# Table S1. Summary of raw and length-filtered MinION data used for assembly of taro contigs.

|  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | Group 1 | Group2 | Group3 | Group4 | Group5 | Group6 | Group7 | Group8 | Group9 | Group10 | Group11 | Length filtered |
| # Reads | 788598 | 1234265 | 1104412 | 988318 | 776269 | 1385620 | 612958 | 1017288 | 789164 | 1681009 | 1924576 | 5801129 |
| Mean L | 4295 | 5461 | 5437 | 6239 | 6379 | 5090 | 5936 | 6549 | 6098 | 5954 | 2416 | 9328 |
| Median L | 2232 | 2915 | 4968 | 4425 | 3651 | 3131 | 3934 | 5069 | 4436 | 4619 | 1189 | 7996 |
| Min L | 5 | 5 | 5 | 18 | 5 | 5 | 73 | 5 | 76 | 5 | 5 | 3500 |
| Max L | 717766 | 2108768 | 66617 | 126766 | 113814 | 95192 | 73341 | 80184 | 78113 | 76935 | 78976 | 147912 |

# Legend: Sequencing data were obtained from n=14 MinIONs cells. Each group represents a single cell or data from a cell that stopped prematurely (n = 3). A total of 12302477 reads were generated to produce 63657010728 nucleotides of sequence data. Of those 6501305 were filtered for short length (<3500 nt) and 43 for long length (> 150 Kb). The remaining 5801129 sequences produced 54118492459 nucleotides of data used for the nanopore genome assembly (~23x coverage @ 1C).