

Figure S3: The sequence similarity of candidate reference genes compared between 84K poplar and *Populus trichocarpa*.

1. ACT7 Sequence similarity: 100%

J803231068_14-1.SEQ	GTGATCTCCTTGCTCATTCGGTCAGCAATACCAGGGAACATAGTGAACCACCCTGAGC	60
J803231068_14-2.SEQRC	GTGATCTCCTTGCTCATTCGGTCAGCAATACCAGGGAACATAGTGAACCACCCTGAGC	60
J803231068_14-3.SEQ	GTGATCTCCTTGCTCATTCGGTCAGCAATACCAGGGAACATAGTGAACCACCCTGAGC	60
J803231068_14-4.SEQ	GTGATCTCCTTGCTCATTCGGTCAGCAATACCAGGGAACATAGTGAACCACCCTGAGC	60
J803231068_14-5.SEQRC	GTGATCTCCTTGCTCATTCGGTCAGCAATACCAGGGAACATAGTGAACCACCCTGAGC	60
POTRI.001G309500-ACT7.SEQRC	GTGATCTCCTTGCTCATTCGGTCAGCAATACCAGGGAACATAGTGAACCACCCTGAGC	60
Consensus	gtgatctccttgctcattcggtcagcaataccagggaaacatagtggaaccaccactgagc	
J803231068_14-1.SEQ	ACAATGTTACCATAACAGATCCTTTCTAATATCCACATCACACTTCATGATTGAGTTGTAT	120
J803231068_14-2.SEQRC	ACAATGTTACCATAACAGATCCTTTCTAATATCCACATCACACTTCATGATTGAGTTGTAT	120
J803231068_14-3.SEQ	ACAATGTTACCATAACAGATCCTTTCTAATATCCACATCACACTTCATGATTGAGTTGTAT	120
J803231068_14-4.SEQ	ACAATGTTACCATAACAGATCCTTTCTAATATCCACATCACACTTCATGATTGAGTTGTAT	120
J803231068_14-5.SEQRC	ACAATGTTACCATAACAGATCCTTTCTAATATCCACATCACACTTCATGATTGAGTTGTAT	120
POTRI.001G309500-ACT7.SEQRC	ACAATGTTACCATAACAGATCCTTTCTAATATCCACATCACACTTCATGATTGAGTTGTAT	120
Consensus	acaatgttaccataacagatcctttctaataatccacatcacacttcatgattgagttgtat	
J803231068_14-1.SEQ	GTAGTCTCGTGGATG	135
J803231068_14-2.SEQRC	GTAGTCTCGTGGATG	135
J803231068_14-3.SEQ	GTAGTCTCGTGGATG	135
J803231068_14-4.SEQ	GTAGTCTCGTGGATG	135
J803231068_14-5.SEQRC	GTAGTCTCGTGGATG	135
POTRI.001G309500-ACT7.SEQRC	GTAGTCTCGTGGATG	135
Consensus	gtagtctcgtggatg	

2. EIF4A Sequence similarity: 99.51%

J803231103_21-1.SEQ	TACATTCATCGAATTGGTCGTTCTGGTCGTTTTGGACGGAAGGGTGTGCTATTAAC TTC	60
J803231103_21-2.SEQRC	TACATTCATCGAATTGGTCGTTCTGGTCGTTTTGGACGGAAGGGTGTGCTATTAAC TTC	59
J803231103_21-3.SEQRC	TACATTCATCGAATTGGTCGTTCTGGTCGTTTTGGACGGAAGGGTGTGCTATTAAC TTC	60
J803231103_21-4.SEQRC	TACATTCATCGAATTGGTCGTTCTGGTCGTTTTGGACGGAAGGGTGTGCTATTAAC TTC	60
J803231103_21-5.SEQ	TACATTCATCGAATTGGTCGTTCTGGTCGTTTTGGACGGAAGGGTGTGCTATTAAC TTC	60
POTRI.005G093900-EIF4A.SEQ	TACATTCATCGAATTGGTCGTTCTGGTCGTTTTGGACGGAAGGGTGTGCTATTAAC TTC	60
Consensus	tacattcatcgaattggtcgttctggtcgTTTTGGACGGAAGGGTGTGCTATTAAC TTC	
J803231103_21-1.SEQ	GTCAAAGTGATGATATCAGGATTTTAAGAGATATTGAACAGTATTACAGCACCAGATT	120
J803231103_21-2.SEQRC	GTCAAAGTGATGATATCAGGATTTTAAGAGATATTGAACAGTATTACAGCACCAGATT	119
J803231103_21-3.SEQRC	GTCAAAGTGATGATATCAGGATTTTAAGAGATATTGAACAGTATTACAGCACCAGATT	120
J803231103_21-4.SEQRC	GTCAAAGTGATGATATCAGGATTTTAAGAGATATTGAACAGTATTACAGCACCAGATT	120
J803231103_21-5.SEQ	GTCAAAGTGATGATATCAGGATTTTAAGAGATATTGAACAGTATTACAGCACCAGATT	120
POTRI.005G093900-EIF4A.SEQ	GTCAAAGTGATGATATCAGGATTTTAAGAGATATTGAACAGTATTACAGCACCAGATT	120
Consensus	gtcaaagtgatgatatcaggatTTTAAGAGATATTGAACAGTATTACAGCACCAGATT	
J803231103_21-1.SEQ	GACGAAATGCCTATGA	136
J803231103_21-2.SEQRC	GACGAAATGCCTATGA	135
