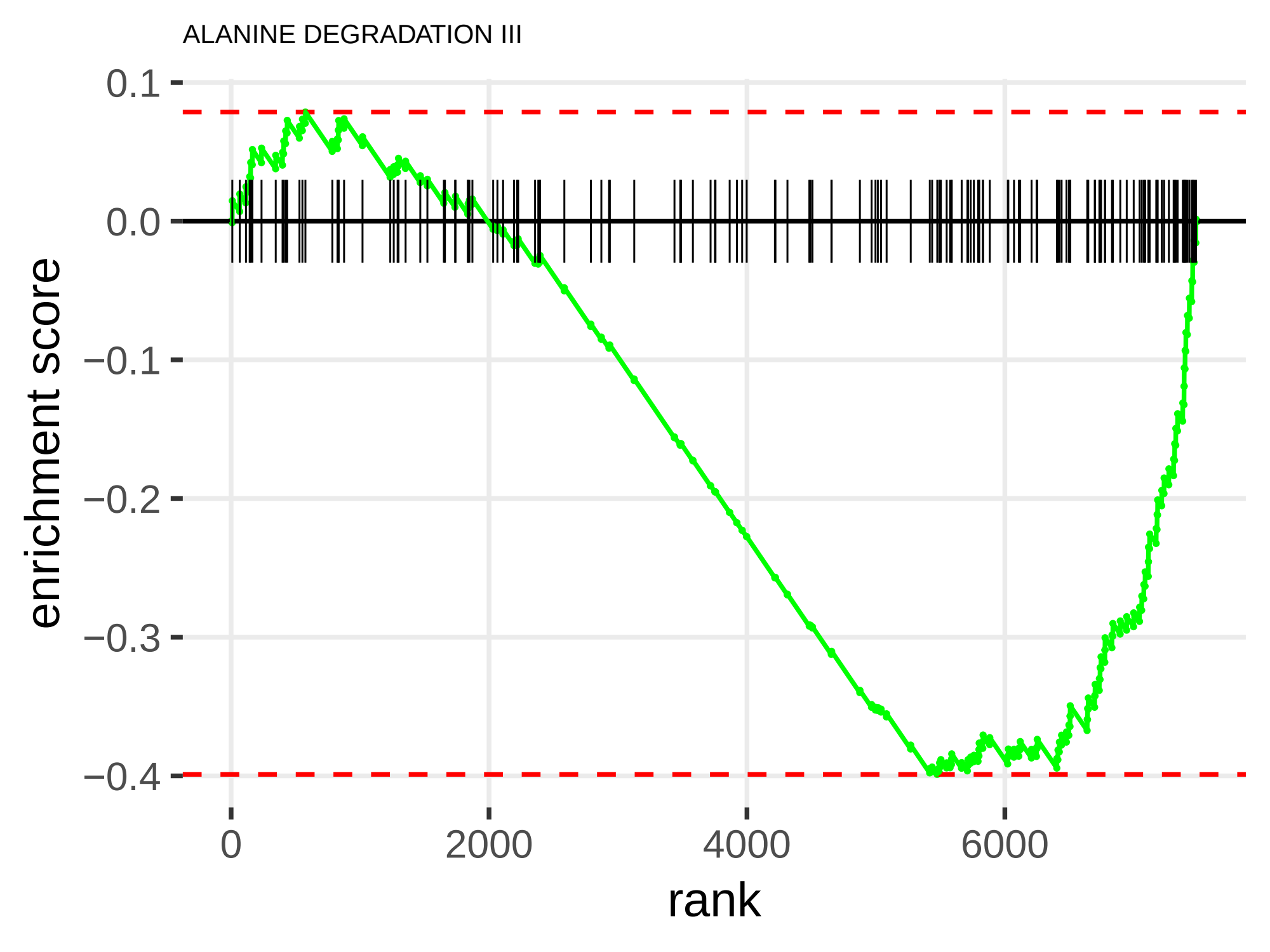

THYMINE DEGRADATION
0.0
−0.1
−0.2
−0.3
−0.4
enrichment score
0
2000
4000
6000
rank

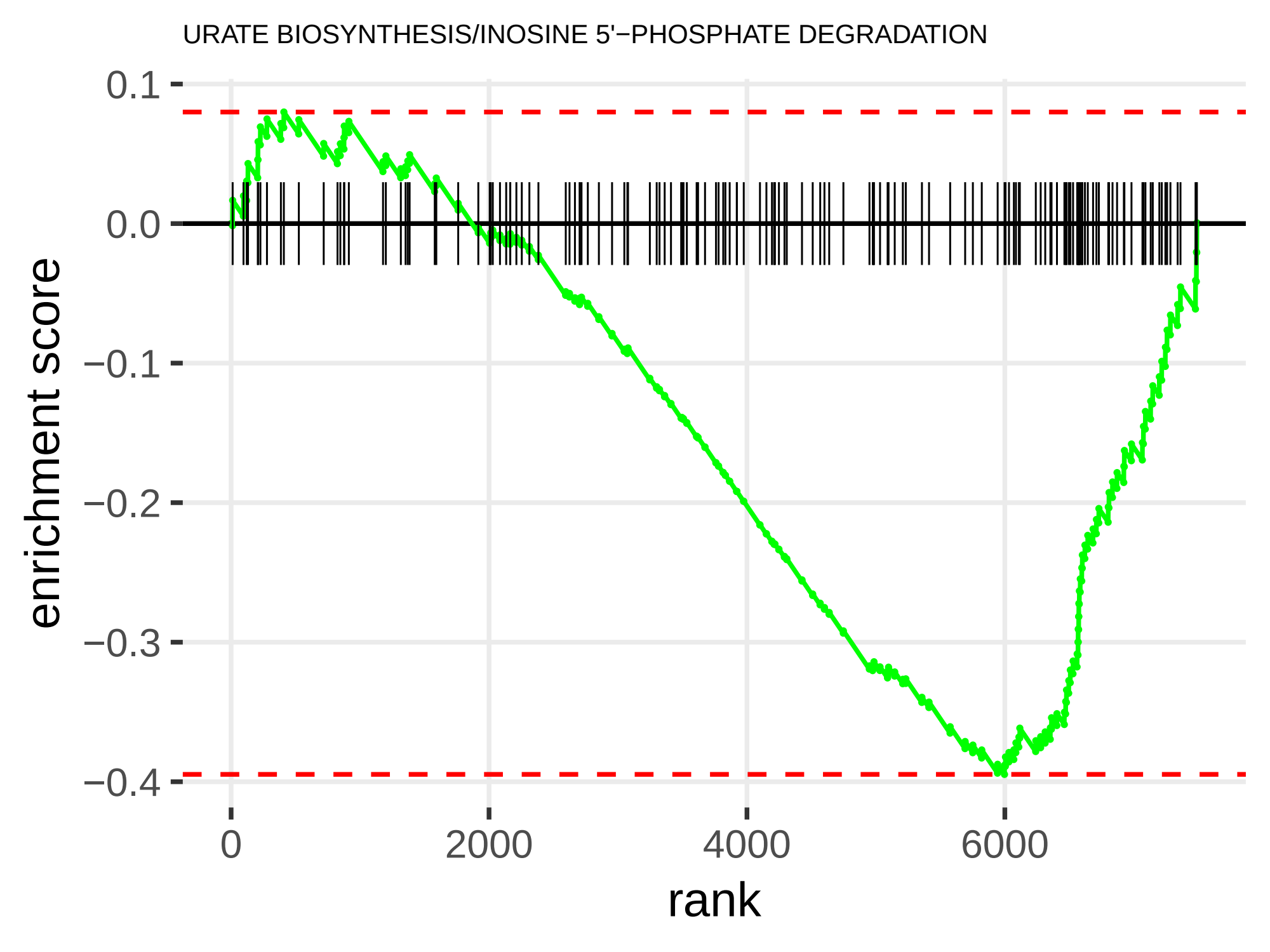

HISTAMINE BIOSYNTHESIS
0.0
−0.1
−0.2
−0.3
−0.4
enrichment score
0
2000
4000
6000
rank

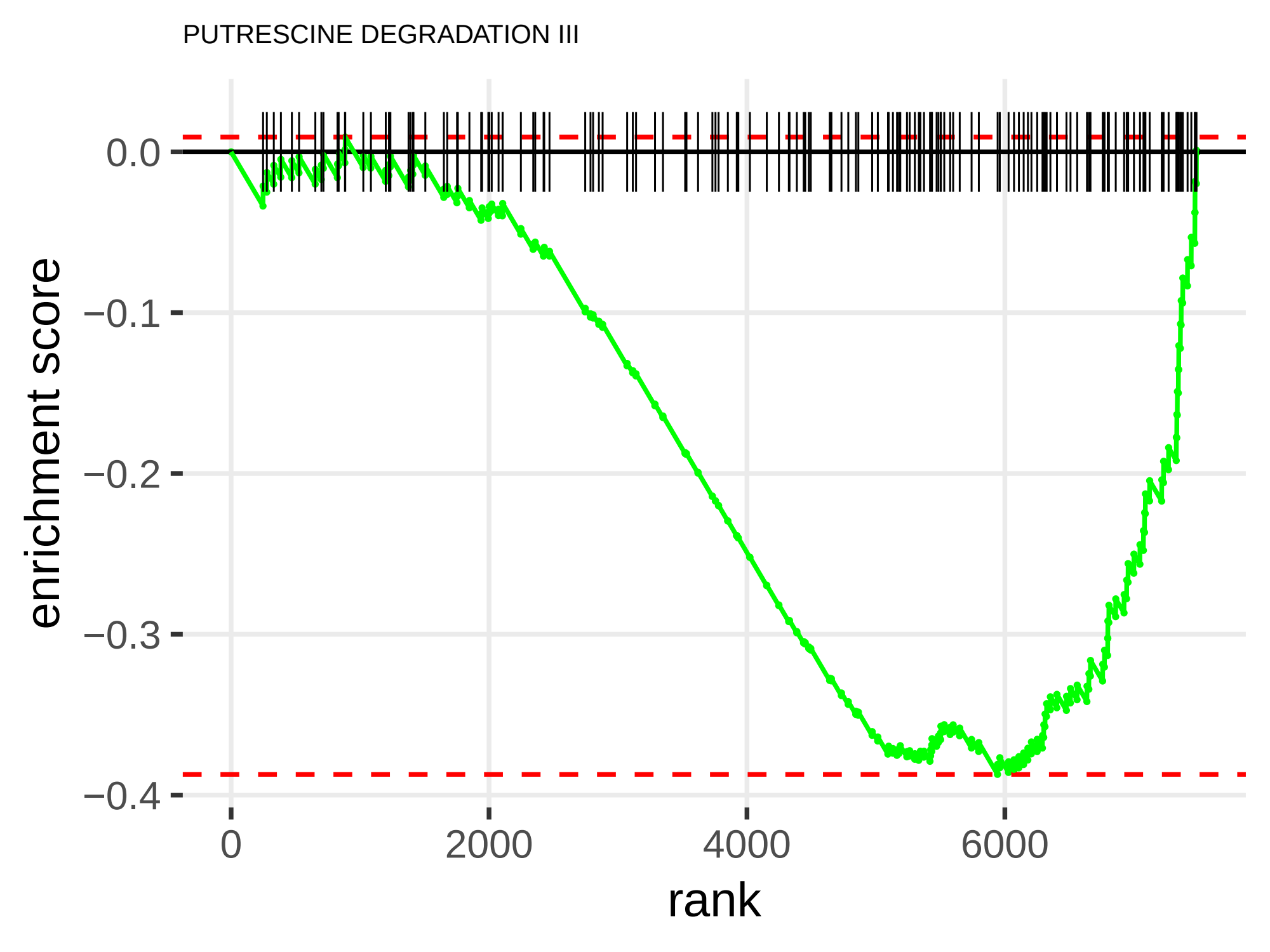

<ITRANS, TRANS</I−FARNESYL DIPHOSPHATE BIOSYNTHESIS
enrichment score
0.0
−0.1
−0.2
−0.3
−0.4
0
2000
4000
6000
rank

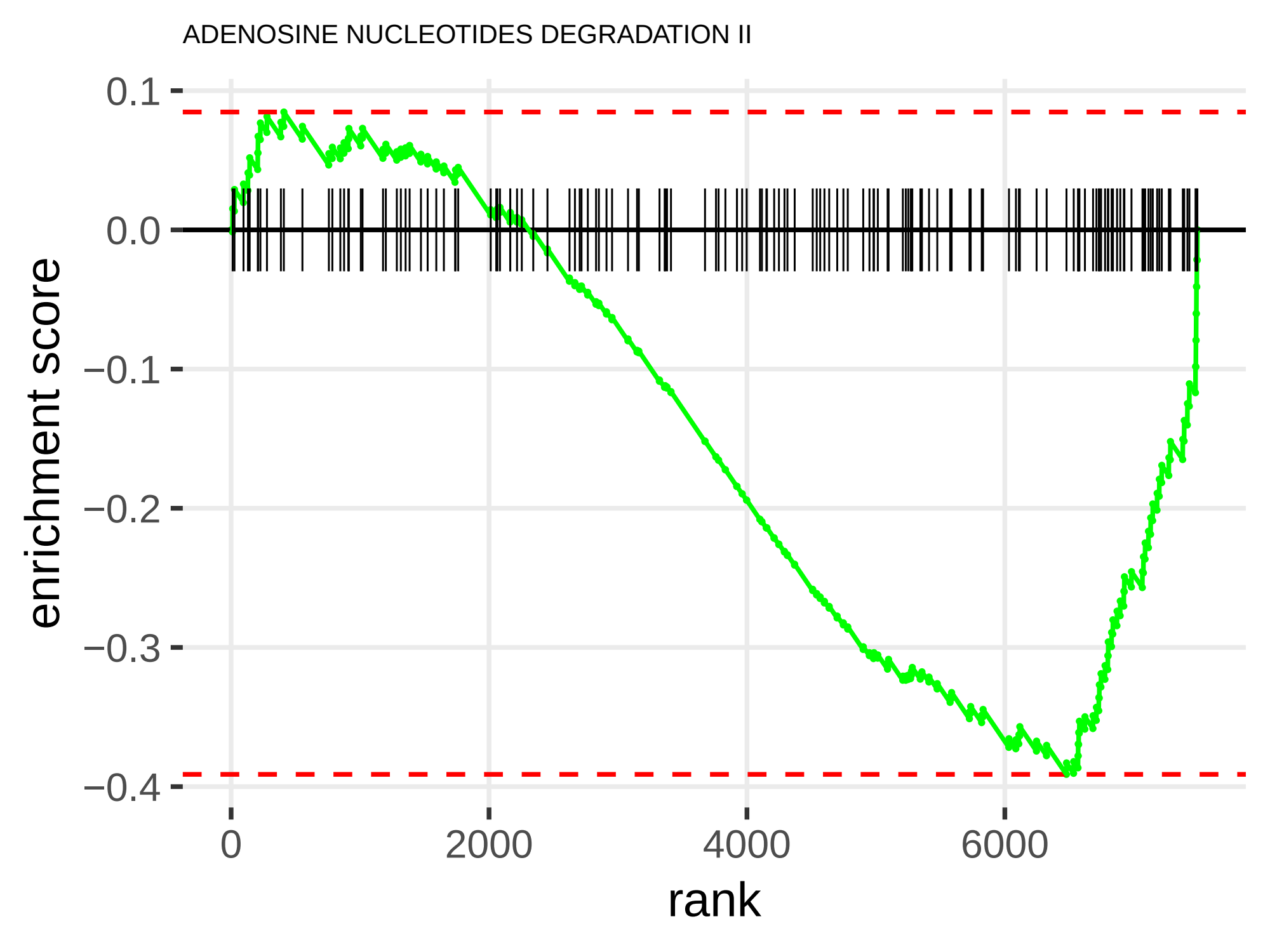

CERAMIDE BIOSYNTHESIS
0.0
−0.1
−0.2
−0.3
−0.4
enrichment score
0
2000
4000
6000
rank

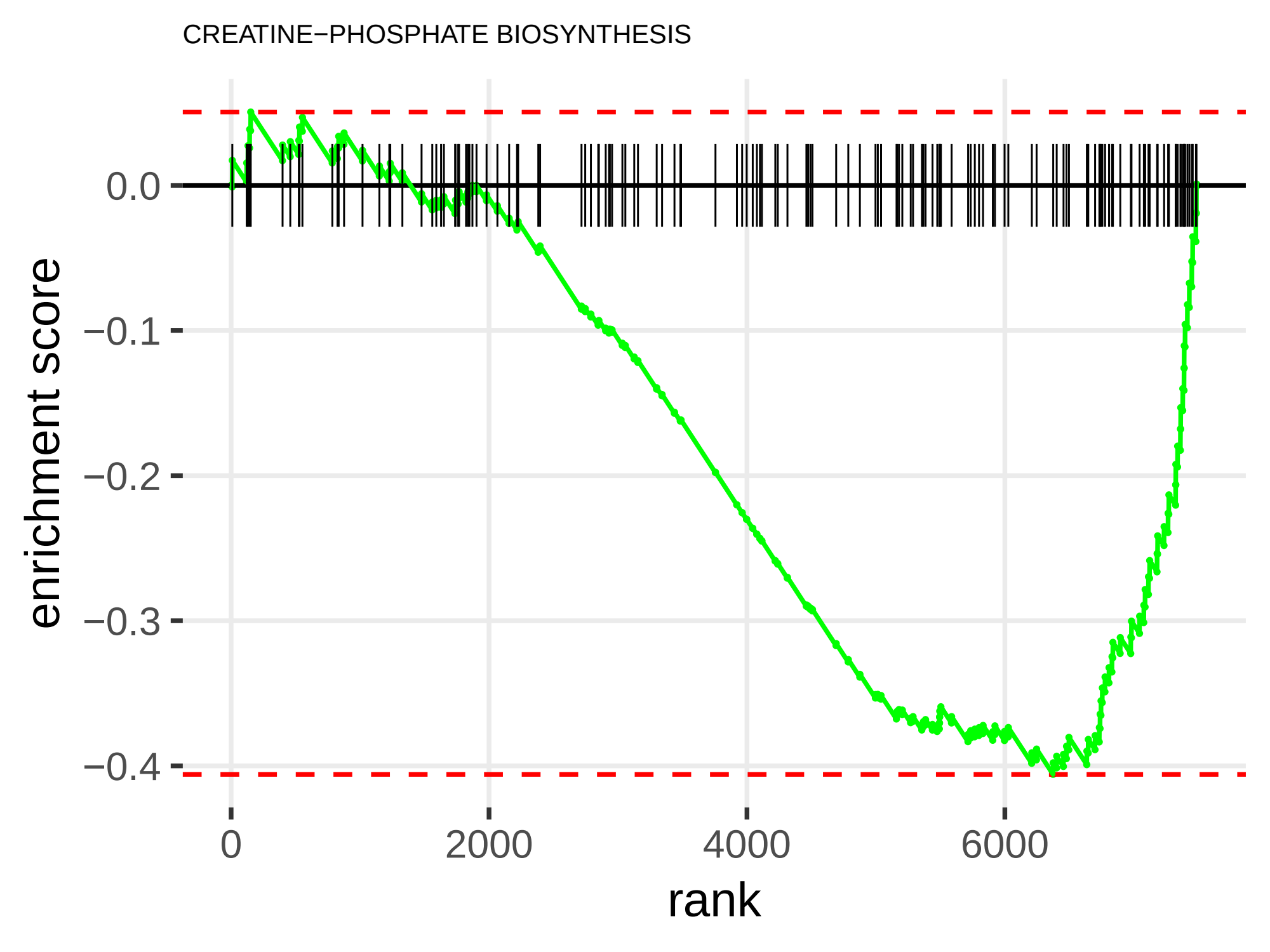

ALANINE BIOSYNTHESIS II
0.1
0.0
−0.1
−0.2
−0.3
−0.4
enrichment score
0
2000
4000
6000
rank

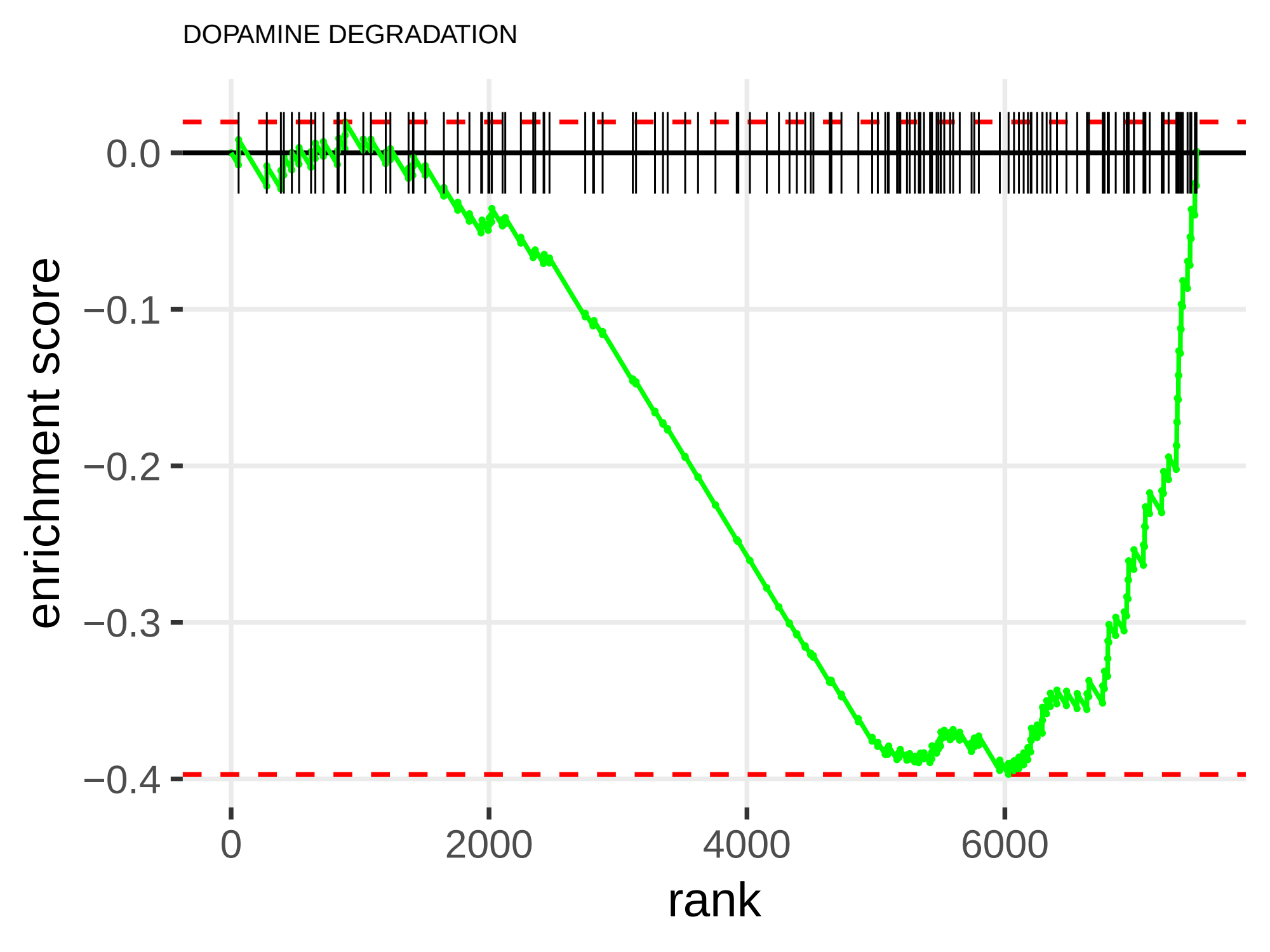

ALANINE DEGRADATION III
0.1
0.0
−0.1
−0.2
−0.3
−0.4
enrichment score
0
2000
4000
6000
rank

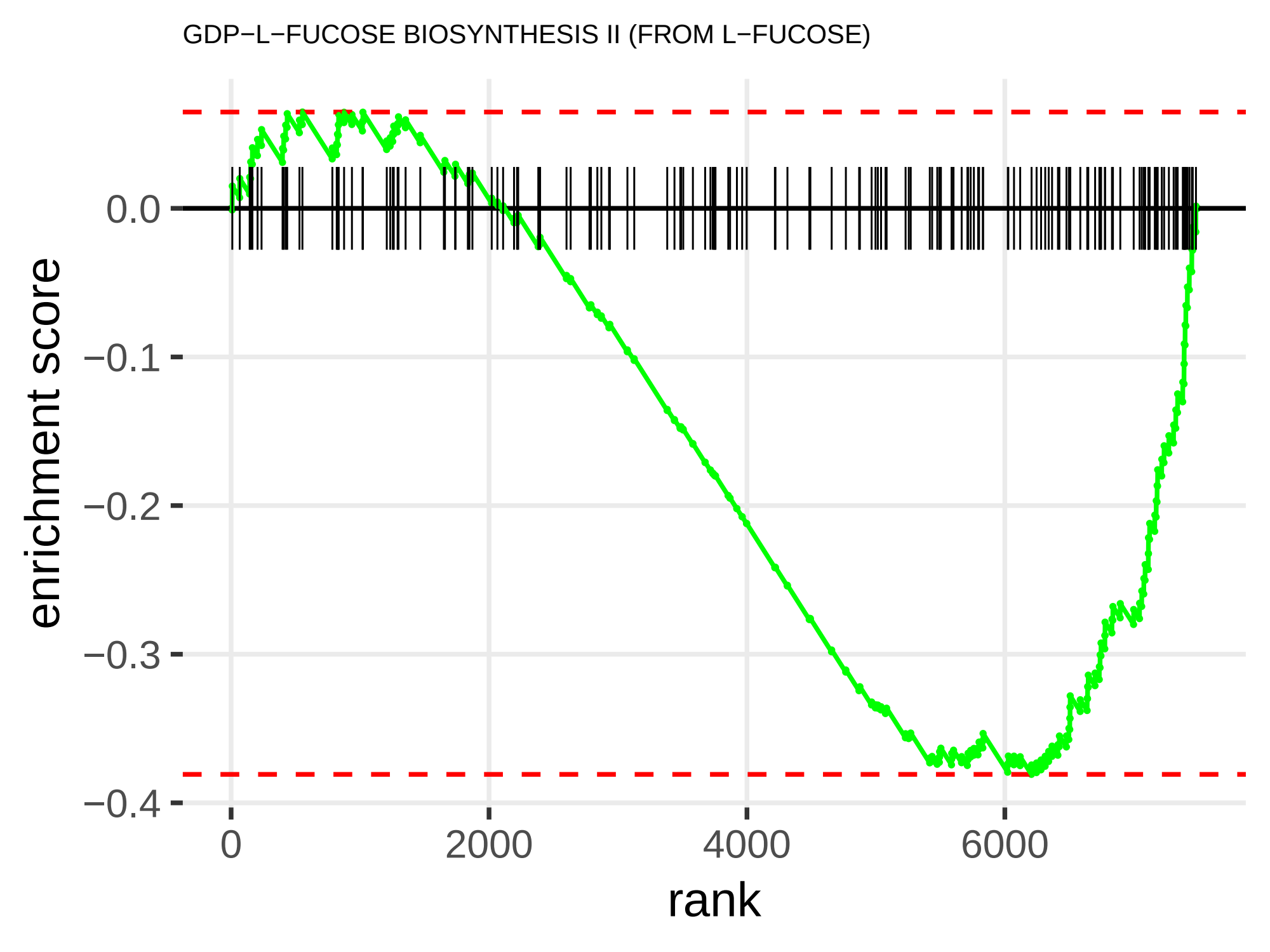

URATE BIOSYNTHESIS/INOSINE 5'−PHOSPHATE DEGRADATION
0.1
0.0
−0.1
−0.2
−0.3
−0.4
enrichment score
0
2000
4000
6000
rank

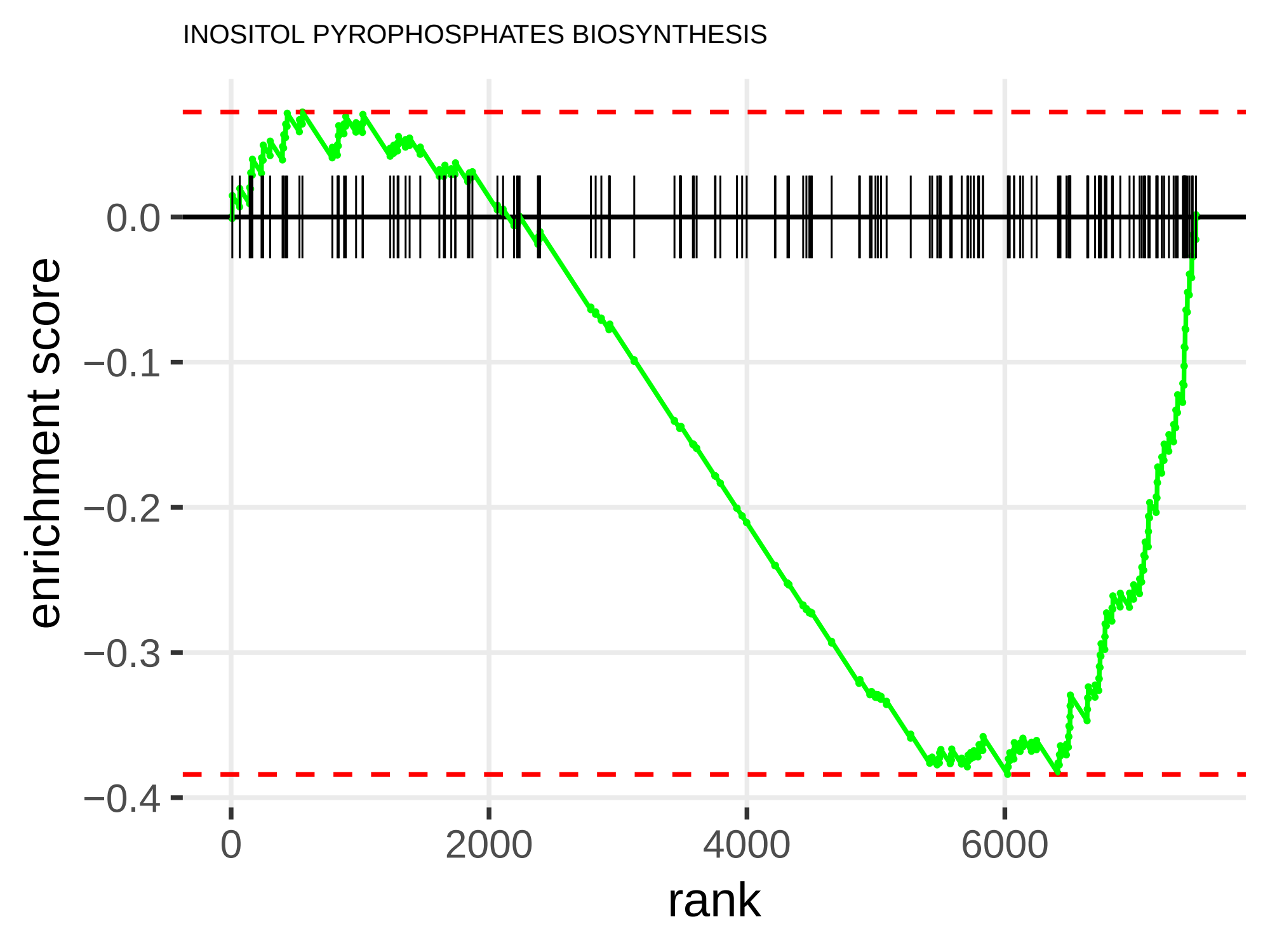

PUTRESCINE DEGRADATION III
0.0
−0.1
−0.2
−0.3
−0.4
enrichment score
0
2000
4000
6000
rank

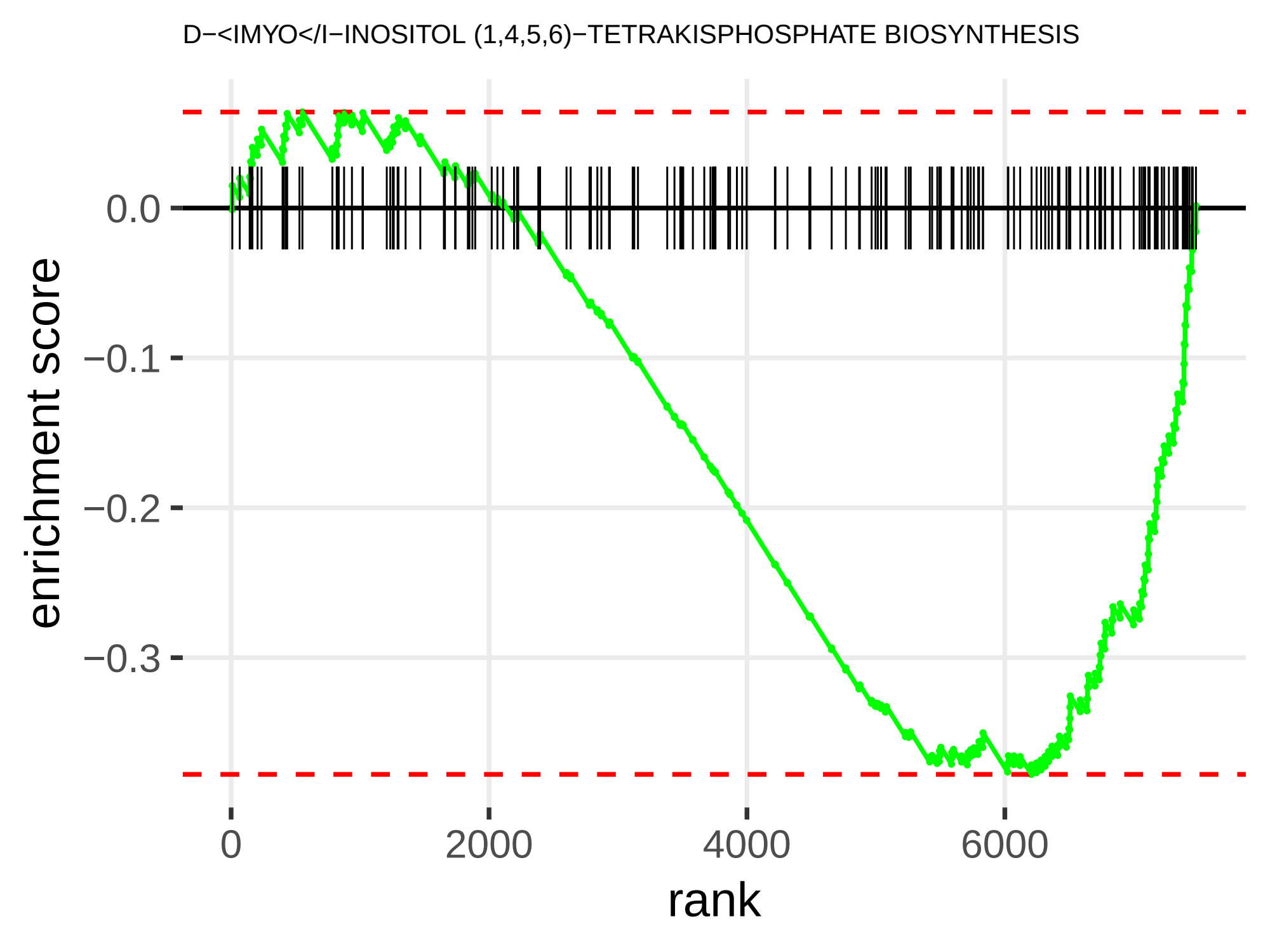

ADENOSINE NUCLEOTIDES DEGRADATION II
enrichment score
0.1
0.0
−0.1
−0.2
−0.3
−0.4
0
2000
4000
6000
rank

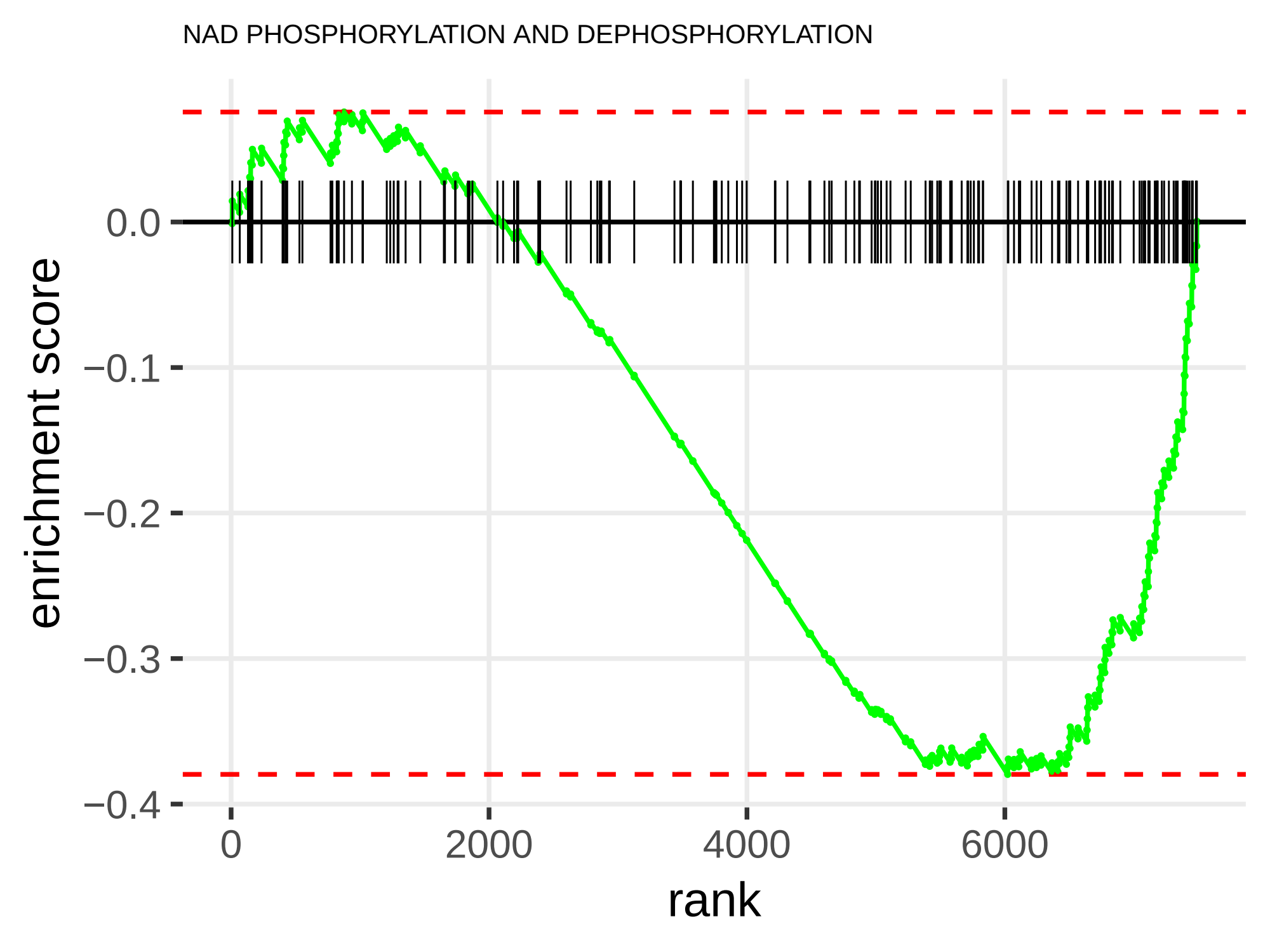

CREATINE−PHOSPHATE BIOSYNTHESIS
0.0
−0.1
−0.2
−0.3
−0.4
enrichment score
0
2000
4000
6000
rank

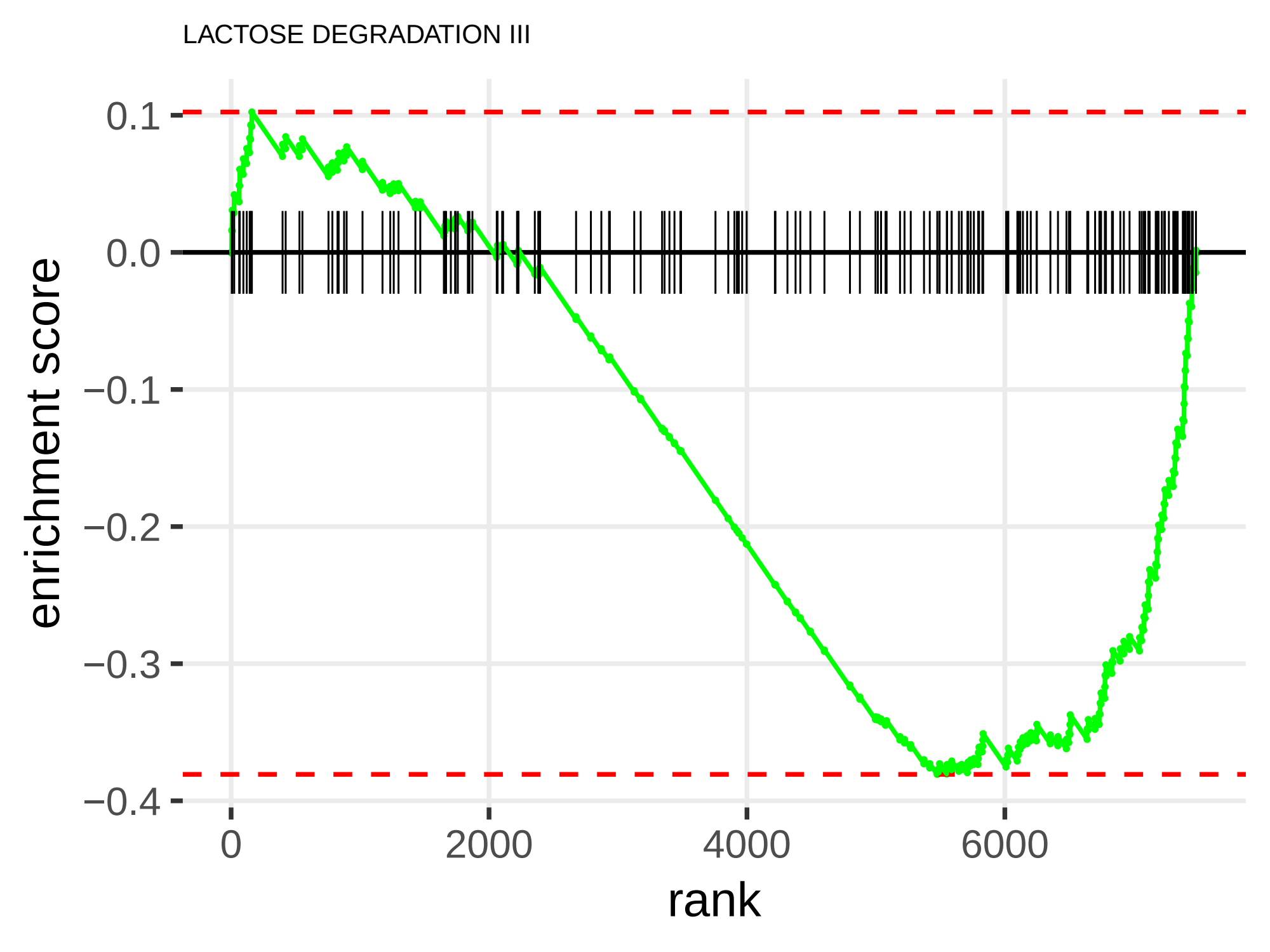

DOPAMINE DEGRADATION
0.0
−0.1
−0.2
−0.3
−0.4
enrichment score
0
2000
4000
6000
rank

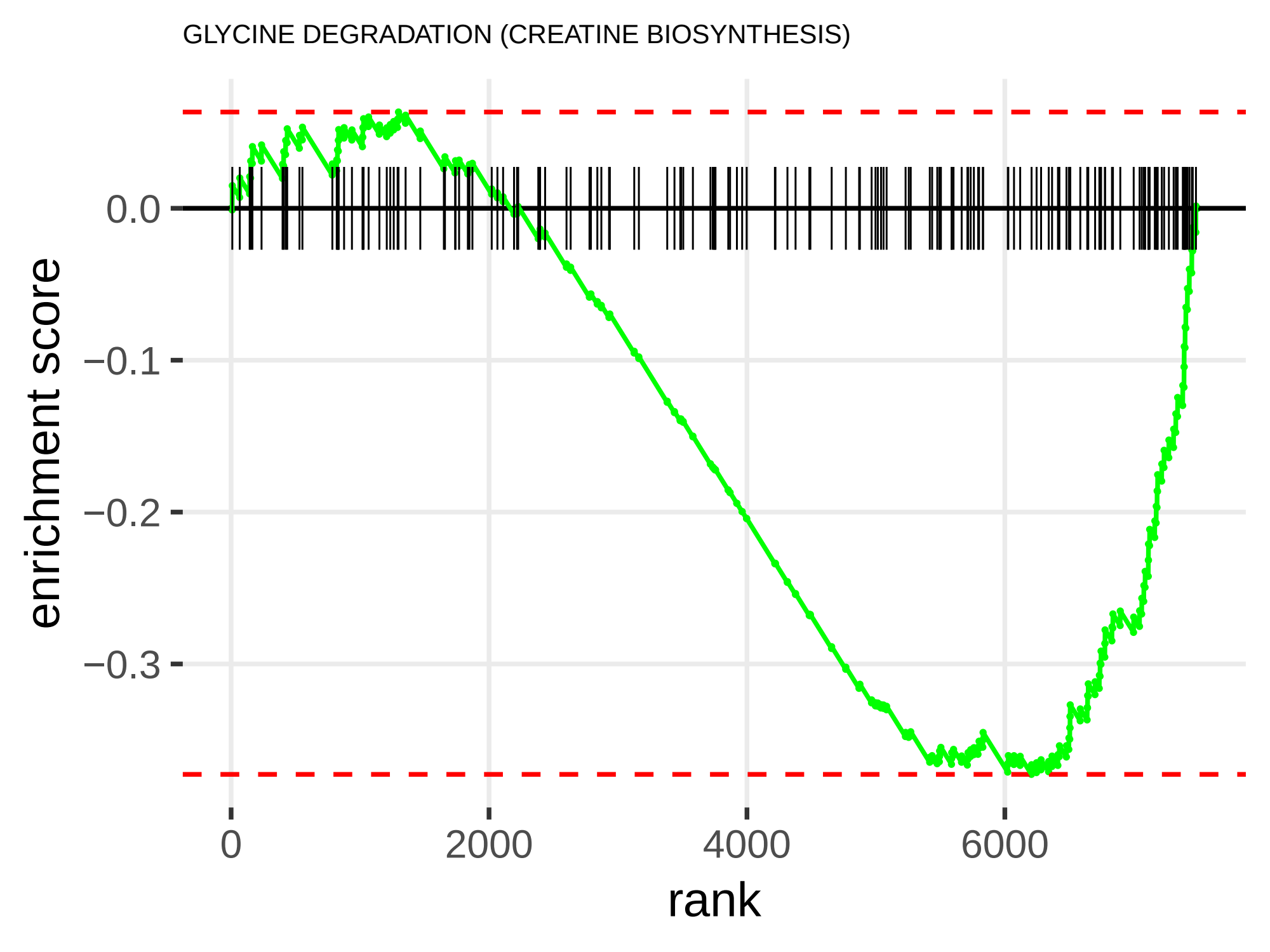

GDP−L−FUCOSE BIOSYNTHESIS II (FROM L−FUCOSE)
enrichment score
0.0
−0.1
−0.2
−0.3
−0.4
0
2000
4000
6000
rank

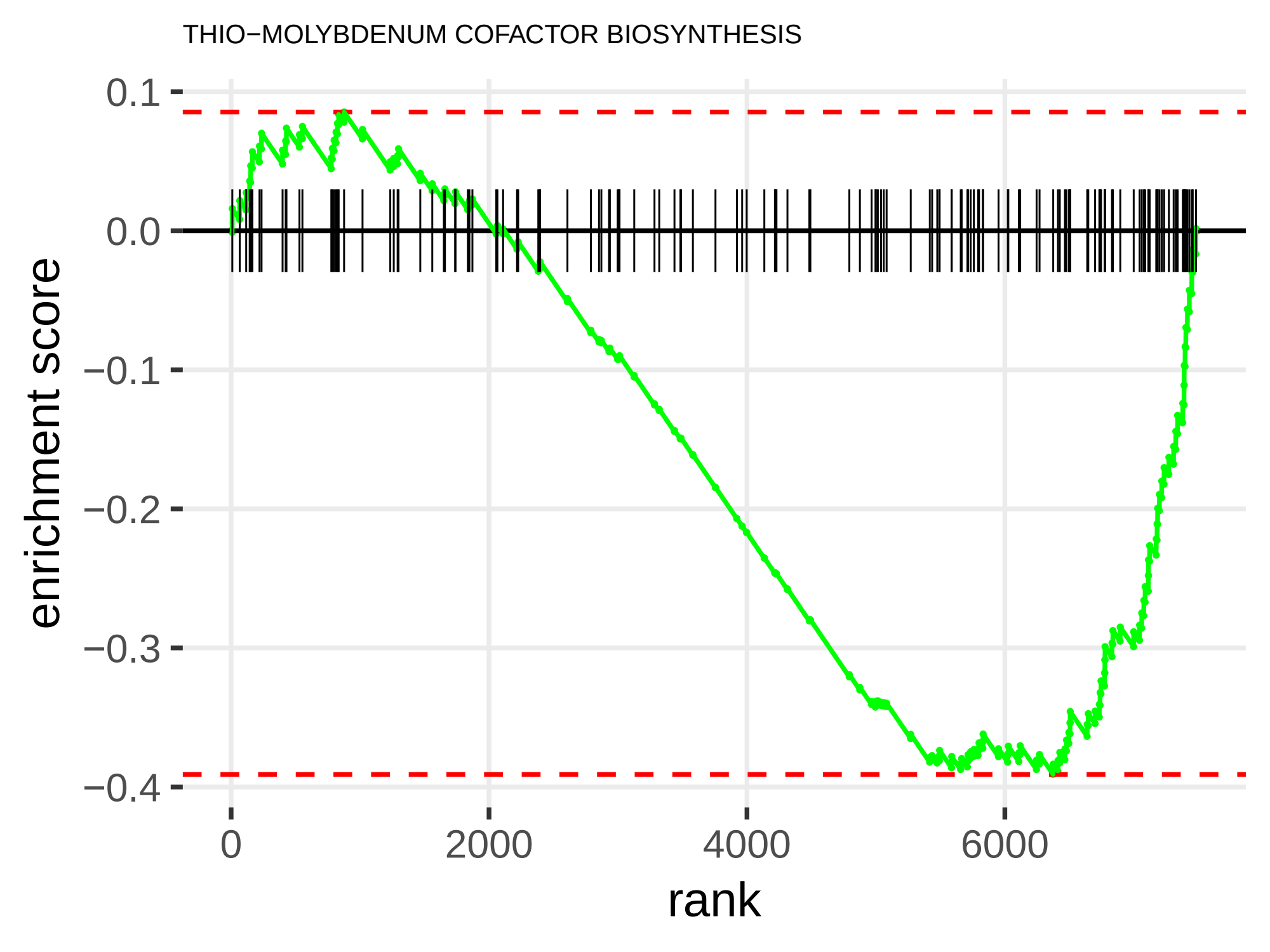

INOSITOL PYROPHOSPHATES BIOSYNTHESIS
enrichment score
0.0
−0.1
−0.2
−0.3
−0.4
0
2000
4000
6000
rank

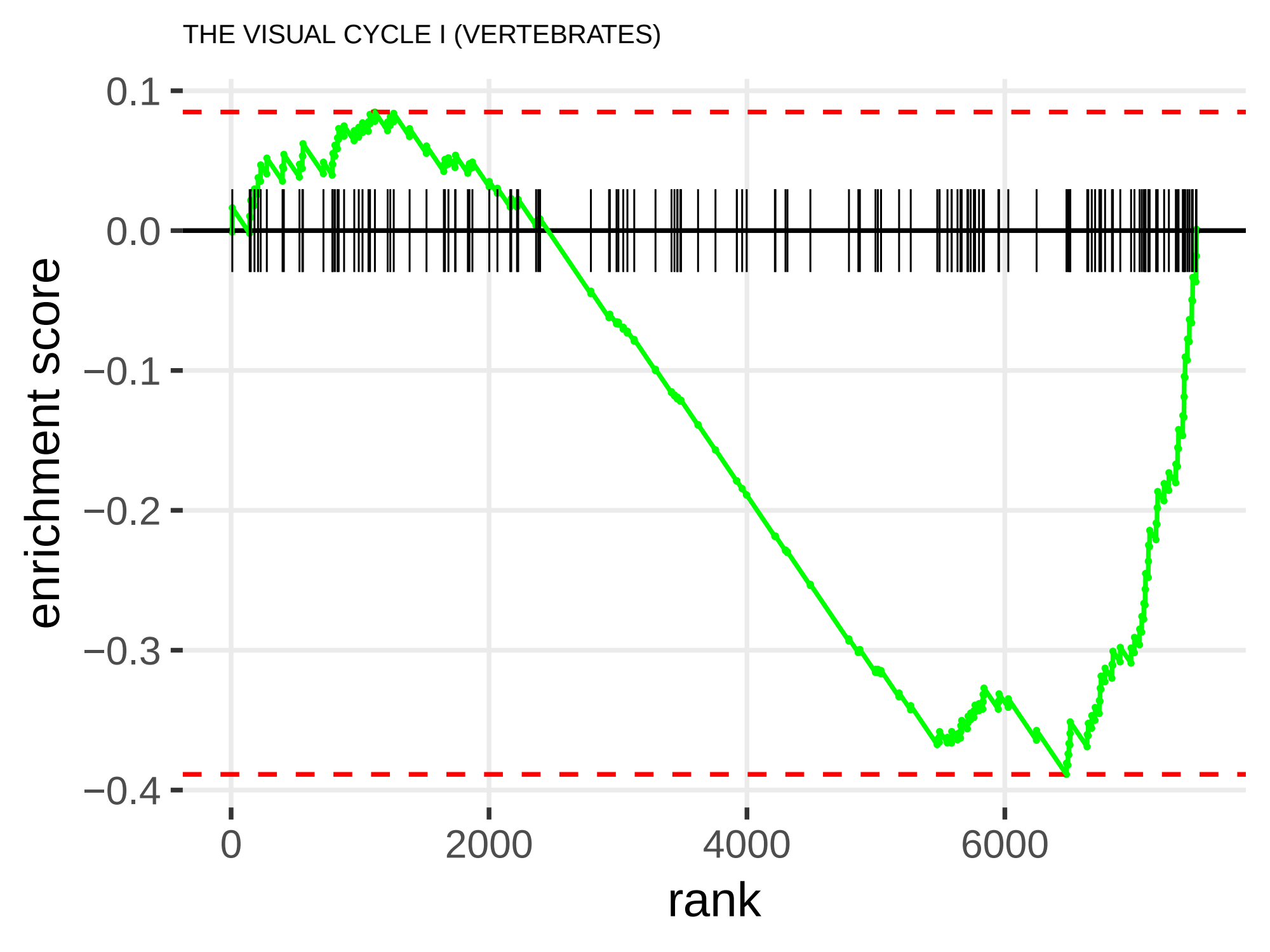

D−<IMYO</I−INOSITOL (1,4,5,6)−TETRAKISPHOSPHATE BIOSYNTHESIS
0.0
−0.1
−0.2
−0.3
enrichment score
0
2000
4000
6000
rank

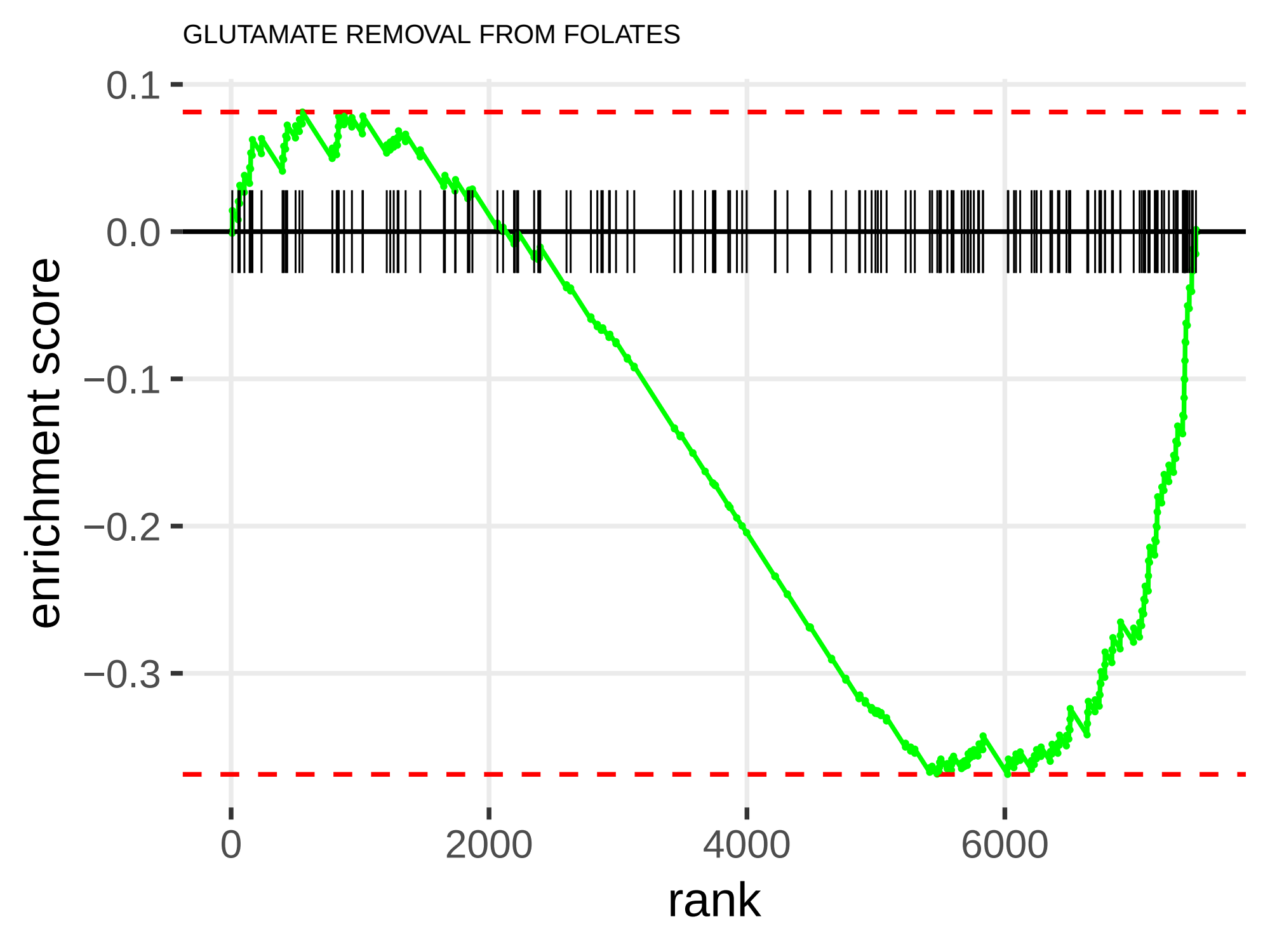

NAD PHOSPHORYLATION AND DEPHOSPHORYLATION
enrichment score
0.0
−0.1
−0.2
−0.3
−0.4
0
2000
4000
6000
rank

