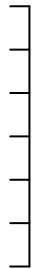


Average coverage per intergenic region

HumanNeuronCulture PositiveSingle E.602 scCLTdegenNuc473

0.0010 0.0016 0.0022



-5kb

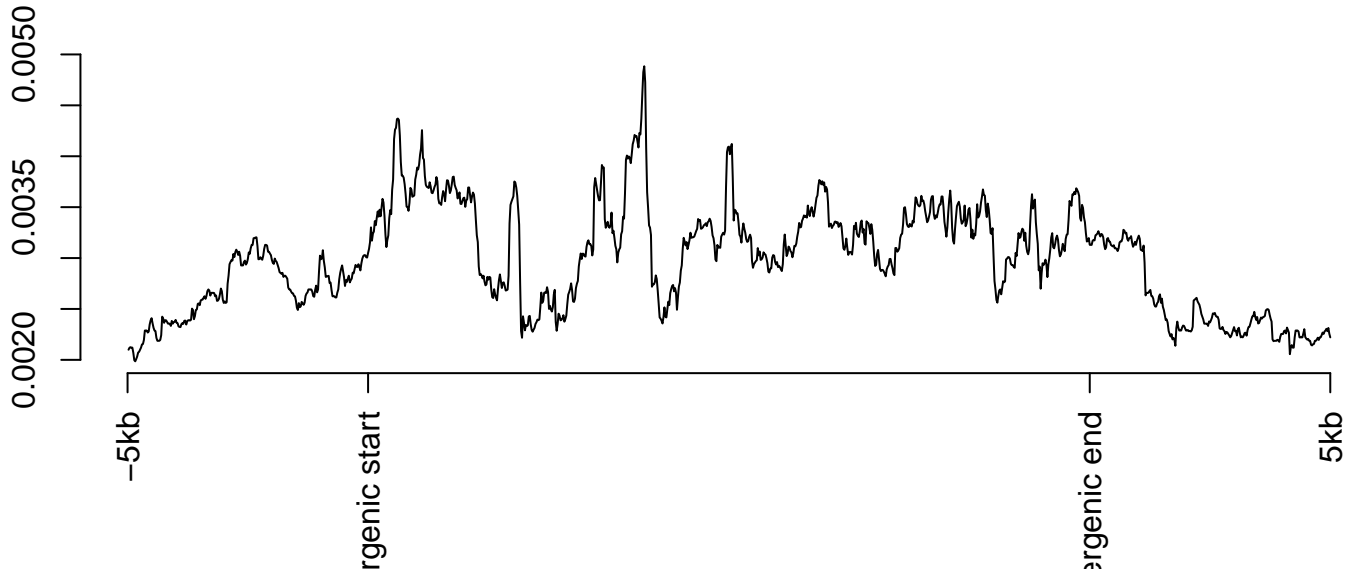
intergenic start

intergenic end

5kb

