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Supplementary information

The genome of *Nautilus pompilius* illuminates eye evolution and biomineralization

In the format provided by the
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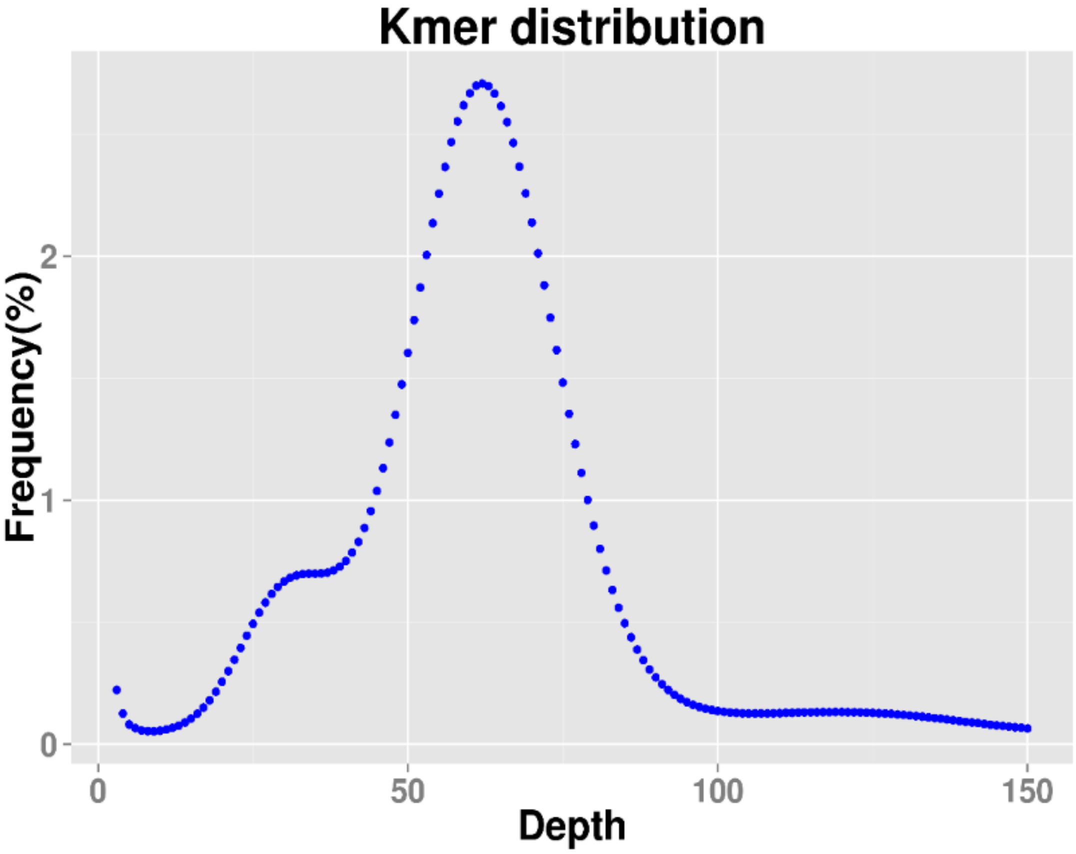
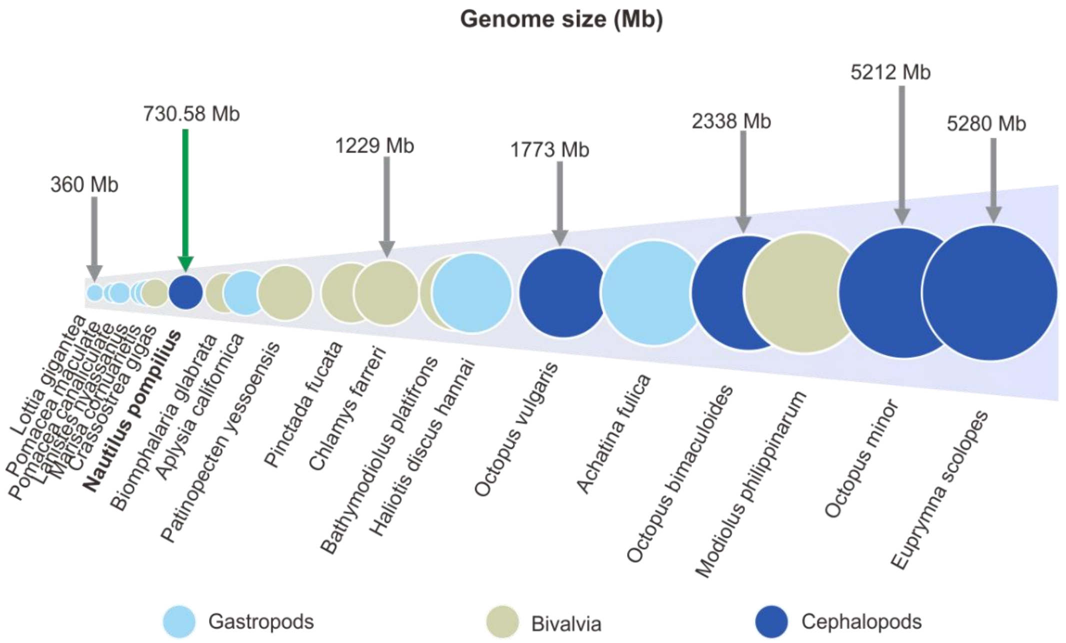
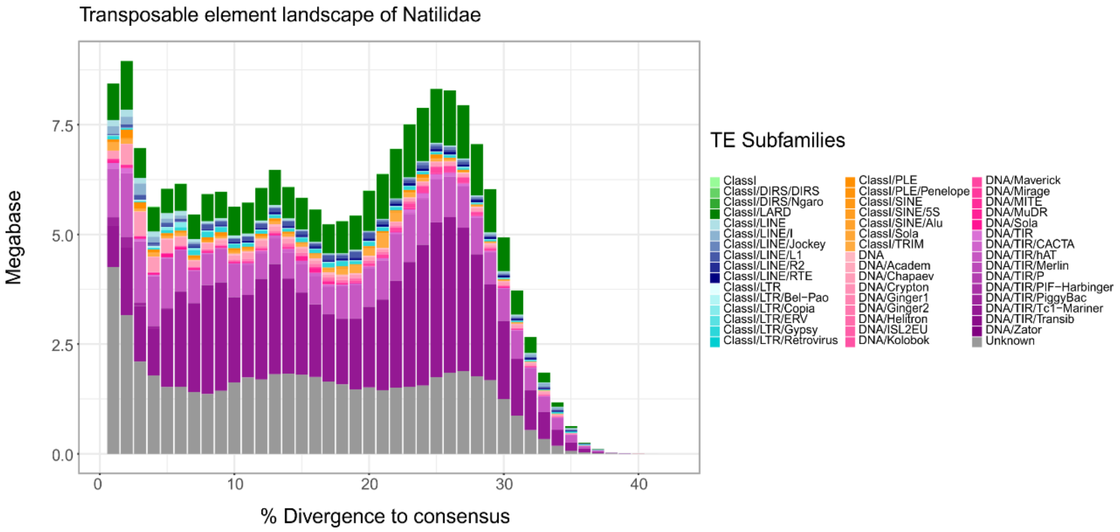
Supplementary Figures



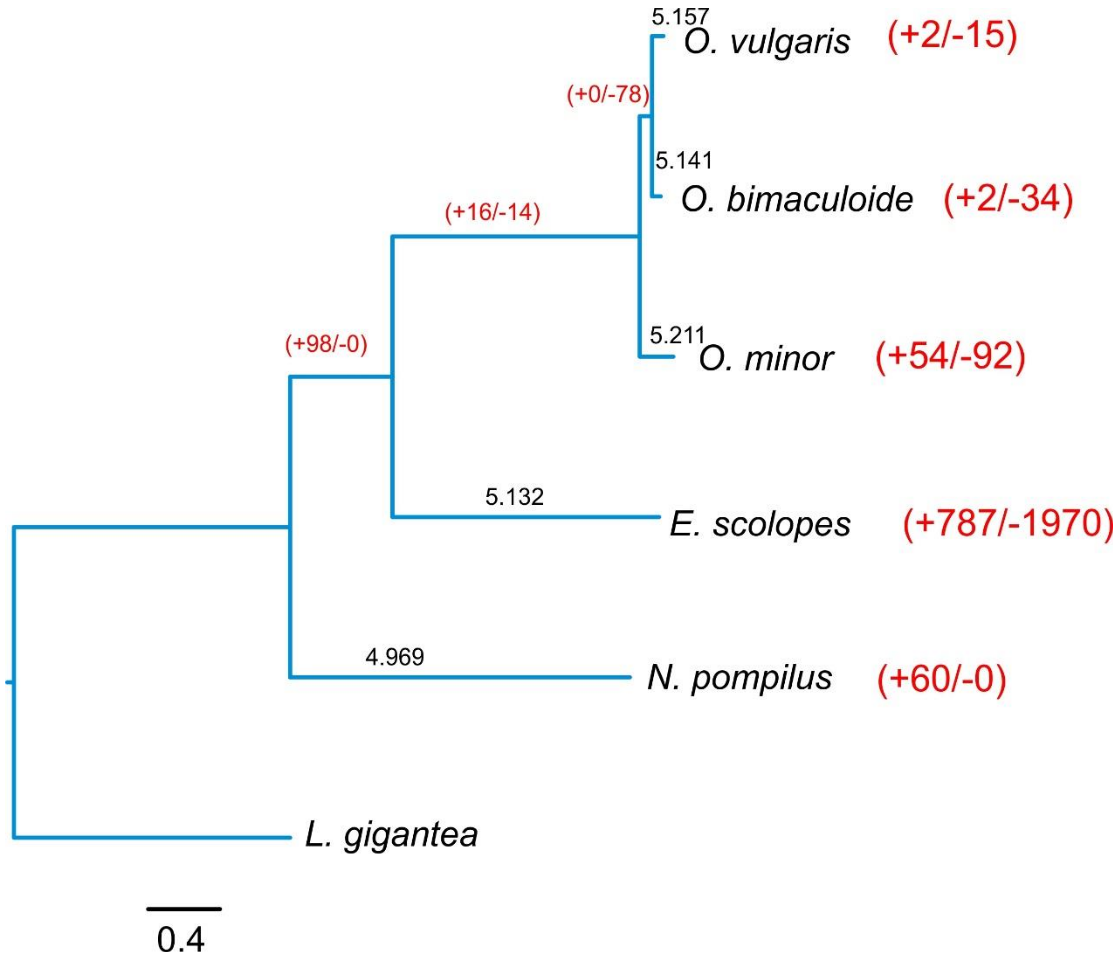
Supplementary Fig. 1 | k-mer distribution of the *N. pompilius* genome. Genome size estimation was performed by the k-mer analysis, and about 59.78 Gb corrected Illumina reads were selected to estimate the genome size. The genome size of *N. pompilius* thus estimated is 753.09 Mb.



