Supplementary Material

Table S1 Summary of the stereology parameters used for the analysis of ganglion cell and photoreceptor cell distributions along with Schaeffer's coefficient of error (CE).

Ganglion cells

Stage	Individual	SL, cm	Lens $\varnothing$, mm	Counting Frame size, μm	Grid size, μm	Site No.	Schaeffer's CE
Adult	ID1	30.6	6.6	90 x 90	1350 x 1350	219	0.042
	ID2	30.8	6.9	90 x 90	1350 x 1350	238	0.041
Juvenile	ID1	13.8	4.7	80 x 80	1000 x 1000	225	0.042
	ID2	15.2	4.9	80 x 80	1000 x 1000	209	0.041
	ID3	15.7	4.5	80 x 80	1000 x 1000	185	0.042
Larval	ID1	3.18	1.4	50 x 50	250 x 250	205	0.034

Photoreceptors

Stage	Individual	SL, cm	Lens $\varnothing$, mm	Counting Frame size, μm	Grid size, μm	Site N	Schaeffer's CE
Adult	ID3	29.7	6.8	90 x 90	1450 x 1450	207	0.047
	ID4	27.7	6.4	90 x 90	1450 x 1450	185	0.050
Juvenile	ID3	13.8	4.5	80 x 80	950 x 950	195	0.045
	ID4	18.5	5.6	80 x 80	950 x 950	210	0.054
Larval	ID2	3.08	1.6	45 x 45	340 x 340	216	0.051
	ID3	3.30	1.5	45 x 45	340 x 340	208	0.053

SL = standard length; $\varnothing$ = diameter.

Table S2: Summary of transcriptomes of *N. brevirostris*, opsin mapping (incl. base pair coverage), and proportional opsin gene expression.

RH1 = rod opsin, *SWS2* = short-wavelength sensitive 2, *RH2* = rhodopsin like 2, *LWS* = long-wavelength sensitive

