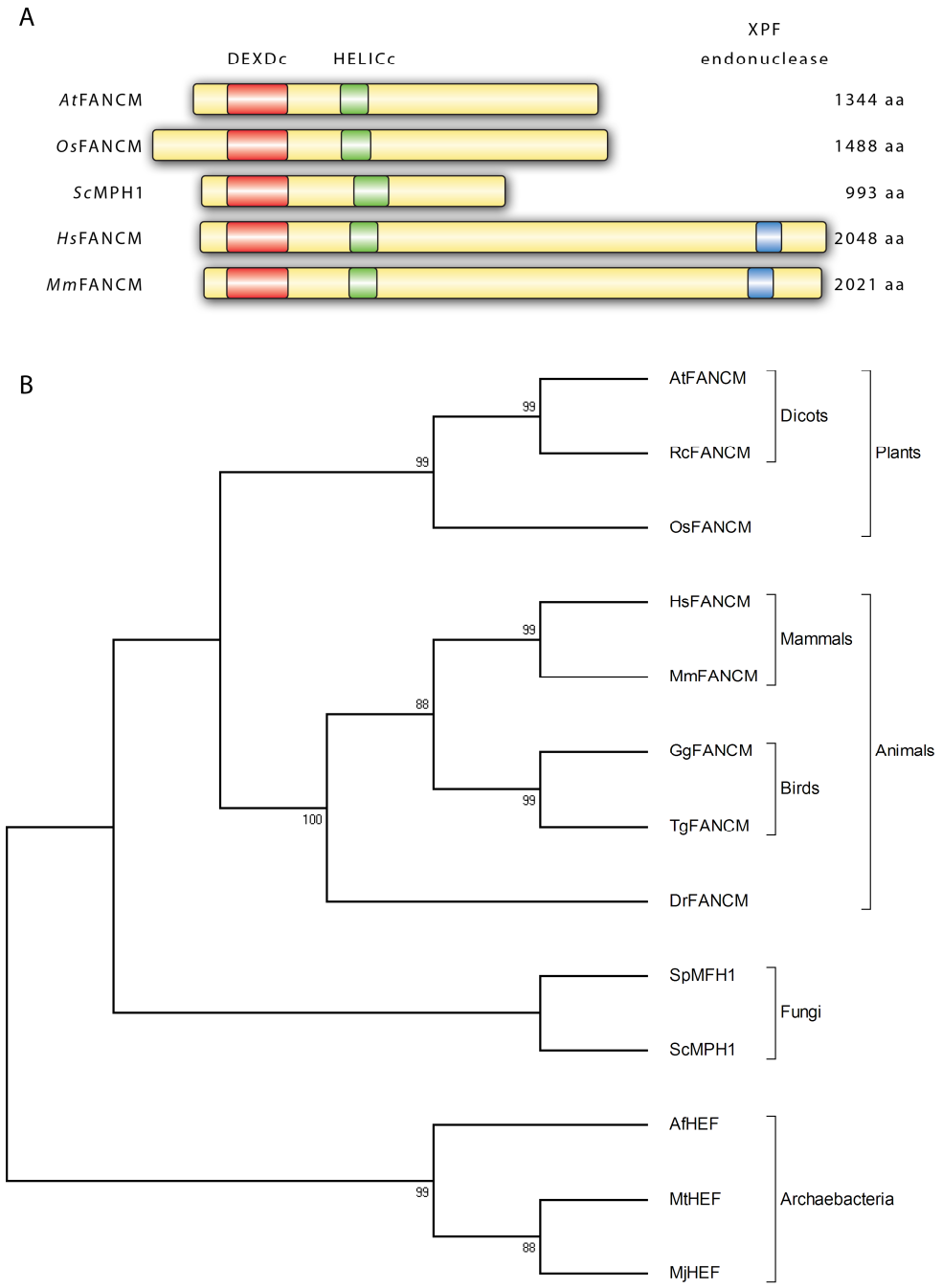
Supplemental Figure 1

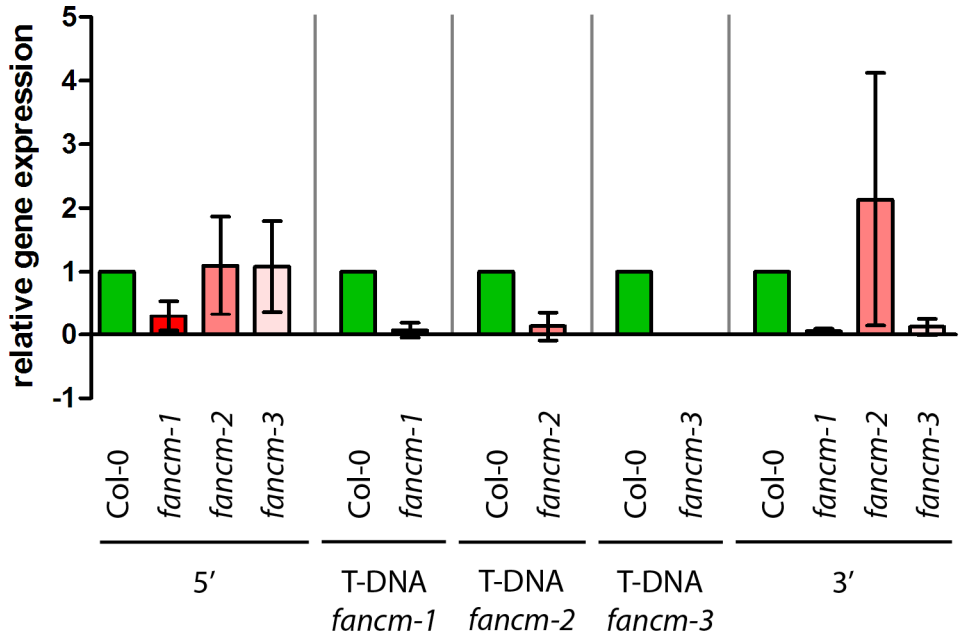


Supplemental Figure 1: Phylogenetic analysis of FANCM homologs. (A) Plant homologs (At-FANCM and Os-FANCM shown) of FANCM share a similar domain composition and length. They possess DEXDc and HELICc domains that together form the helicase domain at their N-terminus. No other domains can be identified. The fungal homologs are shorter, but with a similar domain composition (e.g. Sc-Mph1). Vertebrate FANCM homologs (Mm-FANCM and Hs-FANCM) also possess the DEXDc and HELICc domains at their N-terminus, but are longer than the fungal

and plant homologs and carry a XPF family endonuclease domain at their C-terminus. (B) The evolutionary relationship between 13 FANCM homologs was inferred using the Maximum Parsimony method. Here, the relationship of the different FANCM homologs recapitulates the known relationship of the analyzed taxa. The most parsimonious tree with length = 1703 is shown. Archaebacterial homologs were defined as outgroup. The percentage of replicate trees in which the associated taxa clustered together in the bootstrap test (10000 replicates) are shown next to the branches; bootstrap support values below 70 were omitted. The MP tree was obtained using the Close-Neighbor-Interchange algorithm with search level 3 in which the initial trees were obtained with the random addition of sequences (10 replicates). Phylogenetic analyses were conducted in MEGA4 (Tamura et al., 2007).

