Table S1. Sequencing statistics for UA44 and BY250 before and after Canu-Correction. Canu-corrected reads were used to assemble the genomes with Flye.

Additional Sequencing Statistics

	Total Bases (Gb)	Number of Reads	Mean Read Length	Median Read Length	N50	Coverage
UA44	7.44	2,673,711.0	2,783.80	1,564.00	4,732.0	74.22
Corrected	3.88	597,106.00	6,498.10	4,190.0	8,082.0	38.69
BY250	12.45	4,054,501.0	3,070.00	1,540.00	6,116.0	124.12
Corrected	4.10	344,582.0	11885.10	10,929.0	15109.00	40.84