

enrichment score

0.4

0.3

0.2

0.1

0.0

0

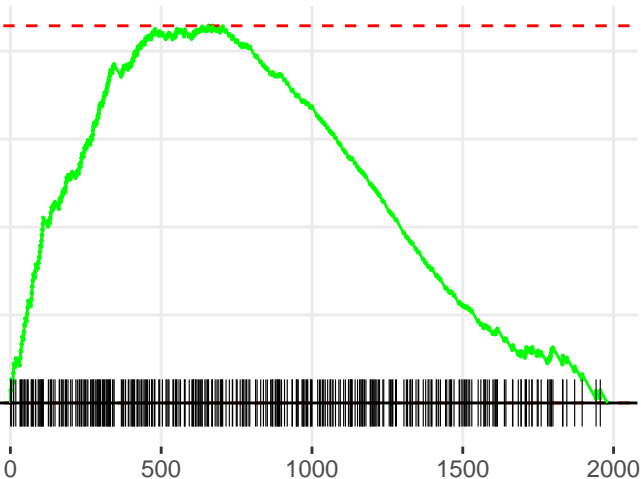
500

1000

1500

2000

rank



GENE EXPRESSION%GOBP%GO:0010467

enrichment score

0.3

0.2

0.1

0.0

0

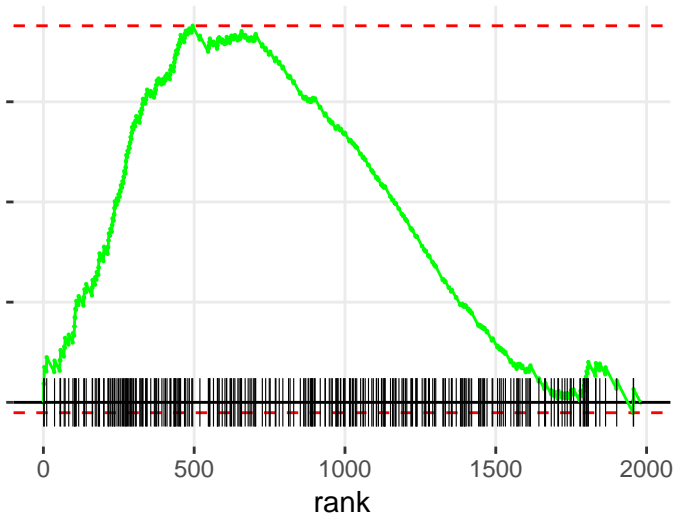
500

1000

1500

2000

rank



enrichment score

0.4

0.3

0.2

0.1

0.0

0

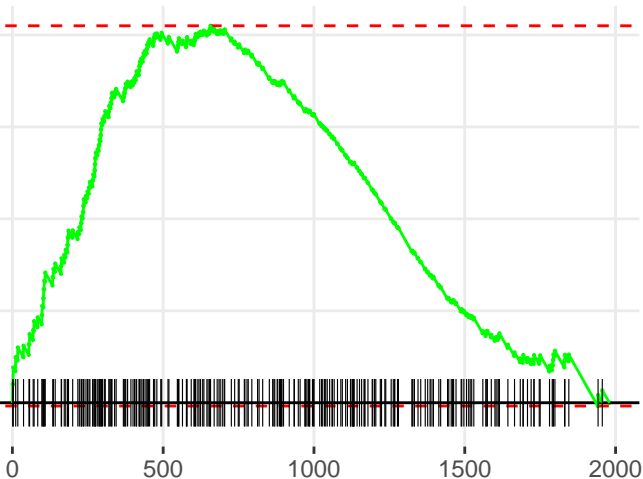
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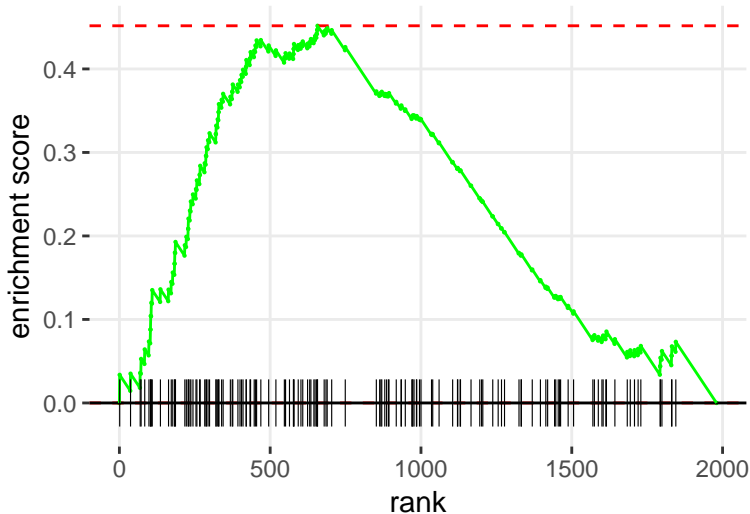
1000

1500

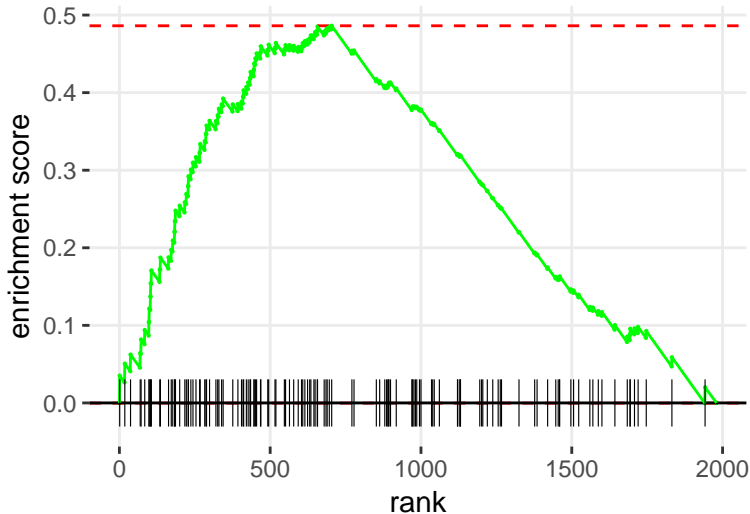
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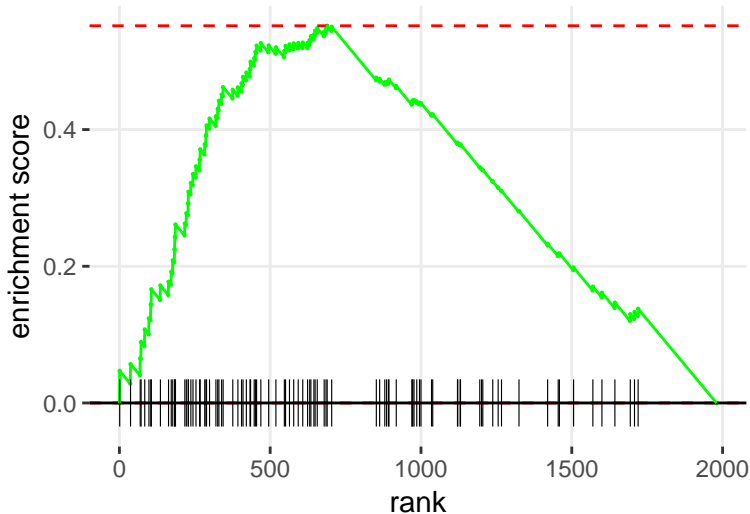
rank





