

Supplementary Table 10. The prediction of gene structures of the *C. goeringii*.

Gene set		Protein coding gene number	Average gene length (bp)	Average CDS length (bp)	Average exon per gene	Average exon length (bp)	Average intron length (bp)
<i>De novo</i>	AUGUSTUS	44,936	5,153.97	725.87	2.98	243.95	2,241.61
	SNAP	73,894	7,133.34	546.41	4.52	120.75	1,868.64
Homolog	<i>A. thaliana</i>	2,497	4,967.47	873.01	3.03	287.97	2,015.32
	<i>O. sativa</i>	77,993	4,610.49	860.92	2.82	305.1	2,058.24
	<i>S. bicolor</i>	69,437	5,163.83	906.94	3.07	295.48	2,057.07
	<i>Z. mays</i>	93,101	3,872.65	700.79	2.62	267.84	1,962.21
	<i>G. elata</i>	61,836	4,612.66	820.03	2.92	280.39	1,970.61
	<i>P. equestris</i>	353,965	1,455.54	447.39	1.57	285.75	1,782.27
	MAKER	30,897	14,860.41	970.03	4.70	206.52	2,699.87
RNA-seq	2,711,296	1,125.36	258.32	1.44	179.61	1,978.41	