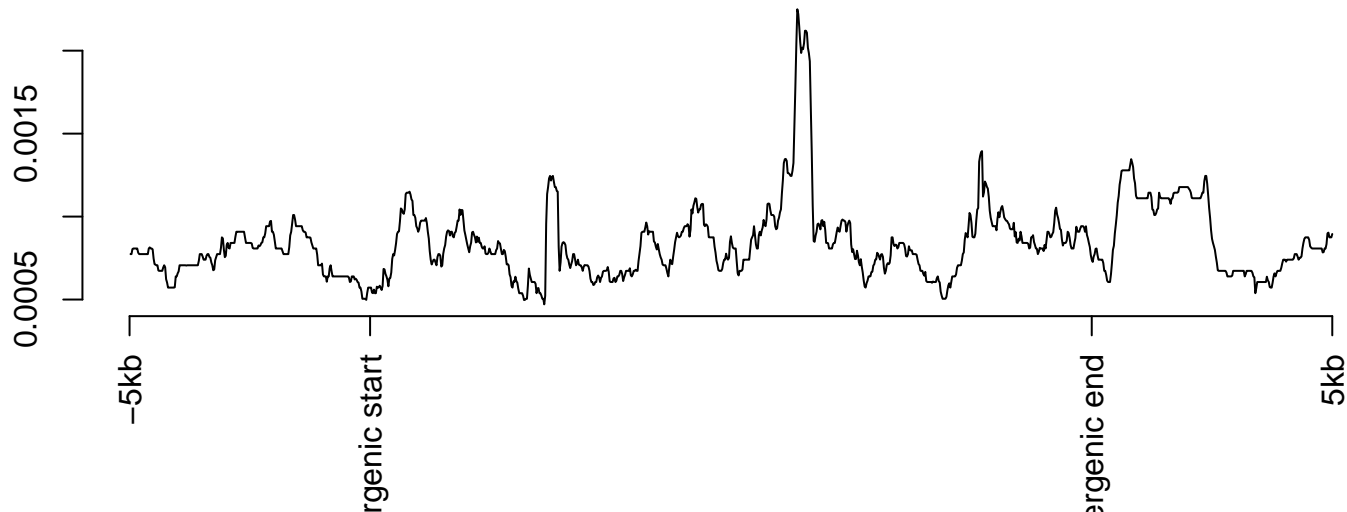


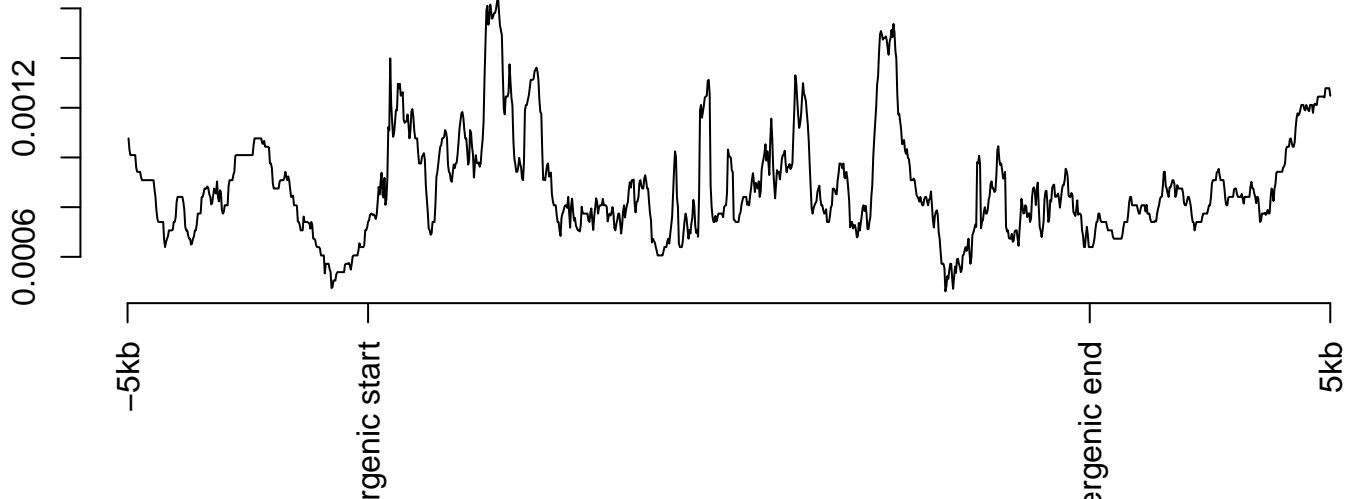
HumanInterneuronCulture PositiveSingle E.658 scCLTdegenNuc735

