1 Supplementary Figures and Tables

1.1 Supplementary Figures

Supplementary Figure 1. Statistics of ortholog group prediction by PortmBL. A total of 22,649 ortholog groups were predicted for the 11 species. (A) Similar ortholog groups with genes of each species. (B) Similar ortholog groups with genes of each species. (C) Similar ortholog groups with genes of each species. (D) Similar ortholog groups with genes of each species. (E) Similar ortholog groups with genes of each species. (F) Similar ortholog groups with genes of each species. (G) Similar ortholog groups with genes of each species. (H) Similar ortholog groups with genes of each species. (I) Similar ortholog groups with genes of each species. (J) Similar ortholog groups with genes of each species. (K) Similar ortholog groups with genes of each species. (L) Similar ortholog groups with genes of each species. (M) Similar ortholog groups with genes of each species. (N) Similar ortholog groups with genes of each species. (O) Similar ortholog groups with genes of each species. (P) Similar ortholog groups with genes of each species. (Q) Similar ortholog groups with genes of each species. (R) Similar ortholog groups with genes of each species. (S) Similar ortholog groups with genes of each species. (T) Similar ortholog groups with genes of each species. (U) Similar ortholog groups with genes of each species. (V) Similar ortholog groups with genes of each species. (W) Similar ortholog groups with genes of each species. (X) Similar ortholog groups with genes of each species. (Y) Similar ortholog groups with genes of each species. (Z) Similar ortholog groups with genes of each species. (AA) Similar ortholog groups with genes of each species. (BB) Similar ortholog groups with genes of each species. (CC) Similar ortholog groups with genes of each species. (DD) Similar ortholog groups with genes of each species. (EE) Similar ortholog groups with genes of each species. (FF) Similar ortholog groups with genes of each species. (GG) Similar ortholog groups with genes of each species. (HH) Similar ortholog groups with genes of each species. (II) Similar ortholog groups with genes of each species. (JJ) Similar ortholog groups with genes of each species. (KK) Similar ortholog groups with genes of each species. (LL) Similar ortholog groups with genes of each species. (MM) Similar ortholog groups with genes of each species. (NN) Similar ortholog groups with genes of each species. (OO) Similar ortholog groups with genes of each species. (PP) Similar ortholog groups with genes of each species. (QQ) Similar ortholog groups with genes of each species. (RR) Similar ortholog groups with genes of each species. (SS) Similar ortholog groups with genes of each species. (TT) Similar ortholog groups with genes of each species. (UU) Similar ortholog groups with genes of each species. (VV) Similar ortholog groups with genes of each species. (WW) Similar ortholog groups with genes of each species. (XX) Similar ortholog groups with genes of each species. (YY) Similar ortholog groups with genes of each species. (ZZ) Similar ortholog groups with genes of each species. (AAAA) Similar ortholog groups with genes of each species. (BBBB) Similar ortholog groups with genes of each species. (CCCC) Similar ortholog groups with genes of each species. (DDDD) Similar ortholog groups with genes of each species. (EEEE) Similar ortholog groups with genes of each species. (FFFF) Similar ortholog groups with genes of each species. (GGGG) Similar ortholog groups with genes of each species. (HHHH) Similar ortholog groups with genes of each species. (IIII) Similar ortholog groups with genes of each species. (JJJJ) Similar ortholog groups with genes of each species. (KKKK) Similar ortholog groups with genes of each species. (LLLL) Similar ortholog groups with genes of each species. (MMMM) Similar ortholog groups with genes of each species. (NNNN) Similar ortholog groups with genes of each species. (OOOO) Similar ortholog groups with genes of each species. (PPPP) Similar ortholog groups with genes of each species. (QQQQ) Similar ortholog groups with genes of each species. (RRRR) Similar ortholog groups with genes of each species. (SSSS) Similar ortholog groups with genes of each species. (TTTT) Similar ortholog groups with genes of each species. (UUUU) Similar ortholog groups with genes of each species. (VVVV) Similar ortholog groups with genes of each species. (WWWW) Similar ortholog groups with genes of each species. (XXXX) Similar ortholog groups with genes of each species. (YYYY) Similar ortholog groups with genes of each species. (ZZZZ) Similar ortholog groups with genes of each species.

