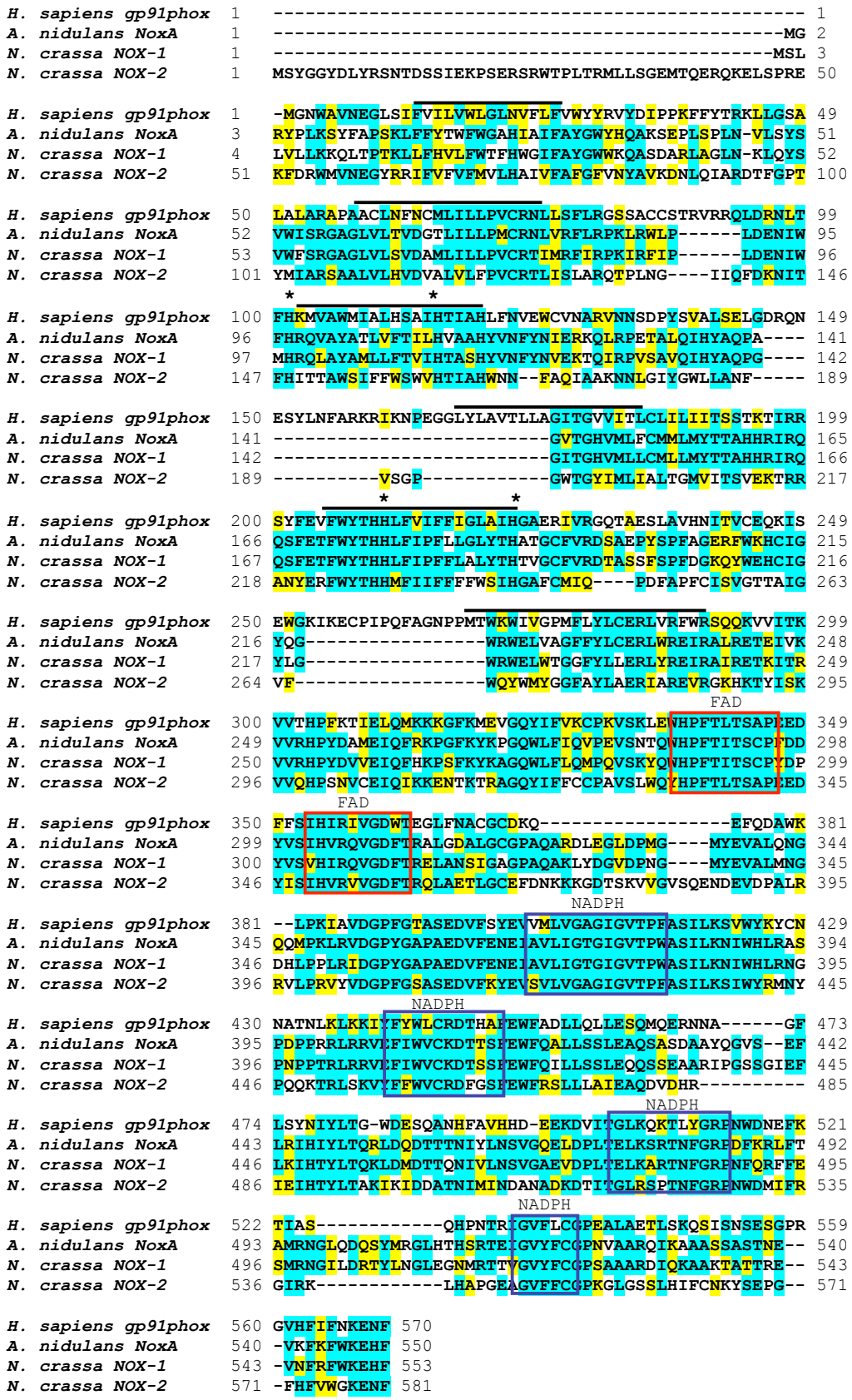

Fig S1. The amino acid sequence of *N. crassa* NADPH oxidases NOX-1 and NOX-2 are aligned, along with *A. nidulans NoxA* and human gp91^{phox} (Nox2). Residues conserved in all proteins are blue shaded. Asterisks indicate candidate histidines for haem ligation. Top black bars show predicted transmembrane regions. FAD and NADPH-binding sites are indicated by red and blue rectangles, respectively.

