

Average coverage per intergenic region

K562 NegCtrlSingle E.571 scCLTdegenNuc383

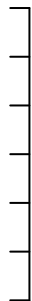
0.00030
0.00015
0.00000

-5kb

intergenic start

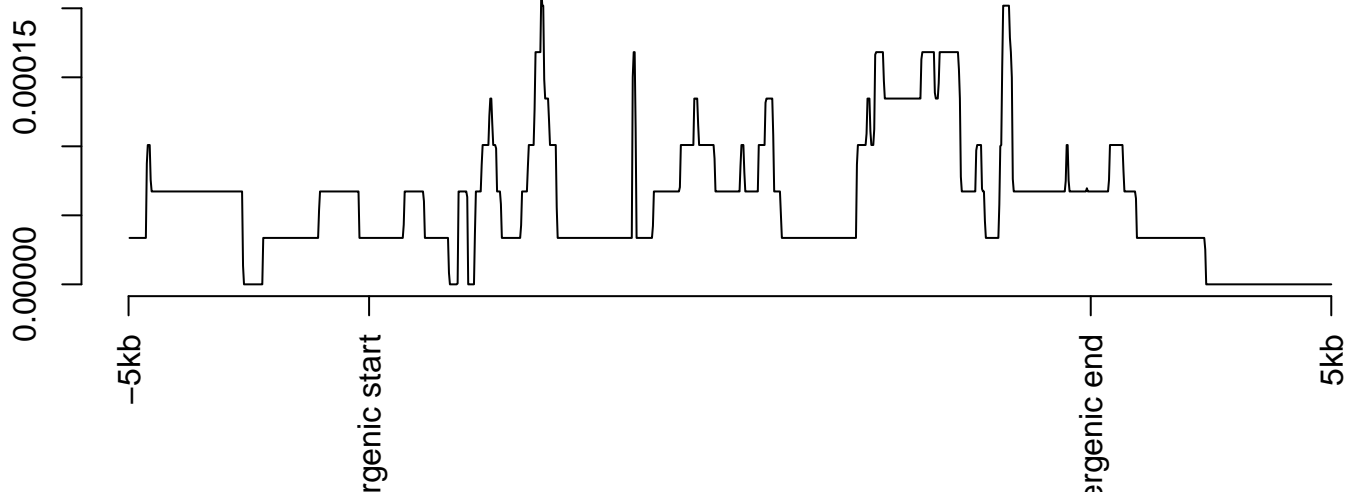
intergenic end

5kb



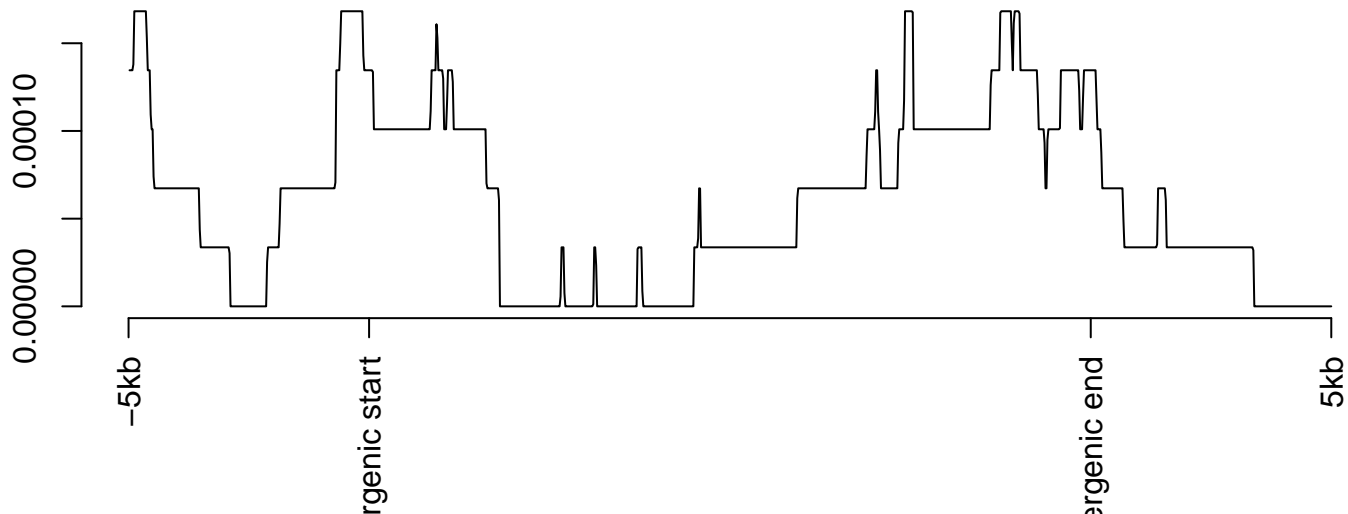
Average coverage per intergenic region

K562 NegCtrlSingle E.571 scCLTdegenNuc384



Average coverage per intergenic region

K562 NegCtrlSingle E.571 scCLTdegenNuc386



Average coverage per intergenic region

K562 NegCtrlSingle E.579 scCLTdegenNuc417

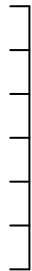
0.00000 0.00020

-5kb

intergenic start

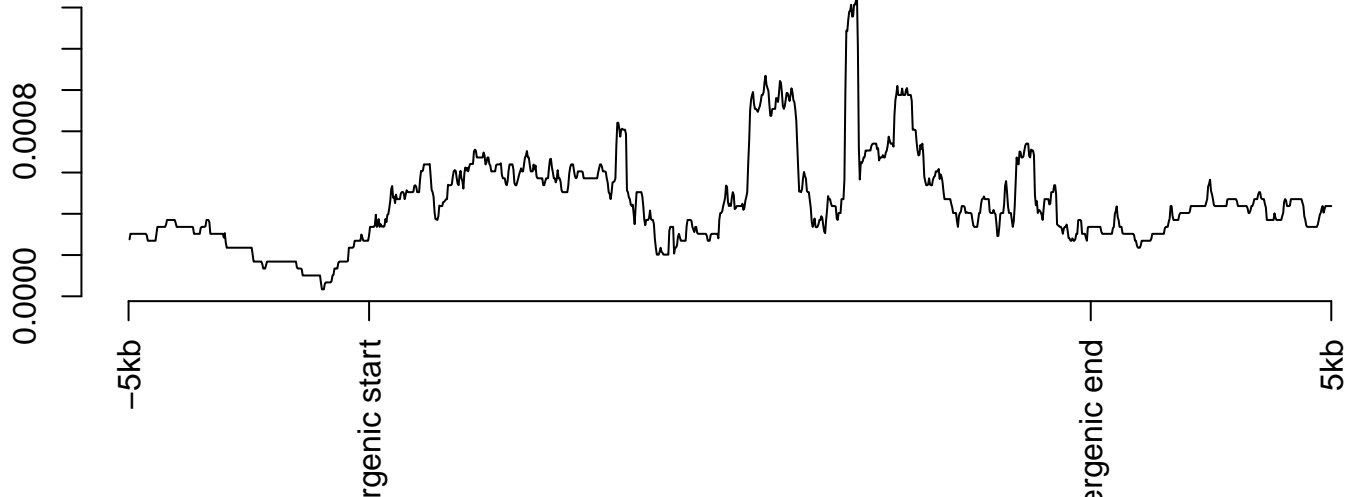
intergenic end

5kb



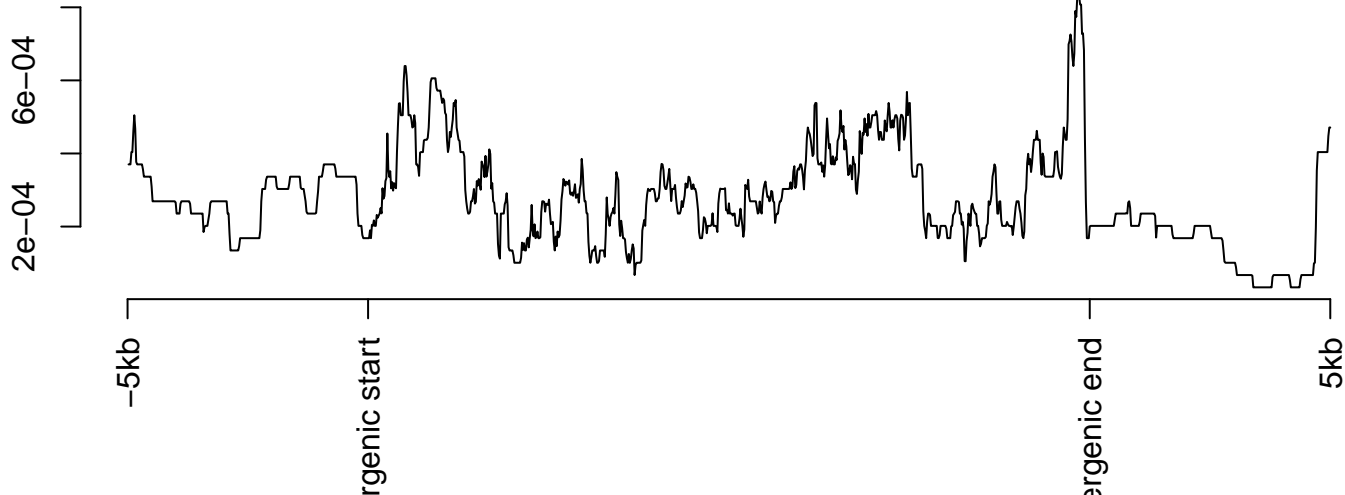
Average coverage per intergenic region

K562 NegCtrlSingle E.579 scCLTdegenNuc418



Average coverage per intergenic region

K562 NegCtrlSingle E.579 scCLTdegenNuc420



Average coverage per intergenic region

K562 NegCtrlSingle E.579 scCLTdegenNuc422

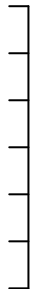
0.0012
0.0006
0.0000

-5kb

intergenic start

intergenic end

5kb



Average coverage per intergenic region

K562 NegCtrlSingle E.579 scCLTdegenNuc423

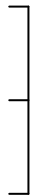
0.0015
0.0005

-5kb

intergenic start

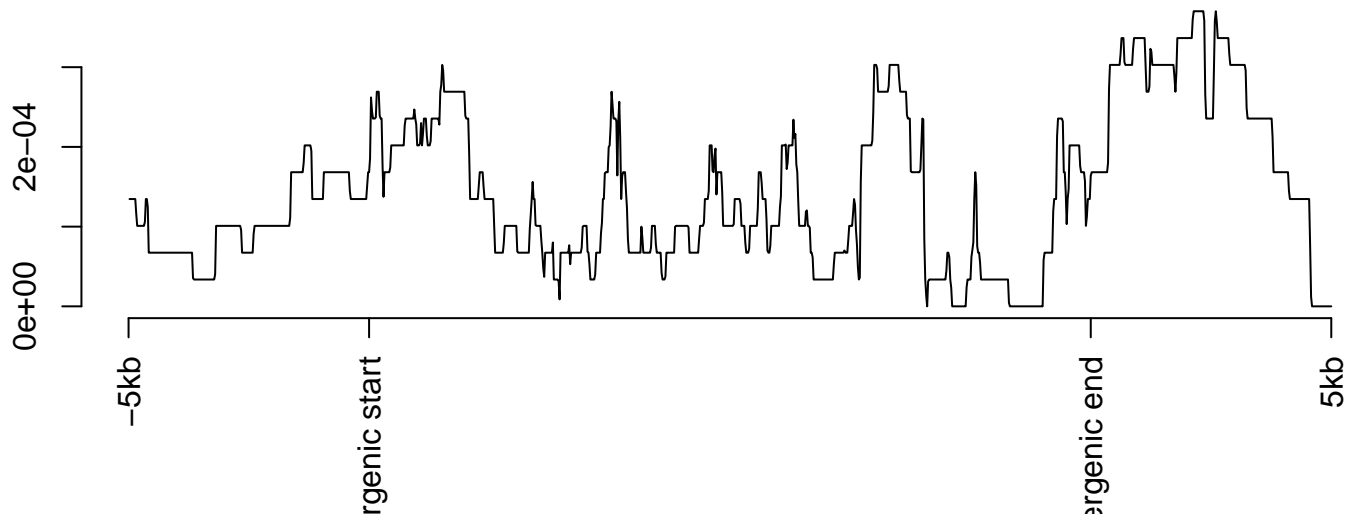
intergenic end

5kb



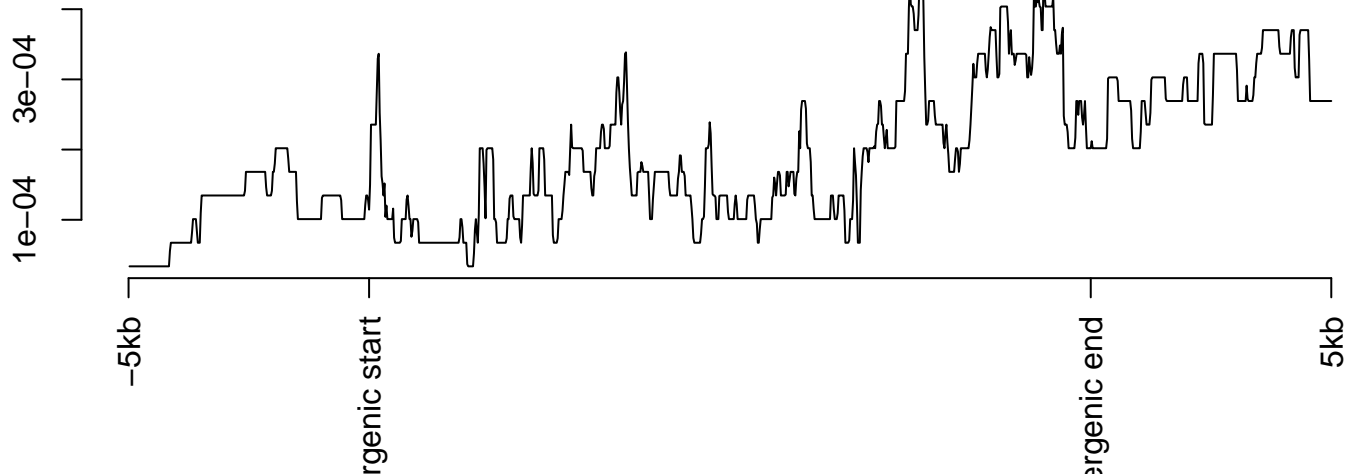
Average coverage per intergenic region

K562 NegCtrlSingle E.579 scCLTdegenNuc424



Average coverage per intergenic region

K562 NegCtrlSingle E.579 scCLTdegenNuc425



Average coverage per intergenic region

K562 NegCtrlSingle E.671 scCLTdegenNuc897

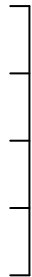
0.010
0.006
0.002

-5kb

intergenic start

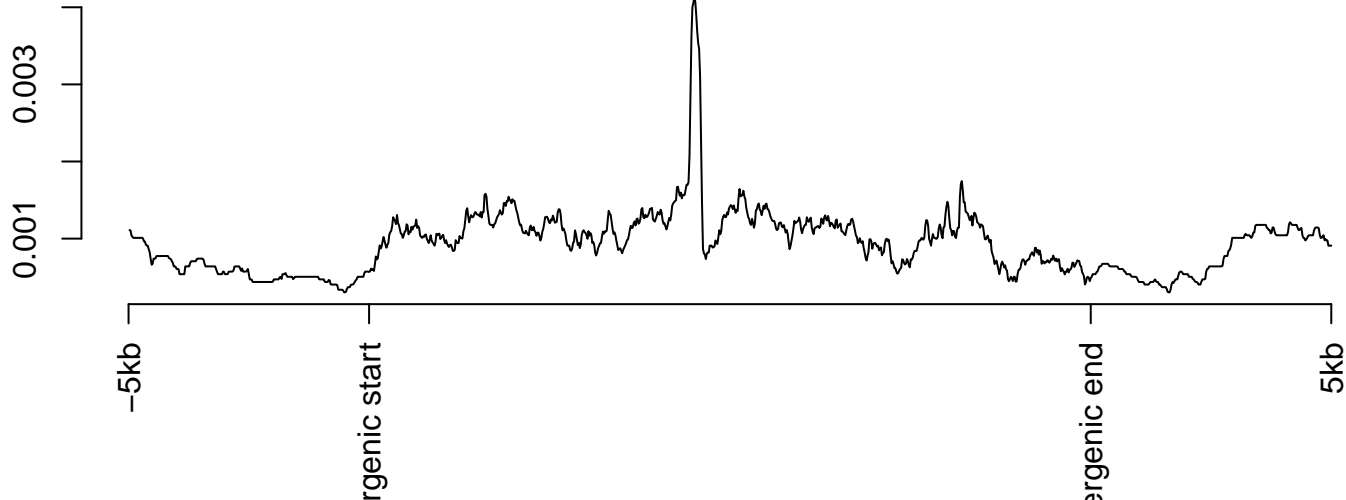
intergenic end

5kb



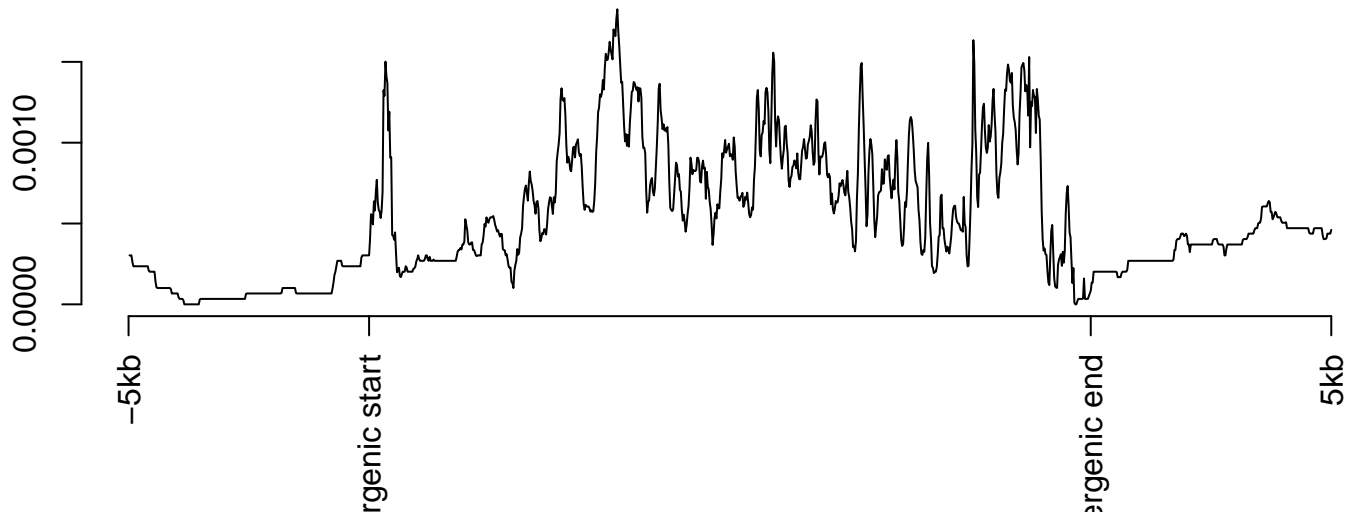
Average coverage per intergenic region

K562 NegCtrlSingle E.671 scCLTdegenNuc898



Average coverage per intergenic region

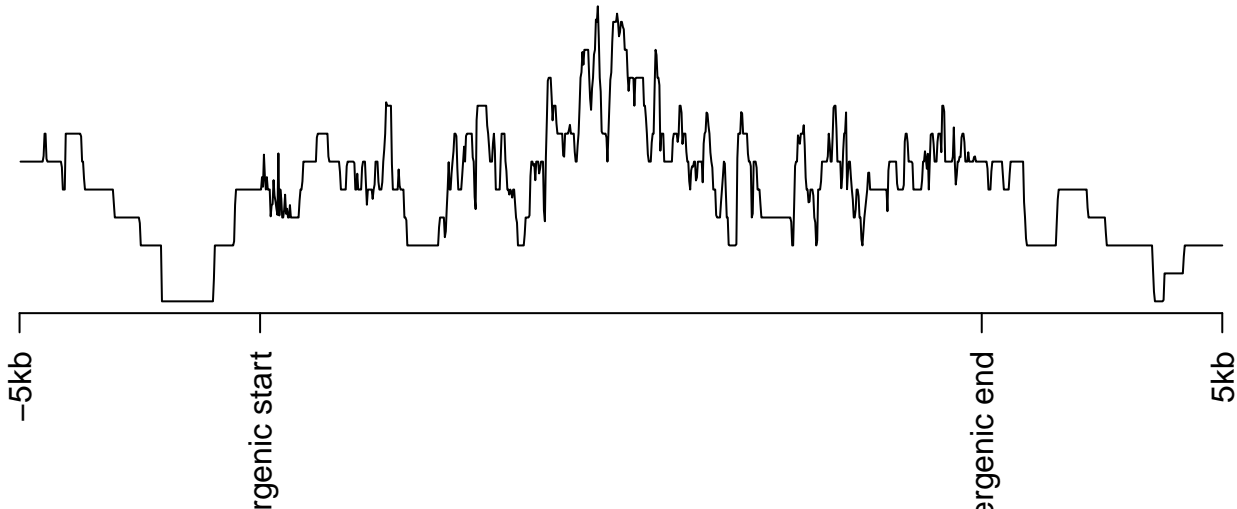
K562 NegCtrlSingle E.671 scCLTdegenNuc900



