

Nterminus

[illegible][illegible]

Cterminus

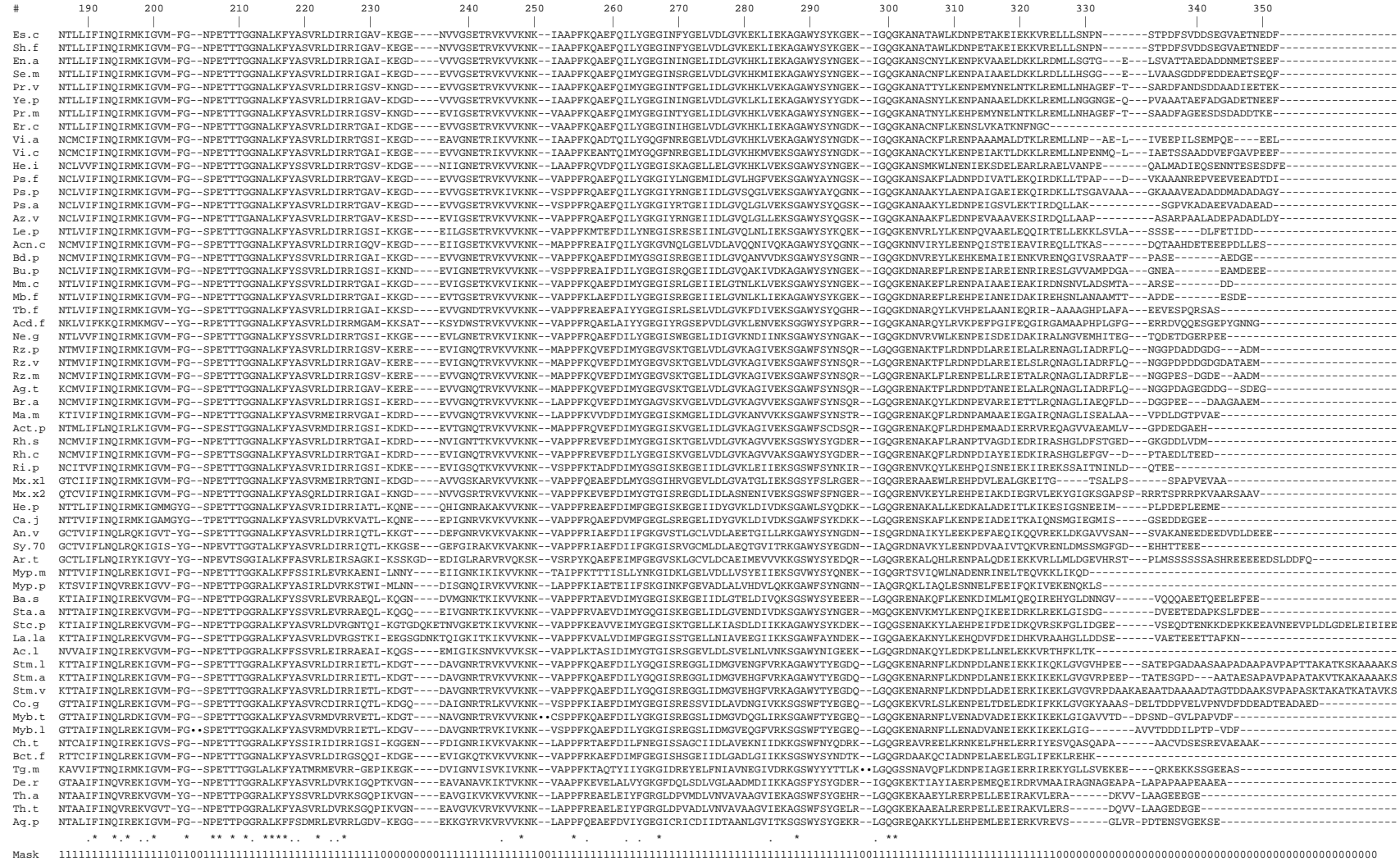


Figure 1. Alignment of complete RecA sequences.

The alignment was generated using the *clustalw* multiple sequence alignment program. Dashes (-) represent alignment gaps. Three insertions that are present in only one sequence each (*Myb.t*, *Myb.l*, and *Tg.m*) and the first 80 aa of the *A. thaliana* protein are left out for space reasons and are indicated by a **. Conservation of alignment positions as determined by the *clustalw* program is indicated by * (identical aa in all) and . (similar aa in all). The alignment positions used in phylogenetic analysis are indicated by the sequence mask (1=used, 0=not used). Sequence abbreviations are described in Table 1.