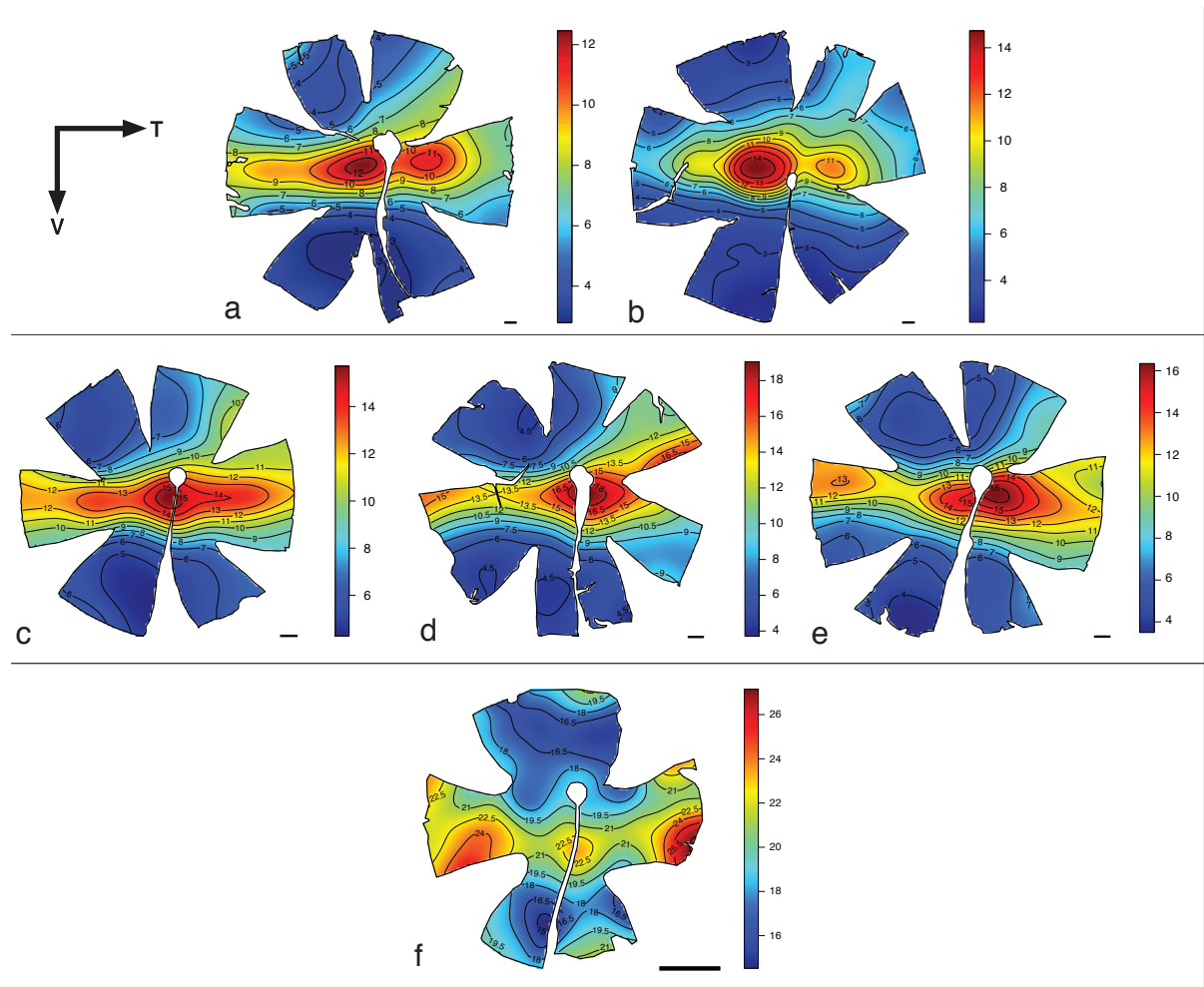| | | RNA sequencing | | | Mapping | | | | | Proportional opsin expression % (normalized to coding sequence length) | | | | | |
| | | Transcriptome | | | Rod | Single cones (SC) | Double cones (DC) | | | Rod vs Cone | | SC | DC | | |
Stage	ID	Standard length (cm)	# raw reads	# filtered reads	*RH1* # reads	*SWS2B* # reads	*RH2B* # reads	*RH2A* # reads	*LWS* # reads	R	C	*SWS2B*	*RH2B*	*RH2A*	*LWS*
Larval	L19	3.18	25,789,980	22,792,356	1,178,462	35,634	39,634	98,812	188	87.1	12.9	100	28.5	71.4	0.1
	L20	3.07	24,433,162	21,718,144	1,125,563	35,125	46,386	84,954	158	87.1	12.9	100	35.2	64.7	0.1
	L26	3.07	25,820,192	22,996,270	1,066,043	47,843	118,750	143,946	602	77.4	22.6	100	45	54.8	0.2
	Mean		25,347,778	22,502,257	1,123,356	39,534	68,257	109,237	316	83.9	16.1	100	36.2	63.6	0.2
	Se		457,391	396,451	32,471	4,157	25,321	17,809	143	3.23		-	4.8	4.8	0.0
Juvenile	FD8	6.5	14,854,726	13,176,755	679,634	39,829	88,651	57,481	3,005	78.2	21.8	100	59.3	38.7	2
	SRG1	15.5	9,043,423	7,458,565	365,928	17,873	34,235	25,225	2,333	82.1	17.9	100	55.3	41	3.7
	SRG21	19.5	9,895,137	6,536,514	631,856	6,452	15,656	10,926	786	94.9	5.1	100	57.1	40.1	2.8
	SRG22	15.2	12,990,170	11,708,074	612,536	11,203	17,282	13,292	1,887	93.3	6.7	100	53.1	41.1	5.8
	SRG28	14.2	2,914,410	2,560,493	133,236	8,445	19,856	12,731	748	76.1	23.9	100	59.5	38.3	2.2
	SRG31_2	15.3	20,785,172	18,299,205	896,430	18,684	41,142	37,840	466	90.1	9.9	100	51.7	47.7	0.6
	Mean		11,747,173	9,956,601	553,270	17,081	36,137	26,249	1,537.5	85.8	14.2	100	56.0	41.2	2.8
	Se		2,460,660	2,277,979	108,772	4,976	11,294	7,519.4	418.1	3.3		-	1.3	1.4	0.7
Adult	SRG2_VT	33.0	21,687,092	17,535,898	1,555,234	75,996	173,683	116,779	17,268	80.2	19.8	100	56.3	38.1	5.6
	SRG4_VT	30.8	13,659,085	12,284,294	1,454,916	72,354	94,914	56,266	8,520	86.2	13.8	100	59.3	35.4	5.3
	SRG7_VT	30.6	22,826,459	18,406,216	1,817,211	76,589	173,392	133,336	21,603	81.8	18.2	100	52.7	40.8	6.5
	Mean		19,390,879	16,075,469	1,609,120	74,980	147,330	102,127	15,797.0	82.7	17.3	100	56.1	38.1	5.8
	Se		2,884,709	1,912,165	108,000	1,324	26,208	23,423.3	3,847.7	1.8		-	1.9	1.6	0.4