Supplementary Figure 2. Normalization of ortholog-group based expression table. (A) (B). Normalizations of expression data. Expression data are aligned from early to late developmental stages in each species. These figures show that normalization of the expression data is necessary to increase its overall resolution for comparison between species. (A) (B) (C) (D) (E) (F) (G) (H) (I) (J) (K) (L) (M) (N) (O) (P) (Q) (R) (S) (T) (U) (V) (W) (X) (Y) (Z) (AA) (BB) (CC) (DD) (EE) (FF) (GG) (HH) (II) (JJ) (KK) (LL) (MM) (NN) (OO) (PP) (QQ) (RR) (SS) (TT) (UU) (VV) (WW) (XX) (YY) (ZZ) (AAAA) (BBBB) (CCCC) (DDDD) (EEEE) (FFFF) (GGGG) (HHHH) (IIII) (JJJJ) (KKKK) (LLLL) (MMMM) (NNNN) (OOOO) (PPPP) (QQQQ) (RRRR) (SSSS) (TTTT) (UUUU) (VVVV) (WWWW) (XXXX) (YYYY) (ZZZZ).
Supplementary Figure 4. Derivation trees considering specific genes. (A) Expression levels of all genes were considered. (B) Genes with expression output at TPM1 were considered. However, both mass variation columns (as indicated with black polygons) in A. Areni became the ogopogos of the other vertebrate species. Notably, among the 19,624 detected specific-specific genes in A. Areni, 9,879 genes were locally expressed from TPM1.

Supplementary Figure 5. Tree considering expression of only 1:1 orthologues. Moreover, all genes of the same species (colored by the same color) fall into clusters together in sub-sections (1–4) and sub-branch (10). Species abbreviations are shown in squares.

Supplementary Figure 6. Trees inferred from other distance methods. Embryos of the same species are denoted by the same color in each of the trees.

Supplementary Figure 7. Least derived stages identified as being within top 2% (top), 5% (middle), and 10% (bottom) lowest derivation indices in each species. The least derived ontogenetical process (top) span multiple embryonic stages, which could be reflected in several embryos having similarly low derivation indices. In this case, biological replicates included (BRI) were not utilized to get statistical support. For each BRI tree, the range of derivation indices of embryos of each species was first calculated, and stages within the lowest 5%–10% range were marked. The percentage of the lowest 5%–10% derivation stages is shown in the cluster for each species (Fisher’s exact test). The results showed consistent tendency with that shown in Figure 4, with similar embryonic, organogenesis stages in vertebrates and gastropoda in echinoderms (except further star) being the least derived.

Supplementary Figure 8. DCOs (derivedness of core orthology groups) showing negative associations across all six vertebrate species (total: 385) with predicted development-related fractions (total: 20). Points highlighted in purple. Y-axis: mean correlation value across the six vertebrate species. Each 0.1 range is further divided into fine bins, and the predicted names of orthology groups within each bin are shown inside.
example, HoxA2 was missed in the genome assembly of P. elegans (turquoise), HoxA7 was not found in the genome assembly of D. rerio (red) while HoxB5, B7 (peach). HoxD3 was missed in P. sinensis (green), X. laevis (blue). Hox genes were split into two orthologous groups: one grouped with the fish orthologs (HoxA, B) and the other one with the other vertebrate orthologs (HoxC, D) (Table 1). Additionally, we calculated Spearman’s correlation coefficient *P. sinensis* - *D. rerio*.

**Supplementary Figure 9.** Negative DCMs across vertebrate species with predicted function involved in signal transduction of (A) Not, (B) Ihh, (C) Bmp, (D) Nodal, and (E) bmp. Location of points appear to differ due to the plotting function when plotting the horizontal location (representing the mean correlation value) remains the same for the same point in all plots.

