



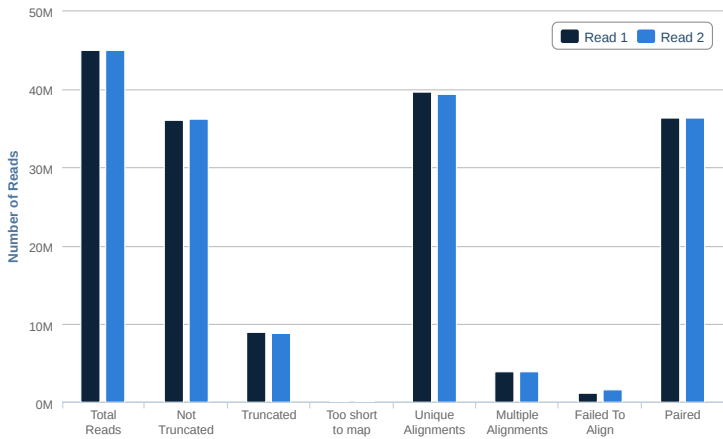
Processing Report

/gpfs/projects/bsc08/shared_projects/IJC_3Dchromatin/PROJECTS/p53_omics/HCT116_KONutlin/results/hicup
E85221050035-43_1.HCT116_KONutlin_1_2_115_000000_HCT116_KO_NUT_BR1_HiC_V300097959_L01_CHKPE85221050035-43_2
idXsgknRDk_16-33-45_28-05-2021

Truncating and Mapping

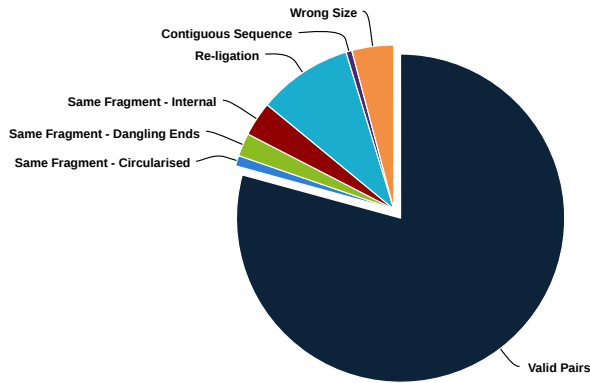
	Read 1	Read 2
Total Reads	44,960,079	44,960,079
Not Truncated	36,037,581	36,172,074
Truncated	8,922,498	8,788,005
Too short to map	253,222	247,979
Average length of truncated sequence	58.67	58.74

	Read 1	Read 2
Unique Alignments	39,630,327	39,231,848
Multiple Alignments	3,908,998	3,894,860
Failed To Align	1,167,532	1,585,392
Paired	36,307,944	36,307,944

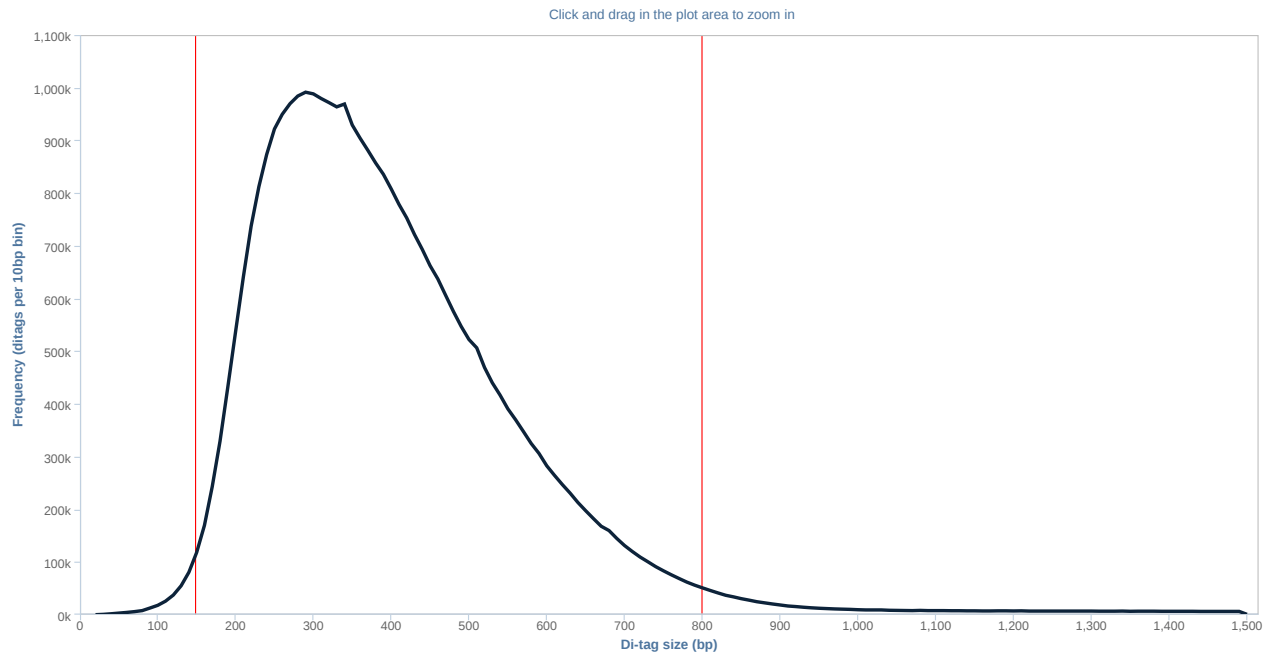


Filtering

	Di-Tag Count
Valid Pairs	28,778,690
Invalid Pairs	7,529,254
Same Circularised	373,580
Same Fragment Dangling Ends	826,628
Same Fragment Internal	1,236,049
Re-ligation	3,384,931
Contiguous Sequence	213,998
Wrong Size	1,494,068
Total Pairs	36,307,944



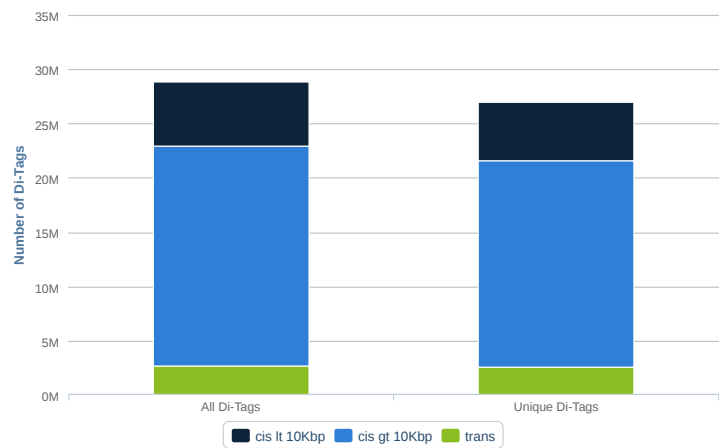
Di-tag length Distribution



De-duplication

Percentage uniques: 93.64

	All Di-Tags	Unique Di-Tags
Read Pairs	28,778,690	26,947,476
Cis-close (< 10Kbp)	5,836,773	5,367,360
Cis-far (> 10Kbp)	20,282,380	19,068,967
Trans	2,659,537	2,511,149



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](#).