Figure S4. CSN6 sequences and MPN domain structure. (A) Sequence alignment of human CSN6 and CSN6 sequences from 10 diverse representative organisms. To obtain this sequence alignment, CSN6 sequences were retrieved with a Blastp step using human CSN6 as the search and 10 diverse sequences from representative organisms were selected in addition to the human one. A multiple sequence alignment using these eleven sequences was done with the Clustal Omega server (default parameters). This procedure was entirely carried out on the Uniprot website (www.uniprot.org). Dm: Drosophila
*melanogaster* (Uniprot entry: Q9VCY3); *Bm: Bombyx mori* (Uniprot entry: Q2F614); *Ag: Anopheles gambiae* (Uniprot entry: Q7Q421); *Bt: Bos taurus* (Uniprot entry: A6QQ21); *Mm: Mus musculus* (Uniprot entry: Q3UIT2); *Hs: Homo sapiens* (Uniprot entry: Q7L5N1); *Xi: Xenopus laevis* (Uniprot entry: Q6NUC2); *Dr: Danio rerio* (Uniprot entry: Q567F8); *Sm: Schistosoma mansoni* (Uniprot entry: G4V7G0); *Os: Oryza sativa* (Uniprot entry: Q6ZKM2); *At: Arabidopsis thaliana* (Uniprot entry: Q8W1P0). A ‘*’ sign indicates a residue strictly conserved among the eleven selected sequences. The residues H44 and V115 discussed in the text are highlighted with an orange box and CSN6 residues involved in the CSN5ΔC/CSN6ΔC complex that we propose in this study are boxed in blue. (B-G) Illustration of (B,C) human CSN6ΔC, (D,E) DmCSN6 fragment (residues 51-187) and (F,G) human Rpn8ΔC (residues 1-186) homodimers. Two orientations (0; 180°) are displayed for each protein. The protomers in dimer are represented in brown ribbons. In human CSN6ΔC and in Rpn8ΔC, the C-terminal helical portion (green) of molecule A is engaged in a helix swap with the molecule A’.

Defined secondary structure elements are labelled. Human CSN6ΔC and Rpn8ΔC contain seven β-strands and four α-helices. DmCSN6ΔC structure contains five β-strands and two to three α-helices, depending on the considered monomer. Structural comparison of the monomeric form of HsCSN6ΔC with HsRpn8ΔC and DmCSN6ΔC using LSQMAN program (2) gave rmsd values of 1.64 Å for 153 Ca pairs and 1.35 Å for 84 Ca pairs, respectively.

Reference.