**Table S1.** Sample RNA quality test results

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Gel image number | sample name | concentration（ng/ul） | total（ug） | OD260/280 | OD260/230 | RIN |
| 1 | BTWZZ\_1\_1 | 644.10  | 19.32 | 2.11 | 2.03 | 6.80  |
| 2 | BTWZZ\_1\_2 | 429.20  | 12.88 | 2.02 | 1.85 | 6.80  |
| 3 | BTWZZ\_1\_3 | 396.90  | 11.91 | 2.00 | 1.09 | 6.70  |
| 4 | BTWZZ\_2\_1 | 1024.20  | 30.37 | 2.15 | 2.25 | 8.60  |
| 5 | BTWZZ\_2\_2 | 820.40  | 24.61 | 2.16 | 2.01 | 7.00  |
| 6 | BTWZZ\_2\_3 | 868.10  | 26.04 | 2.17 | 2.05 | 8.30  |
| 7 | BTWZZ\_3\_1 | 1588.70  | 47.66 | 2.13 | 2.29 | 9.70  |
| 8 | BTWZZ\_3\_2 | 914.30  | 27.43 | 2.18 | 2.26 | 9.30  |
| 9 | BTWZZ\_3\_3 | 1334.90  | 40.05 | 2.14 | 2.27 | 10.00  |
| 10 | BTWZZ\_4\_1 | 967.60  | 29.03 | 2.19 | 2.25 | 9.20  |
| 11 | BTWZZ\_4\_2 | 1404.20  | 42.13 | 2.18 | 2.29 | 9.20  |
| 12 | BTWZZ\_4\_3 | 1482.50  | 44.48 | 2.14 | 2.29 | 8.80  |

**Table S2.** Quality control analysis of sequencing data

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Sample | Raw reads | Raw bases | Clean reads | Clean bases | Error rate(%) | Q20(%) | Q30(%) | GC content(%) |
| BTWZZ1\_1 | 42484926 | 6.42E+09 | 42117998 | 6.24E+09 | 0.0259 | 97.66 | 93.22 | 47.77 |
| BTWZZ1\_2 | 43846230 | 6.62E+09 | 43394836 | 6.38E+09 | 0.0262 | 97.54 | 92.98 | 47.34 |
| BTWZZ1\_3 | 42366630 | 6.4E+09 | 41970972 | 6.19E+09 | 0.0262 | 97.54 | 92.97 | 48.03 |
| BTWZZ2\_1 | 42021326 | 6.35E+09 | 41672264 | 6.15E+09 | 0.0264 | 97.51 | 92.82 | 46.3 |
| BTWZZ2\_2 | 42389598 | 6.4E+09 | 41879996 | 6.2E+09 | 0.0263 | 97.5 | 92.9 | 46.88 |
| BTWZZ2\_3 | 41046292 | 6.2E+09 | 40671764 | 6.0E+09 | 0.0263 | 97.52 | 92.9 | 46.2 |
| BTWZZ3\_1 | 49510464 | 7.48E+09 | 49128000 | 7.26E+09 | 0.0266 | 97.4 | 92.63 | 45.75 |
| BTWZZ3\_2 | 43044560 | 6.5E+09 | 42722736 | 6.32E+09 | 0.0264 | 97.48 | 92.81 | 45.61 |
| BTWZZ3\_3 | 38459736 | 5.81E+09 | 38060746 | 5.63E+09 | 0.0271 | 97.19 | 92.18 | 45.96 |
| BTWZZ4\_1 | 41155630 | 6.21E+09 | 40847194 | 6.03E+09 | 0.0263 | 97.54 | 92.94 | 45.8 |
| BTWZZ4\_2 | 41314288 | 6.24E+09 | 40999058 | 6.04E+09 | 0.0261 | 97.6 | 93.08 | 45.71 |
| BTWZZ4\_3 | 42366052 | 6.4E+09 | 42062376 | 6.24E+09 | 0.0263 | 97.54 | 92.93 | 45.75 |