**Supplementary Material**

Gene Ontology enrichment analysis was performed using GOTools (Kliepstein et al., 2014) with GO terms produced by PANTHER (Tong et al., 2013).
genes. Drosophila each species. (A) cluster with the echinoderm species, which violates criterion 2 (consistent with known phylogeny) as the frog, (B) Tree based on expression data with exome sizes when UTRs are removed are controlled (blue and green) were analyzed and showed similar tendencies. Distances calculated from the 10M depth-controlled data tended to be larger than those calculated from the original expression data (red). In (B), only the distribution between Xenopus laevis (Xlae) and Mus musculus (Mm) is shown. (C) Distribution of pairwise distances between orthologous genes within each species (i.e., chicken, Mm, mouse, A) sea cucumber). In (D), Two random replicates of 10M depth-controlled (blue and green) were compared. The standard deviation of expression among biological replicates of the two images was determined by a smoothing algorithm performed on the original table. (B) Smoothness analysis of the two images. Three of the six descriptions showed that the original table was significantly smoother than the 10M depth-controlled expression tables (two-sample t-test) (blue: original table, red: 10M depth-controlled table; asterisk indicates p value < 0.05, others are not significant). (C) Visualizatio...
Supplementary Figure 16. Transcriptomic distinctness index could potentially be influenced by RNA-seq read depth. (A) To study the effect of read depth, a two-sampling of read-depth in the mouse (also dataset from 38M through 23M, 20M, 15M, 10M, 5M and 0M) was performed (retaining the depth of the dataset of all other species unchanged) to compare with Figure 1A. Reads were randomly divided from both read modes (the total number of all-heterologous reads was around 38M for most of the mouse datasets). The result showed that distinctness index tends to decrease when read depth decreases, and those of phylogenetically related species, such as clones (G) and teleost (T), were also affected. (B) Similar effect was observed when down-sampling was done in the tissue (G) dataset from 150M through 50M, 30M, and 10M. However, even when down-sampling was done to 3M from 38M, distinctness index remained high (the orange box). (Mann-Whitney U test, p < 0.01). These results are consistent with those shown in Figure 1A and Supplementary Figure 14. (C) Pairwise distances (Spearman’s correlation coefficient) among mouse samples only slightly differed when down-sampling was performed (Kruskal-Wallis test, p < 0.01).

Supplementary Figure 17. Pre-metamorphosis and the penta-metamorphic phase display similar sets of genes but at different expression levels in z. spartea. (A) The majority of orthologs (11,080) are up-regulated in the pre-metamorphic phase, while almost none are up-regulated in the penta-metamorphic phase. (B) Developmental genes specifically expressed in either phase (g1 and g6, respectively). (C) Pearson’s analysis of expression levels from early to late developmental stages of ortholog groups supports that most ortholog groups are expressed at different levels in pre-metamorphic and penta-metamorphic phases. Each cluster represents ortholog groups that tend to show similar expression dynamics from early to late development. For instance, ortholog groups in cluster 1 are mostly highly expressed in both developmental phases while those in cluster 3 tend to be expressed more highly in the penta-metamorphic phase (y-axis); early-to-late development, with the appearance of penta-metamorphic stages marked by the blue triangle (Y2/F). y-axis: expression level log2(TPM+1)). Tail line: median expression level of ortholog groups of the cluster. These results tend to suggest that the differences in transcriptomic distinctness indices of the pre-metamorphic and the penta-metamorphic developmental phases could be partly attributed to ortholog groups expressing at different levels rather than displaying different sets of genes during the two phases. K-means and PCA analyses were performed using scikit-learn in Python.

