

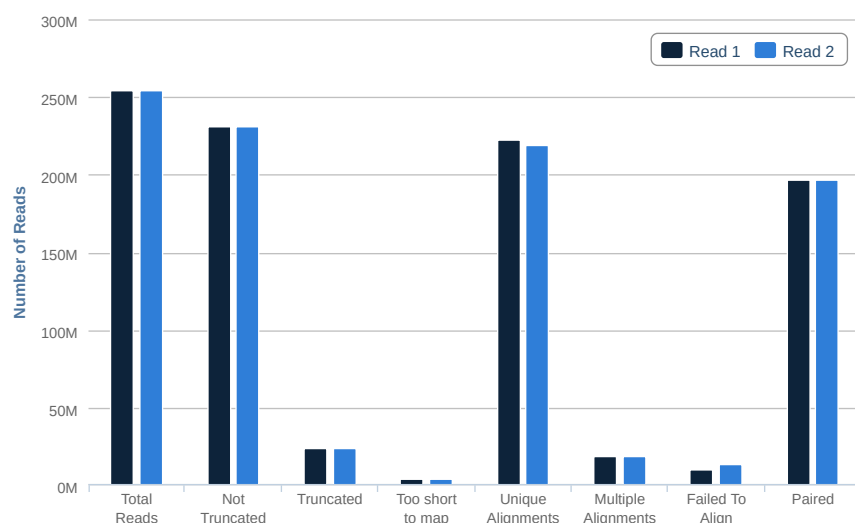
Processing Report

/gpfs/projects/bsc08/bsc08471/PCHiC/p53/HiCUP/NUT2KO/lane3223_HCT116-_-Nutlin3a_2BR-103.1_NoIndex_L006_R1_2
eBMxKSmZwu_15-24-52_25-04-2020

Truncating and Mapping

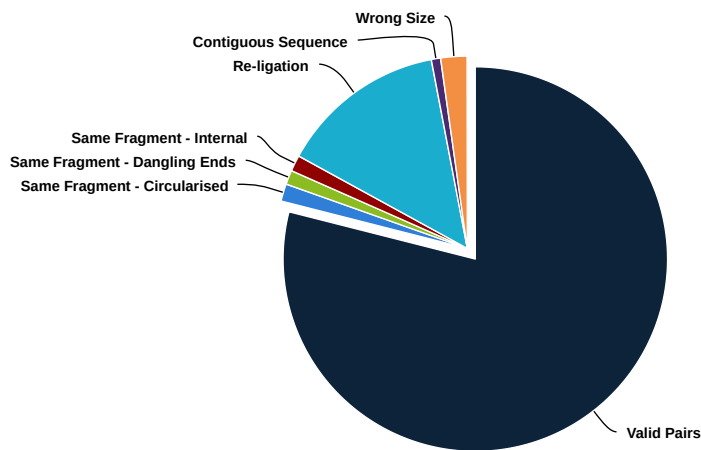
| | Read 1 | Read 2 |
|--------------------------------------|-------------|-------------|
| Total Reads | 254,321,968 | 254,321,968 |
| Not Truncated | 230,545,257 | 231,022,910 |
| Truncated | 23,776,711 | 23,299,058 |
| Too short to map | 3,770,422 | 3,618,186 |
| Average length of truncated sequence | 30.17 | 30.27 |

| | Read 1 | Read 2 |
|---------------------|-------------|-------------|
| Unique Alignments | 222,383,852 | 219,040,487 |
| Multiple Alignments | 18,258,963 | 18,010,077 |
| Failed To Align | 9,908,731 | 13,653,218 |
| Paired | 196,262,561 | 196,262,561 |

