

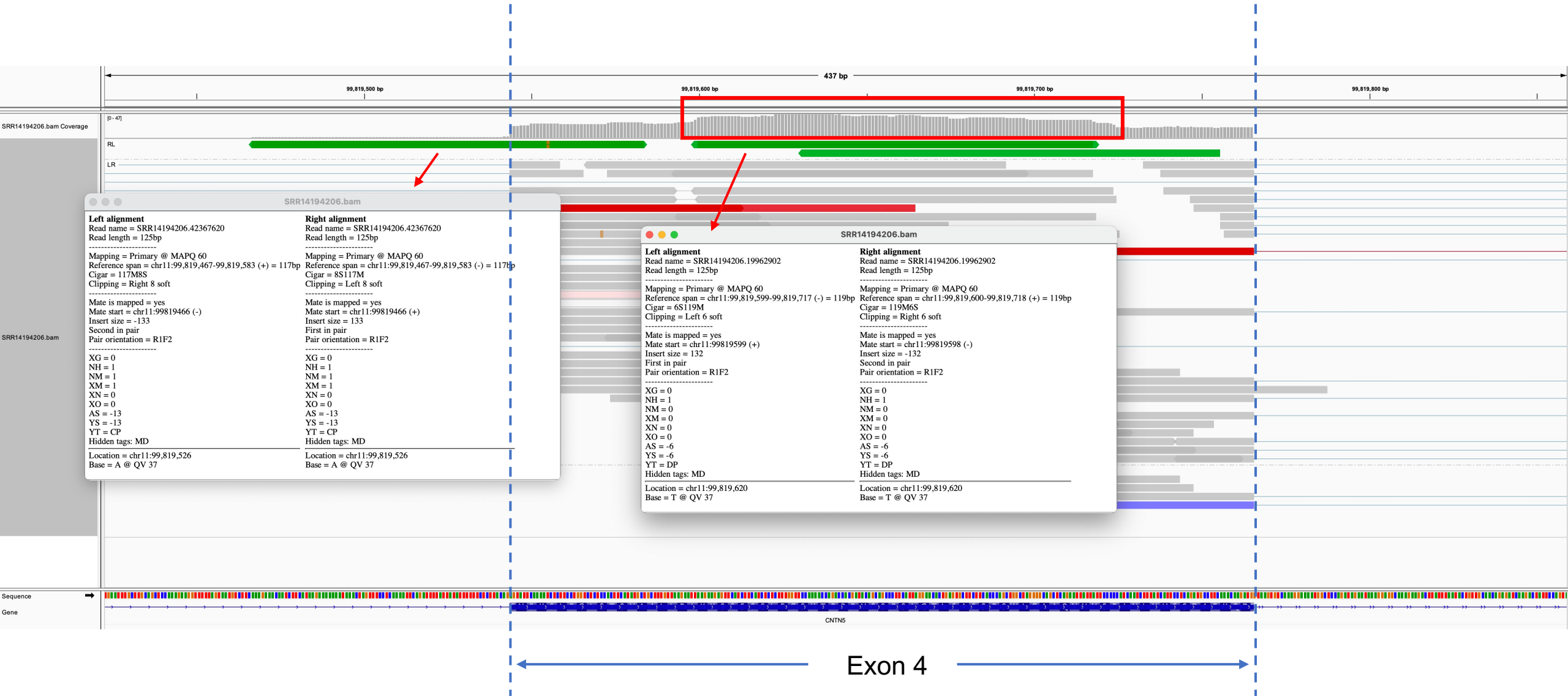
# Supplementary File 5

## RNA-Seq analysis of one CSV at *CNTN5*

### Note:

- The IGV view is grouped by read-pair orientations.
- The region between two dashed blue lines contains *CNTN5* exon 4.
- The red arrow points to the green read-pairs supporting duplicated exon signature and detailed alignment information of supporting read-pairs.
- The read depth increases inside red box compare to read depth outside the red box.