Supplementary Figure 18. Correlation plots between distinctness index of each species and ortholog group matrix (other columns in Supplementary Figure 1). (A) The median of the distinctness index of all developmental stages of each species was plotted to represent the species. (B) Number of ortholog groups (Supplementary Figure 1A) shows a moderately strong correlation with distinctness index. (C) When species-specific genes are considered to influence distinctness index (Supplementary Figure 1B), the number of detected species-specific genes (C) are expression level cutoff (D). expression cutoff at TPM(1) is strongly correlated with the measured distinctness index (R = 0.8; for all panels).
Supplementary Figure 28. DCO (Derivedness correlation orthologs) analysis using the tree covering species-specific genes (Supplementary Figure 4). The proportion of species sharing a multitude of orthologs (>90%) of each developmental stage in echinoderm species did not change dramatically in the tree covering species-specific genes. However, larger differences were observed in (B) vertebrates and (C) chordates. This could be due to the differences in developmental stages of those and zebrafish between the two trees. Extracted orthologs that could be extracted from both trees in vertebrates and chordates are highlighted (indicated by negative correlation coefficients).

**Tables**

**Supplementary Table 2.** Developmental stages included in the study: sea cucumber (Apostichopus japonicus).

| Species abbreviation | General name | Developmental stages | Stage abbreviation | Source |
|----------------------|--------------|----------------------|--------------------|--------|
| *Apostichopus* | | Early planula | Planula | Li et al., 2020 |
| | | Early gastrula | Early gastrula | Muller, 1841 |
| | | Late gastrula | Late gastrula | Muller, 1841 |
| | | Early cystidean larva | Early cystidean larva | Muller, 1841 |
| | | Late cystidean larva | Late cystidean larva | Muller, 1841 |
| | | Early pentacrinoid larva | Early pentacrinoid larva | Muller, 1841 |
| | | Late pentacrinoid larva | Late pentacrinoid larva | Muller, 1841 |
| | | Adult | Adult | Muller, 1841 |

**Supplementary Table 3.** Developmental stages included in the study: sea urchin (Echinus esculentus).

| Species abbreviation | General name | Developmental stages | Stage abbreviation | Source |
|----------------------|--------------|----------------------|--------------------|--------|
| *Echinus esculentus* | | Early blastula | Blastula | Muller, 1841 |
| | | Mid blastula | Mid blastula | Muller, 1841 |
| | | Late blastula | Late blastula | Muller, 1841 |
| | | Early arcuria larva | Early arcuria larva | Muller, 1841 |
| | | Late arcuria larva | Late arcuria larva | Muller, 1841 |
| | | Early pentacrinoid larva | Early pentacrinoid larva | Muller, 1841 |
| | | Late pentacrinoid larva | Late pentacrinoid larva | Muller, 1841 |
| | | Adult | Adult | Muller, 1841 |

**Supplementary Table 4.** Numbers of species-specific genes (SSGs) in different developmental stages of Echinodermata (Apostichopus japonicus), Vertebrata (four species), and Chordata (one species). The species abbreviations for sea cucumber, or "Apostichopus japonicus," are taken from its previous scientific name, "Apostichopus japonicus" (Muller, 1841).

| Species abbreviation | General name | Developmental stages | Stage abbreviation | Source |
|----------------------|--------------|----------------------|--------------------|--------|
| *Apostichopus* | | Early planula | Planula | Li et al., 2020 |
| | | Early gastrula | Early gastrula | Muller, 1841 |
| | | Late gastrula | Late gastrula | Muller, 1841 |
| | | Early cystidean larva | Early cystidean larva | Muller, 1841 |
| | | Late cystidean larva | Late cystidean larva | Muller, 1841 |
| | | Early pentacrinoid larva | Early pentacrinoid larva | Muller, 1841 |
| | | Late pentacrinoid larva | Late pentacrinoid larva | Muller, 1841 |
| | | Adult | Adult | Muller, 1841 |

**Supplementary Table 5.** Numbers of best hits from multi-end samples, (A) Number of all samples; (B) Number of reads that could be mapped to the respective genome, including multi-end reads (selected by "samtools view -F 4") and paired-end reads (selected by "samtools view -f 207"); (C) Number of best-hit reads (selected by "samtools view -f 207"). Error bars represent standard deviations of raw depths for samples of each species.

