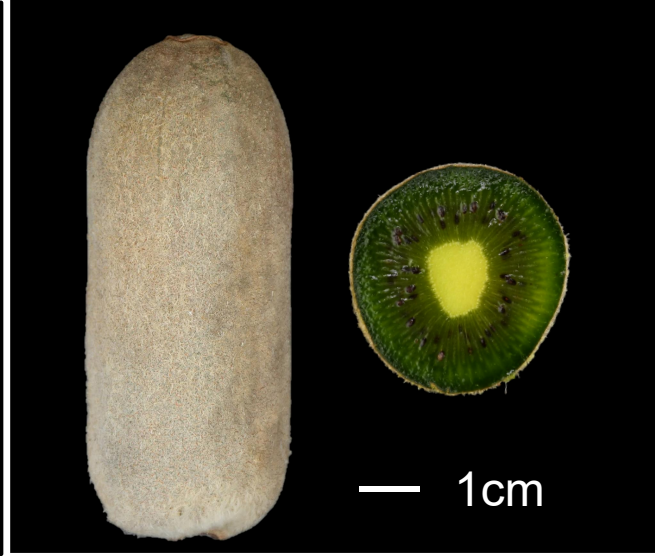
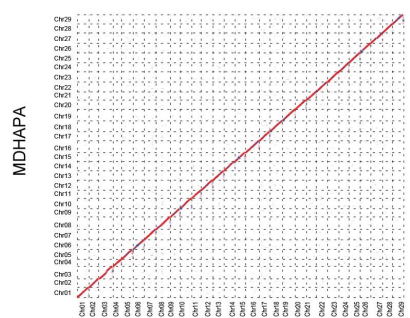
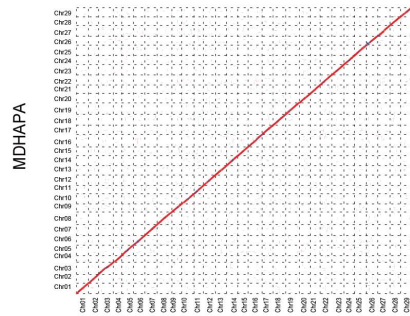




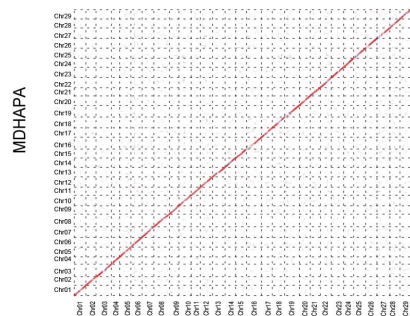
**Supplementary Fig. 1 Tree and fruit of *A. eriantha* ‘Midao 31’.** The average soluble solid content is 19.6 %, the average fruit weight is 76.2 g, the average acidity is 0.88%, and the average ASA content is 695.76 mg/100g.