Fig. S1: Topographic distribution of retinal ganglion cells for adult (a, b), juvenile (c, d, e), and larval (f) stages. Black lines represent isodensity contours, and values are expressed in densities x 10^3 cells/mm^2. V = Ventral, T = temporal. Scale bar = 1 mm.
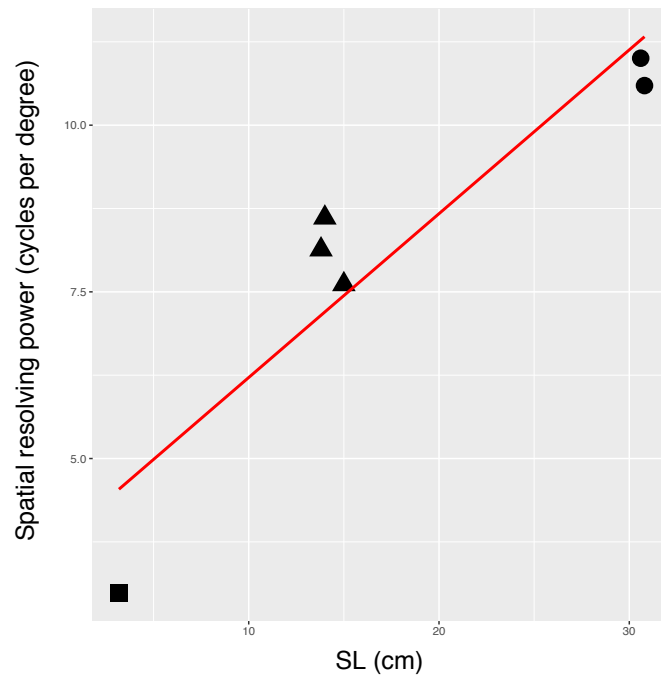
Fig. S2 Relationship between visual acuity **(**spatial resolving power) and body size (standard length, SL) for different life stages of *Naso brevirostris*. Squares = larval stage; triangles = juvenile stage; circles = adult stage.
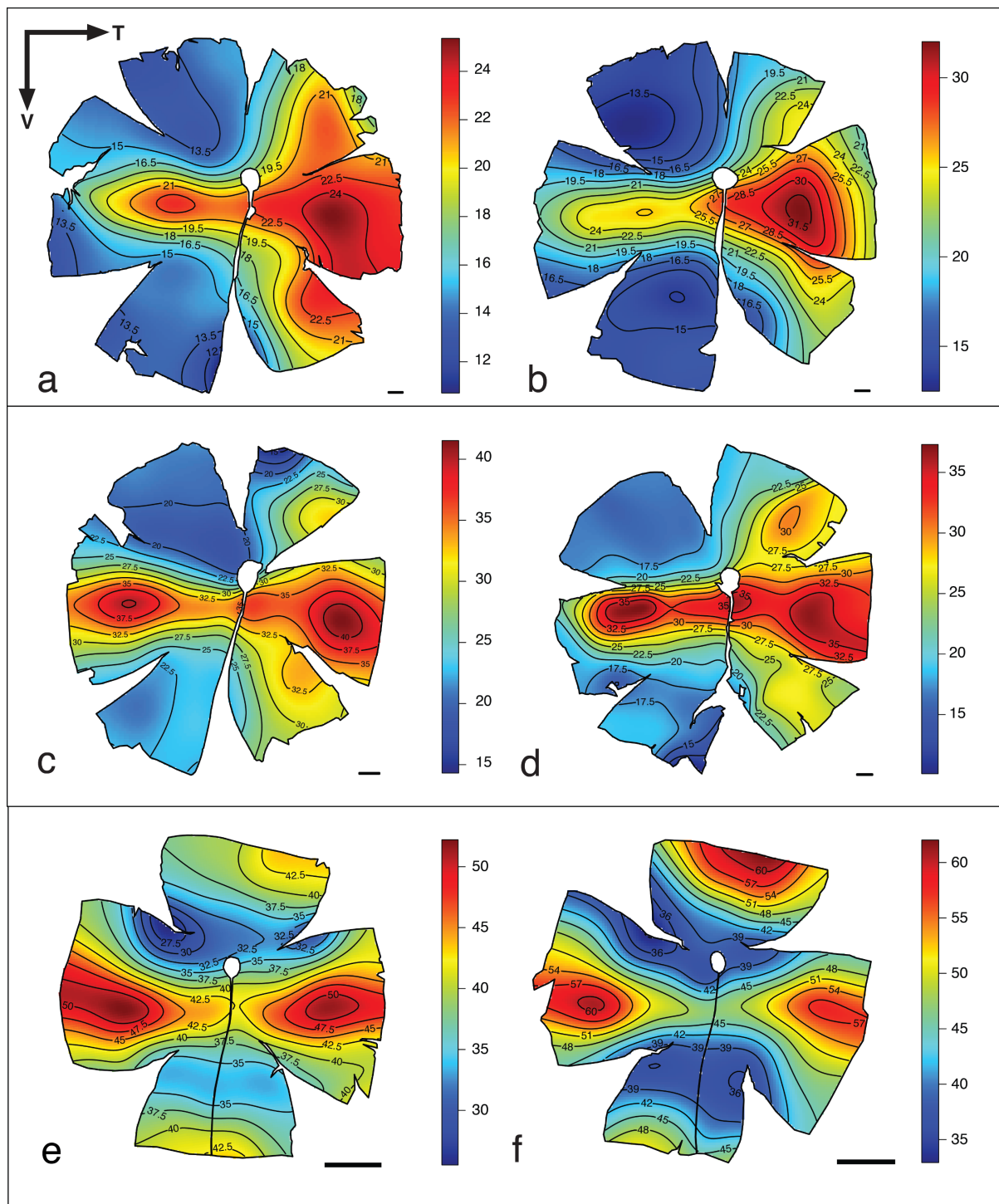