| Source | General name | Developmental stages | Stage abbreviation | Source |
|--------|--------------|----------------------|--------------------|--------|
| *Apostichopus* | | Early planula | Planula | Li et al., 2020 |
| | | Early gastrula | Early gastrula | Muller, 1841 |
| | | Late gastrula | Late gastrula | Muller, 1841 |
| | | Early cystidean larva | Early cystidean larva | Muller, 1841 |
| | | Late cystidean larva | Late cystidean larva | Muller, 1841 |
| | | Early pentacrinoid larva | Early pentacrinoid larva | Muller, 1841 |
| | | Late pentacrinoid larva | Late pentacrinoid larva | Muller, 1841 |
| | | Adult | Adult | Muller, 1841 |
### Supplementary Table 4. Developmental stages included in the study: purple sea urchin (Strongylocentrotus purpuratus)

| Species abbreviation | General name | Developmental stages | Stage abbreviation | Source |
|----------------------|--------------|----------------------|--------------------|--------|
| Purple sea           | Purple sea   | Embryonic egg (6 hpf) | 6hpf               | 1 et al., 2012, 2014 |
|                      |              | Blastula             | 12-hpf             |        |
|                      |              | Mid-gastrula         | 24-hpf             |        |
|                      |              | Late-gastrula        | 36-hpf             |        |
|                      |              | Early neurula        | 48-hpf             |        |
|                      |              | Mid-neurula          | 60-hpf             |        |
|                      |              | Late-neurula         | 72-hpf             |        |
|                      |              | Early larva          | 84-hpf             |        |
|                      |              | Mid-larva            | 96-hpf             |        |
|                      |              | Late larva           | 108-hpf            |        |
|                      |              | Early juvenile        | 120-hpf            |        |
|                      |              | Mid juvenile          | 132-hpf            |        |
|                      |              | Late juvenile         | 144-hpf            |        |
|                      |              | Early adult           | 156-hpf            |        |
|                      |              | Mid adult             | 168-hpf            |        |
|                      |              | Late adult            | 180-hpf            |        |

### Supplementary Table 5. Developmental stages included in the study: amphioxus (Branchiostoma byelense)

Staging was performed as described in (Holland and Kaji, 1996, 1996, 1996, Ya and Holland, 2008).

| Species abbreviation | General name | Developmental stages | Stage abbreviation | Source |
|----------------------|--------------|----------------------|--------------------|--------|
| Amphioxus            | Amphioxus    | Embryonic egg        | 1 day              |        |
|                      |              | Blastula             | 2 day              |        |
|                      |              | Mid-gastrula         | 3 day              |        |
|                      |              | Late-gastrula        | 4 day              |        |
|                      |              | Early neurula        | 5 day              |        |
|                      |              | Mid-neurula          | 6 day              |        |
|                      |              | Late neurula         | 7 day              |        |
|                      |              | Early larva          | 8 day              |        |
|                      |              | Mid larva            | 9 day              |        |
|                      |              | Late larva           | 10 day             |        |
|                      |              | Early juvenile        | 11 day             |        |
|                      |              | Mid juvenile          | 12 day             |        |
|                      |              | Late juvenile         | 13 day             |        |
|                      |              | Early adult           | 14 day             |        |
|                      |              | Mid adult             | 15 day             |        |
|                      |              | Late adult            | 16 day             |        |

### Supplementary Table 6. Developmental stages included in the study: Japanese medaka (Oryzias latipes)

Staging was performed as described in (Ichikawa et al., 2017).

