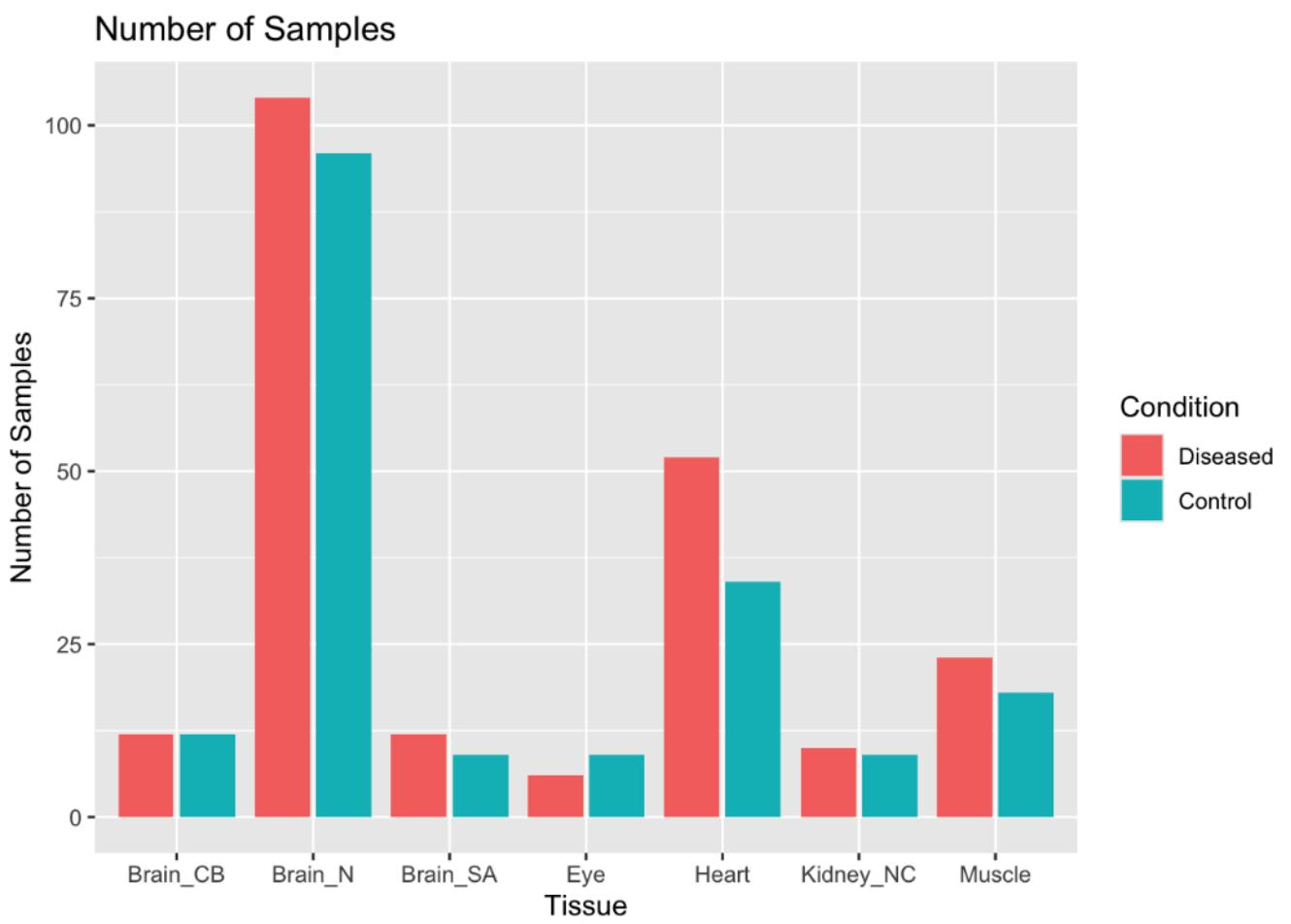


Key QC Metrics across Tissues

2025-09-05

Number of samples

Tissue	Disease	Sample.number
Data Information		
Brain_CB	Late onset AD	12
Brain_CB	Control	12
Brain_N	AD	104
Brain_N	Control	96
Brain_SA	Parkinsons	12
Brain_SA	Control	9
Eye	AMD	6
Eye	Control	9
Heart	CAD	52
Heart	Control	34
Kidney_NC	DKD	10
Kidney_NC	Control	9
Muscle	Aged	23
Muscle	Control	18



