

S1 Table. Fluctuation results of double mutants containing a null mutation of genes in the Rad52 pathway and *mms21-CH*.

Genotype	uGCR rate*	dGCR rate*	Ratio #
Wild type**	2.27x10 ⁻⁹ (1) [1.30x10 ⁻⁹ – 4.78x10 ⁻⁹]	1.97x10 ⁻⁸ (8.7) [1.61x10 ⁻⁸ – 4.32x10 ⁻⁸]	8.7
<i>mms21-CH</i> **	2.08x10 ⁻⁸ (9.1) [0.00x10 ⁻⁸ – 18.2x10 ⁻⁸]	4.2x10 ⁻⁶ (1850) [2.4x10 ⁻⁶ – 22.2x10 ⁻⁶]	202
<i>rad52Δ</i> **	1.67x10 ⁻⁸ (7.4) [0.99x10 ⁻⁸ – 2.74x10 ⁻⁸]	1.09x10 ⁻⁸ (4.8) [0.29x10 ⁻⁸ – 7.08x10 ⁻⁸]	0.7
<i>rad52Δ mms21-CH</i>	1.66x10 ⁻⁷ (73) [2.62x10 ⁻⁸ – 5.64x10 ⁻⁷] {HZY3310/3311}	1.20x10 ⁻⁷ (53) [4.98x10 ⁻⁸ – 3.84x10 ⁻⁷] {HZY3019/3020}	0.7
<i>rad59Δ</i> **	5.85x10 ⁻⁹ (2.6) [0.57x10 ⁻⁹ – 24.7x10 ⁻⁹]	6.94x10 ⁻⁸ (31) [5.17x10 ⁻⁸ – 9.12x10 ⁻⁸]	12
<i>rad59Δ mms21-CH</i>	3.66x10 ⁻⁷ (161) [1.56x10 ⁻⁷ – 8.82 x10 ⁻⁷] {HZY3362/3363}	2.71x10 ⁻⁶ (1194) [1.16x10 ⁻⁶ – 7.30x10 ⁻⁶] {HZY3166/3167}	7.4
<i>rad51Δ</i>	6.19x10 ⁻⁹ (2.7) [2.17x10 ⁻⁹ – 2.99x10 ⁻⁸] {HZY3264}	2.31x10 ⁻⁸ (10)** [1.20x10 ⁻⁸ – 4.35x10 ⁻⁸]	3.7
<i>rad51Δ mms21-CH</i>	2.17x10 ⁻⁸ (9.6) [4.06x10 ⁻⁹ – 4.90x10 ⁻⁸] {HZY3265/3266}	1.91 x10 ⁻⁷ (84) [1.02x10 ⁻⁷ – 5.00x10 ⁻⁷] {HZY3257/3258,JLY380}	8.8
<i>rad55Δ</i>	5.62x10 ⁻⁸ (25) [4.02x10 ⁻⁸ – 6.46x10 ⁻⁸] {HZY3369}	2.95x10 ⁻⁸ (13) [4.28x10 ⁻⁹ – 2.29x10 ⁻⁷] {HZY3021/3368}	0.5
<i>rad55Δ mms21-CH</i>	2.23x10 ⁻⁸ (9.8) [1.15x10 ⁻⁸ – 7.86x10 ⁻⁸] {HZY3245/3246}	1.41x10 ⁻⁷ (62) [6.74x10 ⁻⁸ – 2.23x10 ⁻⁷] {HZY3025/3026}	6.3
<i>rad54Δ</i>	1.4 x 10 ⁻⁸ (6.2) [4.17x10 ⁻⁹ – 1.74x10 ⁻⁸] {HZY3269/3270,JLY406}	2.16x10 ⁻⁸ (9.5) [1.11x10 ⁻⁸ – 1.03x10 ⁻⁷] {HZY3299/3306}	6.1
<i>rad54Δ mms21-CH</i>	1.18x10 ⁻⁷ (52) [4.27x10 ⁻⁸ – 1.15x10 ⁻⁶] {HZY3271/3272}	3.0x10 ⁻⁸ (13) [8.71x10 ⁻⁹ – 9.26x10 ⁻⁸] {HZY3300/3301}	0.3
<i>rdh54Δ</i>	3.72x10 ⁻⁹ (1.6) [2.26x10 ⁻⁹ – 7.75x10 ⁻⁹] {HZY3277,JLY382}	7.85x10 ⁻⁸ (35) [4.36x10 ⁻⁸ – 1.27x10 ⁻⁷] {HZY3274/JLY442}	21
<i>rdh54Δ mms21-CH</i>	5.05x10 ⁻⁸ (22) [7.32x10 ⁻⁸ – 1.88x10 ⁻⁸] {HZY3280/3281}	4.26x10 ⁻⁶ (1877) [2.98x10 ⁻⁶ – 6.56x10 ⁻⁶] {HZY3275/3276,JLY444}	84
<i>mre11Δ</i> **	5.75x10 ⁻⁷ (253) [2.82x10 ⁻⁷ – 19.2x10 ⁻⁷]	1.52x10 ⁻⁶ (670) [0.95x10 ⁻⁶ – 2.77x10 ⁻⁶]	2.6
<i>mre11Δ mms21-CH</i>	1.39x10 ⁻⁶ (612) [1.13x10 ⁻⁶ – 1.58x10 ⁻⁶]	6.66x10 ⁻⁶ (2934) [3.28x10 ⁻⁶ – 1.49x10 ⁻⁵]	4.8

	{HZY2480/2481}	{HZY2476/2477/2516}	
Genotype	uGCR rate*	dGCR rate*	Ratio #
<i>mre11-H125N</i>	2.78x10 ⁻⁷ (122) [1.80x10 ⁻⁷ – 4.01x10 ⁻⁷] {HZY2771/2772}	6.23x10 ⁻⁷ (274) [5.24x10 ⁻⁷ – 9.75x10 ⁻⁷] {HZY2763/2764}	2.2
<i>mre11-H125N mms21-CH</i>	6.35x10 ⁻⁷ (280) [2.73x10 ⁻⁷ – 1.43x10 ⁻⁶] {JLY929/930}	4.17x10 ⁻⁶ (1837) [2.86x10 ⁻⁶ – 5.28x10 ⁻⁶] {JLY973/974/975}	6.6
<i>sae2Δ</i> **	4.23x10 ⁻⁸ (19) [2.92x10 ⁻⁸ – 5.32x10 ⁻⁸]	1.65x10 ⁻⁷ (73) [1.09x10 ⁻⁷ – 2.09x10 ⁻⁷]	3.9
<i>sae2Δ mms21-CH</i>	6.61x10 ⁻⁷ (291) [2.66x10 ⁻⁷ – 1.03x10 ⁻⁶] {HZY2599/2600}	6.03x10 ⁻⁶ (2656) [3.33x10 ⁻⁶ – 8.81x10 ⁻⁶] {HZY2591/2592}	9.1

* Rate of accumulating Can 5-FOA progeny. Number in the parenthesis is the fold increase relative to wild-type uGCR strain.

** Rates taken from (Putnam et al., 2009; 2010; Albuquerque et al., 2013).

The dGCR rate divided by the uGCR rate.

Square brackets represent the upper and lower limits of the 95% confidence intervals of the median.

Strains used to calculate the GCR rate from this study are as indicated in curly braces.