Abstract Submitted
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Base-by-Base Counting of Nucleotide Incorporations by DNA Polymerase MACKENZIE W. TURVEY, O. TOLGA GUL, KAITLIN M. PUGLIESE, DENYS O. MARUSHCHAK, ARITH J. RAJAPAKSE, GREGORY A. WEISS, PHILLIP G. COLLINS, University of California, Irvine — Previously, the catalytic cycle of DNA polymerase has been recorded by tethering single polymerase molecules to single-walled carbon nanotube field effect transistors (FETs) [1]. As the polymerase incorporates nucleotides into a single-stranded DNA template, it generates electrical signals in the SWCNT-FET. Here, we investigate the accuracy of this electronic method by using low concentrations (<10 nM) of DNA template, such that the signal consists of long, diffusion-limited pauses interrupted by template binding and a burst of nucleotide incorporation events. By counting the events generated by as few as 10 template molecules, template length has been correctly determined with <1 base pair resolution. Furthermore, differing template lengths can be identified and correctly enumerated in solutions containing mixtures of templates. Processivity of the Klenow Fragment of DNA polymerase currently limits read lengths to 50-100 base pairs, but the FET technique should work equally well with longer-processivity polymerases. 1. T.J. Olsen, et. al., "Electronic Measurements of Single-Molecule Processing by DNA polymerase I (Klenow fragment)," JACS 135, 7855 (2013).

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