

Table 1 Suppl. Assembly quality for transcript and Unigene of *A. trifoliata*. Total number, the number of sequence entries of the assembled unigene/transcript; total base, the number of bases of all unigenes/transcripts assembled; largest length, the longest unigene/transcript length obtained through assembly; smallest length, the shortest unigene/transcript length obtained through assembly; average length, the average length of all unigenes/transcripts assembled; N50 length, the assembled unigene/transcript sorted in descending order of length, and the length of the transcript accumulated to half of the total length, corresponding to the length of the transcript.

Type	Unigene	Transcript
Total number	82321	127383
Total base	76165113	138563235
Largest length [(bp)]	16296	16296
Smallest length (bp)	201	201
Average length (bp)	925.22	1087.77
N50 length (bp)	1623	1826

Table 2 Suppl. Comparison and statistics of *A. trifoliata* transcriptome sequencing data and assembly results. Clean reads (pair reads) - the number of filtered sequencing data entries; mapped reads - the number of clean reads (pair reads) that can be compared to the assembled transcript; mapped ratio - the percentage of clean reads (pair reads) that can be located on the assembled transcript.

Sample	Clean reads	Mapped reads	Mapped ratio
Control_1	23822238	18857616	79.16%
Control_2	22309643	17686746	79.28%
Control_3	24765330	19765848	79.81%
CUR0_1	24098950	19253469	79.89%
CUR0_2	24587926	19642332	79.89%
CUR0_3	22536391	18029666	80.00%
CUR50_1	24924290	19732547	79.17%
CUR50_2	22736807	18123653	79.71%
CUR50_3	21823176	17294801	79.25%