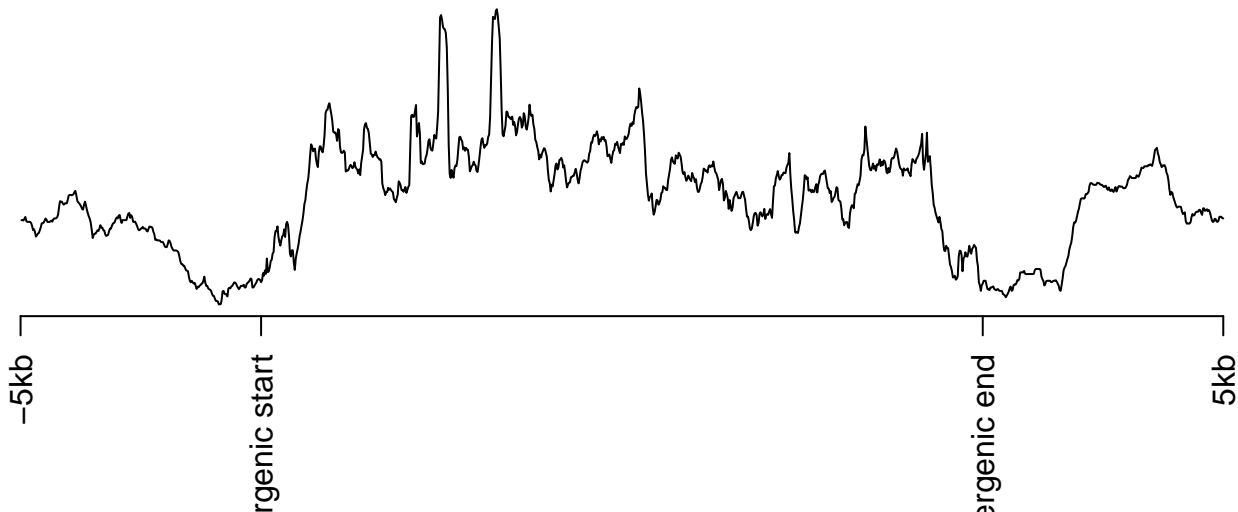


K562TPA1hr PositiveSingle E.644 scCLTdegenNuc631

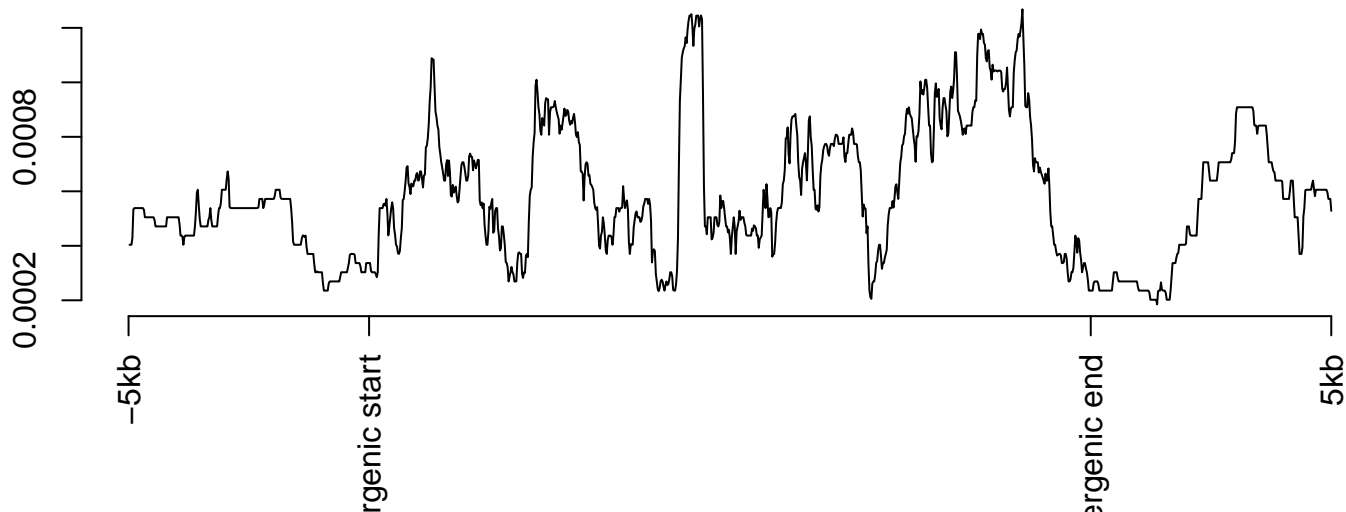
Average coverage per intergenic region

0.005
0.002



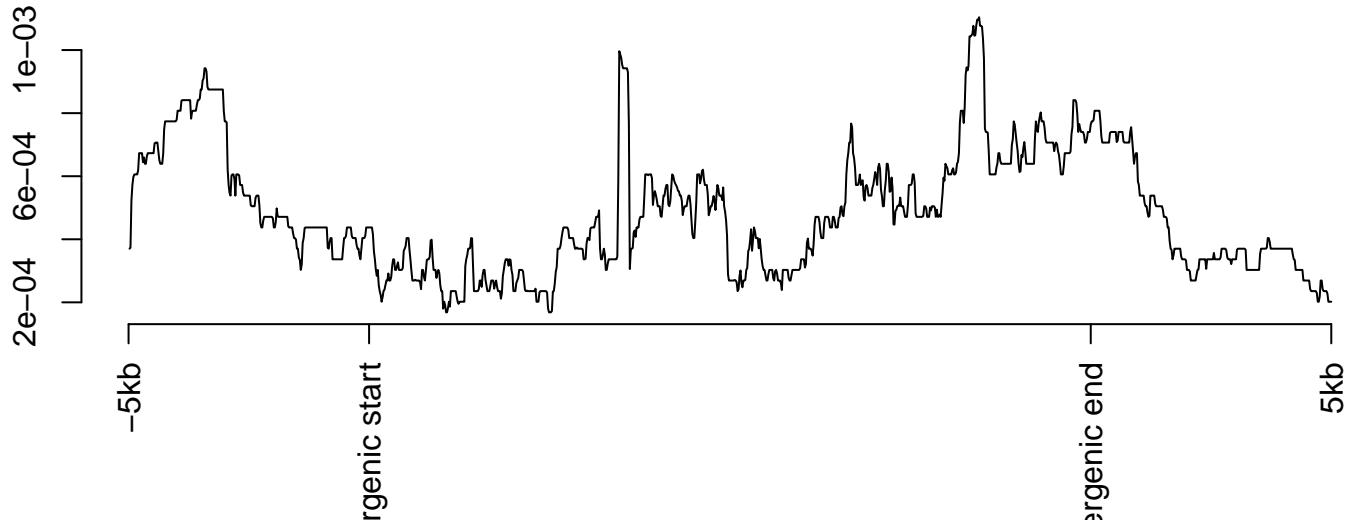
Average coverage per intergenic region