J803231103_21-3.SEQRC	GACGAAATGCCTATGA	136
J803231103_21-4.SEQRC	GACGAAATGCCTATGA	136
J803231103_21-5.SEQ	GACGAAATGCCTATGA	136
POTRI.005G093900-EIF4A.SEQ	GACGAAATGCCTATGA	136
Consensus	gacgaaatgcctatga	

3. GAPDH Sequence similarity: 98.90%

J803231108_22-1.SEQ	AACCGACTTCATPGGTGACAACCGGTC AAGTATCTTTGATGCCAAAGCTGGAATTGCTTT	60
J803231108_22-2.SEQ	AACCGACTTCATPGGTGACAACCGGTC AAGTATCTTTGATGCCAAAGCTGGAATTGCTTT	60
J803231108_22-3.SEQRC	AACCGACTTCATPGGTGACAACCGGTC AAGTATCTTTGATGCCAAAGCTGGAATTGCTTT	60
J803231108_22-4.SEQRC	AACCGACTTCATPGGTGACAACCGGTC AAGTATCTTTGATGCCAAAGCTGGAATTGCTTT	60
J803231108_22-5.SEQ	AACCGACTTCATPGGTGACAACCGGTC AAGTATCTTTGATGCCAAAGCTGGAATTGCTTT	60
POTRI.012G094100-GAPDH.SEQ	AACCGACTTCATPGGTGACAACCGGTC AAGTATCTTTGATGCCAAAGCTGGAATTGCTTT	60
Consensus	aaccgacttcattpggtgacaacccggTC AAGTATCTTTGATGCCAAAGCTGGAATTGCTTT	
J803231108_22-1.SEQ	GAACGATAACTATGTGAAGCTCGTTGCGTGGTATGACAATGAGTG	105
J803231108_22-2.SEQ	GAACGATAACTATGTGAAGCTCGTTGCGTGGTATGACAATGAGTG	105
J803231108_22-3.SEQRC	GAACGATAACTATGTGAAGCTCGTTGCGTGGTATGACAATGAGTG	105
J803231108_22-4.SEQRC	GAACGATAACTATGTGAAGCTCGTTGCGTGGTATGACAATGAGTG	105
J803231108_22-5.SEQ	GAACGATAACTATGTGAAGCTCGTTGCGTGGTATGACAATGAGTG	105
POTRI.012G094100-GAPDH.SEQ	GAACGATAACTATGTGAAGCTCGTTGCGTGGTATGACAATGAGTG	105
Consensus	gaacgataactatgtgaagctcgttgcgtggatgacaatgagtg	

#### 4. Histone Sequence similarity: 94.13%

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J803231113_23-1.SEQ CTTAAAAATCCTGGGCAATTTACGAACAAGACCGCTGGAAAAGGTAACCTTGGCGGATCAAAAAG 60
J803231113_23-2.SEQ CTTAAAAATCCTGGGCAATTTACGAACAAGACCGCTGGAAAAGGTAACCTTGGCGGATCAAAAAG 60
J803231113_23-3.SEQRC CTTAAAAATCCTGGGCAATTTACGAACAAGACCGCTGGAAAAGGTAACCTTGGCGGATCAAAAAG 60
J803231113_23-4.SEQRC CTTAAAAATCCTGGGCAATTTACGAACAAGACCGCTGGAAAAGGTAACCTTGGCGGATCAAAAAG 60
J803231113_23-5.SEQRC CTTAAAAATCCTGGGCAATTTACGAACAAGACCGCTGGAAAAGGTAACCTTGGCGGATCAAAAAG 60
POTRI.005G072300-HISTONE.SEQRC CTTAAAAATCCTGGGCAATTTACGAACAAGACCGCTGGAAAAGGTAACCTTGGCGGATCAAAAAG 60
Consensus cttaaaaatcctggggcaatttcacgaacaagacgctggaaaaggaacttcgcggatcaaaaag
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J803231113_23-1.SEQ CTCAGTACTCTTTCTGACTTACGGATTTACGAAGAGCAACAG 104
J803231113_23-2.SEQ CTCAGTACTCTTTCTGACTTACGGATTTACGAAGAGCAACAG 104
J803231113_23-3.SEQRC CTCAGTACTCTTTCTGACTTACGGATTTACGAAGAGCAACAG 104
J803231113_23-4.SEQRC CTCAGTACTCTTTCTGACTTACGGATTTACGAAGAGCAACAG 104
J803231113_23-5.SEQRC CTCAGTACTCTTTCTGACTTACGGATTTACGAAGAGCAACAG 104
POTRI.005G072300-HISTONE.SEQRC CTCAGTACTCTTTCTGACTTACGGATTTACGAAGAGCAACAG 104
Consensus ctcagtactcttctgatacttacggatttcacgaagagcaaacag
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#### 5. PP2A-2 Sequence similarity: 99.30%

```
J803231004_1-2.SEQ TTTGGCGCACTGAACACTGTAACCACATTTCTTGTCTGGGACCAATTGTATCCTTCCATA 60
J803231005_1-3.SEQ TTTGGCGCACTGAACACTGTAACCACATTTCTTGTCTGGGACCAATTGTATCCTTCCATA 60
