

Average coverage per intergenic region

K562TPA2hr PositiveSingle E.644 scCLTdegenNuc644

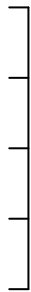
0.0005 0.0015 0.0025

-5kb

intergenic start

intergenic end

5kb



Average coverage per intergenic region

**K562TPA2hr PositiveSingle E.644 scCLTdegenNuc645**

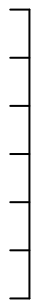
0.0050  
0.0035  
0.0020

-5kb

intergenic start

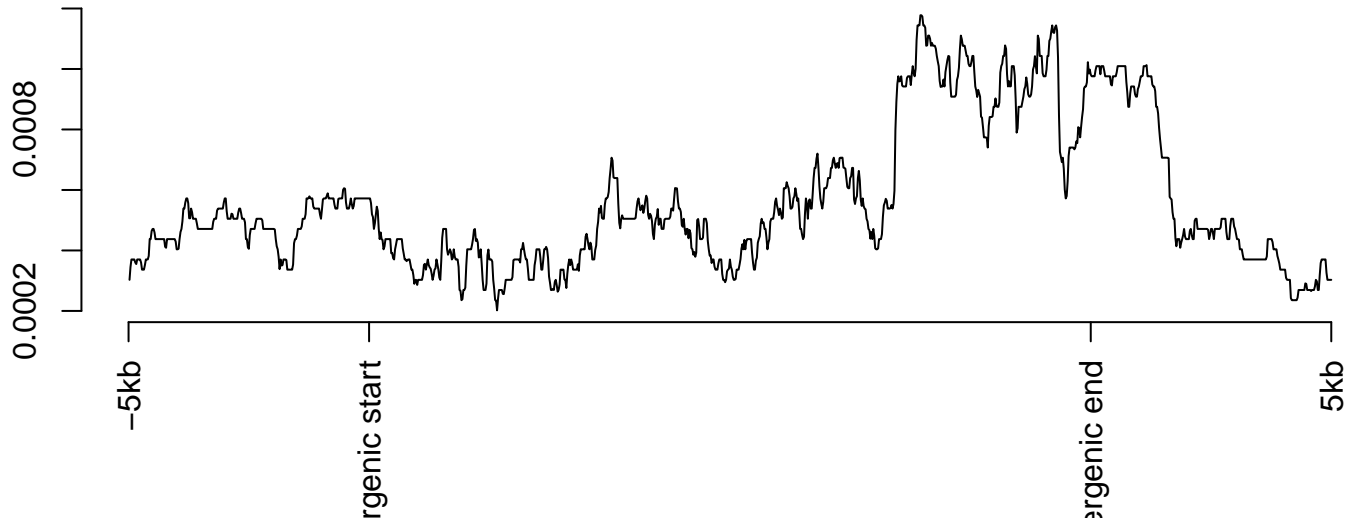