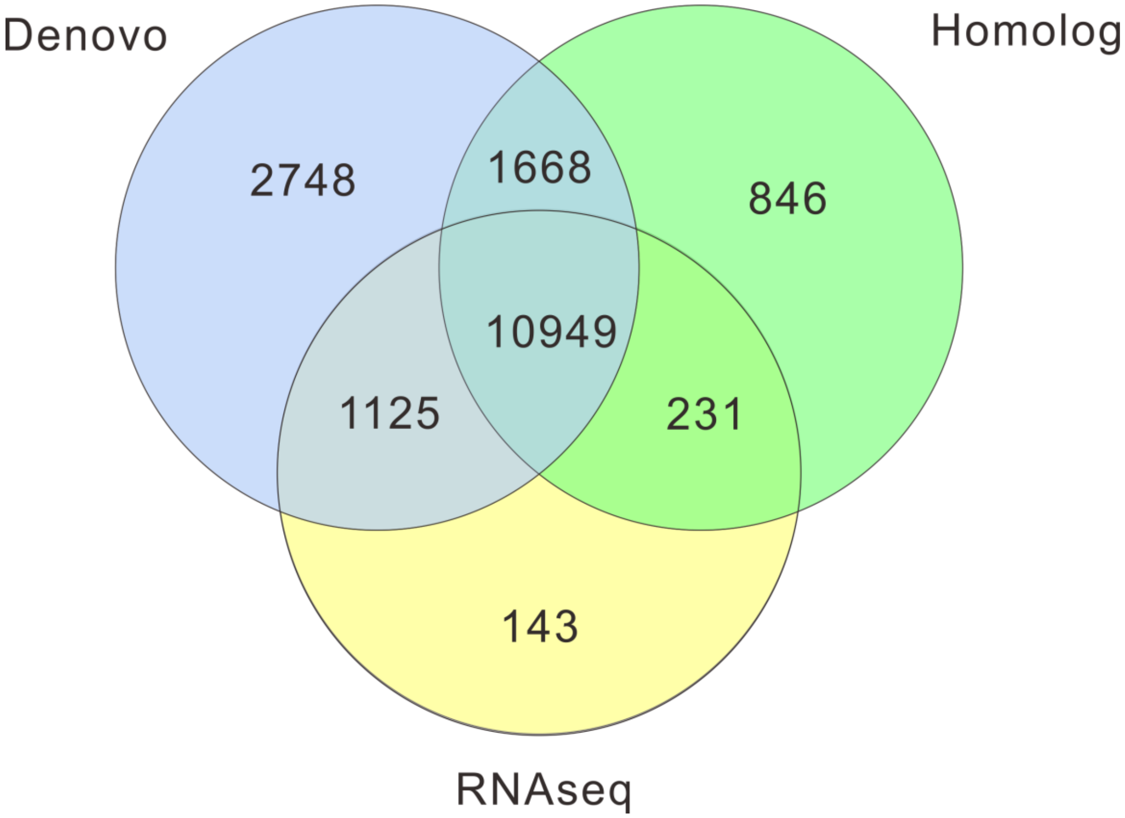
Supplementary Fig. 2 | Distribution of genome size in different molluscan lineages. Molluscan species are lined up according to their genome sizes, ranging from 360 Mb (*L. gigantea*) to 5.28 Gb (*E. scolopes*)[1-11]. Gastropods, bivalvia and cephalopods are indicated by different colors. Notably, the genome size of *N. pompilius* is the smallest among known cephalopods.



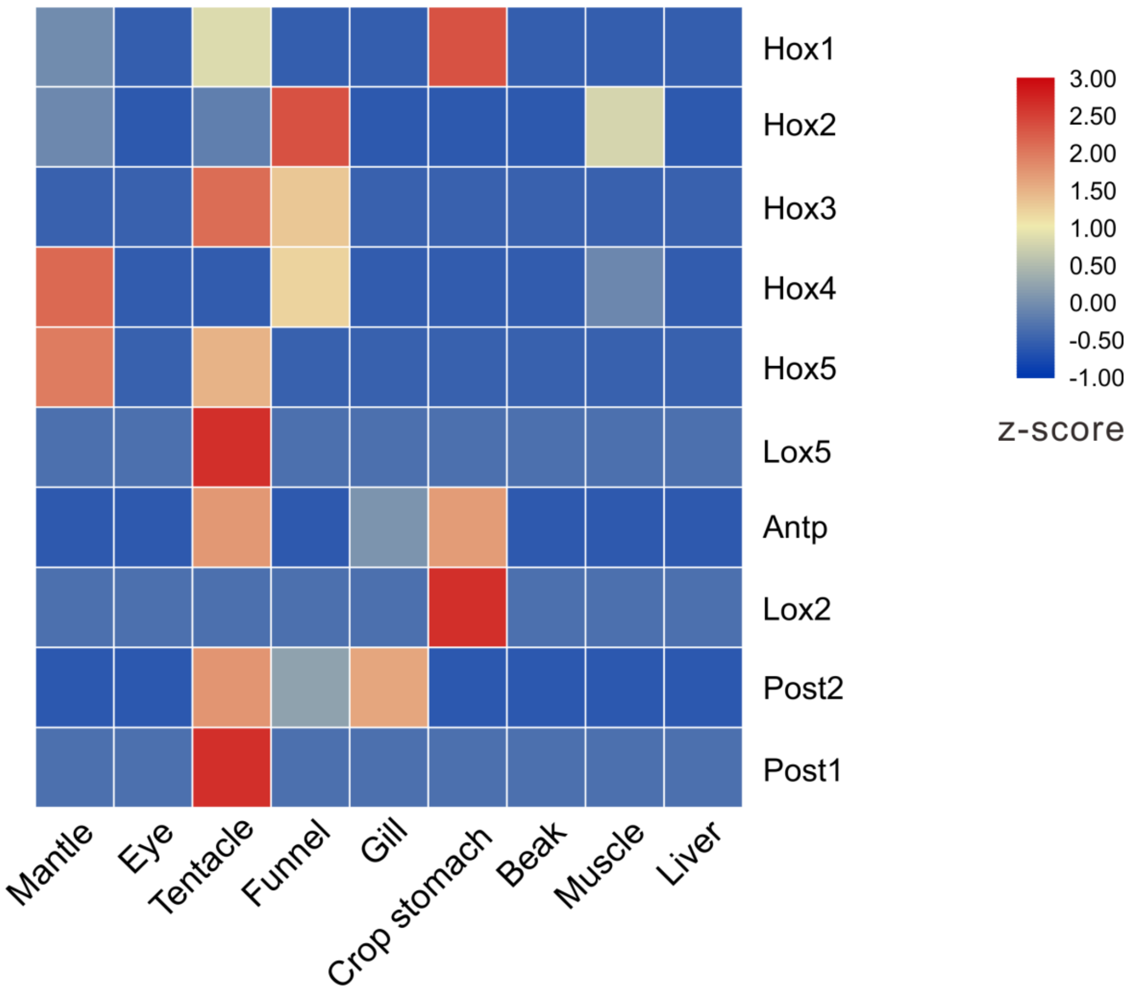
Supplementary Fig. 3 | History of transposable element (TE) accumulation in the *N. pompilius* genome. Temporal changes in transposable element (TE) accumulation in the *N. pompilius* genome based on a Kimura distance-based copy divergence analysis of TEs, with Kimura substitution level (CpG adjusted) illustrated on the *x*-axis, and percentage of the genome represented by each repeat type on the *y*-axis. Repeat type is indicated by different colored bars.



