

Suppl. Fig. S1: Alignment of Kaiso proteins of various species reveals two conserved domains, CD1 and CD2, in addition to the BTB/POZ and zinc finger domains. Multiple sequence alignment of Kaiso protein sequences from mammals (human, chimpanzee, rhesus monkey, horse, mouse, rat) and other vertebrates (chicken, the frog *Xenopus laevis*, zebrafish). RefSeq sequences were obtained from the Entrez Gene database [1] by searching for “Kaiso OR Zbtb33” and aligned with ClustalX2 using default parameters [2]. The shaded background was created with the BoxShade server. The line below every alignment block denotes the type of conservation: “*” for identical residues, “:” for high similarity and “.” for weak similarity. Annotation of the BTB/POZ domain (cyan background) and zinc fingers (green background; red: C and H residues) was based on, respectively, CD-Search [3] and InterPro [4] analyses. Other conserved regions, CD1, CD2 and NLS, are indicated by yellow background. The novel Spindle-Associated domains 1 and 2 (SA1 and SA2) are highlighted in pink. See also Fig. 1 for domain organization.

References

1. Maglott D, Ostell J, Pruitt KD, Tatusova T (2007) Entrez Gene: gene-centered information at NCBI. *Nucleic Acids Res* 35: D26-31.
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4. Hunter S, Apweiler R, Attwood TK, Bairoch A, Bateman A, et al. (2009) InterPro: the integrative protein signature database. *Nucleic Acids Res* 37: D211-215.