# HiCUP

Processing Report

/gpfs/projects/bsc08/shared_projects/IJC_3Dchromatin/PROJECTS/p53_omics/HCT116_WTDMSO/results/hicup
85221050034-49_1.HCT116_WTDMSO_2_2_114_000000_HCT116_WT_DMSO_BR2_HiC_V300097959_L01_CHKPE85221050034-49_2

AhNFXOisYx_10-28-02_28-05-2021

Truncating and Mapping

	Read 1	Read 2
Total Reads	40,734,405	40,734,405
Not Truncated	40,733,546	40,733,520
Truncated	859	885
Too short to map	415,095	399,037
Average length of truncated sequence	50.63	52.34

	Read 1	Read 2
Unique Alignments	52,377,739	51,868,424
Multiple Alignments	5,007,254	4,991,227
Failed To Align	1,399,254	1,940,654
Paired	48,123,210	48,123,210
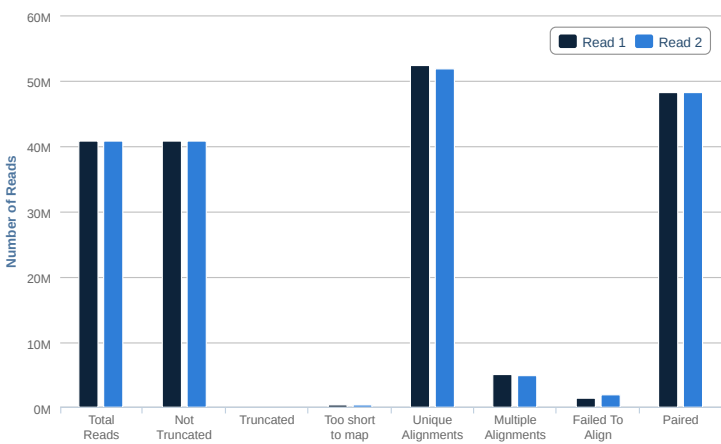
Filtering

	Di-Tag Count
Valid Pairs	36,062,782
Invalid Pairs	12,060,428
Same Circularised	712,911
Same Fragment Dangling Ends	1,072,098
Same Fragment Internal	1,914,774
Re-ligation	6,019,343
Contiguous Sequence	405,416
Wrong Size	1,935,886
Total Pairs	48,123,210
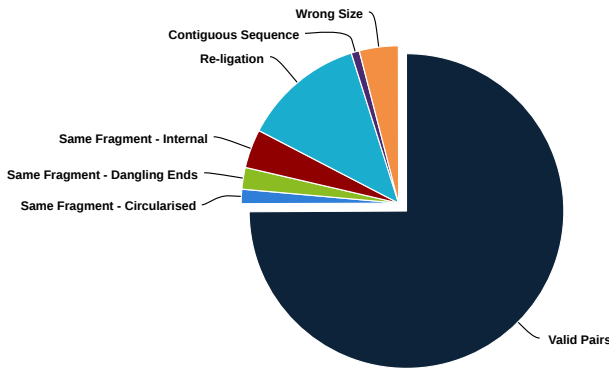
Di-tag length Distribution
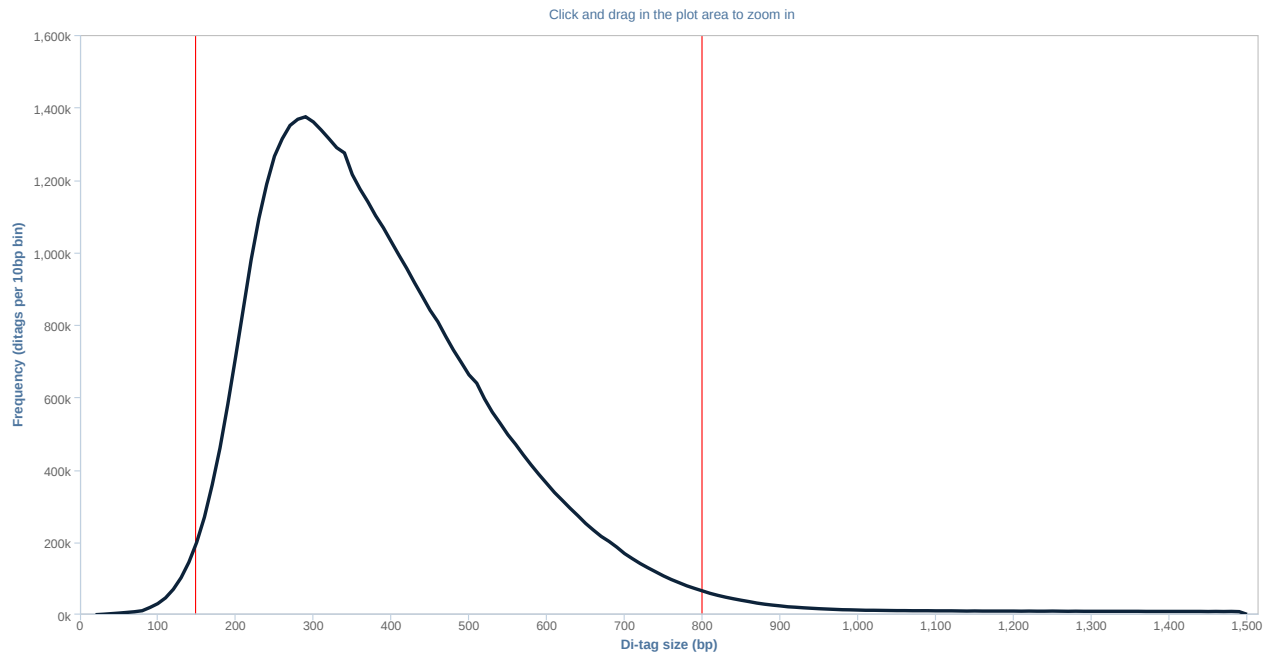
De-duplication

Percentage uniques: 93.11

	All Di-Tags	Unique Di-Tags
Read Pairs	36,062,782	33,579,660
Cis-close (< 10Kbp)	8,835,745	8,109,325
Cis-far (> 10Kbp)	25,064,216	23,446,140
Trans	2,162,821	2,024,195
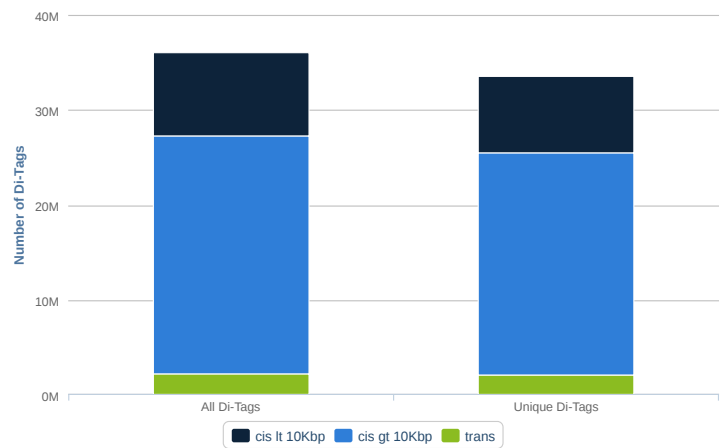
Analysis produced by **HiCUP** (0.7.2) - a tool for mapping and performing quality control on Hi-C data.

Report graphs rendered using jQuery and Highcharts.