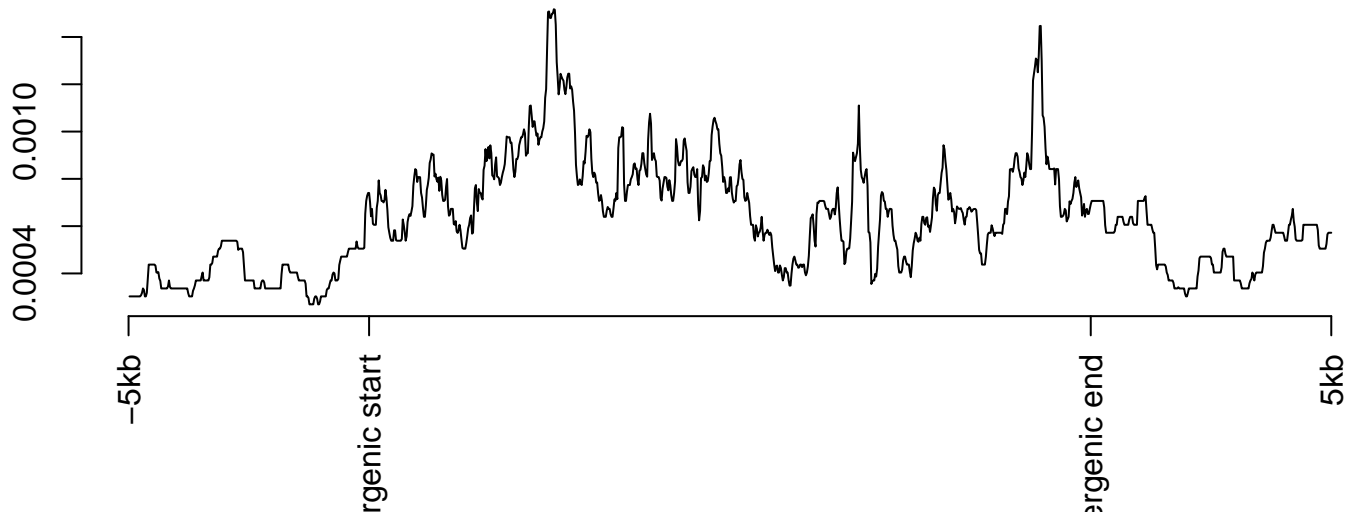


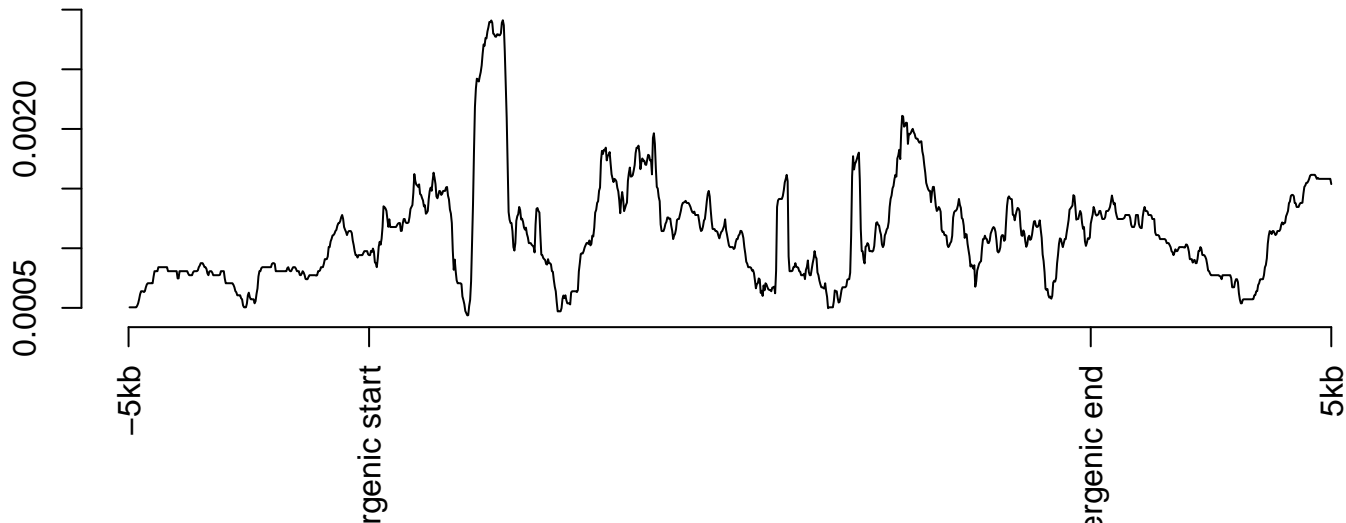
Average coverage per intergenic region

K562TPA15min PositiveSingle E.644 scCLTdegenNuc641



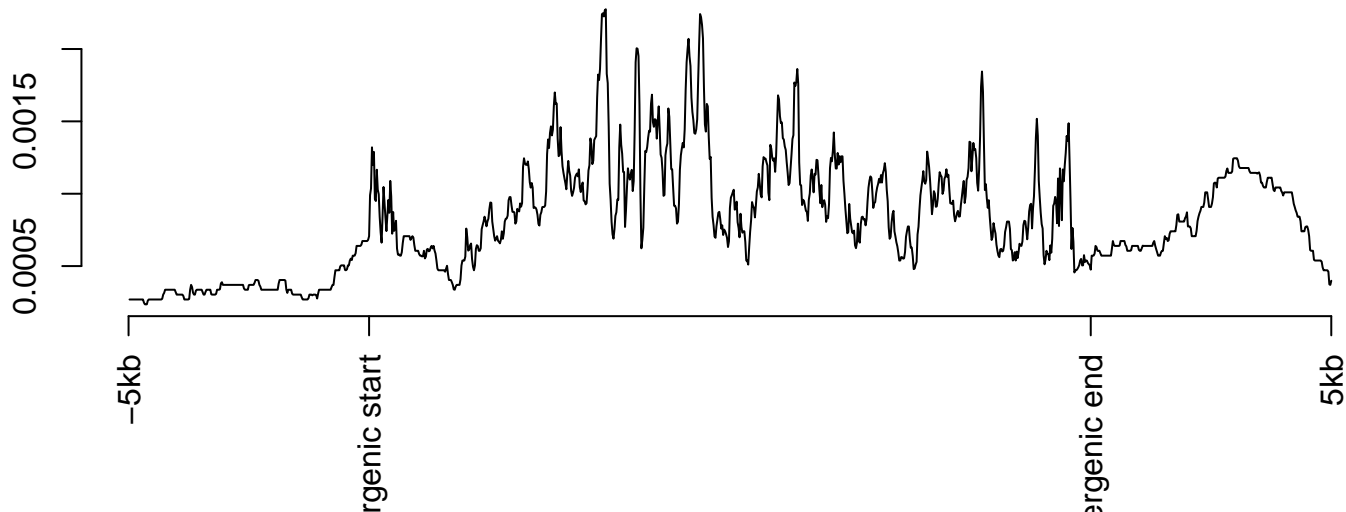
Average coverage per intergenic region

