

SUPPLEMENTAL TABLE S2

Synthetic oligonucleotides used to amplify COG2154 sequences for complementation tests

Restriction sites are underlined. Stop codons in frame with LacZ of the pBluescript vector are in orange. Shine-Dalgarno sequences are in blue. Start codons are in green. Stop anticodons are in red.

Plant COG2154 type 1		
Organism	Forward (5'-3')	Reverse (5'-3')
<i>Arabidopsis thaliana</i>	<u>GGG</u> <u>CTGAAGGAAA</u> CAGCTATGGCTAGAACATTTTGCTC ^a	TAGCTCTCGAGTCACTTAGCAACTTCTTCTT
<i>Chlamydomonas reinhardtii</i>	AGTCACATATGTGCCAGGGGCCGACGCGG	AGTAGGTACCCTAGCTGGAGCCGCGTCCGC
<i>Physcomitrella patens</i>	CTAGGGATCCATGAAGGAAACAGCTATGCAAGAAGG	CTAGGAATCTTAAGCTAGGAGCTGCTTTGGTT
<i>Pinus taeda</i>	CTAGTCTAGAAATGAAGGAAACAGCTATGAAATGTTT	CTAGGAATCTTAAGTCTTTGCAGCTTCTTT
<i>Zea mays</i>	AGTCACATATGTGCCATAGCTCCCTGAGAGT	AGTAGGTACCCTATTAGCTTCTTCTTATAATGCC
Plant COG2154 type 2		
Organism	Forward (5'-3')	Reverse (5'-3')
<i>Arabidopsis thaliana</i>	CTAGTCTAGAAATGAAGGAAACAGCTATGCAAGATTTCTGGTGACTTC	CTAGGAATCTCACGCCCAAGCTCTTTTCC
<i>Chlamydomonas reinhardtii</i>	AGTCACATATGGGAATGTTCCGGCAGAACTTC	AGTAGGTACCCTAGCACCAGAAAGCGTGT
<i>Physcomitrella patens</i>	AGTCACATATGGGGCAGATGTTGGGTGA	AGTAGGTACCCTAGAACCATGTCGGAAG
<i>Pinus taeda</i>	AGTCACATATGGGGATCTTCTAGGTGACTTT	AGTAGGTACCCTAAGCCCAAAATCTTTTCTGG
<i>Zea mays</i>	AGTCACATATGGCCGACCTGCTGGGGAC	AGTAGGTACCCTATGCCACGCCGCTTCTT
Microbial COG2154		
Organism	Forward (5'-3')	Reverse (5'-3')
<i>Bacillus cereus</i>	AGTCACATATGATGCTACGATTAACCTGAAG	AGTAGGTACCCTACTTCTTATAATGGCTTTTGG
<i>Corynebacterium glutamicum</i>	AGTCACATATGTGCCCATTTTAAGGC	AGTAGGTACCCTAAGCCTCTGCCGAAATG
<i>Cytophaga hutchinsonii</i>	AGTCACATATGTATGTATTAGTTAATAAGAACC	AGTAGGTACCCTAATTGTCTGATTATGAGC
<i>Leishmania major</i>	CTAGTCTAGAAATGAAGGAAACAGCTATGCGTCGAACCGCTCCTC	CTAGGAATCTCAATGCCTGCGCATCGCTT
<i>Pseudomonas aeruginosa</i>	AGTCACATATGACCCGACTCACCACAGGCC	AGTAGGTACCCTAATTGCGCCCTCGGCGGT
<i>Saccharomyces cerevisiae</i>	AGTCAGGATCCGTGAAGGAAAGCCATATGCACAAAGATTGTTAGAATC	AGTAGGTACCCTAAGTTGTCATCTCATCGATG
<i>Silicibacter pomeroyi</i>	AGTCACATATGAGCGAACGTTTGTCCGAG	AGTAGGTACCCTAGCAGAGGCTGTCCATCTT
<i>Streptomyces avermitilis</i>	AGTCACATATGCCCGTCGAACCGTTGTGCGC	AGTAGGTACCCTAGCTCGCCGCTGCC
<i>Sulfolobus solfataricus</i>	AGTCACATATGAGTGGGATTTCTCCGA	AGTAGGTACCCTAAGTGTCTTCTTTGTAAAGCT
<i>Synechocystis sp.</i>	AGTCAGGATCCGTGAAGGAAAGCCATATGGCCACCCCAACGT	AGTAGGTACCCTAATCAGCAAAACTATTAGCCTTGGT

^aThe underlined 5'-terminal sequence is a half-*SmaI* restriction site.