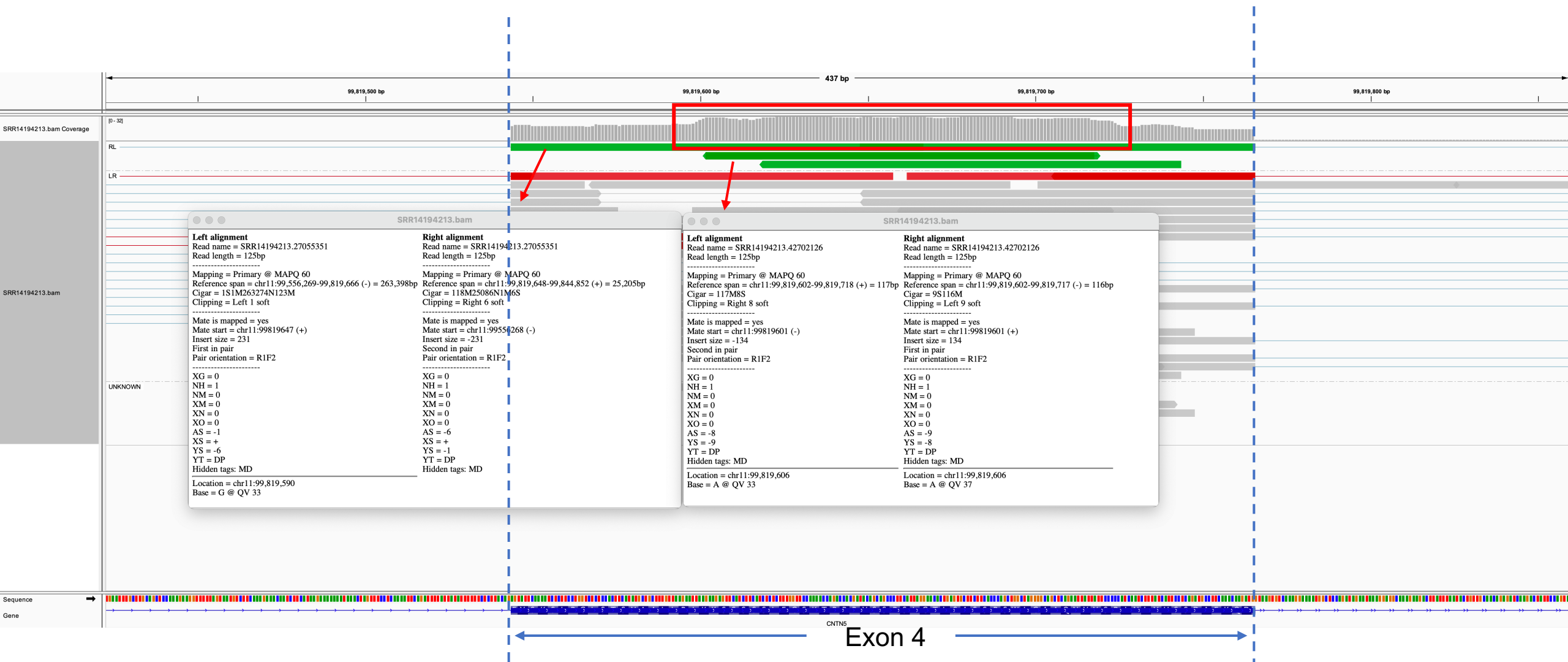
# ❖ SRR14194206, Control\_Male\_Precuneus



