MS ID#: JBC/2010/128611
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Legends to the supplemental figures

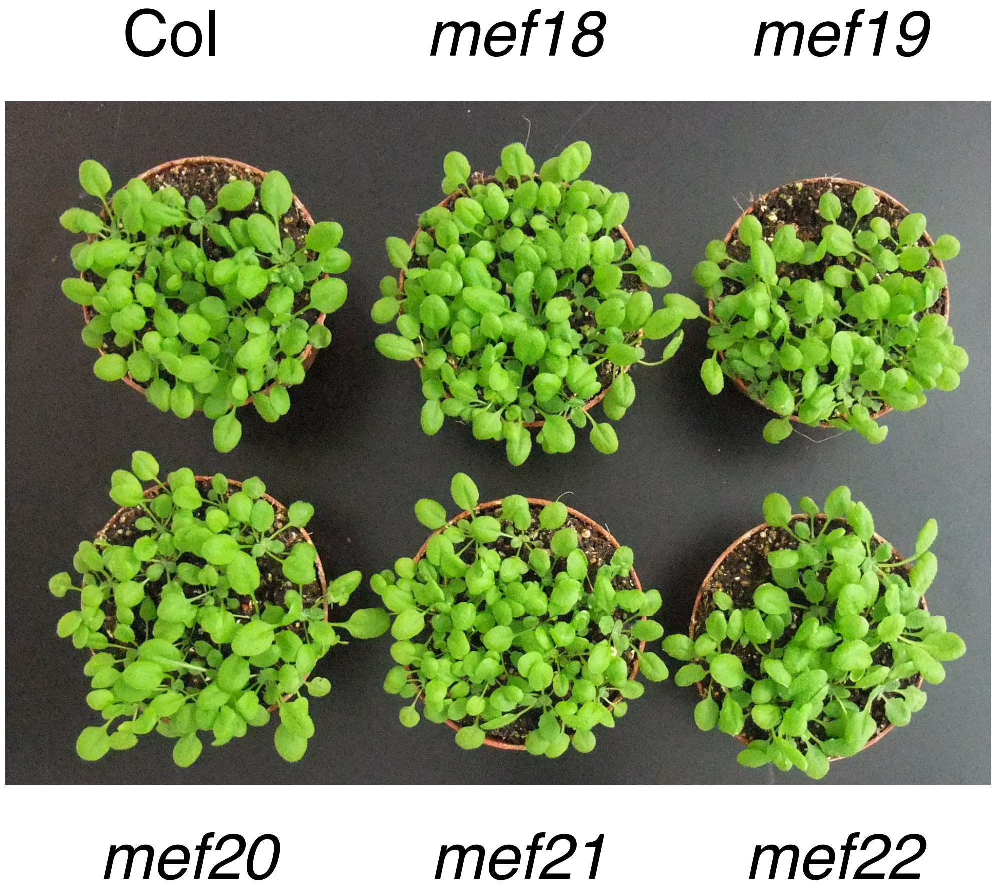
Figure S1. **Growth of mutant plants in comparison to wild type plants.** Homozygous mutant plants with the T-DNA insertions in the genes *MEF18 –MEF22* grow in the greenhouse with phenotypes similar to the Col wild type plants. Pictures of several plants per pot are shown after three weeks of growth.

Figure S2. **Comparison of leaf numbers between mutant and wild type plants. N**umbers of leaves are counted in Col wt and in the mutant plants two and three weeks after seeding from five plants grown in two different pots. Overall numbers of leaves are similar between the mutants and the Col wt plants.

Figure S3. **Mutant plants produce viable pollen similar to wild type plants.** Individual pollen kernels were released from excised anthers from Col wt and the mutant plants and were stained for viability. Pollen viability was analysed by the staining procedure developed by Alexander (Alexander, M.P. (1969) *Stain Technol.* **44,** 117-122). The bar equals 20 µm.

Figure S4. **Comparison of nucleotide and amino acid conservation around the editing sites affected in the *mef18* to *mef22* mutants.** The left alignment compares the nucleotide conservation around the targeted editing sites between the respective mutant and edited sequences in *Arabidopsis* and other plants including dicots, monocots, a moss and a liverwort. The nucleotide whose editing is affected in the mutants is indicated by its position from the AUG. Shared nucleotide identities are highlighted in grey. Editing events are underlined and only the edited U-nucleotide is given.
The amino acid alignments on right show the extensive conservation of shared amino acids between the different plants at and around the residue derived from the editing site altered in the mutants. The positions of these amino acids in the respective proteins are indicated by the numbers above. All sequences are shown 5' to 3' or N- to C-terminus from left to right.

