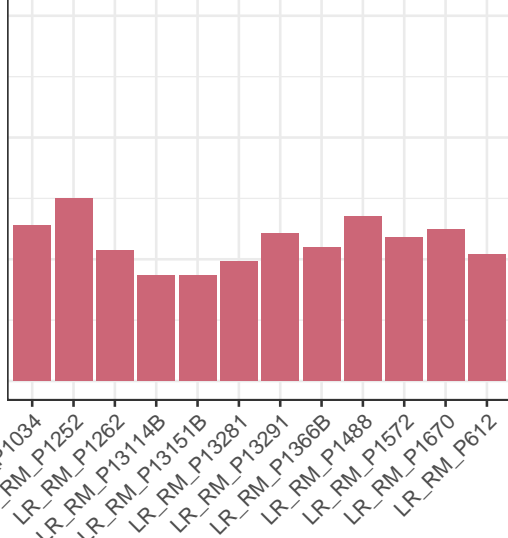
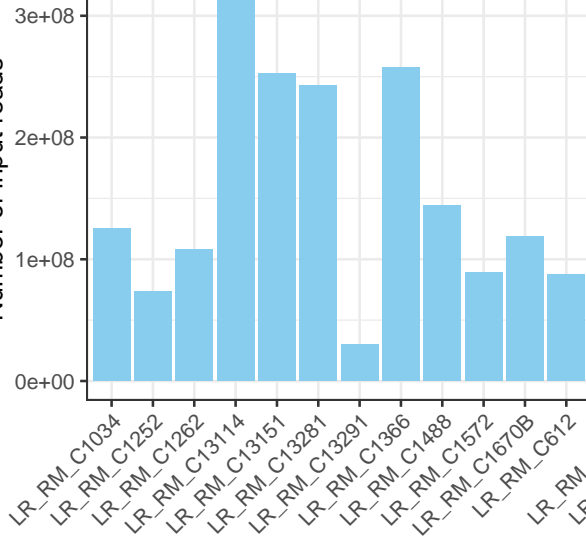


