

Supporting Appendix 1. Tables containing amino acid polymorphisms identified in *Saccharomyces cerevisiae* *MLH* and *MSH* genes

| <i>MLH1</i> | Amino acid position | | | | | | | | | | | | |
|-------------|---------------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------------|
| Strains | 240 | 242 | 271 | 309 | 333 | 375 | 452 | 465 | 470 | 607 | 678 | 703 | 761 |
| S288c | S | D | L | E | E | A | S | D | P | L | D | P | D |
| SK1 | R | D | P | E | K | A | S | D | P | L | N | L | G |
| W303 | S | D | L | E | E | A | S | D | P | L | D | P | D |
| YJM145 | S | D | L | E | E | A | S | D | P | L | D | P | G |
| YJM269 | S | D | P | E | E | A | S | N | P | L | D | P | G |
| YJM627 | S | D | P | E | E | A | G | D | P | F | D | P | G |
| M2-8 | S | D | P | E | E | A | G | D | P | F | D | P | G |
| M5-7 | S | D | P | E | E | A | G | D | P | F | D | P | G |
| M7-8 | S | D | P | E | E | A | G | D | P | F | D | P | G |
| M1-2 a* | S | D | P | D | E | A | G | D | P | F | D | P | G |
| M1-2 b* | S | D | P | E | E | A | S | N | P | Ls | D | P | G |
| YJM280 | S | D | P | E | E | A | S | N | P | L | D | P | D |
| YJM326 | S | E | P | E | E | A | S | D | P | L | D | P | D |
| YJM339 | S | E | P | E | E | T | S | D | S | L | N | L | G |
| YJM320 | S | D | P | E | E | A | S | D | P | L | N | L | G |

*M1-2 is heterozygous for *MLH1*. The original diploid isolate was sporulated and tetrad dissected, and *MLH1* and *PMS1* were sequenced from three of four spore clones.

| <i>PMS1</i> | Amino acid position | | | | | | | | | | | | | | |
|-------------|---------------------|-----|-----|-----|-----|-----|-----|-------|-----|-----|-----|-----|-----|-----|------------|
| Strains | 41 | 112 | 309 | 384 | 392 | 400 | 401 | 416** | 458 | 475 | 513 | 564 | 619 | 768 | 818 |
| S288c | N | S | V | F | E | T | A | T | D | D | Y | A | N | K | R |
| SK1 | S | T | V | V | E | S | A | TCEGT | D | D | F | A | N | K | K |
| W303 | N | S | V | F | E | T | A | T | D | D | Y | A | N | K | R |
| YJM145 | N | S | V | F | E | T | A | T | D | D | Y | A | N | K | R |
| YJM269 | N | S | V | F | E | T | A | T | D | D | Y | A | N | K | R |
| YJM627 | N | S | V | F | E | T | A | T | D | D | Y | A | N | K | R |
| M2-8 | N | S | V | F | E | T | A | T | D | D | Y | A | N | K | R |
| M5-7 | N | S | V | F | E | T | A | T | D | D | Y | A | N | K | R |
| M7-8 | N | S | V | F | E | T | A | T | D | D | Y | A | N | K | R |
| M1-2 a | N | S | V | F | E | T | A | T | D | D | Y | A | N | K | R |
| M1-2 b | N | S | V | F | E | T | A | T | Y | D | Y | A | N | K | R |
| YJM280 | N | S | F | F | E | T | A | T | D | D | Y | A | N | K | R |
| YJM326 | N | S | V | V | E | S | S | TCEGT | D | D | Y | A | I | K | R |
| YJM339 | N | S | V | V | E | S | A | TCEGT | D | N | Y | A | N | K | R |
| YJM320 | N | S | V | V | V | S | S | TCEGT | D | D | Y | V | N | R | K |

Amino acids in bold are implicated in mismatch repair (MMR) incompatibility as described in the text. Sequences have been deposited in the GenBank database (accession nos. DQ356633–DQ356646 for *MLH1* sequences and DQ356628–DQ356632 for *PMS1* sequences).

**Some strains contain a 4-aa insertion after T416.

| <i>MSH2</i> | Amino acid position | | | |
|-------------|---------------------|-----|-----|-----|
| Strains | 277 | 282 | 446 | 505 |
| S288c | E | G | N | T |
| SK1 | K | S | K | A |

| <i>MSH3</i> | Amino acid position | | |
|-------------|---------------------|----|-----|
| Strains | 25 | 31 | 482 |
| S288c | N | A | L |
| SK1 | T | V | F |

| <i>MSH6</i> | Amino acid position | | | | | | | |
|-------------|---------------------|----|-----|-----|-----|-----|-----|-----|
| Strains | 15 | 79 | 221 | 224 | 225 | 237 | 254 | 885 |
| S288c | E | V | Y | S | H | D | N | Q |
| SK1 | K | A | N | L | N | N | T | L |