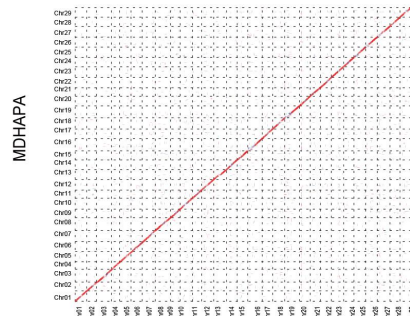
White



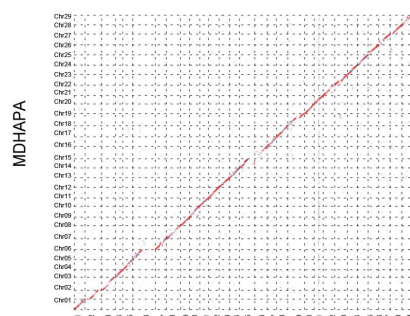
Wild



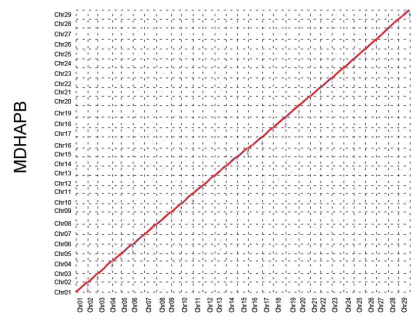
HY4A



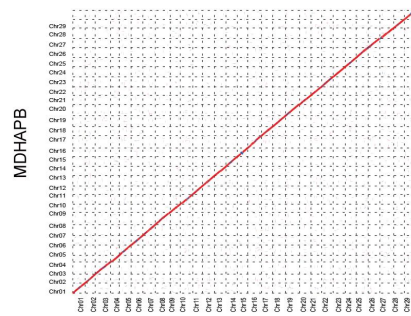
HY4P



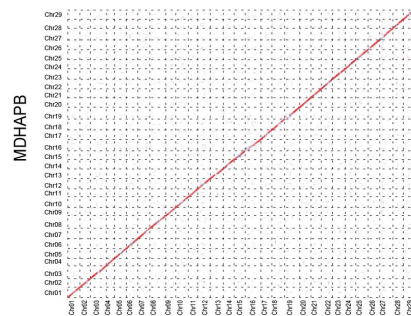
Red5



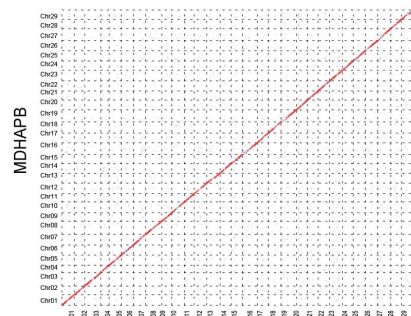
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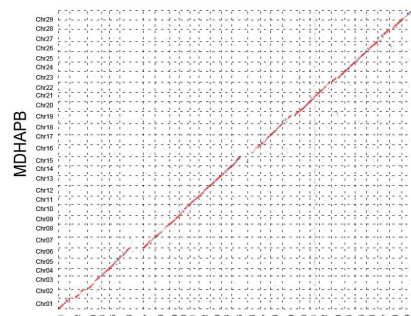
Wild