Average coverage per intergenic region

K562 NegCtrlSingle E.671 scCLTdegenNuc902

0.00020
0.00000



Average coverage per intergenic region

K562 NegCtrlSingle E.671 scCLTdegenNuc903

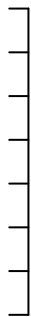
0.0035
0.0020
0.0005

-5kb

intergenic start

intergenic end

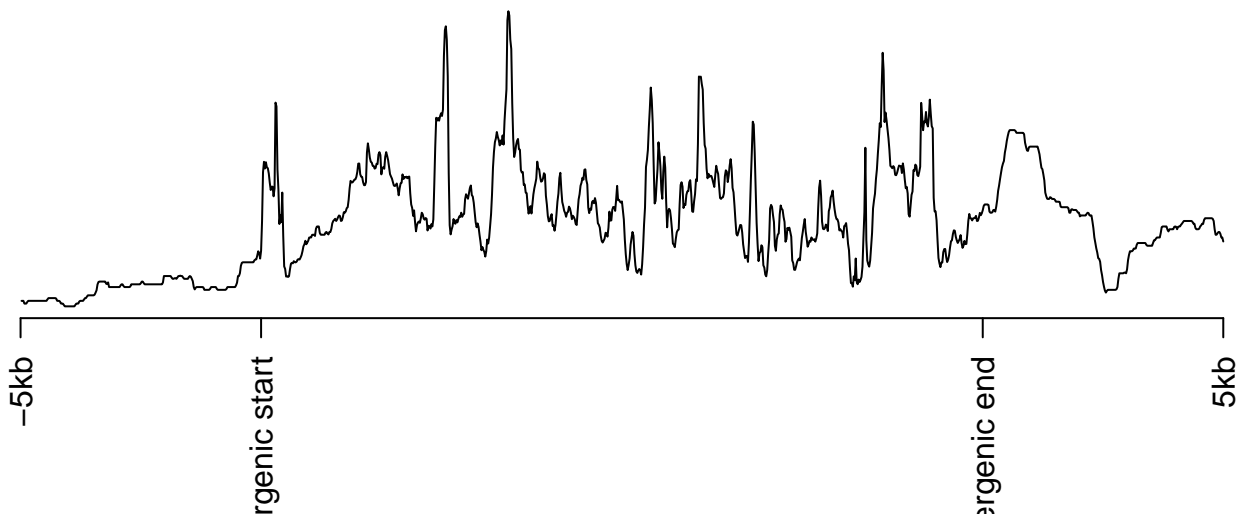
5kb



Average coverage per intergenic region

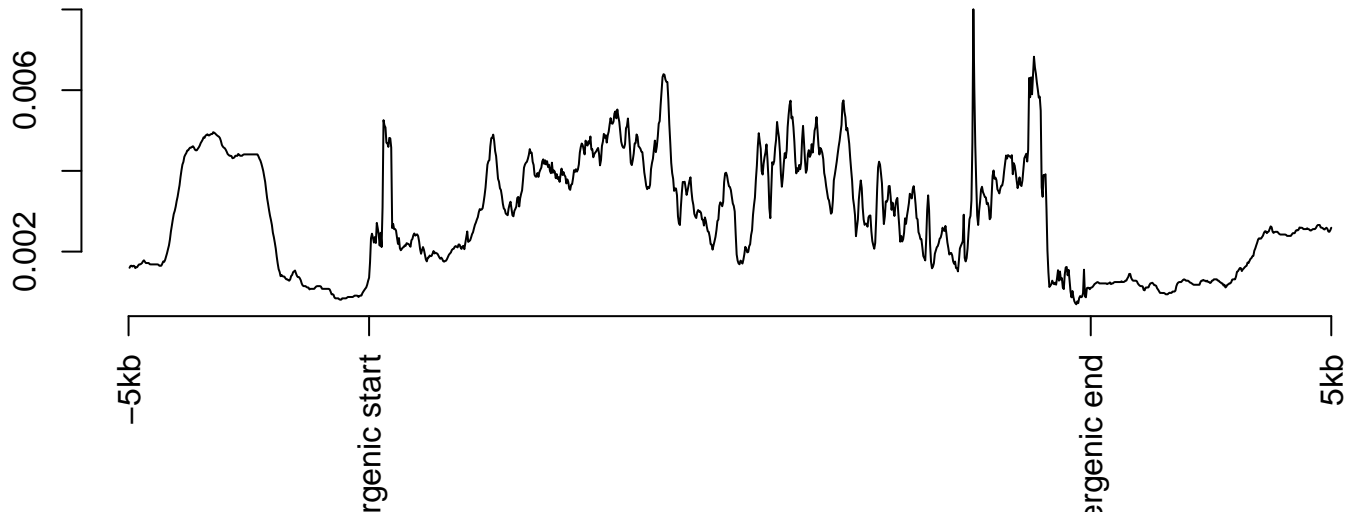
K562 NegCtrlSingle E.676 scCLTdegenNuc950

0.003
0.001



Average coverage per intergenic region

K562 NegCtrlSingle E.678 scCLTdegenNuc957



Average coverage per intergenic region

K562 NegCtrlPooled E.591 scCLTdegenNuc463

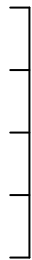
0.004 0.008 0.012

-5kb

intergenic start

intergenic end

5kb



Average coverage per intergenic region

K562 NegCtrlPooled E.591 scCLTdegenNuc464

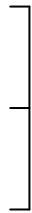
0.015
0.005

-5kb

intergenic start

intergenic end

5kb



Average coverage per intergenic region

K562 NegCtrlMerged E.- K562NegCtrlMerged

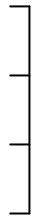
0.010
0.020

-5kb

intergenic start

intergenic end

5kb



Average coverage per intergenic region

K562 NegCtrlAll E.- K562NegCtrlAll

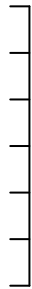
0.045
0.030
0.015

-5kb

intergenic start

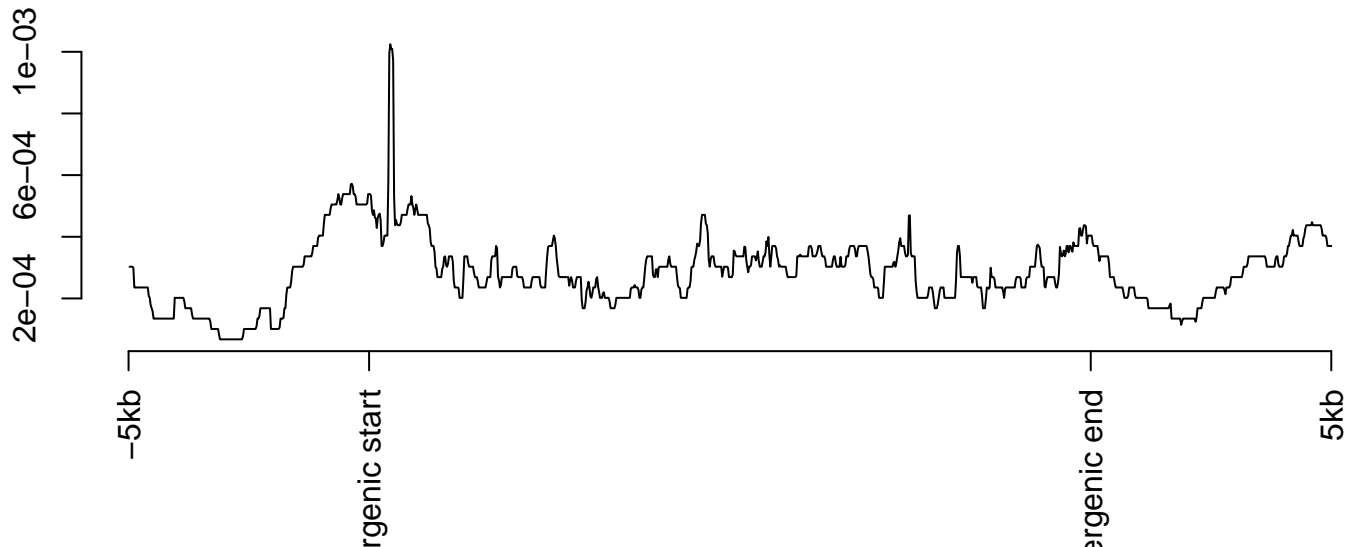
intergenic end

5kb



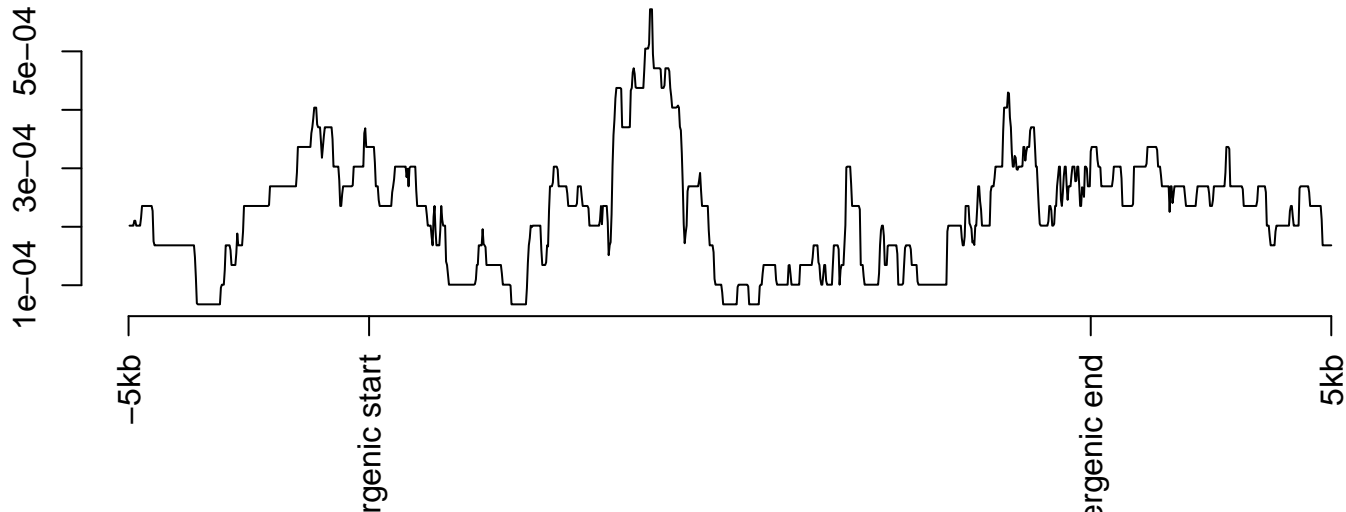
Average coverage per intergenic region

K562 PositiveSingle E.571 scCLTdegenNuc404



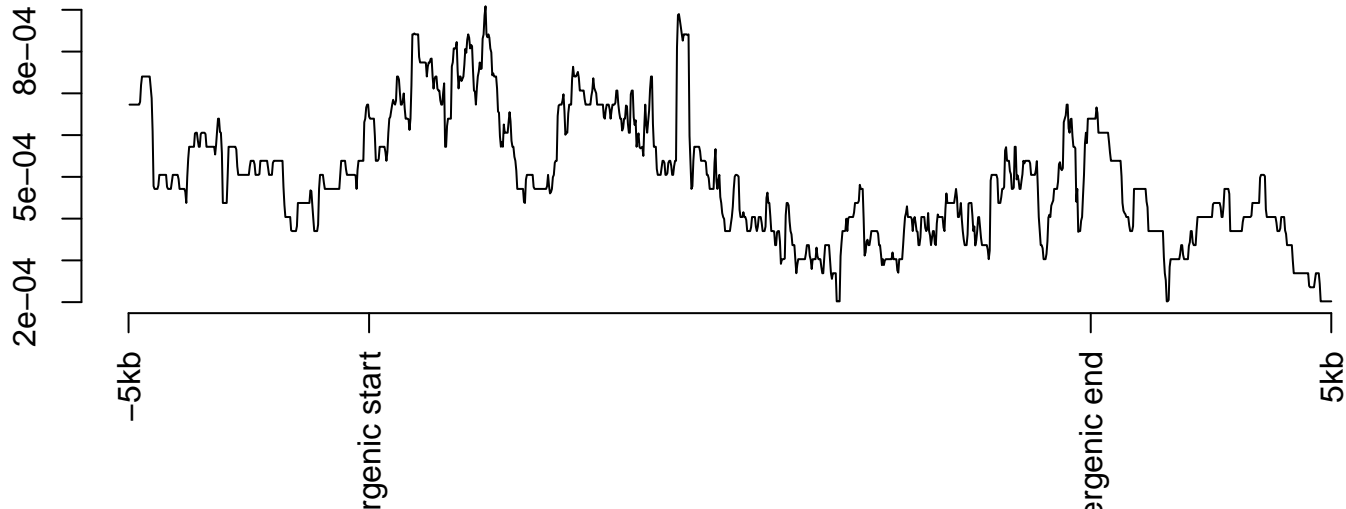
Average coverage per intergenic region

K562 PositiveSingle E.571 scCLTdegenNuc406



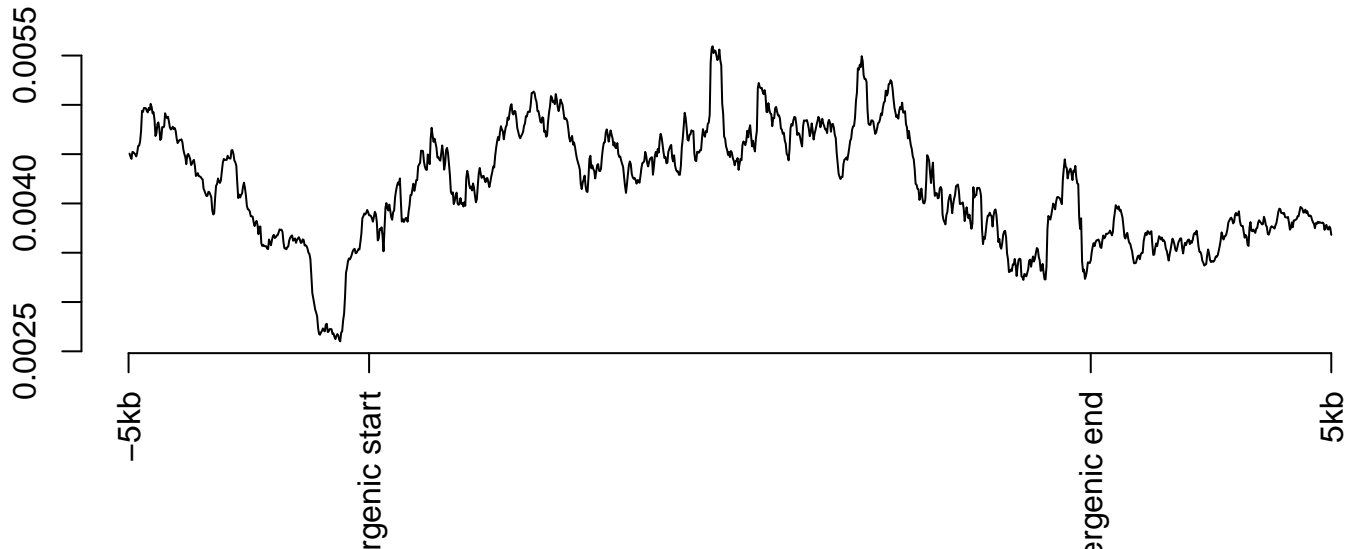
Average coverage per intergenic region

K562 PositiveSingle E.571 scCLTdegenNuc408



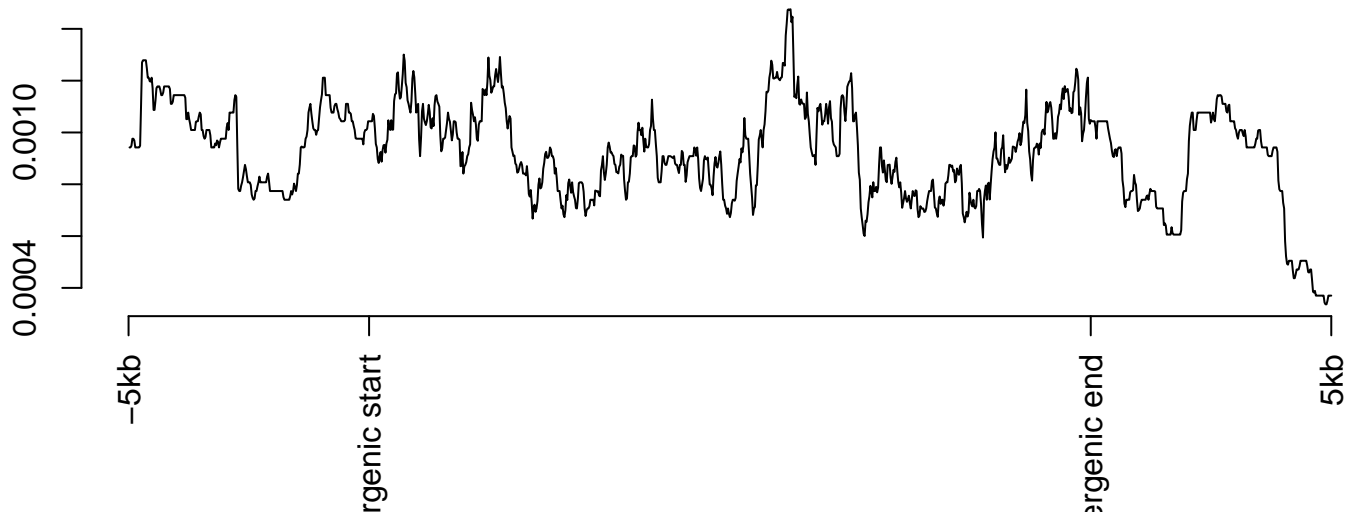
Average coverage per intergenic region

K562 PositiveSingle E.571 scCLTdegenNuc409



Average coverage per intergenic region

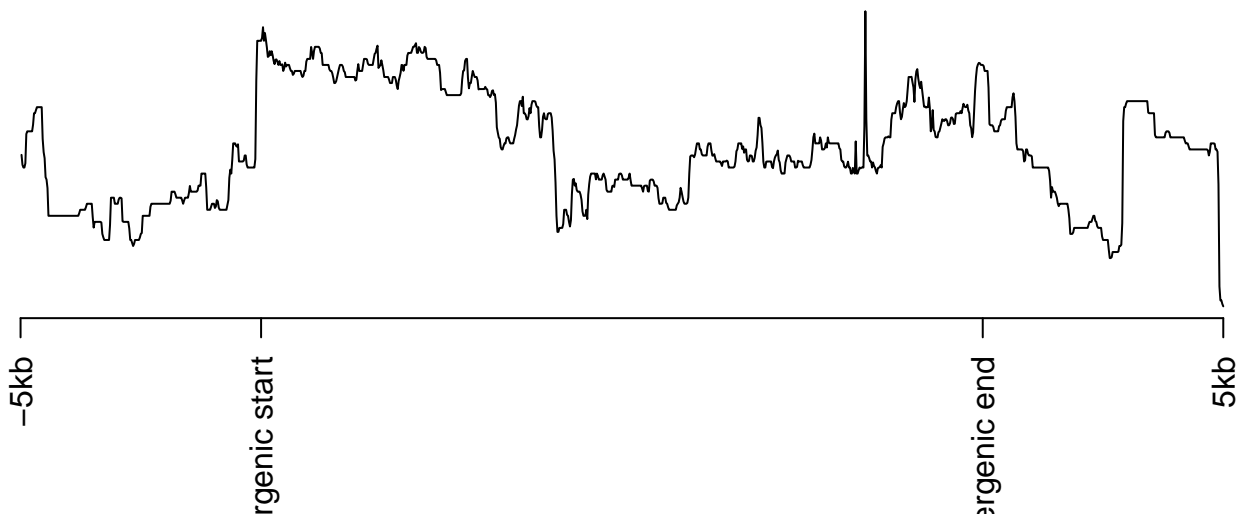
K562 PositiveSingle E.571 scCLTdegenNuc410



Average coverage per intergenic region

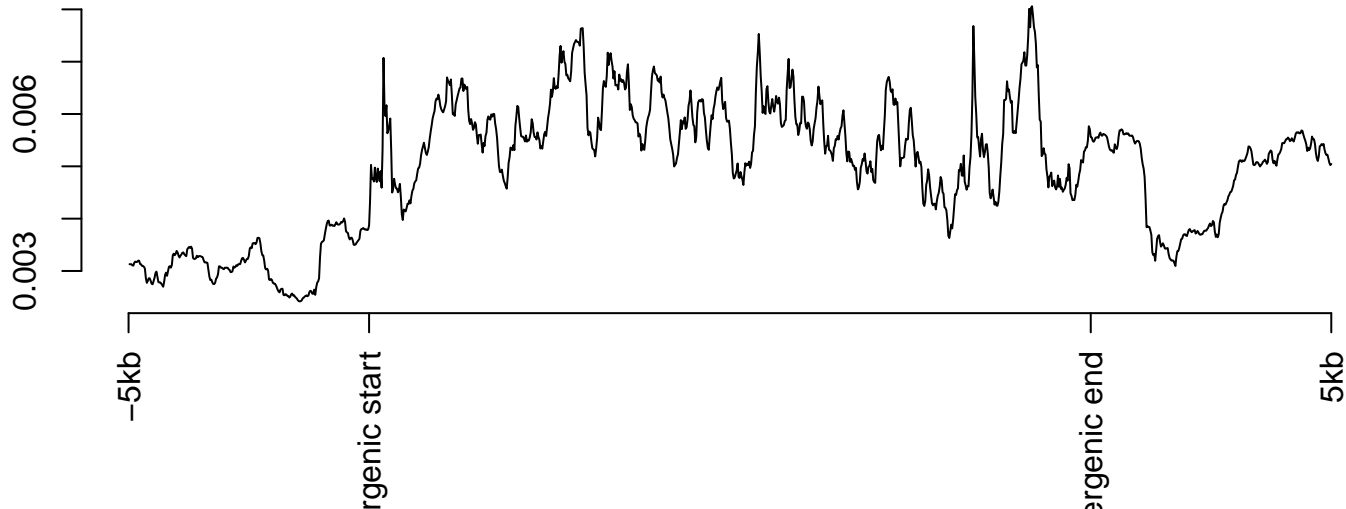
K562 PositiveSingle E.571 scCLTdegenNuc411

