

## Supplementary Data

### Supplementary Figure Legends

**Figure S1.** tAI means of all-IDR proteins compared with SDs of all proteins using DICHOT results. Proteins that consist entirely of IDRs were divided into the first half (DN) and the latter half (DC). They were regarded as middle IDR sections and were analyzed in comparison to SD regions of all proteins. The expected-to-observed ratios are presented as in Figure 2 except for *S. pombe*, in which less than 100 residues in each IDR region were available.

**Figure S2.** tAI means of all-IDR proteins compared with SDs of all proteins using POODLE-L results. tAI means were calculated using POODL-L instead of DICHOT results and presented as in Figure 2.

**Figure S3.** tAI means of IDRs and SDs using DICHOT results with a 36-residue offset. The geometric means of tAI in each species and the overall means of the seven eukaryotes were calculated using DICHOT results with an offset of 36 residues and plotted as in Figure 2.

**Figure S4.** tAI means of IDRs and SDs using POODLE-L results with a 36-residue offset. The geometric means of tAI in each species and the overall means of the seven eukaryotes were calculated using POODLE-L results with a 36-residue offset and plotted as in Figure 2

Figure S1

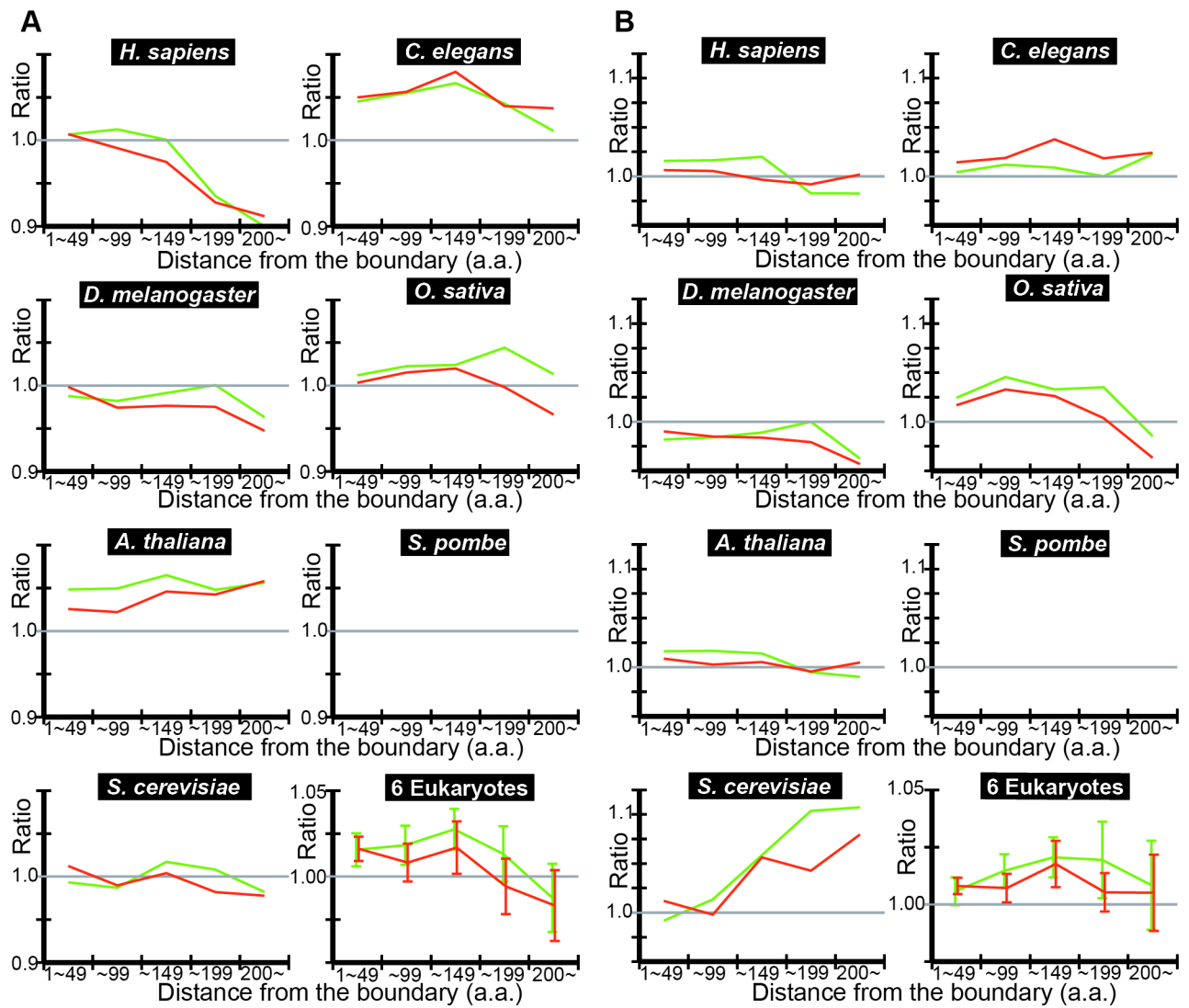


Figure S2

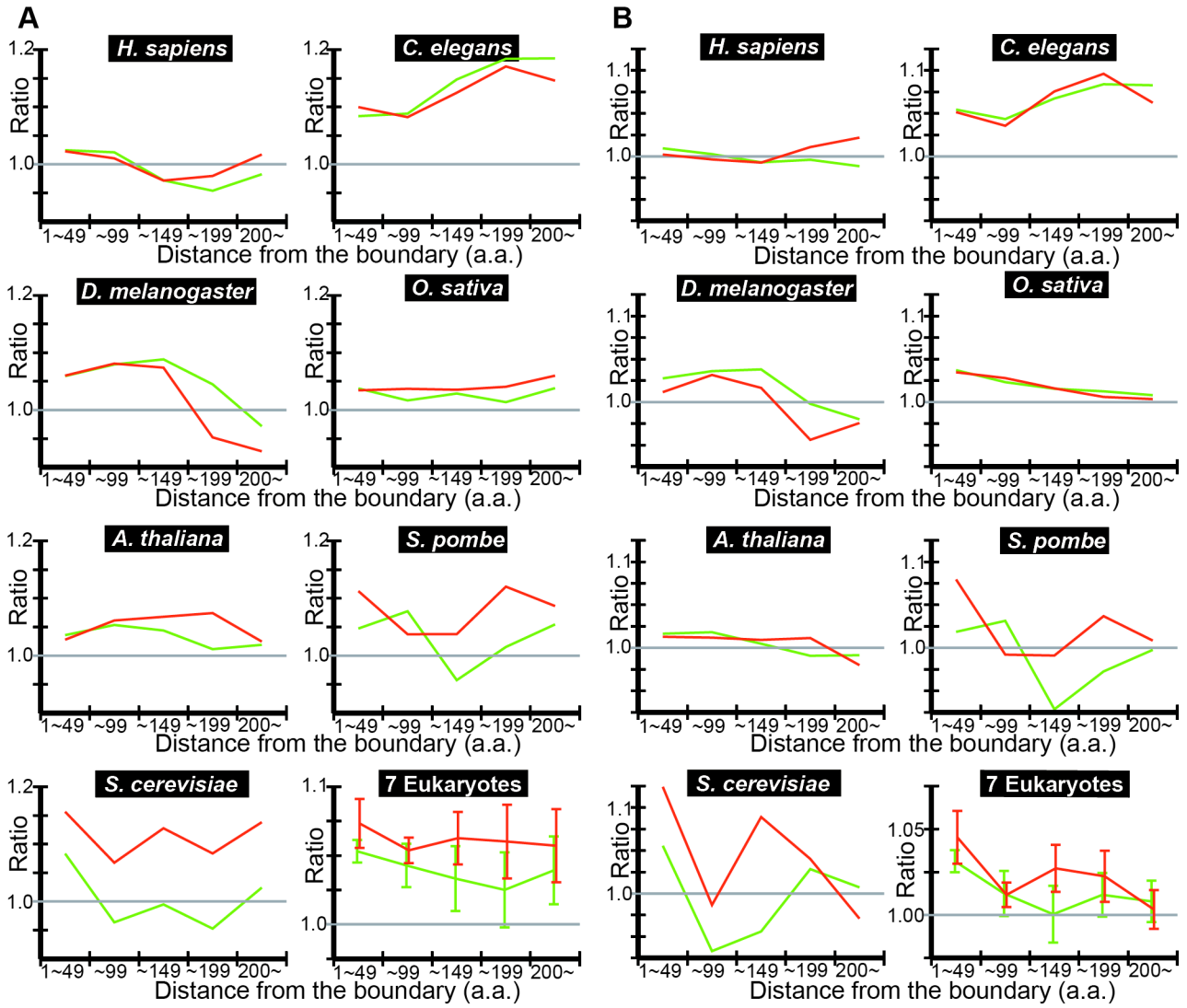


Figure S3

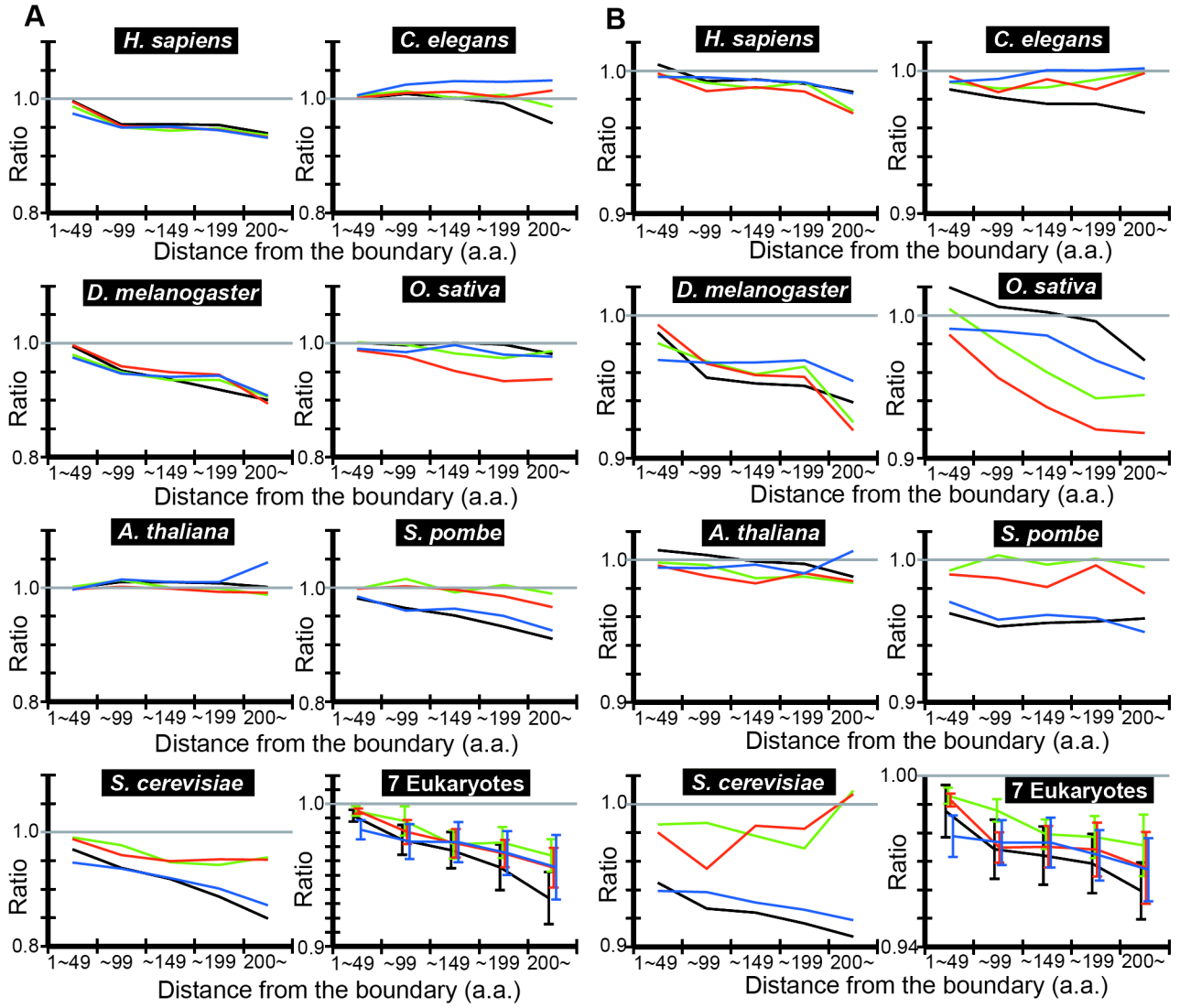


Figure S4

