

Supplementary Figure S1. Spectra of single base errors during copying of undamaged DNA by yeast pol η with and without the accessory proteins RPA, RFC and PCNA. Shown in six horizontal lines is the template sequence of the 407 nucleotide gap used in the forward mutation assay. Base substitutions are shown above the sequence as the base that was detected by sequencing of mutant plaques. Single base insertions (\uparrow) and deletions (Δ) are shown beneath the template sequence. Insertions/deletions occurring in runs are shown in the middle of the run since it is impossible to say exactly which base was affected. Insertions are of the same base the arrow points to, unless indicated with a subscript. A. Sequence changes observed in the absence of RPA, RFC, and PCNA. B. Sequence changes observed in the presence of RPA, RFC, and PCNA.

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      C
      C
    AC   T   C       C   C       C           C   G   C
CTGTTGCCCG TCTCACTGGT GAAAAGAAAA ACCACCCTGG CGCCCAATAC GCAAACCGCC TCTCCCCGCG
                ↑                ↑                    Δ

              C
              C
          C       T C       C           G
          C       T CC  CC  C   C       C   G
CGTTGGCCGA TTCATTAATG CAGCTGGCAC GACAGGTTTC CCGACTGGAA AGCGGGCAGT GAGCGCAACG
                ↑                ↑                ↑                ↑                ↑

      C
      C
      C
      C   C       C           C
      CT C C       AA  C   C   G   AC       CAT C   CC  C   C       CT
CAATTAATGT GAGTTAGCTC ACTCATTAGG CACCCCAGGC TTTACTTTT ATGCTTCCGG CTCGTATGTT
  Δ   ↑                Δ                ↑   ↑                ↑

              C
              C
          C       C C       CCAC  T   G       C   C   G       A   GCC       T
GTGTGGAATT GTGAGCGGAT AACAAATTTCA CACAGGAAAC AGCTATGACC ATGATTACGA ATTCACTGGC
                Δ   ↑A
                Δ

      C C
      CCC
      CCAAC       C   A C C       C       T   C       C       T
CGTCGTTTTTA CAACGTCGTG ACTGGGAAAA CCCTGGCGTT ACCCAACTTA ATCGCCTTGC AGCACATCCC
  Δ   ↑C Δ                ↑                Δ Δ                Δ   Δ

      C   C
CCTTTCGCCA GCTGGCGTAA TAGCGAAGAG GCCCGCACCG ATCGCCCTTC CCAACAGCTG
  Δ

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Start
←

C C C T GT A C T G C G TC T CT C
 CTGTTGCCCG TCTCACTGGT GAAAAGAAAA ACCACCCTGG CGCCCAATAC GCAAACCGCC TCTCCCCGCG
 ↑ Δ ↑ Δ ↑ Δ

C C G T
 C C G G T
 CC C C TC G C C C A G C G A
 AC CC CC C CAGCTGGCAC GACAGGTTTC CCGACTGGAA AGCGGGCAGT GAGCGCAACG
 ↑_G

C T C C C
 CC C C C C GC
 AC C C CT C CA A C ACCC T CCC CAT ATCCCC
 CAATTAATGT GAGTTAGCTC ACTCATTAGG CACCCCAGGC TTTACACTTT ATGCTTCCGG CTCGTATGTT
 Δ ↑ Δ Δ Δ Δ

C C C C T
 G C C CC G C C T
 A A CTC C C TCC GT CTC G C CCC T C
 GTGTGGAATT GTGAGCGGAT AACAAATTTCA CACAGGAAAC AGCTATGACC ATGATTACGA ATTCACTGGC
 Δ Δ Δ

CCC CG
 C C C C
 C C T C C C
 AACC C C T T AC T C CC A
 CGTCGTTTTA CAACGTCGTG ACTGGGAAAA CCCTGGCGTT ACCCAACTTA ATCGCCTTGC AGCACATCCC
 Δ Δ ↑_T Δ Δ Δ Δ ↑
 ↑

T C Start
 G CCC ←
 CCTTTCGCCA GCTGGCGTAA TAGCGAAGAG GCCCGCACCG ATCGCCCTTC CCAACAGCTG
 Δ