

Processing Report

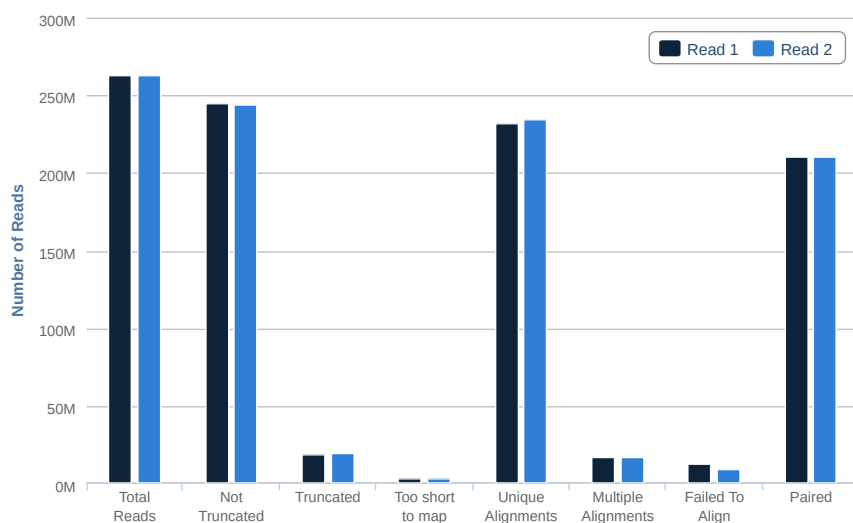
/gpfs/projects/bsc08/bsc08471/PCHiC/p53/HiCUP/MOCK2WT/lane1_NoIndex_L001_R2_1

QUHzDZLHYt_15-24-52_25-04-2020

Truncating and Mapping

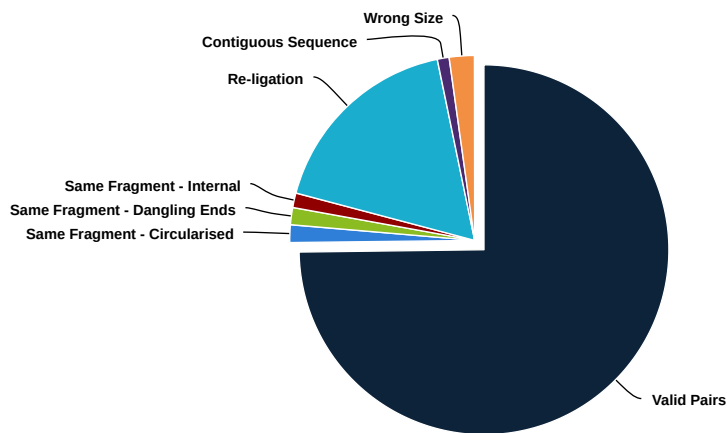
	Read 1	Read 2
Total Reads	262,846,987	262,846,987
Not Truncated	244,168,124	243,349,278
Truncated	18,678,863	19,497,709
Too short to map	2,622,881	2,824,189
Average length of truncated sequence	30.75	30.59

	Read 1	Read 2
Unique Alignments	231,472,455	234,266,415
Multiple Alignments	16,726,334	16,961,649
Failed To Align	12,025,317	8,794,734
Paired	210,134,874	210,134,874