intergenic end

5kb



# K562TPA2hr PositiveSingle E.651 scCLTdegenNuc646

Average coverage per intergenic region



Average coverage per intergenic region

K562TPA2hr PositiveSingle E.651 scCLTdegenNuc647

0.014  
0.010

-5kb

intergenic start

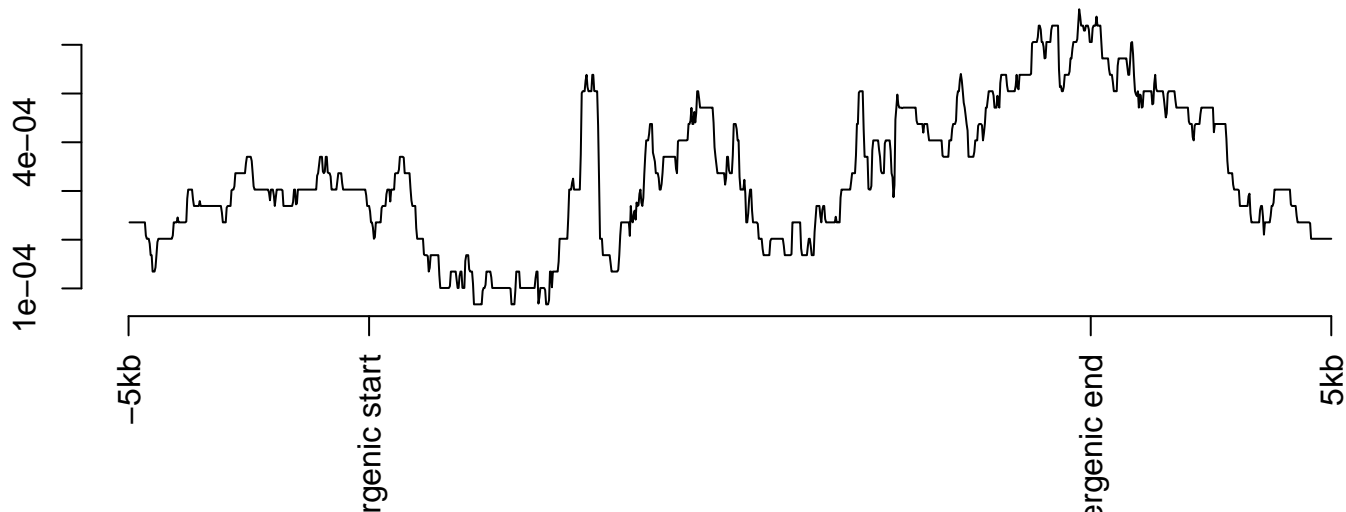
intergenic end

5kb



Average coverage per intergenic region

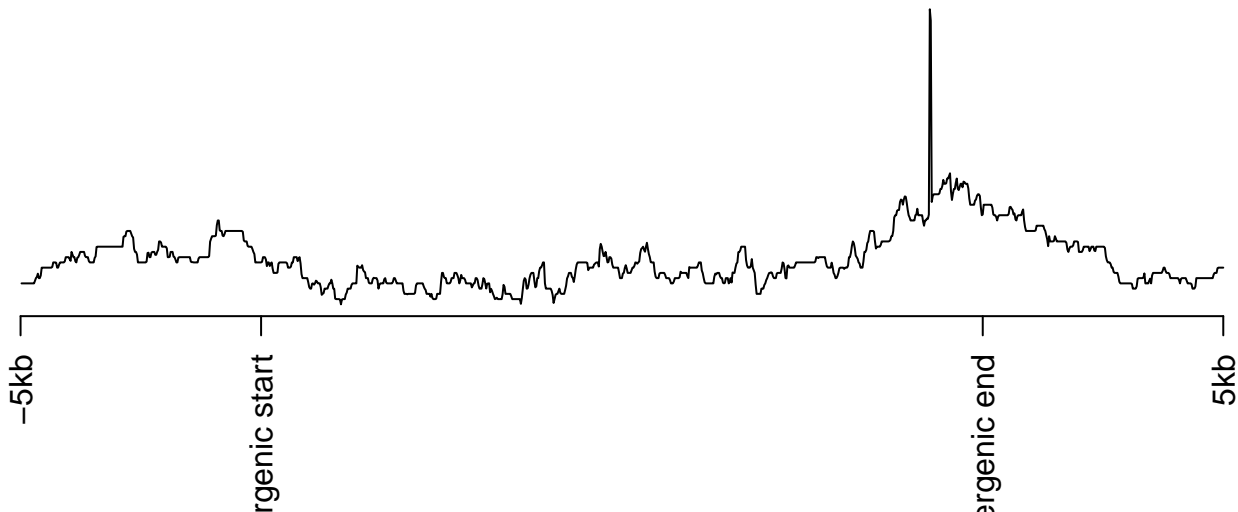
K562TPA2hr PositiveSingle E.651 scCLTdegenNuc648