Average coverage per intergenic region



Average coverage per intergenic region

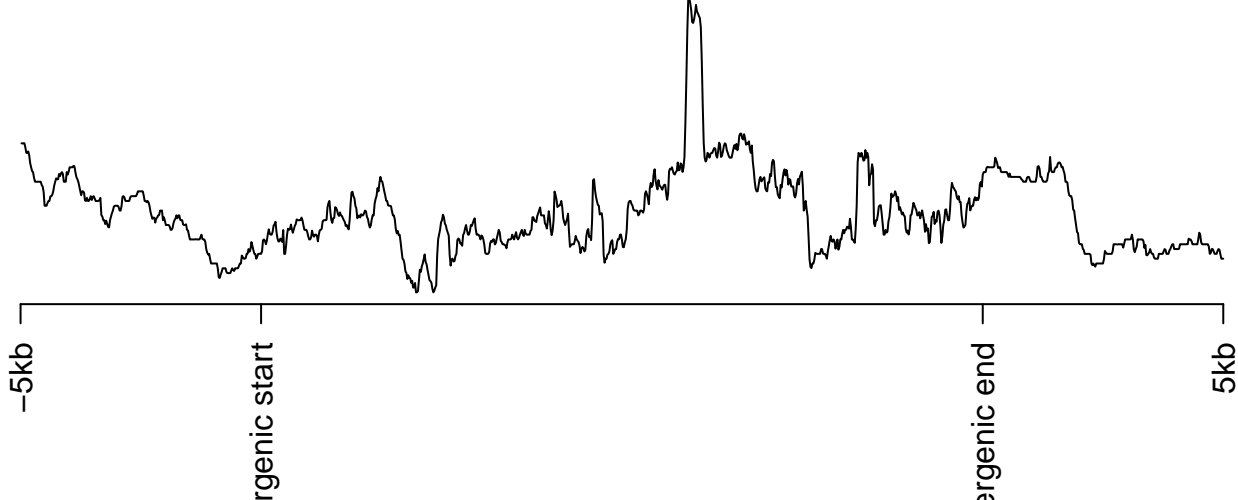
HumanInterneuronCulture PositiveSingle E.658 scCLTdegenNuc736



