S5 Table. Fluctuation results of double mutants containing a null mutation of genes in the BIR pathway and *mms21-CH* or *sgs1Δ.*

Genotype	uGCR rate*	dGCR rate*	Ratio #
Wild type**	2.27x10^{-9} (1)	1.97x10^{-8} (8.7)	8.7
*mms21-CH***	2.08x10^{-8} (9.1)	4.2x10^{-6} (1850)	202
*sgs1Δ***	1.69x10^{-8} (7.4)	1.93x10^{-6} (850)	114
sgs1Δ mms21-CH	1.53x10^{-7} (67) [9.58x10^{-8} – 8.56x10^{-7}] {HZY2478/2479}	2.56x10^{-5} (11278) [1.74x10^{-5} – 3.33x10^{-5}] {HZY2474/2475/2547}	167
*sgs1Δ rad52Δ***	7.75x10^{-8} (34)	8.07x10^{-8} (36)	1.0
sgs1Δ pol32Δ	2.05x10^{-8} (9.0) [8.75x10^{-9} – 3.26x10^{-8}] {JLY1423/1425}	3.35x10^{-6} (1476) [2.16x10^{-6} – 4.11x10^{-6}] {JLY1427/1428}	163
sgs1Δ mre11-H125N	8.07x10^{-7} (355) [7.46x10^{-7} – 2.97x10^{-6}] {JLY1489/1491}	1.25x10^{-5} (5507) [7.31x10^{-6} – 2.36x10^{-5}] {JLY1490/1493}	15
sgs1-3KR	2.10x10^{-9} (0.9) [5.50x10^{-10} – 3.64x10^{-8}] {JLY1534/1535}	9.68x10^{-8} (43) [7.03x10^{-8} – 3.54x10^{-7}] {JLY1537/1538}	46
sgs1-E12G,H13C	6.51x10^{-8} (29) [4.12x10^{-8} – 1.05x10^{-7}] {JLY1569}	4.25x10^{-6} (1872) [3.29x10^{-6} – 6.89x10^{-6}] {JLY1572/1573}	65
sgs1-K706A	2.16x10^{-8} (9.5) [8.91x10^{-9} – 3.86x10^{-8}] {JLY1570/1571}	2.49x10^{-6} (1097) [2.17x10^{-6} –3.32x10^{-6}] {JLY1574/1576}	115
exo1Δ	1.01x10^{-8} (4.4) [5.13x10^{-9} – 2.00x10^{-8}] {HZY2922/3036}	8.44x10^{-8} (37)**	8.4
exo1Δ mms21-CH	1.29x10^{-7} (57) [8.21x10^{-8} – 1.67x10^{-7}] {HZY3196/3197}	4.39x10^{-6} (1934) [2.65x10^{-6} – 1.02x10^{-5}] {HZY3190}	34
*pol32Δ***	3.41x10^{-9} (1.5)	3.15x10^{-8} (14)	9.2
pol32Δ mms21-CH	3.64x10^{-8} (16) [1.24x10^{-8} – 1.52x10^{-7}] {JLY726/727}	2.75x10^{-7} (121) [1.11x10^{-7} – 6.82x10^{-7}] {JLY768/769}	7.6
srs2Δ	9.01x10^{-9} (4.0) [5.83x10^{-9} – 7.17x10^{-8}] {JLY1316}	1.28x10^{-7} (56)**	14.2
srs2Δ mms21-CH	2.03x10^{-7} (89) [1.25x10^{-7} – 2.90x10^{-7}]	3.41x10^{-6} (1502) [2.59x10^{-6} – 4.26x10^{-6}]	17

	{HZY3286/3287}	{HZY3328/3329}	
*pif1Δ***	3.73x10^{-7} (164)	3.61x10^{-7} (159)	1.0
pif1Δ mms21-CH	4.91x10^{-6} (2163) [4.04x10^{-6} – 7.68x10^{-6}] {JLY723/724}	1.21x10^{-5} (5330) [5.56x10^{-6} – 1.93x10^{-5}] {JLY667/668}	2.5
rrm3Δ	1.46x10^{-8} (6.4) [3.33x10^{-9} – 2.00x10^{-7}] {JLY737}	3.87x10^{-8} (17)**	2.7
Genotype	uGCR rate*	dGCR rate*	Ratio #
rrm3Δ mms21-CH	2.37x10^{-8} (10) [4.91x10^{-9} – 8.68x10^{-8}] {JLY773/779}	9.74x10^{-8} (43) [5.77x10^{-8} – 2.28x10^{-7}] {JLY671/672/777}	4.1
*mph1Δ***	2.00x10^{-9} (0.9)	1.05x10^{-7} (46)	53
mph1Δ mms21-CH	3.50x10^{-7} (154) [1.47x10^{-7} – 6.72x10^{-7}] {JLY1452/1453}	8.21x10^{-6} (3617) [2.52x10^{-6} – 9.99x10^{-6}] {JLY1456/1457}	23
csm2Δ	1.12x10^{-8} (4.9) [5.30x10^{-9} – 1.96x10^{-8}] {JLY469/470}	7.19x10^{-8} (32) [4.94x10^{-8} – 8.71x10^{-8}] {JLY483/484}	6.4
csm2Δ mms21-CH	2.85x10^{-7} (126) [5.36x10^{-7} – 2.08x10^{-7}] {JLY485}	2.38x10^{-6} (1048) [1.86x10^{-6} – 3.05x10^{-6}] {JLY467/468}	8.4

* 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.
[ ] 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 { }.