# K562TPA2hr PositiveSingle E.651 scCLTdegenNuc649

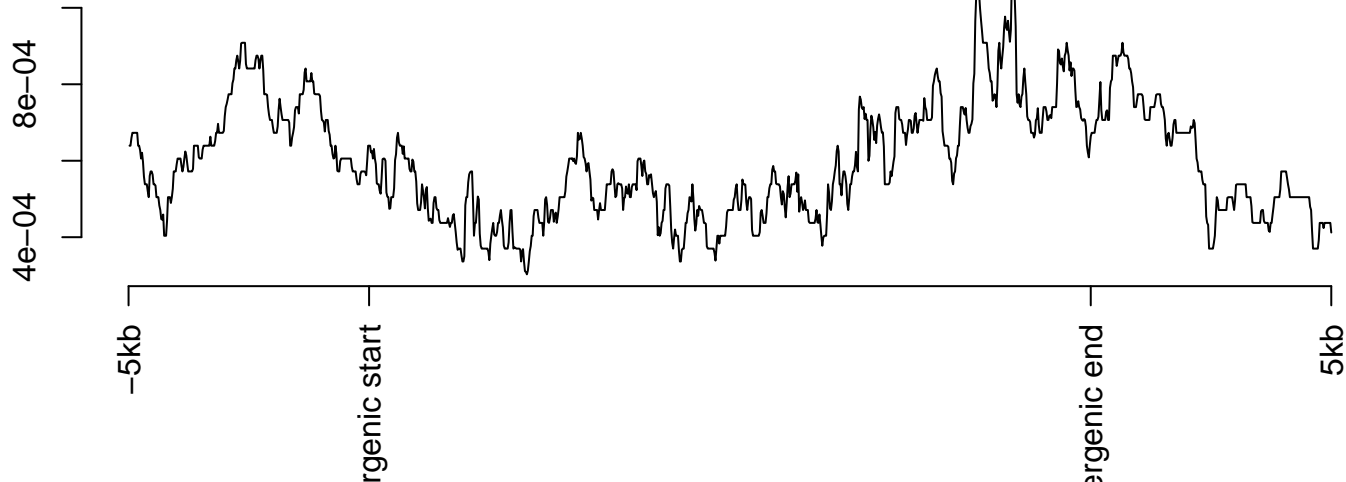
Average coverage per intergenic region

0.0005 0.0015



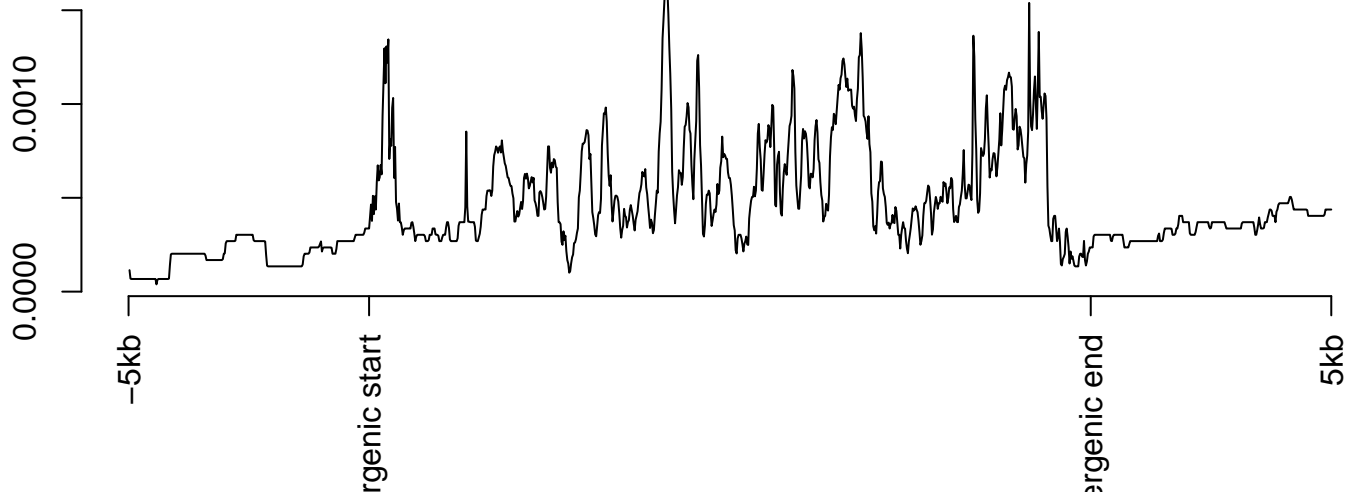
Average coverage per intergenic region

# K562TPA2hr PositiveSingle E.651 scCLTdegenNuc650