HumanInterneuronCulture PositiveSingle E.658 scCLTdegenNuc737

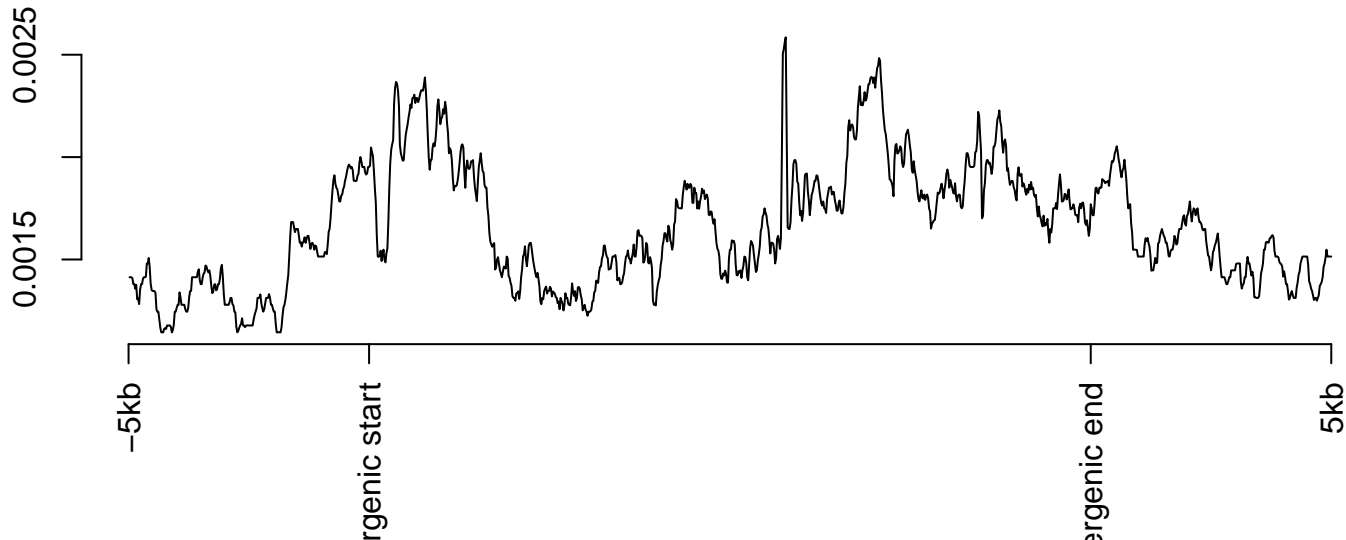
Average coverage per intergenic region

0.0025
0.0015
0.0005



Average coverage per intergenic region

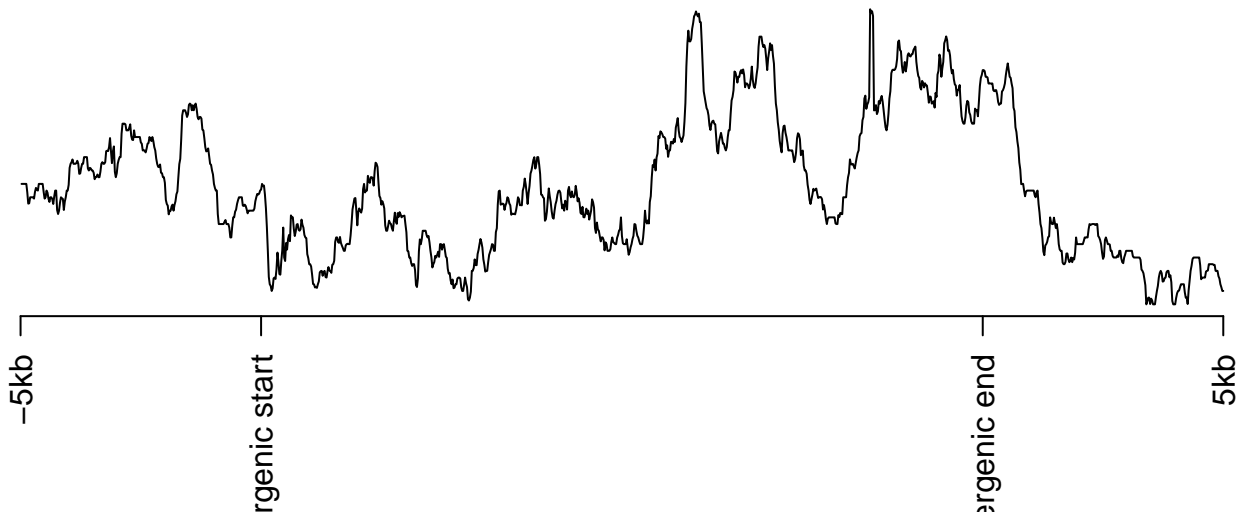
HumanInterneuronCulture PositiveSingle E.658 scCLTdegenNuc738



