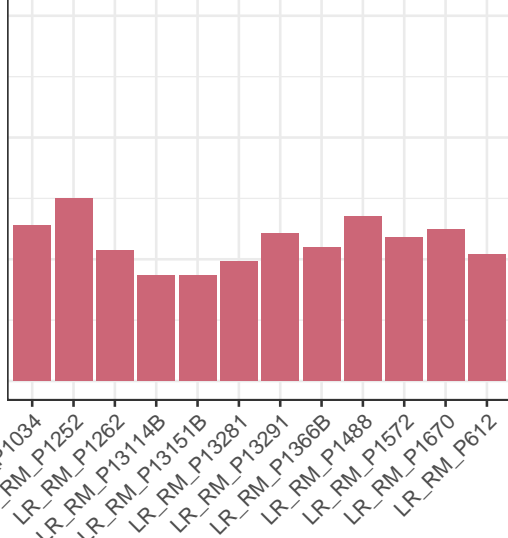
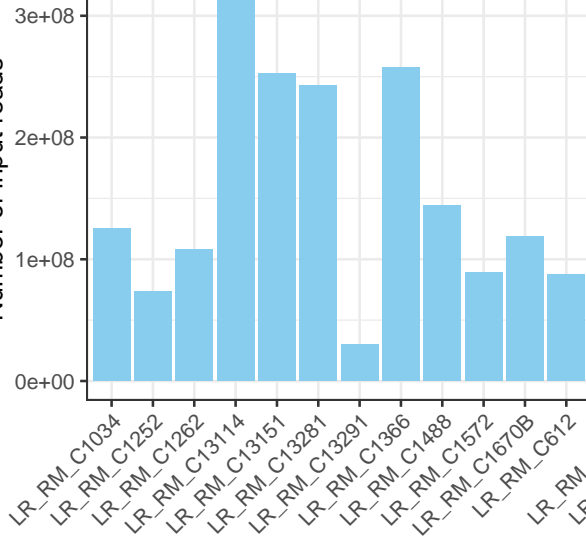


