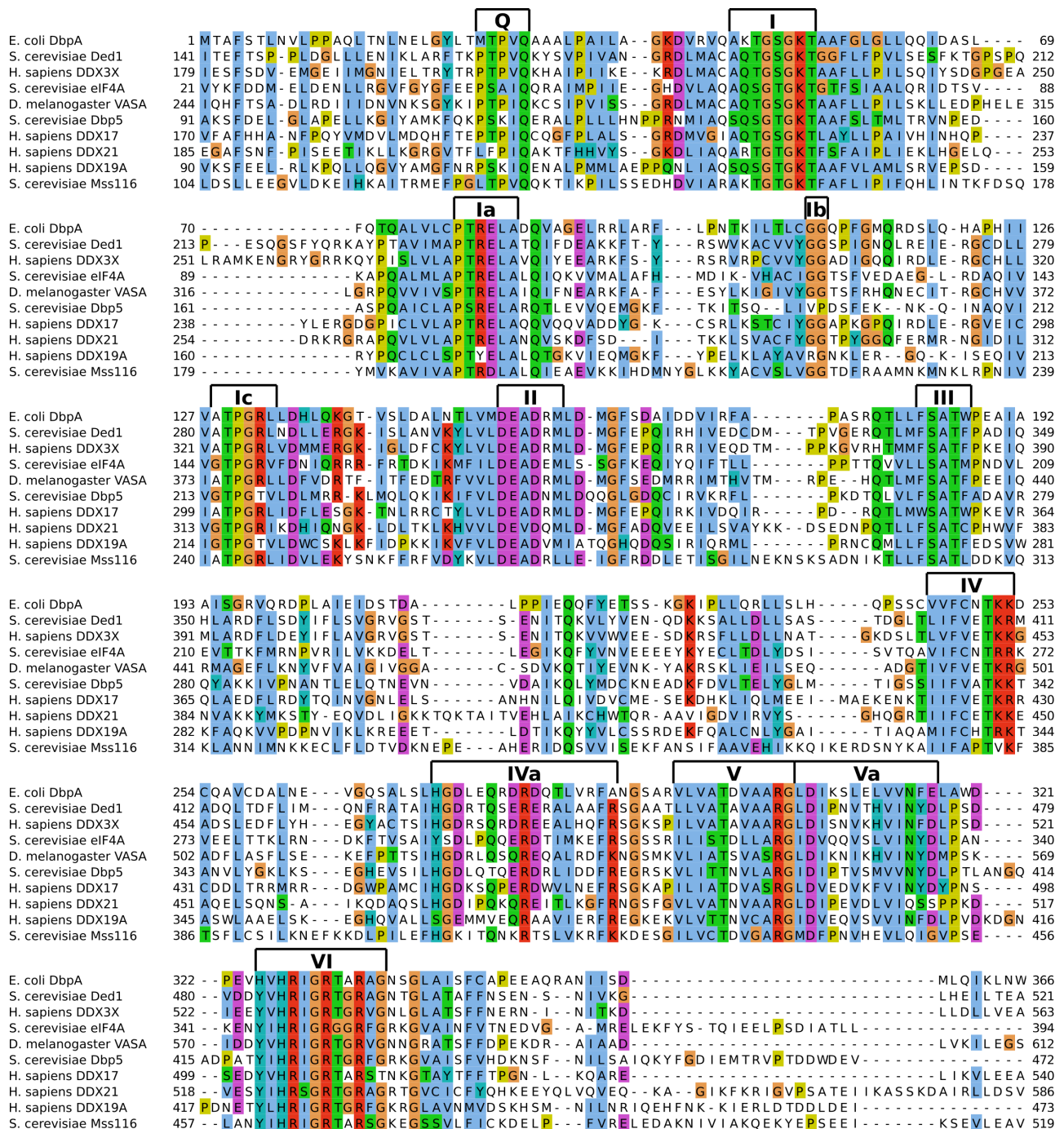




Supplementary Fig. 13: Sequence comparison for DbpA and unrelated DEAD-box helicases

Sequence alignments of the RecA core domains of DbpA (residues 1-366) (top) and nine unrelated DEAD-box helicases. The highly conserved sequence motifs (Q, I-VI (Putnam and Jankowsky, 2013)) of DEAD-box helicases are indicated on top. The sequence alignment was generated using Jalview (Waterhouse et al., 2009) in combination with Clustal Omega (McWilliam et al., 2013).