

Supplementary Table 2. Types of NHEJ repair events in *mre11* mutants.

Mutation types ^a		<i>MRE11</i>	<i>mre11-K62A</i>	<i>mre11-H125N</i>	<i>mre11-R184A</i>	
Original sequence: TCCGCAACAGTATAATT ^b						
Insertion	Total	27 (46.6%) ^c	89 (75.4%)	52 (89.7%)	49 (77.8%)	
	+A	TCCGCAACAAGTATAAT	1 (1.7%)	1 (0.8%)	0	0
	+CA	TCCGCAACAACGTATAAT	13 (22.4)	33 (28.0%)	15 (25.9%)	25 (39.7%)
	+ACA	TCCGCAACAACAGTATAAT	11 (19.0%)	49 (41.5%)	37 (63.8%)	24 (38.1%)
	+AA	TCCGCAAAACAGTATAAT	0	0	0	1 (1.6%)
	+CACA	TCCGCAACACACAGTATAAT	2 (3.4%)	1 (0.8%)	0	0
Deletion	Total	28 (48.3)	27 (22.9%)	2 (3.5%)	11 (17.5%)	
	-A	TTCCGC*ACAGTATAAT	4 (6.9%)	2 (1.7%)	0	3 (4.8%)
		TTCCGCAAC*GTATAAT	0	1 (0.8%)	0	0
	-CA	TCCGCAA**GTATAATT	10 (17.2%)	1 (0.8%)	0	2 (3.2%)
	-ACA	TCCGCA***GTATAATT	13 (22.4%)	14 (11.9%)	1 (1.7%)	2 (3.2%)
	-AACA	TCCGC****GTATAATT	1 (1.7)	2 (1.7%)	0	1 (1.6%)
	-C	TCCG*ACAGTATAAT	1 (1.7%)	1 (0.8%)	0	0
		TCCGCAA*AGTATAAT	0	1 (0.8%)	0	0
	-GC	TCC**AACAGTATAAT	0	0	0	1 (1.6%)
	-G	TCCGCAACA*ATAATT	0	2 (1.7%)	1 (1.7%)	2 (3.2%)
	-GT	TCCGCAACA**ATAATT	1 (1.7%)	0	0	0
	-GTA	TCCGCAACA***TAATT	0	1 (0.8%)	0	0
	-GTAT	TCCGCAACA****AATT	0	2 (1.7%)	0	0
Large deletion (>4bp)		3 (5.2%)	8 (6.8%)	4 (6.9%)	3 (4.8%)	
Total		58 (100%)	118 (100%)	58 (100%)	63 (100%)	

^a Alignment of the sequences flanking the HO cleavage site at the proximal boundary of the Z1 region in the *MATa* locus among survivors after persistent HO expression. ^b The 3' 4-bp overhang created after HO cleavage is underlined, the sequence highlighted by grey indicates inserted sequences whereas those with asterisk indicate deleted sequences.

^c The percentage of relative fractions of a specific repair event in the total number of the repair junction analyzed.