

S2 Table. Diploid strains used to measure % tetratype, spore viability, meiotic progression, genetic map distances and for whole genome recombination mapping.

| Diploid strain | Relevant genotype |
|---|---|
| Spore autonomous fluorescent protein assay [56], meiotic progression assay [93], and Sgs1 overexpression. | |
| EAY3252/EAY3486 | <i>MLH3/mlh3Δ</i> |
| EAY3255/EAY3486 | <i>mlh3Δ/mlh3Δ</i> |
| EAY3490 to EAY3708/EAY3486 | <i>mlh3-1 to mlh3-60/mlh3Δ</i> |
| EAY3339/EAY3552-53 | <i>MLH3/mlh3-32</i> |
| EAY3819-20/EAY3486 | <i>mlh3-D523N/mlh3Δ</i> |
| Tetrad analysis [7] | |
| EAY1112/EAY2413 | <i>MLH3/mlh3Δ</i> |
| EAY1848/EAY2413 | <i>mlh3Δ/mlh3Δ</i> |
| EAY3713-14/EAY2413 | <i>mlh3-6/mlh3Δ</i> |
| EAY3715-16/EAY2413 | <i>mlh3-23/mlh3Δ</i> |
| EAY3717-18/EAY2413 | <i>mlh3-32/mlh3Δ</i> |
| EAY3719-20/EAY2413 | <i>mlh3-42/mlh3Δ</i> |
| EAY3721-22/EAY2413 | <i>mlh3-45/mlh3Δ</i> |
| EAY3723-24/EAY2413 | <i>mlh3-54/mlh3Δ</i> |
| Whole genome recombination mapping [34, 64] | |
| KTY618/KTY610 | <i>SK1-MLH1/mlh1Δ, SK1-MLH3/mlh3Δ</i> |
| KTY618/KTY616 | <i>SK1-MLH1/mlh1Δ, SK1-mlh3-23/mlh3Δ</i> |
| KTY618/KTY614 | <i>SK1-MLH1/mlh1Δ, SK1-mlh3-32/mlh3Δ</i> |
| KTY618/KTY621 | <i>SK1-MLH1/mlh1Δ, SK1-mlh3-D523N/mlh3Δ</i> |
| KTY618/KTY626 | <i>SK1-MLH1/mlh1Δ, mlh3Δ/mlh3Δ</i> |

The indicated haploid strains were mated to form the diploids with the relevant genotype shown.