

Supplemental Material to:

Marie Turner, Sajag Adhikari and Senthil Subramanian

**Optimizing stem-loop qPCR assays through multiplexed
cDNA synthesis of U6 and miRNAs**

Plant Signaling & Behavior 2013; 8(8)

<http://dx.doi.org/10.4161/psb.24918>

www.landesbioscience.com/journals/psb/article/24918

A

CLUSTAL 2.1 multiple sequence alignment

```

Oryza_sativa_cv_japonica      GTCTCTTCGGGAGACATCCGATAAAAATTGGAACGATACAGAGAAGATTAGC 50
Zea_mays                      GTCTCTTCGGGAGACATCCGATAAAAATTGGAACGATACAGAGAAGATTAGC 50
Triticum_aestivum            GCCCCTTCGGGGACATCCGATAAAAATTGGAACGATACAGAGAAGATTAGC 50
Broad_bean                   ----CTTCGGGGACATCCGATAAAAATTGGAACGACACAGAGAAGATTAGC 46
Medicago_truncatula         GTCCCTTTGGGGACATCTGATAAAAATTGGAACGATACAGAGAAGATTAGC 50
Arabidopsis_thaliana         GTCCCTTCGGGGACATCTGATAAAAATTGGAACGATACAGAGAAGATTAGC 50
                               *** ** ***** *****

Oryza_sativa_cv_japonica      ATGGCCCTGCGCAAGGATGACACGCACAAATCGAGAAATGGTCCAAATT 100
Zea_mays                      ATGGCCCTGCGCAAGGATGACACGCACAAATCGAGAAATGGTCCAAATT 100
Triticum_aestivum            ATGGCCCTGCGCAAGGATGACACGCACAAATCGAGAAATGGTCCAAATT 100
Broad_bean                   ATGGCCCTGCGCAAGGATGACACGCACAAATCGAGAAATGGTCCAAATT 96
Medicago_truncatula         ATGGCCCTGCGCAAGGATGACACGCACAAATCGAGAAATGGTCCAAATT 100
Arabidopsis_thaliana         ATGGCCCTGCGCAAGGATGACACGCATAAATCGAGAAATGGTCCAAATT 100
                               *****

Oryza_sativa_cv_japonica      TTT----- 103
Zea_mays                      TTTT----- 105
Triticum_aestivum            TTTTGGAGATT 111
Broad_bean                   TT----- 98
Medicago_truncatula         TTT----- 103
Arabidopsis_thaliana         TTT----- 103
                               **

```

B**Primer Sequences:**

U6 cDNA synthesis primer: 5'-GTGCAGGGTCCGAGGTTTTGGACCATTCTCGAT-3'

U6 qPCR forward primer: 5'-GGAACGATACAGAGAAGATTAGCA-3'

Universal qPCR reverse primer: 5'-GTGCAGGGTCCGAGGT-3'

Figure S1. U6 primer design. **A.** Sequence alignment of U6 sequences from multiple plant species showing a conserved region from which qPCR primers were designed. U6 sequences from multiple plant species were obtained from non-coding RNA database (<http://www.ncrna.org/frnadb/>), NCBI and ncRNAdb. Sequences used to design "Forward" and "Reverse" primers are underlined. **B.** Novel U6 primer sequences designed in this study for multiplexed cDNA synthesis and qPCR. The universal qPCR primer is from Varkonyi-Gasic et al (2007).