**Table S1:** Summary statistics for fosmid and BAC assemblies

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|  | **Fosmid\_19** | **BAC\_156A12** |
| Genotype | ICMP 451 | Tift 23DB |
| Sequencing technology | Roche 454 GLS FX | Roche 454 GLS FX |
| Insert size | 35 kb | 90 kb |
| Average read length | 181 bp | 303 bp |
| Read coverage (X-fold) | 23 | 68 |
| Number of contigs in assembly | 2 | 15 |
| Largest contig | 31,571 bp | 47,002 bp |
| Smallest contig | 6952 bp | 364 bp |