**Table S3.** Transcriptome data functional annotation results

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  | Exp\_Unigene number(percent) | Exp\_Transcript number(percent) | All\_Unigene number(percent) | All\_Transcript number(percent) |
| GO | 52111(0.407) | 83973(0.4536) | 52331(0.4052) | 84337(0.4522) |
| KEGG | 38670(0.302) | 58168(0.3142) | 38909(0.3013) | 58504(0.3137) |
| COG | 63414(0.4952) | 97352(0.5259) | 63753(0.4936) | 97842(0.5246) |
| NR | 62876(0.491) | 100495(0.5428) | 63147(0.4889) | 100929(0.5412) |
| Swiss-Prot | 53580(0.4184) | 83357(0.4503) | 53825(0.4168) | 83744(0.449) |
| Pfam | 57876(0.452) | 87690(0.4737) | 58137(0.4501) | 88086(0.4723) |
| Total\_anno | 76222(0.5953) | 116681(0.6303) | 76659(0.5936) | 117288(0.6289) |
| Total | 128046(1) | 185125(1) | 129151(1) | 186492(1) |

**Table S4**. Statistical result table of DEGs

|  |  |  |  |
| --- | --- | --- | --- |
| diff\_group | total DEGs | up | down |
| BTWZZ1\_vs\_BTWZZ2 | 11748 | 401 | 11347 |
| BTWZZ1\_vs\_BTWZZ3 | 21528 | 3706 | 17822 |
| BTWZZ1\_vs\_BTWZZ4 | 23650 | 5398 | 18252 |
| BTWZZ2\_vs\_BTWZZ3 | 5513 | 2848 | 2665 |
| BTWZZ2\_vs\_BTWZZ4 | 8137 | 4733 | 3404 |
| BTWZZ3\_vs\_BTWZZ4 | 1622 | 1006 | 616 |