| Species abbreviation | General name | Developmental stages | Stage abbreviation | Source |
|----------------------|--------------|----------------------|--------------------|--------|
| Medaka               | Medaka       | Embryonic egg        | 1 day              |        |
|                      |              | Blastula             | 2 day              |        |
|                      |              | Mid-gastrula         | 3 day              |        |
|                      |              | Late-gastrula        | 4 day              |        |
|                      |              | Early neurula        | 5 day              |        |
|                      |              | Mid-neurula          | 6 day              |        |
|                      |              | Late neurula         | 7 day              |        |
|                      |              | Early larva          | 8 day              |        |
|                      |              | Mid larva            | 9 day              |        |
|                      |              | Late larva           | 10 day             |        |
|                      |              | Early juvenile        | 11 day             |        |
|                      |              | Mid juvenile          | 12 day             |        |
|                      |              | Late juvenile         | 13 day             |        |
|                      |              | Early adult           | 14 day             |        |
|                      |              | Mid adult             | 15 day             |        |
|                      |              | Late adult            | 16 day             |        |

### Supplementary Table 7. Developmental stages included in the study: zebrafish (Danio rerio)

Staging was performed as described in (Kim et al., 1995).

| Species abbreviation | General name | Developmental stages | Stage abbreviation | Source |
|----------------------|--------------|----------------------|--------------------|--------|
| Zebrafish            | Zebrafish    | 0 cells              | 0.5 d               |        |
|                      |              | 2 cells              | 1 d                 |        |
|                      |              | 6 cells              | 2 d                 |        |
|                      |              | 12 cells             | 3 d                 |        |
|                      |              | 30 cells             | 4 d                 |        |
|                      |              | 50 cells             | 5 d                 |        |
|                      |              | 75 cells             | 6 d                 |        |
|                      |              | 100 cells            | 7 d                 |        |
|                      |              | 125 cells            | 8 d                 |        |
|                      |              | 150 cells            | 9 d                 |        |
|                      |              | 180 cells            | 10 d                |        |
|                      |              | 200 cells            | 11 d                |        |
|                      |              | 250 cells            | 12 d                |        |
|                      |              | 300 cells            | 13 d                |        |
|                      |              | 350 cells            | 14 d                |        |
|                      |              | 400 cells            | 15 d                |        |
|                      |              | 450 cells            | 16 d                |        |
|                      |              | 500 cells            | 17 d                |        |

### Supplementary Table 8. Developmental stages included in the study: clover frog (Bombina variegata)

Staging was performed as described in (Kuo and Lin, 1994).

| Species abbreviation | General name | Developmental stages | Stage abbreviation | Source |
|----------------------|--------------|----------------------|--------------------|--------|
| clover frog          | clover frog  | Embryonic egg        | 1 day              |        |
|                      |              | Blastula             | 2 day              |        |
|                      |              | Mid-gastrula         | 3 day              |        |
|                      |              | Late-gastrula        | 4 day              |        |
|                      |              | Early neurula        | 5 day              |        |
|                      |              | Mid-neurula          | 6 day              |        |
|                      |              | Late neurula         | 7 day              |        |
|                      |              | Early larva          | 8 day              |        |
|                      |              | Mid larva            | 9 day              |        |
|                      |              | Late larva           | 10 day             |        |
|                      |              | Early juvenile        | 11 day             |        |
|                      |              | Mid juvenile          | 12 day             |        |
|                      |              | Late juvenile         | 13 day             |        |
|                      |              | Early adult           | 14 day             |        |
|                      |              | Mid adult             | 15 day             |        |
|                      |              | Late adult            | 16 day             |        |

### Supplementary Table 9. Developmental stages included in the study: African clawed frog (Xenopus laevis)

Staging was performed as described in (Nieuwkoop and Faber, 1994).