0.0015
0.0005



Average coverage per intergenic region

K562 PositiveSingle E.574 scCLTdegenNuc334



Average coverage per intergenic region

K562 PositiveSingle E.574 scCLTdegenNuc335

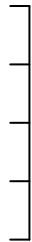
0.003 0.005 0.007

-5kb

intergenic start

intergenic end

5kb



Average coverage per intergenic region

K562 PositiveSingle E.574 scCLTdegenNuc336

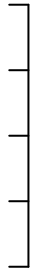
0.004 0.008 0.012

-5kb

intergenic start

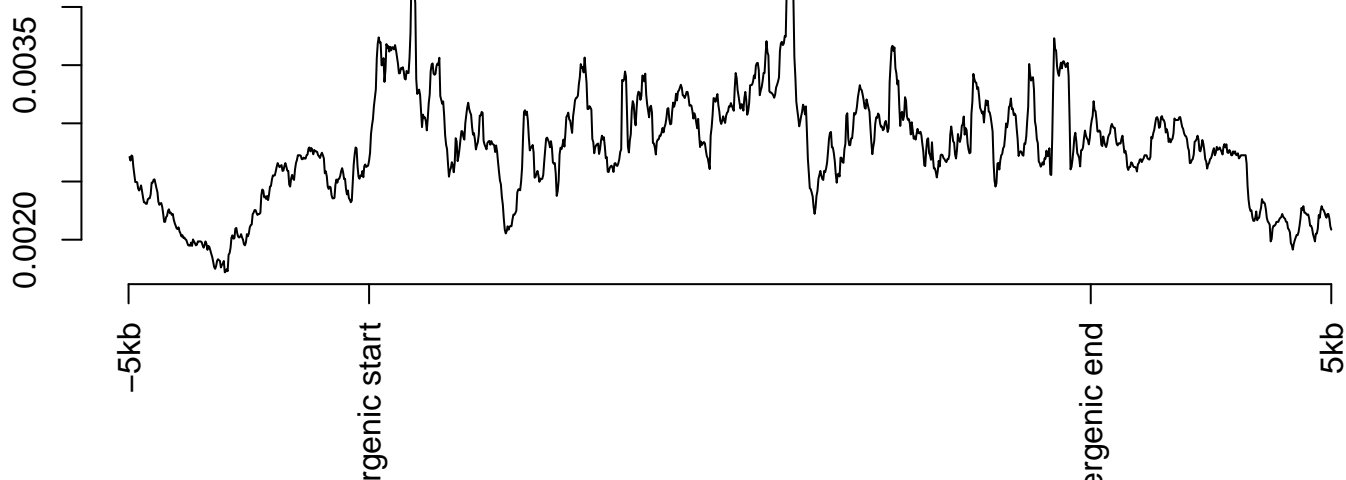
intergenic end

5kb



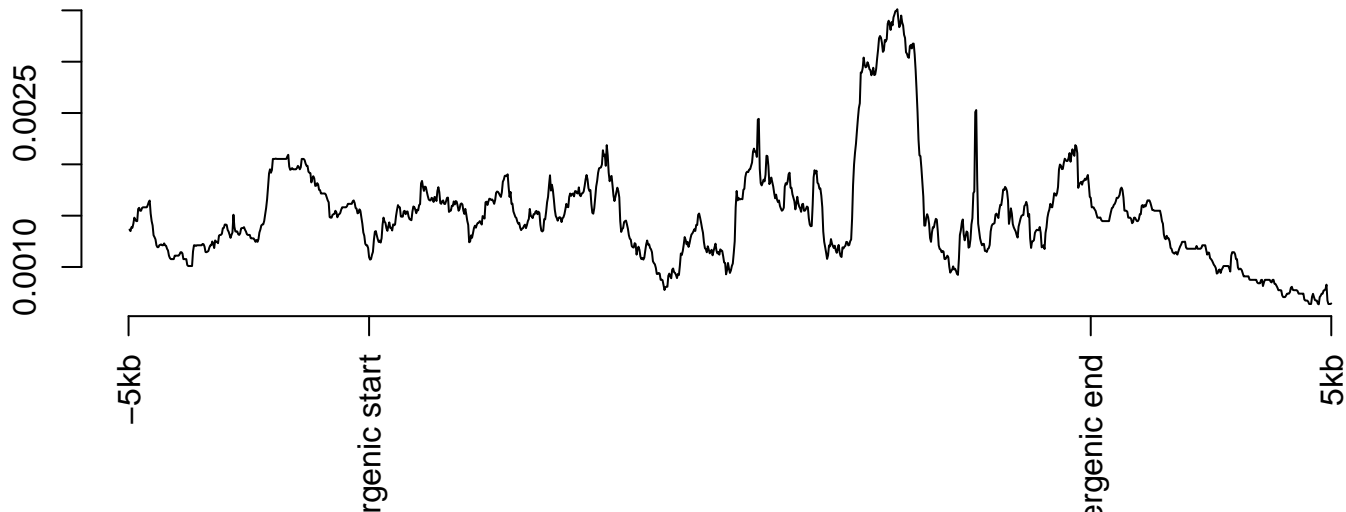
Average coverage per intergenic region

K562 PositiveSingle E.579 scCLTdegenNuc337



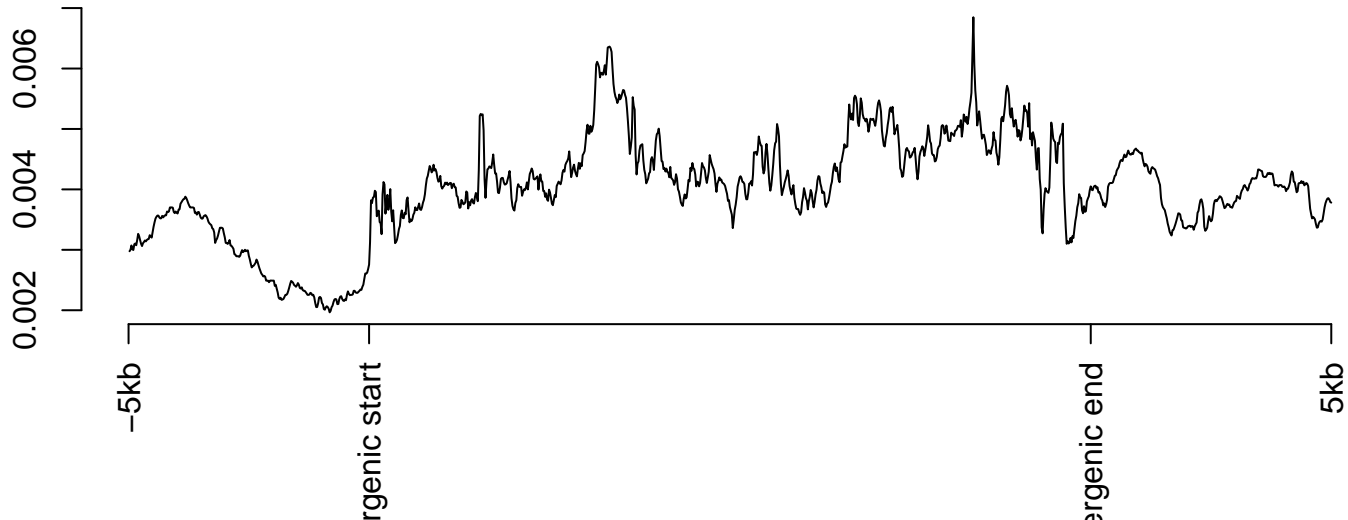
Average coverage per intergenic region

K562 PositiveSingle E.579 scCLTdegenNuc338



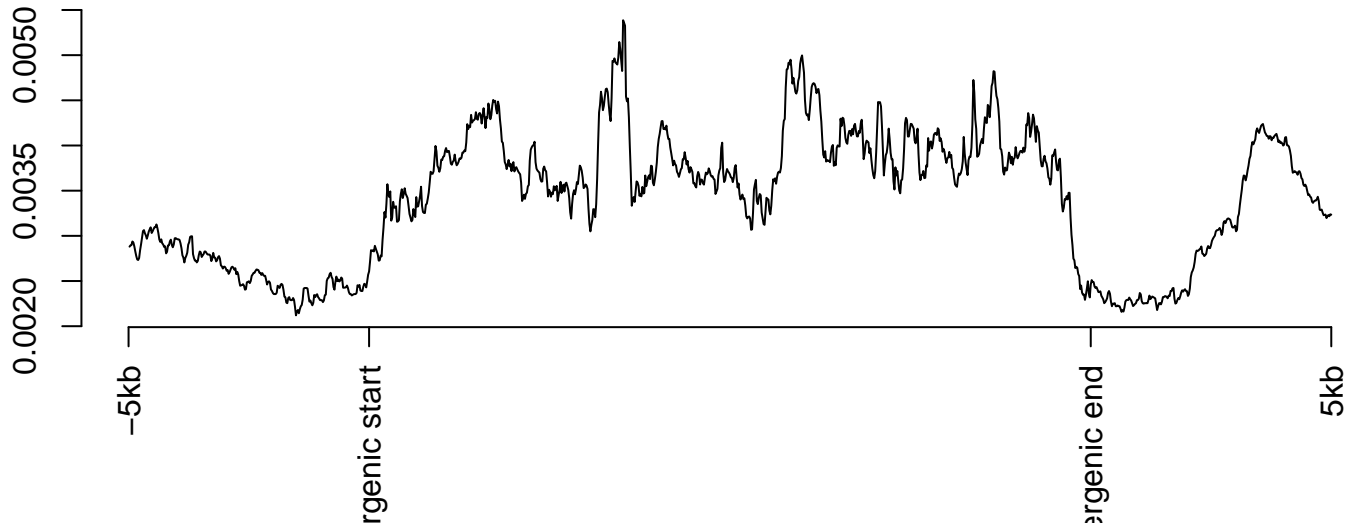
Average coverage per intergenic region

K562 PositiveSingle E.579 scCLTdegenNuc339



Average coverage per intergenic region

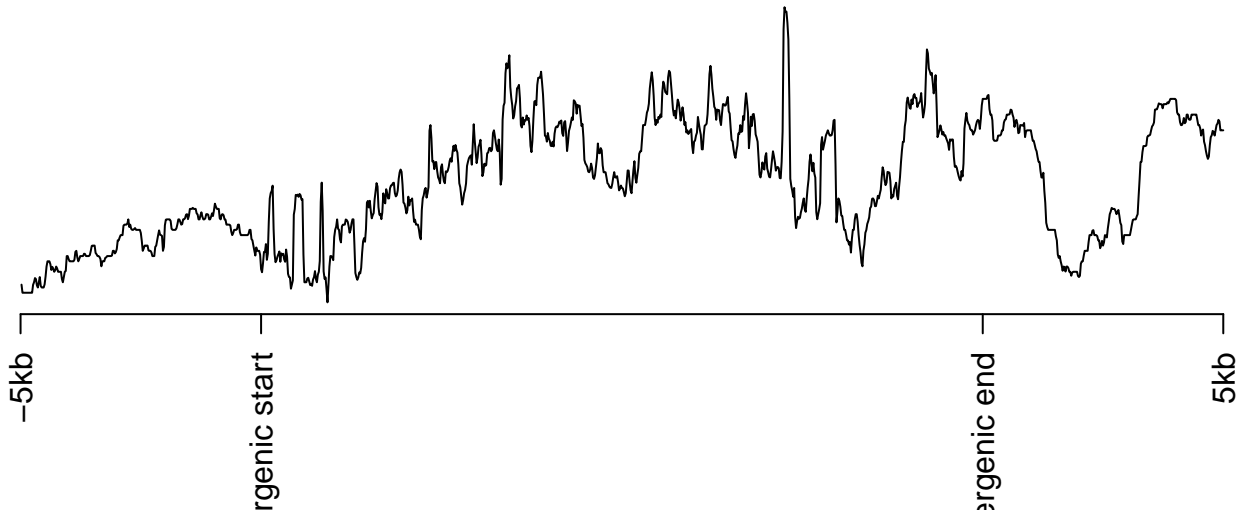
K562 PositiveSingle E.579 scCLTdegenNuc340



Average coverage per intergenic region

K562 PositiveSingle E.579 scCLTdegenNuc341

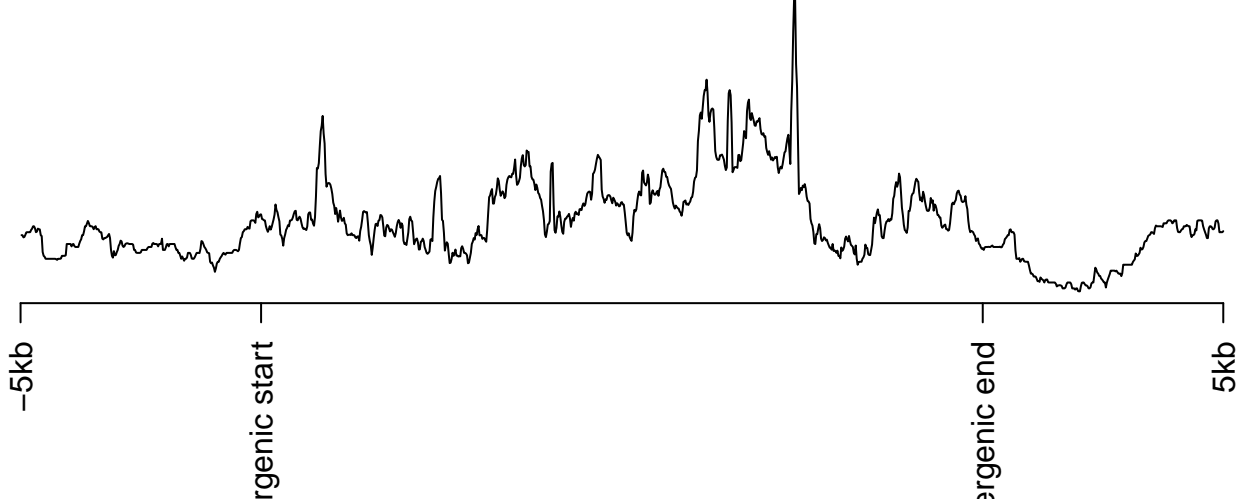
0.0010 0.0020



Average coverage per intergenic region

K562 PositiveSingle E.580 scCLTdegenNuc342

0.0010 0.0025 0.0040



Average coverage per intergenic region

K562 PositiveSingle E.580 scCLTdegenNuc343

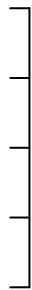
0.0030
0.0020
0.0010

-5kb

intergenic start

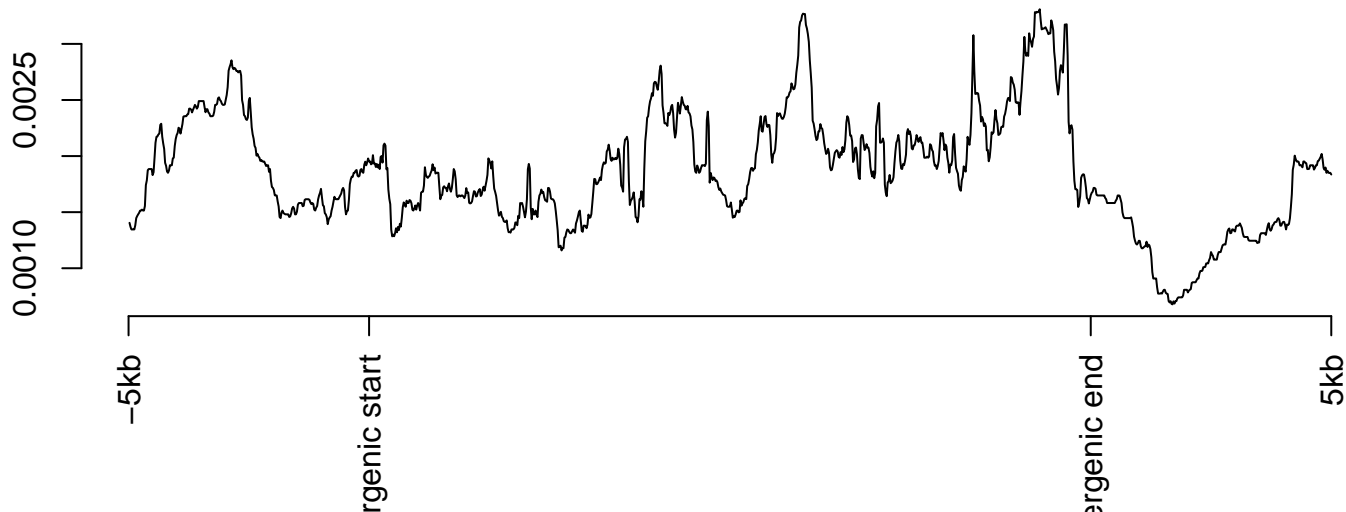
intergenic end

5kb



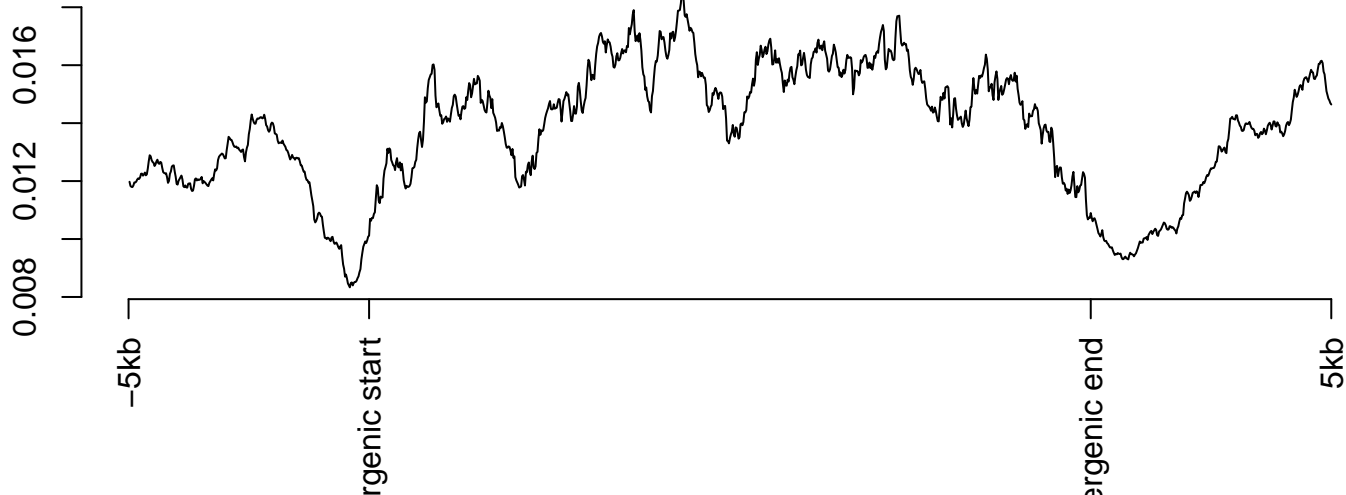
Average coverage per intergenic region

K562 PositiveSingle E.580 scCLTdegenNuc345



Average coverage per intergenic region

K562 PositiveSingle E.580 scCLTdegenNuc428



Average coverage per intergenic region

K562 PositiveSingle E.588 scCLTdegenNuc323

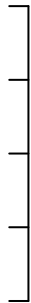
0.0005 0.0015 0.0025

-5kb

intergenic start

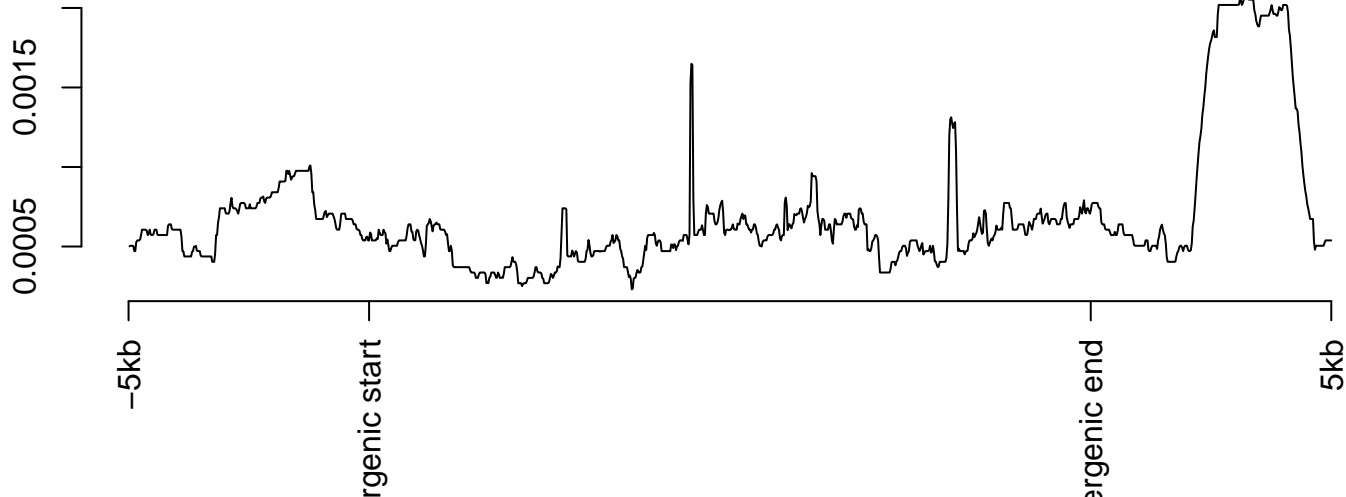
intergenic end

5kb



Average coverage per intergenic region

K562 PositiveSingle E.588 scCLTdegenNuc324



Average coverage per intergenic region

K562 PositiveSingle E.588 scCLTdegenNuc325

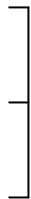
0.0015
0.0005

-5kb

intergenic start

intergenic end

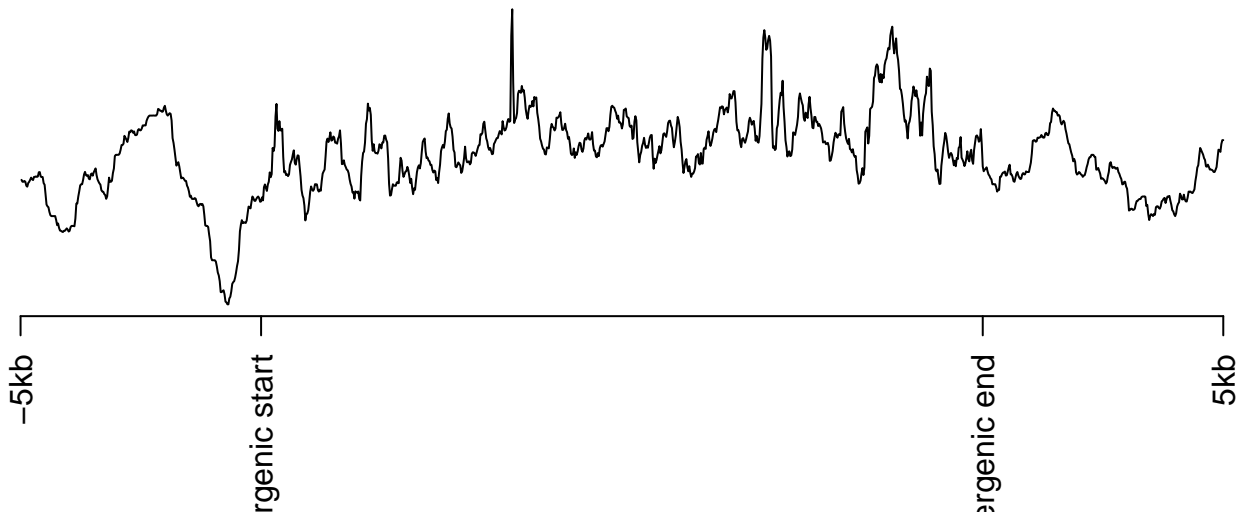
5kb



Average coverage per intergenic region

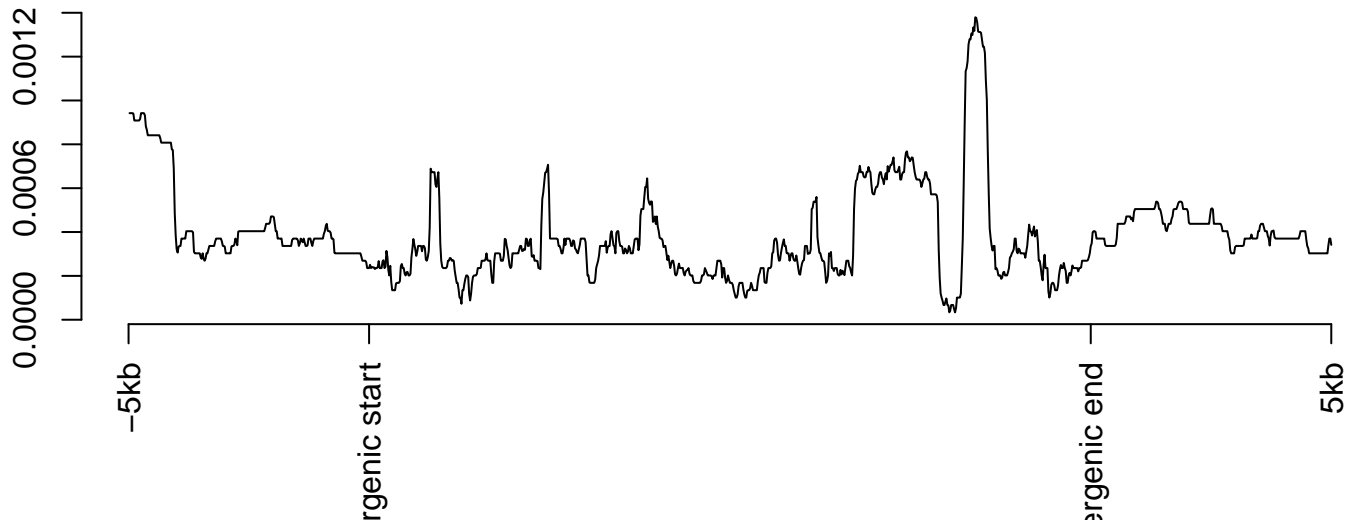
K562 PositiveSingle E.588 scCLTdegenNuc446

