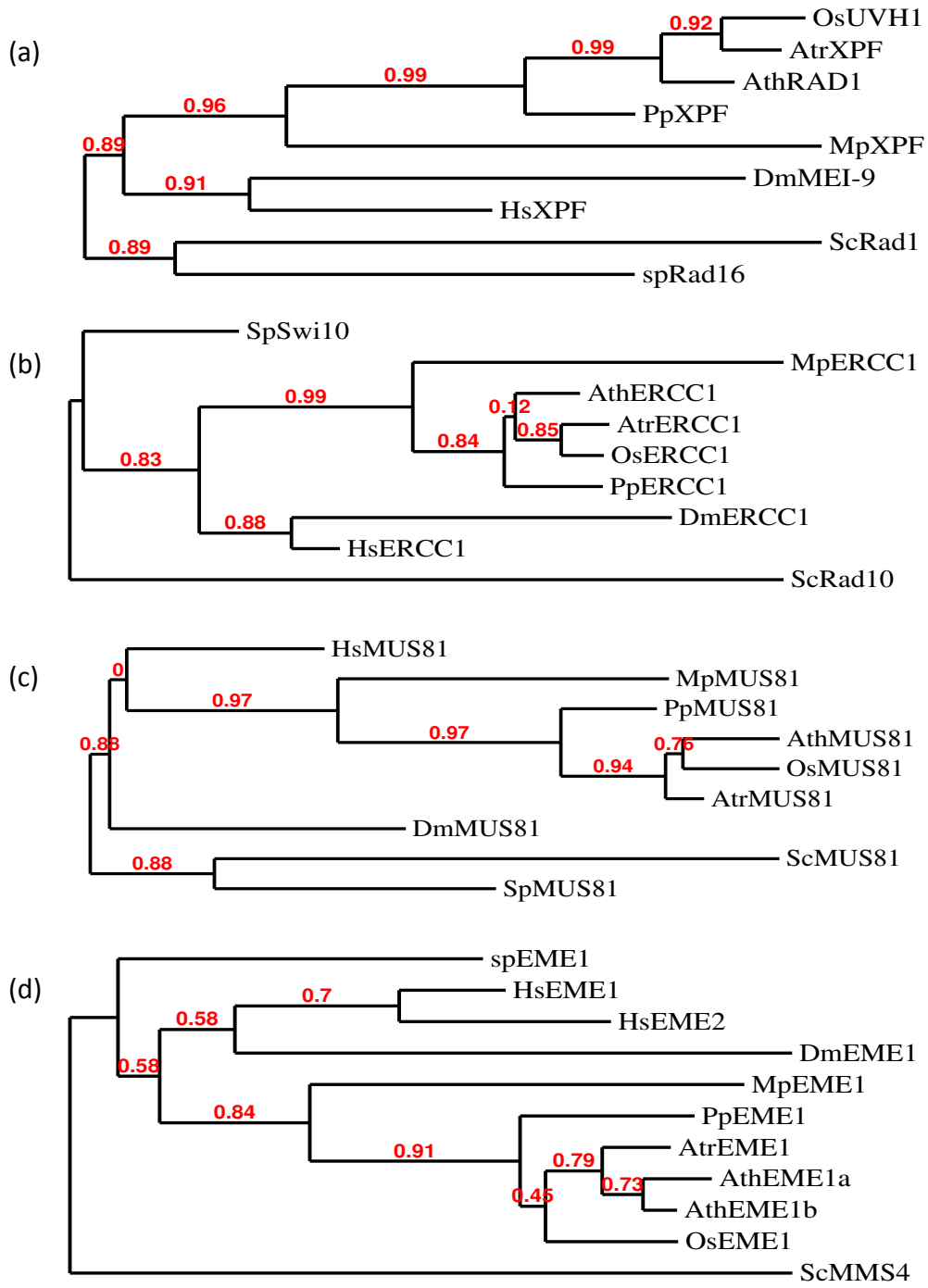

Figure S1. Physcomitrella genome encodes homologs of ERCC1 and XPF. The dendrograms illustrate the sequence relationships between several XPF (a), ERCC1 (b), MUS81 (c) and EME1 (d) proteins within the XPF super family of structure specific endonucleases. The branch lengths are proportional to the sequence divergence.

