Supplementary material
A COP9 signalosome-like complex is a regulator of mating pheromone response in *S. cerevisiae*.

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Supplementary Tables and Figures

Supplementary Table 1.

A

	yCsn9	yCsn10	yCsn12	yPci8/Csn11
hCsn1	17.0	11.8	14.6	10.8
hCsn2	16.0	11.8	10.7	**16.2**
hCsn3	11.9	11.7	**14.4**	6.7
hCsn4	12.2	**16.0**	14.0	11.0
hCsn7a	**16.9**	10.6	12.5	8.5
hCsn7b	**17.8**	13.5	10.6	8.5
hCsn8	8.0	10.6	7.8	6.9

B

	yCsn5
hCsn5	**52.2**
hCsn6	18.9

Table 1.
Pairwise identity values of CSN subunits from human and the newly identified complex in budding yeast.
A. The CSN-like complex identified in S. cerevisiae contains four PCI subunits that co-interact while the CSN from other eukaryotes contains 6 PCI proteins. The % identities between all PCI components are shown. The best match is shown in bold, however, the extremely low levels of % identities obstruct assignment of direct orthologs between the PCI subunits from budding yeast and those from other organisms (human in this case).
B. ydl216c encodes for a homologous subunit of Csn5 from other eukaryotes and is referred to as Csn5. The % homology of this MPN subunit with its presumed ortholog, Csn5 is shown as well as with Csn6, an additional MPN protein that is found in the CSN from other eukaryotes but not present in budding yeast.

Supplementary Figure 1

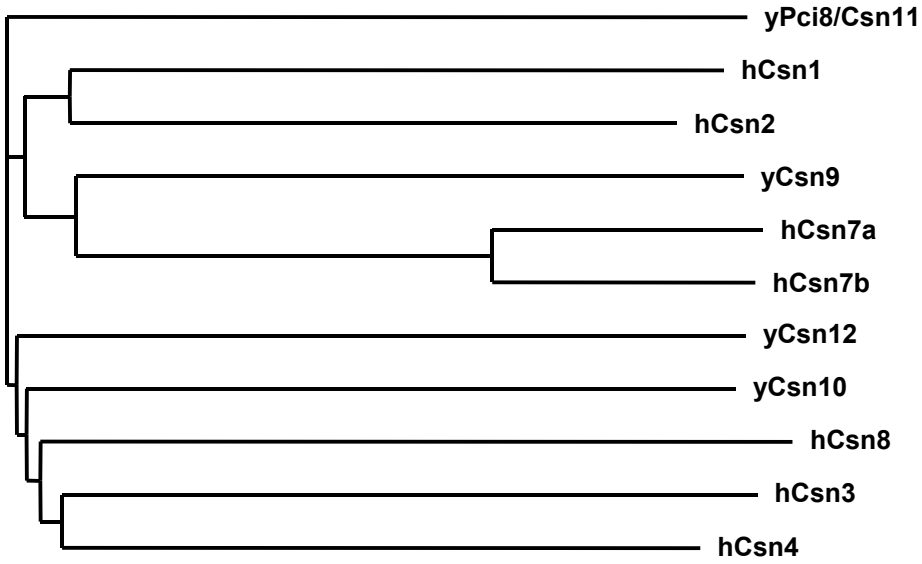
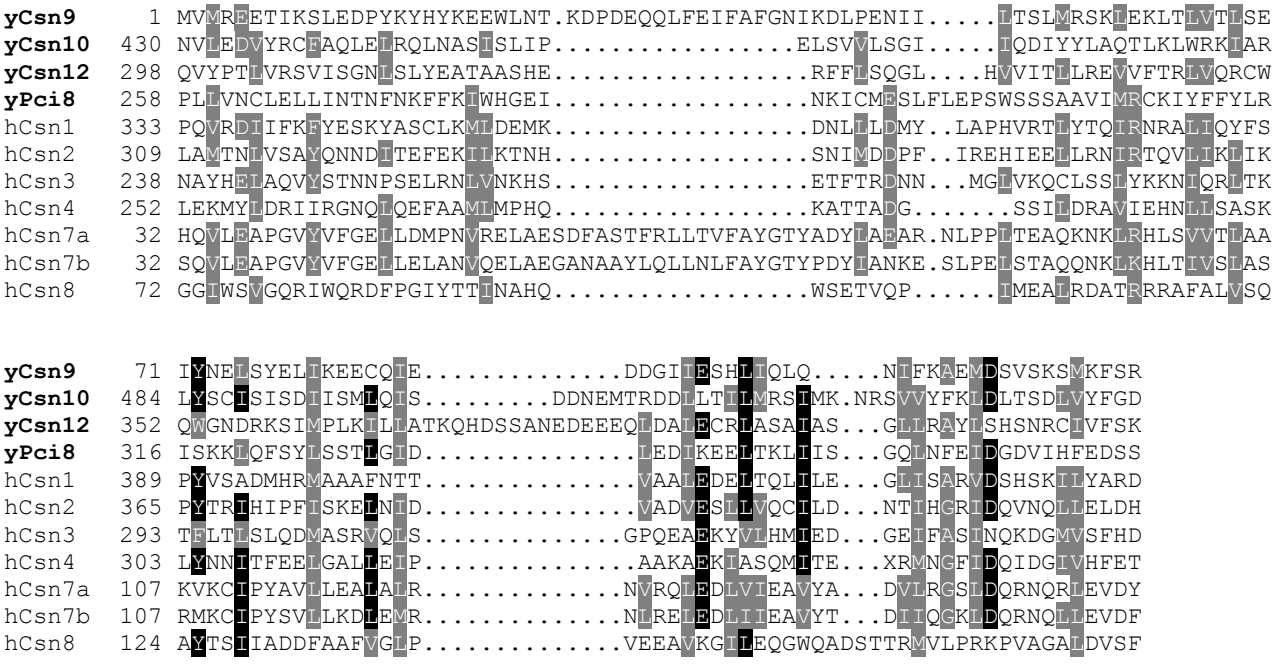


Figure 1. Dendrogram analysis of PCI subunits from yeast and human. All subunits have a common evolutionary precursor. Notice that evolutionary distance is not always correlated with the % identity of each possible pair (shown in Table 1). For this reason, a direct ortholog relationship is not claimed for newly identified CSN and they are given numerical suffixes that do not correspond to previously identified CSN subunits.

Supplementary Figure 2

A



B

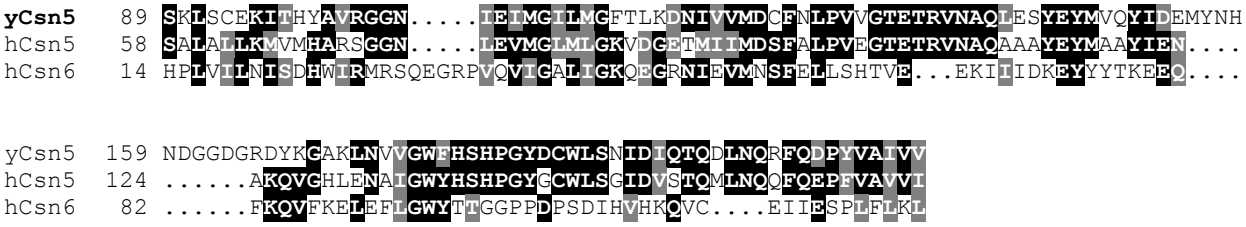


Figure 2. Definition of PCI and MPN motifs. Sequence alignment of PCI domain (A) or MPN domain (B) is shown for all CSN subunits from yeast and human.