0.004
0.002



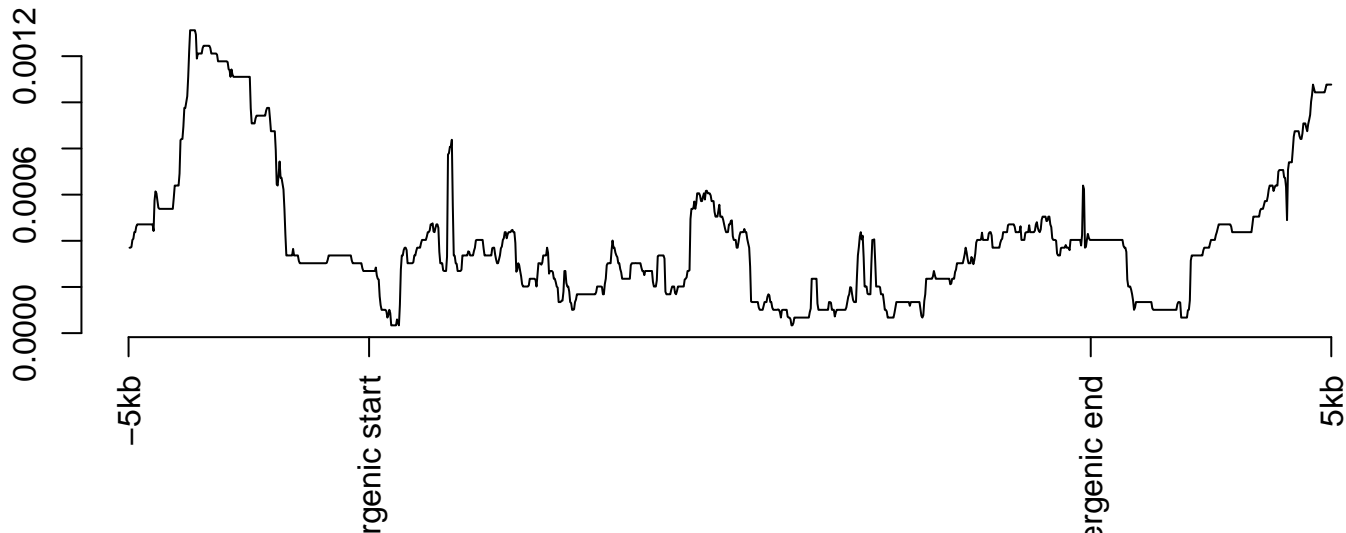
Average coverage per intergenic region

K562 PositiveSingle E.588 scCLTdegenNuc447



Average coverage per intergenic region

K562 PositiveSingle E.588 scCLTdegenNuc448



Average coverage per intergenic region

K562 PositiveSingle E.588 scCLTdegenNuc452

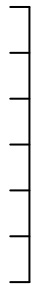
0.0020 0.0035 0.0050

-5kb

intergenic start

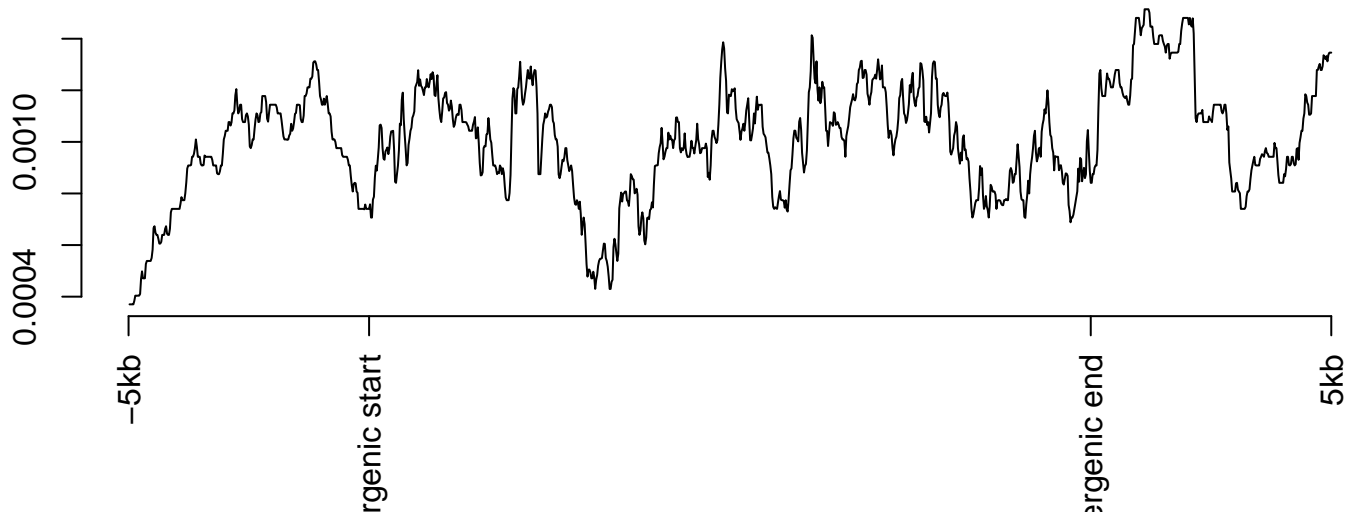
intergenic end

5kb



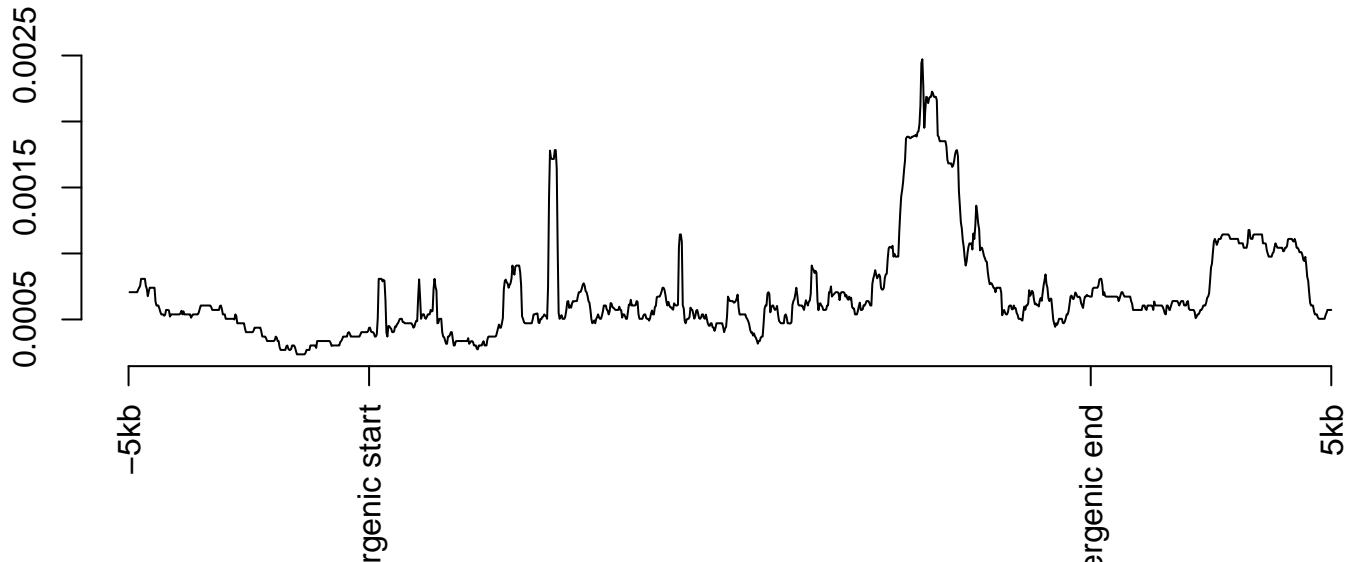
Average coverage per intergenic region

K562 PositiveSingle E.588 scCLTdegenNuc454



Average coverage per intergenic region

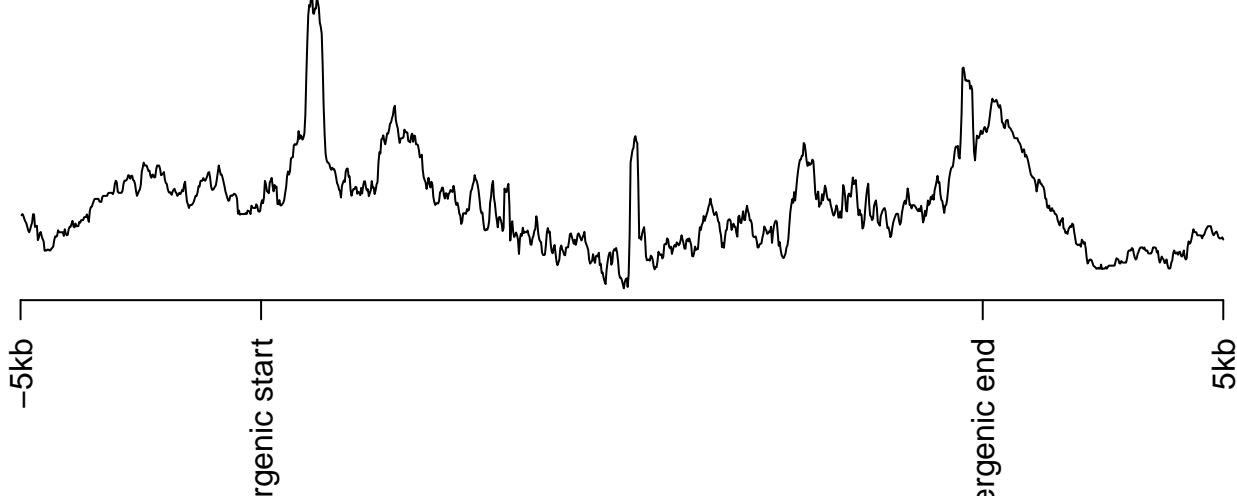
K562 PositiveSingle E.588 scCLTdegenNuc455



Average coverage per intergenic region

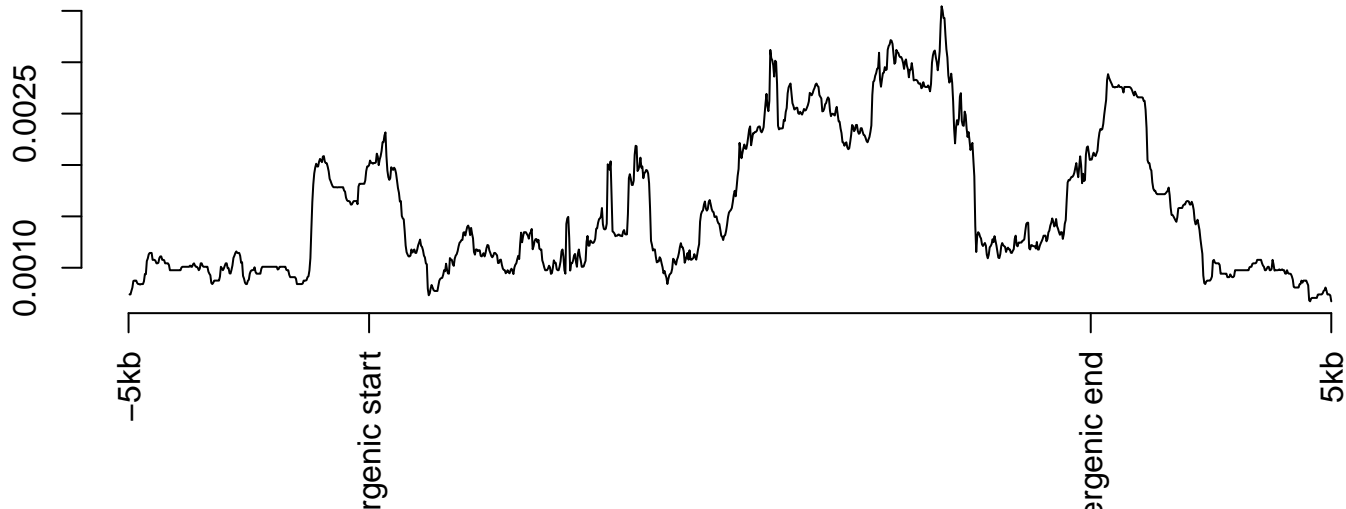
K562 PositiveSingle E.588 scCLTdegenNuc456

0.0015 0.0030 0.0045



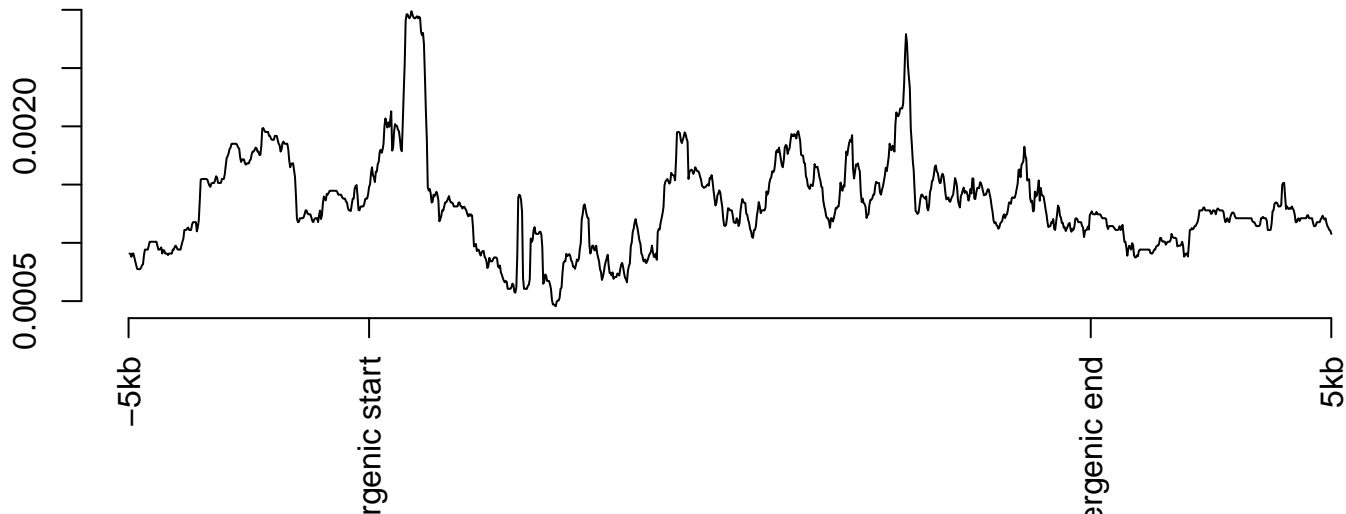
Average coverage per intergenic region

K562 PositiveSingle E.589 scCLTdegenNuc326



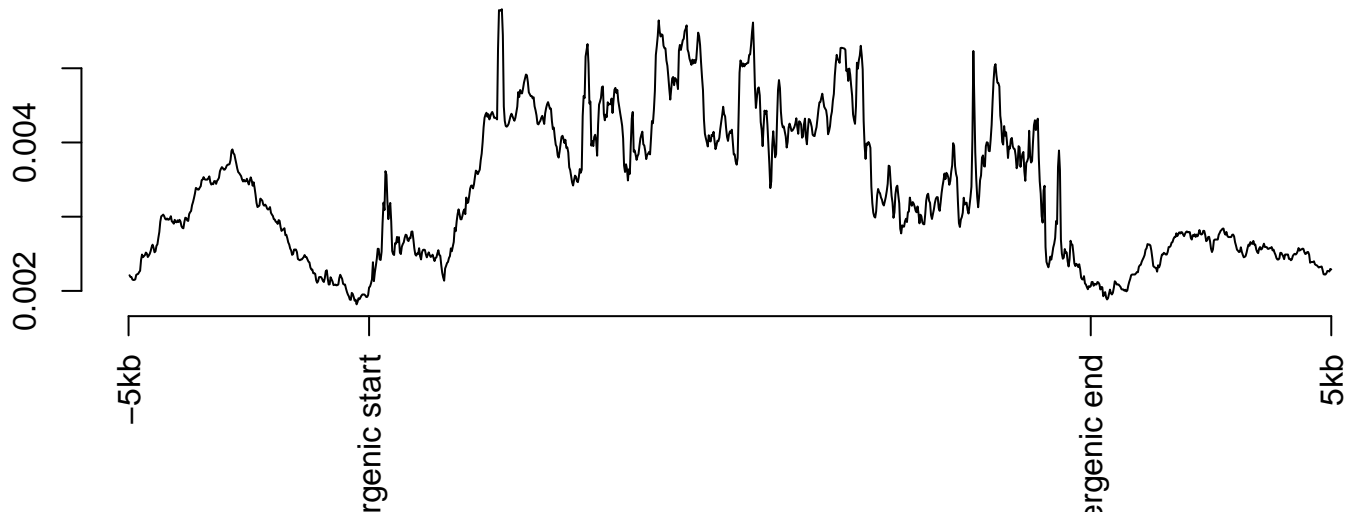
Average coverage per intergenic region

K562 PositiveSingle E.589 scCLTdegenNuc348



Average coverage per intergenic region

K562 PositiveSingle E.665 scCLTdegenNuc766



Average coverage per intergenic region

K562 PositiveSingle E.665 scCLTdegenNuc767

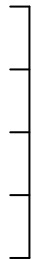
0.007
0.005
0.003

-5kb

intergenic start

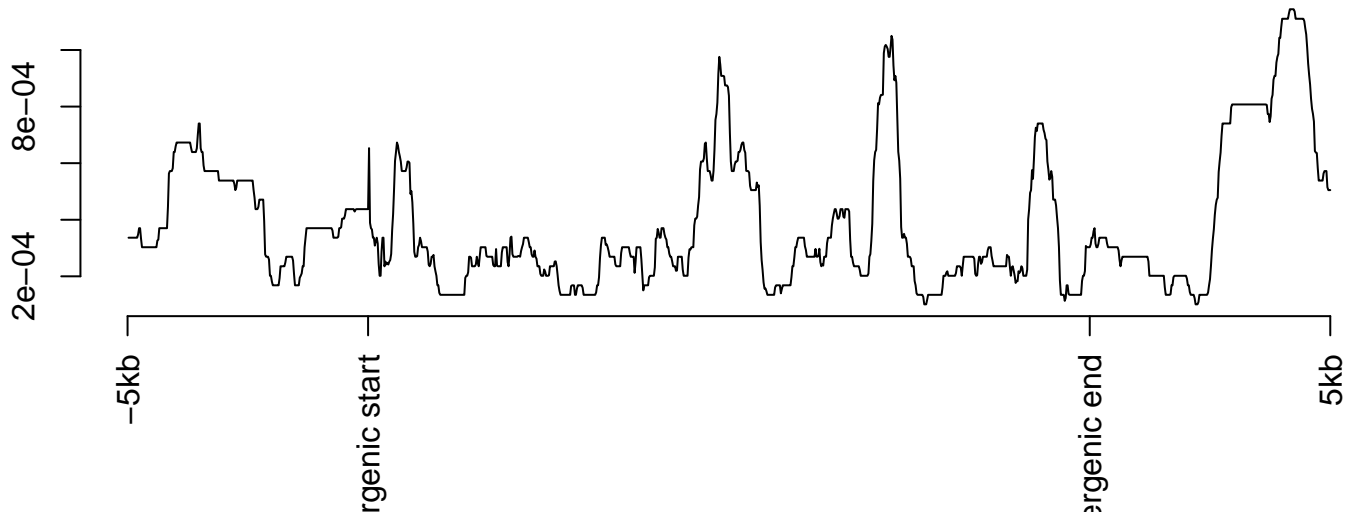
intergenic end

5kb



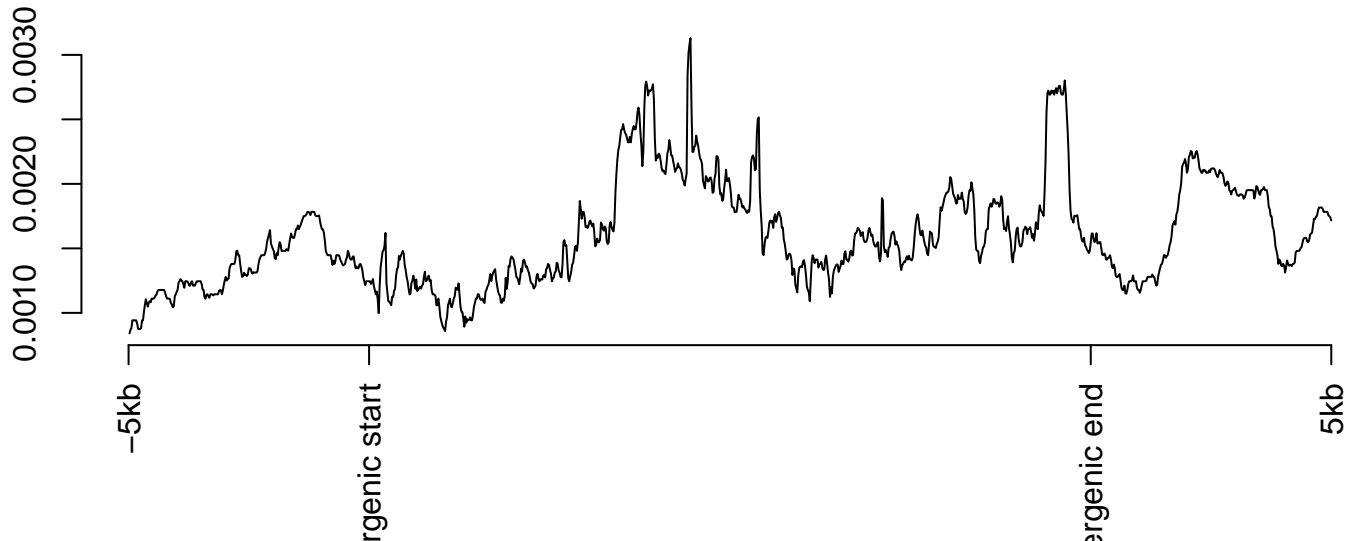
Average coverage per intergenic region

K562 PositiveSingle E.665 scCLTdegenNuc768



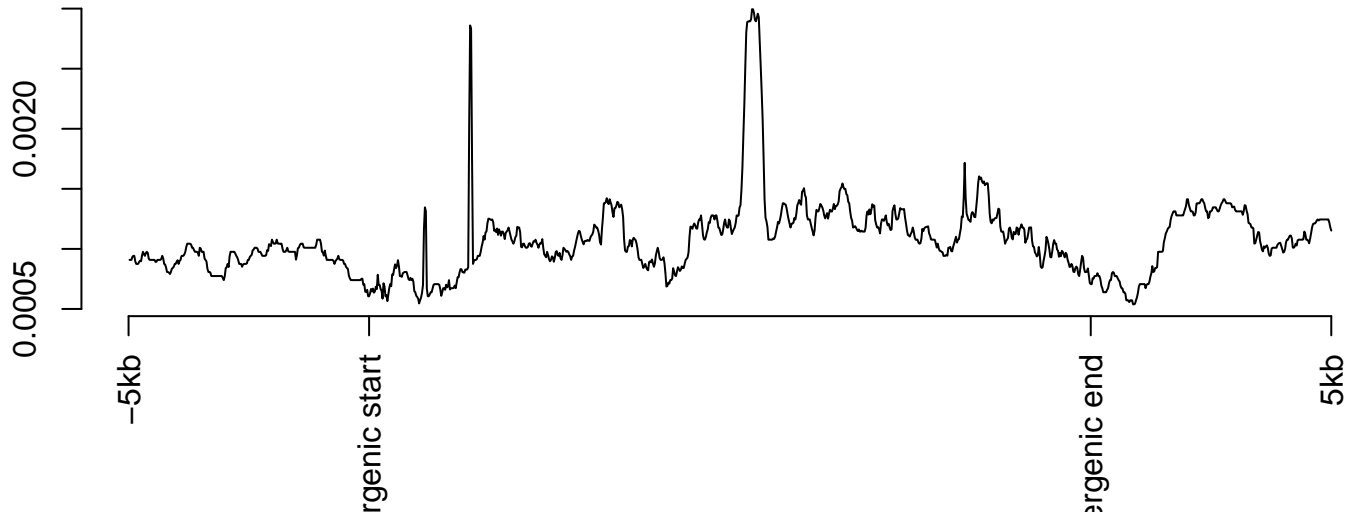
Average coverage per intergenic region

K562 PositiveSingle E.665 scCLTdegenNuc769



Average coverage per intergenic region

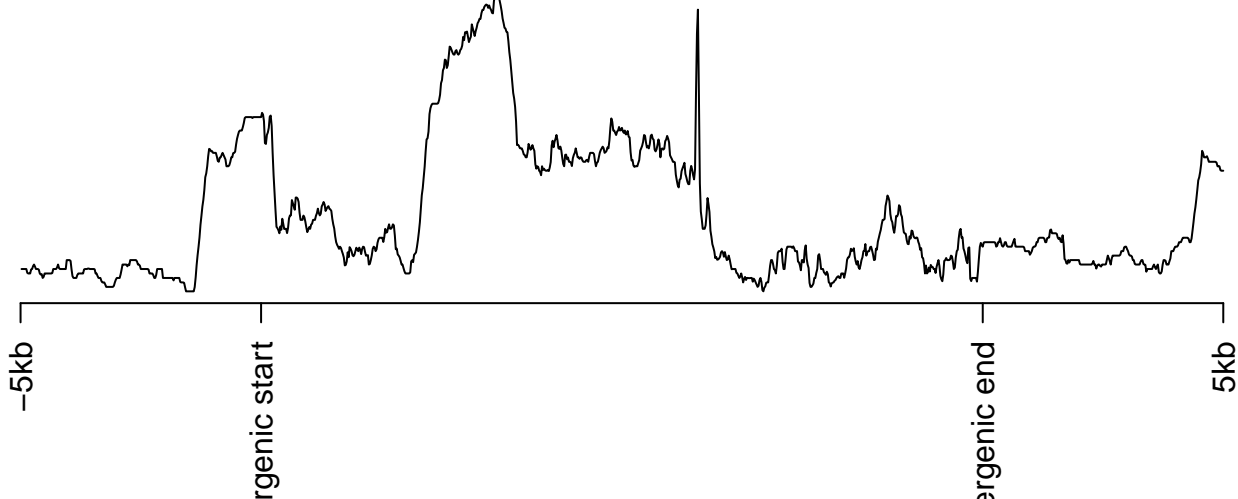
K562 PositiveSingle E.665 scCLTdegenNuc770