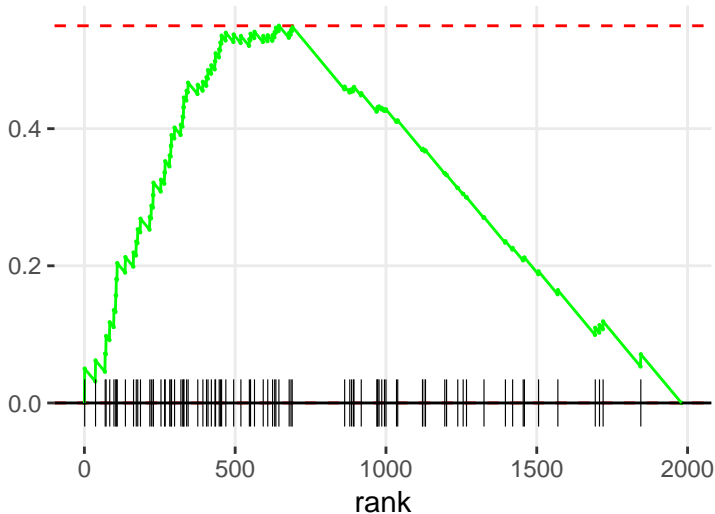
MRNA METABOLIC PROCESS%GOBP%GO:0016071



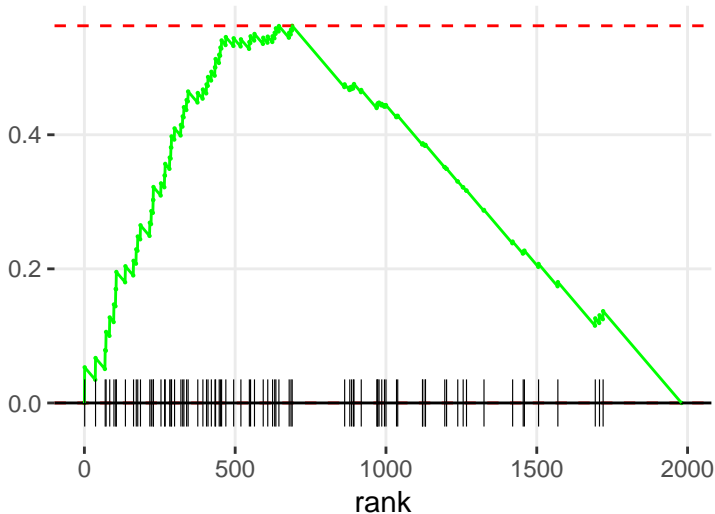


RNA SPLICING%GOBP%GO:0008380

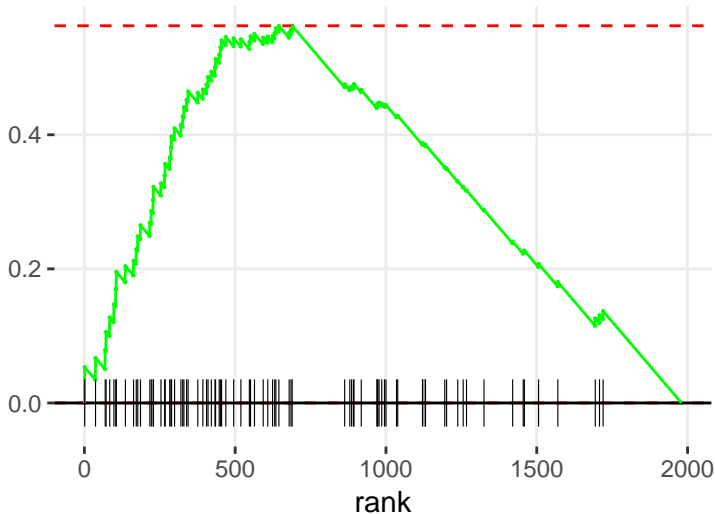
enrichment score



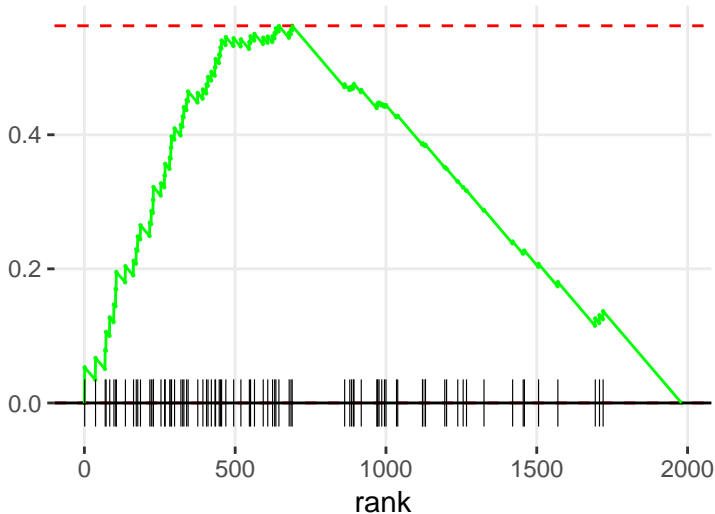
enrichment score

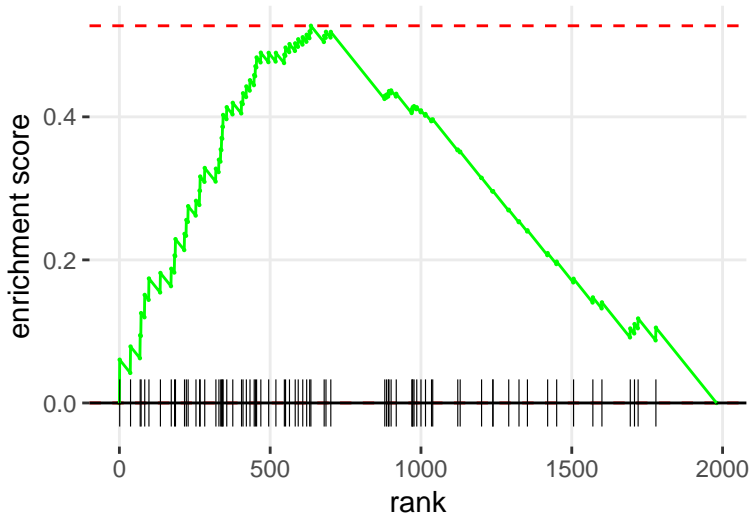


enrichment score

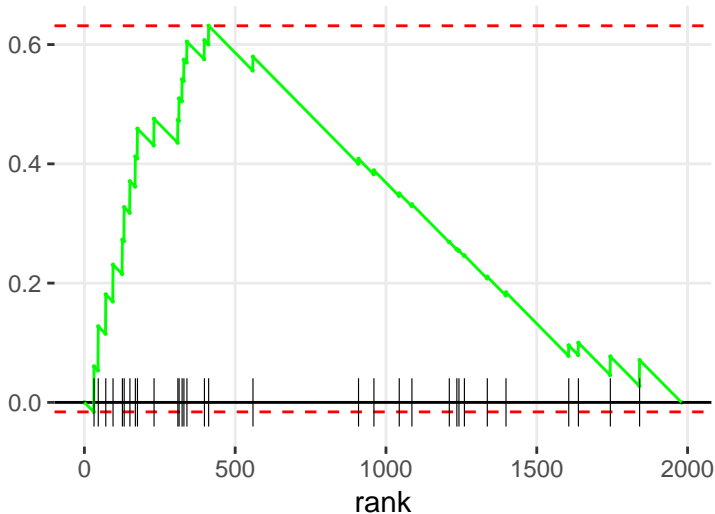


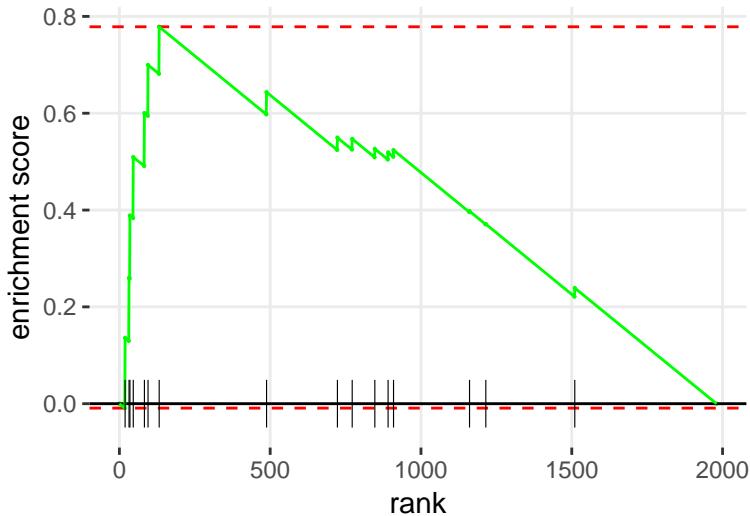
enrichment score



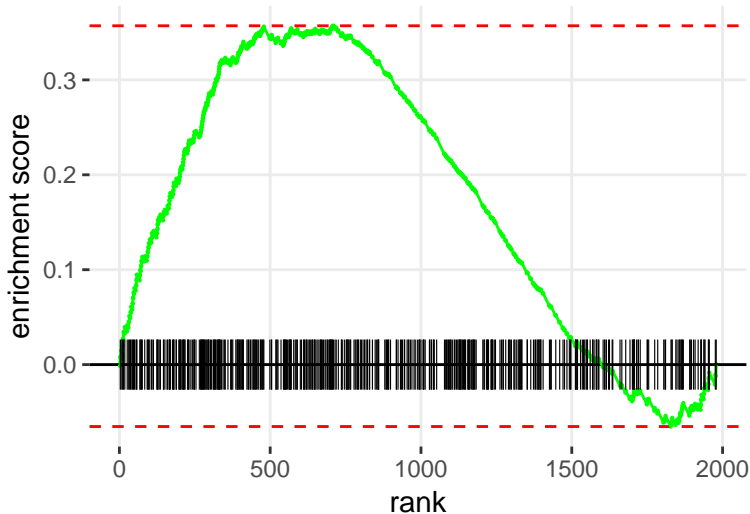


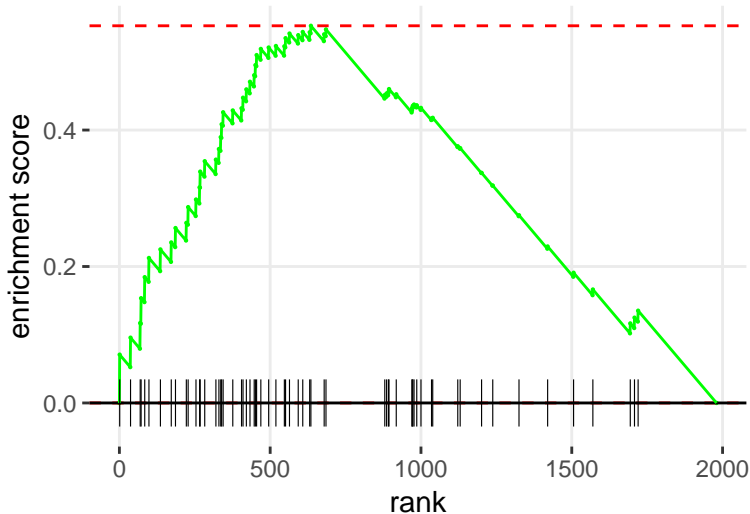
enrichment score

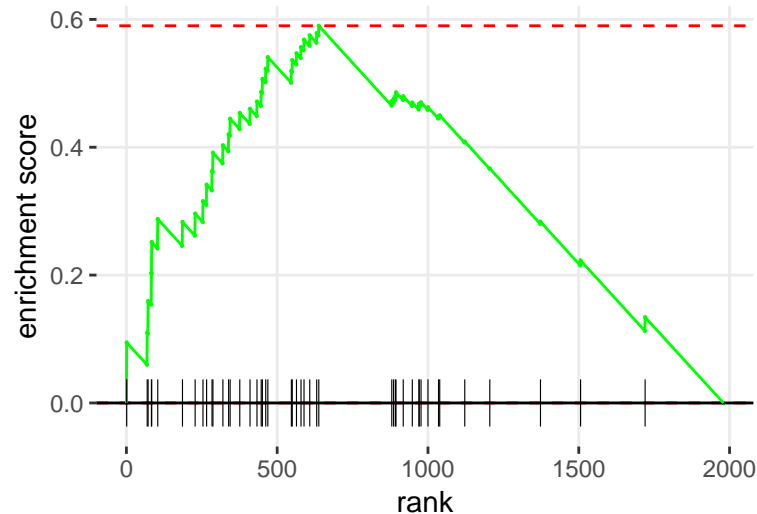


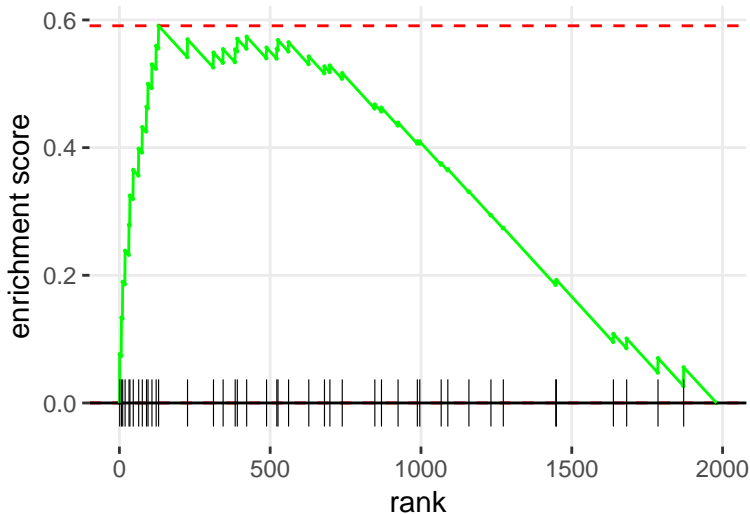


REGULATION OF RNA METABOLIC PROCESS%GOBP%GO:0051252









enrichment score

0.0

-0.2

-0.4

-0.6

0

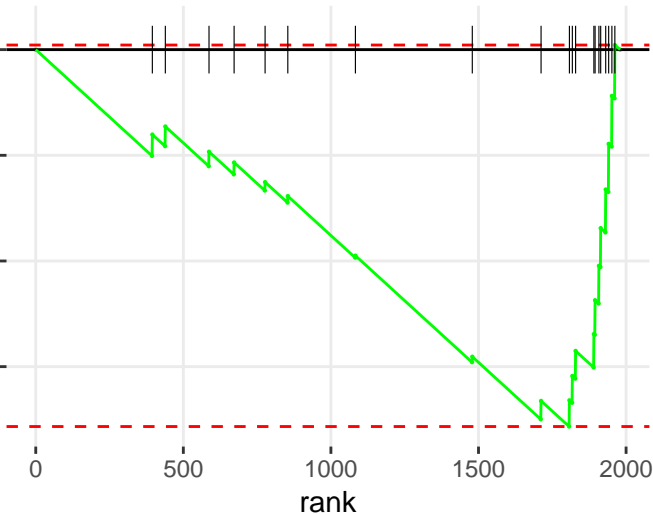
500

1000

1500

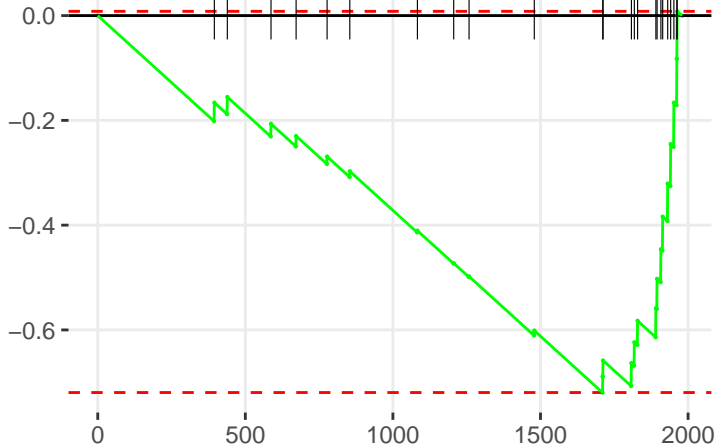