HumanInterneuronCulture PositiveSingle E.658 scCLTdegenNuc739

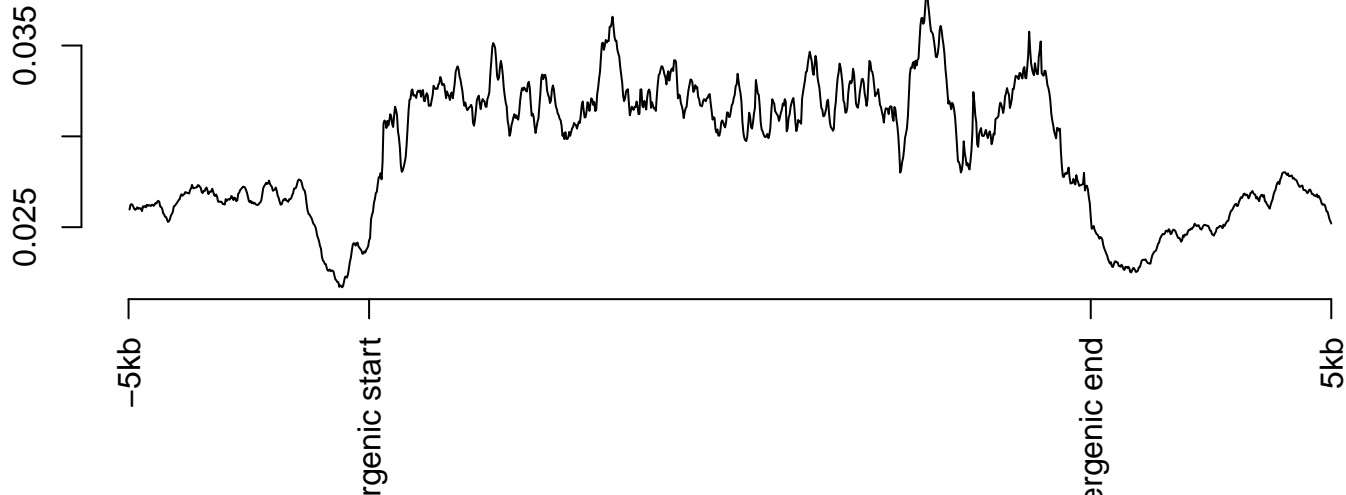
Average coverage per intergenic region

0.0020
0.0010



Average coverage per intergenic region

HumanInterneuronCulture PositiveSingle E.663 scCLTdegenNuc740



HumanInterneuronCulture PositiveSingle E.663 scCLTdegenNuc741

Average coverage per intergenic region

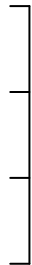
0.0020
0.0010

-5kb

intergenic start

intergenic end

5kb



HumanInterneuronCulture PositiveSingle E.663 scCLTdegenNuc742