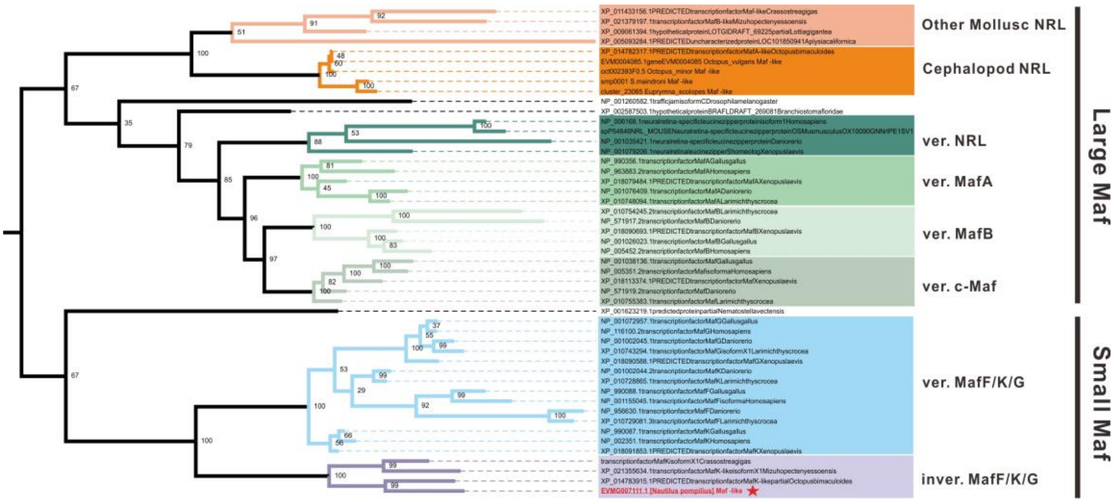
Supplementary Fig. 4 | Neutral tree and intron gain/loss event. Neutral tree of five cephalopods and *L. gigantea* is based on fourfold degenerate sites and pairwise distances to *L. gigantean* are shown for each species above their respective branches. Intron gain/loss events are shown in red besides taxon labels and at the ancestral nodes.



Supplementary Fig. 5 | Genome annotation in *N. pompilius.* Whole-genome annotation was performed by integrating multiple methods, which eventually generated 17,710 protein coding genes.



Supplementary Fig. 6 | Tissue distribution of Hox cluster in *N. pompilius.* Heatmap shows the expression profile of Hox cluster genes in different tissues. *x*-axis displays different tissues and *y*-axis shows the degree of expression of different Hox genes. Colored bars represent *Z*-score calculated from RPKM-values of a target gene in different tissues.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EVM0004085.1geneEVM0004085 Octopus_vulgaris Maf -like
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smp0001 S.maindroni Maf -like
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NP_001079206.1neuralretinaleucinezipperShomeologXenopuslaevis
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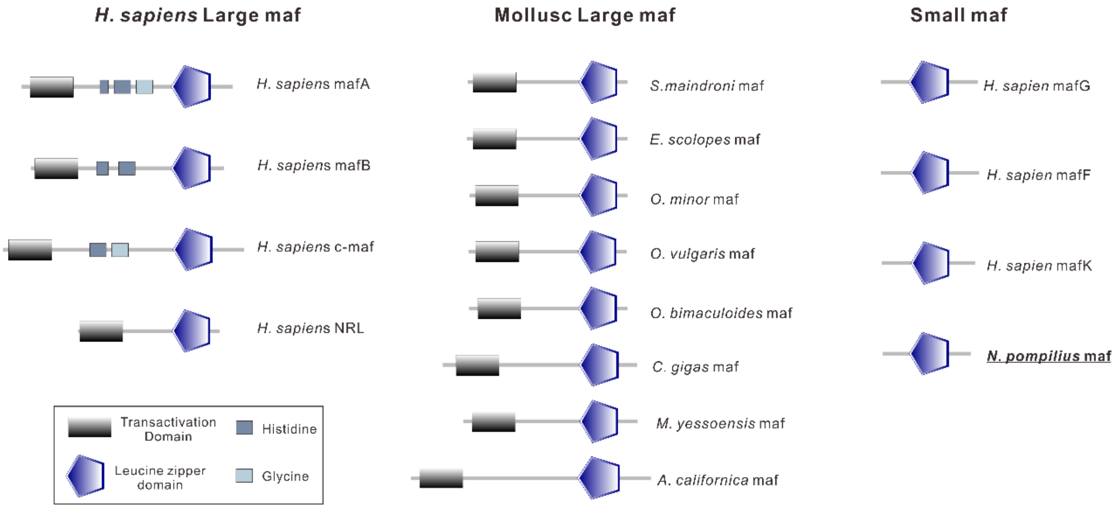
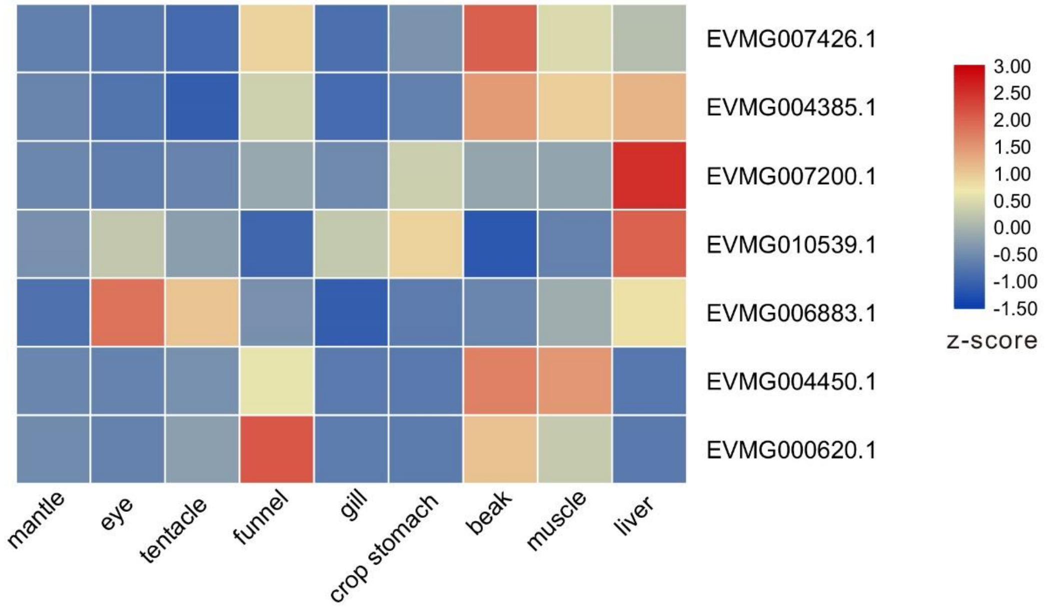
XP_014783915.1PREDICTEDtranscriptionfactorMafK-likepartialOctopusbimaculoides
EVMG007111.1 [Nautilus pompilius] Maf -like ★
Other Mollusc NRL
Cephalopod NRL
ver. NRL
ver. MafA
ver. MafB
ver. c-Maf
ver. MafF/K/G
inver. MafF/K/G
Large Maf
Small Maf

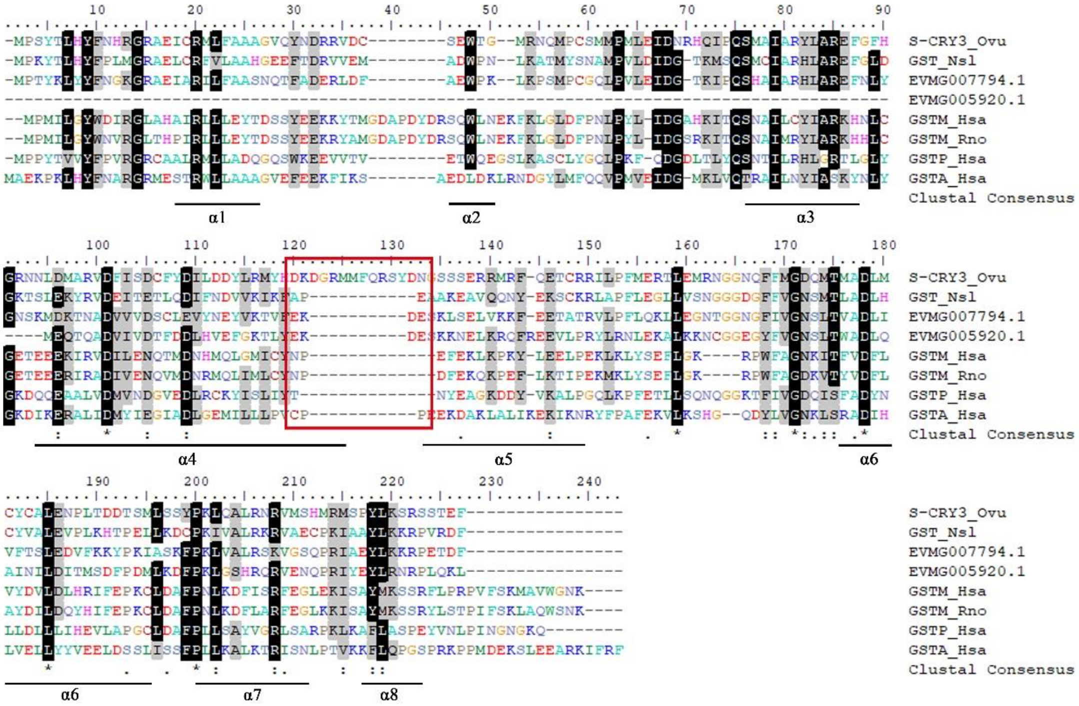
Supplementary Fig. 7 | Phylogenetic tree of the Maf/NRL superfamily. Multiple alignment was performed by using three methods including MAFFT 7.221[12], MUSCLE[13] and T-coffee[14]. The best alignment was applied to phylogenetic analysis beads on MUMSA scores[15]. Then, the phylogenetic tree was constructed by MrBayes 3.2.1[16] under a mixed model of amino acid substitution. Two independent runs with one cold and three heated chains were set for 15,000,000 generations. Starting trees were random and the trees were sampled every 1,000th generation. The ancestor of Maf/NRL was divided into the large and the small Maf clades. Each clade evolves independently and expands specifically in vertebrates. In the large Maf clades, the ancestor of Maf was continuously duplicated three times and generated four members (NRL, Maf A, Maf B and c-Maf) in vertebrates, but preserved one copy of NRL in mulloscan lineages. Similarly, the small Maf clade was divided into Maf F, Maf G and Maf K after vertebrate-specific duplications, while one copy of Maf K was preserved in mulloscan lineages. In contrast, the *N. pompilius* genome only encodes one Maf K gene but lost NRL. ver., vertebrate; inver., invertebrate.



