

Supplementary Materials

Table S1 Overview of the tea leaves metagenomic sequencing

| Sample | Raw Reads | Clean Reads | Clean Base(G) | Error Rate(%) |
|---------------|-----------|-------------|---------------|---------------|
| M1-1 | 52880364 | 52001448 | 7.80 | 0.03 |
| M1-2 | 58706344 | 57655662 | 8.65 | 0.03 |
| M1-3 | 59114616 | 58008120 | 8.70 | 0.03 |
| M2-1 | 55994064 | 54941134 | 8.24 | 0.03 |
| M2-2 | 41541042 | 40792498 | 6.12 | 0.03 |
| M2-3 | 47635590 | 46977510 | 7.05 | 0.03 |
| M3-1 | 47603320 | 46802894 | 7.02 | 0.03 |
| M3-2 | 47587670 | 46660894 | 7.00 | 0.03 |
| M3-3 | 43976934 | 42789208 | 6.42 | 0.03 |
| Total/Average | 455039944 | 446629368 | 67.00 | 0.03 |

Note: M1: Control; M2: The Mg concentration is 0.4m mol/L; M3: The Mg concentration is 0.8 mmol/L

Table S2 Efficiency statistics of transcriptome data compared with reference genomes

| Sample | Total Reads | Reads mapped | Unique mapped | Multi mapped | Read1 mapped | Read2 mapped | '+' mapped | '-' mapped |
|--------|-------------|------------------|------------------|----------------|------------------|------------------|------------------|------------------|
| M1-1 | 46802894 | 41082667(87.78%) | 38496896(82.25%) | 2585771(5.52%) | 19424164(41.50%) | 19072732(40.75%) | 19267507(41.17%) | 19229389(41.09%) |
| M1-2 | 46660894 | 40138661(86.02%) | 37624398(80.63%) | 2514263(5.39%) | 19000175(40.72%) | 18624223(39.91%) | 18831651(40.36%) | 18792747(40.28%) |
| M1-3 | 42789208 | 37701908(88.11%) | 35349290(82.61%) | 2352618(5.50%) | 17766723(41.52%) | 17582567(41.09%) | 17693883(41.35%) | 17655407(41.26%) |
| M2-1 | 52001448 | 45341865(87.19%) | 42480283(81.69%) | 2861582(5.50%) | 21415440(41.18%) | 21064843(40.51%) | 21255910(40.88%) | 21224373(40.81%) |
| M2-2 | 57655662 | 50225362(87.11%) | 47036125(81.58%) | 3189237(5.53%) | 23787066(41.26%) | 23249059(40.32%) | 23534996(40.82%) | 23501129(40.76%) |
| M2-3 | 58008120 | 50528574(87.11%) | 47346941(81.62%) | 3181633(5.48%) | 23890368(41.18%) | 23456573(40.44%) | 23689649(40.84%) | 23657292(40.78%) |
| M3-1 | 54941134 | 49168624(89.49%) | 46164824(84.03%) | 3003800(5.47%) | 23162596(42.16%) | 23002228(41.87%) | 23108951(42.06%) | 23055873(41.96%) |
| M3-2 | 40792498 | 36168709(88.67%) | 33998852(83.35%) | 2169857(5.32%) | 17136903(42.01%) | 16861949(41.34%) | 17020649(41.72%) | 16978203(41.62%) |
| M3-3 | 46977510 | 42034975(89.48%) | 39542729(84.17%) | 2492246(5.31%) | 19830648(42.21%) | 19712081(41.96%) | 19796912(42.14%) | 19745817(42.03%) |

Note: M1: Control; M2: The Mg concentration is 0.4 mmol/L; M3: The Mg concentration is 0.8 mmol/L; The reference genome was GCF_004153795.1_AHAU_CSS_1_genomic.fna.gz. Download address: https://ftp.ncbi.nlm.nih.gov/genomes/all/GCF/004/153/795/GCF_004153795.1_AHAU_CSS_1/; Total Reads: Total number of clean reads; Reads mapped: The number of reads compared to the reference genome; Unique mapped: The number of reads only compared to the reference genome; Multi mapped: The number of reads multiple compared to the reference genome; Read1 mapped: Number of successes comparison in read1; Read2 mapped: Number of successes comparison in read2; '+' mapped: Number of reads successfully comparison on the positive chain of the genome; '-' mapped: Number of reads successfully comparison on the negative chain of the genome.