Number of input reads

Caudate

Putamen



Sample

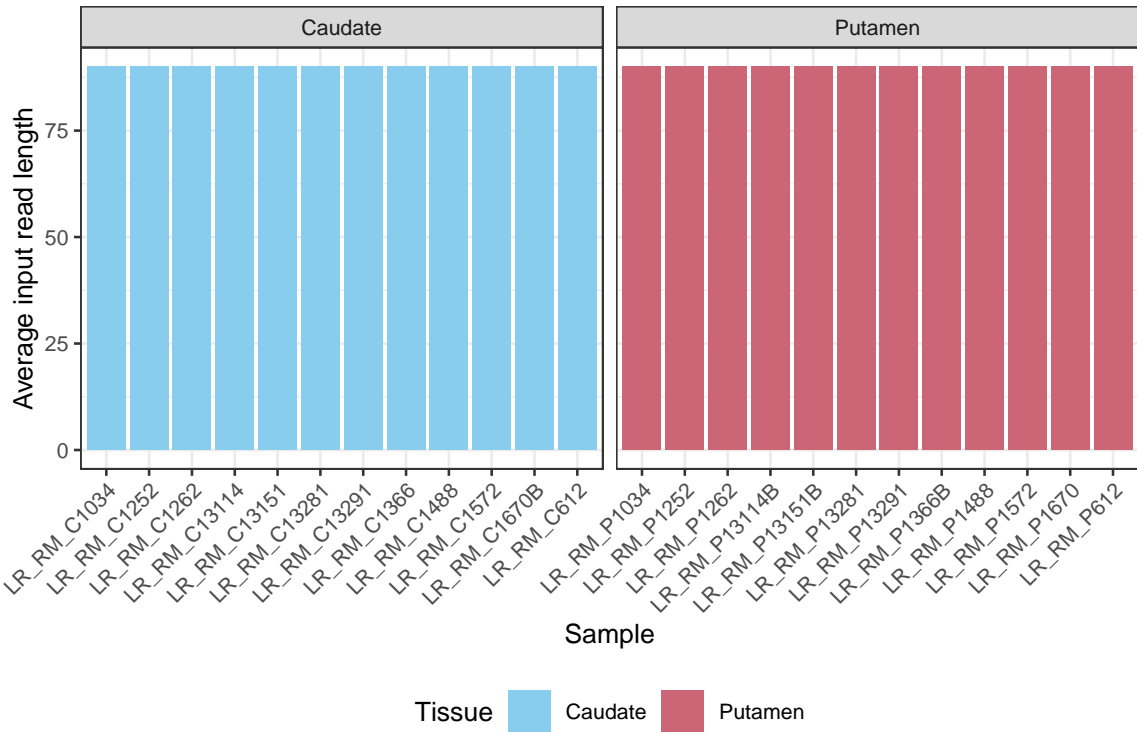
Tissue

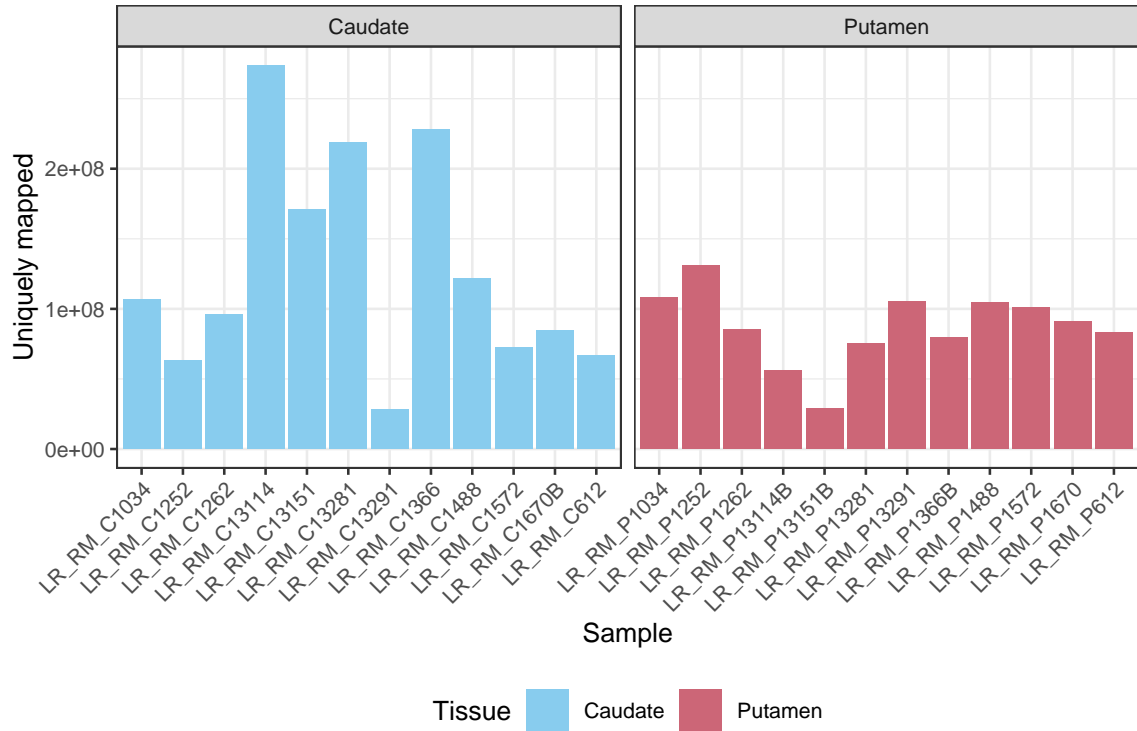


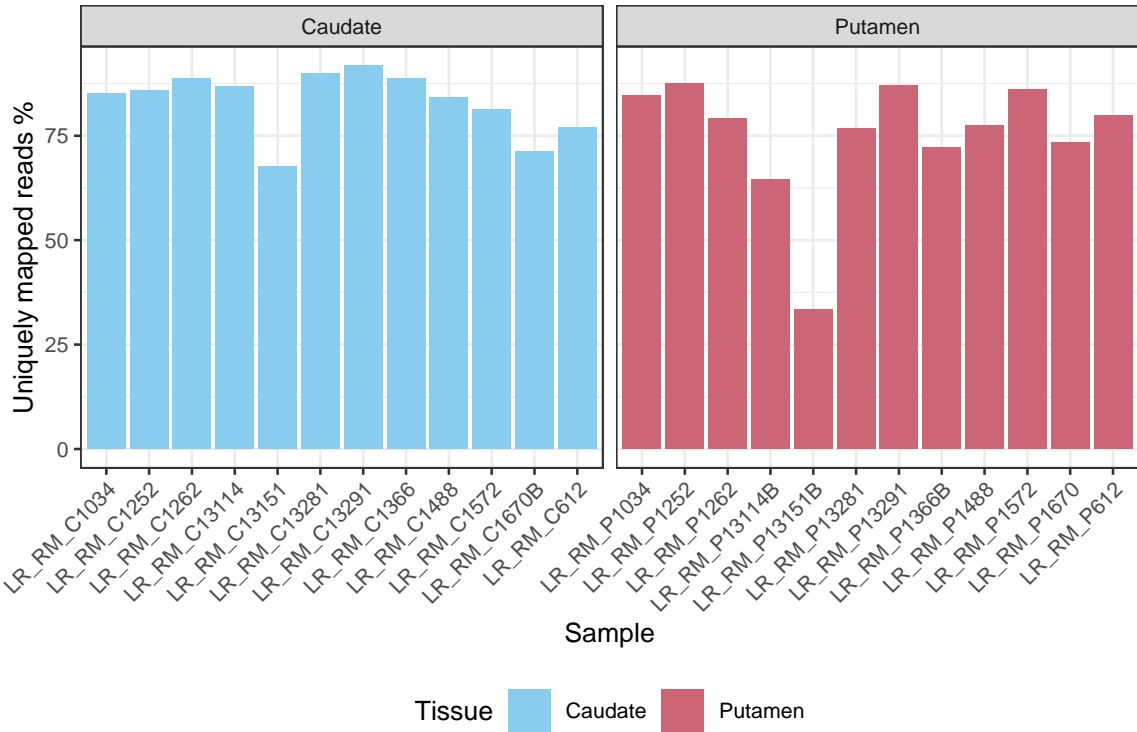
Caudate

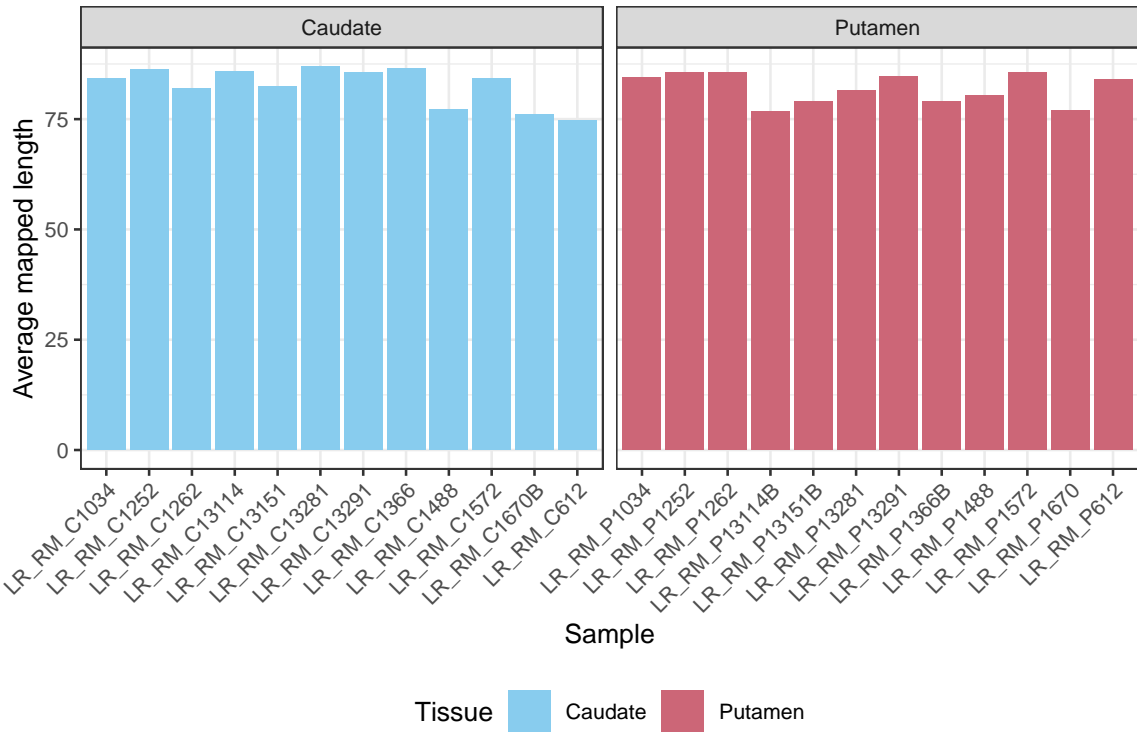