Number of input reads

Caudate

Putamen



Sample

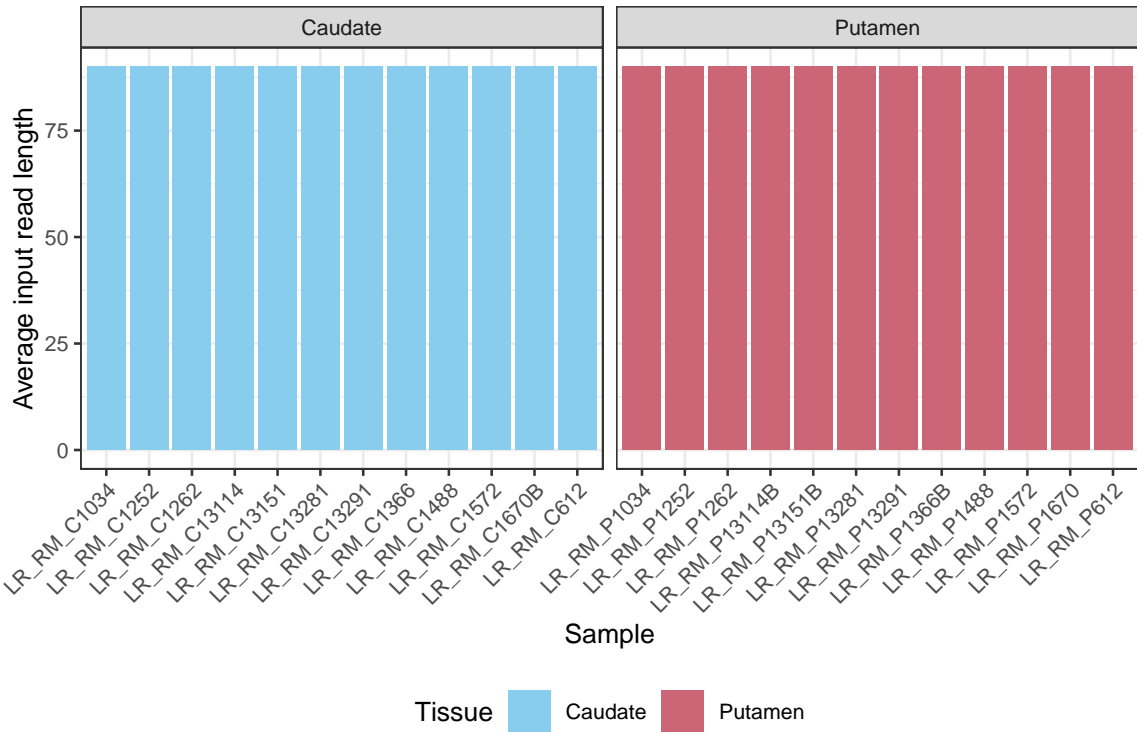
Tissue

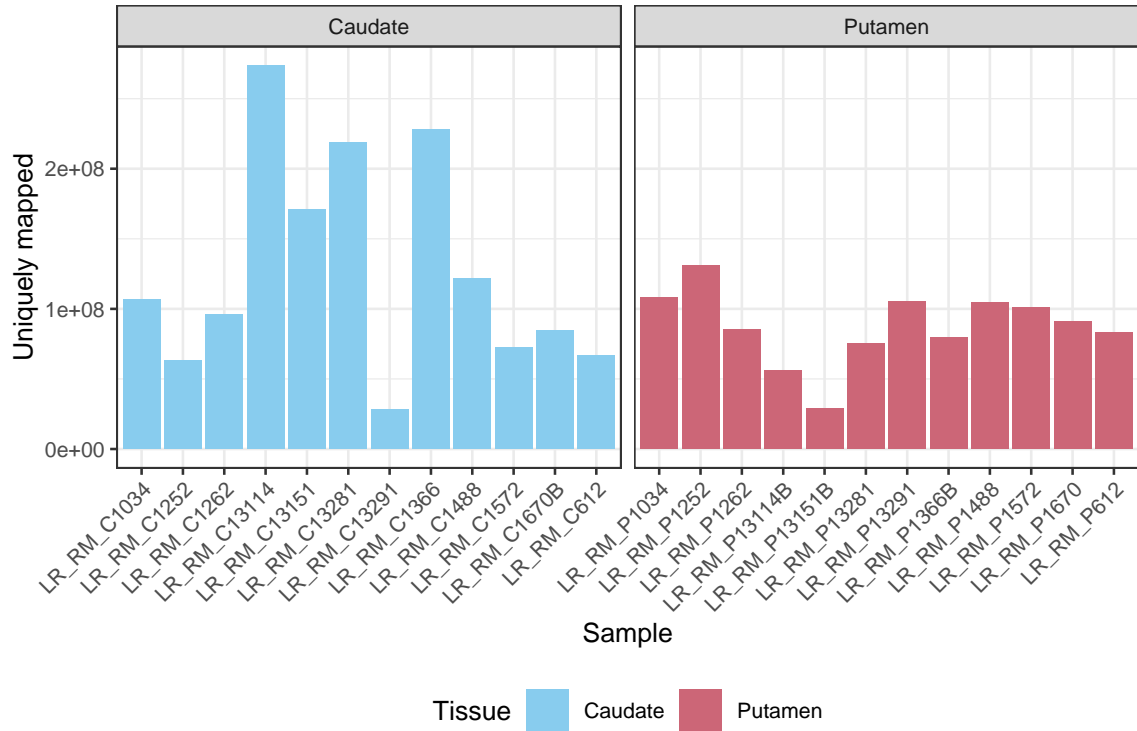


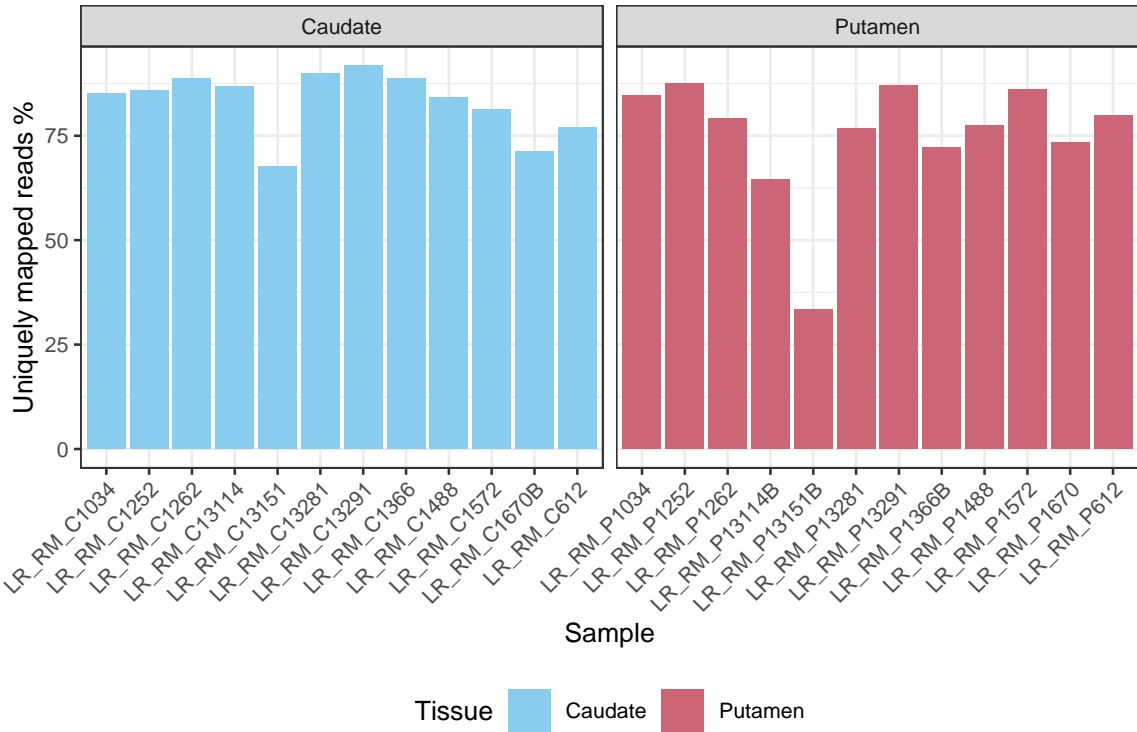
Caudate

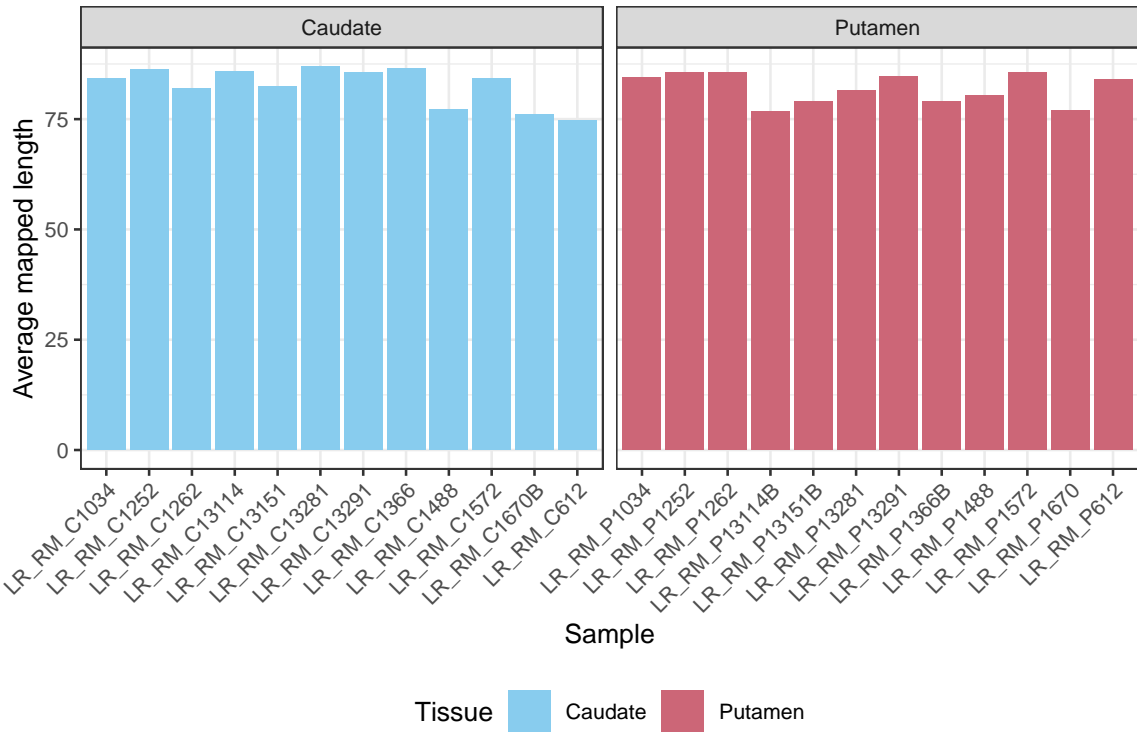


