

Table S3 Genome completeness evaluation based on Reads alignment, CEGs and BUSCOs

Type 1	Total reads	Mapped reads	Mapped(%)	Properly mapped reads	Properly mapped(%)	
Reads alignment analysis	180,095,649	174,858,550	97.09	160,219,616	90.51	
Type 2	Number of CEGs present in <i>V. bracteatum</i>	Percentage of 458 CEGs present in assembly (%)	Number of 248 highly conserved CEGs present in assembly	Percentage of 248 highly conserved CEGs present (%)		
Core gene integrity assessment	431	94.10%	202	81.45%		
Type 3	Complete BUSCOs(C)	Complete and single-copy BUSCOs(S)	Complete and duplicated BUSCOs(D)	Fragmented BUSCOs(F)	Missing BUSCOs(M)	Total Lineage BUSCOs
BUSCO assessment	1468 (90.95%)	1397 (86.56%)	71 (4.40%)	16 (0.99%)	130 (8.05%)	1,614