**Table S1. Yeast Strains**

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| **Strain #** | **Relevant Genotype** | **Description** |
| SJR3782 | *MATα* | Craven *et al.* 2002 |
| SJR3848 | *MATa lys2::I-SceI can1::lys2Δ3′,I-SceIncSNP8 his3Δ::kanMX-pGAL-I-SceI mlh1Δ::LEU2* | Complete SNP8 I-SceI (*mlh1Δ*) system  |
| SJR4015 | *MATa lys2::CORE* | Hum and Jinks-Robertson 2019 |
| SJR4016  | *MATα can1::lys2Δ3′,I-SceIncSNP8* | Hum and Jinks-Robertson 2019 |
| SJR4029 | *MATα can1::lys2Δ3′::CORE-UK*  | CORE-UK inserted in *lys2Δ3′* donor allele of SJR4016 |
| SJR4195 | *MATa hisG-lys2::I-SceI* | Hum and Jinks-Robertson 2019 |
| SJR4258 | *MATα hisG-lys2::I-SceI can1::lys2Δ3′,I-SceIncSNP8-URA3-hisG his3Δ::hph-pGAL-I-SceI* | Complete *I-SceI* SNP8 (*mlh1Δ*) system with CO-NCO phenotypic distinction; Hum and Jinks-Robertson 2019 |
| SJR4582 | *MATa hisG-lys2:ZFN can1::lys2Δ3′, ZFNncSNP7-URA3-hisG leu2-3,112:ryB-ZFN:LEU2 his3-11,15:ryA-ZFN:HIS3 mlh1Δ::loxP-TRP1-loxP*  | Complete ZFN SNP7 (*mlh1Δ*) system with CO-NCO phenotypic distinction  |
| SJR4686 | *MATα can1::lys2Δ3′,I-SceIncSNP22*  | CORE in SJR4029 replaced with *I-SceI*nc and SNP22  |
| SJR4727 | *MATα can1::lys2Δ3′,I-SceIncSNP22-URA3-hisG*  | SJR4686 transformed with *URA3-hisG* fragment  |
| SJR4748 | *MATa lys2::ISceI can1::lys2Δ3′,I-SceIncSNP22-URA3-hisG his3Δ::kanMX-pGAL-I-SceI mlh1Δ::LEU2* | *I-SceI* SNP22 (*mlh1Δ*) system; spore from SJR4727 x SJR3848  |
| SJR4813 | *MATα can1::lys2Δ3′,ZFNncSNP22*  | CORE in SJR4029 replaced with ZFNnc and SNP22 |
| SJR4815 | *Isolate 1- MATa, Isolate 2- MATα hisG-lys2::ISceI can1::lys2Δ3′,I-SceIncSNP22-URA3-hisG his3Δ::kanMX-pGAL-I-SceI mlh1Δ::LEU2* | Complete *I-SceI SNP22* (*mlh1Δ*) System with CO-NCO phenotypic distinction; spore from SJR4748 x SJR4258  |
| SJR4814 | *MATα can1::lys2Δ3′::ZFNnc22-URA3-hisG*  | Transformed SJR4813 with *URA3-hisG* fragment |
| SJR5022 | *Isolate 1- MATa, Isolate 2- MATα hisG-lys2:ZFN can1::lys2Δ3′,ZFNncSNP22-URA3-hisG leu2-3,112:ryB-ZFN:LEU2 his3-11,15:ryA-ZFN:HIS3 mlh1Δ::loxP-TRP1-loxP*  | Complete ZFN SNP22 (*mlh1Δ*) system with CO-NCO phenotypic distinction; spore from SJR4814 x SJR4582 |

Craven R. J., P. W. Greenwell, M. Dominska, and T. D. Petes, 2002 Regulation of genome stability by TEL1 and MEC1, yeast homologs of the mammalian ATM and ATR genes. Genetics 161: 493–507.

Hum Y. F., and S. Jinks-Robertson, 2019 Mismatch recognition and subsequent processing have distinct effects on mitotic recombination intermediates and outcomes in yeast. Nucleic Acids Res. 47: 4554–4568.