# HiCUP

Processing Report

/gpfs/projects/bsc08/bsc08471/PCHiC/p53/HiCUP/MOCK2KO/lane3_NoIndex_L003_R2_1

IziVFKVKCa_15-24-52_25-04-2020

## Truncating and Mapping

	Read 1	Read 2
Total Reads	238,997,995	238,997,995
Not Truncated	221,594,521	220,935,772
Truncated	17,403,474	18,062,223
Too short to map	2,521,312	2,703,612
Average length of truncated sequence	30.62	30.46

	Read 1	Read 2
Unique Alignments	210,092,040	212,427,796
Multiple Alignments	15,228,891	15,377,475
Failed To Align	11,155,752	8,489,112
Paired	190,543,734	190,543,734
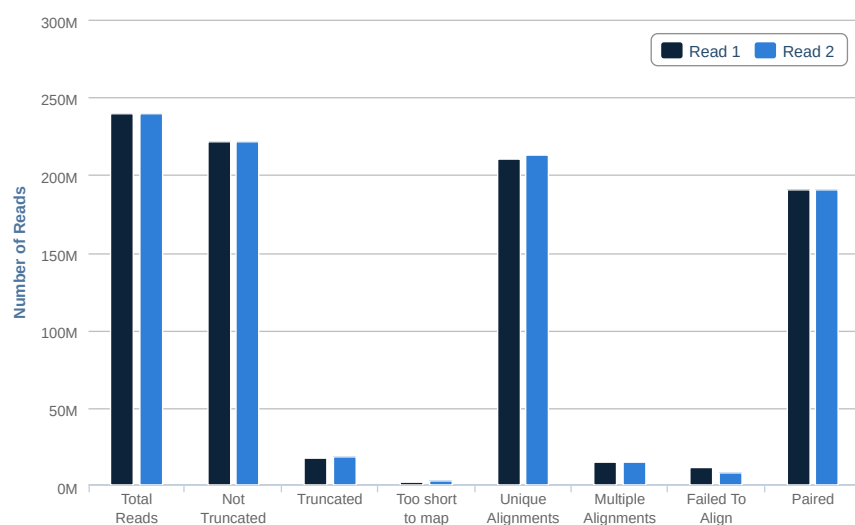
Filtering

	Di-Tag Count
Valid Pairs	143,277,381
Invalid Pairs	47,266,353
Same Circularised	3,247,979
Same Fragment Dangling Ends	2,575,495
Same Fragment Internal	2,529,251
Re-ligation	33,418,568
Contiguous Sequence	1,960,735
Wrong Size	3,534,325
Total Pairs	190,543,734
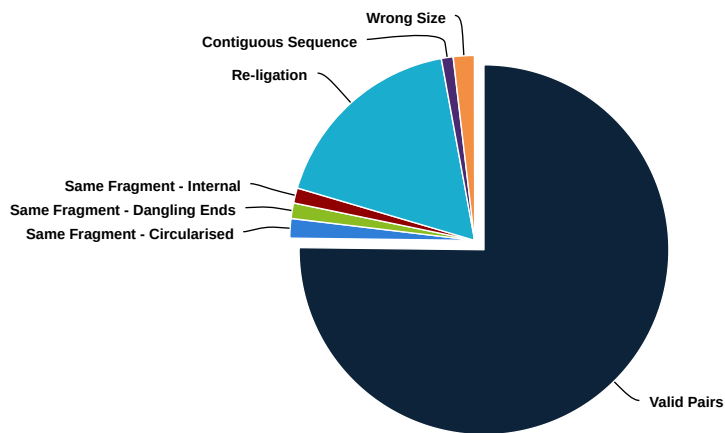
Di-tag length Distribution