Figure S5. **Analysis of the T-DNA insertion sites in the *mef18-mef22* mutant plants.** The insertion sites of the T-DNA were investigated by PCR assays with right-border (RB) and left border (LB) primers and with primers in the predicted adjacent gene sequence. RB-gene primer combinations gave a product only for *mef22* with the downstream sequence. LB-gene primer combinations gave products with upstream and downstream sequences for *mef18-mef21* and only with the upstream sequence for *mef22*. All PCR products were sequenced which yielded the following information: In *mef18* a left border - left border T-DNA fragment is inserted downstream of nucleotide 1148 from the A in the ATG start codon. Nucleotides 1149-1248 are deleted and instead 41 nucleotides of unknown origin are inserted. The lost nucleotides code for one of the central repeats (PPR). In *mef19* a left border - left border T-DNA fragment is inserted in the E-domain downstream of nucleotide 1549 from the A in the ATG start codon. Nucleotides 1550-1599 are deleted. In *mef20* a left border - left border T-DNA fragment is inserted just upstream of the first predicted L-type PPR downstream of nucleotide 228 from the A in the ATG start codon. Nucleotides 229-313 are deleted, while 773 nucleotides of plasmid vector origin are inserted just upstream of the T-DNA. In *mef21* a left border - left border T-DNA fragment is inserted downstream of nucleotide 964 from the A in the ATG start codon. Nucleotides 965-979 are missing. In *mef22* a left border - right border T-DNA fragment is inserted downstream of nucleotide 1840 from the A in the ATG start codon. Nucleotides 1841-2087 are deleted, which cover much of the E-domain and the N-terminus of the DYW-region. Downstream of the T-DNA 36 nucleotides of unknown origin are inserted.



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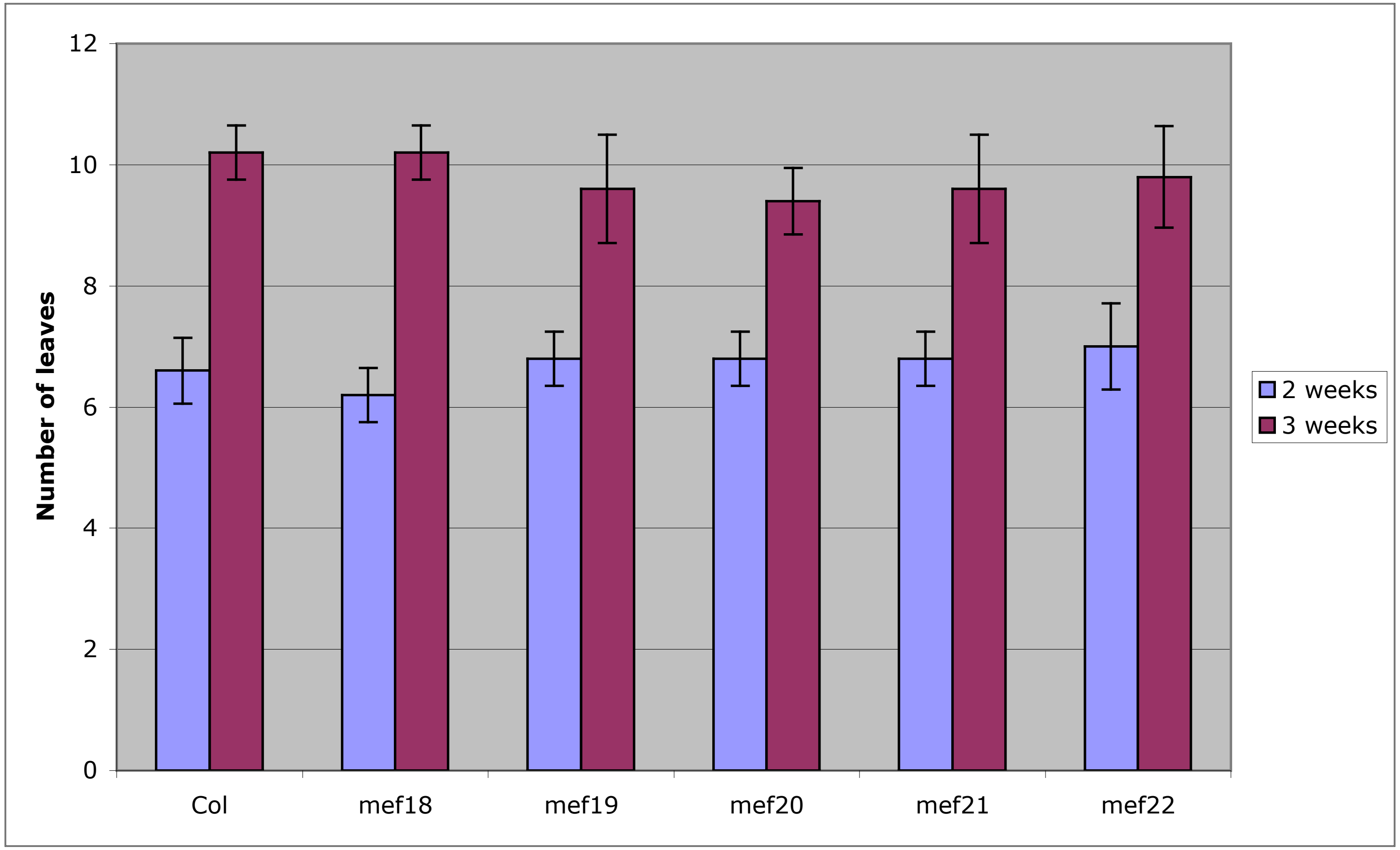

