

Table S5. Oligonucleotides used in this study.

Oligonucleotide	Description	Sequence (5' to 3')
F1	<i>CDC11</i> UTR ¹ +406 F	CATCTACAAAAGCAGGTTATAGCTCCG TTAAAC
F7	<i>CDC11</i> UTR +330 F	CACAACATGGAACATAACATTTAAACAT CGTTCTCAATC
R1	<i>CDC11</i> UTR -327 R	GCTAAGTGATGTTCTGGTCTTTCCAAAA TTCTC
F2	<i>CDC11</i> UTR +101 F	GATCGAAAAGTAAAATAGGTAGACACC ACGTATTG
R2	<i>CDC11</i> Int ² +75 R1	CACAGTGAAGGTTATACCTCTTTTCAAA TGCTTTC
F3	<i>CDC11</i> Int +1233 F	GAAGCCAGGTTGGAAAAAGAGGCGAAA ATC
R3	<i>CDC11</i> UTR -89 R	TAATATACCAGATGTATTTACTTATATAC AACACTCACTC
F4	<i>SHS1</i> UTR +800 F	CATTACTAGAGTTTGCTGGTGTTCAG ATCG
F8	<i>SHS1</i> UTR +500 F	GTTCTCCGGTTTAAACTGATCCATAGT GATAG
R4	<i>SHS1</i> Int +999 R	ACGGTAATTCTCGTAAAGCAAATTTTGC GTGG
R5	Int Hyg R	CTCCTACATCGAAGCTGAAAGCACGAG
F5	Cas9 Int +2903 F	CTGAAGTCTAAGCTGGTCTCAGATTTCA GAAA
F9	Cas9 Int +3477 F	GTGGAGAAAGGGAAGTCTAAAAAACTC AAAAGC
R6	Int Kan R	GAACACTGCCAGCGCATCAACAATATT TTC
F6	<i>HIS3</i> UTR +992 F	GGGTCAGTTATTTTCATCCAGATATAACC CG
F10	<i>HIS3</i> UTR +500 F	TTCTCGACGTGGGCCTTTTTCTTGCCAT AT

R7	<i>HIS3</i> UTR -497 R	GTAACCACCACGACGGTTGTTGCTAAA GAA
F11	<i>CDC11</i> UTR +30 F	CACAAGGCCTAAAGTTGCTAACCACCA GCCATGTCCGGAATAATTGACGCATCT TCTGCA
R8	<i>CDC11</i> UTR -30 R	AAGAAATAAGTGAGGAAGCCAAAAGCG GACTCATTCTTCCTGTTTGATTTTCGCC TCTTTTTCC
F12	<i>SHS1</i> UTR +30 F	TATAATTGCTAGAAAAATATATTATTAAT CATGAGCACTGCTTCAAC
R9	<i>SHS1</i> UTR -30 R	GCTCAGCTTTGGATTTTGTACAGATACA ACACTGGATGGCGGCGTTAGTATCGAA TC
F13	<i>HIS3</i> UTR +30 F	AATGAGCAGGCAAGATAAACGAAGGCA AAG
R10	<i>HIS3</i> UTR -30 R	GTATGCTGCAGCTTTAAATAATCGGTGT CA
F14	Int Kan F	CGTTGCATTCGATTCCTGTTTGTAATT GTCC
R11	<i>SHS1</i> UTR -469 R	CCACTAGAGCATTGGCAGAATTATATG GTAGT

¹UTR +/- designates sequence upstream (5') or downstream (3') of the specified gene.

²"Int" designates a position internal to the coding sequence of the specified ORF.