J803231006_1-4.SEQ TTTGGCGCACTGAACACTGTAACCACATTTCTTGTCTGGGACCAATTGTATCCTTCCATA 60
J803231007_1-5.SEQ TTTGGCGCACTGAACACTGTAACCACATTTCTTGTCTGGGACCAATTGTATCCTTCCATA 60
POTRI.015G068300-PP2A-2.SEQRC TTTGGCGCACTGAACACTGTAACCACATTTCTTGTCTGGGACCAATTGTATCCTTCCATA 60
Consensus tttggcgcaactgaacactgtaaccacatttcttgtctgggaccaattgtatccttccata
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J803231004_1-2.SEQ ACAAGCTGGTGAGCTCTAGAAATGAGAGCGAGGCCATTAGTGTGGTTGAACTG 113
J803231005_1-3.SEQ ACAAGCTGGTGAGCTCTAGAAATGAGAGCGAGGCCATTAGTGTGGTTGAACTG 113
J803231006_1-4.SEQ ACAAGCTGGTGAGCTCTAGAAATGAGAGCGAGGCCATTAGTGTGGTTGAACTG 113
J803231007_1-5.SEQ ACAAGCTGGTGAGCTCTAGAAATGAGAGCGAGGCCATTAGTGTGGTTGAACTG 113
POTRI.015G068300-PP2A-2.SEQRC ACAAGCTGGTGAGCTCTAGAAATGAGAGCGAGGCCATTAGTGTGGTTGAACTG 113
Consensus acaagctggtgagctctagaaatgagagcgaggccattagtggttgaactg
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#### 6. PP2A-A2 Sequence similarity: 98.69%

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J803231008_2-1.SEQ CAATGCCTATCCTCTGCAAGCTCAACAATTGCTGGCAATAGTGATTGGGAAGCAATCA 60
J803231009_2-2.SEQ CAATGCCTATCCTCTGCAAGCTCAACAATTGCTGGCAATAGTGATTGGGATAGTAGATCA 60
J803231010_2-3.SEQ CAATGCCTATCCTCTGCAAGCTCAACAATTGCTGGCAATAGTGATTGGGATAGTAGATCA 60
J803231011_2-4.SEQRC CAATGCCTATCCTCTGCAAGCTCAACAATTGCTGGCAATAGTGATTGGGATAGTAGATCA 60
J803231012_2-5.SEQRC CAATGCCTATCCTCTGCAAGCTCAACAATTGCTGGCAATAGTGATTGGGATAGTAGATCA 60
POTRI.010G127500-PP2A-A2.SEQRC CAATGCCTATCCTCTGCAAGCTCAACAATTGCTGGCAATAGTGATTGGGATAGTAGATCA 60
Consensus caatgcctatcctctgcaagctcaacaattgctggcaatagtgattgggatagtatgatca
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J803231008_2-1.SEQ ATCCCAATAACCTGATTGACTTGATCAAGCTTGCTGATAATGTTTCAGTCGCACATCAGGA 120
J803231009_2-2.SEQ ATCCCAATAACCTGATTGACTTGATCAAGCTTGCTGATAATGTTTCAGTCGCACATCAGGA 120
J803231010_2-3.SEQ ATCCCAATAACCTGATTGACTTGATCAAGCTTGCTGATAATGTTTCAGTCGCACATCAGGA 120
J803231011_2-4.SEQRC ATCCCAATAACCTGATTGACTTGATCAAGCTTGCTGATAATGTTTCAGTCGCACATCAGGA 120
J803231012_2-5.SEQRC ATCCCAATAACCTGATTGACTTGATCAAGCTTGCTGATAATGTTTCAGTCGCACATCAGGA 120
POTRI.010G127500-PP2A-A2.SEQRC ATCCCAATAACCTGATTGACTTGATCAAGCTTGCTGATAATGTTTCAGTCGCACATCAGGA 120
Consensus atcccaataaactgattgacttgatcaagcttgctgataatgtttcagtcgcacatcagga
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J803231008_2-1.SEQ AATTCA 126
J803231009_2-2.SEQ AATTCA 126
J803231010_2-3.SEQ AATTCA 126
J803231011_2-4.SEQRC AATTCA 126
J803231012_2-5.SEQRC AATTCA 126
POTRI.010G127500-PP2A-A2.SEQRC AATTCA 126
Consensus aattca
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## 7. RPS18 Sequence similarity: 99.74%

J803231013_3-1.SEQ	AGGCTCATCATCTTATCAAATCCCTCTCTACAAATGCA	CCTTCAGATAAATGGATTGGAG	60
J803231014_3-2.SEQ	AGGCTCATCATCTTATCAAATCCCTCTCTACAAATGCA	CCTTCAGATAAATGGATTGGAG	60
J803231015_3-3.SEQ	AGGCTCATCATCTTATCAAATCCCTCTCTACAAATGCA	CCTTCAGATAAATGGATTGGAG	60
J803231015_3-4.SEQ	AGGCTCATCATCTTATCAAATCCCTCTCTACAAATGCA	CCTTCAGATAAATGGATTGGAG	60