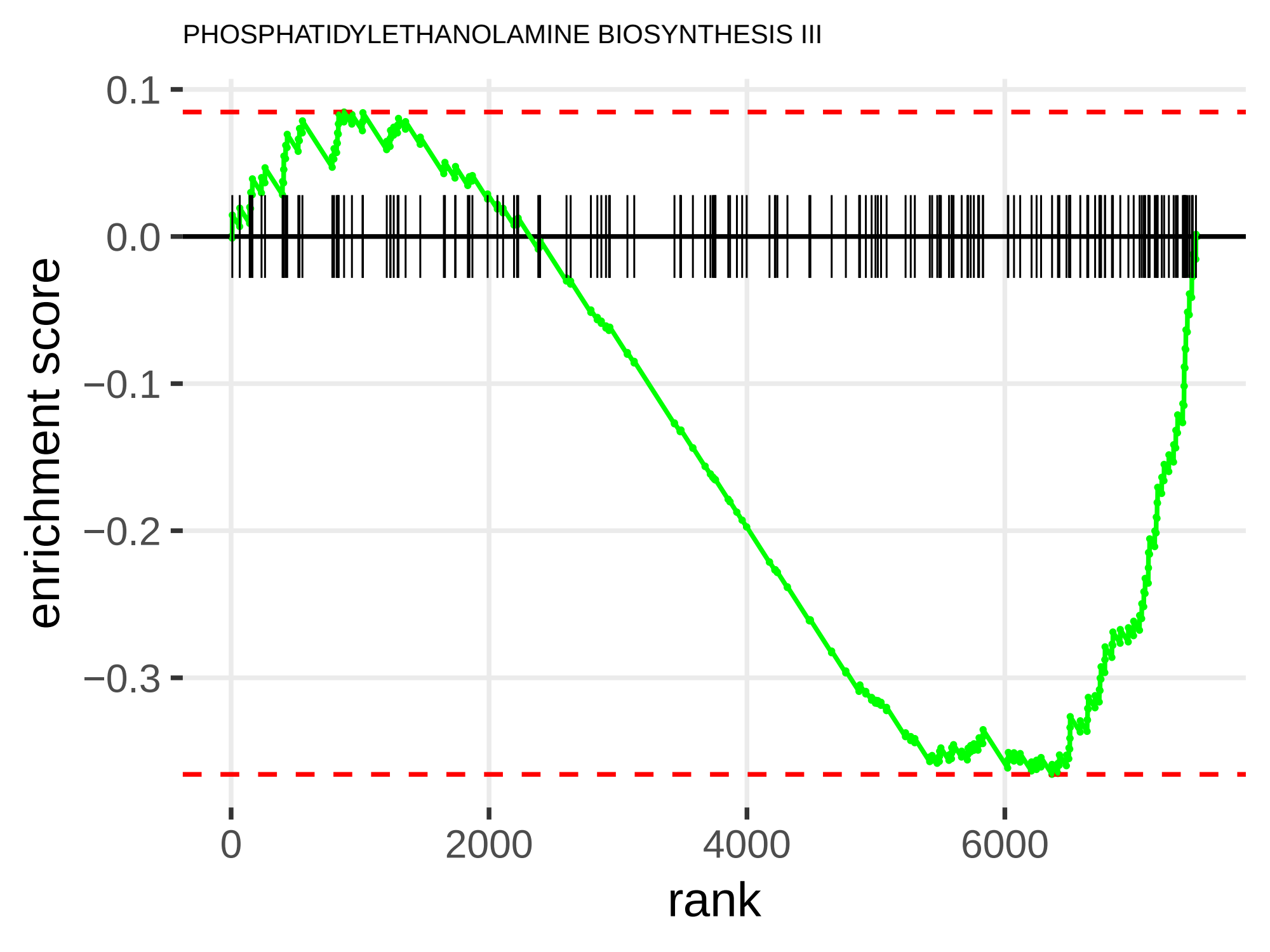

LACTOSE DEGRADATION III
0.1
0.0
−0.1
−0.2
−0.3
−0.4
enrichment score
0
2000
4000
6000
rank

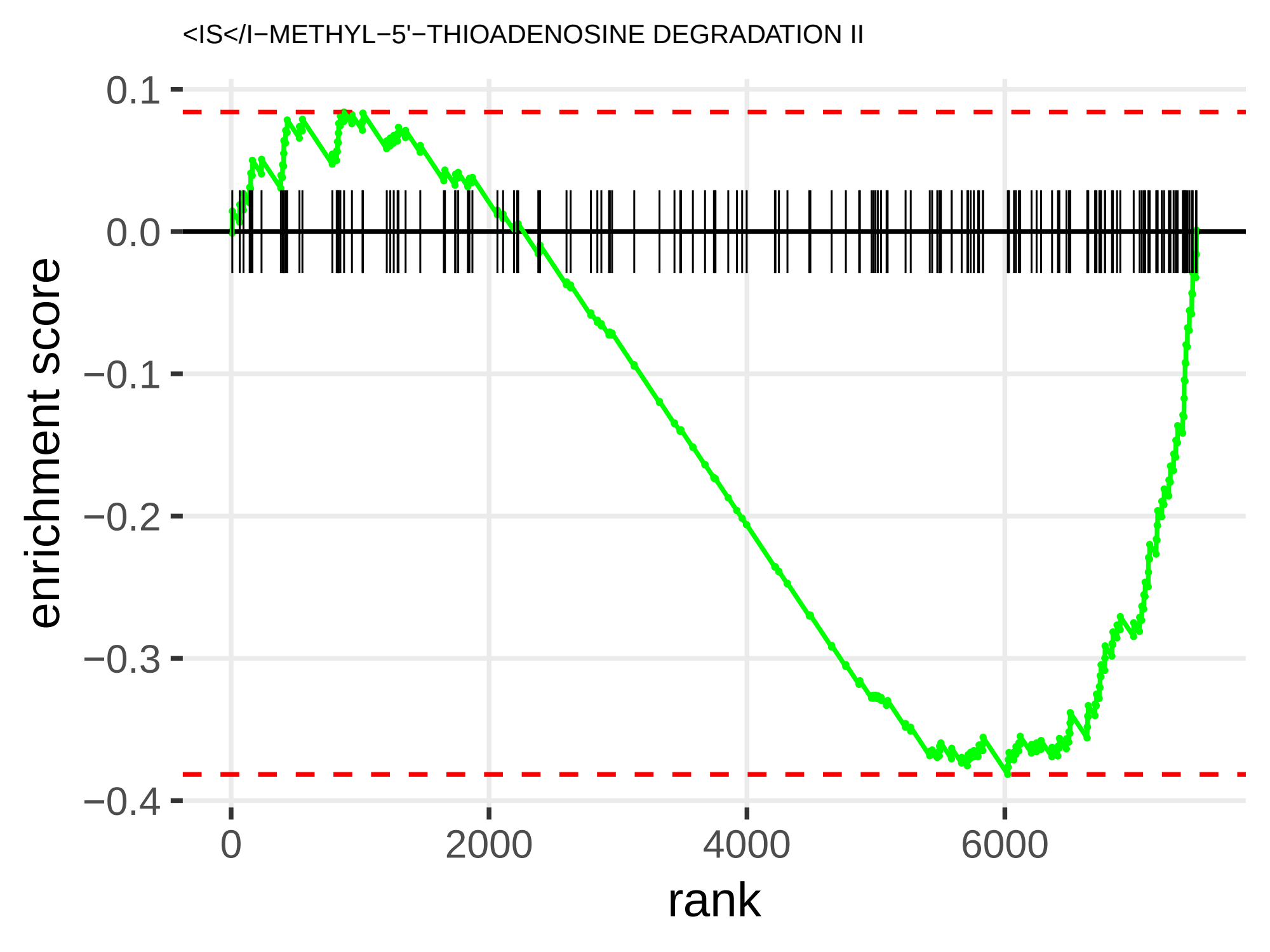

GLYCINE DEGRADATION (CREATINE BIOSYNTHESIS)
enrichment score
0.0
−0.1
−0.2
−0.3
0
2000
4000
6000
rank

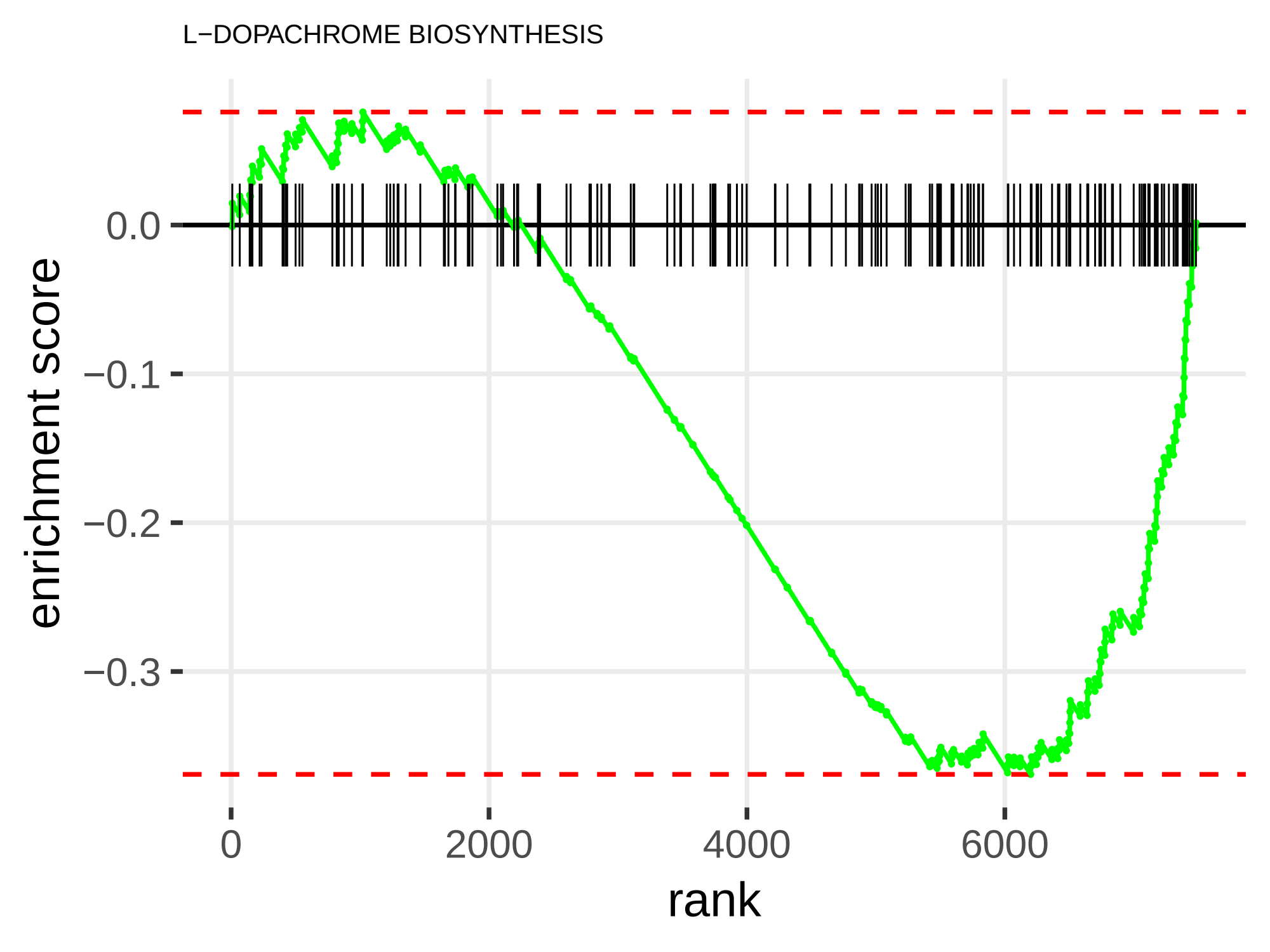

THIO−MOLYBDENUM COFACTOR BIOSYNTHESIS
0.1
0.0
−0.1
−0.2
−0.3
−0.4
enrichment score
0
2000
4000
6000
rank

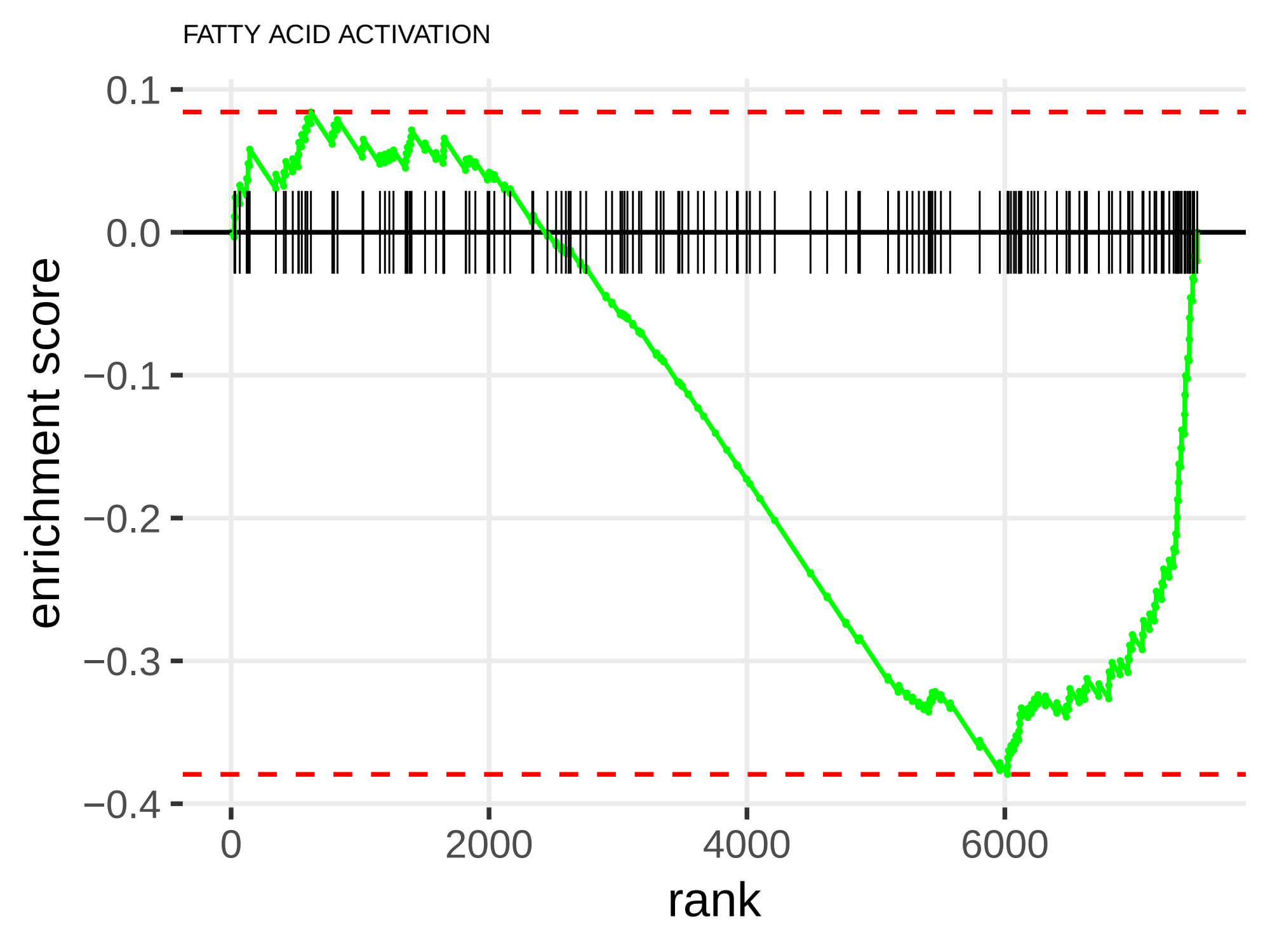

THE VISUAL CYCLE I (VERTEBRATES)
0.1
0.0
−0.1
−0.2
−0.3
−0.4
enrichment score
0
2000
4000
6000
rank

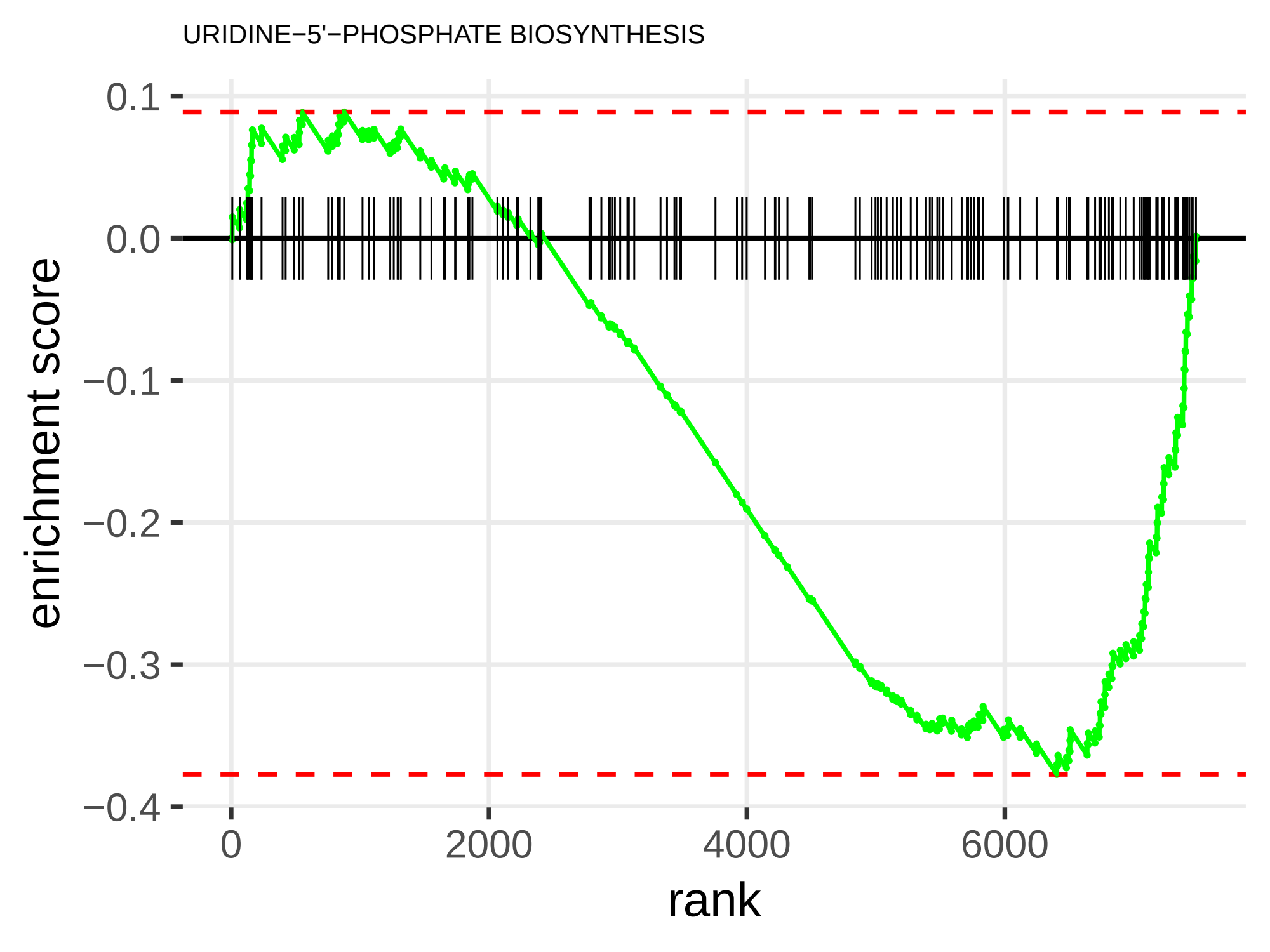

GLUTAMATE REMOVAL FROM FOLATES
0.1
0.0
−0.1
−0.2
−0.3
enrichment score
0
2000
4000
6000
rank

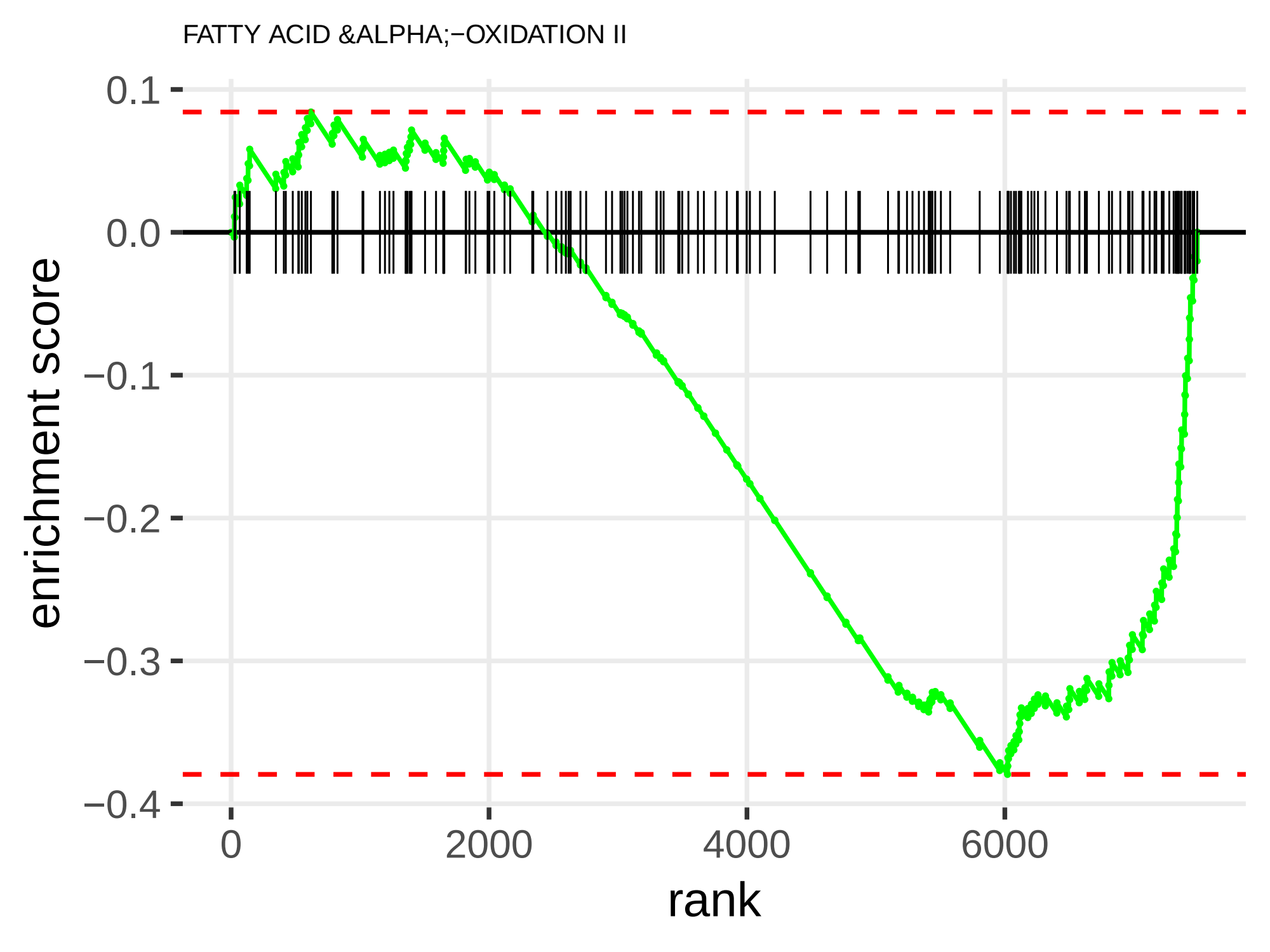

PHOSPHATIDYLETHANOLAMINE BIOSYNTHESIS III
0.1
0.0
−0.1
−0.2
−0.3
enrichment score
0
2000
4000
6000
rank

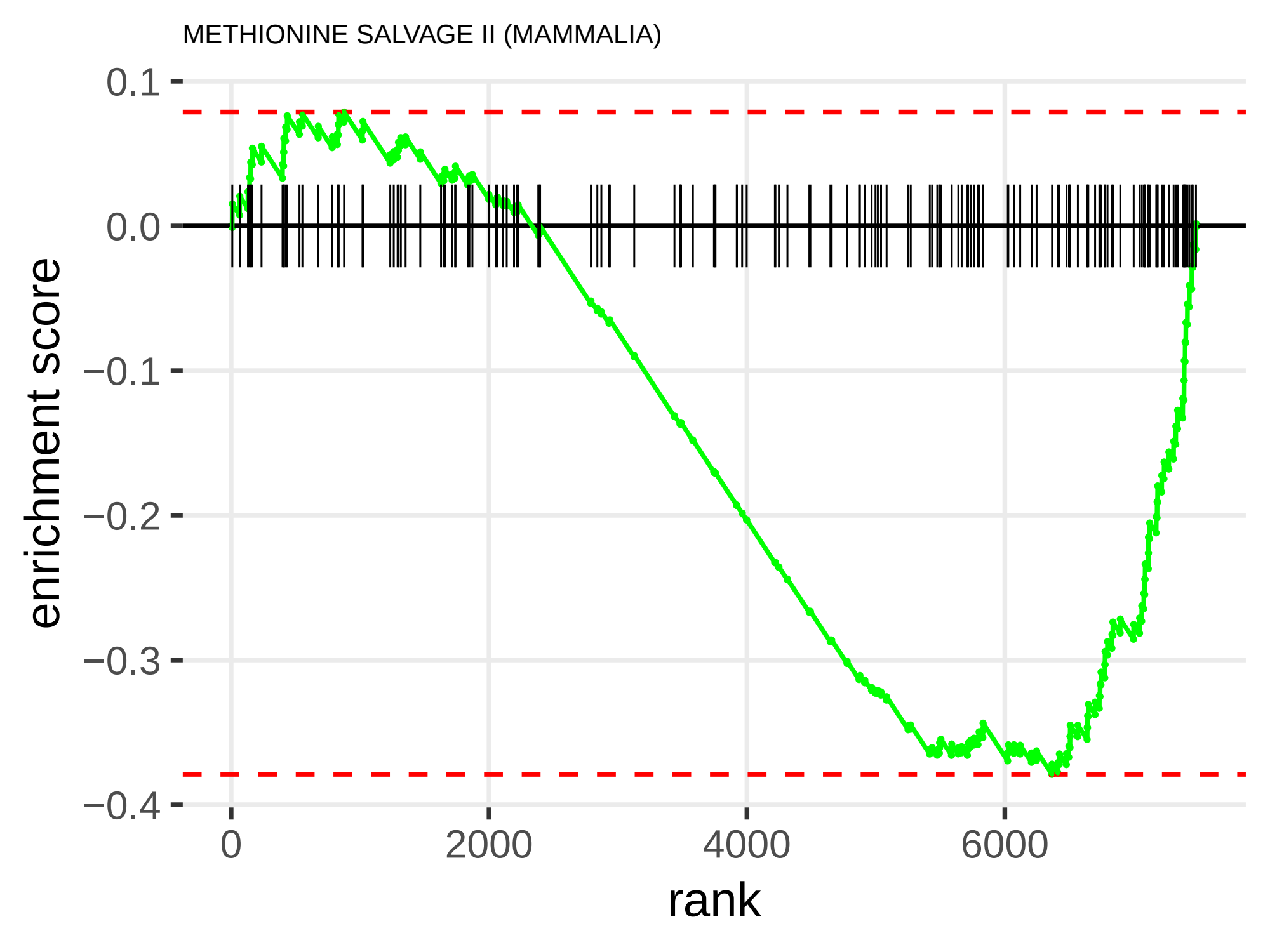

<IS</I−METHYL−5'−THIOADENOSINE DEGRADATION II
0.1
0.0
−0.1
−0.2
−0.3
−0.4
enrichment score
0
2000
4000
6000
rank

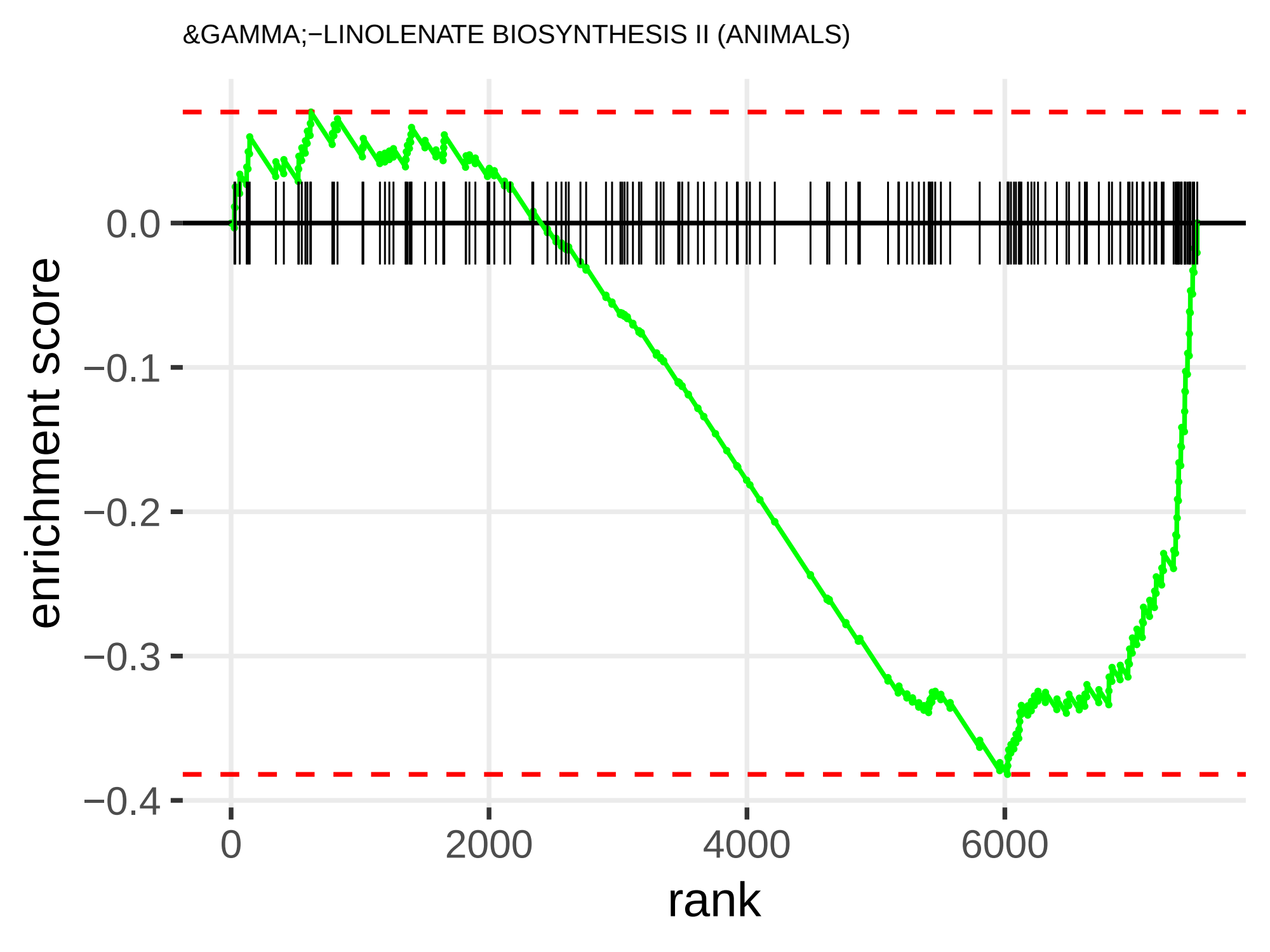

L−DOPACHROME BIOSYNTHESIS
enrichment score
0.0
−0.1
−0.2
−0.3
0
2000
4000
6000
rank

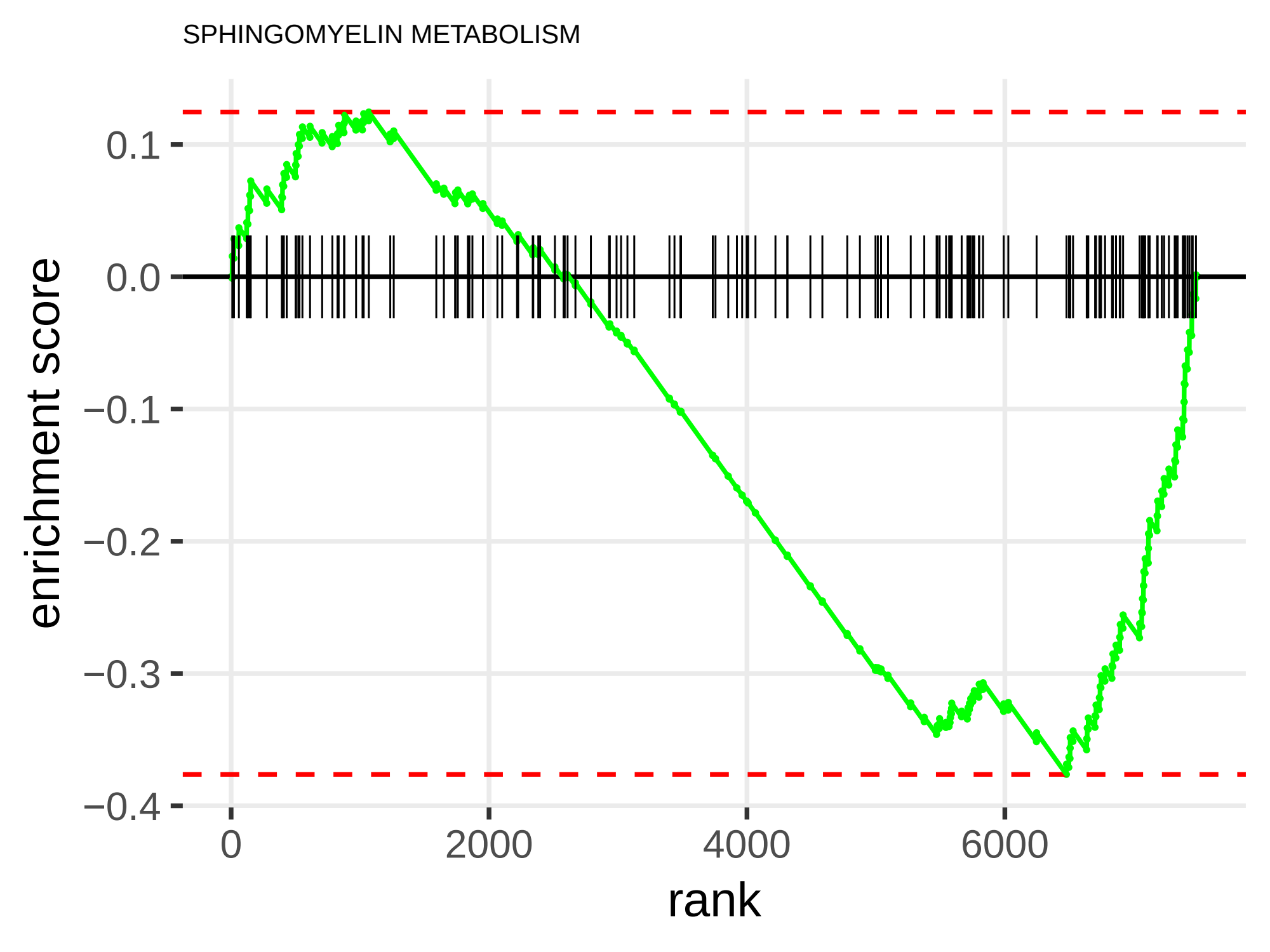

FATTY ACID ACTIVATION
0.1
0.0
−0.1
−0.2
−0.3
−0.4
enrichment score
0
2000
4000
6000
rank

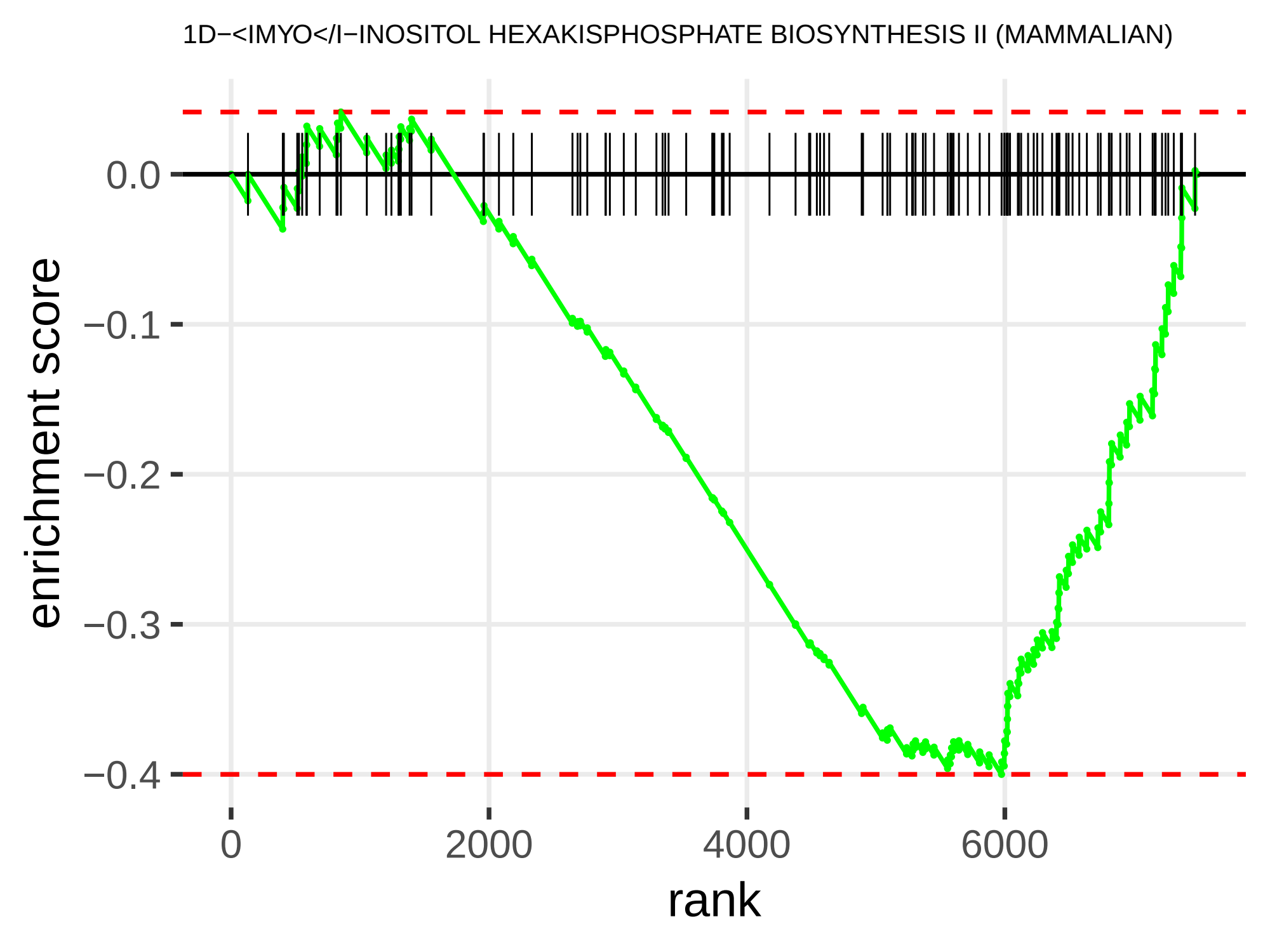

URIDINE−5'−PHOSPHATE BIOSYNTHESIS
0.1
0.0
−0.1
−0.2
−0.3
−0.4
enrichment score
0
2000
4000
6000
rank

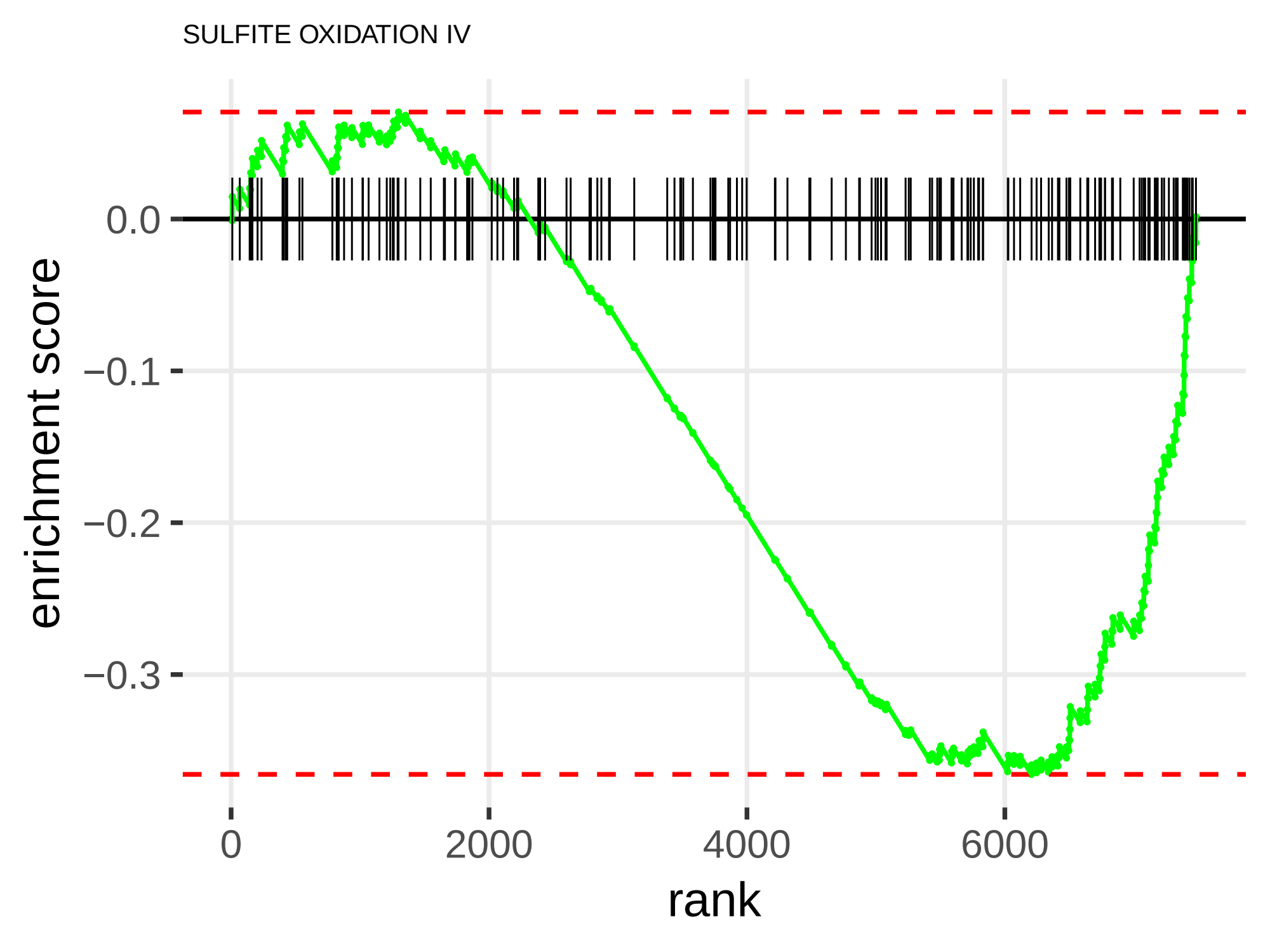

FATTY ACID &ALPHA;−OXIDATION II
0.1
0.0
−0.1
−0.2
−0.3
−0.4
enrichment score
0
2000
4000
6000
rank

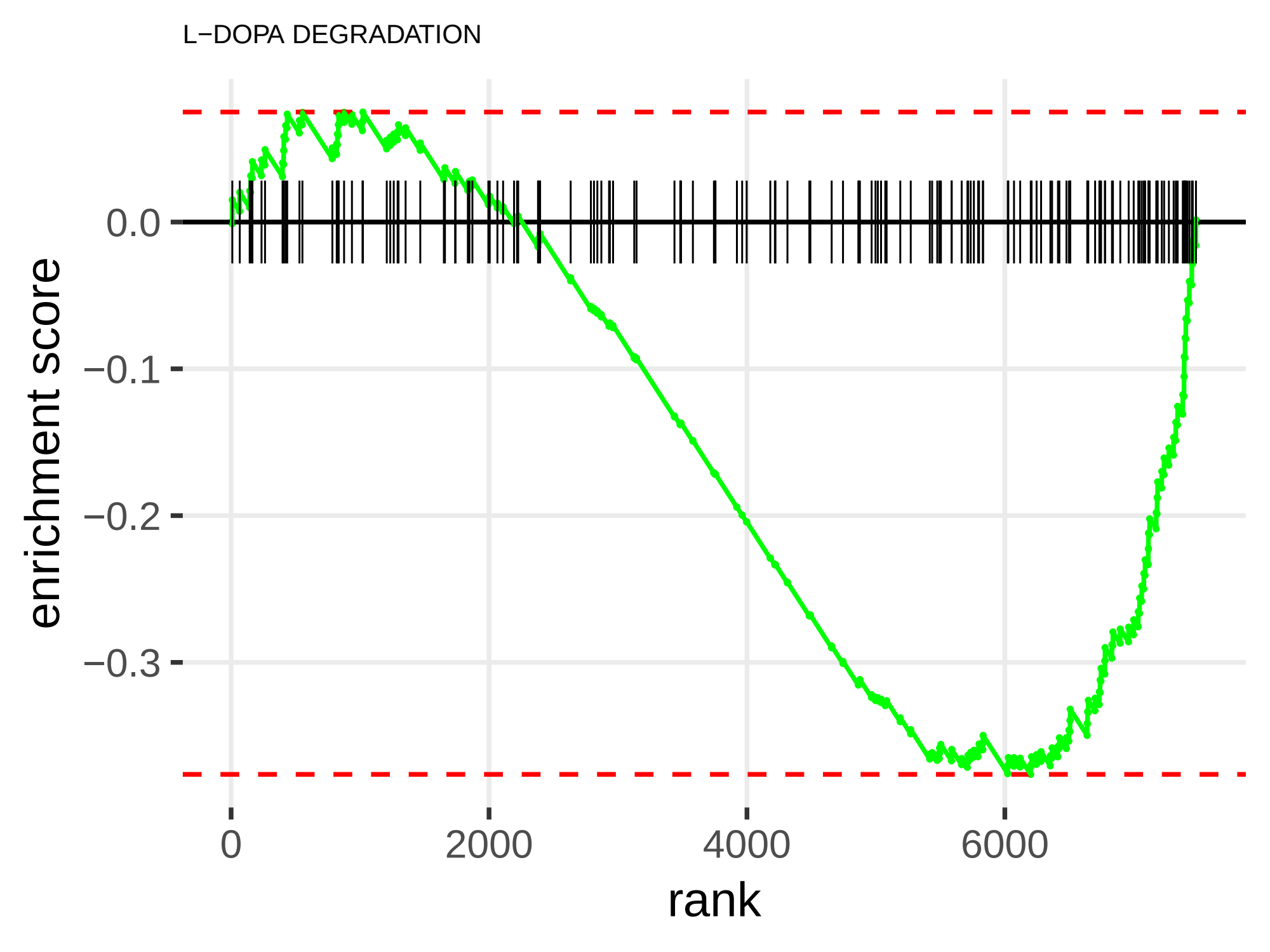

METHIONINE SALVAGE II (MAMMALIA)
0.1
0.0
−0.1
−0.2
−0.3
−0.4
enrichment score
0
2000
4000
6000
rank

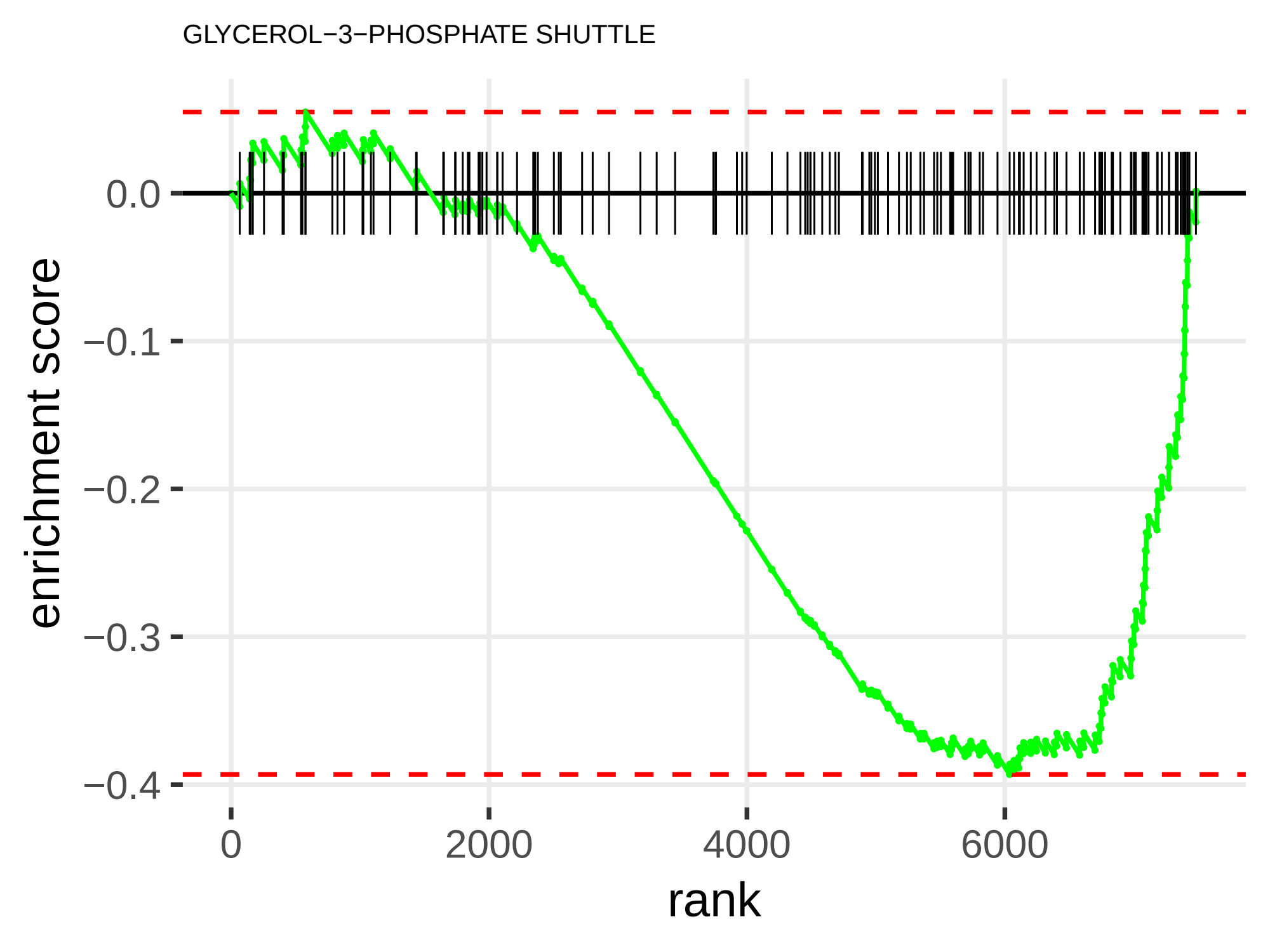

&GAMMA;−LINOLENATE BIOSYNTHESIS II (ANIMALS)
enrichment score
0.0
−0.1
−0.2
−0.3
−0.4
0
2000
4000
6000
rank

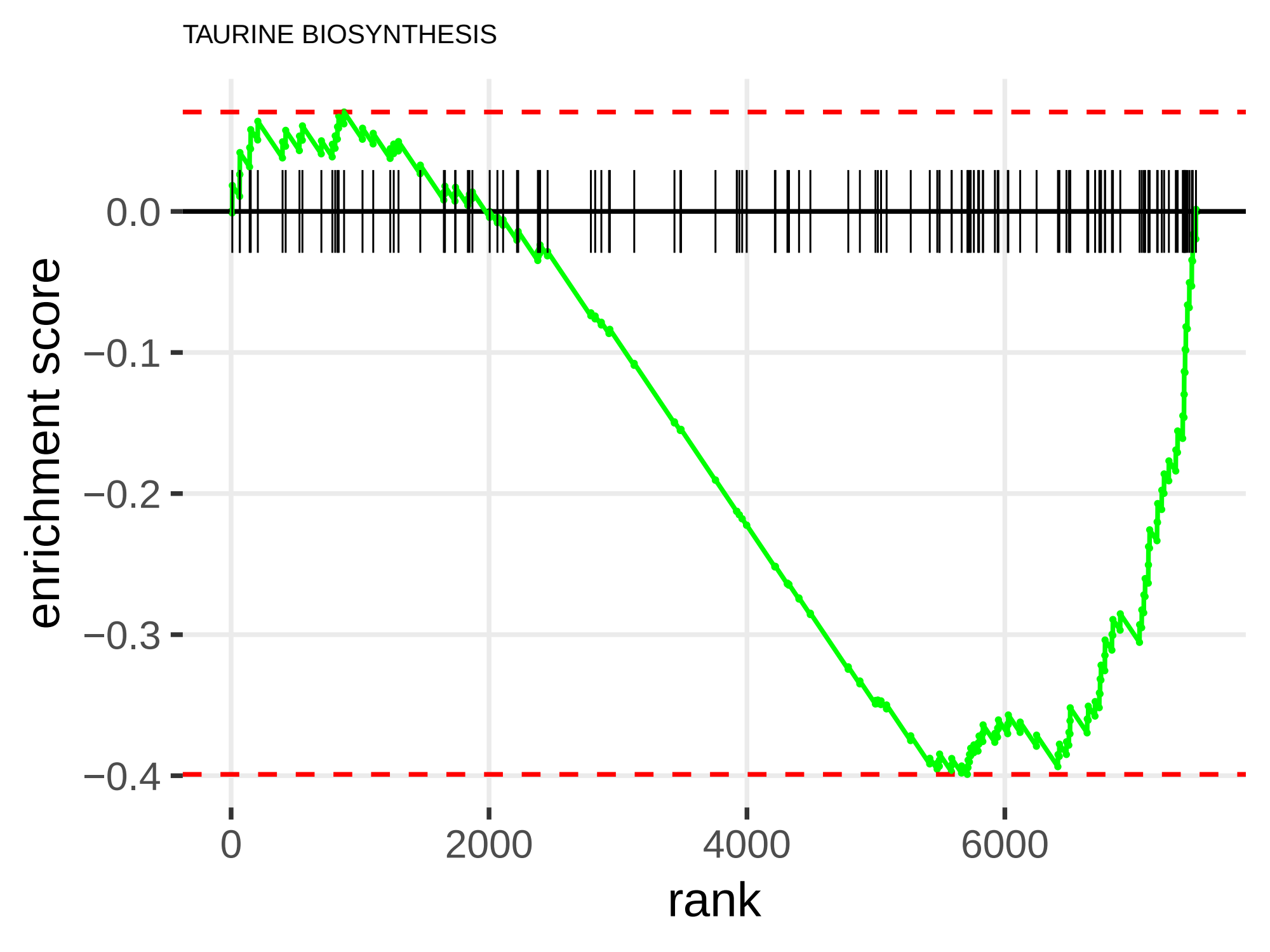

SPHINGOMYELIN METABOLISM
enrichment score
0.1
0.0
−0.1
−0.2
−0.3
−0.4
0
2000
4000
6000
rank

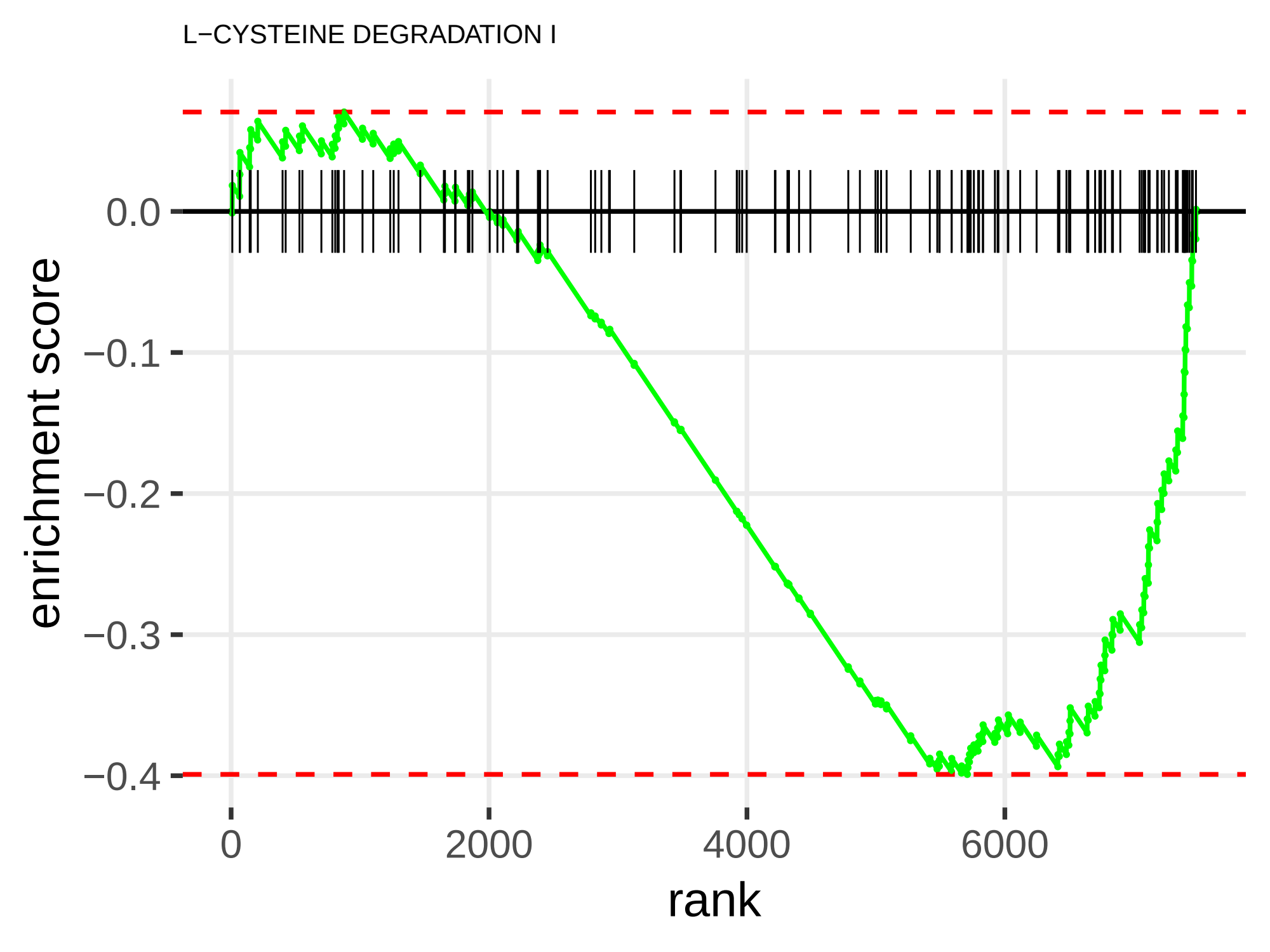

1D−<IMYO</I−INOSITOL HEXAKISPHOSPHATE BIOSYNTHESIS II (MAMMALIAN)
0.0
−0.1
−0.2
−0.3
−0.4
enrichment score
0
2000
4000
6000
rank