Accession numbers used in this analysis are, for *Physcomitrella patens*: PpXPF (XP_024403241), PpERCC1 (XP_024378954), PpMUS81 (XP_024398365), PpEME1 (XP_024376616), for *Arabidopsis thaliana*: AthXPF (NP_001031991), AthERCC1 (NP_187172), AthMUS81 (NP_194816), AthEME1a (NP_001189572), AthEME1b (NP_179804), for *Oryza sativa*: OsUVH1 (XP_015630768), OsERCC1 (XP_015612964), OsMUS81 (XP_015622535), OsEME1 (XP_015637261), for *Amborella trichopoda*: AtrXPF (XP_020519892), AtrERCC1 (XP_020525873), AtrMUS81 (XP_020522223), AtrEME1 (XP_020530544), for *Micromonas pusilla*: MpXPF (XP_003058408), MpERCC1 (XP_003056392), MpMUS81 (XP_003055357), MpEME1 (XP_003060706), for *Drosophila melanogaster*: DmMEI9 (AAC46917), DmERCC1 (NP_477468), DmMUS81 (NP_569873), DmEME1(), for *Homo sapiens*: HsXPF (NP_005227), HsERCC1 (NP_001974), HsMUS81 (AAL28065), HsEME1 (NP_689676), HsEME2 (NP_001244299), for *Saccharomyces cerevisiae*: ScRad1 (AJW05769), ScRad10 (NP_013614), ScMus81 (EDN60717), ScMms4 (CBK39173), for *Schizosaccharomyces pombe*: SpRad16 (NP_587855), ScSwi10 (NP_596115), SpMus81 (NP_001343019), SpEme1 (NP_594132).

Figure S2. Physcomitrella genome encodes an XPF homolog. Clustal Omega alignment of the 250 C terminal amino acids of XPF proteins from *P. patens*, *A. thaliana*, *S. pombe* and *H. sapiens*. The restriction endonuclease type II-like domain or ERCC4 domain (pfam02732 (819-946) and the RuvA 2-like domain (978-1042) or HhH domain (SMART **HHH_5** 987-1040) are indicated with green and blue lines, respectively. Green box contains the residues required for nuclease activity. Accession numbers used in this analysis are as follows: PpXPF (P_024403241), AtXPF (NP_001031991), SpRAD16 (NP_587855) and HsXPF (NP_005227).