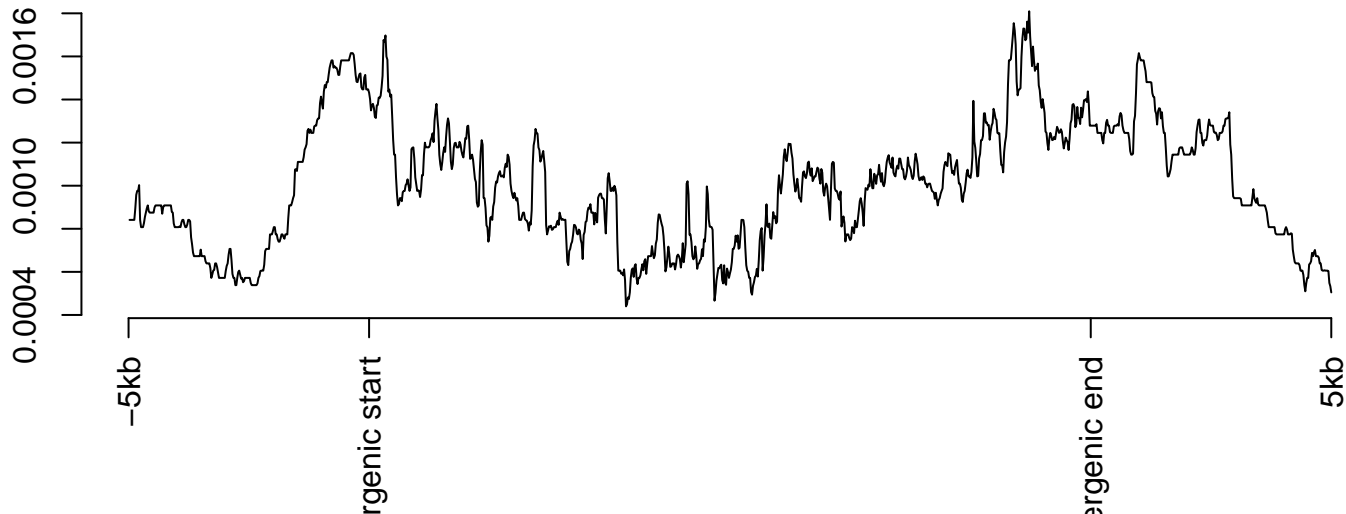
Average coverage per intergenic region

HumanNeuronCulture PositiveSingle E.602 scCLTdegenNuc474



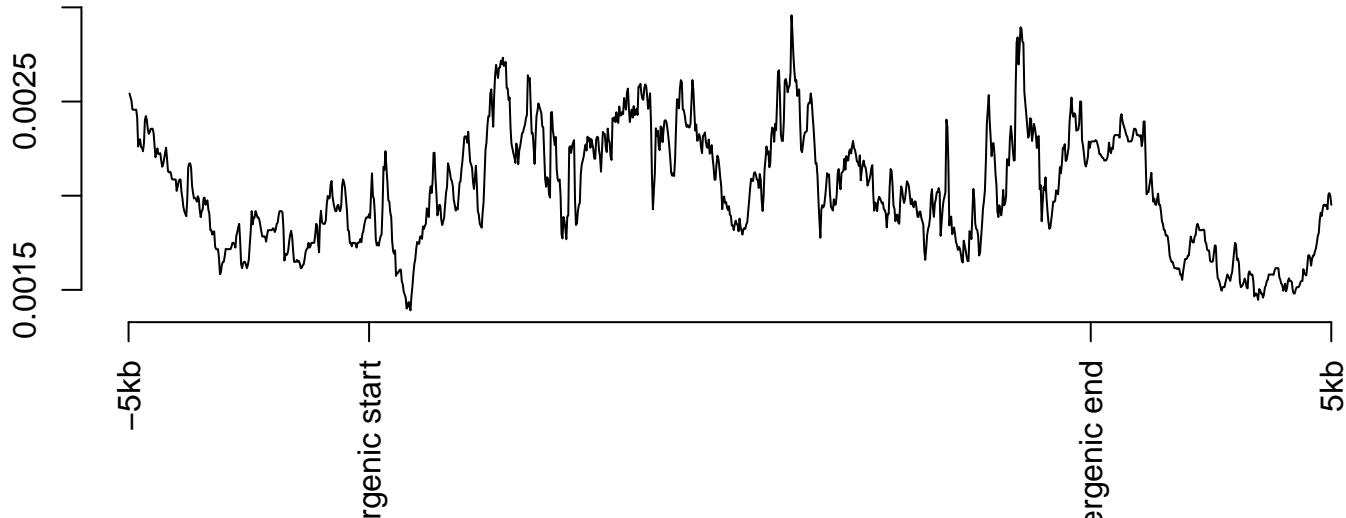
Average coverage per intergenic region

HumanNeuronCulture PositiveSingle E.602 scCLTdegenNuc475