2000

rank

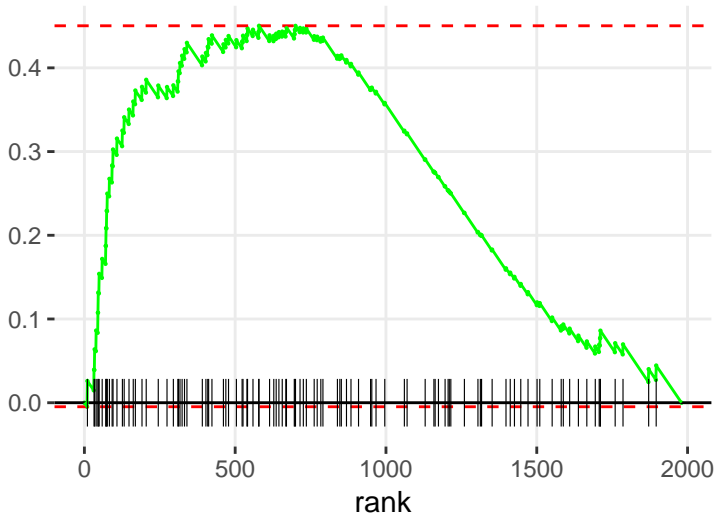


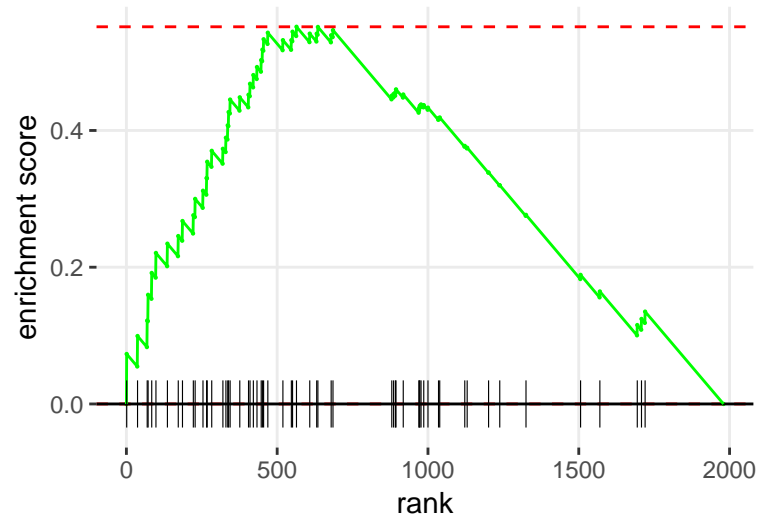
enrichment score

rank

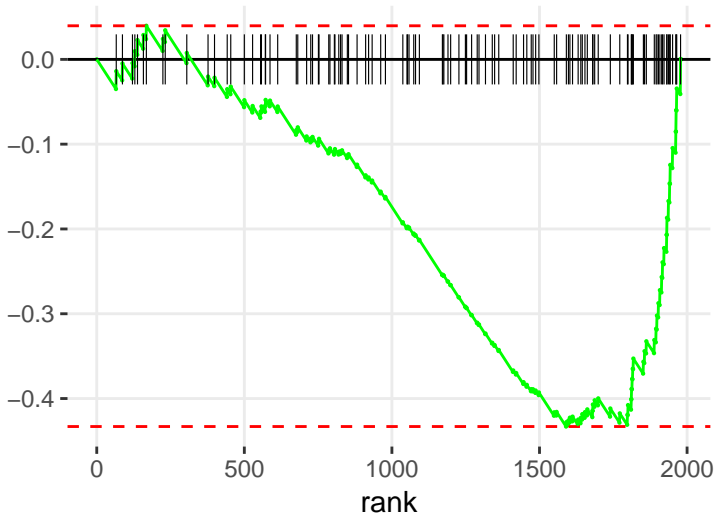


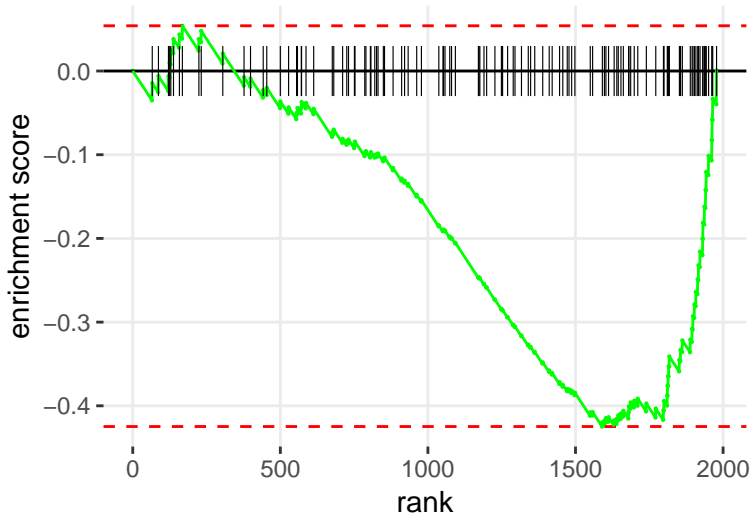
enrichment score

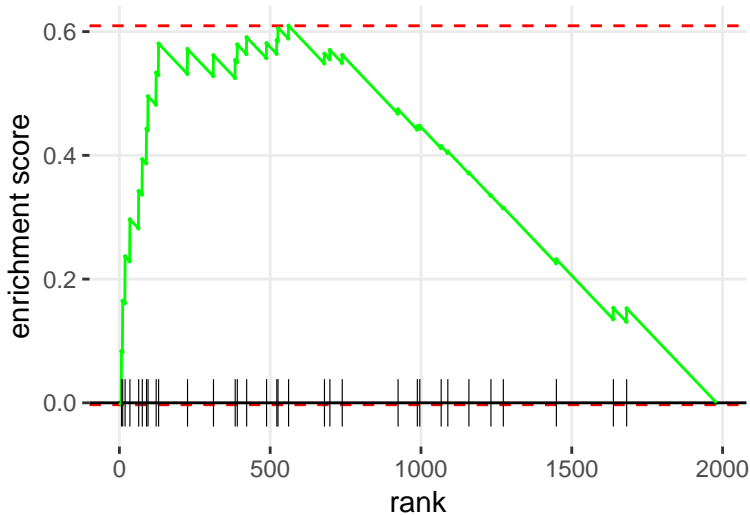


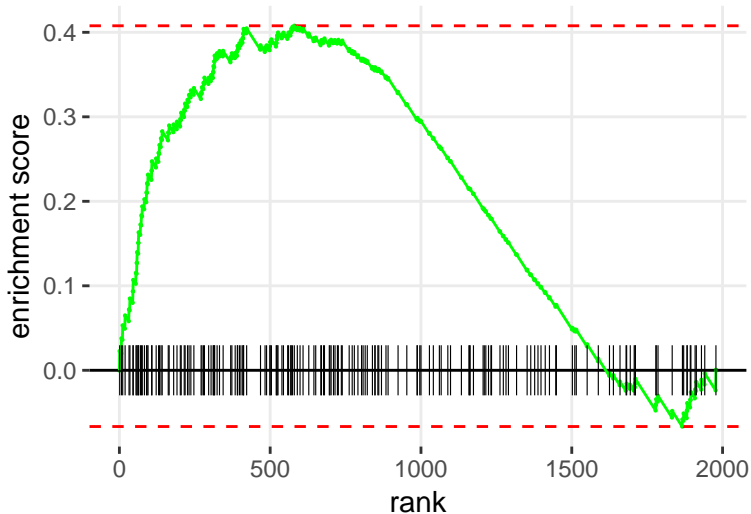


enrichment score

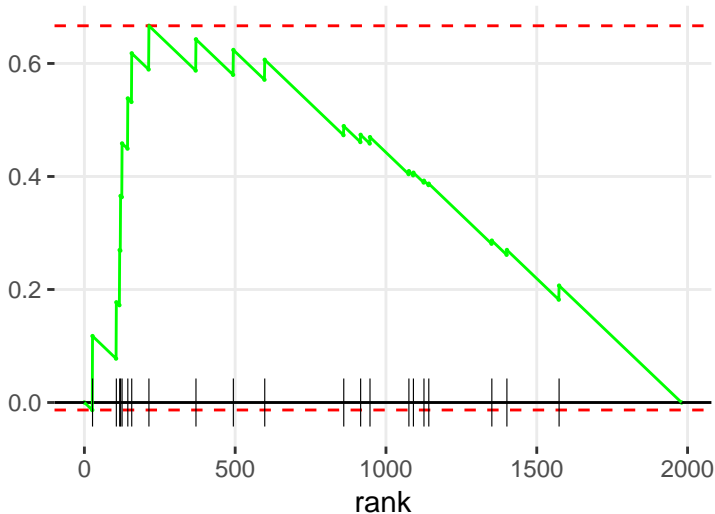




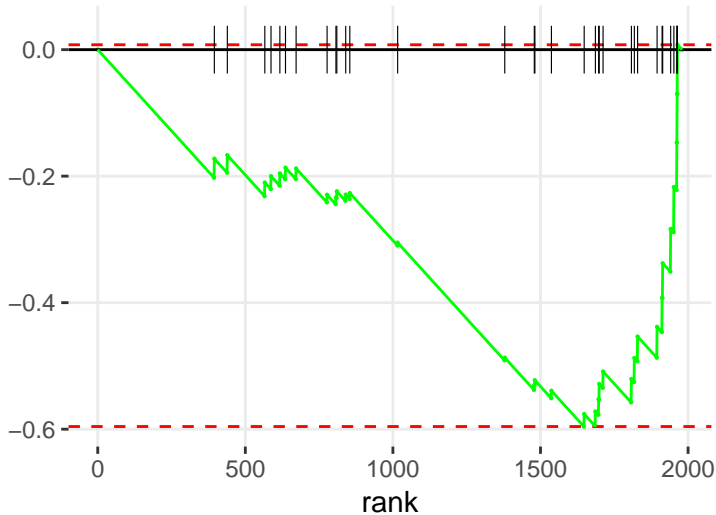




enrichment score



enrichment score



enrichment score

0.0

-0.2

-0.4

0

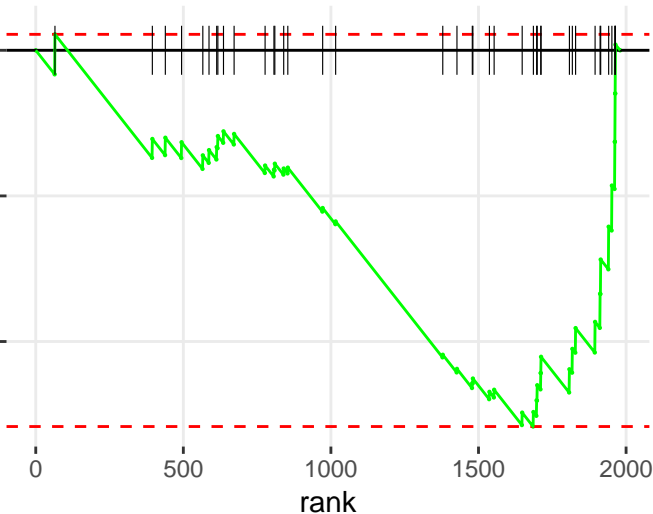
500

1000

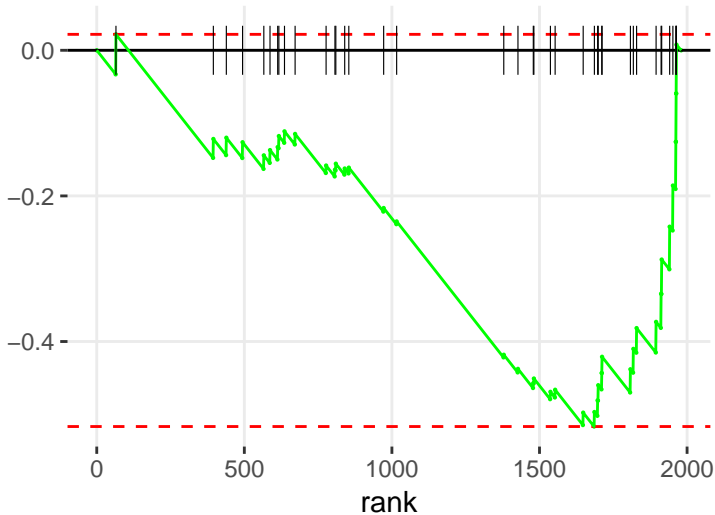
1500

2000

rank



enrichment score



enrichment score

0.0
-0.1
-0.2
-0.3
-0.4

0

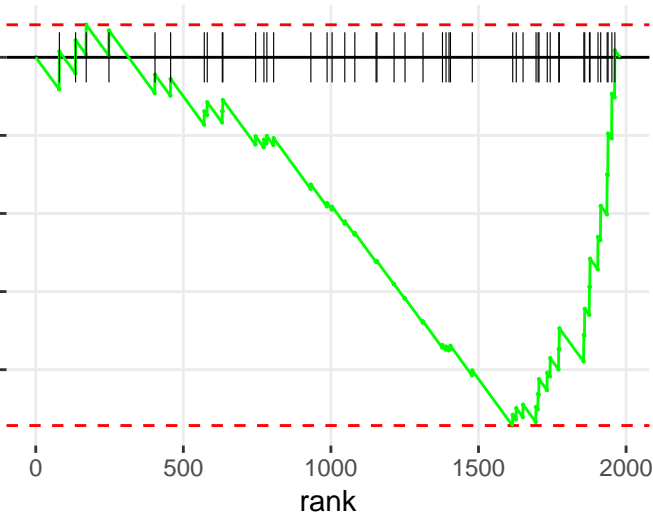
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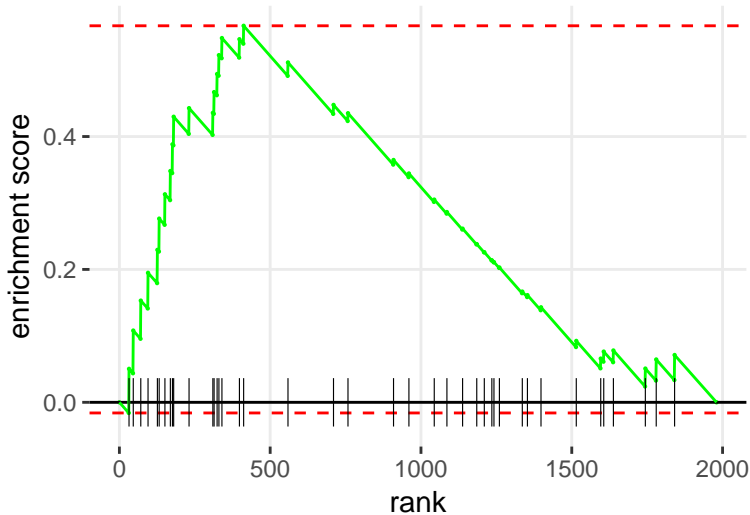
1000