**Table S5.** The CDS of the six core protein genes

|  |  |  |
| --- | --- | --- |
| **gene\_id** | **gene\_name** | **CDS** |
| TRINITY\_DN6507\_c0\_g1 | AUX1 | ATGTTGAATCAAAAGCAAGCTGAAGAAGCTATTGTCGCCAACTACAACGAGACAGATAATGATGGTAACAGTCAACAGGTTAAAAAAGATGGAGAAGATGATGAGTCAGACTCCATGTTCAATGTCAAAAGCTTCCTCTGGCATGGTGGCTCTGCGTATGATGCTTGGTTCAGCTGTGCTTCCAATCAAGTGGCGCAAGTGCTGTTAACTCTGCCATACTCGTTCTCACAACTGGGAATGCTCTCAGGAATAATATTTCAGATATTTTATGGTATCATGGGAAGCTGGACAGCTTATCTTATCAGTGTGTTATACATTGAGTACCGAACTAGAAAAGAGAAAGAAAACAAAAACTTCAAGAACCATGTTATTCAGTGGTTTGAAGTACTTGATGGGCTTCTTGGCCCTTACTGGAAAGCAATTGGCCTGGCCTTCAACTGTACCTTCCTTCTCTTTGGTTCAGTCATCCAACTCATAGCCTGTGCCAGTAACATATATTACATAAATGATCGATTGGATAAGCGGACTTGGACGTATATCTTCGGGGCGTGTTGTGCGACGACTGTGTTCATACCTTCCTTTCACAATTACCGGATTTGGTCGTTTCTAGGGCTTGGCATGACTACATATACTGCTTGGTATATGACCATTGCCGCAATCGTTCACGGCCAGGTTGAGGGTGTGACTCACAGTGGACCCAAAAAATTGGTTTTGTATTTCACTGGTGCCACTAATATACTGTATACTTTCGGTGGACATGCTGTCACTGTAGAAATTATGCATGCAATGTGGAAGCCGCAGAAGTTCAAGTACATCTACCTAGGAGCTACCTTATATGTATTCACACTAACGCTTCCATCGGCTACTGCTGTTTACTGGGCTTTCGGCGATGAGCTTCTTACTCACGCCAATGCGTTCTCACTTCTCCCCAAGAACGGGTTCCGTGATGCTGCCGTTATACTCATGCTTATCCACCAGTTCATCACATTCGGTTTCGCATGTACCCCCTTGTATTTTGTGTGGGAGAAGGTAATTGGAATGCACGACACGAAGAGCATATGTCTACGGGCAATTGCCCGTTTGCCCGTGGTGGTGCCCATTTGGTTCTTGGCTATCATCTTCCCTTTCTTTGGACCTATCA |
| TRINITY\_DN51284\_c0\_g4 | IAA19 | ATGGCAACAGAAGCCGTAAGTGTTGGGAGTGAGATCACCACTGAGCTGAGTTTGGGTCTTCCAGGGGGCTCTCTTTCAGCTGCATCAGGGAAGAATGAGAAGAAGAGGCTGTTCTCTGAAATAGATGTTGATGATCGGAATAGCTCGAACACCGATCACAATAAGAGCCAAGTTGTAGGATGGCCGCCCGTTTGTTCATATAGAAGAAAAAACCATGTTAGCGAAGCATCAAAATTTTACGTCAAAGTTAGTATGGACTGTACTCCTTATATGCGAAAAATTGATTTGAAGAATCACAAAGGGTATTCAGATCTTTTTCTTGCCTTCGAGAAGCTCTTCAGCTGTCTCTACAATGGTGGAGTGTTGAAGGATTCAGAGAATACAGAATATACACCAATATATGAAGACAAAGATGGGGACTGGTTGCTTGTAGGAGATGTCCCCTGGGAGTTGTTTACCAAATCATGCAAGAGGTTGAGAATATTGAAGCAGGGGATTCAAAAGAAGTTCAACTGACAAGAACGAAAATTTTATGTGCCTGGTGTTCAGTTTATTAGCAGGAGTGATAGTTAA |
| TRINITY\_DN11146\_c0\_g1 | ABI1 | ATGGAGAAACAACAGCAACAGCAGCAGCAACAGCAACATGAAGAAGTTGAAGATCTCCGGCGAGAAGATTCGACGACTGAATCATCGCTGTTTGGAACTGAAGACAACAACAACAACAGCAACAACATTCGTTGTAACAGCTCAGGTGACTTGTCCATTTGTAGTAGTAGCTCCTCTTCCGGTGAAATTCCGGCGGGAGTGATCGAAGAGGCTGTGGTTGTGGTGGTTCCGAAGCCGCTATCGACGGACGTTAGCGGAGAGGTAACGGTAACAGCAACGGCAACGGCGGTGAGTAGAGAGAGAGAACCTTGTTGTGTTGGCAGGAGAAATAAAGGAGTGTCTTGGGGGTTTACTTCAGTGATTGGTAGGAGGAGAGAGATGGAAGACGCCGTTGCCGTCATTCCCGGATTCATGTCTCGCACGTGCGATCACGTGGGTGGCTGTACTGCTCCCGGGAGCAAAATCTCCGGTGAGATCTCACCCGTCCACTTCTTCGGAGTGTTCGATGGGCACGGCGGTTCTCAGGTGGCTAAGTTTTGTGCTGAACGAATGCACGAGGTGATTGCAGAACAATGGGAAAAGGGAAAAGTCGATGGAAATGGATGGCGTCACAGGTGGGAGGAGGCATTCTCTAGTGGATTTGAGCGAACTGATAATGAAGTTTCCGAGGAATCCATTGCACCAGAAATAGTTGGTTCAACCGCTGTGGTAGTAGCTTTATCTGGATGTCAGATAATAACATCCAACTGTGGCGATTCAAGGGCGATACTTTGCAGAGGAACCCAAACTATCCAGTTATCAACTGATCACAAGCCGGATAGGGAGGATGAGCTAGTTAGAATTGAAGGAGGCGGAGGGAAAGTAATCTACTGGAATGGTGCCAGAGTACTAGGTGTACTTGCTATGTCGAGGTCCATAGGTGACCGGTATATGAGACCTTGGATTATACCAGATCCTGAAGTTACATTCACCACAAGGACTGAAGAAGATGACTGTTTGATAGTGGCTAGCGATGGGCTTTGGGATGTTATGTCCAATAATGAGGTTGGGGAAATAGCTCGTCATCTGTTCAGGAGGATGAGGCGTTCTGCAATGGCTGATGAGACCTCGCCTTCTCCAGCACAAGCTGTTGCTGACCACCTCACCGACATAGCTTTTAGGAAGAACAGCTCAGACAATATTTCAGTGGTCGTCGTTGATTTAAAACTGAGGAGGAAGCGTCATCCGAGGCAACCATCAAAATGA |
| TRINITY\_DN52899\_c0\_g1 | ABI5 | ATGGGACCTGAAACCAAAGCACCAAGCTATAAAGAAGCTGGACAGGGGTCAGCTCTGCCTTCACAGCAGCCACTACCAACTTCACAACCGGAAGAAGCCTCAAAGGCCAATAATCCACTCACTTTTCTGGGGCGACAGTCCTCAATATACTCTCTCACCCTGGACGAATTTCAGAACACGATATGTGGCGAAAATGGCAAGACGTTTGGTTCTATGAACATGGATGAGTTTCTTACCAATATATGGACAGCTGAAGAACATCAGGCTGCCATTGAAGATGAGGAGGGCATTACTTCTACTCCAAATGATGCCTCAGAGAACAAATCCTCAGCTACTCAACCTGGTCTGCATCGACAAGGCTCTCTCACTCTTCCGGCTCCTCTTTGTAGGAAGACTGTGGAAGAAGTTTGGTCAGAGATCCACAAGGAACAGCAGCAGCAGCAACAACAAAAACACCATCCTGGAAATGCTAGTAGGCAACCTACCTTTGGAGAGATGACCTTGGAGGATTTCTTAGTAAAGGCAGGAGTTGTTCGTGAGCCAATTGCTTCTTCATCTCACCACCACGCTCAACCAACCGTTGTGCCACCACCTCCTCCTTCACAACAGTTATGTCTTTATCCAAACAACAATGCAGTAGATCCAAATTATGGTGTTGGCCCTGTCATGAGTCTTGGATTCCCTGATCACCGCAGTGCTCCCAATGGTGTATCAGGTGGCATACCTGCTTACCAAACTTACCCCCAGTCTAGTGGCATGGTTGGTGAATCTTCAAGTTATGCTGCAGGTAATGGTAAGAGAAATGGTGGTTACGCGCCTGGAATGTGTTTCAATGGTAGAATGGGAAATGGAGGTGGGTATGCTCCGGCTGTGACAATTGGTACTGGATCTCCAGTGAGTCCTGTGTCATCTGATGGACTGGTCGCAAACCCTGTTGACAATTCGAACTCTGCTGGCCAGTATGGGGTGGACATGGGAGGCACTAGAGGGGGGAGGAAGAGGATCATAGATGGGCCTGTAGAGAAAGTAGTGGAGAGAAGACAAAGGAGGATGATCAAGAACAGGGAATCCGCTGCAAGGTCCAGGGCAAGGAAACAGGTGTGTGTTTATCTATCCATAATTTCTAGCCATTTATTCGCTTTATGGTAG |
| TRINITY\_DN55822\_c0\_g1 | RGA1 | ATGGACAGTGGTAAGGCTAAGATATGGGATGATTCTGCAACTGCTGGAGAGGATGAACTTCTTGCGATTCTTGGGTATAAGGTGAGATCTTCTGATATGGCTGATGTTGCTCAGAAGATGGAGCAACTTGACATGATGATCGGTTCTGGATGTACTGATGATGGAGCTGGTTTGCTTACTCATCTTGGCTCTGATATCGTTCATTACAATCCATCAGATTTGTCTACTTGGTTAGAAACCATGTTATCTGGAGCTGAAACCAATATCCCCCCAAATCCATCTTTCCAAAACAACCTTCCATTCGTACCTACTGCTGAATCCTCCACAATTACTACCATTGATTACCCACTCCCACACACATCGATTTATGATGAACCCGTTTGTTCCGATTATGATCTCAGTGCCATCCCCGGCGATGCCATTTTCGGTGAACGTGACAGGAAGCGCCCCAAGCAAGAATTAGCAATGGTCAATTCTACCATAATCCCATTCCCAAACCCAAACCCAAACCCAAGCCCGTTGATGATGAACGGTGGTCAGATTGGGGTTGGGGGGATGATGAATATGGCTGAGCCGAGTCGGCCAGTGGTCCTGGTTGACTCACAAGAAAACGGTATCCGTCTTGTCCACACCTTAATGGCATGTGCGGAAGCTGTACAGCAAGATAACCTCAAGCTAGCTGAGTCACTCGTTAAGCAAGTGAGTCTACTCGCTGCTTCACAAGCGGGTGCGATGAGGAAAGTCGCTACGTATTTCGCTGAAGCTCTTGCAAGGAGGATTTACCGGTTCTACCCTCAGCCGTCTCTTGATTCATCCTTTTCGGACATTCTCCAAATCCATTTTTACGAGACCTGCCCTCACCTCAAGTTCGCGCATTTTACAGCTAATCAGGCGATTCTCGACTCAGTGATTGACTCAAGCCGGGTCCATATCATTGATTTCAGTATGAAGCAAGGGATTCAGTGGCCGGCCTTGATGCAAGCTCTTGCAATGCGTCCAAATGGTGGGCCGAGCATCCGGATCACGGGTATTGGCCCGCCCCAACCGGATAACTCTGACGCGTTACAGCAAGTCGGTTGGAAGCTCGCTCAGTTCGCTGAGAATCTGTGCGTTGAGTTCGAGTACAGAGGATTCGTCACCAACAGTCTAGCGGATCTGGATGCTTCAATGCTGGATCTCCGACCCGGGGAAACCGTTGTTGTGAATTCGGTTTTTGAACTGCACCCGTTACTGGCCCGACCCGGTGCGATCGAGAAGGTTCTAGGTACGGTCAGGGATTTGAATCCCAAGATTGTCACTGTGGTCGAACAAGAAGCGAATCATAATGGTCCGATTTTCATGGATAGGTTCACTCAGGCTTTGCATTATTACTCAACCCTGTTTGACTCACTGGAAGGGGGTGCTCTGACCCCAGTAAGCGGTCAGGATTTGCTGATGTCTGAGATGTATTTTGGGCGGCAGATCTGTAATTTGGTGGCGTGTGAAGGCGTGGATCGGGTTGAAAGGCATGAGAGCCTGAGTCAGTGGAGAGATCGGTTCGAATCGGCTGGGTTGGAGCTGAGTCCACTCGGGTCGAATTCGTTTAGACAGGTGTGTCACTTGCTGGGCATGGTTGATGGTGCGAGCGGTTACAGGGTGGATGAAAGGGAAGGGTGTTTGATGCTTGGGTGGCATACTCGGCCACTTGTCACTTCCTCAGTGTGGCAAATCGCGGACATTGACTCGGATTGA |
| TRINITY\_DN8581\_c0\_g1 | GAI | ATGAAAAGAGAGCACCACCAATATCATCAAACTGTTTCTTCAACTGCCATGGCAGTGAATACCAAGAAGAAGATAGAGATGGAACAGCTCGTACCGGATGCAGGCGTTGATGAGCTTCTTGCTGTTTTGGGCTACAAAGTCAGGTCATCTGATATGGCTGAAGTCGCCCAGAAGCTTGAACAGCTTGAAATGGCTATGGCTGCAGGTAGCATGGGAGGGGGTGTTTGTAATAATATGGGGACTGTTCAAGATGACTCCCTCATCTCTCATGTTAATCCGTCTGATCTCTCGACGTATCTTCAATCCATGTTGTCTGAGATCAATCCGGATCTTGATGATCCGGTCCTGGCAGCGGCCGCTGCCGGATGTGATGATCTCAGCGCGATTCCAGGTGGAGCTATCTGTGCTCCACCTGAACGCGAAACAAAGAGACTGAAACAATCAACTAGTACAACTGACATAACTCGTCCCGTTGTGCTAGTTGACTCGCAAGAGAACGGCATCAGATTGGTGCATACTCTGCTAGCATGTGCAGAAGCGATCCAGCAAGAGAATCTGCAATTAGCTGAAGCGTTAGTGAGTCAAATCGGGTTACTAGCTGTTTCTCAAGCTGGAGCTATGAAGAAAGTGGCTACTTACTTCGCAGAAGCTCTGGCTCGTCGGATTTACCGATTCCAGTTGTTCCCTCAAGACTCACTGGACTCACCATCATTGTCTGAAATCCTGGAAATGCATTTCTATGAGACGTGCCCTTATTTGAAATTCGCGCATTTCACGGCAAATCAGGCTATTCTGGATGCATTTGAAGGTATGAACCATGTACACGTGGTTGATTTCAGTATGAAGCAAGGGATTCAGTGGCCAGCATTGATTCAGGCCTTGGCGTTACGCCCAGGCGGTCCGCCAACGTTCCGGTTAACCGCTATTGGGCCGCCGCAGCCGGATAATAAGGATGCGTTGCAGCAGGTGGGATGGAGGTTGGCCCAGTTGGCTGAGACTGTTCATATTGAGTTCGAGTACAGAGGGTTTGTGGCTAGTAGCATAGCTGACATCGATGCGGAGATGCTGAATTTACGCCCCAGTGAGATCGAAGCGGTGGCGGTGAACTCAGTGTTCGAGATGCATCAGCTGTTAGCCCAACCGGGCGCAATGGAAAAGGTCTTGAGGTCGATCAGAGCAATGAAACCAAAAATCGTGACTATTGTTGAGCAAGAAGCGAACCACAATGGACCGGTGTTCCTGGACCGGTTCACCGAGTCGCTACATTATTATTCGACCCTGTTTGACTCGTTGGAAGGGGGCGGGGGGAGTAGTAGGGAGGACCAAATGATGTCCGAGGTGTACCTGGGGAAACAGATCTACAACGTGGTGGCTTGTGAGGGAGTCGAGCGAGTGGAACGGCACGAGACGTTGAGCCAGTGGCGAGTCAGGATGGGATCGGCTGGGTTCGCCCCGGTTCATCTTGGTTCGAAAGCGTTTAAACAGGCTAGTATGTTGTTGTCACTGTTTGGAGGTGTGGATGGGTACAGGGTGGAAGAGAATCAAGGGTGCTTGATGCTTGGTTGGCATACTCGGCCACTTATTGCGACTTCCGCGTGGCGACCGGGACCAATAATTGAGAGCTATTGA |