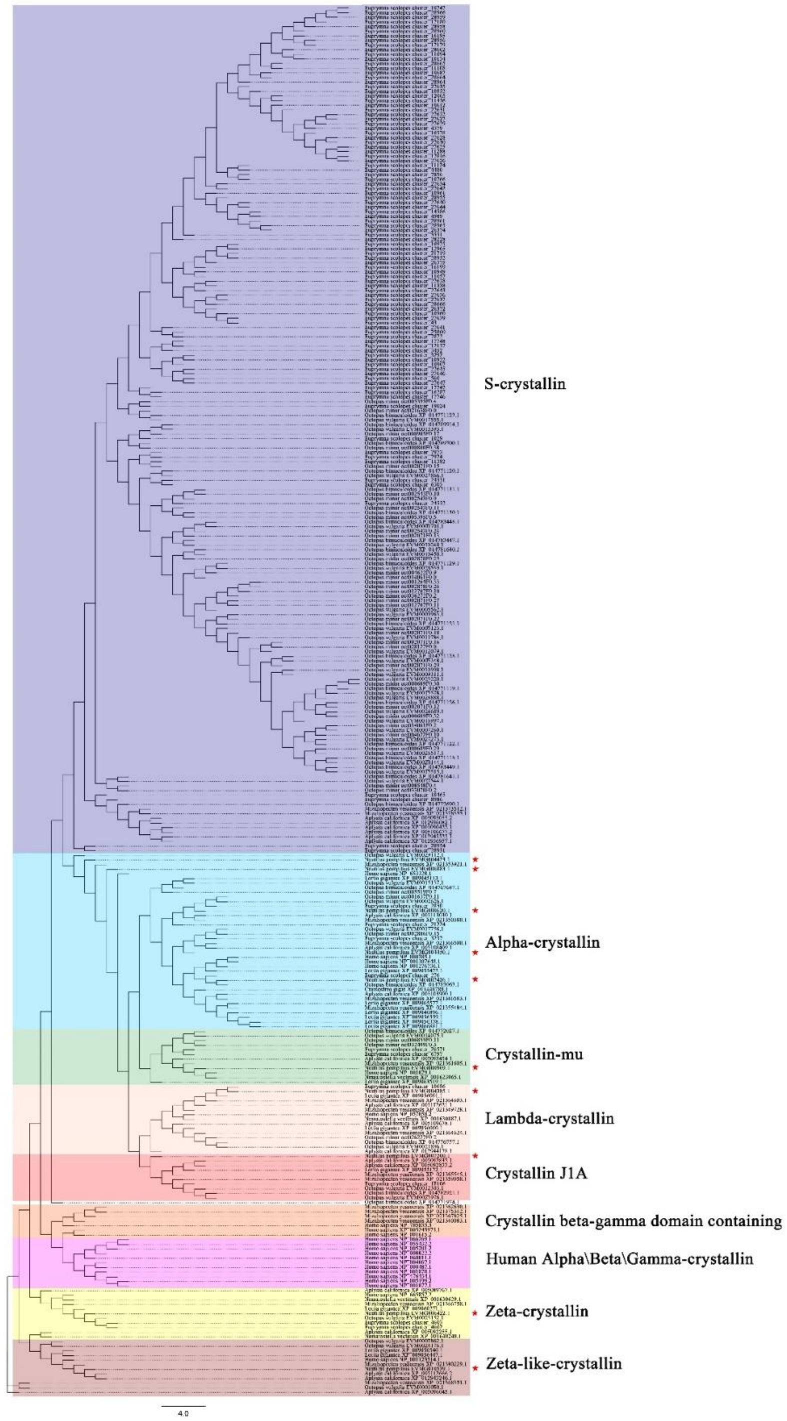
Supplementary Fig. 8 | Domain composition of Maf/NRL family members across different metazoans. MafA, MafB, c-Maf and NRL belong to large Maf family, and Maf K Maf G and Maf F belong to the small Maf family. The only extant homologue of Maf in the *N. pompilius* genome is the member of small Maf. Domain architecture was predicted and constructed by the software SMART[17].



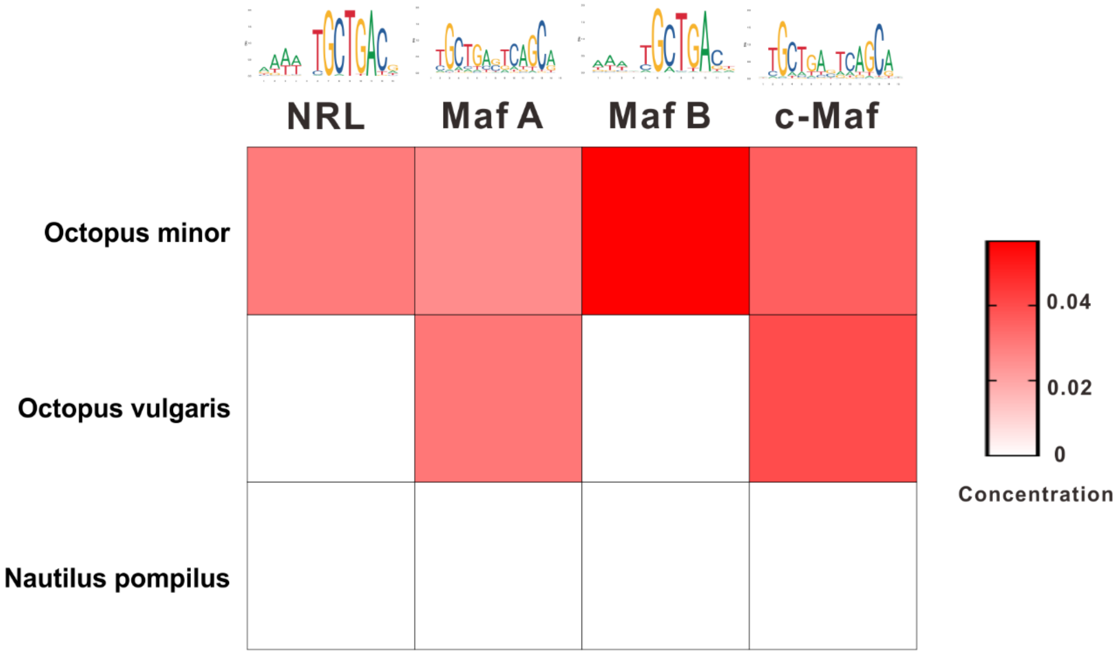
Supplementary Fig. 9 | Tissue distribution of crystallin-like genes in *N. pompilius.* Heatmap shows the expression profile of crystallin genes in different tissues, in which 3 of crystallin genes without expression are excluded. *x*-axis displays different tissues and *y*-axis shows the degree of expression of different crystallin genes. Colored bars represent *Z*-score calculated from RPKM-values of a target gene in different tissues.



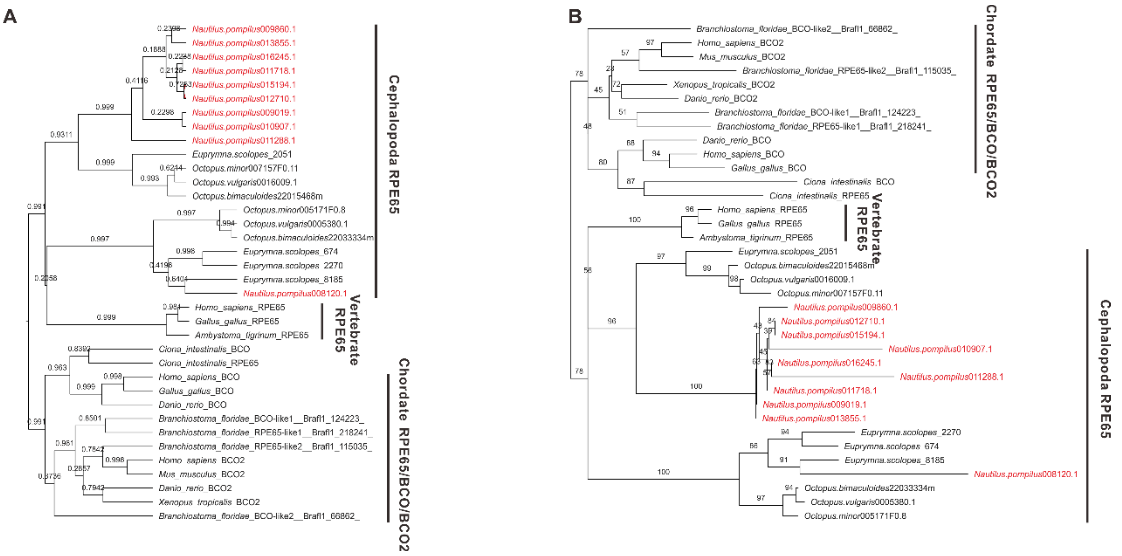
Supplementary Fig. 10 | Pairwise alignment of the potential S-crystallin of *N. pompilius* with cephalopods S-crystallin, Glutathione S-transferase (GST) and other classes of GST. The a-helices in S-crystallin are underlined and labeled. Compared with other classes of GST, the cephalopods S-crystallin has an 11-amino acid residues insertion between the conserved a4 and a5 helices (red box). Ovu, *Octopus vulgaris*; Nsl, *Nototodarus sloanii*; Has, *Homo sapiens*; Rno, *Rattus norvegicus.*



Supplementary Fig. 11 | Phylogenetic tree of the crystallin gene family. Phylogenetic tree of crystallin family were constructed by MrBayes methods as described above. Crystallin genes from *Homo sapiens*, *Euprymna scolopes*, *Octopus minor*, *Octopus bimaculoides*, *Octopus vulgaris*, *Nautilus pompilius*, *Aplysia californica*, *Lottia gigantea*, *Mizuhopecten yessoensis*, *Crassostrea gigas* and *Nematostella vectensis* are used. Different types of crystallin are labeled with separate colors. *N. pompilus* genome only contains a total of 10 crystallin genes (by red pentacle) and lacking S-crystallin which constitutes the major lens protein in cephalopods, featuring the least number of crystallins in metazoans.