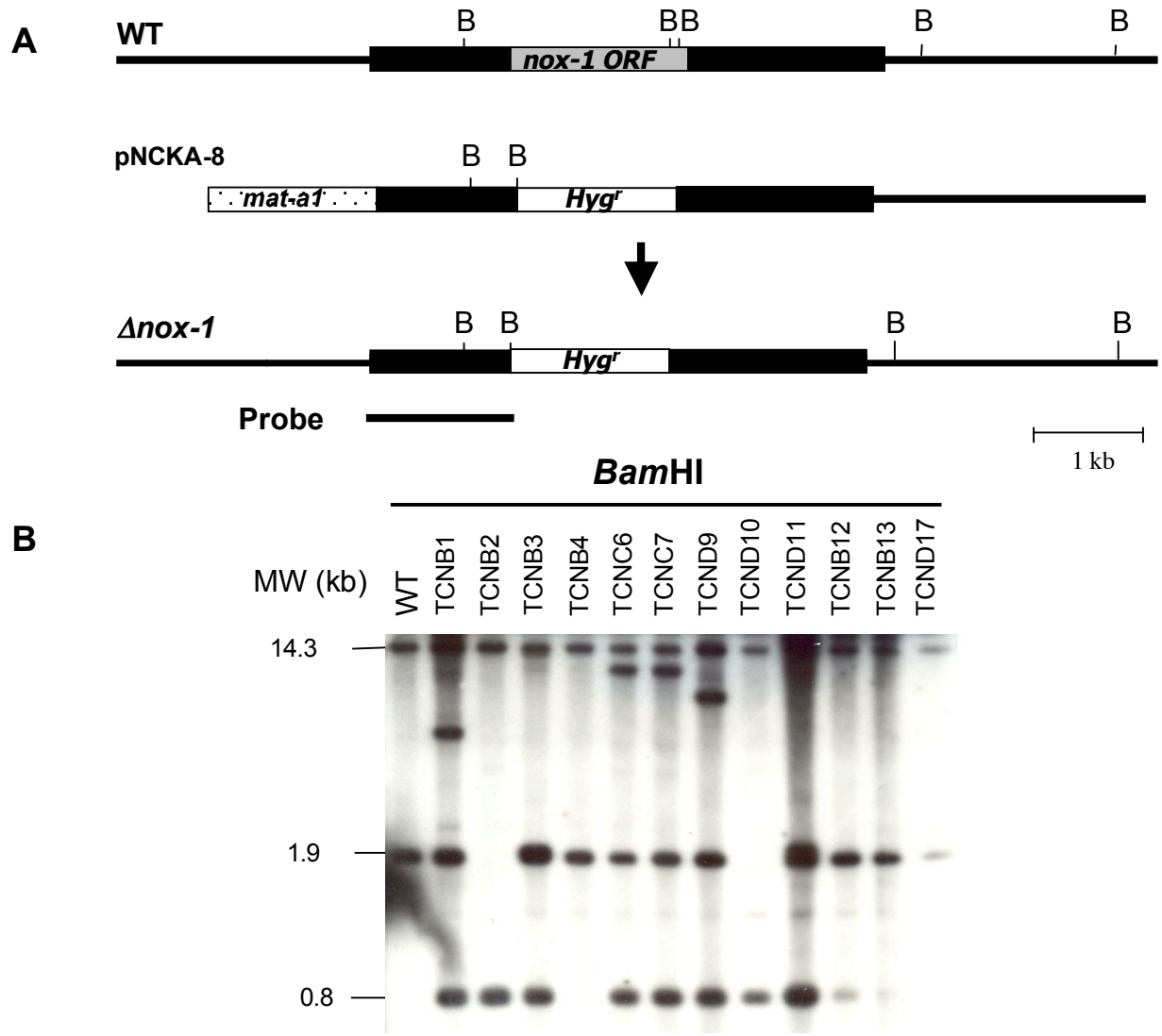

Fig. S2. Deletion of the *nox-1* gene. (A) The *nox-1* deletion plasmid pNCKA-8 containing the *mat-a1* gene, as counter selection marker, and the hygromycin resistance marker Hyg^r was used to transform strain RPNCR3A. A double recombination event results in replacement of the wild type *nox-1* gene. B indicates *Bam*HI sites. (B) DNA from the WT and hygromycin resistance transformants was digested with *Bam*HI and used for Southern blot analysis with the indicated probe. The wild type *Bam*HI pattern corresponds to bands of 14.3 and 1.9 kb, while the *nox-1* deletion pattern corresponds to bands of 14.3 and 0.8 kb (strains TCNB2 and TCND10).

