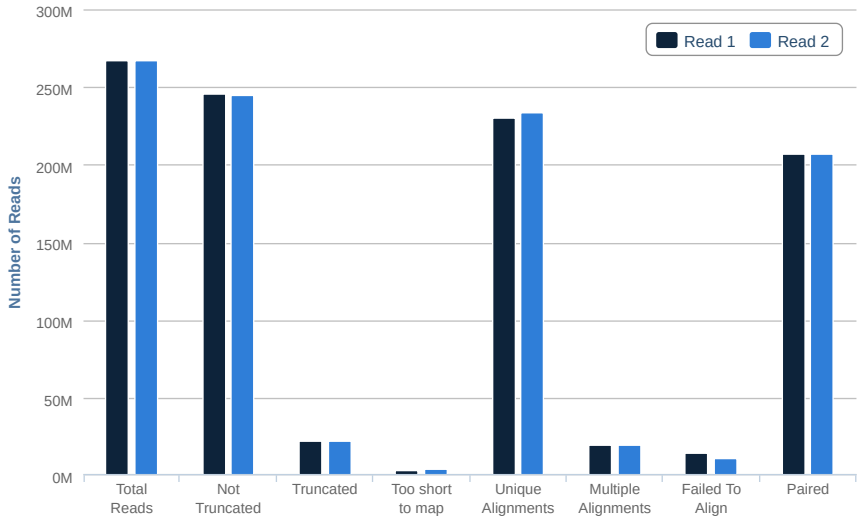
Processing Report

/gpfs/projects/bsc08/bsc08471/PCHiC/p53/HiCUP/NUT2WT/lane3222_HCT116_Nutlin3a_2BR-102.1_NoIndex_L005_R2_1
LiaLMRvGhu_15-24-52_25-04-2020

Truncating and Mapping

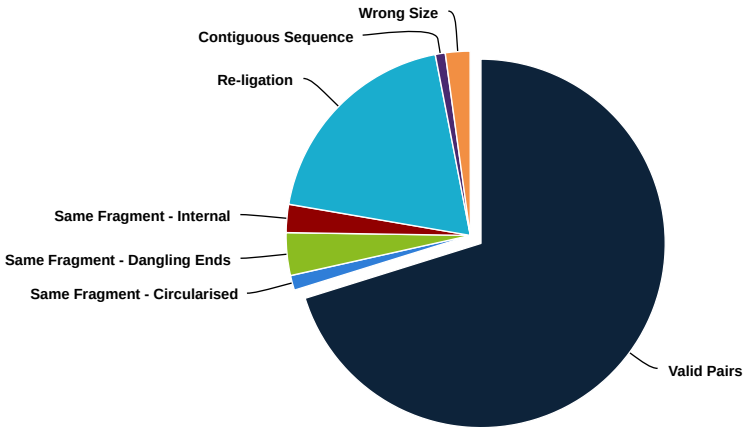
	Read 1	Read 2
Total Reads	267,094,677	267,094,677
Not Truncated	245,451,408	244,838,689
Truncated	21,643,269	22,255,988
Too short to map	3,283,318	3,462,112
Average length of truncated sequence	30.35	30.22

	Read 1	Read 2
Unique Alignments	229,943,623	233,208,196
Multiple Alignments	19,385,856	19,690,134
Failed To Align	14,481,880	10,734,235
Paired	206,896,517	206,896,517

