## Supplemental Table 6. Effect of *CDC73* truncations on dGCR rates.

| | **Wild-type *YKU80*** | | ***yku80*Δ Mutation** | |
|---|---|---|---|---|
| ***Genotype*** | ***RDKY*** | ***Can$^R$ 5FOA$^R$ Rate$^{\dagger}$*** | ***RDKY*** | ***Can$^R$ 5FOA$^R$ Rate$^{\dagger}$*** |
| Wild-type | 7635 | 8.1 [6.4-15] x $10^{-8}$ (1) | 8339 | 3.29 [1.5-10] x $10^{-7}$ (4.1) |
| *cdc73Δ2-91* | 8358 | 1.37 [0.8-3.8] x $10^{-7}$ (1.7) | 8369 | 1.51 [1.0-3.8] x $10^{-7}$ (1.9) |
| *cdc73Δ2-124* | 8362 | 1.42 [1.1-2.7] x$10^{-7}$ (1.7) | 8373 | 1.32 [0.7-4.3] x $10^{-7}$ (1.6) |
| *cdc73Δ2-229* | 8357 | 6.73 [4.0-23] x $10^{-7}$ (8.3) | 8368 | 1.32 [0.2-3.8] x $10^{-5}$ (163) |
| *cdc73Δ92-147* | 8360 | 4.51 [1.4-9.9] x $10^{-7}$ (5.6) | 8371 | 6.98 [3.2-16] x $10^{-7}$ (8.6) |
| *cdc73Δ92-229* | 8359 | 1.07 [0.4-11] x $10^{-6}$ (13.2) | 8370 | 1.09 [0.2-4.5] x$10^{-5}$ (135) |
| *cdc73Δ125-229* | 8363 | 1.40 [0.8-3.3] x $10^{-6}$ (17.3) | 8374 | 7.95 [0.3-14] x $10^{-6}$ (98.1) |
| *cdc73Δ148-229* | 8361 | 6.08 [4.3-16] x $10^{-7}$ (7.5) | 8372 | 1.21 [0.6-2.6] x $10^{-6}$ (14.9) |
| *cdc73Δ230-393* | 8356 | 1.31 [0.9-2.4] x $10^{-7}$ (1.6) | 8367 | 2.01 [1.2-6.8] x $10^{-7}$ (2.5) |
| *cdc73:125-229* | 8364 | 2.09 [1.0-3.2] x $10^{-7}$ (2.6) | 8375 | 2.26 [1.9-4.9] x $10^{-7}$ (2.8) |

[†] Rate of accumulating Can$^R$ 5FOA$^R$ progeny. The numbers in square brackets [ ] are the 95% confidence interval limits. The number in parenthesis is the fold increase relative to the wild-type dGCR assay. n.d., not determined.