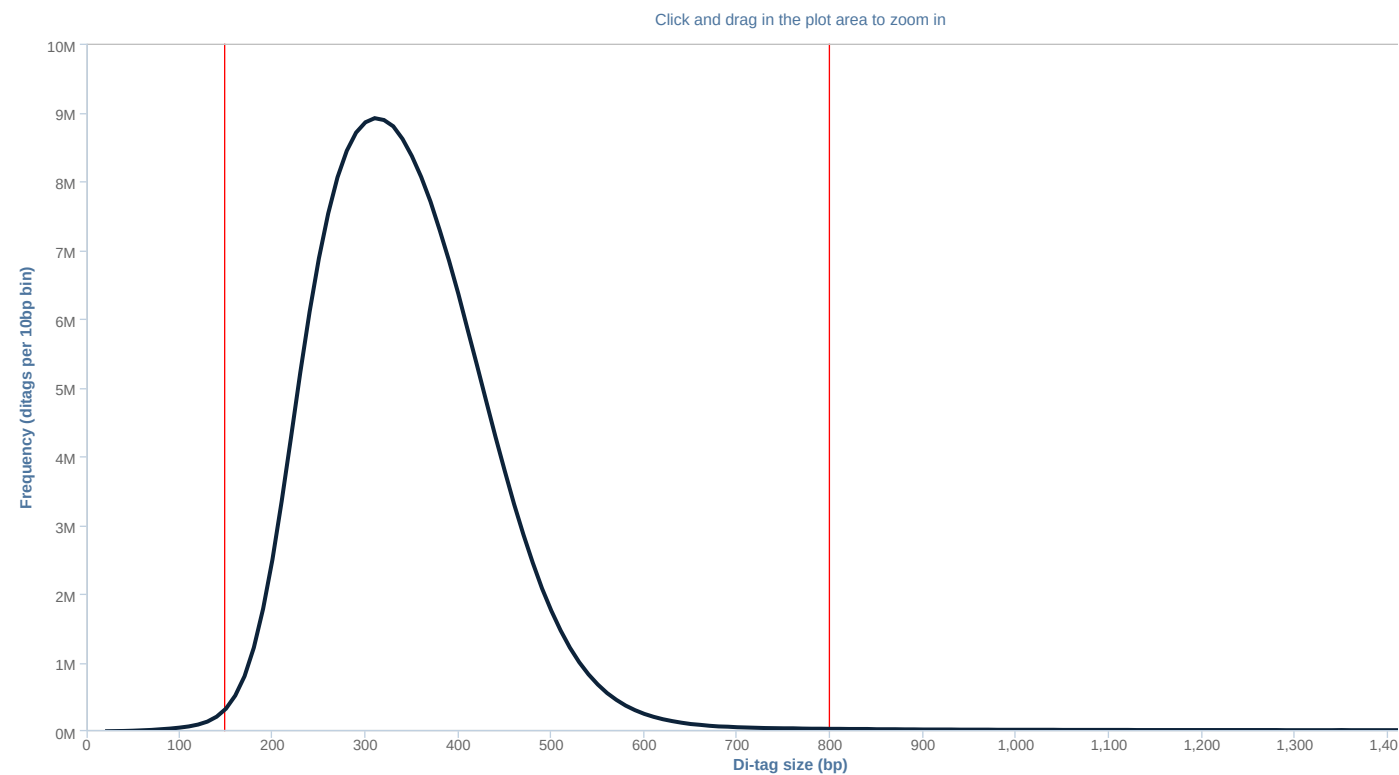


Filtering

	Di-Tag Count
Valid Pairs	157,219,580
Invalid Pairs	52,915,294
Same Circularised	3,231,704
Same Fragment Dangling Ends	3,136,114
Same Fragment Internal	2,683,921
Re-ligation	37,065,523
Contiguous Sequence	2,182,908
Wrong Size	4,615,124
Total Pairs	210,134,874



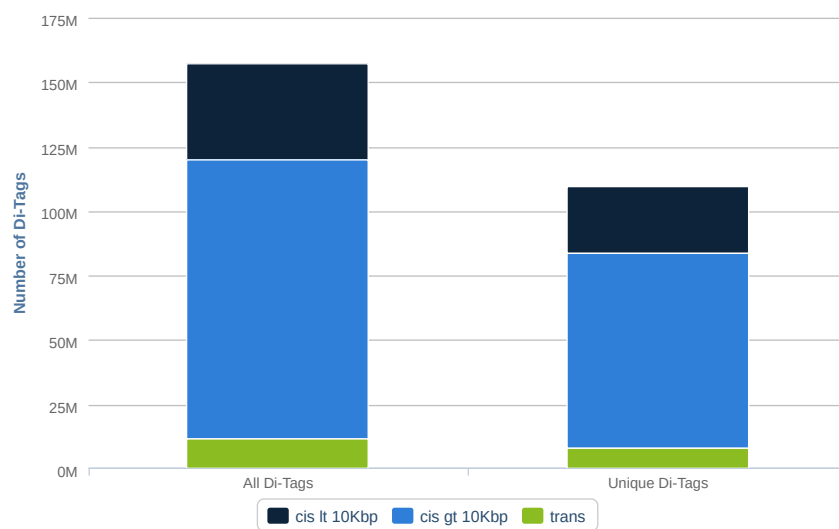
Di-tag length Distribution



De-duplication

Percentage uniques: 69.50

	All Di-Tags	Unique Di-Tags
Read Pairs	157,219,580	109,269,204
Cis-close (< 10Kbp)	37,519,662	25,455,372
Cis-far (> 10Kbp)	108,180,145	75,737,034
Trans	11,519,773	8,076,798



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](#).