



Figure S1 Multiple sequence alignment of human, *Arabidopsis thaliana*, *Tetrahymena thermophila* and *Tetrahymena borealis* Msh4 and Msh5 sequences spanning their MutS_II, MutS_III, MutS_IV and most of MutS_V domain regions. Colored bars below the alignment indicate the position of these domains according to PFAM domain analysis and are color-coded as explained in Figure S2. The alignment was generated using MAFFT (KATO, K., and D. M. STANDLEY, 2013 MAFFT multiple sequence alignment software version 7: improvements in performance and usability. *Mol. Biol. Evol.* 30: 772-780) and visualized with the default Clustal color scheme. Sequences extracted from the NCBI protein database can be found under the accessions NP_002431, NP_193469, NP_002432, NP_188683.