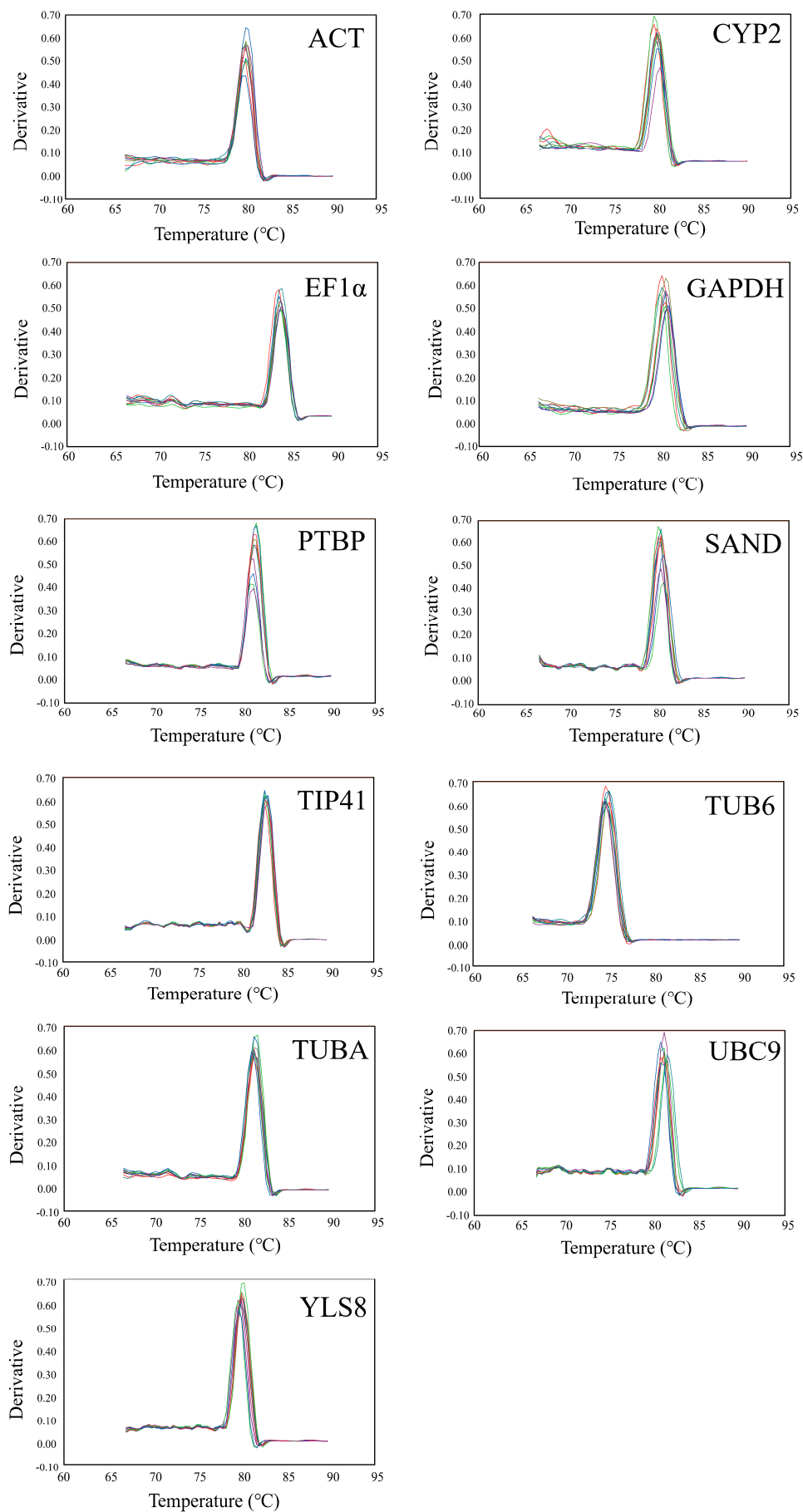


**Figure S1.** Agarose gel (1.0 %) electrophoresis showing amplification of a specific PCR product of the expected size for each gene. M represents a 500 bp DNA marker.



**Figure S2.** Melting curves of 11 candidate reference genes tested in this study.

**Table S1.** Information of all candidate genes and target gene in *A. dahurica*.

**Gene abbreviation-** *SAND*. **Gene ID-** TRINITY\_DN30497\_c0\_g1\_i3

**Gene sequence-**

CTGGCGGTACATTAACAATTCAGGTGCTTCTATTGCAATATTGCAAAATTGTAGGTTGGCCTCAATGAA  
ATATACCTAGAGATGGATTACAGACTTAGCATACAAACATACAGTAAATGACAAATACATCTGATGA  
TACATTCAACGAACATAAGGATTGATATATTATGATCGGCATAATCTTGCTGTGTTAGAACCTTGTTT  
AAAAATCAAACTAGTATACATGAATAACATACTTTTCTGGAAACATCACCATGAAAAGGGGCTTGCT  
CCCAACAAAAAACTTCATTTTCCACATCTTTAACCCATTGGCATACTCGGTTGCATGTCTTTATAGCC  
AGTGCCTTGTCTGCTAGAGGATCAAATGCTGCATAAAGTTCAAAATCCTGAGTAACCCAGCAGAGTAT  
AACATAGTTCTCATCCCTTCTAAACTGGGTTTTGTGAGGACCAAGTTCTCTATCATGCATAGAAGTATA  
CAGCTTCTGATATGCTCTATATAATCTTTTCTGTTGTTTAGGGGTGTTGATCGGTGATGAGAACTCAGAA  
GATACATATTGATCTAGATACATACTGCGGTAAACGAAGTGCCAAAGCCCAGCAGGACCACCTAACAA  
GTGCCTTACACCTATCTGCGGAGTCCAGTGGAGGTCTAGGCTGACCTAAATGAGATGACAAAGATCCC  
GAGCGAGGAGATGGATTAACAGGCAAATCTTCGACACGCATGCCACCATCCAACATCGACCTTTGAG  
CTTCATTAAGAACATTTGACTTCAGAAGGACCATTTCGATACGGATCCTCCAATCTTTTAGACGATGAA  
ATGCATCAGGATTAGCAGTAAGCAACATCAAATATGTATCAGCATCAAGATAATACACATAACTATAT  
AAAAATGCCATTGGATTGTATCTCGGCAGACAGATTGGAGAGAAAGATTCAGATGTCTCTGAATGATTC  
AGATGACATCACAAAGTTGGCAAGCAAAAGCATATCATCAGGATGAAGAGATGCTTTTTGTGCACCA  
ACCAGACTGATGACCTTGTGTTTACACATTAATATCGGAAGAGGACACCTGACTCAGCAACATCCTG  
CAATATGGCACCGGCGGCTTGCCTTGTGGATAAGCAAGGGGAAGACAAGAGTAGGCATGAAGAAA  
AGTGGCAGGGTTCCAATAAACGAGTGGATGAGAGAAGAGAACACAGCATCTGTTCCCCCAAGCAA  
AGGCATCATATCAAATTTTCGGATTCTTCTCAAAGCATCTATTTATAGACTTTGTGAGAATAAGTATCAT  
CTGGCCATAAAGAAGTTCCAGTTGTTCACTGAGGGATTCATGAGGCTCTTCTGTACAGCTTATGCAAAC  
TAGATATATAGGTCCTTTAACAAGAAAAACCACCTGGTGTTCCTCCGCCCTAACCAACTTCACACGAT  
CTCCCCCATTCTCCACGAAGGAAATGATGGCTTGCAAAGTTGCTGAAAATCCTGCTAGTCTGTGTTTCAT  
CTCCATATCTTGAATATATTGGTTTTCCGGAATGGCTTAAGATAAAAAAATGCTTCTTCCTTTTCTCCA  
TGAAGCAGAAGCATCATCTTCATTAACATGCCATTTCCAGGGACCCATTCCGAATCCACACTACAAC  
CAAAAGAACCACTCCTGTTATCCACCTCATCATCGCCACTAATCTCCTCGATACCTGAACCACTTATAC  
CACTACTACTAGTCCCTTTTCTCCAGCATATCCACTACTACTCGGACTCCCTTGCCCTTCCACCTC  
AACTTCCACATCCGAATTATTCCTCCACAACACTCCTTCGCCTCTCGAATTTCCAATACTTCTCTCTCT  
ACTTCTGTATACGAATCCGAACCTAATATATCCACTTCTCCAGAATTTTCAACTACTTCTCCGACTCGC  
GAATGTGAATCTGAAAGTAATGTACCGGTATTTTCTGGATTTTCAGCTACTGCTACTTGTTCGAGTTGC  
AAATGTGAATCAGAAGGTAATGTATCGATAGTTTGGGGATTCTCAGCTACTTCGAGTTGCGAATGTGA  
ATCGGAAGGTAATGTATCGATATTTTCGAGATTTTCAGCTACTACTTCGAGTTGCGAATGCGAATCGGA  
AGGTAATGTAGCGGCATTTTGGAGATGAGGGGGTATTAGGGGTTTTGAGTTGTGGTGATTGAGTGAAA  
TAGAGGTTAATTGACCTTCAATAGCGTCGAGAGATTGGTCAATAGAATCATGAATACAAGCTGAATTA  
GGAGTAGCAGATGATGACCCTGCAATGCTAGTAGATAAGCTCCCAAGTTCTGTTCCAGTCTCATTGTGT  
ACAATTTCTTTGAATCAGAAGATACAGAGTCTGAATTAGCTACTGCTGCGATTCCGATATCGATCGCC  
GTTGAATTCTCCATTTTGATCGAAATTTTAGCACTTATAAACAGAGTTGTGTATATATACACTTATACA  
GGAAGGAGAGAGAGAGGGGGGGGAGAGAGTATAAAACAATCAGAGAAGAGAGAGAGAGATTATAA  
AACAAAGAGATGGTGTATAAAATAAAGAGAGAGAGAAAG