1500

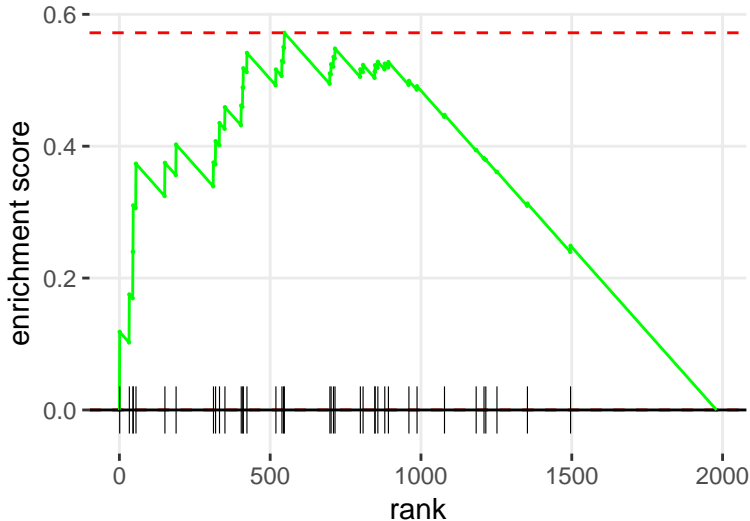
2000

rank





POSITIVE REGULATION OF CHROMOSOME ORGANIZATION%GOBP%GO:2001252



IMPORT INTO CELL%GOBP%GO:0098657

enrichment score

0.0
-0.1
-0.2
-0.3
-0.4

0

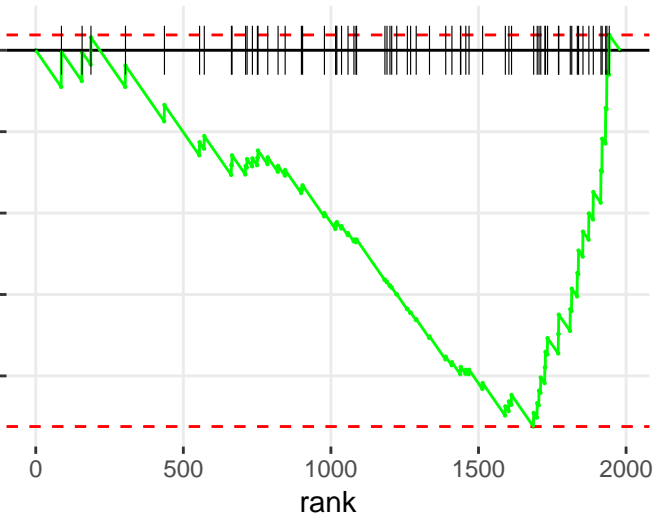
500

1000

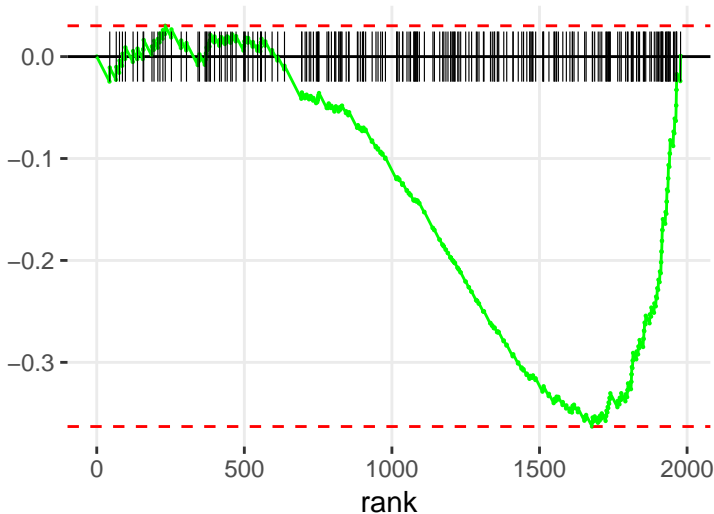
1500

2000

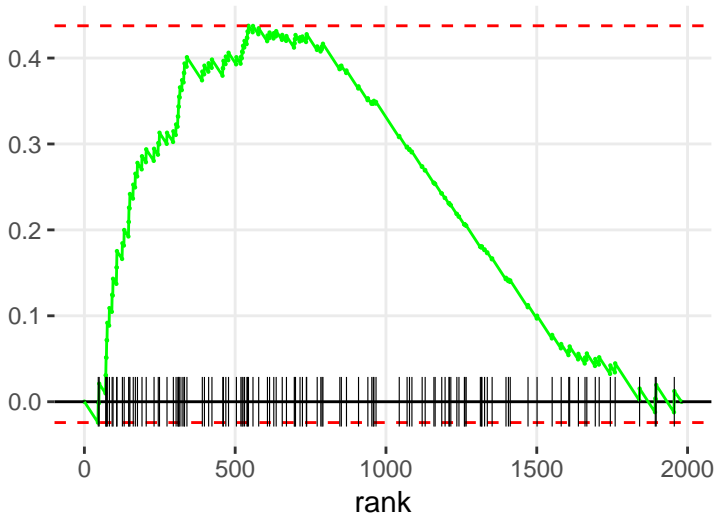
rank



enrichment score



enrichment score



enrichment score

0.0

-0.2

-0.4

-0.6

0

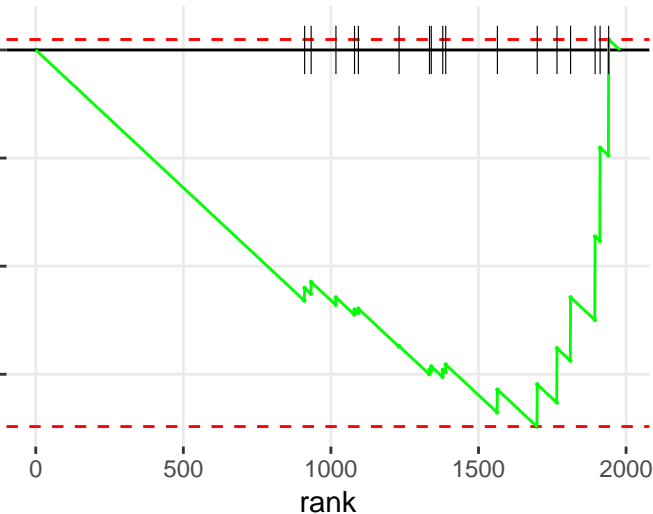
500

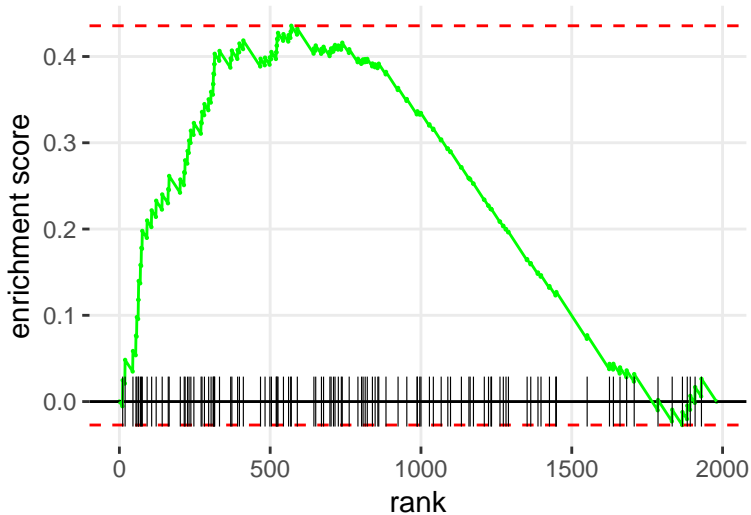
1000

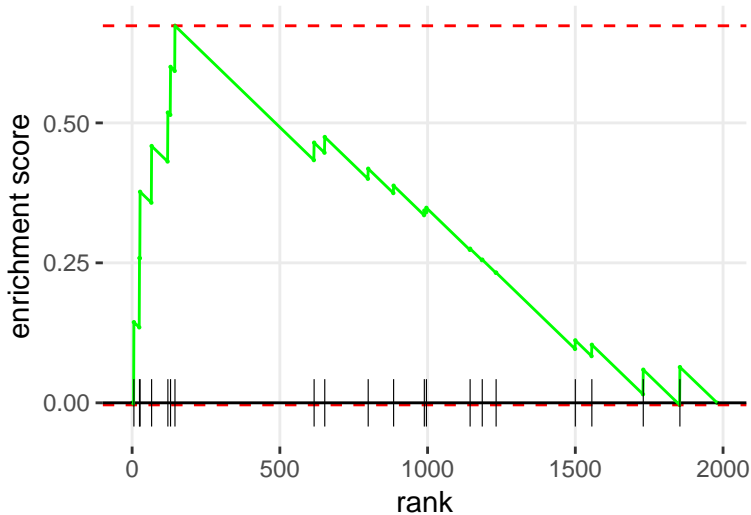
1500

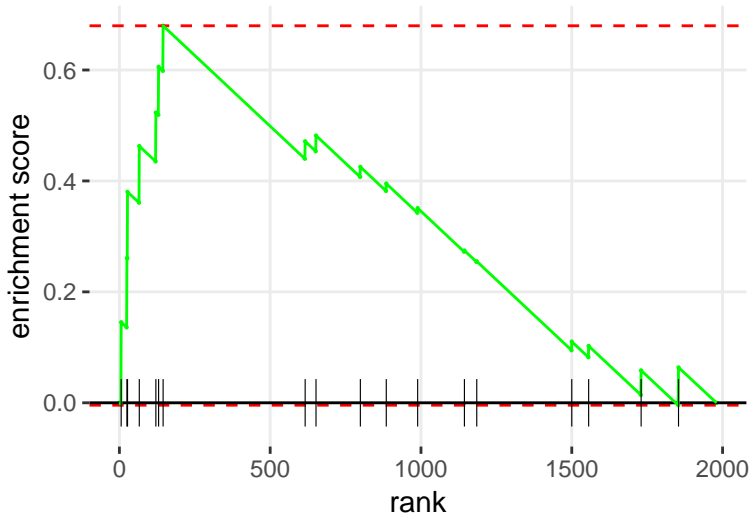
2000

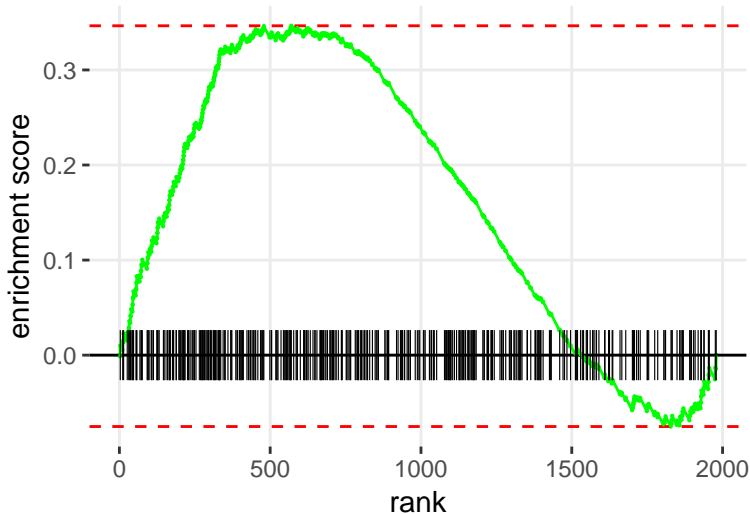
rank











enrichment score

0.3

0.2

0.1

0.0

0

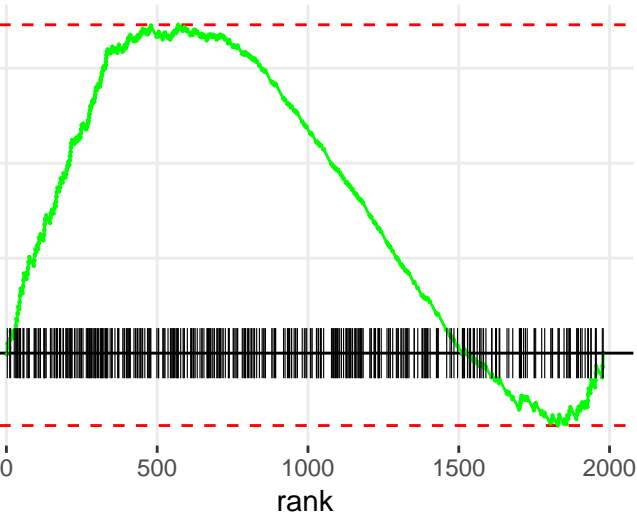
500

1000

1500

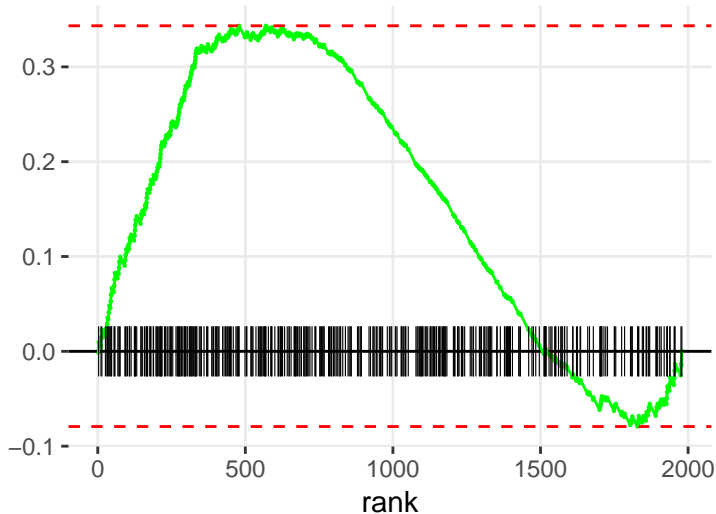
2000

rank



REGULATION OF RNA BIOSYNTHETIC PROCESS%GOBP%GO:2001141

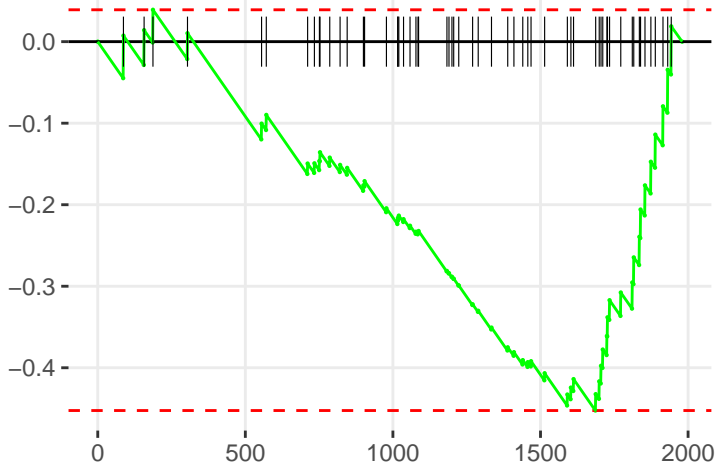
enrichment score