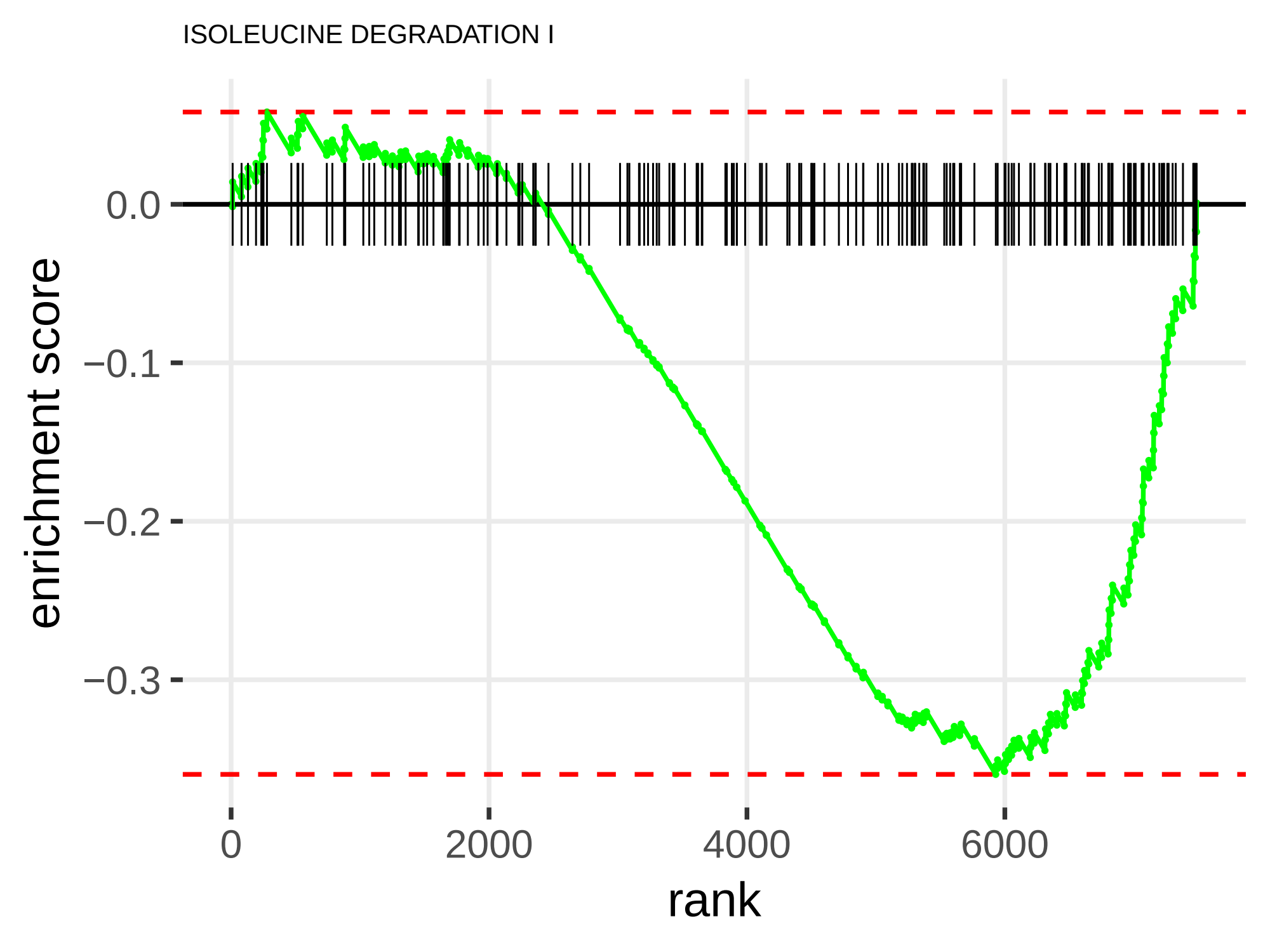

SULFITE OXIDATION IV
0.0
−0.1
−0.2
−0.3
enrichment score
0
2000
4000
6000
rank

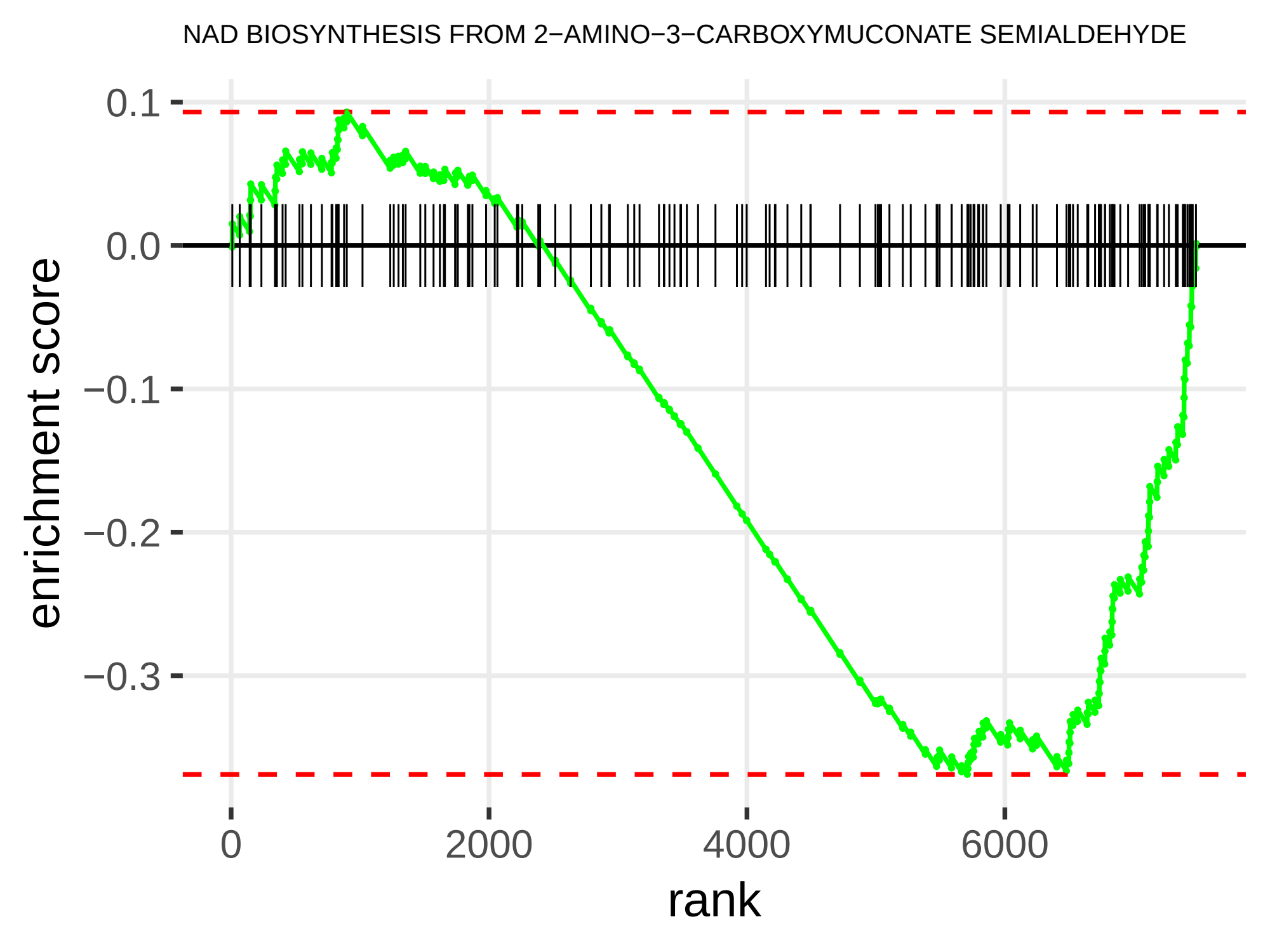

L−DOPA DEGRADATION
enrichment score
0.0
−0.1
−0.2
−0.3
0
2000
4000
6000
rank

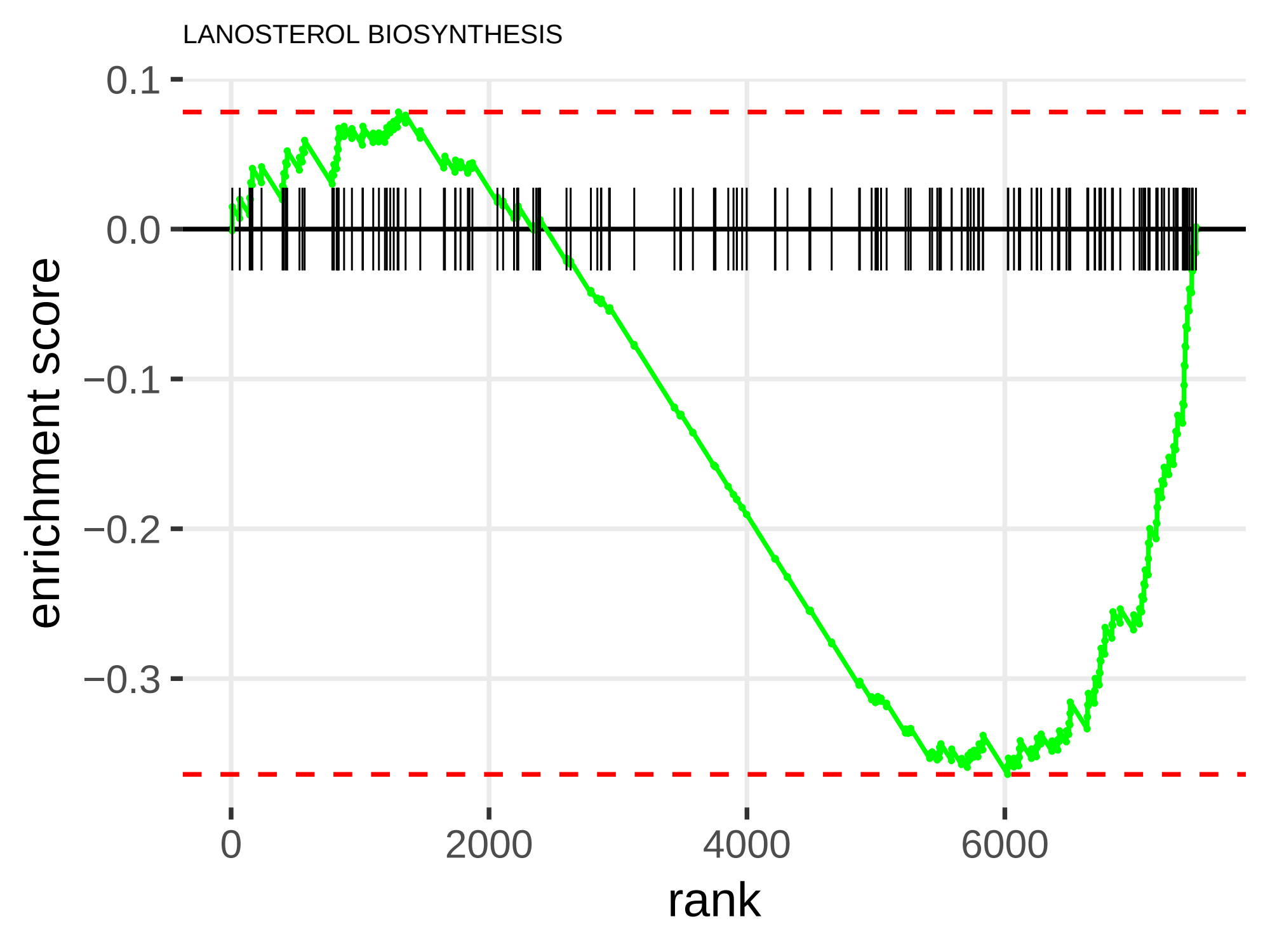

GLYCEROL−3−PHOSPHATE SHUTTLE
enrichment score
0.0
−0.1
−0.2
−0.3
−0.4
0
2000
4000
6000
rank

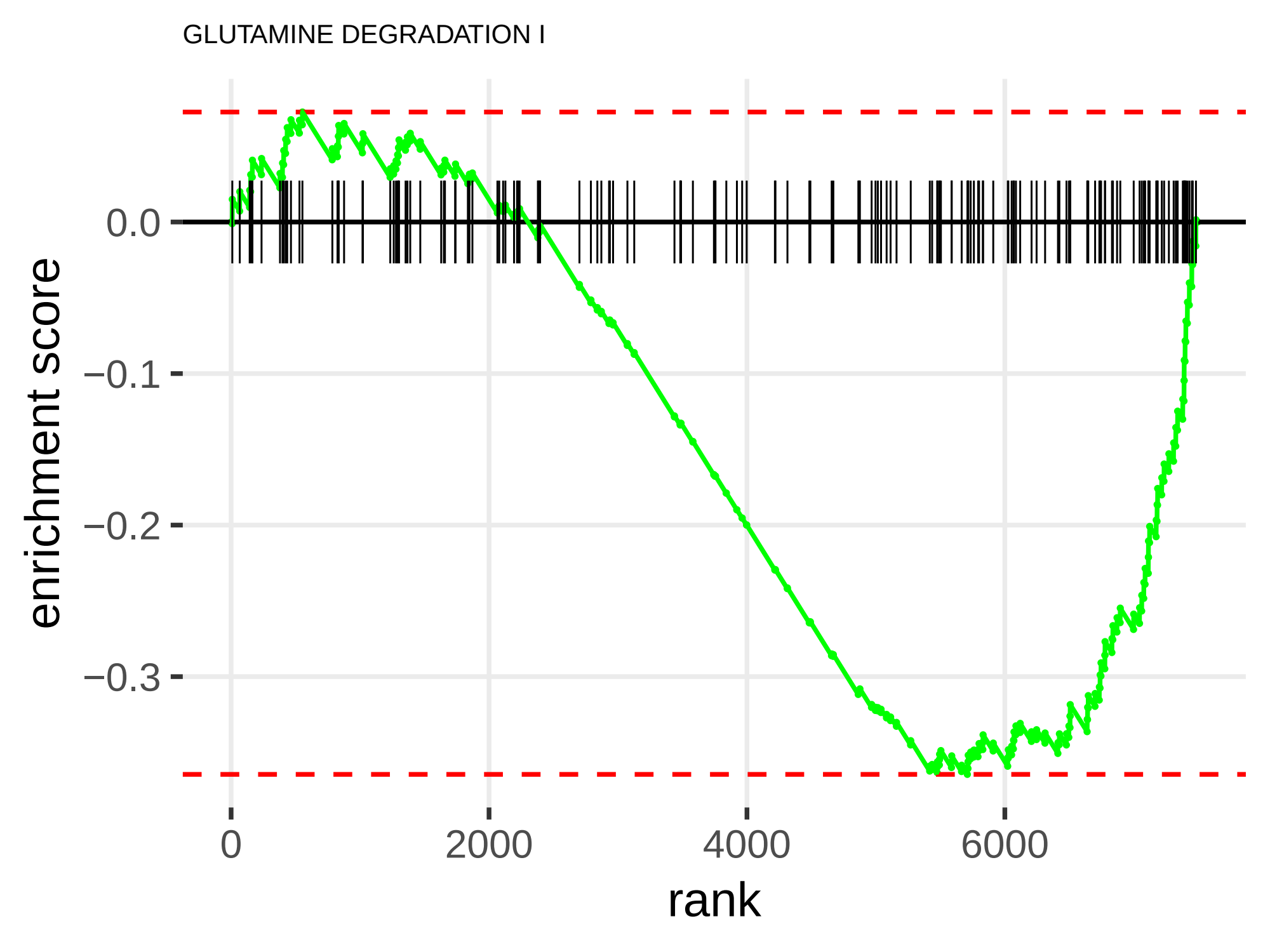

TAURINE BIOSYNTHESIS
0.0
−0.1
−0.2
−0.3
−0.4
enrichment score
0
2000
4000
6000
rank

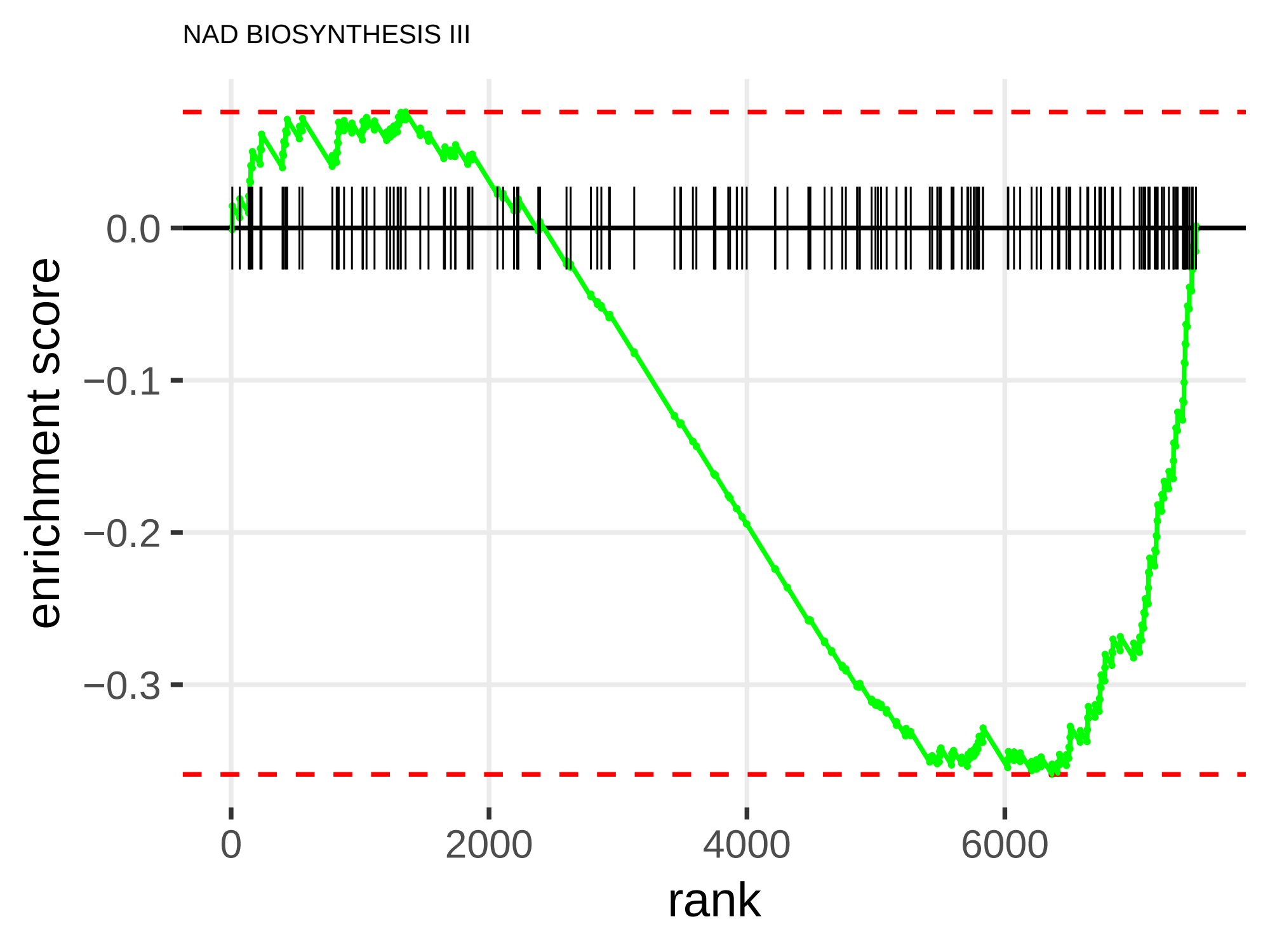

L−CYSTEINE DEGRADATION I
enrichment score
0.0
−0.1
−0.2
−0.3
−0.4
0
2000
4000
6000
rank

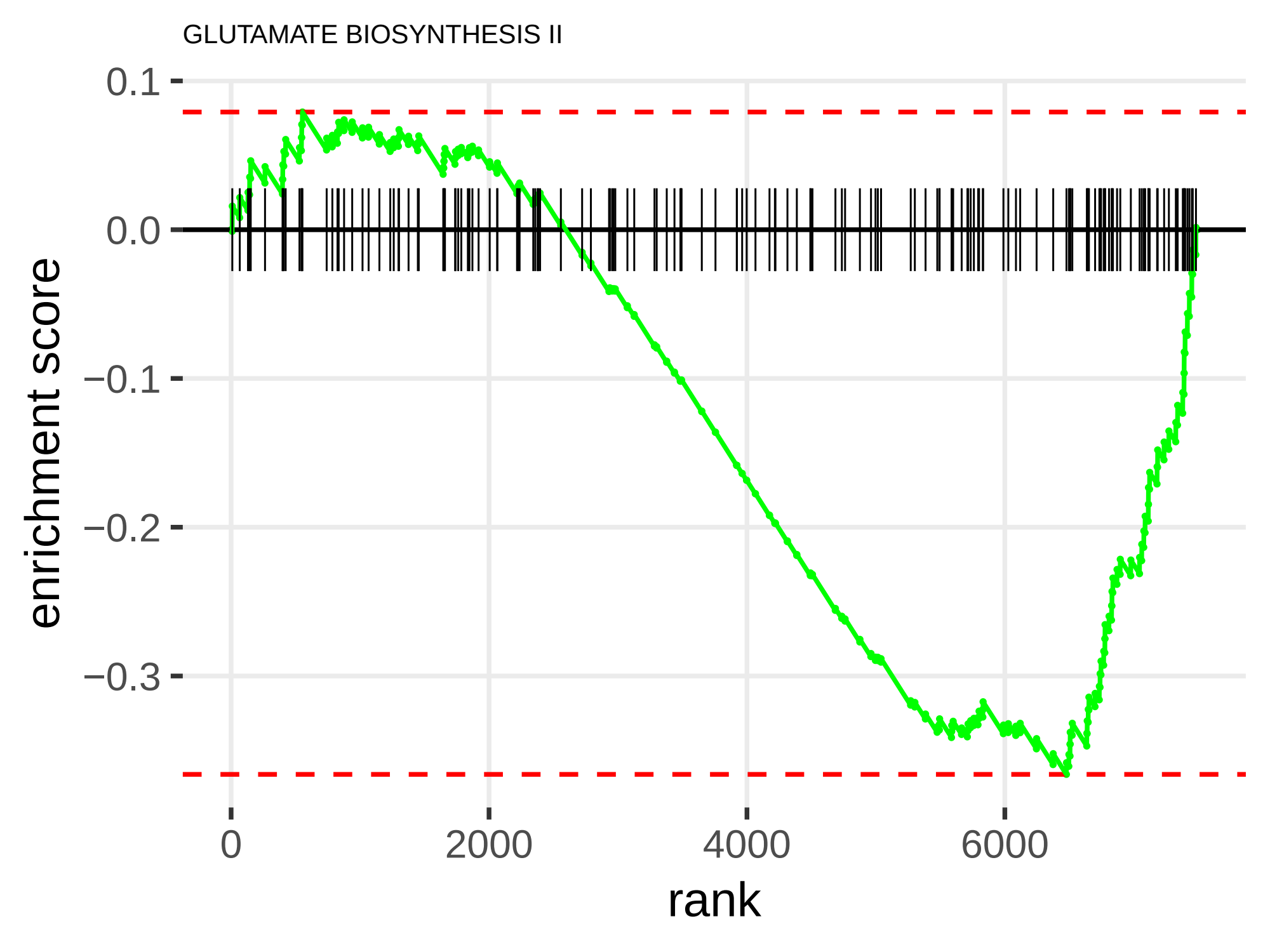

ISOLEUCINE DEGRADATION I
0.0
−0.1
−0.2
−0.3
enrichment score
0
2000
4000
6000
rank

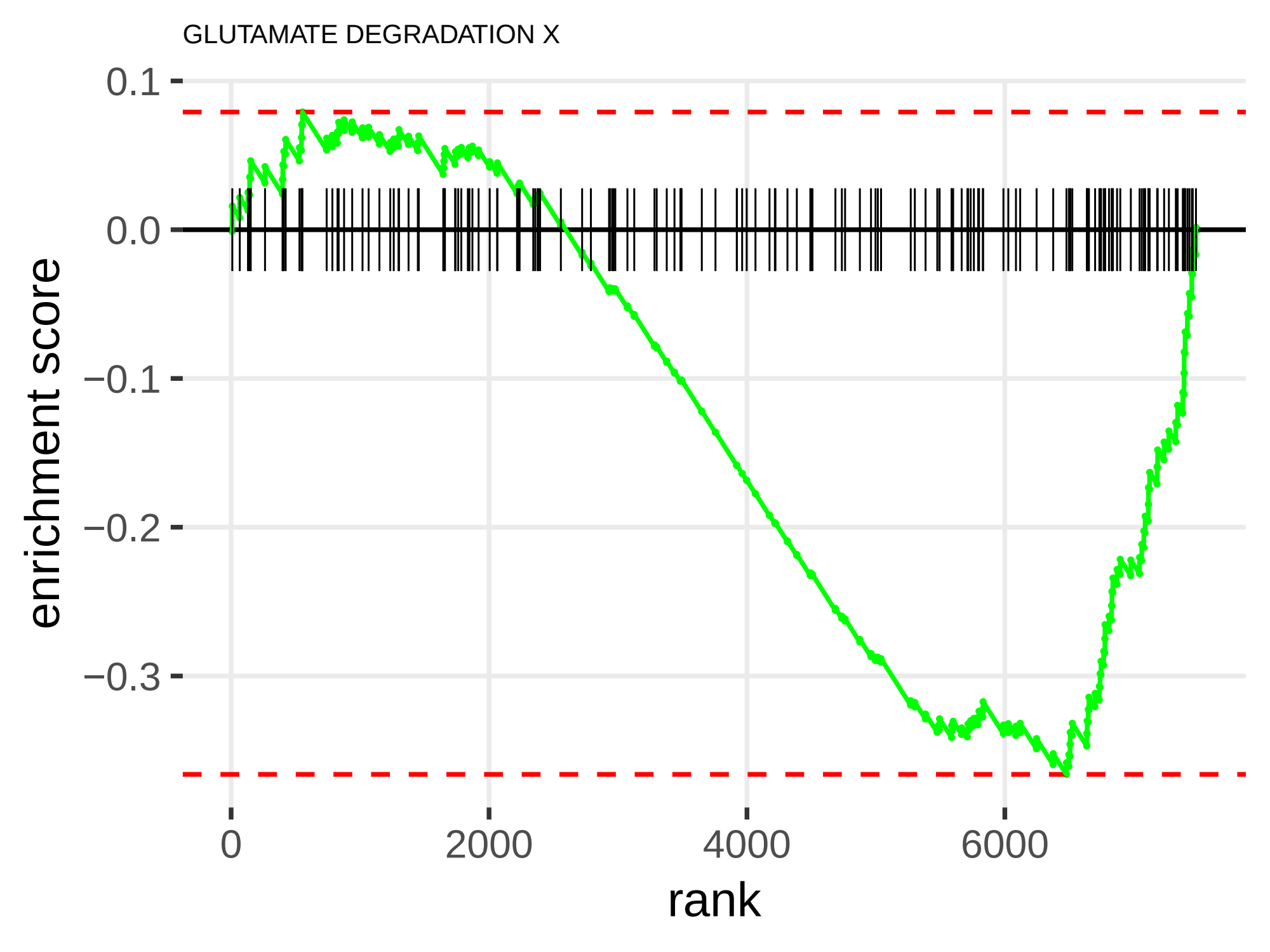

NAD BIOSYNTHESIS FROM 2−AMINO−3−CARBOXYMUCONATE SEMIALDEHYDE
0.1
0.0
−0.1
−0.2
−0.3
enrichment score
0
2000
4000
6000
rank

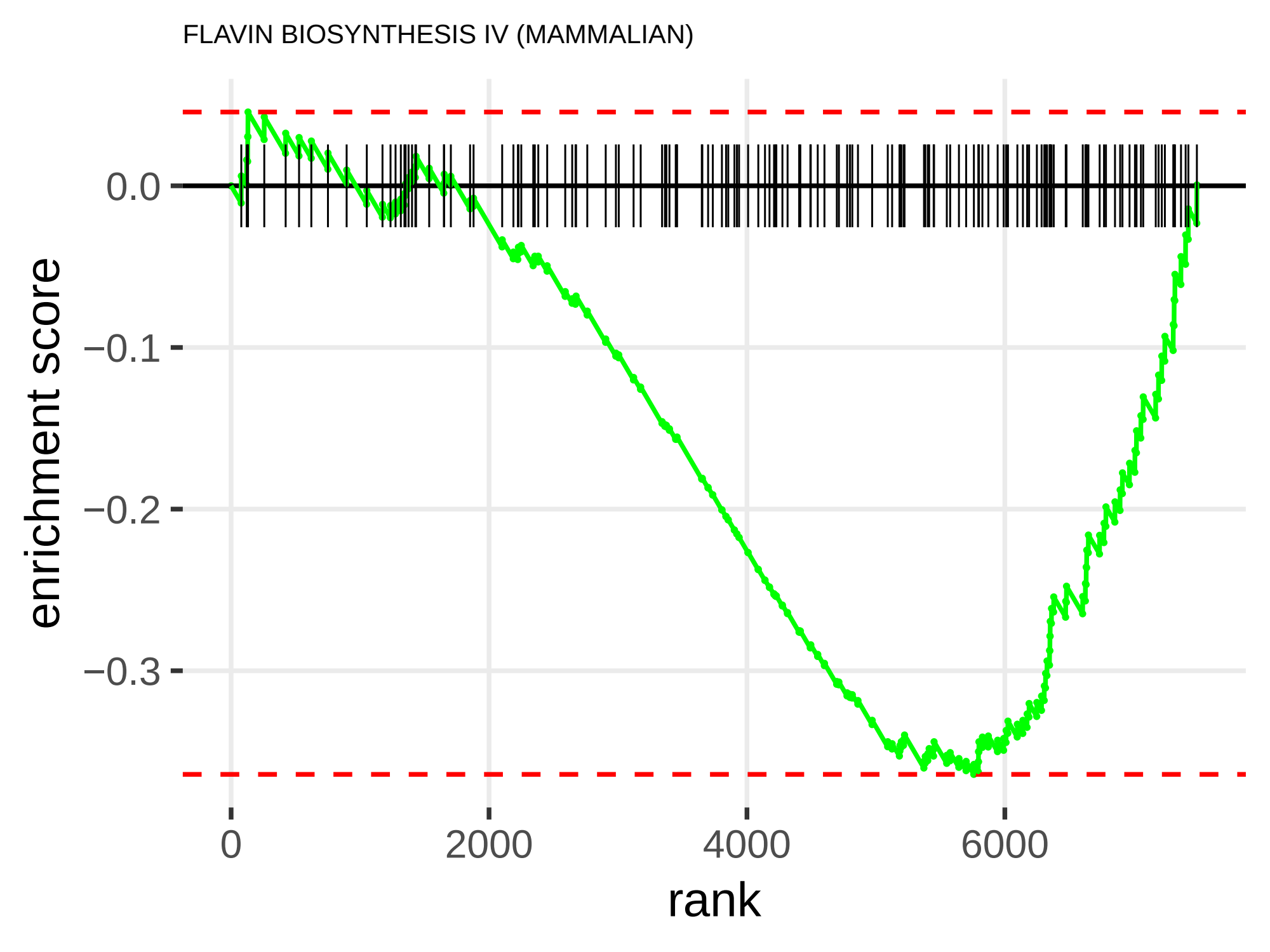

LANOSTEROL BIOSYNTHESIS
0.1
0.0
−0.1
−0.2
−0.3
enrichment score
0
2000
4000
6000
rank

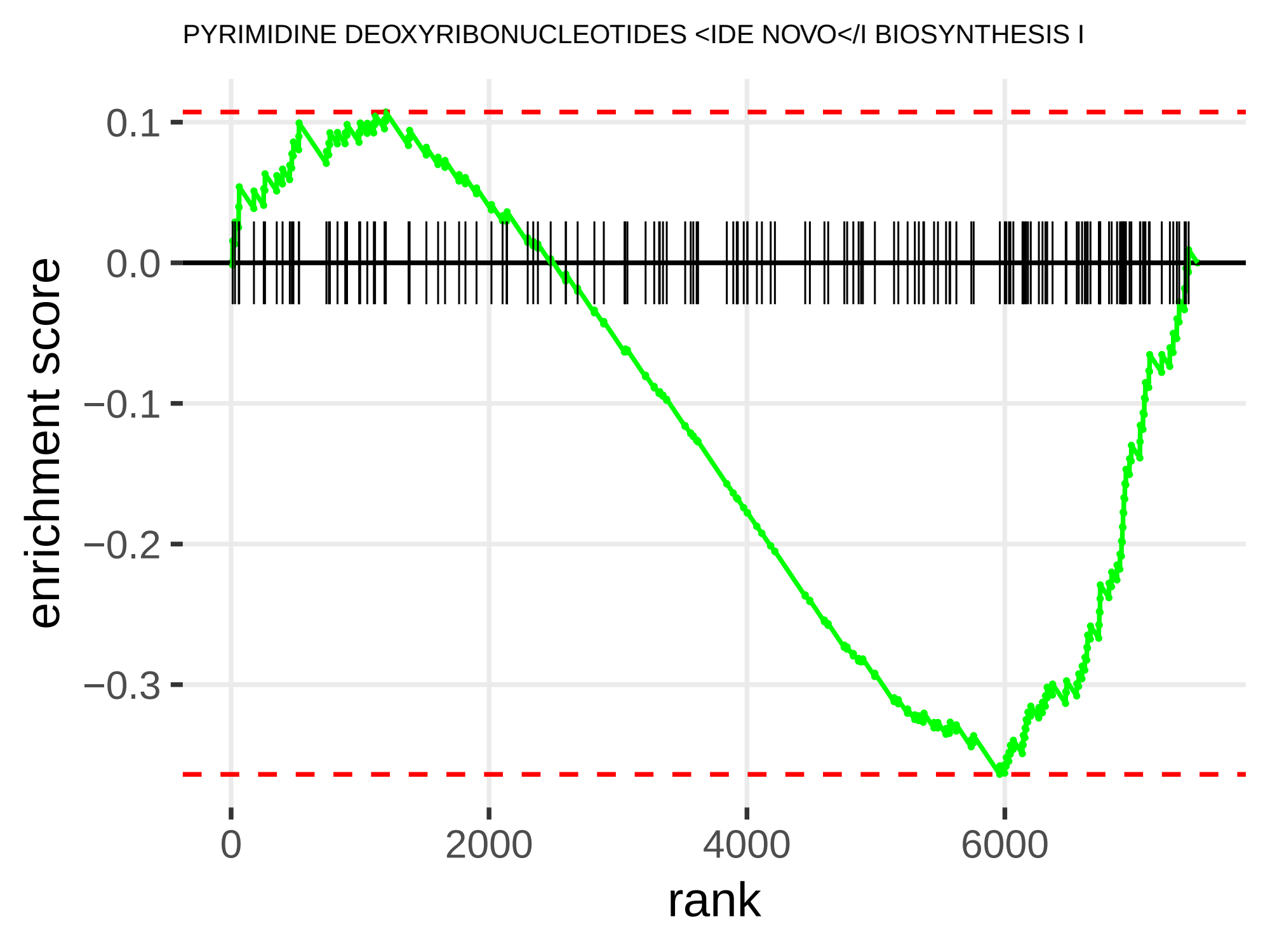

GLUTAMINE DEGRADATION I
enrichment score
0.0
−0.1
−0.2
−0.3
0
2000
4000
6000
rank

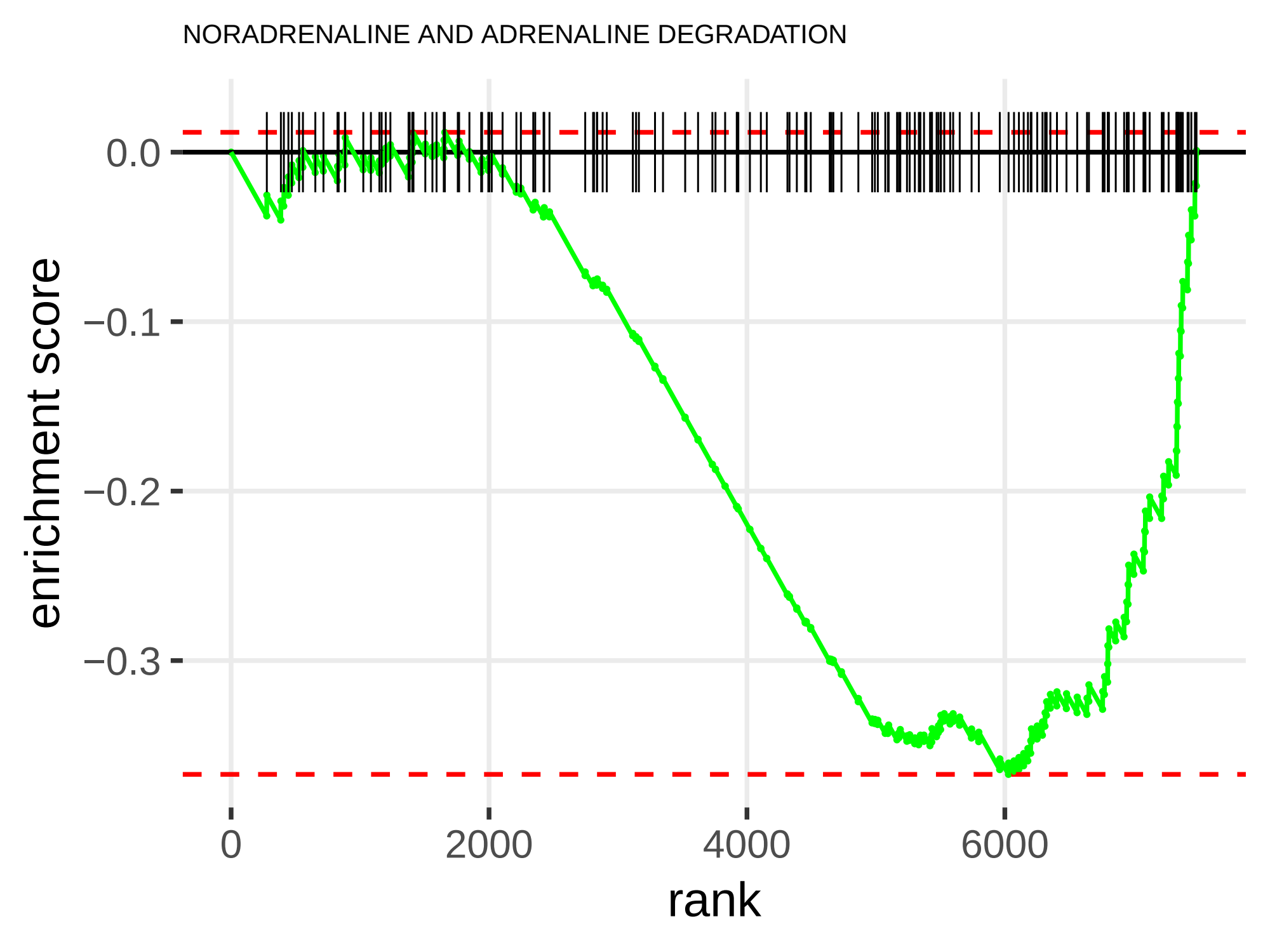

NAD BIOSYNTHESIS III
enrichment score
0.0
−0.1
−0.2
−0.3
0
2000
4000
6000
rank

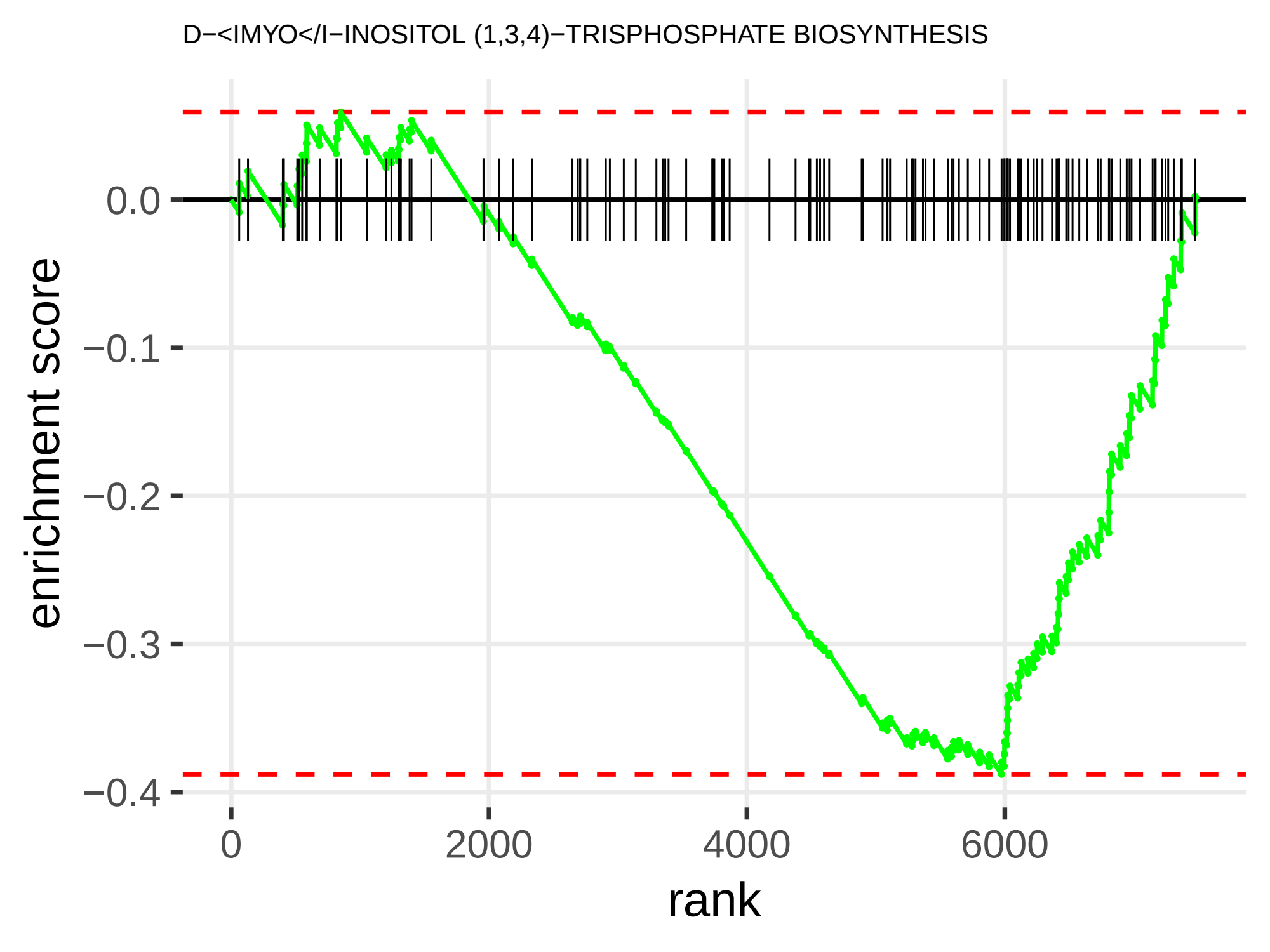

GLUTAMATE BIOSYNTHESIS II
0.1
0.0
−0.1
−0.2
−0.3
enrichment score
0
2000
4000
6000
rank

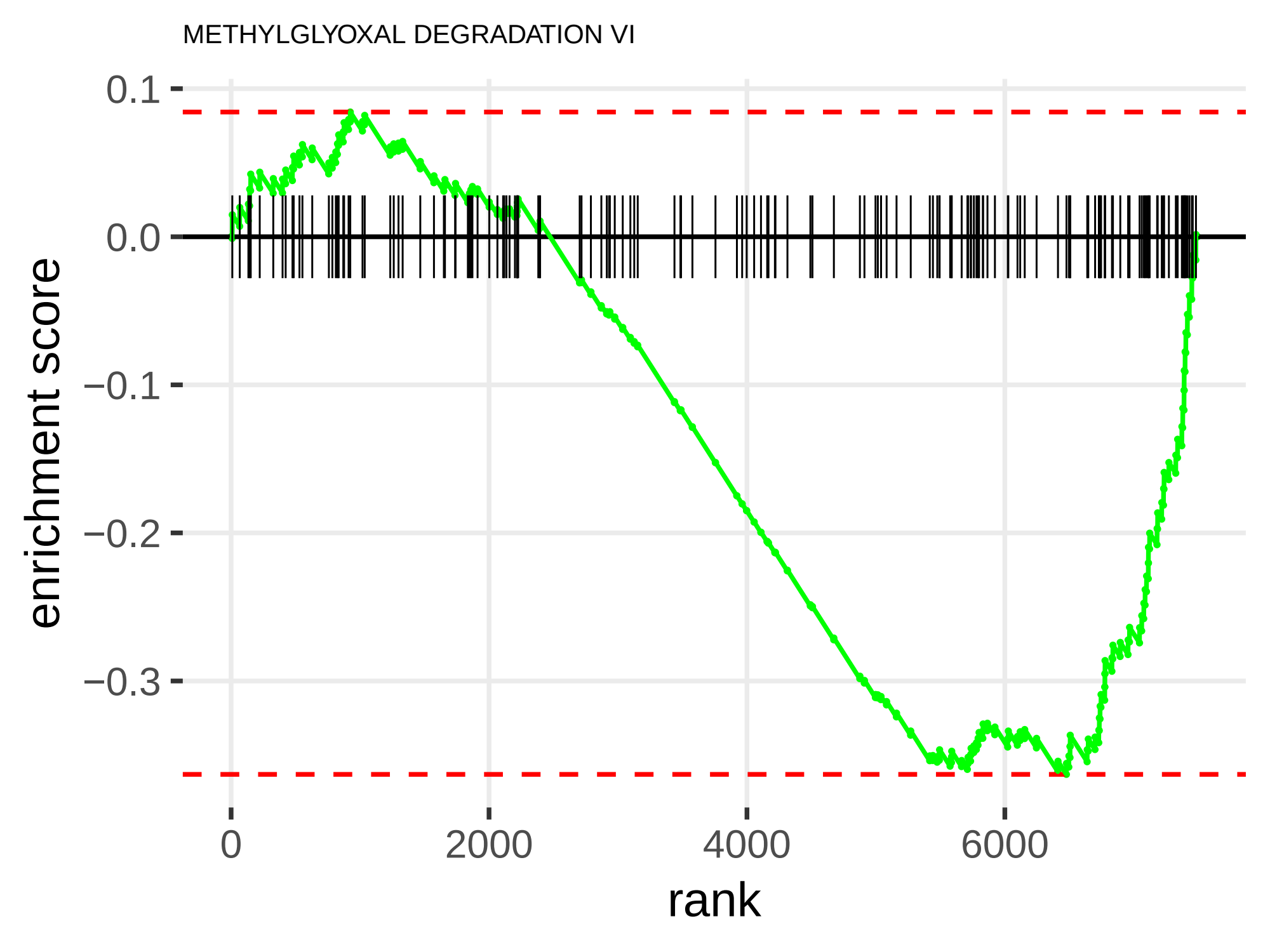

GLUTAMATE DEGRADATION X
0.1
0.0
−0.1
−0.2
−0.3
enrichment score
0
2000
4000
6000
rank

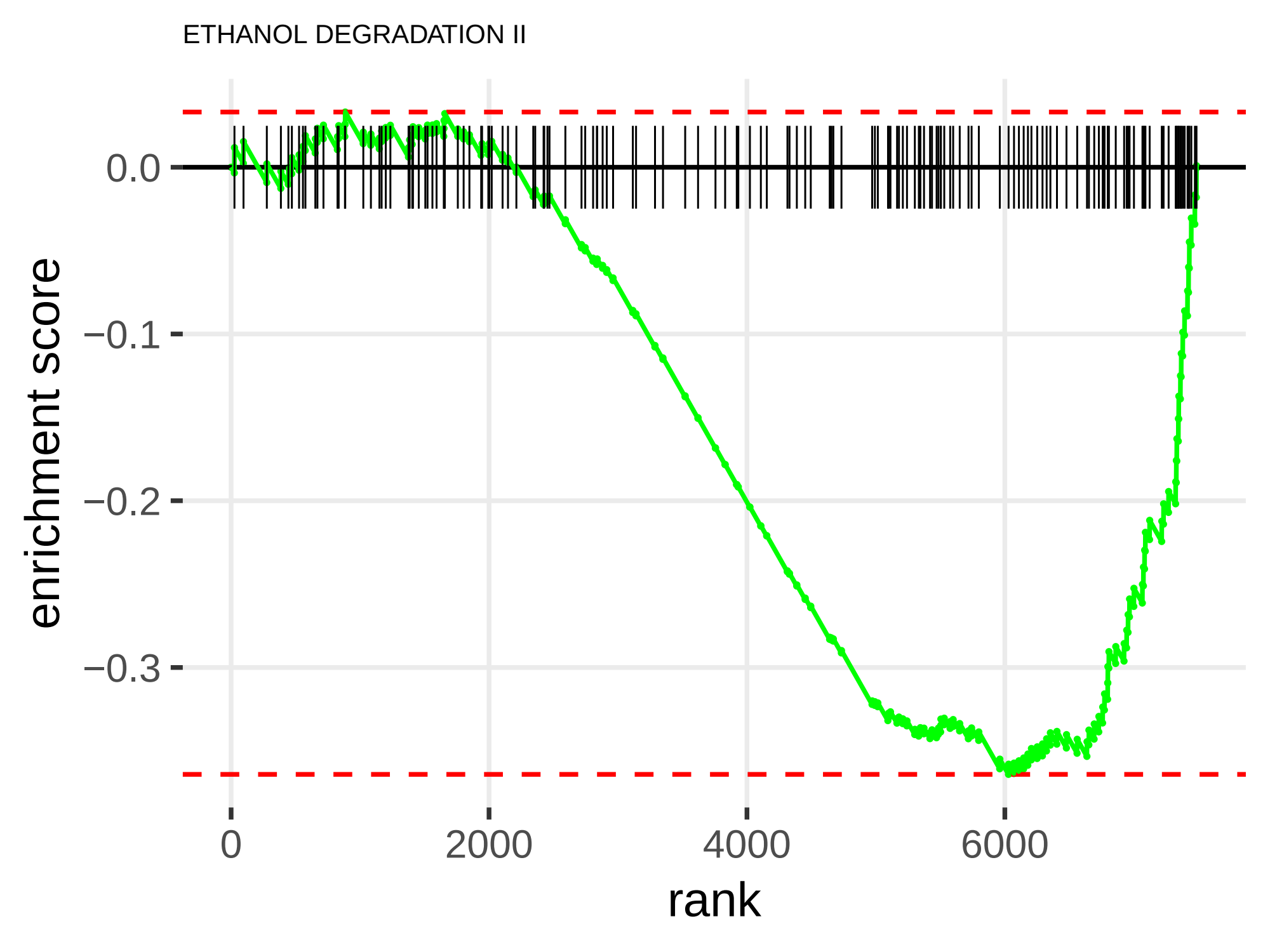

FLAVIN BIOSYNTHESIS IV (MAMMALIAN)
0.0
−0.1
−0.2
−0.3
enrichment score
0
2000
4000
6000
rank

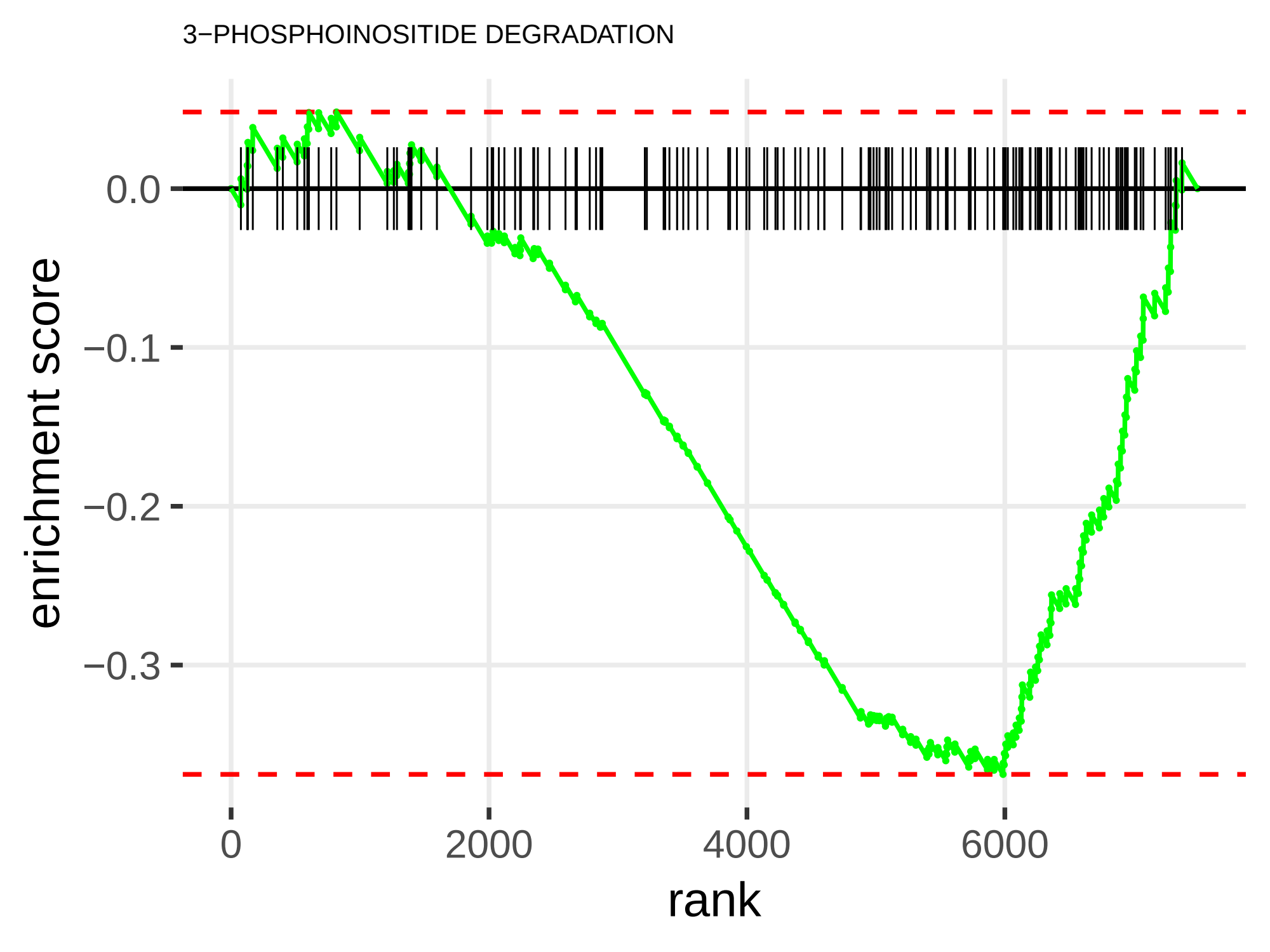

PYRIMIDINE DEOXYRIBONUCLEOTIDES <IDE NOVO</I BIOSYNTHESIS I
0.1
0.0
−0.1
−0.2
−0.3
enrichment score
0
2000
4000
6000
rank

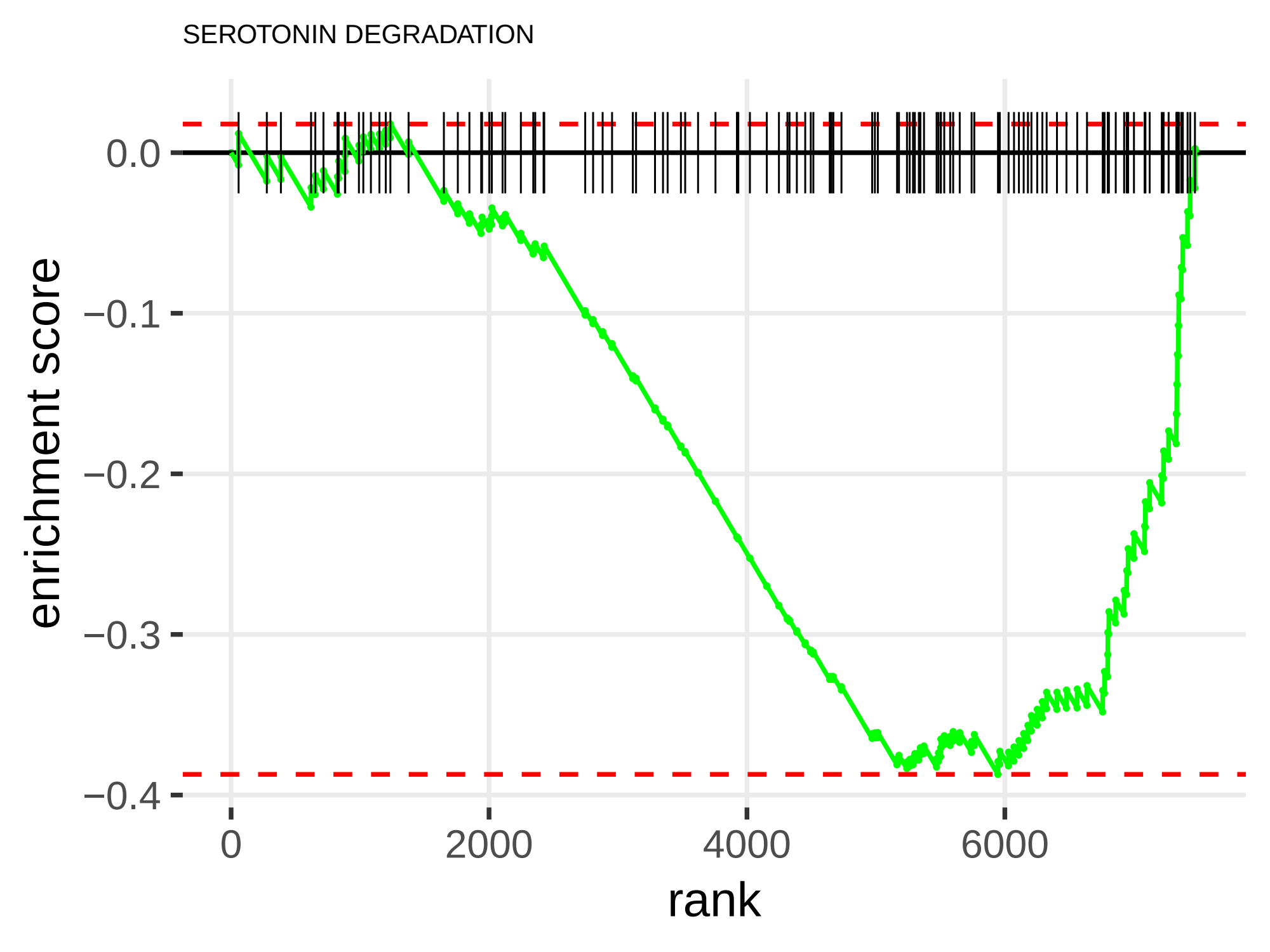

NORADRENALINE AND ADRENALINE DEGRADATION
0.0
−0.1
−0.2
−0.3
enrichment score
0
2000
4000
6000
rank

