Supplemental Figure legends

Fig. S1. Sequence alignment of the GmERD15 deduced amino acid sequence with other ERD15-like proteins from plants. ERD15-like proteins identified in the soybean genome and in other plants genomes were compared with respect to their amino acid sequences. The species and accession numbers are shown in the alignment. The ERD15 protein from the soybean genome identical to GmERD15 is marked in gray. The PABP (poly-A-binding protein)-interacting motif PAMP2 at the N-terminus is indicated by a black bar. The conserved residues in all sequences are highlighted in blue, while residues that are conserved in more than half of the proteins are marked in green**.** The multiple alignment was created using ClustalW.

Fig. S2. Expression and purification of a His-tagged GmERD15 fusion protein. The recombinant protein was purified by affinity chromatography from total protein extract (lane 1) prepared from an IPTG-induced culture of E. coli expressing His-tagged GmERD15 fusion protein. The samples were separated by SDS-PAGE and stained with Coomassie blue dye. Lanes 2, 3 and 4 are eluted fractions from nickel-affinity chromatography. The positions of molecular mass markers are indicated in M.

Fig. S3. Negative controls for specificity of GmERD15:NRP-B DNA complex formation. A. GmERD15 does not bind to a 350-bp promoter fragment of soyBiPD gene. A 350-bp biotin-labeled DNA fragment of the soyBiPD promoter (lane 1) was incubated with purified His-tagged GmERD15 in the absence (lane 2) and presence of 4 pmol of unlabeled probe DNA (lane 3) for 20 min at RT. The products were separated by electrophoresis in a 5% polyacrylamide gel in TB buffer. Bands corresponding to the free DNA are designated by the arrow. B. An unrelated gluthathione S-transferase (GST) does not bind to the 187-bp NRP-B promoter DNA fragment. A 187-bp biotin-labeled DNA fragment of GmNRP-B 5'flanking sequences (positions -330 to -517; lane 1) was incubated with *E. coli*-produced GST protein in the absence (lane 2) and presence of unlabeled DNA as a competitor (lane 3).

Fig. S4. Time course of NRP-A and NRP-B induction by wounding and CDE treatment. Soybean leaves were wounded (A) or treated with cell-wall degrading enzymes (CDE; B) for the indicated number of hours. After incubation, total RNA was isolated from treated leaves and expression was monitored by qRT-PCR.

Fig. S5. Putative cis-regulatory elements for dsDNA- or ssDNA-binding transcription factors on the NRP-B promoter region. A. 1-kb NRP-B 5'-flanking sequences. NRP-B sequences extend until the ATG (purple) translational initiation codon of NRP-B. Numbers indicate the position relative to the translation start codon. The sequence in gray corresponds to the 187-bp NRP-B target promoter DNA. Several putative cis-regulatory elements are indicated in other colors. These include a putative CCAAT box (blue), MYC recognition sites (pink boxes), RAV1 binding sites (red) and an unfolded protein response element (yellow). Sequences in green are palindromic sequences. B. Hairpin formation within the 187-bp fragment. Potential hairpins are from the palindromic sequences in (A) shown in green.