Average coverage per intergenic region

K562 PositiveSingle E.665 scCLTdegenNuc771

0.0005 0.0015 0.0025



Average coverage per intergenic region

K562 PositiveSingle E.665 scCLTdegenNuc772

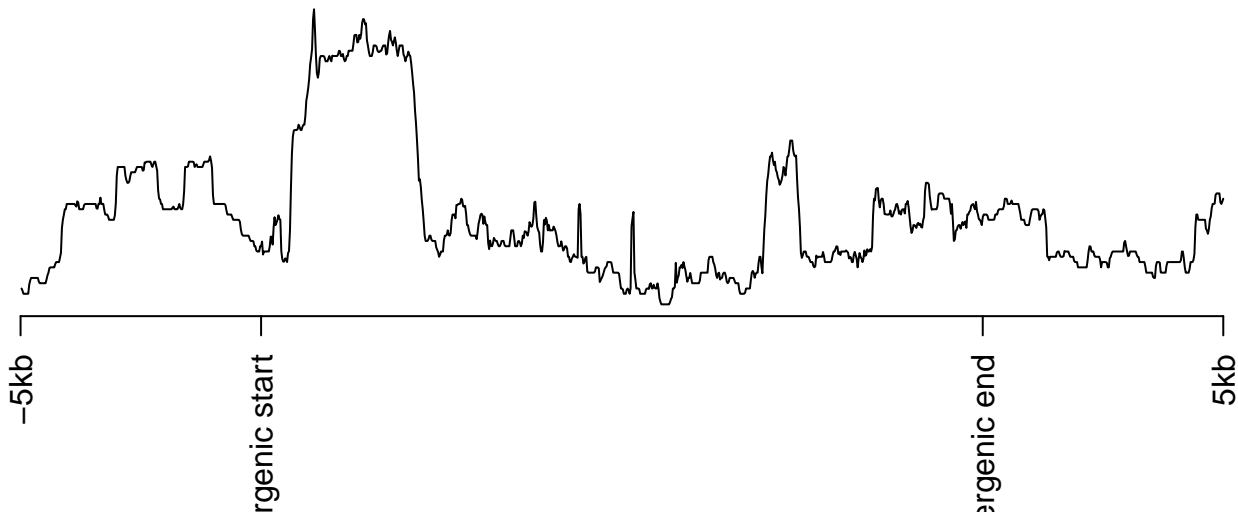
0.0015
0.0005

-5kb

intergenic start

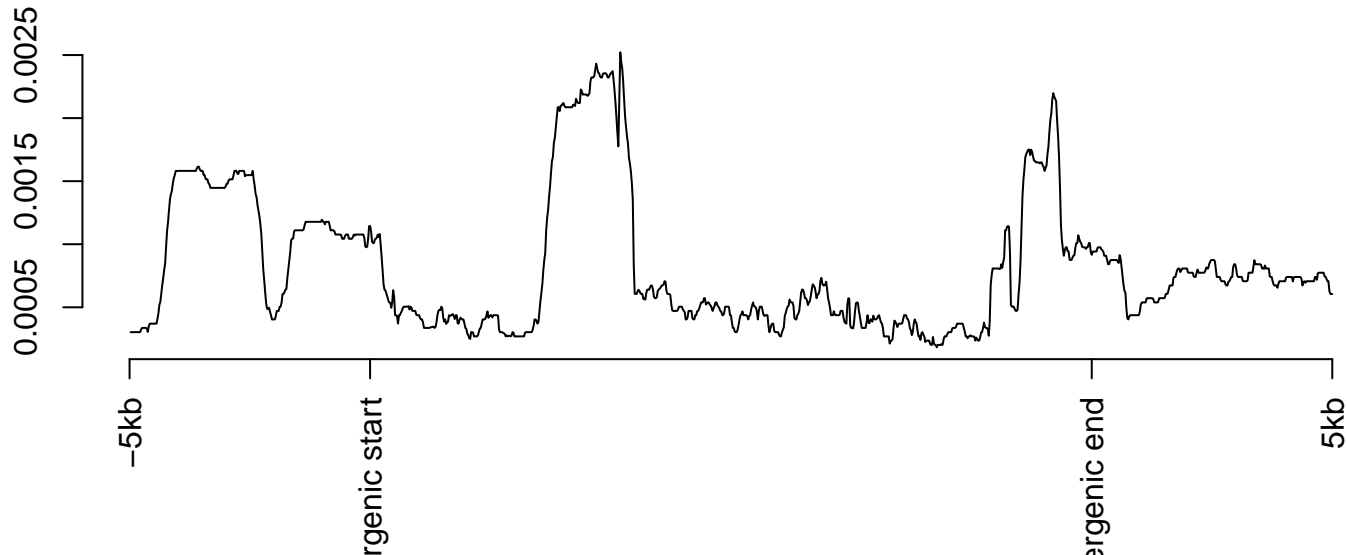
intergenic end

5kb



Average coverage per intergenic region

K562 PositiveSingle E.665 scCLTdegenNuc773



Average coverage per intergenic region

K562 PositiveSingle E.665 scCLTdegenNuc774

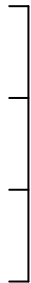
0.0000
0.0010

-5kb

intergenic start

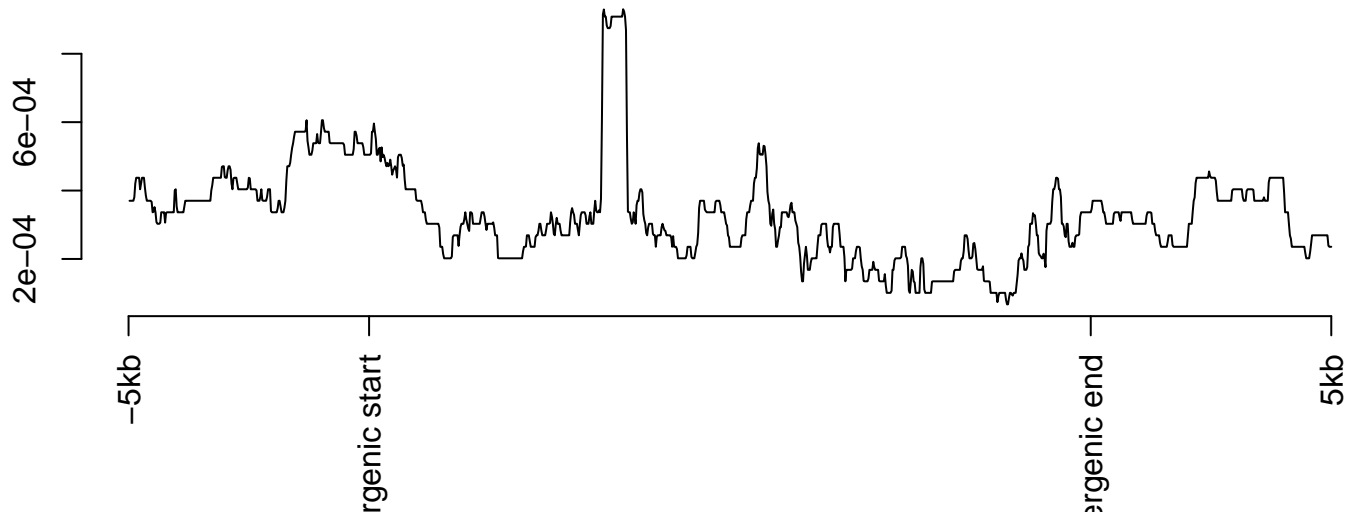
intergenic end

5kb



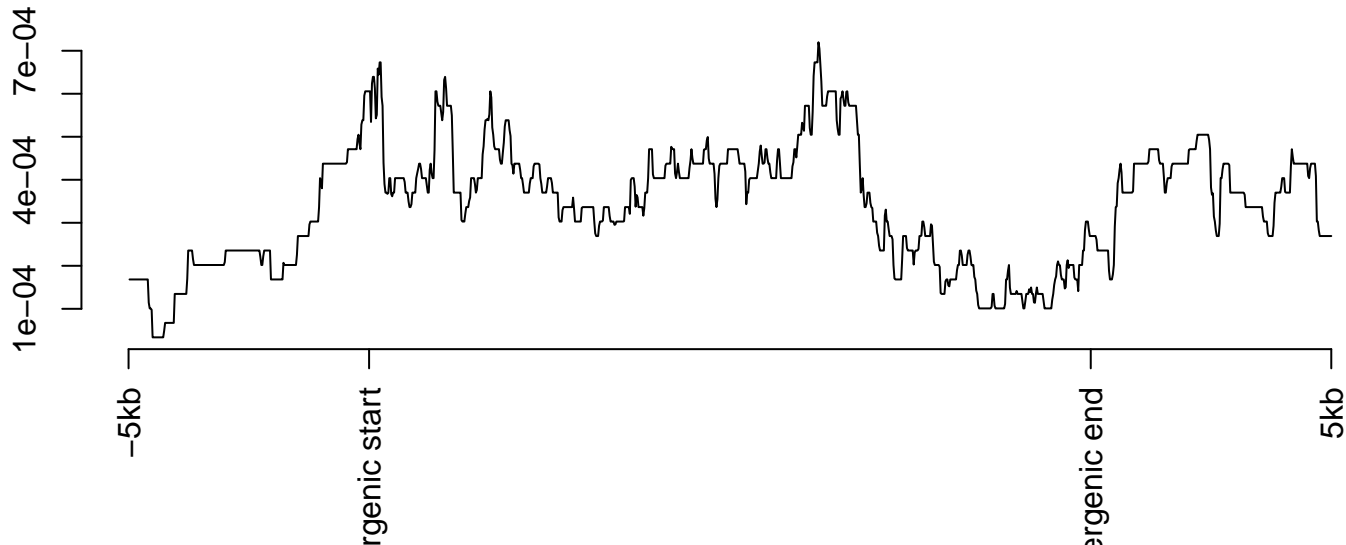
Average coverage per intergenic region

K562 PositiveSingle E.665 scCLTdegenNuc775



Average coverage per intergenic region

K562 PositiveSingle E.673 scCLTdegenNuc906_b



Average coverage per intergenic region

K562 PositiveSingle E.673 scCLTdegenNuc907_b

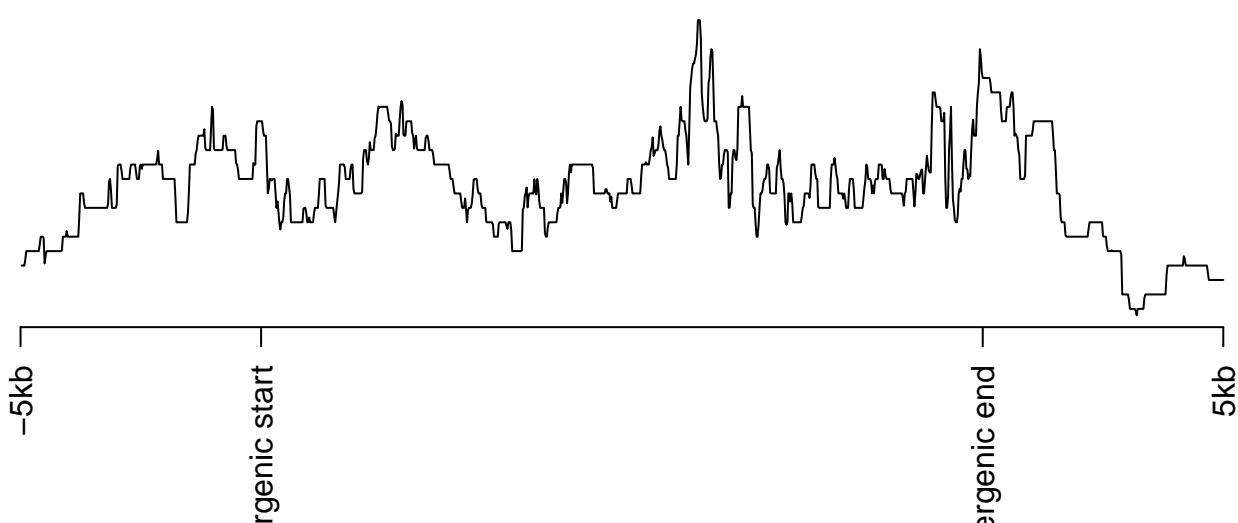
1e-04
4e-04
7e-04

-5kb

intergenic start

intergenic end

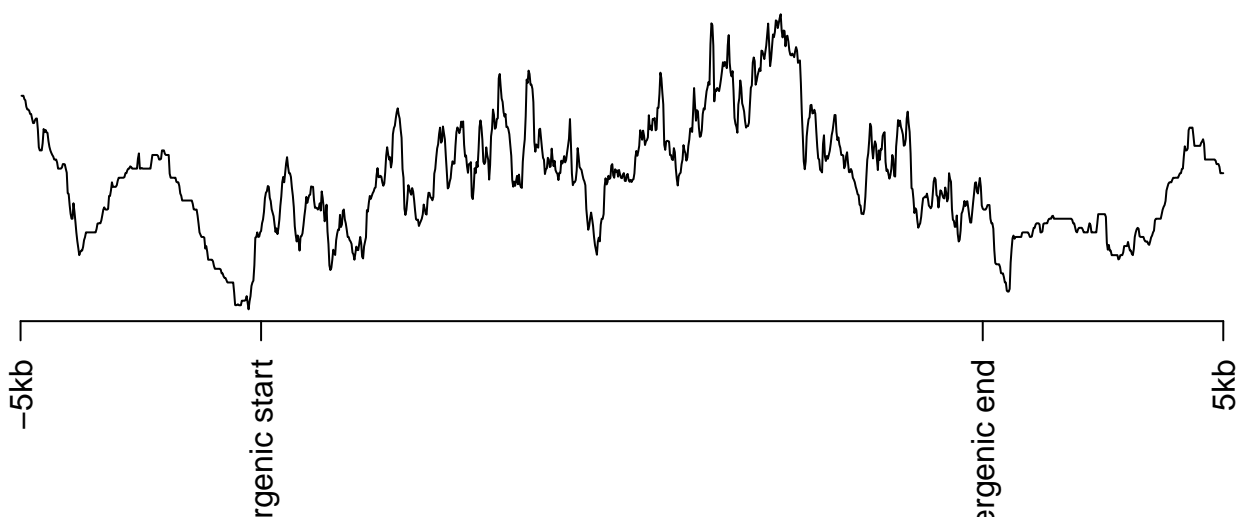
5kb



Average coverage per intergenic region

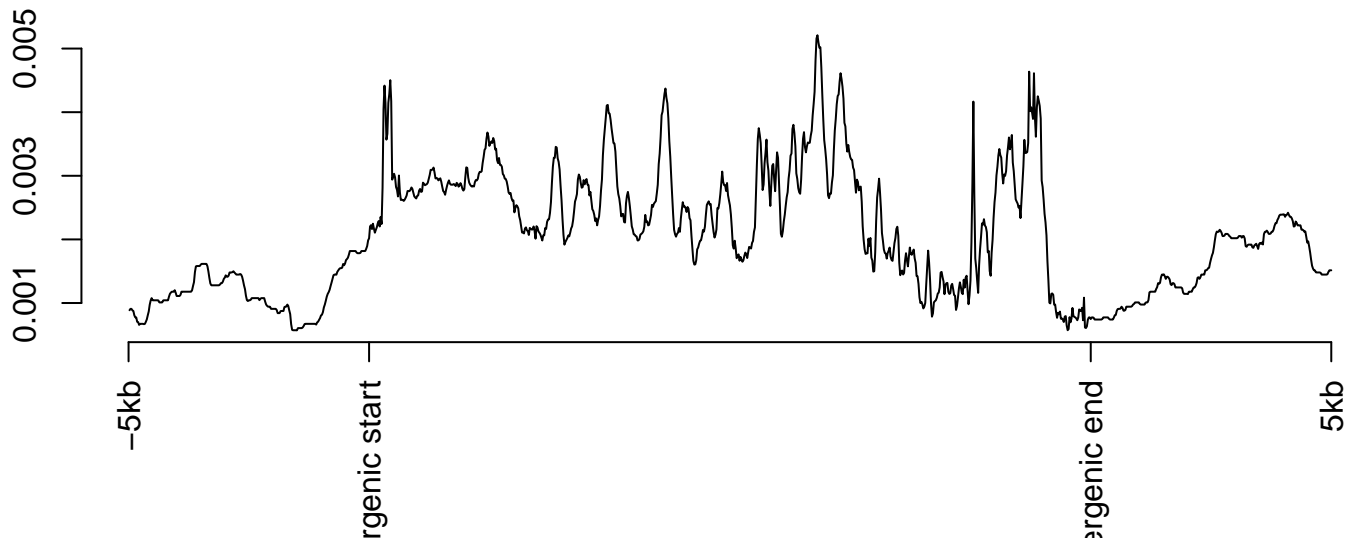
K562 PositiveSingle E.673 scCLTdegenNuc908_b