**Table S6.** Analysis of AUX1 Gene Homology

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| No. | Scientific Name | Max Score | Total Score | Query Cover | E value | Per. ident | Acc. Len | Accession |
| 1 | Papaver somniferum | 798 | 798 | 0.91 | 0 | 80.6 | 1946 | XM\_026569782.1 |
| 2 | Papaver somniferum | 798 | 798 | 0.91 | 0 | 80.6 | 1960 | XM\_026569781.1 |
| 3 | Papaver somniferum | 798 | 798 | 0.91 | 0 | 80.6 | 2447 | XM\_026569780.1 |
| 4 | Papaver somniferum | 798 | 798 | 0.91 | 0 | 80.6 | 2450 | XM\_026569779.1 |
| 5 | Ipomoea nil | 789 | 789 | 0.9 | 0 | 80.54 | 2266 | XM\_019331370.1 |
| 6 | Ipomoea nil | 789 | 789 | 0.9 | 0 | 80.54 | 2303 | XM\_019331369.1 |
| 7 | Ipomoea nil | 789 | 789 | 0.9 | 0 | 80.54 | 2254 | XM\_019331368.1 |
| 8 | Ipomoea triloba | 784 | 784 | 0.9 | 0 | 80.37 | 2211 | XM\_031246991.1 |
| 9 | Carya illinoinensis | 776 | 776 | 0.89 | 0 | 80.45 | 2492 | XM\_043100006.1 |
| 10 | Tripterygium wilfordii | 776 | 776 | 0.88 | 0 | 80.57 | 2418 | XM\_038833357.1 |
| 11 | Papaver somniferum | 763 | 763 | 0.89 | 0 | 80.16 | 2077 | XM\_026558534.1 |
| 12 | Tripterygium wilfordii | 758 | 758 | 0.89 | 0 | 80.23 | 2042 | XM\_038845336.1 |
| 13 | Mercurialis annua | 756 | 756 | 0.89 | 0 | 80 | 2301 | XM\_050356504.1 |
| 14 | Mercurialis annua | 756 | 756 | 0.89 | 0 | 80 | 2368 | XM\_050356503.1 |
| 15 | Camellia sinensis | 747 | 747 | 0.99 | 0 | 78.69 | 2184 | XM\_028253504.1 |
| 16 | Camellia sinensis | 747 | 747 | 0.99 | 0 | 78.69 | 2430 | XM\_028253503.1 |
| 17 | Populus euphratica | 737 | 737 | 0.9 | 0 | 79.55 | 1863 | XM\_011020837.1 |
| 18 | Populus euphratica | 737 | 737 | 0.9 | 0 | 79.55 | 2486 | XM\_011020836.1 |
| 19 | Populus euphratica | 737 | 737 | 0.9 | 0 | 79.55 | 2629 | XM\_011020835.1 |
| 20 | Pisum sativum | 736 | 736 | 0.89 | 0 | 79.73 | 2203 | XM\_051056681.1 |
| 21 | Populus alba | 732 | 732 | 0.9 | 0 | 79.46 | 2589 | XM\_035058139.1 |
| 22 | Populus alba | 732 | 732 | 0.9 | 0 | 79.46 | 2725 | XM\_035058138.1 |

