**Table S2:** Comparison between the previously reported *Artocarpus heterophyllus* sequence and BARI Kanthal-3 sequence

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| --- | --- | --- |
| **Parameters** | **Previously reported *A. heterophyllus* sequence** | **BARI Kanthal-3 sequence**  |
| 1. No. of scaffolds
 | * 1. M scaffolds totaling 982 Mb
 | 218,562 scaffolds totaling 843 Mb |
| 1. Size of N50s in the scaffolds
 | 548 kb with the longest being 3.1 Mb | 425 kb and with the longest being 2.6 Mb |
| 1. GC content (%)
 | 32.9 % | 34.10%. |
| 1. BUSCO results
 | 1369 (95%) complete BUSCOs where 932 (64.7%) BUSCO genes were “complete single-copy”, 437 (30.3%) were “complete duplicated”, 15 (1%) were “fragmented”, and 56 (4%) were “missing” | 1569 (97.2%) were complete BUSCOs in which 1094 (67. 8%) BUSCO genes were “complete single-copy”, 475 (29.4%) were “complete duplicated”, 21 (1.3%) were “fragmented”, and 24 (1.5%) were “missing” |
| 1. Genome size
 | The estimated genome size was 1.01 Gbp | The estimated genome size was 1.04 Gbp |