**Gene abbreviation-** *PTBP*. **Gene ID-** TRINITY\_DN27766\_c3\_g2\_i10

**Gene sequence-**

GACAAAAATAGGTAAGTGGGTAAGAACCCCCCAGAATAACCAAAAAAAAAAAAAAGCTTTCCAGTCA  
ATGTCACTCAAACGTGTGACCTAGAAACATATTTATCACGCCACTAGAATTTTAAGTAGAACACAGTAC  
AATCTGCCATCCGCTACTTGATGTTTACAAGGATATGCACACATATCCTTGGTTGGACACCAAAGGAC  
AGTAAATAGAACAAAAACAATTTGAAGAATTCAAGTCTACTGAACAGAACTGATACAACCTTACTATC  
AGTAAGGTGGGTGGTGGTGATTATGTGGGGAAGAACTATCATGTTGCATATTTGACTGATTCCCAGGC  
TGACCTCCACTTGCTGAAGAACTGGGATTGATTGGCTGCTGTGTCCAAGAGGTGAGGAACCAGCAGG  
AGAGGCCATAAGATTATAAGCCTGACCAGAGGGAGGCCATAAGTTTGTCCAAGTAATGTGTTAGGG  
CCTGAAACAAAGGAGGGTCTGCTAAGCTGCATGGCTGGATTCCAAGATGGAGTTTGTCCAGGCGGGC  
CCTGCATGGGAGGTCCGTGGGCAGGAGGTCCTTGCCCGGAGGTCCGTGGTCAGGTGGACCTTGACCG  
GAAGGACCGTGGCCAGGAGGTCCCTTGACCGGGAGGGCCGTGGCCAGGAGGTCCTTGACCGGGAGGG  
CCGTGGCCAGGAGGTCCCTTGACCGGGAGGACCGTGGCCAGAAGGTCCTTGACCGGGAGGGCCTTGAG  
GCTGCCCATTAATTGATACTAGAAAATTCGCTCCCAATAAAGACCGGAGCAGCATGAGGATTCTGCCAT  
ACTGTTGCTCCAGCAGGCAGACCAGCAGCAAAACCGGACTCTGGTACTGTATAATCCCTACTTTTATC

GCTGAAGGCCTTTACATTGAGATCAGTATGACGAGAGTATGATATATGAAGCTTACAGTAGCCACCAT  
CATATATGCAGTGTCCCTCTAGAGCATCTTTAGCTACAGCGGCAGTGTTGACATCAGGATACTGAATTA  
GAGCCTGAGTTGTCGCGTTCTTCTCGAATATAGCAATTTTCTGAACCGTACCAAATGCAGAGAATACC  
GTGTTAAGAACATCTACAGTGACATCATAGATCCTATTTTCAATTGAGGCAAGAAGTACATTACTCTCC  
GGTTCTTTTTTCTTCCGTCAGGACCTACAACAGGCTGGACAAATCCCTCAATTGCAGTTGCATTAACA  
GGAAGATATGGATTTGTATAGTCCCGGCTACGGTGTGATTGGAACCTGATGTTTAGATCTGTGTGAGCT  
GAATATGAGATGCGCAGATTGCAAGAACCAACATGTTCTGGAAGCAAGTACCTTGAATACTTCTGCC  
ATCTAAAGCTTCCCTTGCTGAAAGAGCAGTCTCAGCATCAGTAACTGGATTAGTGCCTGGAAACCTG  
CTGCCTTCTCAAAAGTAGCAATCTTGTGCACAAATCCAAAAGCCGAGAAGACCAAGTGAATCACATC  
AATGCTTACATCACCGGCTTCTACACCCTCAATGGTTACCAGCAAGACATTTCCCGGAACATCACCTG  
GACCTTGTGTGTGACAATTTTCATGTCTGTTTGAATACTGTATATAAACATGTTTACCCCGAACAGATG  
CAGGTTCCGATGATGAAGCATAATATGAAACCATATTAATGGCCTGATTAAGATCCACAAATTCAACG  
AAGGCTTGATTGCGATTAGCGCCGACATTGCACTTGGTGTTAACGATCTTACCAAAGGCTTGCAAAG  
CTCAACGAGCTCTTCTTCGATACACTCCCAAGGCAAGTTACGCAAGTGAAGCACTTTAGATGGAGTCT  
GTGTGTATCGAAATTGAGGCTGATTTGAATTCGACATCCGCTCACTTTTGATTCAATTAGGGTTTTGTTT  
GTGTGTATATATATATGTAGTATTATTTGTATGGTGGTGCTGAATATGCAGAGGAGAGCTGAACGTTT  
T

**Gene abbreviation-** *GAPDH*. **Gene ID-** TRINITY\_DN26270\_c0\_g5\_i1

**Gene sequence-**

CAAAAATATCATCTCTTATCTTATAGAAATCTCTACATTTATCCTCACCACACACTCAGTTTGTAACCTC  
AAGATGCATATTCAGCATTAATACTTATATAGTTTCTCTTTTGCAAGGAACTTTTAAATAATATTTGTT  
CAATTTAATAAAGACAATATCTTAATAGAAAAAAATACAGAATAACACAAAATTAACCTTGAGATGG  
AACTAATGAGGAGTTCAATTAAGCTGCATGATAGAGTTGGAAGTAAAATGTAAGTGTATTATGTATAA  
ACACTGAAAAATAAGAAGAAAAAAGTAGGTATTCTCTGAGTCTTTAGTTGCAGCAATGGCTTGTA  
AGCAGCTCTGGTTTCTTCAAGCCTTCCAGTAAATATTAGACTTCCATCTAGAAGCTCTTATTCTTTCCCT  
GCTCATTGCTCCTCCAAGAGACTTGAAGTAGCTGAGTTTCCGGGCTCCGATCCAGTGTTTCGCTCACA  
TATTCAAAGAATGCTAGTGAAGGATCTTTCTTTGATGTGGTGGCTTCCCAACTTTCTCCTGAGACTTCA  
GGATTATCCCCTGTTAGAGGACAAACAGTTGCCAAATTGAAGGTAGCAATCAATGGTTTCGGACGCAT  
TGGCAGGAATTTTCTTCGTTGCTGGCATGGACGCAAGGACTCTCCACTCGAAGTTATTGTTGTCAATGA  
CAGTGGTGGTGTCAAGAATGCATCGCACTTGCTCAAGTACGACTCAATGCTGGGCACTTTCAAGGCAG  
ATGTTAAGATTGTAGACAGTGAGACCATCAGTGTTGATGGAAAGCACATCAAGGTTGTCTCCAACAGA  
GATCCACTCCAGCTTCCTTGGGCTGAGATGGGAATCGACATTGTTATTGAGGGTACTGGTGTGTTTGT  
GATGGCCCTGGGGCTGGGAAGCACATCCAAGCAGGGGCAAAGAAAGTTATTATCACCGCACCAGCA  
AAAGGAGCTGATATCCAACCTACGTTGTTGGCGTGAATGAGAAAGATTATGGTGATGACGTTGCTAA  
CATCATAAGCAATGCTTCTTGCACTACAACTGTTTAGCTCCTTTTGTGAAGATCTTAGATGAAGAATT  
CGGTATCATTAAGGGAACCATGACAACCACTCATTCTTATACAGGAGACCAGAGGCTTTTAGATGCTT  
CTCATCGGGACTTGAGGAGAGCCAGAGCTGCAGCTTTGAACATAGTCCCAACAAGTACTGGTGCAGC  
CAAGGCTGTATCTTTAGTGCTACCCCAACTGAAGGGTAAGCTGAATGGCATTGCACTCCGGGTGCCCA  
CGCCTAATGTATCCGTTGTTGACCTTGTTATAAATGTCGAGAAGAAAGGACTTACTGCTGAAGACGTC  
AATGCTGCCTTTAGAAAGGCTGCTCAAGGACCACTGAAGGGAATTCTGGAGGTCTGTGATTTGCCTCT  
AGTGTGCGGTGGATTTCCGGTGCTCTGATGTTTCATGCTCCATCGATTTCATCATTGACAATGGTCATGGG  
GGATGACATGGTCAAGGTCGTAGCCTGGTACGACAACGAATGGGGATACAGCCAAAGAGTTGTAGAT  
TTGGCAGATTTGGTAGCAAGCAAATGGCCAGGTGCAGCAGTAACTGGAAGTGGTGATCCATTAGAAG  
AGTTTTGCGAGACAAACCCTGCTGATGAGGAATGCAAAGTTTATGAATAATTTACCTTTGTTCCACCTT  
TATGCTTCCCAATTAAGTTGTTTAGGTGGTTGTTAAGTTCAAGTCATTGATGTGTTAGTGCGTCATGAT  
TTGTTTCGGAAGTGCAAGTATAATATGGAATCAGAGGATGGGGAGAGTCGGTCTAAACTACCAAGTG  
CAGGGGAAGGTATCGGAAATATGCTGGTTCTTGCAATTATTAGATTGGTGCATAATTGGGTAAATTTGAA  
ATGAACTGGTGACTGAAATAAGATCTGTGGGGAACATCAAGATATTGATGTTTTCAAAGATAGATGCC  
TGCTGTGTTTCAAAATTATTAAGCTTTGTTTTAATTATTACTCTTGACCGAATGGCCAACATAGAGGCTGC  
AACTGTTTTCTTGCTCTGCCTTTTACTGCTGTTTTTCTCTCCTTAATTAGTGGCAACATTTGATAATGCTT  
AGCAGCTGTAAGAGCTCCAACCTGCATAAAAGTAAACATACCATGACAATGTGCTCATACGGACTCGA  
CCAAGTCAAGAAAATAGACAGCAACCTCGCTCATGTAAGTATTCCCACCTAAACCAGCTAATAGAT  
AGACCTCCAACTTACTTGTAAGCAACTTTTGTAGCAGCACCAAACACTCCAACTTCTGAGCAGCTG  
AAGTGCTATACATTACAATGGCTCATTCTCTCATTTTTTC

