

Additional file 3 – Sequencing and *de novo* assembly metrics of chloroplast genomes of four *Urochloa* species

Species	Reads (bp)	N50	Minimum size (bp)	Maximum size (bp)	Mean size (bp)	Contigs	Total (bp)	cpDNA assembly size (bp)	% recovery of assembled genome*
<i>U. ruziziensis</i>	20,211,010,488	1,704	200	57,461	754	382,380	288,171,438	136,733	98.5%
<i>U. brizantha</i>	8,643,705,720	505	200	86,745	464	380,899	176,721,916	134,165	96.5%
<i>U. humidicola</i>	8,476,910,040	485	200	80,478	448	476,044	213,428,620	138,213	99.45%
<i>U. decumbens</i>	9,018,811,776	491	200	38,791	455	408,401	185,680,658	129,056	92.89%

*Size of *de novo* assemblies when compared to assemblies using *P. virgatum* cpDNA as a reference