

Suppl. Table I: Primers used for gene cloning, subcloning, and RT-PCR

Primers are given in 5'→3' orientation. The restriction sites and introduced point mutations are underlined.

Gene/construct	Analysis	ORF modification	Forward/reverse primer
Gene (sub-)cloning:			
AtHsp15.7 in pGEMT	gene cloning	full-length (aa 1 to 137)	for.: <u>CGGTCTAGAATGGCAGACAGAGGAATATTCTTG</u> rev.: AATCCCGGGTCAAAGCTTGCTAGTAAT
EYFP:AtHsp15.7 in pCAT-Nfus	PTS1 analysis	full-length (aa 1 to 137)	for.: ACATAAGAT <u>TGCCGCCGCTATGGCAGACAGAGGAATATTC</u> rev.: CCT <u>CTAGATCAAAGCTTGCTAGTAAT</u>
EYFP:AtHsp15.7ΔPTS1 in pCAT-Nfus	PTS1 analysis	PTS1 deletion (aa 1 to 123)	for.: ACATAAGAT <u>TGCCGCCGCTATGGCAGACAGAGGAATATTC</u> rev.: ATAT <u>CTAGATCACGATGAAGTGTCCCTTAGG</u>
AtHsp15.7:EYFP in pCAT-Cfus	mitochondrial targeting analysis	PTS1 deletion (aa 1 to 123)	for.: GATCCATGGCAGACAGAGGAATATT rev.: ATACCATGGATGAAGTGTCCCTAGGAAC
AtHsp15.7ΔPTS1 in pYES2.1	yeast complementation	PTS1 deletion (aa 1 to 134)	for.: GAATATGGCAGACAGAGGAAT rev.: GTATCAAGTAATATTAACATTCCTAAC
AtAcd31.2 in pGEMT	gene cloning	full-length (aa 1 to 285)	for.: ACTGCGGCCGCTATGGAGCATGAATCTATCAC rev.: TCAAAGCTTTGGAATTACTATTCTCAG
AtAcd31.2:EYFP in pCAT-Cfus	PTS2 analysis	full-length (aa 1 to 285)	for.: CACTAACCATGGAGCATGAATCTATCAC rev.: TGCTCACCATGGAAAGCTTTGGAATTACTATTC
AtAcd31.2ΔPTS2:EYFP in pCAT-Cfus	PTS2 analysis	PTS2 deletion (aa 30 to 285)	for.: CACTAACCATGGAGCATCTCGTCCCCCTTG rev.: TGCTCACCATGGAAAGCTTTGGAATTACTATTC
AtAcd31.2:EYFP(H→D) in pCAT-Cfus	PTS2 analysis	PTS2 mutation (aa 1 to 285, H18→D)	for.: AGGCTCGCTGCCTTCGCCGCGGACTTCCCAGCAACAGTTACGATTCCG rev.: CGGAATCGTAACCTGGTTGCCGGAAGTCCGCGGCAAGGCAGCGAGCCCT
EYFP:AtAcd31.2 in pCAT-Nfus	PTS1 analysis	full-length (aa 1 to 285)	for.: ACTGCGGCCGCTATGGAGCATGAATCTATCAC rev.: TCAAAGCTTTGGAATTACTATTCTCAG
EYFP:AtAcd31.2ΔPTS1 in pCAT-Nfus	PTS1 analysis	PTS1 deletion (aa 1 to 282)	for.: ACTGCGGCCGCTATGGAGCATGAATCTATCAC rev.: GATCAAATTACTATTCTCAGAATCC
EYFP-AtAcd31.2(K→E) in pCAT-Nfus	PTS1 analysis	PTS1 mutation (aa 1 to 285, K284→E)	for.: GGGATTCTGAGAATAGTAATTCCAGAGCTCTGAGCGGCCGCTCTAGAG rev.: CTCTAGAGCGGCCGCTCAGAGCTCTGGAATTACTATTCTCAGAATCC
AtAcd31.2ΔPTS1 in pYES2.1	yeast complementation, PTS1 deletion	PTS1 deletion (aa 1 to 282)	for.: AGAGATGGAGCATGAATCTATC rev.: GATCAAATTACTATTCTCAGAATCC
AtAcd31.2ΔPTS1+2 in pYES2.1	yeast complementation, PTS1/2 deletion	PTS1 and PTS2 deletion (aa 30 to 282)	for.: CACTAACCATGGAGCATCTCGTCCCCCTTG rev.: GATCAAATTACTATTCTCAGAATCC
RT-PCR:			
AtHsp15.7			for.: CGGTCTAGAATGGCAGACAGAGGAATATTCTTG rev.: AATCCCGGGTCAAAGCTTGCTAGTAAT
AtAcd31.2			for.: CACTAACCATGGAGCATGAATCTATCAC rev.: GATCAAATTACTATTCTCAGAATCC
AtpMDH			for.: CTCTGTAATCGGACGGGAAAAC rev.: ACTTCTCTGCTCCTGTACGG
Ubiquitin			for.: GATCTTTGCCGAAAACAATTGGAGGATGGT rev.: CGACTTGTATTAGAAAAGAGATAACAGG