Processing Report

Truncating and Mapping

	Read 1	Read 2
Total Reads	260,220,163	260,220,163
Not Truncated	235,680,822	237,180,471
Truncated	24,539,341	23,039,692
Too short to map	3,636,518	3,312,742
Average length of truncated sequence	30.48	30.68

|	Read 1	Read 2
Unique Alignments	225,269,321	222,599,191
Multiple Alignments	21,219,285	20,944,830
Failed To Align	10,095,039	13,363,400
Paired	199,380,409	199,380,409
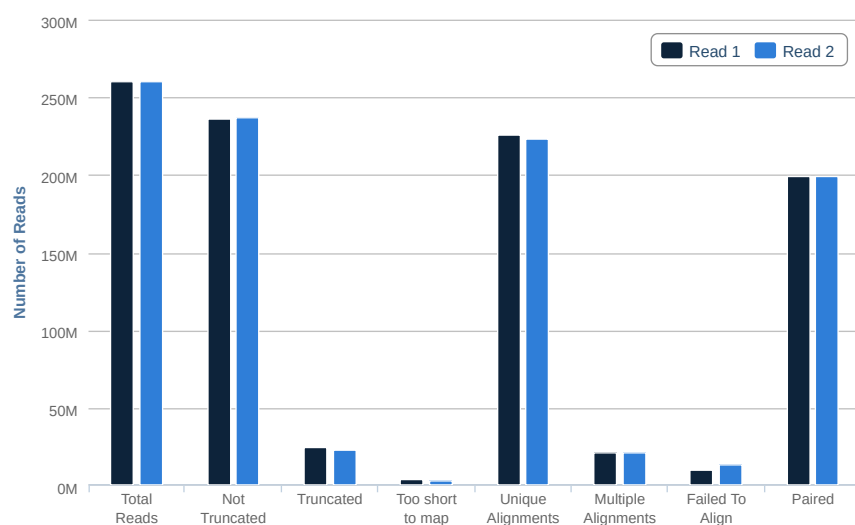
Filtering

|	Di-Tag Count
Valid Pairs	150,356,474
Invalid Pairs	49,023,935
Same Circularised	4,032,537
Same Fragment Dangling Ends	3,869,234
Same Fragment Internal	3,409,417
Re-ligation	29,674,629
Contiguous Sequence	1,964,153
Wrong Size	6,073,965
Total Pairs	199,380,409
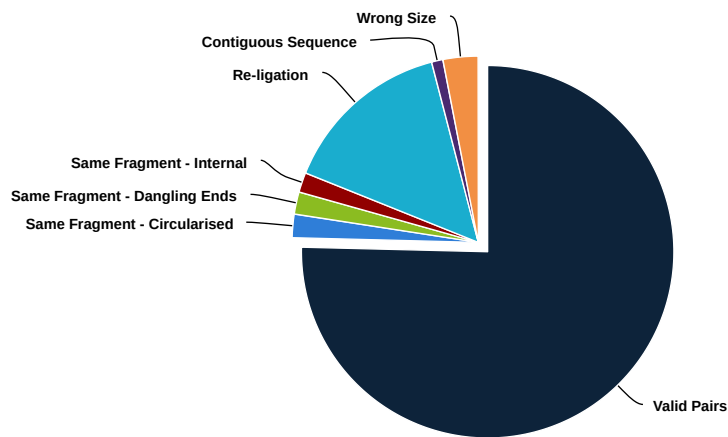
Di-tag length Distribution