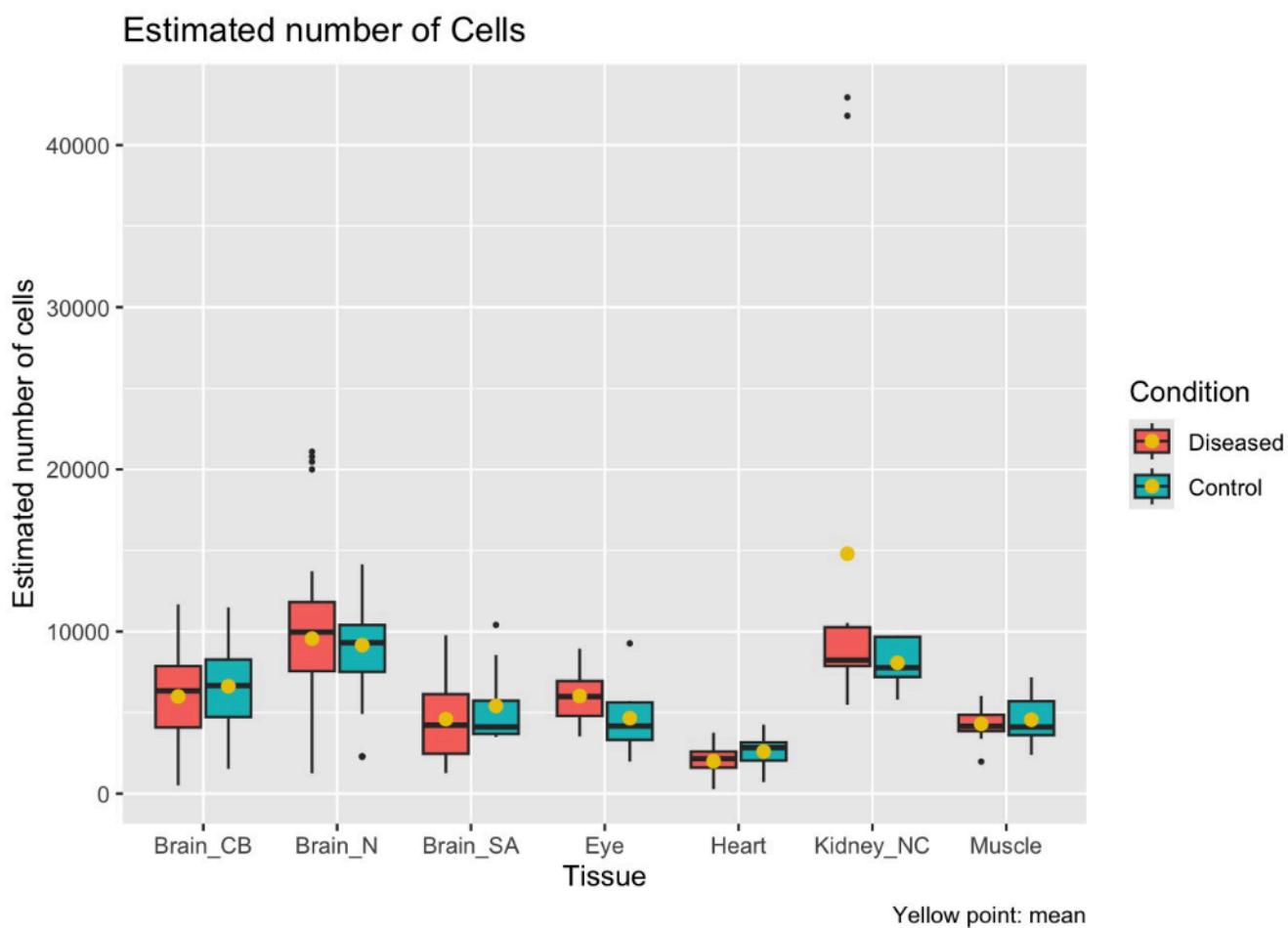
Estimated number of Cells

Mean Estimated number of cells

Tissue Condition Estimated.number.of.cells

Brain_CB	Diseased	5989.917
Brain_CB	Control	6625.083
Brain_N	Diseased	9554.894
Brain_N	Control	9161.990
Brain_SA	Diseased	4591.667
Brain_SA	Control	5406.444
Eye	Diseased	6016.000
Eye	Control	4651.889
Heart	Diseased	2000.846
Heart	Control	2599.059