Supplementary Fig. 12 | Enrichment analysis on NRL/MAF binding motifs on the promoter of the cephalopod crystallin gene family. 2,000 bp of 5'-flanking regions of crystallin genes were extracted from the genomes of *O. minor, O. vulgaris* and *N. pompilus*. NRL, Maf A, Maf B and c-Maf binding motif matrices were downloaded from a JASPAR database. Enrichment analysis for NRL/MAF bingding motifs in the crystallin promoter regions were analyzed by CentriMo[18]. Search parameters are set as follows: (1) 0-order background model generated from supplied sequences; (2) motif sites on either strand is considered; (3) motif sites only are considered, if they have a match score ≥ 5; and (4) regions are only reported, if they have a *E*-value ≤ 1.


A
0.2398
Nautilus.pompilus009860.1
Nautilus.pompilus013855.1
0.1888
0.2288
Nautilus.pompilus016245.1
0.2128
Nautilus.pompilus011718.1
0.4116
0.7253
Nautilus.pompilus015194.1
Nautilus.pompilus012710.1
0.999
0.2298
Nautilus.pompilus009019.1
Nautilus.pompilus010907.1
0.9311
Nautilus.pompilus011288.1
Euprymna.scolopes_2051
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0.6244
Octopus.minor007157F0.11
0.993
Octopus.vulgaris0016009.1
Octopus.bimaculoides22015468m
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0.997
Octopus.minor005171F0.8
0.994
Octopus.vulgaris0005380.1
0.997
Octopus.bimaculoides22033334m
0.998
Euprymna.scolopes_674
0.4196
Euprymna.scolopes_2270
0.2358
0.6404
Euprymna.scolopes_8185
Nautilus.pompilus008120.1
Cephalopoda RPE65
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Homo_sapiens_RPE65
0.999
Gallus_gallus_RPE65
Ambystoma_tigrinum_RPE65
Vertebrate RPE65
0.8392
Ciona_intestinalis_BCO
0.963
Ciona_intestinalis_RPE65
0.998
Homo_sapiens_BCO
0.999
Gallus_gallus_BCO
Danio_rerio_BCO
0.991
0.8501
Branchiostoma_floridae_BCO-like1__Brafl1_124223_
Branchiostoma_floridae_RPE65-like1__Brafl1_218241_
0.981
0.7842
Branchiostoma_floridae_RPE65-like2__Brafl1_115035_
0.998
Homo_sapiens_BCO2
0.2857
Mus_musculus_BCO2
0.3736
0.7942
Danio_rerio_BCO2
Xenopus_tropicalis_BCO2
Branchiostoma_floridae_BCO-like2__Brafl1_66862_
Chordate RPE65/BCO/BCO2
B
Branchiostoma_floridae_BCO-like2__Brafl1_66862_
97
Homo_sapiens_BCO2
57
Mus_musculus_BCO2
78
23
Branchiostoma_floridae_RPE65-like2__Brafl1_115035_
72
Xenopus_tropicalis_BCO2
45
Danio_rerio_BCO2
51
Branchiostoma_floridae_BCO-like1__Brafl1_124223_
48
Branchiostoma_floridae_RPE65-like1__Brafl1_218241_
68
Danio_rerio_BCO
94
Homo_sapiens_BCO
80
Gallus_gallus_BCO
87
Ciona_intestinalis_BCO
Ciona_intestinalis_RPE65
Chordate RPE65/BCO/BCO2
96
Homo_sapiens_RPE65
100
Gallus_gallus_RPE65
Ambystoma_tigrinum_RPE65
Vertebrate RPE65
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Euprymna.scolopes_2051
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99
Octopus.bimaculoides22015468m
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Octopus.vulgaris0016009.1
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Nautilus.pompilus009860.1
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Nautilus.pompilus012710.1
49
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Nautilus.pompilus015194.1
96
45
Nautilus.pompilus010907.1
63
82
Nautilus.pompilus016245.1
78
57
Nautilus.pompilus011288.1
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Nautilus.pompilus011718.1
Nautilus.pompilus009019.1
Nautilus.pompilus013855.1
94
Euprymna.scolopes_2270
86
Euprymna.scolopes_674
91
Euprymna.scolopes_8185
100
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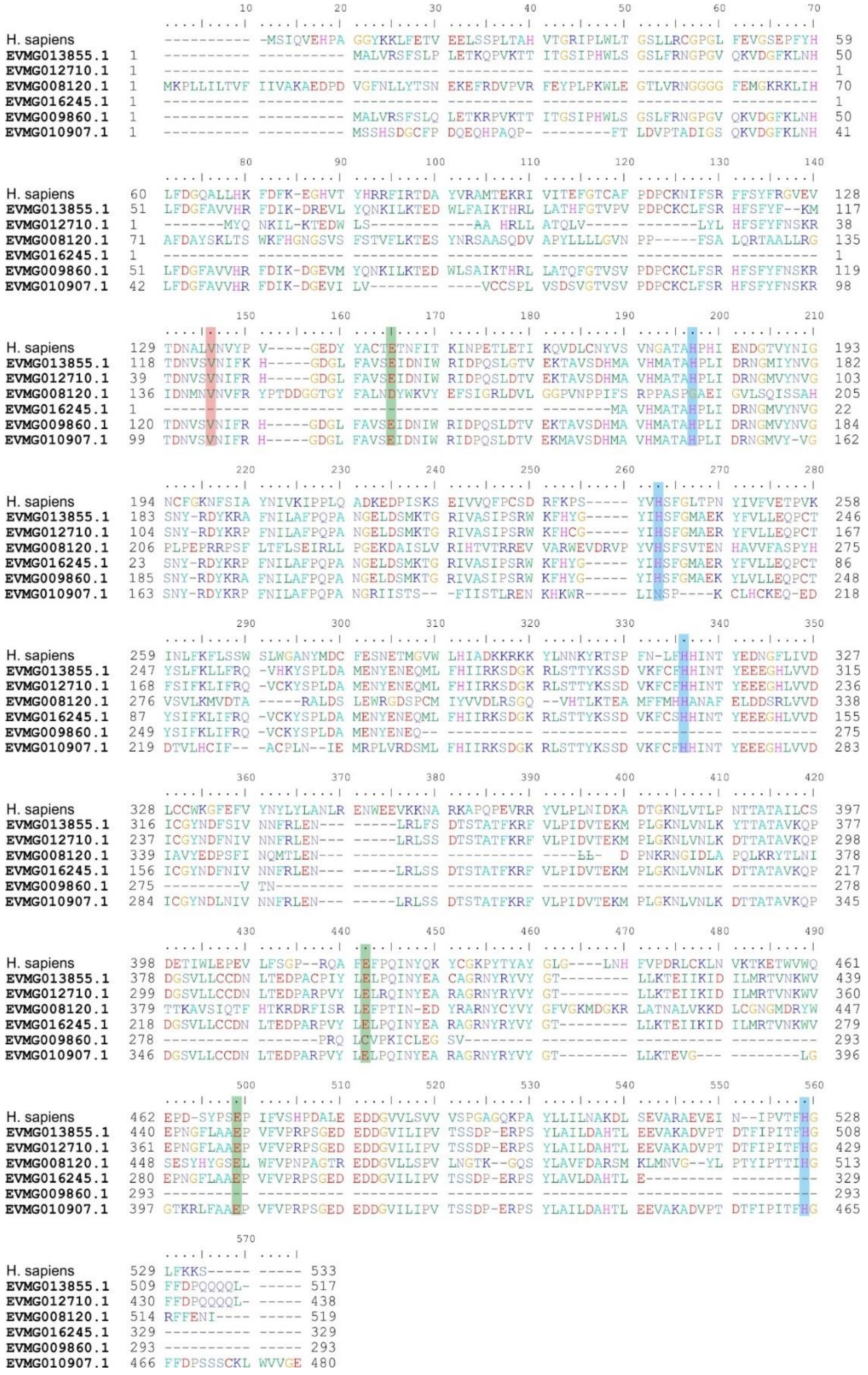
94
Octopus.bimaculoides22033334m
97
Octopus.vulgaris0005380.1
Octopus.minor005171F0.8
Cephalopoda RPE65

Supplementary Fig. 13 | RPE65 family expansion in *N. pompilus*. RPE65 domain containing proteins in cephalopods were applied to construct a phylogenetic tree by MrBayes method (A) as described above and ML method (B, model: LG+G4; bootstrap: 1000), respectively. The cephalopod RPE65 are homologs of vertebrates RPE65. Moreover, the *N. pompilus* genome contains a total of 10 RPE65 proteins, among which 9 of them were expanded and specifically clustered into one independent clade, and 1 of them was clustered with coleoids and formed one other clade.