Putamen

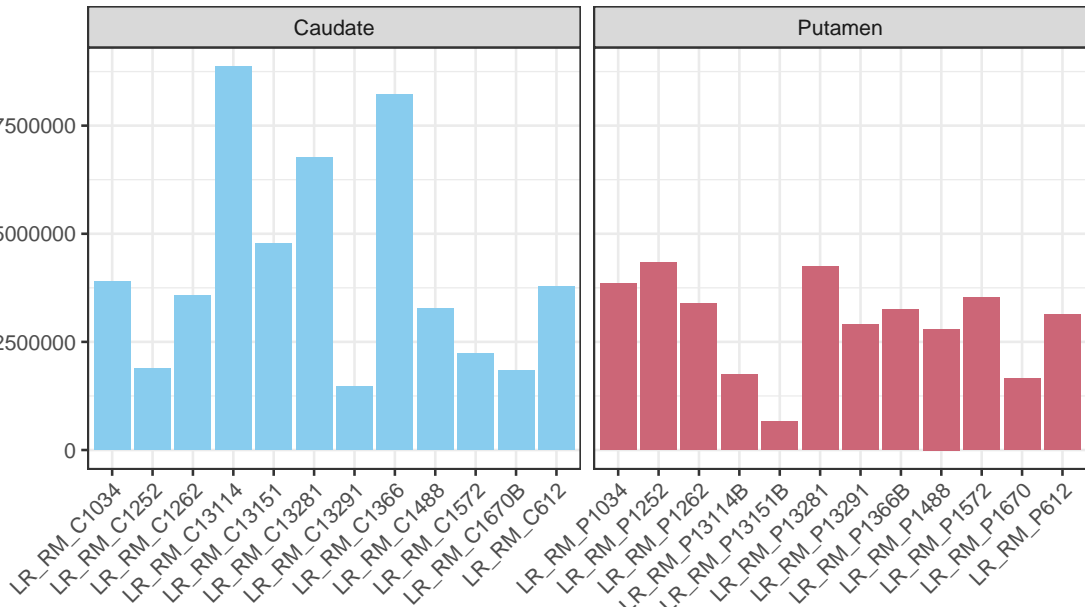








Number of splices: Total



Sample

Tissue

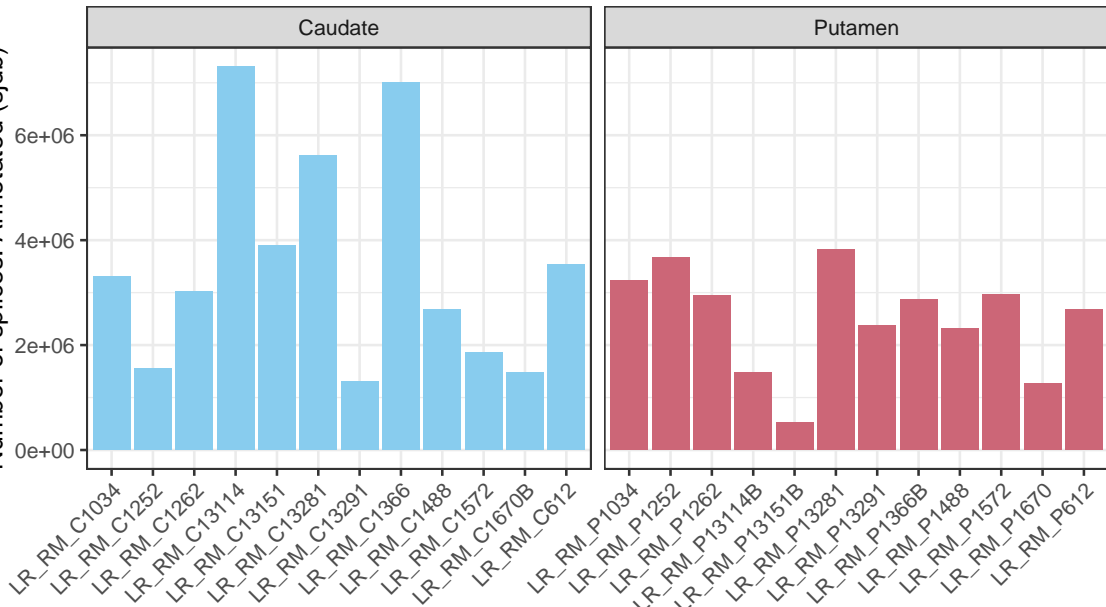


Caudate



Putamen

Number of splices: Annotated (sjdb)



