

**Table S2 Statistics of polymerase read results**

| Library                   | Cell Number | Total Reads | Total Base(GB) | MaxLength(bp) | MeanLength(bp) | N50 Length(bp) |
|---------------------------|-------------|-------------|----------------|---------------|----------------|----------------|
| WHARTmjIEA<br>AA0-5RAAPBI | 1           | 1428605     | 84.81          | 336177        | 59367.63       | 118122         |

**Table S3 Statistics of subread results**

| Sample | Library                   | Cell Number | Total Reads | Total Base(GB) | MaxLength(bp) | MeanLength(bp) | N50 Length(bp) |
|--------|---------------------------|-------------|-------------|----------------|---------------|----------------|----------------|
| Qiai   | WHARTmjIEAA<br>A0-5RAAPBI | 1           | 63281536    | 80.18          | 262660        | 1267.11        | 1571           |

**Table S4 Statistics of CCS results**

| Sample | Library                   | Cell Number | Reads of Insert | Mean Read Length of Insert(bp) | Mean Read Quality of Insert | Mean Number of Passes |
|--------|---------------------------|-------------|-----------------|--------------------------------|-----------------------------|-----------------------|
| Qiai   | WHARTmjIEAAA<br>0-5RAAPBI | 1           | 888748          | 1616                           | 0.99                        | 46                    |

**Table S5 PacBio single-molecular long-read sequencing of *A. argyi***

| Sample | Library                       | Cell Number | Classified ROI | Full-length non-chimeric reads | Mean FL per ROI | Mean Read Quality | Mean Number of Passes | Mean full-length non-chimeric read length(bp) |
|--------|-------------------------------|-------------|----------------|--------------------------------|-----------------|-------------------|-----------------------|-----------------------------------------------|
| Qiai   | WHARTmjI<br>EAAA0-5R<br>AAPBI | 1           | 740702         | 855813                         | 1               | 0.99              | 42                    | 1268                                          |

**Table S6 Statistics of isoform results**

| Sample | Library               | Cell Number | Total isoforms | Mean Quality | Mean isoforms length(bp) | Mean Full length coverage |
|--------|-----------------------|-------------|----------------|--------------|--------------------------|---------------------------|
| Qiai   | WHARTmjlEAAA0-5RAAPBI | 1           | 241963         | 0.99         | 1395                     | Qiai                      |

**Table S7 The number of transcripts of *A. argyi***

| Library                    | sLibrary_genes | [AllSamples]_genes |
|----------------------------|----------------|--------------------|
| Qiai_WHARTmjlEAAA0-5RAAPBI | 76,158         | 69,178             |
| TOTAL                      | 76,158         | 69,178             |

**Table S8 Statistics of transcripts after redundant sequence removal**

| Total_number | Total_length | N50   | N90 | Max_length | Min_length | Sequence_GC(%) |
|--------------|--------------|-------|-----|------------|------------|----------------|
| 69,178       | 92,392,860   | 1,619 | 795 | 5,657      | 200        | 40.71%         |

**Table S9 Statistics of CDS prediction results**

| Total_number | Total_length | N50  | N90 | Max_length | Min_length | Sequence_GC(%) |
|--------------|--------------|------|-----|------------|------------|----------------|
| 53,136       | 59,241,828   | 1242 | 582 | 5125       | 297        | 43.02%         |

**Table S10 Functional annotation and classification of assembled unigenes in *A. argyi***

| Values     | Total  | Nr     | Nt     | Swissprot | KEGG   | KOG    | Pfam   | GO     | Intersection | Overall |
|------------|--------|--------|--------|-----------|--------|--------|--------|--------|--------------|---------|
| Number     | 69,178 | 64,747 | 54,149 | 52,983    | 52,917 | 52,029 | 53,299 | 53,710 | 32,691       | 65,893  |
| Percentage | 100%   | 93.59% | 78.27% | 76.59%    | 76.49% | 75.21% | 77.05% | 77.64% | 47.26%       | 95.25%  |

**Table S12 Primers for qRT-PCR**

| Primer  | Sequence (5'- 3')         |
|---------|---------------------------|
| HMGR1_F | GACGATGGTAGCTCATGCGA      |
| HMGR1_R | TTGTCAACCCATGGATGCCT      |
| HDS7_F  | TCGTGCCCATCTTGTGGTAG      |
| HDS7_R  | GGAGCACCACCGACATATCC      |
| HDR1_F  | CTCGCACAGACTACCTCTCC      |
| HDR1_R  | ATTGCGTTGACGATGACGTG      |
| HDR3_F  | CCACTCAGGAGCGACAAGAT      |
| HDR3_R  | TGTTGCTCGAGTTGAACCCA      |
| TPS2_F  | TGTAAAGGAGATGAAGATTTTGCTG |
| TPS2_R  | GCATTTCCAGTAAACCCGTCAT    |
| TPS5_F  | CCTGTTGTCTGCAGCATTCTCG    |
| TPS5_R  | ATCCATAGATCCTCCAACATCG    |
| GAPDF-F | GACCAGAGGCTATTGGACGCT     |
| GAPDH-R | ACATTAGGGGTGGGGACACGAAG   |