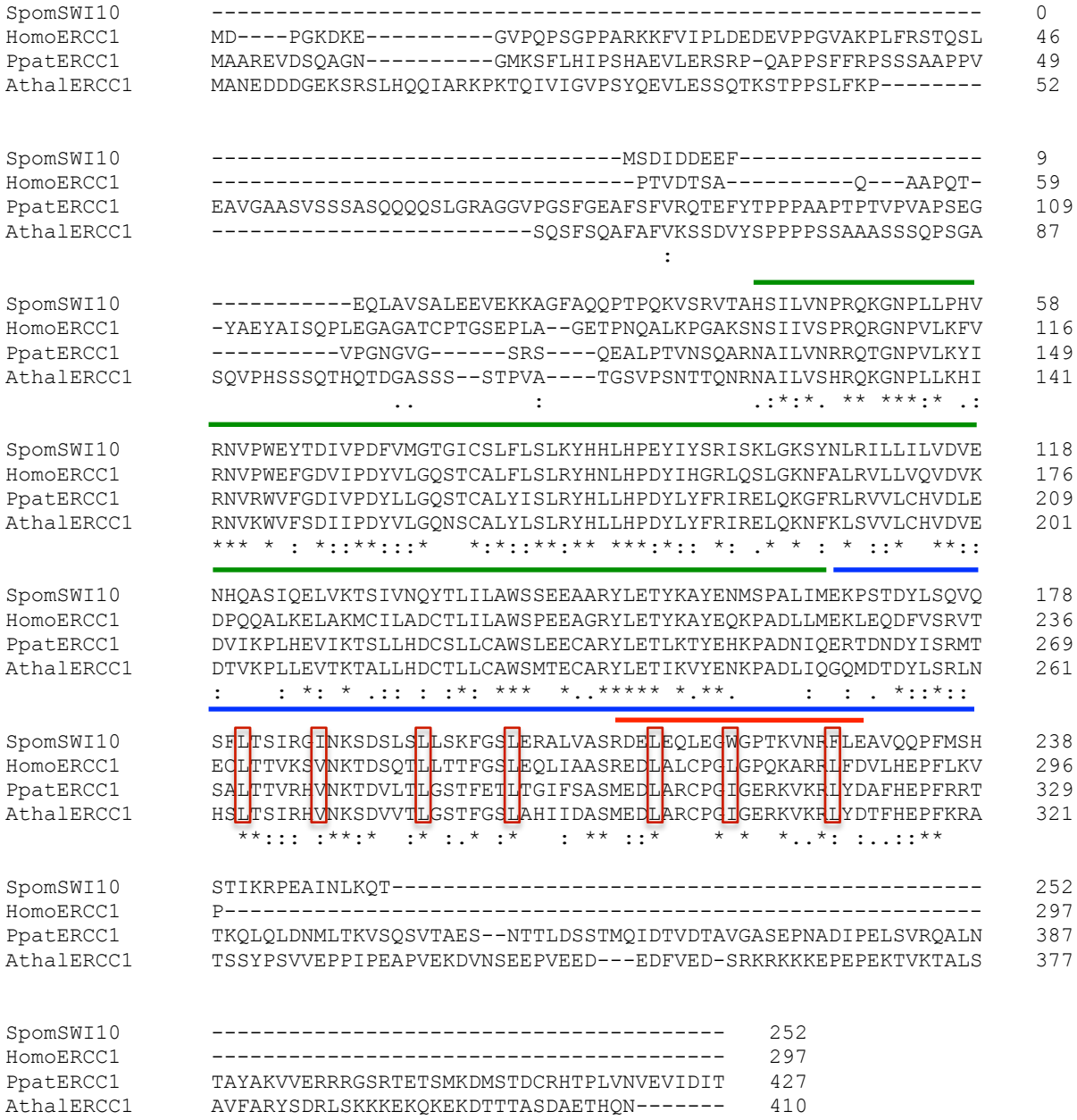

Figure S3. Physcomitrella genome encodes an ERCC1 homolog. Clustal Omega alignment of ERCC1 sequences from moss (Ppat), Arabidopsis (Athal), Human (homo) and fission yeast (Spom). Restriction endonuclease type II-like domain (132-257), RuvA 2-like domain (259-328) and Helix-hairpin-helix DNA-binding motif (305-321) are indicated with green, blue and red lines respectively. Hydrophobic amino acids critical for the formation of the HhH motifs are indicated with brown boxes. Accession numbers used in this analysis are as follows: PpERCC1 (XP_024378954), AtERCC1 (NP_187172), Spombe SWI10 (NP_596115) and HsERCC1(NP_005227).

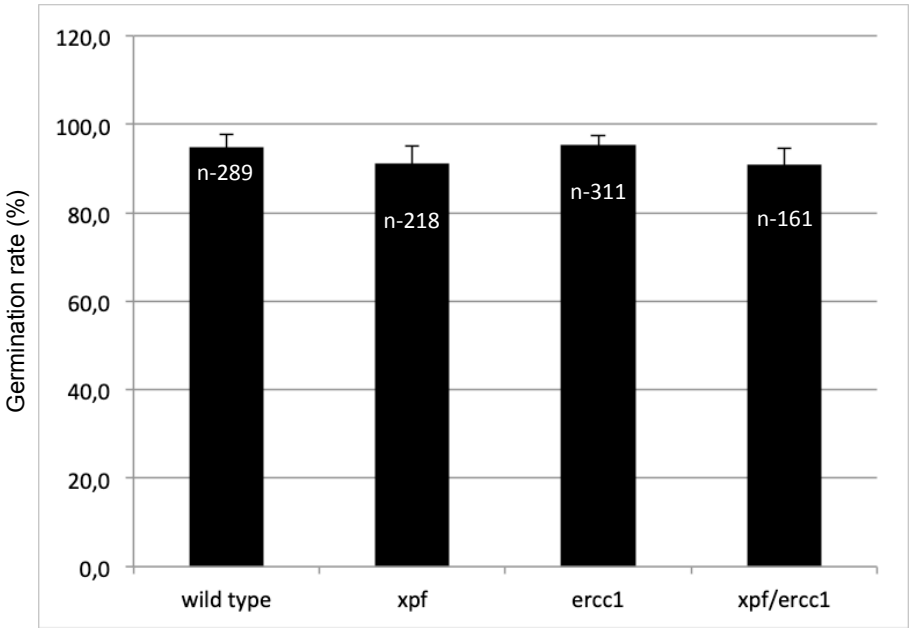

Figure S4. Germination rate of wild type *and xpf*, *ercc1* and *xpf/ercc1* mutants spores. Freshly harvested spores from wild type *and xpf*, *ercc1* and *xpf/ercc1* capsules were sown on PpNH4 medium. Percentages of germination were calculated three days after sowing. Error bars indicate SD based on three independent experiments.