**Gene abbreviation-** *ACT*. **Gene ID-** TRINITY\_DN29396\_c0\_g2\_i4

**Gene sequence-**

AATATAAACATGTGTTGCAGTAAAAGGAAAGAAAATGAAATTAAGTATTTAATAATTGGATAGGAA  
AATCAACATAACAACTCAACTCTAAGCATCCTACTAACAAGTCACAATTTTCTTTAACATACAGACT  
GATATACCAAACATAGTAGACAAAGAGTAGATGCATCAAAATCATTTTATCCTCTCTCCCAATTGTCA  
ACCCATCACAGGTAACCAAGTTCACATGAAAAATTACATTAAGCCAAATAAATTGAAAAAGAAA  
CTCCGAGTTCCAATGCATATAATACTGTAGAACTTAGAAGCACTTCCTGTGCACGATTGATGGGCCAG  
ACTCATCATATTCACCCTTGGAGATCCACATCTGTTGGAAGGTGCTCAGTGATGCAAGAATGGATCCT  
CCAATCCAGACACTGTATTTTCTCTCAGGTGGTGCAACAACCTTGATCTTCATGCTGCTGGGAGCAAGA  
GCAGTGATTTCCTTGCTCATACGATCTGCAATACCGGGGAACATTGTCGAACCACCACTGAGCACTAT  
GTTTCCATAGAGATCCTTCTGATATCAACATCACACTTCATGATGGAGTTGTAAGTAGTTTCGTGAAT  
TCCTGCAGCTTCCATTCCGATCAAAGATGGCTGGAACAGAACCTCAGGGCAACGGAATCTTTCAGCTC  
CAATTGTAATAACTTGACCATCAGGCAATTCATAATTCTTTTCCACAGAAGAGCTACTCTTCGAAGTTT  
CAAGTTCTGCTCATAGTCGAGGGCAACATAAGCAAGCTTCTCCTTCATGTCACGCACAATTTCCCGCT  
CGGCAGTGGTGGTGAACATGTAACCTCTCTCAGTTAAGATCTTCATGAGAGAATCAGTGAGATCACGC  
CCAGCAAGATCAAGACGAAGAATGGCATGGGGAAGGGCATAACCTTCATAAATTGGTACAGTATGGC  
TCACACCATCACCAGAGTCGAGCACAATACCAGTAGTACGTCCACTTGCATATAGAGAAAGGACGGC  
CTGGATCGCAACATACATAGCAGGAACATTAAATGTCTCAAACATGATTTGAGTCATCTTCTCCCTGTT  
GGCCTTAGGGTTGAGTGGTGCCTCAGTTAGAAGAACTGGGTGTTCTCTGGAGCAACTCGAAGCTCAT  
TGTAAGAAAGTGTGATGCCATATTTTCTCCATGTCATCCCAATTACTTACAATACCATGCTCAATTGGAT  
ATTTCAAGGTAAGAATACCTCTCTTCGACTGGGCTTCGTCACCAACATAAGCATCCTTCTGTCCCATCC  
CAACCATCACACCAGTATGTCTTGGTCTCCCAACAATACTGGGGAACACCGCTCTGGGAGCATCATCA  
CCAGCAAAACCAGCCTTCACCATTCCAGTTCCATTGTCACAACTAGGGGCTGGATATCCTCAGCATC  
GGCCATTTTATGTTACTGATAAAGAGTTGCTTTATCTCTCTCGATAATCTCTCTCTCGATAATCTCTCT  
CTGTTGTAACGATGAAGCGGATATGAGAGTAGTG

**Gene abbreviation-** *TIP41*. **Gene ID-** TRINITY\_DN25936\_c0\_g1\_i2

**Gene sequence-**

TAAAAAGATGTATAATGCAGAAGGTGTTTACATGCCTCTGGAAAATTTGTCTCAAATCTCAATTCAAGA  
GCAAGGAATATGGTAATGTATGCAGCTGGATGCCAAAGTAAAGATAAAAAACATTATGCAGTAAAAAG  
TAAAAACTGTGAAGATATAAATAAACTTTCCAGCATGTAATGATAAAATACAGCATTTCCATACT  
ATAAAGGATTAGTATAAGCGCACTGCGTACATGTTAATCAGGAATTATAAGCTTTTGGGTCTTATGCA  
AAATGATAGGAAGTCTTTGGCTGATGCTGCTTGGATCAATATACGCAGCACAATCAGAAGGATATCCT  
TTAGAAGCTAGTGCTTGAAATGTGGCTTCTCTCCAGCAACATTCTCTCAGAATAACTGGTTTTTTACCCT  
CACCAAAAATGCAATGGATGCGTGTGTCTTTAAACGCATAAGCACACCATCAACTCTAAGCCAAAA  
ACGCAAGAGAAGAAACCAACAGCTTGGCATCACTCTCACTTTTACTGTTAAAGCGCACTCCACTAT  
CAGCCAATTCATCTTCATAGAAGATCACCTCATCATAGAAGAGAATAGGCTCTTTTGATGCAAGTGCA  
GTCAAATTAATTCGTTCCCTCGCAGTCCTCCCAACGAAGCTTGCAACTGCCCTTCATCAGAGATTGTATCC  
CTCTCTGAGTTTTTCTCAACAGTTTCACTTCCACAATATGGTGTGTAAATGTGTAGTCATAATCTAATA  
TCACCTGCTGGAAAGGTTTGCATCTAAATTTCCAATTTGCTGCTGCAGGGACCTCAACTGGCGGTAATT  
TTTCTGCTTCCAACCAACTAGAGAATCAAATGCGTTGAAATGAATCTTACATCGCTCTTCAAGTGCT  
TGAGAACCAATGAACTTTCCCCAAAAACCATTTCTGGCAAGTGAGAGGTCTGAAGCTTTTGTTCAC  
AATTGGACGTTGACTGAGTTGAGGATGGGGAACCTGCGAGTTTCAATCTCCAATCGTTAATTATTA  
CCAGTTCTTCCGTCAGGAAGGAGCTGAGCTCCGGCAGCTTTAAGCTCTTCTTGTGATCTCAACTTCC  
ATATTCCGACTTGTTTACCTGATCAGCCGGTCACCAGTTGCCTATATATATCTTCAAGTGACAGCGAGC  
TCTAATGATTCTTTTTCCGATTTTCA

**Gene abbreviation-** *CYP2*. **Gene ID-** TRINITY\_DN25407\_c0\_g2\_i1

**Gene sequence-**

TTAGTTAAAAAAACACACACAAAACACATACAACCTCTCTCCGATCTCTCCACCGTCGTTGATCTCTC  
TCCGGCAGGCTTGAAGGTGGGAGCTAGACGGGAACCTCAGGCTCGTGCCTTGATGCCAGGTGTAGCT  
TGACAAGTGCACGTTTGTATGCTGTGTTCAGTTATAGAAAATATGGGTTCTTTCTGCAGTAAACAGCGA  
CATAATCAAGCTGATTCCGAAGAAAATGCACAGACTGCAGAAATAGAAAGGCGAATTGAGCTAGAA  
ACAAAGGCAGAGAAACATATACATAAGCTTCTTTTACTTGGTGTGAGAGTCAGGAAAATCAACAA  
TCTTTAAGCAGATAAACTTCTATTTAGACCCGGCTTTAATGAGGCTGAGCTAAAGAGCTACATTACA  
GTTATTCATGCAAATGTGTATCAGATAATAAAAAATATTATATGATGGGGCAAAGGAATTGGCTCAAAA  
TGAAGAAGAATCCTCAAAATATGCTTTATCGGTTGAAATCAAGGAAATAGGAGAGAAACTATCGGAA  
ATTGGTGGCAGGTTGGATTATCCTCGCCTCAGTAAAGAGCTTGCTCAAGAAATAGAACTCTCTGGAA