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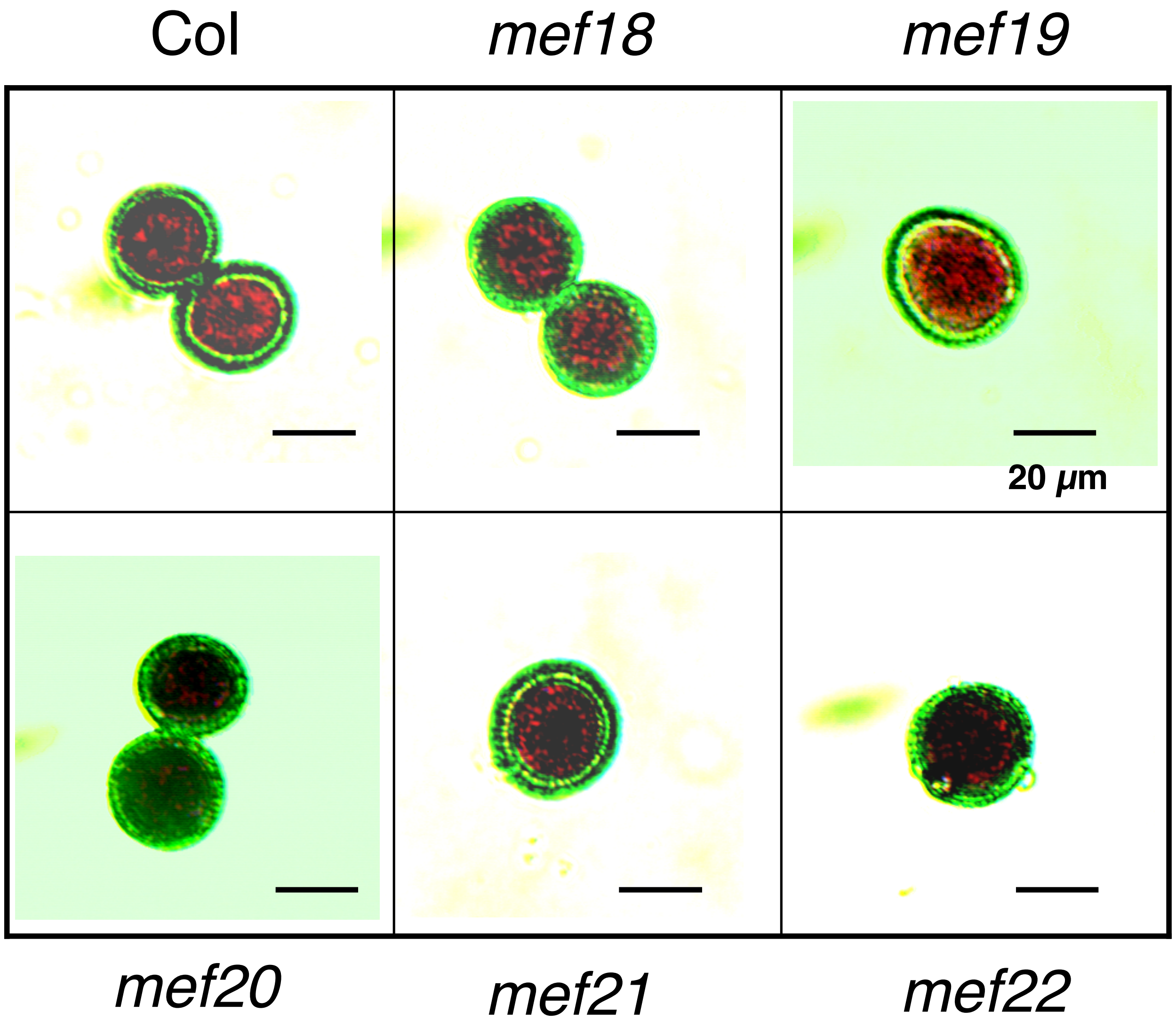

