

# Supporting Information

Sontz et al. 10.1073/pnas.1120063109

Table S1. Binding density ratios for AFM samples

Sample	BDR*, <sup>†</sup>	Long strands	Proteins	Short strands	Proteins	Error (%) <sup>‡</sup>	Prot/kbp
0.6 μM XPD	0.94	307	216	360	142	5.3	0.19
0.6 μM XPD (C:A)	1.54	354	304	323	95	5	0.20
0.3 μM XPD	1.08	304	123	502	99	6.7	0.11
0.3 μM XPD (C:A)	1.38	376	271	354	97	5.2	0.18
L325V 0.6 μM	1.05	221	149	251	85	6.5	0.18
L325V 0.6 μM (C:A)	1.14	311	236	415	145	5	0.19
XPD/EndoIII 1:1	1.02	221	127	257	76	7	0.15
XPD/EndoIII 1:1 (C:A)	1.75	253	150	370	66	7.6	0.13
XPD/Y82A 1:1	1.11	468	183	665	123	6	0.10
XPD/Y82A 1:1 (C:A)	0.98	496	258	538	150	5	0.14
EndoIII/L325V 1:1	0.94	327	263	412	186	4.7	0.22
EndoIII/L325V 1:1	1.02	361	217	553	171	5.1	0.16
XPD/L325V 1:1	0.90	309	174	408	134	5.7	0.16
XPD/L325V 1:1 (C:A)	0.88	564	329	653	227	4.2	0.16

\*Binding Density Ratio (BDR) is reported as [number of proteins bound on long strands (3.8 kbp) /number of long strands] divided by the [number of proteins on short strands (1.9 kbp)/number of short strands] normalized for length. (C:A) represents samples with long mismatched strands.

<sup>†</sup>These data represent three individual samples with 10–20 images per sample. L325V is a mutant of wild type XPD, and Y82A is a mutant of wild type EndoIII.

<sup>‡</sup>Error is reported as the (total number of proteins divided by the square root of the total number of proteins counted) times 100 for each type of sample.