Supplementary Figure 1: Sequence alignment of the GERMN domain.

The alignment was formatted with Jalview (Clamp et al., 2004) and annotated with the PSIPRED (Jones, 1999) prediction for the top sequence. Sequences were extracted from a full alignment so that no pair shares more than 60% sequence identity. The sequences are sorted by domain context, from top to bottom, N-terminal domains from twin GERMN proteins (top 6 sequences), then C-terminal domains from twin GERMN proteins (17 sequences), domains from single GERMN proteins (19), domains from GERMN+GMA1 proteins (13) and finally domains from GERMN+GMAD2 proteins (5).

References