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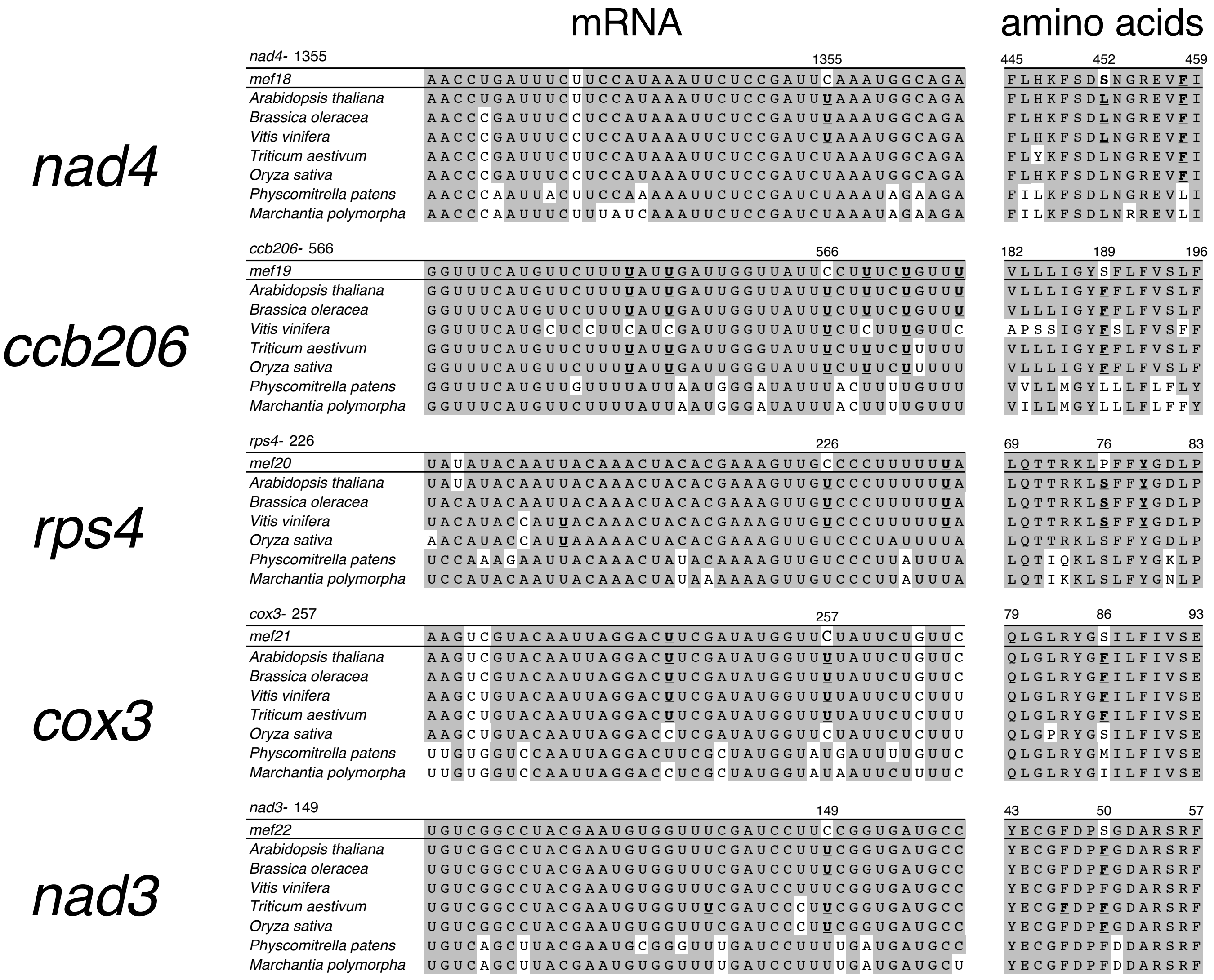