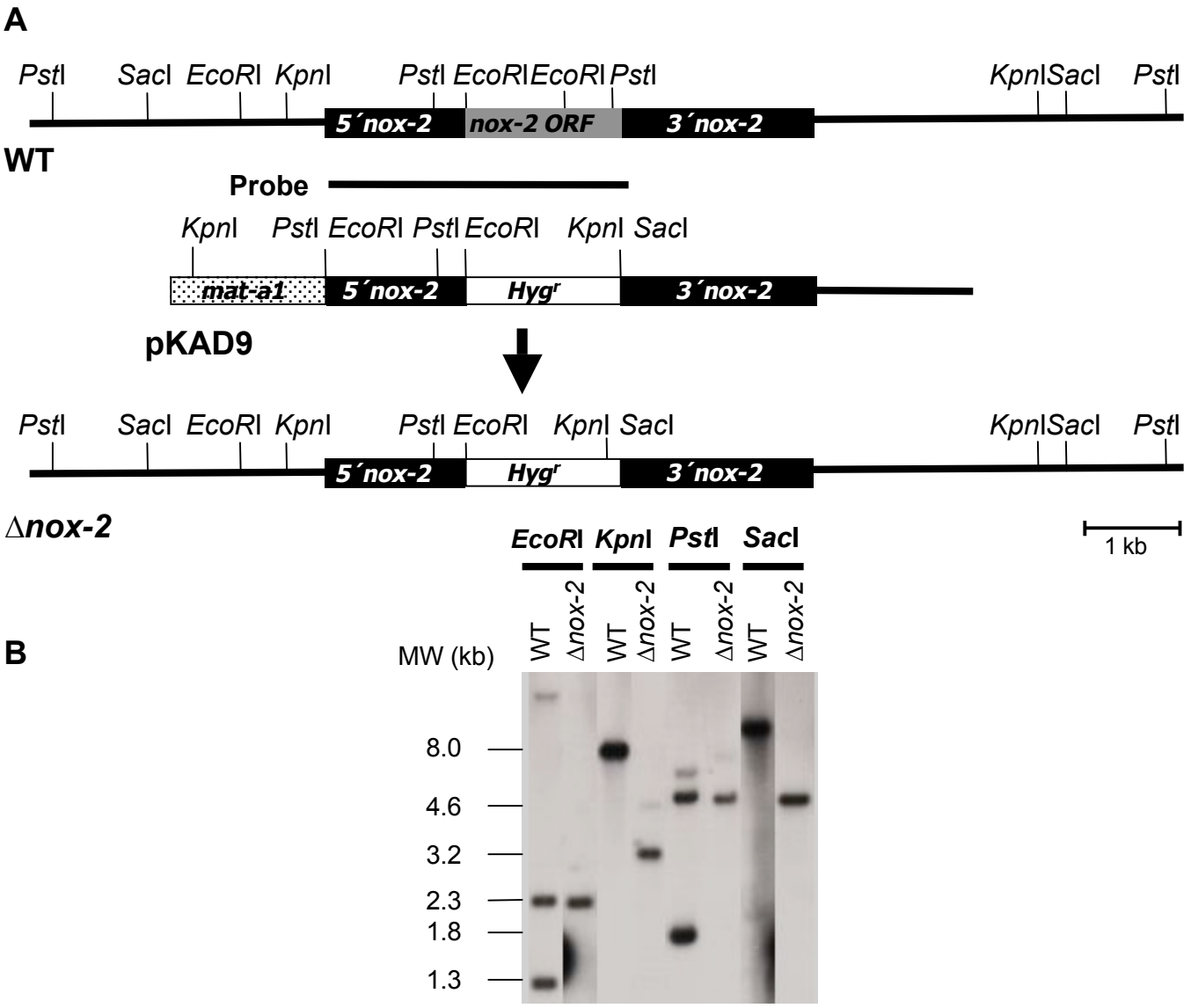

Fig. S3. Deletion of the *nox-2* gene. (A) In plasmid pKAD9 85% of *nox-2* ORF was replaced by the hygromycin resistance marker *Hyg*^{r}. (B) To verify *nox-2* deletion, DNA from WT and hygromycyn resistance transformants was digested with *Pst*I, *Sac*I, *Eco*RI and *Kpn*I and used for Southern blot analysis with the probe indicated in (A).

