Processing Report

Truncating and Mapping

	Read 1	Read 2
Total Reads	256,945,663	256,945,663
Not Truncated	233,091,580	233,703,845
Truncated	23,854,083	23,241,818
Too short to map	3,674,019	3,502,934
Average length of truncated sequence	30.25	30.36

	Read 1	Read 2
Unique Alignments	223,212,597	219,883,055
Multiple Alignments	19,514,372	19,211,373
Failed To Align	10,544,675	14,348,301
Paired	196,570,229	196,570,229
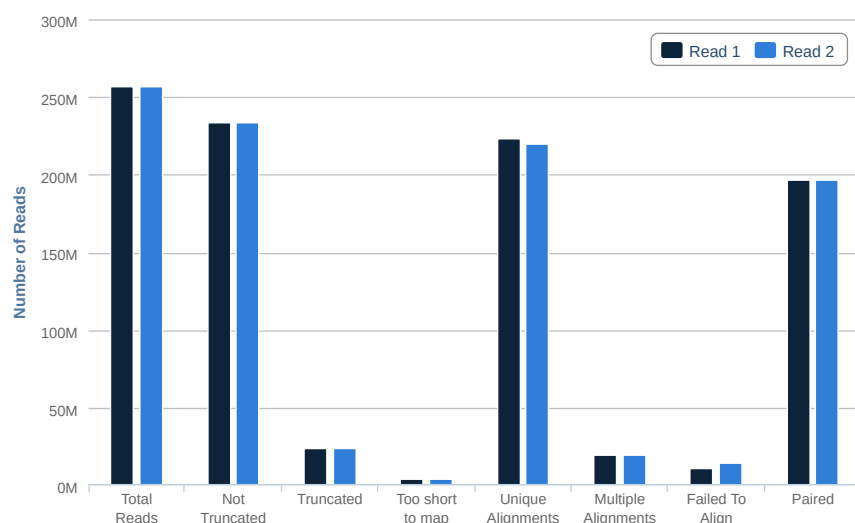
Filtering

	Di-Tag Count
Valid Pairs	153,286,821
Invalid Pairs	43,283,408
Same Circularised	2,861,675
Same Fragment Dangling Ends	3,431,353
Same Fragment Internal	3,271,191
Re-ligation	28,028,813
Contiguous Sequence	1,435,159
Wrong Size	4,255,217
Total Pairs	196,570,229
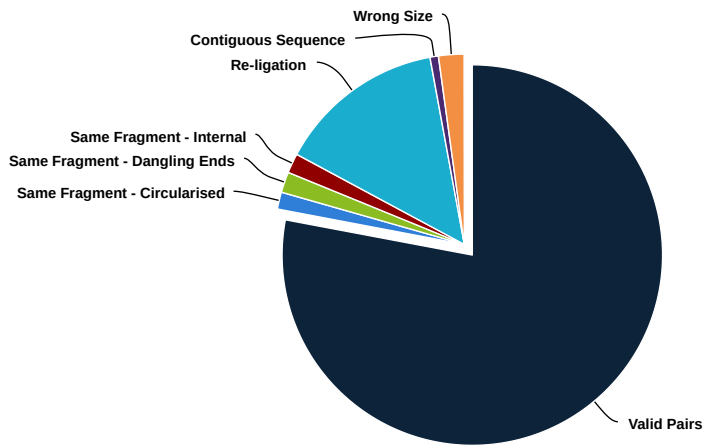
Di-tag length Distribution