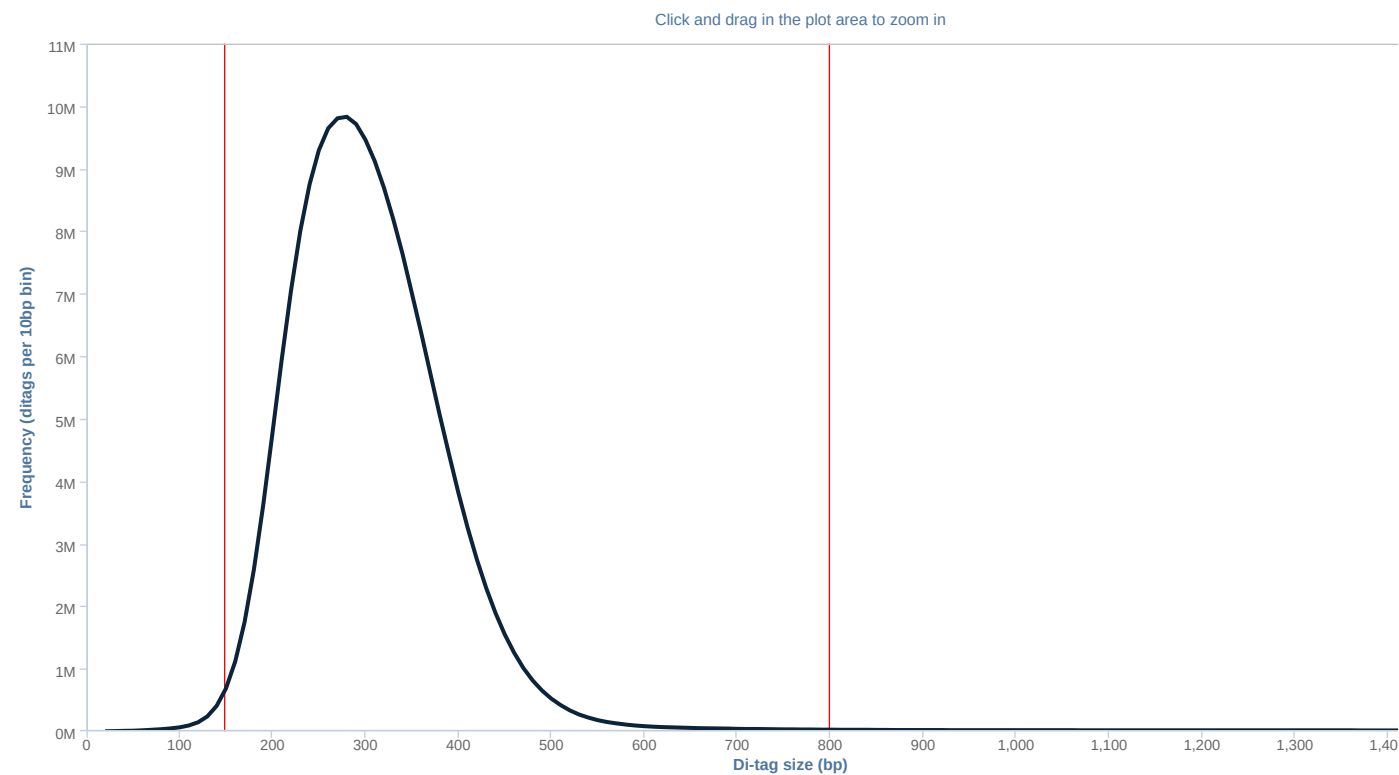


Filtering

| | Di-Tag Count |
|-----------------------------|--------------|
| Valid Pairs | 154,978,896 |
| Invalid Pairs | 41,283,665 |
| Same Circularised | 2,896,538 |
| Same Fragment Dangling Ends | 2,339,752 |
| Same Fragment Internal | 2,652,751 |
| Re-ligation | 27,498,222 |
| Contiguous Sequence | 1,545,528 |
| Wrong Size | 4,350,874 |
| Total Pairs | 196,262,561 |



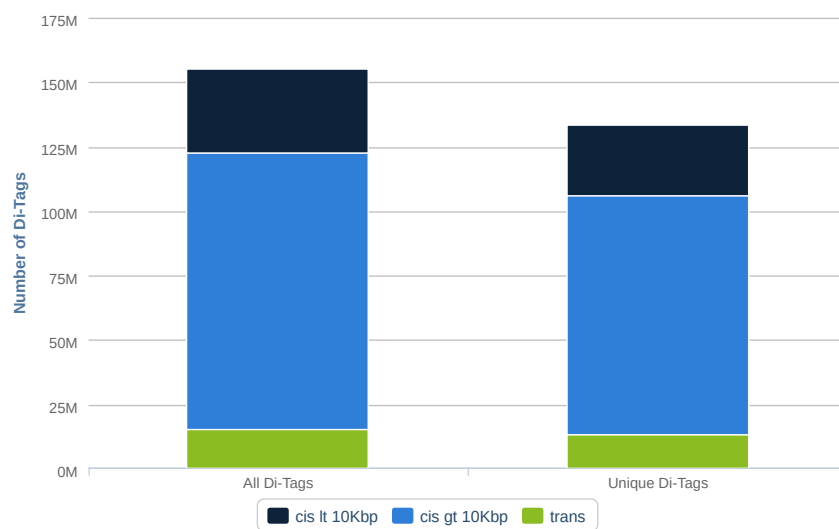
Di-tag length Distribution



De-duplication

Percentage uniques: 86.02

| | All Di-Tags | Unique Di-Tags |
|---------------------|-------------|----------------|
| Read Pairs | 154,978,896 | 133,305,826 |
| Cis-close (< 10Kbp) | 32,615,575 | 27,359,854 |
| Cis-far (> 10Kbp) | 107,050,681 | 92,673,429 |
| Trans | 15,312,640 | 13,272,543 |



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](#).