AGACGACGCGATACAGGAAACATATTCTCGGGGTAATGAACTCCAAGTTCCTGACTGCACTCTTTATT  
TCATGGAAAATTTACAAAGGTTGGCTGTTGCGGATTATATTCCGACAAAGGAGGATGTTCTTTATGCA  
AGGATCCGTACAACCTGGTGTGTAGAAATTCAGTTCAGCCCGTTGGAGAGAAACAAAAAAGTGGCG  
AAGTATATAGATTATTTGATGTTGGAGGTCAGAGAAATGAGAGAAGGAAATGGATTTCATCTGTTTGAA  
GGTGTACAGCTGTGATTTTTTGTGCTGCCGTTAGTGAGTATGATCAGACTCTTTTTGAGGACGAGAAC  
AGGAACAGAATGATGGAGACAAGAGAACTCTTTGAGTGGGTCCTCAAGCAGCCATGTTTCGAGAAAA  
CATCCTTCATGCTGTTTCTGAACAAATTTGATATATTTGAGAAGAAGGTTCTAGATGTGCCACTAAATG  
TATGCGATTGGTTTAAAGATTACCAACCAGTATACTCGGGAAAGCAGGAAGTCGAGCATGCATATGA  
GTTTGTCAAAAAGAAATTTGAGGAGCTATATTTCAAAGCACTGCCCTCACTGCGTGGACCGAGTTTT  
TAAGATATATAGGACAACCTGCTCTTGACCAGAAGCTTGTGAAAAAGACTTTCAAGCTGGTAGACGAG  
ACCTTAAGAAGGCGAAACCTCTTCGAAGCGGTTTGTGTGATAGTGGATTTTCATCCGAAAGGAAATG  
TTAATATCTTGAAAAGCTAGATTCTGCAGTGAGGTGGGAACACTCATTAAACTCTTTACACCGTAATT  
TACAGGTAAAAAATGGCTGTTTGGTATACCCTCTGTAATAGGAACTTGATGTTACCCCTGTTTCTTTTT  
GCCTTAAAAGAAGTCCCCAAGATTTTGTCTGTTTGTAGCATACCGCTAGTTGGAGAAGCAAGCAA  
GTATATCAAAAGTTTTTTTATACCTTAATTTGTTTTTGTTTTTTACAGTGATCTGTTTTATGTTTTACCT  
AAGAATTG

**Gene abbreviation-** *EF1α*. **Gene ID-** TRINITY\_DN32140\_c1\_g3\_i6

**Gene sequence-**

CAAGAATTGAGGTCAATAACAAAAAAATACTAATATCGTCCATTTCATTTAAAGATTTTTTCTCTAT  
ATAAAGTTTCTATCAAGTTTTACAACACCAGTCTCTTCTTTCATCAAGGCCTTTTTTGTCAACATATATA  
GAGTTCATCTCTTTGACAAGTTAGTAGCTGATCACAATGGGCAAGGAGAAGGTTACATCAGCATTGT  
GGTGATTGGCCATGTGGATTCCGGAAGTCAACCACCCTGGTCATCTCATCTACAAGCTTGGCGGGA  
TTGACAAGCGCGTGATTGAGAGGTTGAGAGAAAGAAGCAGCTGAGATGAACAAGCGTTCGTTCAAGTA  
TGCGTGGGTGCTTGACAAGCTCAAGGCTGAGCGTGAGCGTGGTATCACTATTGATATTGCTCTGTGGA  
AGTTTGAGACTAACAAGTACTACTGCACTGTCATTGATGCCCTGGACATCGTGATTTTCATCAAGAAT  
ATGATTACTGGAACCTCTCAGGCTGACTGTGCTGTTCTTATCATTGATTCAACTACTGGAGGTTTCGAA  
GCTGGTATCTCCAAGGATGGGCAGACGCGTGAGCATGCCTTGCTTGCTTTCACACTTGGTGTCAAGCA  
GATGATTTGTTGCTGCAATAAGATGGATGCCACAACCTCCAAGTACTCCAAGGGTAGGTATGAAGAA  
ATTGTGAAGGAGTTTTCTTCGATTTGAAGAAGTTGGGTACAACCCCGACAAAATTGCATTTCATTCCC  
ATCTCTGGATTTGAGGGTGACAACATGATTGATAGGTCTACCAACCTTGACTGGTACAAGGGACCGAC  
TCTTCTGAAGCTCTTGACCAGATCTCTGAGCCCAAGAGACCATCAGACAAGCCCCCTTCGTCTCCCACT  
TCAGGATGTTTACAAGATTGGAGGTATTGGAACCTGTTCCAGTGGGACGTGTTGAAACTGGTGTGATCA  
AGCCTGGTATGGTTGTGACTTTTGGTCCCTCAGGGTTGACCACTGAAGTCAAGTCTGTTGAGATGCATC  
ATGAGGCTCTCCAGGAGGCTCTTCTGGTGACAATGTTGGATTCAATGTTAAGAATGTTGCTGTTAAGG  
ATCTCAAGCGTGATATGTTGCCTCCAACCTCCAAGGATGATCCCGCCAAAGAGGCTGCCAACTTCACT  
GCTCAAGTTATCATCATGAACCACCCTGGTCAGATCTCAAATGGTTATGCTCCAGTTCCTTGATTGCCAC  
ACCTGTCACATTGCTGTTAAGTTTGTGAAATCCAAACCAAGATTGATCGTCGATCGGGTAAGGAGCT  
TGAGAAGGAGCCCAAGTTTTTGAAGAATGGTGATGCTGGATTGTTAAGATGATTCCAACCAAGCCAA  
TGGTGGTTGAGACCTTTATGACCTACCCTCCTTGGAAAGTTTGTGTTAGGGACATGAGGCAGACTG  
TTGCTGTGGGAGTCATCAAGAGTGTGGAGAAGAAGGAACCTACCGAGCCAAGGTCACAAAGGCGG  
CAATCAAGAAGAAATGAACCGGTGCTGTTGGTGGGTATCGGTGTGGTAATACTGCAGGCTGGATTGCT  
CTTGTTGGTTTTAATATTAAGTCAAGTTTCTGTTATGTTTCGTGTCATGTGTTTTGCTGTGTCAGCCACCTG  
GTCGCAGAATTGGGTGCTTGACAGGCGGTGGTGTGGCTATTATTAGCCTGTTATCCTTGTTGCTTTTT  
CTTCTTGTTTTCTTCTGTTTTTAAAAGACTACCGTGTTATTTGATGTTATATGACAGACCAGCCGTTGA  
TTTTGGTGTATGTTGCCCTTGAGTGTGTGATTCTTTTTTGCCAAGTTTATATGTTTAGTTTCATCTACG  
AAAGACTGCCGTTTTGTTTAGATATCTTGACAATGTTATTTACCAGGTAAGATTGAAGTGGAAATTGT  
TTCTTCAAGTGTAACAGTAACGTGGTTAGTCATCCATGTATGTATGTTTGAACCTCCATCTCATTTCGG  
AAAATTGCTTTTTTC

**Gene abbreviation-** *UBC9*. **Gene ID-** TRINITY\_DN32451\_c0\_g1\_i7

**Gene sequence-**

CACGCTACTATCATCATTTTTCTCTACATCTTCCACTTCATTTACAGCTTCCATCTTTCACATTTCTTGGTAA  
GTAGTTGACGATGGCTTCTAAGAGGATTTTGAAGGAACTTAAGGATCTTCAGAAGGATCCTCCTACTTC  
TTGTAGCGCTGGCCCTGTTGCTGAAGATATGTTTCACTGGCAAGCTACAATTATGGGCCCTCCAGATAG  
TCCTTATTTCTGGTGGGGTTTTCTCGTTACCATAACATTTCCCTCCAGATTATCCGTTCAAGCCACCAAAG  
GTGGCATTTAGAACAAAGGTTTTCCACCCGAATATAAACAGCAACGGGAGCATATGCCTAGACATTCT  
GAAAGAACAATGGAGCCCTGCTCTGACCATTTCGAAGGTTTTGCTGTCAATATGCTCCTTGCTGACAG  
ACCCAAATCCGGATGACCCTTGGTGCCCGAGATAGCTCACATGTACAAGACAGACAGAAACAAGTA