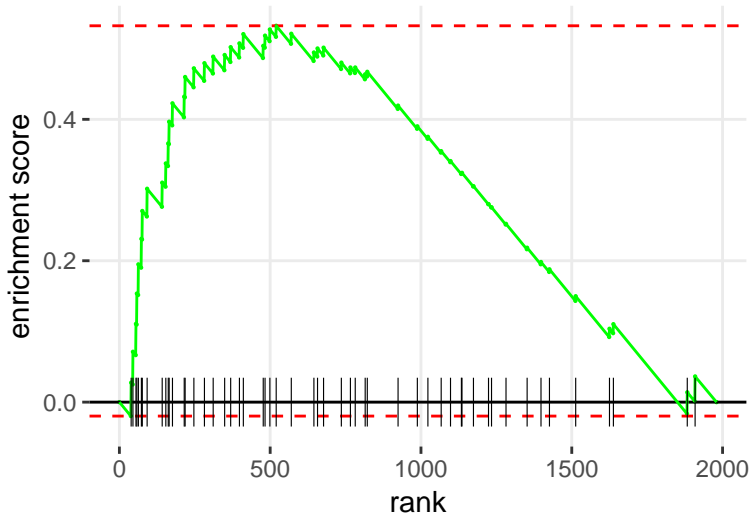


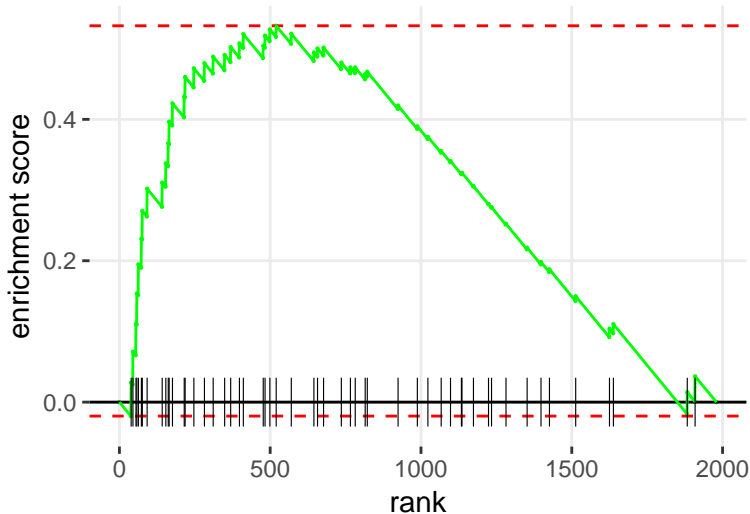
ENDOCYTOSIS%GOBP%GO:0006897

enrichment score

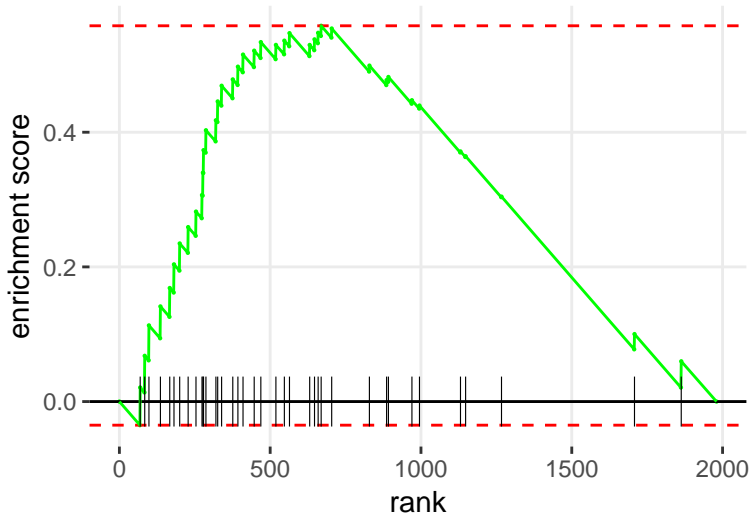
rank



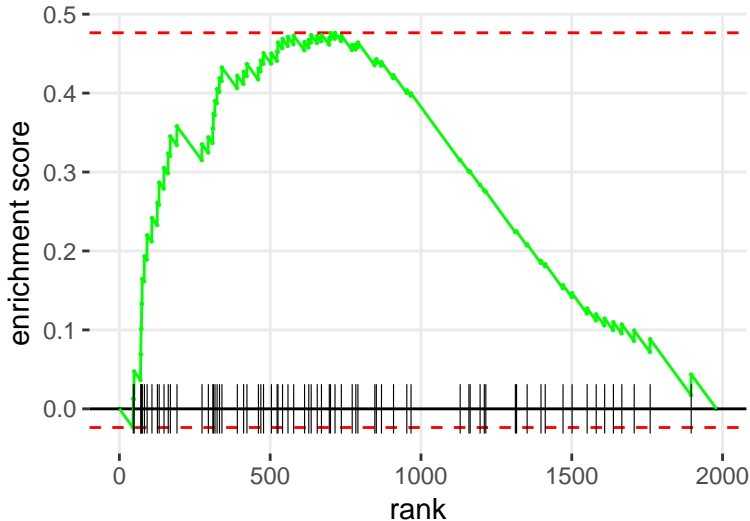


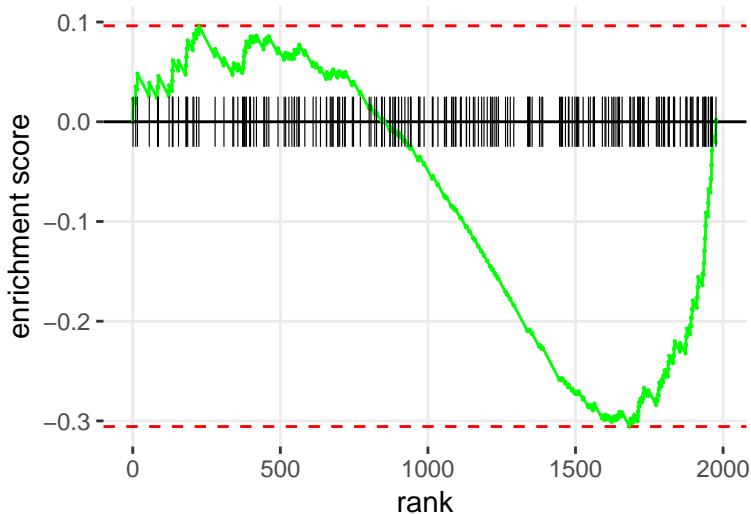


REGULATION OF MRNA SPLICING, VIA SPLICEOSOME%GOBP%GO:0048024

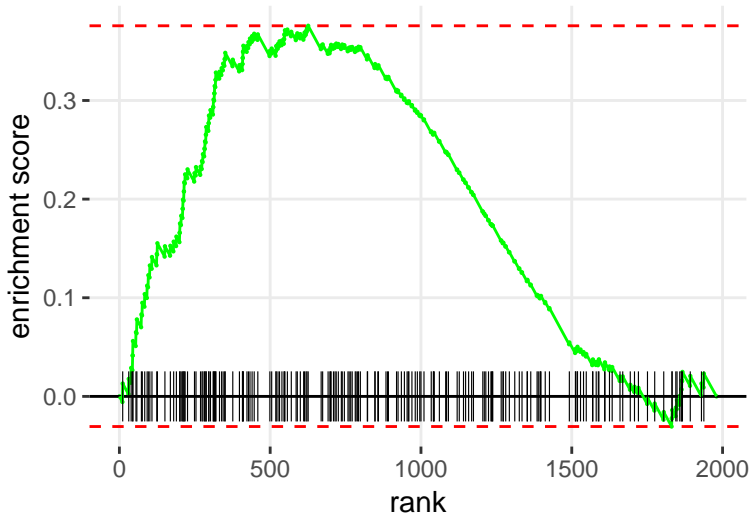


DNA REPAIR%GOBP%GO:0006281

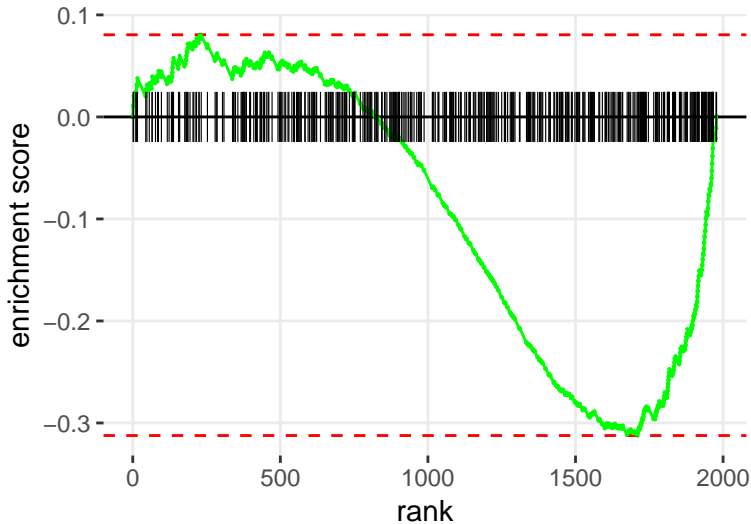




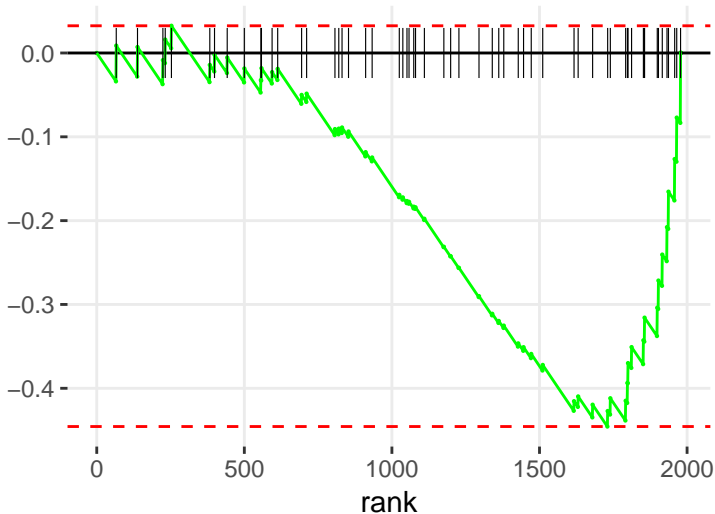
NEGATIVE REGULATION OF NUCLEOBASE-CONTAINING COMPOUND METABOLIC PROC



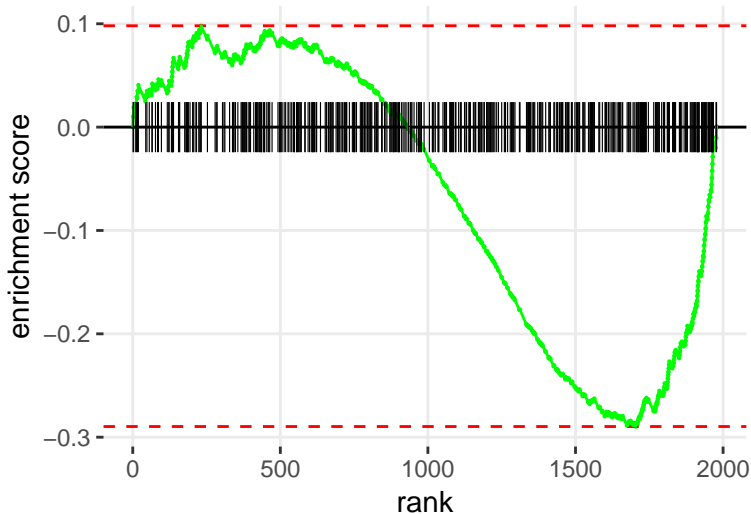
TRANSPORT%GOBP%GO:0006810



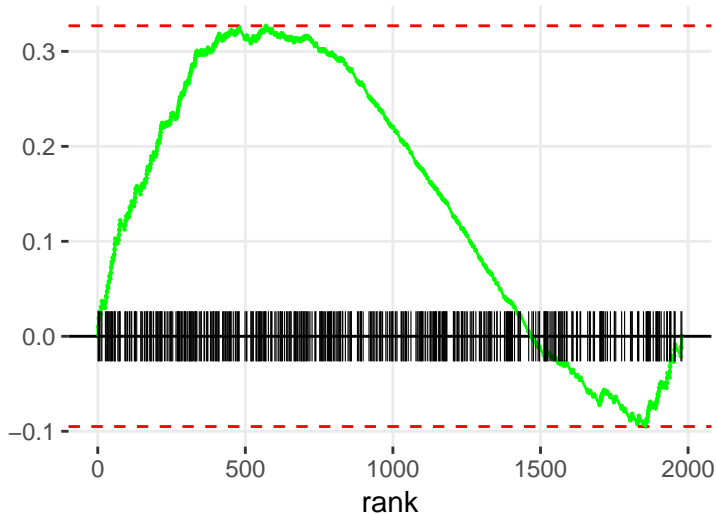
enrichment score



ESTABLISHMENT OF LOCALIZATION%GOBP%GO:0051234

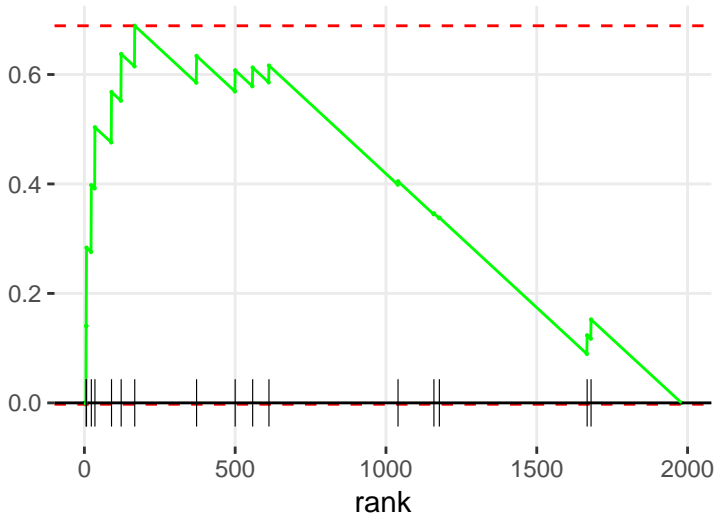


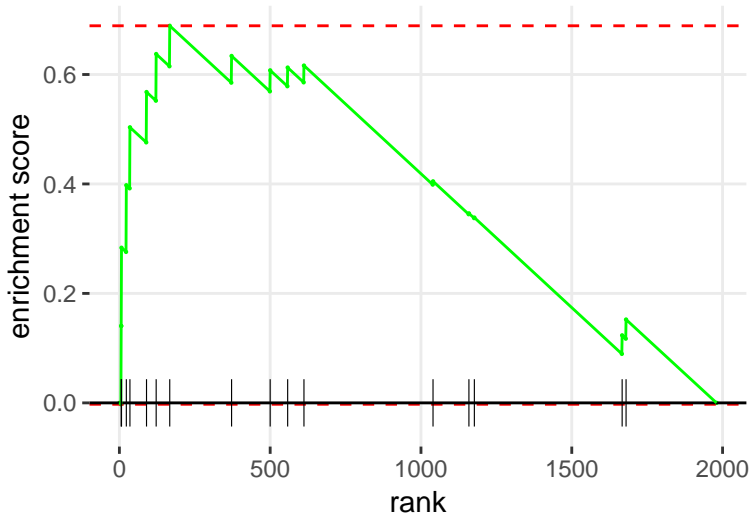
enrichment score

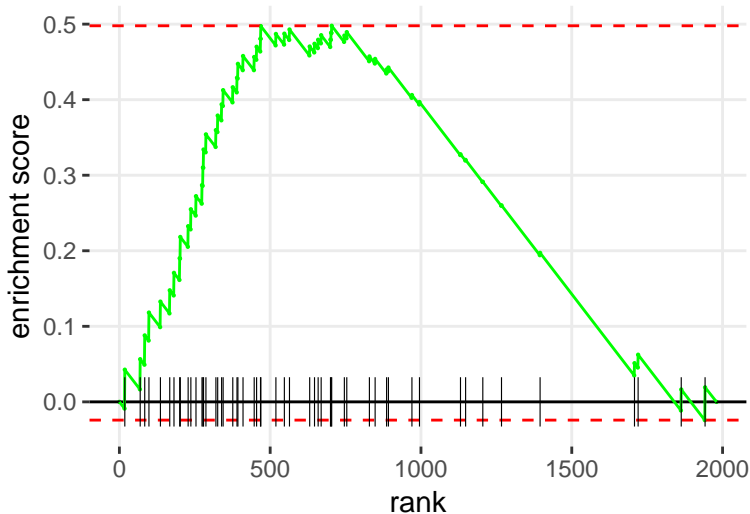


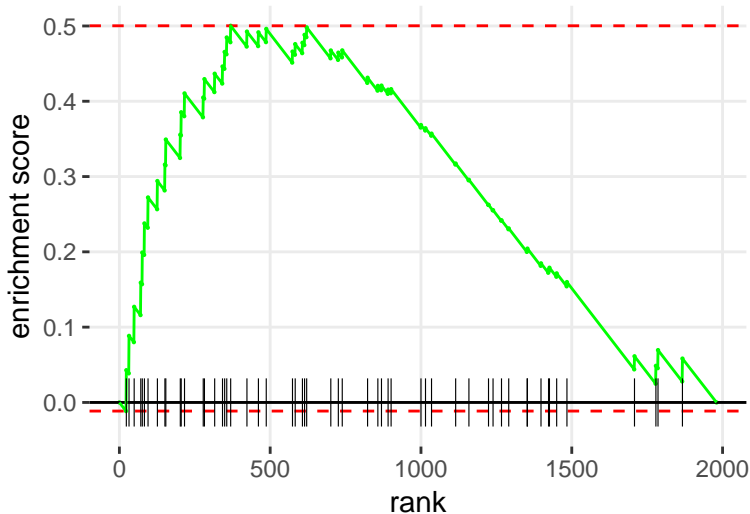
PID_AURORA_B_PATHWAY%MSIGDB_C2%PID_AURORA_B_PATHWAY