Click and drag in the plot area to zoom in
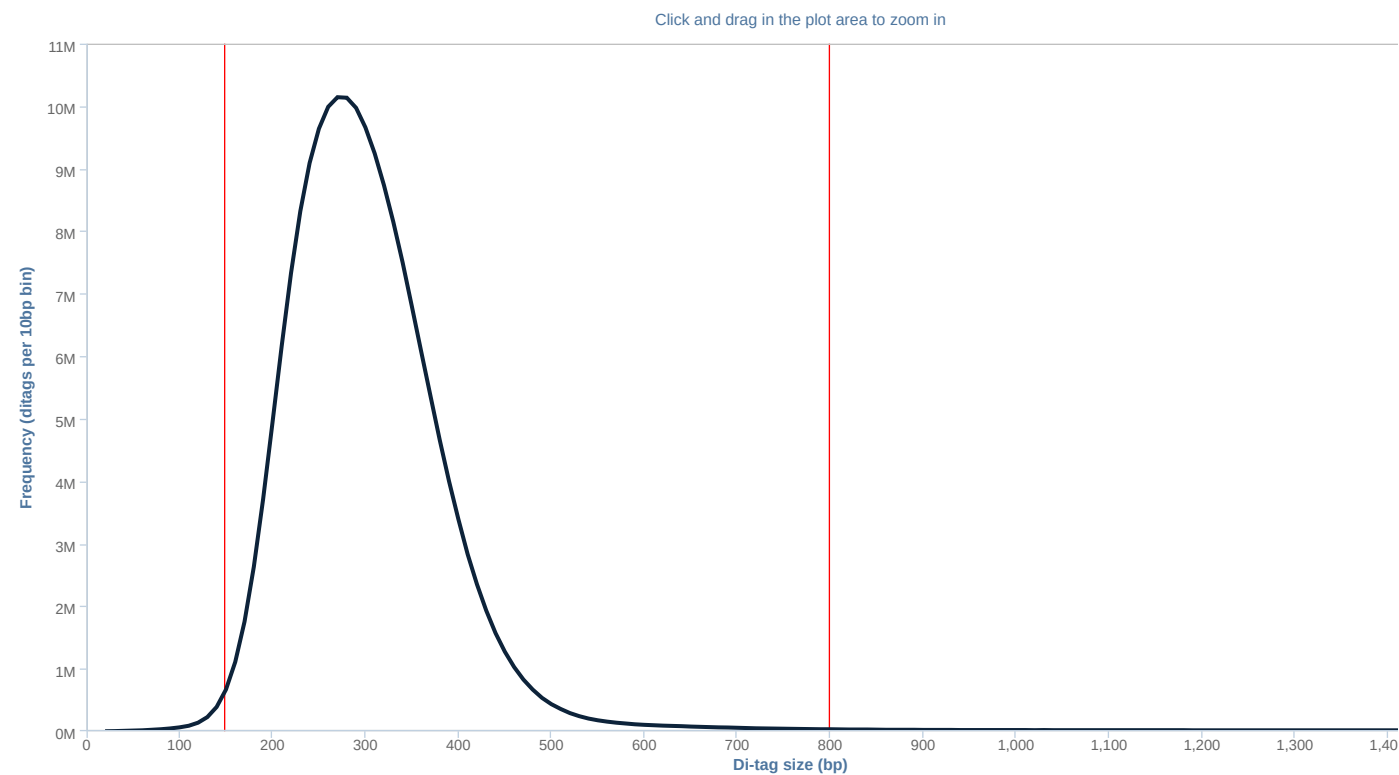
De-duplication

Percentage uniques: 85.44

	All Di-Tags	Unique Di-Tags
Read Pairs	153,286,821	130,971,918
Cis-close (< 10Kbp)	31,366,204	26,223,310
Cis-far (> 10Kbp)	107,687,407	92,515,211
Trans	14,233,210	12,233,397
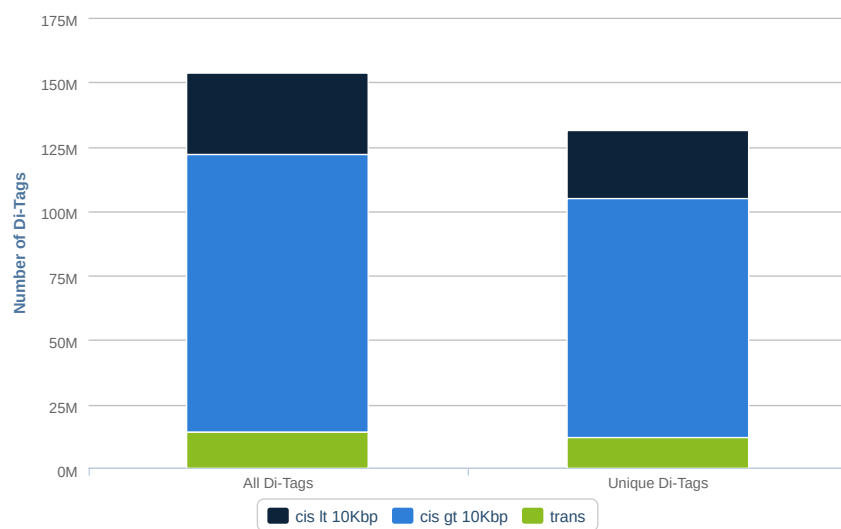
Analysis produced by **HiCUP** (0.7.2) - a tool for mapping and performing quality control on Hi-C data.

Report graphs rendered using jQuery and Highcharts.