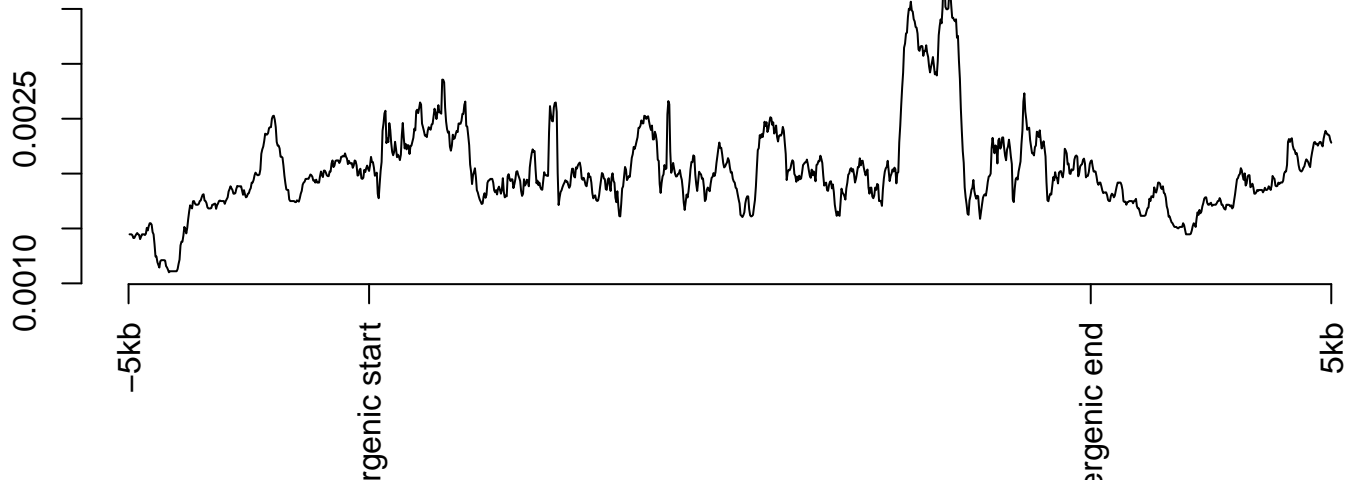
HumanNeuronCulture PositiveSingle E.602 scCLTdegenNuc476

Average coverage per intergenic region



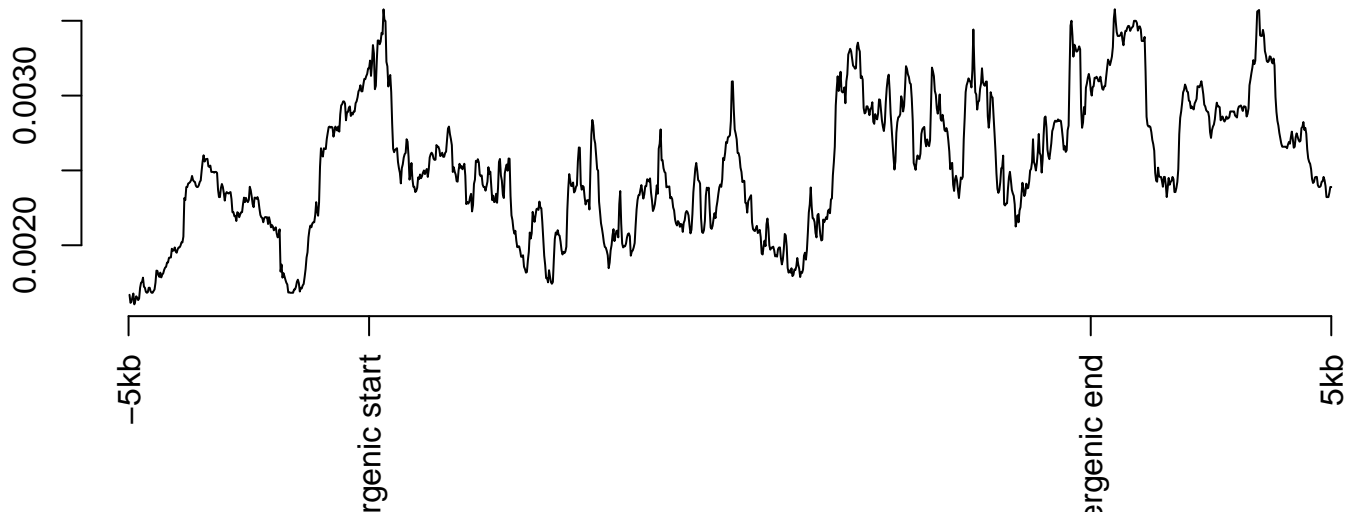
HumanNeuronCulture PositiveSingle E.602 scCLTdegenNuc477

