**Supplementary Table 3.** *De novo* assembly of the floral transcriptomes of *Aristolochia fimbriata* at two different developmental stages.

|  |  |
| --- | --- |
| **Sample** | **Transcriptome assembly statistics (TRINITY)** |
| ***Aristolochia fimbriata*****(Limb S6)** | Total length of sequence: 173083699 bpTotal number of sequences: 96132Average contig length is: 1800 bpLargest contig: 17324 bpShortest contig: 201 bpN25 stats: 25% of total sequence length is contained in the 8035 sequences >= 4055 bpN50 stats: 50% of total sequence length is contained in the 21058 sequences >= 2766 bpN75 stats: 75% of total sequence length is contained in the 40487 sequences >= 1768 bpTotal GC count: 73740853 bpGC %: 42.60 %Number of Ns: 0Ns %: 0.00 % |
| ***Aristolochia fimbriata*****(Tube S6)** | Total length of sequence: 88849014 bpTotal number of sequences: 66217Average contig length is: 1341 bpLargest contig: 13435 bpShortest contig: 201 bpN25 stats: 25% of total sequence length is contained in the 6413 sequences >= 2707 bpN50 stats: 50% of total sequence length is contained in the 16174 sequences >= 1946 bpN75 stats: 75% of total sequence length is contained in the 29968 sequences >= 1305 bpTotal GC count: 38610430 bpGC %: 43.46 %Number of Ns: 0Ns %: 0.00 % |
| ***Aristolochia fimbriata*****(Utricle S6)** | Total length of sequence: 184564520 bpTotal number of sequences: 101267Average contig length is: 1822 bpLargest contig: 17241 bpShortest contig: 201 bpN25 stats: 25% of total sequence length is contained in the 8397 sequences >= 4131 bpN50 stats: 50% of total sequence length is contained in the 22175 sequences >= 2779 bpN75 stats: 75% of total sequence length is contained in the 42823 sequences >= 1777 bpTotal GC count: 78795454 bpGC %: 42.69 %Number of Ns: 0Ns %: 0.00 % |
| ***Aristolochia fimbriata*****(Limb S9)** | Total length of sequence: 124735043 bpTotal number of sequences: 90543Average contig length is: 1377 bpLargest contig: 15080 bpShortest contig: 201 bpN25 stats: 25% of total sequence length is contained in the 6769 sequences >= 3431 bpN50 stats: 50% of total sequence length is contained in the 18222 sequences >= 2212 bpN75 stats: 75% of total sequence length is contained in the 36313 sequences >= 1311 bpTotal GC count: 53347519 bpGC %: 42.77 %Number of Ns: 0Ns %: 0.00 % |
| ***Aristolochia fimbriata*****(Tube S9)** | Total length of sequence: 150478482 bpTotal number of sequences: 123439Average contig length is: 1219 bpLargest contig: 14074 bpShortest contig: 201 bpN25 stats: 25% of total sequence length is contained in the 9846 sequences >= 2841 bpN50 stats: 50% of total sequence length is contained in the 26269 sequences >= 1877 bpN75 stats: 75% of total sequence length is contained in the 52141 sequences >= 1101 bpTotal GC count: 64319073 bpGC %: 42.74 %Number of Ns: 0Ns %: 0.00 % |
| ***Aristolochia fimbriata*****(Utricle S9)** | Total length of sequence: 145574976 bpTotal number of sequences: 123214Average contig length is: 1181 bpLargest contig: 16531 bpShortest contig: 201 bpN25 stats: 25% of total sequence length is contained in the 9698 sequences >= 2797 bpN50 stats: 50% of total sequence length is contained in the 26012 sequences >= 1812 bpN75 stats: 75% of total sequence length is contained in the 52079 sequences >= 1054 bpTotal GC count: 62305178 bpGC %: 42.80 %Number of Ns: 0Ns %: 0.00 % |