K562TPA15min PositiveSingle E.644 scCLTdegenNuc642



Average coverage per intergenic region

K562TPA15min PositiveSingle E.644 scCLTdegenNuc643



Average coverage per intergenic region

K562TPA15min PositiveSingle E.651 scCLTdegenNuc639

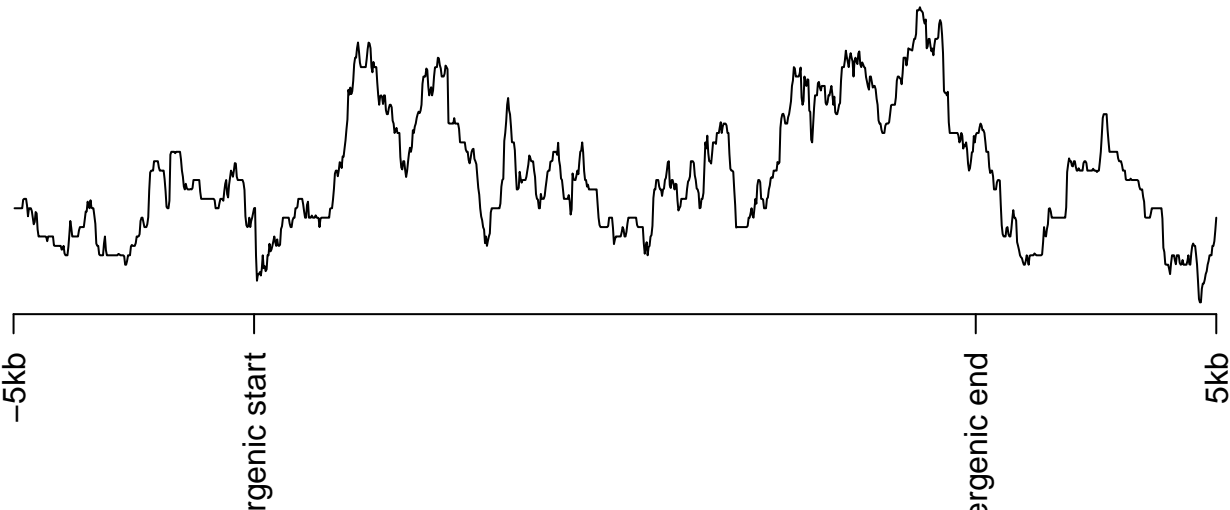
0.0012  
0.0006