HY4A



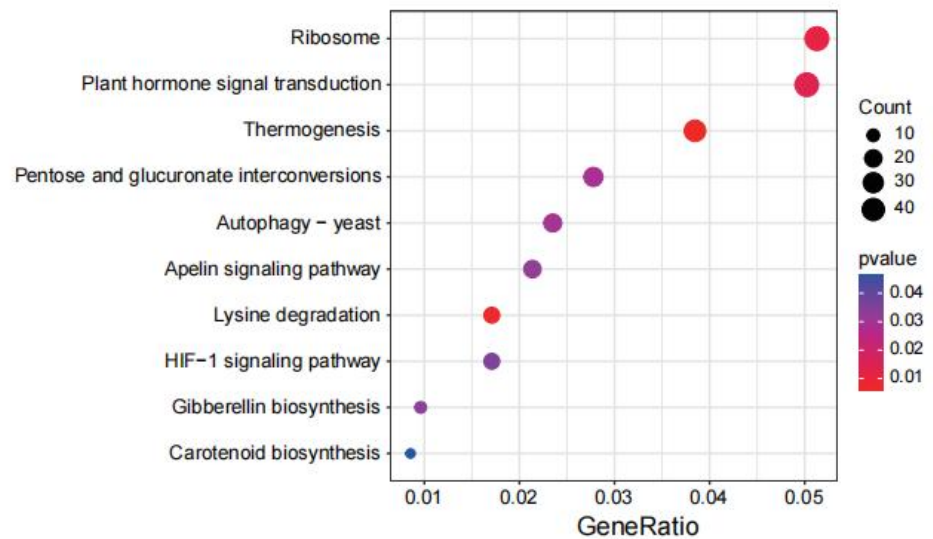
HY4P



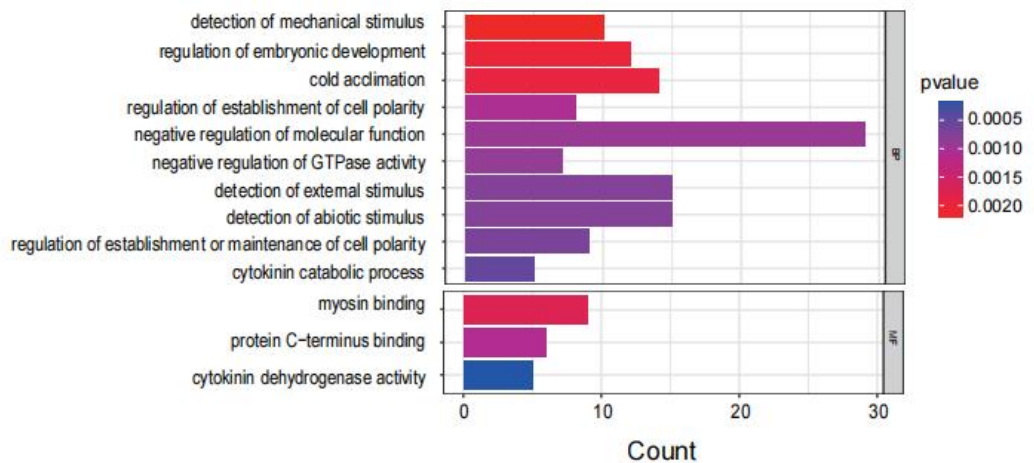
Red5

**Supplementary Fig. 2** Sequence alignment between MDHAPs and other genomes.

a

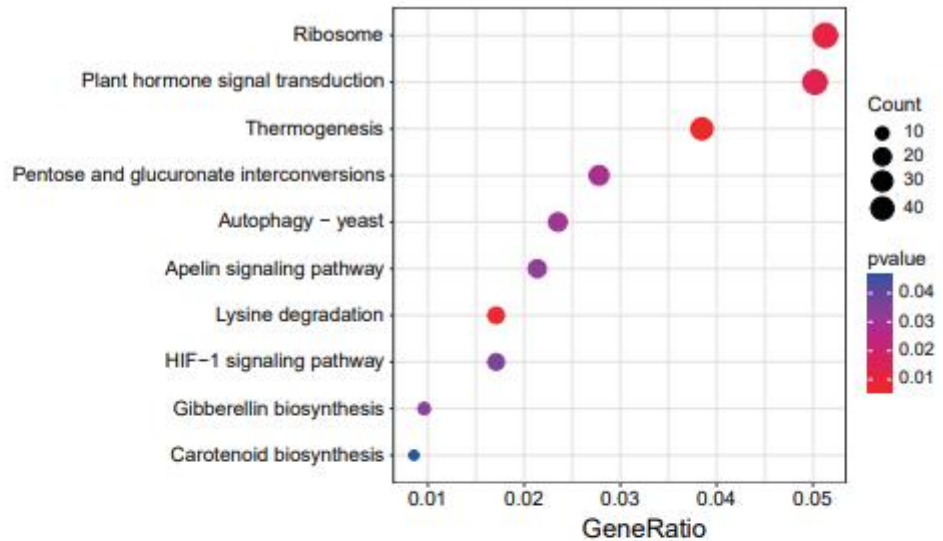


b

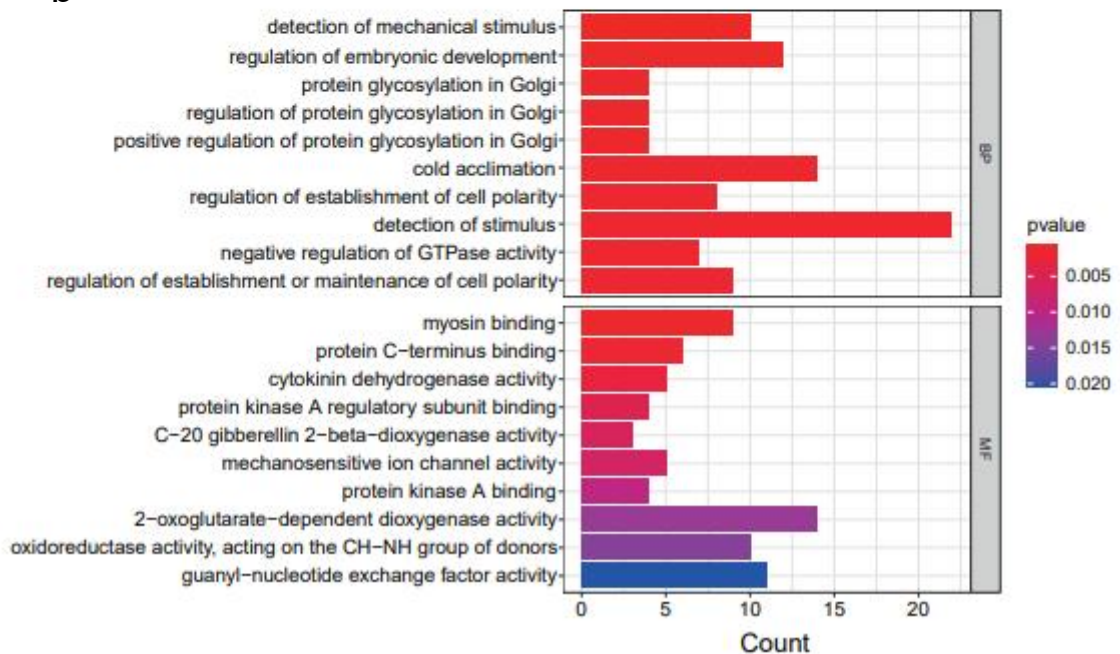


**Supplementary Fig.3** KEGG(a) and GO(b) enrichment of newly predicted genes in MDHAPA.

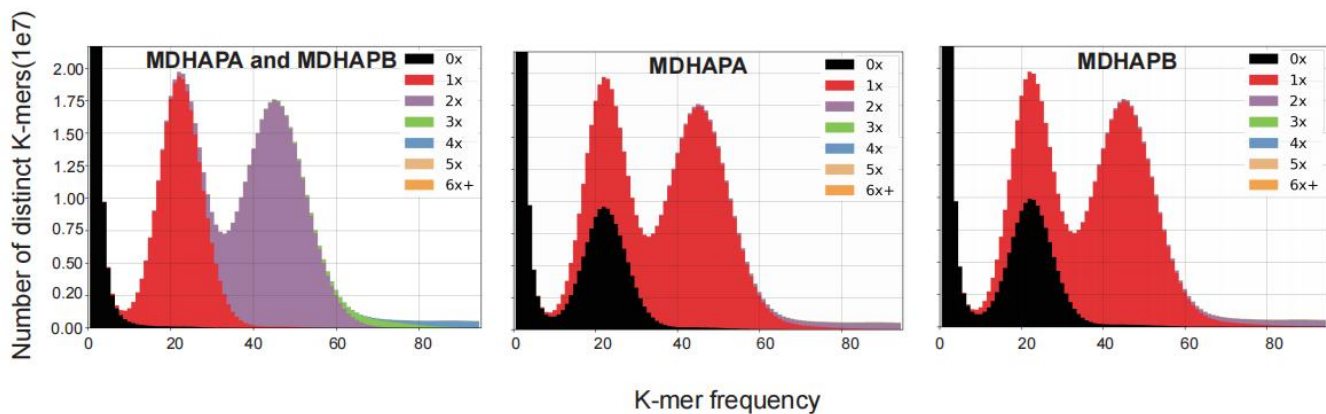