Putamen

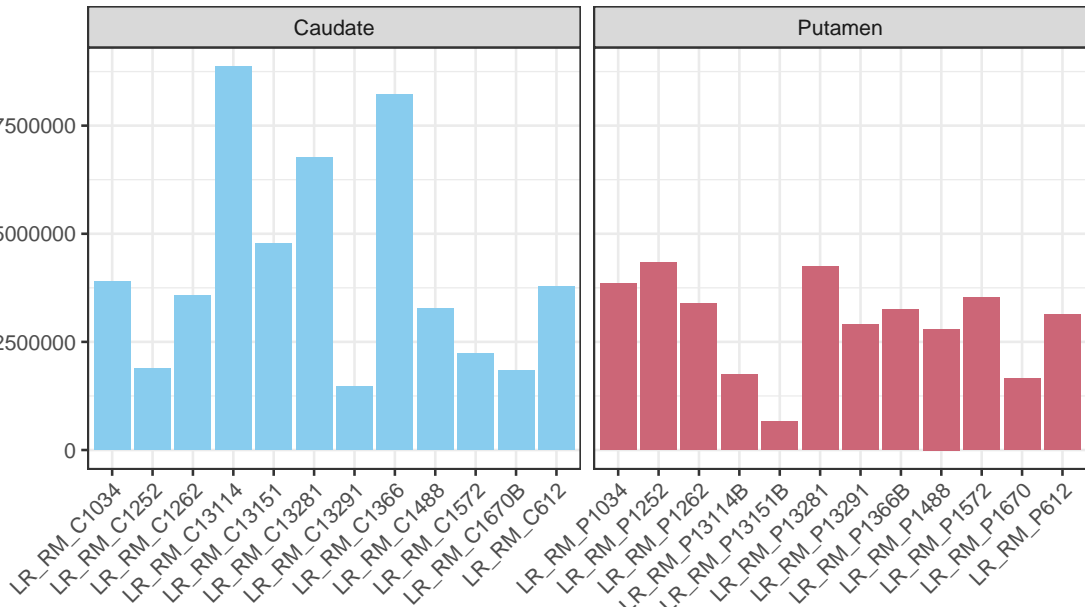








Number of splices: Total



Sample

Tissue

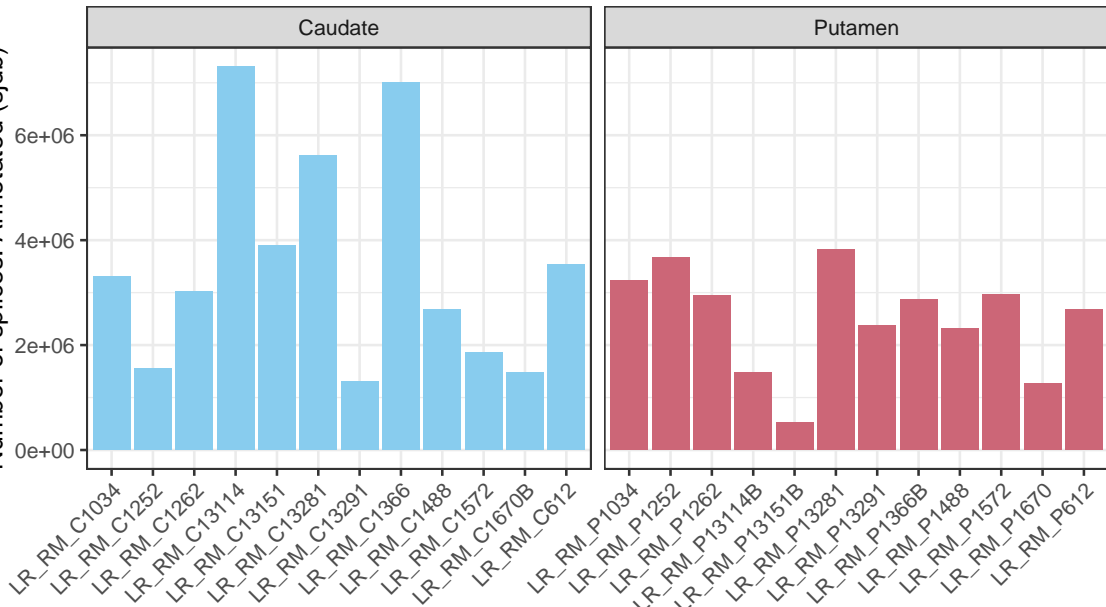


Caudate



Putamen

Number of splices: Annotated (sjdb)



