

**Fig. S1. Molecular phylogenetic tree of bHLHs transcription factors**, generated by maximum-likelihood using RAxML with 100 bootstrap replications. This tree is based in the alignment of bHLHs orthologous sequences of *S. roscoffensis* with those of the species *H. sapiens*, *N. vectensis*, *D. melanogaster*, *A. digitifera* and *H. magnipapillata*. The data was provided by F. Gyoja, (Gyoja et al., 2012, Simionato et al., 2007). We are keeping the original orthologous family names used in previous studies. We use the names given by Gyoja et al. (Gyoja et al., 2012) and Simionato et al. (Simionato et al., 2007), which are based on accession number or FlyBase IDs, adding an abbreviation for the species name followed by the, generic, orthologous family names. The sequences domains of two other species, *S. kowalevski* and *C. teleta* were added from the PFAM database, preserving their original identification codes. The monophyletic groups are shown and gene families are grouped by colours. Numbers at the branches are the statistical support obtained by bootstrap; only bootstrap values above 50% are shown, except for a few cases. The bHLHs family members identified in *S. roscoffensis* are indicated by black arrows.

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**Fig. S2. Phylogenetic analysis of *X.bocki* bHLHs transcription factors.** The represented tree is generated by maximum-likelihood using RAxML. This tree is the outcome from a multiple alignment of bHLHs orthologous sequences of *X.bocki* and those of the species *H. sapiens*, *N. vectensis*, *D. melanogaster*, *A. digitifera* and *H. magnipapillata* (Gyoja et al., 2012, Simionato et al., 2007). Basically, the bHLHs sequences from these species conserve the names given by Gyoja et al. (Gyoja et al., 2012) and Simionato et al. (Simionato et al., 2007), which are based on accession number or FlyBase IDs, adding an abbreviation for the species name followed by the generic orthologous family names. Two new species sequences domains were included in our analysis (*S. kowalevski* and *C. teleta*), all downloaded from the PFAM database and keeping their original identification codes. The gene families are clustered and highlighted within colour boxes, with the inside grouping of all monophyletic groups. Numbers at the branches are the times that a node was supported in 100 bootstrap pseudoreplications; only values higher than 50% are shown, except for few cases. Black arrows designate the bHLHs family members of *X.bocki* found.

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**Fig. S3. Glutamate\_tree.** Phylogenetic relationships between glutamate GPCR family members of the species *Amphimedon queenslandica*, *Nematostella vectensis*, *Saccoglossus kowalevskii*, *H. sapiens*, *Capitella teleta*, *D. melanogaster* and the acoel *Symsagittifera roscoffensis*. GenBank or ENSEMBL proteins IDs are shown in the sequence name of the 6 first species (sequences from de Mendoza et al., 2014). Trees are generated with RAxML bestree with 100 bootstrap pseudoreplications. Bootstrap values lower than 50% are not shown. Glutamate subfamilies are highlighted using different colours. Acoel sequences are marked with a black arrow.

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**Fig. S4. Frizzled\_tree.** Phylogenetic relationships between frizzled GPCR of the species *Amphimedon queenslandica*, *Nematostella vectensis*, *Saccoglossus kowalevskii*, *H. sapiens*, *Capitella teleta*, *D. melanogaster* and the acoel *Symsagittifera roscoffensis*. GenBank or ENSEMBL proteins IDs shown in the sequence name of the 6 first species (sequences from de Mendoza et al., 2014). Trees are generated with RAxML bestree with 100 bootstrap replicates. Bootstrap values lower than 50% are not shown. Frizzled subfamilies are highlighted using different colours. Acoel sequences are marked with a black arrow.

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**Fig. S5. A/S\_tree.** Phylogenetic relationships between adhesion and secretin GPCR of the species *Amphimedon queenslandica*, *Nematostella vectensis*, *Saccoglossus kowalevskii*, *H. sapiens*, *Capitella teleta*, *D. melanogaster* and the acoel *Symsagittifera roscoffensis*. GenBank or ENSEMBL proteins IDs are shown in the sequence name of the 6 first species (sequences from de Mendoza et al., 2014). Trees are generated with  $N=100$  RAxML bestree with 100 bootstrap replicates. Bootstraps  $<50$  are generally not shown. A/S subfamilies are highlighted using different colours. Acoel sequences are marked with a black arrow.

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**Fig. S6. Complete multiple alignment for the analysis of the bHLHs orthologous protein sequences of the acoel *Symsagittifera roscoffensis*, performed in MAFFT with all the bHLHs sequences used in this study.** The bHLHs sequences of the species *H. sapiens*, *N. vectensis*, *D. melanogaster*, *A. digitifera* and *H. magnipapillata* were provided by F. Gyoja (Gyoja et al., 2012, Simionato et al., 2007). The sequences domains of two other species, *S. kowalevski* and *C. teleta* were added from the PFAM database, preserving their original identification codes. The file in fasta format results from the selection of conserved regions using the Geneious software (<http://www.geneious.com/>).

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**Fig. S7. Multiple alignment used in the analysis of the bHLHs orthologous protein sequences in the xenoturbellid *X.bocki*, performed in MAFFT with the total group of bHLHs sequences used in this study.** The bHLHs sequences of the species *H. sapiens*, *N. vectensis*, *D. melanogaster*, *A. digitifera* and *H. magnipapillata* were provided by F. Gyoja (Gyoja et al., 2012, Simionato et al., 2007). The sequences domains of two other species, *S. kowalevski* and *C. teleta* were added from the PFAM database, preserving their original identification codes. The file is in FASTA format and contains the conserved regions manually selected from the original alignment using the Geneious software.

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**Fig. S8. Multiple alignment used in the analysis of the Glutamate orthologous proteins in the acoel *S. roscoffensis*,** performed in MAFFT with the reference sequences of *A. queenslandica*, *H. Sapiens*, *D. melanogaster*, *S. kowalevski*, *N. vectensis*, and *C. teleta* provided by A. de Mendoza (de Mendoza et al., 2014). The file is in FASTA format and contains the conserved regions manually selected from the original alignment using Geneious software.

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**Fig. S9. Multiple alignment used in the analysis of the Frizzled orthologous proteins in the acoel *S. roscoffensis*,** performed in MAFFT with the reference sequences of *A. queenslandica*, *H. sapiens*, *D. melanogaster*, *S. kowalevski*, *N. vectensis*, and *C. teleta* provided by A. de Mendoza (de Mendoza et al., 2014). The file is in FASTA format and contains the conserved regions manually selected from the original alignment using Geneious software.

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**Fig. S10. Multiple alignment used in the analysis of the Adhesion and Secretin orthologous proteins in the acoel *S. roscoffensis*,** performed in MAFFT with the reference sequences of *A. queenslandica*, *H. sapiens*, *D. melanogaster*, *S. kowalevski*, *N. vectensis*, and *C. teleta* provided by A. de Mendoza (de Mendoza et al., 2014). The file is in FASTA format and contains the conserved regions manually selected from the original alignment using Geneious software.

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