-5kb

intergenic start

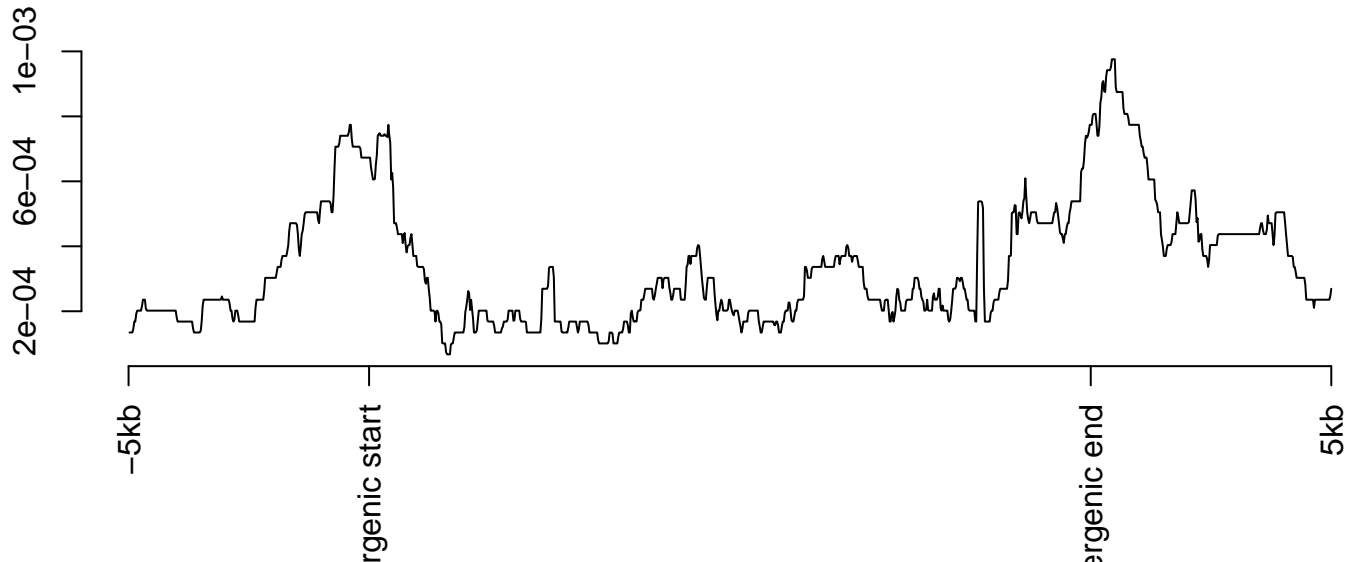
intergenic end

5kb



Average coverage per intergenic region

K562TPA15min PositiveSingle E.651 scCLTdegenNuc640



Average coverage per intergenic region

K562TPA15min PositiveMerged E.- K562TPA15minPositiveMerged