K562TPA1hr PositiveSingle E.644 scCLTdegenNuc633



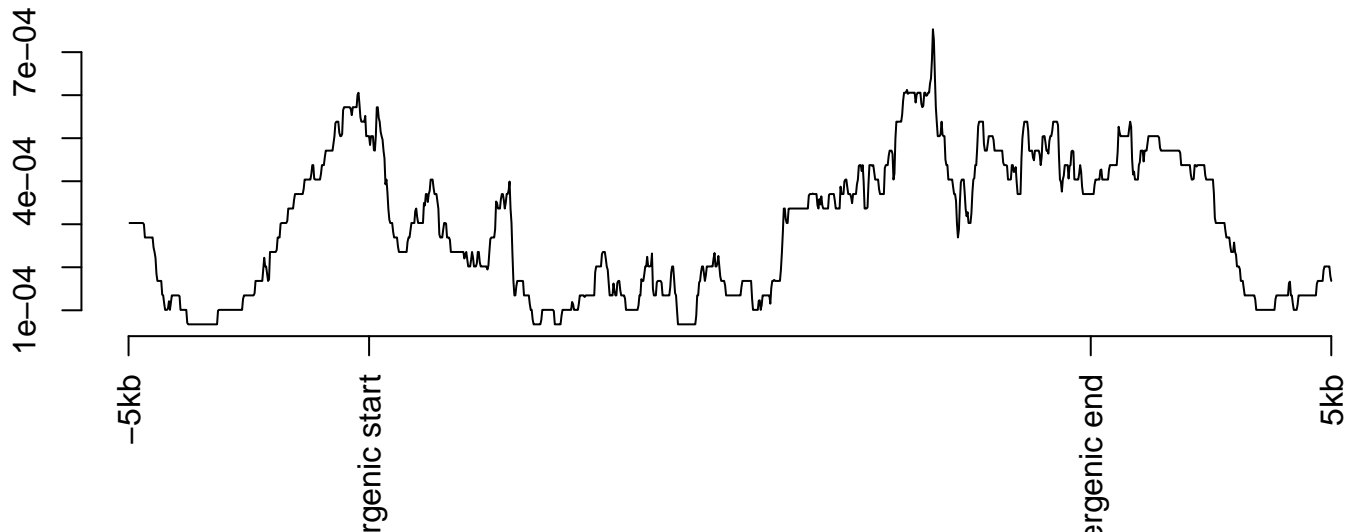
Average coverage per intergenic region

K562TPA1hr PositiveSingle E.651 scCLTdegenNuc651



Average coverage per intergenic region

K562TPA1hr PositiveSingle E.651 scCLTdegenNuc652