# ❖ SRR14194208, Control\_Female\_Precuneus



# ❖ SRR14194213, Alzheimer\_Disease\_Female\_Precuneus



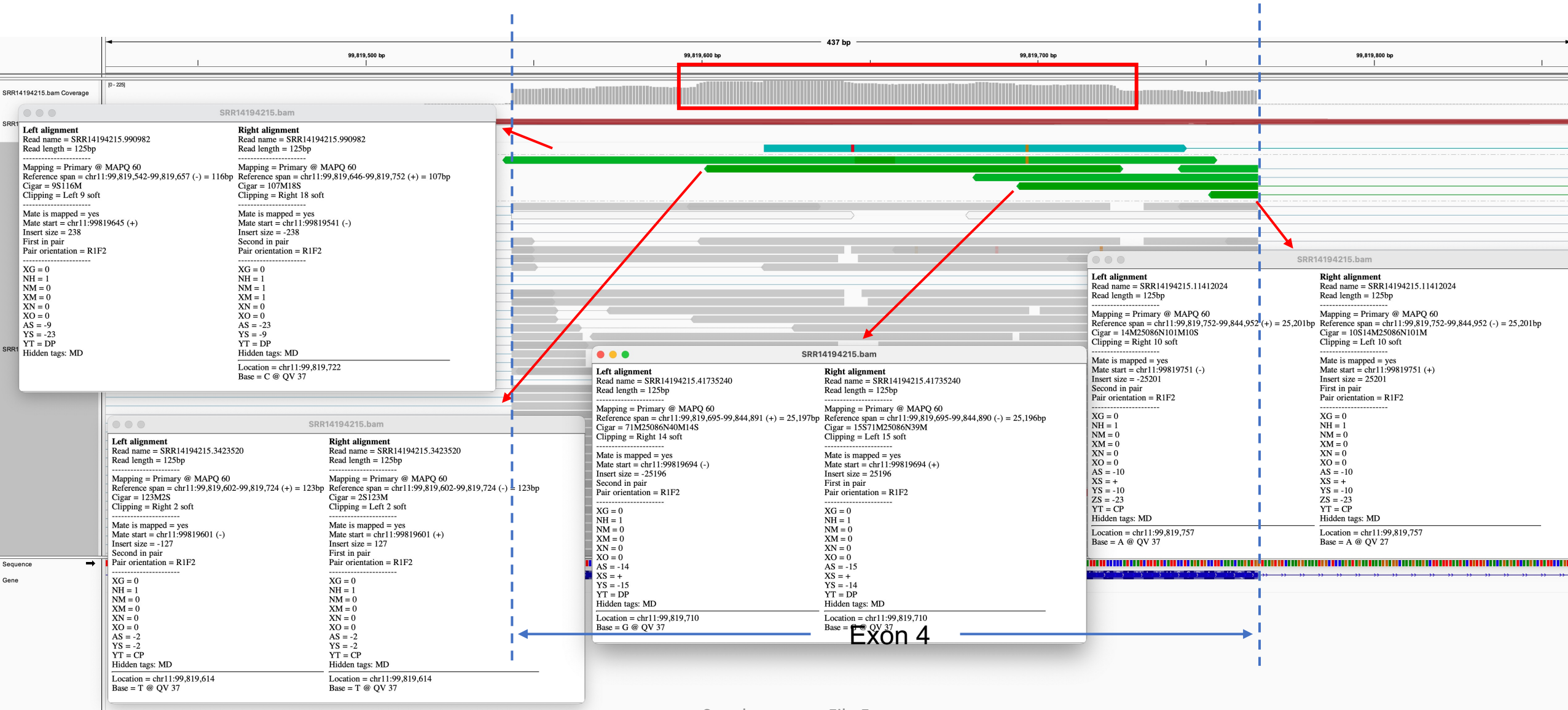
# ❖ SRR14194223, Control\_Male\_Primary\_Visual\_Cortex