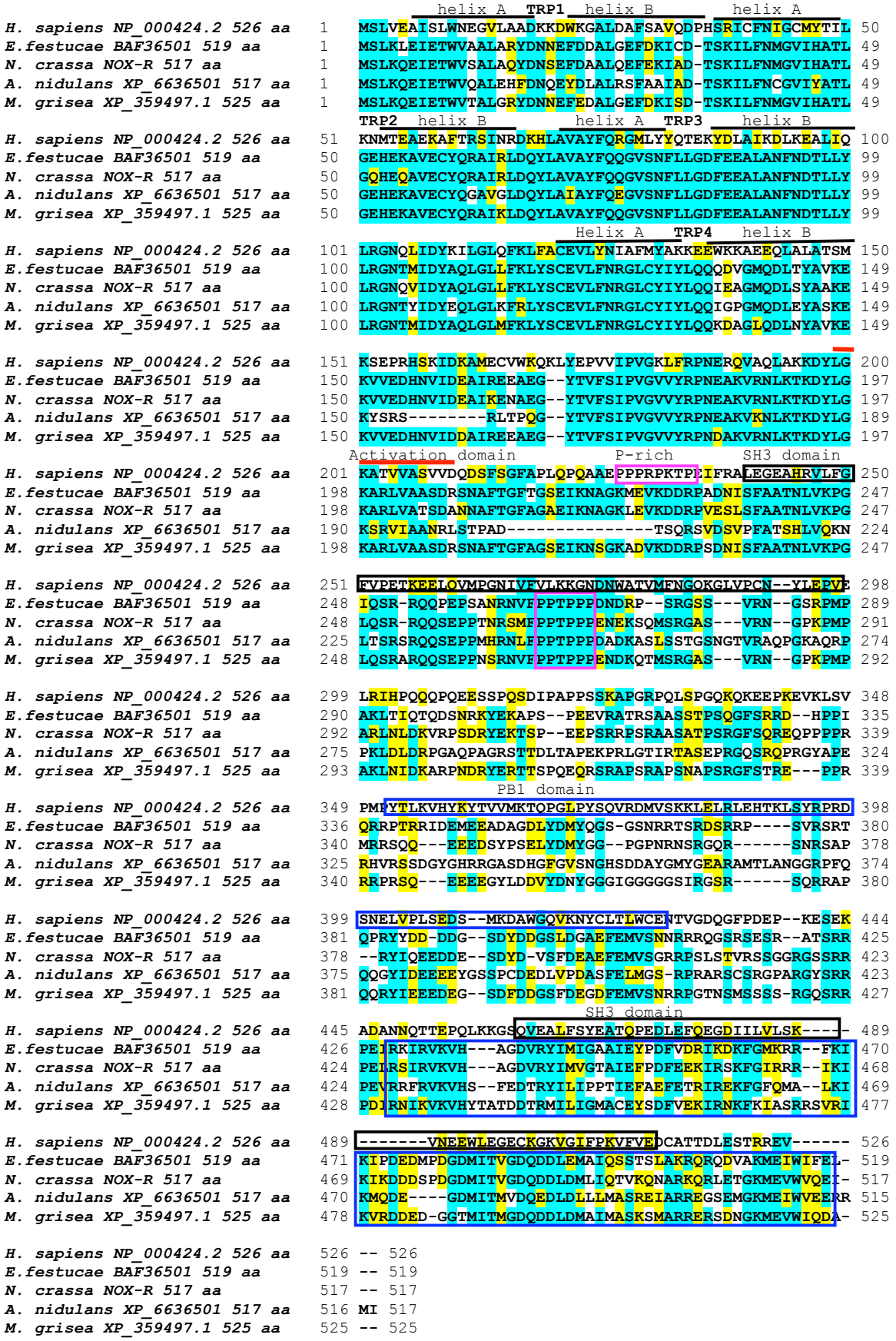

Fig. S4. The amino acid secuence of *N. crassa* NOR-1 is aligned with human p67^{phox}, *E. festucae* NoxR and orthologs from *A. nidulans* and *M. griseae.* Sequences are identified by species name, GenBank accession and protein size. Top red bar indicates the active domain. Top black bars show the helices between tetratricopetide domains (TRP). Proline rich region, SH3 and PB1 domains are indicated by pink, black and blue rectangles, respectively.

