Table S1 Sequencing data used for genome assembly and annotation of *V. bracteatum*

Sequencing type	platform	Library size(bp)	Data (Gb)	Depth (x)	Q20(%)	Q30(%)	Application
Fragment library	Illumina HiSeq 4000	350 (sequenced)	26.51	45.76	97.64	93.49	Genome survey and assessment
		350	3	4.24			
Third generation library	Pacbio	20Kb	57	100x			
Nanopore reads	Nanopore platform	20,000	76.41	114.60			Nanopore sequencing analysis of fine map
Hi-C reads	Illumina HiSeq 4000	300–700	67.25				Chromosome assembly