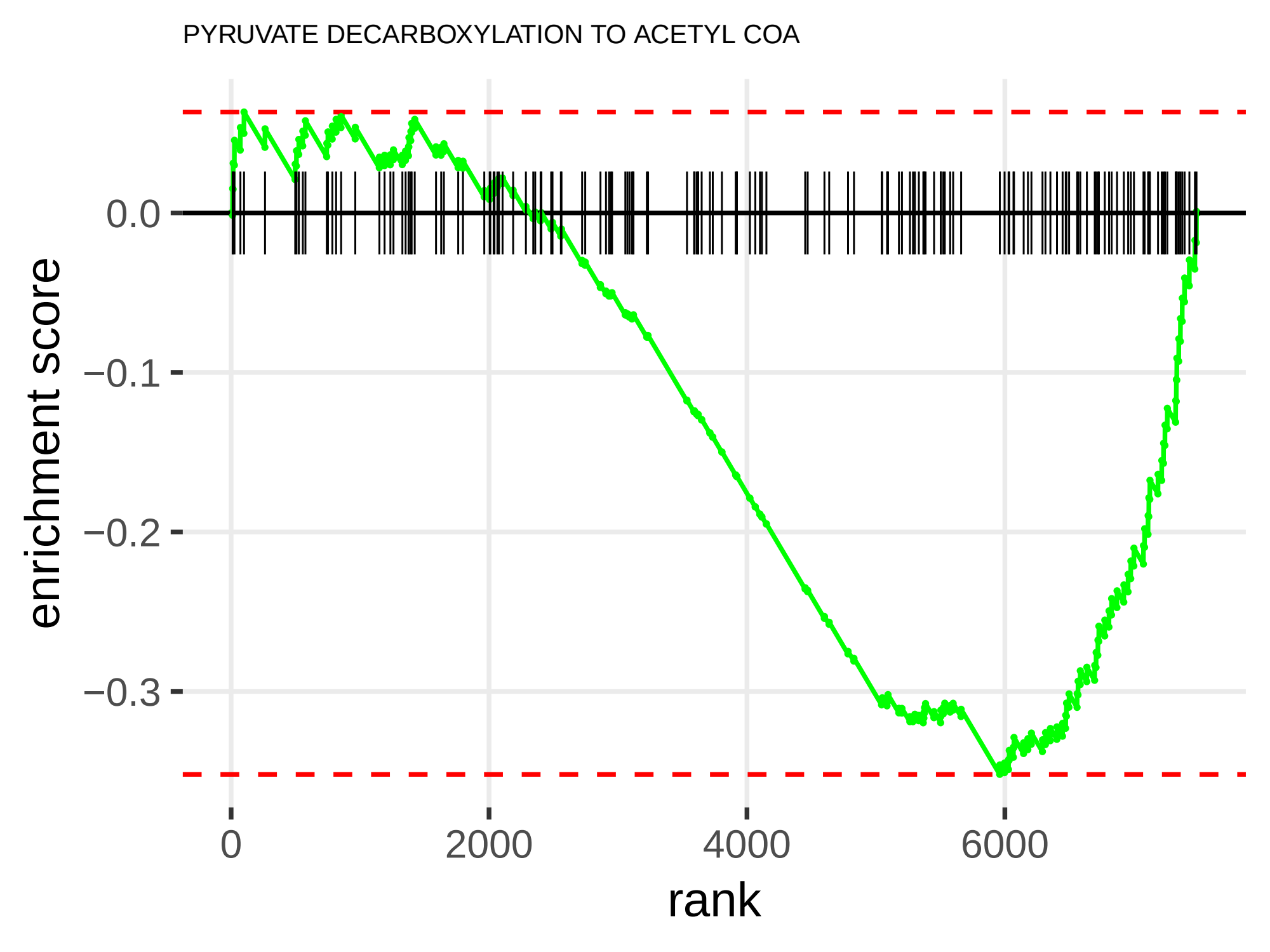

D−<IMYO</I−INOSITOL (1,3,4)−TRISPHOSPHATE BIOSYNTHESIS
enrichment score
0.0
−0.1
−0.2
−0.3
−0.4
0
2000
4000
6000
rank

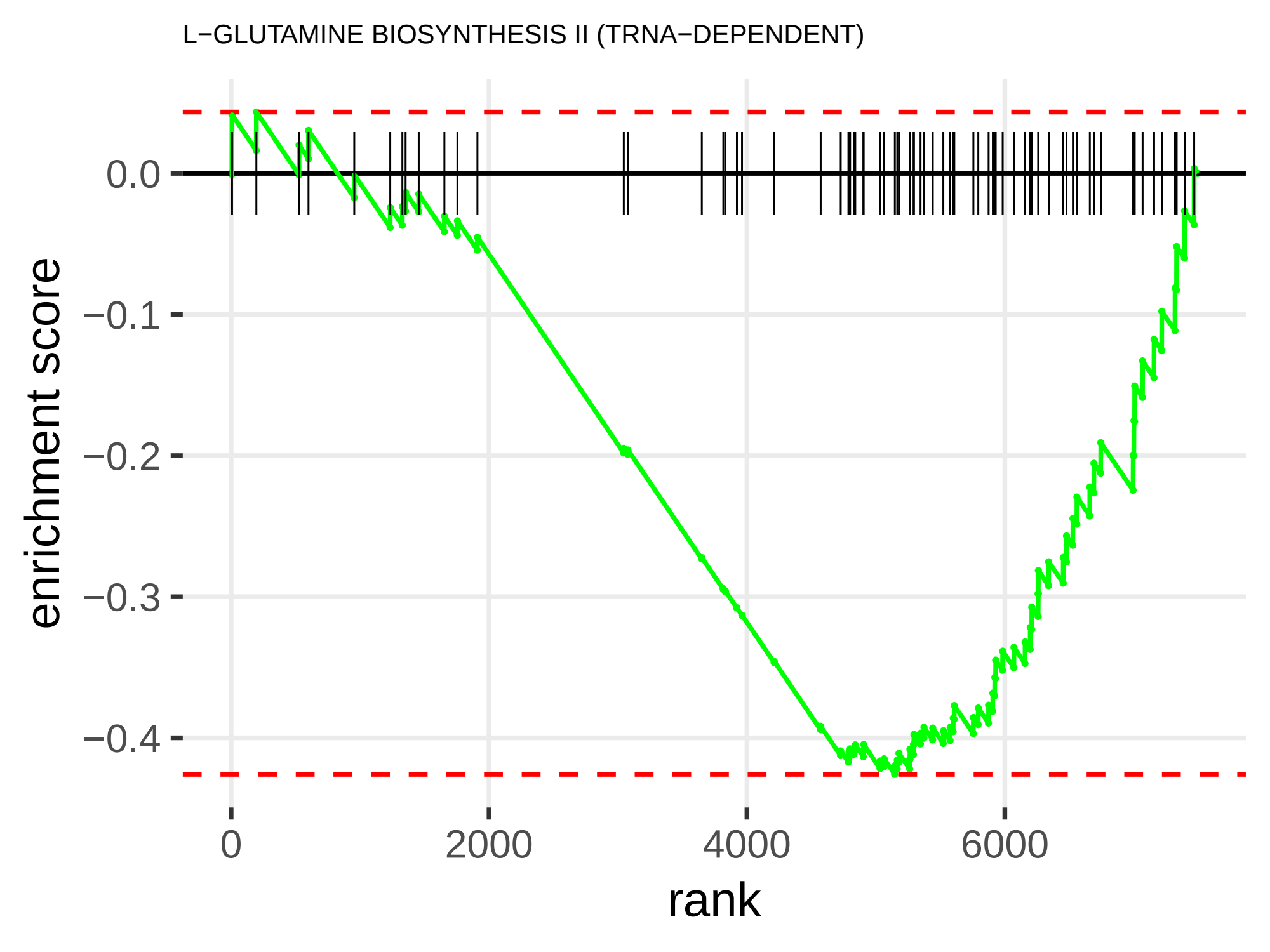

METHYLGLYOXAL DEGRADATION VI
0.1
0.0
−0.1
−0.2
−0.3
enrichment score
0
2000
4000
6000
rank

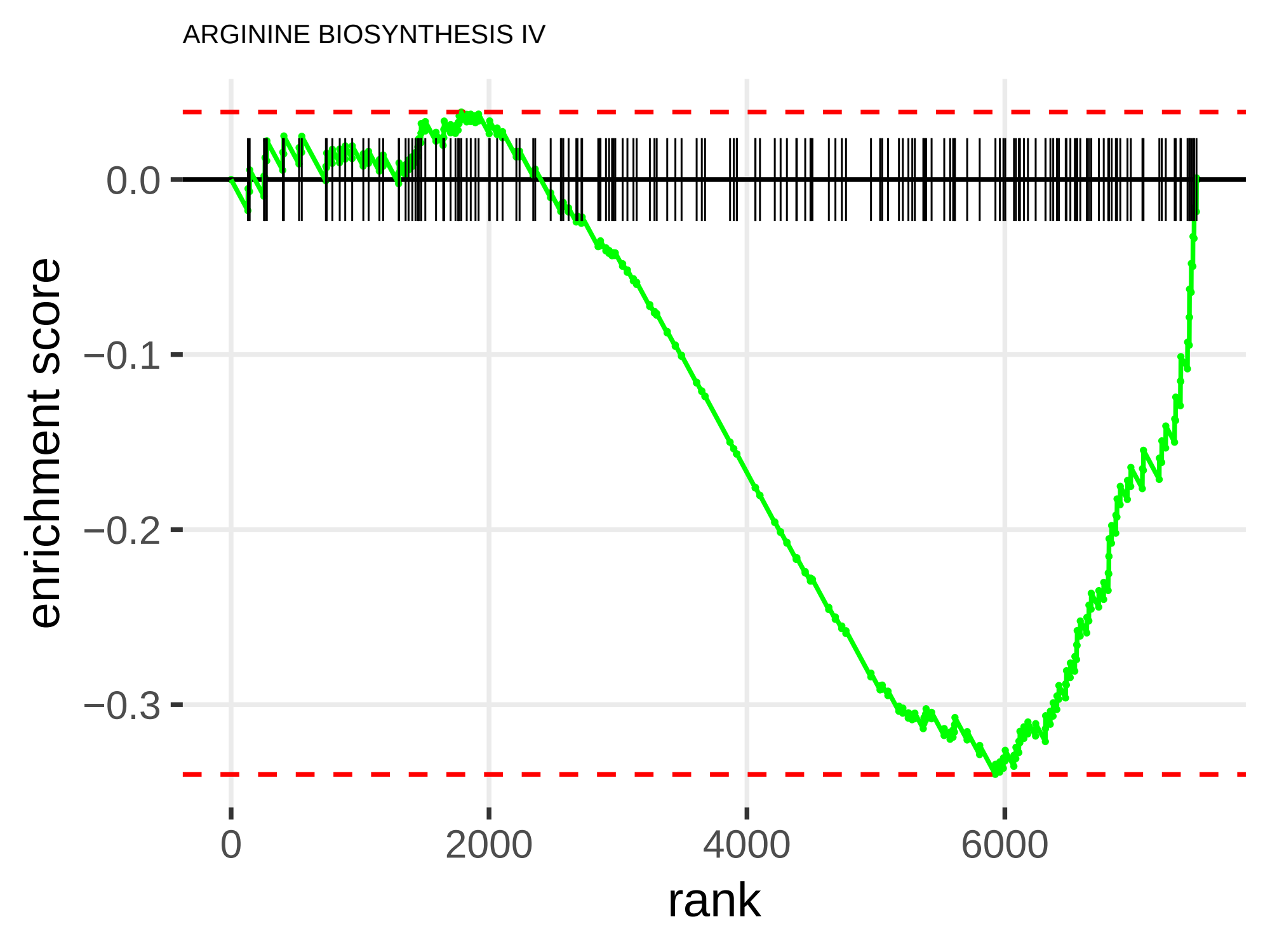

ETHANOL DEGRADATION II
0.0
−0.1
−0.2
−0.3
enrichment score
0
2000
4000
6000
rank

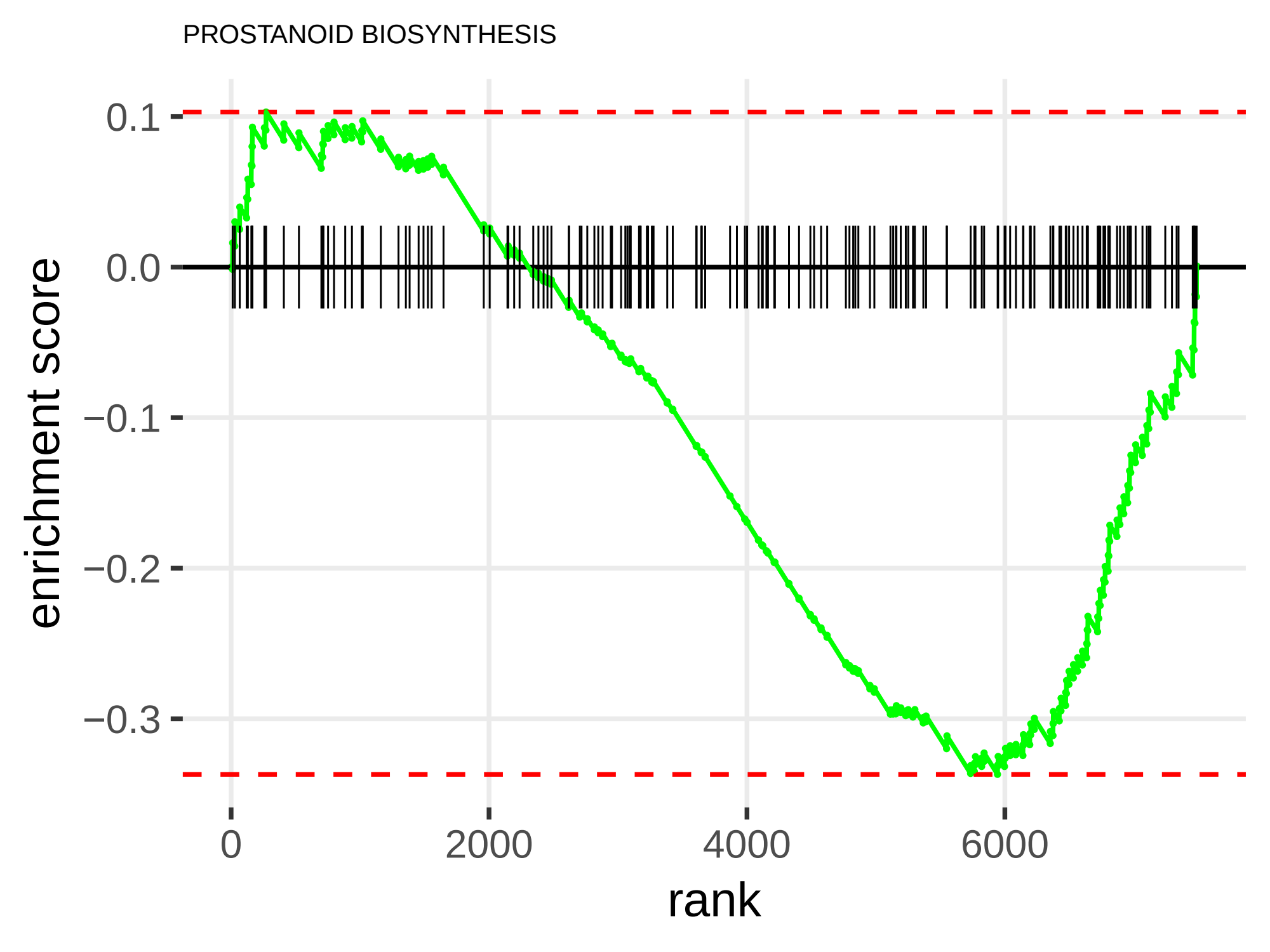

3−PHOSPHOINOSITIDE DEGRADATION
0.0
−0.1
−0.2
−0.3
enrichment score
0
2000
4000
6000
rank

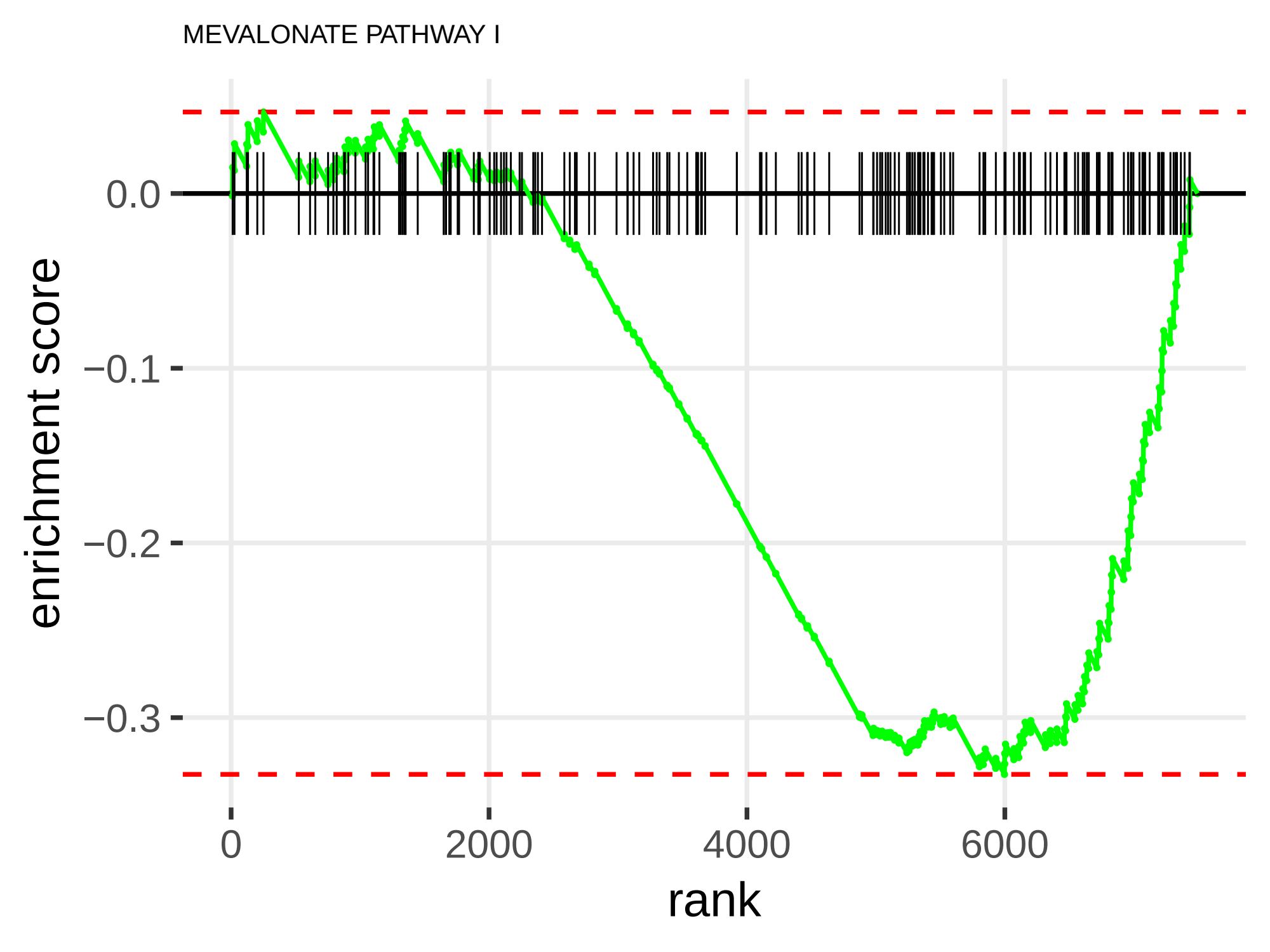

SEROTONIN DEGRADATION
0.0
−0.1
−0.2
−0.3
−0.4
enrichment score
0
2000
4000
6000
rank

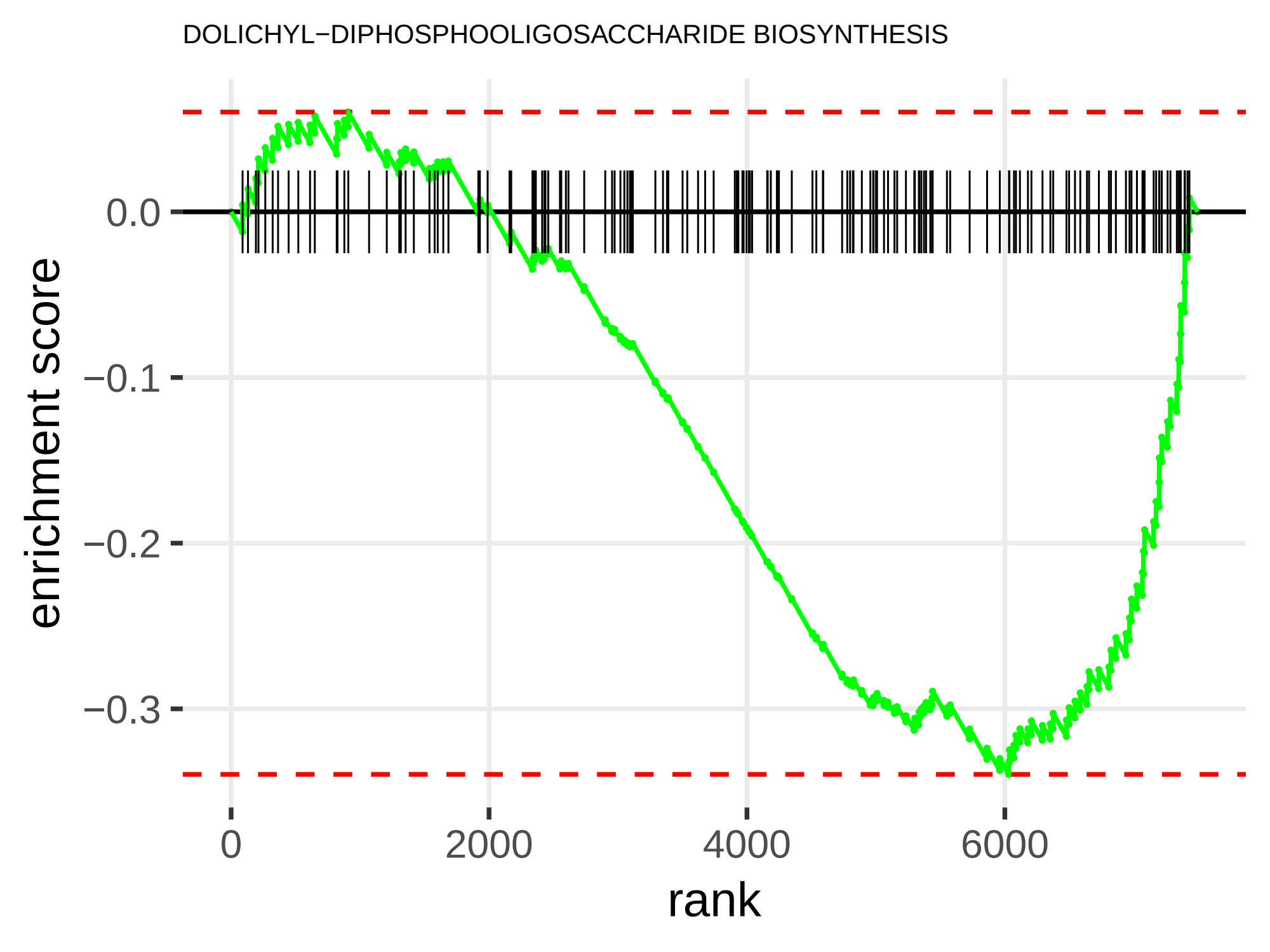

PYRUVATE DECARBOXYLATION TO ACETYL COA
enrichment score
0.0
−0.1
−0.2
−0.3
0
2000
4000
6000
rank

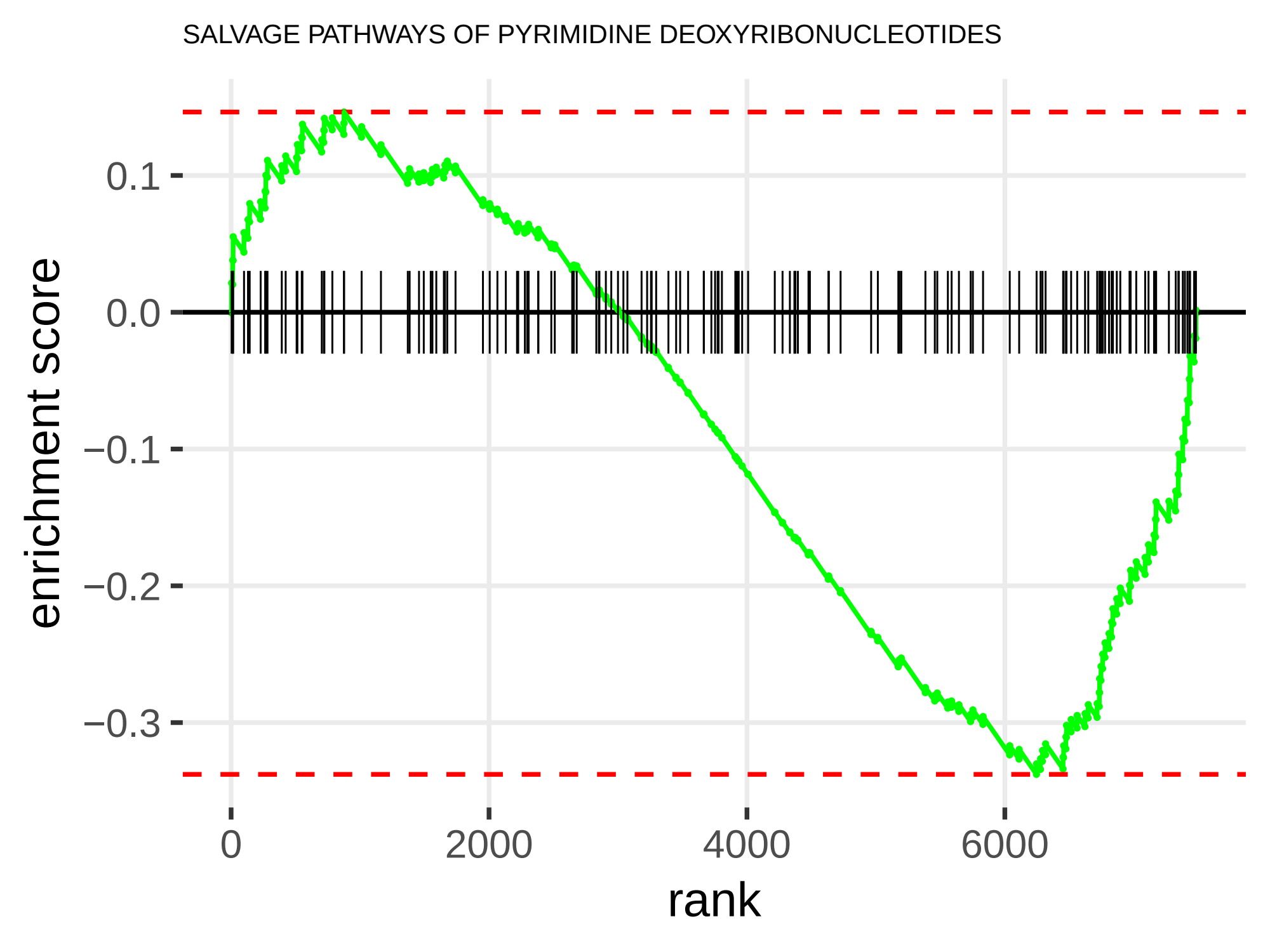

L−GLUTAMINE BIOSYNTHESIS II (TRNA−DEPENDENT)
0.0
−0.1
−0.2
−0.3
−0.4
enrichment score
0
2000
4000
6000
rank

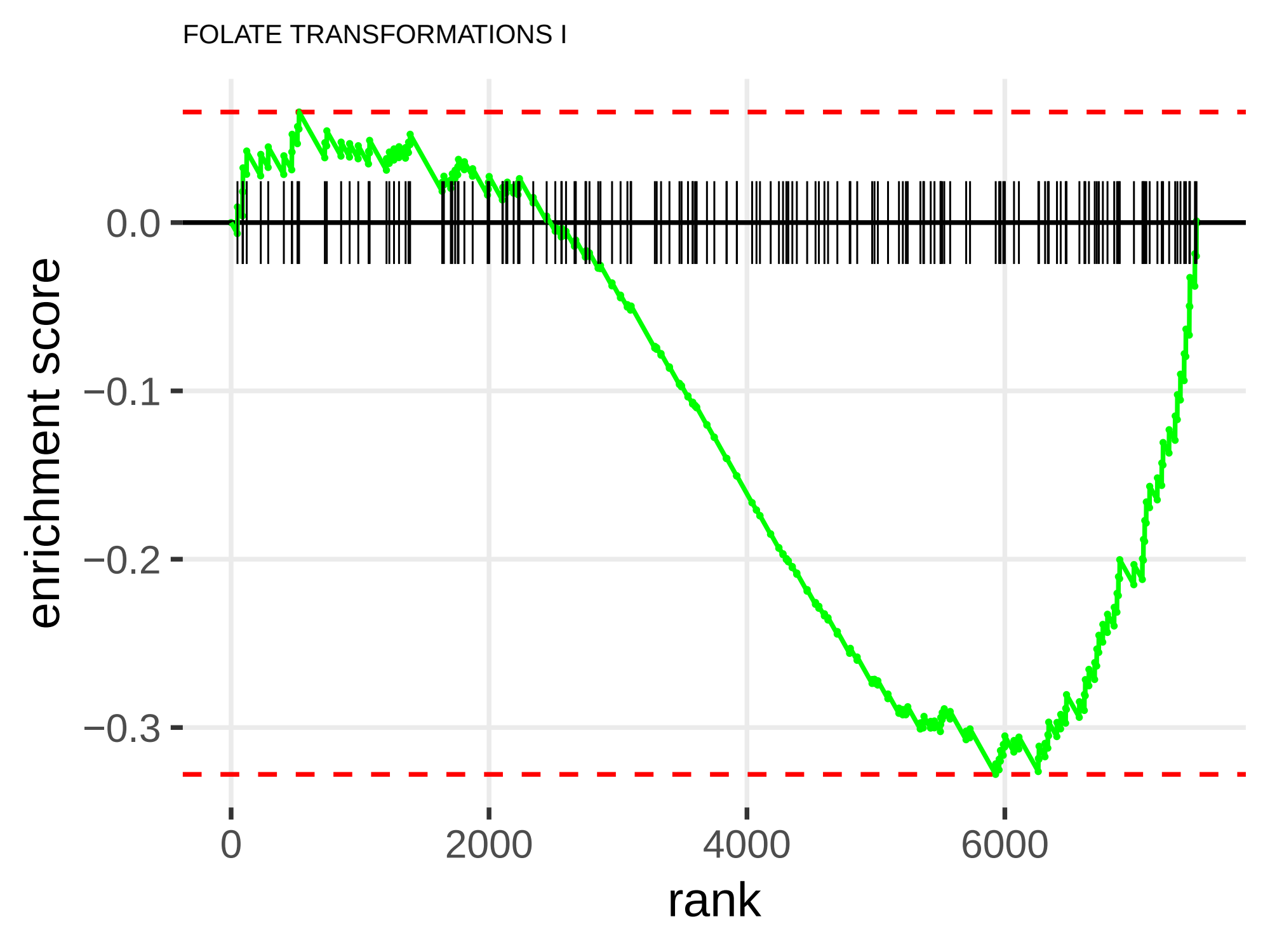

ARGININE BIOSYNTHESIS IV
0.0
−0.1
−0.2
−0.3
enrichment score
0
2000
4000
6000
rank

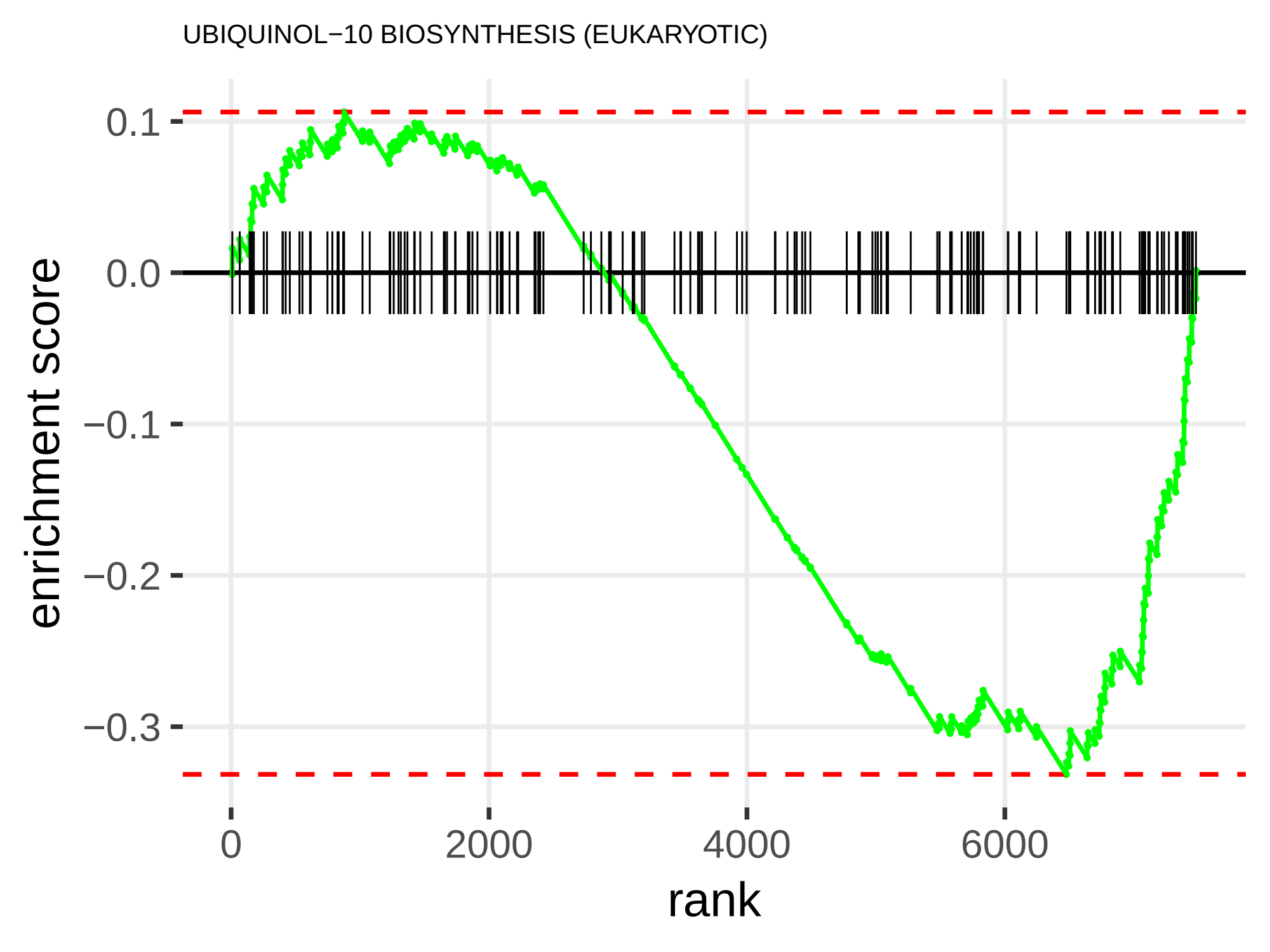

PROSTANOID BIOSYNTHESIS
0.1
0.0
−0.1
−0.2
−0.3
enrichment score
0
2000
4000
6000
rank

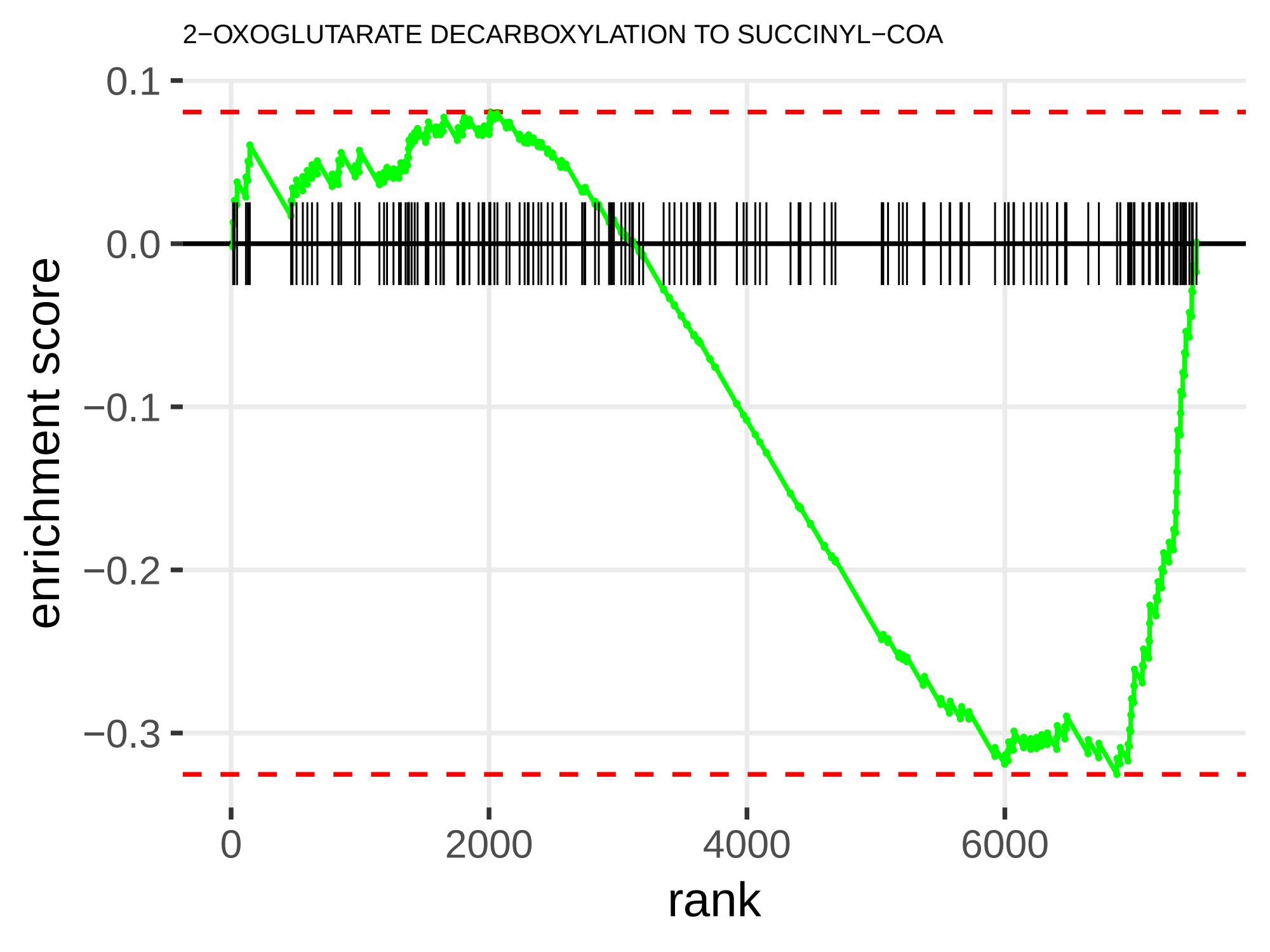

MEVALONATE PATHWAY I
0.0
−0.1
−0.2
−0.3
enrichment score
0
2000
4000
6000
rank

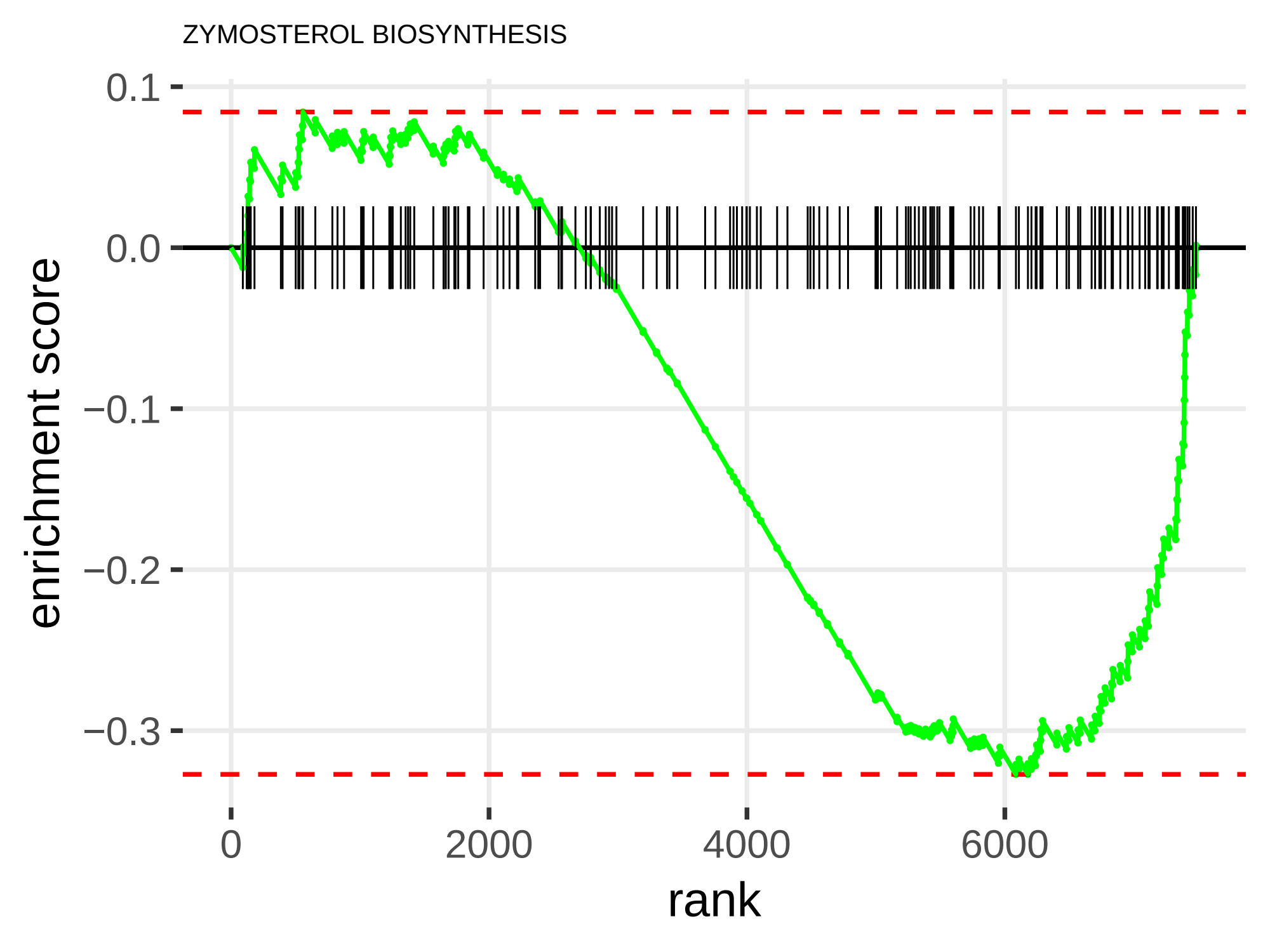

DOLICHYL−DIPHOSPHOOLIGOSACCHARIDE BIOSYNTHESIS
enrichment score
0.0
−0.1
−0.2
−0.3
0
2000
4000
6000
rank

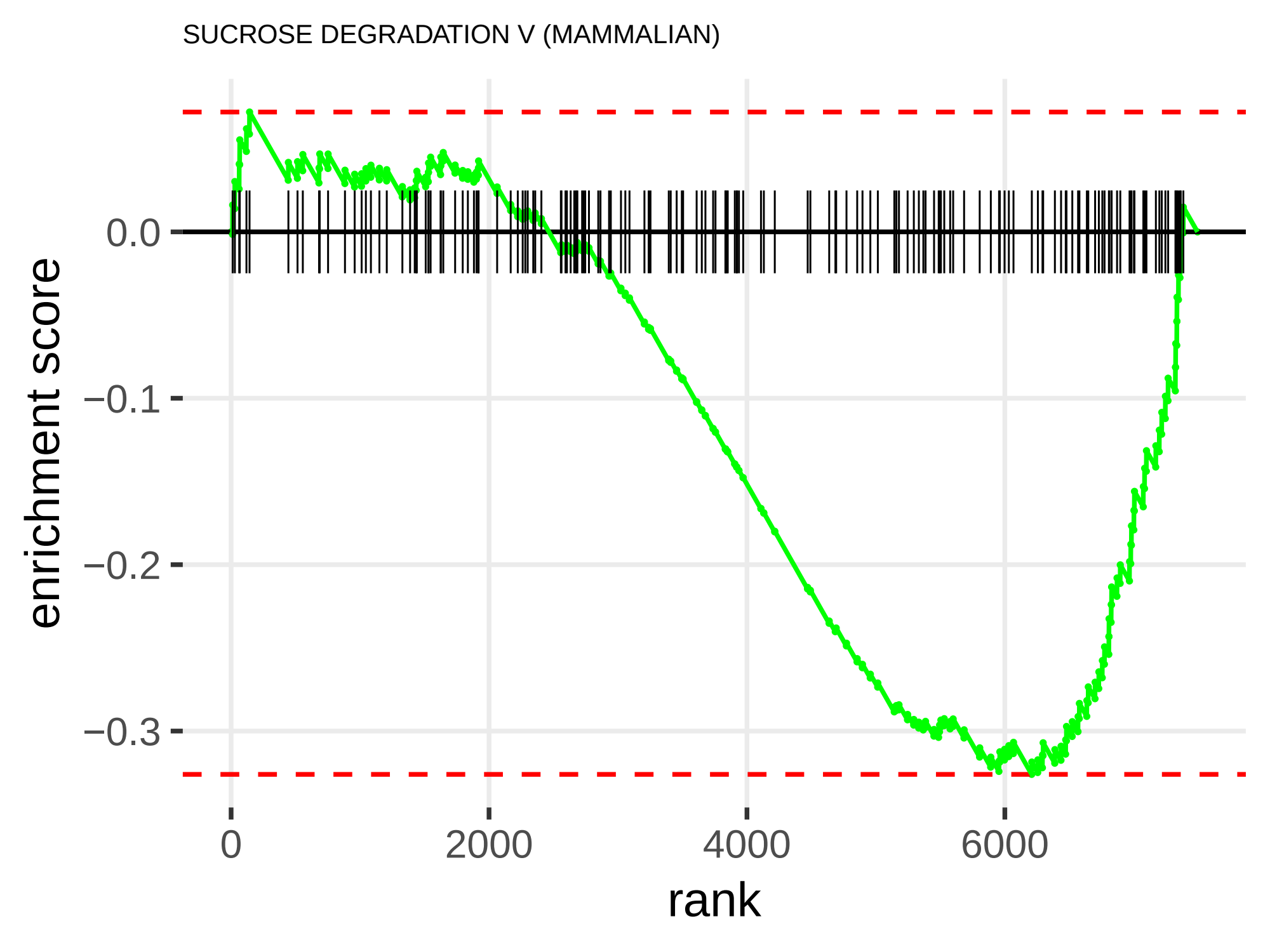

SALVAGE PATHWAYS OF PYRIMIDINE DEOXYRIBONUCLEOTIDES
enrichment score
0.1
0.0
−0.1
−0.2
−0.3
0
2000
4000
6000
rank

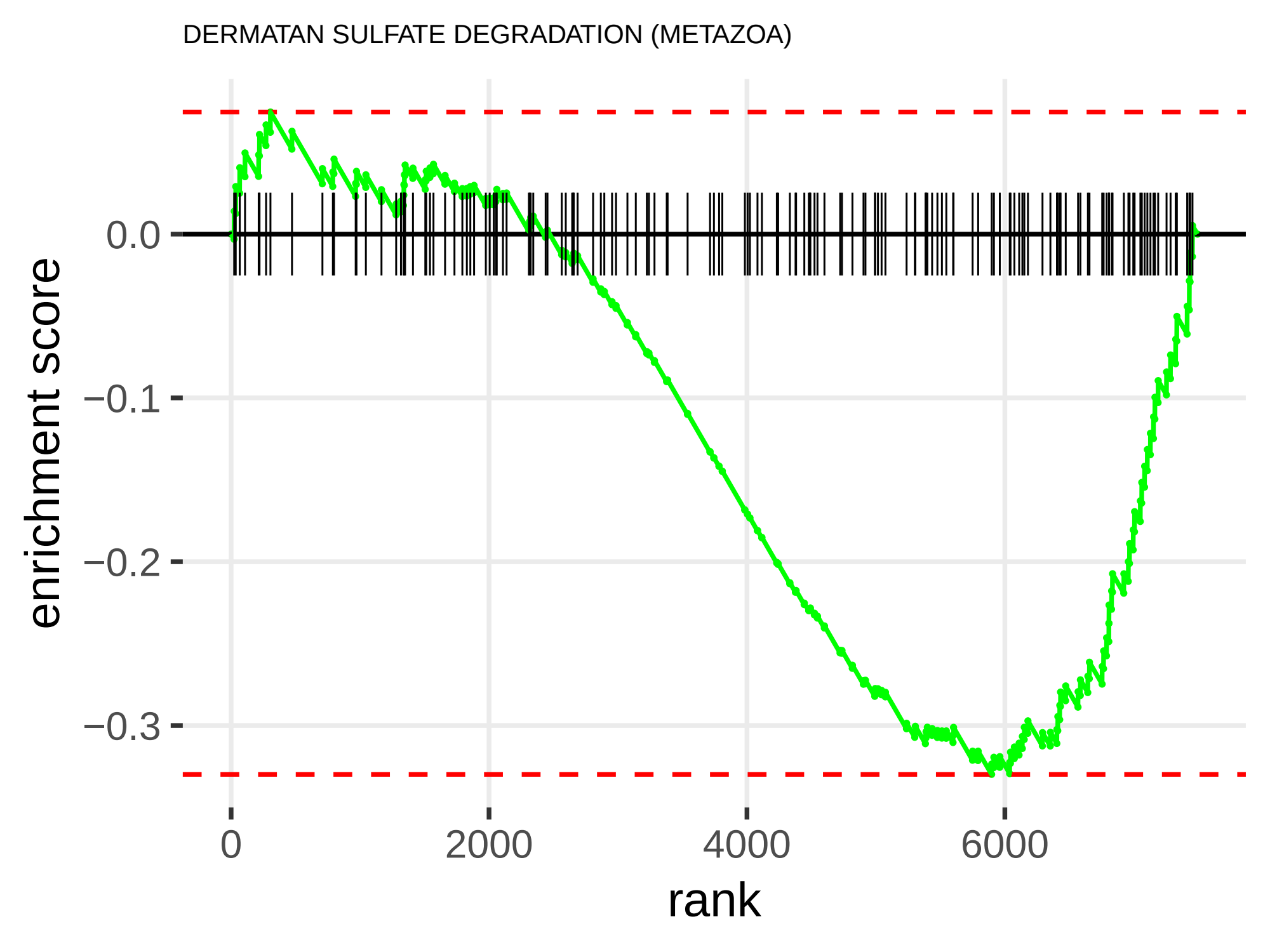

FOLATE TRANSFORMATIONS I
enrichment score
0.0
−0.1
−0.2
−0.3
0
2000
4000
6000
rank

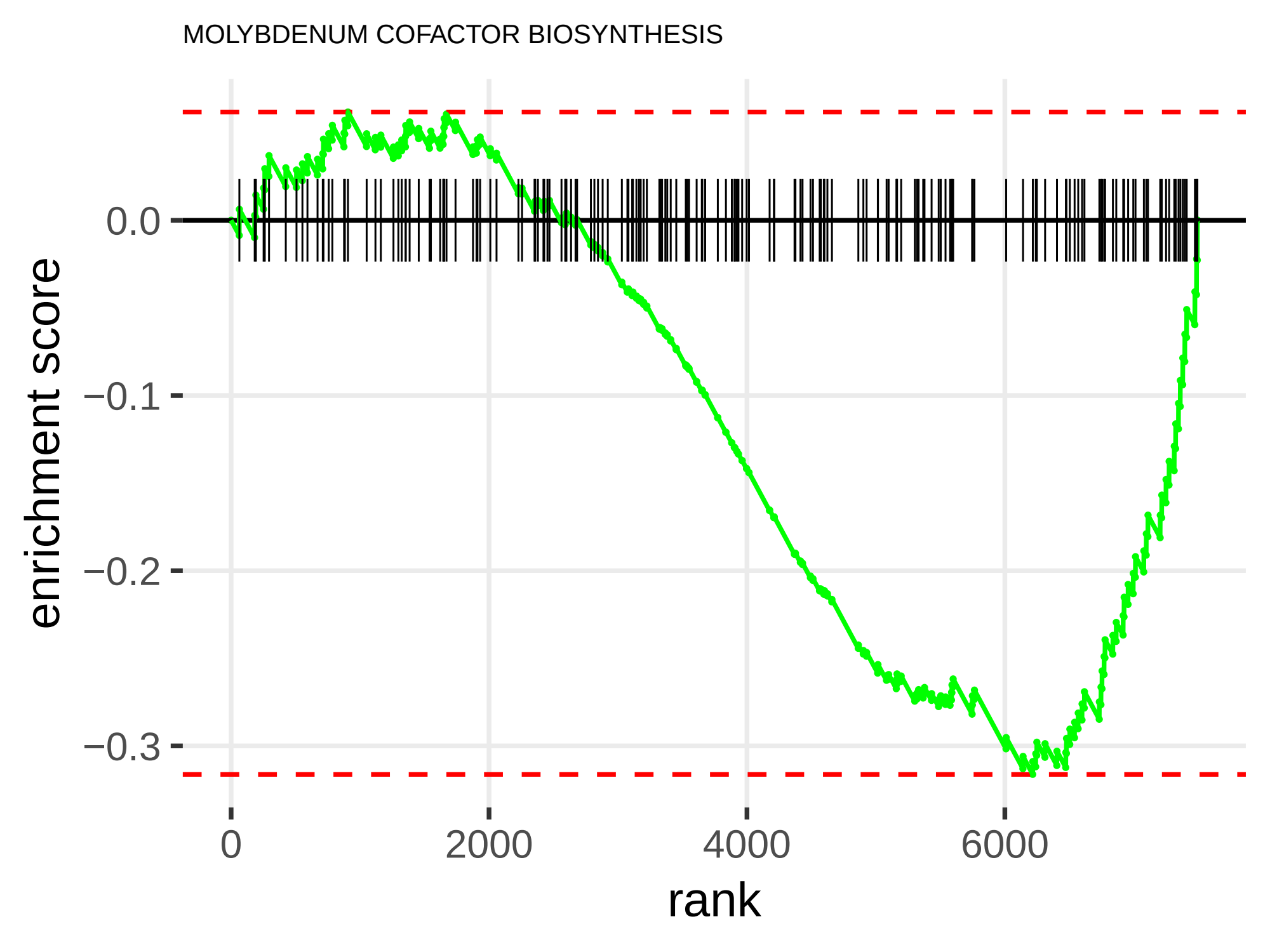

UBIQUINOL−10 BIOSYNTHESIS (EUKARYOTIC)
0.1
0.0
−0.1
−0.2
−0.3
enrichment score
0
2000
4000
6000
rank

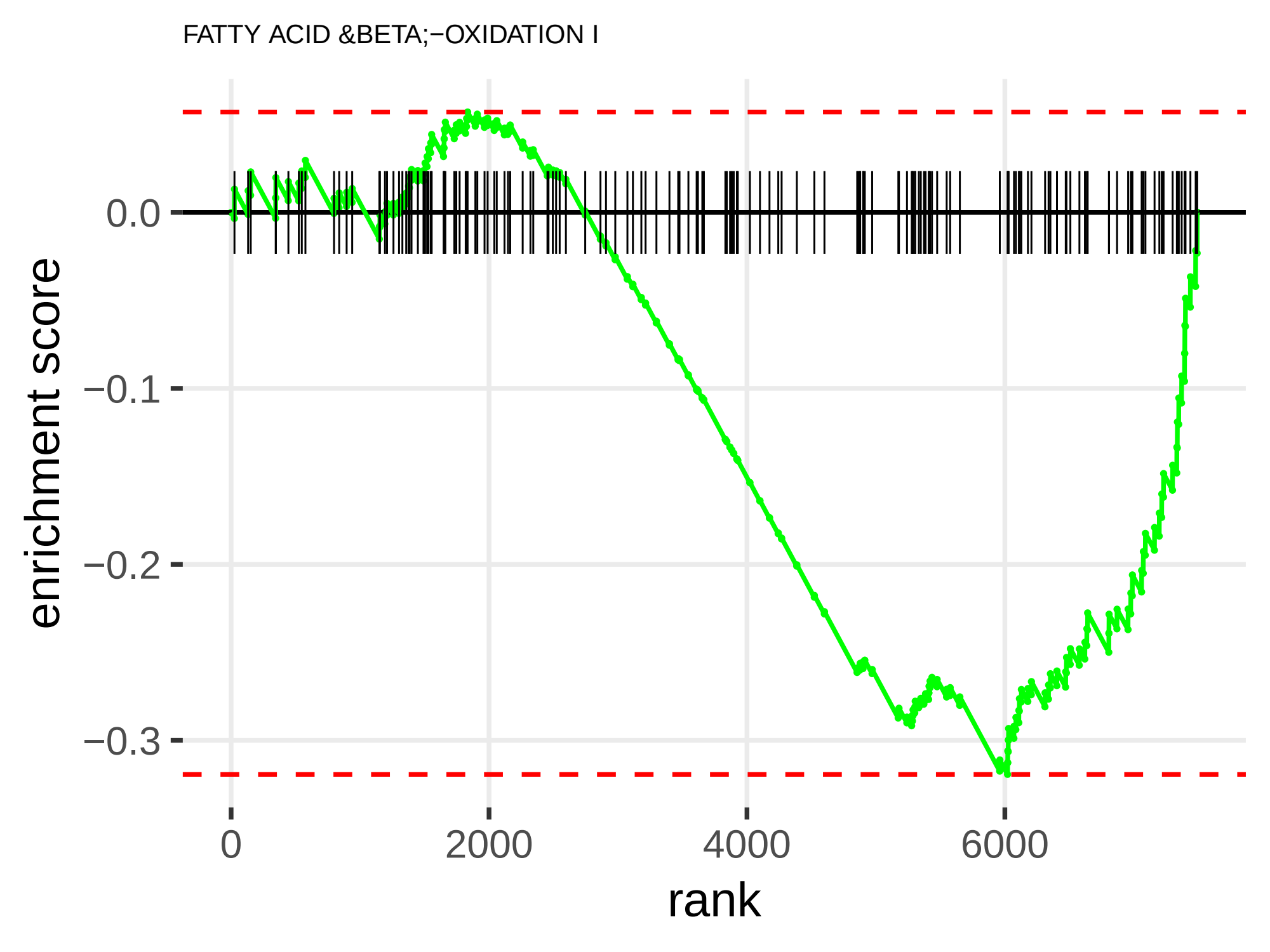

2−OXOGLUTARATE DECARBOXYLATION TO SUCCINYL−COA
0.1
0.0
−0.1
−0.2
−0.3
enrichment score
0
2000
4000
6000
rank