| Species abbreviation | General name | Developmental stages | Stage abbreviation | Source |
|----------------------|--------------|----------------------|--------------------|--------|
| African clawed frog  | African clawed frog | Embryonic egg | 1 day |        |
|                      |              | Blastula             | 2 day              |        |
|                      |              | Mid-gastrula         | 3 day              |        |
|                      |              | Late-gastrula        | 4 day              |        |
|                      |              | Early neurula        | 5 day              |        |
|                      |              | Mid-neurula          | 6 day              |        |
|                      |              | Late neurula         | 7 day              |        |
|                      |              | Early larva          | 8 day              |        |
|                      |              | Mid larva            | 9 day              |        |
|                      |              | Late larva           | 10 day             |        |
|                      |              | Early juvenile        | 11 day             |        |
|                      |              | Mid juvenile          | 12 day             |        |
|                      |              | Late juvenile         | 13 day             |        |
|                      |              | Early adult           | 14 day             |        |
|                      |              | Mid adult             | 15 day             |        |
|                      |              | Late adult            | 16 day             |        |
| Species abbreviation | General name | Developmental stages | Stage abbreviation | Source |
|----------------------|--------------|----------------------|--------------------|--------|
| Oyster               | Crassostrea gigas | Spat, Pediveliger, Late umbo larva, Umbo larva, Early umbo larva, D, D5, D6, D7, ED1, ED2, Early gastrula, Free swimming, Rotary movement, Blastula, Morula, 2 cells, Eggs, TK27, TK23, TK17, TK13, TK8, TK4, TK2, TK, Long tubule buds,输卵管, JK, JKL, Cameral cell, Cameral (pigmentation), JK, JKL, Green-bluish body color, TK25 | | |
| Softshell turtle     | Pelodiscus sinensis | 2 cells, Eggs, TK27, Brownish body color, TK23, Carapace pigmentation, Carapacial ridge, Long limb buds, 27 somites, 14 somites, 7 somites, 3, 13.75 d, 18.19 d, 15.73 d, 26 somites, 22 somites, 18 somites, 13 somites, 4 somites, 1, 56 somites, 40 somites, 28 somites, 20 somites, 13 somites, 8 somites, 4 somites, 2, 13.75 d, 18.19 d, 15.73 d, 26 somites, 22 somites, 18 somites, 13 somites, 8 somites, 4 somites, 2 | | |

**Supplementary Table 13.** Developmental stages included in the study: chicken (Gallus gallus), Oyster (Crassostrea gigas).

Staging was performed as described in (Tokita and Kuratani, 2001).

**Supplementary Table 14.** Information of RNA-seq samples utilized for this study:

| Species abbreviation | General name | Accession number | Library preparation methods | Single-end (SE) paired-end (PE) | Sequencing platform |
|----------------------|--------------|------------------|-----------------------------|---------------------------------|-------------------|
| Chicken              | Gallus gallus | PRJNA553681      | TruSeq PE, 100 bp           | PE, 100 bp                      | Illumina Hiseq 2000 |
| Sea cucumber         | Cucumis sativus | PRJNA553681      | TruSeq PE, 100 bp           | PE, 100 bp                      | Illumina Hiseq 2000 |
| Purple sea urchin    | Paracentrotus lividus | PRJNA81157 | TruSeq PE, 78 bp | PE, 78 bp | Illumina Genome Analyze Bx |
| Amphiprion             | PRJNA553681 | TruSeq PE, 100 bp | PE, 100 bp | Illumina Hiseq 2000 |
| Transcript            | PRJNA553681 | TruSeq PE, 100 bp | PE, 100 bp | Illumina Hiseq 2000 |
| Zebrafish             | PRJNA553681 | TruSeq PE, 100 bp | PE, 100 bp | Illumina Hiseq 2000 |
| Medaka                | Oryzias latipes | PRJNA553681 | TruSeq PE, 100 bp | PE, 100 bp | Illumina Genome Analyze Bx |
| Frog                   | PRJNA553681 | TruSeq PE, 100 bp | PE, 100 bp | Illumina Hiseq 2000 |
| Softshell turtle      | Pelodiscus sinensis | PRJNA553681 | TruSeq PE, 100 bp | PE, 100 bp | Illumina Hiseq 2000 |
| Chicken               | Gallus gallus | PRJNA553681 | TruSeq PE, 100 bp | PE, 100 bp | Illumina Hiseq 2000 |
| Softshell turtle      | Pelodiscus sinensis | PRJNA553681 | TruSeq PE, 100 bp | PE, 100 bp | Illumina Hiseq 2000 |