Average coverage per intergenic region



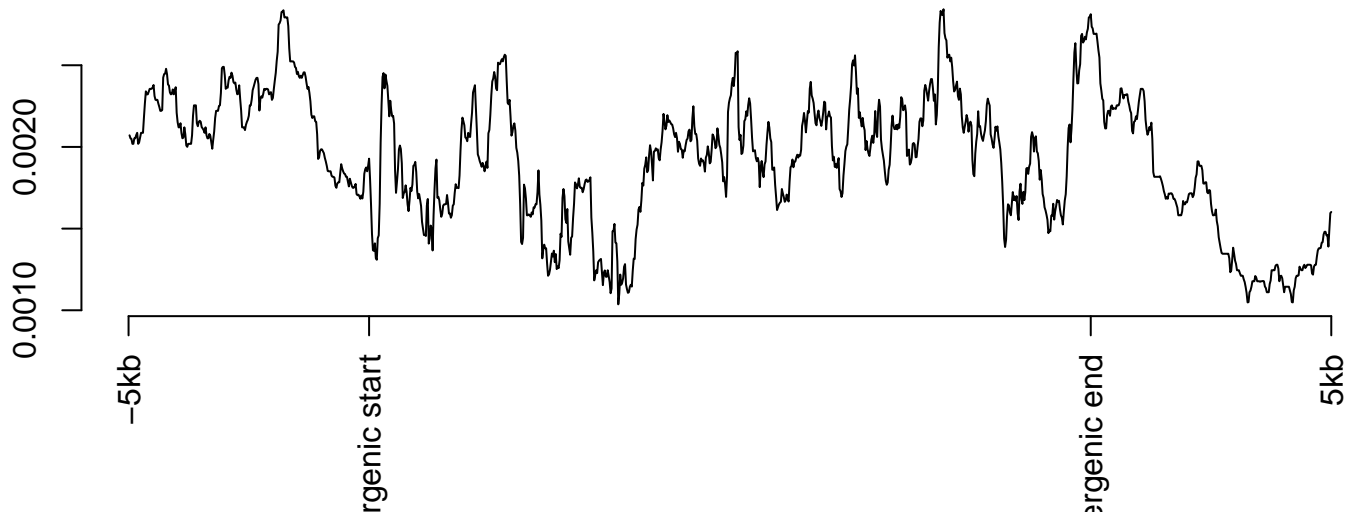
Average coverage per intergenic region

HumanNeuronCulture PositiveSingle E.602 scCLTdegenNuc478



Average coverage per intergenic region

HumanNeuronCulture PositiveSingle E.602 scCLTdegenNuc480



HumanNeuronCulture PositiveSingle E.602 scCLTdegenNuc481

Average coverage per intergenic region

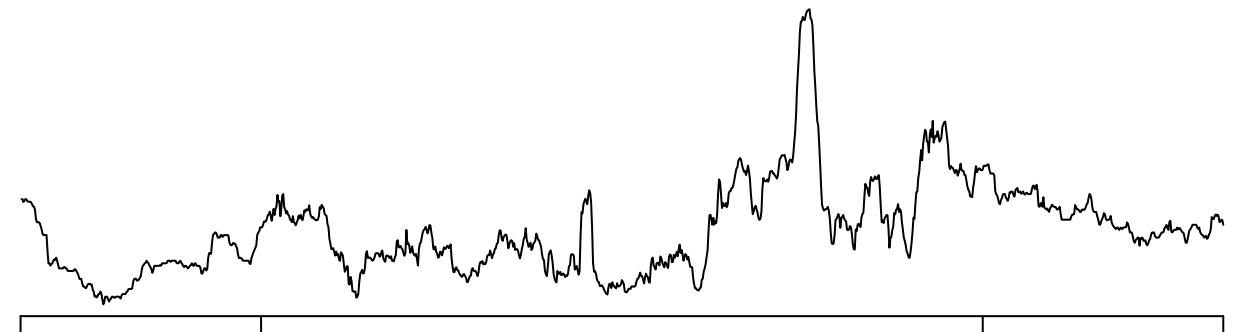