J803231015_3-5.SEQ	AGGCTCATCATCTTATCAAATCCCTCTCTACAAATGCA	CCTTCAGATAAATGGATTGGAG	60
POTRI.006G170500-RPS18.SEQ	AGGCTCATCATCTTATCAAATCCCTCTCTACAAATGCT	CCTTCAGATAAATGGATTGGAG	60
Consensus	aggctcatcatcttatacaaatccctctctacaaatgca	ccttcagataaattggattggag	
J803231013_3-1.SEQ	ACAATCAAAGCTCCAATTCTTTTGTGCTGCTGATGGCTTTGAGCAACGAATATT	TGGTG	120
J803231014_3-2.SEQ	ACAATCAAAGCTCCAATTCTTTTGTGCTGCTGATGGCTTTGAGCAACGAATATT	TGGTG	120
J803231015_3-3.SEQ	ACAATCAAAGCTCCAATTCTTTTGTGCTGCTGATGGCTTTGAGCAACGAATATT	TGGTG	120
J803231015_3-4.SEQ	ACAATCAAAGCTCCAATTCTTTTGTGCTGCTGATGGCTTTGAGCAACGAATATT	TGGTG	120
J803231015_3-5.SEQ	ACAATCAAAGCTCCAATTCTTTTGTGCTGCTGATGGCTTTGAGCAACGAATATT	TGGTG	119
POTRI.006G170500-RPS18.SEQ	ACAATCAAAGCTCCAATTCTTTTGTGCTGCTGATGGCTTTGAGCAACGAATATT	TGGTG	120
Consensus	acaatcaaagctccaattcttttgtgctgctgattggctttgagcaacgaatatt	tgggtg	
J803231013_3-1.SEQ	GCATTG		126
J803231014_3-2.SEQ	GCATTG		126
J803231015_3-3.SEQ	GCATTG		126
J803231015_3-4.SEQ	GCATTG		126
J803231015_3-5.SEQ	GCATTG		125
POTRI.006G170500-RPS18.SEQ	GCATTG		126
Consensus	gcattg		

## 8. UBQ10 Sequence similarity:99.22%

J803231028_6-1.SEQ	GTTGATTTTTGCTGGGAAGCAGCTTGAAGATGGGAGA	A	ACTCTTGCTGACTACAACATTCA	60	
J803231029_6-2_.SEQ	GTTGATTTTTGCTGGGAAGCAGCTTGAAGATGGGAGA	A	ACTCTTGCTGACTACAACATTCA	60	
J803231030_6-3.SEQ	GTTGATTTTTGCTGGGAAGCAGCTTGAAGATGGGAGA	A	ACTCTTGCTGACTACAACATTCA	60	
J803231031_6-4.SEQRC	GTTGATTTTTGCTGGGAAGCAGCTTGAAGATGGGAGA	A	ACTCTTGCTGACTACAACATTCA	60	
J803231032_6-5.SEQRC	GTTGATTTTTGCTGGGAAGCAGCTTGAAGATGGGAGA	A	ACTCTTGCTGACTACAACATTCA	60	
POTRI.001G418500-UBQ10.SEQ	GTTGATTTTTGCTGGGAAGCAGCTTGAAGATGGGAGA	A	ACTCTTGCTGACTACAACATTCA	60	
Consensus	gttgatttttctgggaagcagcttgaagatgggagaa	a	actcttgctgactacaacattca		
J803231028_6-1.SEQ	GAAGGAGTCAACCCCTTCACT	TGGTGC	TGCGTCTCCGTGGAGGAATGCAG	TTTTTGTCAA	120
J803231029_6-2_.SEQ	GAAGGAGTCAACCCCTTCACT	TGGTGC	TGCGTCTCCGTGGAGGAATGCAG	TTTTTGTCAA	120
J803231030_6-3.SEQ	GAAGGAGTCAACCCCTTCACT	TGGTGC	TGCGTCTCCGTGGAGGAATGCAG	TTTTTGTCAA	120
J803231031_6-4.SEQRC	GAAGGAGTCAACCCCTTCACT	TGGTGC	TGCGTCTCCGTGGAGGAATGCAG	TTTTTGTCAA	120
J803231032_6-5.SEQRC	GAAGGAGTCAACCCCTTCACT	TGGTGC	TGCGTCTCCGTGGAGGAATGCAG	TTTTTGTCAA	120
POTRI.001G418500-UBQ10.SEQ	GAAGGAGTCAACCCCTTCACT	TGGTGC	TGCGTCTCCGTGGAGGAATGCAG	TTTTTGTCAA	120
Consensus	gaaggagtcaacccttcacttgggtgctgctctccgtggaggaatgcagatttttgtcaa				
J803231028_6-1.SEQ	GACTTTGACCGGAAAGACCATCAC	CTGGAGGTCGAGAGCTC	GACACCATTGACAACGT	180	
J803231029_6-2_.SEQ	GACTTTGACCGGAAAGACCATCAC	CTGGAGGTCGAGAGCTC	GACACCATTGACAACGT	180	
J803231030_6-3.SEQ	GACTTTGACCGGAAAGACCATCAC	CTGGAGGTCGAGAGCTC	GACACCATTGACAACGT	180	
J803231031_6-4.SEQRC	GACTTTGACCGGAAAGACCATCAC	CTGGAGGTCGAGAGCTC	GACACCATTGACAACGT	180	
J803231032_6-5.SEQRC	GACTTTGACCGGAAAGACCATCAC	CTGGAGGTCGAGAGCTC	GACACCATTGACAACGT	180	
POTRI.001G418500-UBQ10.SEQ	GACTTTGACCGGAAAGACCATCAC	CTGGAGGTCGAGAGCTC	GACACCATTGACAACGT	180	
Consensus	gactttgaccggaaagaccatcacctggaggtcgagagctcgacaccattgacaacgt				