a



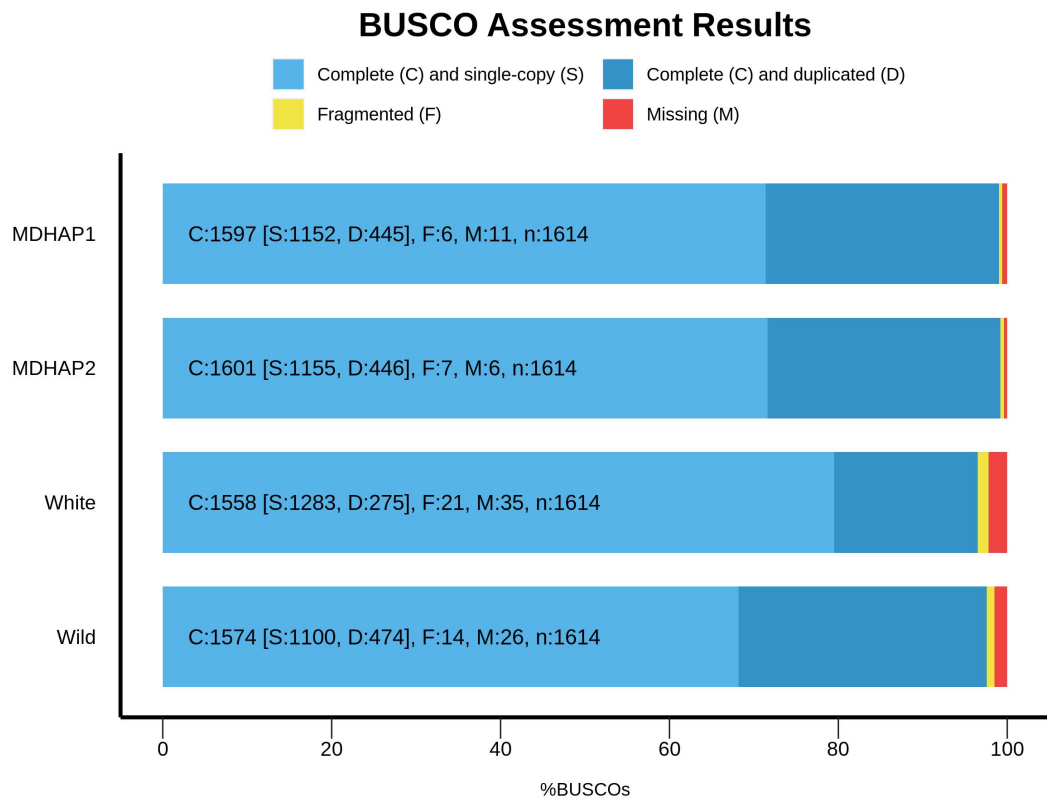
b



**Supplementary Fig.4** KEGG(a) and GO(b) enrichment of newly predicted genes in MDHAPB.

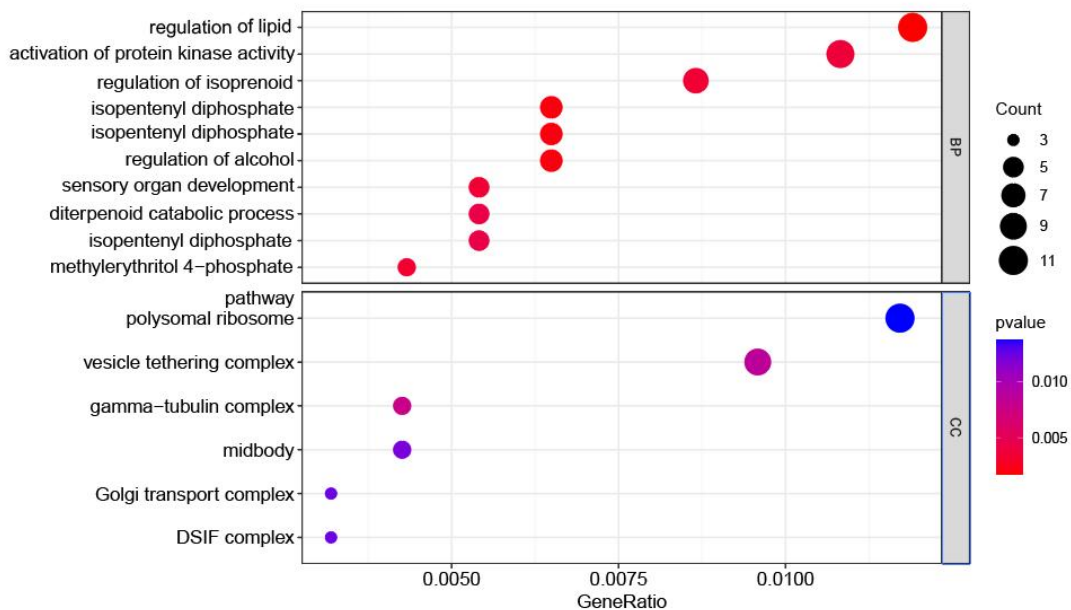


**Supplementary Fig. 5** K-mer spectrum analysis. The plots are colored to illustrate how many times of special K-mers from the hifi reads appearing in the assembly.

