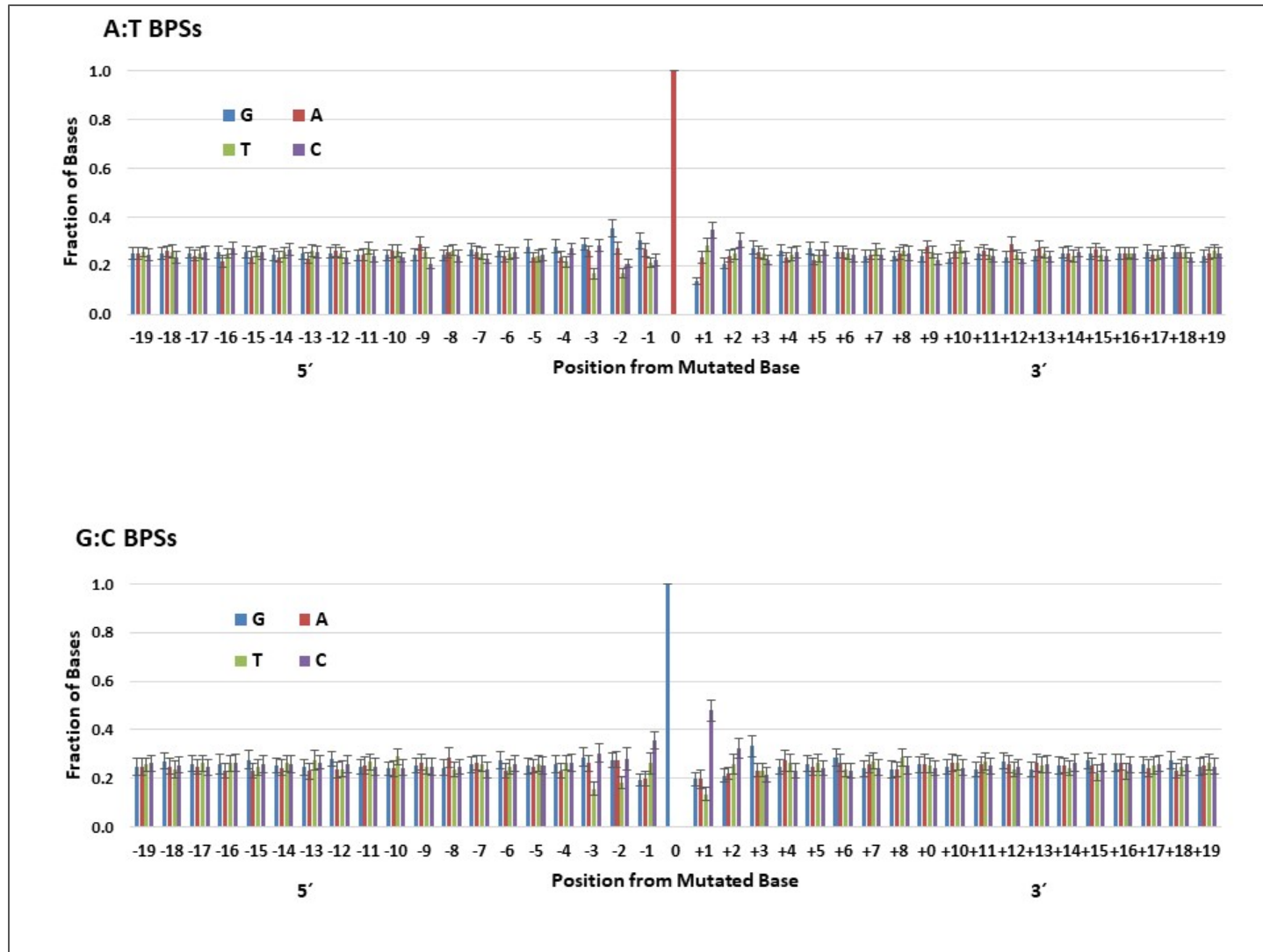
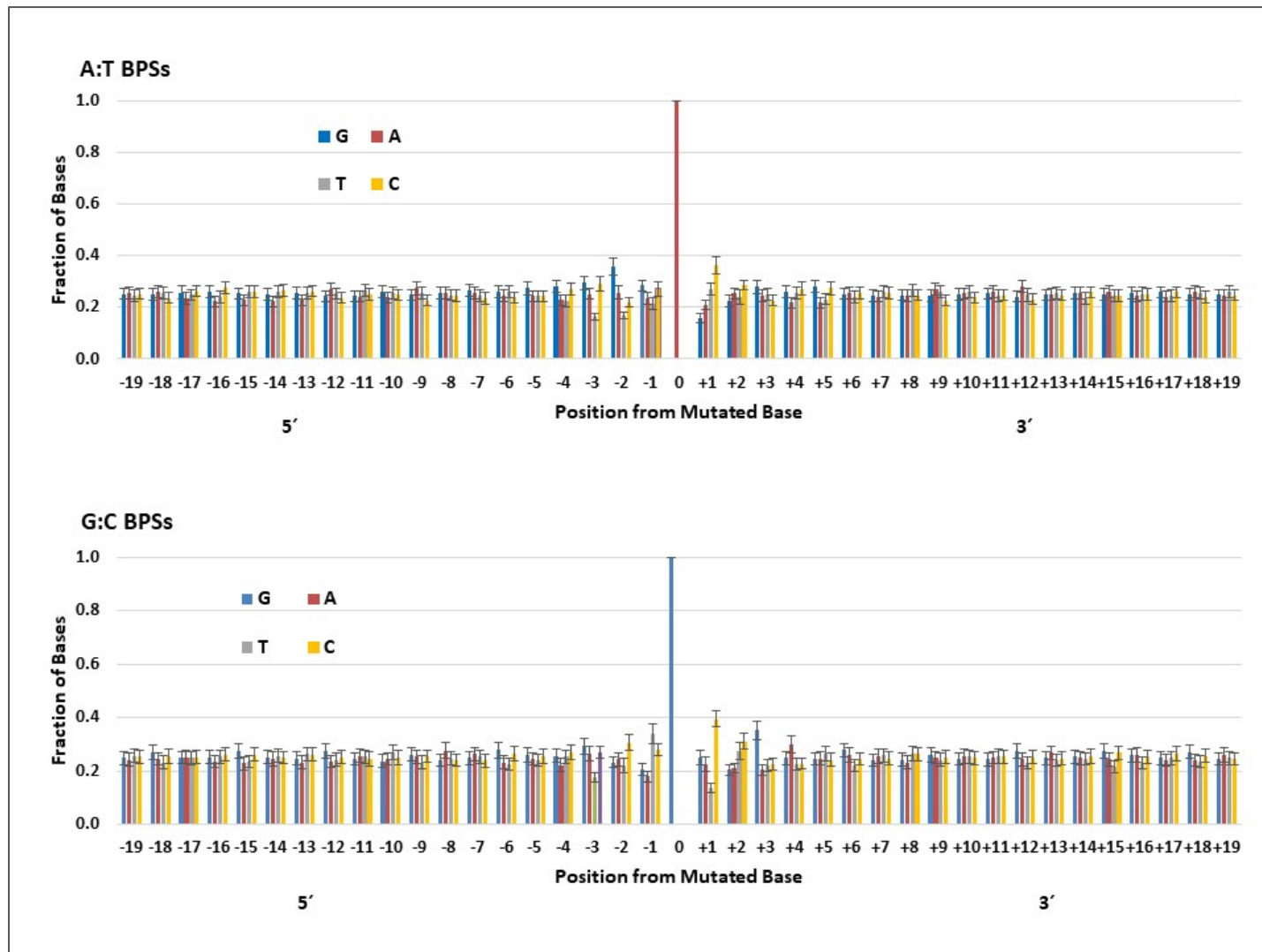


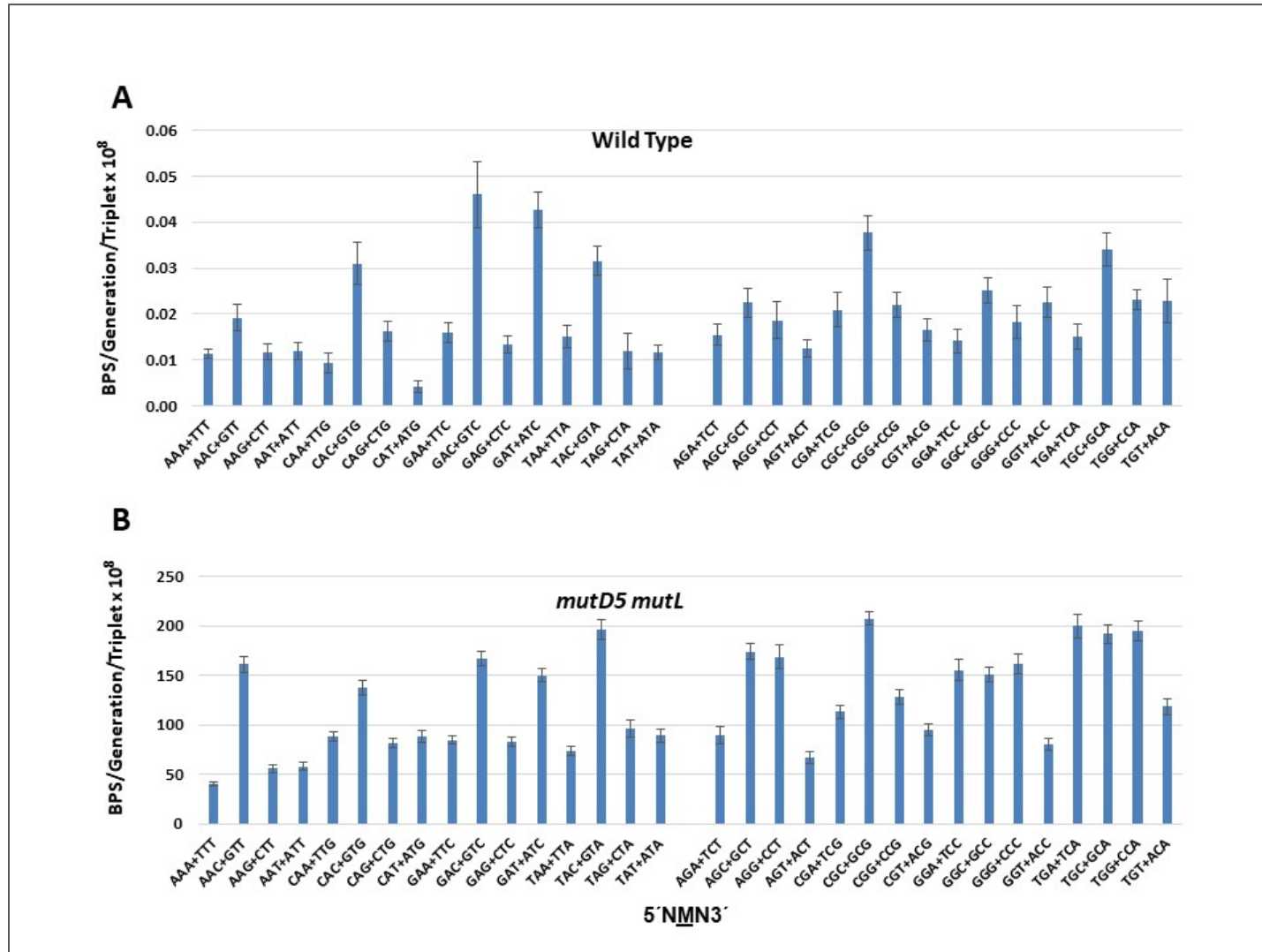
FILE S3. SUPPLEMENTAL FIGURES



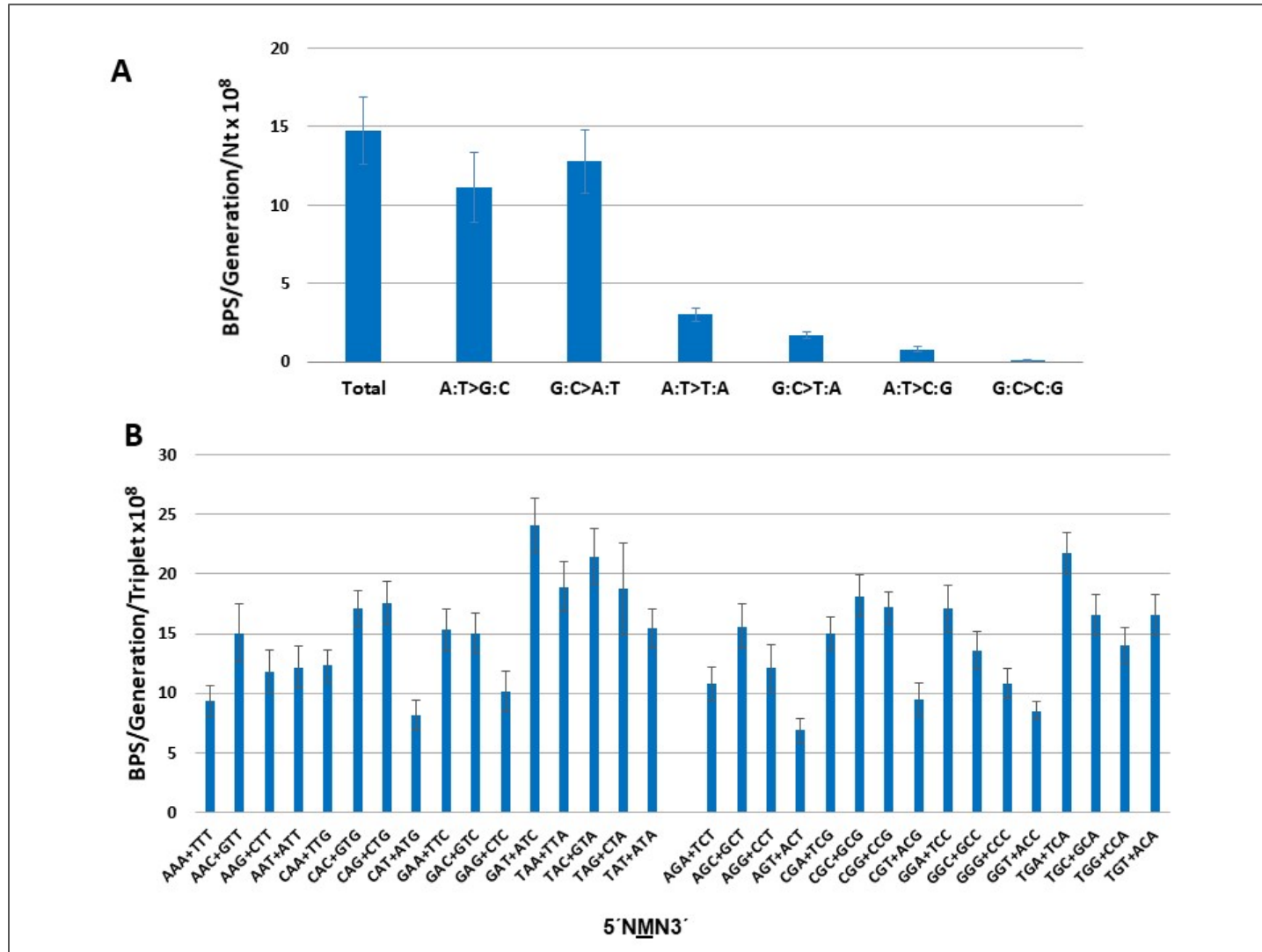
Supplemental Figure S1. The influence of the local sequence context on BPS frequencies in the mutD5 mutant strain. The sequences or the reverse complements of the 19 bases on each side of each mutated base or were oriented so to flank the purine member of the mutated base pair. The rate at which each base appeared in each of the 38 flanking positions was calculated using the same method as used to calculate the mutation rate (see Supplemental Materials and Methods). The resulting numbers were then normalized to the number of that base in the genome, and then divided by the overall sum of all 4 bases. The resulting fraction of each base in each position is shown with the 95% CL. The data are from strain PFM163.