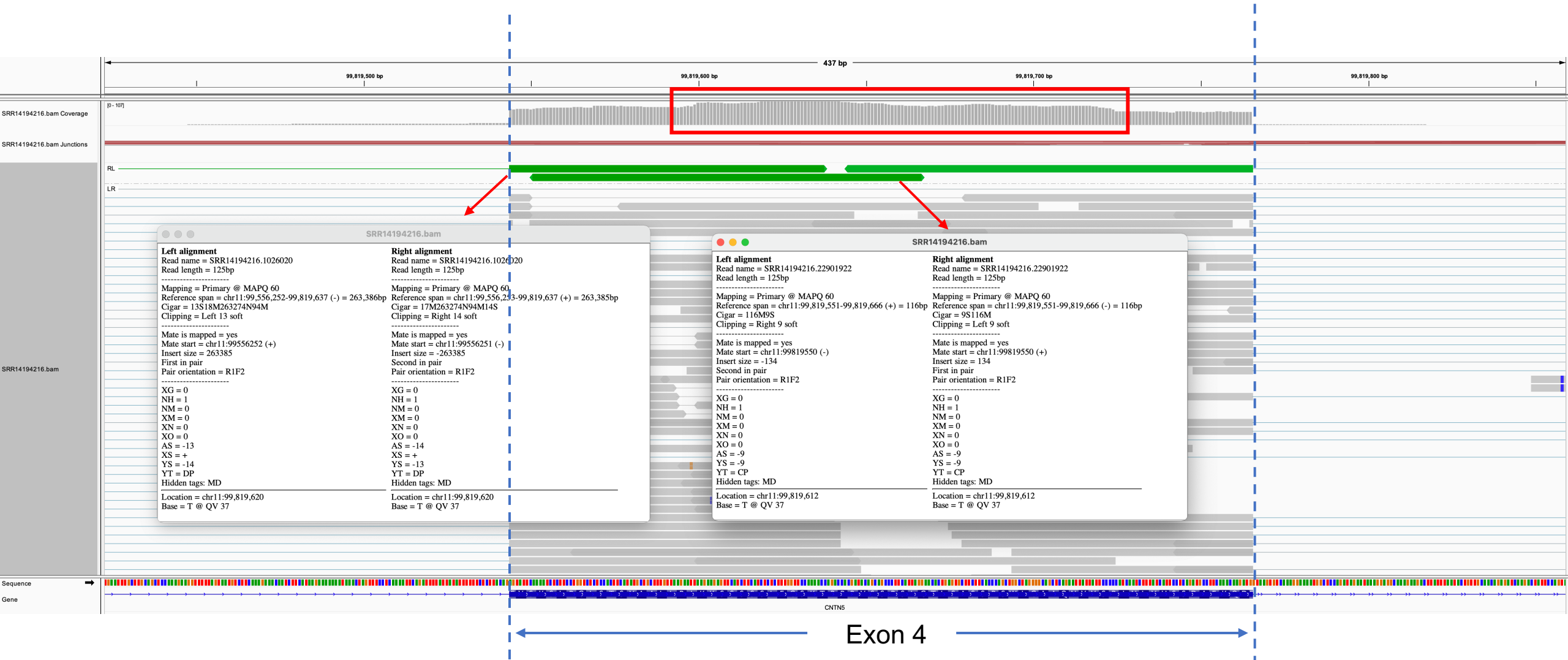
SRR14194223.bam

Left alignment	Right alignment
Read name = SRR14194223.19087773	Read name = SRR14194223.19087773
Read length = 125bp	Read length = 125bp
Mapping = Primary @ MAPQ 60	Mapping = Primary @ MAPQ 60
Reference span = chr11:99,819,604-99,819,723 (+) = 120bp	Reference span = chr11:99,819,604-99,819,723 (-) = 120bp
Cigar = 120M5S	Cigar = 5S120M
Clipping = Right 5 soft	Clipping = Left 5 soft
Mate is mapped = yes	Mate is mapped = yes
Mate start = chr11:99819603 (-)	Mate start = chr11:99819603 (+)
Insert size = -130	Insert size = 130
Second in pair	First in pair
Pair orientation = R1F2	Pair orientation = R1F2
-----	-----
XG = 0	XG = 0
NH = 1	NH = 1
NM = 0	NM = 0
XM = 0	XM = 0
XN = 0	XN = 0
XO = 0	XO = 0
AS = -5	AS = -5
YS = -5	YS = -5
ZS = -5	YT = CP
YT = CP	Hidden tags: MD
Hidden tags: MD	Location = chr11:99,819,709
Location = chr11:99,819,709	Base = A @ QV 37
Base = A @ QV 37	

