

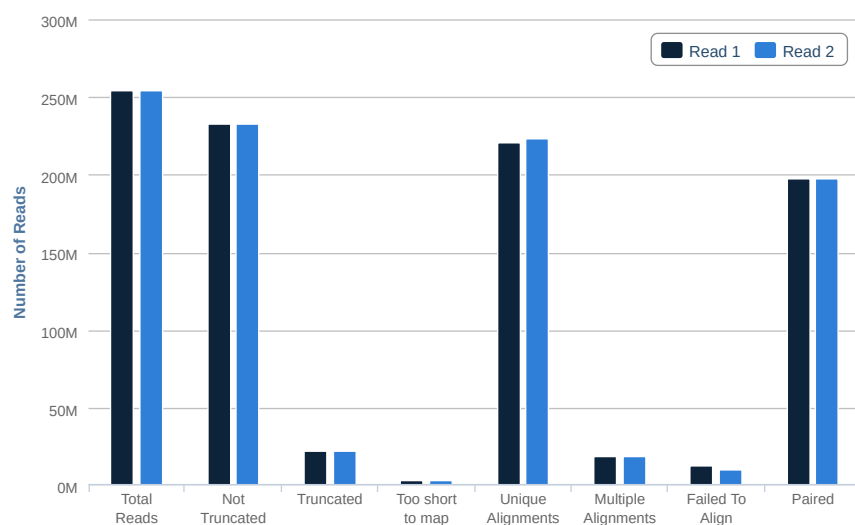
Processing Report

/gpfs/projects/bsc08/bsc08471/PCHiC/p53/HiCUP/NUT1KO/lane3221_HCT116-_-Nutlin3a_1BR-101.1_NoIndex_L004_R2_1
 HlchcCLByJ_15-24-52_25-04-2020

Truncating and Mapping

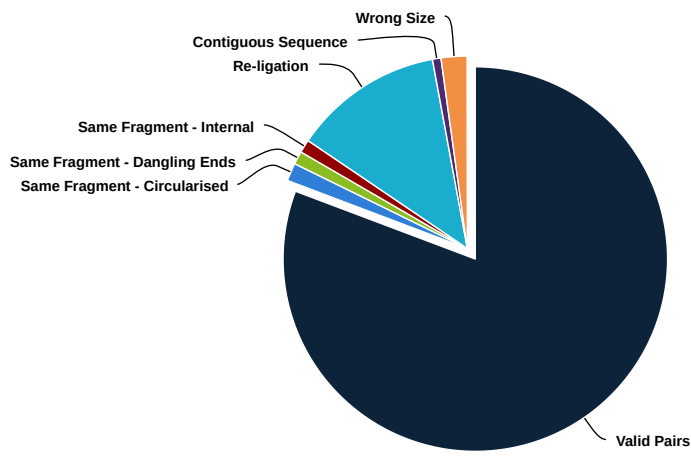
	Read 1	Read 2
Total Reads	254,246,572	254,246,572
Not Truncated	232,542,012	232,114,002
Truncated	21,704,560	22,132,570
Too short to map	3,227,600	3,348,599
Average length of truncated sequence	30.40	30.31

	Read 1	Read 2
Unique Alignments	220,277,091	222,959,303
Multiple Alignments	18,119,934	18,282,403
Failed To Align	12,621,947	9,656,267
Paired	197,626,650	197,626,650