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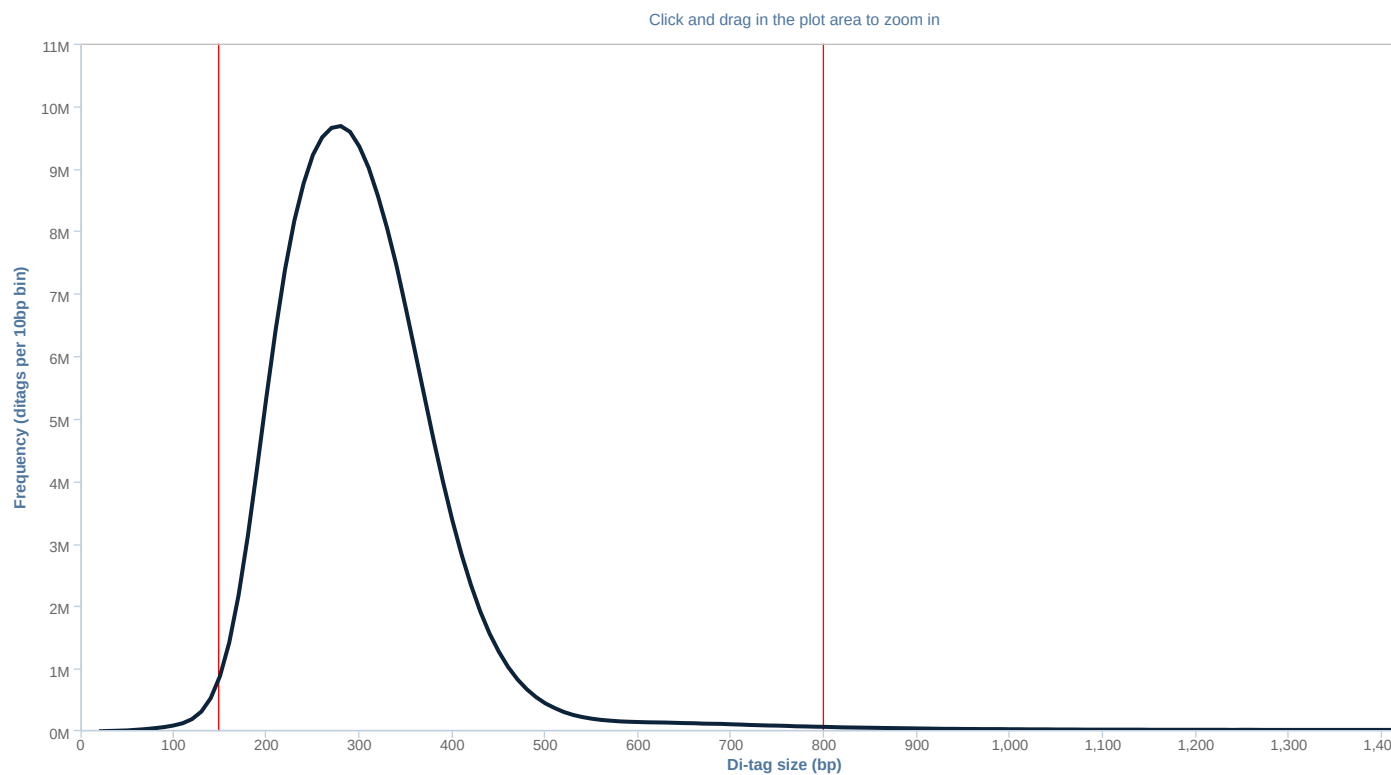
De-duplication

Percentage uniques: 61.31

	All Di-Tags	Unique Di-Tags
Read Pairs	150,356,474	92,188,914
Cis-close (< 10Kbp)	38,953,686	23,513,623
Cis-far (> 10Kbp)	99,348,757	61,327,198
Trans	12,054,031	7,348,093
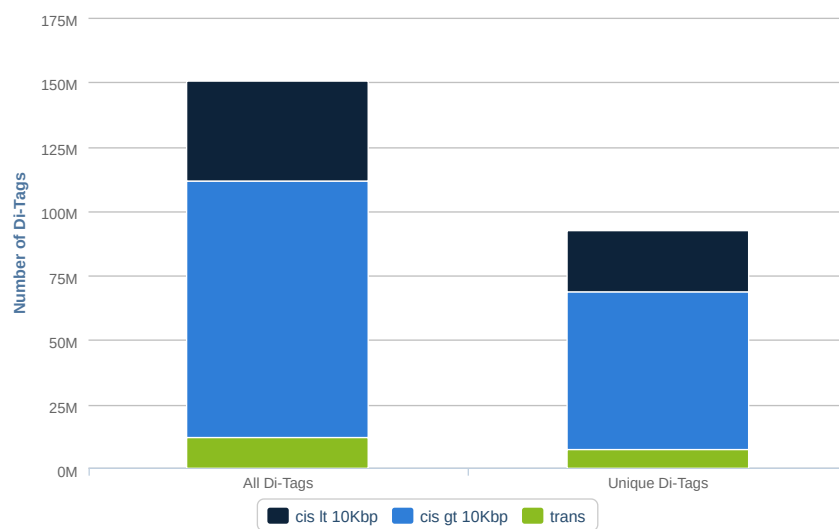
Analysis produced by **HiCUP** (0.7.2) - a tool for mapping and performing quality control on Hi-C data.

Report graphs rendered using jQuery and Highcharts.