J803231028_6-1.SEQ	GAAGGCCAAGAT			192	
J803231029_6-2_.SEQ	GAAGGCCAAGAT			192	
J803231030_6-3.SEQ	GAAGGCCAAGAT			192	
J803231031_6-4.SEQRC	GAAGGCCAAGAT			192	
J803231032_6-5.SEQRC	GAAGGCCAAGAT			192	
POTRI.001G418500-UBQ10.SEQ	GAAGGCCAAGAT			192	
Consensus	gaaggccaagat				

### 9. ATPase Sequence similarity: 97.99%

J803231073_15-1.SEQ	ACTCATCCCACCCCTGATCTTACGGGATACATCACAGAGGGACAGATTTATATTGACAGG	60
J803231073_15-2.SEQRC	ACTCATCCCACCCCTGATCTTACGGGATACATCACAGAGGGACAGATTTATATTGACAGG	60
J803231073_15-4.SEQ	ACTCATCCCACCCCTGATCTTACGGGATACATCACAGAGGGACAGATTTATATTGACAGG	60
J803231073_15-5.SEQRC	ACTCATCCCACCCCTGATCTTACGGGATACATCACAGAGGGACAGATTTATATTGACAGG	60
POTRI.004G177500-ATPASE.SEQ	ACTCATCCCACCCCTGATCTTACGGGATACATCACAGAGGGACAGATTTATATTGACAGG	60
Consensus	actcatcccacccctgatcttacgggatacatcacagagggacagatttatattgacagg	
J803231073_15-1.SEQ	CAGCTACA CAATAGCAGATTTATCCTCCAATCAATGTCCTCCCATCTCTGCTCTCGTCTC	120
J803231073_15-2.SEQRC	CAGCTACA CAATAGCAGATTTATCCTCCAATCAATGTCCTCCCATCTCTGCTCTCGTCTC	120
J803231073_15-4.SEQ	CAGCTACA CAATAGCAGATTTATCCTCCAATCAATGTCCTCCCATCTCTGCTCTCGTCTC	120
J803231073_15-5.SEQRC	CAGCTACA CAATAGCAGATTTATCCTCCAATCAATGTCCTCCCATCTCTGCTCTCGTCTC	120
POTRI.004G177500-ATPASE.SEQ	CAGCTACA CAATAGCAGATTTATCCTCCAATCAATGTCCTCCCATCTCTGCTCTCGTCTC	120
Consensus	cagctacacaatagacagatttatcctccaatcaatgtcctcccatctctgtctctcgctctc	
J803231073_15-1.SEQ	ATGAAGAGTGCC.ATTGG	137
J803231073_15-2.SEQRC	ATGAAGAGTGCC.ATTGG	138
J803231073_15-4.SEQ	ATGAAGAGTGCC.ATTGG	137
J803231073_15-5.SEQRC	ATGAAGAGTGCC.ATTGG	137
POTRI.004G177500-ATPASE.SEQ	ATGAAGAGTGCC.ATTGG	137
Consensus	atgaagagtgcc attgg	

### 10. UBP Sequence similarity: 99.10%

J803231048_10-1.SEQ	GGCTTTGTTTCATTCCSTAATCAGCAGGAGGCCAAAAGTGCTATTAATGACTAACTGGT	60
J803231048_10-2.SEQ	GGCTTTGTTTCATTCCSTAATCAGCAGGAGGCCAAAAGTGCTATTAATGACTAACTGGT	60
J803231048_10-3.SEQRC	GGCTTTGTTTCATTCCSTAATCAGCAGGAGGCCAAAAGTGCTATTAATGACTAACTGGT	60
J803231048_10-4.SEQRC	GGCTTTGTTTCATTCCSTAATCAGCAGGAGGCCAAAAGTGCTATTAATGACTAACTGGT	60
J803231048_10-5.SEQRC	GGCTTTGTTTCATTCCSTAATCAGCAGGAGGCCAAAAGTGCTATTAATGACTAACTGGT	60
POTRI.006G279600-UBP.SEQ	GGCTTTGTTTCATTCCSTAATCAGCAGGAGGCCAAAAGTGCTATTAATGACTAACTGGT	60
Consensus	ggctttgtttcattccstaatcagcagaggccacaaaagtgctattaatgacttaactggt	
J803231048_10-1.SEQ	AAATGGCTTGGAAACAGGCAGATAAGATGCAATTGGGCAACTAAAGGTGT	110
J803231048_10-2.SEQ	AAATGGCTTGGAAACAGGCAGATAAGATGCAATTGGGCAACTAAAGGTGT	110
J803231048_10-3.SEQRC	AAATGGCTTGGAAACAGGCAGATAAGATGCAATTGGGCAACTAAAGGTGT	110
J803231048_10-4.SEQRC	AAATGGCTTGGAAACAGGCAGATAAGATGCAATTGGGCAACTAAAGGTGT	110
J803231048_10-5.SEQRC	AAATGGCTTGGAAACAGGCAGATAAGATGCAATTGGGCAACTAAAGGTGT	110
POTRI.006G279600-UBP.SEQ	AAATGGCTTGGAAACAGGCAGATAAGATGCAATTGGGCAACTAAAGGTGT	110
Consensus	aaatggcttggaacaggcagataaagatgcaattgggcaactaaaggtgt	

### 11. bHLH Sequence similarity: 97.73%

J803231078_16-1.SEQ	ATCTGAATCGTGTAGTGCGTCTAGCTCCAAAGCATGTAGGGAAAAGTTGCGAAGGGATAG	60