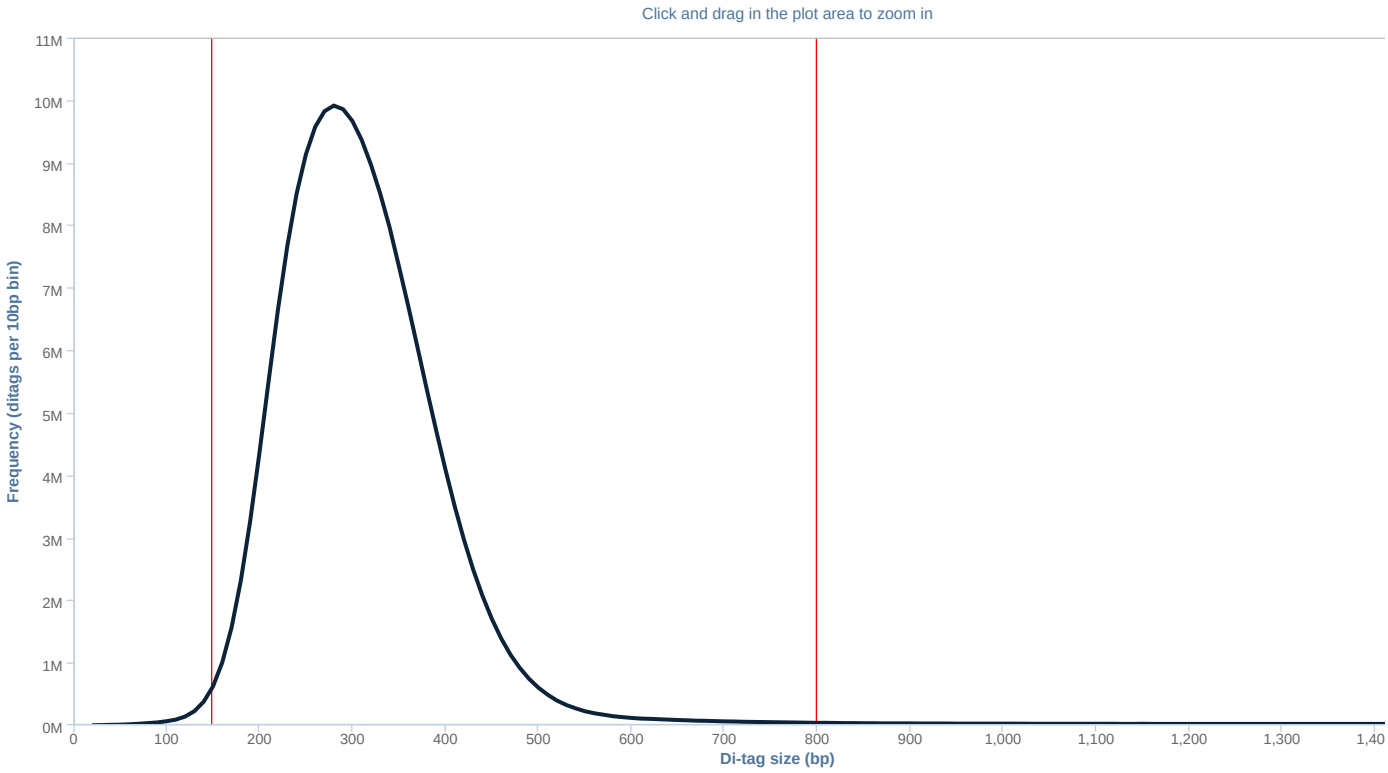


Filtering

	Di-Tag Count
Valid Pairs	145,245,887
Invalid Pairs	61,650,630
Same Circularised	2,690,781
Same Fragment Dangling Ends	7,740,238
Same Fragment Internal	5,099,724
Re-ligation	39,827,041
Contiguous Sequence	1,816,617
Wrong Size	4,476,229
Total Pairs	206,896,517



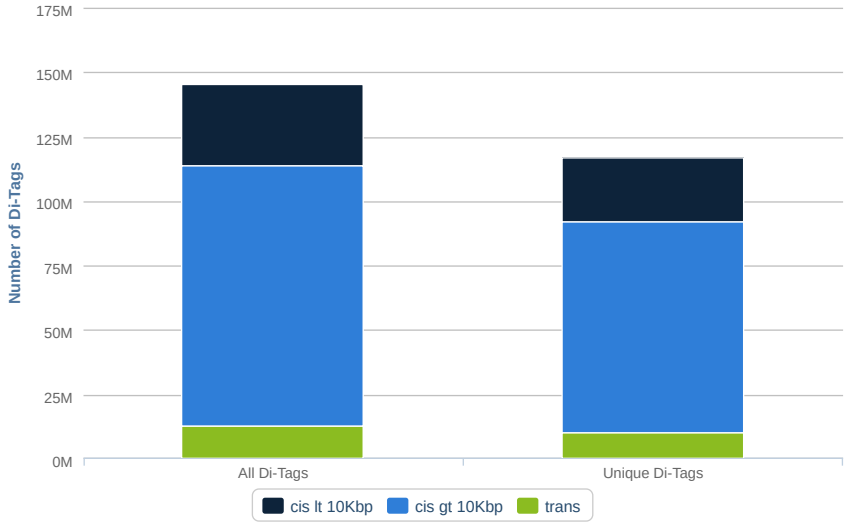
Di-tag length Distribution



De-duplication

Percentage uniques: 80.40

	All Di-Tags	Unique Di-Tags
Read Pairs	145,245,887	116,773,849
Cis-close (< 10Kbp)	31,757,682	24,991,710
Cis-far (> 10Kbp)	101,009,029	81,700,166
Trans	12,479,176	10,081,973



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.

Babraham Bioinformatics