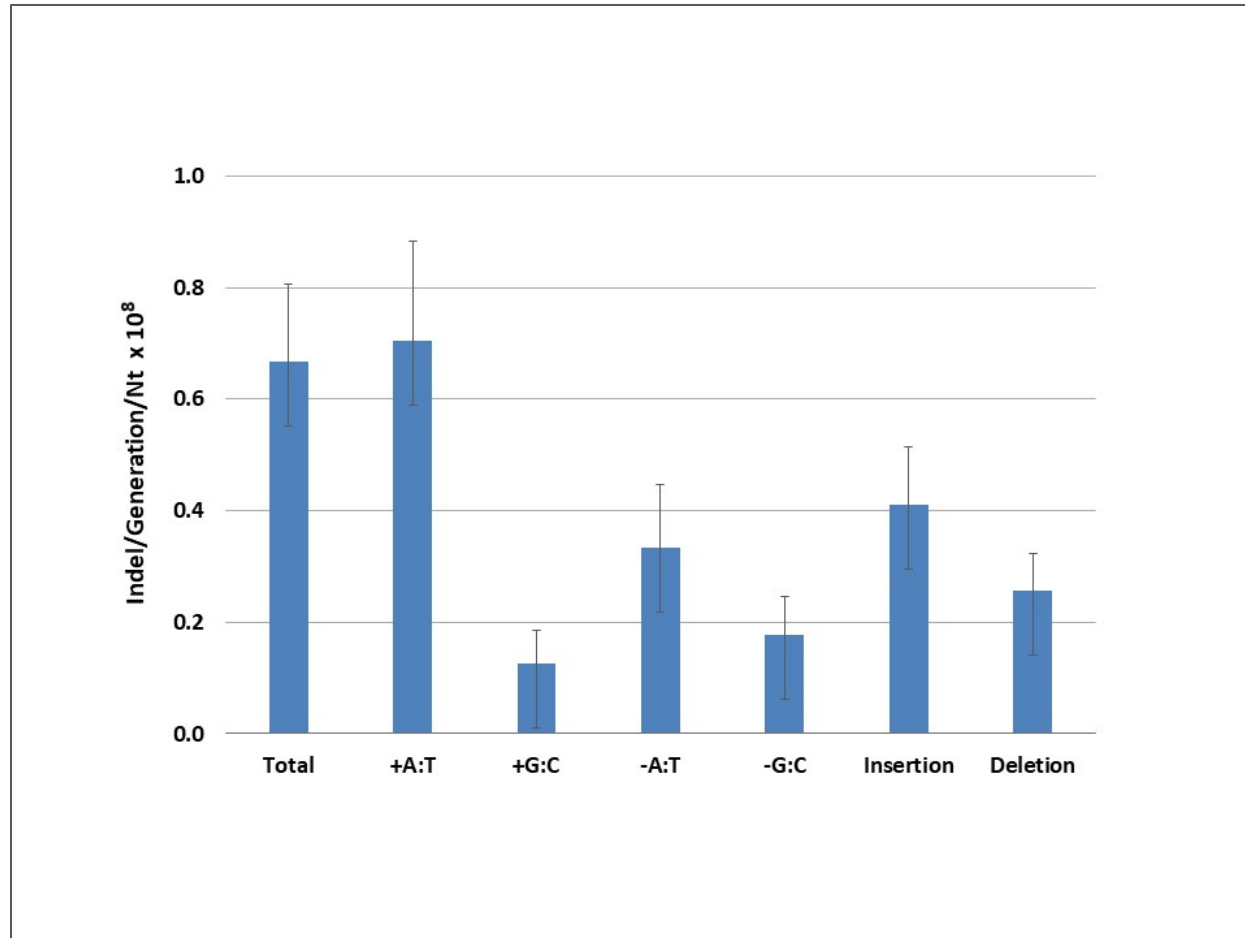
Supplemental Figure S2. The influence of the local sequence context on BPS frequencies in the *mutD5 mutL* mutant strain. The sequences or the reverse complements of the 19 bases on each side of each mutated base were oriented so to flank the purine member of the mutated base pair. The rate at which each base appeared in each of the 38 flanking positions was calculated using the same method as used to calculate the mutation rate (see Supplemental Materials and Methods). The resulting numbers were then normalized to the number of that base in the genome, and then divided by the overall sum of all 4 bases. The resulting fraction of each base in each position is shown with the 95% CL. The data are combined from strains PFM165, 397, and 399.



Supplemental Figure S3. The context bias of the base-pair substitutions accumulated by wild-type and *mutD5 mutL*⁻ mutant strains. The X-axis labels are the 32 non-redundant triplets oriented 5'NMN3' with the mutated base in the center. The bars represent the BPS per generation per triplet in the genome; the error bars are 95% CLs. A. Data for 8 wild-type experiments from Foster et al, accompanying paper. B. Data for the *mutD5 mutL*⁻ mutant strains reproduced from Figure 2A.



Supplemental Figure S4. BPS spectrum (A) and context dependent mutation rates (B) of the *mutD5* mutant strain, PFM163, grown on minimal medium. The bars represent the BPSs per generation per number of A:T or G:C base pairs in the genome; the error bars are 95% CLs. The X-axis labels in B are the 32 non-redundant triplets oriented 5'NMN3' with the mutated base in the center.



Supplemental Figure S5. The conditional rates and spectra of the indels accumulated by the *mutD5* mutant strain, PFM163, grown on minimal glucose medium. The bars represent the indels per generation per number of relevant base pairs in the genome; the error bars are 95% CLs