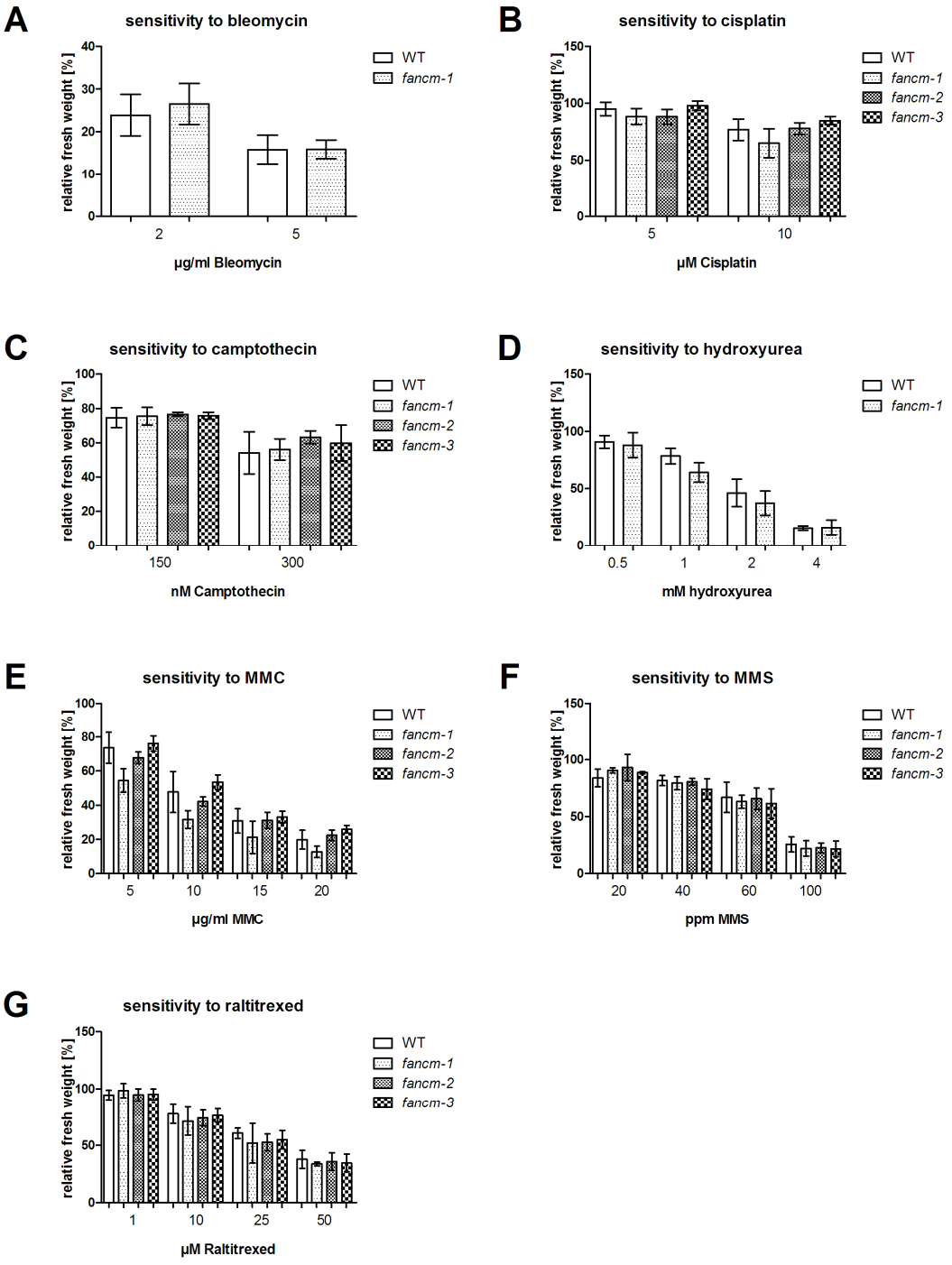
Tamura, K., Dudley, J., Nei, M., and Kumar, S. (2007). MEGA4: Molecular Evolutionary Genetics Analysis (MEGA) software version 4.0. Mol Biol Evol 24, 1596-1599.

Supplemental Figure 2



Supplemental Figure 2: Expression analysis of the At-*FANCM* locus in *fancm* mutant lines. To assess the effect of T-DNA insertion in lines *fancm-1*, *fancm-2* and *fancm-3*, regions of cDNA from these lines and the isogenic wild-type Col-0 were amplified in realtime qPCRs. Primers were placed in coding regions 5' and 3' of all three insertions to test expression upstream and downstream of the inserted T-DNAs. In each *fancm* line the expression of a third region was tested where the primer pair was located at both sides of the insertion to exclude splicing of the T-DNAs since they are located in introns. Expression levels of *fancm* lines are given relative to Col-0 in each region, respectively, after normalization to the geometric mean of reference genes At3g18780 (ACT2) and At4g34270. Across each T-DNA insertion, only minor levels of expression could be found in mutant lines. 5' of the T-DNA insertions, *fancm-2* and *fancm-3* were expressed at similar levels as Col-0, while in *fancm-1* expression was reduced to a third of Col-0. 3' of the T-DNA insertions, expression of both *fancm-1* and *fancm-3* was much lower than Col-0, at 0,05 and 0,12 times, respectively. At this 3' region, expression of *fancm-2* was about 2 times higher than Col-0, although with a high variance. Error bars represent SD after three biological replicates, where each biological replicate contains reverse transcribed RNA isolated from 100 mg of 2 weeks old whole seedlings.

Supplemental Figure 3



Supplemental Figure 3: Genotoxin sensitivity assays. Wild-type Col-0 plants as well as *fancm-1*, *fancm-2* and *fancm-3* were treated with different concentrations of the genotoxins bleomycin, cisplatin, camptothecin, hydroxyurea, Mitomycin C (MMC), methyl methanesulfonate (MMS) and raltitrexed. All *fancm* lines tested were not more sensitive to these genotoxins in the shown concentration ranges than wild-type.