TGAAACAACCTGCAAGGAGCTGGACCCAGAAGTATGCCATGGGTAAAGAAGCTATGCGTTTATGATGG  
AATTGCCTTTCTCTTAAAAATAATT

**Gene abbreviation-** *TUB6*. **Gene ID-** TRINITY\_DN9948\_c0\_g1\_i1

**Gene sequence-**

CTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCATGTGTAGATCTACGAATGTTGGCAATGTA  
AATGAACTCGTTGAAATGTGTCCATATTTTGTATATATATTCTGATTTTGTATGGTATTTGTTTATT  
ATTGTTGAAGATGAGATGACTACAGATCTTCGAGTATTGGTTATTTATATGAAGTTGTTGAAATGTTTG  
TGTGTGTGTGCATGCATAGATCTGCGAGTATTGATGTGTAAATGAACTTGTGAGATGCGTGTATATAT  
GTGTGTGTATGAGATAAGGAAGAGTAGTGTGTTTACTAATTGTTTTTTGATTATTATTCACATTACGTA  
TTGCTCGAGCTGTATCCCTTTATGCCTATGTTTGTATTAAGTATACAAGTGTATTATGTTTTGTGCTG  
ATCTGATTCATATCTTCGTGATTTGTATGTTTTATTCAGTCTCTAGGTCATACTGTAAGACAGTAATG  
TATATACAGATCTGTATAGATTTAAACAAGCATGTGATTCTCGAATGTTCTGTATGGGTGTCAATTAAC  
TGAGCACATTCTGTTTGTAGGTTTATATGCAGGTGTTTGTCTCATGTGTTTCTCATGATTTGGTTTT  
AGAGATTTATATGATGTTGTGAGGTCTTTATTATTTTAATTTGAGAACTAATGCTAGACTTGATATGA  
CATGTGTGTATGTATAAGATTTAGATATTGTGCTGATTATTA

**Gene abbreviation-** *YLS8*. **Gene ID-** TRINITY\_DN29984\_c0\_g1\_i5

**Gene sequence-**

GGTGAGAGAGATGAGCGAGAGAGATGAGACAGAGAGGAGAGAGTTCGTTGTGTGAAAGGGGGGTGAT  
TGATAGTTGATACAATCGTCTATACCTAGATATCGAGAGAGAGATCGAGAGAGATCGAGATCGAGCG  
AGAGAGAGAGAGGAGAAGATGTCGTATTTGCTTCCACACTTGCCTCAGGATGGGCAGTAGACCAGG  
CGATTCTCGCTGAGGAAGAACGCCTCGTCGTATTTCGCTTCGGTCACGATTGGGATGAACTTGTATGC  
AGATGGATGAAGTACTAGCTTCTGTTGCGGAGACGATAAAGAAGCTTGTCTGTCATTTATCTCGTGGATA  
TTACTGAGGTGCCCGATTTCAACACTATGTACGAACTGTACGATCCTTCTACTGTTATGTTCTTTTTCAG  
GAACAAGCATATTATGATTGATCTTGGCACTGGGAACAACAATAAGATTAATTGGGCAATGAAGGAC  
AAGCAGGAGTTTATTGACATTATTGAAACGGTTTATCGTGGAGCAAGGAAAGGCCGTGGATTGGTCAT  
TGCACCCAAAGATTACTCCACCAAGTACCGCTATTAGTCTGTCTGCATCATTTGGCAGGTTGACGAG  
GCTAAACAATACTTTAACTGTTGAAAAGTATTATGTGACATCAAATTGTTCAAGTGAGTTGGGCCTTAA  
GGACTGTGTGCACCTTGAATGTGTGAAGGAACAAGGACATGGCAGAAATACCACTGAAGTTGCAGCG  
TCAATTTGCTACGTTCTTCAACAGGGTAGTCTCTAGCTCTACTCTTAATTTACTGTGTGCACCTTGAAT  
GTGTGAAGGAACAAGGACATGGCAGAAATACCACTGAAGTTGCAGCGTCAATTTGCTACGTTCTTCA  
ACAGGGTAGTCTCTAGCTCTACTCTTAATTTACT

**Gene abbreviation-** *TUBA*. **Gene ID-** TRINITY\_DN27287\_c1\_g6\_i1

**Gene sequence-**

CTTTGGTGATCTCAACCACTTGATTTCGGCCACAATGTCTGGTGTTACATGTTGCTTGCCTTCCCTGGT  
CAGTTGAACTCTGACCTCAGGAAGTTGGCTGTAAATCTAATCCCCTTCCCTAGGCTTCACCTCTTTATG  
GTGGGTTTTGCACCTCTTACATCCCGTGGTTCCCAACAGTATCGTGCTTTGAGTGTGCCTGAGCTTACCC  
AACAGATGTGGGATTCCAAGAACATGATGTGTGCGGCTGATCCCCGCCATGGTAGATACTTGACAGCT  
TCTGCTGTGTTGAGAGAAAGATGAGCACCAAGGAGGTTGATGAGCAGATGATCAATGTTGAGAACAA  
AGAACTCATCTTACTTTGTTGAATGGATCCCAACAATGTGAAGTCAACTGTTTGTGATATCCACCGA  
CTGGCTTGAATAATGGCTTCTACTTTTATTGGGAATTCGACTTCAATTCAGGAGATGTTGAGGCGTGTGA  
GTGAGCAGTTTACTGCTATGTTGAGGAGAAAGGCCTTTTTGCATTGGTACACAGGCGAAGGTATGGAC  
GAGATGGAATTCACCGAGGCTGAAAGCAATATGAACGATCTTGTCTGAGTATCAGCAGTACCAGG  
ATGCAACTGCTGATGAGGAGGGAGAATATTTTGAAGATGAAGAAGAGGAGGGGCAAGAAATGTAAG  
GTGTGTTCTGCCATGAGTGTACTGTGTGAACTGCTGAGTATGTAGGATGCTGCAACTGTGTGTTGCCTTT  
TGGGCAGTCTTCTGAAGCTGTTGTCTAGCTATTATGTGGTTTGTAAATTTCTCAAAGACAGTTTGCGA  
AATCTTGTTAAGAATTTAACTTGGCTTTGTTATTATATTCAGTTTATTTGCAGATTTAGTAGTTTTGGT  
TGCTTGGGTTACAAAAGCAAAGTTTACTTAATGATT

**Gene abbreviation-** *PAL*. **Gene ID-** TRINITY\_DN30247\_c1\_g2\_i1

**Gene sequence-**

ATGGATTGCCAGACCAAGAATGTTGTGTGAGTAAACGGGACAGGTGATTCGCTATGCATGCAGAAAG  
ATCCTTTGAACTGGGGAATGGCTGCGGAGTCATTGAAAGGAAGTCATTTGGACGAAGTTAAGAGGAT  
GGTGGCTGAGTTTAGGAAGCCTATGGTGCAGCTGGGTGGAGAGACATTGACGGTTTCTCAAGTGGCCG  
CTATTGCTTCCGGTTACGTCAAGGTTGAGTTATCGGAGACGGCAAGGGCTGGAGTTAAAGCTAGTAGT

GATTGGGTGATGGAGAGTATGAATAAAGGAACCGATAGTTATGGTGTTACTACCGGTTTTGGTGCTAC  
TTCTCATAGGAGGACTAAACAAGGTGGTGCTTTGCAGAAAGAACTTATTAGGTTTTGAATGCTGGAA  
TCTTTGGAAATGGAAGTGATTCTTCCAACACATTACCACATTCAGCAACAAGAGCAGCAATGCTTGTG  
AGGATCAACACACTTCTCCAAGGTTACTCTGGCATTTCGATTTGAGATCCTTGAAGCAATTACAAAAGTTT  
CTCAACCAAAAACATTACTCCTTGTTTGCCACTCCGCGGAACAATCACTGCTTCTGGTGATCTCGTTCCC  
TTATCCTACATTGCTGGACTTCTAACAGGACGTCCCAATTCTAAGGCGGTCGGACCCACTGGAGAAAA  
TCTAACCGCTGCAGAAGCATTTAAACTTGCTGGAGTTGATGGTGGATTCTTTGAGCTGCAGCCAAAAG  
AAGGCCTTGCTTTAGTCAATGGAACGGCTGTTGGTTCTGGGATGGCTTCGATGGTTCTCTTTGAGACCA  
ATATACTTGCTGTGTTAGCTGAGGTTATGTCAGCTATATTTGCTGAAAGTGATGCAGGGCAAACCAGAAT  
TCACTGACCACTTGACACATAAGTTGAAGCATCATCCAGGACAAATTGAAGCCGCGGCCATCATGGA  
ACACATATTGGACGGTAGCTCTTACGTTAAGGCTGCTCAGAAGCAACATGAAATGGATCCCCTGCAAA  
AACCAAAACAAGATAGATATGCTCTTAGGACGTCTCCACAATGGCTTGGACCGCAGATTGAAGTAATT  
CGATCATCAACAAAAATGATAGAAAGGGAGATCAATTCTGTCAATGATAACCCTTTGATTGATGTGTC  
AAGGAACAAGGCCATACATGGTGGTAACTTCCAGGGTACCCCTATTGGAGTTTCTATGGACAATACAA  
GGTTGGCTATTGCAGCCATTGGAAAGCTCATGTTTGCCCAATTTTCGGAGCTTGTGAATGATTTTTATA  
ACAATGGGCTGCCATCTAATCTATCCGGAGGACGTAATCCAAGTTTGGATTATGGTTTCAAGGGTGCT  
GAAATTGCTATGGCTTCTTACTGCTCTGAGCTGCAATTTTTGGGCAATCCAGTCACCAACCATGTCCAA  
AGTGCTGAGCAACATAATCAGGACGTGAACTCCCTGGGTTTAATCTCCTCGAGGAAAACAGCAGAAG  
CTGTTGAAATCTTGAAGCTCATGTCTACCACATTTTTGGTAGGCCTCTGCCAAGCTGTAGACCTGAGGC  
ATCTGGAGGAGAACTTGAAGAGCACTGTGAAGAACACTGTAAGCCAAGTAGCCAAGAAAGTCCTAA  
CTATGGGTGTCAACGGTGAGCTTCATCCTTCAAGATTTTGCGAGAAGGATTTGCTTAGAGTTGTTGACC  
GAGAGTACATTTTGCATACATTGACGACCCCTGCAGTGCAACCTACCCATTGATGCAAAAATAAGA  
CAAGTACTAGTTGAACACGCACTGAAGAATGGCGAAACTGAGAAGAACTTGAGCACTTCAATCTTCC  
AAAAGATTGCAGCTTTTGAAGATGAATTGAAGACCCTTTTGCCAAAGGAGGTTGAAAGTGCTAGGGCT  
GTGCTTGAGAGTGGAATCCTGCCATTCTAACAGAATTAAGGAGTGCAGGTCTTATCCATTGTACAA  
GTTTGTAAGGGAAGAGTTGGGAACAGTTTATTTAACCGGTGAGAAAGTGACATCGCCTGGAGAGGAG  
TTTGACAAGGTGTTACGGCAATGTGCAAAGGACAGATCATTGATCCTCTGATGGAGTGTCTACAGAG  
CTGGAATGGAGCTCCTCTACCAATTTCTTAG