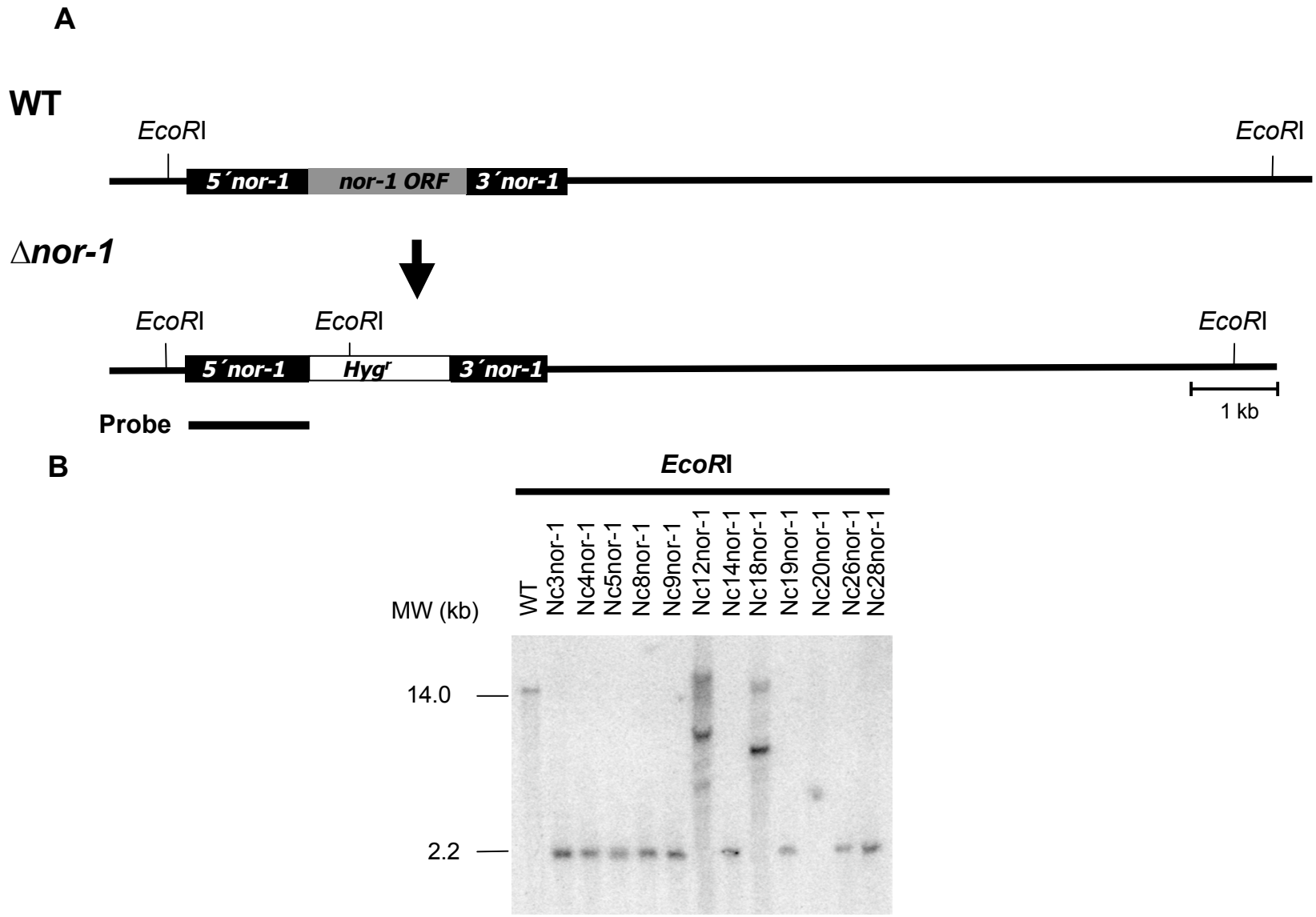

Fig. S5. Deletion of the *nor-1* gene. (A) The *nor-1* deletion construct, containing the hygromycin resistance gene, was generated by double-joint PCR and used to transform strain Δ*mus-51*. A double recombination event results in replacement of the wild type locus by the deletion construct. (B) To verify *nor-1* deletion, DNA from WT and hygromycin resistance transformants was digested with *EcoR*I and used for Southern blot analysis with the indicated probe. The wild type *EcoR*I pattern corresponds