Ciliary photoreceptors in sea urchin larvae indicate pan-deuterostome cell type conservation

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Figure S1. Expression of opsin genes in putative photoreceptors in sea urchin larvae. (A) Developmental time course of opsin gene expression based on transcriptome data from Tu et al 2014. (B) Spatial expression of opsin 3.2 and opsin 2 in 72h sea urchin larvae. OV, oral view; LLV, left lateral view.
**Figure S2.** Phylogenetic analysis of opsin. (A) Phylogenetic tree of opsin. Values in bold indicate the Bayesian posterior probability, values in italics indicate SH-aLTR bootstrap values, values underlined indicate ultrafast bootstrap (1000 replicates). Major opsin clades are color coded. The three group topology where R-opsins are a sister group of C-opsins and RGR/Go-opsins is well supported. (B) Phylogenetic tree as in (A) with focus on Go-opsins. Opsin 3.2 is a co-ortholog of Go-opsin1 of *Platynereis dumerilii*, which was recently shown to be sensitive to cyan blue light.
Fig. S3. Expression of synaptotagmin but not serotonin in photoreceptors. (A) Co-localization of Opsin3.2 and SynaptotagminB. Confocal projection from a left lateral perspective showing the projection of a SynaptotagminB containing axon into the basal neuropil of the Apical Organ (AO). (B) Co-immunostaining of Opsin3.2 and Serotonin indicates that PRCs do not contain serotonin. The apical organ is known to include serotonergic neurons on the dorsal margin, and the photoreceptor cells project axons into the apical organ, but do not contain Serotonin.
**Figure S4.**

Expression of additional regulatory genes in PRCs. Double fluorescent WMISH of *opsin3.2* and (A) *awh* or (B) *six3* confirming expression in PRCs. OV, oral view
### Table S1

| Gene name | Transcript ID | Forward | Reverse |
|-----------|--------------|---------|---------|
| Awh       | WHL22.9369.1 | CATAACATCCCATCAATAAAATCC | TAAATCGACTCATATAGGGAGATGCACGCACTCTATTTTCAATC |
| Dac       | WHL22.169355 | GATGCGAACCTGTTCTACG | TAATACGACTCATATAGGGAGAATGACTTGTTACCCGCA |
| Eya       | WHL22.168736 | STAATTGGAGAGGGGCTCAA | TAAATCGACTCATATAGGGAGATGGGCTTGTTACCAGCA |
| FoxG      | WHL22.389872.0 | GCCTTATCTCCTTATATTCTACCC | GTCTTTAGTTGAAATGGGAAACC |
| Hbn       | WHL22.523959.1 | TCATTTCTCTCTGAGGTTACC | CATGAAAGCTCTGATCTG |
| Ia1       | WHL22.769122.0 | ACCCTCTACAGTGAATCTGAAACA | ATGGGCAAGCTGTCAGTAAATAA |
| Id        | WHL22.467043  | CGTCTTAATTAAAAAGCTTGTTGGA | AAATATGCTTTTTGCGTGTCAGT |
| Nkx2.1    | WHL22.739581.0 | AACAGCAGAGAATACCTGTGCAAGAATGCTATTATGCTTCTATGCAAGC |
| Opsin2    | WHL22.272775  | GTTAAATGTCCTACAGGCTGCTC | TAAATCGACTCATATAGGGAGACTTTGGGCAAGACAGCAGAT |
| Opsin3.2  | WHL22.338995  | CGGTAAACATCAGGTGCTCTTT | TAAATCGACTCATATAGGGAGAGTTGGGCAAGACAGCAGAT |
| Otx       | WHL22.532435.1 | AACACAGGCAACAGCAACAG | AGAGCTGCGTCTGACAGGTCAT |
| Pax6      | WHL22.585512.0 | CGCAATCAGGAAGAAGCAGCAA | TTGGCCAGCAGAAGGAAA |
| Rx        | WHL22.523971.0 | AAGAGCAAGGGTGGAAATTAAAC | GCTGATTATACGCTGCAGGCAAGA |
| Six1/2    | WHL22.121485.0 | GCCAATACTTTCTAGGCGATCTAA | TAAATCGACTCATATAGGGAGATGTTCAGTAGTGTGCTTTCGACTG |
| Six3      | WHL22.121654.0 | CTCATAGACACACCCACACA | AGGATGGGAGATCTTCTT |
| SoxB2     | WHL22.104525.0 | ATCAAGACCTTTCCCCATCATC | TAAATCAGCTCAGATAGGAGATGTTGACAGATCTGTGTTGAC |
| SoxC      | WHL22.622787.0 | GCACAAATAGGAGAGGAGAG | TAAATCGACTCATATAGGGAGAATGCTGCTGAGT |
| Tbx2/3    | WHL22.457020.0 | TCACAAAGGAGGACAGAGAAATGG | TAAATCGACTCATATAGGGAGAGGAGAGAGAGGATGGGCTCTAATAACTG |
| Zic       | WHL22.331651.0 | CAATTGGTTCTGACTAC | ACCTGACATTTCAGATGTCG |

**Table S1. Primers used for generation of WMISH probes.** The transcript ID refers to the transcriptome-based gene model defined in [1]. Gene sequences can be found on Echinobase ([http://www.echinobase.org/Echinobase/](http://www.echinobase.org/Echinobase/)).