**Table S2.** Ct values of 11 candidate genes of *A. dahurica*.

Treatments	Replicates	<i>SAND</i>	<i>PTBP</i>	<i>GAPDH</i>	<i>ACT</i>	<i>TIP41</i>	<i>CYP2</i>	<i>EF1<math>\alpha</math></i>	<i>UBC9</i>	<i>TUB6</i>	<i>YLS8</i>	<i>TUBA</i>
control (Sterile water)	1	26.7796	24.9754	20.5092	21.7106	25.2387	23.4786	18.5456	21.8313	26.9064	21.8604	18.9995
		26.0154	26.2328	21.3897	21.7227	24.7191	23.247	18.3417	21.6811	27.0457	21.6851	19.9748
		25.6375	25.3116	20.5816	21.5386	24.4656	23.5801	18.37	21.6032	26.7851	21.5499	19.4524
	2	24.7305	25.2539	20.5479	21.3273	25.2951	23.7765	18.58	22.0090	26.4068	21.7510	18.7972
		24.6274	25.3785	20.4767	21.4485	24.4048	23.9245	18.461	21.8286	27.0241	22.2643	18.8000
		24.5452	25.1263	20.6160	21.6452	24.3100	23.7071	18.5504	21.7288	26.5058	22.0746	18.6702
	3	25.2893	25.3798	20.3741	21.5655	24.8711	23.5564	18.5320	21.6482	26.7834	21.7418	19.2246
		25.4773	25.2239	20.3689	21.4896	24.7389	23.6190	18.4750	21.7803	26.7790	21.8642	19.1157
		25.4013	25.3357	21.3177	21.6414	24.6067	23.6816	18.4180	21.9154	26.7746	21.9866	19.0068
SA	1	21.7174	22.0633	18.6099	19.1928	22.7132	22.5562	16.5078	19.5212	25.6771	18.2956	17.8476
		21.9887	22.2833	18.4669	18.6875	22.976	22.2217	16.2551	19.4069	25.3198	18.0057	18.3292
		22.0935	22.3328	18.6546	19.5741	22.4223	22.9421	16.8064	19.0596	25.661	18.5891	17.6858
	2	22.0703	22.1887	18.5610	19.0431	22.3472	22.6054	16.4208	19.3074	26.1895	18.2997	18.5005
		21.9299	22.5842	18.8041	19.0439	22.0014	22.217	16.1815	19.2369	25.5632	18.1296	17.8355
		21.6310	22.6219	18.4918	18.8719	22.0394	22.0648	16.1237	19.1375	25.7548	18.1235	18.3066
	3	21.7614	22.2724	19.1491	18.7479	22.9699	22.6789	16.1549	19.163	26.0422	18.0615	18.1982
		21.9723	22.6694	18.4285	19.0275	22.0327	22.1581	16.3631	19.3403	25.4211	18.1858	17.7485
		22.3478	22.4948	18.3379	19.3941	22.4056	22.1642	16.105	19.1987	25.8507	18.0646	18.5728
NaCl	1	28.1626	27.6881	24.4006	23.8432	28.2176	27.2359	21.7818	23.3076	31.4448	22.6736	22.2059
		26.7949	26.3821	23.0588	24.0683	28.4427	26.1603	21.4205	23.2034	32.0233	22.1394	21.4259
		28.3305	26.7041	23.0741	24.5837	27.2681	26.4281	21.9248	23.1291	30.1621	22.1998	20.7281

	2	26.9465	26.6733	23.2006	23.5006	27.1249	26.6582	21.6848	23.0029	30.1340	22.4139	20.8482
		26.1030	26.8729	23.0847	23.7186	27.0179	25.9805	21.6646	23.2386	29.7338	22.3048	21.0040
		26.7713	27.5248	24.3431	24.8678	28.0863	27.4021	22.1602	23.5704	30.2343	23.3645	21.7983
	3	26.6052	27.0890	23.2472	24.5346	27.1836	26.0972	22.1598	23.0597	31.9393	22.4572	20.9445
		28.0183	26.7022	23.2406	23.6792	27.1727	26.6678	22.0168	23.0690	30.7128	22.4195	20.4672
		26.5768	26.8850	23.3479	24.0502	27.1328	26.0810	21.9005	22.9463	30.8291	22.3408	20.5944
MeJA	1	24.3847	22.8734	18.3225	18.8426	22.2894	22.3278	16.8268	19.3080	25.2183	18.6305	18.0991
		22.9342	22.2495	18.2781	19.2405	23.0147	22.0847	16.9592	19.2496	24.0228	18.2840	18.0059
		22.5406	22.4879	18.9565	19.7952	22.8795	22.2989	17.0654	19.1088	25.5384	18.4930	18.5912
	2	22.4508	22.4930	18.5868	20.0964	22.2652	22.364	16.8964	19.2758	26.0537	18.4089	18.0945
		22.6849	22.3192	18.4791	19.0890	22.3308	22.2729	16.6704	19.1972	25.9867	18.2951	17.7949
		22.5326	22.3650	18.6733	19.1450	22.4726	22.1747	17.0311	19.3972	26.0454	18.8597	17.7558
	3	22.4611	22.3332	18.6051	19.4749	22.6395	22.489	17.0059	19.2645	25.4616	18.5307	17.9584
		22.8289	22.4818	18.8528	20.1567	22.4409	22.357	16.9658	19.3586	25.6906	18.4776	18.1372
		23.0577	22.5166	18.7774	19.5848	22.3452	22.4686	17.0911	19.4295	25.6976	18.7601	17.6551
CuSO <sub>4</sub>	1	24.0607	22.6570	18.8603	19.9596	22.7376	22.9057	17.5603	19.1686	27.276	18.1021	19.0073
		22.7708	22.4717	19.0393	20.1678	22.6403	23.4852	17.7866	19.1898	27.6375	17.9916	18.8502
		22.8999	22.7428	18.9328	20.1775	23.0452	23.0228	17.4818	19.2384	27.4543	18.069	19.0701
	2	22.7396	22.8036	18.9603	20.4849	22.6968	22.7883	17.7583	19.155	26.9114	18.0533	18.9489
		23.0127	22.6337	19.0128	20.3243	23.0193	22.9378	17.9536	19.2114	26.9023	18.1965	19.1975
		22.6950	22.4650	19.0761	19.9690	23.1276	23.0891	17.8238	19.2117	27.1723	18.4890	19.1018
	3	22.9718	22.9853	19.0278	18.9623	22.6176	23.2046	17.8569	19.1174	26.2809	18.0823	19.0054
		22.8171	22.4113	19.0395	20.2295	22.5242	22.8805	17.5526	19.1426	26.3443	18.4341	18.792
		23.0119	22.8497	19.3903	22.1814	22.6575	23.1692	17.6109	19.1524	26.9404	18.4422	18.5365