Sample

Tissue



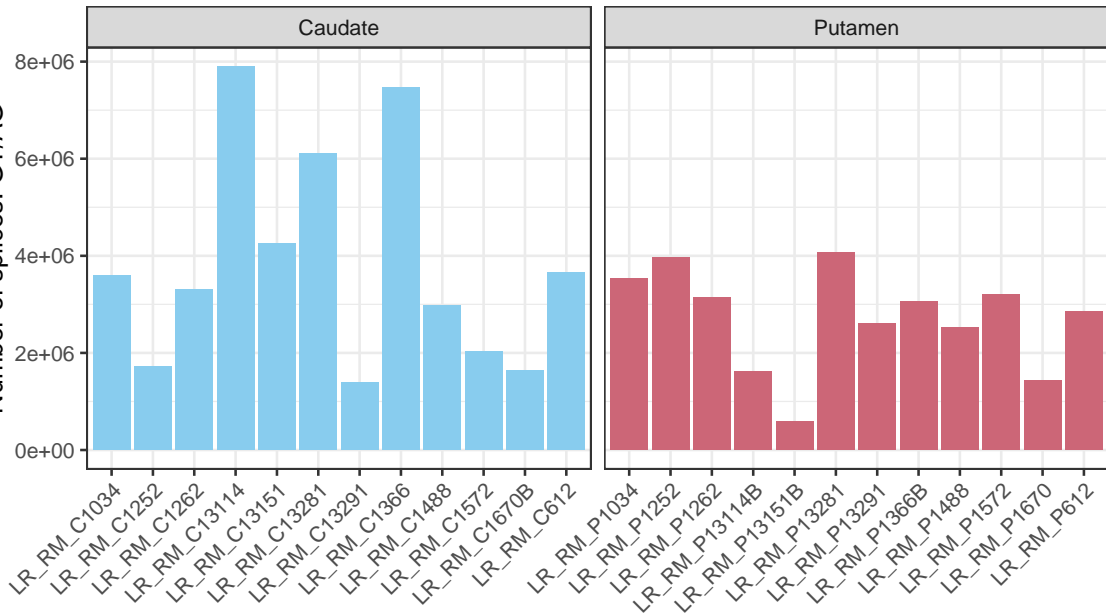
Caudate



Putamen



Number of splices: GT/AG



Sample

Tissue

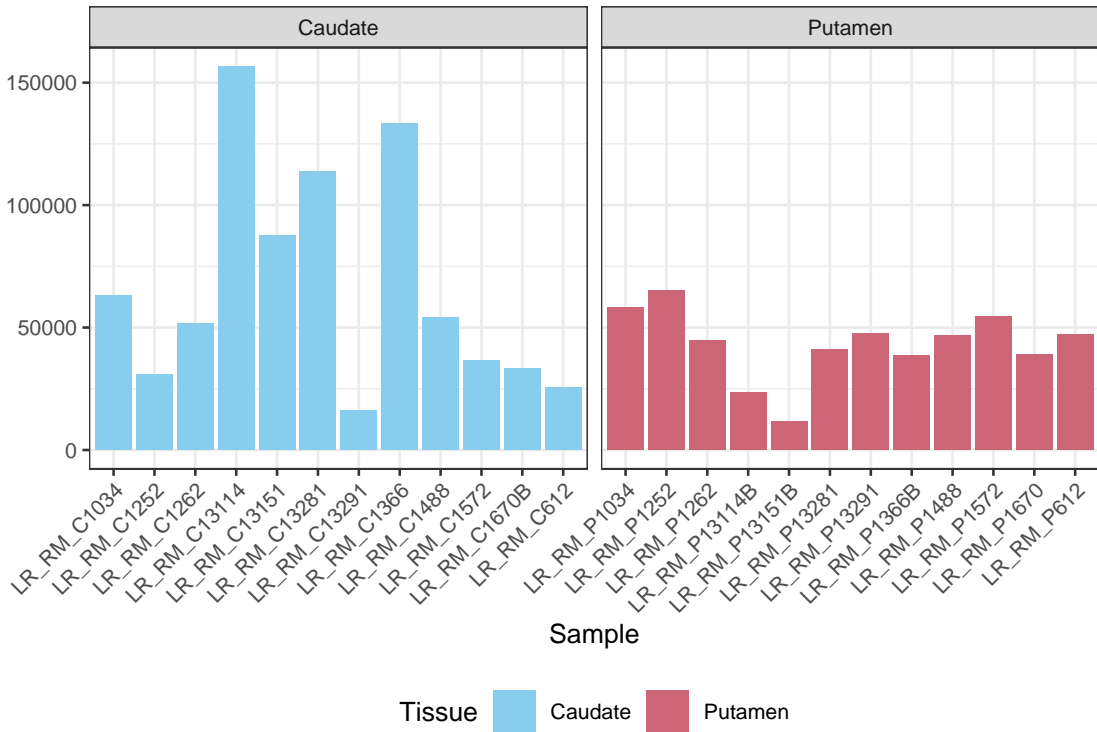


Caudate

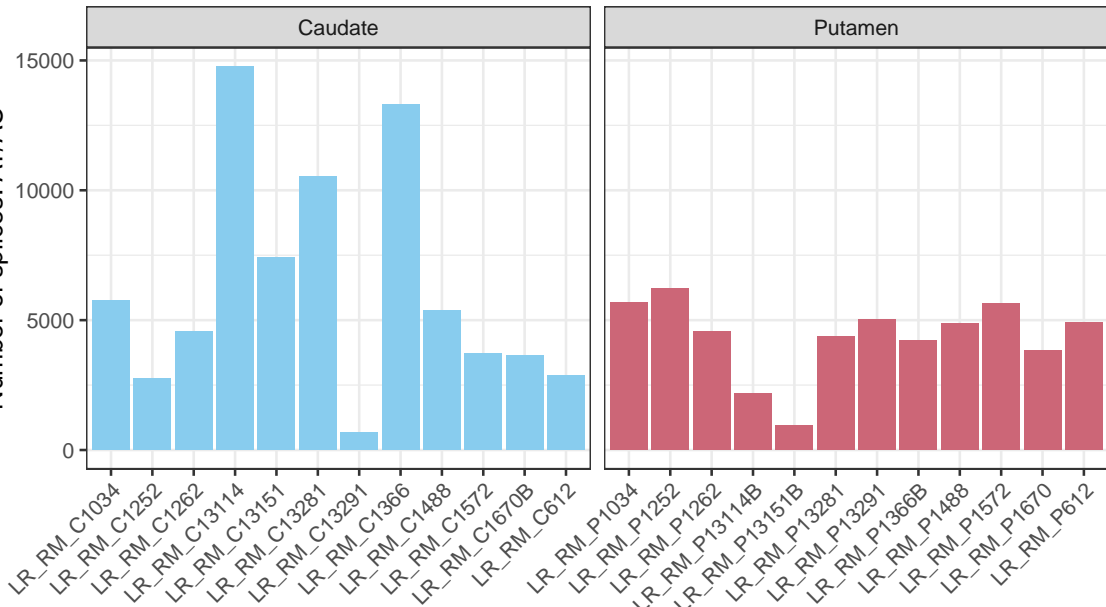


Putamen

