

S6 Table. Fluctuation results of double mutants containing a null mutation of genes in the DNA damage checkpoint pathways 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>mec1Δ sml1Δ</i> **	2.34x10 ⁻⁸ (10) [1.29x10 ⁻⁸ – 4.02x10 ⁻⁸]	1.50x10 ⁻⁷ (66) [0.55x10 ⁻⁷ – 2.74x10 ⁻⁷]	6.4
<i>mec1Δ sml1Δ mms21-CH</i>	3.87x10 ⁻⁷ (170) [8.45x10 ⁻⁸ – 7.34x10 ⁻⁷] {HZY2927/2928}	7.81x10 ⁻⁷ (344) [2.20x10 ⁻⁷ – 2.74x10 ⁻⁶] {HZY2836/2837}	2.0
<i>tel1Δ</i> **	4.99x10 ⁻⁹ (2.2) [0.0x10 ⁻⁹ – 9.20x10 ⁻⁹]	2.87x10 ⁻⁸ (13) [1.81x10 ⁻⁸ – 5.68x10 ⁻⁸]	5.8
<i>tel1Δ mms21-CH</i>	1.41x10 ⁻⁸ (6.2) [8.04x10 ⁻⁹ – 5.72x10 ⁻⁸] {HZY3145}	3.80x10 ⁻⁶ (1674) [2.66x10 ⁻⁶ – 7.67x10 ⁻⁶] {HZY2974/2975}	270
<i>rad9Δ</i> **	2.17x10 ⁻⁸ (9.6) [0.98x10 ⁻⁸ – 4.81x10 ⁻⁸]	3.82x10 ⁻⁸ (17) [0.0x10 ⁻⁸ – 9.93x10 ⁻⁸]	1.8
<i>rad9Δ mms21-CH</i>	1.14x10 ⁻⁷ (50) [2.39x10 ⁻⁸ – 3.38x10 ⁻⁷] {HZY3082/3083}	1.74x10 ⁻⁷ (77) [1.40x10 ⁻⁷ – 2.86x10 ⁻⁷] {HZY2940/2941}	1.5
<i>mrc1Δ</i> **	3.35x10 ⁻⁹ (1.5) [0.0x10 ⁻⁹ – 16.4x10 ⁻⁹]	3.75x10 ⁻⁷ (165) [2.79x10 ⁻⁷ – 5.16x10 ⁻⁷]	112
<i>mrc1Δ mms21-CH</i>	9.50x10 ⁻⁷ (419) [6.05x10 ⁻⁸ – 1.75x10 ⁻⁶] {HZY3112/3113}	7.30x10 ⁻⁶ (3216) [4.66x10 ⁻⁶ – 1.03x10 ⁻⁵] {HZY2964/2965}	7.7
<i>mrc1-aq</i> **	1.51x10 ⁻⁹ (0.7) [0.0x10 ⁻⁹ – 5.19x10 ⁻⁹]	1.23x10 ⁻⁷ (54) [0.64x10 ⁻⁷ – 5.29x10 ⁻⁷]	81
<i>mrc1-aq mms21-CH</i>	1.06x10 ⁻⁷ (47) [7.52x10 ⁻⁸ – 1.89x10 ⁻⁷] {JLY1460/1461}	4.60x10 ⁻⁶ (2026) [3.18x10 ⁻⁶ – 7.06x10 ⁻⁶] {JLY1464/1465}	43
<i>rad53Δ sml1Δ</i> **	5.60x10 ⁻⁸ (25) [2.53x10 ⁻⁸ – 11.0x10 ⁻⁸]	3.05x10 ⁻⁷ (134) [1.16x10 ⁻⁷ – 7.31x10 ⁻⁷]	5.4
<i>rad53Δ sml1Δ mms21-CH</i>	7.19x10 ⁻⁸ (32) [2.89x10 ⁻⁸ – 9.05x10 ⁻⁸] {HZY3008}	5.48x10 ⁻⁷ (241) [2.73x10 ⁻⁷ – 9.80x10 ⁻⁷] {HZY2805/3236}	7.6
<i>chk1Δ</i> **	1.76x10 ⁻⁸ (7.8) [7.5x10 ⁻¹⁰ – 6.02x10 ⁻⁸]	1.96x10 ⁻⁷ (86) [0.86x10 ⁻⁷ – 4.37x10 ⁻⁷]	11
<i>chk1Δ mms21-CH</i>	6.75x10 ⁻⁸ (30) [3.99x10 ⁻⁶ – 9.75x10 ⁻⁶] {HZY3158}	4.02x10 ⁻⁶ (1771) [3.02x10 ⁻⁶ – 5.93x10 ⁻⁶] {HZY2987/2988}	60

Genotype	uGCR rate*	dGCR rate*	Ratio #
<i>dun1Δ</i>	1.26x10 ⁻⁸ (5.6) [7.70x10 ⁻⁹ – 2.25x10 ⁻⁸] {HZY2876/2877}	5.52x10 ⁻⁷ (243) [4.13x10 ⁻⁷ – 1.04x10 ⁻⁶] {HZY2864/2865}	44
<i>dun1Δ mms21-CH</i>	5.96x10 ⁻⁷ (263) [4.91x10 ⁻⁸ – 6.01x10 ⁻⁶] {HZY3154}	3.39x10 ⁻⁶ (1493) [2.51x10 ⁻⁶ – 5.76x10 ⁻⁶] {HZY2839/2995}	5.7
<i>mec3Δ</i>	1.02x10 ⁻⁸ (4.5) [2.56x10 ⁻⁹ – 6.33x10 ⁻⁸] {HZY3088}	3.77x10 ⁻⁷ (166) [2.29x10 ⁻⁷ – 7.37x10 ⁻⁷] {HZY2632/2633}	37
<i>mec3Δ mms21-CH</i>	1.01x10 ⁻⁷ (44) [4.74x10 ⁻⁸ – 2.14x10 ⁻⁷] {HZY3092}	6.15x10 ⁻⁷ (271) [4.13x10 ⁻⁷ – 8.78x10 ⁻⁷] {HZY2634/2635}	6.1
<i>rad24Δ**</i>	2.00x10 ⁻⁸ (8.8) [0.99x10 ⁻⁸ – 3.06x10 ⁻⁸]	1.97x10 ⁻⁷ (87) [1.43x10 ⁻⁷ – 2.52x10 ⁻⁷]	9.9
<i>rad24Δ mms21-CH</i>	1.68x10 ⁻⁷ (74) [5.41x10 ⁻⁸ – 5.29x10 ⁻⁷] {HZY3103/3104}	1.84x10 ⁻⁶ (811) [9.73x10 ⁻⁷ – 3.87x10 ⁻⁶] {HZY2698/2699}	11

* 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 using curly braces.