Sample

Tissue



Caudate

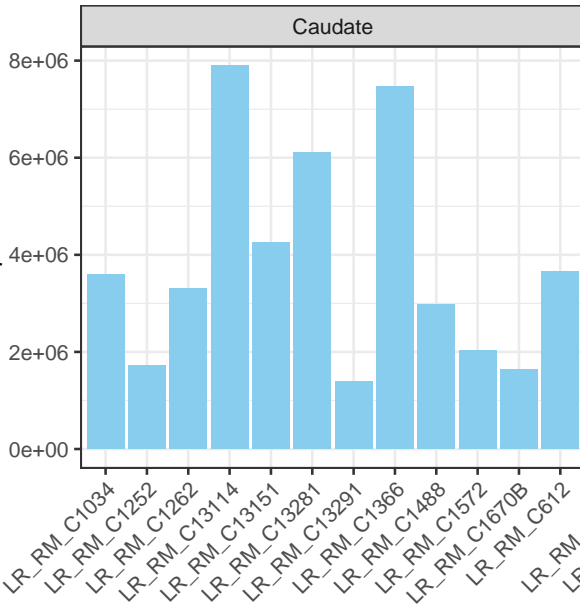


Putamen

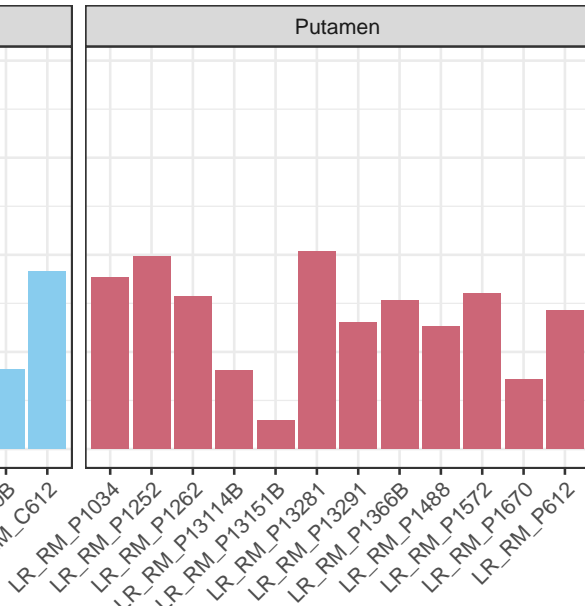


Number of splices: GT/AG

Caudate



Putamen



Sample

Tissue

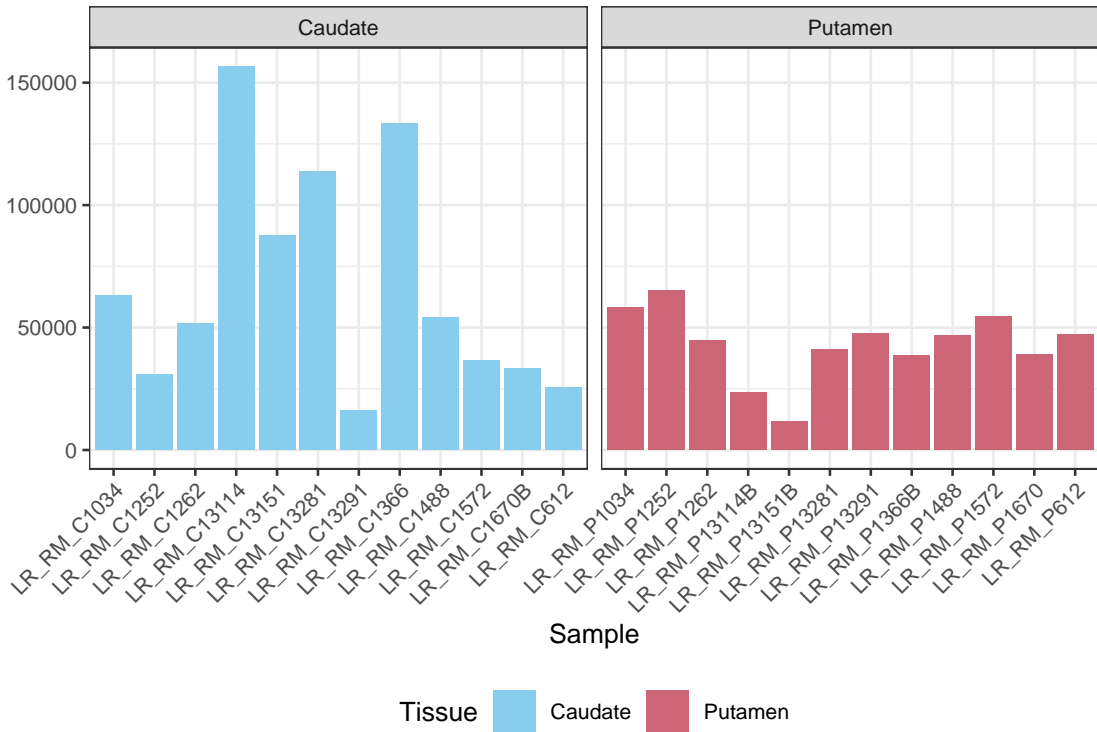


Caudate