Average coverage per intergenic region

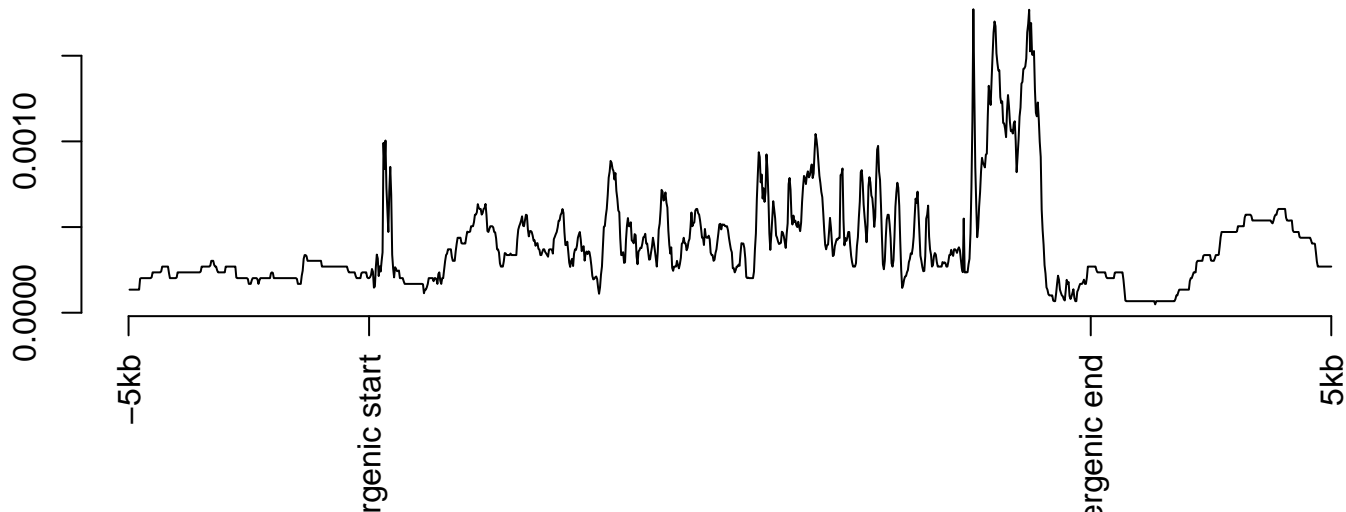
K562TPA2hr PositiveSingle E.673 scCLTdegenNuc922\_b





Average coverage per intergenic region

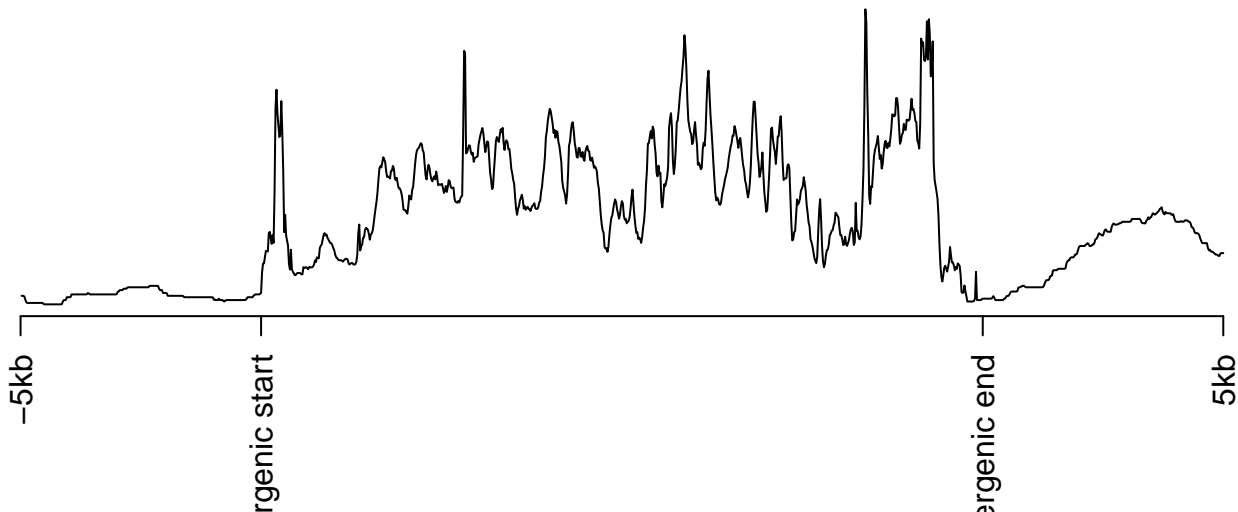
K562TPA2hr PositiveSingle E.673 scCLTdegenNuc923\_b



