



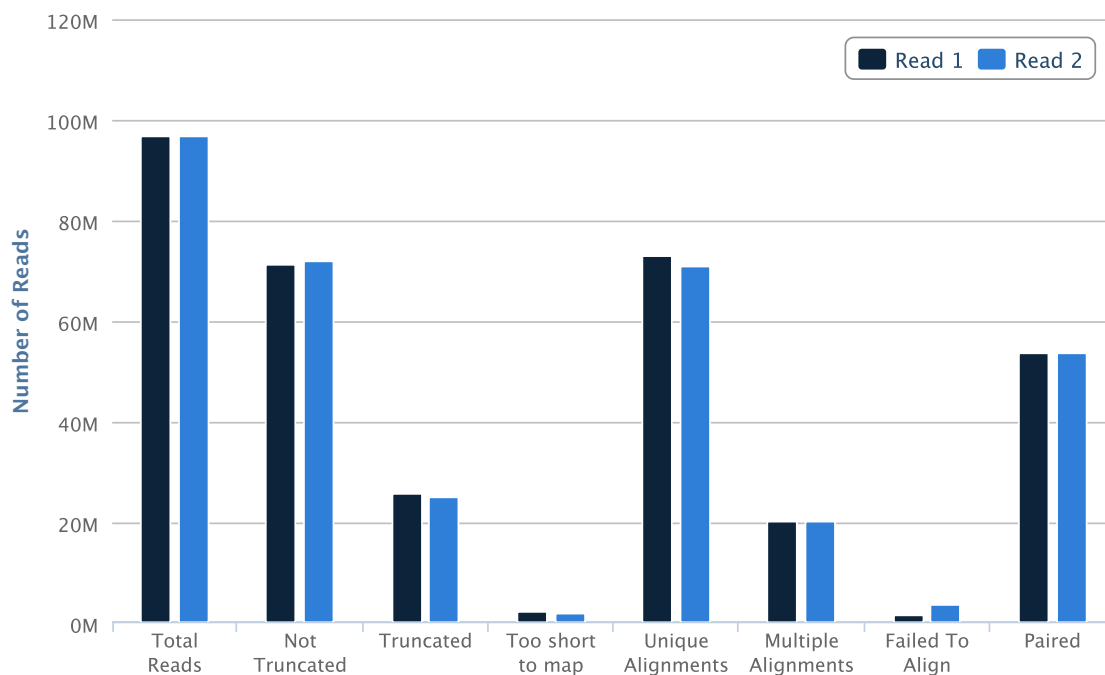
HAEC_R1_2
13-59-13_11-09-2017

Processing Report

Truncating and Mapping

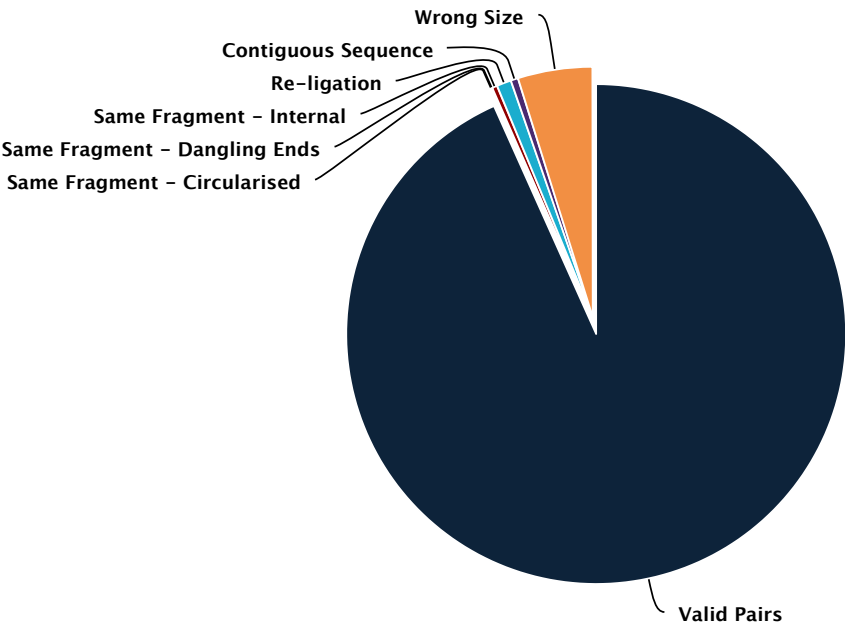
	Read 1	Read 2
Total Reads	96,871,628	96,871,628
Not Truncated	71,068,057	71,862,396
Truncated	25,803,571	25,009,232
Too short to map	2,066,801	2,020,406
Average length of truncated sequence	53.92	53.72

