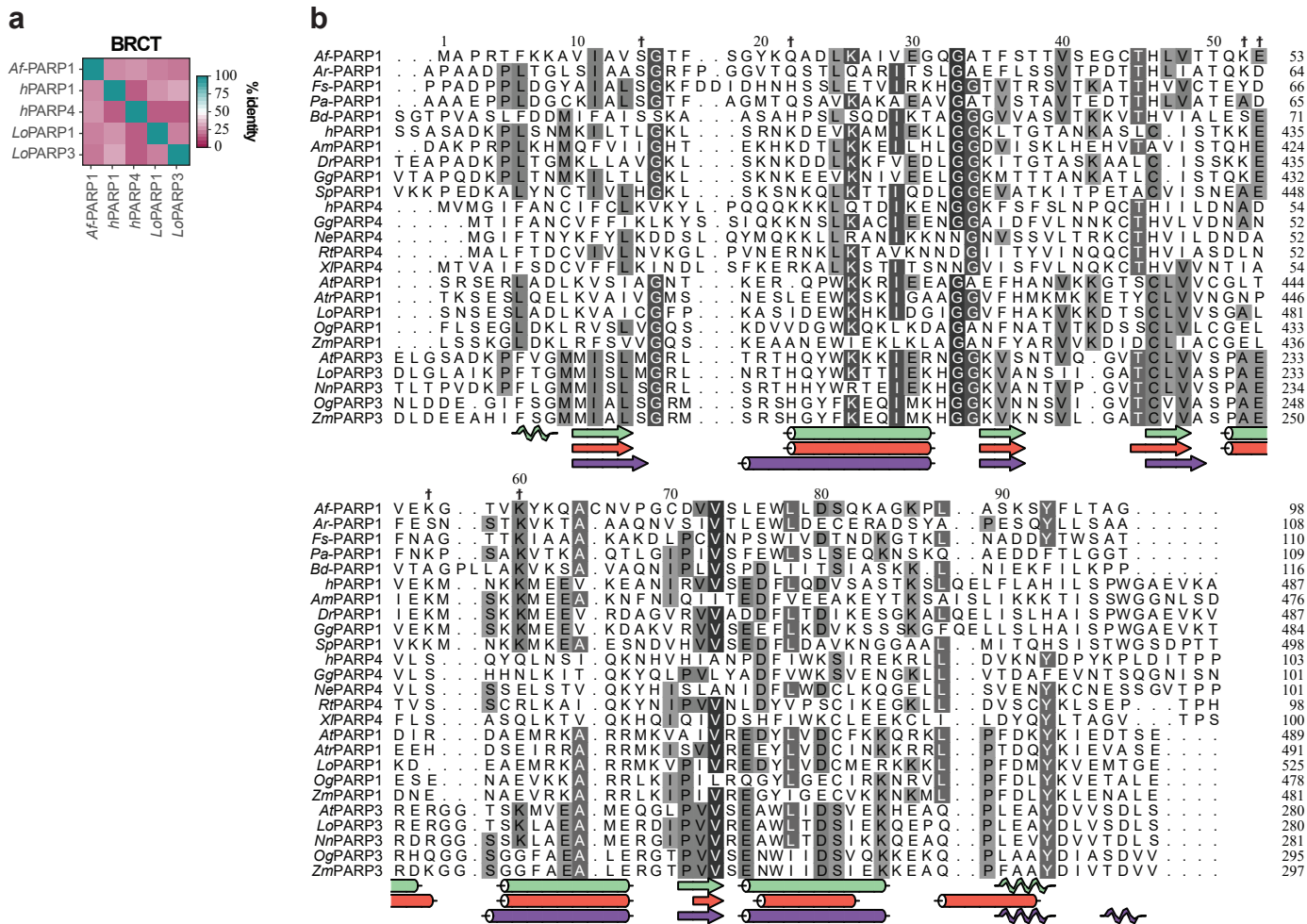




Extended Data Figure 6. PARP-derived BRCT domain show little conservation between homologues.

(a) Pairwise identity matrix of isolated BRCT domains was calculated from multiple sequence alignments using Biostrings⁷⁹ and visualised using heatmapper⁸⁰.

(b) Multiple sequence alignment of PARP-derived BRCT domains from *Fungi*, *Animalia*, and *Plantae*. Residues contributing to the predicted DNA interaction surface are indicated above the alignment by dei (†). Secondary structures of *Af*-PARP (green; AlphaFold 3-derived), *h*PARP1 (red; PDB 2COK), and *h*PARP4 (purple; PDB 9DEV) are given below the alignment. Indexing indicates *Af*-PARP1 residue position.