0.0005 0.0015 0.0025



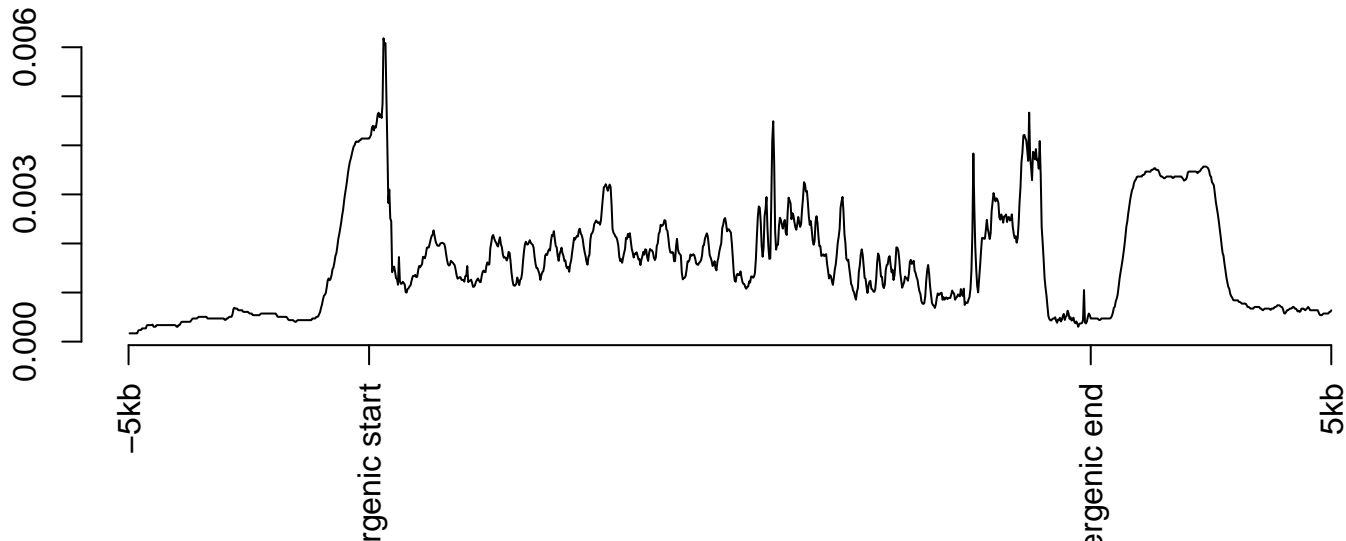
Average coverage per intergenic region

K562 PositiveSingle E.675 scCLTdegenNuc933



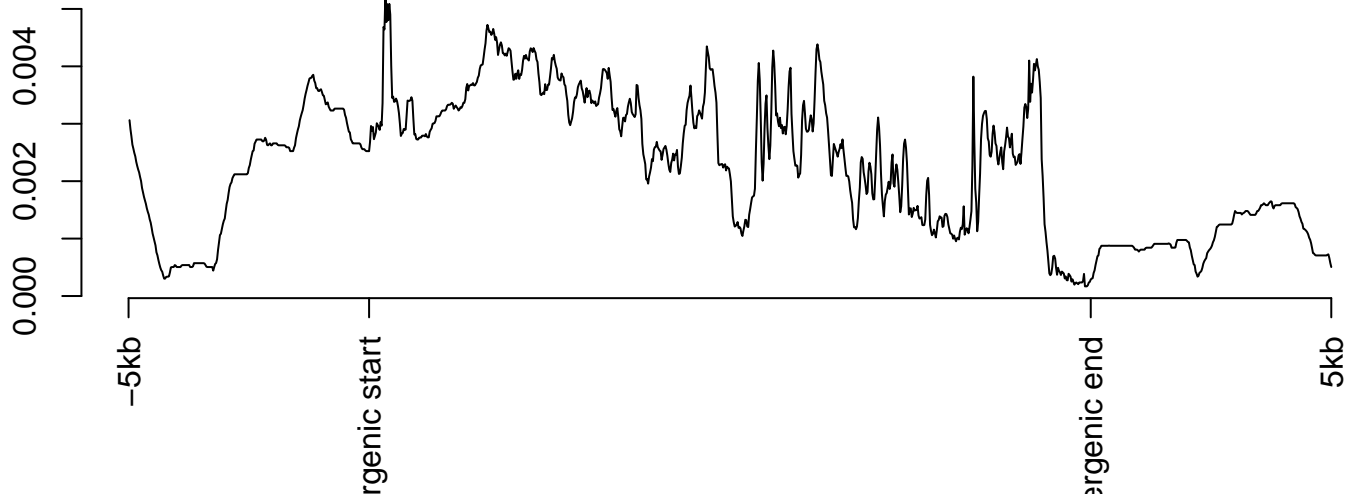
Average coverage per intergenic region

K562 PositiveSingle E.675 scCLTdegenNuc935



Average coverage per intergenic region

K562 PositiveSingle E.675 scCLTdegenNuc936



Average coverage per intergenic region

K562 PositiveSingle E.675 scCLTdegenNuc938

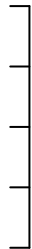
0.001 0.003 0.005

-5kb

intergenic start

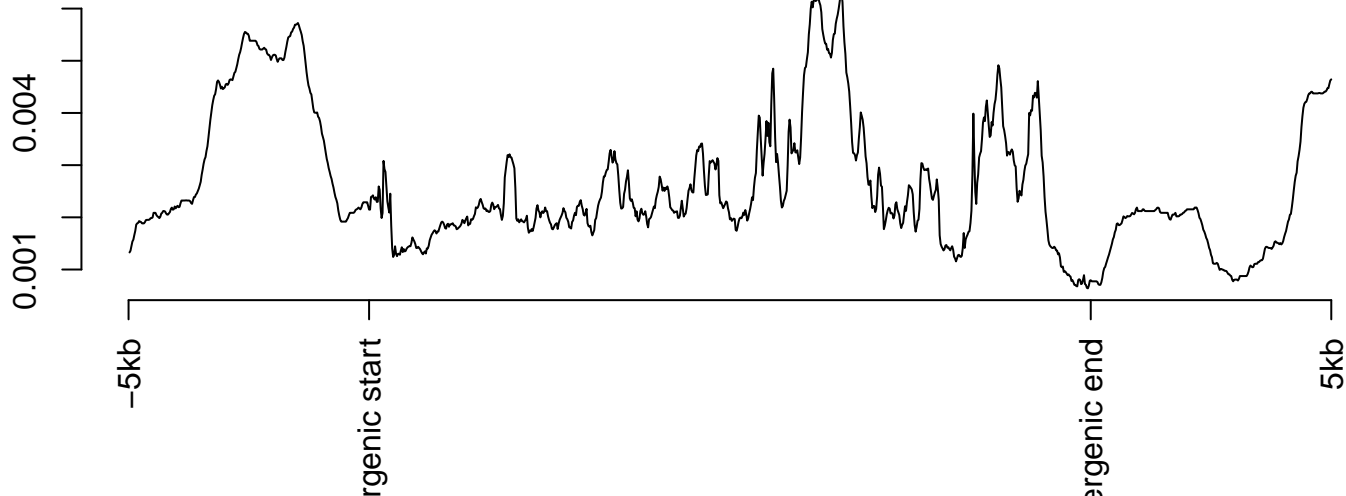
intergenic end

5kb



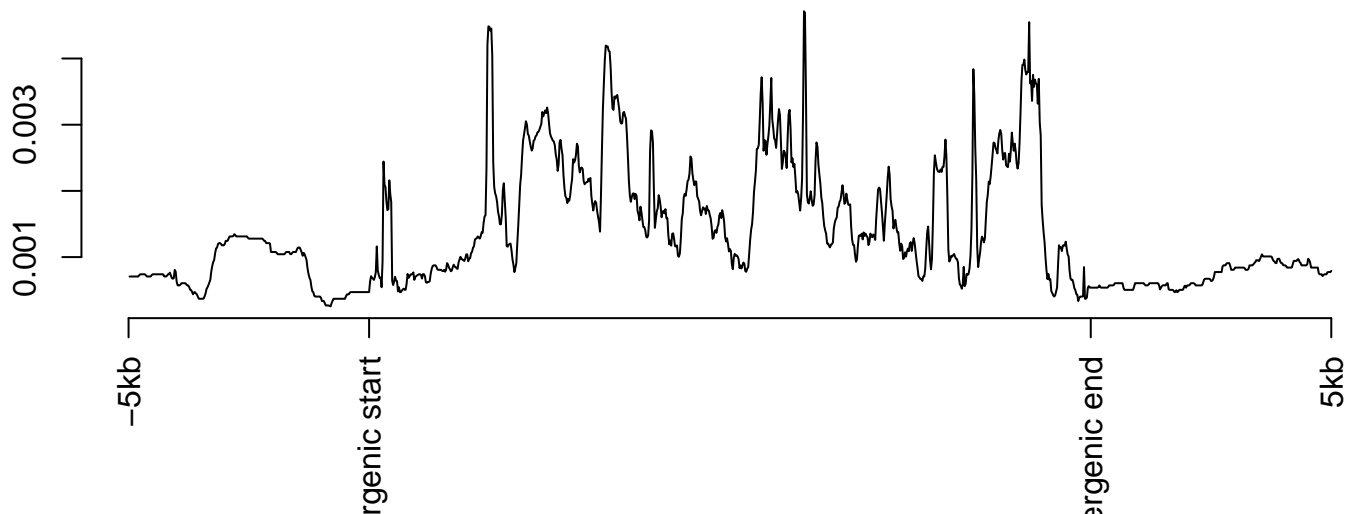
Average coverage per intergenic region

K562 PositiveSingle E.675 scCLTdegenNuc942



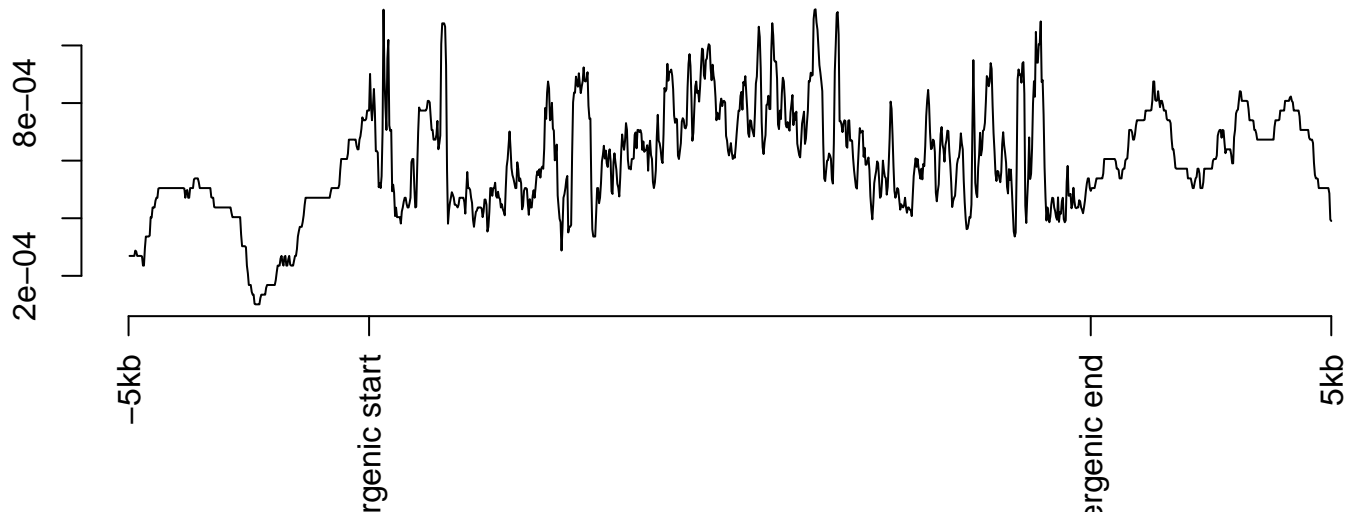
Average coverage per intergenic region

K562 PositiveSingle E.675 scCLTdegenNuc943



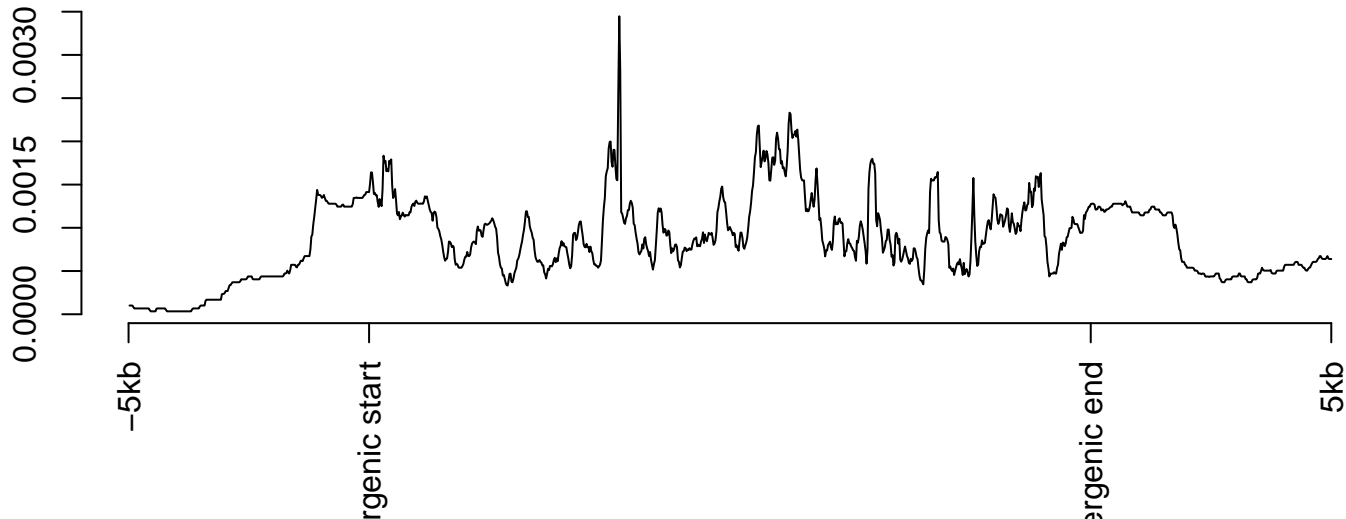
Average coverage per intergenic region

K562 PositiveSingle E.676 scCLTdegenNuc944



Average coverage per intergenic region

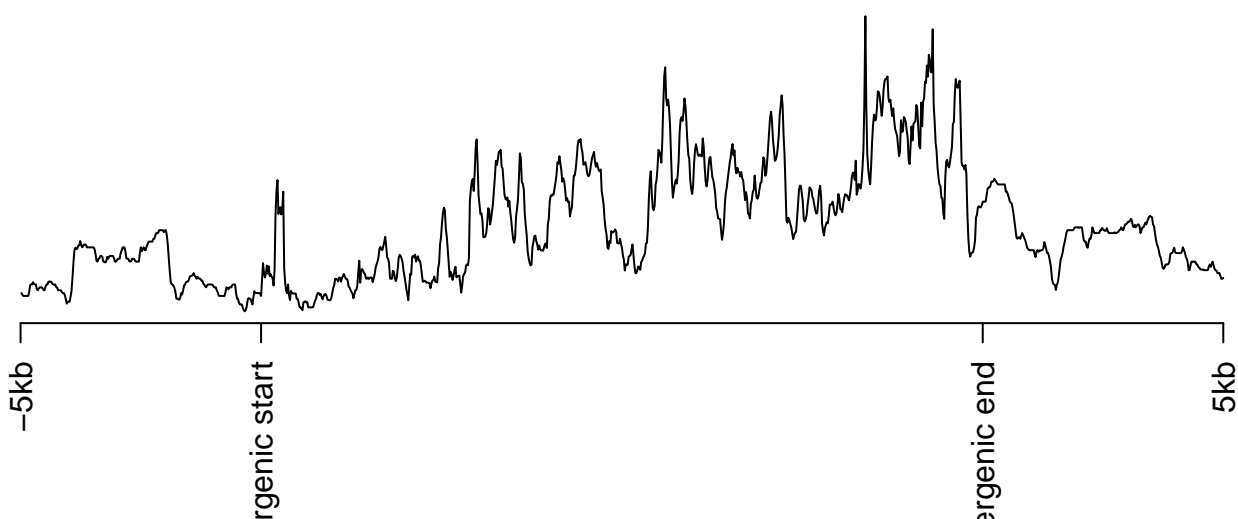
K562 PositiveSingle E.676 scCLTdegenNuc945



Average coverage per intergenic region

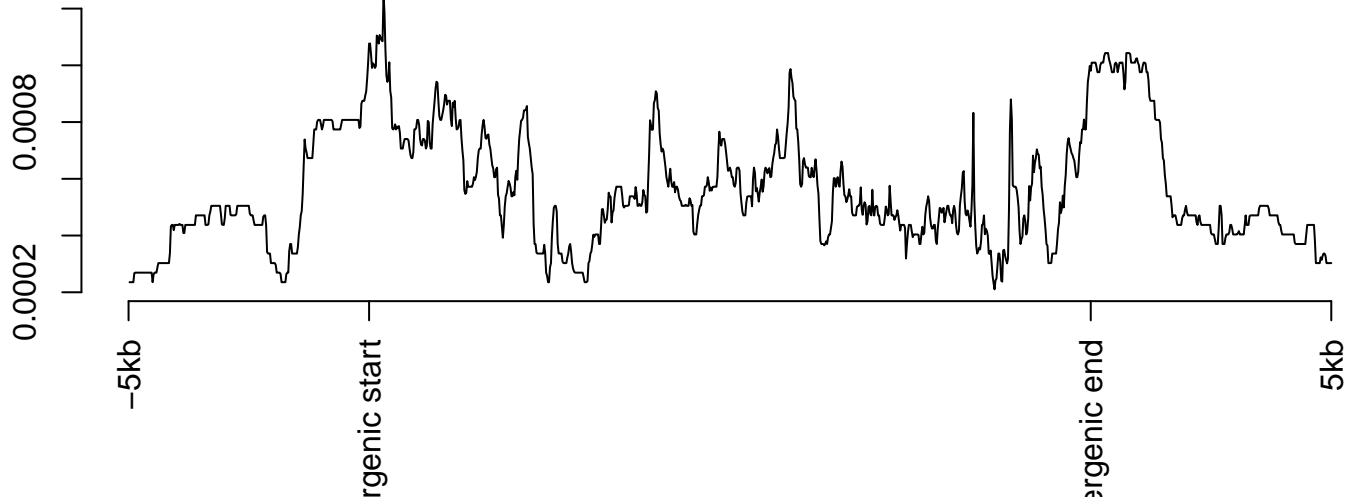
K562 PositiveSingle E.676 scCLTdegenNuc946

0.0010 0.0025 0.0040



Average coverage per intergenic region

K562 PositiveSingle E.676 scCLTdegenNuc947



Average coverage per intergenic region

K562 PositiveSingle E.676 scCLTdegenNuc948

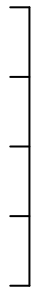
0.0000 0.0010 0.0020

-5kb

intergenic start

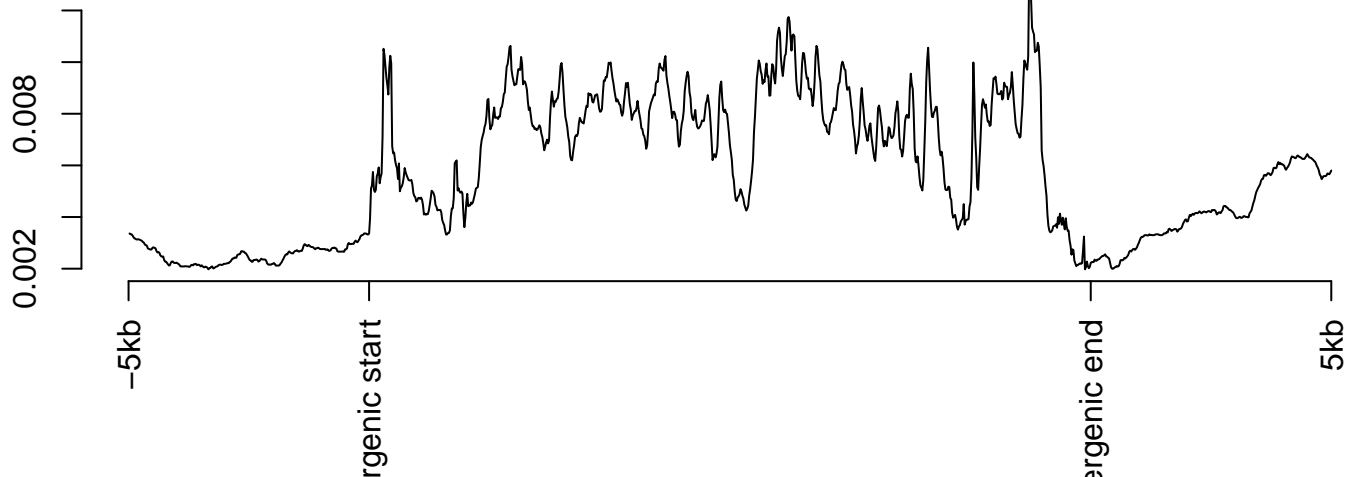
intergenic end

5kb



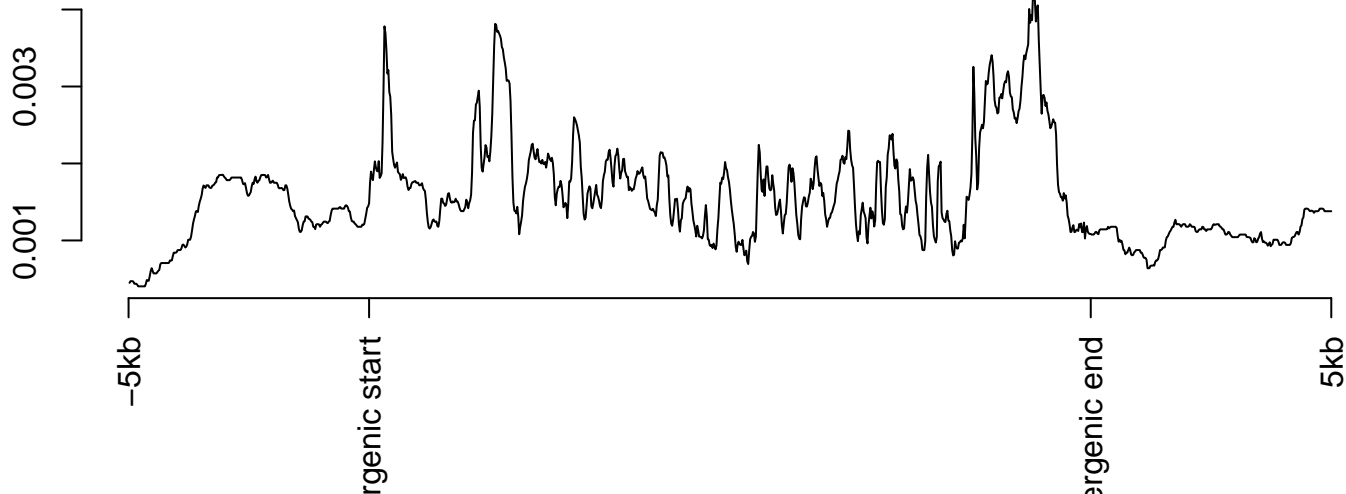
Average coverage per intergenic region

K562 PositiveSingle E.676 scCLTdegenNuc949



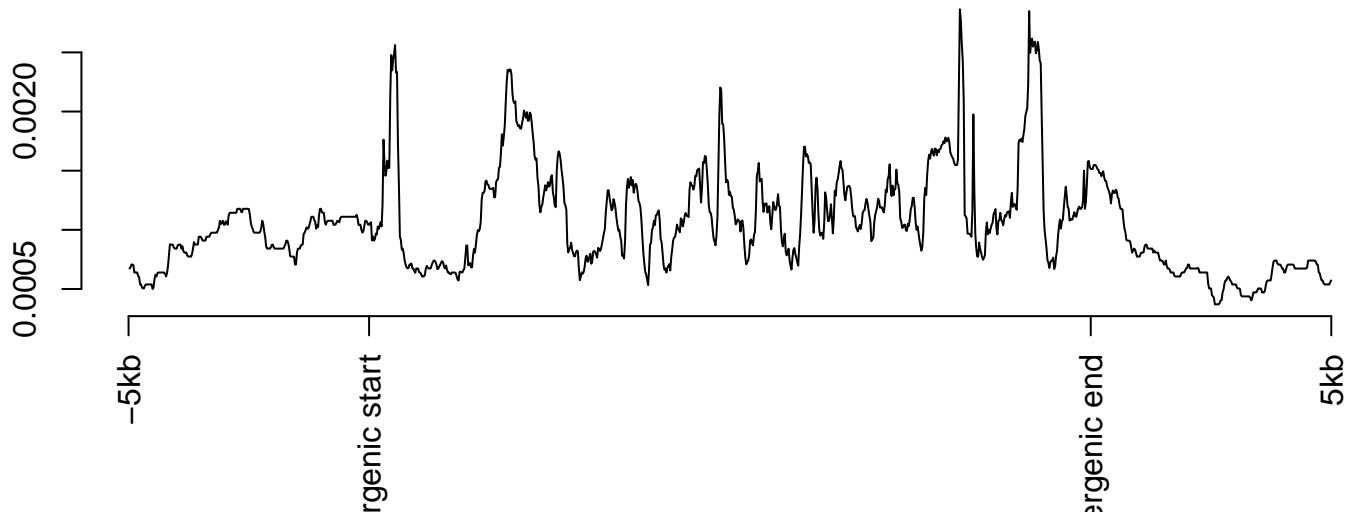
Average coverage per intergenic region

K562 PositiveSingle E.678 scCLTdegenNuc951



Average coverage per intergenic region

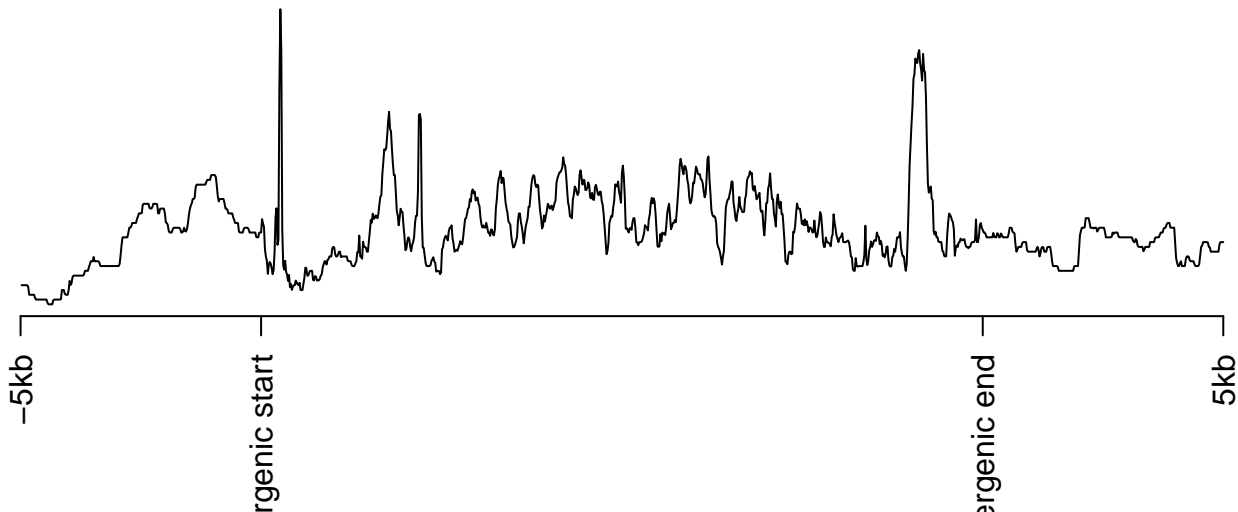
K562 PositiveSingle E.678 scCLTdegenNuc952



