

Additional file 1. List of predicted amino acid sequences used for the phylogenetic analysis of the *Gmubi* genes. The *Gmubi* genes were identified in the soybean genome assembly (accessed in April, 2009; ftp://ftp.jgi-psf.org/pub/JGI_data/Glycine_max/Glyma1/annotation/) based on the presence of the highly conserved ubiquitin-coding unit.

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