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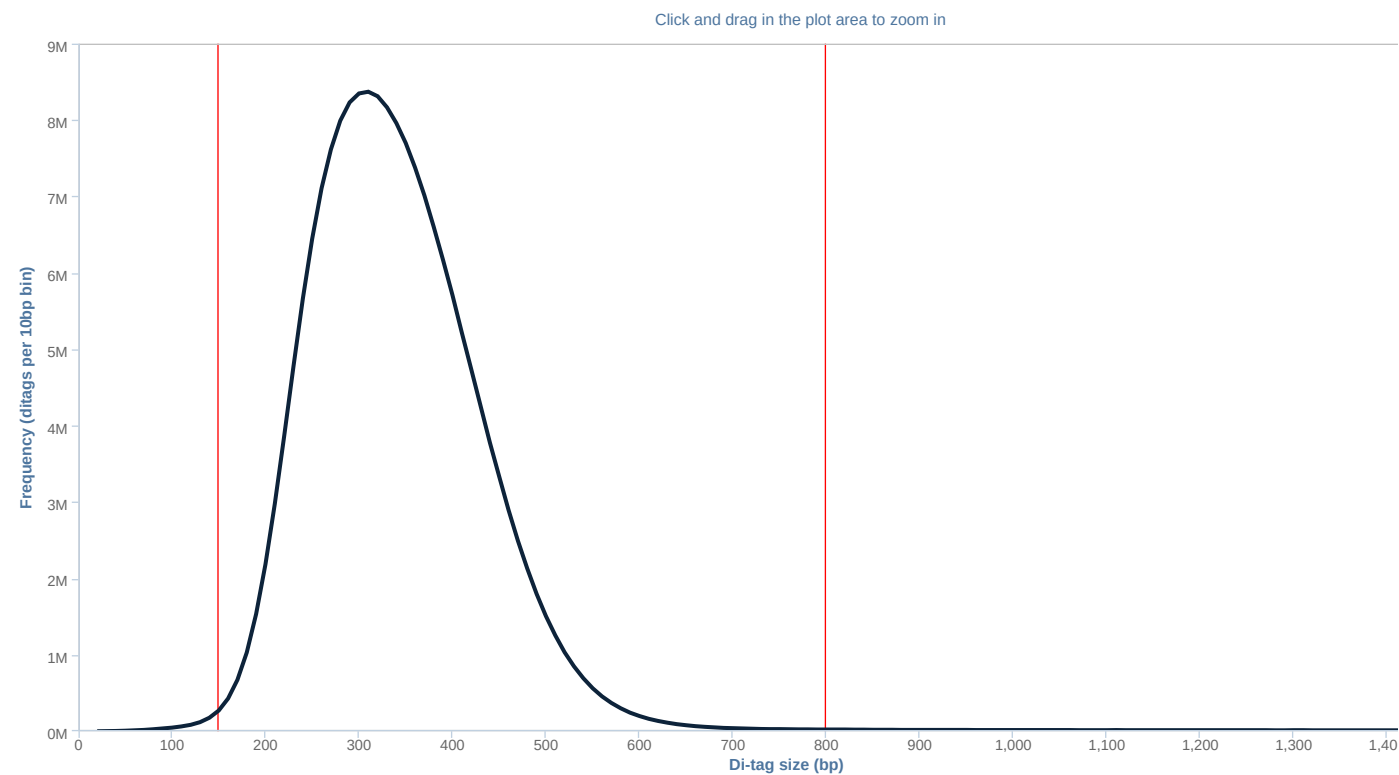
De-duplication

Percentage uniques: 72.25

	All Di-Tags	Unique Di-Tags
Read Pairs	143,277,381	103,520,686
Cis-close (< 10Kbp)	34,667,708	24,536,025
Cis-far (> 10Kbp)	96,962,386	70,512,261
Trans	11,647,287	8,472,400
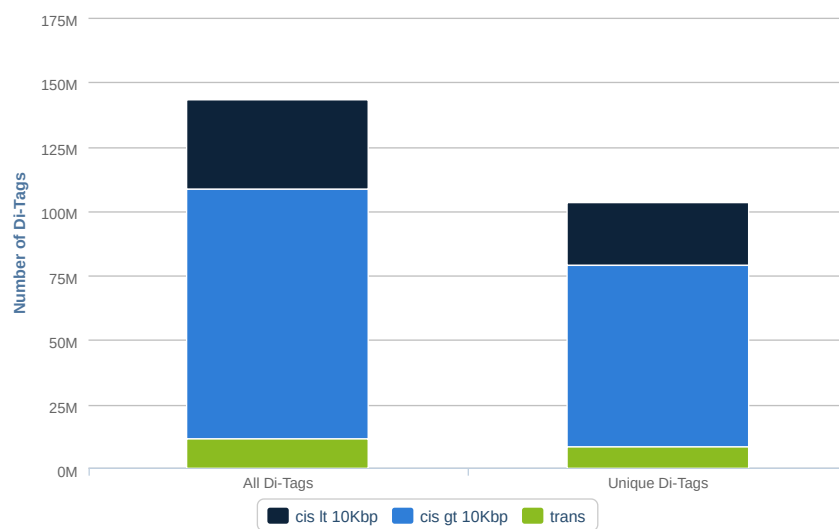
Analysis produced by **HiCUP** (0.7.2) - a tool for mapping and performing quality control on Hi-C data.

Report graphs rendered using jQuery and Highcharts.

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