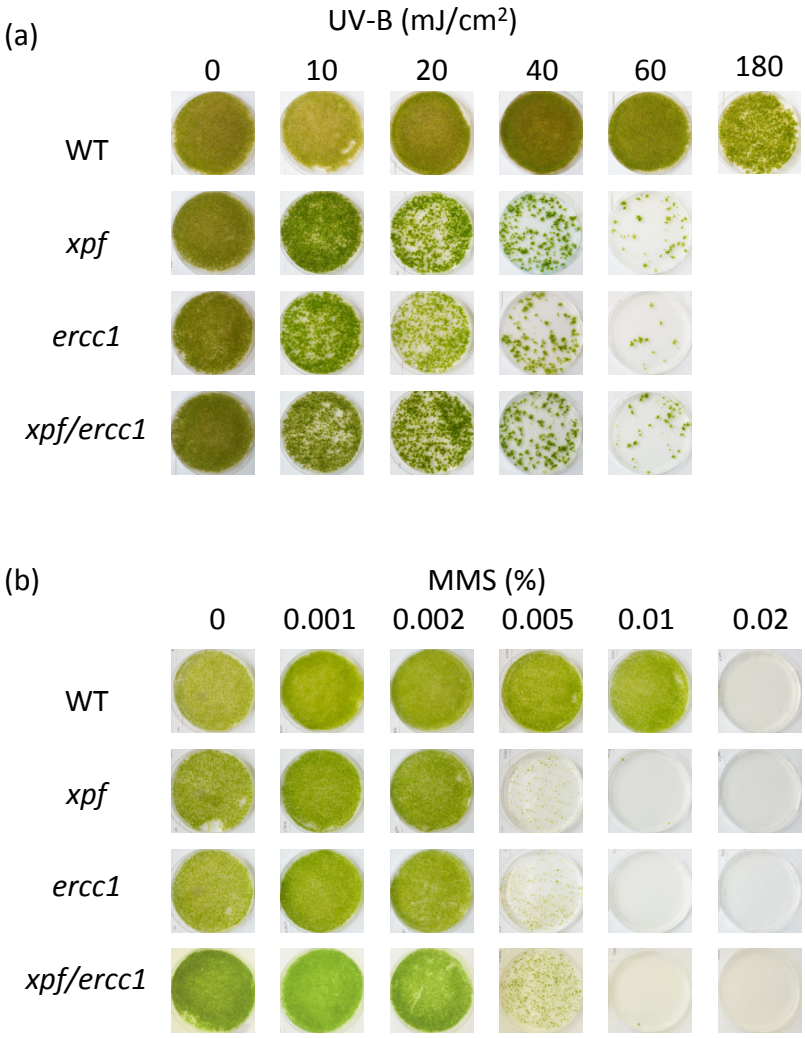

Figure S5. Sensitivity of the wild-type (WT) and of the *xpf*, *ercc1* and *xpf/ercc1* mutants towards genotoxic agents. 3 weeks old plates of WT and the 3 mutants exposed to low doses of UV-B light B (a) or to increasing doses of MMS (b).

