# Processing Report

**/gpfs/projects/bsc08/bsc08471/PCHiC/p53/HiCUP/MOCK1WT/lane3_NoIndex_L003_R1_2**

## Truncating and Mapping

|  | Read 1 | Read 2 |
|---|---|---|
| **Total Reads** | 237,206,273 | 237,206,273 |
| **Not Truncated** | 215,855,743 | 217,284,462 |
| **Truncated** | 21,350,530 | 19,921,811 |
| **Too short to map** | 3,168,487 | 2,869,826 |
| **Average length of truncated sequence** | 30.43 | 30.63 |

|  | Read 1 | Read 2 |
|---|---|---|
| **Unique Alignments** | 202,774,198 | 201,074,276 |
| **Multiple Alignments** | 21,448,640 | 21,245,398 |
| **Failed To Align** | 9,814,948 | 12,016,773 |
| **Paired** | 179,267,942 | 179,267,942 |
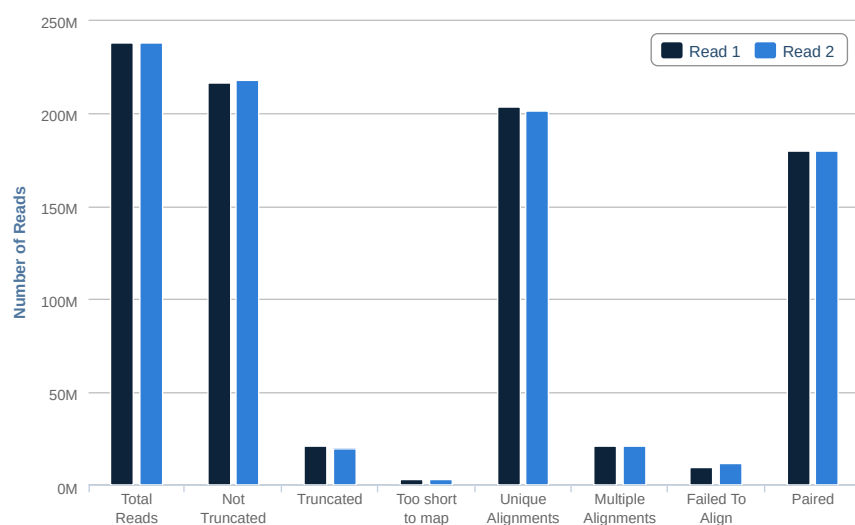


## Filtering

|  | Di-Tag Count |
|---|---|
| **Valid Pairs** | 137,856,713 |
| **Invalid Pairs** | 41,411,229 |
| **Same Circularised** | 3,505,164 |
| **Same Fragment Dangling Ends** | 2,228,245 |
| **Same Fragment Internal** | 2,361,660 |
| **Re-ligation** | 26,707,387 |
| **Contiguous Sequence** | 1,861,146 |
| **Wrong Size** | 4,747,627 |
| **Total Pairs** | 179,267,942 |
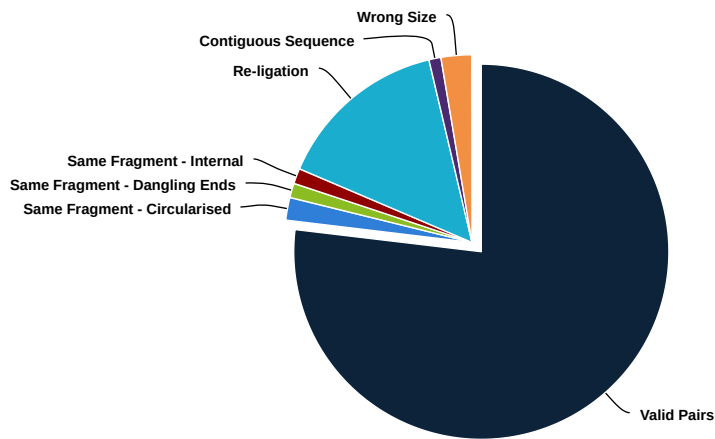
## Di-tag length Distribution

