



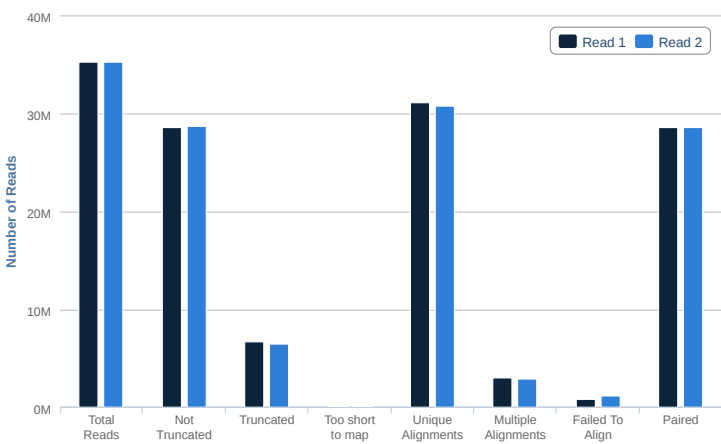
Processing Report

/gpfs/projects/bsc08/shared_projects/IJC_3Dchromatin/PROJECTS/p53_omics/HCT116_KONutlin/results/hicup
E85221050036-45_1.HCT116_KONutlin_2_2_116_000000_HCT116_KO_NUT_BR2_HiC_V300097959_L01_CHKPE85221050036-45_2
jDPaVLIHnl_19-41-35_28-05-2021

Truncating and Mapping

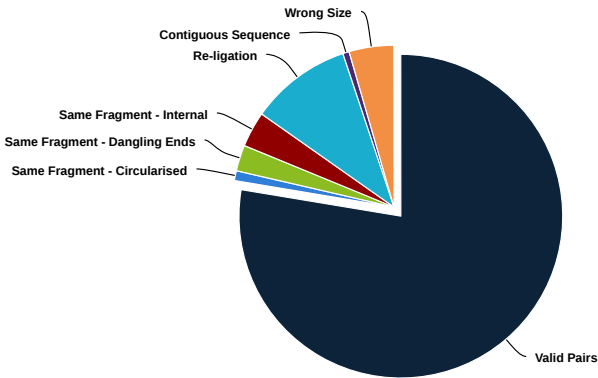
	Read 1	Read 2
Total Reads	35,173,719	35,173,719
Not Truncated	28,511,530	28,674,333
Truncated	6,662,189	6,499,386
Too short to map	192,796	185,623
Average length of truncated sequence	58.70	58.94

	Read 1	Read 2
Unique Alignments	31,064,228	30,771,284
Multiple Alignments	3,020,236	2,980,612
Failed To Align	896,459	1,236,200
Paired	28,522,413	28,522,413

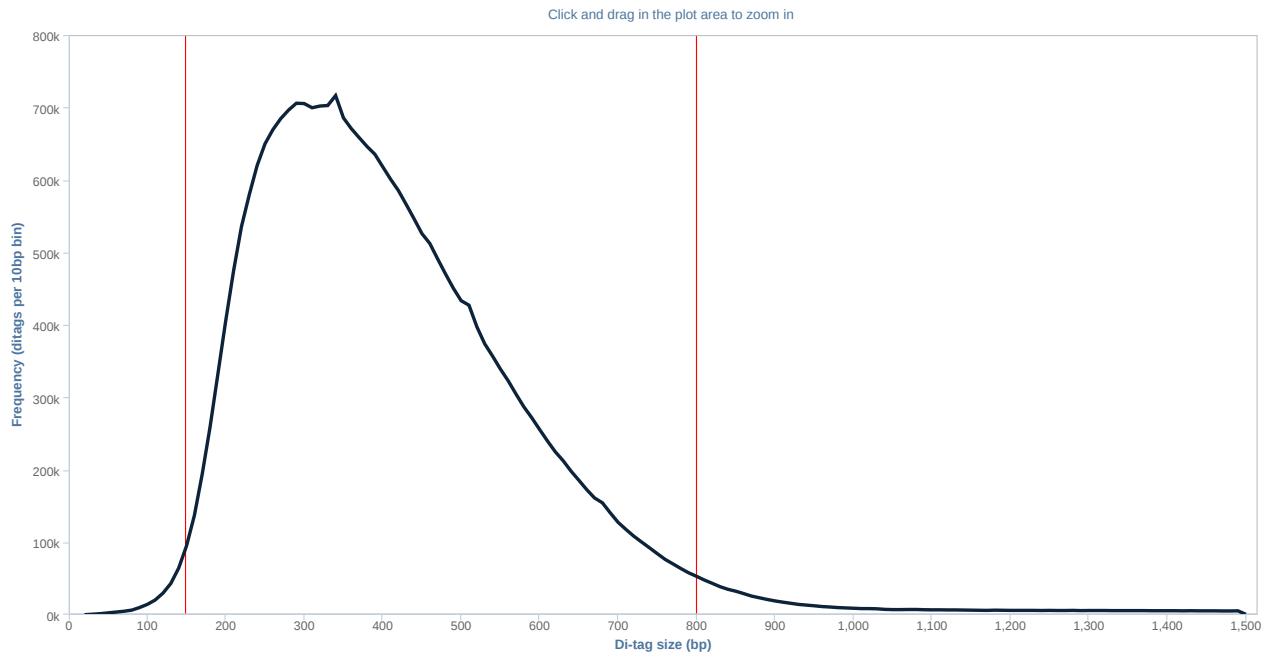


Filtering

	Di-Tag Count
Valid Pairs	22,142,115
Invalid Pairs	6,380,298
Same Circularised	280,276
Same Fragment Dangling Ends	742,416
Same Fragment Internal	1,009,380
Re-ligation	2,888,266
Contiguous Sequence	183,672
Wrong Size	1,276,288
Total Pairs	28,522,413



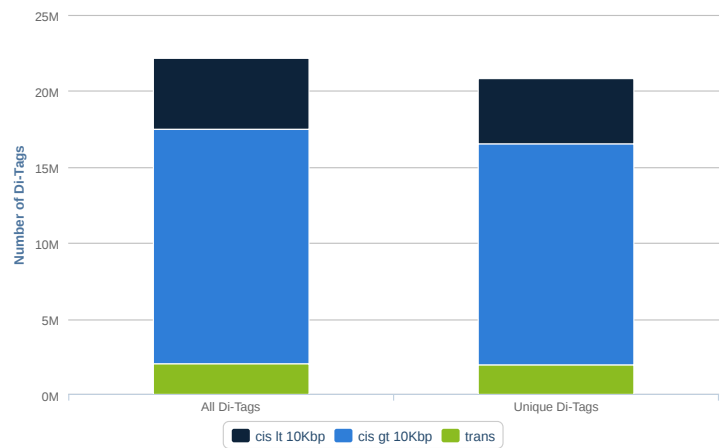
Di-tag length Distribution



De-duplication

Percentage uniques: 93.92

	All Di-Tags	Unique Di-Tags
Read Pairs	22,142,115	20,796,538
Cis-close (< 10Kbp)	4,701,956	4,304,380
Cis-far (> 10Kbp)	15,391,982	14,544,941
Trans	2,048,177	1,947,217



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](#).