Kidney_NC	Diseased	14795.400

Tissue	Condition	Estimated.number.of.cells
Kidney_NC	Control	8073.222
Muscle	Diseased	4301.478
Muscle	Control	4558.056



Median High-Quality Fragments per Cell

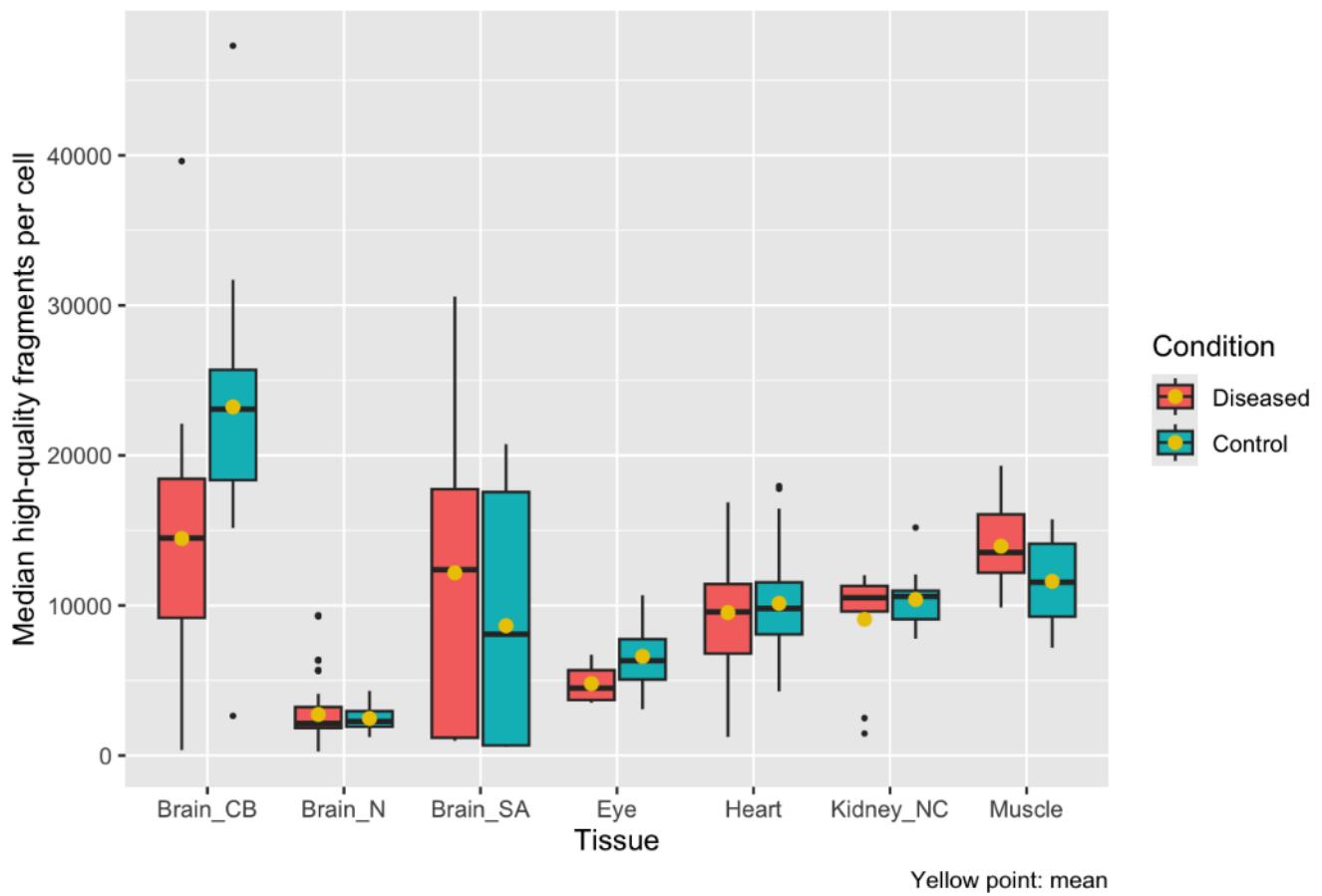
High-quality fragments are defined as read pairs with a valid barcode that map to the nuclear genome with mapping quality > 30, are not chimeric and not duplicate.