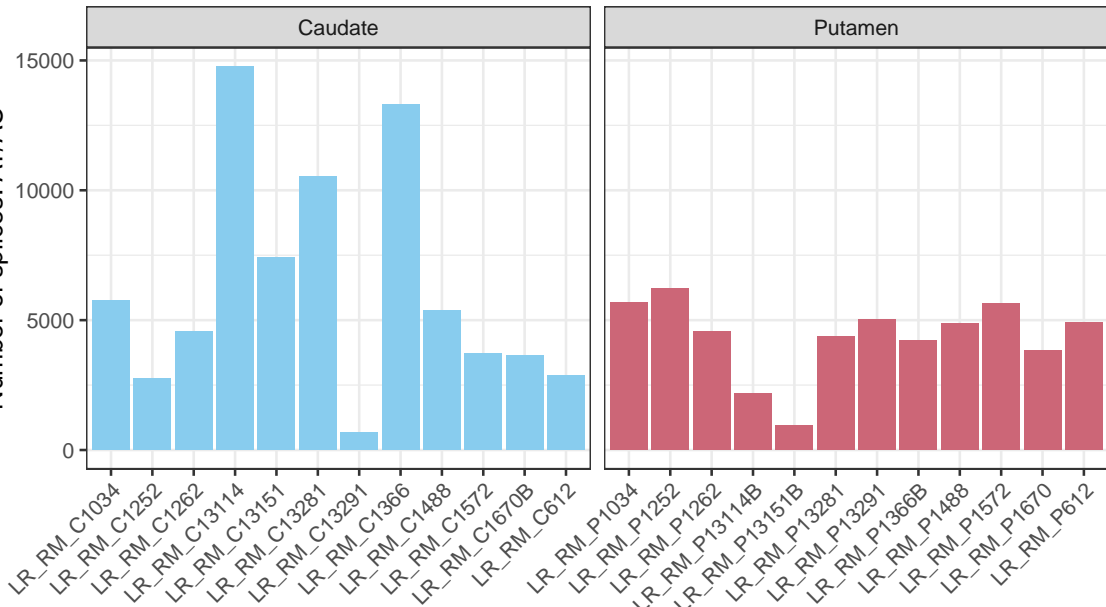


Putamen

Number of splices: GC/AG



Number of splices: AT/AC



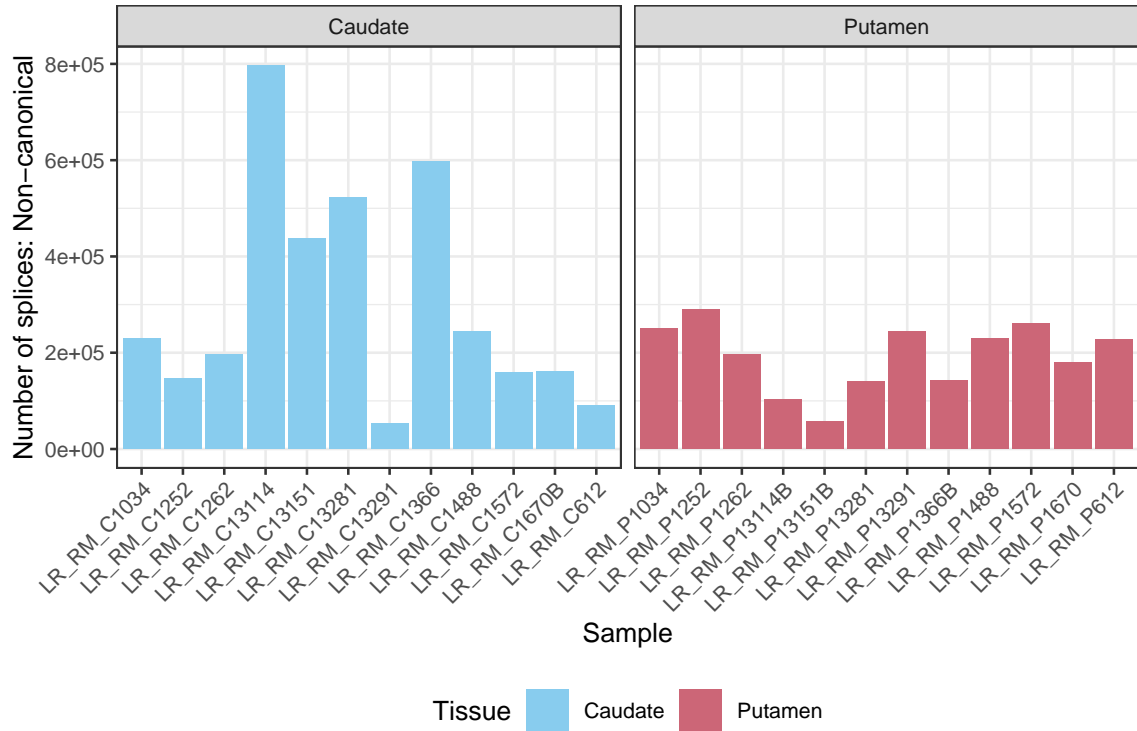
Tissue

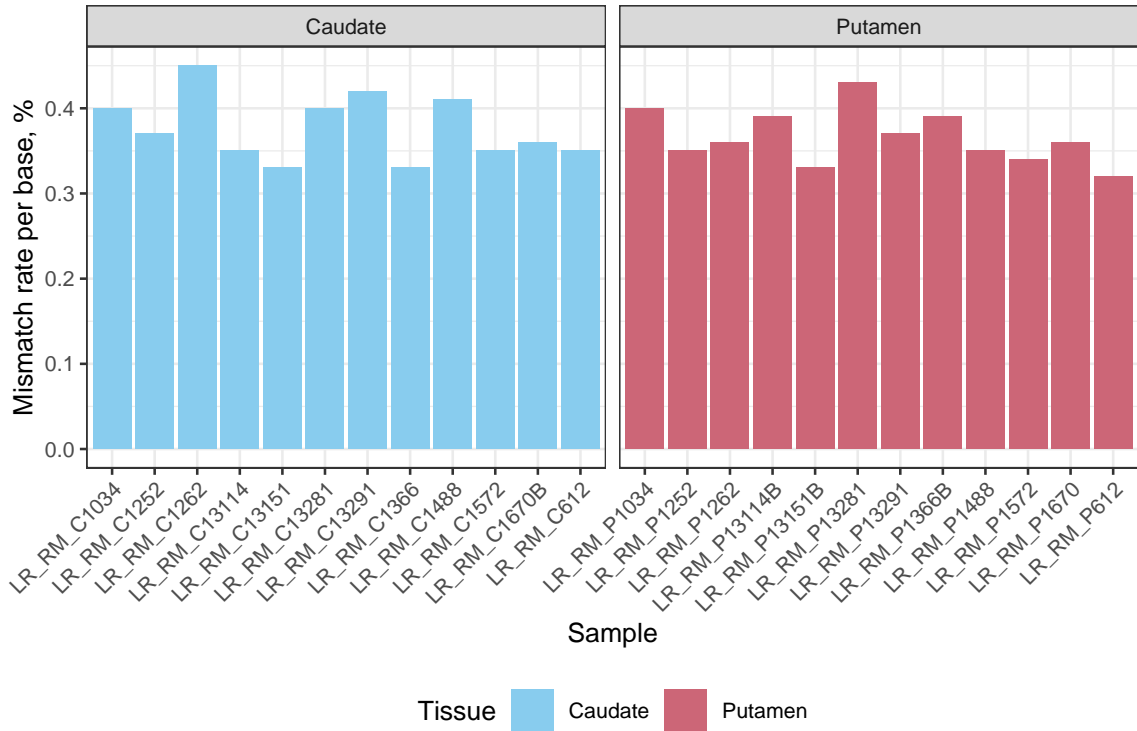


Caudate

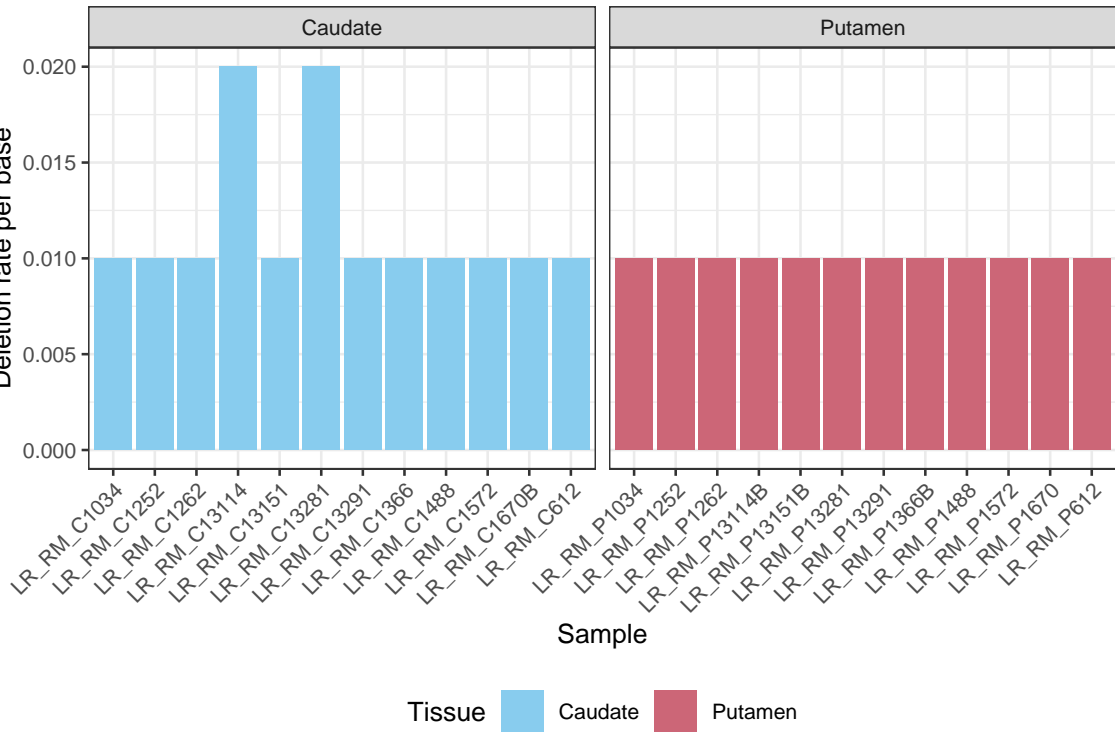


