

Table S4. Statistics of the cp genome assemblies of the 18 sweetpotato cultivars and the *I. triloba* line NCNSP-0323. Contigs were constructed with CANU for Nanopore reads and with SPAdes for Illumina reads. Scaffolds were constructed by anchoring the SPAdes contigs according to the mapping position on the Tanzania cp genome.

Samples	Contigs					Scaffold		Final/polished	
	Number	Size	N50	Min	Max	Number	Size	Number	Size
Tanzania †	-	-	-	-	-	1	161,092	1	161,274
Beauregard	197	207,483	11,829	151	42,933	1	161,198	1	161,198
Dimbuka-Bukulula	156	207,158	6,206	131	39,838	1	161,392	1	161,392
Ejumula	77	168,947	42,510	137	42,933	1	161,303	1	161,303
Huarmeyano	138	196,380	9,992	131	39,840	1	161,392	1	161,392
Magabali	114	184,750	24,420	137	42,308	1	161,429	1	161,429
Mugande	110	182,827	18,137	131	42,506	1	161,393	1	161,393
NASPOT 1	92	174,794	23,994	137	42,310	1	161,393	1	161,393
NASPOT 10 O/f ‡	128	192,961	14,442	131	42,506	1	161,393	1	161,393
NASPOT 10 O/s §	165	217,712	12,330	137	42,510	1	161,393	1	161,393
NASPOT 11	127	193,751	9,997	131	42,491	1	161,428	1	161,428
NASPOT 5	91	175,407	27,308	137	42,932	1	161,509	1	161,509
NASPOT 5/58	122	190,087	23,994	137	42,510	1	161,393	1	161,393
NASPOT 7	76	169,016	42,510	137	42,933	1	161,303	1	161,303
NK259L	193	229,272	6,269	131	42,491	1	161,428	1	161,428
New Kawogo	111	186,122	24,420	137	42,806	1	161,429	1	161,429
Resisto	184	221,669	5,895	131	41,409	1	161,375	1	161,375
SPK004	163	214,907	12,330	131	42,506	1	161,393	1	161,393
Wagabolige	101	182,269	27,654	137	42,931	1	161,339	1	161,339
NCNSP-0323	128	205,788	6,328	131	36,181	1	161,360	1	161,360

† reference cp genome constructed from the Nanopore sequence data.

‡ sample collected from field.

§ sample collected from screen house.