

Haplotype-resolved genome assembly of the tetraploid Youcha tree *Camellia meiocarpa* Hu

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Table S1. Statistics of the RNA-seq data

Sample	TotalReads	TotalBases	MappedReads	MappedBases	MappedReadsRate
Adult Leaf	165479778	24821966700	117180721	17577108150	0.7081
Stem	145488426	21823263900	102317357	15347603550	0.7033
Bark	136641270	20496190500	98417503	14762625450	0.7203
Young Fruit	137345480	20601822000	94535785	14180367750	0.6883
Shoot	167744664	25161699600	94244062	14136609300	0.5618
Full-length RNA-seq	62796	133279315	47703	100295656	0.7597

Table S2. Assessments of gene structure annotations using BUSCO and OMArk

Program	BUSCO	OMArk
A	97.3	98.03
B	96.7	96.99
C	96.4	97.29
D	97.8	97.63