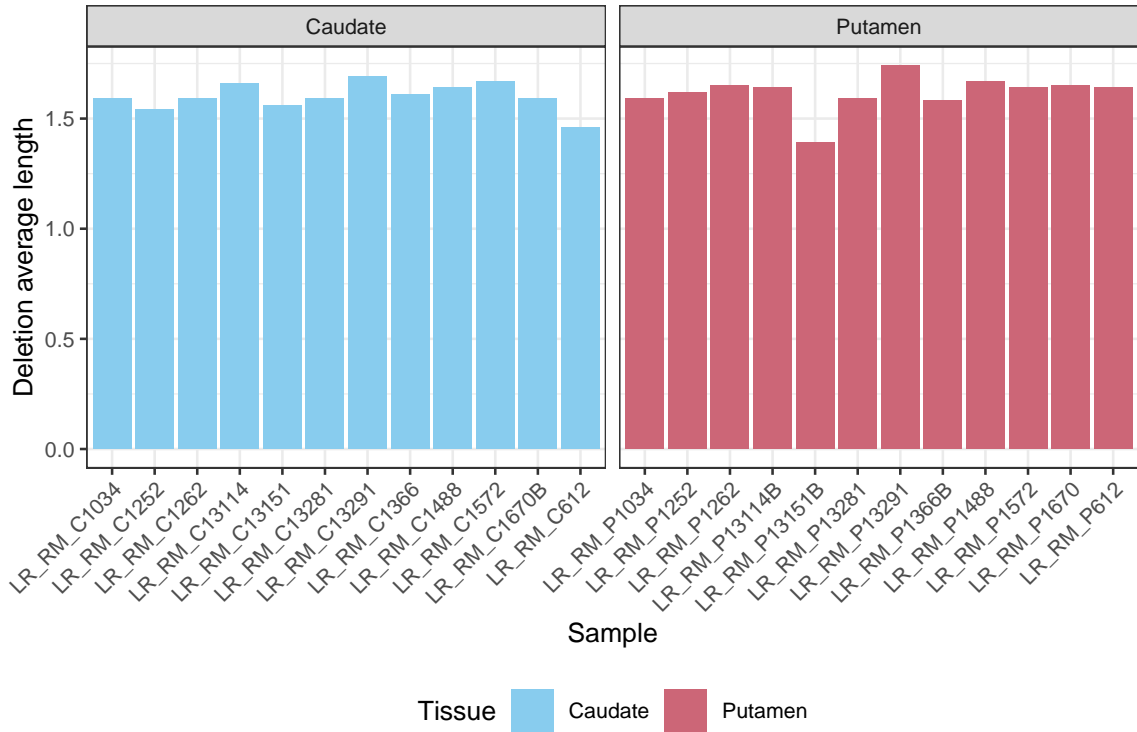
Putamen



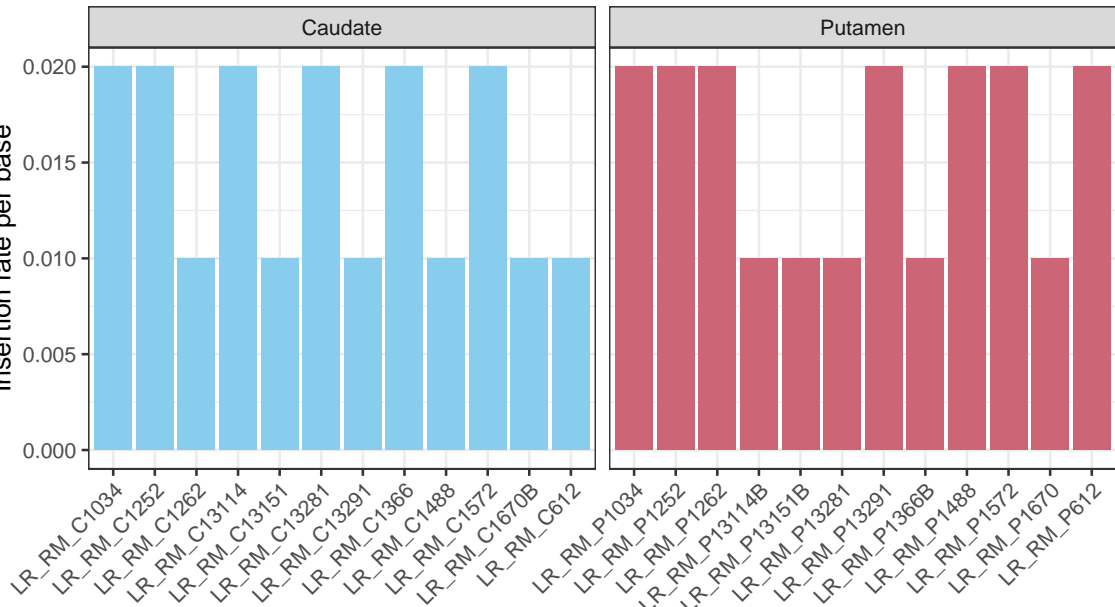


Deletion rate per base





Insertion rate per base



Sample

Tissue

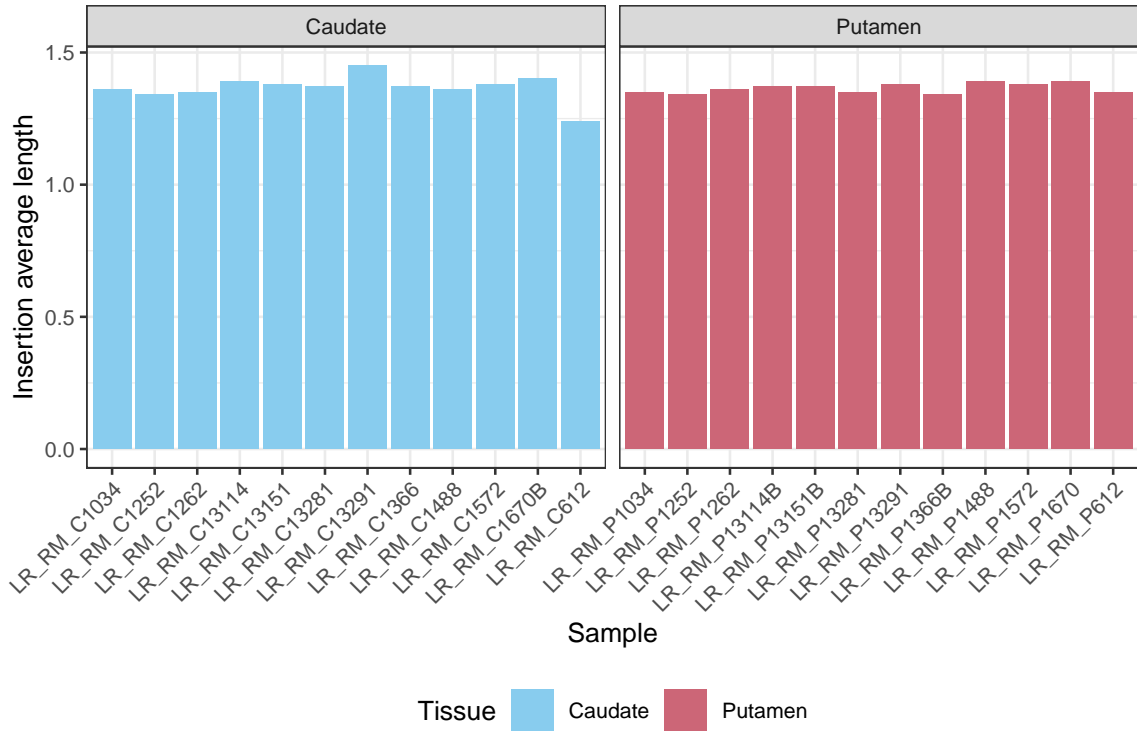


Caudate

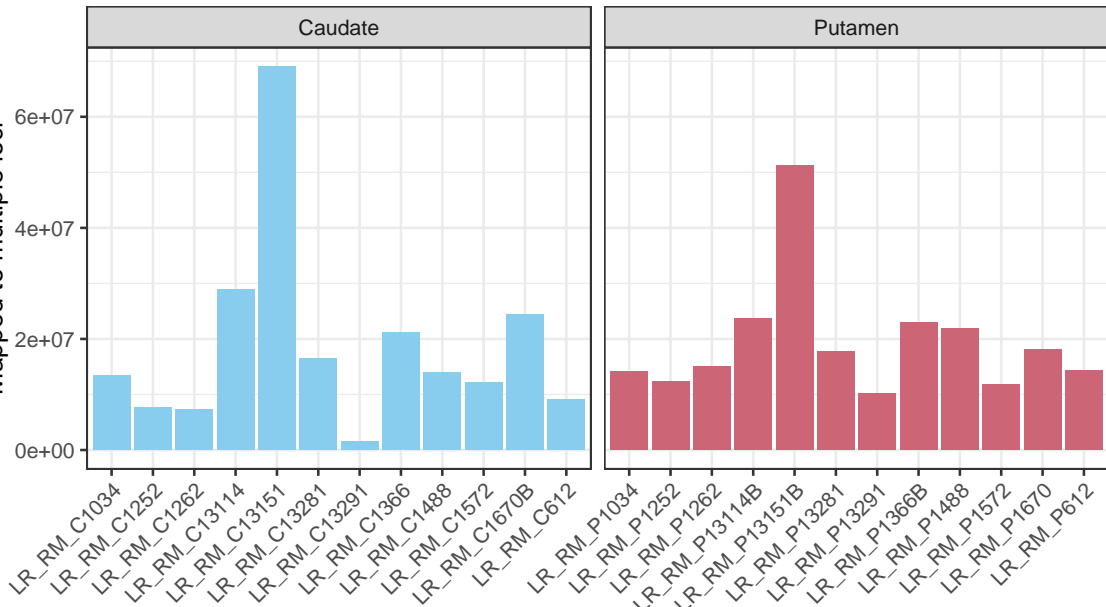


Putamen