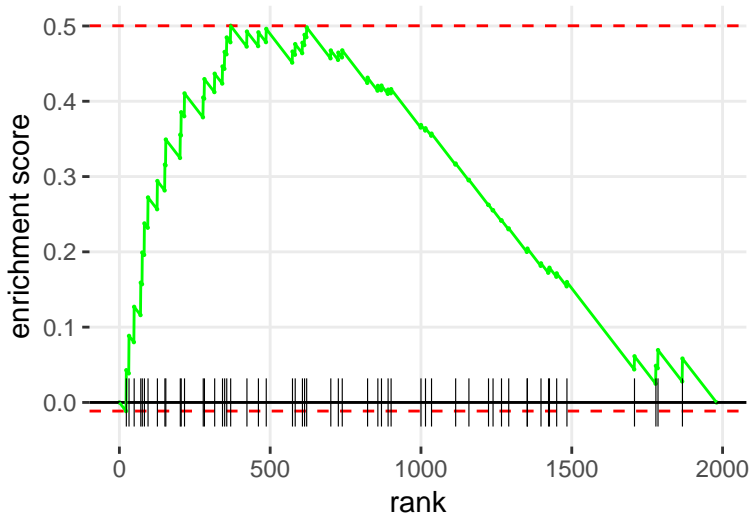
enrichment score



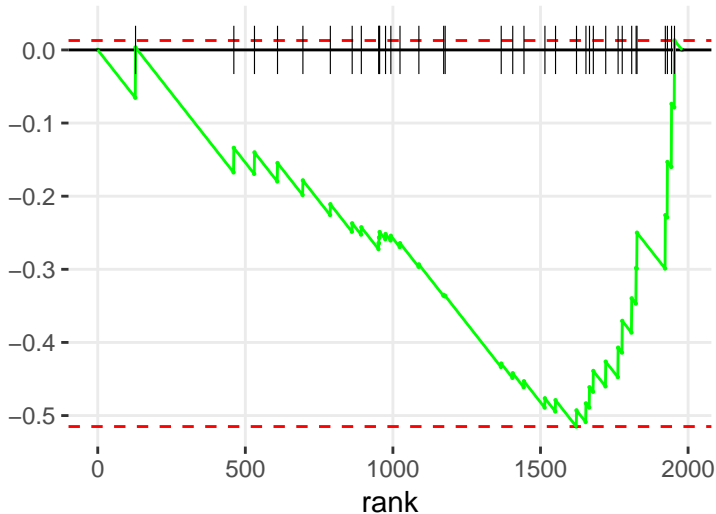




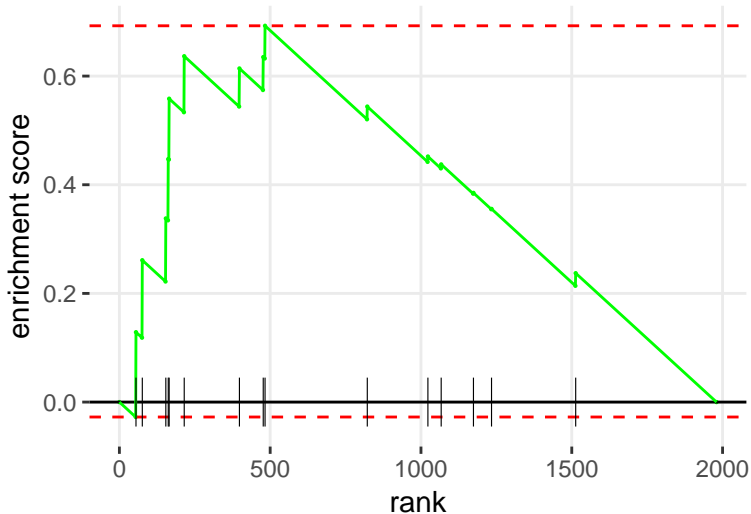




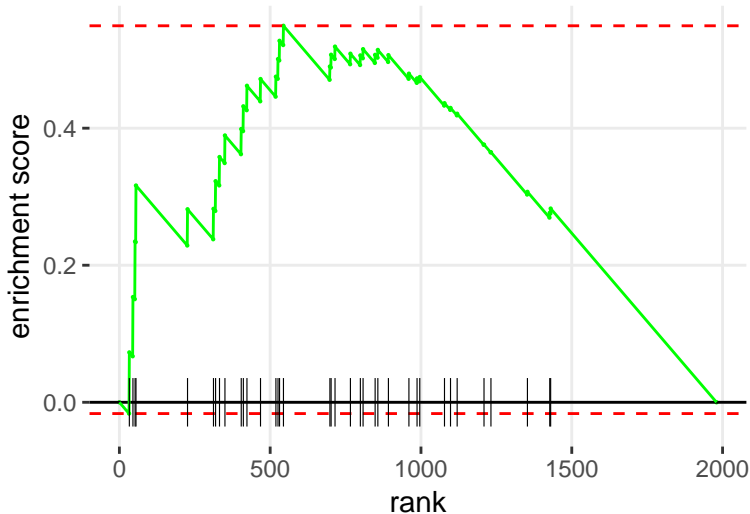
enrichment score

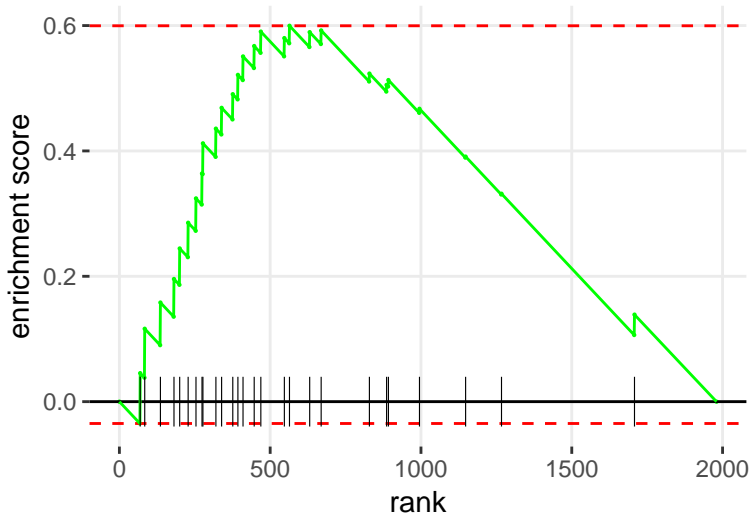


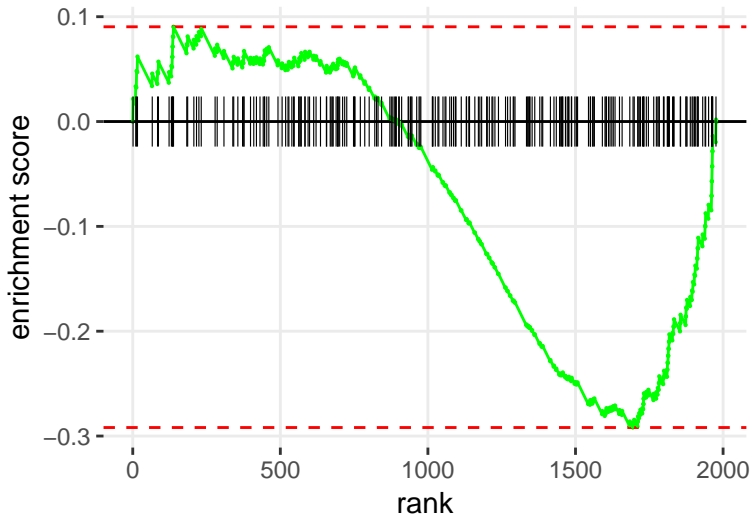
PKMTS METHYLATE HISTONE LYSINES%REACTOME%R-HSA-3214841.3