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                            10         20         30         40         50         60         70
                    ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
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EVMG013855.1     1      ---------- ---------- MALVRSFSLP LETKQPVKTT ITGSIPHWLS GSLFRNGPGV QKVDGFKLNH  50
EVMG012710.1     1      ---------- ---------- ---------- ---------- ---------- ---------- ----------  1
EVMG008120.1     1      MKPLLILTVF IIVAKAEDPD VGFNLLYTSN EKEFRDVPVR FEYPLPKWLE GTLVRNGGGG FEMGKRKLIH  70
EVMG016245.1     1      ---------- ---------- ---------- ---------- ---------- ---------- ----------  1
EVMG009860.1     1      ---------- ---------- MALVRSFSLQ LETKRPVKTT ITGSIPHWLS GSLFRNGPGV QKVDGFKLNH  50
EVMG010907.1     1      ---------- ---------- MSSHSDGCFP DQEQHPAQP- --------FT LDVPTADIGS QKVDGFKLNH  41

                            80         90        100        110        120        130        140
                    ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
H. sapiens       60     LFDGQALLHK FDFK-EGHVT YHRRFIRTDA YVRAMTEKRI VITEFGTCAF PDPCKNIFSR FFSYFRGVEV  128
EVMG013855.1     51     LFDGFAVVHR FDIK-DREVL YQNKILKTED WLFAIKTHRL LATHFGTVPV PDPCKCLFSR HFSYF--KM  117
EVMG012710.1     1      -------MYQ NKIL-KTEDW LS-------- ---AA HRLL ATQLV----- -------LYL HFSFYFNSKR  38
EVMG008120.1     71     AFDAYSKLTS WKFHGNGSVS FSTVFLKTES YNRSAASQDV APYLLLLGVN PP-----FSA LQRTAALLRG  135
EVMG016245.1     1      ---------- ---------- ---------- ---------- ---------- ---------- ----------  1
EVMG009860.1     51     LFDGFAVVHR FDIK-DGEVM YQNKILKTED WLSAIKTHRL LATQFGTVSV PDPCKCLFSR HFSFYFNSKR  119
EVMG010907.1     42     LFDGFAVVHR FDIK-DGEVI LV-------- ----VCCSPL VSDSVGTVSV PDPCKCLFSR HFSFYFNSKR  98

                           150        160        170        180        190        200        210
                    ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
H. sapiens       129    TDNALVNVYP V-----GEDY YACTETNFIT KINPETLETI KQVDLCNYVS VNGATAHPHI ENDGTVYNIG  193
EVMG013855.1     118    TDNVSVNIFK H-----GDGL FAVSEIDNIW RIDPQSLGTV EKTAVSDHMA VHMATAHPLI DRNGMIYNVG  182
EVMG012710.1     39     TDNVSVNIFR H-----GDGL FAVSEIDNIW RIDPQSLDTV EKTAVSDHMA VHMATAHPLI DRNGMVYNVG  103
EVMG008120.1     136    IDNMNVNVFR YPTDDGGTGY FALNDYWKVY EFSIGRLDVL GGPVNPPIFS RPPASPGAEI GVLSQISSAH  205
EVMG016245.1     1      ---------- ---------- ---------- ---------- --------MA VHMATAHPLI DRNGMVYNVG  22
EVMG009860.1     120    TDNVSVNIFR H-----GDGL FAVSEIDNIW RIDPQSLDTV EKTAVSDHMA VHMATAHPLI DRNGMVYNVG  184
EVMG010907.1     99     TDNVSVNIFR H-----GDGL FAVSEIDNIW RIDPQSLDTV EKMAVSDHMA VHMATAHPLI DRNGMVY-VG  162

                           220        230        240        250        260        270        280
                    ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
H. sapiens       194    NCFGKNFSIA YNIVKIPPLQ ADKEDPISKS EIVVQFPCSD RFKPS----- YVHSFGLTPN YIVFVETPVK  258
EVMG013855.1     183    SNY-RDYKRA FNILAFPQPA NGELDSMKTG RIVASIPSRW KFHYG----- YIHSFGMAEK YFVLLEQPCT  246
EVMG012710.1     104    SNY-RDYKRP FNILAFPQPA NGELDSMKTG RIVASIPSRW KFHCG----- YIHSFGMAER YFVLLEQPCT  167
EVMG008120.1     206    PLPEPRRPSF LTFLSEIRLL PGEKDAISLV RIHTVTRREV VARWEVDRVP YVHSFSVTEN HAVVFASPYH  275
EVMG016245.1     23     SNY-RDYKRP FNILAFPQPA NGELDSMKTG RIVASIPSRW KFHYG----- YIHSFGMAER YFVLLEQPCT  86
EVMG009860.1     185    SNY-RDYKRA FNILAFPQPA NGELDSMKTG RIVASIPSRW KFHYG----- YIHSFGMAEK YLVLLEQPCT  248
EVMG010907.1     163    SNY-RDYKRP FNILAFPQPA NGRIISTS-- -FIISTLREN KHKWR----- LINSP----K CLHCKEQ-ED  218

                           290        300        310        320        330        340        350
                    ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
H. sapiens       259    INLFKFLSSW SLWGANYMDC FESNETMGVW LHIADKKRKK YLNNKYRTSP FN-LFHHINT YEDNGFLIVD  327
EVMG013855.1     247    YSLFKLLFRQ -VHKYSPLDA MENYENEQML FHIIRKSDGK RLSTTYKSSD VKFCFHHINT YEEEGHLVVD  315
EVMG012710.1     168    FSIFKLIFRQ -VCKYSPLDA MENYENEQML FHIIRKSDGK RLSTTYKSSD VKFCFHHINT YEEEGHLVVD  236
EVMG008120.1     276    VSVLKMVDTA -----RALDS LEWRGDSPCM IYVVDLRSGQ --VHTLKTEA MFFMHHANAF ELDDSRLVVD  338
EVMG016245.1     87     YSIFKLIFRQ -VCKYSPLDA MENYENEQML FHIIRKSDGK RLSTTYKSSD VKFCSHHINT YEEEGHLVVD  155
EVMG009860.1     249    YSIFKLIFRQ -VCKYSPLDA MENYENEQ-- ---------- ---------- ---------- ----------  275
EVMG010907.1     219    DTVLHCIF-- -ACPLN--IE MRPLVRDSML FHIIRKSDGK RLSTTYKSSD VKFCFHHINT YEEEGHLVVD  283

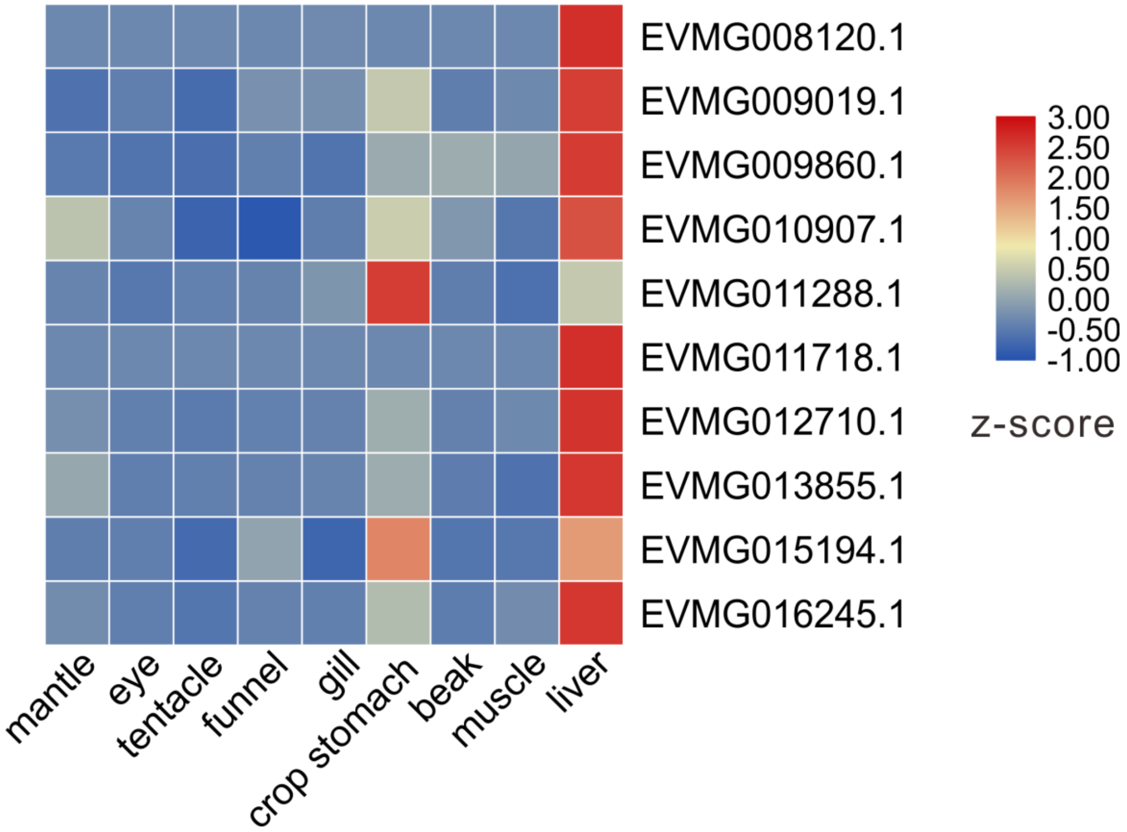
                           360        370        380        390        400        410        420
                    ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
H. sapiens       328    LCCWKGFEFV YNYLYLANLR ENWEEVKKNA RKAPQPEVRR YVLPLNIDKA DTGKNLVTLP NTTATAILCS  397
EVMG013855.1     316    ICGYNDFSIV NNFRLEN--- -----LRLFS DTSTATFKRF VLPIDVTEKM PLGKNLVNLK YTTATAVKQP  377
EVMG012710.1     237    ICGYNDFNIV NNFRLEN--- -----LRLSS DTSTATFKRF VLPIDVTEKM PLGKNLVNLK DTTATAVKQP  298
EVMG008120.1     339    IAVYEDPSFI NQMTLEN--- ---------- ---------- ----LL-  D PNKRNGIDLA PQLKRYTLNI  378
EVMG016245.1     156    ICGYNDFNIV NNFRLEN--- -----LRLSS DTSTATFKRF VLPIDVTEKM PLGKNLVNLK DTTATAVKQP  217
EVMG009860.1     275    ---------V TN-------- ---------- ---------- ---------- ---------- ----------  278
EVMG010907.1     284    ICGYNDLNIV NNFRLEN--- -----LRLSS DTSTATFKRF VLPIDVTEKM PLGKNLVNLK DTTATAVKQP  345