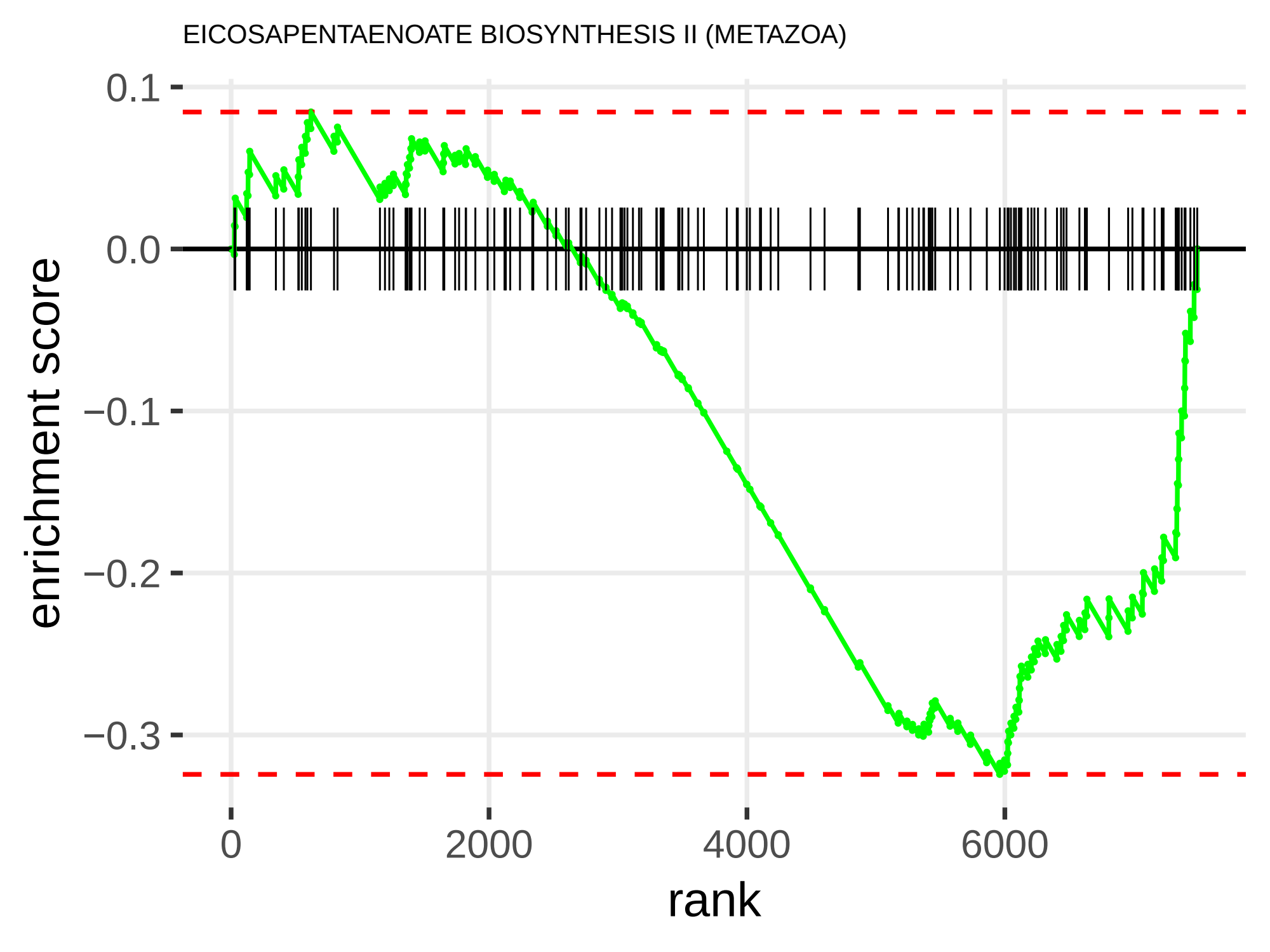

ZYMOSTEROL BIOSYNTHESIS
0.1
0.0
−0.1
−0.2
−0.3
enrichment score
0
2000
4000
6000
rank

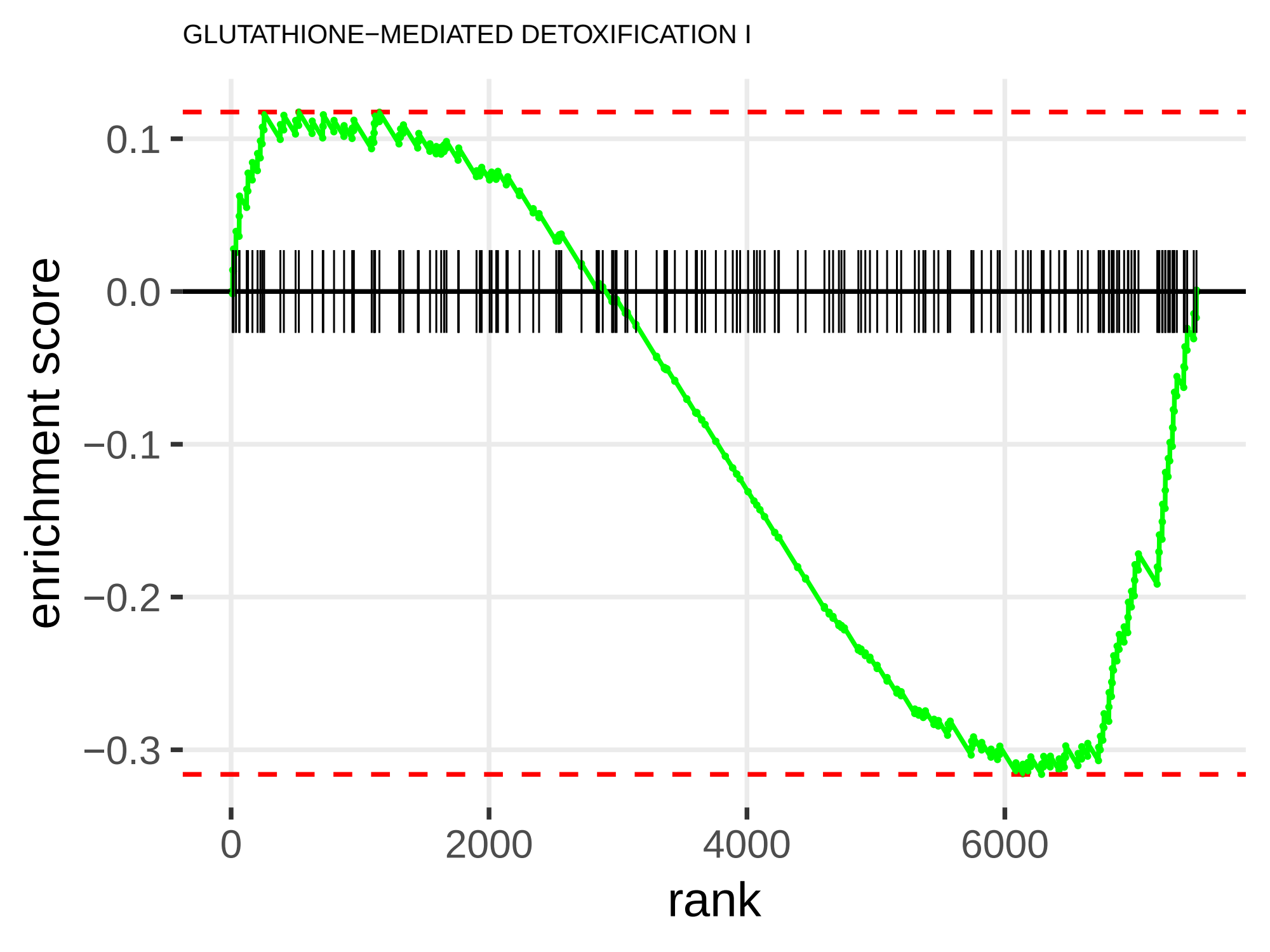

SUCROSE DEGRADATION V (MAMMALIAN)
0.0
−0.1
−0.2
−0.3
enrichment score
0
2000
4000
6000
rank

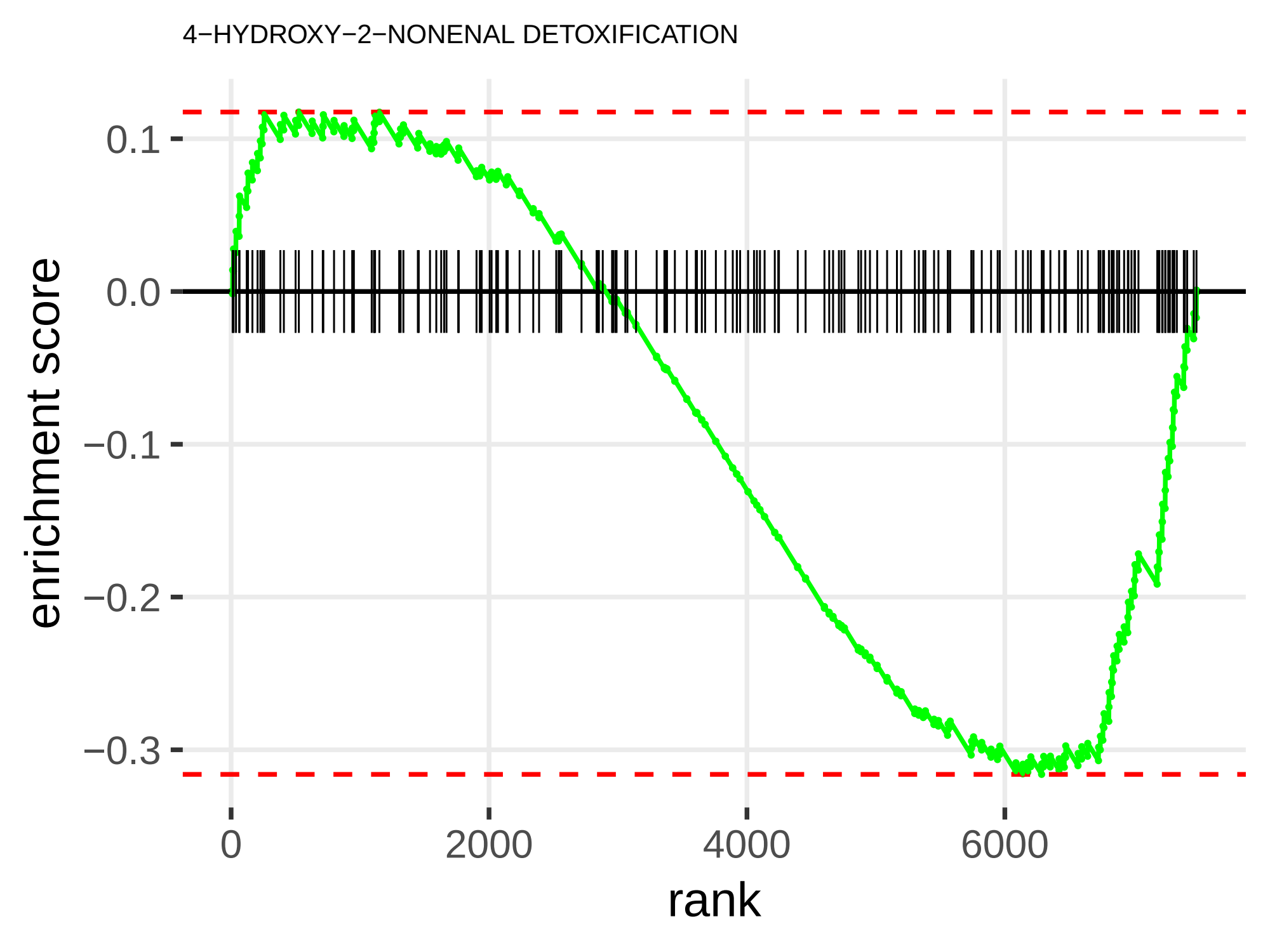

DERMATAN SULFATE DEGRADATION (METAZOA)
enrichment score
0.0
−0.1
−0.2
−0.3
0
2000
4000
6000
rank

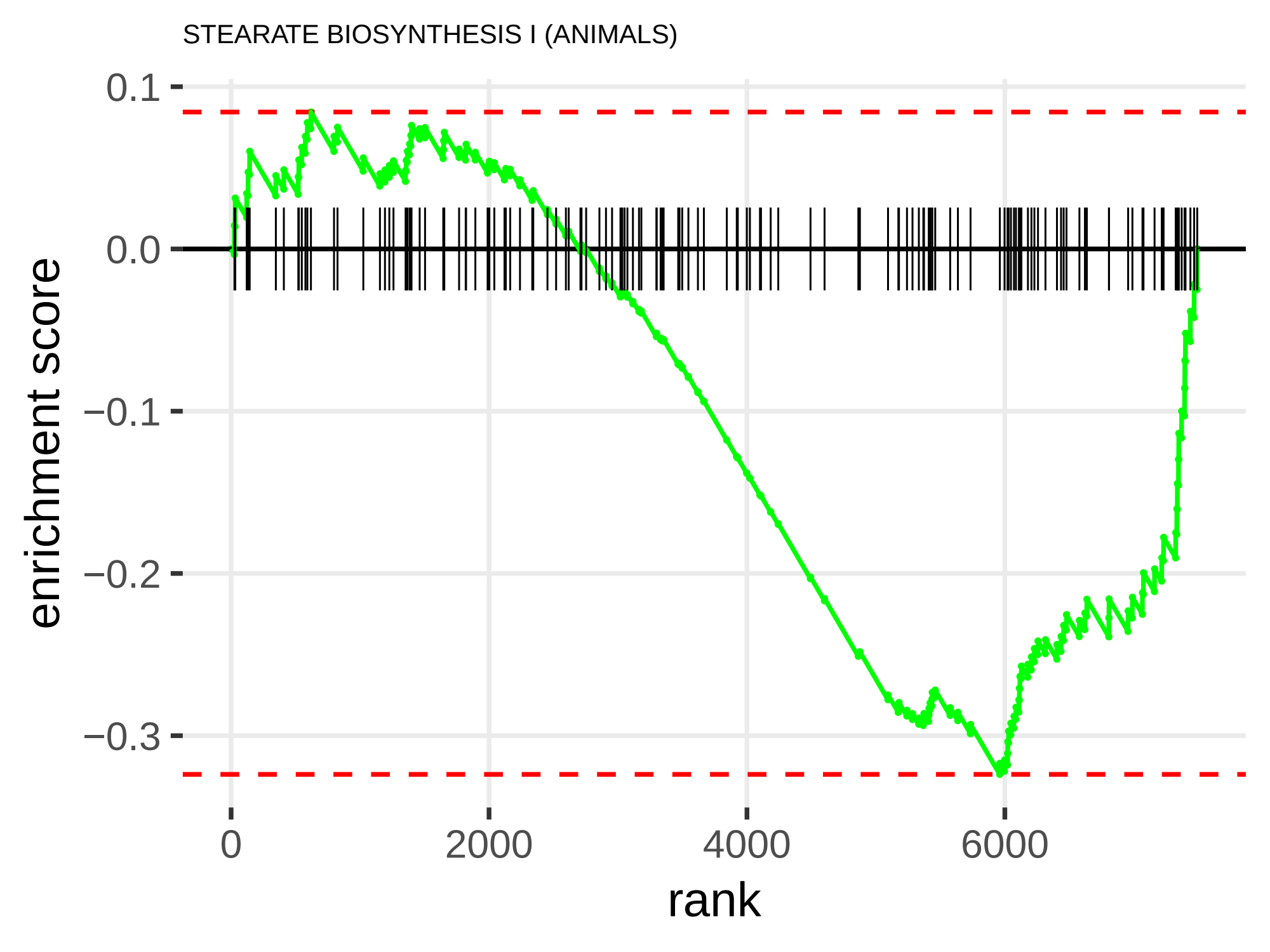

MOLYBDENUM COFACTOR BIOSYNTHESIS
enrichment score
0.0
−0.1
−0.2
−0.3
0
2000
4000
6000
rank

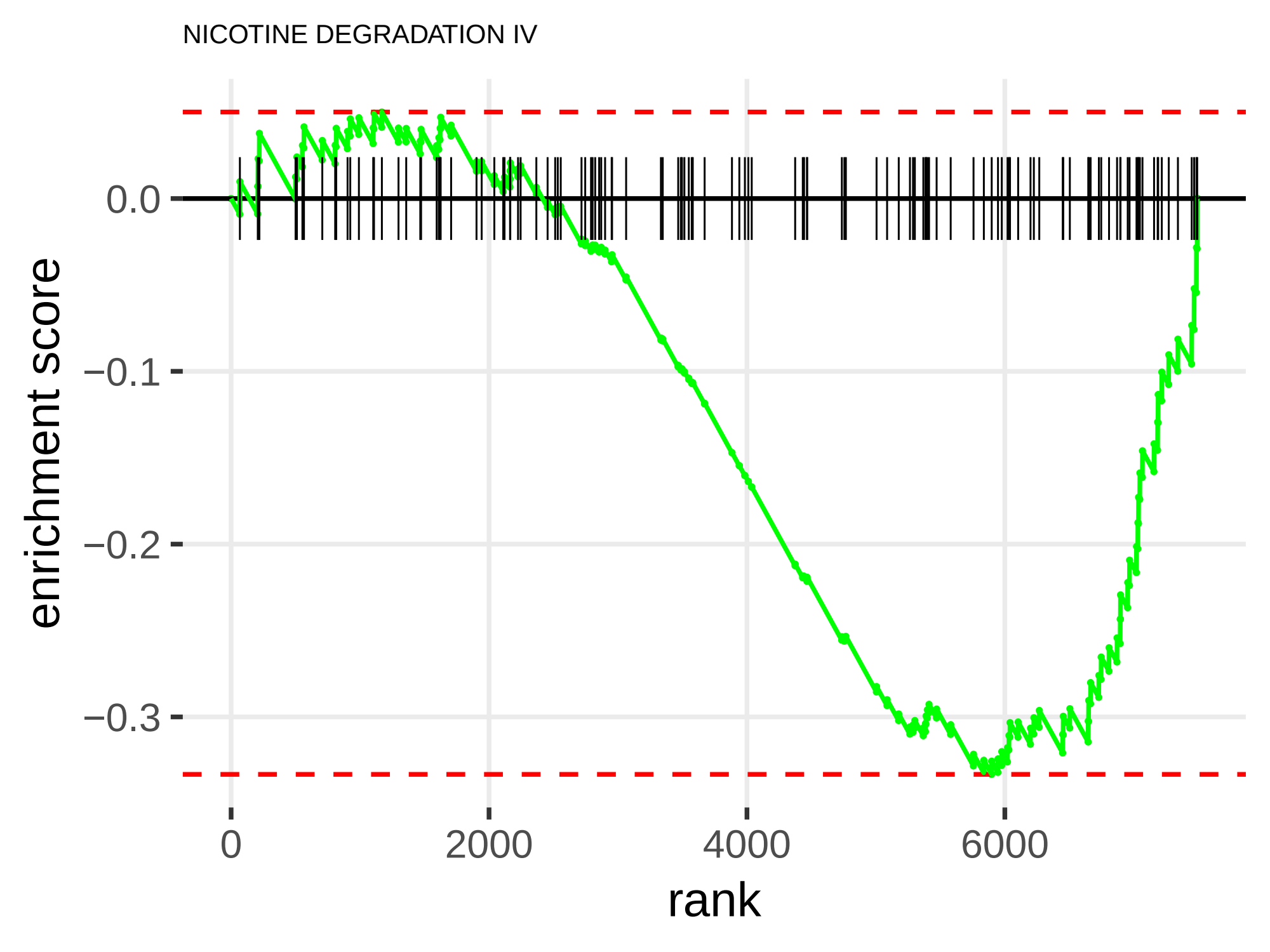

FATTY ACID &BETA;−OXIDATION I
0.0
−0.1
−0.2
−0.3
enrichment score
0
2000
4000
6000
rank

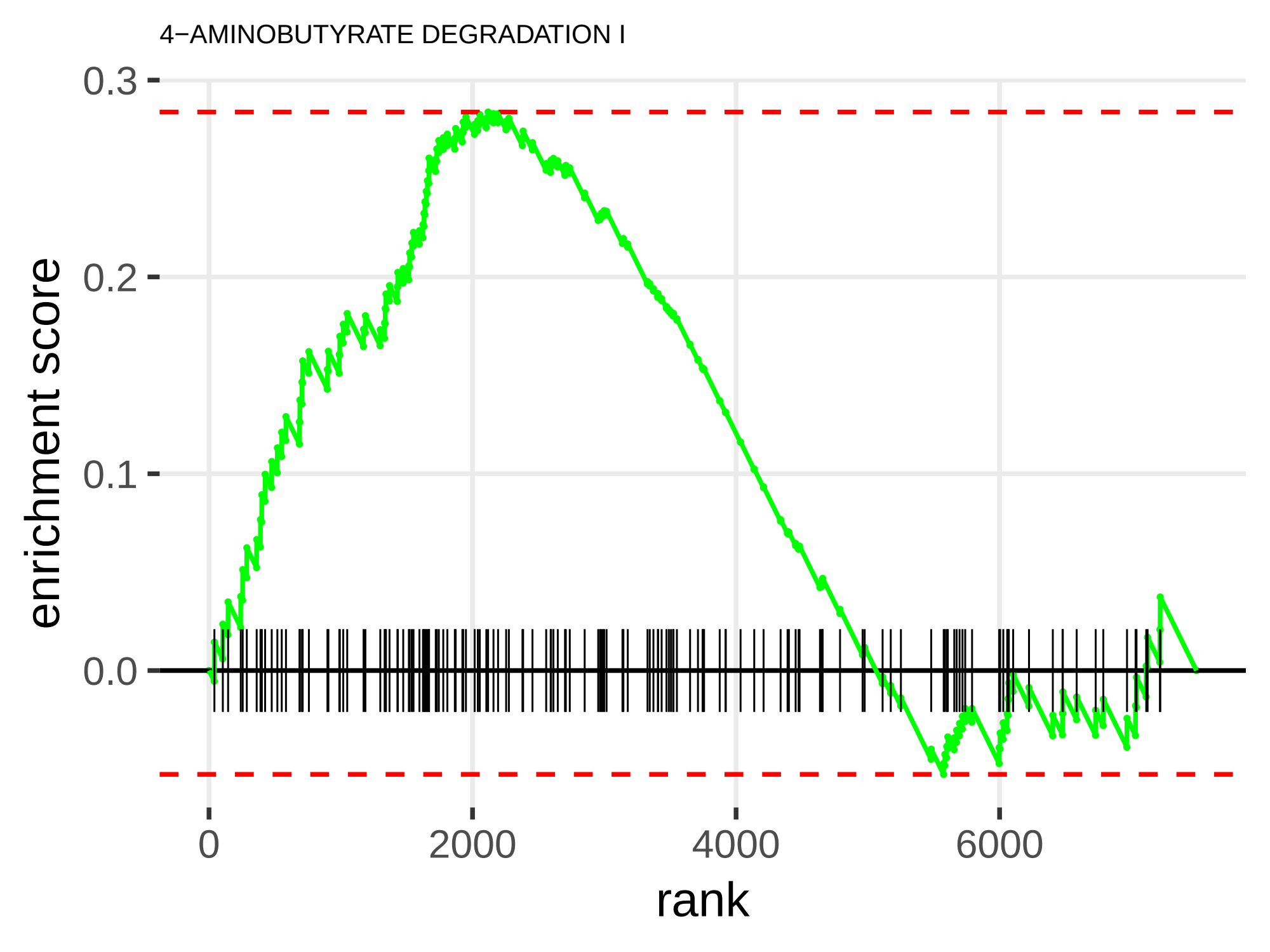

EICOSAPENTAENOATE BIOSYNTHESIS II (METAZOA)
0.1
0.0
−0.1
−0.2
−0.3
enrichment score
0
2000
4000
6000
rank

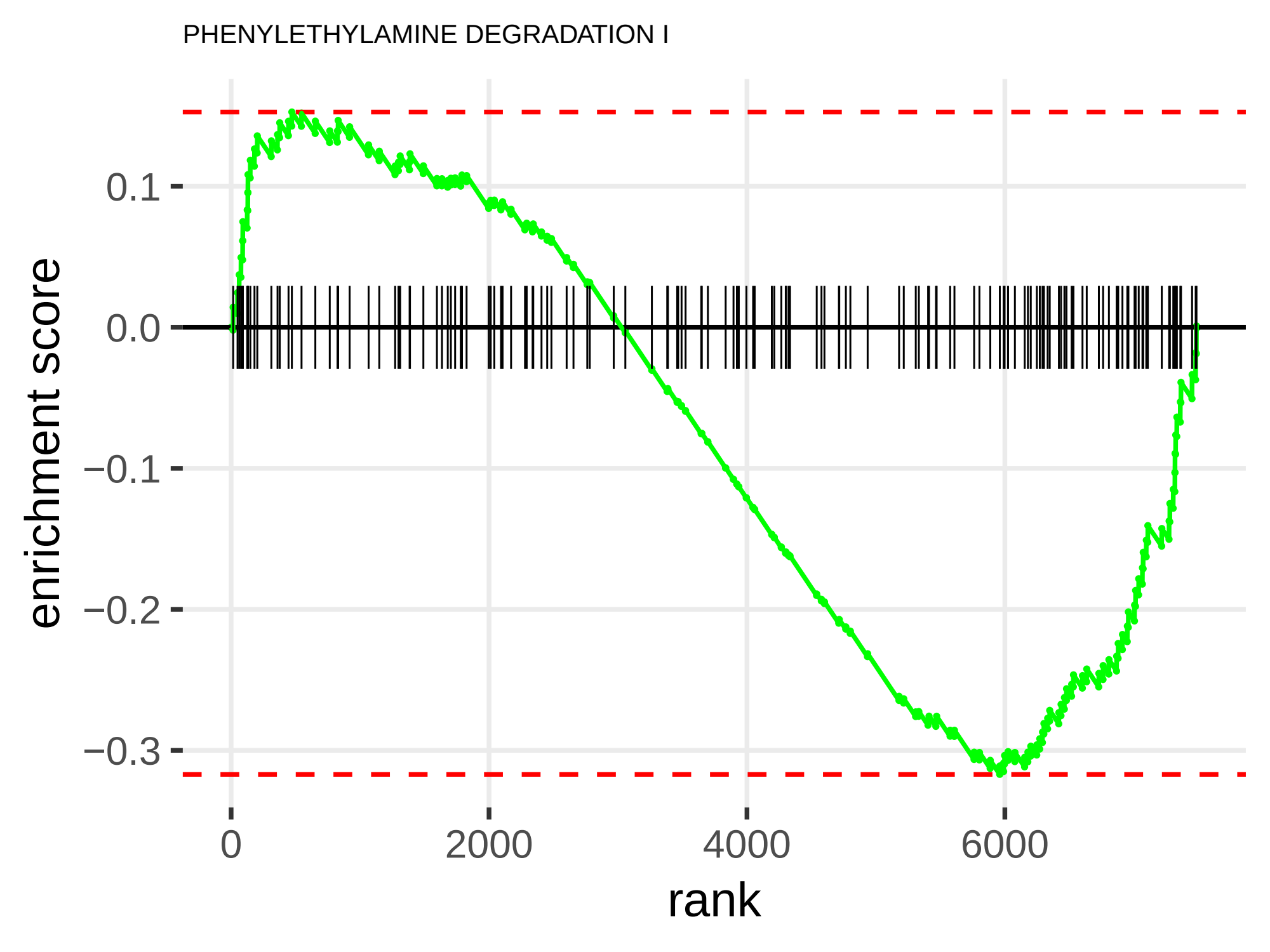

GLUTATHIONE−MEDIATED DETOXIFICATION I
enrichment score
0.1
0.0
−0.1
−0.2
−0.3
0
2000
4000
6000
rank

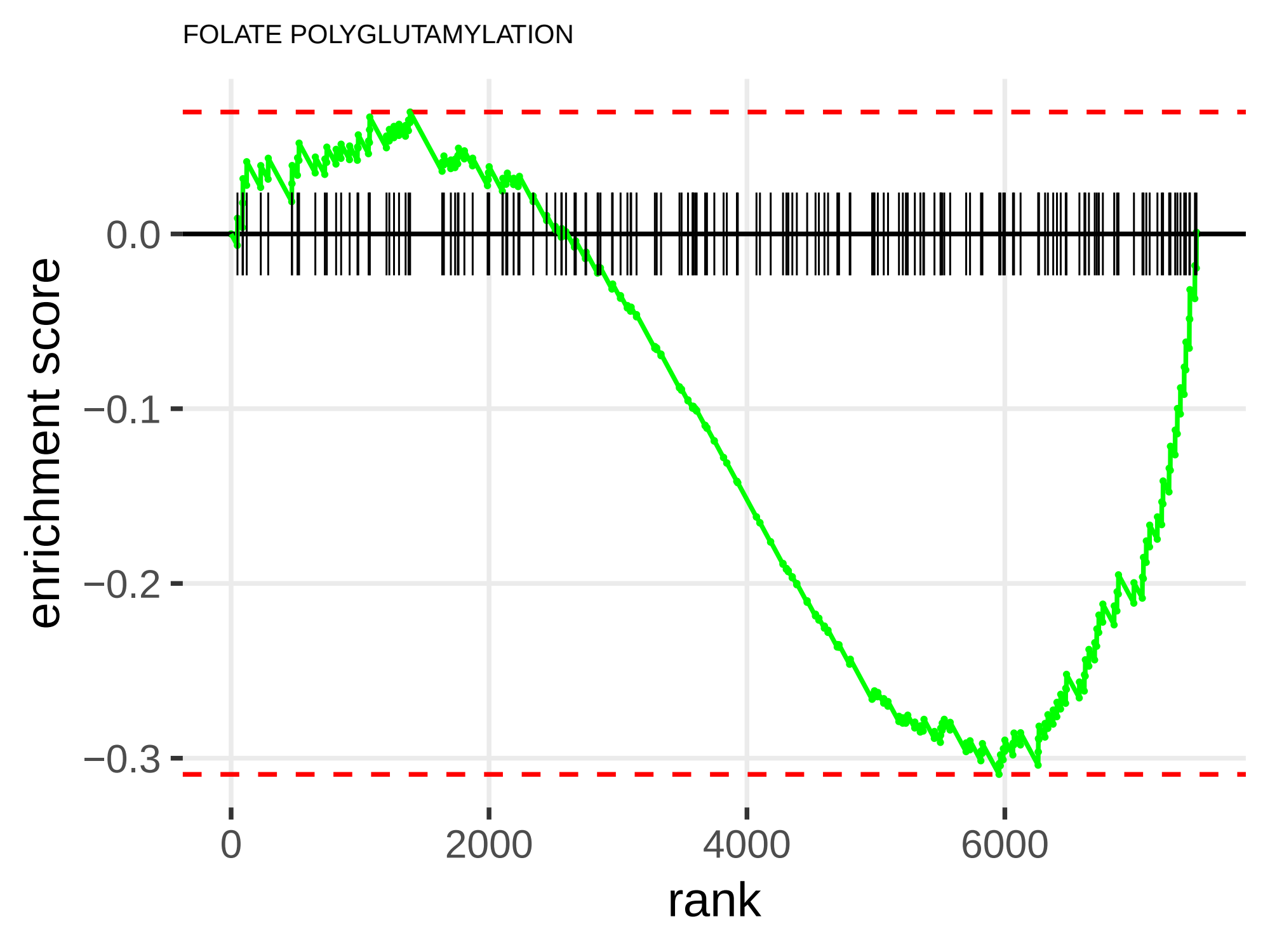

4−HYDROXY−2−NONENAL DETOXIFICATION
enrichment score
0.1
0.0
−0.1
−0.2
−0.3
0
2000
4000
6000
rank

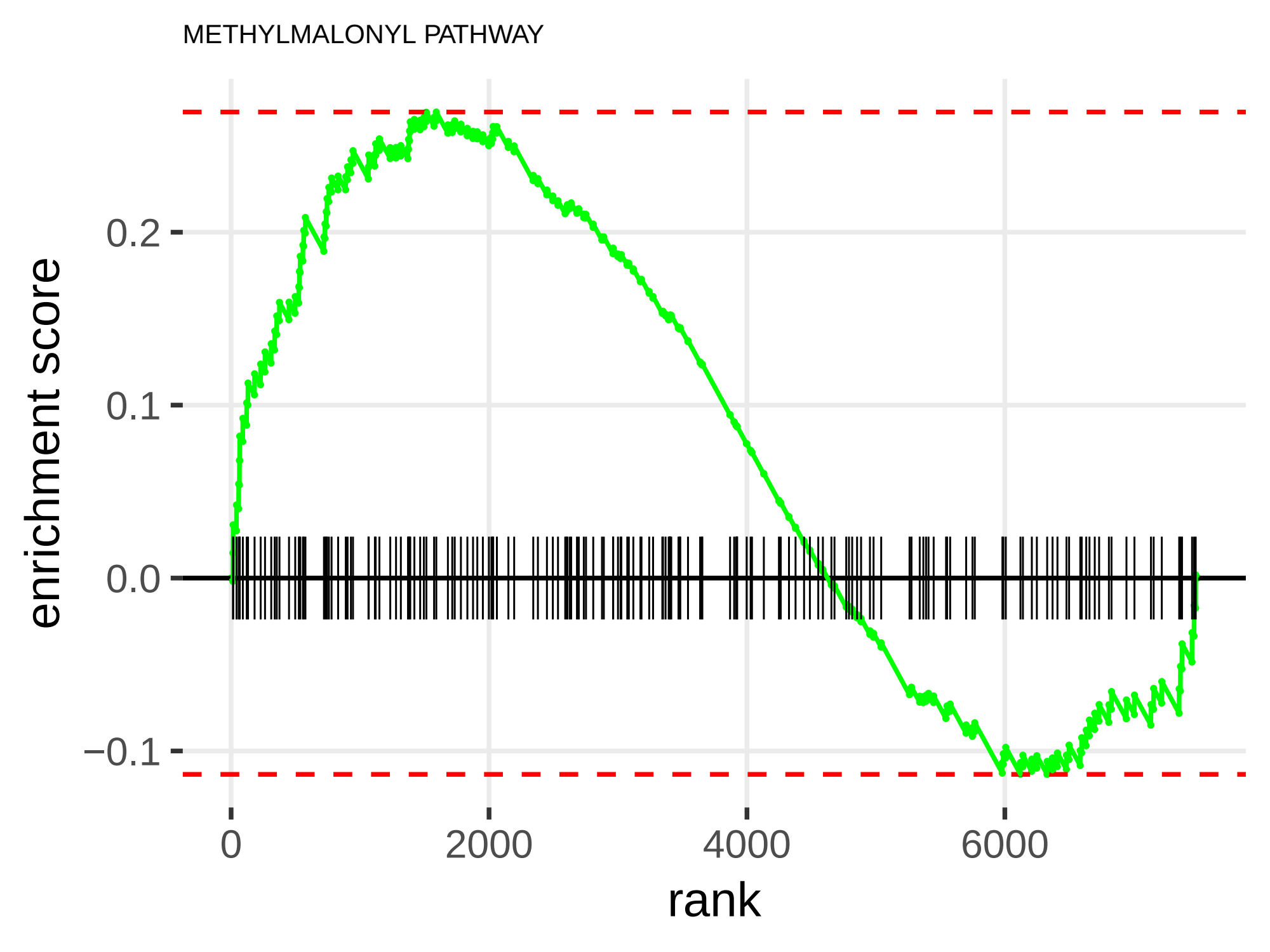

STEARATE BIOSYNTHESIS I (ANIMALS)
0.1
0.0
−0.1
−0.2
−0.3
enrichment score
0
2000
4000
6000
rank

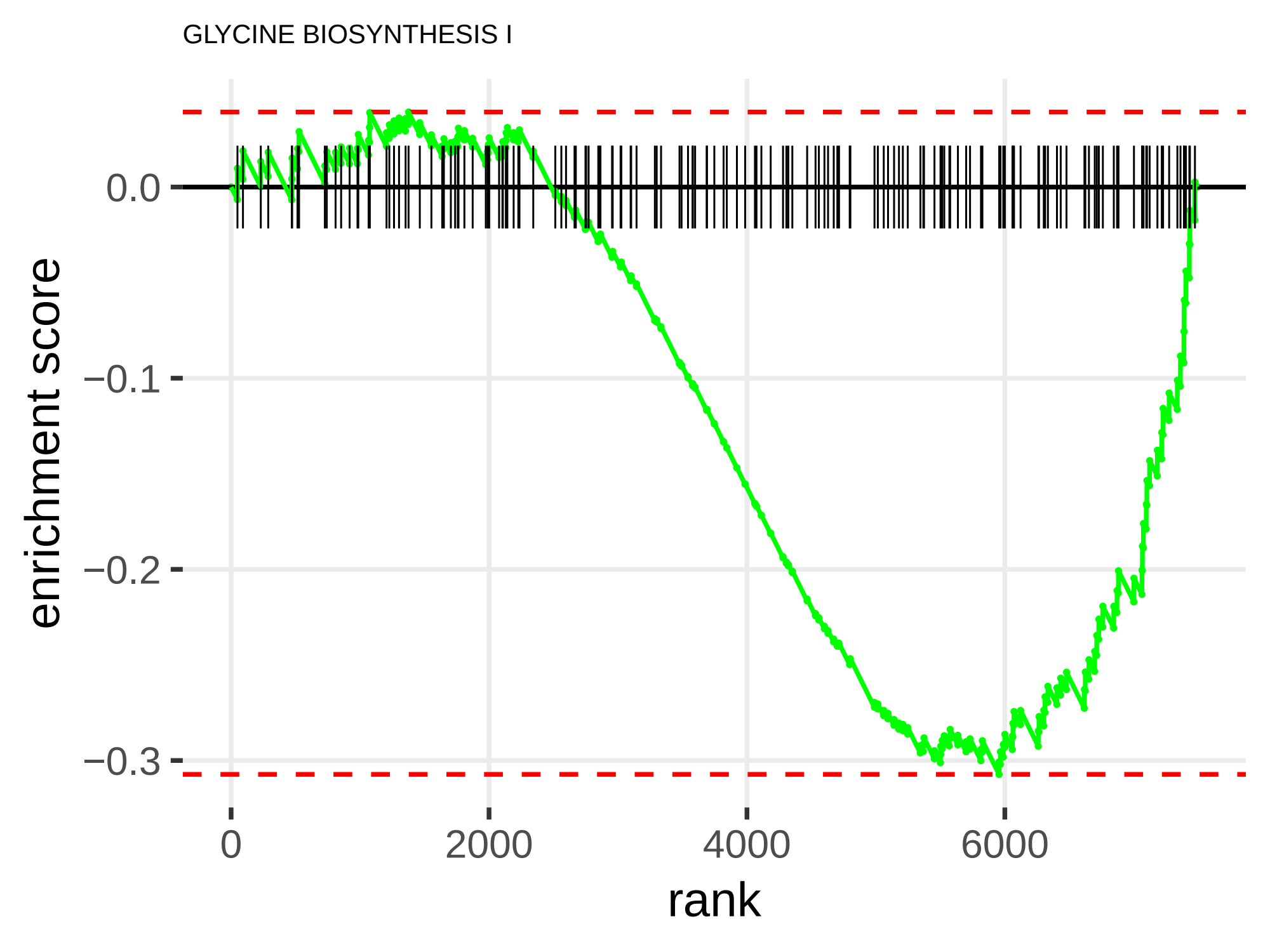

NICOTINE DEGRADATION IV
enrichment score
0.0
−0.1
−0.2
−0.3
0
2000
4000
6000
rank

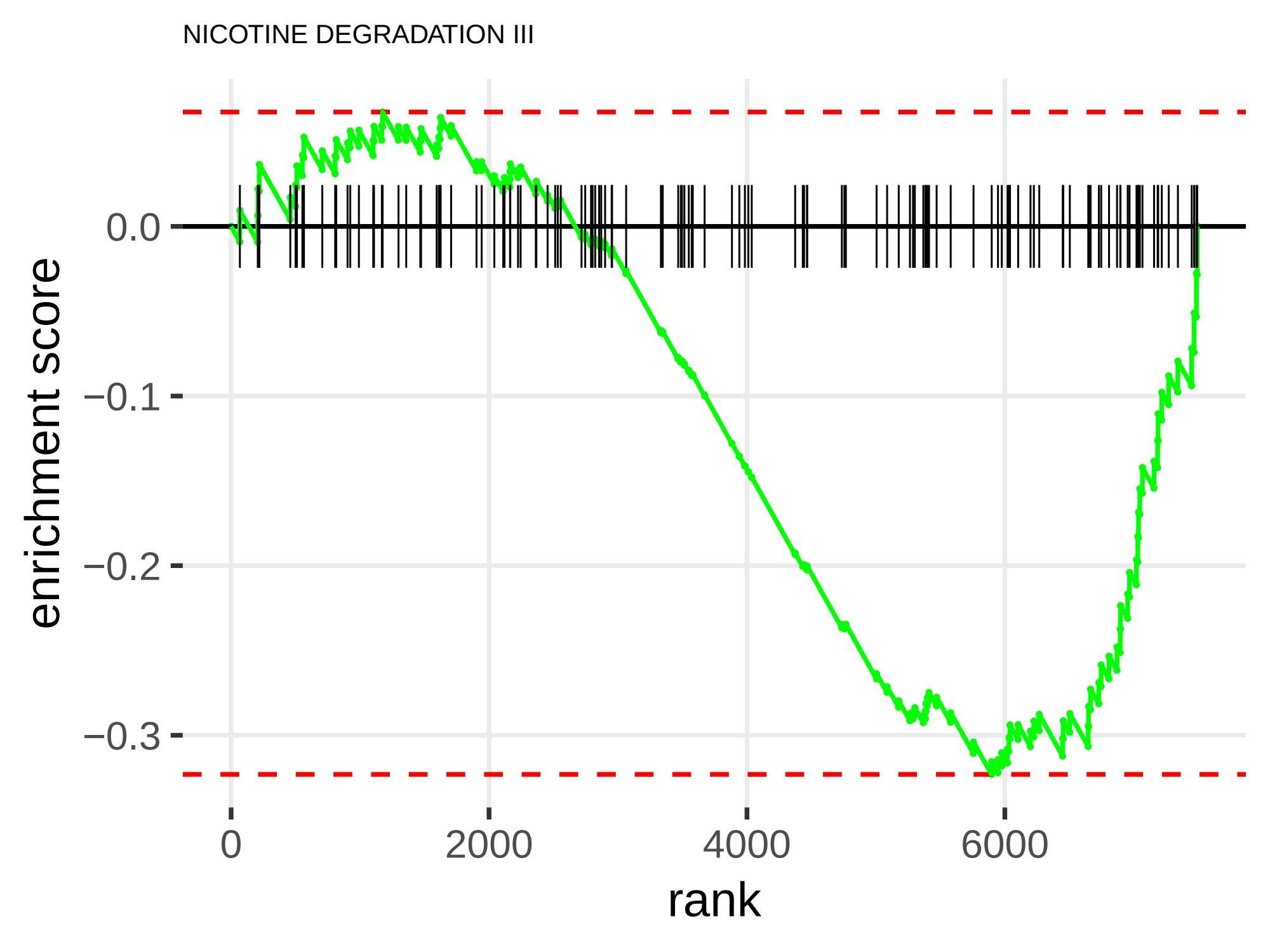

4−AMINOBUTYRATE DEGRADATION I
0.3
0.2
0.1
0.0
enrichment score
0
2000
4000
6000
rank

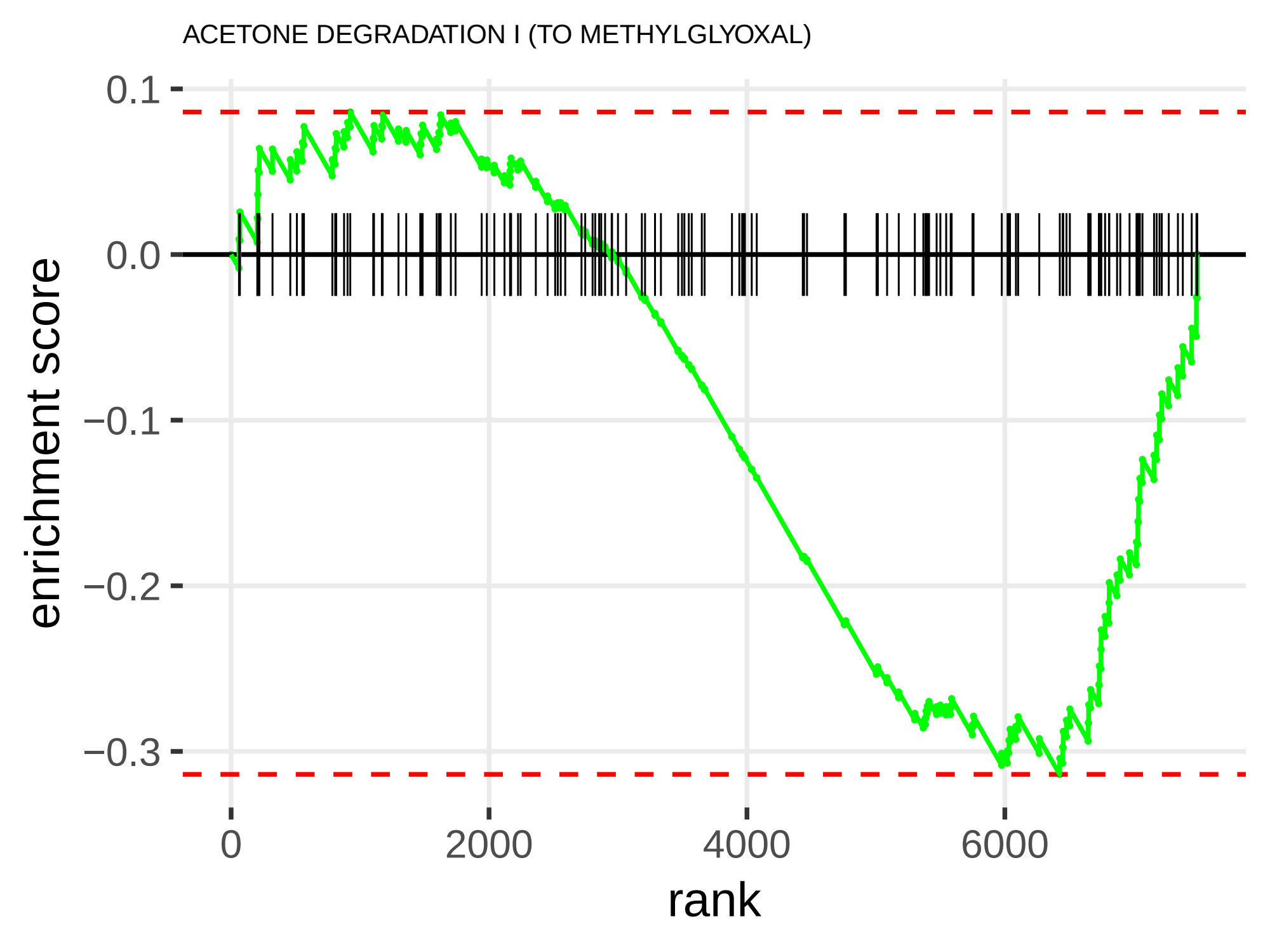

PHENYLETHYLAMINE DEGRADATION I
enrichment score
0.1
0.0
−0.1
−0.2
−0.3
0
2000
4000
6000
rank

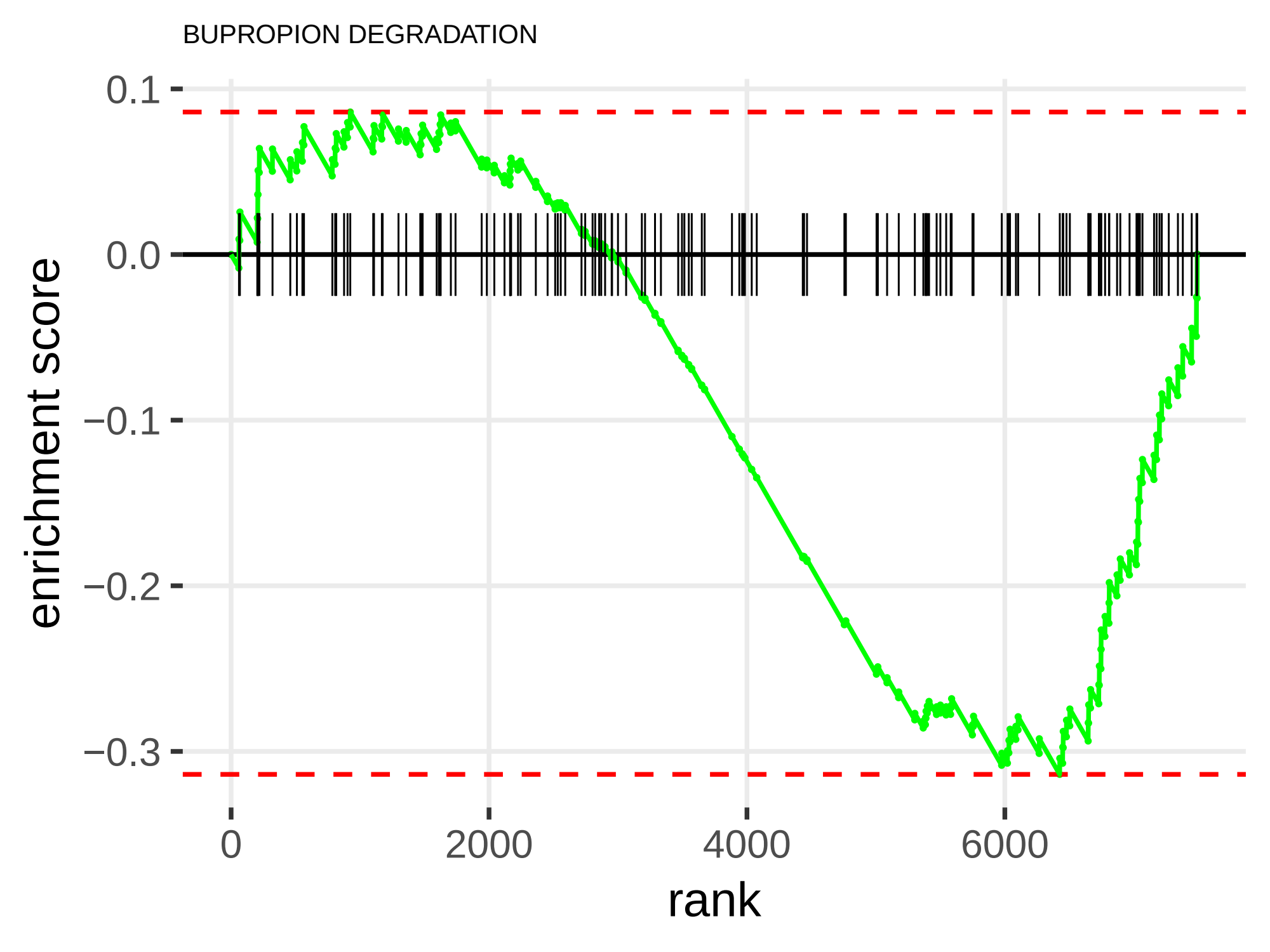

FOLATE POLYGLUTAMYLATION
enrichment score
0.0
−0.1
−0.2
−0.3
0
2000
4000
6000
rank

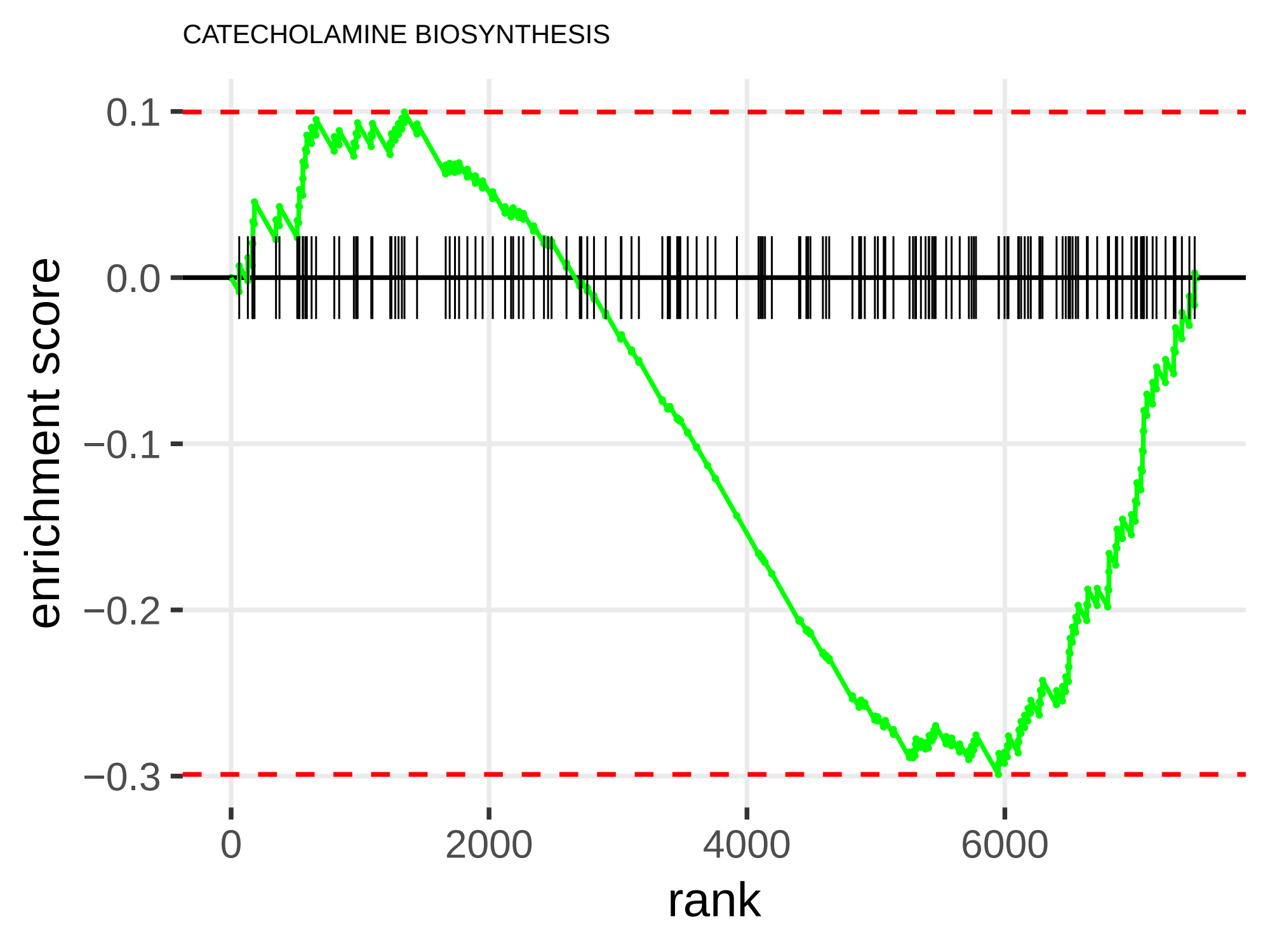

METHYLMALONYL PATHWAY
enrichment score
0.2
0.1
0.0
−0.1
0
2000
4000
6000
rank

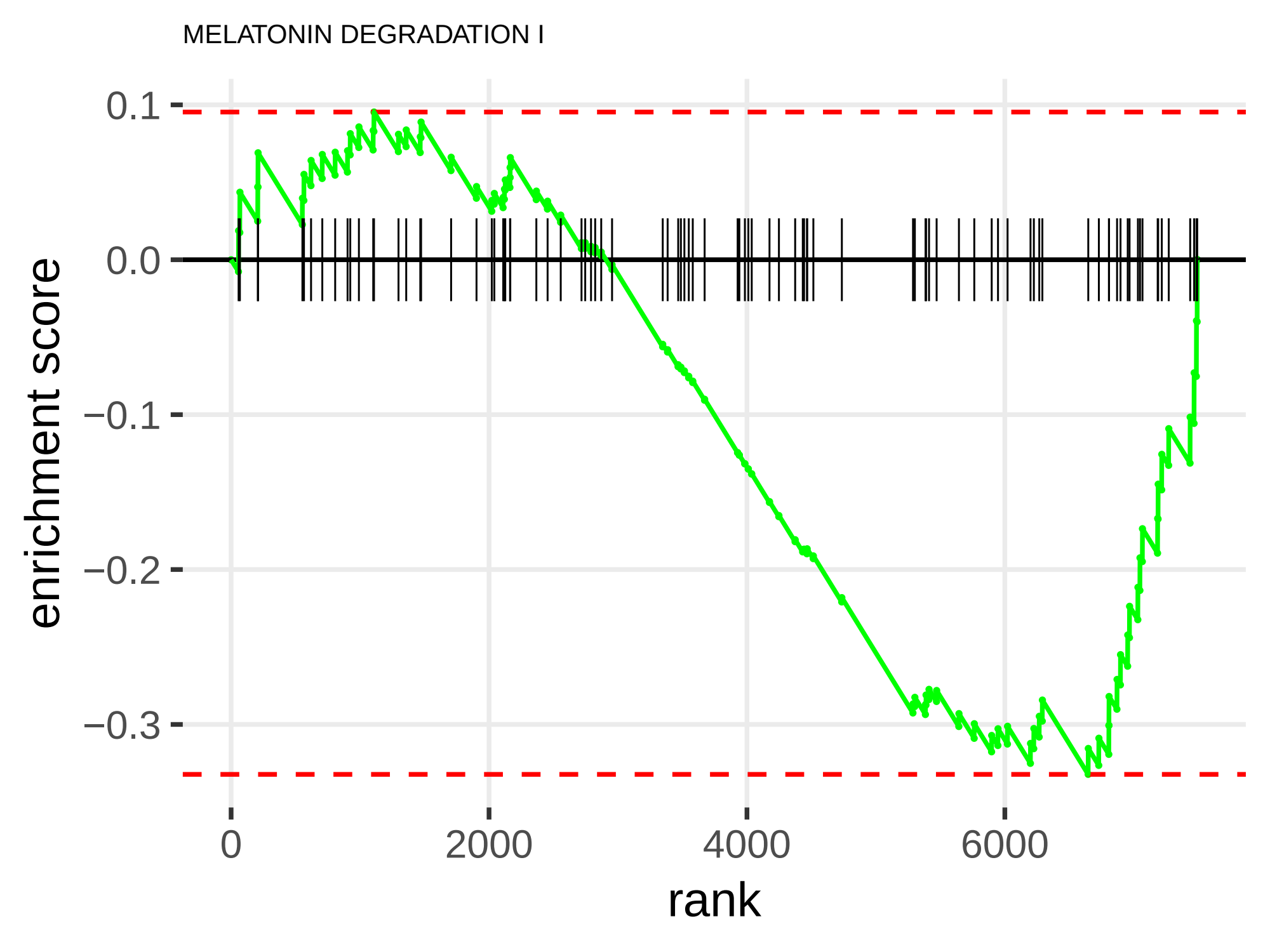

GLYCINE BIOSYNTHESIS I
0.0
−0.1
−0.2
−0.3
enrichment score
0
2000
4000
6000
rank

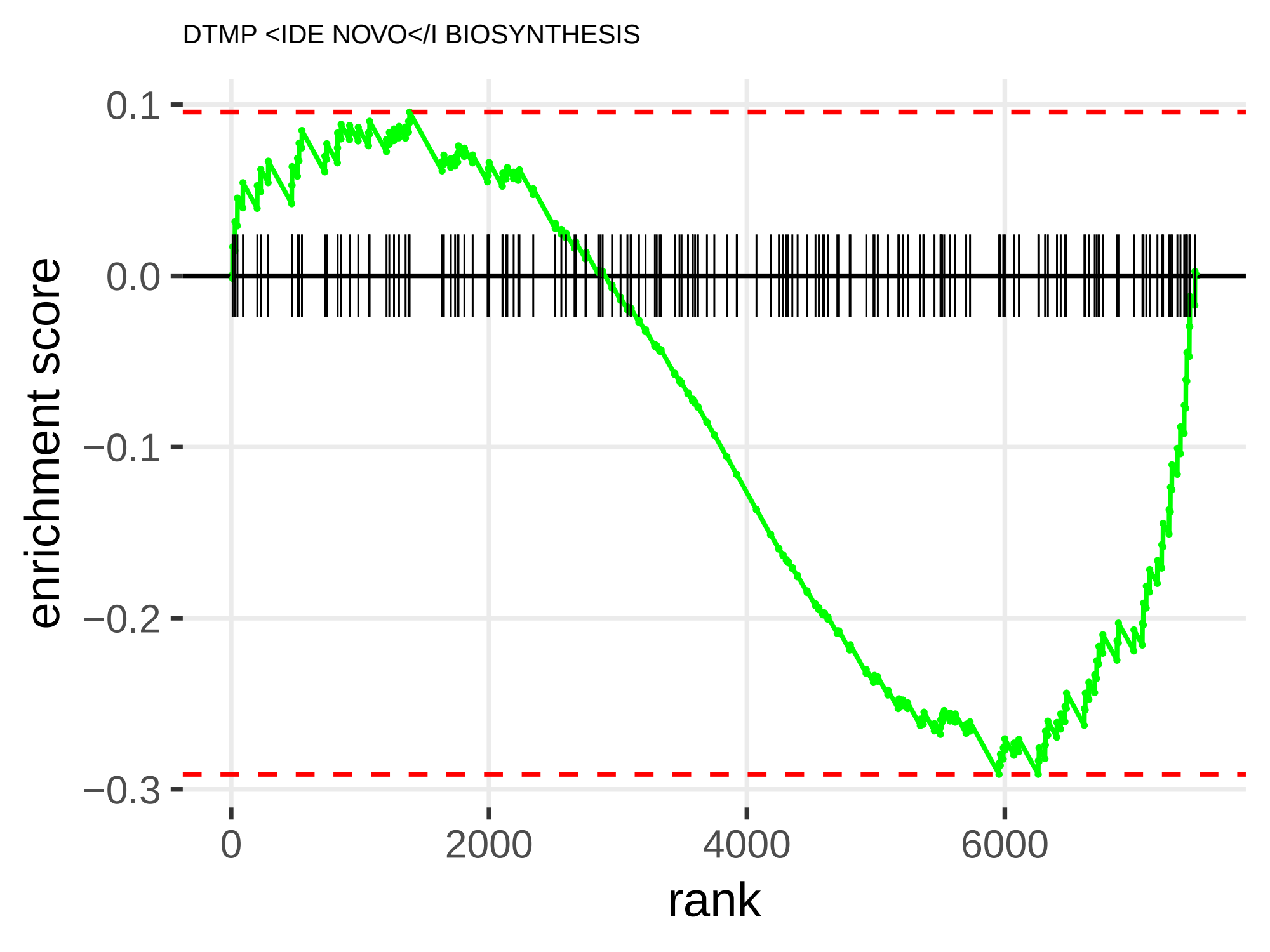

NICOTINE DEGRADATION III
enrichment score
0.0
−0.1
−0.2
−0.3
0
2000
4000
6000
rank