REGULATION OF CHROMATIN ORGANIZATION%GOBP%GO:1902275







REGULATION OF TRANSCRIPTION BY RNA POLYMERASE II%GOBP%GO:0006357

enrichment score

0.3

0.2

0.1

0.0

0

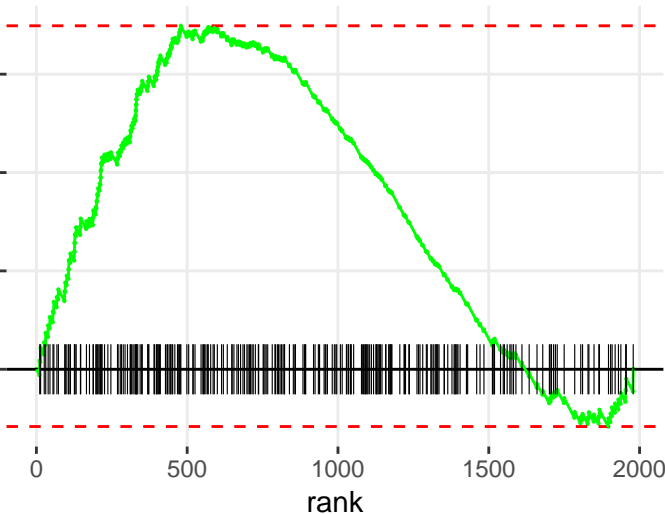
500

1000

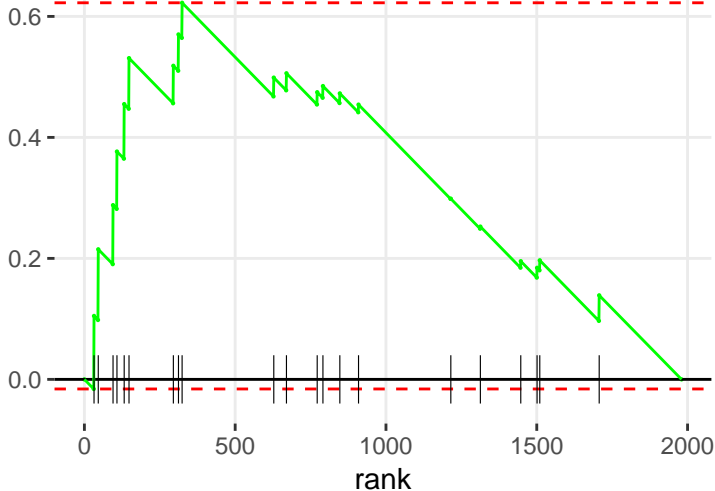
1500

2000

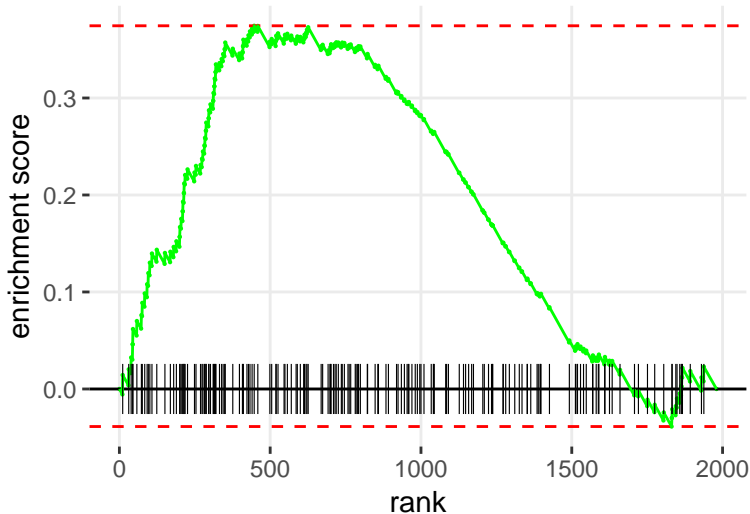
rank



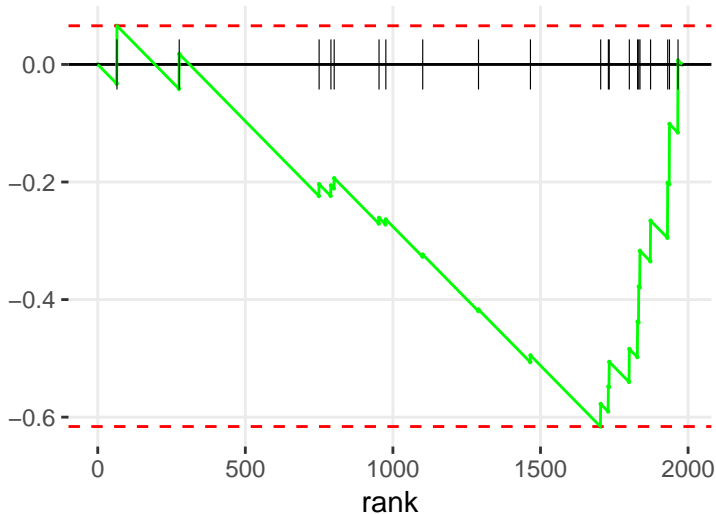
enrichment score

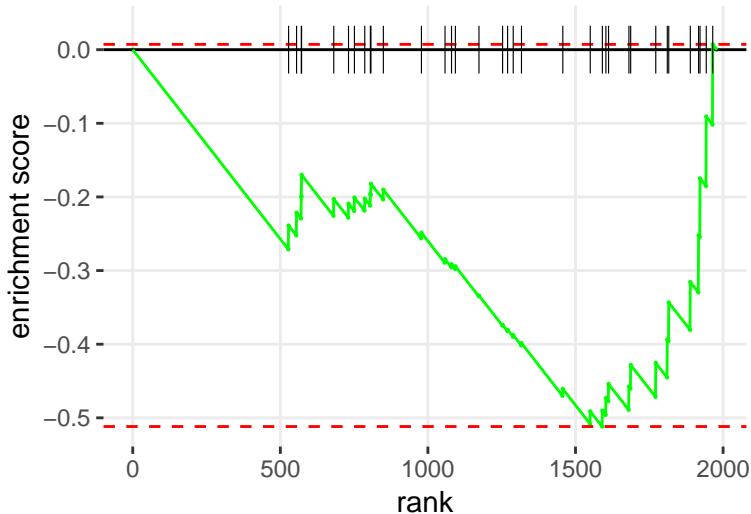


NEGATIVE REGULATION OF RNA METABOLIC PROCESS%GOBP%GO:0051253



enrichment score





PROTEIN LOCALIZATION TO NUCLEUS%GOBP%GO:0034504

enrichment score

0.4
0.2
0.0

0

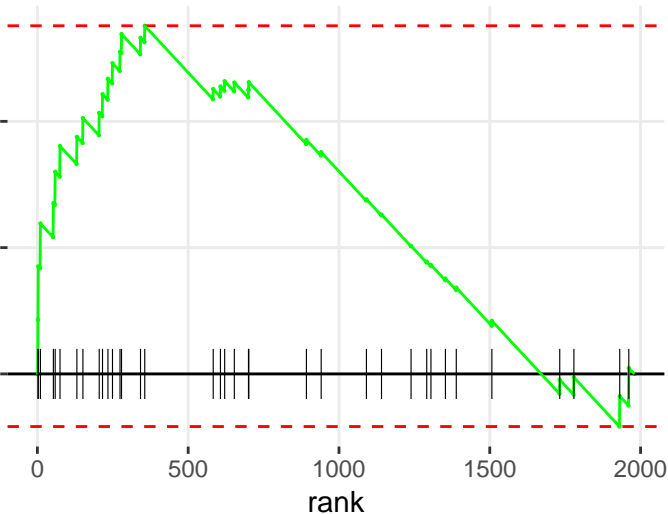
500

1000

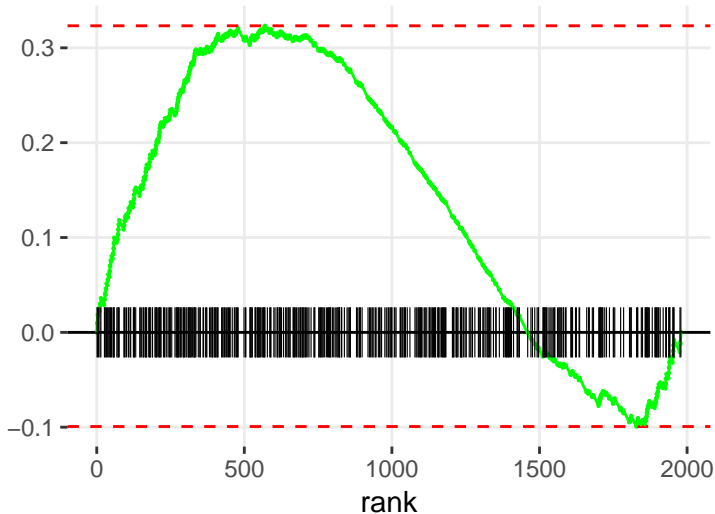
1500

2000

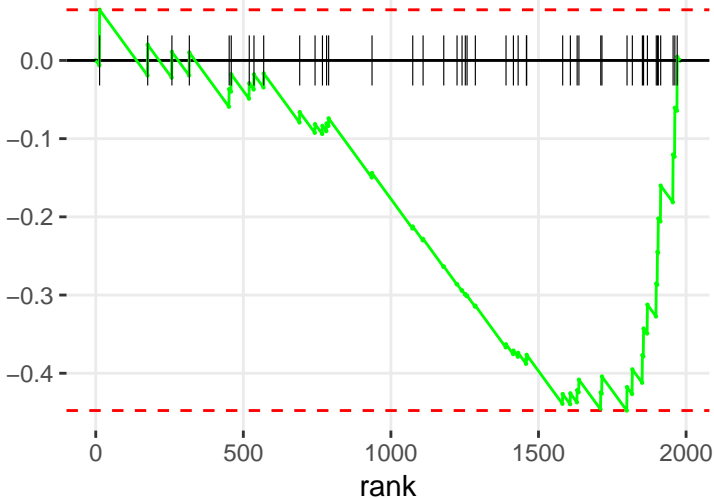
rank



enrichment score

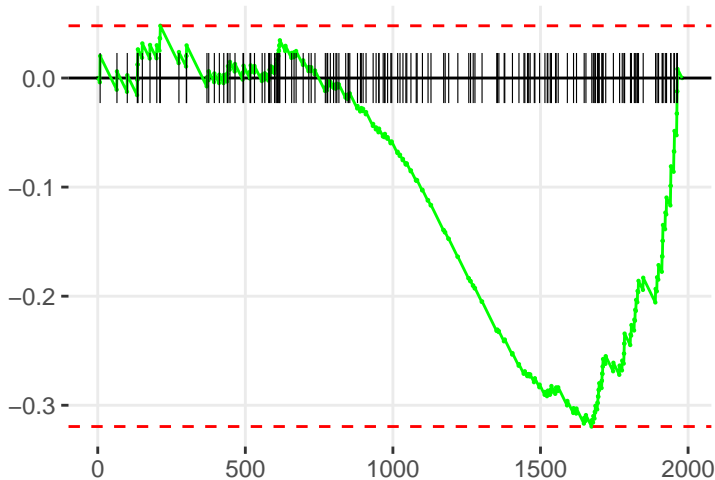


enrichment score

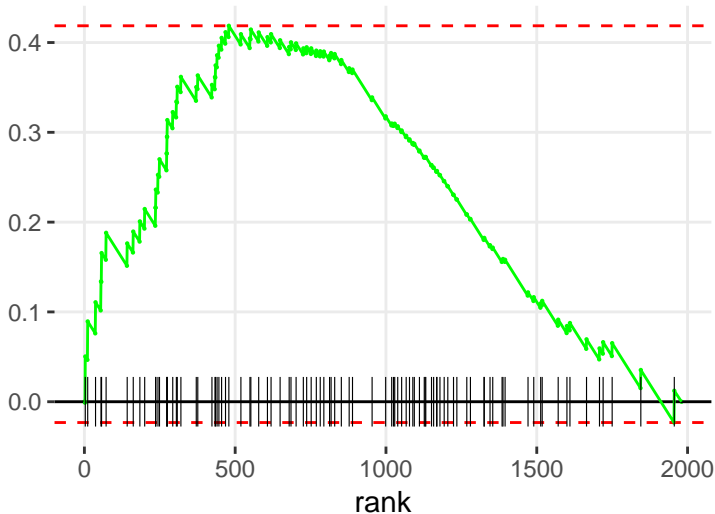


enrichment score

rank



enrichment score



TRANSCRIPTION, DNA-TEMPLATED%GOBP%GO:0006351

enrichment score

0.4

0.3

0.2

0.1

0.0

0

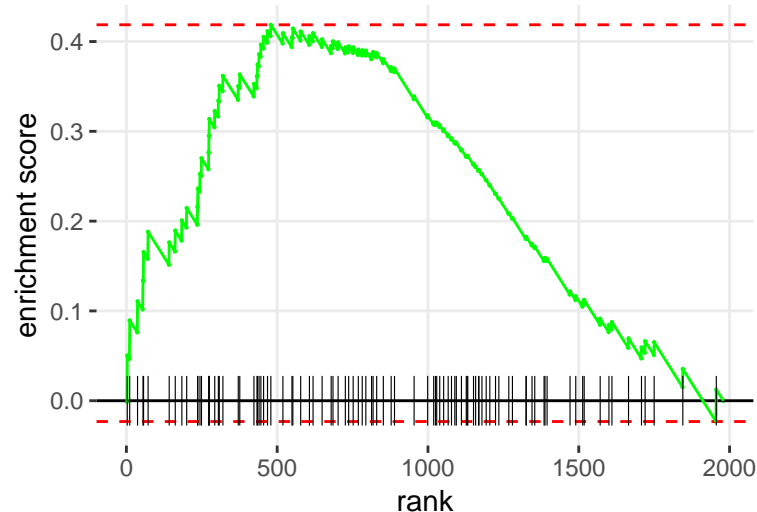
500

1000

1500

2000

rank



RNA BIOSYNTHETIC PROCESS%GOBP%GO:0032774

enrichment score

0.4

0.3

0.2

0.1

0.0

0

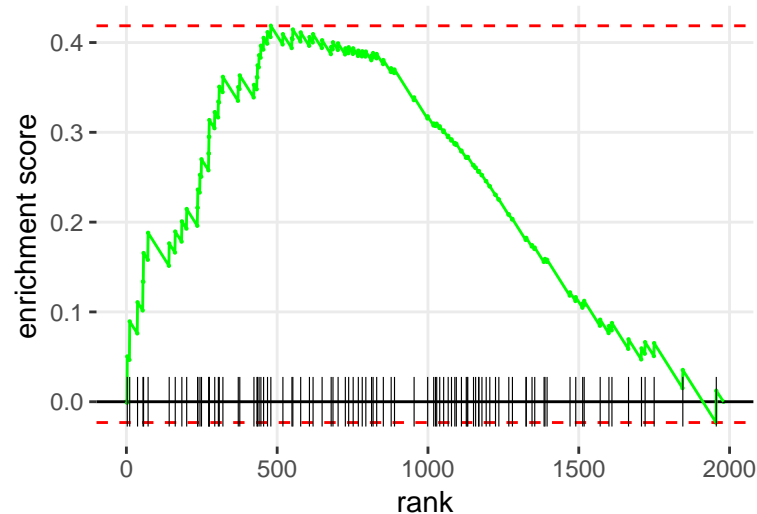
500

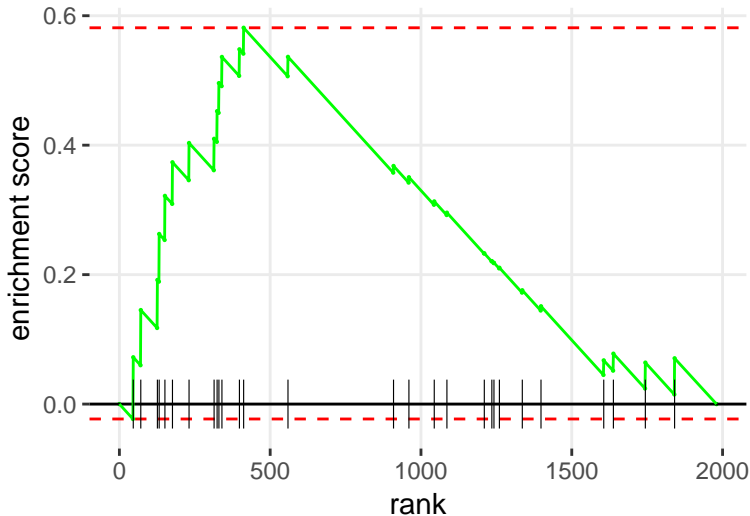
1000

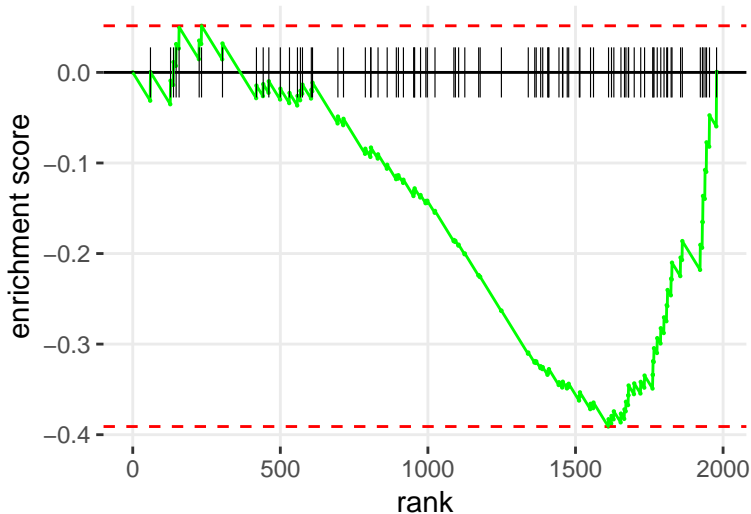
1500

2000

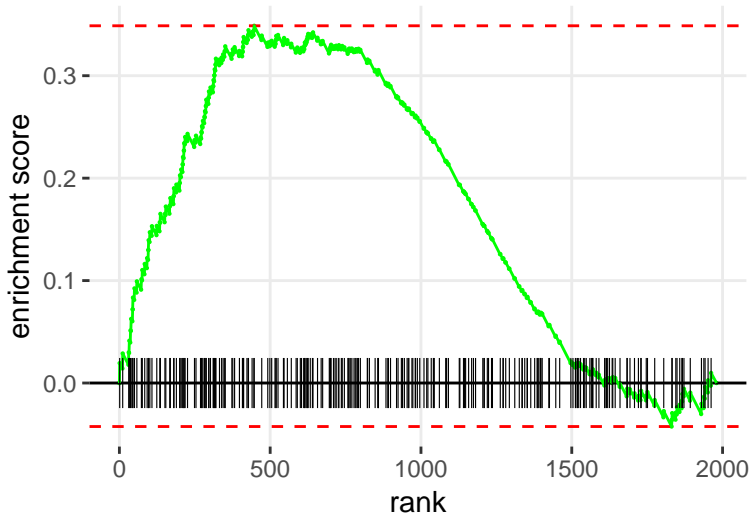
rank



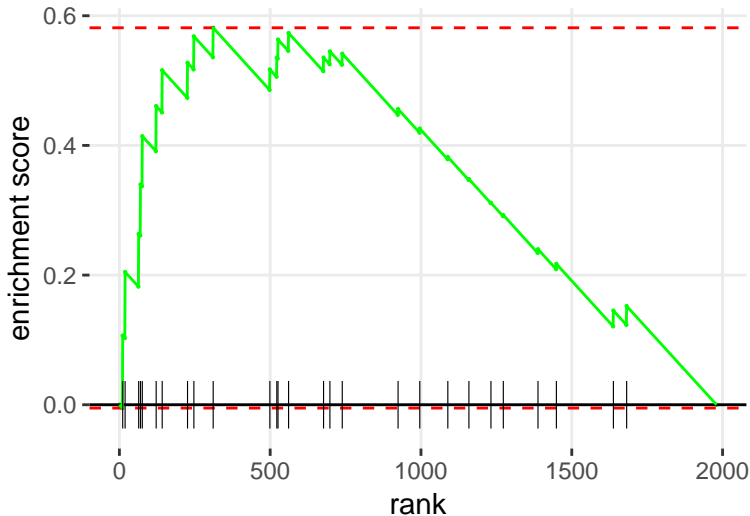




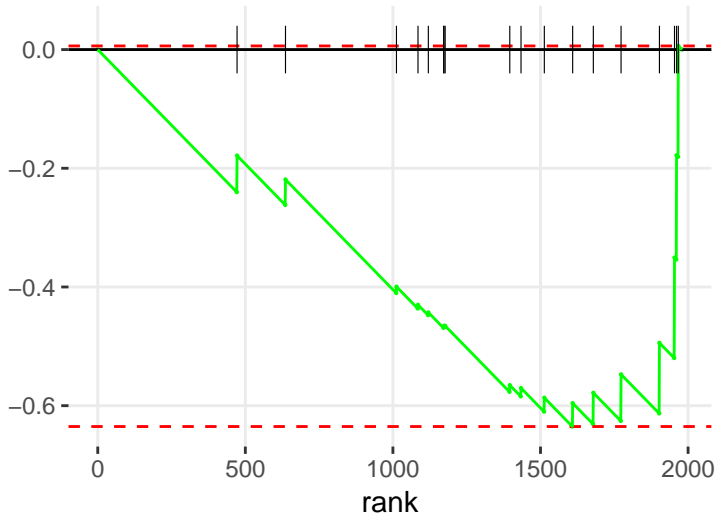
NEGATIVE REGULATION OF GENE EXPRESSION%GOBP%GO:0010629

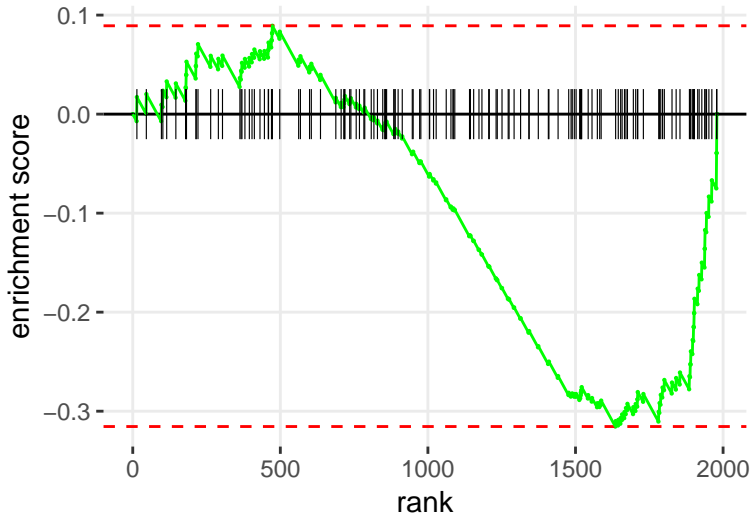


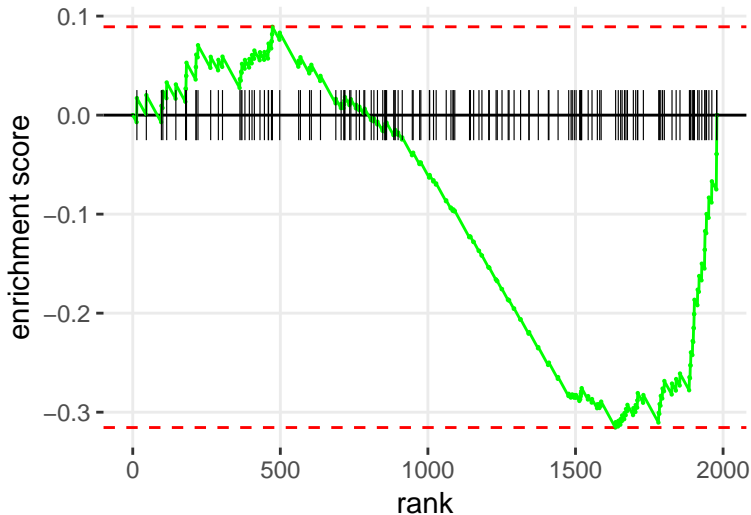
CHROMATIN ASSEMBLY OR DISASSEMBLY%GOBP%GO:0006333