J803231078_16-2.SEQRC	ATCTGAATCGTGTAGTGCGTCTAGCTCCAAAGCATGTAGGGAAAAGTTGCGAAGGGATAG	60
J803231078_16-3.SEQRC	ATCTGAATCGTGTAGTGCGTCTAGCTCCAAAGCATGTAGGGAAAAGTTGCGAAGGGATAG	60
J803231078_16-4.SEQRC	ATCTGAATCGTGTAGTGCGTCTAGCTCCAAAGCATGTAGGGAAAAGTTGCGAAGGGATAG	60
J803231078_16-5.SEQRC	ATCTGAATCGTGTAGTGCGTCTAGCTCCAAAGCATGTAGGGAAAAGTTGCGAAGGGATAG	60
POTRI.011G132400-bHLH.SEQ	ATCTGAATCGTGTAGTGCGTCTAGCTCCAAAGCATGTAGGGAAAAGTTGCGAAGGGATAG	60
Consensus	atctgaatcgtgtagtgcgctctagctccaaagcatgtagggaaaagctgcaagggatag	
J803231078_16-1.SEQ	GCTAAATGACAAGTTTATGGAATGGGCTCTATCTTGGATCCTGGGAGAGCTCCCAAAAC	120
J803231078_16-2.SEQRC	GCTAAATGACAAGTTTATGGAATGGGCTCTATCTTGGATCCTGGGAGAGCTCCCAAAAC	120
J803231078_16-3.SEQRC	GCTAAATGACAAGTTTATGGAATGGGCTCTATCTTGGATCCTGGGAGAGCTCCCAAAAC	120
J803231078_16-4.SEQRC	GCTAAATGACAAGTTTATGGAATGGGCTCTATCTTGGATCCTGGGAGAGCTCCCAAAAC	120
J803231078_16-5.SEQRC	GCTAAATGACAAGTTTATGGAATGGGCTCTATCTTGGATCCTGGGAGAGCTCCCAAAAC	120
POTRI.011G132400-bHLH.SEQ	GCTAAATGACAAGTTTATGGAATGGGCTCTATCTTGGATCCTGGGAGAGCTCCCAAAAC	120
Consensus	gctaaatgacaagtttatagaatgggctctatcttggagcctggaagaactcccaaaac	
J803231078_16-1.SEQ	GGACAAGGCTGCTATTTTGGTTGATG	146
J803231078_16-2.SEQRC	GGACAAGGCTGCTATTTTGGTTGATG	146
J803231078_16-3.SEQRC	GGACAAGGCTGCTATTTTGGTTGATG	146
J803231078_16-4.SEQRC	GGACAAGGCTGCTATTTTGGTTGATG	146
J803231078_16-5.SEQRC	GGACAAGGCTGCTATTTTGGTTGATG	146
POTRI.011G132400-bHLH.SEQ	GGACAAGGCTGCTATTTTGGTTGATG	146
Consensus	ggacaaggctgctatTTTTGGTTGATG	

12. *DNAJ 2* Sequence similarity: 99.78%

J803231003_1-1.SEQ	AGGCAATTAATGACAAGGACCGTTGCCCTCAATGCAAGGGTGAGAAGGTGGTCCAAGAGA	60
J803231088_18-1.SEQ	AGGCAATTAATGACAAGGACCGTTGCCCTCAATGCAAGGGTGAGAAGGTGGTCCAAGAGA	60
J803231088_18-2.SEQ	AGGCAATTAATGACAAGGACCGTTGCCCTCAATGCAAGGGTGAGAAGGTGGTCCAAGAGA	60
J803231088_18-3.SEQ	AGGCAATTAATGACAAGGACCGTTGCCCTCAATGCAAGGGTGAGAAGGTGGTCCAAGAGA	60
J803231088_18-4.SEQRC	AGGCAATTAATGACAAGGACCGTTGCCCTCAATGCAAGGGTGAGAAGGTGGTCCAAGAGA	60
J803231088_18-5.SEQ	AGGCAATTAATGACAAGGACCGTTGCCCTCAATGCAAGGGTGAGAAGGTGGTCCAAGAGA	60
POTRI.010G243100-DNAJ.SEQ	AGGCAATTAATGACAAGGACCGTTGCCCTCAATGCAAGGGTGAGAAGGTGGTCCAAGAGA	60
Consensus	aggcaathtaagacaaggaccgttgccctcaatgcaagggtgagaaggtgggtccaagaga	
J803231003_1-1.SEQ	AAAAAGTTTGGAGTAGTTGTTGAGAAGGGCATGCAAAATGCACAGAGGATTACTTTCC	120
J803231088_18-1.SEQ	AAAAAGTTTGGAGTAGTTGTTGAGAAGGGCATGCAAAATGCACAGAGGATTACTTTCC	120
J803231088_18-2.SEQ	AAAAAGTTTGGAGTAGTTGTTGAGAAGGGCATGCAAAATGCACAGAGGATTACTTTCC	120
J803231088_18-3.SEQ	AAAAAGTTTGGAGTAGTTGTTGAGAAGGGCATGCAAAATGCACAGAGGATTACTTTCC	120
J803231088_18-4.SEQRC	AAAAAGTTTGGAGTAGTTGTTGAGAAGGGCATGCAAAATGCACAGAGGATTACTTTCC	120
J803231088_18-5.SEQ	AAAAAGTTTGGAGTAGTTGTTGAGAAGGGCATGCAAAATGCACAGAGGATTACTTTCC	120
POTRI.010G243100-DNAJ.SEQ	AAAAAGTTTGGAGTAGTTGTTGAGAAGGGCATGCAAAATGCACAGAGGATTACTTTCC	120
Consensus	aaaaagtttggagtagttgttggagaagggcatgcaaaatgcacagaggattactttcc	
J803231003_1-1.SEQ	CTGGAGAGGC	130
J803231088_18-1.SEQ	CTGGAGAGGC	130
J803231088_18-2.SEQ	CTGGAGAGGC	130
