# Processing Report

/gpfs/projects/bsc08/shared_projects/IJC_3Dchromatin/PROJECTS/p53_omics/HCT116_WTDMSO/results/hicup
85221050033-47_1.HCT116_WTDMSO_1_2_113_000000_HCT116_WT_DMSO_BR1_HiC_V300097959_L01_CHKPE85221050033-47_2

hHKIWAHdiv_09-58-38_28-05-2021

Truncating and Mapping

	Read 1	Read 2
Total Reads	38,121,969	38,121,969
Not Truncated	29,862,030	29,887,639
Truncated	8,259,939	8,234,330
Too short to map	263,976	261,857
Average length of truncated sequence	58.15	58.19

|	Read 1	Read 2
Unique Alignments	33,759,184	33,471,640
Multiple Alignments	3,184,174	3,172,002
Failed To Align	914,635	1,216,470
Paired	31,042,557	31,042,557
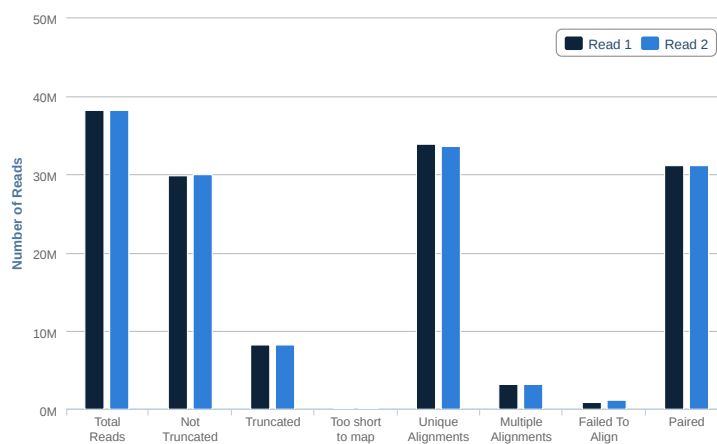
Filtering

|	Di-Tag Count
Valid Pairs	24,166,802
Invalid Pairs	6,875,755
Same Circularised	472,206
Same Fragment Dangling Ends	446,945
Same Fragment Internal	1,022,766
Re-ligation	3,481,560
Contiguous Sequence	266,562
Wrong Size	1,185,716
Total Pairs	31,042,557
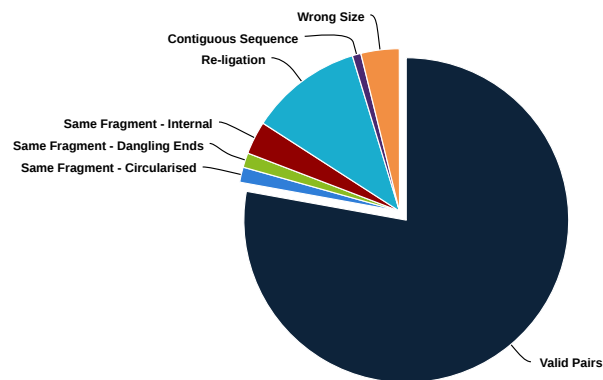
Di-tag length Distribution

Click and drag in the plot area to zoom in
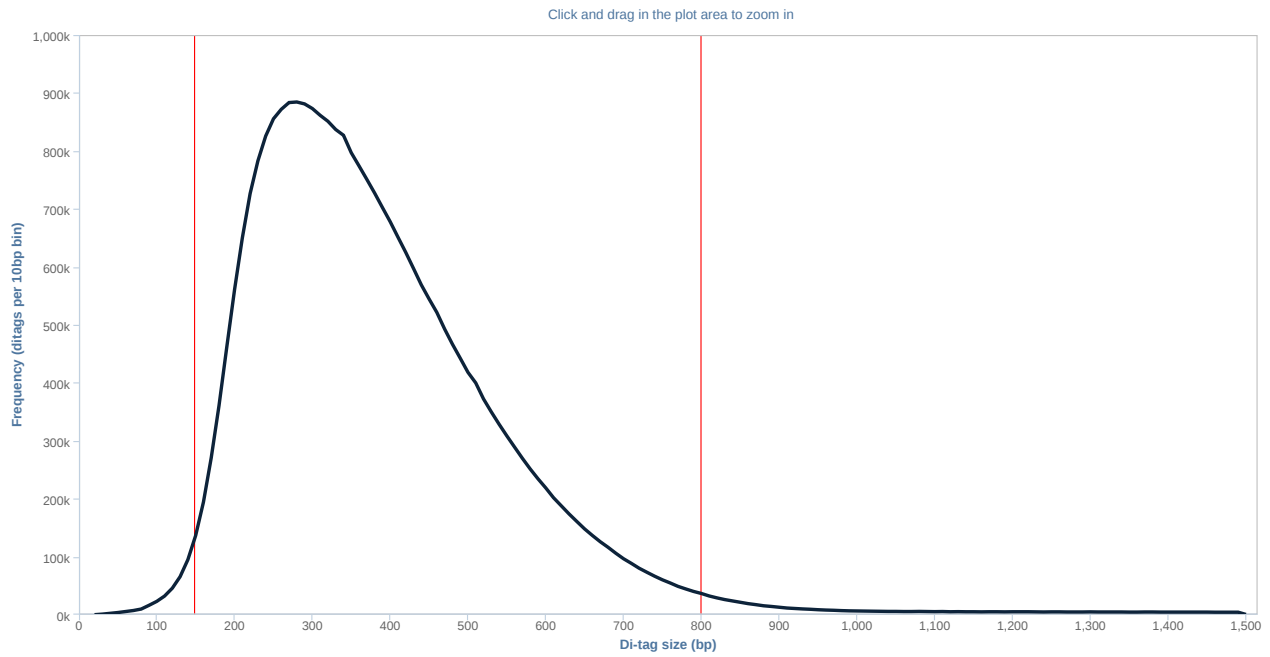
De-duplication

Percentage uniques: 93.22

	All Di-Tags	Unique Di-Tags
Read Pairs	24,166,802	22,527,545
Cis-close (< 10Kbp)	6,009,240	5,545,187
Cis-far (> 10Kbp)	16,598,490	15,518,163
Trans	1,559,072	1,464,195
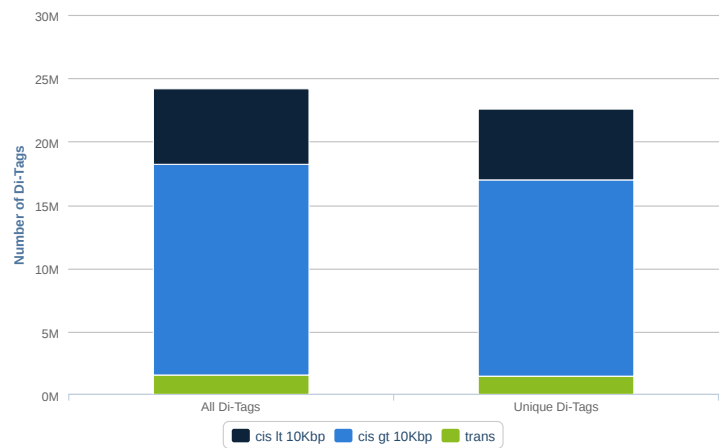
Analysis produced by **HiCUP** (0.7.2) - a tool for mapping and performing quality control on Hi-C data.

Report graphs rendered using jQuery and Highcharts.