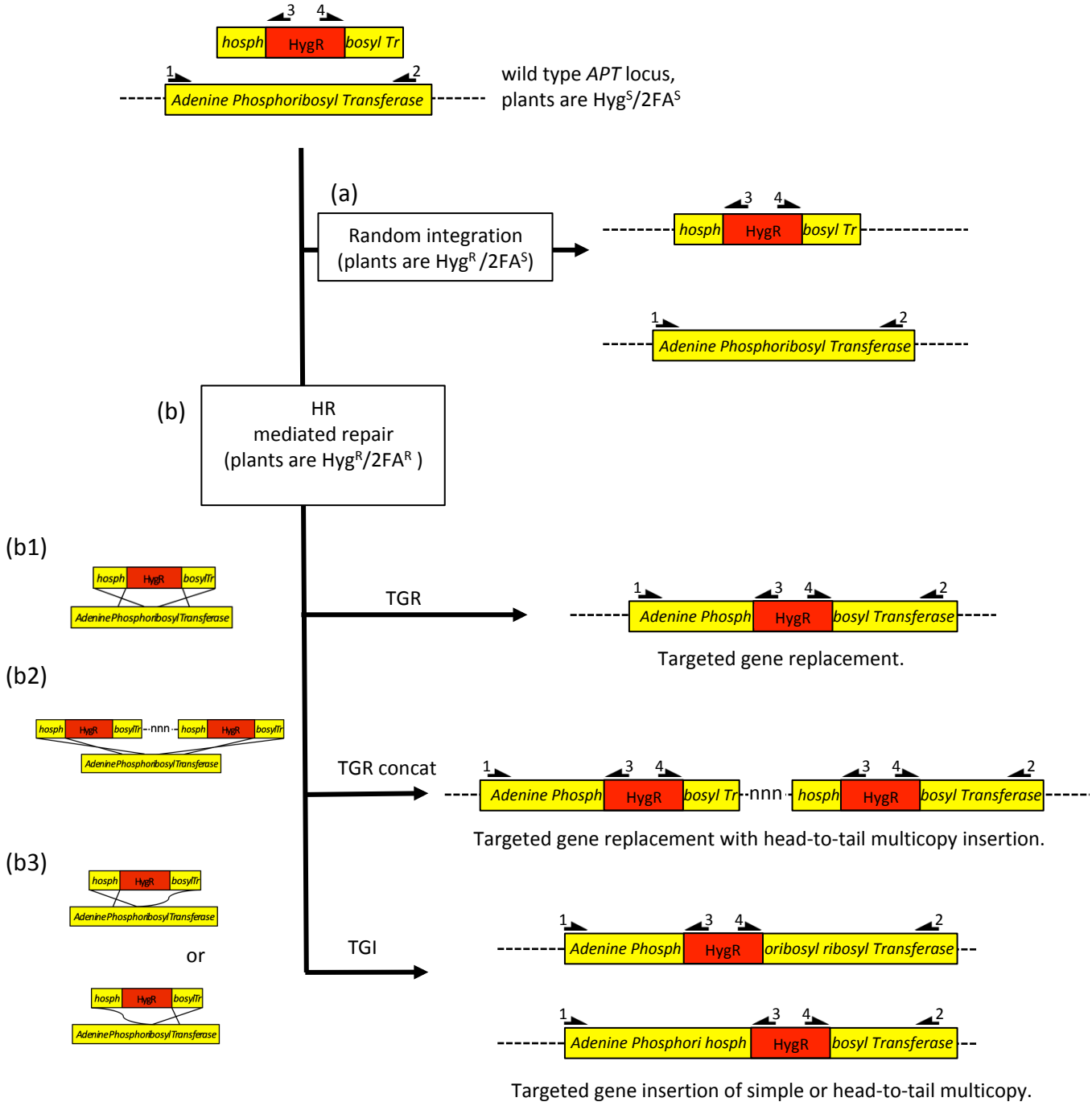

Figure S6. Different outputs of repair of a CRISPR-Cas9 induced DSB in presence of a donor template. Integration of the Donor DNA can be random (a) and in this case plants are resistant to hygromycine but sensitive to 2FA, or via gene targeting (b). As targeting of the *APT* gene leads to resistance to 2FA, selection of hygromycin resistant plants on this compound will permit selection of clones that experienced an HR mediated integration of the donor DNA at the targeted locus. HR mediated integration of the donor template can lead to TGR (b1), TGR with concatemers (b2) or TGI (b3). For a given 2FA and Hygromycin resistant clone, analysis of PCR products 1+3 and 4+2 will permit to determine whether it results from a TGR or TGI integration. Furthermore analysis of PCR products 1+2 will permit to determine whether it is or it is not a monocopy insertions. In this study primers 1, 2, 3 and 4 correspond to PpAPT#2, PpAPT#20, ProRev and TerFwd respectively (Table S1).