Number of splices: GC/AG



Number of splices: AT/AC



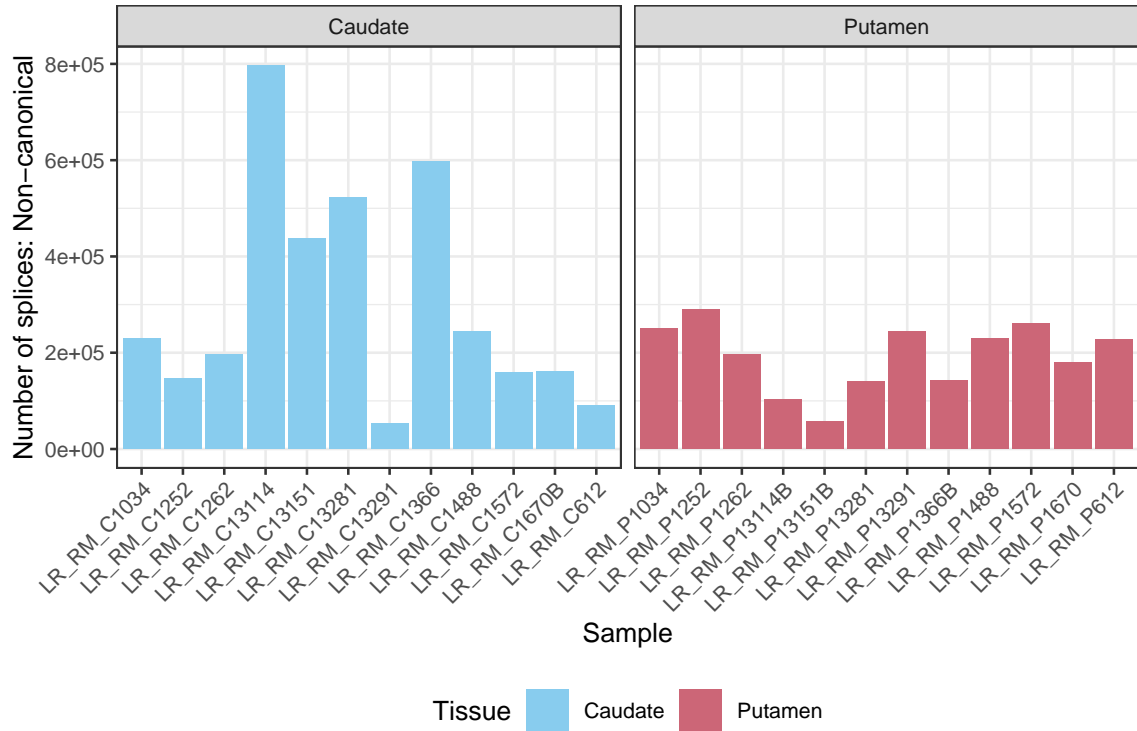
Tissue

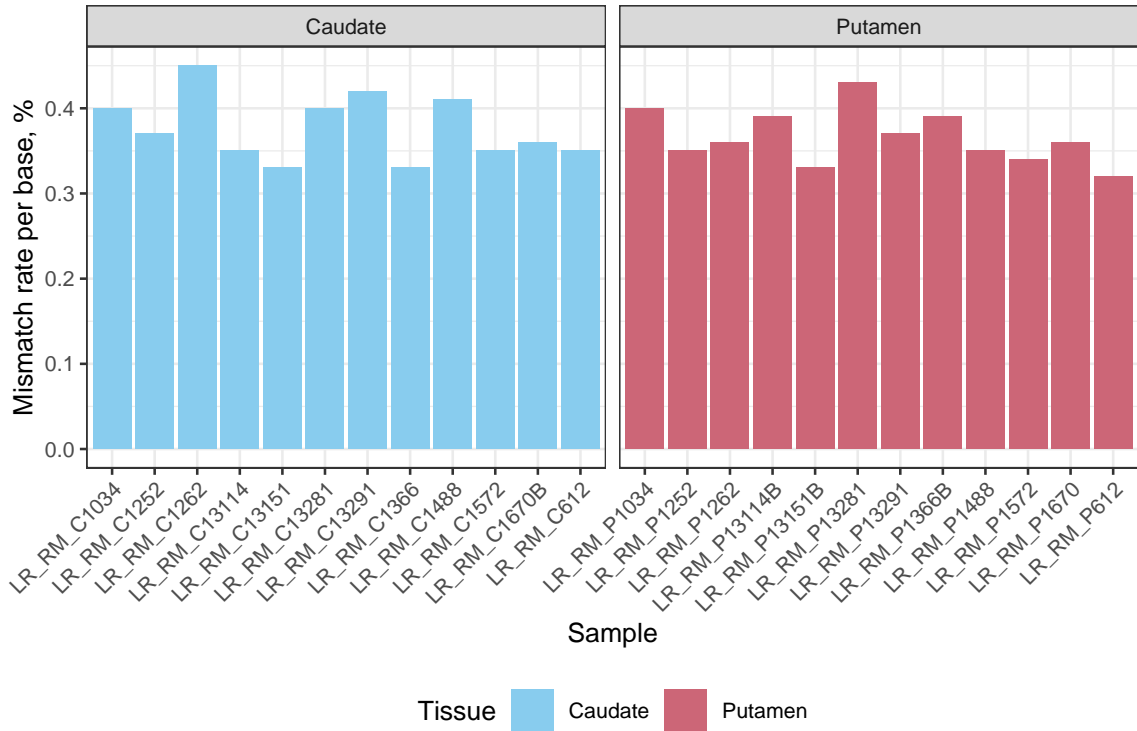


Caudate

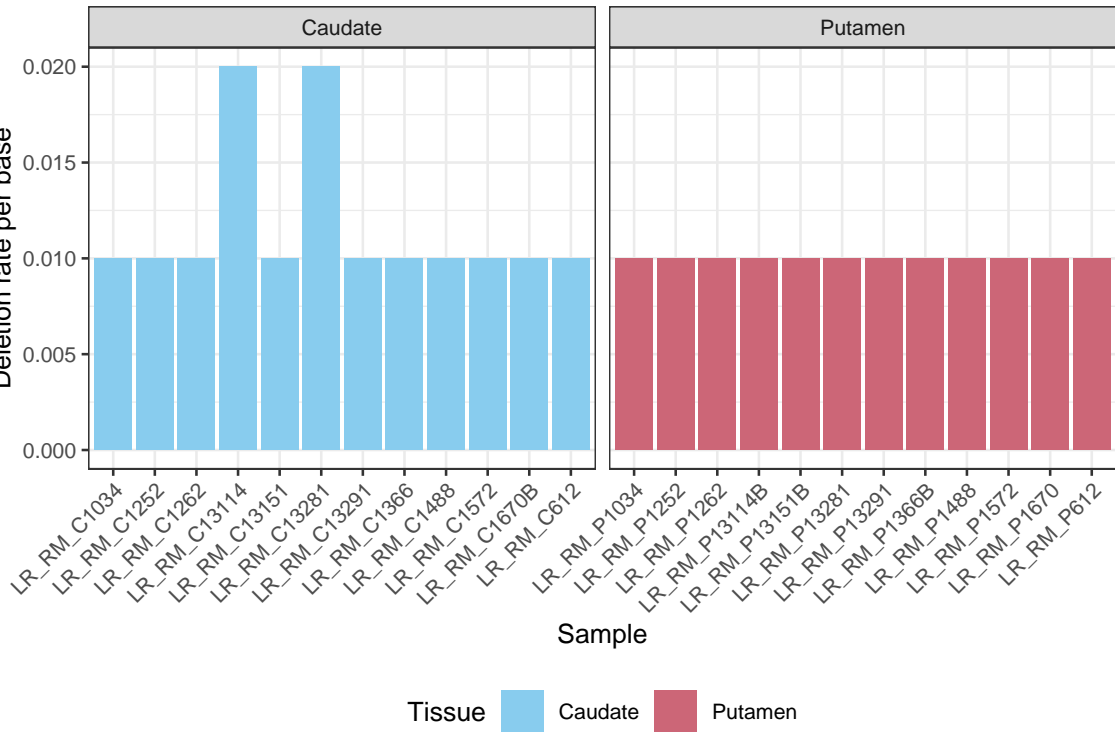


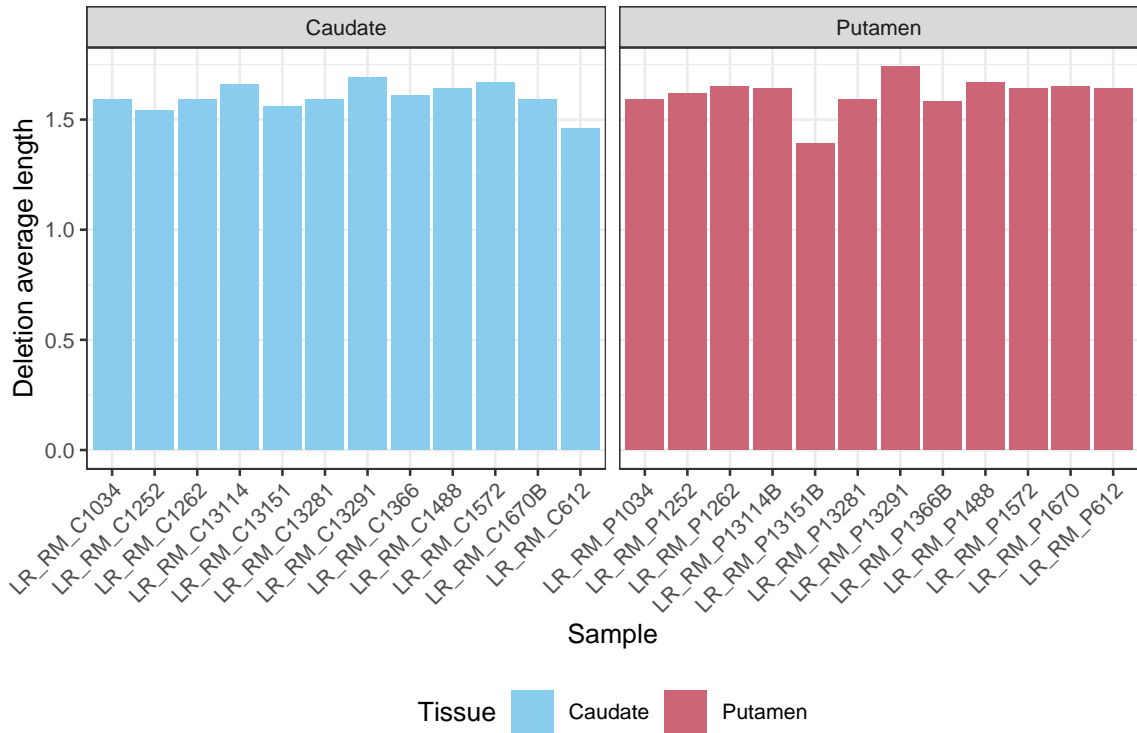
Putamen