J803231088_18-3.SEQ	CTGGAGAGGC	130
J803231088_18-4.SEQRC	CTGGAGAGGC	130
J803231088_18-5.SEQ	CTGGAGAGGC	130
POTRI.010G243100-DNAJ.SEQ	CTGGAGAGGC	130
Consensus	ctggagaggc	

13. *U6-1* Sequence similarity: 98.54%

J803231018_4-2.SEQRC	GTGACCTTTATTGCGACATCCACTTGGGTCTATATGTAATTCGTGGCGAGAATGTTGTCT	60
J803231018_4-3.SEQRC	GTGACCTTTATTGCGACATCCACTTGGGTCTATATGTAATTCGTGGCGAGAATGTTGTCT	60
J803231018_4-4.SEQ	GTGACCTTTATTGCGACATCCACTTGGGTCTATATGTAATTCGTGGCGAGAATGTTGTCT	60
J803231018_4-5.SEQ	GTGACCTTTATTGCGACATCCACTTGGGTCTATATGTAATTCGTGGCGAGAATGTTGTCT	60
POTRI.001G166600-U6-1.SEQ	GTGACCTTTATTGCGACATCCACTTGGGTCTATATGTAATTCGTGGCGAGAATGTTGTCT	60
Consensus	gtgacctttattgcgacatccacttgggtctatatgtaattcgtggcgagaatgttgtct	
J803231018_4-2.SEQRC	TAATTGGGAGCTGGATTGGAGAGGGAGGAACTTCCACCACATATGACTCGTGTTCAG	120
J803231018_4-3.SEQRC	TAATTGGGAGCTGGATTGGAGAGGGAGGAACTTCCACCACATATGACTCGTGTTCAG	120
J803231018_4-4.SEQ	TAATTGGGAGCTGGATTGGAGAGGGAGGAACTTCCACCACATATGACTCGTGTTCAG	120
J803231018_4-5.SEQ	TAATTGGGAGCTGGATTGGAGAGGGAGGAACTTCCACCACATATGACTCGTGTTCAG	119
POTRI.001G166600-U6-1.SEQ	TAATTGGGAGCTGGATTGGAGAGGGAGGAACTTCCACCACATATGACTCGTGTTCAG	120
Consensus	taattgggagctggattggagagggaggaaacttccaccacatataactcgtgtttcag	
J803231018_4-2.SEQRC	AA	122
J803231018_4-3.SEQRC	AA	122
J803231018_4-4.SEQ	AA	122
J803231018_4-5.SEQ	AA	121
POTRI.001G166600-U6-1.SEQ	AA	122
Consensus	aa	

14. *U6-2* Sequence similarity: 99.22%

J803231023_5-1.SEQ	TTCCGCGGATGAAAGCATCACCATATTTGTTTTTCAGTTGGCCATTTACATATCTCTCTG	60
J803231024_5-2.SEQ	TTCCCTCGTATGAAAGCATCACCATATTTGTTTTTCAGTTGGCCATTTACATATCTCTCTG	60
J803231025_5-3.SEQRC	TTCCCTCGTATGAAAGCATCACCATATTTGTTTTTCAGTTGGCCATTTACATATCTCTCTG	60
J803231026_5-4.SEQRC	TTCCCTCGTATGAAAGCATCACCATATTTGTTTTTCAGTTGGCCATTTACATATCTCTCTG	60
J803231026_5-5.SEQ	TTCCCTCGTATGAAAGCATCACCATATTTGTTTTTCAGTTGGCCATTTACATATCTCTCTG	60
POTRI.008G078400-U6-2.SEQRC	TTCCCTCGTATGAAAGCATCACCATATTTGTTTTTCAGTTGGCCATTTACATATCTCTCTG	60
Consensus	ttcctcgtatgaaagcatcaccatatttgTTTTTCAGTTGGCCATTTACATATCTCTCTG	
J803231023_5-1.SEQ	TTTGTTCATTGCTATGTTTCATGTACCCATCAAGACAAGCTAAAAACCTCTATAATCAA	120
J803231024_5-2.SEQ	TTTGTTCATTGCTATGTTTCATGTACCCATCAAGACAAGCTAAAAACCTCTATAATCAA	120
J803231025_5-3.SEQRC	TTTGTTCATTGCTATGTTTCATGTACCCATCAAGACAAGCTAAAAACCTCTATAATCAA	120
J803231026_5-4.SEQRC	TTTGTTCATTGCTATGTTTCATGTACCCATCAAGACAAGCTAAAAACCTCTATAATCAA	120
J803231026_5-5.SEQ	TTTGTTCATTGCTATGTTTCATGTACCCATCAAGACAAGCTAAAAACCTCTATAATCAA	120
POTRI.008G078400-U6-2.SEQRC	TTTGTTCATTGCTATGTTTCATGTACCCATCAAGACAAGCTAAAAACCTCTATAATCAA	120
Consensus	tttgttcattgctatgtttcatgtacccatcaagacaagctaaaaacctctataatcaa	
J803231023_5-1.SEQ	CTCCAGAAATTGAGCTTAACCACAACAGG	148
J803231024_5-2.SEQ	CTCCAGAAATTGAGCTTAACCACAACAGG	148
J803231025_5-3.SEQRC	CTCCAGAAATTGAGCTTAACCACAACAGG	148
J803231026_5-4.SEQRC	CTCCAGAAATTGAGCTTAACCACAACAGG	148
J803231026_5-5.SEQ	CTCCAGAAATTGAGCTTAACCACAACAGG	148
POTRI.008G078400-U6-2.SEQRC	CTCCAGAAATTGAGCTTAACCACAACAGG	148