**Supplementary Table 15.** Genomes were utilized for RNA-seq mapping and ortholog group prediction:

| Species abbreviation | General name | Genome version | Source |
|----------------------|--------------|----------------|--------|
| Chicken              | Gallus gallus | GRCg38          | Ensembl |
| Sea cucumber         | Cucumis sativus | ASM275485v1     | NCBI   |
| Purple sea urchin    | Paracentrotus lividus | GCF_AB0022354    | NCBI   |
| Amphiprion           | PRJNA81157   | PRJNA553681     | Ensembl |
| Transcript           | PRJNA553681   | PRJNA553681     | Ensembl |
| Zebrafish            | PRJNA553681   | PRJNA553681     | Ensembl |
| Medaka               | Oryzias latipes | PRJNA553681     | Ensembl |
| Frog                 | PRJNA553681   | PRJNA553681     | Ensembl |
| Softshell turtle     | Pelodiscus sinensis | PRJNA553681     | Ensembl |
| Chicken              | Gallus gallus | PRJNA553681     | Ensembl |
| Softshell turtle     | Pelodiscus sinensis | PRJNA553681     | Ensembl |

**Supplementary Table 16.** Developmental stages included in the study: chicken (Gallus gallus), Oyster (Crassostrea gigas).

Staging was performed as described in (Hamburger and Hamilton, 1951).
**Supplementary Table 16.** Descriptions of smoothness algorithms (Gonzalez and Woods, 2007).

| Parameter | Formula | Range of values |
|-----------|---------|----------------|
| Homogeneity | $r = \frac{n}{\sum_{i=1}^{n} (x_i - \bar{x})^2}$ | $-1 < r < 1$ |
| Dissimilarity | $d = \frac{1}{n} \sum_{i=1}^{n} \left| x_i - x_j \right|$ | $0 < d < 1$ |
| Contrast | $c = \frac{1}{n} \sum_{i=1}^{n} \left( x_i - x_j \right)^2$ | $0 < c < 1$ |
| Uniformity (Energy) | $E = \frac{\sum_{i=1}^{n} x_i^2}{n}$ | $0 < E < 1$ |

**Supplementary Table 17.** Bioinformatics tools used in the study.

| Tool | Description |
|------|-------------|
| DNAseq | DNA sequencing software (Bolger et al., 2014) |
| BCBio | Bioinformatics tools used in the study (Haas et al., 2003) |
| PASA | Promoter analysis software (Haas et al., 2003) |
| FANTOM |-FANTOM-5 consists of 36,279 unique genes identified in mouse embryonic stem cells: genomic organization (Kuwano et al., 2009) |
| Skimia | Image processing software (Bolstad, 2019) |

**Supplementary Table 18.** Read depth was adjusted proportionally to the exon size of each specie. The total exon size was calculated using the genomic line reported in the Methods section. As regions annotated with exons were recalculated with UTRs, the total exon size could change after the UTRs were removed from the genomic annotation file (translated exons). The number of reads for each specie was calculated to maintain the same depth of exon size ratio for each specie. The total exon size could change after the UTRs were removed from the genomic annotation file (translated exons).

| Species | Exon size in the original annotation file (bp) | Depth-controlled number of reads with UTRs removed (bp) | Depth-controlled number of reads with UTRs removed (bp) |
|---------|---------------------------------------------|------------------------------------------------------|------------------------------------------------------|
| E. angustata | 6,758,976 | 6,758,976 | 6,758,976 |
| G. gramineus | 5,976 | 5,976 | 5,976 |
| M. musculus | 3,217 | 3,217 | 3,217 |

**Supplementary Table 19.** 195 DCs (differential-correlation under filtering groups) showing negative correlations with the E3 ubiquitin ligase 7.

**Supplementary Table 20.** 26 echinoderm DCs across eight echinoderm species.

**Supplementary Table 21.** 2,514 genes DCs across three echinoderm species.