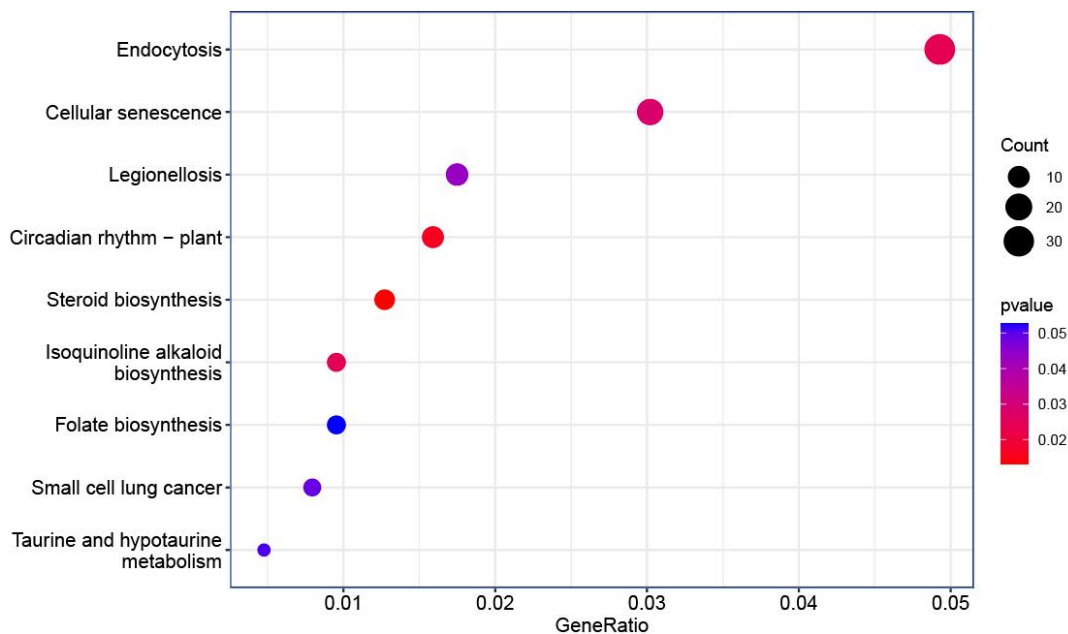


**Supplementary Fig. 6** BUSCO assessment of *A. eriantha* genome assemblies.

a



b

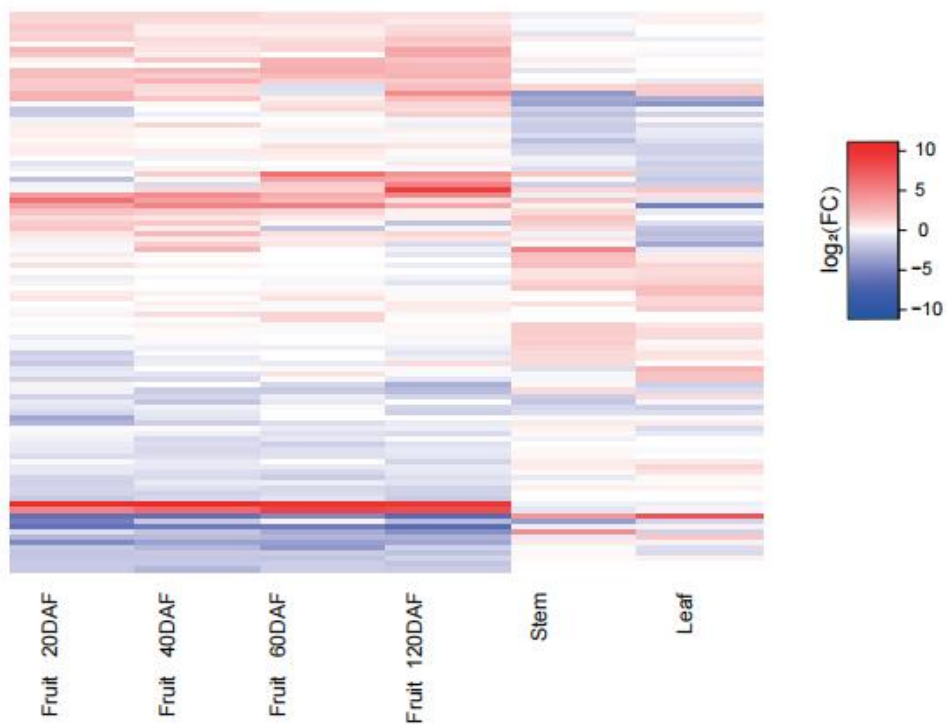


Supplementary Fig.7 GO(a) and KEGG(b) enrichment of ASES.

a



b



**Supplementary Fig. 8** Consistent and inconsistent allele-specific expression (ASE) pattern across six samples. (a) Consistent ASEs. (b) inconsistent ASEs. The color bar represents  $\log_2(\text{FC})$  values. FC indicates fold change of FPKM values between allele A and allele B. Red color suggests that expression in allele A is significantly higher than allele B and blue color means that expression in allele B is significantly higher than allele A. DAF means day after fruiting.