Average coverage per intergenic region

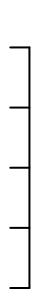
0.020 0.030 0.040

-5kb

intergenic start

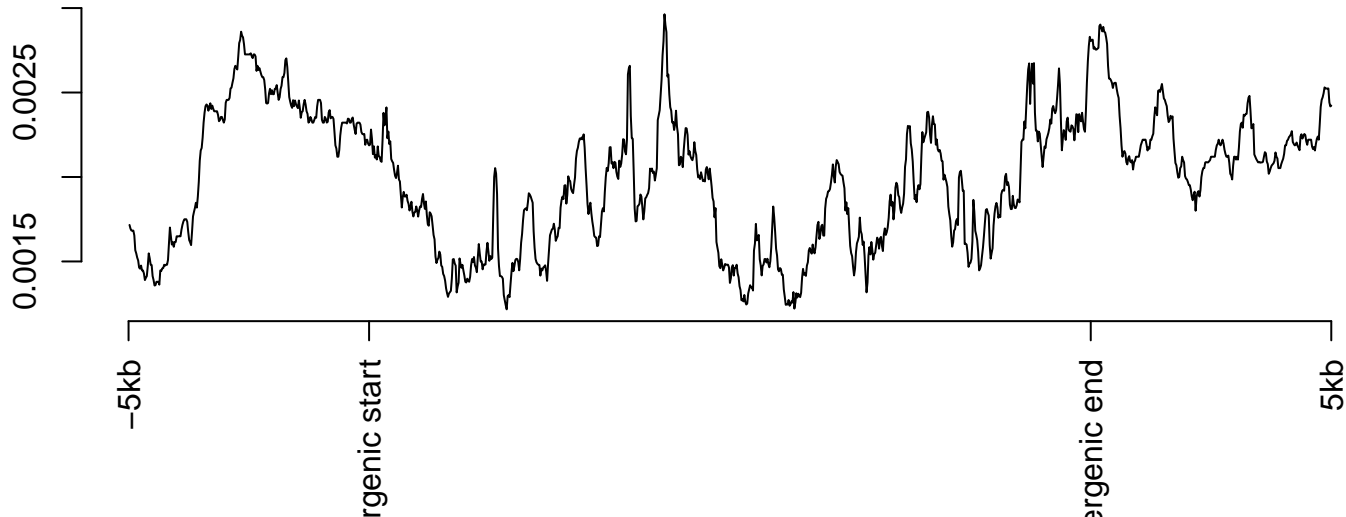
intergenic end

5kb



Average coverage per intergenic region

HumanInterneuronCulture PositiveSingle E.663 scCLTdegenNuc743



Average coverage per intergenic region

HumanInterneuronCulture PositiveSingle E.663 scCLTdegenNuc744

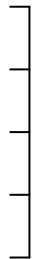
0.0015 0.0025 0.0035

-5kb

intergenic start

intergenic end

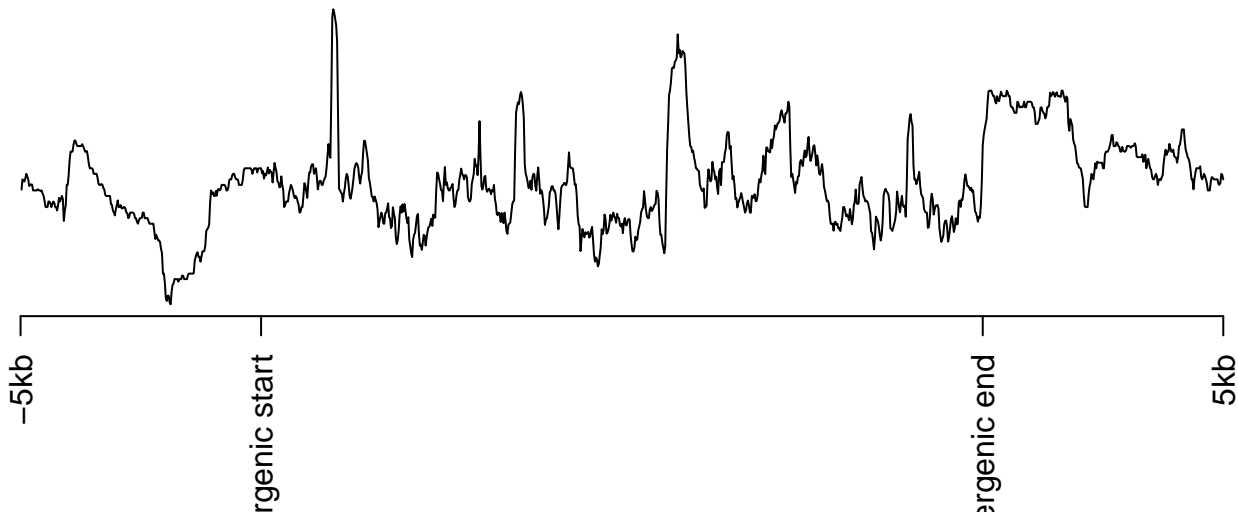