                           430        440        450        460        470        480        490
                    ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
H. sapiens       398    DETIWLEPEV LFSGP--RQA FEFPQINYQK YCGKPYTYAY GLG----LNH FVPDRLCKLN VKTKETWVWQ  461
EVMG013855.1     378    DGSVLLCCDN LTEDPACPIY LELPQINYEA CAGRNYRYVY GT-------- LLKTEIIKID ILMRTVNKWV  439
EVMG012710.1     299    DGSVLLCCDN LTEDPARPVY LELRQINYEA RAGRNYRYVY GT-------- LLKTEIIKID ILMRTVNKWV  360
EVMG008120.1     379    TTKAVSIQTF HTKRDRFISR LEFPTIN-ED YRARNYCYVY GFVGKMDGKR LATNALVKKD LCGNGMDRYW  447
EVMG016245.1     218    DGSVLLCCDN LTEDPARPVY LELPQINYEA RAGRNYRYVY GT-------- LLKTEIIKID ILMRTVNKWV  279
EVMG009860.1     278    ---------- -------PRQ LCVPKICLEG SV-------- ---------- ---------- ----------  293
EVMG010907.1     346    DGSVLLCCDN LTEDPARPVY LELPQINYEA RAGRNYRYVY GT-------- LLKTEVG--- --------LG  396

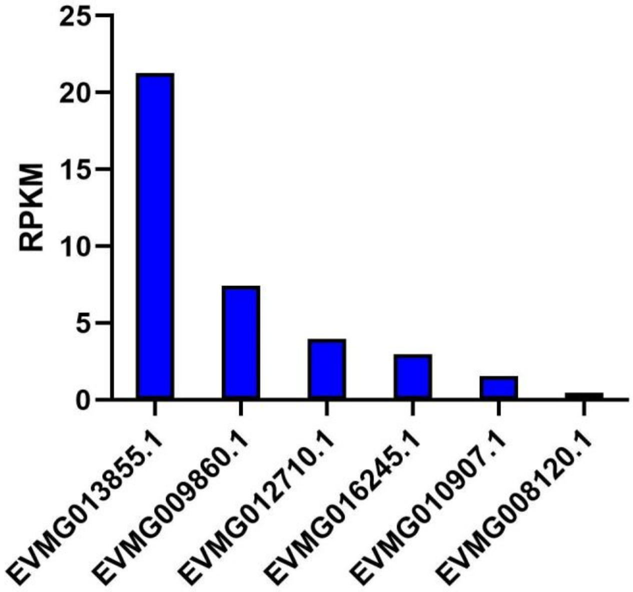
                           500        510        520        530        540        550        560
                    ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
H. sapiens       462    EPD-SYPSEP IFVSHPDALE EDDGVVLSVV VSPGAGQKPA YLLILNAKDL SEVARAEVEI N--IPVTFHG  528
EVMG013855.1     440    EPNGFLAAEP VFVPRPSGED EDDGVILIPV TSSDP-ERPS YLAILDAHTL EEVAKADVPT DTFIPITFHG  508
EVMG012710.1     361    EPNGFLAAEP VFVPRPSGED EDDGVILIPV TSSDP-ERPS YLAILDAHTL EEVAKADVPT DTFIPITFHG  429
EVMG008120.1     448    SESYHYGSEL WFVPNPAGTR EDDGVLLSPV LNGTK--GQS YLAVFDARSM KLMNVG--YL PTYIPTTIHG  513
EVMG016245.1     280    EPNGFLAAEP VFVPRPSGED EDDGVILIPV TSSDP-ERPS YLAVLDAHTL E--------- ----------  329
EVMG009860.1     293    ---------- ---------- ---------- ---------- ---------- ---------- ----------  293
EVMG010907.1     397    GTKRLFAAEP VFVPRPSGED EDDGVILIPV TSSDP-ERPS YLAILDAHTL EEVAKADVPT DTFIPITFHG  465