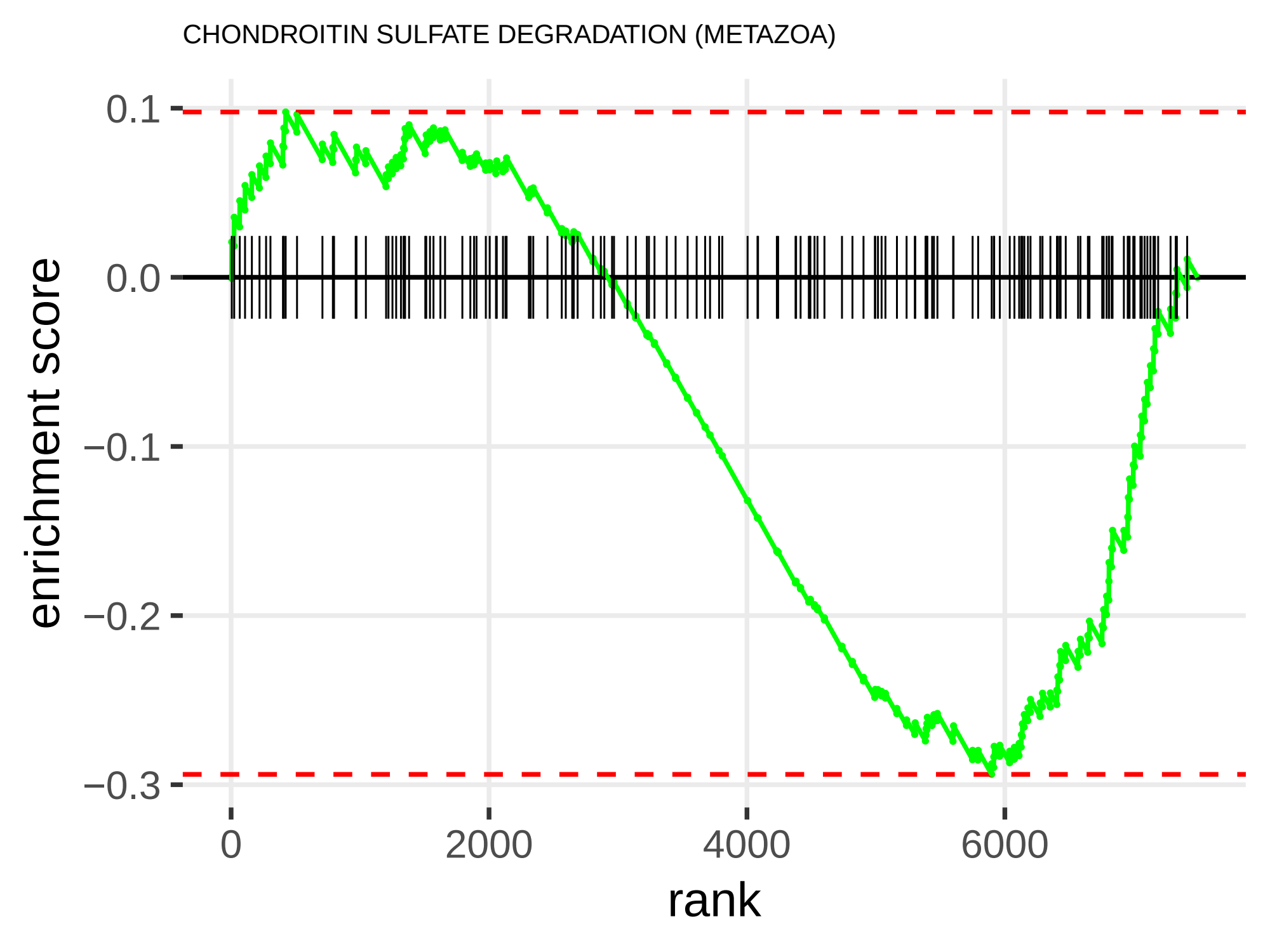

ACETONE DEGRADATION I (TO METHYLGLYOXAL)
0.1
0.0
−0.1
−0.2
−0.3
enrichment score
0
2000
4000
6000
rank

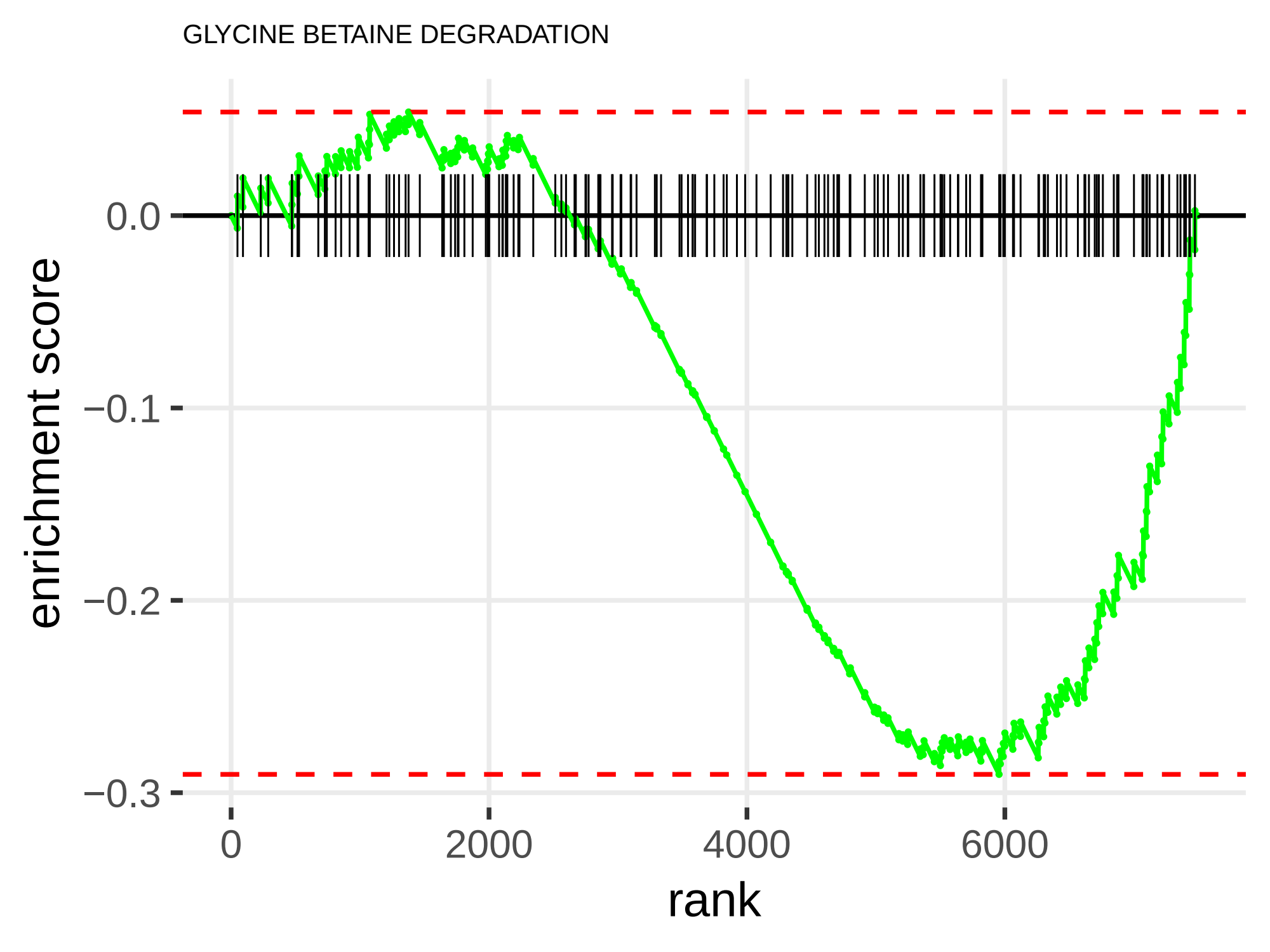

BUPROPION DEGRADATION
0.1
0.0
−0.1
−0.2
−0.3
enrichment score
0
2000
4000
6000
rank

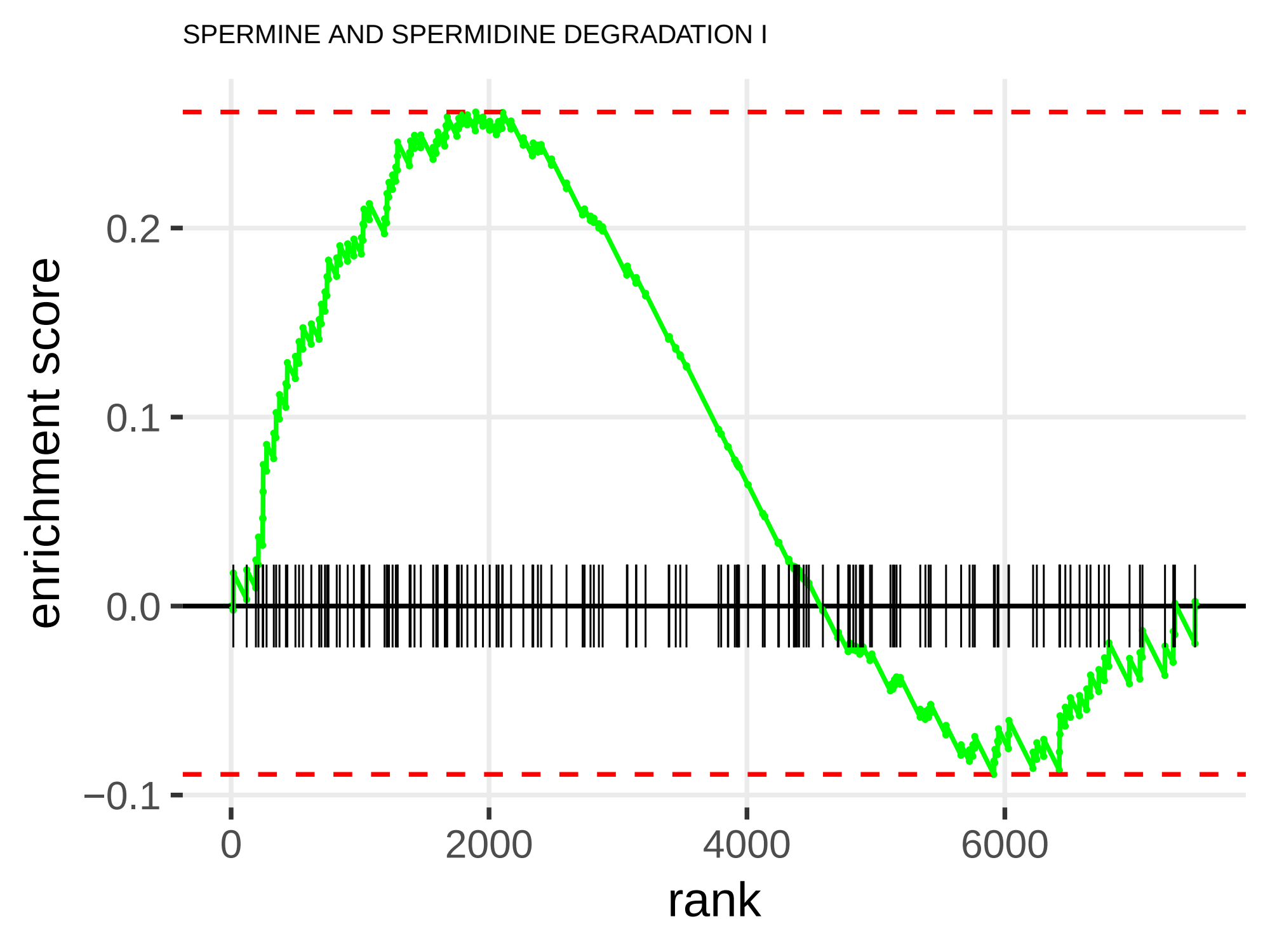

CATECHOLAMINE BIOSYNTHESIS
0.1
0.0
−0.1
−0.2
−0.3
enrichment score
0
2000
4000
6000
rank

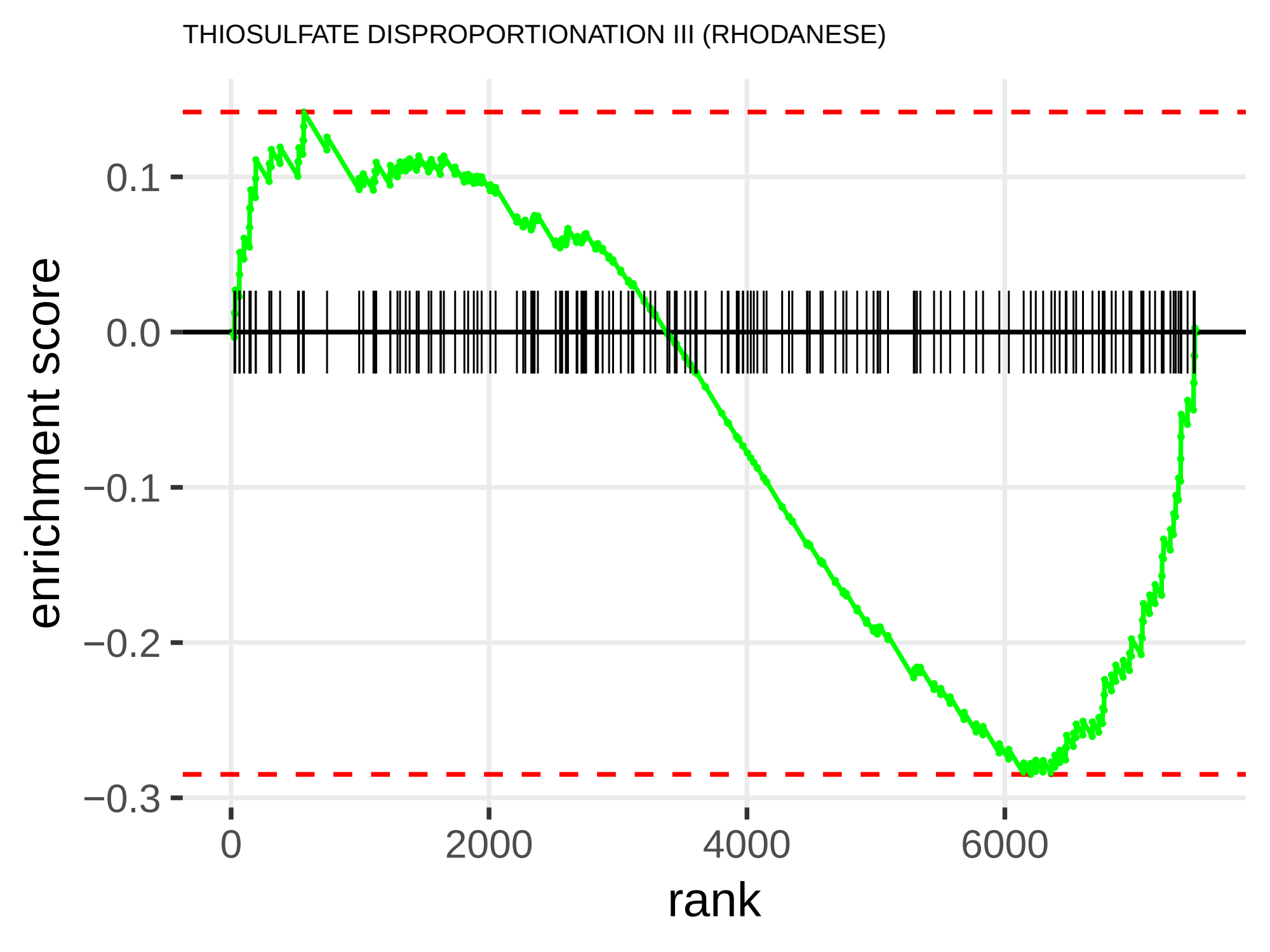

MELATONIN DEGRADATION I
0.1
0.0
−0.1
−0.2
−0.3
enrichment score
0
2000
4000
6000
rank

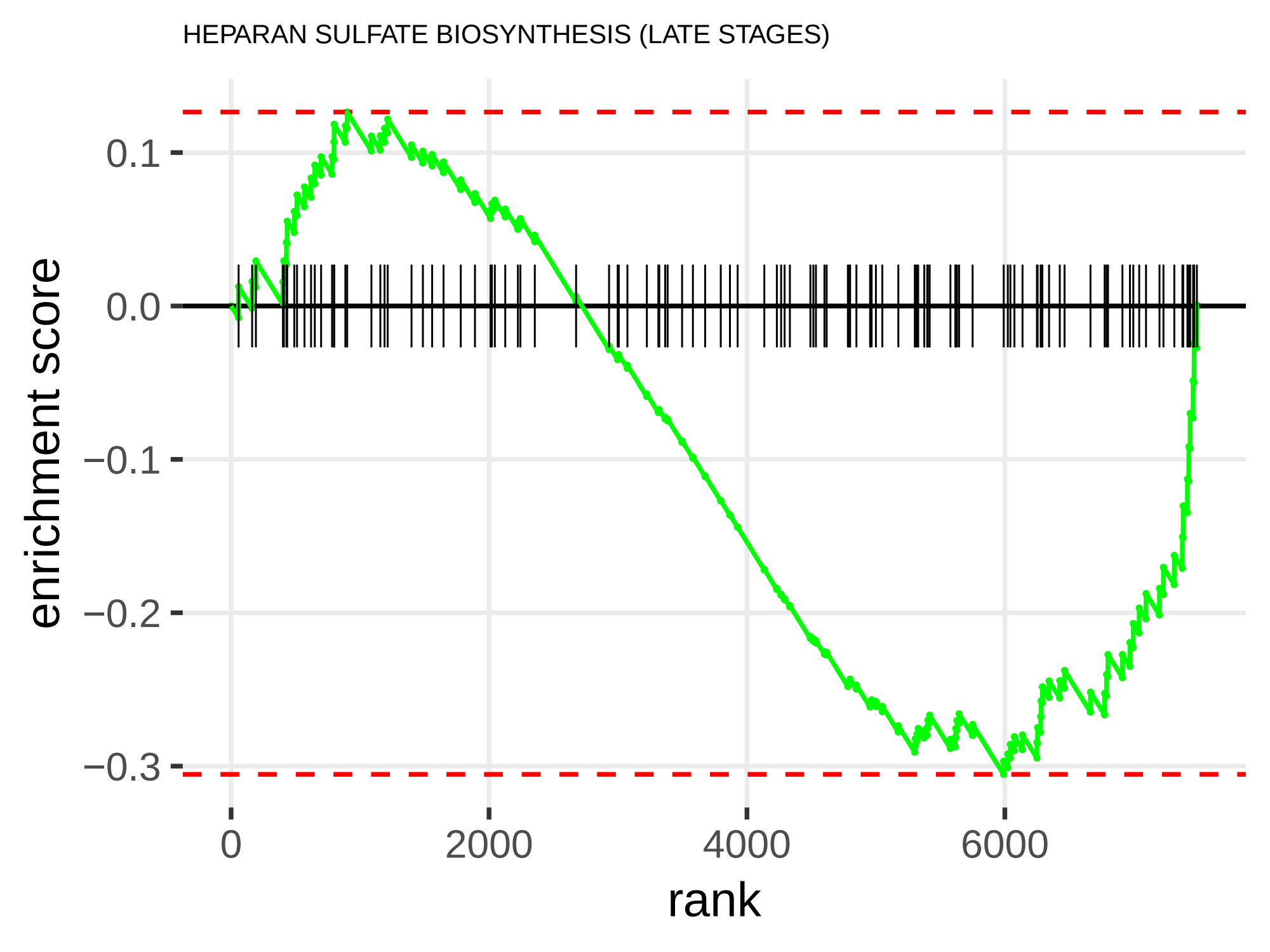

DTMP <IDE NOVO</I BIOSYNTHESIS
0.1
0.0
−0.1
−0.2
−0.3
enrichment score
0
2000
4000
6000
rank

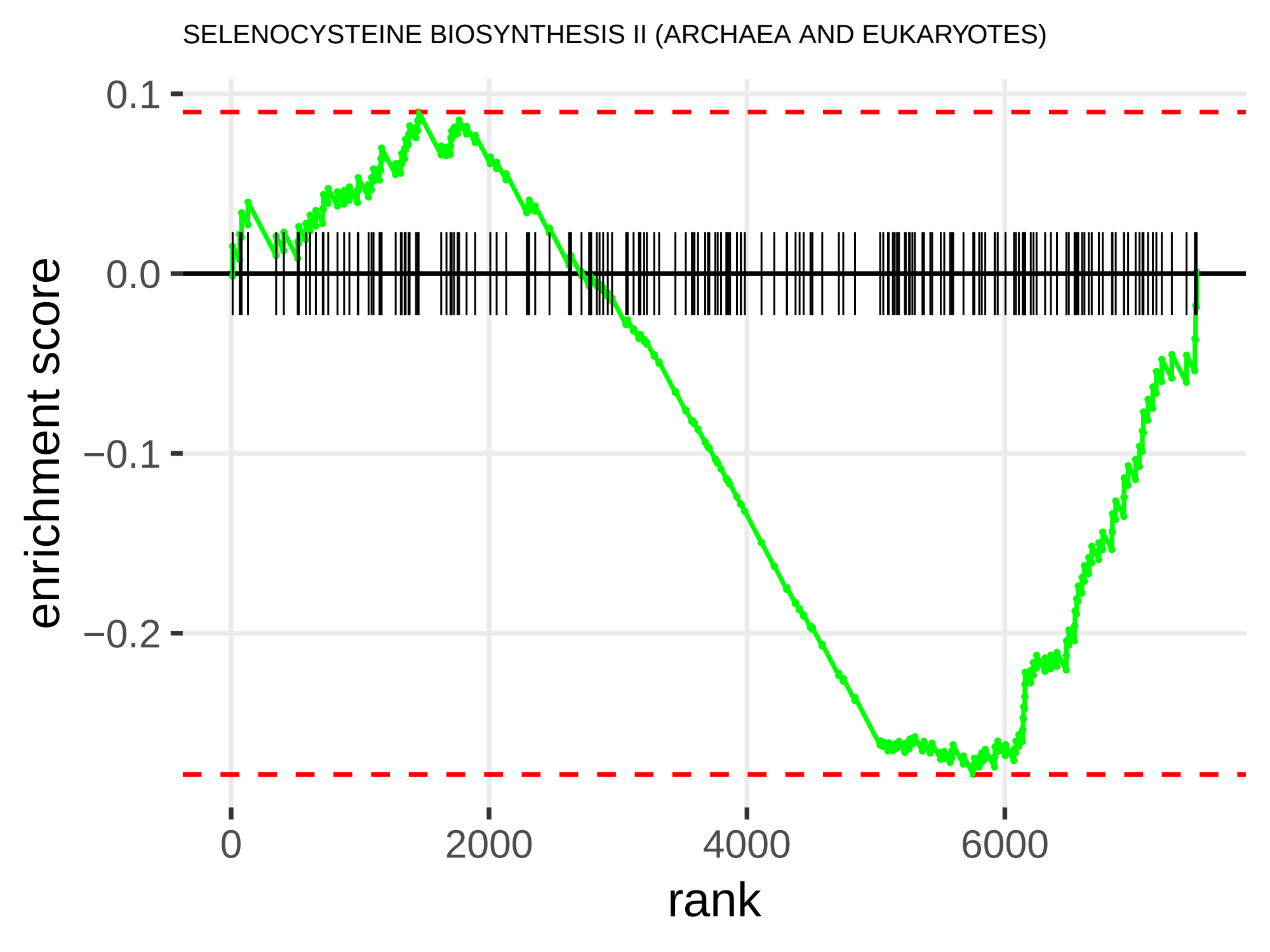

CHONDROITIN SULFATE DEGRADATION (METAZOA)
0.1
0.0
−0.1
−0.2
−0.3
enrichment score
0
2000
4000
6000
rank

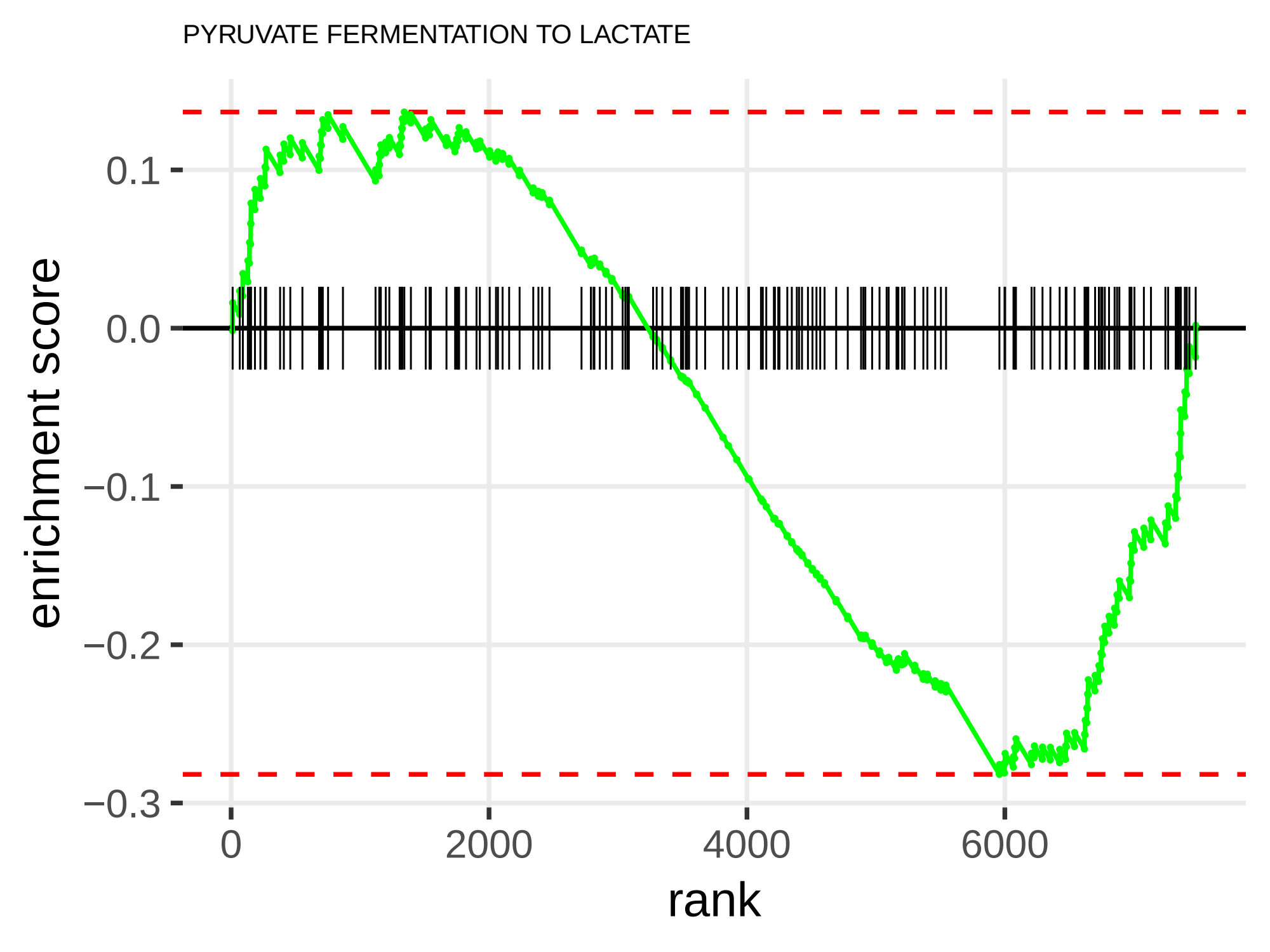

GLYCINE BETAINE DEGRADATION
enrichment score
0.0
−0.1
−0.2
−0.3
0
2000
4000
6000
rank

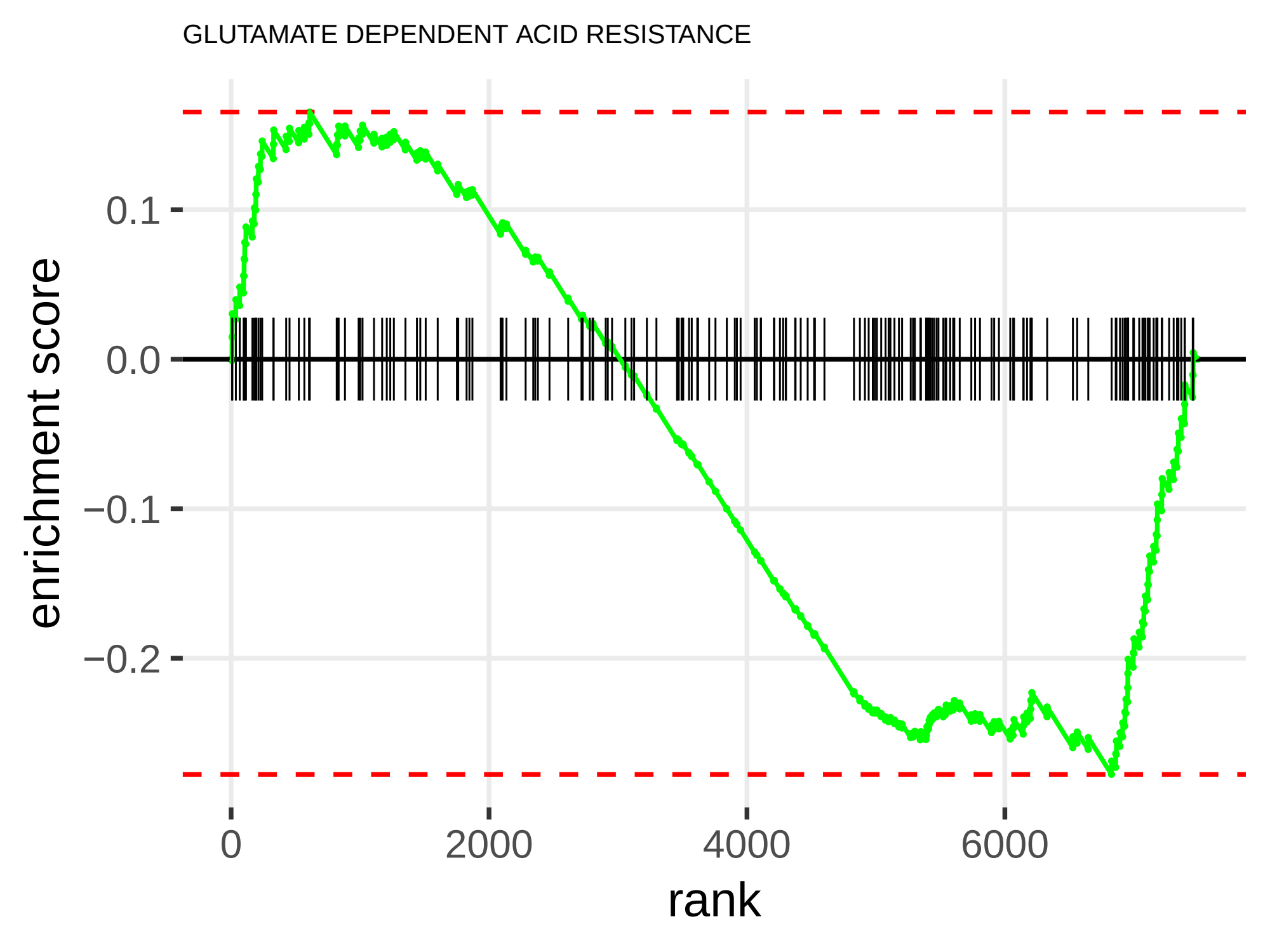

SPERMINE AND SPERMIDINE DEGRADATION I
enrichment score
0.2
0.1
0.0
−0.1
0
2000
4000
6000
rank

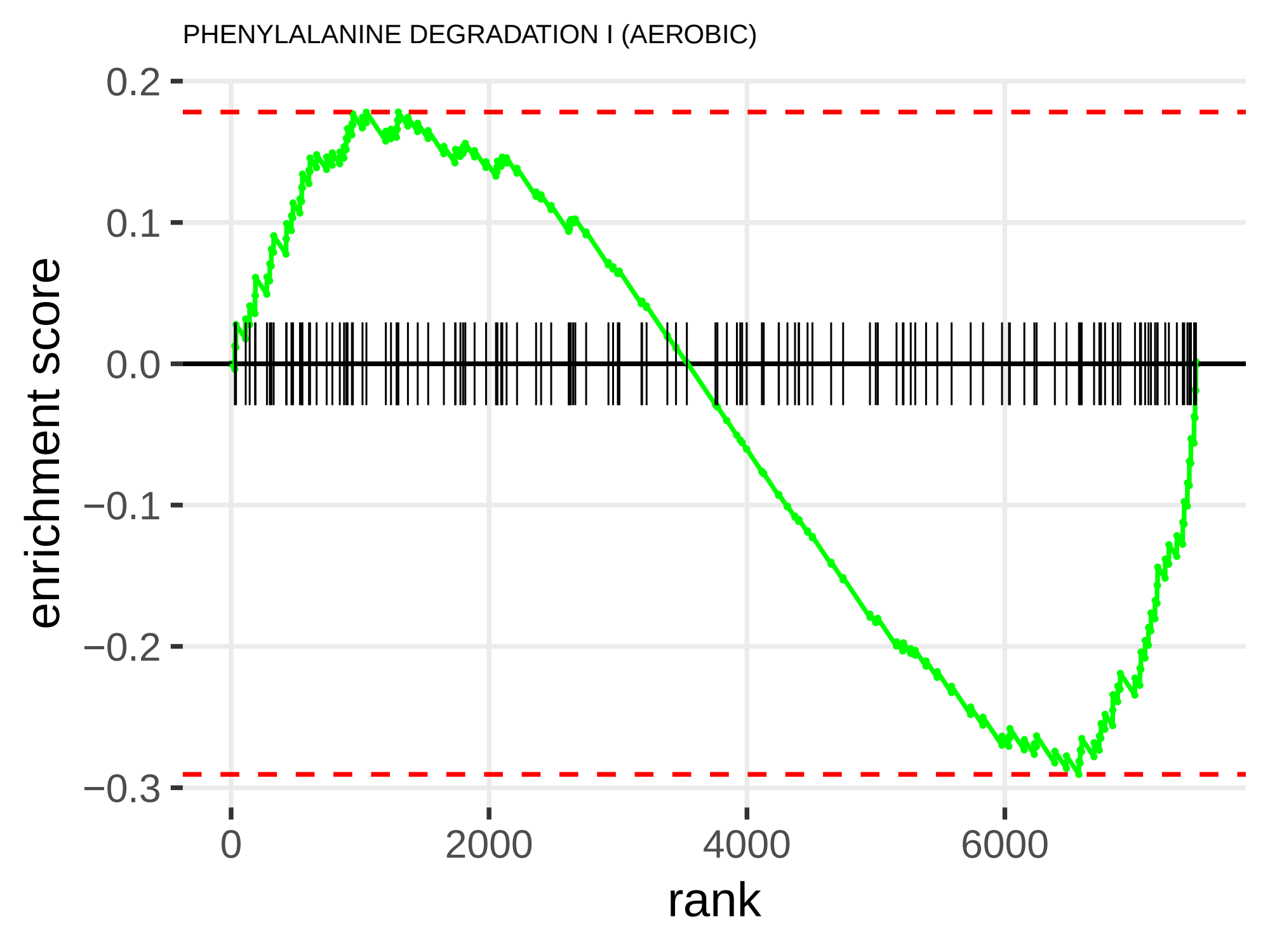

THIOSULFATE DISPROPORTIONATION III (RHODANESE)
enrichment score
0.1
0.0
−0.1
−0.2
−0.3
0
2000
4000
6000
rank

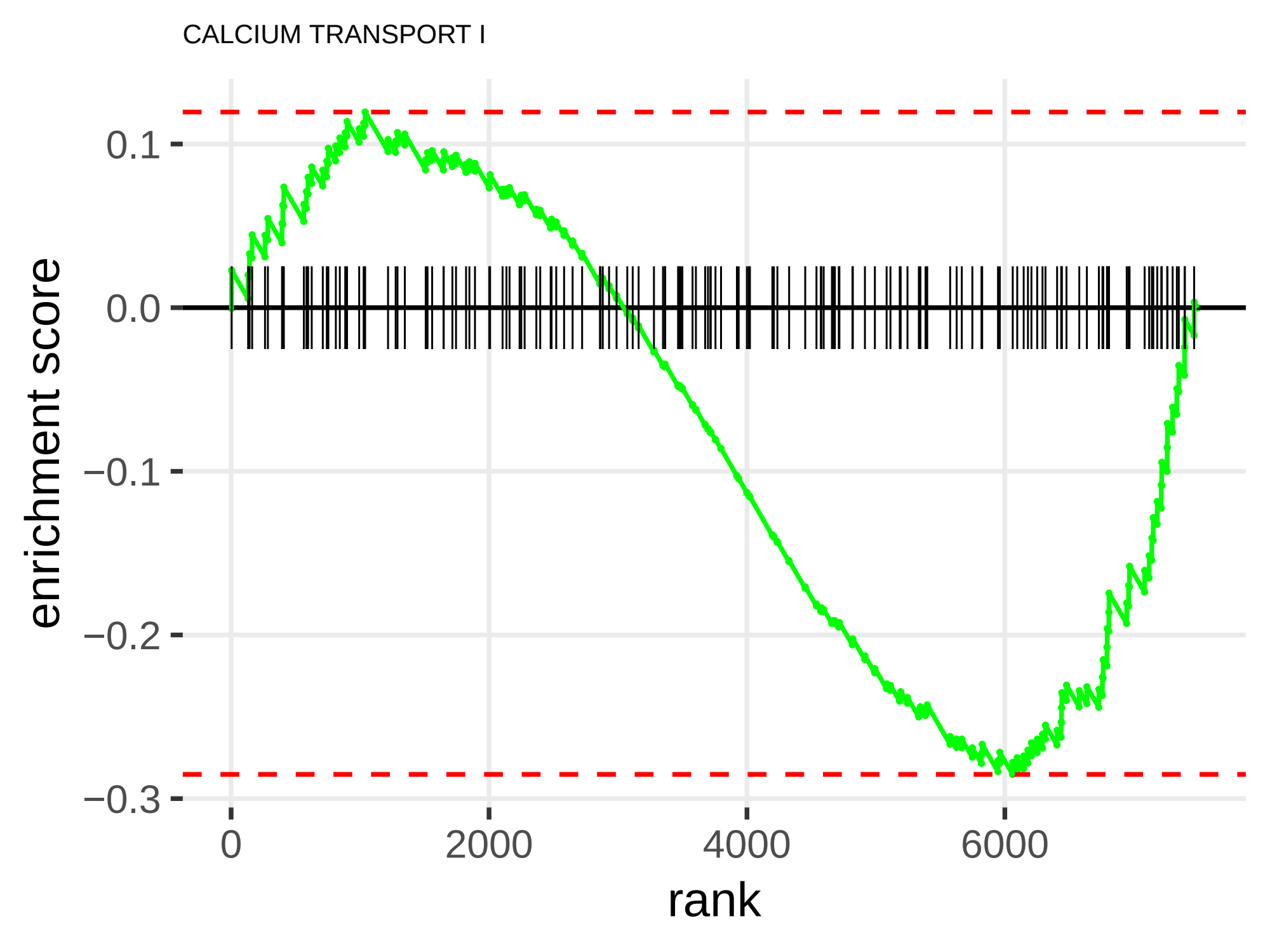

HEPARAN SULFATE BIOSYNTHESIS (LATE STAGES)
enrichment score
0.1
0.0
−0.1
−0.2
−0.3
0
2000
4000
6000
rank

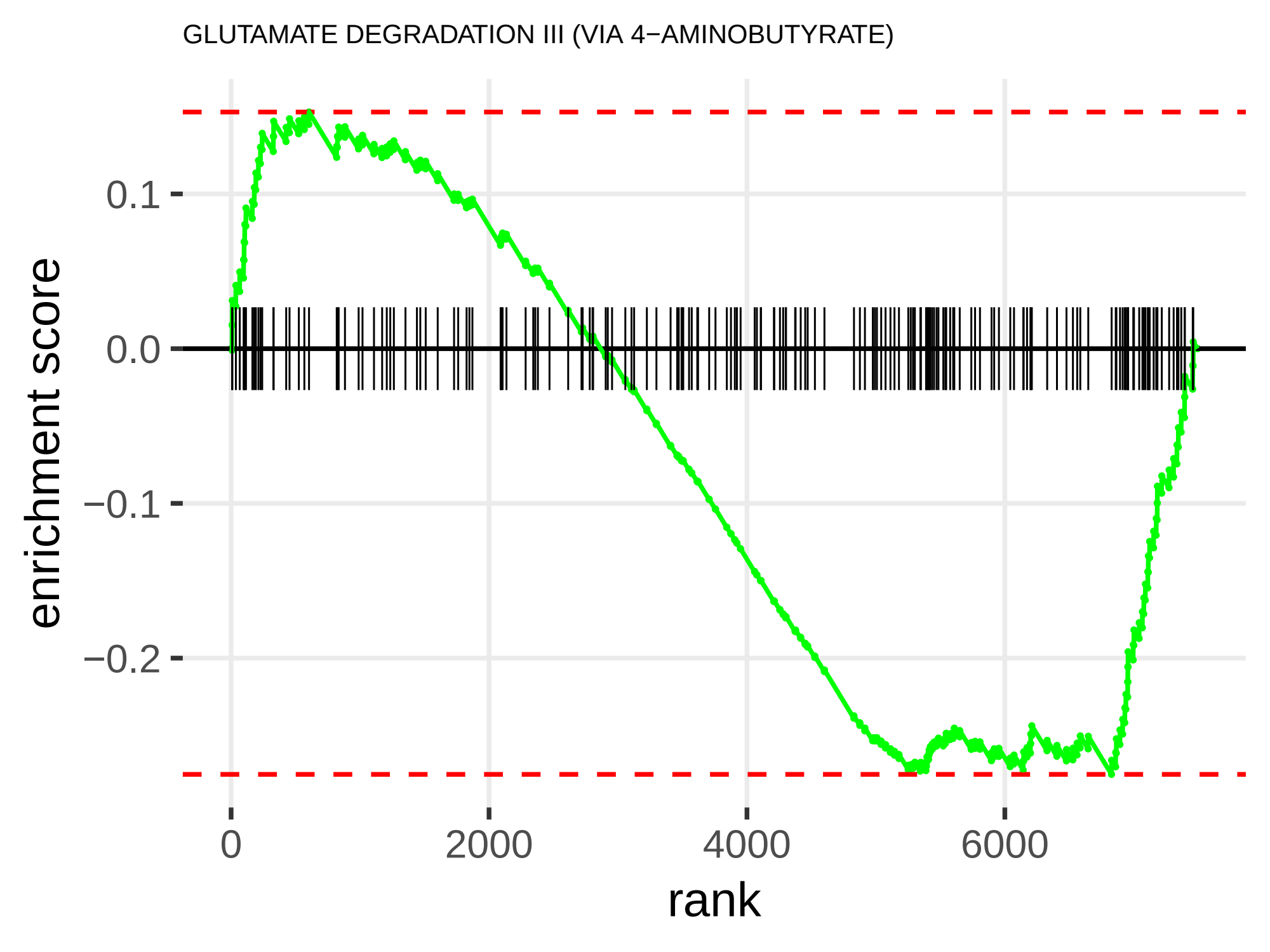

SELENOCYSTEINE BIOSYNTHESIS II (ARCHAEA AND EUKARYOTES)
0.1
0.0
−0.1
−0.2
enrichment score
0
2000
4000
6000
rank

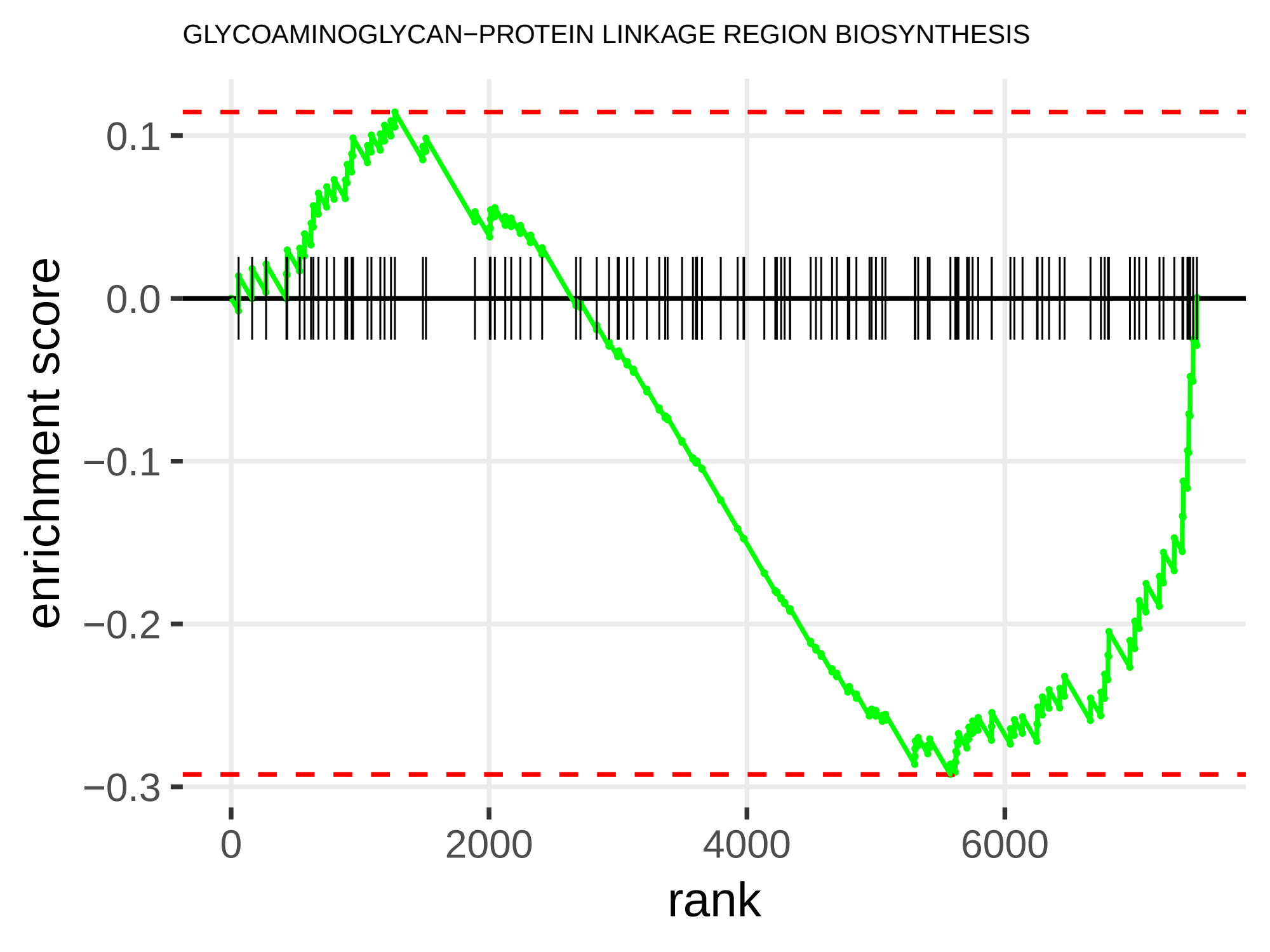

PYRUVATE FERMENTATION TO LACTATE
enrichment score
0.1
0.0
−0.1
−0.2
−0.3
0
2000
4000
6000
rank

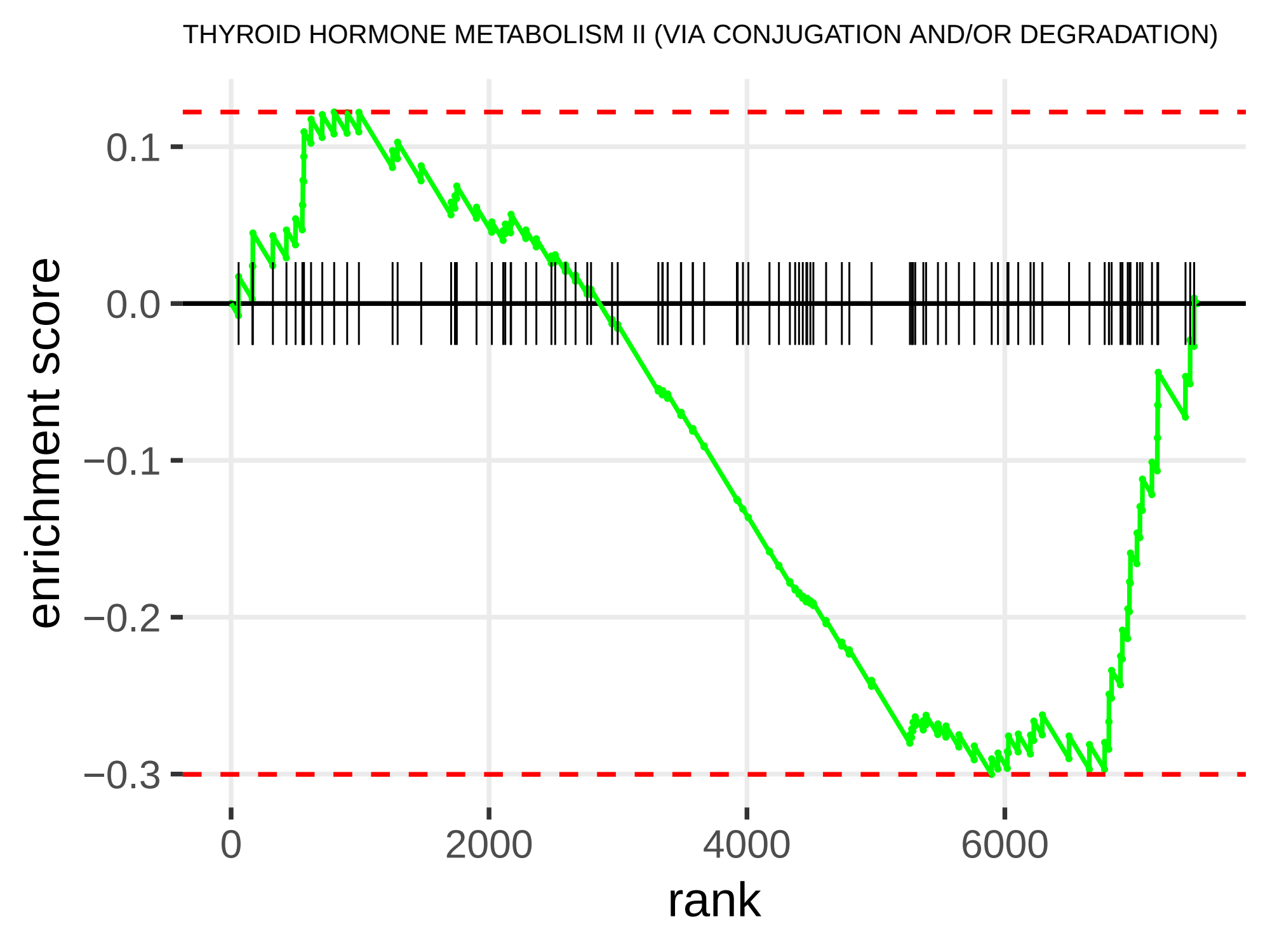

GLUTAMATE DEPENDENT ACID RESISTANCE
enrichment score
0.1
0.0
−0.1
−0.2
0
2000
4000
6000
rank

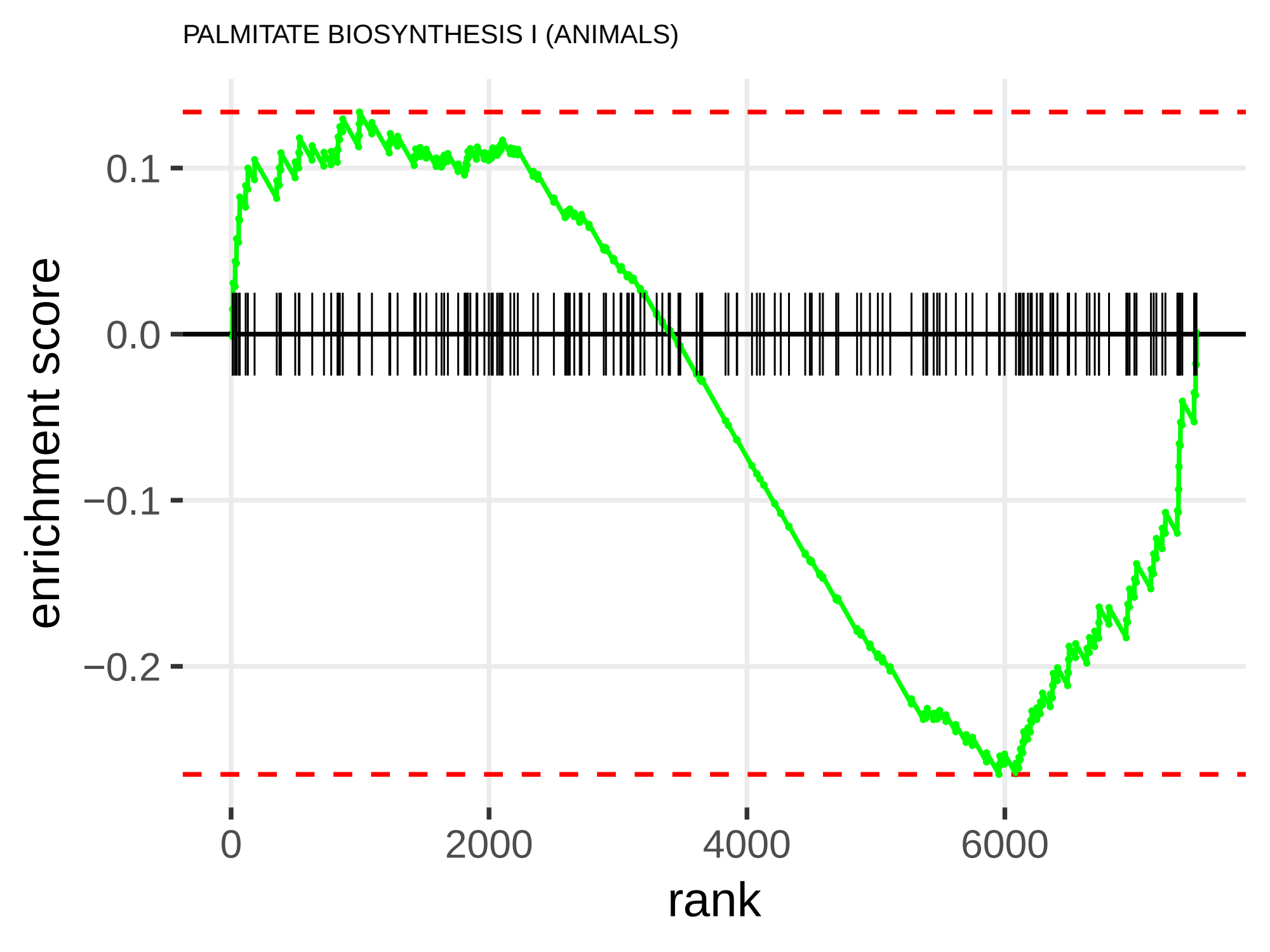

PHENYLALANINE DEGRADATION I (AEROBIC)
0.2
0.1
0.0
−0.1
−0.2
−0.3
enrichment score
0
2000
4000
6000
rank