Mean Median High-Quality Fragments per Cell

Tissue	Condition	Median.high.quality.fragments.per.cell
Brain_CB	Diseased	14459.833
Brain_CB	Control	23232.458
Brain_N	Diseased	2739.620
Brain_N	Control	2470.781
Brain_SA	Diseased	12175.000
Brain_SA	Control	8644.722

Tissue	Condition	Median.high.quality.fragments.per.cell
Eye	Diseased	4787.750
Eye	Control	6604.167
Heart	Diseased	9527.250
Heart	Control	10138.647
Kidney_NC	Diseased	9080.300
Kidney_NC	Control	10396.556
Muscle	Diseased	13948.609
Muscle	Control	11609.778

Median High-Quality Fragments per Cell



Number of Peaks

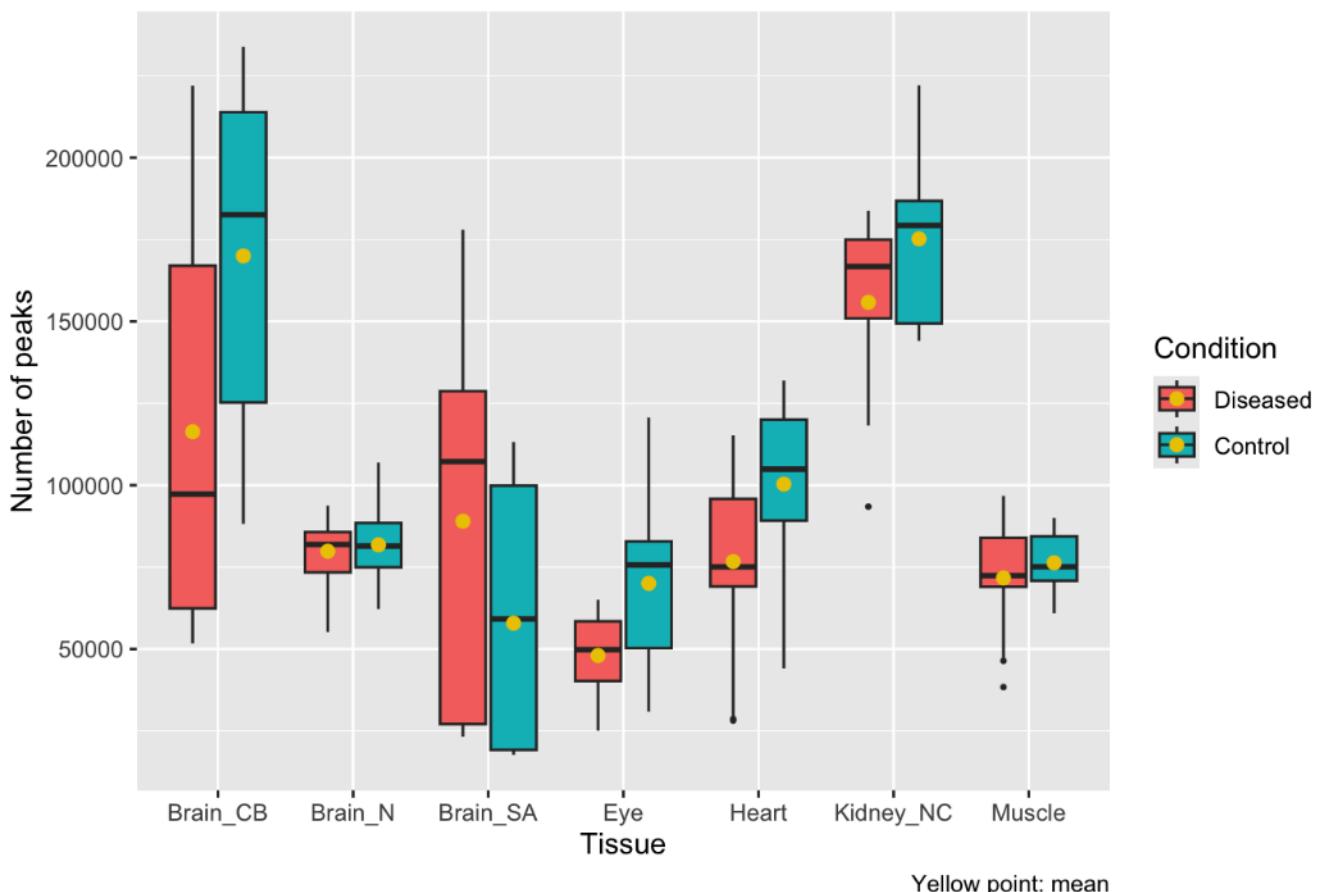
Mean Number of Peaks

Tissue	Condition	Number.of.peaks
Brain_CB	Diseased	116327.17

Tissue Condition Number.of.peaks

Brain_CB	Control	170019.83
Brain_N	Diseased	79854.00
Brain_N	Control	81795.19
Brain_SA	Diseased	89010.92
Brain_SA	Control	57877.33
Eye	Diseased	48010.17
Eye	Control	70029.89
Heart	Diseased	76714.98
Heart	Control	100339.76
Kidney_NC	Diseased	155832.10
Kidney_NC	Control	175219.00
Muscle	Diseased	71686.65
Muscle	Control	76312.89