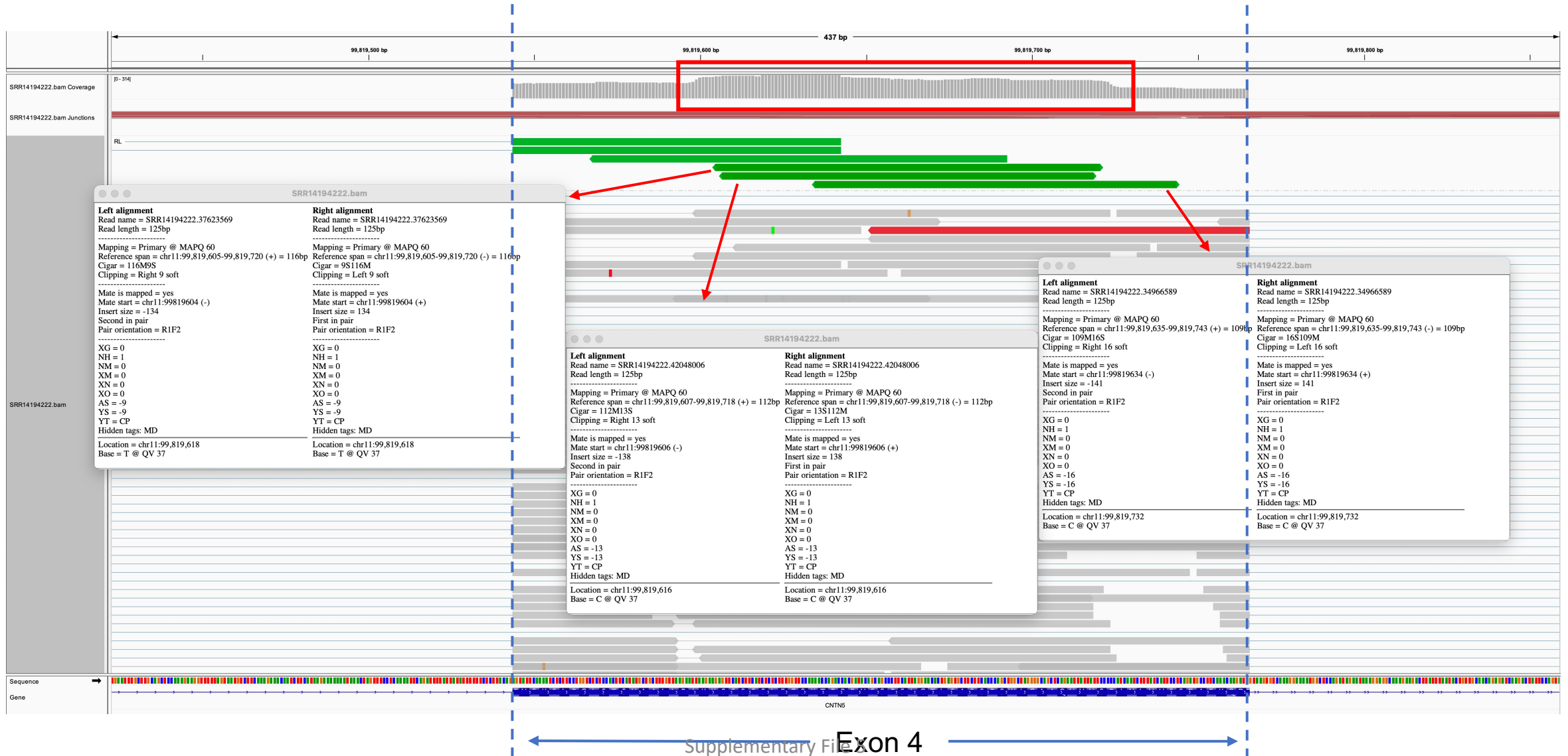
# ❖ SRR14194215, Control\_Female\_Primary\_Visual\_Cortex