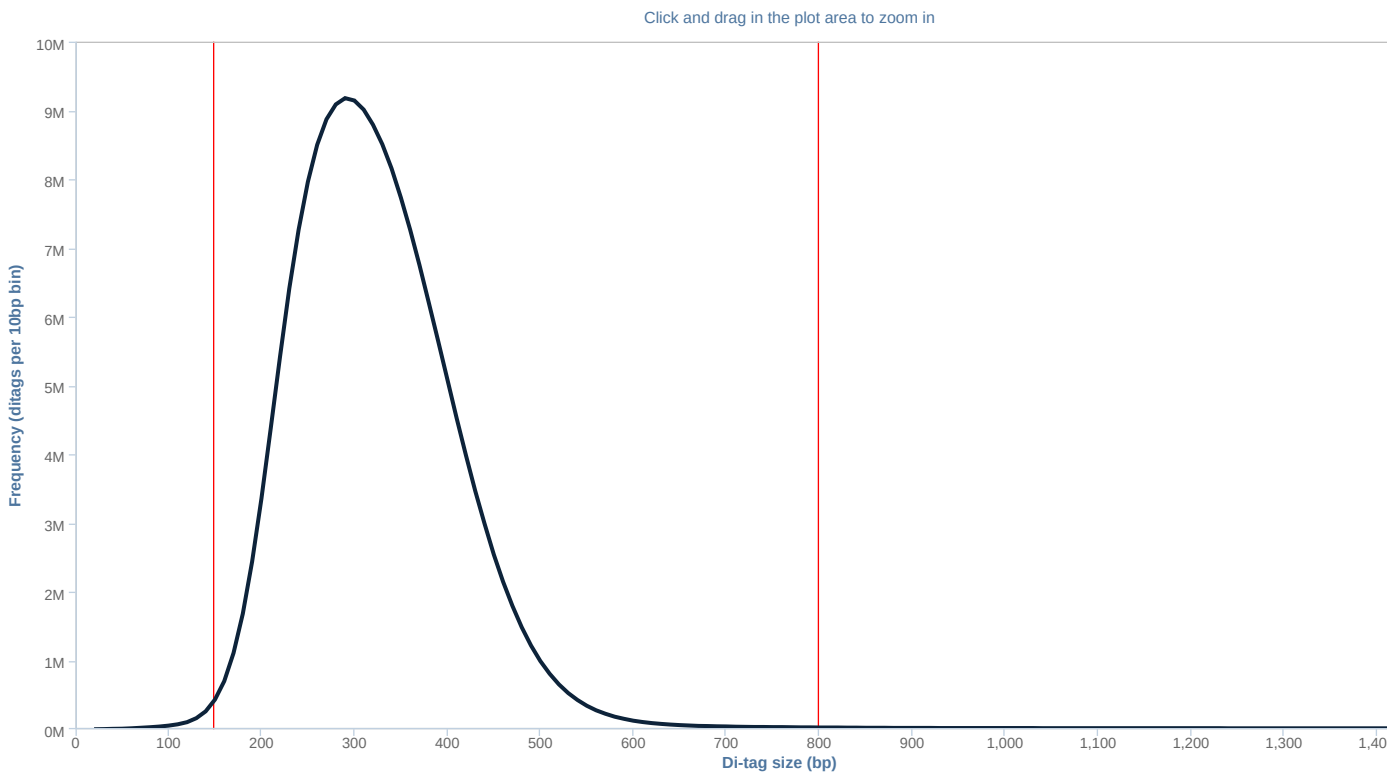


Filtering

	Di-Tag Count
Valid Pairs	159,589,869
Invalid Pairs	38,036,781
Same Circularised	2,982,392
Same Fragment Dangling Ends	2,160,120
Same Fragment Internal	2,200,455
Re-ligation	24,942,953
Contiguous Sequence	1,442,178
Wrong Size	4,308,683
Total Pairs	197,626,650



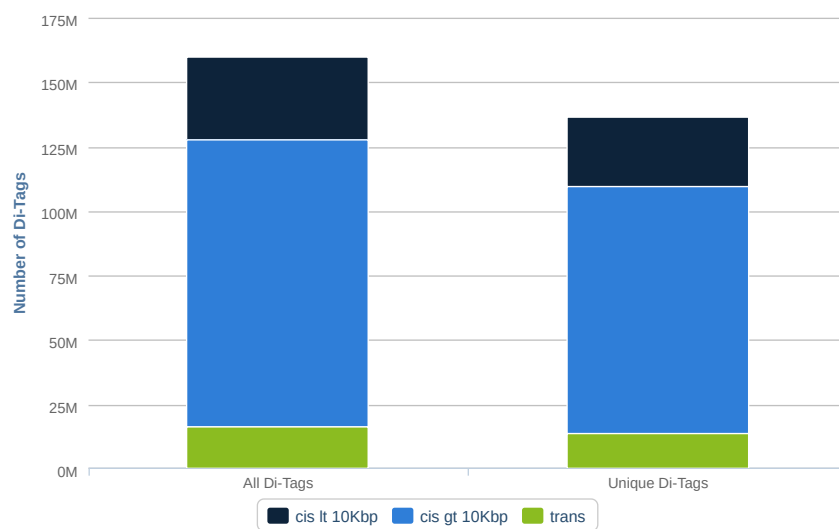
Di-tag length Distribution



De-duplication

Percentage uniques: 85.54

	All Di-Tags	Unique Di-Tags
Read Pairs	159,589,869	136,509,044
Cis-close (< 10Kbp)	32,097,743	26,817,855
Cis-far (> 10Kbp)	111,322,605	95,761,764
Trans	16,169,521	13,929,425



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](#).