to a single band of 14.0 kb, while the Δ*nor-1* pattern corresponds to one band of 2.2 kp.

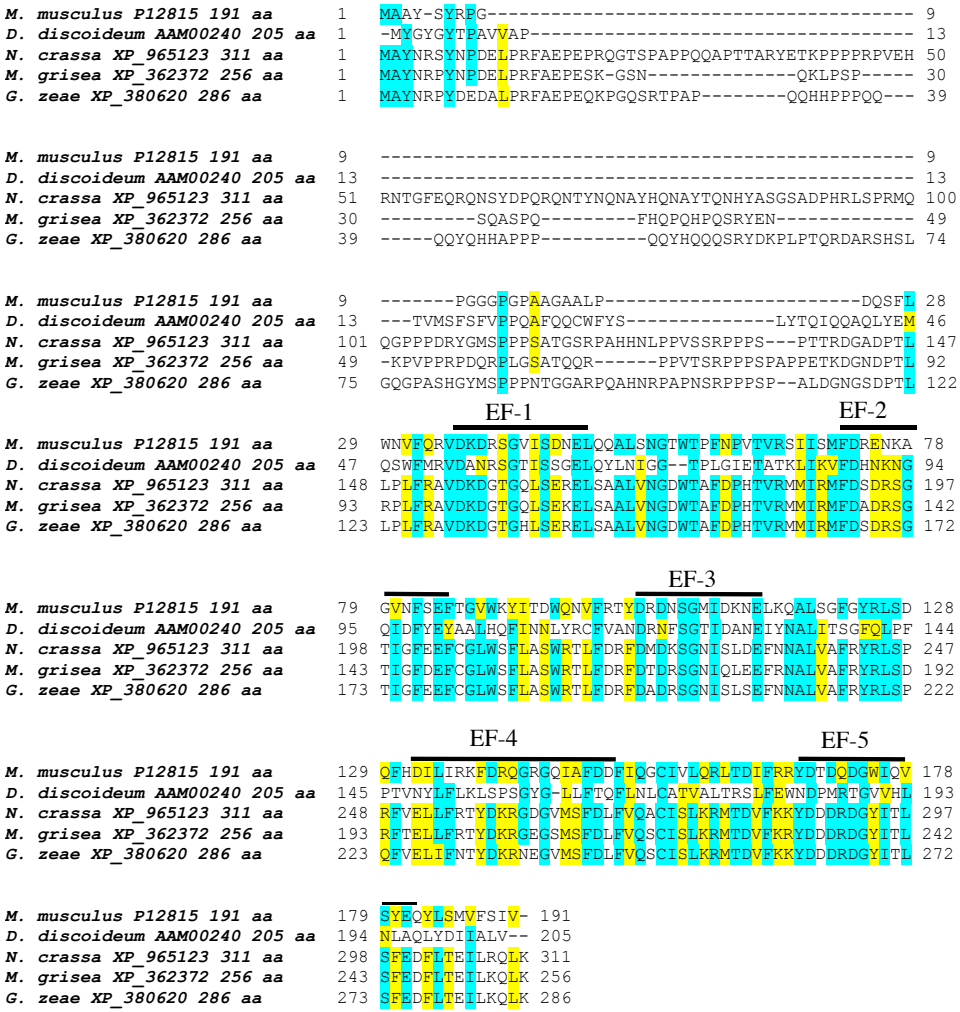

Fig. S6. *N. crassa* predicted PEF-1 protein is aligned with *Mus musculus* (mouse) Alg-2, *Dictyostelium discoideum* Alg-2b and hypothetical orthologs from *Magnaporta grisea* and *Giberella zea*. Secuences are identified by species name, followed by GeneBank accession or contig number and protein size. Top bars indicate EF-hand domains as deduced from Expasy-Prosite database (http://www.expasy .org/prosite/).

