**Supplementary Figure 1.** Branch-specific relaxation in *Caenorhabditis* UGGTs recognition (top) and catalytic (bottom) domains. Branches are color-coded according to the selection strength parameter k, inferred under the general descriptive RELAX model. Low k values (<1) indicate purifying selection relaxation, whereas high k values (>1) indicate selection intensification.

**Supplementary Figure 2.** Branch-specific relaxation in vertebrate UGGTs recognition (left) and catalytic (right) domains. Branches are color-coded according to the selection strength parameter k, inferred under the general descriptive RELAX model. Low k values (<1) indicate purifying selection relaxation, whereas high k values (>1) indicate selection intensification.

**Supplementary Figure 3.** Expression of *Sp*UGGT, *Ce*-UGGT-a, *Ce*-UGGT-b and chimeric proteins in *alg6/gpt1-* cells. Microsomal proteins derived of *S.pombe alg6/gpt1* transformed with pREP3X-*uggt*-b (lane1), pREP3X-*uggt*-a (lane 2), pREP3X-*gpt1+* (lane 3), pREP3X-chimera I (*Ce*-N-term-*uggt*-a-C-term-*gpt1+c-myc*) (lane 4), pREP3X-chimera II (*Ce*-N-term-*uggt-b*-C-term *gpt1+*-*c-myc*) (lane 5) and pREP3X (lane 6) were analyzed in 8 % SDS PAGE and submitted to Western-blot analysis using a commercial anti c-Myc antibody.

**Table S1.** Templates and primers used in the PCR amplification of the sequences encoding the N- and C-terminal domains of *S. pombe* UGGT, *Ce*-UGGT-a, and *Ce*-UGGT-b.

**Table S2.** Templates and primers used in the PCR amplification of the full-length fragments encoding chimeric UGGTs

**Table S3.** List of DNA primers used in this work

**Additional File 1**. **(xls).** Species names, phyla, database and Accession Numbers of the 195 UGGT (and UGGT-like) sequences included in this study. The criteria for excluded sequences is detailed.

**Additional File 2. (fas).** Unaligned 195 UGGT (and UGGT-like) protein sequences.

**Additional File 3. (fas).** Alignment of 195 UGGT (and UGGT-like) protein sequences used for phylogenetic inference.

**Additional File 4. (doc).** Aminoacidic positions corresponding to each UGGT domain taken as reference sequences.

**Additional File 5. (doc).** Table S1, Table S2, Table S3 and Suppementary Figure S3.