Supplementary Note 1

Structure based sequence alignment of zebrafish, human and mouse RAG1 and RAG2 core region

Sequence alignment in the core regions of zebrafish, human and mouse RAG1 (**a**) and RAG2 (**b**). Secondary structures of zRAG1 and zRAG2 were assigned based on the 3.4 Å model of the nicked DNA complex. The secondary structures are colored as in Fig. 1a based on the domain organization. Four catalytic residues are

indicated by black arrows. β4-β5 and α15-α16 loop regions are indicated by lines. The sequence alignment was generated in Espript[1].

1.   Robert, X. & Gouet, P. Deciphering key features in protein structures with the new ENDscript server. *Nucleic Acids Res* **42**, W320-4 (2014).