Click and drag in the plot area to zoom in
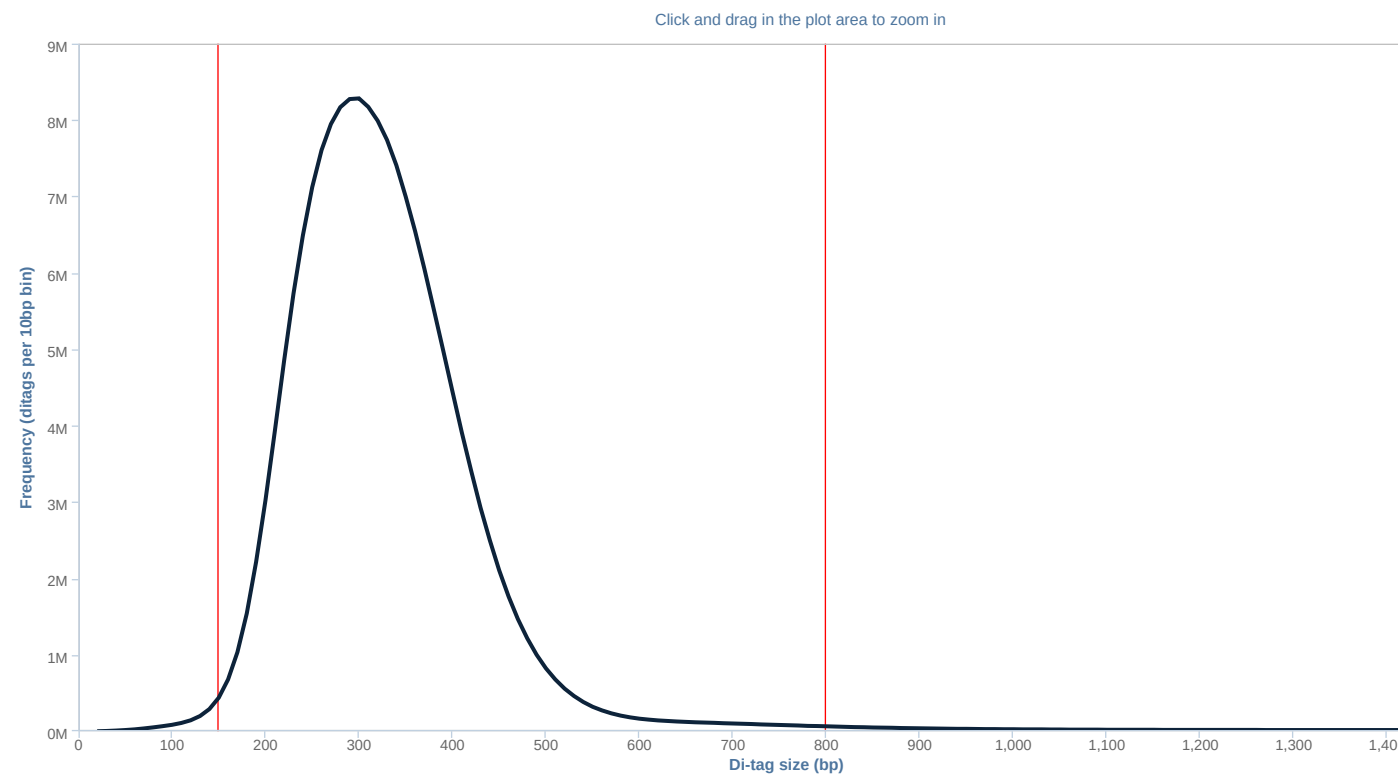


## De-duplication

### Percentage uniques: 79.98

|  | All Di-Tags | Unique Di-Tags |
|---|---|---|
| **Read Pairs** | 137,856,713 | 110,258,841 |
| **Cis-close (< 10Kbp)** | 35,372,353 | 27,768,184 |
| **Cis-far (> 10Kbp)** | 92,857,185 | 74,762,080 |
| **Trans** | 9,627,175 | 7,728,577 |
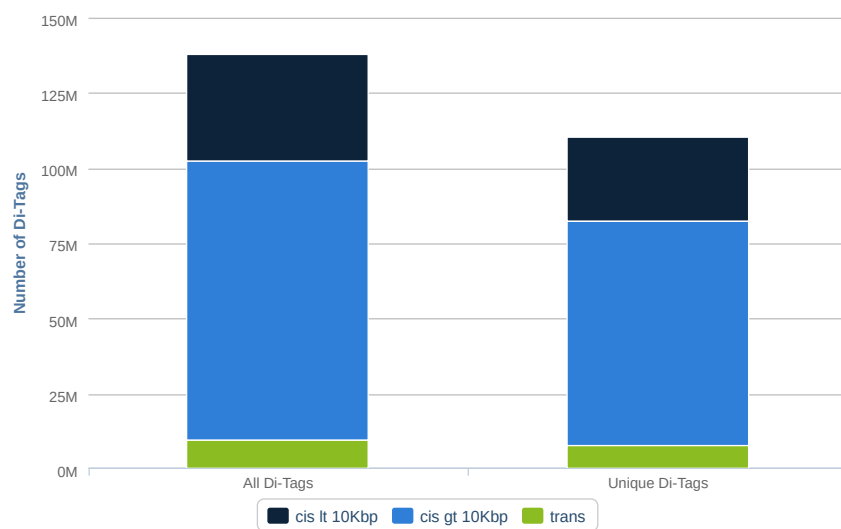
Analysis produced by **HiCUP** (0.7.2) - a tool for mapping and performing quality control on Hi-C data.

Report graphs rendered using jQuery and Highcharts.