5kb



Average coverage per intergenic region

HumanInterneuronCulture PositiveSingle E.663 scCLTdegenNuc745

0.0020
0.0010



Average coverage per intergenic region

HumanInterneuronCulture PositiveSingle E.663 scCLTdegenNuc746

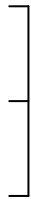
0.0020
0.0010

-5kb

intergenic start

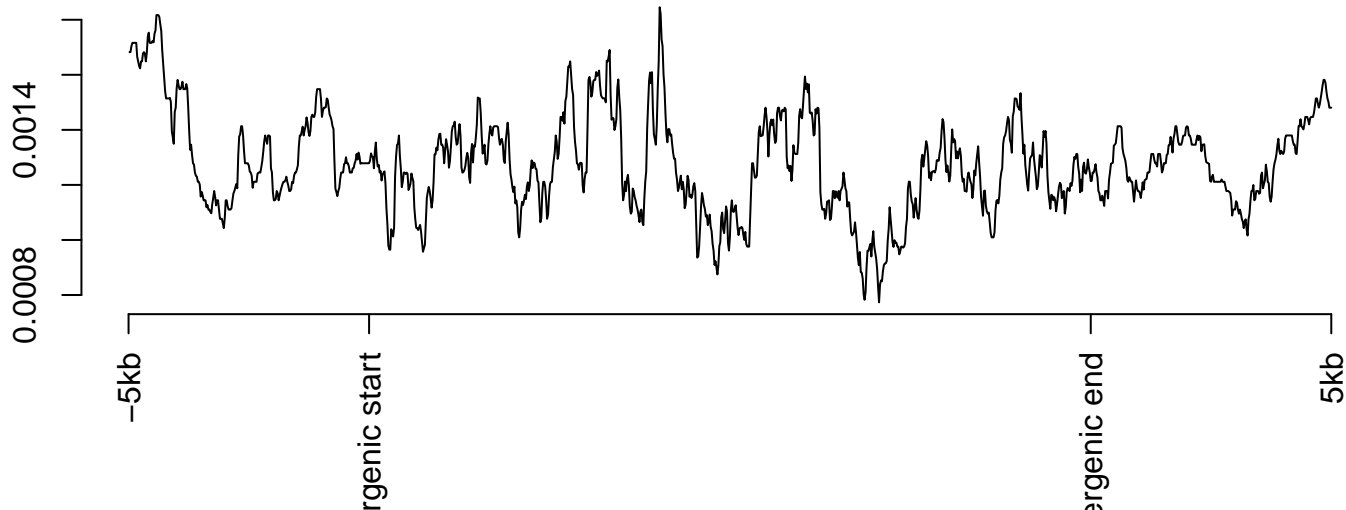
intergenic end

5kb



Average coverage per intergenic region

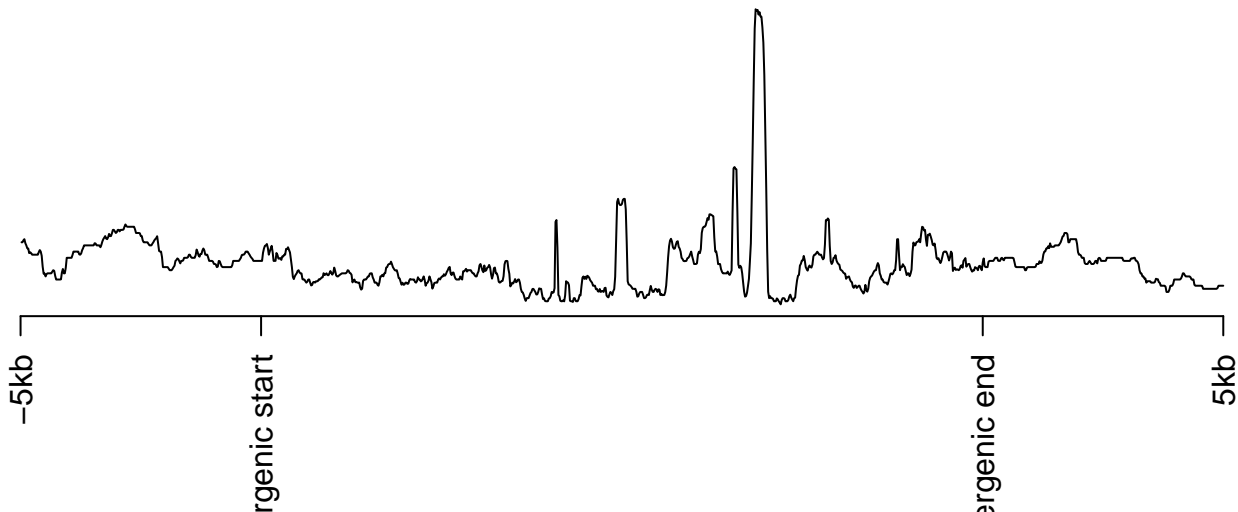
HumanInterneuronCulture PositiveSingle E.663 scCLTdegenNuc747