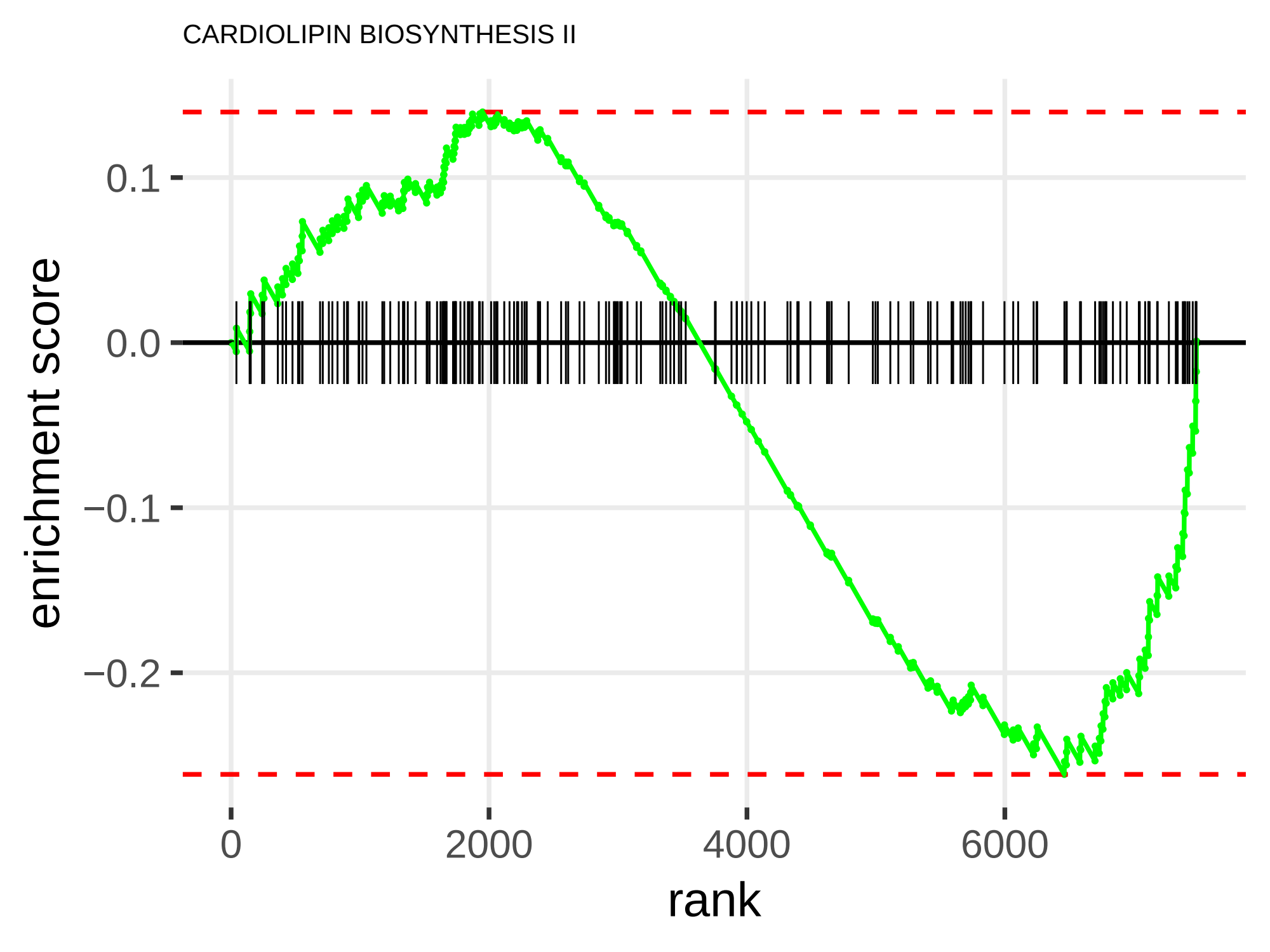

CALCIUM TRANSPORT I
enrichment score
0.1
0.0
−0.1
−0.2
−0.3
0
2000
4000
6000
rank

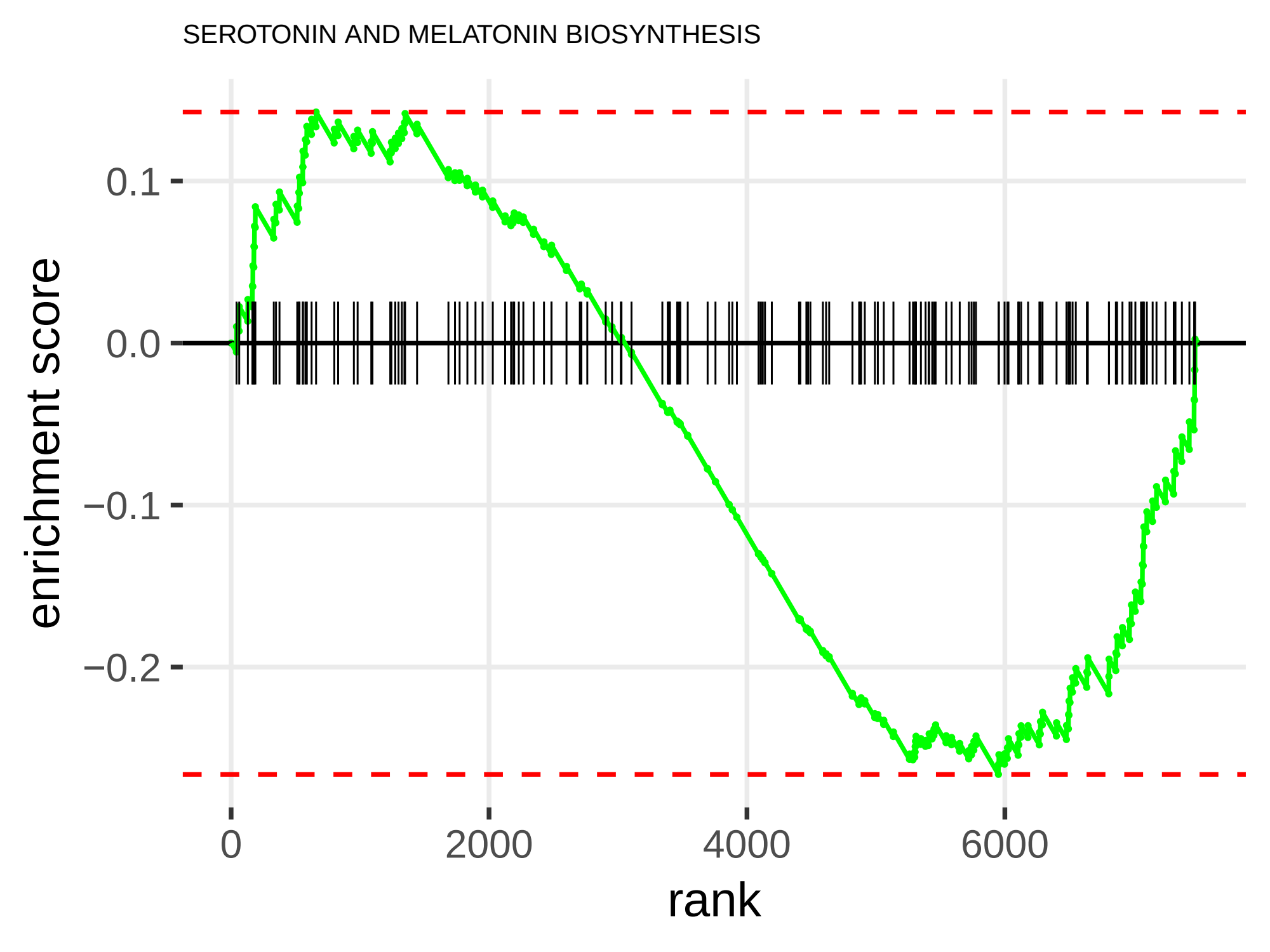

GLUTAMATE DEGRADATION III (VIA 4−AMINOBUTYRATE)
enrichment score
0.1
0.0
−0.1
−0.2
0
2000
4000
6000
rank

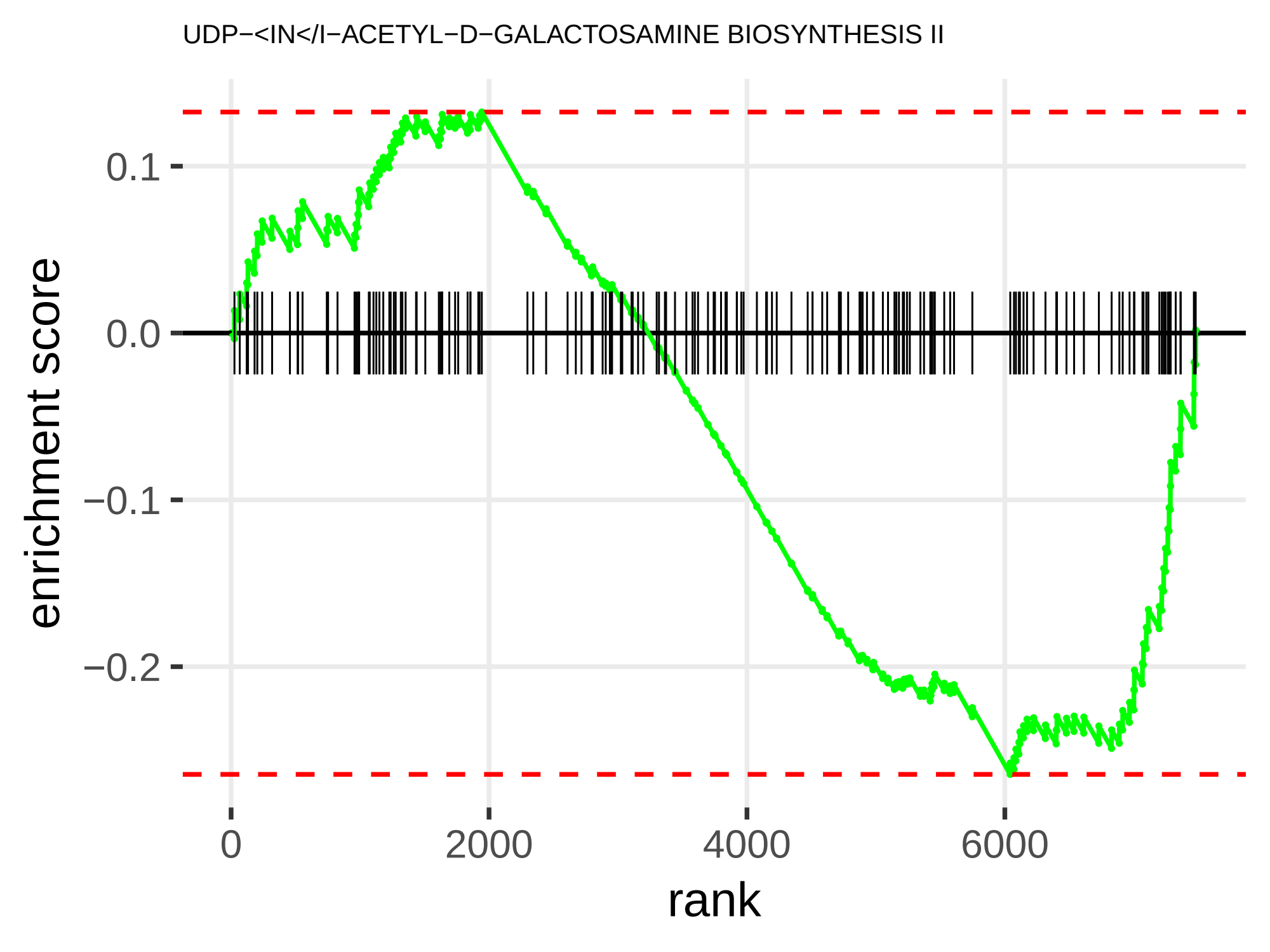

GLYCOAMINOGLYCAN−PROTEIN LINKAGE REGION BIOSYNTHESIS
enrichment score
0.1
0.0
−0.1
−0.2
−0.3
0
2000
4000
6000
rank

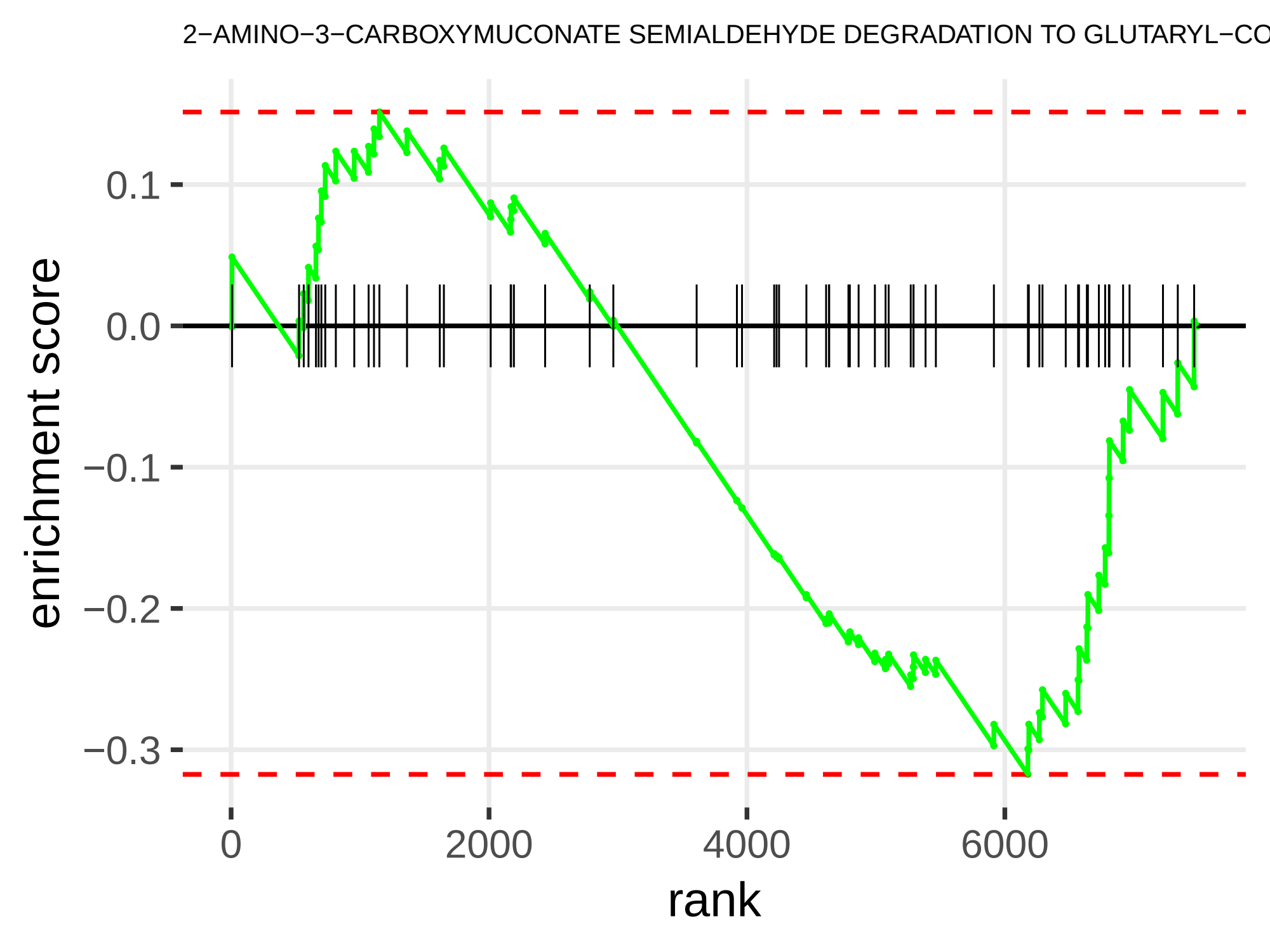

THYROID HORMONE METABOLISM II (VIA CONJUGATION AND/OR DEGRADATION)
enrichment score
0.1
0.0
−0.1
−0.2
−0.3
0
2000
4000
6000
rank

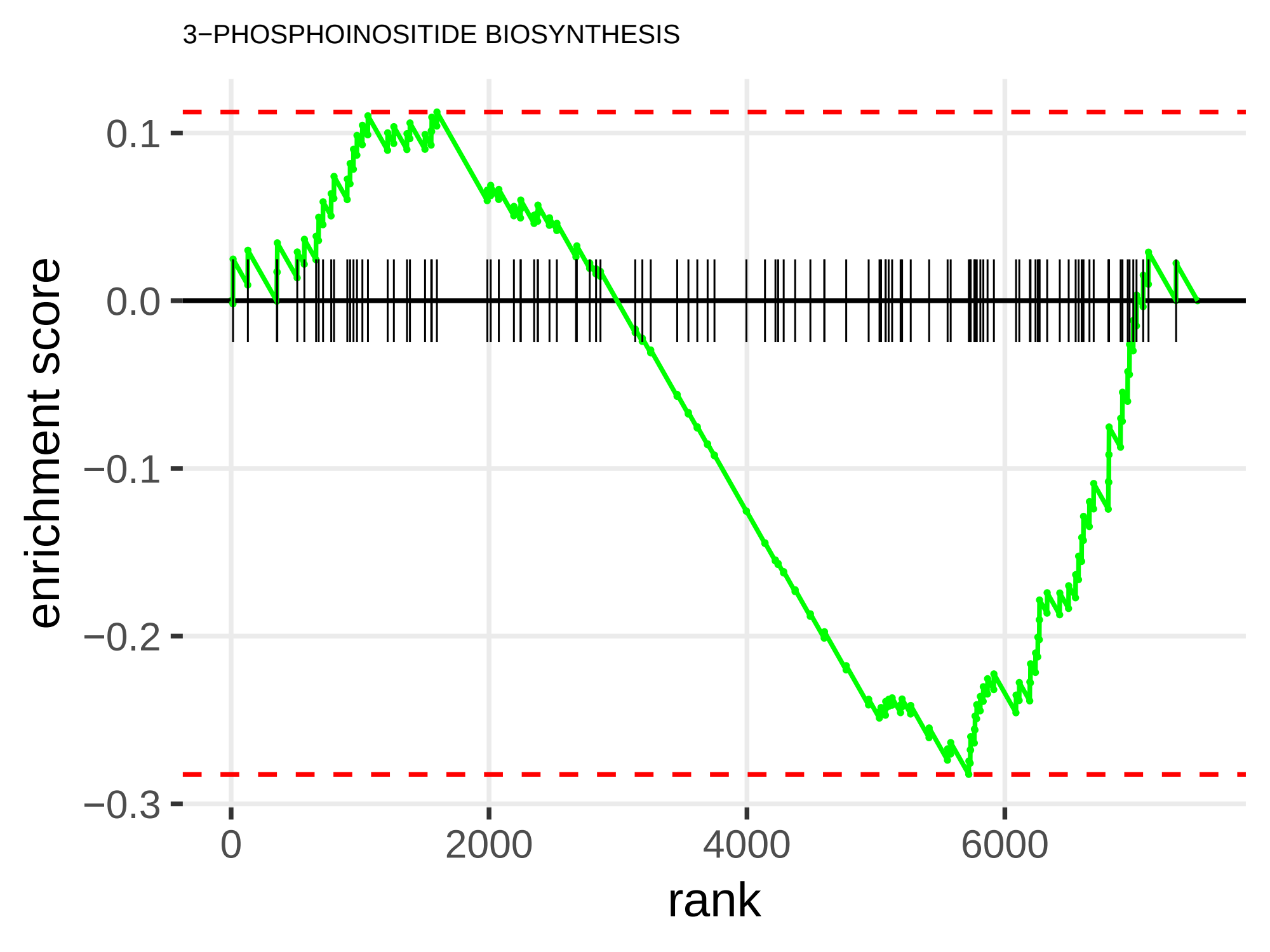

PALMITATE BIOSYNTHESIS I (ANIMALS)
enrichment score
0.1
0.0
−0.1
−0.2
0
2000
4000
6000
rank

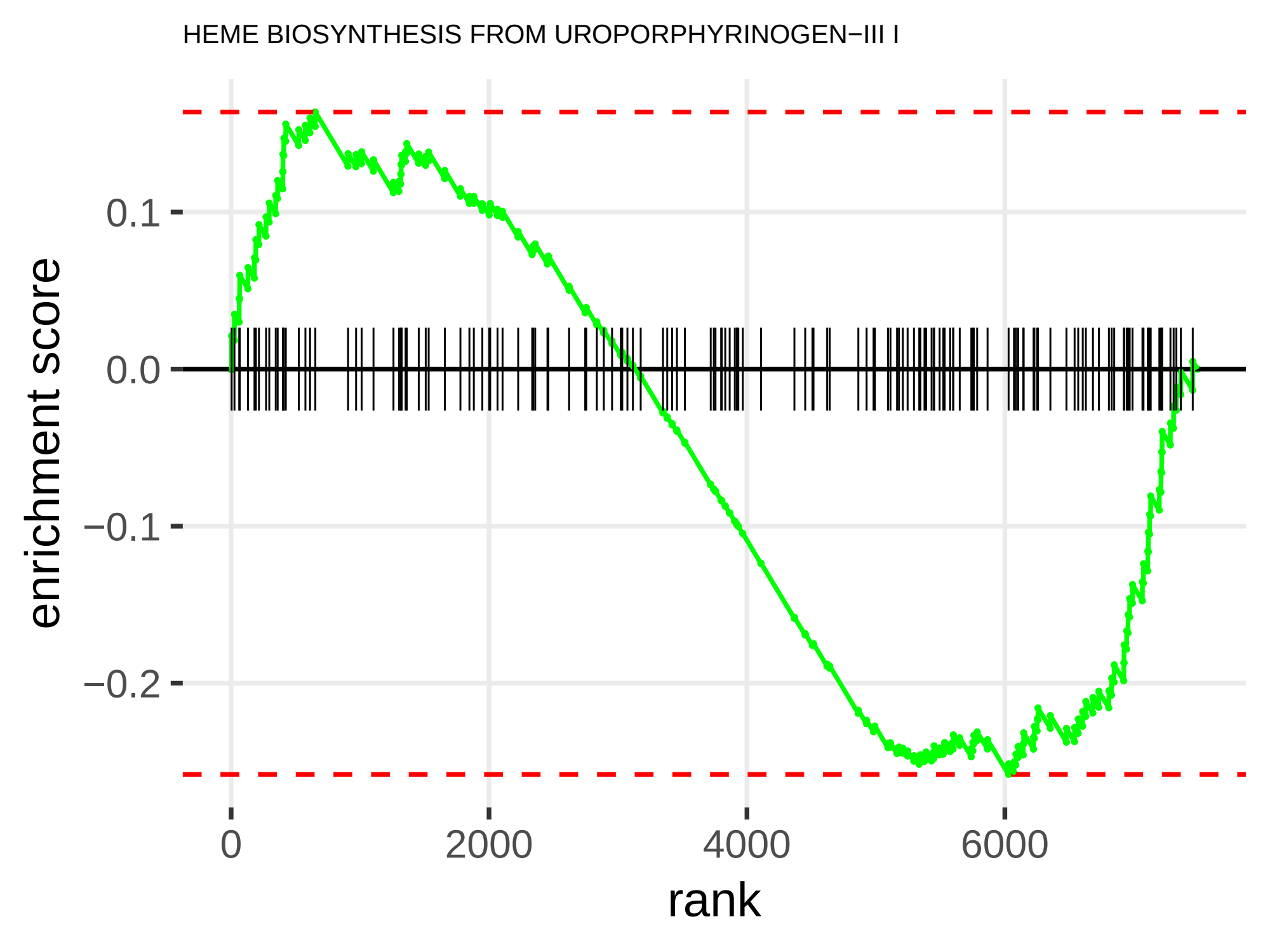

CARDIOLIPIN BIOSYNTHESIS II
enrichment score
0.1
0.0
−0.1
−0.2
0
2000
4000
6000
rank

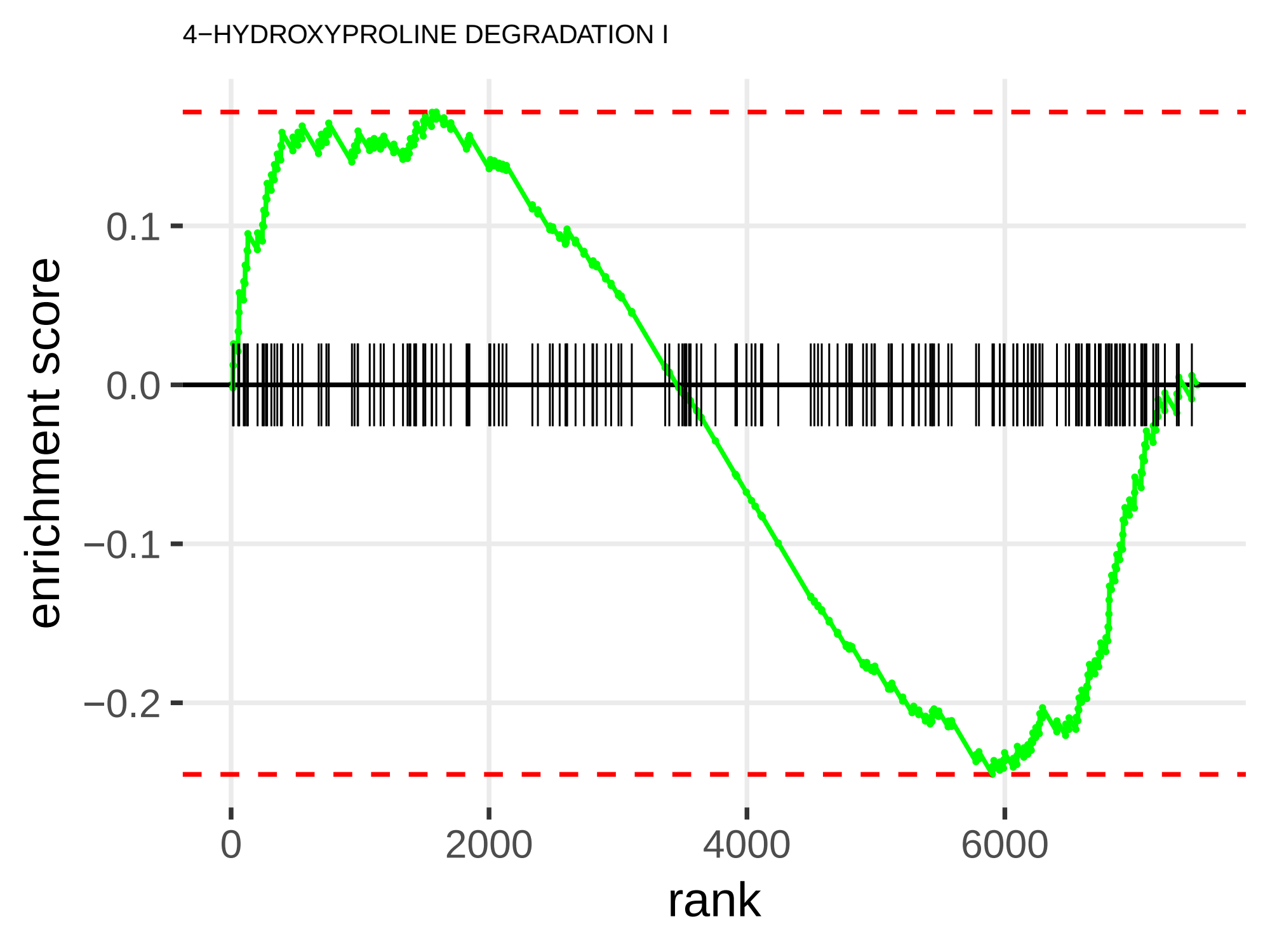

SEROTONIN AND MELATONIN BIOSYNTHESIS
enrichment score
0.1
0.0
−0.1
−0.2
0
2000
4000
6000
rank

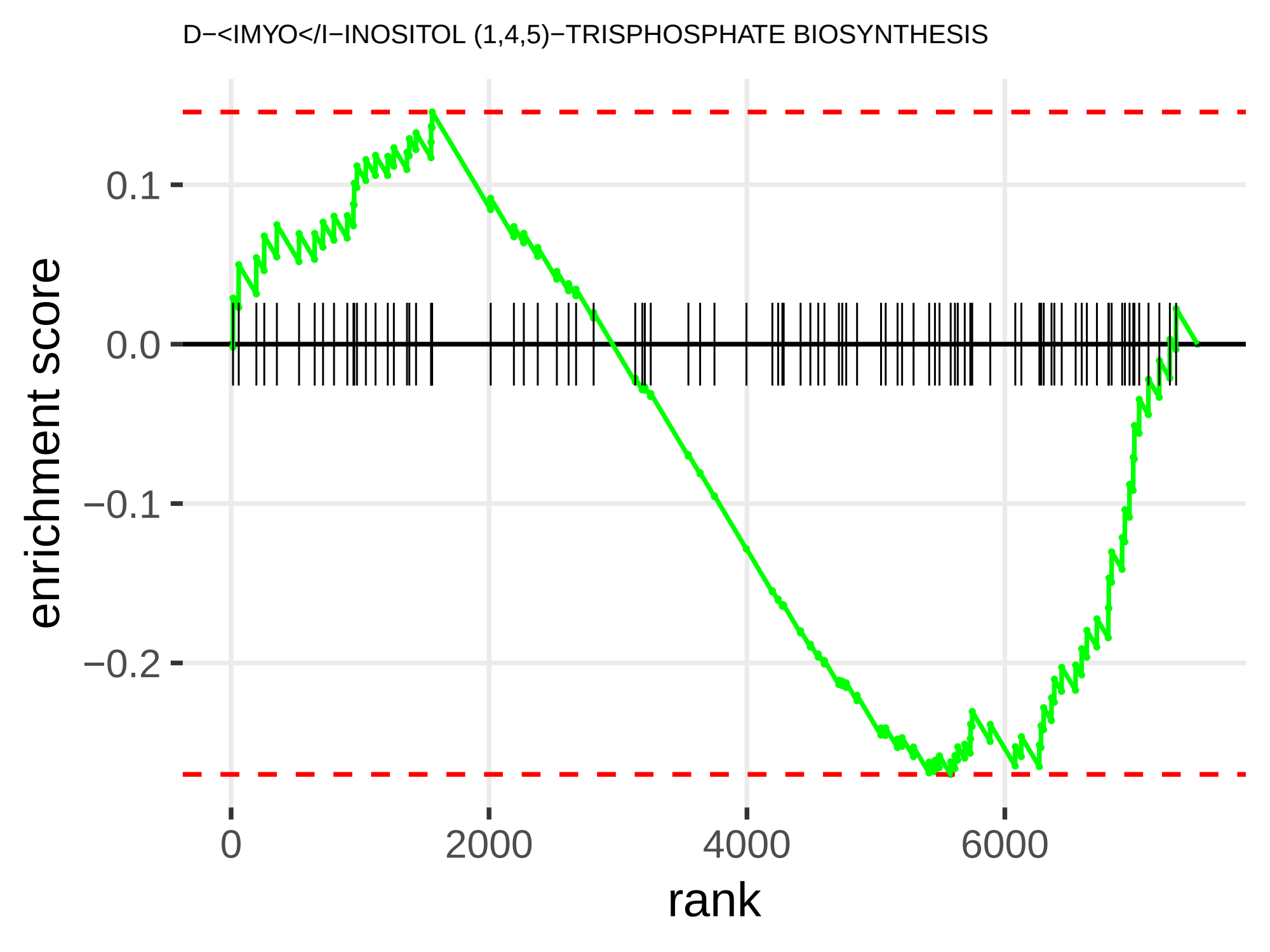

UDP−<IN</I−ACETYL−D−GALACTOSAMINE BIOSYNTHESIS II
enrichment score
0.1
0.0
−0.1
−0.2
0
2000
4000
6000
rank

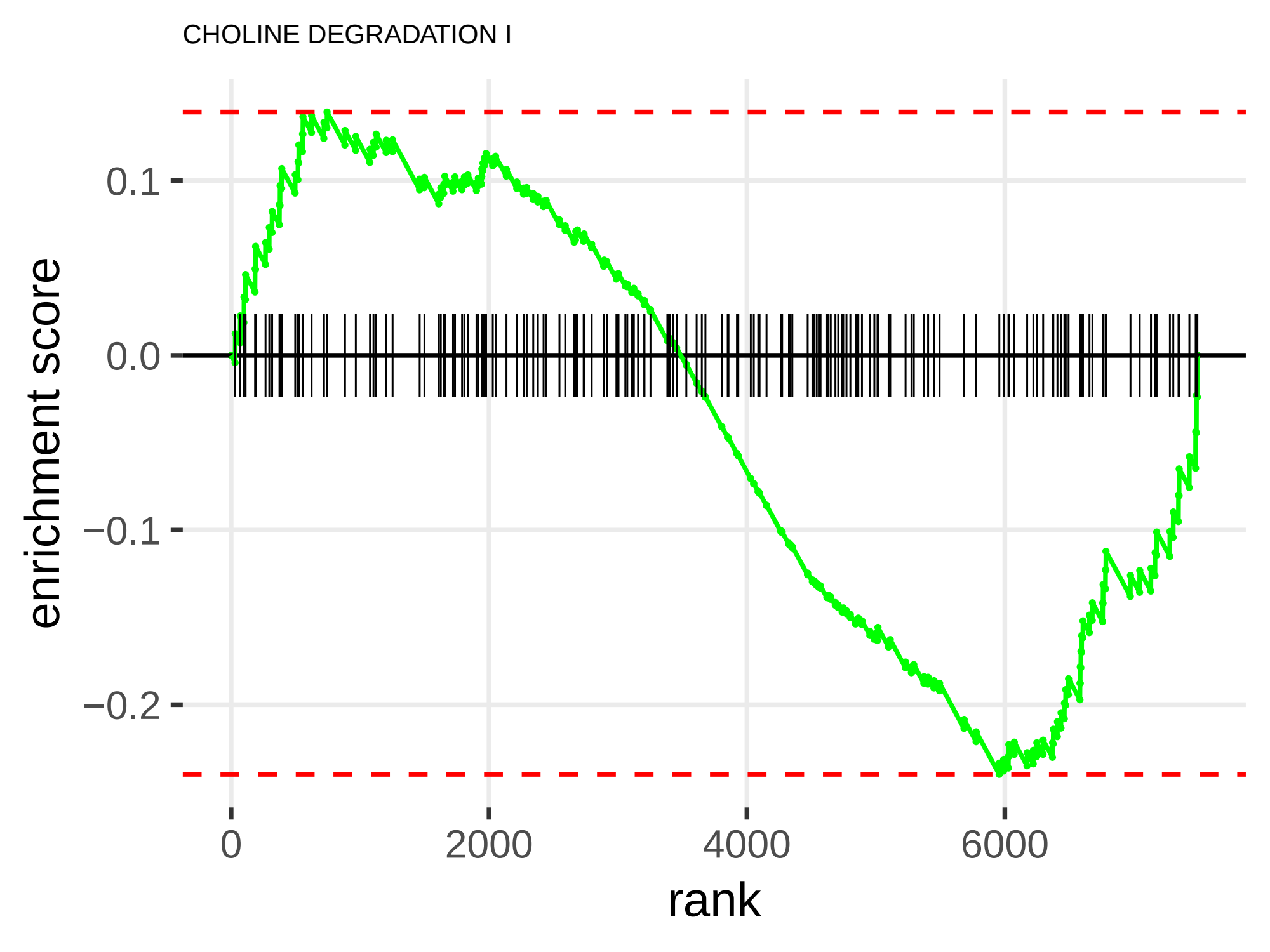

2−AMINO−3−CARBOXYMUCONATE SEMIALDEHYDE DEGRADATION TO GLUTARYL−CO
enrichment score
0.1
0.0
−0.1
−0.2
−0.3
0
2000
4000
6000
rank

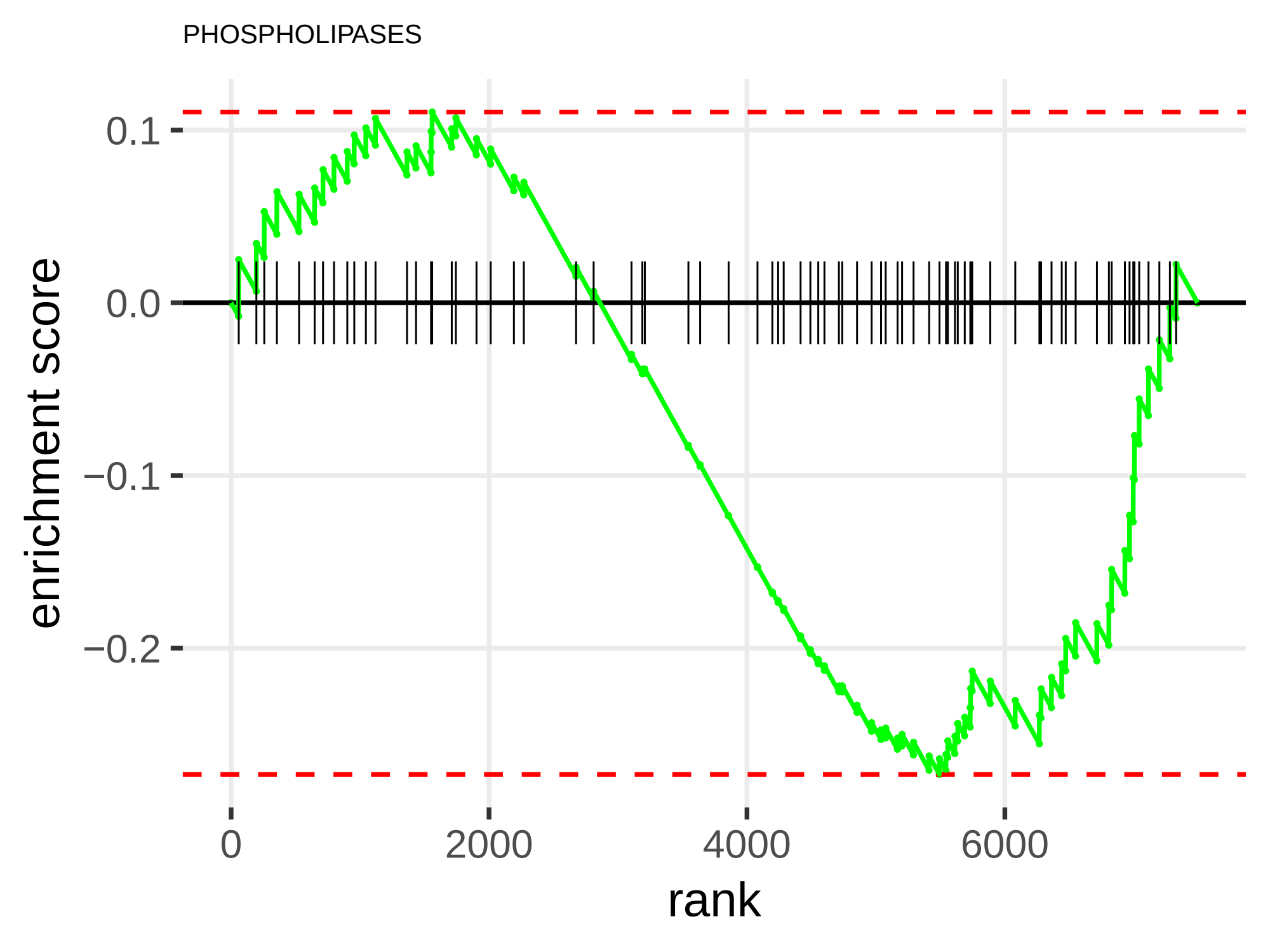

3−PHOSPHOINOSITIDE BIOSYNTHESIS
enrichment score
0.1
0.0
−0.1
−0.2
−0.3
0
2000
4000
6000
rank

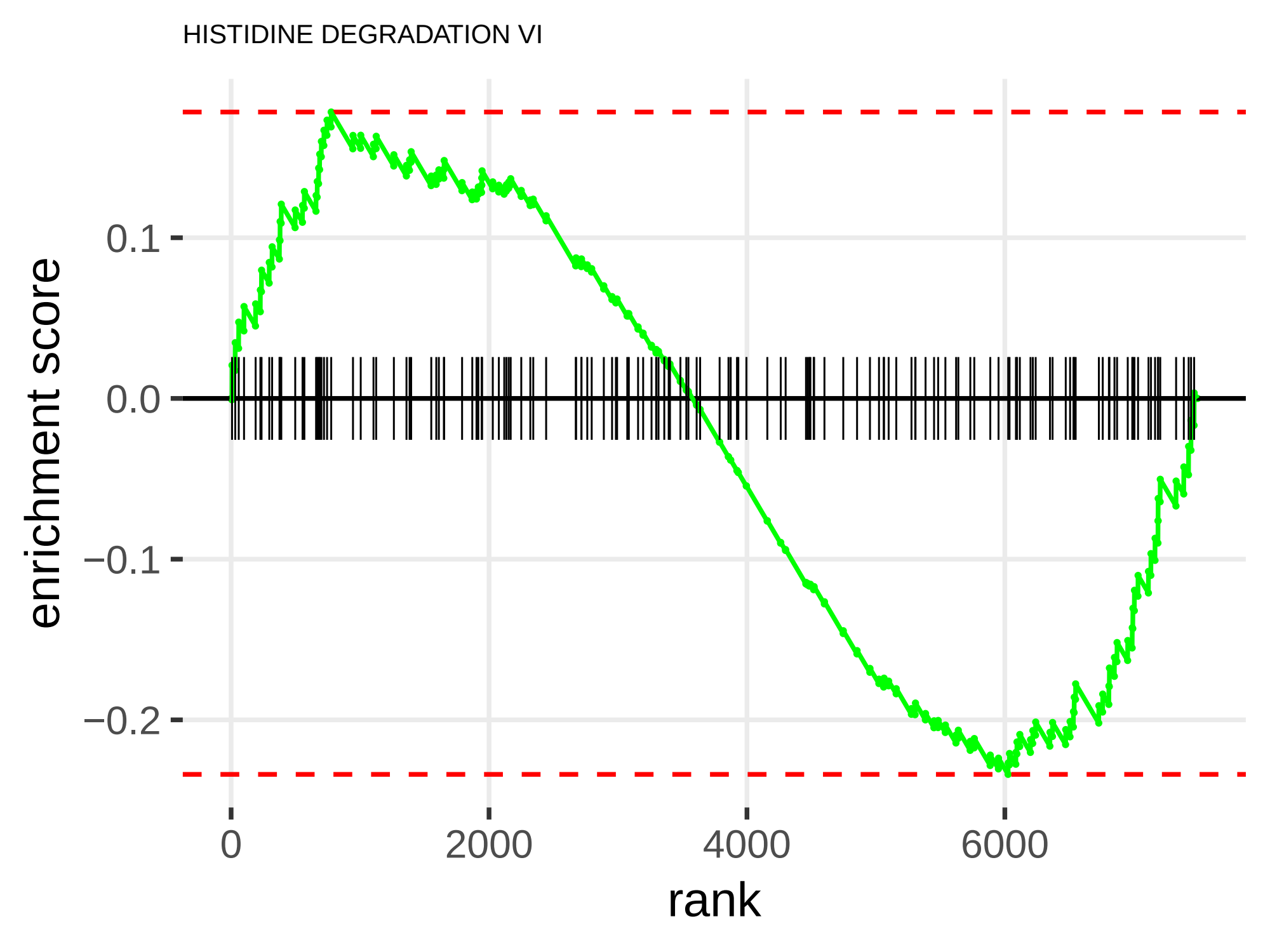

HEME BIOSYNTHESIS FROM UROPORPHYRINOGEN−III I
enrichment score
0.1
0.0
−0.1
−0.2
0
2000
4000
6000
rank

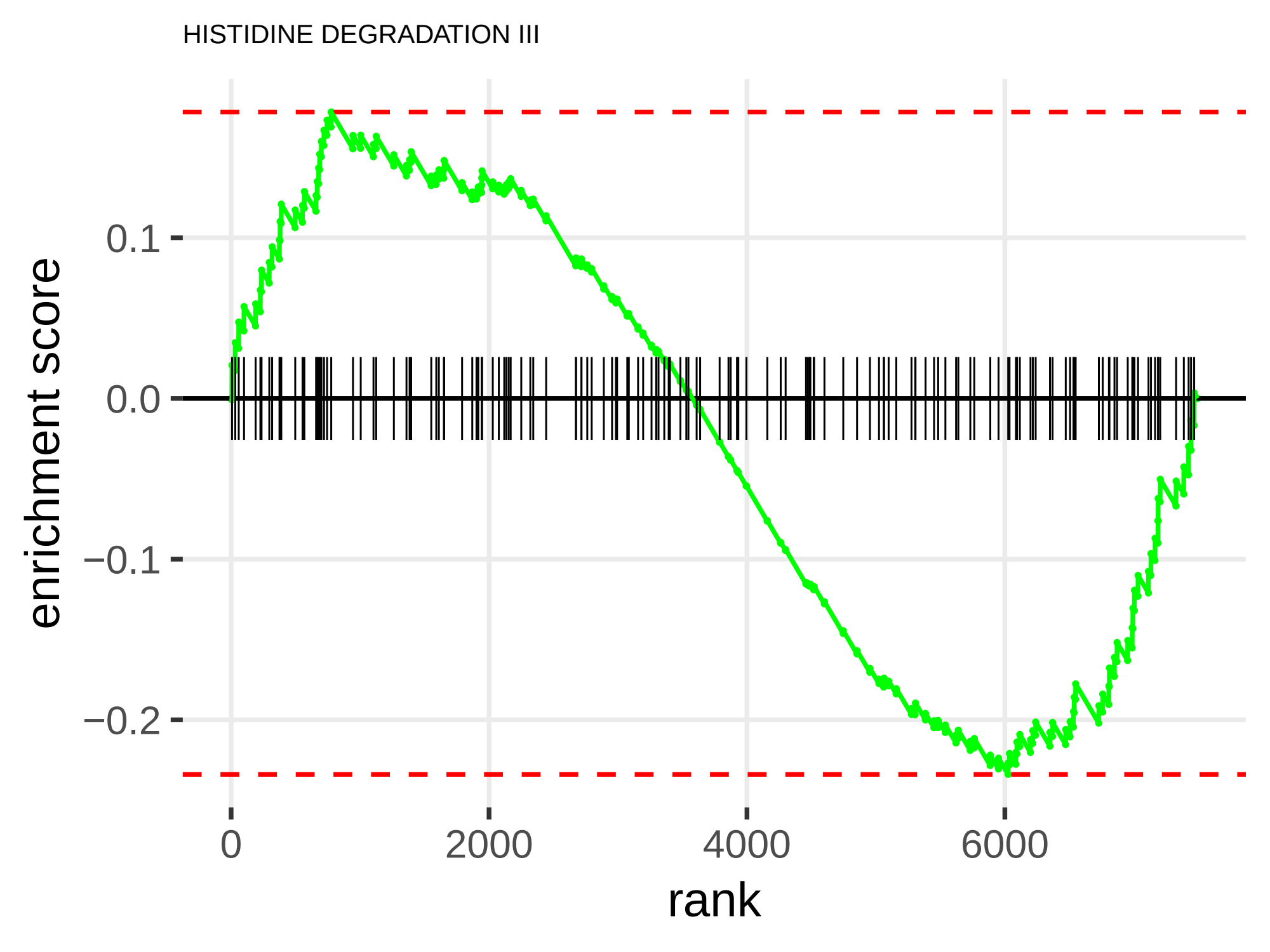

4−HYDROXYPROLINE DEGRADATION I
enrichment score
0.1
0.0
−0.1
−0.2
0
2000
4000
6000
rank

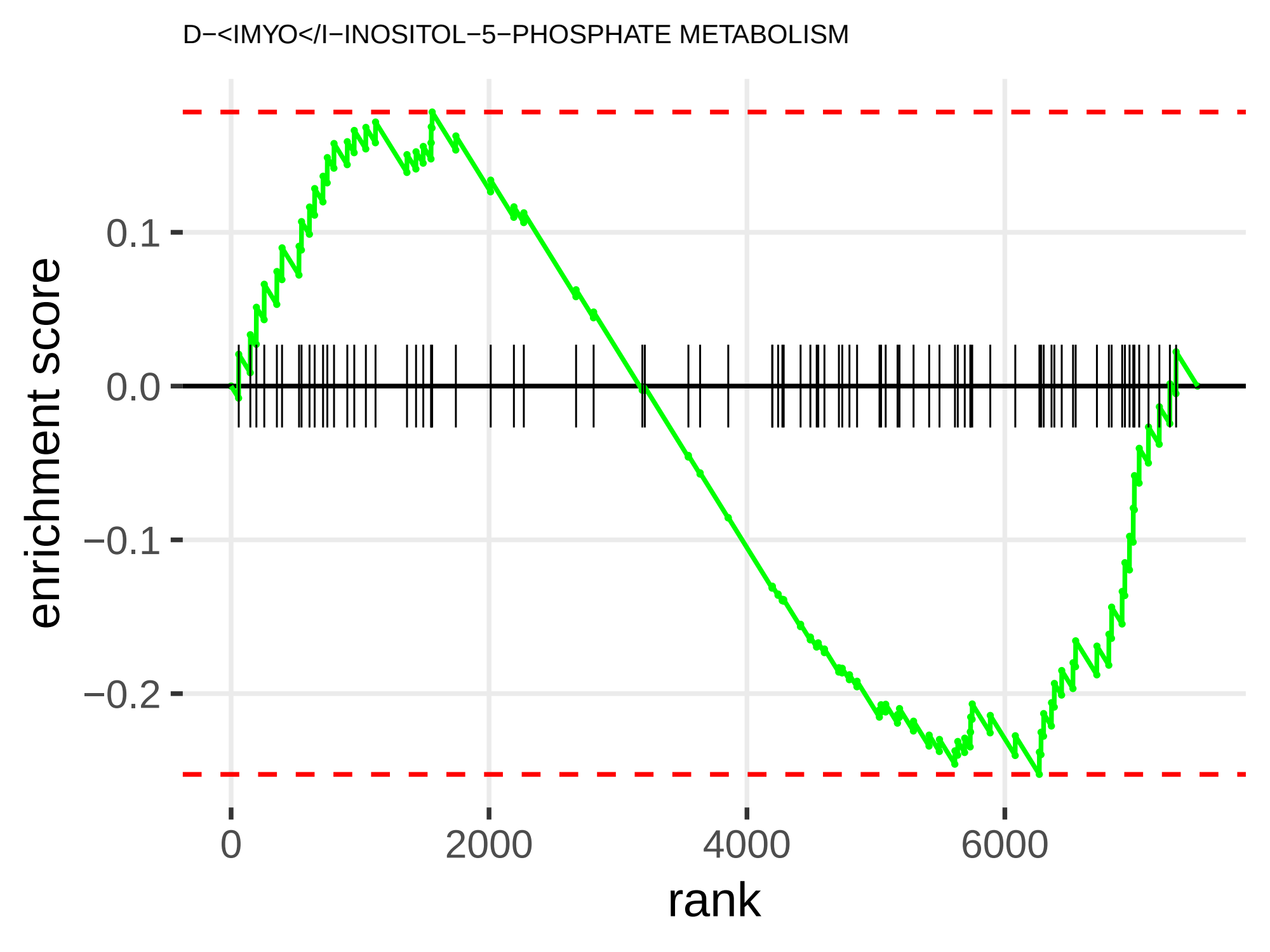

D−<IMYO</I−INOSITOL (1,4,5)−TRISPHOSPHATE BIOSYNTHESIS
enrichment score
0.1
0.0
−0.1
−0.2
0
2000
4000
6000
rank

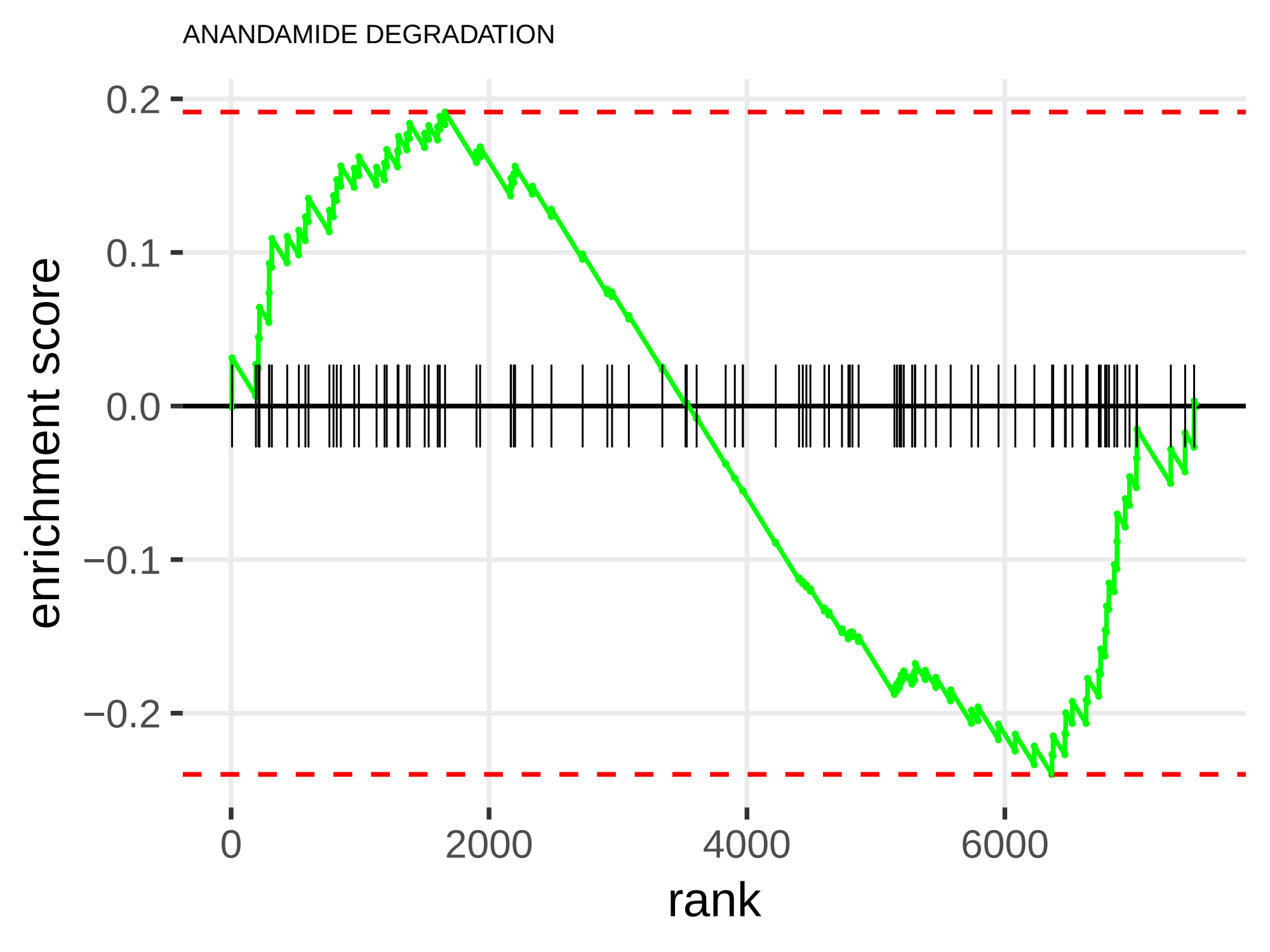

CHOLINE DEGRADATION I
enrichment score
0.1
0.0
−0.1
−0.2
0
2000
4000
6000
rank

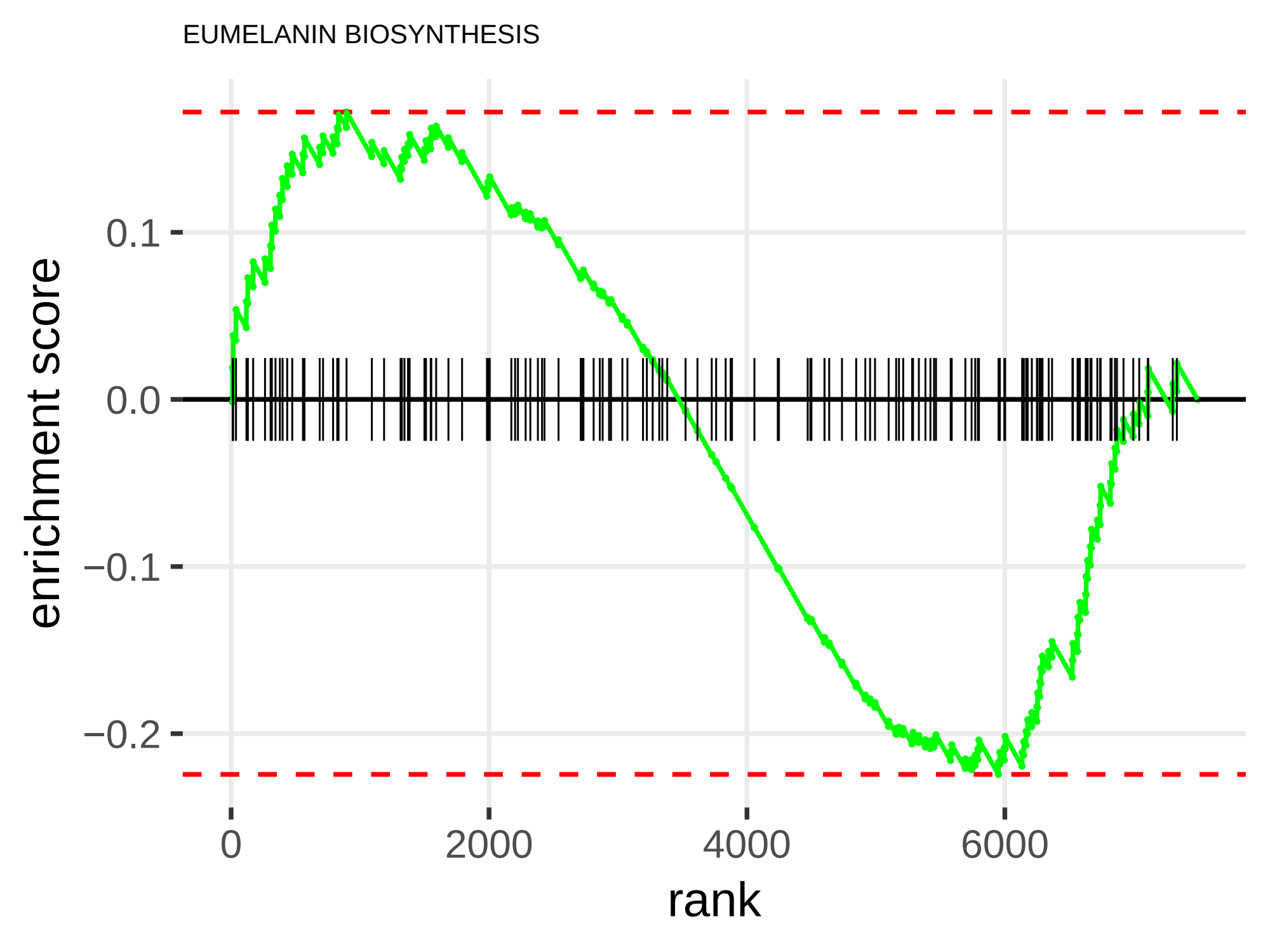

PHOSPHOLIPASES
0.1
0.0
−0.1
−0.2
enrichment score
0
2000
4000
6000
rank

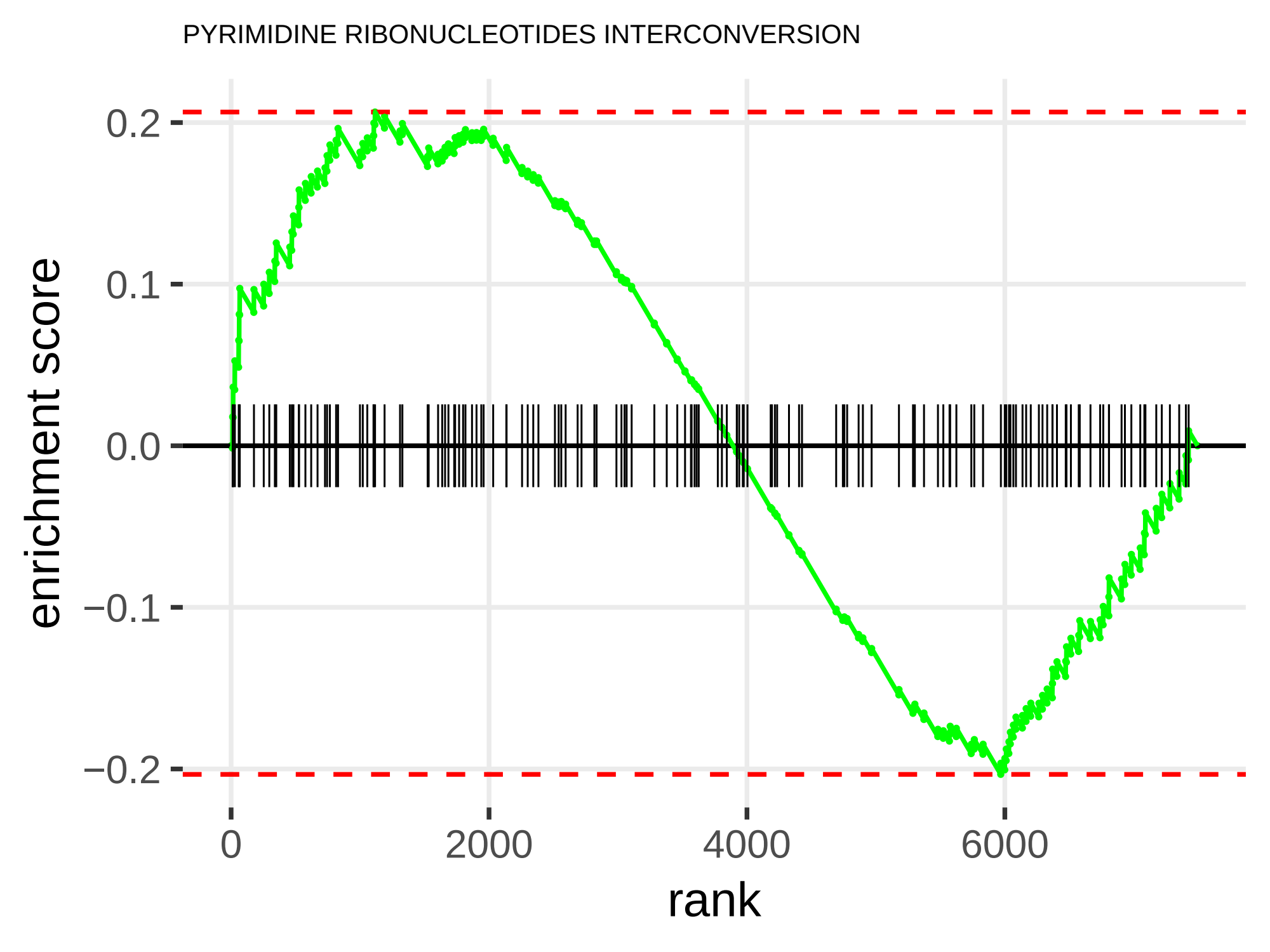

HISTIDINE DEGRADATION VI
enrichment score
0.1
0.0
−0.1
−0.2
0
2000
4000
6000
rank