|             |                                                                                                               |     |
|-------------|---------------------------------------------------------------------------------------------------------------|-----|
| MDHAPA_Ch07 | .....TTTGAAAAATATGATGCAACAAATTTCTGACTTTGAAPATTGGTT.CCPACTTT.APAATTTGGTAGCAACAAATTTCTGCTTT                     | 85  |
| MDHAPA_Ch09 | ..ATTTTCAAAGTCAAAAATTTGTTGCTAGCAATTTTTCAAAC.TTGCAACCCACATTT.TCPAAGTCAGAPATTGTTGCTACTAATTTTCAPAC.TTT           | 94  |
| MDHAPA_Ch10 | .....TTTTCAAAC.TTGAAATCAAAATTT.TCPAAGTCAGAPATTGTTGCTAACCAATTTTCAPAC.TT                                        | 62  |
| MDHAPA_Ch11 | .....TTGCTAGCAATTTTTCAAAC.TTGAAATCACATTT.TCPAAGTCAGAPATTGTTGCTAACCAATTTTCAPAC.TT                              | 74  |
| MDHAPA_Ch14 | .....TTTGAAAAATTTGGTAGCTATAATTTCTGACTTTGAAPATTGGTT.CCPAGTTT.GAPAAATTTGGTAGCAACAAATTTCTGCTTT                   | 84  |
| MDHAPA_Ch15 | .....TTGCTAGCAATTTTTCAAAC.TTGAAATCAAAATTT.TCPAAGTCAGAPATTGTTGCTAACCAATTTTCAPAC.TT                             | 74  |
| MDHAPA_Ch23 | CACATTTTCAAAGTCAGAAATTTGCTGCTATCAATTTTTCAAAG.TAGCAACCCACATTT.TCPAAGTCAGAPATTGTTGCTAACCAATTTTCAPAC.TTT         | 98  |
| MDHAPA_Ch28 | .....AAAAATTTGGTAGCAATTAATTTATGACTTTGAAPATTGGTT.CTAPAGTTT.GAPAAATTTGGTAGCAACAAATTTCTGCTTT                     | 80  |
| MDHAPA_Ch29 | .....TTGCTAGCAATTTTTCAAAC.TTGGAATCAAAATTT.TCPAAGTCAGAPATTGTTGCTAACCAATTTTCAPAC.TT                             | 74  |
| MDHAPB_Ch01 | ..ATTTTCAAAGTCAGAAATTTGTTGCTAACATATTTTTCAAAG.TTGGAATCAAAATTT.TCPAAGTCAGAPATTGTTGCTAACCAATTTTCAPAC.TTT         | 93  |
| MDHAPB_Ch02 | .....TAGCAACAAATTTCTGACTTTGAAPATTGGTT.ACPACTTTT.GAPAAATATGCTAGCAATATTTTATGCTTT                                | 71  |
| MDHAPB_Ch05 | .....TAGCAACAAATTTCTGACTTTGAAPATTGGTT.ACPACTTTT.GAPAAATATGCTAGCAATATTTTATGCTTT                                | 71  |
| MDHAPB_Ch07 | .....AATTTGTTGCTATGCAATTTTTCAAAGTTGCAACCCACATTT.TCPAAGTCAGAPATTGTTGCTAACCAATTTTCAPAC.TTT                      | 81  |
| MDHAPB_Ch09 | ..ATTTTCAAAGTCAGAAATTTGTTGCTAGCAATTTTTCAAAC.TTGCAACCCACATTT.TCPAAGTCAGAPATTGTTGCTAACCAATTTTCAPAC.TTT          | 94  |
| MDHAPB_Ch10 | .....CCGAGCTTGACCAAGCTCCGAGCTTGCCGATATTTTTCAAAG.TTGGAATCAAAATTT.TCPAAGTCAGAPATTGTTGCTAACCAATTTTCAPAC.TTT      | 92  |
| MDHAPB_Ch18 | ..ATTTTCAAAGTCAGAAATTTGTTGCTAGCAATTTTTCAAAG.TTGGAATCAAAATTT.TCPAAGTCAGAPATTGTTGCTAACCAATTTTCAPAC.TTT          | 94  |
| MDHAPB_Ch19 | .....CTTGGAAPATTGGTT.GCPACTTTTATPAAATTTGGTAGCAACAAATTTCTGCTTT                                                 | 56  |
| MDHAPB_Ch20 | .....AAAAATTTGATAGCAACAAATTTCTGACTTTGAAPATTGGTT.TAPAGTTT.GAPAAATTTGGTAGCAACAAATTTCTGCTTT                      | 81  |
| HY4P_Ch01   | .....CTTGGAAPATTGGTT.GCPACTTTT.GAPAAATTTGGTAGCAACAAATTTCTGCTTT                                                | 55  |
| HY4P_Ch04   | .....TTGCTATGCAATTTTTCAAAT.TTGGAATCAAAATTT.TCPAAGTCAGAPATTGTTGCTAACCAATTTTCAPAC.TTT                           | 75  |
| HY4P_Ch09   | .....TTGCTAGCAATTTTTCAAAG.TTGGAATCAAAATTT.TCPAAGTCAGAPATTGTTGCTAACCAATTTTCAPAC.TTT                            | 75  |
| HY4P_Ch10   | .....TTTTCAAAC.TTGGAATCAAAATTT.TCPAAGTCAGAPATTGTTGCTAACCAATTTTCAPAC.TTT                                       | 63  |