HumanInterneuronCulture PositiveSingle E.663 scCLTdegenNuc748

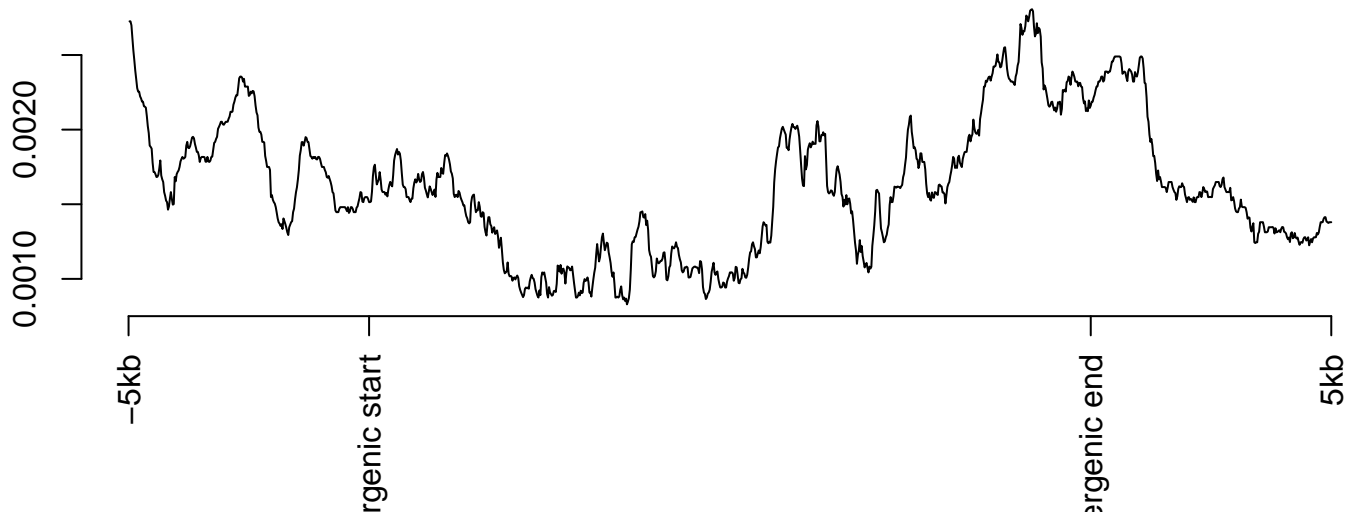
Average coverage per intergenic region

0.0035
0.0020
0.0005



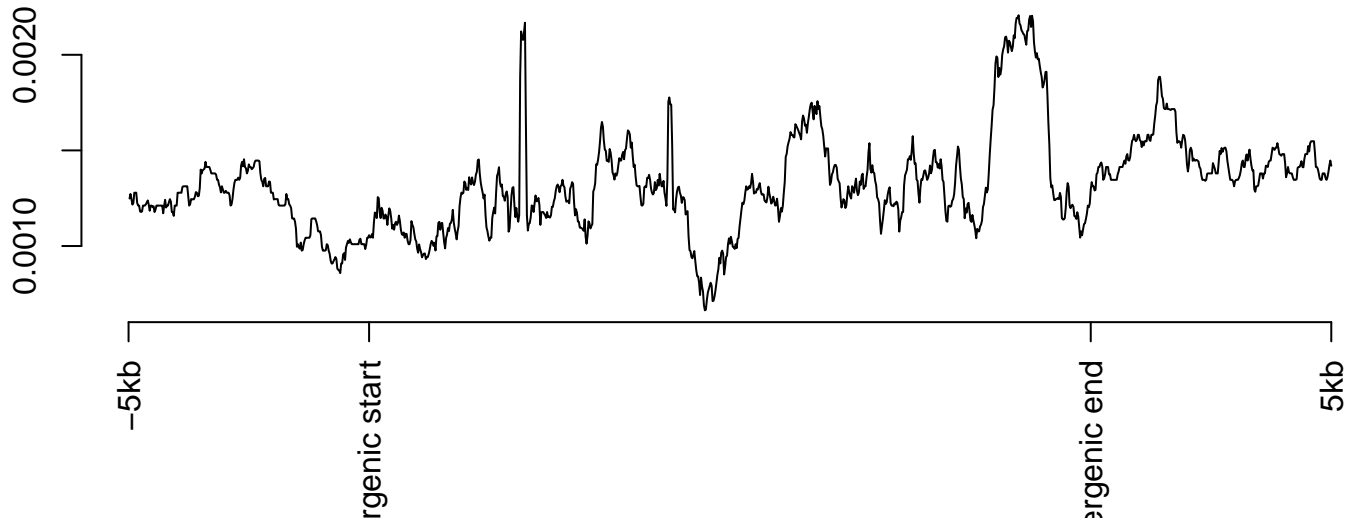
Average coverage per intergenic region

HumanInterneuronCulture PositiveSingle E.663 scCLTdegenNuc749



Average coverage per intergenic region

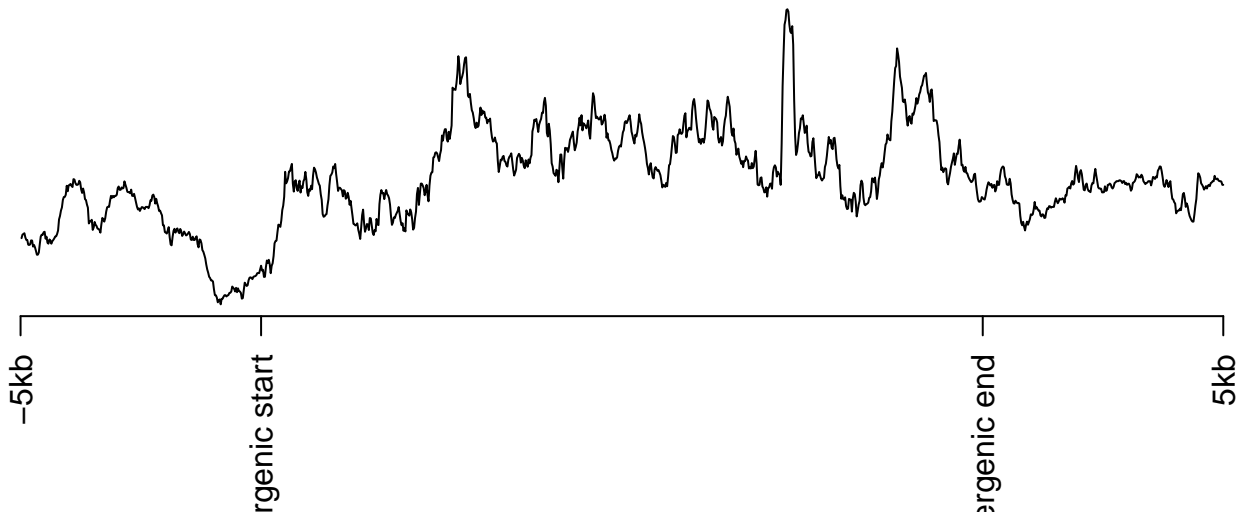
HumanInterneuronCulture PositiveSingle E.663 scCLTdegenNuc750