Mapped to multiple loci



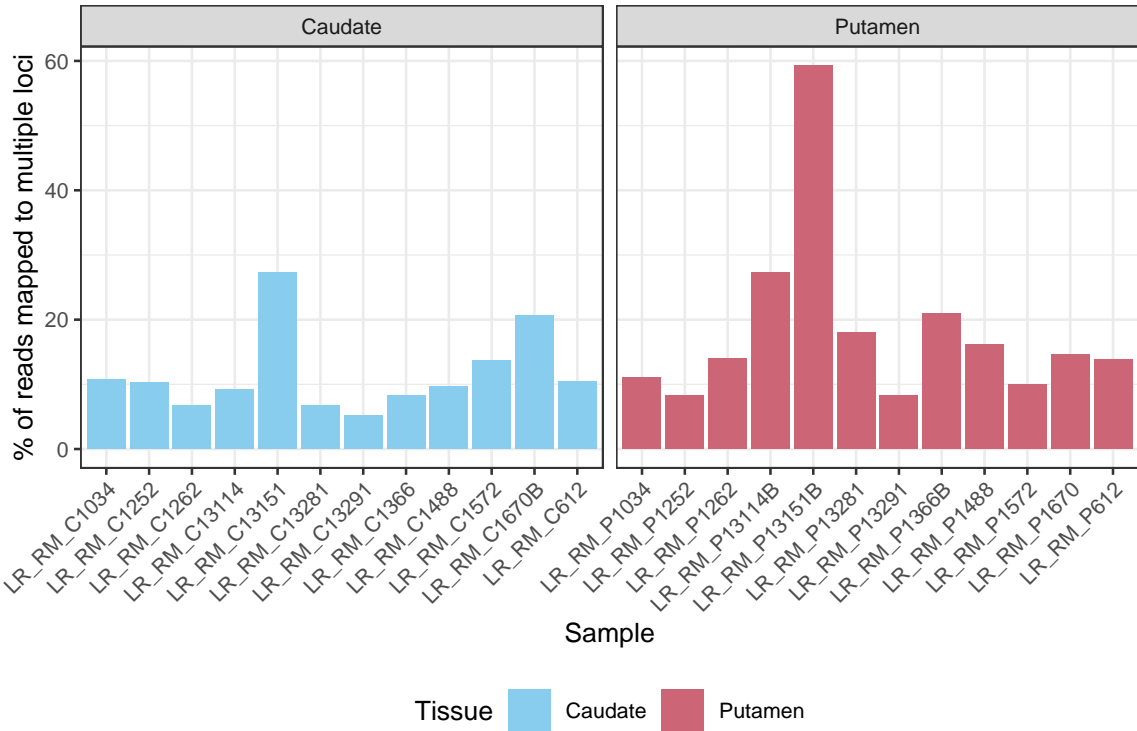
Tissue



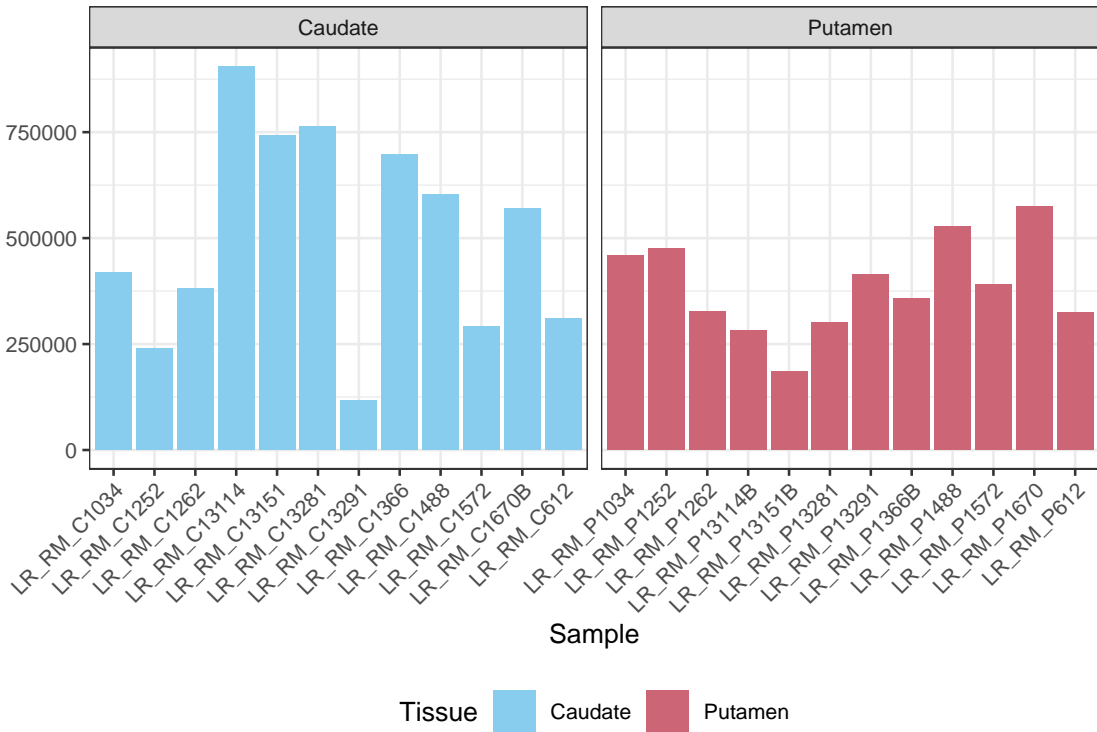
Caudate

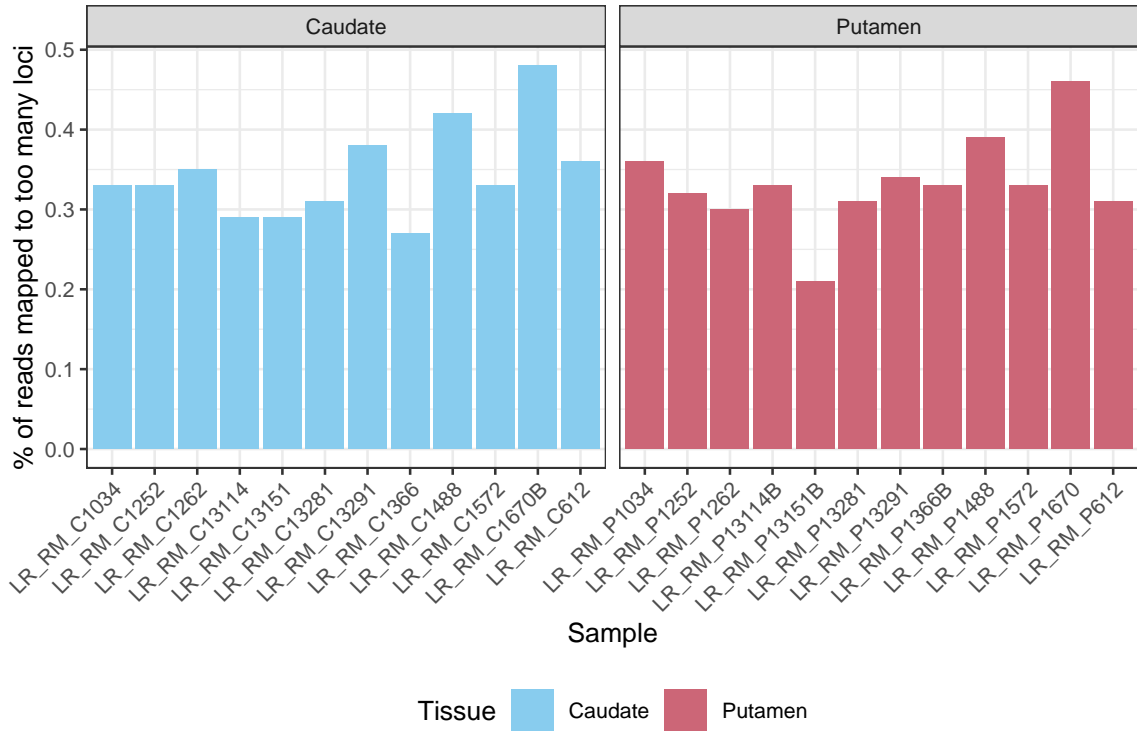


Putamen

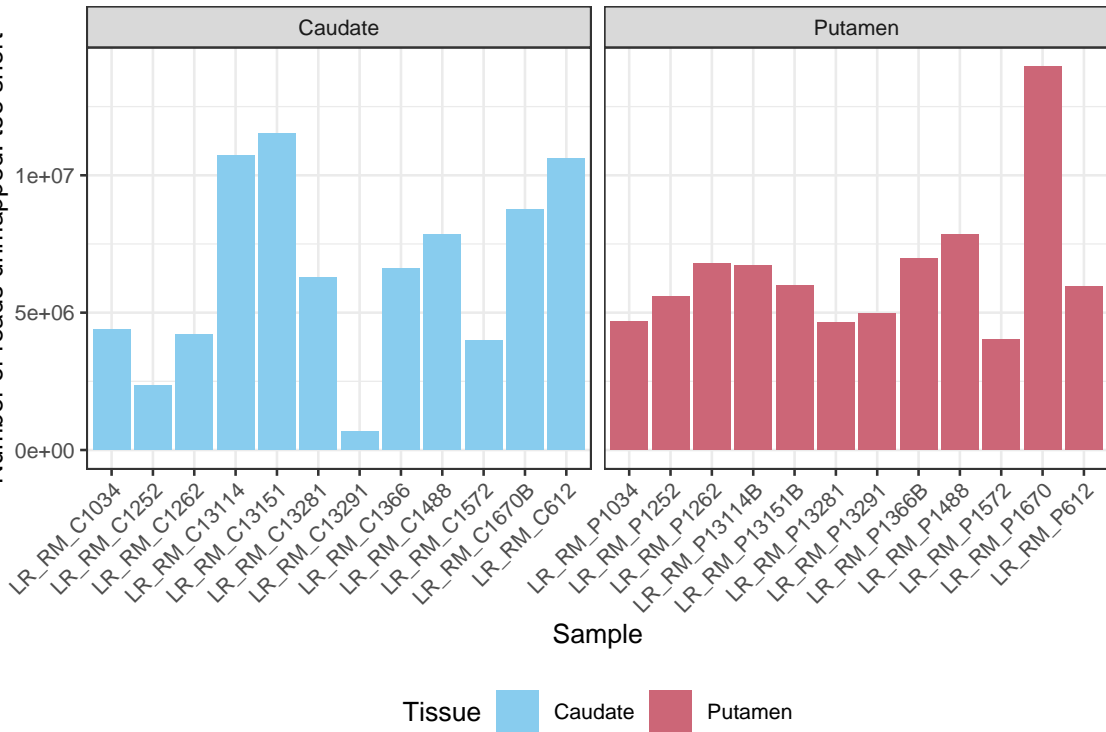


Mapped to too many loci