**Table S7.** Analysis of ABI1 Gene Homology

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| No. | Scientific Name | Max Score | Total Score | Query Cover | E value | Per. ident | Acc. Len | Accession |
| 1 | Prunus avium | 403 | 403 | 0.6 | 3E-107 | 76.39 | 1820 | XM\_021951435.1 |
| 2 | Pyrus x bretschneideri | 387 | 387 | 0.71 | 3E-102 | 74.89 | 1867 | XM\_048586580.1 |
| 3 | Prunus mume | 375 | 375 | 0.6 | 7E-99 | 75.73 | 1820 | XM\_008244275.2 |
| 4 | Prunus persica | 348 | 348 | 0.6 | 2E-90 | 75.07 | 1874 | XM\_007202060.2 |
| 5 | Vigna angularis | 327 | 327 | 0.59 | 2E-84 | 74.93 | 1655 | XM\_017586752.1 |
| 6 | Vigna angularis | 327 | 327 | 0.59 | 2E-84 | 74.93 | 1767 | XM\_017586750.1 |
| 7 | Vigna umbellata | 316 | 316 | 0.59 | 4E-81 | 74.66 | 1919 | XM\_047323018.1 |
| 8 | Pyrus x bretschneideri | 196 | 196 | 0.38 | 6E-45 | 74.33 | 1512 | XM\_048578713.1 |
| 9 | Prunus persica | 97.1 | 97.1 | 0.13 | 6E-15 | 77.78 | 3131 | XM\_020556493.1 |
| 10 | Drosophila hydei | 65.8 | 65.8 | 0.03 | 0.00002 | 95.12 | 2173 | XM\_023318101.2 |
| 11 | Drosophila novamexicana | 63.9 | 63.9 | 0.02 | 0.00006 | 100 | 2704 | XM\_030711399.1 |
| 12 | Alosa alosa | 62.1 | 62.1 | 0.02 | 0.0002 | 97.22 | 1834 | XM\_048244535.1 |
| 13 | Drosophila takahashii | 62.1 | 62.1 | 0.03 | 0.0002 | 95 | 3325 | XM\_044392753.1 |

**Table S8.** Analysis of ABI5 Gene Homology

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| No. | Scientific Name | Max Score | Total Score | Query Cover | E value | Per. ident | Acc. Len | Accession |
| 1 | Prunus avium | 403 | 403 | 60% | 3.00E-107 | 76.39 | 1820 | XM\_021951435.1 |
| 2 | Pyrus x bretschneideri | 387 | 387 | 71% | 3.00E-102 | 74.89 | 1867 | XM\_048586580.1 |
| 3 | Prunus mume | 375 | 375 | 60% | 7.00E-99 | 75.73 | 1820 | XM\_008244275.2 |
| 4 | Prunus persica | 348 | 348 | 60% | 2.00E-90 | 75.07 | 1874 | XM\_007202060.2 |
| 5 | Vigna angularis | 327 | 327 | 59% | 2.00E-84 | 74.93 | 1655 | XM\_017586752.1 |
| 6 | Vigna angularis | 327 | 327 | 59% | 2.00E-84 | 74.93 | 1767 | XM\_017586750.1 |
| 7 | Vigna umbellata | 316 | 316 | 59% | 4.00E-81 | 74.66 | 1919 | XM\_047323018.1 |
| 8 | Pyrus x bretschneideri | 196 | 196 | 38% | 6.00E-45 | 74.33 | 1512 | XM\_048578713.1 |
| 9 | Prunus persica | 97.1 | 97.1 | 13% | 6.00E-15 | 77.78 | 3131 | XM\_020556493.1 |
| 10 | Drosophila hydei | 65.8 | 65.8 | 3% | 2.00E-05 | 95.12 | 2173 | XM\_023318101.2 |
| 11 | Drosophila novamexicana | 63.9 | 63.9 | 2% | 6.00E-05 | 100 | 2704 | XM\_030711399.1 |
| 12 | Alosa alosa | 62.1 | 62.1 | 2% | 2.00E-04 | 97.22 | 1834 | XM\_048244535.1 |
| 13 | Drosophila takahashii | 62.1 | 62.1 | 3% | 2.00E-04 | 95 | 3325 | XM\_044392753.1 |