0.001 0.003

-5kb

intergenic start

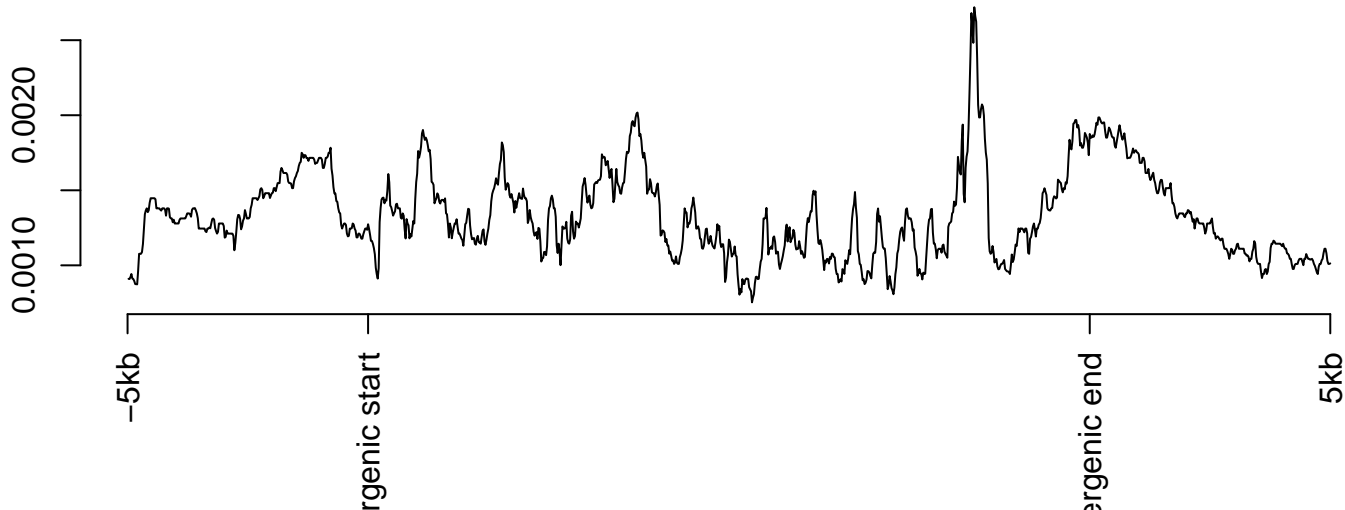
intergenic end

5kb



Average coverage per intergenic region

HumanNeuronCulture PositiveSingle E.602 scCLTdegenNuc482



HumanNeuronCulture PositiveSingle E.602 scCLTdegenNuc483

Average coverage per intergenic region

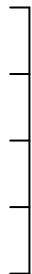
0.0010 0.0020 0.0030

-5kb

intergenic start

intergenic end