Average coverage per intergenic region

K562TPA1hr PositiveSingle E.652 scCLTdegenNuc653

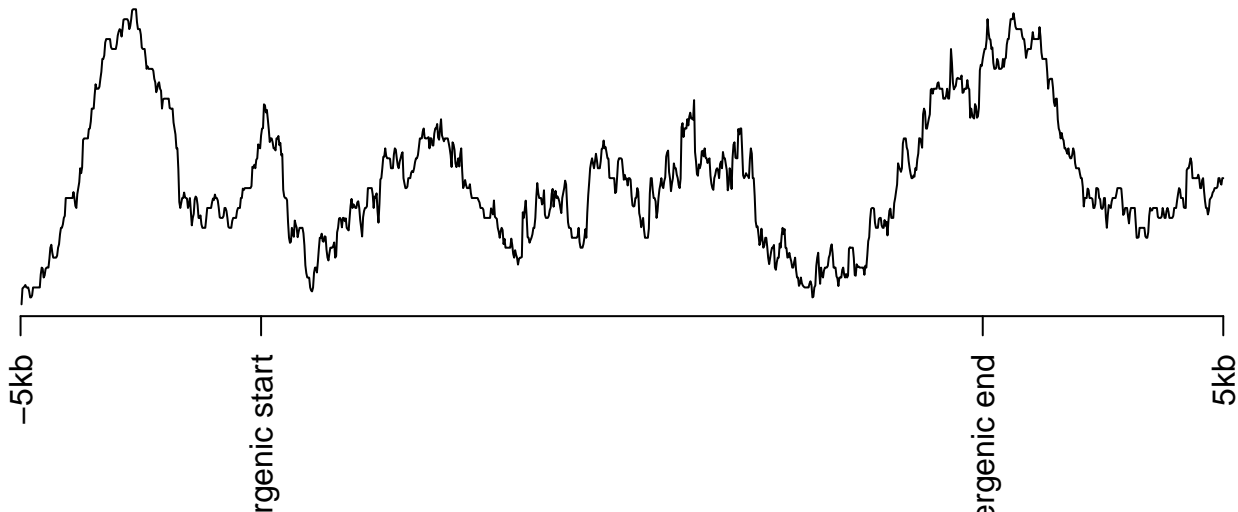
0.0012
0.0006

-5kb

intergenic start

intergenic end

5kb



Average coverage per intergenic region

K562TPA1hr PositiveMerged E.- K562TPA1hrPositiveMerged