Number of Peaks

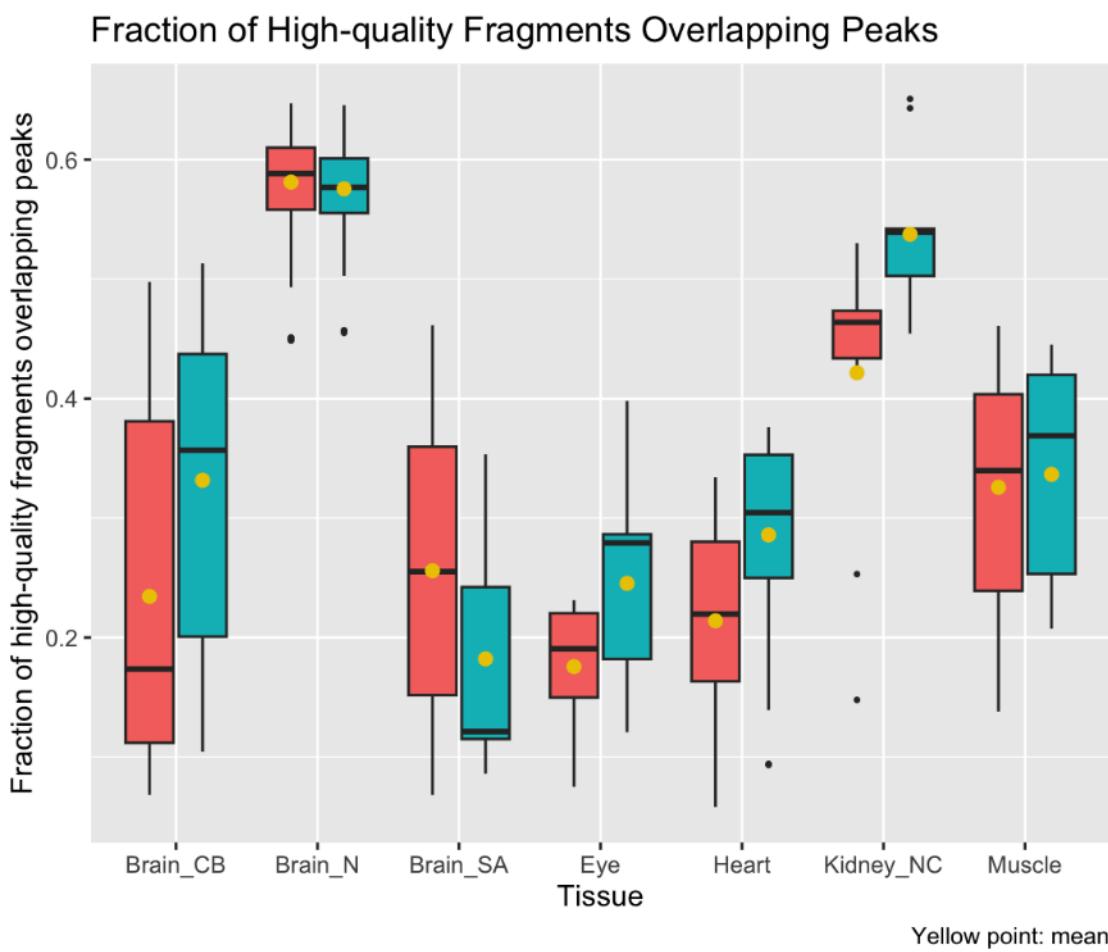


Fraction of High-quality Fragments Overlapping Peaks

High-quality fragments are defined as read pairs with a valid barcode that map to the nuclear genome with mapping quality > 30, are not chimeric and not duplicate.

Mean Fraction of High-quality Fragments Overlapping Peaks

Tissue	Condition	Fraction.of.high.quality.fragments.overlapping.peaks
Brain_C B	Diseased	0.2344333
Brain_C B	Control	0.3316333
Brain_N	Diseased	0.5811356
Brain_N	Control	0.5756177
Brain_S A	Diseased	0.2558917
Brain_S A	Control	0.1821333
Eye	Diseased	0.1756500
Eye	Control	0.2453222
Heart	Diseased	0.2139596
Heart	Control	0.2859088
Kidney_- NC	Diseased	0.4215800
Kidney_- NC	Control	0.5375778
Muscle	Diseased	0.3257522
Muscle	Control	0.3365333



TSS Enrichment Score

Maximum value of the transcription-start-site (TSS) profile. The TSS profile is the summed accessibility signal (defined as number of cut sites per base) in a window of 2,000 bases around all the annotated TSSs, normalized by the minimum signal in the window.

Mean TSS Enrichment Score

Tissue	Condition	TSS.enrichment.score
Brain_CB	Diseased	4.980225
Brain_CB	Control	5.691908
Brain_N	Diseased	11.235238
Brain_N	Control	11.184020
Brain_SA	Diseased	5.275808
Brain_SA	Control	4.951356
Eye	Diseased	3.860583
Eye	Control	4.691244
Heart	Diseased	5.022463

Tissue	Condition	TSS.enrichment.score
Heart	Control	5.906176
Kidney_NC	Diseased	6.440280
Kidney_NC	Control	7.699333
Muscle	Diseased	6.805217
Muscle	Control	7.297778

TSS Enrichment Score