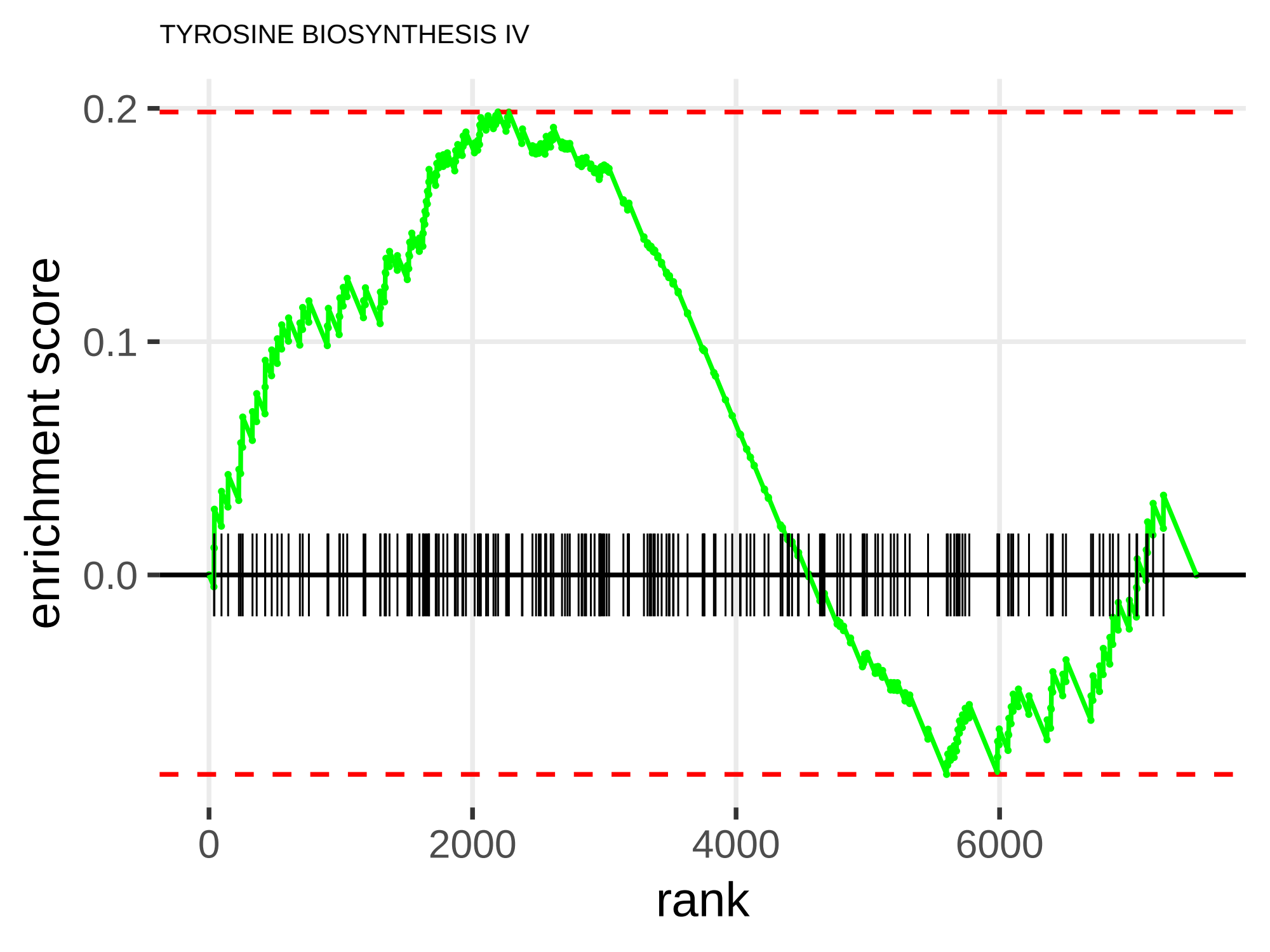

HISTIDINE DEGRADATION III
enrichment score
0.1
0.0
−0.1
−0.2
0
2000
4000
6000
rank

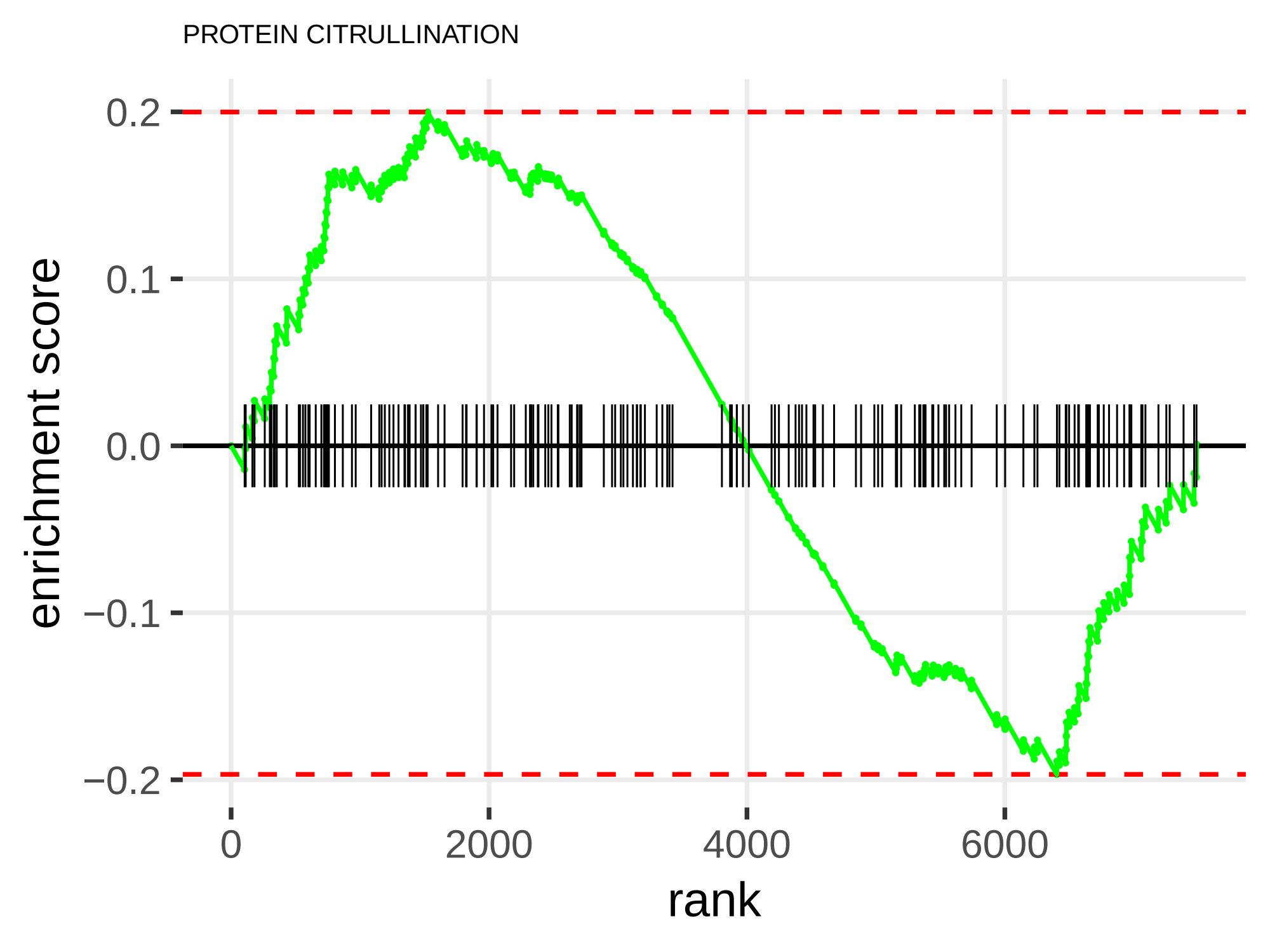

D−<IMYO</I−INOSITOL−5−PHOSPHATE METABOLISM
enrichment score
0.1
0.0
−0.1
−0.2
0
2000
4000
6000
rank

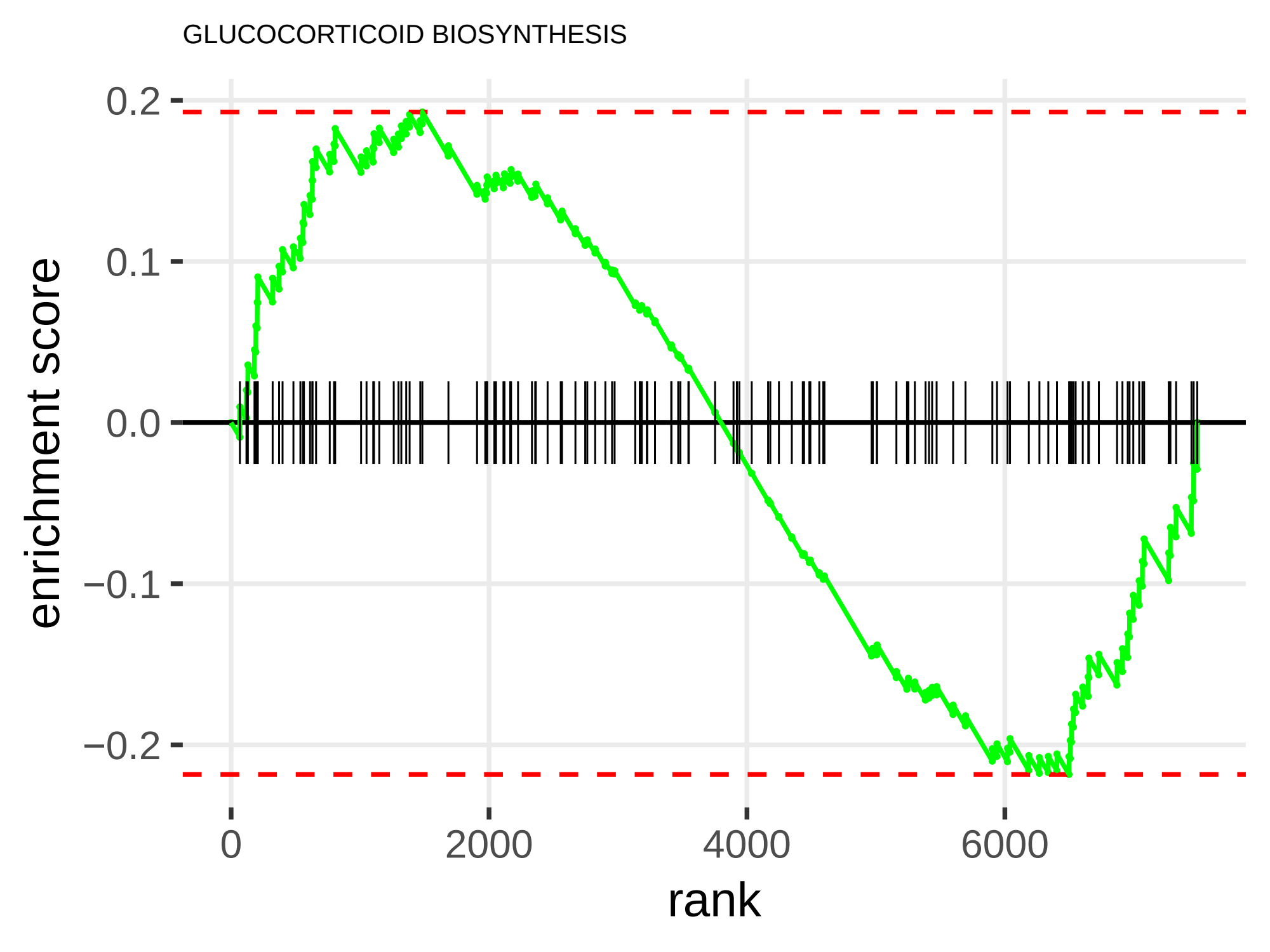

ANANDAMIDE DEGRADATION
0.2
0.1
0.0
−0.1
−0.2
enrichment score
0
2000
4000
6000
rank

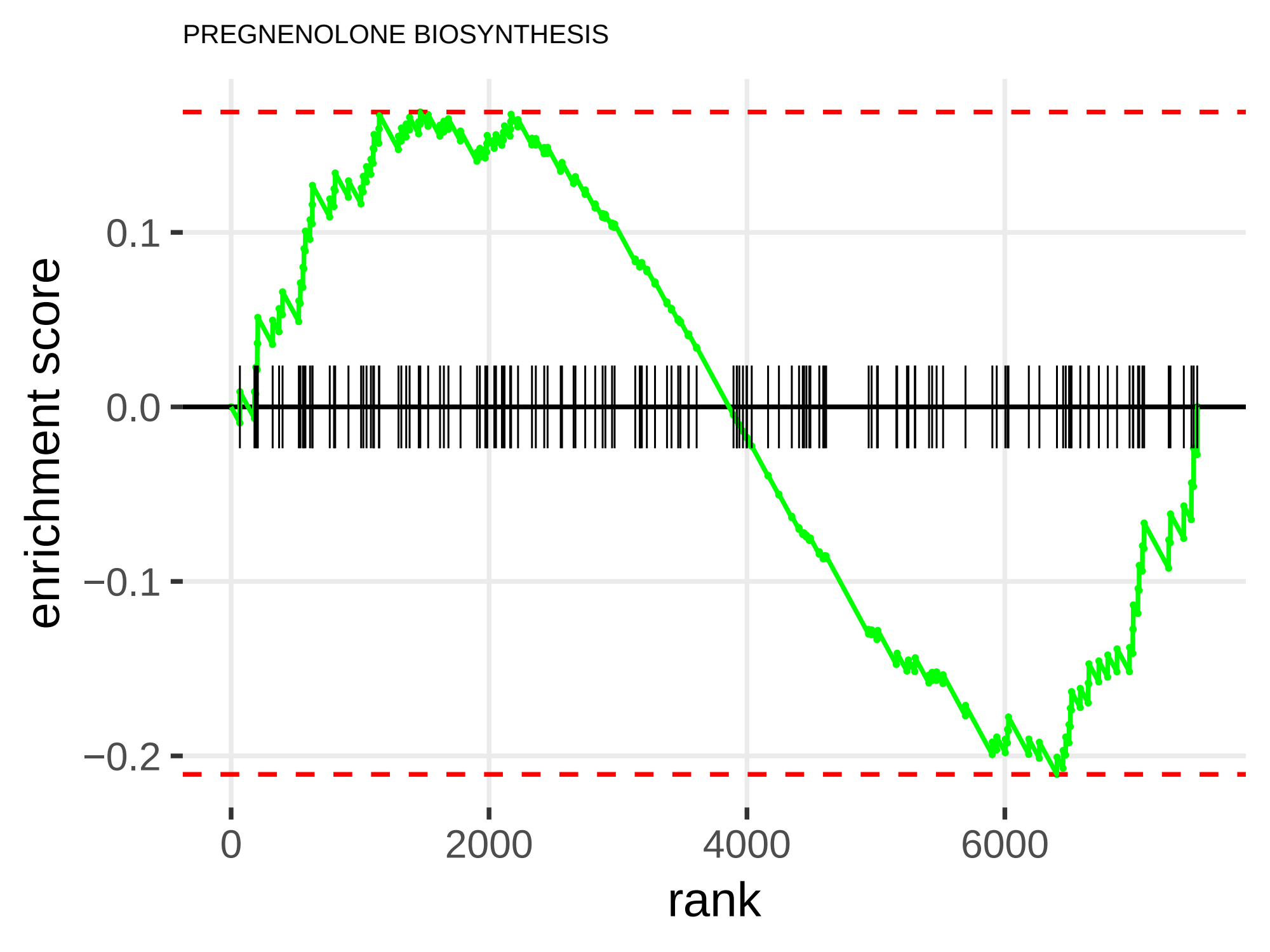

EUMELANIN BIOSYNTHESIS
enrichment score
0.1
0.0
−0.1
−0.2
0
2000
4000
6000
rank

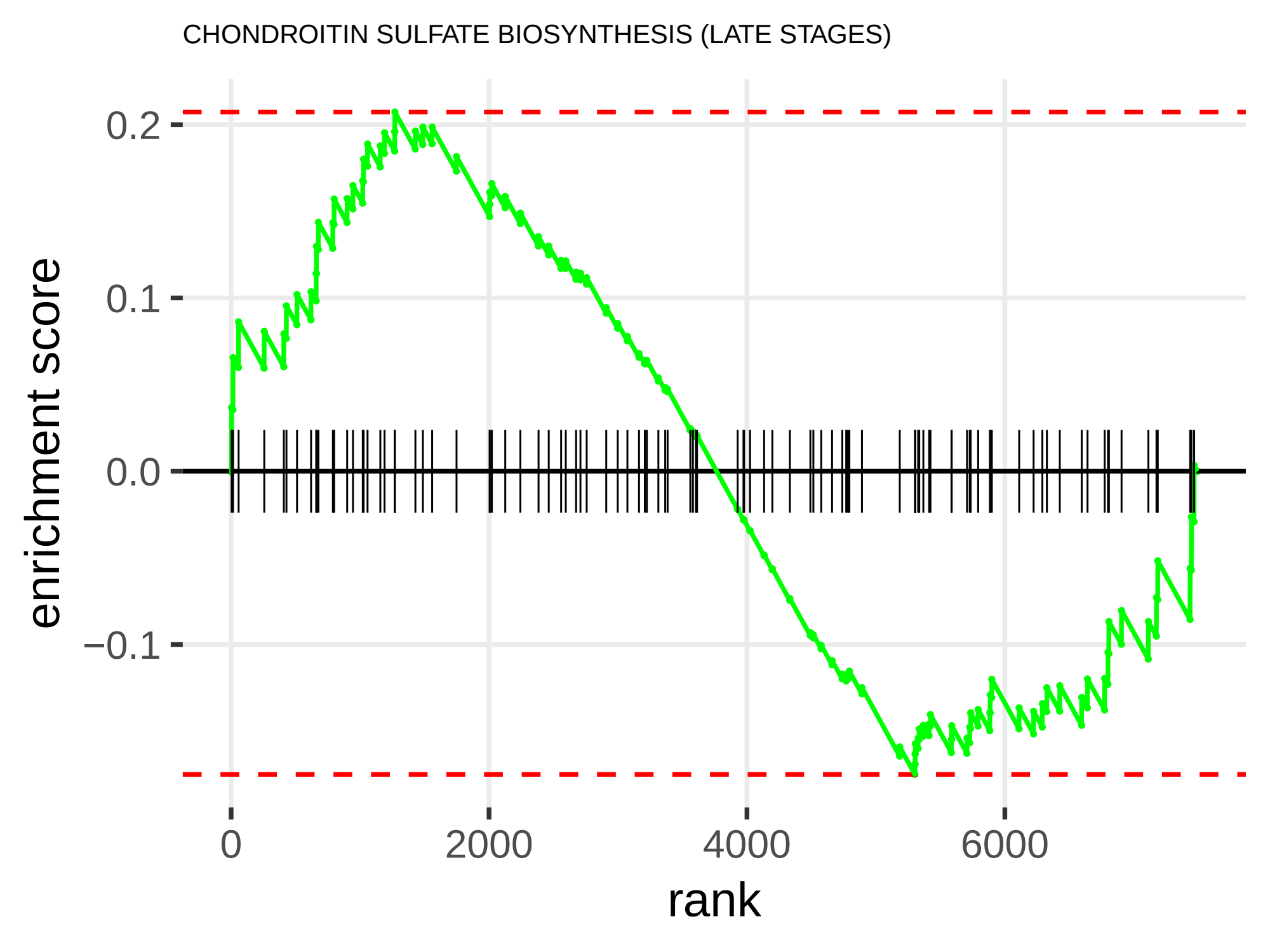

PYRIMIDINE RIBONUCLEOTIDES INTERCONVERSION
enrichment score
0.2
0.1
0.0
−0.1
−0.2
0
2000
4000
6000
rank

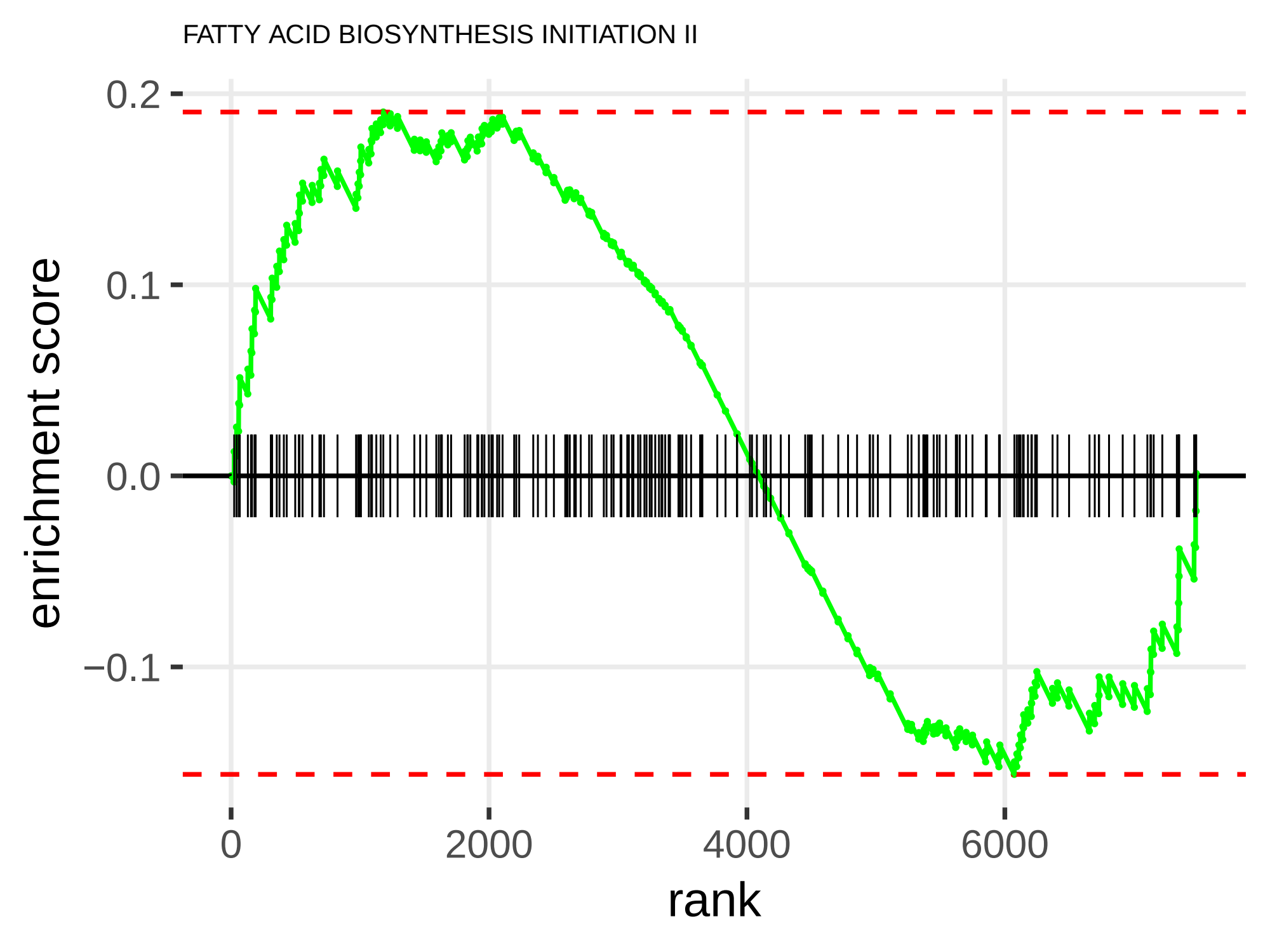

TYROSINE BIOSYNTHESIS IV
0.2
0.1
0.0
enrichment score
0
2000
4000
6000
rank

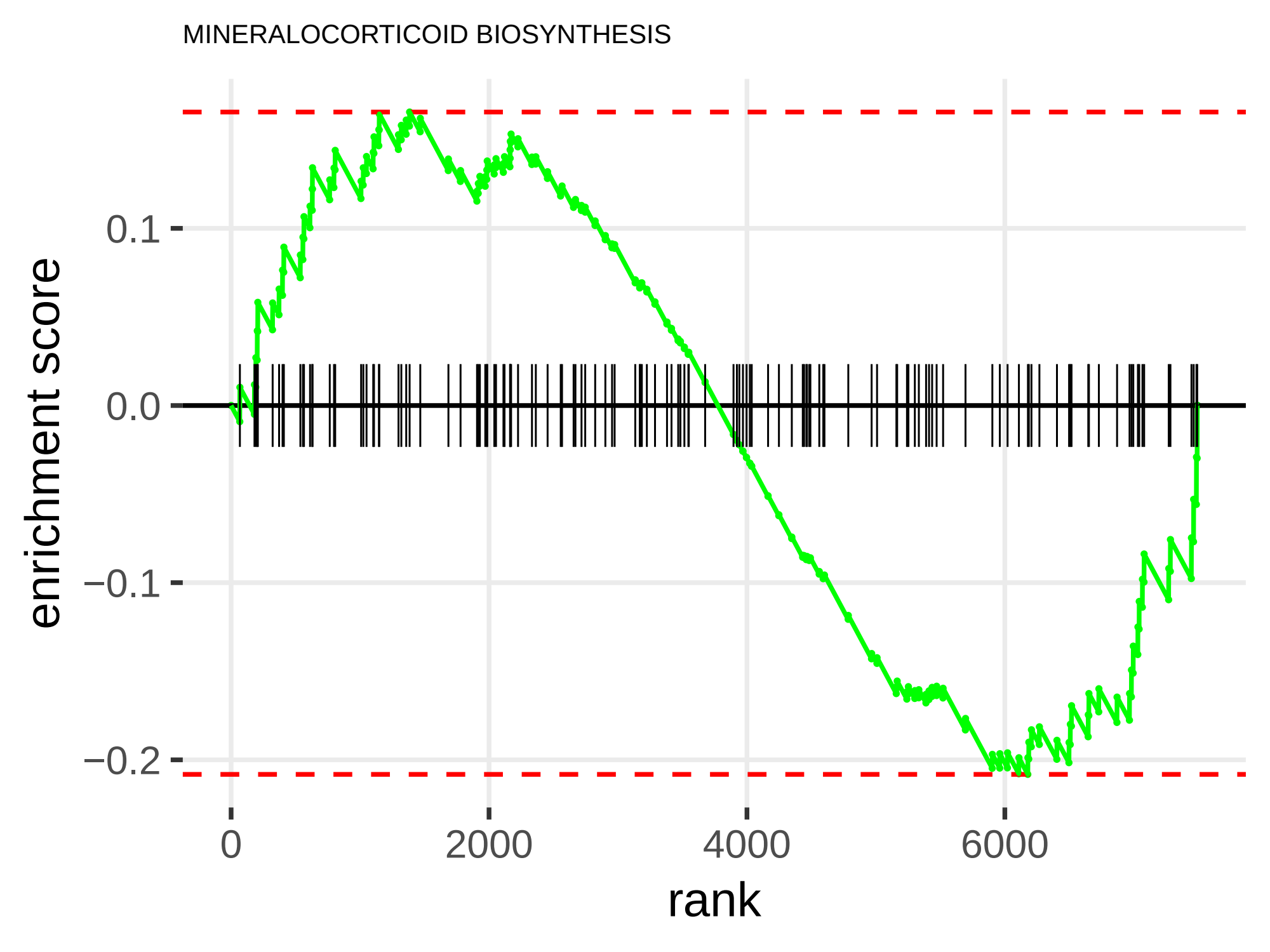

PROTEIN CITRULLINATION
0.2
0.1
0.0
−0.1
−0.2
enrichment score
0
2000
4000
6000
rank

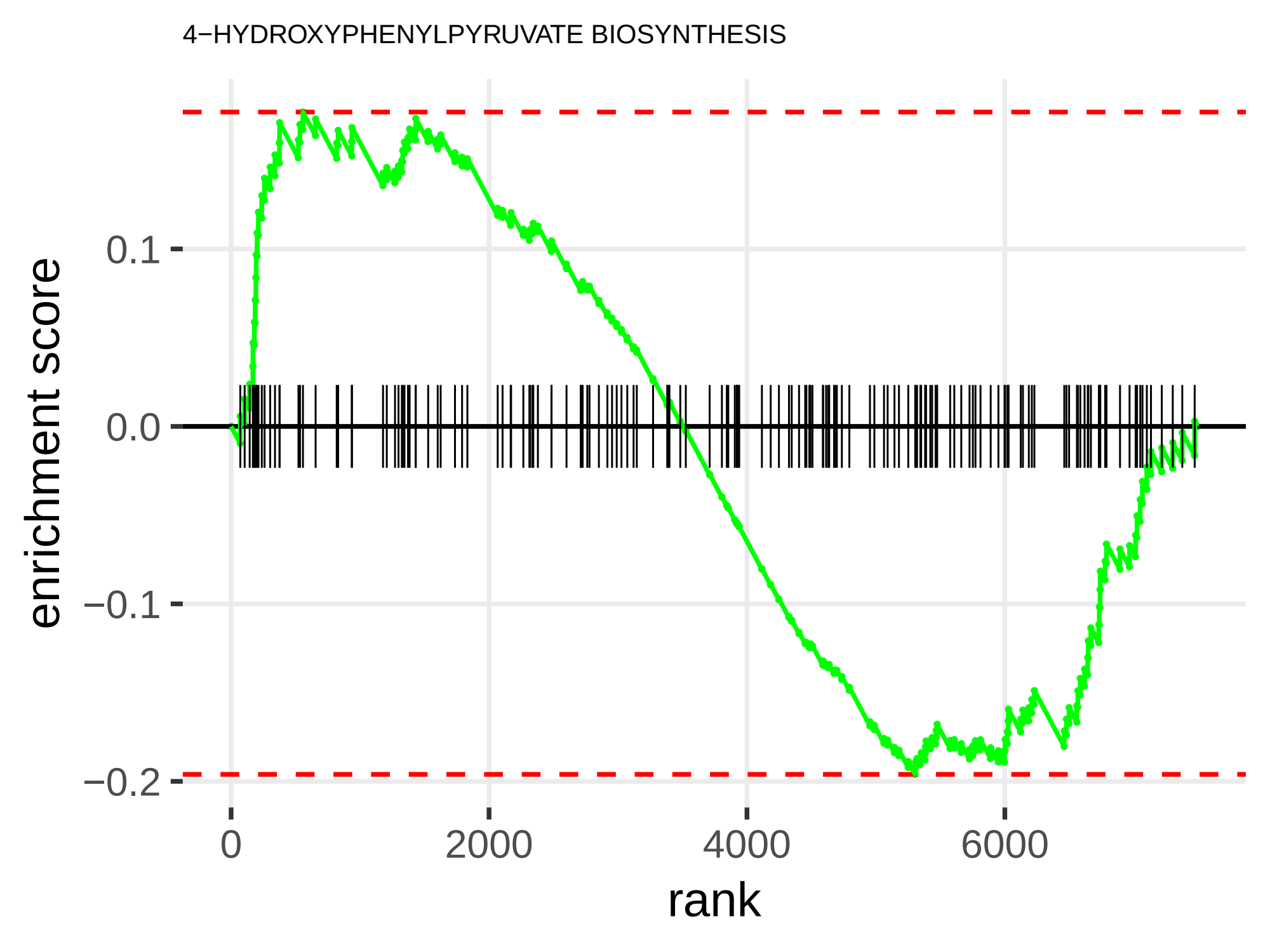

GLUCOCORTICOID BIOSYNTHESIS
0.2
0.1
0.0
−0.1
−0.2
enrichment score
0
2000
4000
6000
rank

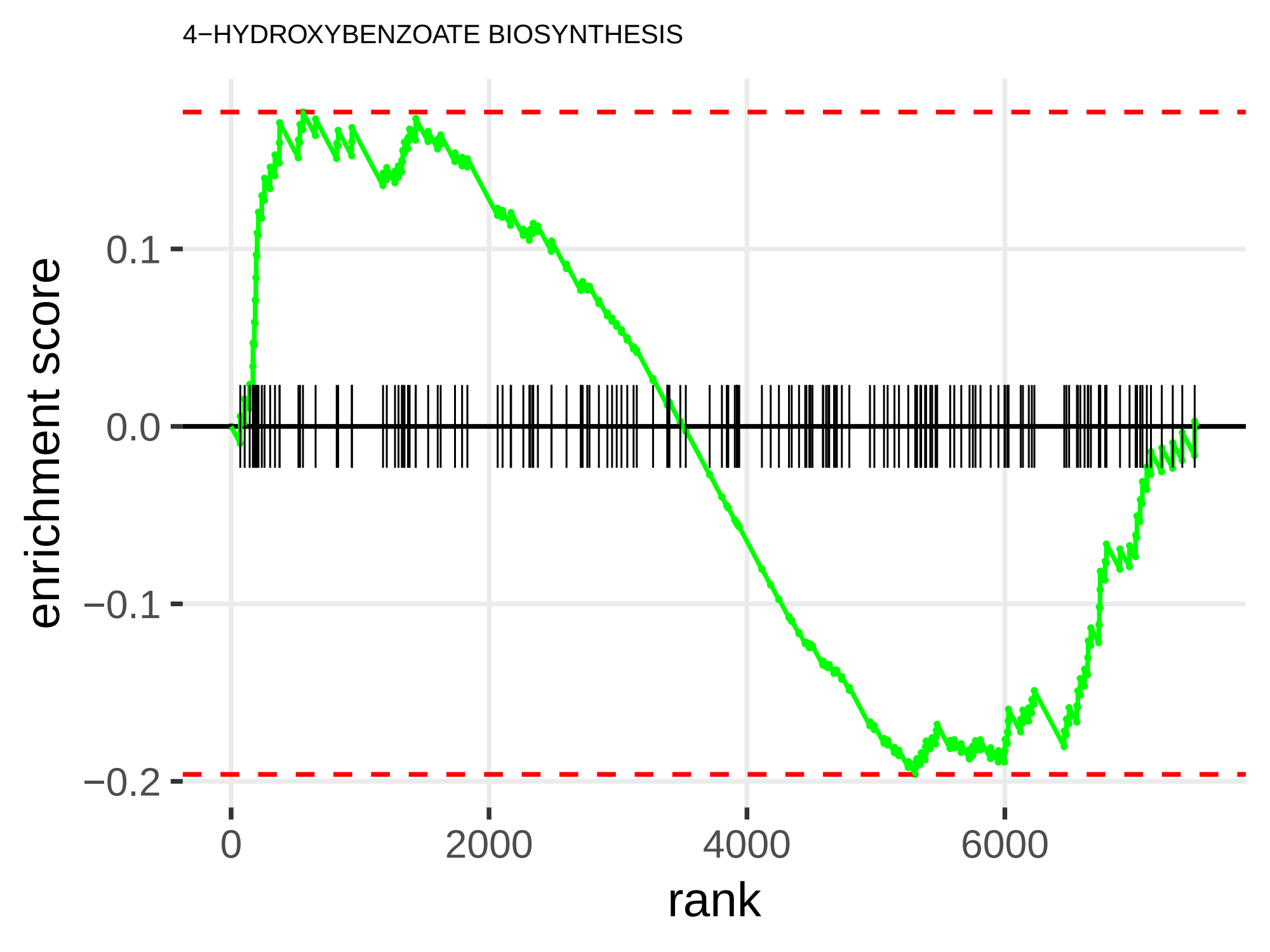

PREGNENOLONE BIOSYNTHESIS
enrichment score
0.1
0.0
−0.1
−0.2
0
2000
4000
6000
rank

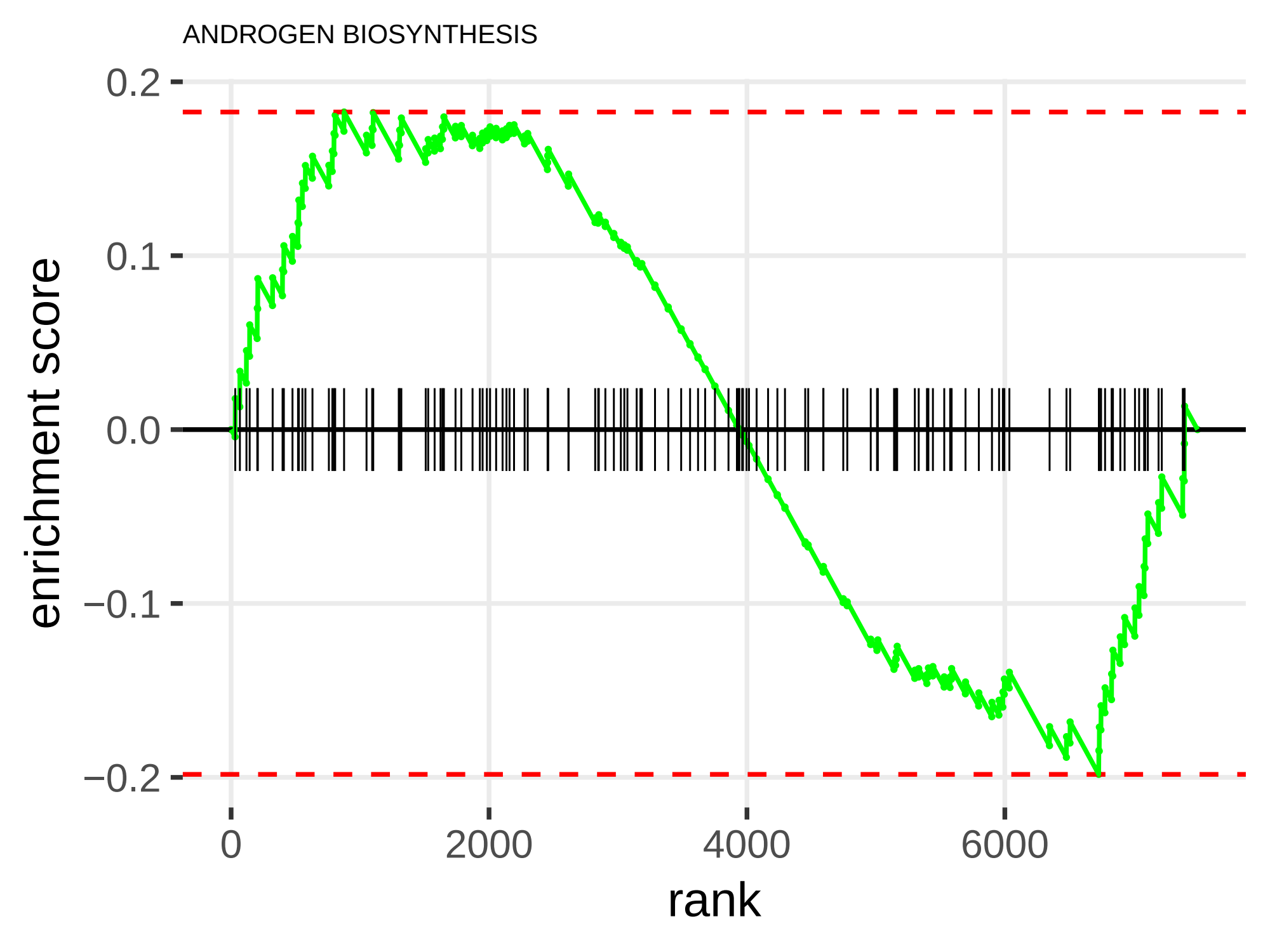

CHONDROITIN SULFATE BIOSYNTHESIS (LATE STAGES)
enrichment score
0.2
0.1
0.0
−0.1
0
2000
4000
6000
rank

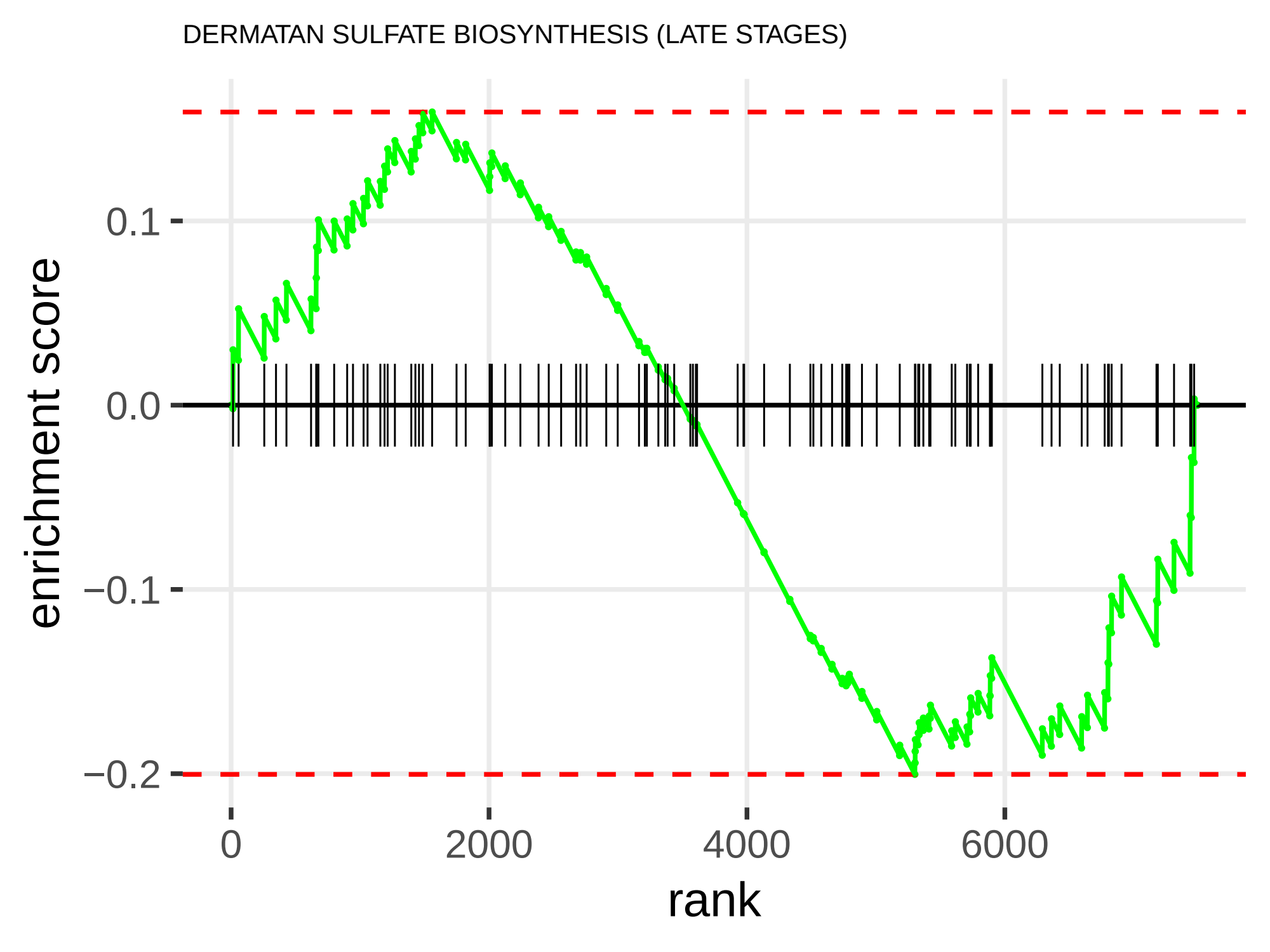

FATTY ACID BIOSYNTHESIS INITIATION II
0.2
0.1
0.0
−0.1
enrichment score
0
2000
4000
6000
rank

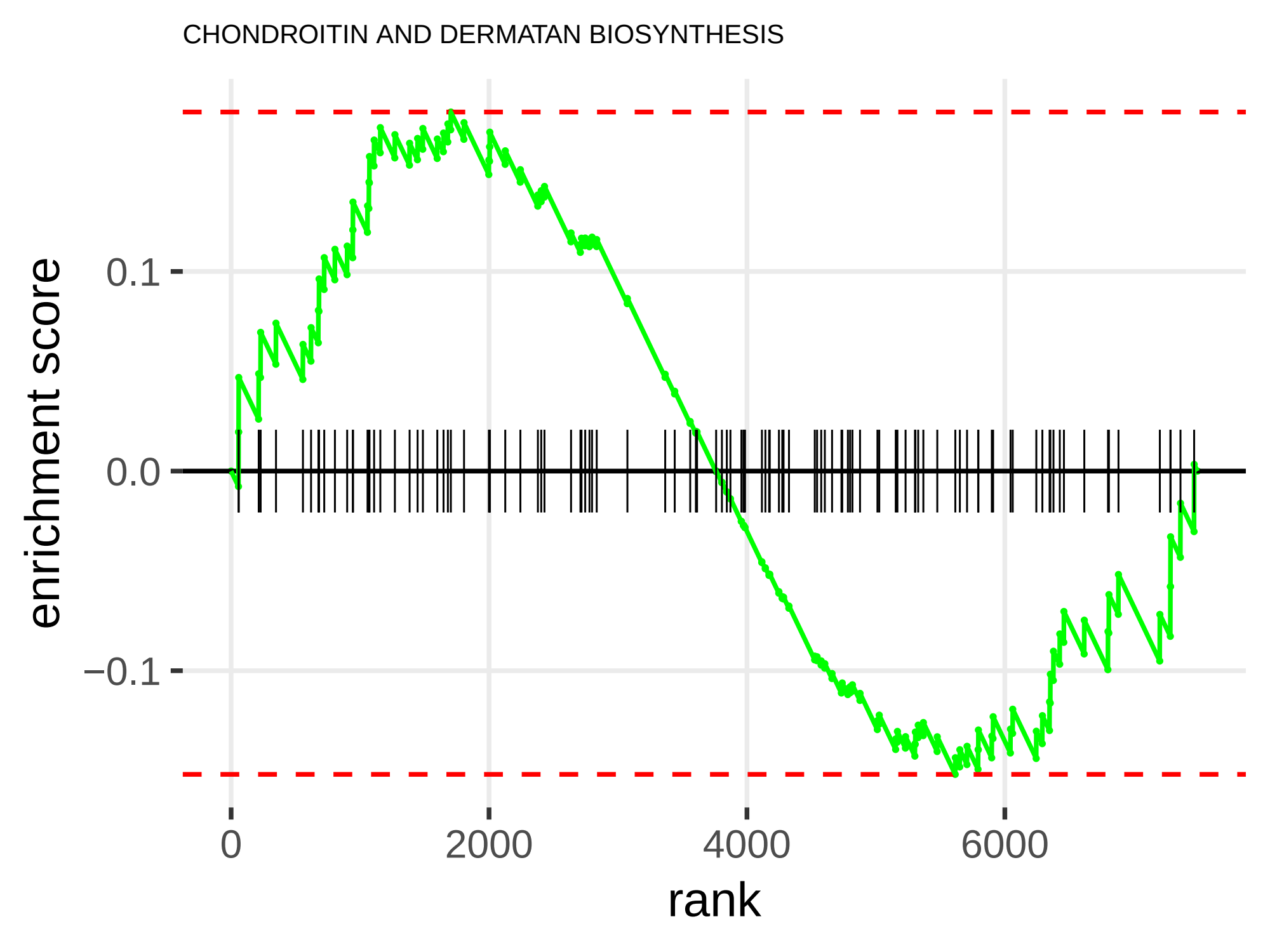

MINERALOCORTICOID BIOSYNTHESIS
enrichment score
0.1
0.0
−0.1
−0.2
0
2000
4000
6000
rank

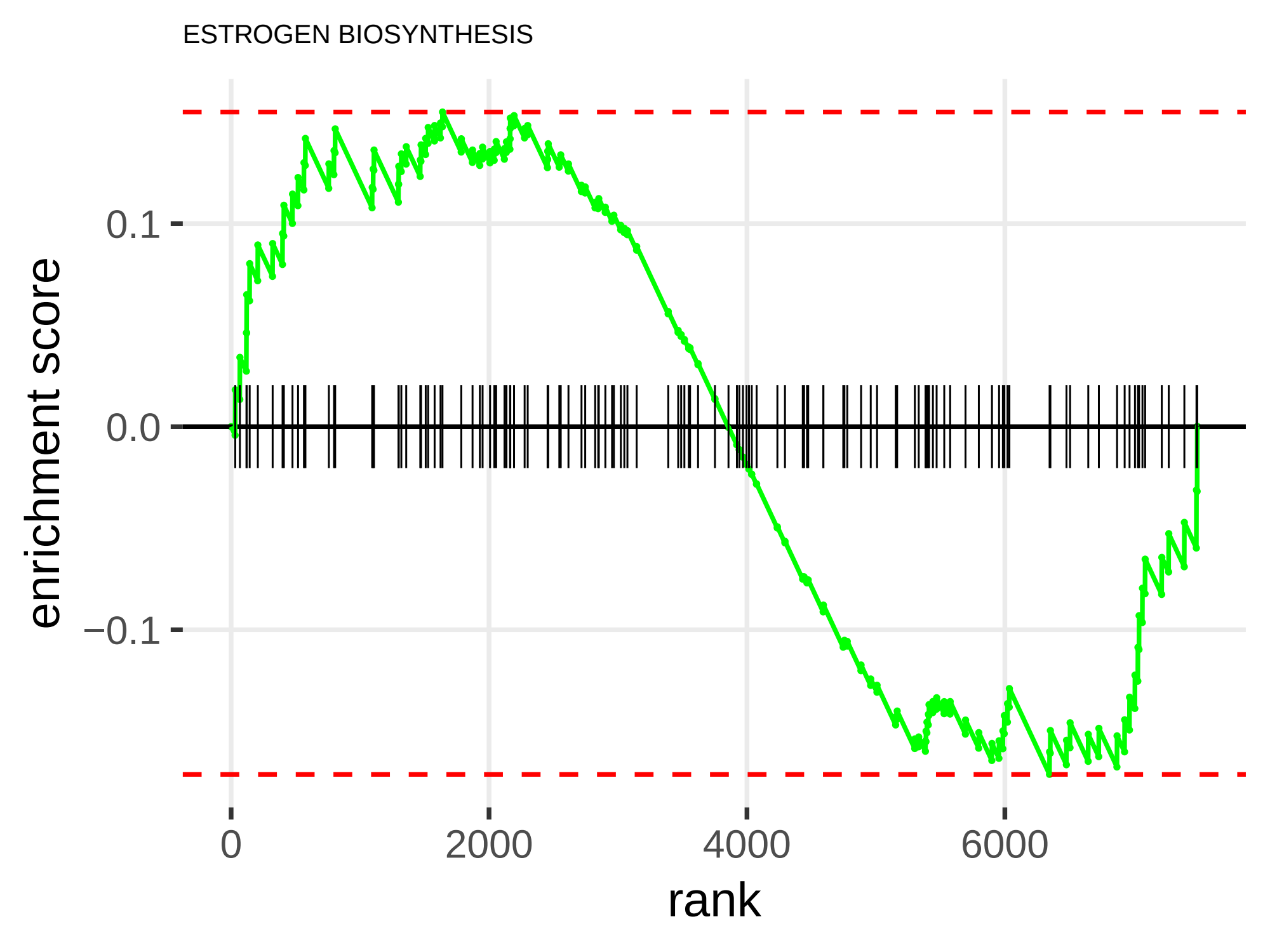

4−HYDROXYPHENYLPYRUVATE BIOSYNTHESIS
enrichment score
0.1
0.0
−0.1
−0.2
0
2000
4000
6000
rank

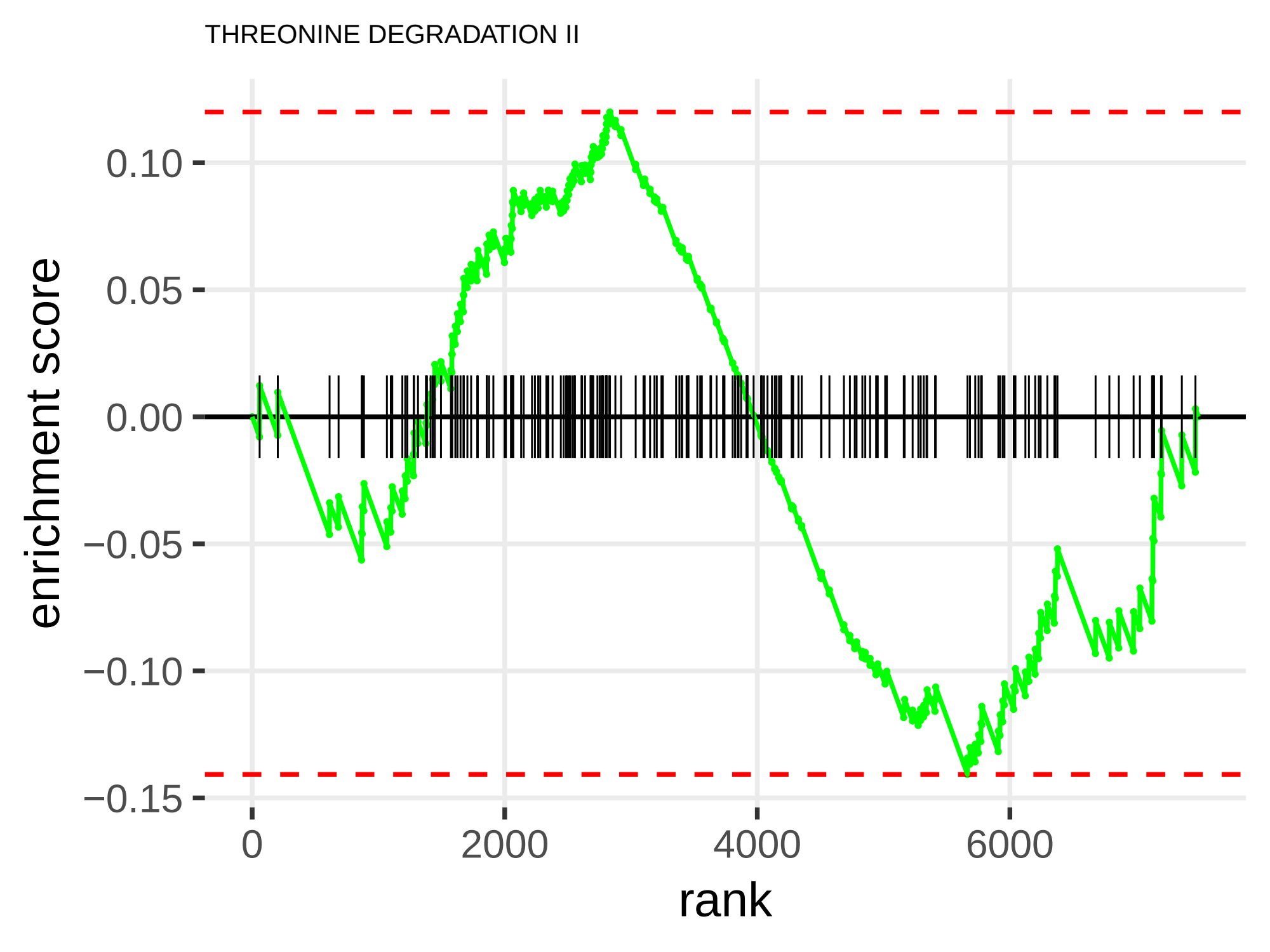

4−HYDROXYBENZOATE BIOSYNTHESIS
enrichment score
0.1
0.0
−0.1
−0.2
0
2000
4000
6000
rank


ANDROGEN BIOSYNTHESIS
0.2
0.1
0.0
−0.1
−0.2
enrichment score
0
2000
4000
6000
rank


DERMATAN SULFATE BIOSYNTHESIS (LATE STAGES)
enrichment score
0.1
0.0
−0.1
−0.2
0
2000
4000
6000
rank


CHONDROITIN AND DERMATAN BIOSYNTHESIS
enrichment score
0.1
0.0
−0.1
0
2000
4000
6000
rank


ESTROGEN BIOSYNTHESIS
enrichment score
0.1
0.0
−0.1
0
2000
4000
6000
rank


THREONINE DEGRADATION II
enrichment score
0.10
0.05
0.00
−0.05
−0.10
−0.15
0
2000
4000
6000
rank