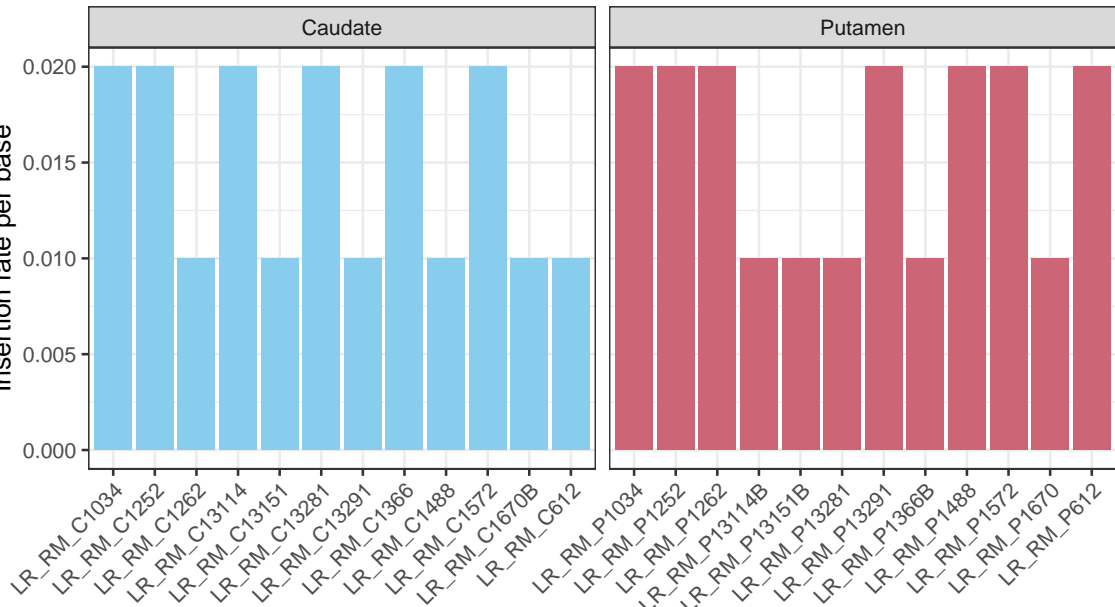


Deletion rate per base





Insertion rate per base



Tissue

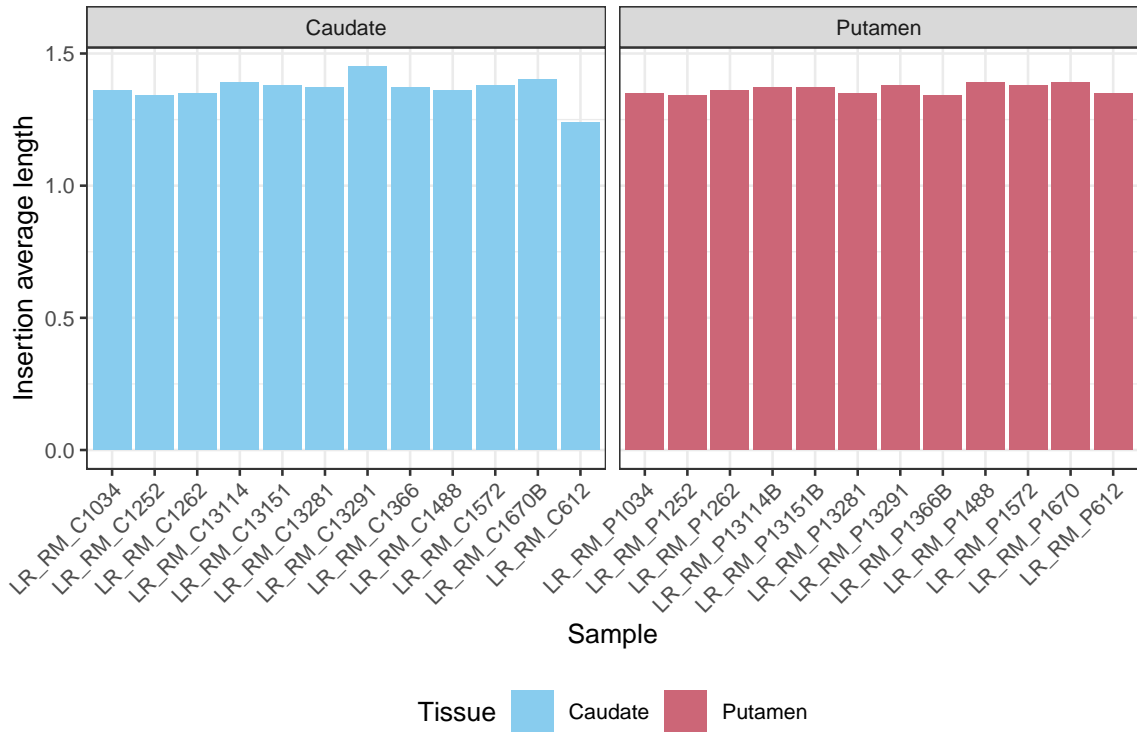


Caudate

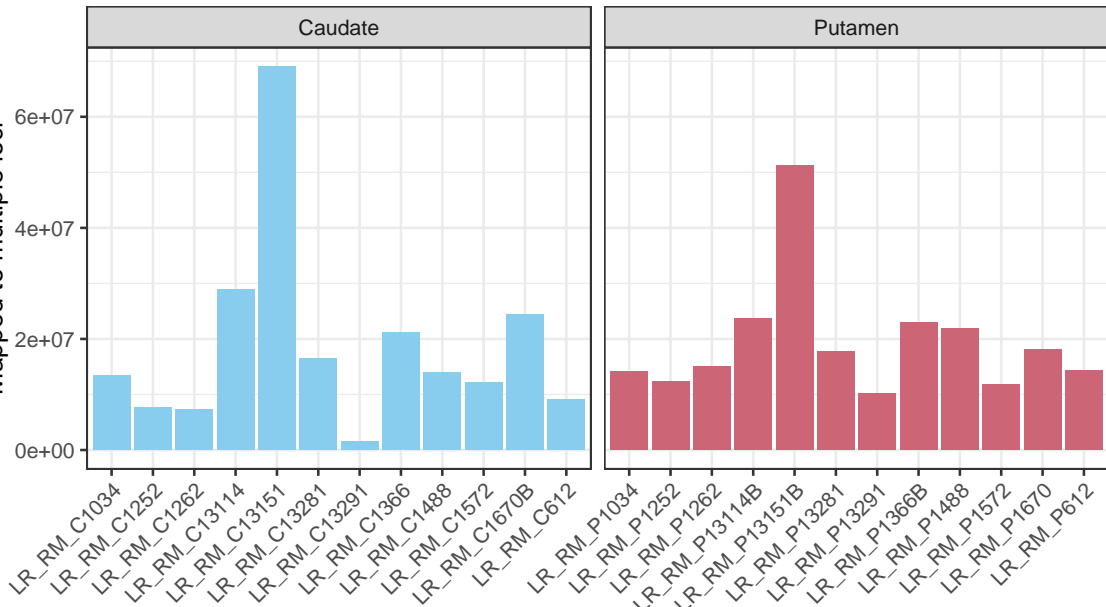


Putamen





Mapped to multiple loci