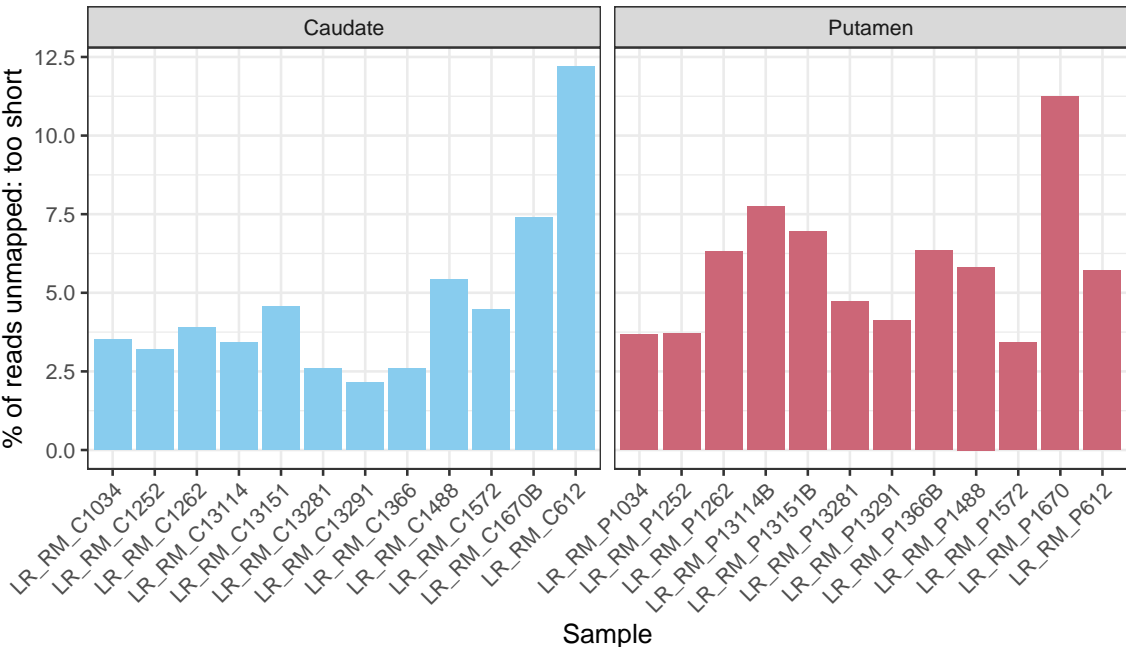




Number of reads unmapped: too short



% of reads unmapped: too short



Tissue

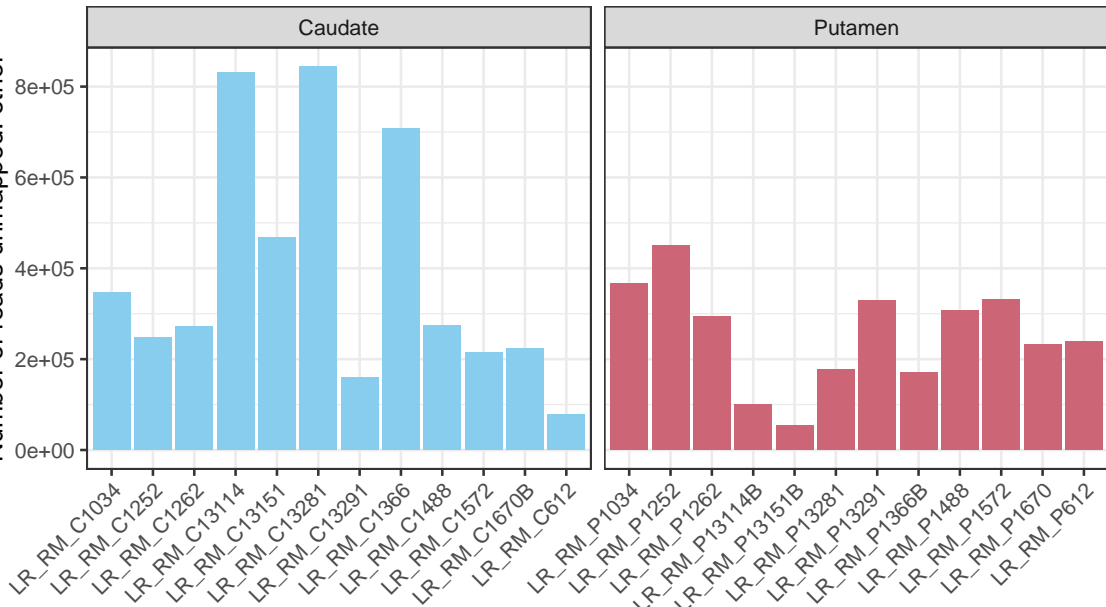


Caudate



Putamen

Number of reads unmapped: other



Tissue



Caudate



Putamen



