Table S1: BLAST analyses of opsin sequences from *Hirudo verbana*

Contig	Library	Top hit with function	Identification	BLAST E-value	Match to UV-associated annelid opsin*
139791	Leech	AID66634	opsin B, partial [*Helobdella robusta*]	0	Modest, 3.37×10^{-8}
	Inverte-brate	BBA21101	rhodopsin [*Ambigolimax valentianus*]	1.93×10^{-103}	
	Arthro-poda	BAG80976	opsin [*Triops granarius*]	8.85×10^{-67}	
156444	Leech	AID66633	opsin A, partial [*Helobdella robusta*]	1.95×10^{-27}	Strong, 2.47×10^{-35}
	Inverte-brate	XP_021373098	rhodopsin, GQ-coupled-like [*Mizuhopecten yessoensis*]	3.86×10^{-14}	
	Arthro-poda	ANF89420	arthopsin 1, partial [*Limulus polyphemus*]	6.72×10^{-13}	

*Based on comparison to opsin (AY692353.1) from Tsukamoto et al. (2017).

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>Contig139791
AAATAACAAAACCTCAAATATTAAATATATTTATCCGAGCCAATCACGAAAACTCTCAGG
CCATTTATCGATGACCATCAATGTCAAAATGACGATGAGGCAATCTTGGCTGGGGAGCTG
GTTTCTTCTGGTTTCGCTGCCTCTGAAGGGTTTGGTTCAGTAGATGGATGGAATTCTATT
GTTGGAACCTCGGCCTGTTCCTTCTGACCAGTGGAGGCAGGAGGGGGGTTGTCGGCAGTC
CTAGTTTCCCTGACAGAACCAGAAGATGACATCTCTGACATTCTGGTATTAGCCACCGAA
ACCTCGGACTTGGTTGGTTTGCTCAAACAGTAACGGAATGGCAGCTTGCTCTTCCTCAGT
GCTTCCCTGTACCTCGGATGGCTGAGGGCATAAATTATGGGGTTCCACGCGCCAGAGGCT
TTGGCCAGCATGACAGGAATCTCAGTGGTATATGGAGTGACCAAGTTGCTGTGCCCAGCC
ACGCCCAACATAGCCACTGTGACGTAGGGCACCCAGGTGATGATGAACATTATCACGTTC
ACGGCGACGACTTTTGCAATCTGGATTTCCTGCTTCTGCTGGTTGGCAGTTTCCTTATTC
ATCCTTGACATTTCCTTCCTGTTCTTGGCTACGGCAGAAATAATACCGACATAGCAAAGC
AAGATCAGGGTGACTGGAACTACAAACTGGAAAACGACGAAGCACAAATTGAAGGAGATG
TTGTTCCAGGTCTGGGTCAAGTAGTCCCAGGTGCAGCTGAAACCGAAACCCTCCAACATG
AAGGCCCCCCAGCCGAACCACGGGGCAGACACCCAGCACACGGCATGGACCCAGACGAAT
GCGATCTGCTGGAGAGTTCTAGATTTTGAAGCAGCGTGCAACATGTACATGGGCTTGGCA
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ACTCCAGCCACAAAAGCGTACCACTGGCATCCGAAGAAGCCCCACATCCAGTAGCGCCTG
AAACAGGCCAGGGCCATCATCGGGAAACCGATAATGGCGGAGAACATGAGGTCACAAATG
GCCAGGTTAATGACGAAGAGATTGGAGGGAGTCTTTAAGGATGGAGTTGTCCCGAAGACA
TATAGGACAATGAGGTTGCCAAAGGTACCGATAAAAGCCACTAAGGTTATGTAGATGCCA
AGAAGGATCATAAACTCTCCTGGGGCCTCGTCAATGACCTCCCTGTACTGATCCCAGTGG
GGGTGGAGGTACAGGCCGTGCTCATCGTACCTTCTGGGGGTAGTAGGGAAAGTGGTGTTG
CTGAGGTTAAAGTAAGAAAGGGATGAATTCCAGTCTTCGTACAGGGGGGTATGGAAGGAT
GTCGGAAACGATGATGTGGTGGAGAGGAGTGAGAAATGTTGTTGATGGCTTGTTGTCATC
TCGCGTTGATCTTCTTGTTGTTGCCGAGGATGTTGCTCGTTCGCCTTCCTGCCTTTTTTG
TGCCTGGTGTTCTCCAATTCAAGTTACTCAAGTAGCATCTTCATTCCTTCTGGAAGAGAT
GACACGTCTAGCTTTTTTCTCGTGATGGAATAAAGCCACAAGGAAAAATCAGAACTCCTC
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Fig. S1. Contig139791.fa. Sequence of contig corresponding to putative green opsin.

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>Contig156444
GCCGTTCGCGGCTGACGATGTCCGACGTGAGTGACGTAAAATCCTTGCGATGCTTCATCA
CGACTCTGACGATGCCAATGTATGAACAGATGATGATGAAAACTGGAAGAAGAAAGCAGA
GAGAAAAGAGAGCCAAGTTGAATGCGATATTGGAAGGGGTACGAGTGAGGTAGTCGAAGG
TGCAGCTGAAACCGAAACCCTCCAACATGAAGGCCCCCCAGCCGAACCA
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Fig. S2. Contig156444.fa. Sequence of contig corresponding to putative UV opsin.