	Read 1	Read 2
Unique Alignments	72,917,498	70,909,258
Multiple Alignments	20,263,180	20,309,902
Failed To Align	1,624,149	3,632,062
Paired	53,541,864	53,541,864

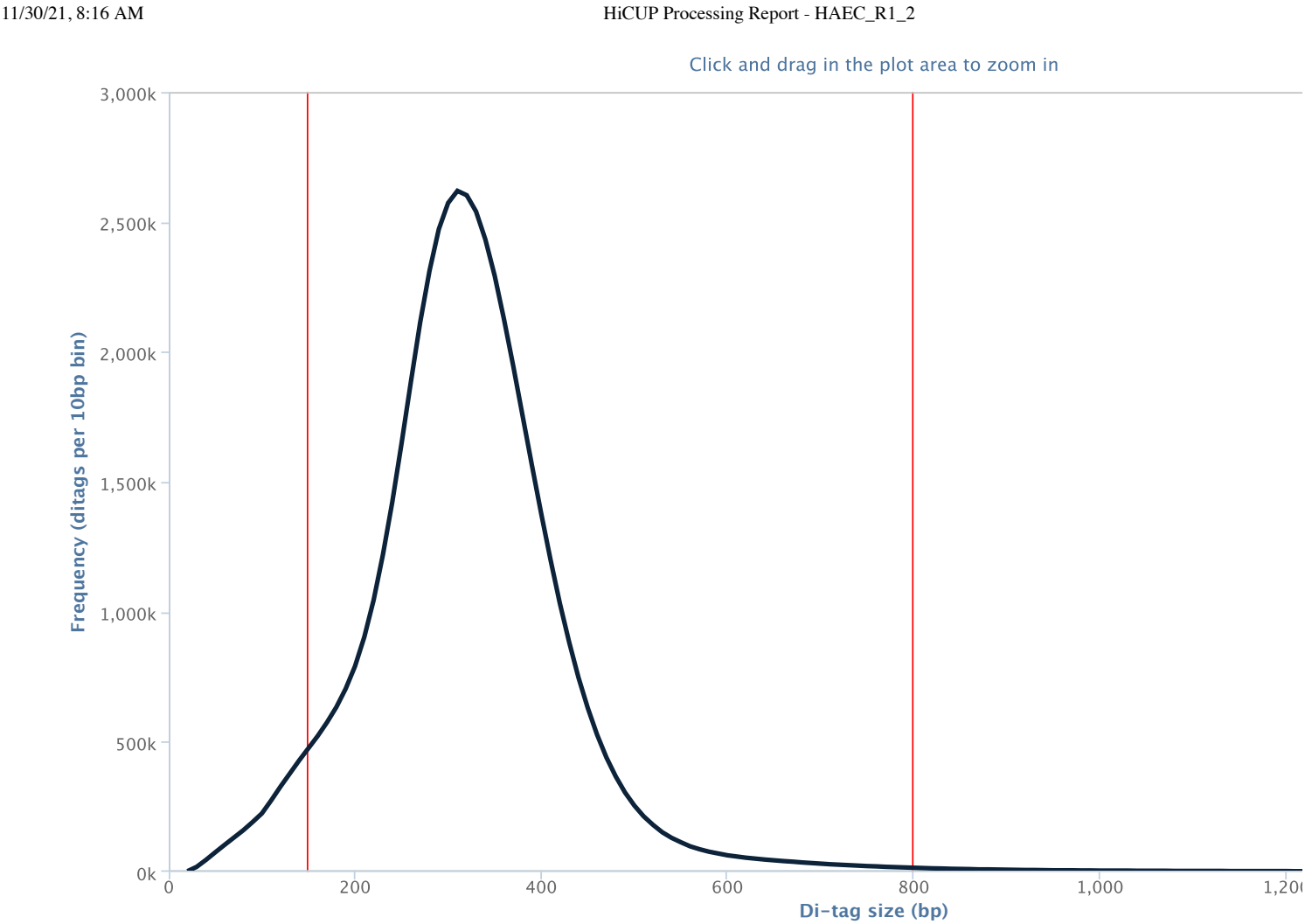


Filtering

	Di-Tag Count
Valid Pairs	49,962,317
Invalid Pairs	3,579,547
Same Circularised	25,505
Same Fragment Dangling Ends	29,973
Same Fragment Internal	181,177
Re-ligation	503,105
Contiguous Sequence	254,024
Wrong Size	2,585,763
Total Pairs	53,541,864