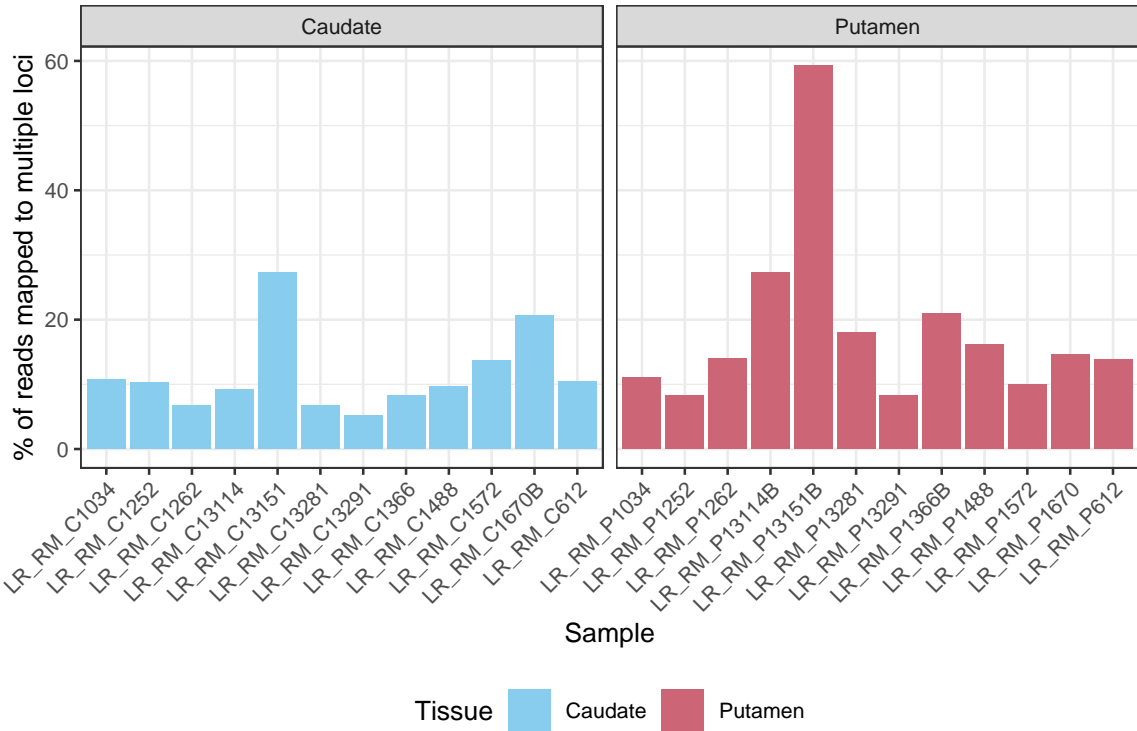
Tissue



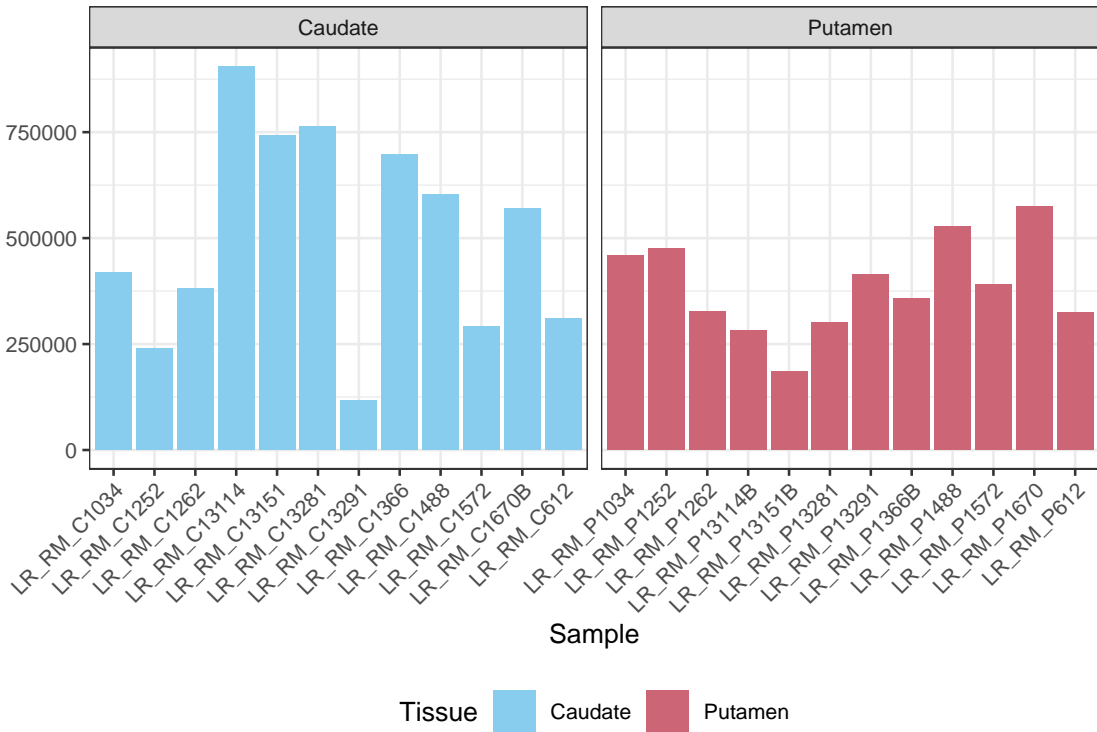
Caudate

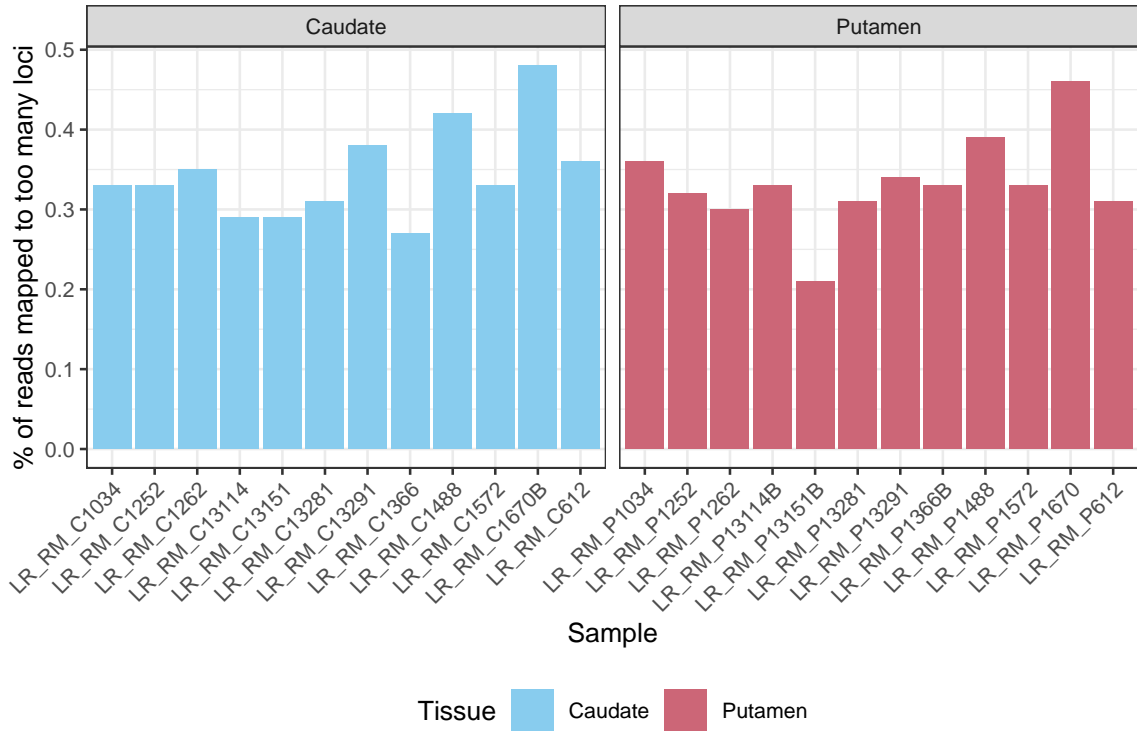


Putamen

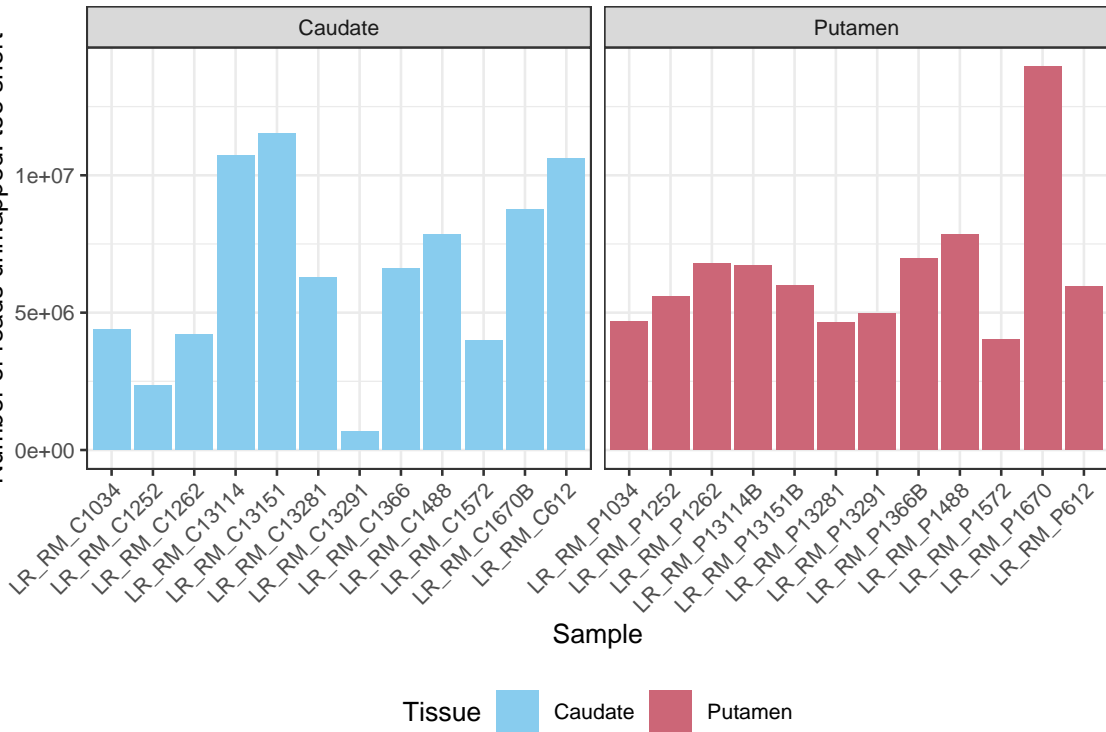


Mapped to too many loci

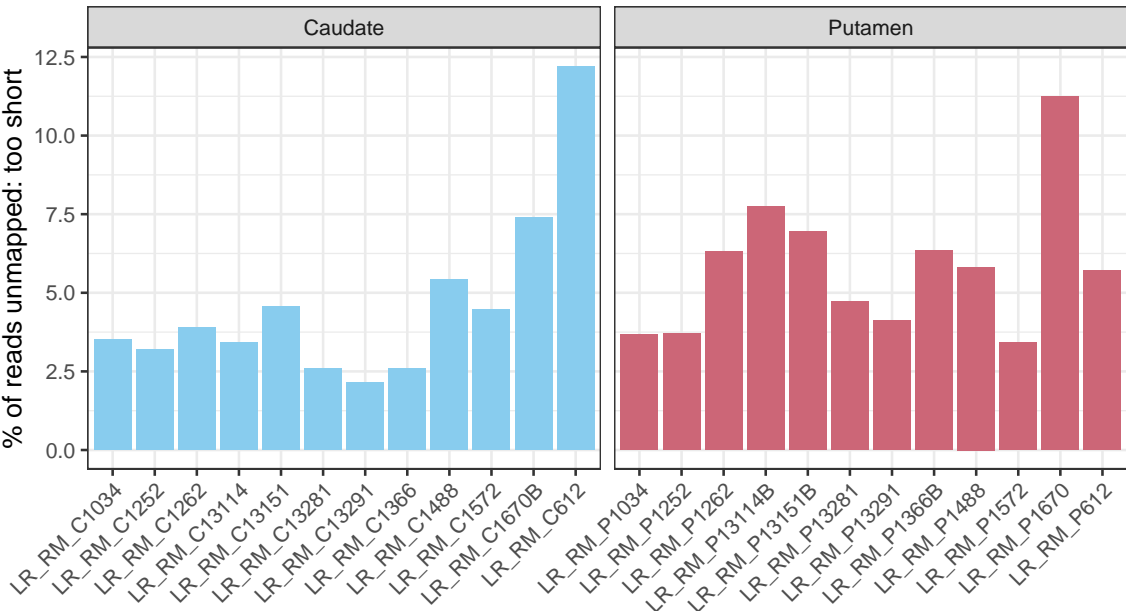