Average coverage per intergenic region

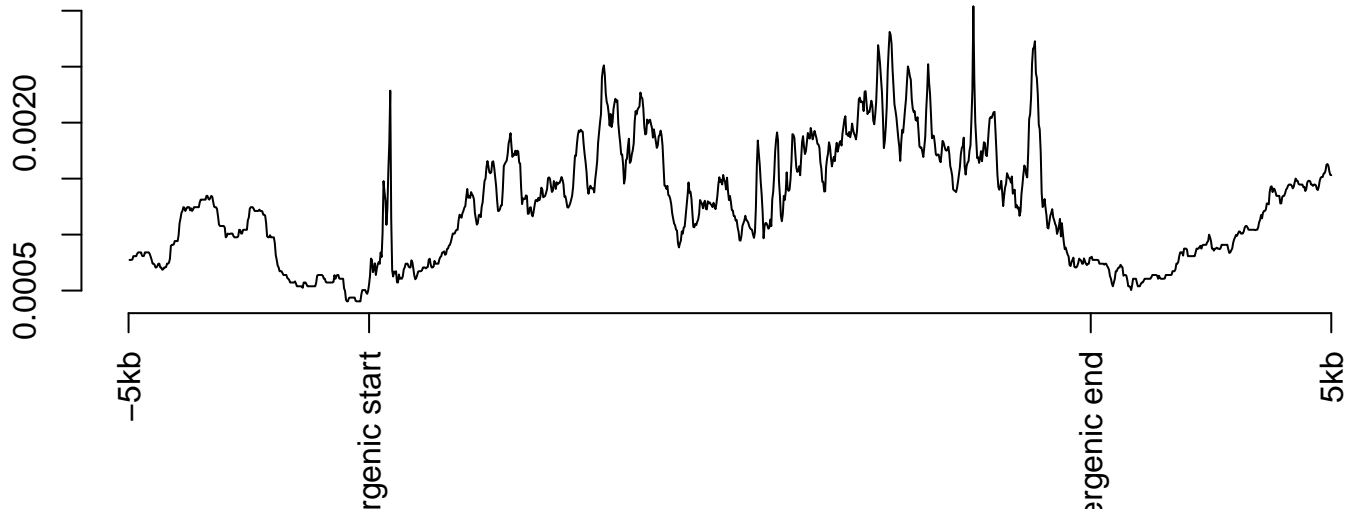
K562TPA2hr PositiveSingle E.673 scCLTdegenNuc927\_b

