



**Figure S3** - Multiple sequence alignment of predicted amino acid sequences of DGAT3 proteins. The DGAT3 sequences from *G. max* (Gma), *A. thaliana* (Ath) and *O. sativa* (Osa) were aligned. Identical residues are shaded black, and similar residues are shaded gray. The color boxes indicate the conserved motifs on protein sequences shown in Figure 2B and 2C.