Number of reads unmapped: too short



% of reads unmapped: too short



Sample

Tissue

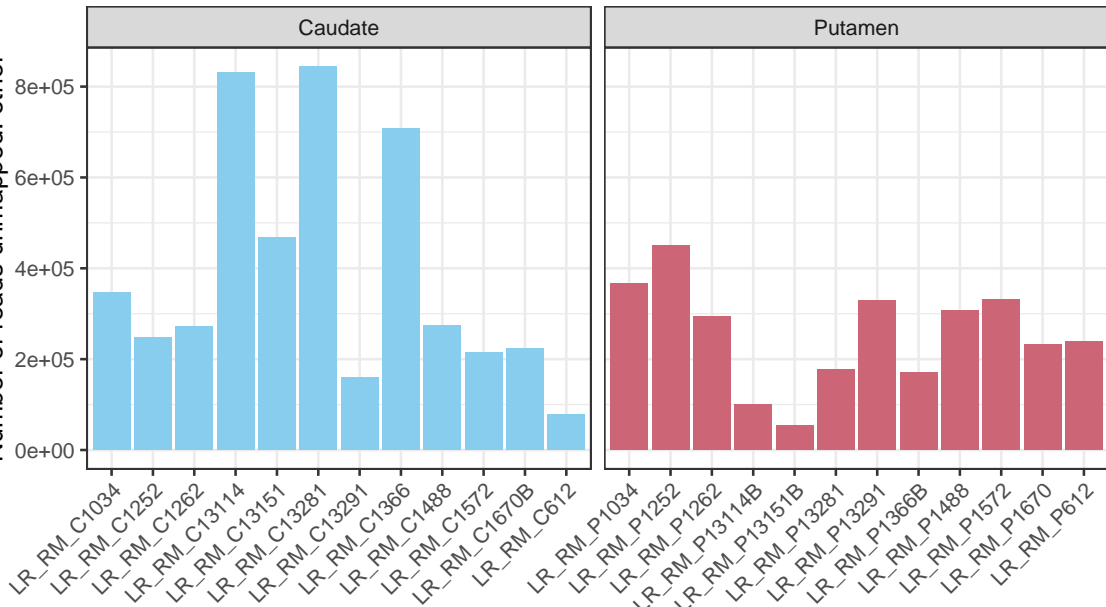


Caudate



Putamen

Number of reads unmapped: other



Tissue



Caudate



Putamen



