

Table 3. Representative examples of breakpoint sequences detected in *rrm3 sgs1* and *rrm3 sgs1 mec3* mutants

Relevant genotype	Breakpoint type	Representative breakpoint sequence
<i>rrm3 sgs1</i> RDKY5577*	telomere addition	GGTACTGAACTAGTTGGTATCACTGCTGGTGAAGtgggtgtgggtgtgggtgtgggtgtgg (32539)
	translocation (MH)	V32573 32506 <u>AGGTACTGAACTAGTTGGTATCACTGCTGGTGAAGCT</u> : GCAAACCCAGAAAATCCGTTCCAAGAGCC <u>AGAAAATTGTTATGACTGCCTCTGCTGCCATTAAAACT</u> : CCGCAAATGACTTTGCCATCTGGAATGAT XV964650 964716
	translocation (NH)	V34294 34228 <u>GCAACAAGTGATAGAGGGCCATTATGAATAC</u> : GCACCTCTATGTATTTCCGAGATACGATTACTCCA <u>CACACATCGCTGCAGTTTCATAATATCTGTCA</u> : CTCACCTGATGCAATAATTAAGTGACGAAATTATAT II259354 259410
	independent mutations	<i>CAN1</i> wildtype ATAGGTGATGAAGATGAAGGAGAAGTACAGAAC I G D E D E G E V Q N mutant ATAGGTGATGAAGATTAAGGAGAAGTACAGAAC I G D E D * <i>URA3</i> deletion
<i>rrm3 sgs1 mec3</i> RDKY5579	telomere addition	GGGCACAAACCCTTGAAAATAGCTTAGCATTTCGcgtgggtgtgggtgtgggtgtgggtgt (34400)
	translocation (MH)	V33208 33142 <u>GAGCTTAAGCAAAGACATATTGGTATGATTGC</u> : CCTTGGTGGTACTATTGGTACAGGTCTTTTCATTG <u>GCCTTGAAGCAAAGACACATTGGTATGATTGC</u> : ACTAGGTGGTACAATCGGTACTGGTCTTTTCGTTG XIV138873 138939
		V34105 34039 <u>GAAAAAAAAACAAAAAAAAAGAAAATAAATAACG</u> : GCAAACAGCAAAGGCCACAGAACCCTATTTCATGTT <u>AAAAAAAAAAAAAAAAAAAAAAAAAACAAAGAGCCA</u> : GCAAACCTGACATTAACATTTGATCAATAAATAAGA XIV779308 779367
	complex inversion [†]	normal chromosome V V34342 34277 CCAGTTTCTTTTTTTTTTATCACTTATCAGTCTTATTCGGAGATACAGGCAACAAAGTGATAGAGGG rearranged chromosome V CCAGTTTCTTTTTTTTTTATCACTTGTTCCTGTATCTCCGAATAGGtgtgggtgtgggtgtgtgtg

For translocations, the numbers above and below the sequences are the SGD coordinates for the first and last nucleotide listed; the chromosome number is indicated by a roman numerical. For telomere additions, the number indicates the last recognizable SGD nucleotide coordinate of chromosome V. The underlined nucleotides indicate those present in the translocation chromosome. Nucleotides in bold indicate identities. In the case of the complex inversion, the dotted lines indicate the inverted repeat, the double line indicates those nucleotides lost in the rearranged chromosome and the boxed nucleotides are inverted in the rearranged chromosome. MH, microhomology; NH, nonhomology.

* The diploid strain RDKY5577 was used to generate *rrm3 sgs1* double mutant spores directly for GCR analysis.

† For a model of the mutational mechanism see Fig. 5.