## Processing Report

/gpfs/projects/bsc08/shared_projects/IJC_3Dchromatin/PROJECTS/p53_omics/HCT116_KODMSO/results/hicup
85221050038-44_1.HCT116_KODMSO_2_2_118_000000_HCT116_KO_DMSO_BR2_HiC_V300097959_L01_CHKPE85221050038-44_2
jCnCkBtDoD_23-03-06_28-05-2021

Truncating and Mapping

	Read 1	Read 2
Total Reads	39,216,359	39,216,359
Not Truncated	31,624,066	31,721,351
Truncated	7,592,293	7,495,008
Too short to map	243,243	234,662
Average length of truncated sequence	58.26	58.45

	Read 1	Read 2
Unique Alignments	34,597,515	34,270,802
Multiple Alignments	3,444,733	3,417,561
Failed To Align	930,868	1,293,334
Paired	31,852,371	31,852,371
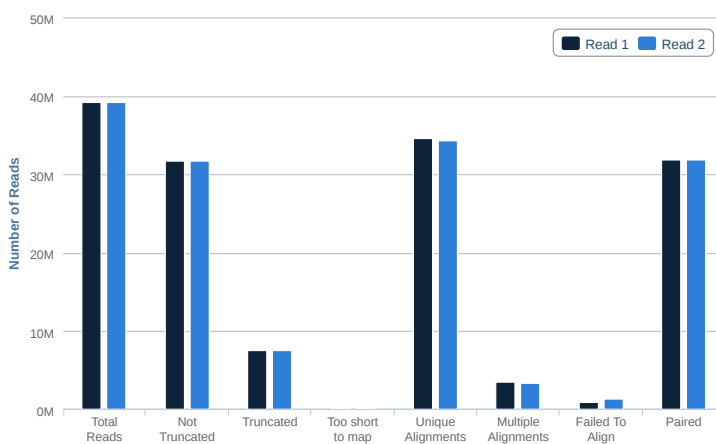
Filtering

	Di-Tag Count
Valid Pairs	23,902,100
Invalid Pairs	7,950,271
Same Circularised	422,770
Same Fragment Dangling Ends	840,934
Same Fragment Internal	1,174,551
Re-ligation	3,966,674
Contiguous Sequence	273,979
Wrong Size	1,271,363
Total Pairs	31,852,371
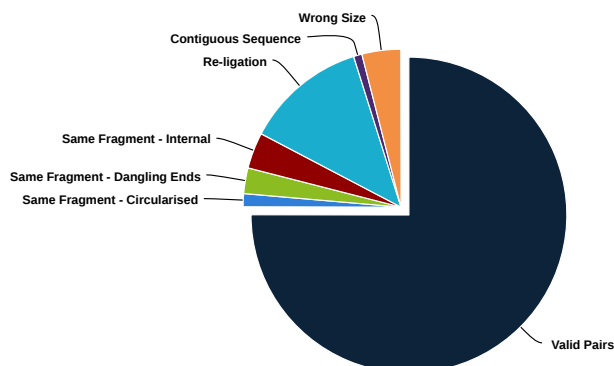
Di-tag length Distribution
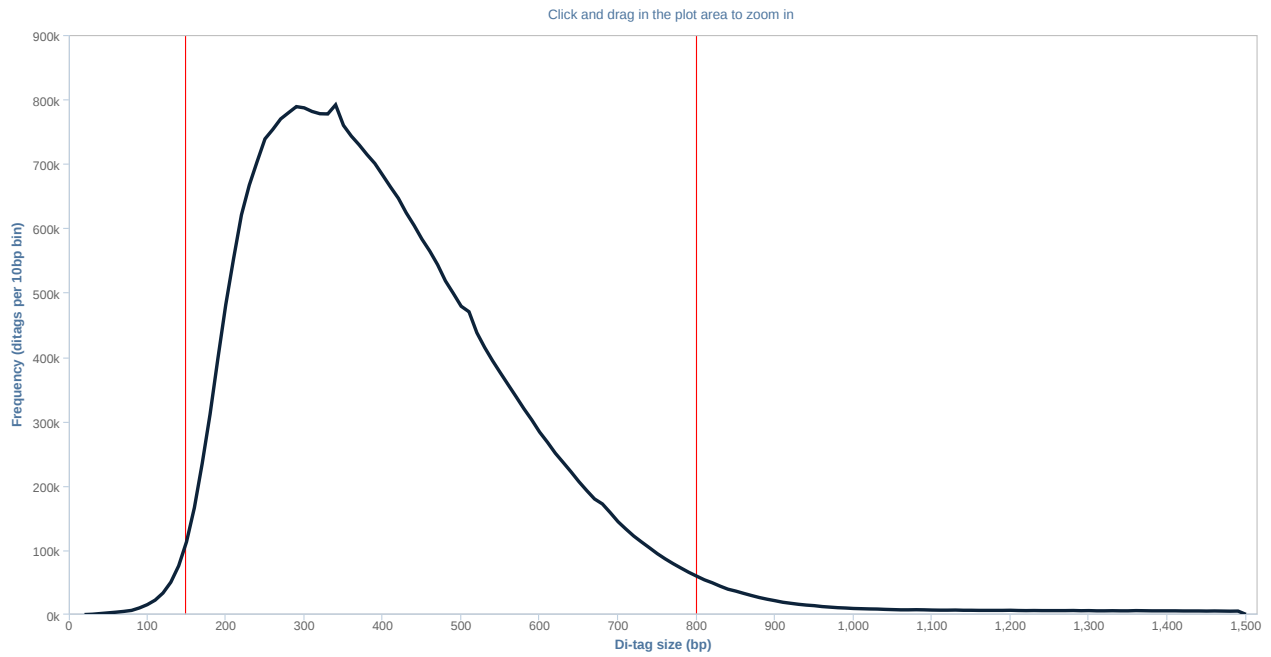
De-duplication

Percentage uniques: 93.11

	All Di-Tags	Unique Di-Tags
Read Pairs	23,902,100	22,254,194
Cis-close (< 10Kbp)	6,004,748	5,473,598
Cis-far (> 10Kbp)	16,314,436	15,295,729
Trans	1,582,916	1,484,867
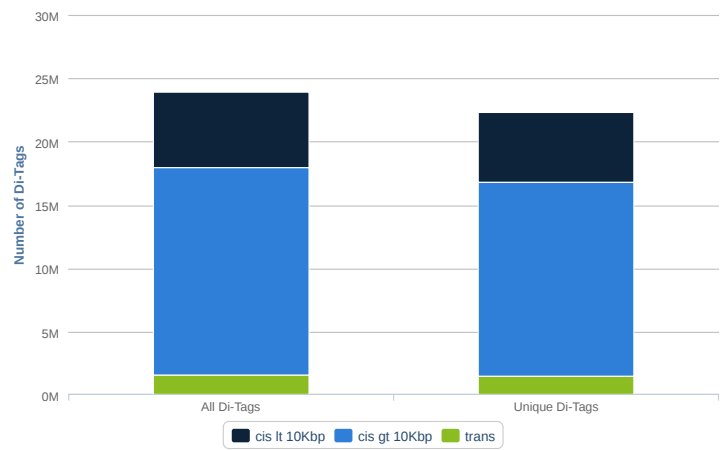
Analysis produced by **HiCUP** (0.7.2) - a tool for mapping and performing quality control on Hi-C data.

Report graphs rendered using jQuery and Highcharts.