                           570
                    ....|....| ....|
H. sapiens       529    LFKKS----- ----- 533
EVMG013855.1     509    FFDPQQQQL- ----- 517
EVMG012710.1     430    FFDPQQQQL- ----- 438
EVMG008120.1     514    RFFENI---- ----- 519
EVMG016245.1     329    ---------- ----- 329
EVMG009860.1     293    ---------- ----- 293
EVMG010907.1     466    FFDPSSSCKL WVVGE 480
```

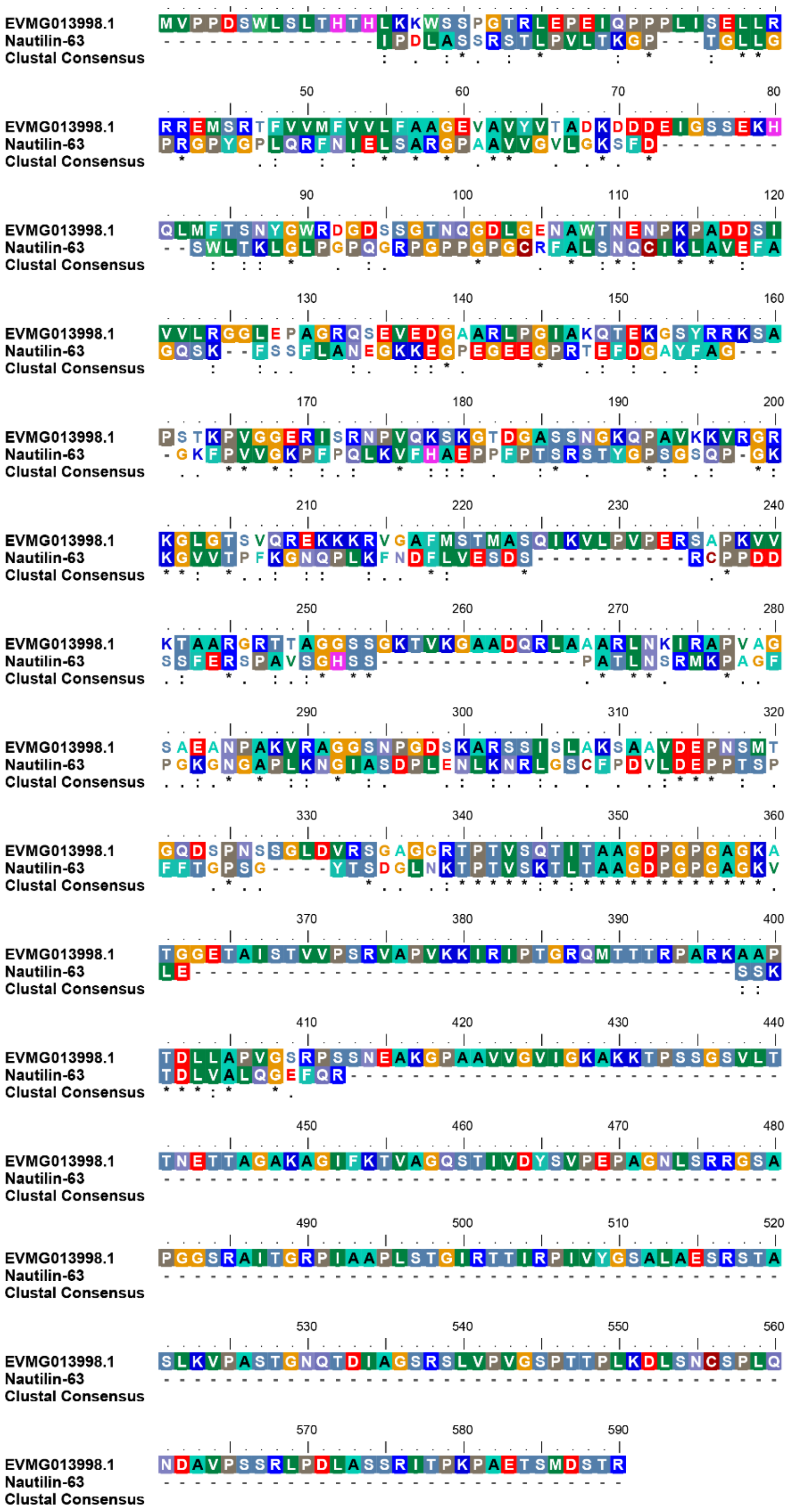
Supplementary Fig. 14 | Sequence alignment of *N. pompilius* and RPE65 of *H. sapiens*. Sequence alignment was conducted and displayed using Bioedit software, between six RPE65 sequences of *N. pompilius* and one of *H. sapiens*. The conserved residues in RPE65 were marked with color background, and EVMG013855.1 retained the conserved domains as in *H. sapiens* RPE65.



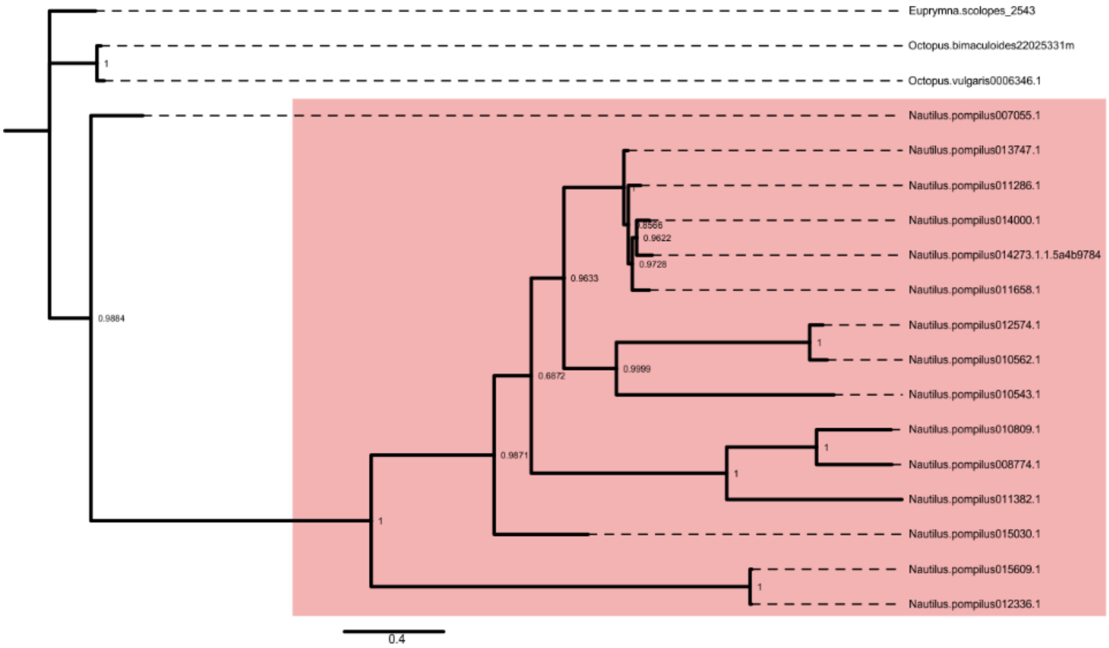
Supplementary Fig. 15 | Expression pattern of RPE65 family in *N. pompilus*. Expression level of RPE65 gene family were analyzed by using transcriptomic data in different tissues, which showed high expression of RPE65 genes in the liver.



Supplementary Fig. 16 | The expression pattern of RPE65 families in the Nautilus eye. Six members of the RPE65 family genes were detected to be expressed in the eye.



Supplementary Fig. 17 | Sequence alignment between Nautilin-63 in *Nautilus macromphalus* and EVMG013998.1 in *N. pompilius*. The identical, highly conserved, and less conserved amino acid residues are indicated by ‘*’, ‘:’ and ‘.’, respectively.


Euprymna.scolopes_2543
Octopus.bimaculoides22025331m
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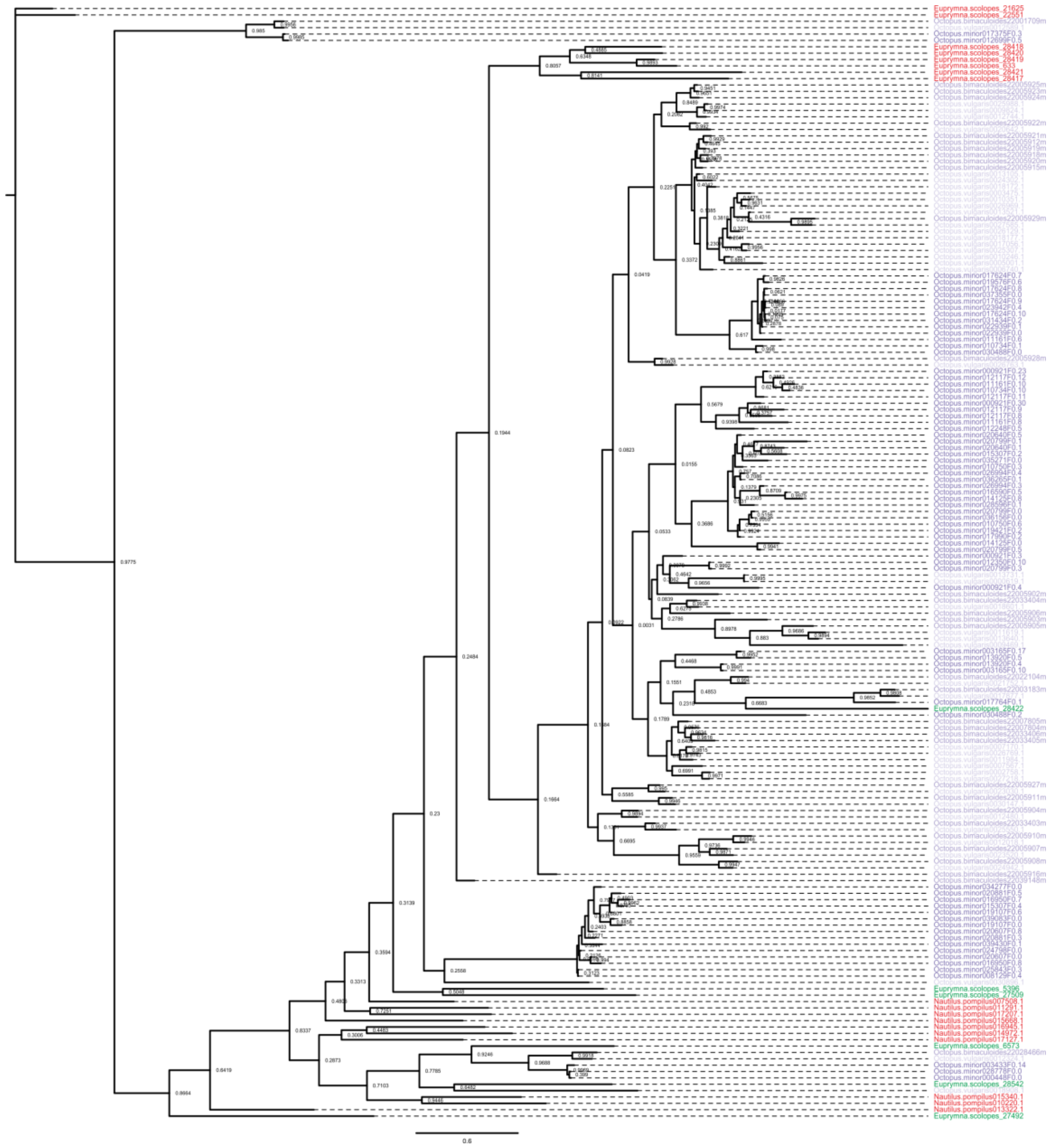
Octopus.vulgaris0006346.1
Nautilus.pompilus007055.1
Nautilus.pompilus013747.1
Nautilus.pompilus011286.1
Nautilus.pompilus014000.1
.8566
0.9622
Nautilus.pompilus014273.1.1.5a4b9784
0.9728
Nautilus.pompilus011658.1
0.9633
0.9884
Nautilus.pompilus012574.1
1
Nautilus.pompilus010562.1
0.9999
0.6872
Nautilus.pompilus010543.1
Nautilus.pompilus010809.1
1
0.9871
Nautilus.pompilus008774.1
1
Nautilus.pompilus011382.1
1
Nautilus.pompilus015030.1
Nautilus.pompilus015609.1
1
Nautilus.pompilus012336.1
0.4

Supplementary Fig. 18 | Expansion of IFN-inducible GTPases (IIG) gene family in the *N. pompilus* genome. Phylogenetic tree of IIG proteins in cephalopods was constructed by using MrBayes methods as described above, and contains 15 of IIG proteins in *N. pompilus*, and only single IIG proteins in other cephalopods.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Euprymna.scolopes_28419
Euprymna.scolopes_633
Euprymna.scolopes_28421
Euprymna.scolopes_28417
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Octopus.bimaculoides22005912m
Octopus.bimaculoides22005919m
Octopus.bimaculoides22005918m
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Octopus.bimaculoides22005915m
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Octopus.vulgaris0024302.1
Octopus.vulgaris0018172.1
Octopus.vulgaris0003475.1
Octopus.vulgaris0010351.1
Octopus.vulgaris0026969.1
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Octopus.vulgaris0018177.1
Octopus.vulgaris0017056.1
Octopus.vulgaris0025307.1
Octopus.vulgaris0010246.1
Octopus.vulgaris0005001.1
Octopus.vulgaris0006740.1
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Octopus.minor017624F0.8
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Octopus.bimaculoides22005911m
Octopus.vulgaris0030147.1
Octopus.bimaculoides22005904m
Octopus.vulgaris0012480.1
Octopus.bimaculoides22033403m
Octopus.vulgaris0025550.1
Octopus.bimaculoides22005910m
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Octopus.minor000448F0.0
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Supplementary Fig. 19 | Phylogenetic tree of interleukin-17 (IL-17) gene family in cephalopods. Phylogenetic tree of IL-17 was constructed by MrBayes method as described above, and includes 10 of IL-17 in *N. pompilus*, 14 of IL-17 in *E. scolopes*, 34 of IL-17 in *O. bimaculoides*, 72 of IL-17 in *O. minor* and 45 of IL-17 in *O. vulgaris*. Independent expansion of IL-17 gene family was found in three octopus species, strongly suggestive of a crucial role of IL-17 in octopus immune defense.

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