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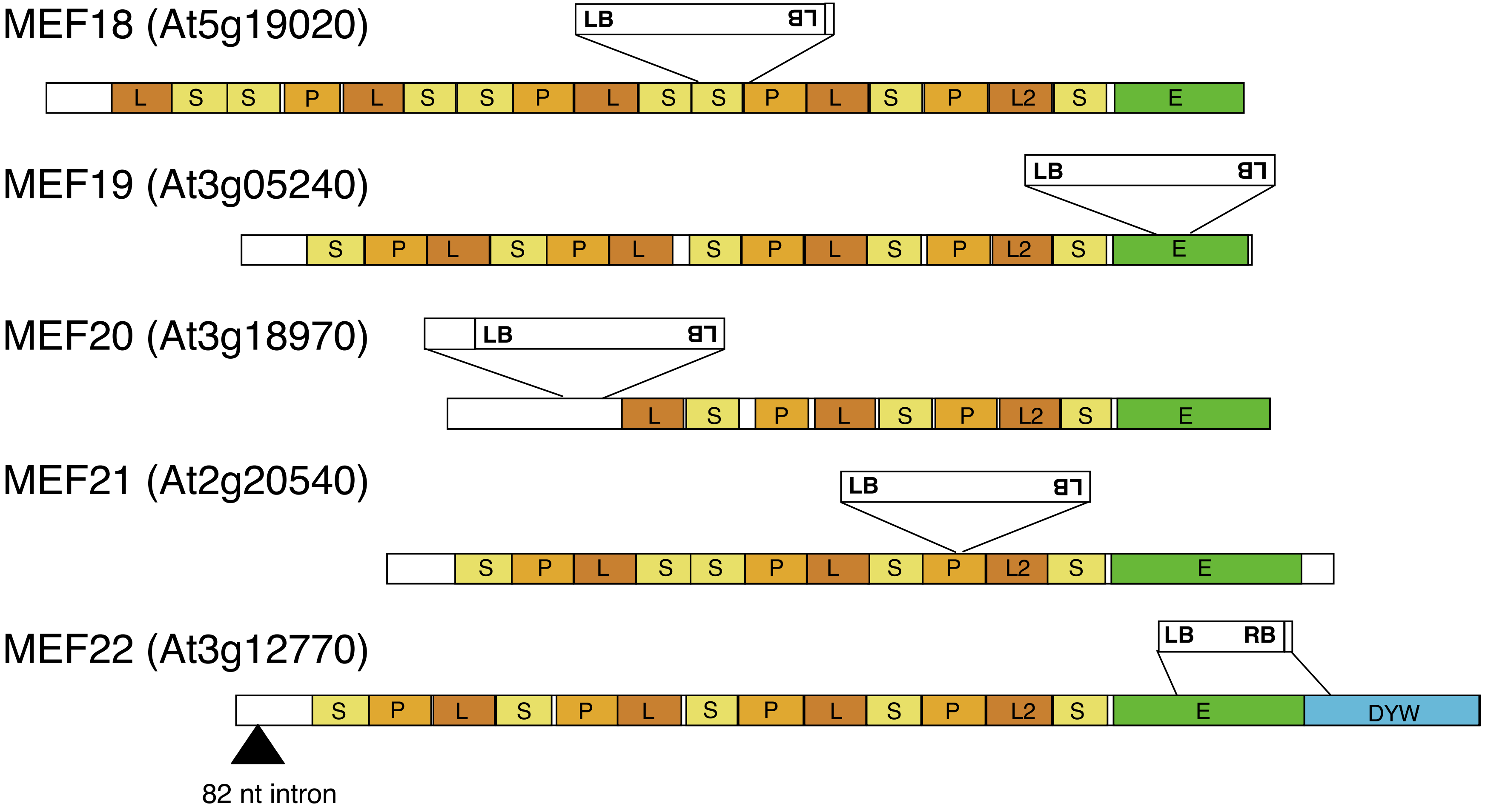

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