**Table 1 Features of Hi-C reads with human datasets**

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| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Datasets | Read pairs | Percentage of unmapped reads (%) | Percentage of reads with PCR duplication (%) | ICI rate (%) | Accessibility | N50 (Mb) | N20 (Mb) | N10 (Mb) |
| Arima V2  NA12878-CEU | 352,429,304 | 20.9 | 6.8 | 12.7 | 0.596 | 47.9 | 96.3 | 130.3 |
| Arima V2  NA24385-AJ | 413,162,798 | 24.8 | 6.1 | 16.2 | 0.529 | 47.2 | 104.9 | 141.9 |
| Arima V1  NA12878-CEU | 415,173,112 | 28.6 | 10.1 | 18.5 | 0.328 | 28.2 | 63.1 | 100.0 |

*Note*: For each dataset, we present the individual accessibility metrics — the unmapped rate, the PCR duplication rate, and the ICI rate, using Equation 2 to compute the final accessibility. We also present the standard N10, N20, and N50 measures. Hi-C, high-throughput chromosome conformation capture; ICI, inter-chromosomal interaction; PCR, polymerase chain reaction.