HumanInterneuronCulture PositiveSingle E.663 scCLTdegenNuc751

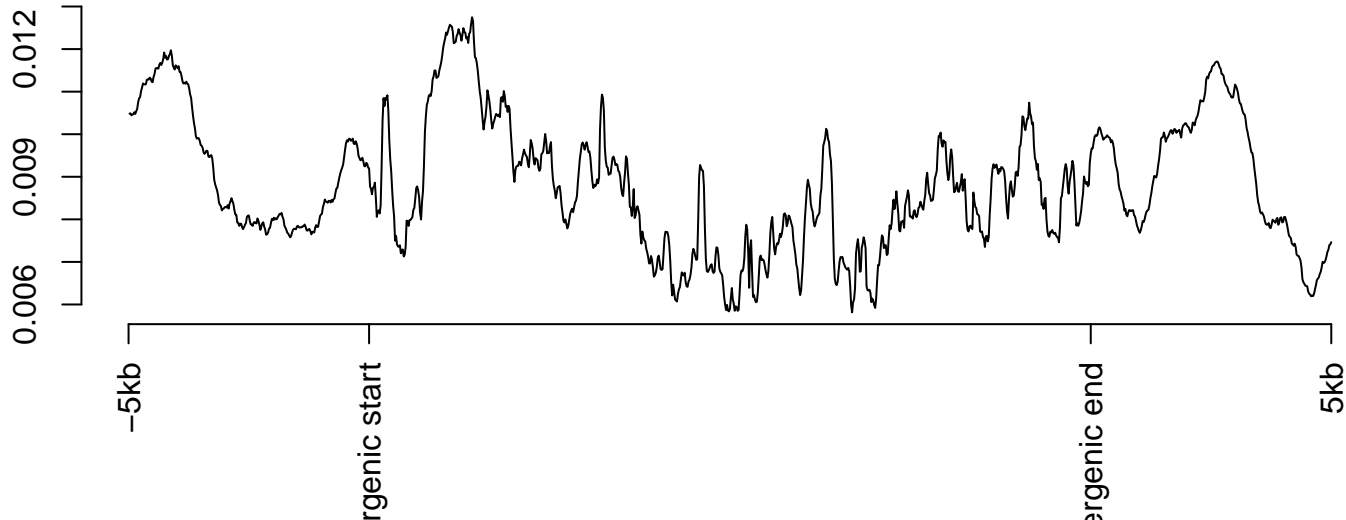
Average coverage per intergenic region

0.0020 0.0035



Average coverage per intergenic region

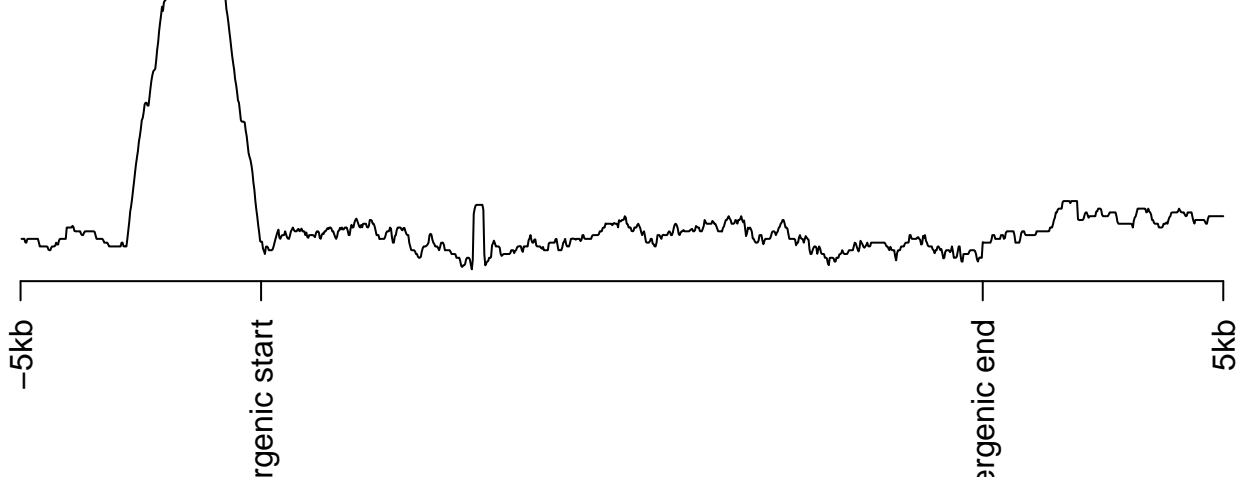
HumanInterneuronCulture PositiveSingle E.664 scCLTdegenNuc752



HumanInterneuronCulture PositiveSingle E.664 scCLTdegenNuc753

Average coverage per intergenic region

0.0020
0.0005



Average coverage per intergenic region

HumanInterneuronCulture PositiveSingle E.664 scCLTdegenNuc754

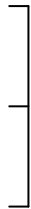
0.0015
0.0005

-5kb

intergenic start

intergenic end

5kb



Average coverage per intergenic region

HumanInterneuronCulture PositiveMerged E.– HumanInterneuronCulturePositiveMerged