# ❖ SRR14194216, Control\_Female\_Primary\_Visual\_Cortex

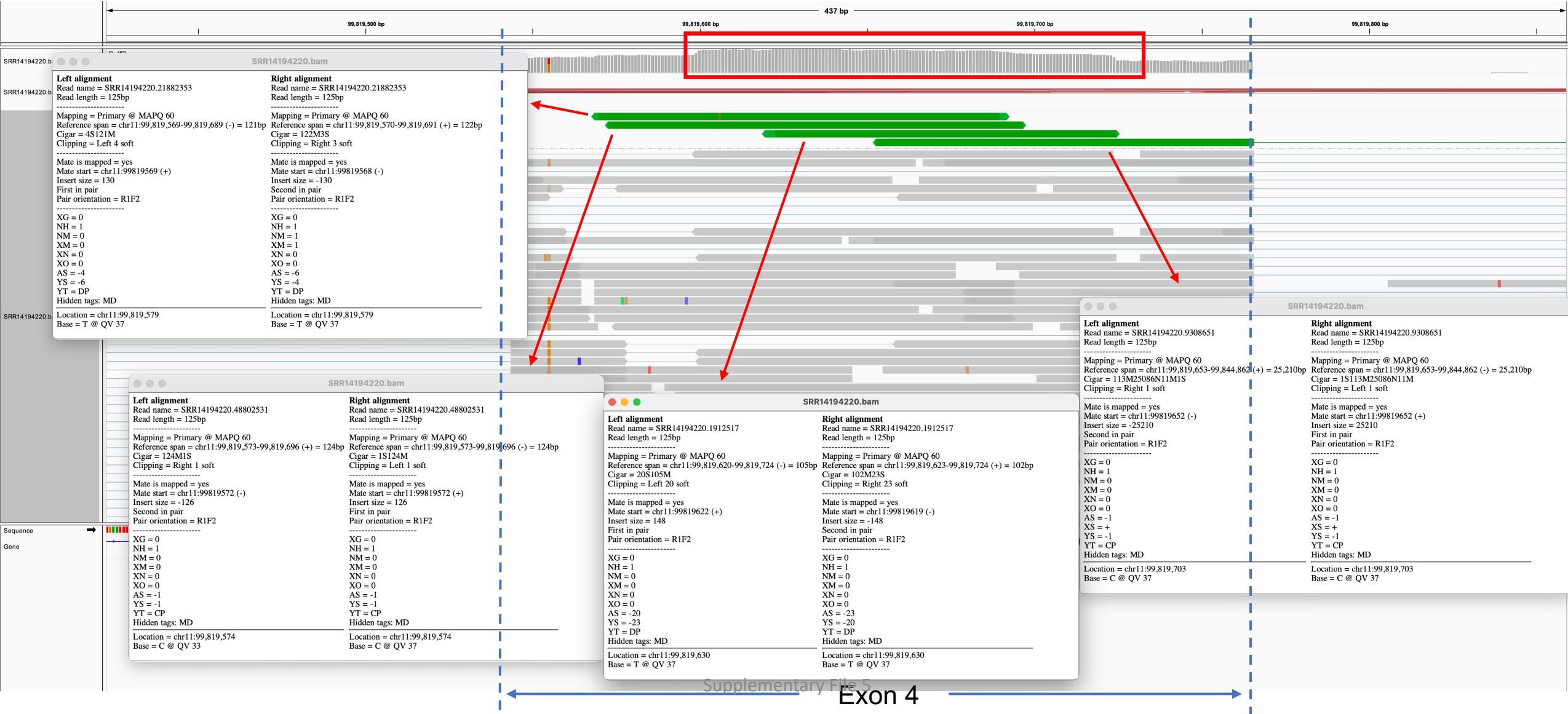


# ❖ SRR14194222, Alzheimer\_Disease\_Male\_Primary\_Visual\_Cortex





# ❖ SRR14194220, Alzheimer\_Disease\_Female\_Primary\_Visual\_Cortex



# ❖ SRR14194221, Alzheimer\_Disease\_Female\_Primary\_Visual\_Cortex