ETH	1	24.0966	20.6716	19.4353	18.9626	22.1293	20.0265	15.3937	19.1778	22.5001	18.1724	17.5492
		22.2369	20.4885	19.3298	18.9295	22.202	20.1662	15.6543	19.1699	21.9569	18.0848	17.417
		22.2467	20.7675	19.4226	18.9295	22.3121	19.9637	15.6087	19.4549	22.2923	18.1503	17.567
	2	22.2198	20.4324	19.5191	18.5836	22.0438	20.0572	15.6818	19.1448	21.8028	18.153	17.6431
		22.1774	20.4908	19.3958	19.0139	22.198	20.0246	15.7348	19.2686	22.0942	18.1609	17.5624
		22.0925	20.6835	19.7655	18.96	22.1717	20.0511	15.5777	19.2127	22.0105	18.3093	17.7466
	3	22.1983	20.6159	19.5304	18.928	22.2718	19.9943	15.5919	19.1625	22.2176	18.1849	17.8276
		22.2761	20.6559	19.6523	19.038	22.4386	20.087	15.7288	19.2283	22.3136	18.3114	17.7013
		22.4342	20.7286	19.4575	19.0204	22.1388	19.8966	15.6619	19.1548	22.0905	18.2378	17.6076
ABA	1	24.0077	22.5018	18.6524	19.1425	22.4655	22.1150	17.0420	19.7961	25.9089	18.3758	18.1349
		22.5823	22.3677	18.3390	18.1592	22.3470	22.2609	16.9196	19.2394	25.3115	18.3895	18.4216
		22.503	22.4611	18.6017	17.8520	22.1654	22.1051	16.9700	19.6825	25.3457	18.4803	17.6571
	2	22.5648	22.4203	19.2503	19.1916	22.2034	22.3039	16.7970	19.5989	26.5266	18.5078	17.6909
		22.2935	22.3245	18.9597	19.0963	22.5591	22.5924	16.9992	19.2933	25.8303	18.2199	17.7087
		22.5785	22.3098	18.5620	18.8621	22.2503	21.4463	17.0097	19.2701	25.5646	18.3540	17.6348
	3	22.3953	22.2074	18.5930	19.144	22.8901	22.4471	16.9291	19.3318	25.8438	18.4100	18.0863
		22.5240	22.4512	18.6340	19.2493	22.4294	22.3467	17.0162	19.3795	25.4276	18.4294	17.9449
		22.5337	22.3306	18.9883	19.8925	22.4138	23.0516	17.0604	19.5821	26.6910	19.1248	18.1537
mannitol	1	23.6581	21.8339	18.5137	19.0340	23.0985	21.1474	17.1646	20.2980	25.3128	18.3299	18.3832
		23.0597	21.4194	18.1239	18.2811	22.6946	21.1759	17.0115	19.1138	24.1675	18.6536	17.6903
		21.7865	21.3175	18.0425	18.7388	21.8179	21.0569	16.7867	20.4627	24.1910	18.6319	17.6852
	2	22.1652	21.8928	17.9240	18.1075	22.0898	21.4011	16.538	19.4848	24.1948	19.0621	18.1225
		21.2043	21.7542	18.4471	18.4762	21.6968	21.1170	16.9242	19.1340	24.6625	18.7812	17.7654
		22.2585	21.3455	18.5044	18.5512	22.7588	21.2373	17.1875	19.1273	25.0264	19.1060	18.1050

	3	21.3127	21.3485	18.3480	18.3805	21.7800	21.0833	17.2081	18.9498	24.3364	18.6725	17.5479
		22.2673	21.6331	18.4876	18.8006	21.7237	21.1166	17.0849	19.2776	24.5377	18.9303	17.7540
		21.2497	21.6899	18.4707	18.8202	22.2075	21.2919	17.0132	19.1814	24.4406	18.7935	17.7887

**Table S3.** Pairwise variation ( $V_{n/n+1}$ ) analysis of 11 candidate reference genes calculated using geNorm.

	control	ETH	ABA	CuSO <sub>4</sub>	mannitol	SA	NaCl	MeJA	total
<b>V<sub>2/3</sub></b>	0.068	0.061	0.134	0.162	0.126	0.088	0.159	0.127	0.179
<b>V<sub>3/4</sub></b>	0.054	0.064	0.098	0.113	0.097	0.091	0.117	0.094	0.131
<b>V<sub>4/5</sub></b>	0.054	0.104	0.099	0.154	0.086	0.077	0.107	0.075	0.117
<b>V<sub>5/6</sub></b>	0.052	0.077	0.088	0.124	0.078	0.082	0.101	0.076	0.115
<b>V<sub>6/7</sub></b>	0.056	0.106	0.078	0.097	0.065	0.096	0.083	0.080	0.110
<b>V<sub>7/8</sub></b>	0.053	0.103	0.078	0.092	0.073	0.083	0.081	0.073	0.098
<b>V<sub>8/9</sub></b>	0.052	0.094	0.077	0.096	0.077	0.076	0.096	0.073	0.085
<b>V<sub>9/10</sub></b>	0.047	0.105	0.079	0.097	0.082	0.089	0.093	0.078	0.083
<b>V<sub>10/11</sub></b>	0.078	0.093	0.067	0.108	0.079	0.077	0.104	0.069	0.099

**Table S4.** Stability rank of 11 candidate genes by NormFinder.

Rank	control	ETH	ABA	CuSO <sub>4</sub>	mannitol	SA	NaCl	MeJA	total
<b>1</b>	<i>ACT</i>	<i>EF1α</i>	<i>UBC9</i>	<i>GAPDH</i>	<i>GAPDH</i>	<i>EF1α</i>	<i>ACT</i>	<i>GAPDH</i>	<i>TIP41</i>
	0.01	0.015	0.123	0.150	0.153	0.095	0.218	0.101	0.258
<b>2</b>	<i>EF1α</i>	<i>ACT</i>	<i>GAPDH</i>	<i>TIP41</i>	<i>TUB6</i>	<i>UBC9</i>	<i>GAPDH</i>	<i>UBC9</i>	<i>ACT</i>
	0.075	0.070	0.145	0.201	0.171	0.126	0.22	0.172	0.277
<b>3</b>	<i>UBC9</i>	<i>UBC9</i>	<i>TIP41</i>	<i>EF1α</i>	<i>CYP2</i>	<i>ACT</i>	<i>TUBA</i>	<i>ACT</i>	<i>EF1α</i>
	0.091	0.145	0.213	0.319	0.182	0.135	0.271	0.217	0.317
<b>4</b>	<i>TUB6</i>	<i>TIP41</i>	<i>EF1α</i>	<i>UBC9</i>	<i>ACT</i>	<i>GAPDH</i>	<i>TIP41</i>	<i>EF1α</i>	<i>UBC9</i>
	0.127	0.218	0.252	0.376	0.205	0.149	0.3	0.218	0.325
<b>5</b>	<i>GAPDH</i>	<i>CYP2</i>	<i>ACT</i>	<i>CYP2</i>	<i>TIP41</i>	<i>TIP41</i>	<i>CYP2</i>	<i>TIP41</i>	<i>GAPDH</i>
	0.175	0.260	0.316	0.424	0.254	0.242	0.302	0.241	0.389
<b>6</b>	<i>YLS8</i>	<i>YLS8</i>	<i>PTBP</i>	<i>ACT</i>	<i>UBC9</i>	<i>PTBP</i>	<i>PTBP</i>	<i>CYP2</i>	<i>CYP2</i>
	0.2	0.278	0.382	0.431	0.284	0.343	0.346	0.332	0.412
<b>7</b>	<i>CYP2</i>	<i>SAND</i>	<i>CYP2</i>	<i>PTBP</i>	<i>YLS8</i>	<i>CYP2</i>	<i>UBC9</i>	<i>PTBP</i>	<i>PTBP</i>
	0.208	0.468	0.383	0.454	0.324	0.444	0.375	0.360	0.468
<b>8</b>	<i>PTBP</i>	<i>TUBA</i>	<i>TUBA</i>	<i>SAND</i>	<i>EF1α</i>	<i>TUB6</i>	<i>EF1α</i>	<i>TUBA</i>	<i>SAND</i>
	0.253	0.596	0.420	0.504	0.425	0.480	0.435	0.427	0.539
<b>9</b>	<i>TUBA</i>	<i>TUB6</i>	<i>TUB6</i>	<i>TUBA</i>	<i>TUBA</i>	<i>TUBA</i>	<i>SAND</i>	<i>TUB6</i>	<i>TUBA</i>
	0.311	0.636	0.491	0.577	0.523	0.544	0.583	0.458	0.542
<b>10</b>	<i>TIP41</i>	<i>PTBP</i>	<i>SAND</i>	<i>TUB6</i>	<i>PTBP</i>	<i>YLS8</i>	<i>YLS8</i>	<i>YLS8</i>	<i>YLS8</i>
	0.312	0.697	0.497	0.728	0.528	0.561	0.689	0.513	0.580
<b>11</b>	<i>SAND</i>	<i>GAPDH</i>	<i>YLS8</i>	<i>YLS8</i>	<i>SAND</i>	<i>SAND</i>	<i>TUB6</i>	<i>SAND</i>	<i>TUB6</i>
	0.654	0.699	0.518	0.810	0.597	0.579	0.786	0.516	0.743