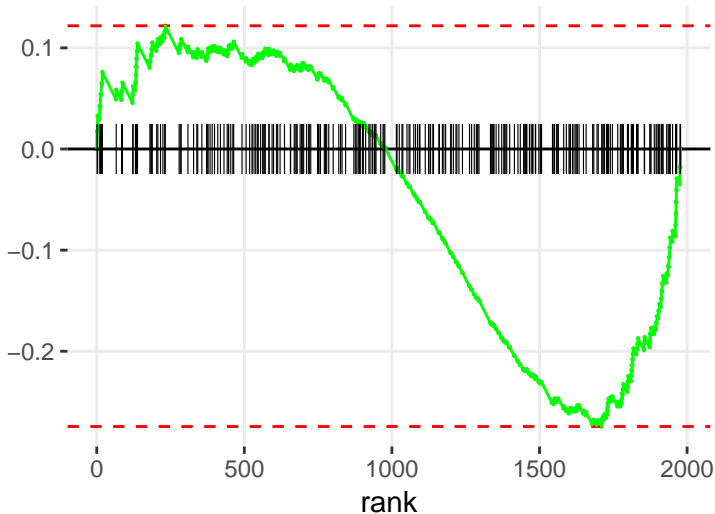
enrichment score



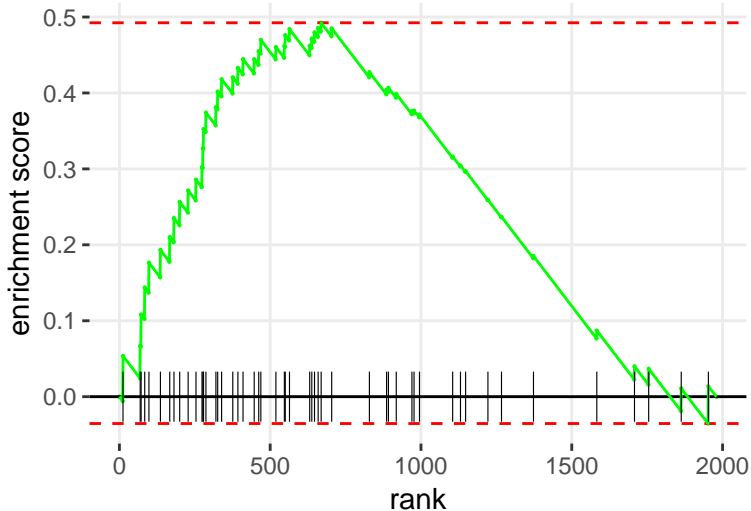




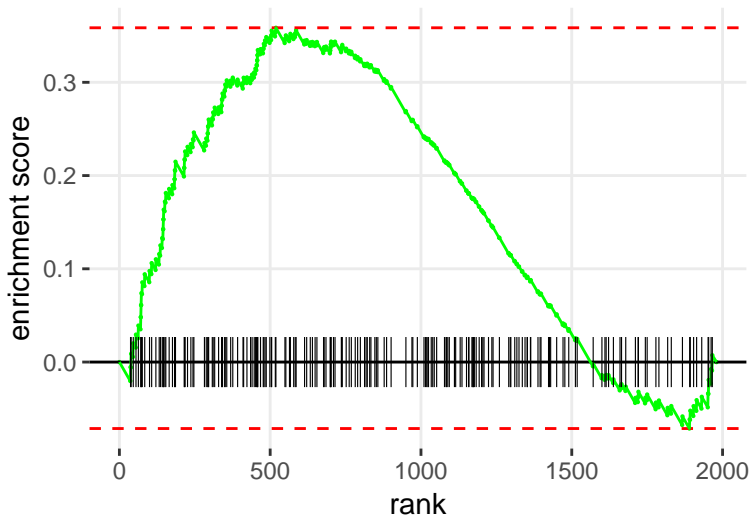
enrichment score

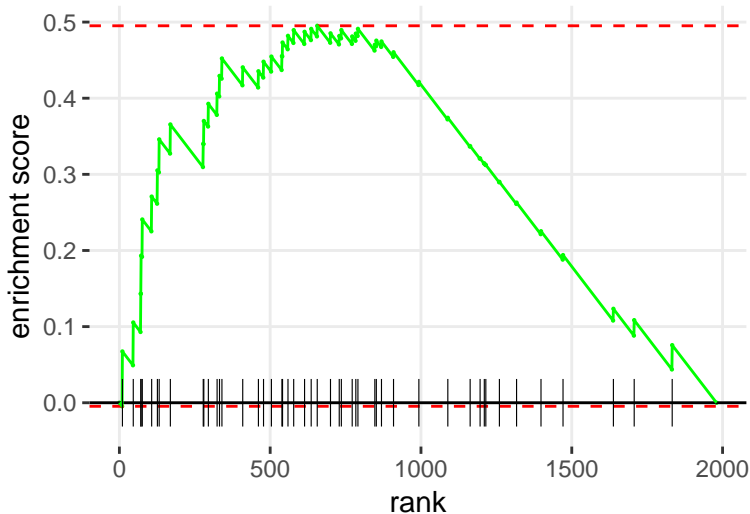


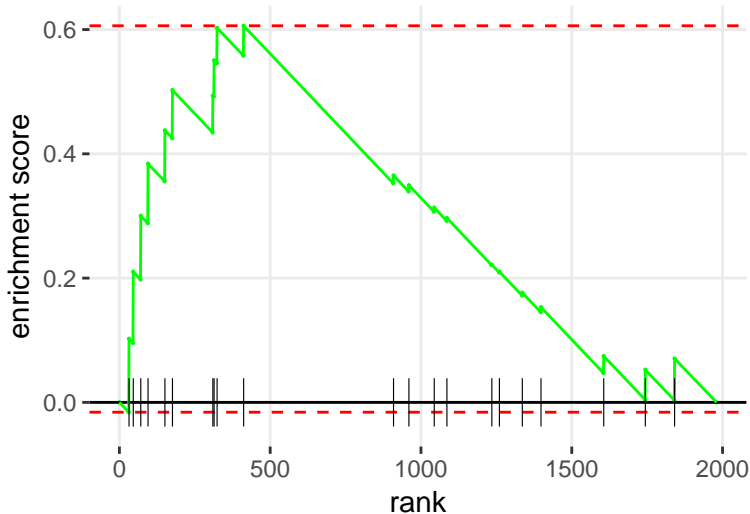
REGULATION OF RNA SPLICING%GOBP%GO:0043484

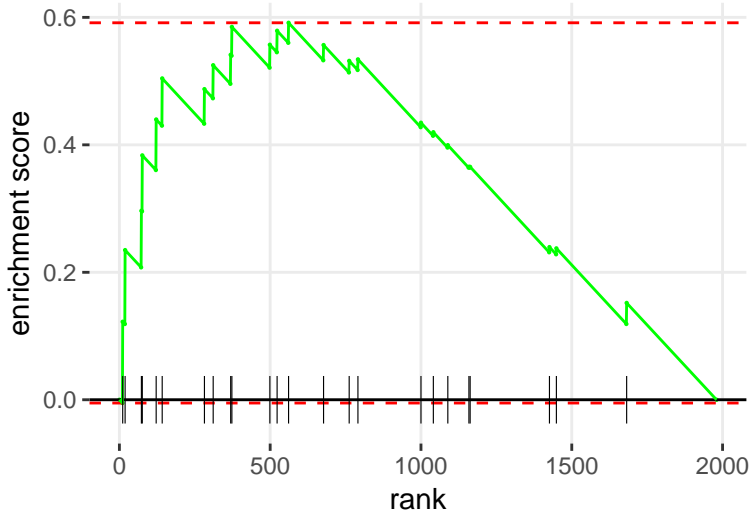


GENE EXPRESSION (TRANSCRIPTION)%REACTOME%R-HSA-74160.7

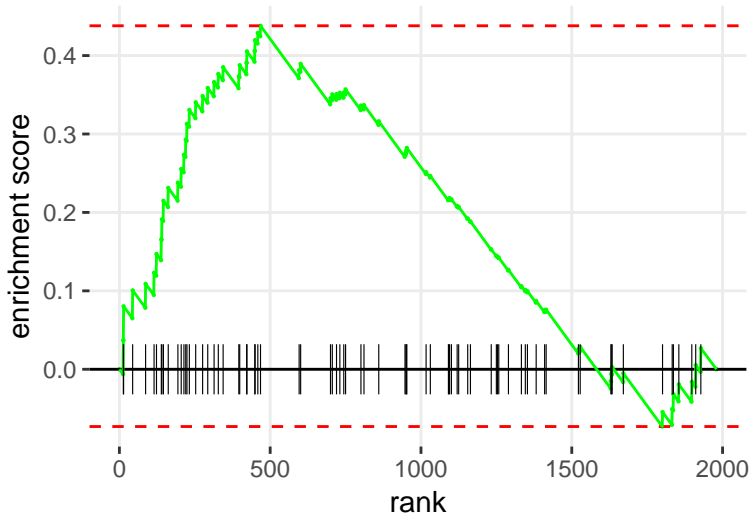


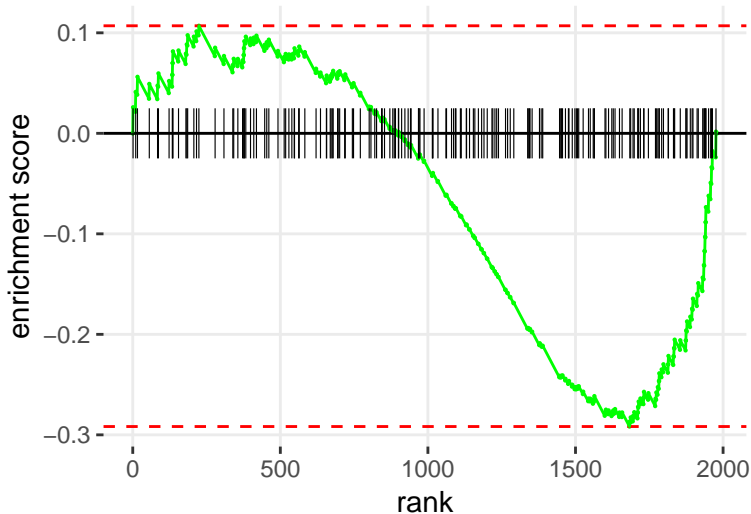




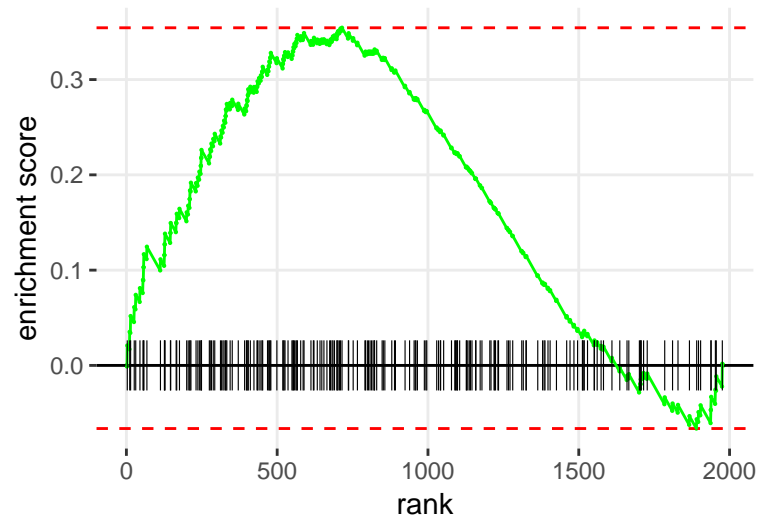


REGULATION OF PROTEIN TRANSPORT%GOBP%GO:0051223



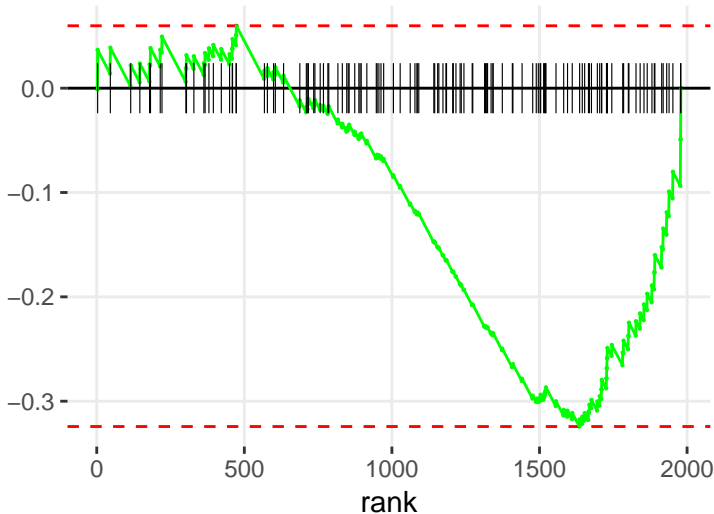


POSITIVE REGULATION OF NUCLEIC ACID-TEMPLATED TRANSCRIPTION%GOBP%GO:1



REGULATION OF KINASE ACTIVITY%GOBP%GO:0043549

enrichment score



PID_TRKR_PATHWAY%MSIGDB_C2%PID_TRKR_PATHWAY

enrichment score

0.0

-0.2

-0.4

-0.6

0

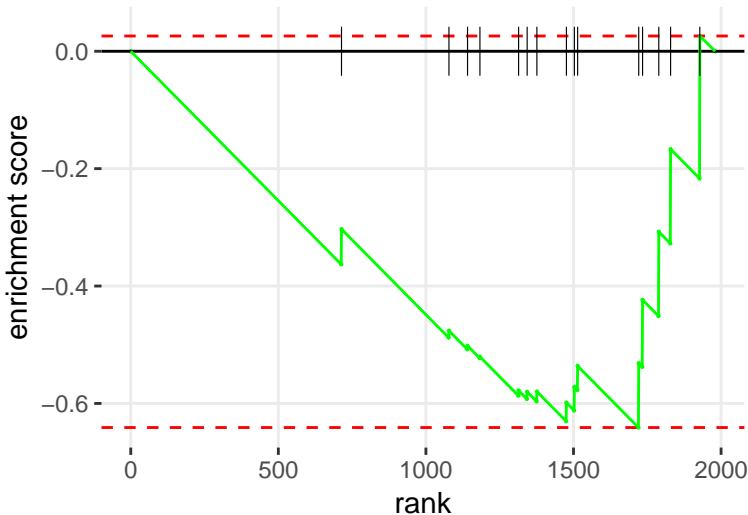
500

1000

1500

2000

rank



POSITIVE REGULATION OF RNA BIOSYNTHETIC PROCESS%GOBP%GO:1902680

enrichment score

0.3

0.2

0.1

0.0

0

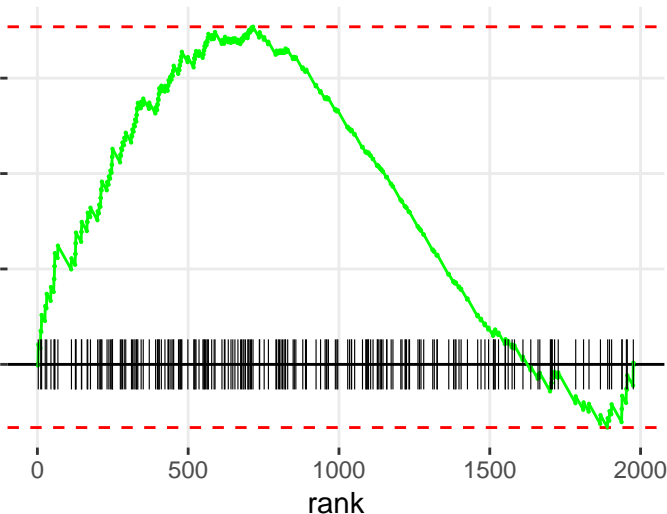
500

1000

1500

2000

rank



REGULATION OF PROTEIN KINASE ACTIVITY%GOBP%GO:0045859

enrichment score