Average coverage per intergenic region

K562 PositiveSingle E.678 scCLTdegenNuc953

0.0005 0.0015



Average coverage per intergenic region

K562 PositiveSingle E.678 scCLTdegenNuc954

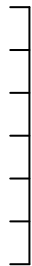
0.0005 0.0020 0.0035

-5kb

intergenic start

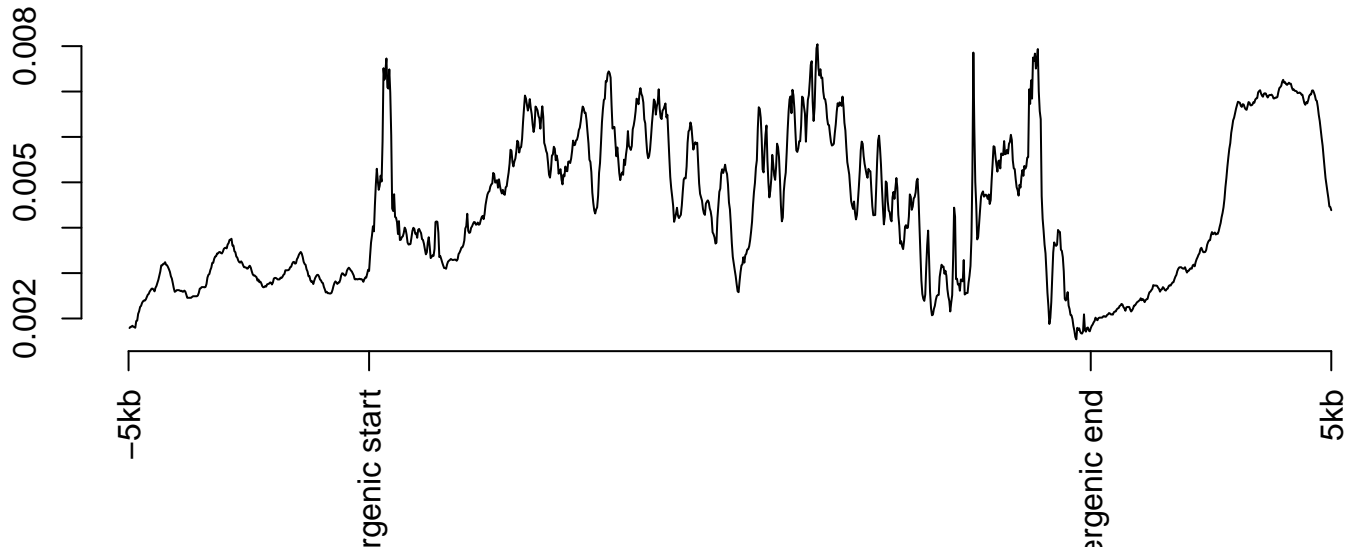
intergenic end

5kb



Average coverage per intergenic region

K562 PositiveSingle E.678 scCLTdegenNuc955



Average coverage per intergenic region

K562 PositiveSingle E.678 scCLTdegenNuc956

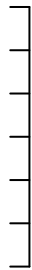
0.0005 0.0020 0.0035

-5kb

intergenic start

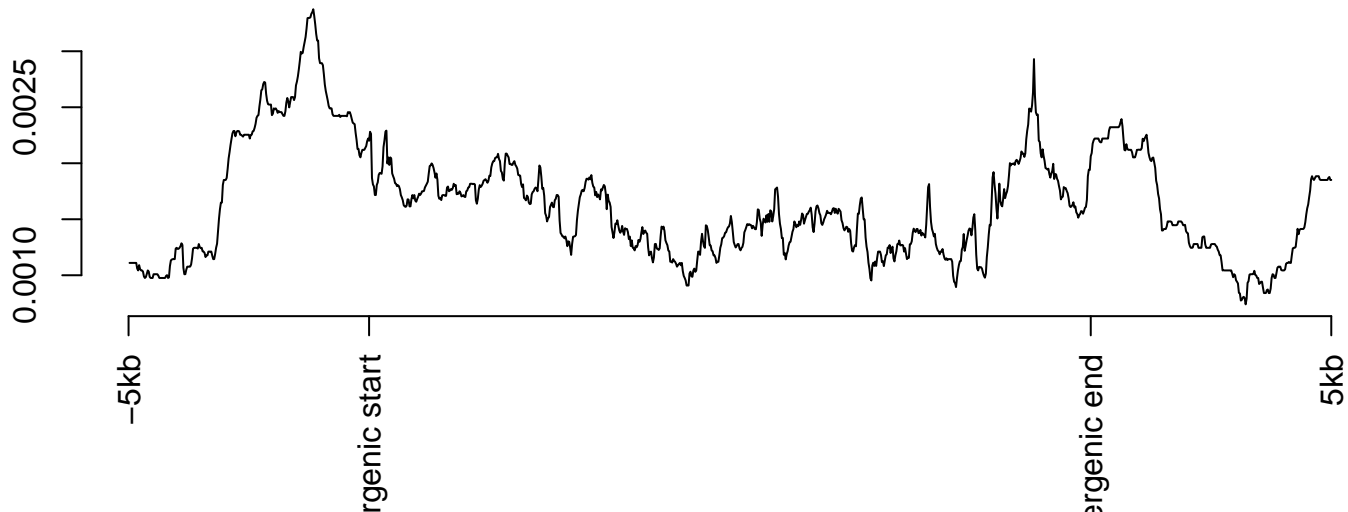
intergenic end

5kb



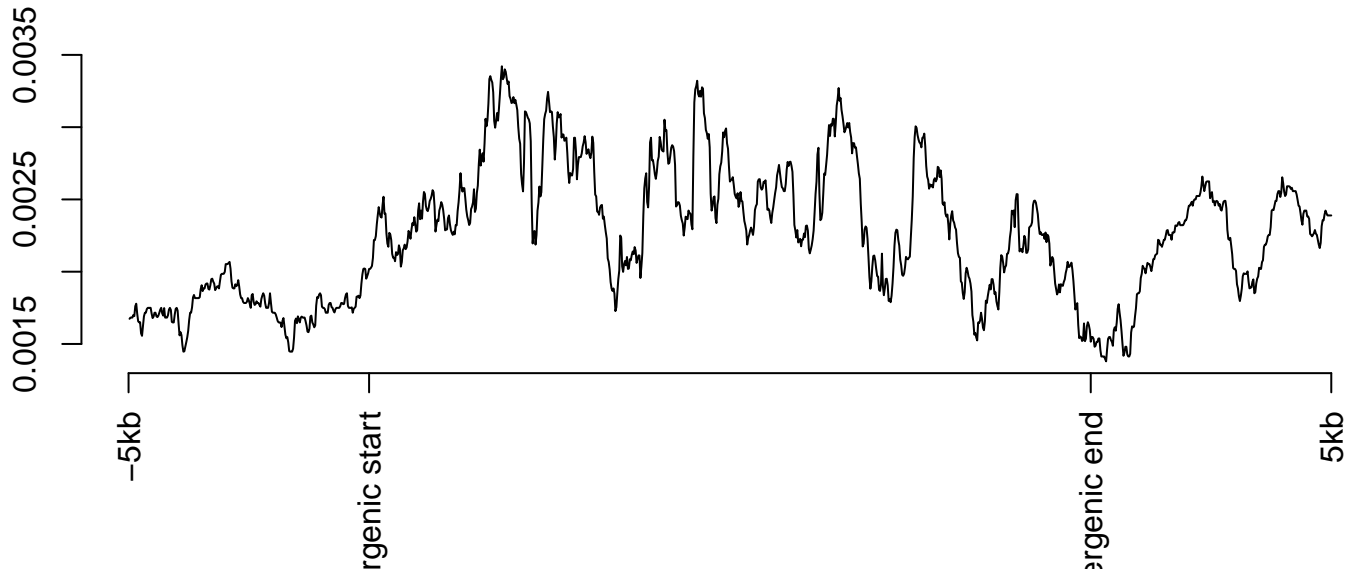
Average coverage per intergenic region

K562 PositiveSingle E.683 scCLTdegenNuc1004



Average coverage per intergenic region

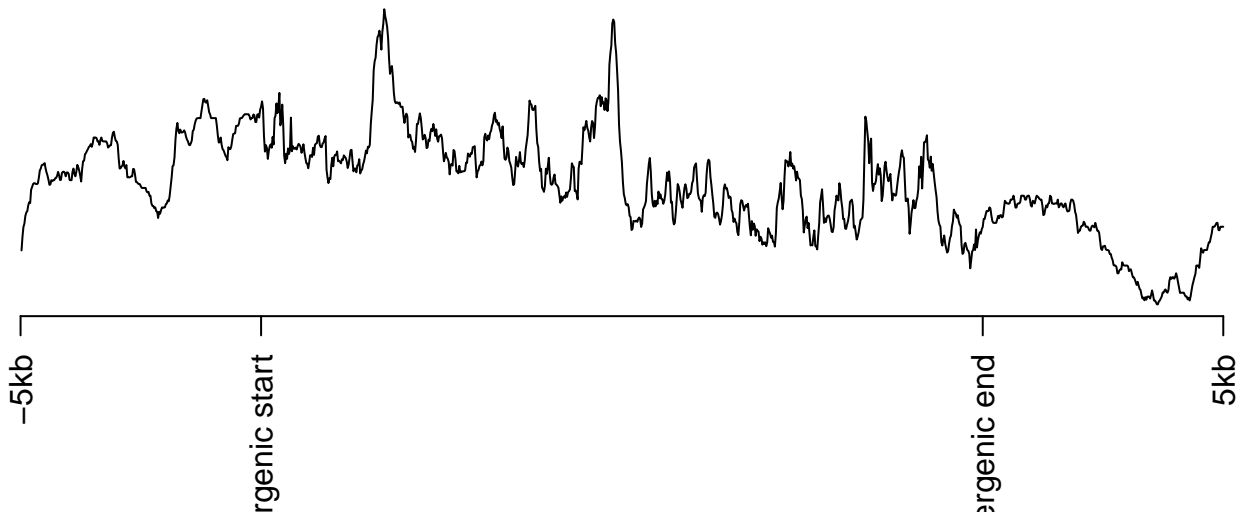
K562 PositiveSingle E.683 scCLTdegenNuc1005



Average coverage per intergenic region

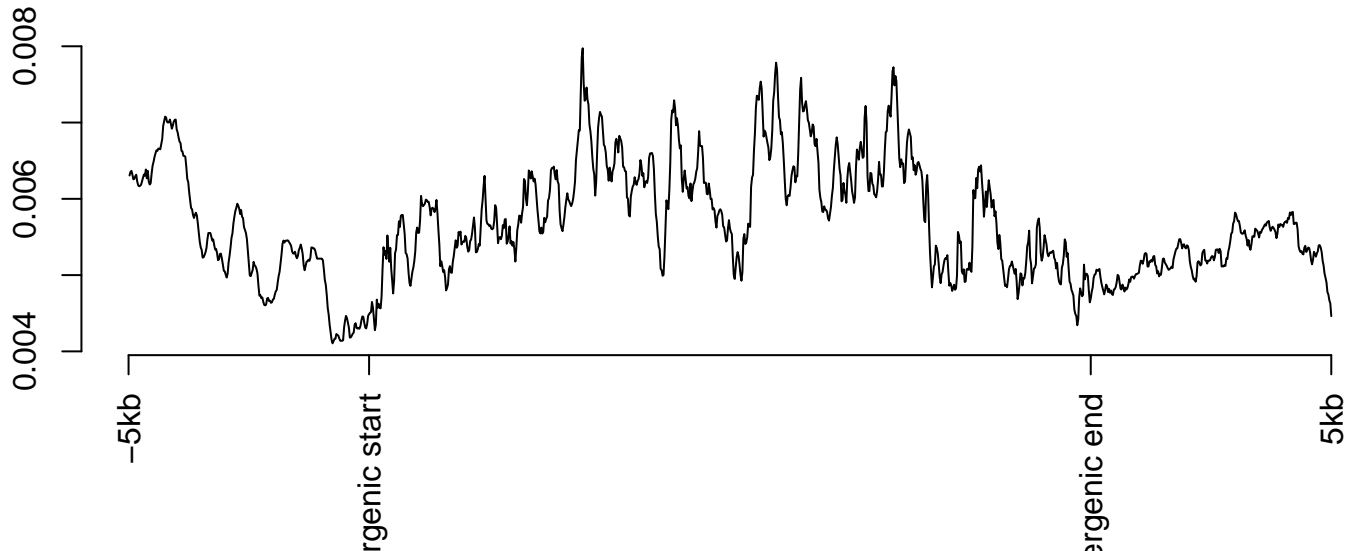
K562 PositiveSingle E.683 scCLTdegenNuc1006

