



FIGURE S1. Sequence alignment of SUN domains. The indicated SUN domain sequences were aligned using ClustalW2. Conserved residues are shown in red and similar residues in green. Cysteine residues thought to participate in intramolecular disulfide bond and in formation of a disulfide bond with the KASH domain are highlighted in yellow (SOSA et al. 2012; ZHOU et al. 2012). These residues do not appear to be conserved in the plant or fungal SUN domains. Secondary structure elements are shown above the aligned sequences and are based on crystallographic data from human Sun2, which was also used to predict residues involved in association with the KASH domain or in formation of the SUN domain pocket (SOSA et al. 2012; ZHOU et al. 2012). Boxed residues indicate key residues that have been shown by mutagenesis to affect SUN-KASH binding or SUN protein function in vivo, including the three *mps3* alleles described (JASPERSEN et al. 2002; JASPERSEN et al. 2006; MALONE et al. 1999; NISHIKAWA et al. 2003; SOSA et al. 2012; ZHOU et al. 2012). The black and magenta dashed lines indicate the regions deleted in *mps3ΔSUN1* (415-480) and *mps3ΔSUN2* (524-645), respectively.