Consensus	ctccagaattgagcttaaccacaacagg	

15. 5.8S Sequence similarity: 99.66%

5.8S-1.SEQ	ACGTCTGCCTGGGTGTCACGCATCGTCGCCCTCTCCCTCGGCTCGCGAGGGCGGGG	60
5.8S-2.SEQ	ACGTCTGCCTGGGTGTCACGCATCGTCGCCCTCTCCCTCGACTCGCGAGGGCGGGG	60
5.8S-3.SEQ	ACGTCTGCCTGGGTGTCACGCATCGTCGCCCTCTCCCTCGACTCGCGAGGGCGGGG	60
5.8S-4.SEQ	ACGTCTGCCTGGGTGTCACGCATCGTCGCCCTCTCCCTCGGCTCGCGAGGGCGGGG	60
5.8S-5.SEQ	ACGTCTGCCTGGGTGTCACGCATCGTCGCCCTCTCCCTCGACTCGCGAGGGCGGGG	60
5.8S.SEQ	ACGTCTGCCTGGGTGTCACGCATCGTCGCCCTCTCCCTCGGCTCGCGAGGGCGGGG	60
Consensus	acgtctgcctgggtgtcacgcacgctcgccccctctcccctcgactcgcgagggcgggg	
5.8S-1.SEQ	CGGATACTGGTCTCCCGCGCGCTCCCGCTCGCGGTGGGCCAAAATCGAGTCTCGGCGA	120
5.8S-2.SEQ	CGGATACTGGTCTCCCGCGCGCTCCCGCTCGCGGTGGGCCAAAATCGAGTCTCGGCGA	120
5.8S-3.SEQ	CGGATACTGGTCTCCCGCGCGCTCCCGCTCGCGGTGGGCCAAAATCGAGTCTCGGCGA	120
5.8S-4.SEQ	CGGATACTGGTCTCCCGCGCGCTCCCGCTCGCGGTGGGCCAAAATCGAGTCTCGGCGA	120
5.8S-5.SEQ	CGGATACTGGTCTCCCGCGCGCTCCCGCTCGCGGTGGGCCAAAATCGAGTCTCGGCGA	120
5.8S.SEQ	CGGATACTGGTCTCCCGCGCGCTCCCGCTCGCGGTGGGCCAAAATCGAGTCTCGGCGA	120
Consensus	cggatactggtctcccgcgctcccgctcgcggtgggccaaaatcgagtctcggcga	
5.8S-1.SEQ	CGGTCGCCACGACGAGCGGTGGTTG	145
5.8S-2.SEQ	CGGTCGCCACGACGAGCGGTGGTTG	145
5.8S-3.SEQ	CGGTCGCCACGACGAGCGGTGGTTG	145
5.8S-4.SEQ	CGGTCGCCACGACGAGCGGTGGTTG	145
5.8S-5.SEQ	CGGTCGCCACGACGAGCGGTGGTTG	145
5.8S.SEQ	CGGTCGCCACGACGAGCGGTGGTTG	145
Consensus	cggtcgccacgacgagcgggtggtt	

16. miR171 Sequence similarity: 98.33%

miR171-1.SEQ	AGATTGAGCCGCGCCAATATCAAAAAAAAAAAGTCTGTCTCGTCTCGT	49
miR171-2.SEQ	AGATTGAGCCGCGCCAATATCAAAAAAAAAAAGTCTGTCTCGTCTCGT	49
miR171-3.SEQ	AGATTGAGCCGCGCCAATATCAAAAAAAAAAG..TCTGTCTCGTCTCGT	47
miR171-4.SEQ	AGATTGAGCCGCGCCAATATCAAAAAAAAAAAGTCTGTCTCGTCTCGT	49
miR171-5.SEQ	AGATTGAGCCGCGCCAATATCAAAAAAAAAA..GTCTGTCTCGTCTCGT	48
ptc-miR171c.SEQ	AGATTGAGCCGCGCCAATATCAAAAAAAAAA..GTCTGTCTCGTCTCGT	48
Consensus	agattgagccgcgccaatatcaaaaaaaaaaagtctgtctcgtctcgt	

17. miR403 Sequence similarity: 98.62%

J803231058_12-2.SEQ	CGCGTTAGATTACAGCACAAACTCGAAAAAAAAAAAAA..GTCTGTCGTCGTCTCGT	55
J803231058_12-3.SEQRC	CGCGTTAGATTACAGCACAAACTCGAAAAAAAAAAAAAAGTCTGTCGTCGTCTCGT	57
J803231058_12-4.SEQRC	CGCGTTAGATTACAGCACAAACTCAAAAAAAAAAAAAAAGTCTGTCGTCGTCTCGT	57
J803231058_12-5.SEQ	CGCGTTAGATTACAGCACAAACTCGAAAAAAAAAAAAA..GTCTGTCGTCGTCTCGT	56
Ptc-miR403.SEQ	CGCGTTAGATTACAGCACAAACTCGAAAAAAAAAAAAAAGTCTGTCGTCGTCTCGT	57
Consensus	cgcgttagattacagcacaaactcgaaaaaaaaaaaaaagtctgtcgtcgtctcgt	

18. miR482 Sequence similarity: 98.69%

MIR482-1.SEQ	CCTACTCCTCCATTCCAAAAAAAAAAAAAAAAAAGTCTGTCGTCGTCTCGT	50
MIR482-2.SEQ	CCTACTCCTCCATTCCAAAAAAAAAAAAAAAAAAGTCTGTCGTCGTCTCGT	50
MIR482-3.SEQ	CCTACTCCTCCATTCCAAAAAAAAAAAAAAAAA..GTCTGTCGTCGTCTCGT	49
MIR482-4.SEQ	CCTACTCCTCCATTCCAAAAAAAAAAAAAAAAA..GTCTGTCGTCGTCTCGT	49
MIR482-5.SEQ	CCTACTCCTCCATTCCAAAAAAAAAAAAAAAAA..GTCTGTCGTCGTCTCGT	49
ptc-miR482.SEQ	CCTACTCCTCCATTCCAAAAAAAAAAAAAAAAA..GTCTGTCGTCGTCTCGT	49
Consensus	cctactcctccattccaaaaaaaaaaaaaaaaa gtctgtcgtcgtctcgt	