0.006  
0.003  
0.000



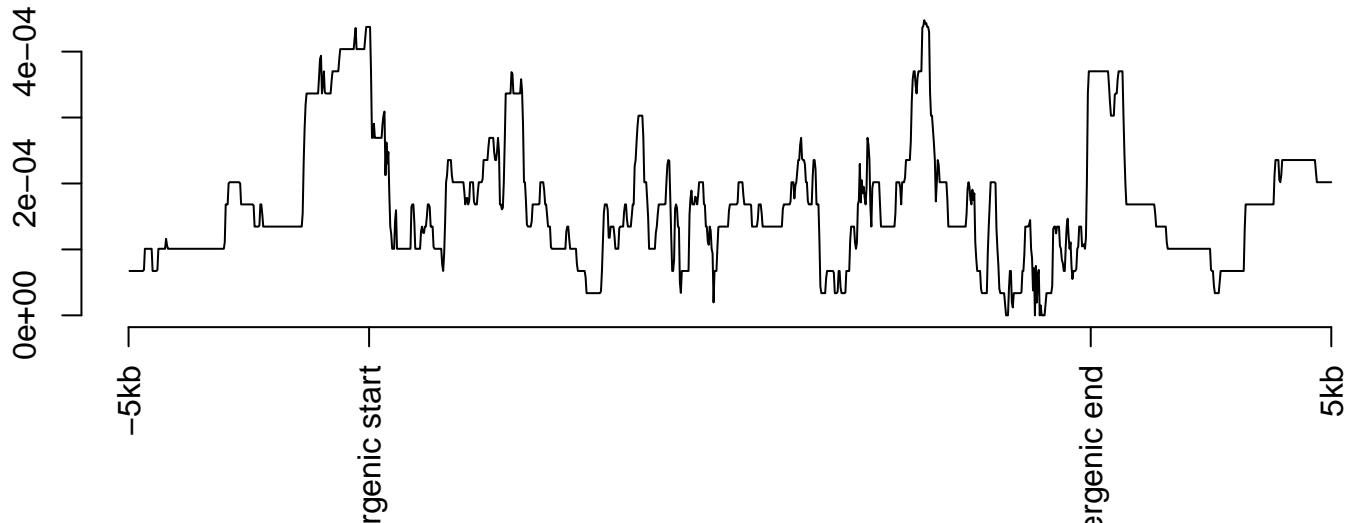
Average coverage per intergenic region

K562TPA2hr PositiveSingle E.673 scCLTdegenNuc928\_b



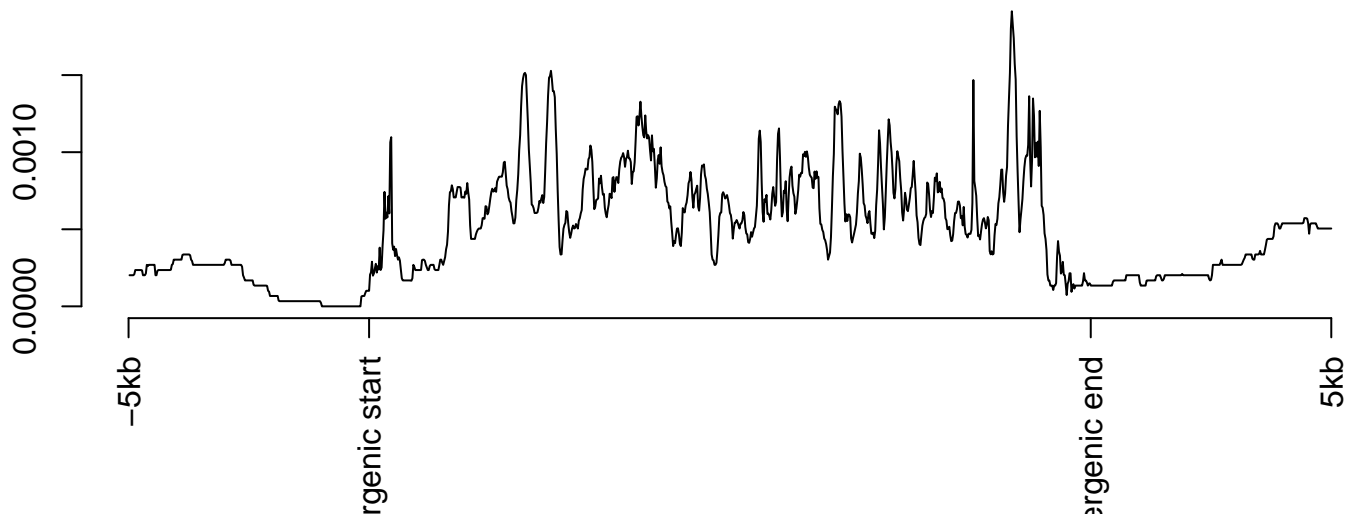
Average coverage per intergenic region

K562TPA2hr PositiveSingle E.673 scCLTdegenNuc930\_b



Average coverage per intergenic region

K562TPA2hr PositiveSingle E.673 scCLTdegenNuc931\_b



Average coverage per intergenic region

K562TPA2hr PositiveMerged E.– K562TPA2hrPositiveMerged