| HY4P_Ch19   | .....AAAAATATGCTAGCAACAAATTTCTGACTTTGAAPATTGGTT.ACPACTTTT.GAPAAATATGCTAGCAACAAATTTCTGCTTT                     | 81  |
| HY4P_Ch24   | .....AAAAATATGCTAGCAACAAATTTCTGACTTTGAAPATTGGTT.CCPAGTTT.GAPAAATTTGGTAGCAACAAATTTCTGCTTT                      | 81  |
| HY4P_Ch25   | .....AAAAATATGCTAGCAACAAATTTCTGACTTTGAAPATTGGTT.ACPAGTTT.GAPAAATTTGGTAGCAACAAATTTCTGCTTT                      | 81  |
| HY4P_Ch26   | .....AATTTCTGACTTTGAAPATTGGTT.CCPACTTTTGAAPATATGCTAGCAACAAATTTCTGCTTT                                         | 65  |
| HY4A_Ch01   | .....AATTTCTGACTTTGAAPATTGGTT.CCPACTTTTGAAPATATGCTAGCAACAAATTTCTGCTTT                                         | 64  |
| HY4A_Ch02   | .....TTGCTAGCAATTTTTCAAAC.TTGGAATCAAAATTT.TCPAAGTCAGAPATTGTTGCTAACCAATTTTCAPAC.TTT                            | 75  |
| HY4A_Ch06   | .....AAAAATATGCTAGCAACAAATTTCTGACTTTGAAPATTGGTT.ACPACTTTT.GAPAAATTTGGTAGCAACAAATTTCTGCTTT                     | 81  |
| HY4A_Ch10   | .....TTTTCAAAC.TTGGAATCAAAATTT.TCPAAGTCAGAPATTGTTGCTAACCAATTTTCAPAC.TTT                                       | 63  |
| HY4A_Ch14   | .....CTTGGAAPATTGGTT.CCPACTTTT.GAPAAATTTGGTAGCAACAAATTTCTGCTTT                                                | 55  |
| HY4A_Ch18   | CAAAATTTCAAAGTCAGAAATTTGTTGCTAGCAATTTTTCAAAC.TTGGAATCAAAATTT.TCPAAGTCAGAPATTGTTGCTAACCAATTTTCAPAC.TTT         | 97  |
| HY4A_Ch20   | .....TTGCTAGCAATTTTTCAAAC.TTGGAATCAAAATTT.TCPAAGTCAGAPATTGTTGCTAACCAATTTTCAPAC.TTT                            | 75  |
| Consensus   | .....t aa tt a t a ta tt a                                                                                    |     |
| MDHAPA_Ch07 | GAAAAATGTAATCCAAATTTGAPAA.ATITGG.TAGCAACAAATTTATGACTTTGAAPATGTGGTTCCAAACG.....                                | 153 |
| MDHAPA_Ch09 | GCAACCAAAATTTCAAAGTCAGAPAAATTTGCTAGCAATTTTTCAAAC.CTTGTTATTA.....                                              | 153 |
| MDHAPA_Ch10 | GCAATCAAAATTTCAAAGTCAGAPAAATTTTACTACAA.ATTTTITAA.CTTGCTPCCAAATTTCAAAGTCAGAAATTTGTTGCTATCCAAAT.....            | 153 |
| MDHAPA_Ch11 | GCAATCAAAATTTCAAAGTCAGAPAAATTTGCTAGCAATTTTTCAAAC.ATTTCCPCCACATTTCAAAGTCAGAAATTTA.....                         | 153 |
| MDHAPA_Ch14 | GAAAAATGTAATCCAAATTTAAPAAATTTGATAGCAACAAATTTCTGACTTTGAPATGTGGTTCCAAAC.....                                    | 153 |
| MDHAPA_Ch15 | GCAACCAAAATTTCAAAGTCAGAPAAATTTGCTAGCAATTTTTCAAAC.CTTGATPCCAAATTTCAAAGTCAGAAATTTA.....                         | 153 |
| MDHAPA_Ch23 | ACAAACCAAAATTTCAAAGTCAGAPAAATTTTACTA.CAAATTTTTCAAAC.CTTCCAC.....                                              | 153 |
| MDHAPA_Ch28 | GAAAAATTTGATTTCCAACTTTTAPAAATTTGGTAGCAACAAATTTCTGACTTTGAPATGTGGTTCCAACTTTG.....                               | 153 |
| MDHAPA_Ch29 | GAAATCAAAATTTCAAAGTCAGAPAAATTTGCTAGCAATTTTTCAAAC.CTTGATPCCAAATTTCAAAGTCAGAAATTTA.....                         | 153 |
| MDHAPB_Ch01 | CAATCAAAATTTCAAAGTCAGAPAAATTTGCTAGCAATTTTTCAAAC.CTTGAPCCCA.....                                               | 152 |
| MDHAPB_Ch02 | GAAAAATTTGGTTCCAACTTTGAPAA.ATITGGTAGCAACAAATTTCTGACTTTGAPATGTGATTTCCAAATTTGAAAA.ATITGGA.....                  | 153 |
