



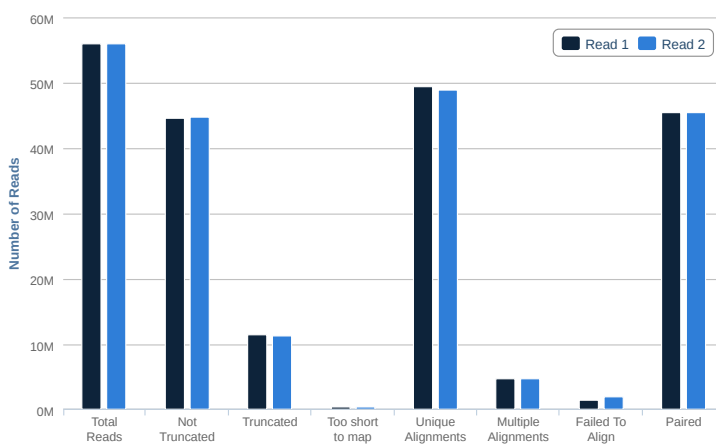
Processing Report

/gpfs/projects/bsc08/shared_projects/IJC_3Dchromatin/PROJECTS/p53_omics/HCT116_KODMSO/results/hicup
 35221050037-42_1.HCT116_KODMSO_1_2_117_000000_HCT116_KO_DMSO_BR1_HiC_V300097959_L01_CHKPE85221050037-42_2
 aTyLMJhEWD_20-57-53_28-05-2021

Truncating and Mapping

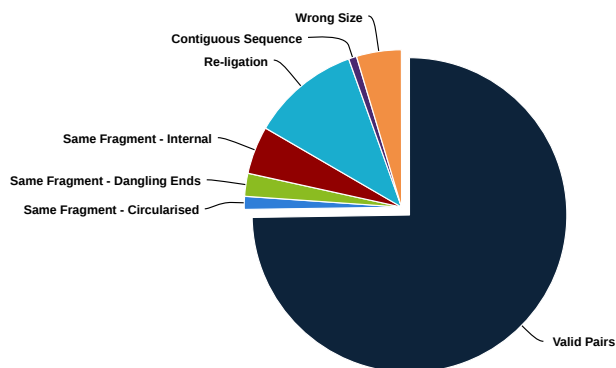
	Read 1	Read 2
Total Reads	55,980,877	55,980,877
Not Truncated	44,519,628	44,674,822
Truncated	11,461,249	11,306,055
Too short to map	359,661	348,615
Average length of truncated sequence	58.32	58.44

	Read 1	Read 2
Unique Alignments	49,378,394	48,934,933
Multiple Alignments	4,800,496	4,782,977
Failed To Align	1,442,326	1,914,352
Paired	45,351,392	45,351,392

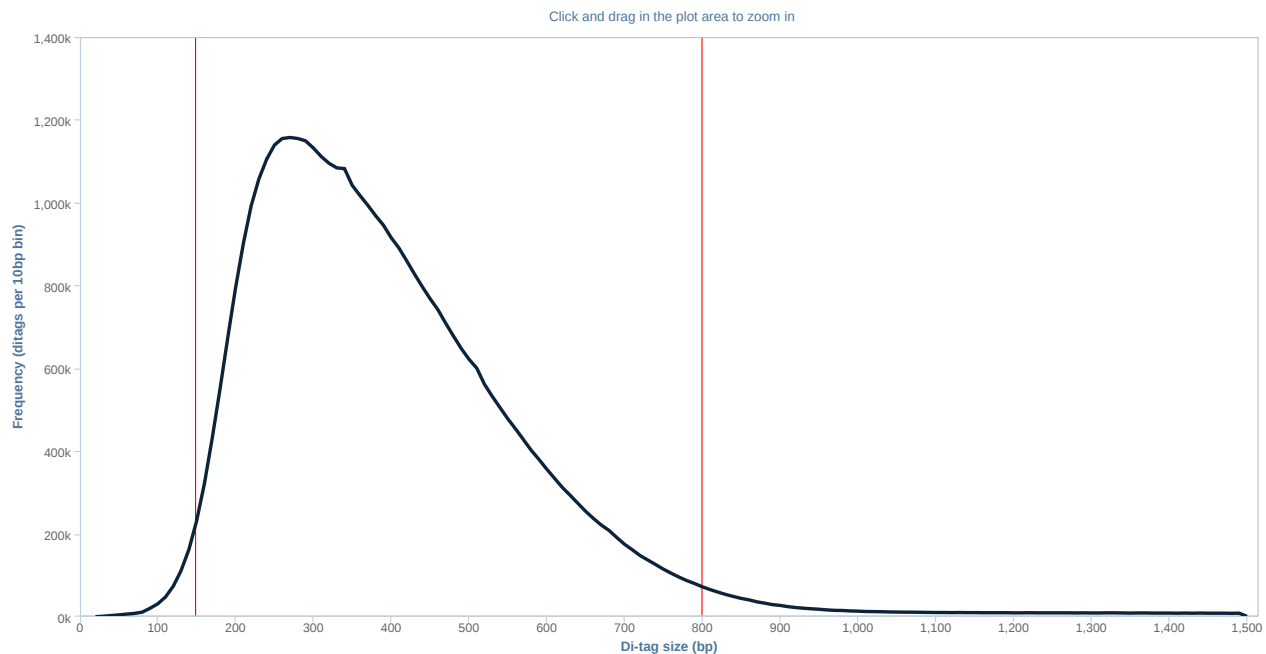


Filtering

	Di-Tag Count
Valid Pairs	33,906,025
Invalid Pairs	11,445,367
Same Circularised	605,079
Same Fragment Dangling Ends	1,074,945
Same Fragment Internal	2,224,595
Re-ligation	5,072,141
Contiguous Sequence	372,541
Wrong Size	2,096,066
Total Pairs	45,351,392



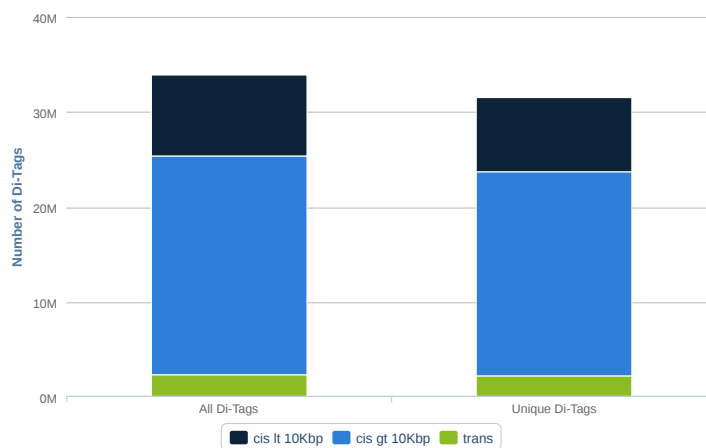
Di-tag length Distribution



De-duplication

Percentage uniques: 92.96

	All Di-Tags	Unique Di-Tags
Read Pairs	33,906,025	31,519,511
Cis-close (< 10Kbp)	8,542,876	7,802,685
Cis-far (> 10Kbp)	23,046,536	21,548,967
Trans	2,316,613	2,167,859



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](#).