

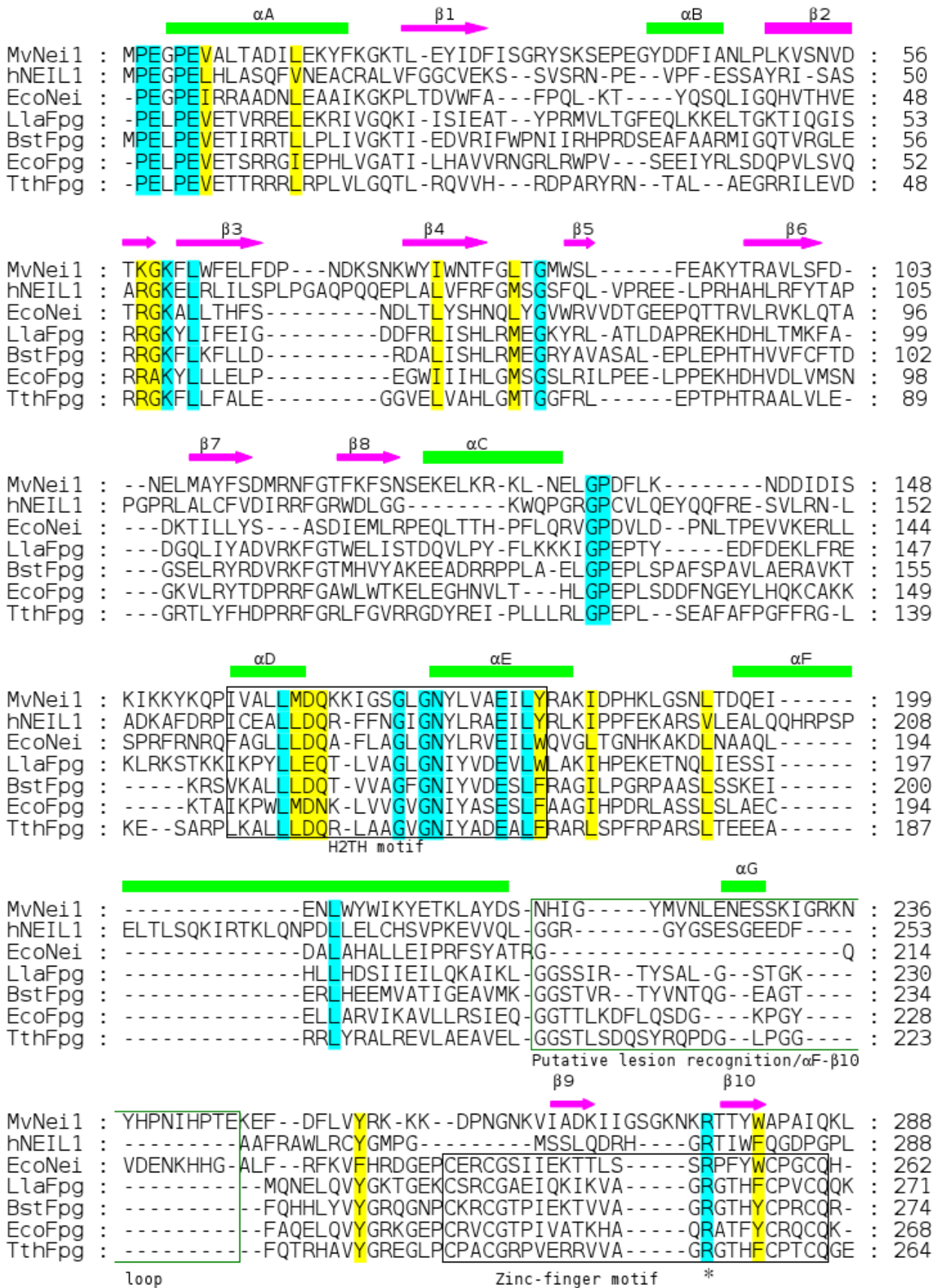
## Supplemental information

**Suppl. Fig. 1** Structure-based sequence alignment of MvNei1 with human endonuclease VIII (Nei)-like 1 (hNEIL1; PDB code 1TDH (29)), *Escherichia coli* Nei (EcoNei; PDB code 1K3W (23)), *Lactococcus lactis* Fpg (LlaFpg; PDB code 1XC8 (50)), *Bacillus stearothermophilus* Fpg (BstFpg; PDB code 1R2Y (48)), *Escherichia coli* Fpg (EcoFpg; PDB code 1K82 (22)) and *Thermus thermophilus* Fpg (TthFpg; PDB code 1EE8 (24)). Secondary structure elements are shown above the aligned sequences ( $\beta$ -strands as red arrows and  $\alpha$ -helices as green tubes). Conserved residues are highlighted in blue, and the two DNA-binding motifs (helix-two-turns-helix and zinc finger) are boxed. The location of the  $\alpha$ F- $\beta$ 9/10 loop of Fpg and putative lesion recognition of MvNei1 is indicated by a dark green box. The conserved arginine residue at the tip of the zinc(less) finger (277 in MvNei1 and hNEIL1, and 252 in EcoNei) is indicated with an asterisk.

**Suppl. Fig. 2** Void filling residues in Fpg/Nei enzymes

(A) EcoNei-DNA (PDB code 1K3W; (23)). (B) MvNei1-DNA (PDB code 3A46). (C) LlaFpg-DNA (PDB code 1KFV; (53)). Void filling amino acid residues are shown in gray for EcoNei, in green for MvNei1 and in beige for LlaFpg. The deoxyribose moiety (dRbl or PED: pentane-3,4-diol-5-phosphate), THF and Pr (1,3-propanediol) are shown in pink.

# Supplemental Fig. 1



# Supplemental Fig. 2

