Table S1. Oligos used in this study.

Name	Site	Size	Sequence
AB	*Nco*I	80	5’GGCGGATAATGCCTTTAGCGGCTTAACTGTGCCCT**CCATGG**AAAAATCAGTCAAGATATCCACATGTGTTTTTAGTAAAC
CD	*Nco*I	80	5’GTTTACTAAAAACACATGTGGATATCTTGACTGATTTTT**CCATGG**AGGGCACAGTTAAGCCGCTAAAGGCATTATCCGCC
AB_S	*Sac*I	80	5’GGCGGATAATGCCTTTAGCGGCTTAACTGTGCCCTC**GAGCTC**AAAATCAGTCAAGATATCCACATGTGTTTTTAGTAAAC
CD_S	*Sac*I	80	5’GTTTACTAAAAACACATGTGGATATCTTGACTGATTTT**GAGCTC**GAGGGCACAGTTAAGCCGCTAAAGGCATTATCCGCC
AB_X	*Xba*I	80	5’GGCGGATAATGCCTTTAGCGGCTTAACTGTGCCCTC**TCTAGA**AAAATCAGTCAAGATATCCACATGTGTTTTTAGTAAAC
CD_X	*Xba*I	80	5’GTTTACTAAAAACACATGTGGATATCTTGACTGATTTT**TCTAGA**GAGGGCACAGTTAAGCCGCTAAAGGCATTATCCGCC
A20B60$_S$	*Sac*I	80	5’AAGAGTAAAAAATTGTACTTGGCGGATAATGCCTTTAGCGGCTTAACTGTGCCCTC**GAGCTC**AAAATCAGTCAAGATATC
C60D20$_S$	*Sac*I	80	5’GATATCTTGACTGATTTT**GAGCTC**GAGGGCACAGTTAAGCCGCTAAAGGCATTATCCGCCAAGTACAATTTTTTACTCTT
e1		80	5’TCCGAAGCTGGCCAATTGATACAATTAATTGACATCAGCAGACAGCAAATGCACTTGATATACGCAGCTTAAAGCAAGGG
f1		80	5’CCCTTGCTTTAAGCTGCGTATATCAAGTGCATTTGCTGTCTGCTGATGTCAATTAATTGTATCAATTGGCCAGCTTCGGA
R1		80	5’GTTGTATATACCACTACTCTGTGATTTTTTTTCACTCTTGGGAAGGAAAGAAAAAGTGAAAACATCAACTGGTAAGTGTC
R2		80	5’GACACTTACCAGTTGATGTTTTCACTTTTTCTTTCCTTCCCAAGAGTGAAAAAAAATCACAGAGTAGTGGTATATACAAC
Trp5.A3-F		80	5'GTCTAAGAGAGTTGGAAAAGGGTTTTGATGAAGCTGTCGCCATGGAGGGCACAGTTAAGCCGCTAAAGGCATTATCCGCC
Trp5.A3-R		80	5’GGCGGATAATGCCTTTAGCGGCTTAACTGTGCCCTCCATGGCGACAGCTTCATCAAAACCCTTTTCCAACTCTCTTAGAC
Trp5.UR-F		80	5’TGTTTACTAAAAACACATGTGGATATCTTGACTGATTTTTCCGATCCCACATTCTGGGAAGACTTCAAATCCTTGTATTCT
Trp5.UR-R		80	5'AGAATACAAGGATTTGAAGTCTTCCCAGAATGTGGGATCGGAAAAATCAGTCAAGATATCCACATGTGTTTTTAGTAAACA

The structures of the oligos used in this study are described from the 5′ end, with restriction endonuclease site sequences shown in bold and underlined. The presence of the *Sac*I site within the AB_S and CD_S oligo sequence changes the 69th serine codon (TCC) of *URA3* and the 70th methionine codon (ATG) to glutamine (GAG) and leucine (CTC), respectively. The presence of the *Xba*I site within the AB_X and CD_X oligo sequence creates a silent mutation on codon 69th serine of *URA3* (TCC to TCT) and changes the 70th codon methionine to arginine codon (ATG to AGA). These changes into the *URA3* coding sequence do not alter the functionality of the Ura3 protein.