



Supplementary Figure S1. Model for repair of AP sites arising from C:G pairs in plants. ARP preferentially repaired AP sites arising from cytosine deamination, whereas FPG favoured those derived from guanine oxidation or alkylation. See text for details.

Supplementary Table S1. Probability of methylation of DNA substrates used depending on the orphan base opposite the AP site.

Sequence Context	Orphan Base	Sequence	Probability of Methylation ^a	
			Plants	Humans
A	G	TCG <u>A</u> PCCG AGC G GGC	Low	Low
B	G	CGC <u>A</u> PCGT GCG G GCA	Medium	Low
C	G	TCG <u>A</u> PGCG AGC G CGC	High	High
A	C	TCG <u>A</u> PCCG AGC <u>C</u> GGC	Medium	Low
B	C	CGC <u>A</u> PCGT GCG <u>C</u> GCA	High	High
C	C	TCG <u>A</u> PGCG AGC <u>C</u> CGC	Medium	Low

^a Probability of cytosine methylation at the underlined position.

Supplementary Table S2. Relative efficiency of native enzymes from *Arabidopsis* on DNA substrates with an AP site in three different sequence contexts and opposite G or C as the orphan base.

Enzyme	Sequence Context	Orphan Base	P _{max} (nM)	T ₅₀ (min)	E _{rel}
ARP	A	G	19.40 ± 0.11	6.27	3.10 ± 0.02
ARP	A	C	19.01 ± 1.84	97.63	0.19 ± 0.02
ARP	B	G	19.17 ± 0.28	13.92	1.38 ± 0.02
ARP	B	C	19.21 ± 0.24	25.48	0.75 ± 0.01
ARP	C	G	19.43 ± 0.12	6.66	2.91 ± 0.02
ARP	C	C	18.55 ± 0.76	49.16	0.38 ± 0.02
FPG	A	G	12.37 ± 0.97	88.87	0.14 ± 0.01
FPG	A	C	15.88 ± 0.93	68.63	0.23 ± 0.01
FPG	B	G	n.d. ^a	n.a. ^b	n.a. ^b
FPG	B	C	16.10 ± 0.39	50.23	0.32 ± 0.01
FPG	C	G	7.82 ± 0.33	74.53	0.10 ± 0.00
FPG	C	C	6.65 ± 0.17	94.95	0.07 ± 0.00

^a n.d.–not determined. ^b n.a.–not applicable.

Supplementary Table S3. Relative efficiency of recombinant or native human APE1 on DNA substrates with an AP site in three different sequence contexts and opposite G or C as the orphan base.

APE1	Sequence Context	Orphan Base	P _{max} (nM)	T ₅₀ (min)	E _{rel}
Recombinant	A	G	78.11 ± 0.93	8.55	9.14 ± 0.11
Recombinant	A	C	78.70 ± 0.53	8.55	9.21 ± 0.06
Recombinant	B	G	77.95 ± 0.60	9.71	8.03 ± 0.06
Recombinant	B	C	81.16 ± 0.85	17.37	4.67 ± 0.05
Recombinant	C	G	76.84 ± 1.63	15.40	4.99 ± 0.11
Recombinant	C	C	77.49 ± 1.69	15.86	4.89 ± 0.11
Native	A	G	19.32 ± 0.03	3.41	5.67 ± 0.01
Native	A	C	19.54 ± 0.17	5.48	3.56 ± 0.03
Native	B	G	18.98 ± 0.31	8.15	2.33 ± 0.04
Native	B	C	19.18 ± 0.64	21.94	0.87 ± 0.03
Native	C	G	19.20 ± 0.44	14.75	1.30 ± 0.03
Native	C	C	19.38 ± 0.47	19.25	1.01 ± 0.02