0.0030
0.0015



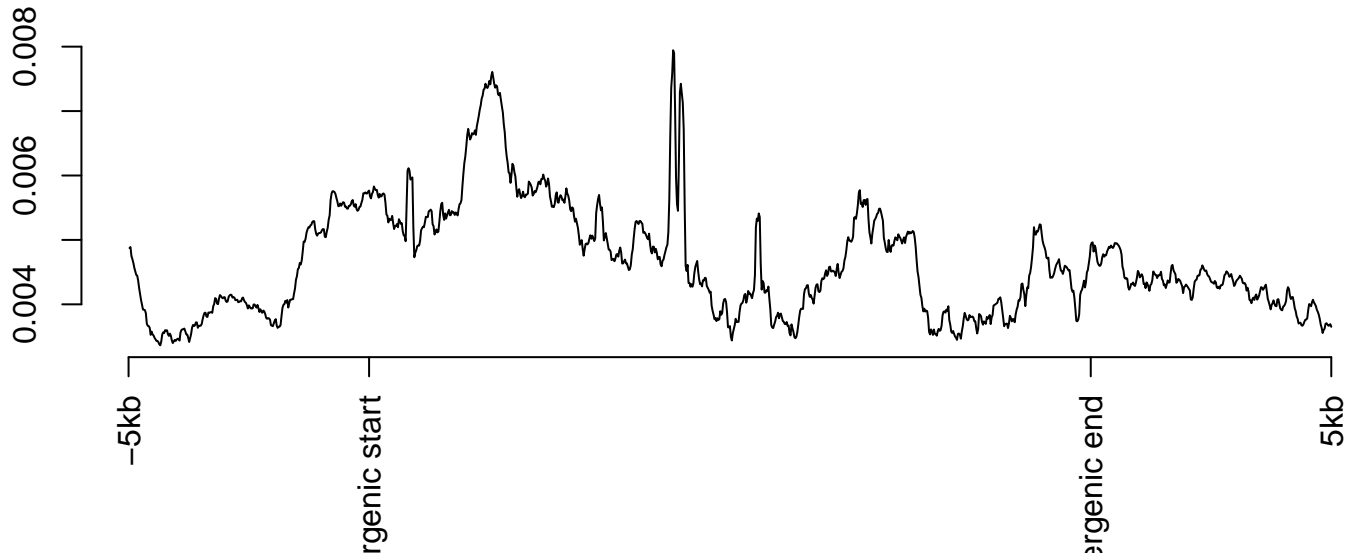
Average coverage per intergenic region

K562 PositiveSingle E.683 scCLTdegenNuc1007



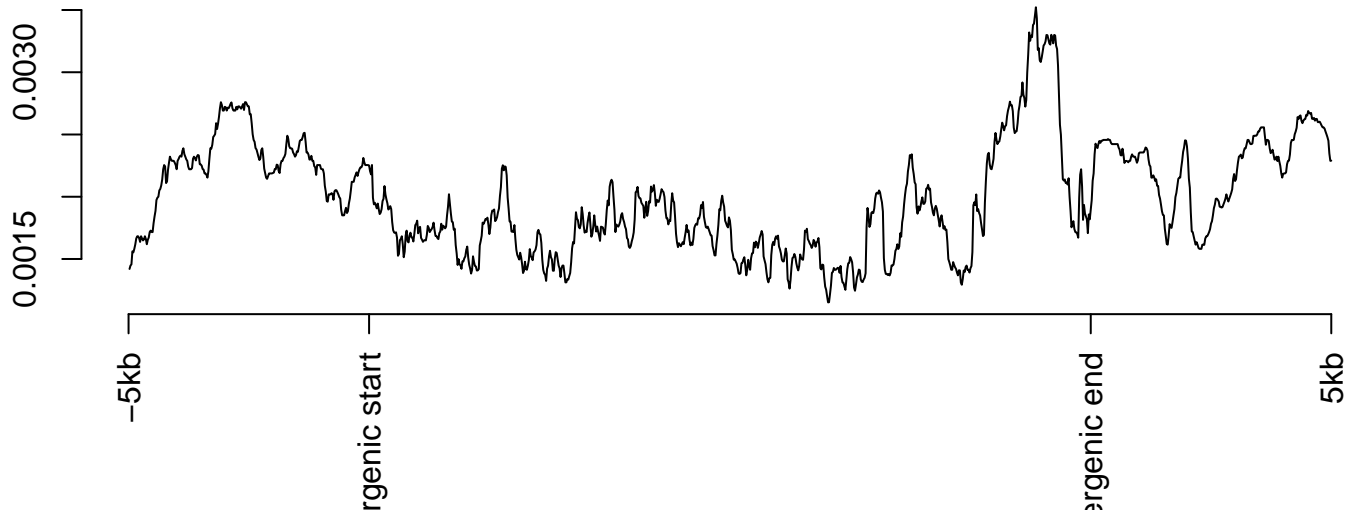
Average coverage per intergenic region

K562 PositiveSingle E.683 scCLTdegenNuc1008



Average coverage per intergenic region

K562 PositiveSingle E.683 scCLTdegenNuc1009



Average coverage per intergenic region

K562 PositiveSingle E.683 scCLTdegenNuc1010

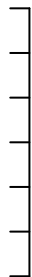
0.0015 0.0030 0.0045

-5kb

intergenic start

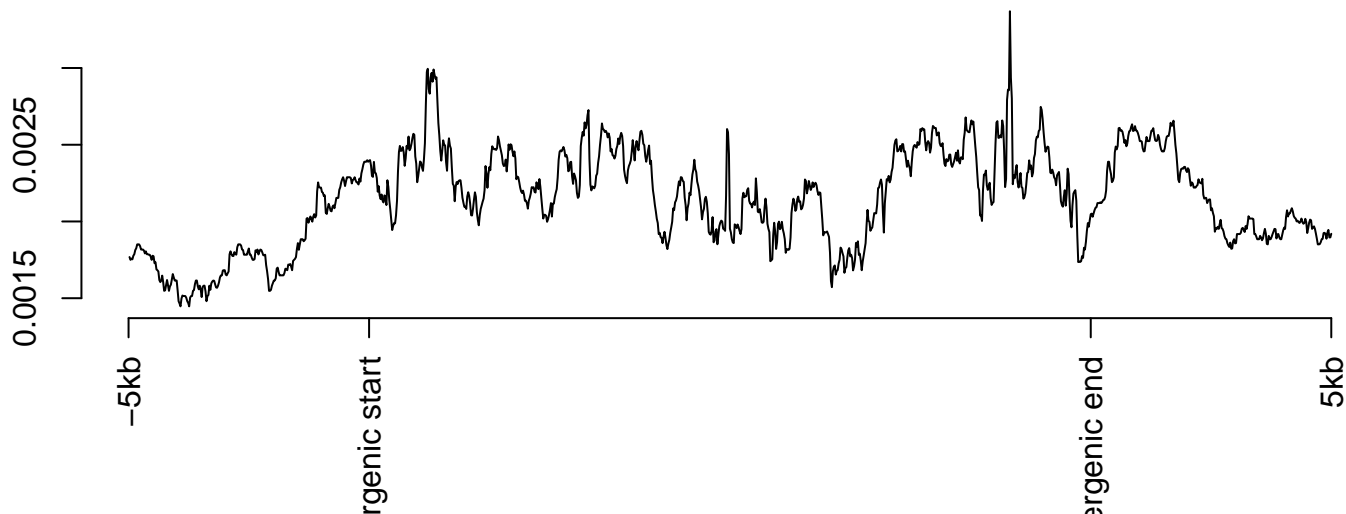
intergenic end

5kb



Average coverage per intergenic region

K562 PositiveSingle E.683 scCLTdegenNuc1012



Average coverage per intergenic region

K562 PositiveSingle E.683 scCLTdegenNuc1013

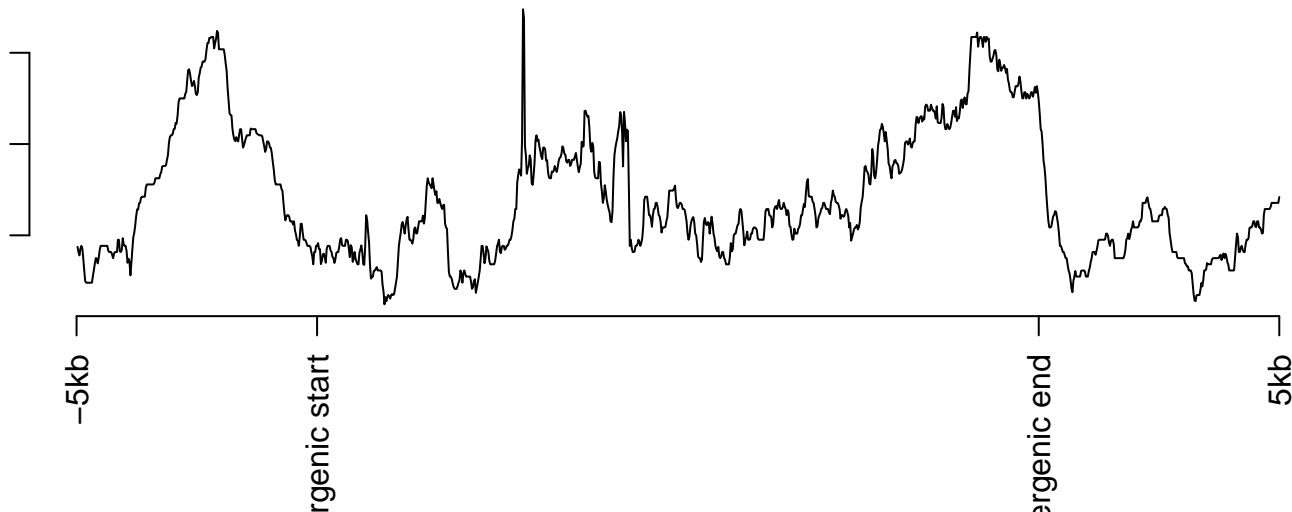
0.0010
0.0020

-5kb

intergenic start

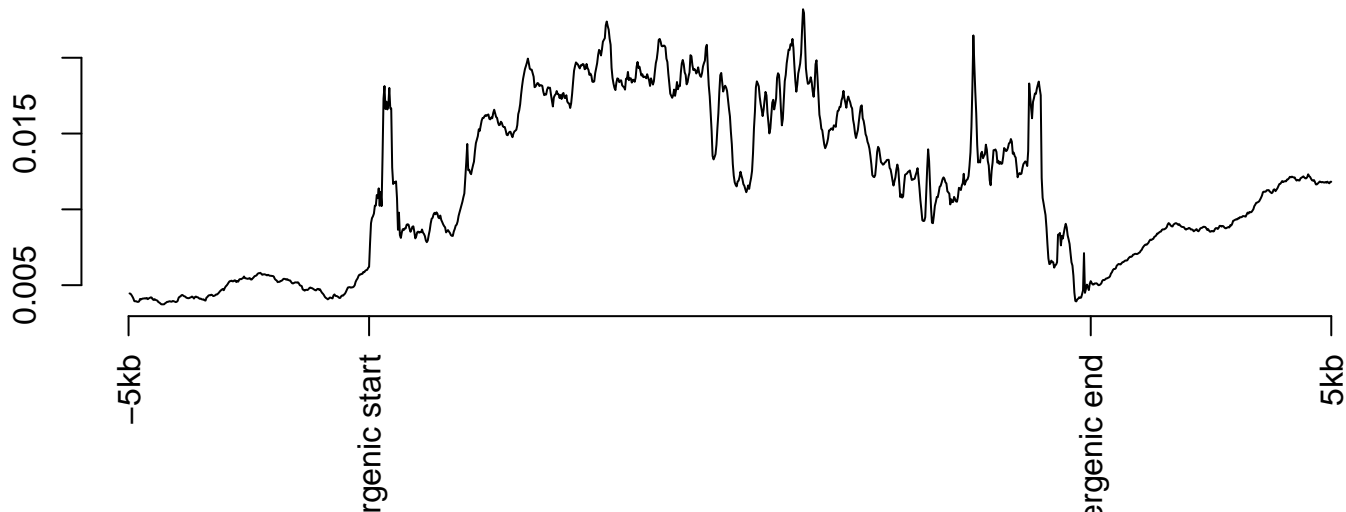
intergenic end

5kb



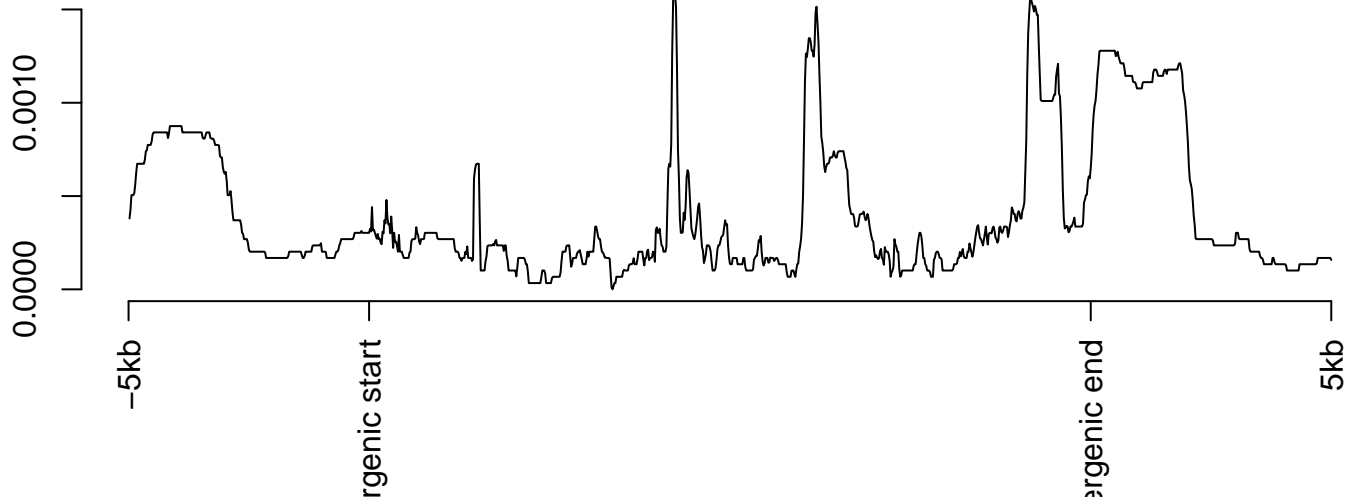
Average coverage per intergenic region

K562 PositiveSingle E.683 scCLTdegenNuc979



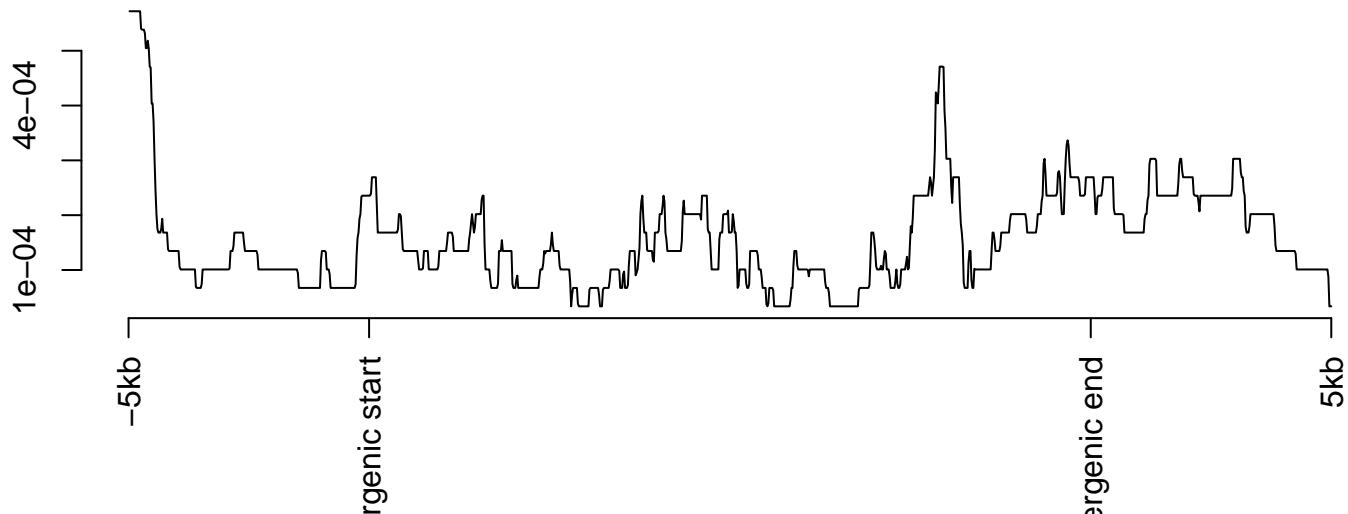
Average coverage per intergenic region

K562 PositiveSingle E.694 scCLTdegenNuc1077



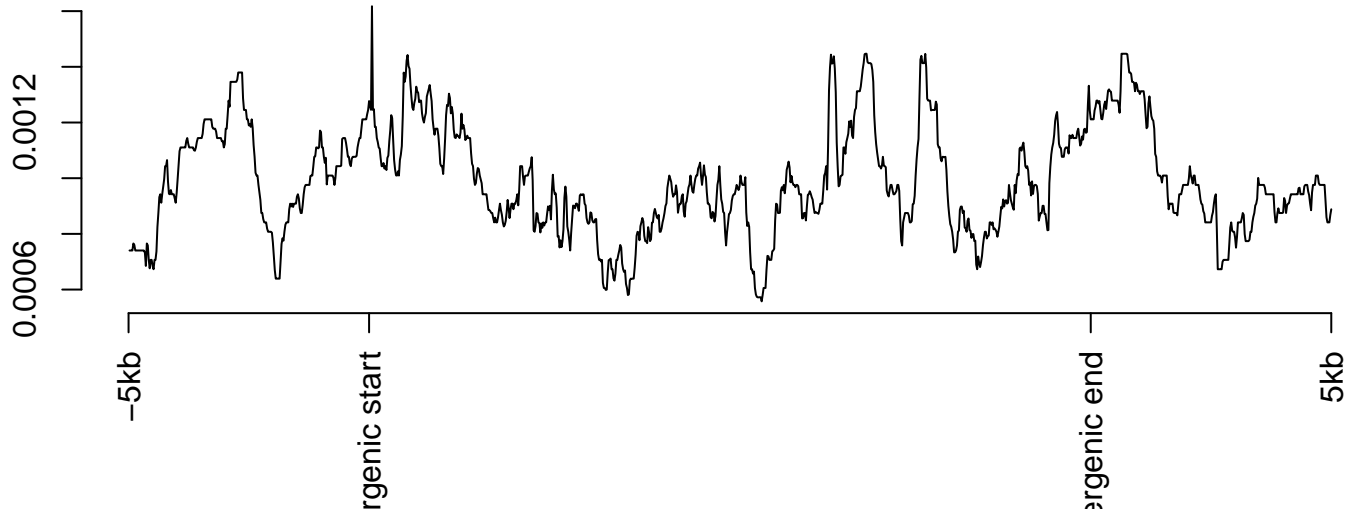
Average coverage per intergenic region

K562 PositiveSingle E.694 scCLTdegenNuc1078



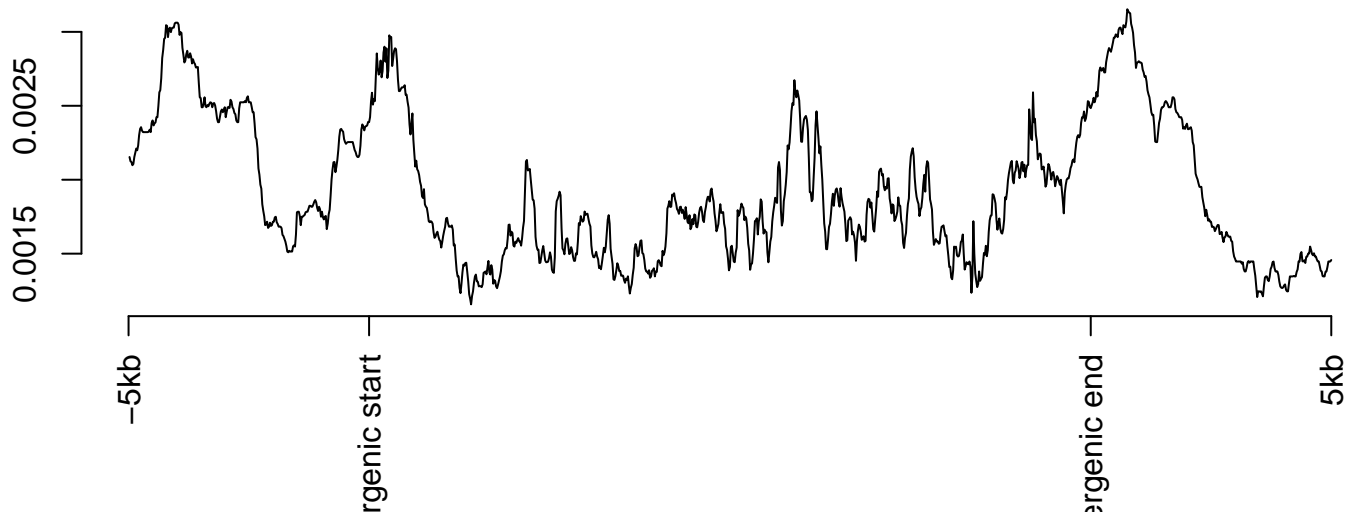
Average coverage per intergenic region

K562 PositiveSingle E.694 scCLTdegenNuc1079



Average coverage per intergenic region

K562 PositiveSingle E.694 scCLTdegenNuc1080



Average coverage per intergenic region

K562 PositivePooled E.574 scCLTdegenNuc333

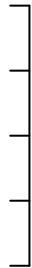
0.010 0.020 0.030

-5kb

intergenic start

intergenic end

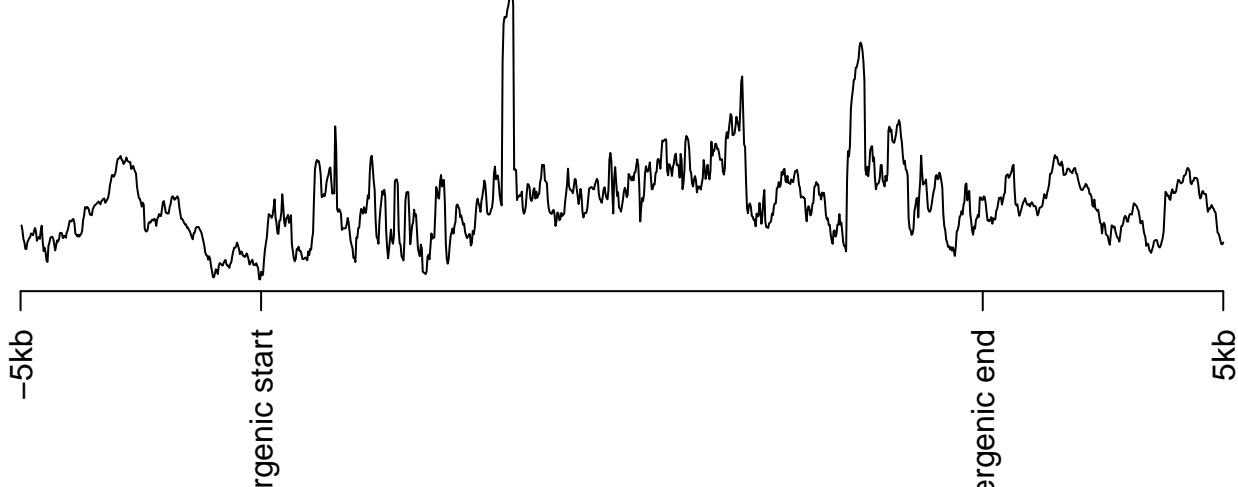
5kb



Average coverage per intergenic region

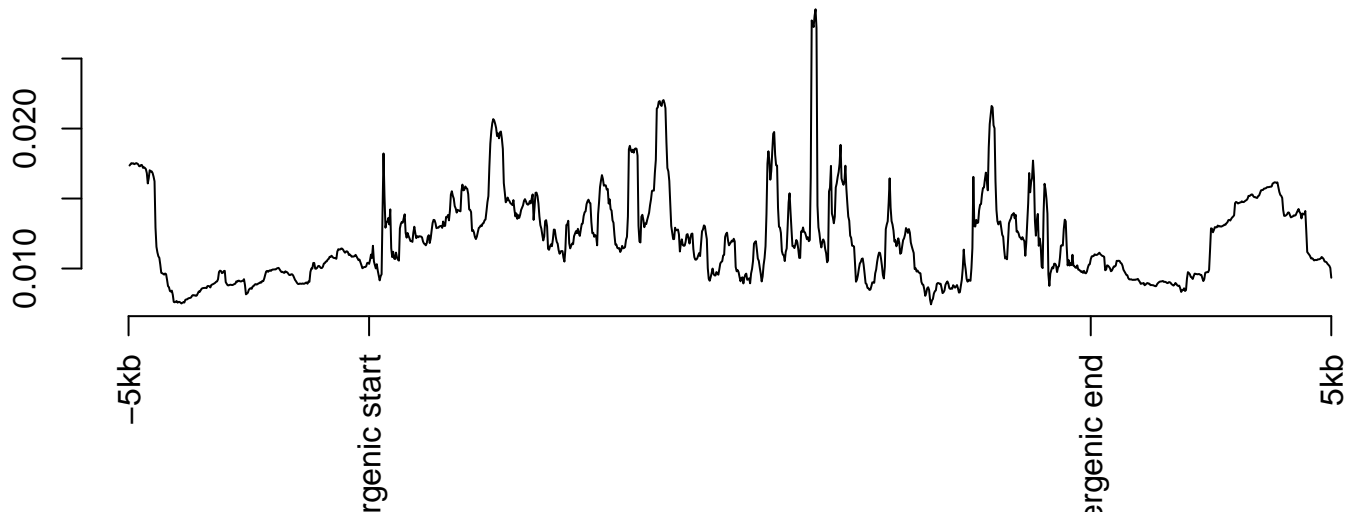
K562 PositivePooled E.588 scCLTdegenNuc451

0.016 0.020 0.024



Average coverage per intergenic region

K562 PositivePooled E.588 scCLTdegenNuc457



Average coverage per intergenic region

K562 PositivePooled E.652 scCLTdegenNuc656

0.020
0.035

-5kb

intergenic start

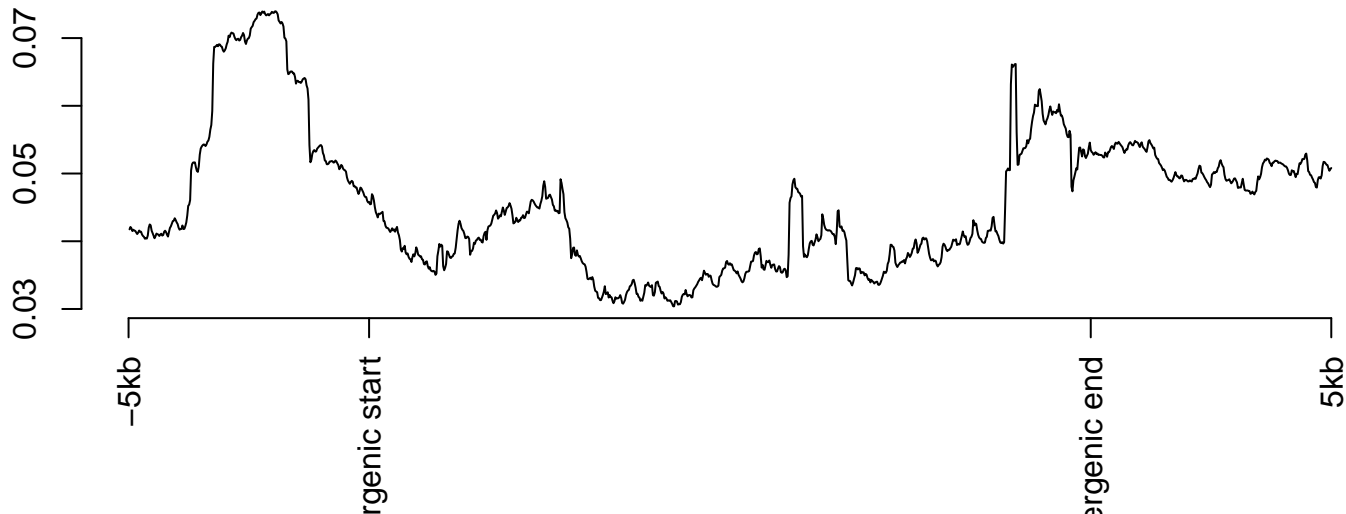
intergenic end

5kb



Average coverage per intergenic region

K562 PositivePooled E.652 scCLTdegenNuc657



Average coverage per intergenic region

K562 PositivePooled E.683 scCLTdegenNuc1011

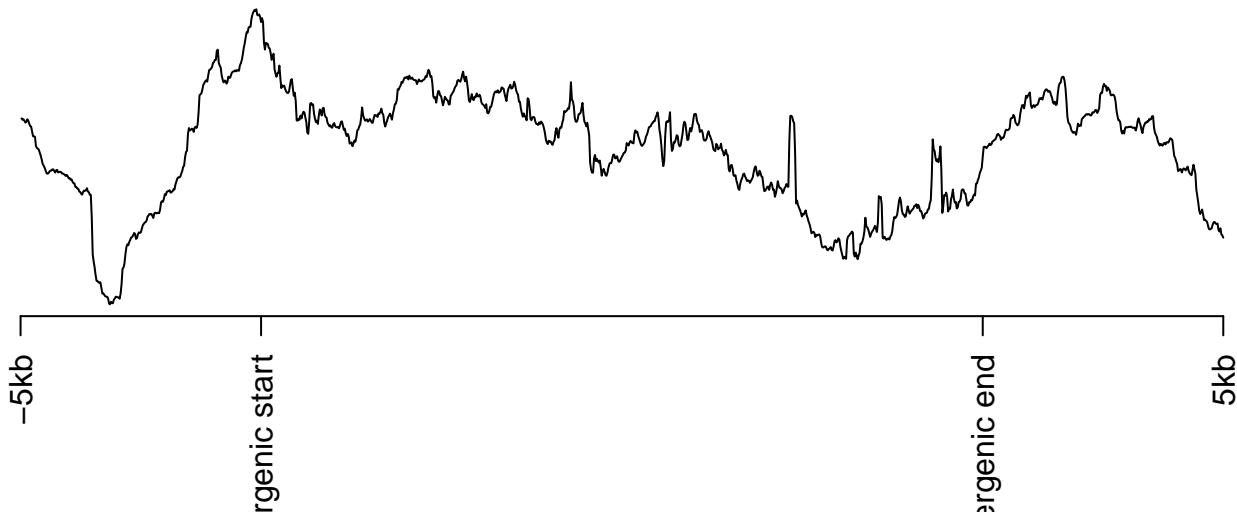
0.025
0.040
0.055

-5kb

intergenic start

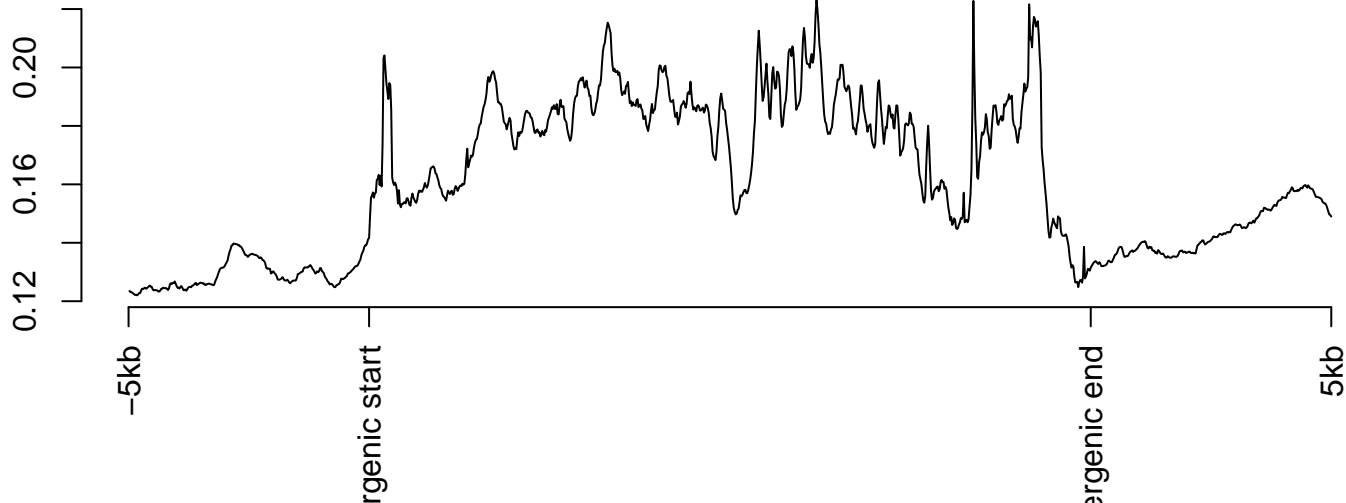
intergenic end

5kb



Average coverage per intergenic region

K562 PositiveMerged E.– K562PositiveMerged



Average coverage per intergenic region

K562 PositiveAll E.- K562PositiveAll

0.30 0.35 0.40

-5kb

intergenic start

intergenic end

5kb