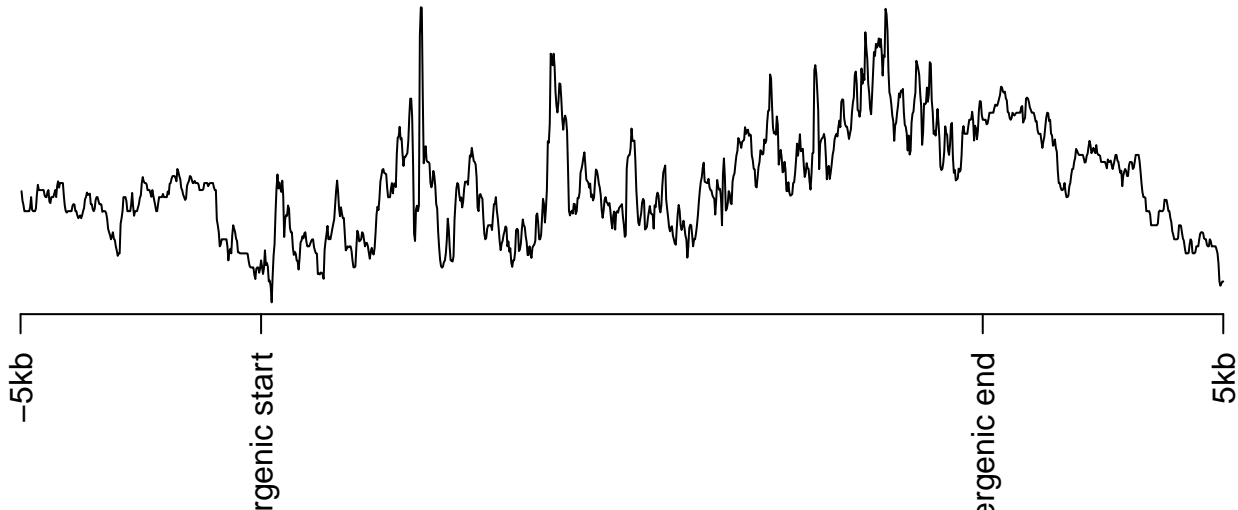
5kb



Average coverage per intergenic region

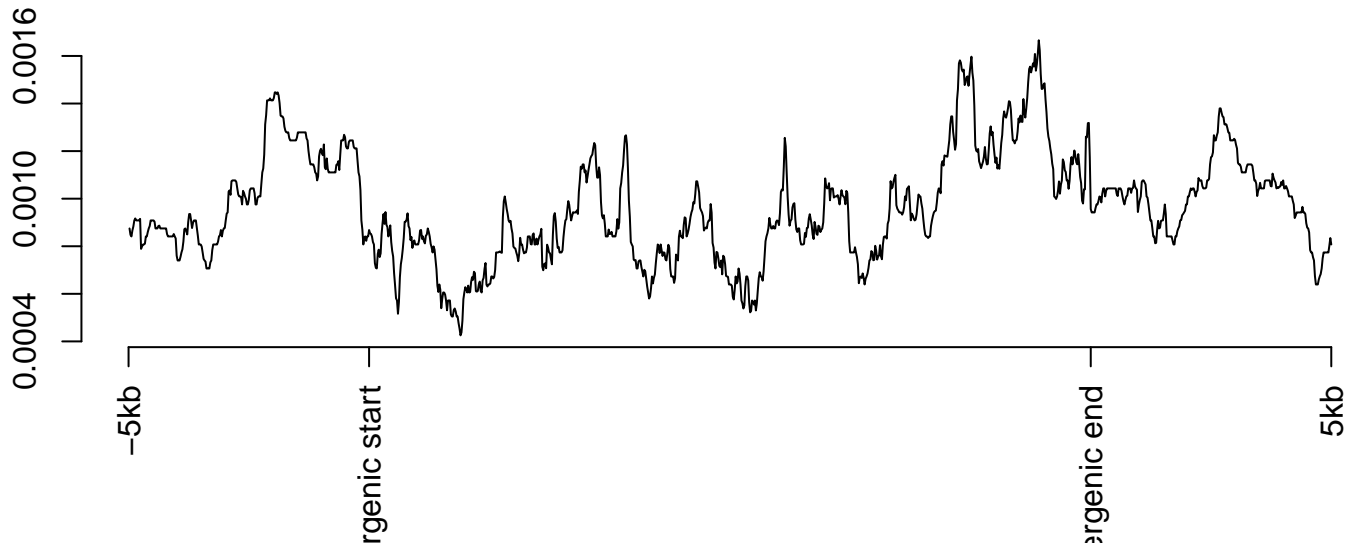
HumanNeuronCulture PositiveSingle E.602 scCLTdegenNuc484

0.0008 0.0014 0.0020



Average coverage per intergenic region

HumanNeuronCulture PositiveSingle E.602 scCLTdegenNuc485



Average coverage per intergenic region

HumanNeuronCulture PositiveMerged E.– HumanNeuronCulturePositiveMerged