| MDHAPB_Ch05 | GAAAAATTTGGTTCCAACTTTGAPAA.ATITGGTAGCAACAAATTTCTGACTTTGAPATGTGATTTCCAAATTTGAAAA.ATITGGA.....                  | 153 |
| MDHAPB_Ch07 | GCAACCAACATTTCAAAGTCAGAPAAATTTTACTACCA.ATTTTTCAAAC.GTTCCPCCACATTTCAAAGTCAGAA.....                             | 154 |
| MDHAPB_Ch09 | GCAACCAAAATTTCAAAGTCAGAPAAATTTGCTAGCAATTTTTCAAAC.CTTGTTATTA.....                                              | 153 |
| MDHAPB_Ch10 | ACCGAAGCTGCTTTGTTCTGCTTTAA..TTCAAGTAGCA..CTTGCAAPATCTGAGGGGAAAGCTAG.....                                      | 154 |
| MDHAPB_Ch18 | GGAAACAAATTTCAAAGTCAGAPAAATTTGCTAGCAATTTTTCAAAC.CTTGTTATTA.....                                               | 154 |
| MDHAPB_Ch19 | GAAAAATGTGGTTGCAACTTTTAPAAATTTGGTAGCAACAAATTTCTGACTTTGAPATGTGGTTGCAACTTTGAAAA.ATITGG.TAGCAACAAATTTCTG.....    | 153 |
| MDHAPB_Ch20 | GAAAAATTTGATTTCCAACTTTGAPAA.ATATGTTAGCAACAAATTTCTGACTTTTAPAAATTTGCTTTCCAACTTTG.....                           | 153 |
| HY4P_Ch01   | GAAAAATTTGATTTCAAGTTT.CAPAAATTTGGTAGCAACAAATTTCTGACTTTGAPATGTGATTTCCAACTTTGAAAA.ATITGGCTAACCAACAAATTTCTG..... | 152 |
| HY4P_Ch04   | GCAACTACATTTCAAAGTCAGAPAAATTTCTTACCA.ATTTTTCAAAC.GTTGCAACCAATTTCAAAGTCAGAAATTTA.....                          | 153 |
| HY4P_Ch09   | GCAACTATATTTTAAAGTCAGAPAAATTTTCTTCCA.ATTTTTCAAAC.GTTGCAACCAATTTCAAAGTCAGAAATTTG.....                          | 153 |
| HY4P_Ch10   | GCAACTACATTTCAAAGTCAGAPAAATTTCTTACCA.ATTTTTCAAAC.GTTGCAACCAATTTCAAAGTCAGAAATTTGTTGCTAGCATAT.....              | 153 |
| HY4P_Ch19   | GAAAAATTTGATTTCAAGTTTGAPAA.ATITGGTAGCAACAAATTTCTGACTTTGAPATTTGATTTCCAAATTTTC.....                             | 153 |
| HY4P_Ch24   | GAAAAATGTGATTTGCAATTTTGAAPAA.ATATGCTAGCAACAAATTTCTGACTTTGAPATTTTAAATTTCCAAATTTA.....                          | 153 |
| HY4P_Ch25   | GAAAAATTTGATTTCAATTTTGAAPAA.ATITGGTAGCAACAAATTTCTGACTTTGAPATTTGATTTCCAAATTTA.....                             | 153 |
| HY4P_Ch26   | GAAAAATGTGGTTGCAACTTTTGAAPAA.ATITGG.TAAGAGAAATTTCTGACTTTGAPATGTAGTTGCAACTTTTGAAPAA.ATITGGTAGCAAC.....         | 153 |
| HY4A_Ch01   | GAAAAATTTGATTTCAAGTTTGAAPAA.ATITGG.TAAGAGAAATTTCTGACTTTGAPATGTAGTTGCAACTTTTGAAPAAATTTGATAGCAAC.....           | 153 |
| HY4A_Ch02   | GCAACTACATTTCAAAGTCAGAPAAATTTCTTACCA.ATTTTTCAAAC.ATTTGCAACCAATTTCAAAGTCAGAAATTTA.....                         | 153 |
| HY4A_Ch06   | GAAAAATTTGATTTCAATTTTAAAPAA.ATITGGTAGCAACAAATTTCTGACTTTGAPATGTGATTTCCAAATTTG.....                             | 153 |
| HY4A_Ch10   | GCAACTACATTTCAAAGTCAGAPAAATTTCTTACCA.ATTTTTCAAAC.GTTGCAACCAATTTCAAAGTCAGAAATTTGTTGCTAGCATAT.....              | 153 |
| HY4A_Ch14   | GAAAAATGTGATTTCCAACTTT.GAPAAATTTGATAGCAACAAATTTCTTACTTTGAPATTTGATTTCCAACTTTGAAAA.ATITGTTAGCAACAAATTTCTG.....  | 152 |
| HY4A_Ch18   | GAAATCAAAATTTCAAAGTCAGAPAAATTTTACTAGCAACAAATTTTCAAAC.ATITGGAT.....                                            | 153 |
| HY4A_Ch20   | GCAACTAAATTTCAAAGTCAGAPAAATTTCTTACCA.ATTTTTCAAAC.GTTGCAACCAATTTCAAAGTCAGAAATTTG.....                          | 153 |
| Consensus   | .....t aa t t a t a                                                                                           |     |

**Supplementary Fig. 9** Sequence alignment of *A. eriantha* and *A.chinensis* representative centromere (153bp) monomers.