**Table S5.** Stability rank of 11 candidate genes by Bestkeeper.

Rank	control	ETH	ABA	CuSO <sub>4</sub>	mannitol	SA	NaCl	MeJA	total
1	<i>EF1α</i>	<i>GAPDH</i>	<i>TUB6</i>	<i>TUBA</i>	<i>TUBA</i>	<i>TUBA</i>	<i>YLS8</i>	<i>TUBA</i>	<i>TUBA</i>
CV±SD	0.45±0.08	2.85±0.57	2.15±0.56	1.21±0.23	3.26±0.60	2.64±0.49	1.42±0.32	2.98±0.55	3.94±0.74
2	<i>UBC9</i>	<i>TUBA</i>	<i>TUBA</i>	<i>TUB6</i>	<i>EF1α</i>	<i>TUB6</i>	<i>UBC9</i>	<i>TUB6</i>	<i>CTP2</i>
CV±SD	0.50±0.11	3.93±0.72	3.08±0.57	1.10±0.29	4.05±0.71	1.97±0.51	2.95±0.67	2.34±0.61	5.00±1.15
3	<i>ACT</i>	<i>TIP41</i>	<i>CYP2</i>	<i>CYP2</i>	<i>TUB6</i>	<i>CYP2</i>	<i>PTBP</i>	<i>CYP2</i>	<i>EF1α</i>
CV±SD	0.59±0.13	5.22±1.21	2.91±0.66	1.30±0.30	4.22±1.07	2.59±0.59	2.86±0.75	2.74±0.63	6.46±1.16
4	<i>CYP2</i>	<i>UBC9</i>	<i>EF1α</i>	<i>EF1α</i>	<i>UBC9</i>	<i>GAPDH</i>	<i>SAND</i>	<i>EF1α</i>	<i>GAPDH</i>
CV±SD	0.78±0.18	6.07±1.23	4.11±0.72	2.04±0.37	5.55±1.13	5.12±1.00	3.53±0.93	4.18±0.73	5.94±1.18
5	<i>YLS8</i>	<i>ACT</i>	<i>GAPDH</i>	<i>GAPDH</i>	<i>GAPDH</i>	<i>EF1α</i>	<i>TUBA</i>	<i>GAPDH</i>	<i>TUB6</i>
CV±SD	0.93±0.20	6.33±1.27	4.81±0.94	1.02±0.79	5.90±1.14	6.01±1.03	4.72±0.96	5.12±0.99	5.01±1.32
6	<i>TUB6</i>	<i>EF1α</i>	<i>UBC9</i>	<i>ACT</i>	<i>CYP2</i>	<i>TIP41</i>	<i>ACT</i>	<i>ACT</i>	<i>UBC9</i>
CV±SD	0.80±0.22	8.16±1.37	5.45±1.11	3.88±0.81	5.28±1.17	4.74±1.11	5.26±1.21	4.90±1.00	6.58±1.36
7	<i>GAPDH</i>	<i>SAND</i>	<i>TIP41</i>	<i>TIP41</i>	<i>TIP41</i>	<i>ACT</i>	<i>GAPDH</i>	<i>TIP41</i>	<i>TIP41</i>
CV±SD	1.13±0.23	6.26±1.48	4.78±1.12	3.98±0.94	5.23±1.22	5.98±1.20	5.92±1.32	4.55±1.07	5.88±1.40
8	<i>PTBP</i>	<i>CYP2</i>	<i>ACT</i>	<i>SAND</i>	<i>ACT</i>	<i>UBC9</i>	<i>TIP41</i>	<i>UBC9</i>	<i>ACT</i>
CV±SD	1.12±0.28	8.03±1.72	6.27±1.25	4.85±1.16	7.26±1.43	5.96±1.21	5.05±1.33	5.90±1.20	6.94±1.43
9	<i>TIP41</i>	<i>YLS8</i>	<i>SAND</i>	<i>UBC9</i>	<i>YLS8</i>	<i>PTBP</i>	<i>CYP2</i>	<i>SAND</i>	<i>SAND</i>
CV±SD	1.42±0.35	8.95±1.76	5.65±1.34	6.18±1.25	7.41±1.48	6.08±1.44	5.50±1.39	5.33±1.27	6.66±1.60
10	<i>TUBA</i>	<i>TUB6</i>	<i>PTBP</i>	<i>PTBP</i>	<i>SAND</i>	<i>SAND</i>	<i>EF1α</i>	<i>PTBP</i>	<i>YLS8</i>
CV±SD	2.09±0.40	9.28±2.23	6.12±1.44	5.48±1.30	6.86±1.61	7.09±1.65	7.92±1.62	5.94±1.40	8.88±1.79
11	<i>SAND</i>	<i>PTBP</i>	<i>YLS8</i>	<i>YLS8</i>	<i>PTBP</i>	<i>YLS8</i>	<i>TUB6</i>	<i>YLS8</i>	<i>PTBP</i>
CV±SD	2.97±0.75	10.16±2.29	8.20±1.63	8.93±1.76	7.89±1.82	8.96±1.76	6.61±1.93	8.07±1.60	7.65±1.82

**Table S6.** Expression stability values of 11 candidate genes calculated using the RefFinder.

Rank	control	SA	NaCl	MeJA	CuSO <sub>4</sub>	ETH	ABA	mannitol	total
1	<i>EF1α</i>	<i>EF1α</i>	<i>GAPDH</i>	<i>GAPDH</i>	<i>GAPDH</i>	<i>EF1α</i>	<i>UBC9</i>	<i>GAPDH</i>	<i>TIP41</i>
	1.565	1.495	1.934	1.495	2.115	1.565	1.565	1.495	1.627
2	<i>ACT</i>	<i>UBC9</i>	<i>ACT</i>	<i>ACT</i>	<i>TIP41</i>	<i>UBC9</i>	<i>GAPDH</i>	<i>TUB6</i>	<i>UBC9</i>
	1.968	2.378	2.632	2.913	3.027	2.449	2.783	1.861	2.913
3	<i>UBC9</i>	<i>ACT</i>	<i>CYP2</i>	<i>UBC9</i>	<i>UBC9</i>	<i>ACT</i>	<i>TIP41</i>	<i>CYP2</i>	<i>ACT</i>
	2.213	3.705	3.663	3.13	3.464	2.783	2.817	3.568	3.364
4	<i>TUB6</i>	<i>GAPDH</i>	<i>TUBA</i>	<i>EF1α</i>	<i>EF1α</i>	<i>TIP41</i>	<i>EF1α</i>	<i>ACT</i>	<i>EF1α</i>
	4.12	4	3.873	3.936	3.663	3.722	4	4.757	3.663
5	<i>CYP2</i>	<i>TUBA</i>	<i>TIP41</i>	<i>TUBA</i>	<i>PTBP</i>	<i>GAPDH</i>	<i>TUB6</i>	<i>TUBA</i>	<i>GAPDH</i>
	5.091	5.196	4.681	4.601	4.527	5.609	4.88	5.196	4.162
6	<i>YLS8</i>	<i>TIP41</i>	<i>PTBP</i>	<i>CYP2</i>	<i>CYP2</i>	<i>CYP2</i>	<i>CYP2</i>	<i>UBC9</i>	<i>CYP2</i>
	5.180	5.233	5.045	5.045	4.606	5.623	5.01	5.422	4.559
7	<i>GAPDH</i>	<i>TUB6</i>	<i>UBC9</i>	<i>TIP41</i>	<i>TUBA</i>	<i>TUBA</i>	<i>TUBA</i>	<i>EF1α</i>	<i>TUBA</i>
	5.916	5.657	5.118	5.144	5.196	5.657	5.264	5.657	5.335
8	<i>PTBP</i>	<i>CYP2</i>	<i>YLS8</i>	<i>TUB6</i>	<i>ACT</i>	<i>YLS8</i>	<i>ACT</i>	<i>TIP41</i>	<i>PTBP</i>
	7.737	5.664	5.623	6.000	6.481	6.64	6.325	5.916	7.837
9	<i>TUBA</i>	<i>PTBP</i>	<i>SAND</i>	<i>PTBP</i>	<i>TUB6</i>	<i>SAND</i>	<i>PTBP</i>	<i>YLS8</i>	<i>SAND</i>
	9.24	6.64	7.348	8.149	6.687	7	7.841	6.853	8.485
10	<i>TIP41</i>	<i>YLS8</i>	<i>EF1α</i>	<i>YLS8</i>	<i>SAND</i>	<i>TUB6</i>	<i>SAND</i>	<i>PTBP</i>	<i>TUB6</i>
	9.74	10.241	8.459	10.241	8	9.487	10.215	10.241	9.032
11	<i>SAND</i>	<i>SAND</i>	<i>TUB6</i>	<i>SAND</i>	<i>YLS8</i>	<i>PTBP</i>	<i>YLS8</i>	<i>SAND</i>	<i>YLS8</i>
	11	10.741	11	10.462	11	10.741	10.488	10.741	9.457