TABLE S3 Oligonucleotides used to generate the 3348*slo*dm and 3348Δ*slo* strains

Name	Sequence[a]	Description[a]/Orientation[b]	5'-Terminal restriction site
F*slo*SOE1	GGATCCCTTAGCAGAGATTGATGC	631bp upstream of SLO start/F	BamHI
R*slo*SOE1	*ATAATTGATTTCATC*TGGTTGCTCATTTGTCGT	132bp downstream of SLO start/R	None
F*slo*SOE2	*ACAAATGAGCAACCA*GATGAAATCAATTATGATGAC	1443bp downstream of SLO start/F	None
R*slo*SOE2	CTCGAGCCATATAACCTTGACCGG	2309bp downstream of SLO start/R	XhoI
F*slo*EXT	AAAGCGGAGCTTCTCACGTTACAAGT	1041bp upstream of SLO start/F	None
R*slo*EXT	GTCTATGAAGGTATCTCATAGAC	1806bp downstream of SLO start/R	None

[a]Oligonucleotide sequences were derived from the sequenced *slo* locus in M1-3348. Where indicated, additional nucleotides were added to the 5' terminus to create specific restriction enzyme cutting sites (underlined). The sequences indicated in italics are complementary and used to fuse PCR fragments by SOEing.

[b]F, forward (coding strand); R, reverse (non coding strand).