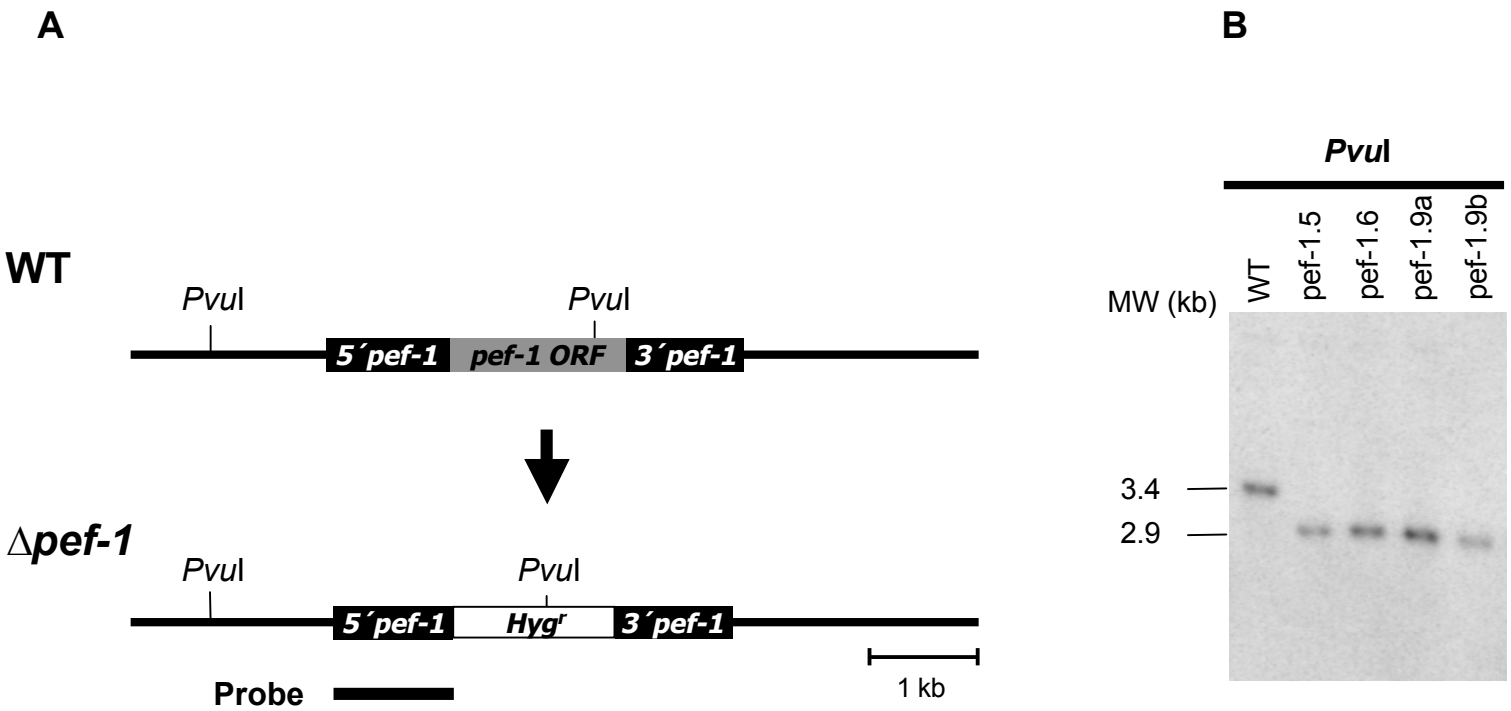

Fig. S7. Deletion of the *pef-1* gene. (A) A *pef-1* deletion construct based on the hygromycin resistance gene was generated by double-joint PCR and used to transform strain Δ*mus-51*. Double recombination results in replacement of the wild type *pef-1* locus. (B) To verify *pef-1* deletion, DNA from WT and hygromycyn resistance transformants was digested with *Pvu*I and used for Southern blot analysis with the probe indicated in (A). The wild type *Pvu*I pattern corresponds to one band of 3.4 kb; the Δ*pef-1* pattern corresponds to a band of 2.9 kb.