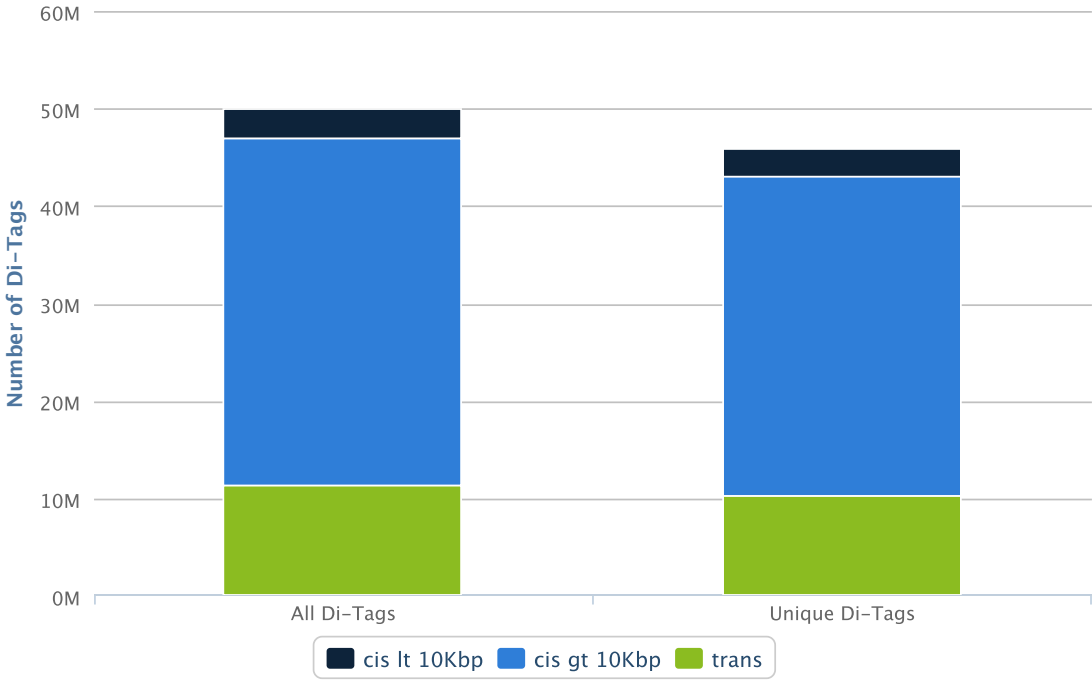
Di-tag length Distribution



De-duplication

Percentage uniques: 91.65

	All Di-Tags	Unique Di-Tags
Read Pairs	49,962,317	45,791,879
Cis-close (< 10Kbp)	3,080,996	2,822,436
Cis-far (> 10Kbp)	35,645,267	32,683,082
Trans	11,236,054	10,286,361



Analysis produced by [HiCUP](#) (0.5.9) - a tool for mapping and performing quality control on Hi-C data.

Report graphs rendered using [jQuery](#) and [Highcharts](#).

