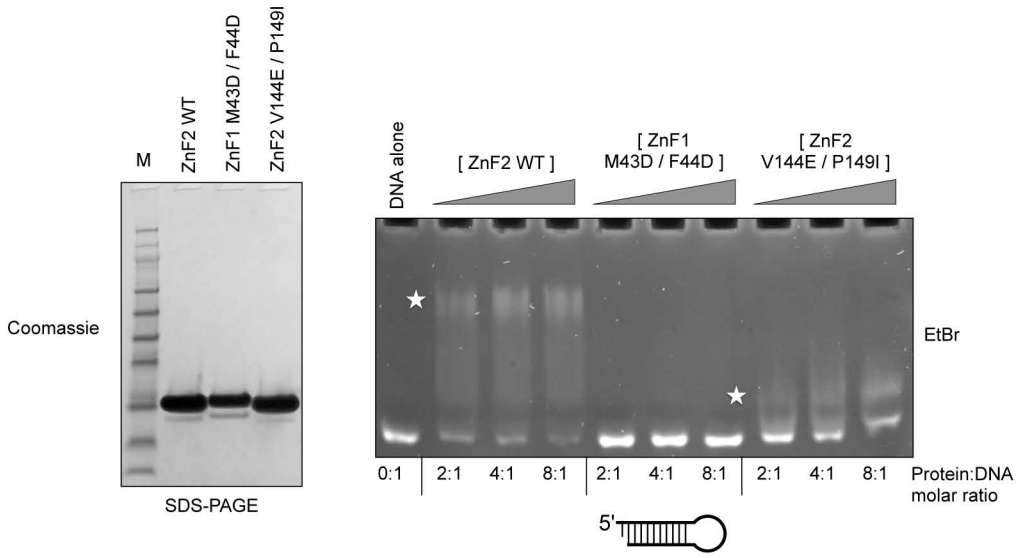
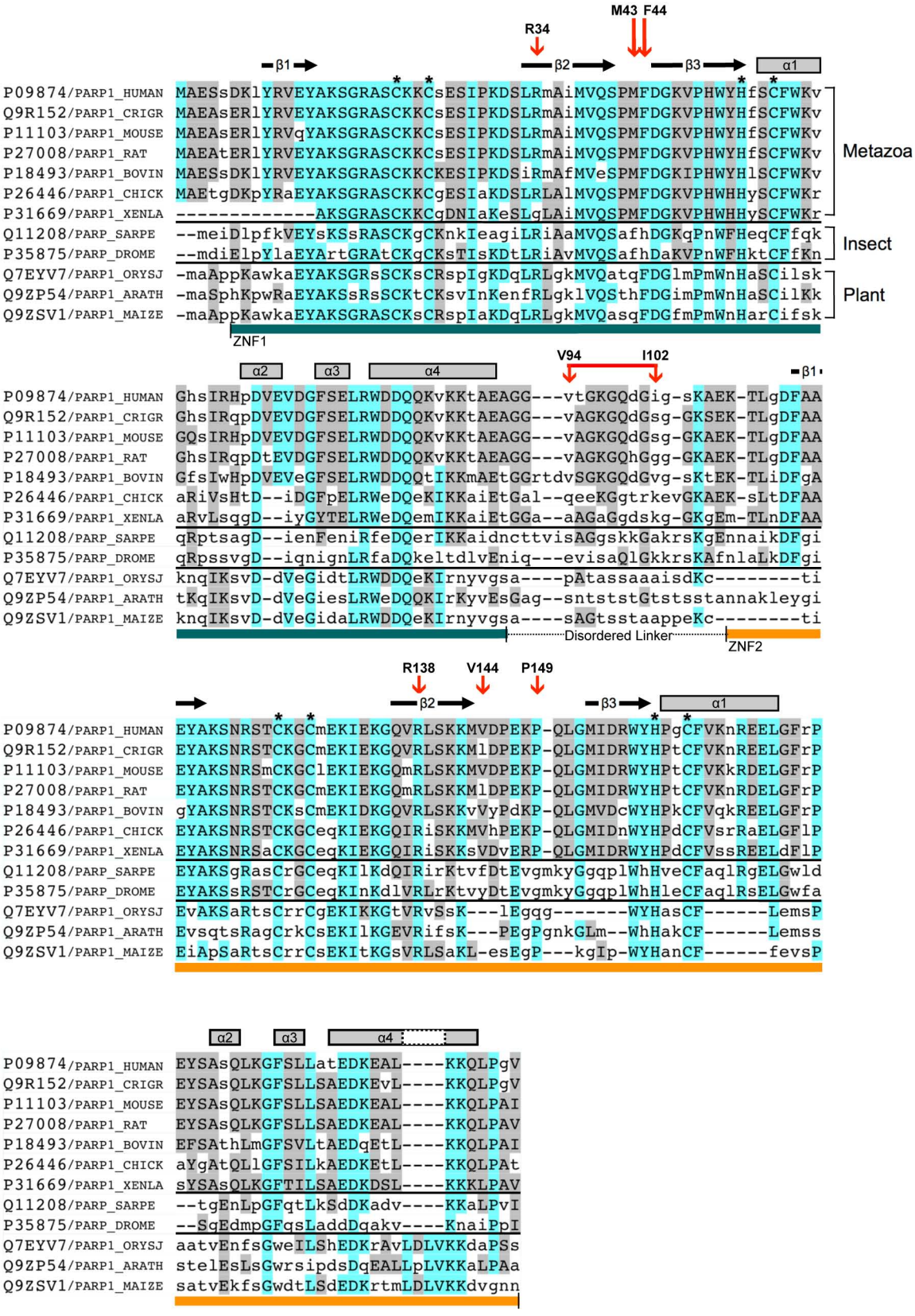


Supplementary Figure 1. Electrophoretic mobility shift assay of isolated zinc-finger constructs

(left) Coomassie stained SDS-PAGE of purified protein for wild-type ZnF2, ZnF1-M43D F44D, and ZnF2 V144E P149I.
(right) Electrophoretic mobility shift assay, showing weak DNA binding by the isolated wild-type ZnF2 and the isolated ZnF2 V144E P149I mutant intended to disrupt protein-protein interactions with ZnF1. The DNA complex with the ZnF2 V144E P149I mutant (★) runs faster in the gel due to the increased negative charge of the mutant protein. The isolated ZnF1-M43D F44D mutant show no DNA binding, reflecting the involvement of the mutated residues, which form part of the protein-protein interface in the intact PARP1-DBD, to mediate DNA interaction independently of ZnF2, in isolation.



Supplementary Figure 2. Multiple sequence alignment of human PARP-1 homologues.

Amino acid sequences for human PARP-1 orthologues were obtained from the Swissprot / Uniprot database, using the indicated accession codes. The program MUSCLE[1] was then used to generate a multiple sequence alignment over the region spanning the PARP1-DBD construct (aa 5-202) used in this study. Conserved amino acids are indicated in upper case, with either a cyan (strongly-conserved with human PARP-1) or grey (partially-conserved) background. Secondary structure elements are also shown, along with the position of the point mutants (red arrows) and linker deletion generated for the laser-damage microscopy assay. Amino acids highlighed with an asterisk are involved in Zinc coordination.

1. Edgar, R.C. MUSCLE: multiple sequence alignment with high accuracy and high throughput. *Nucleic Acids Res.* **32**,1792-1797 (2004).