Fig. S3: Topographic distribution of total cone photoreceptors for adult (a, b), juvenile (c, d), and larval (e, f) stages. The topographic maps for single and double cones for all individuals are provided on Dryad. Black lines represent isodensity contours, and values are expressed in densities x 10^3 cells/mm^2. V = Ventral, T = temporal. Scale bar = 1 mm.
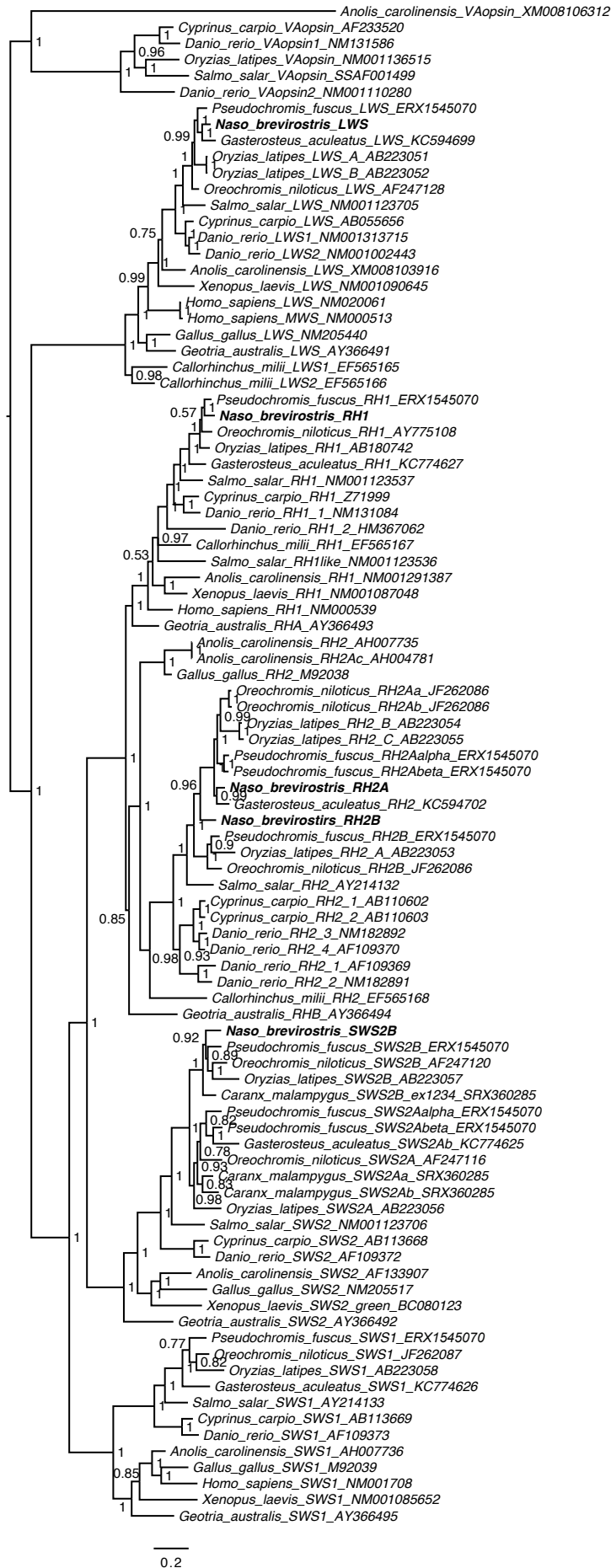
Fig. S4: Vertebrate opsin phylogeny. The different *Naso brevirostris* opsins (extracted from the transcriptomes) are shown in bold. Bayesian support values as indicated. *RH1* = rhodopsin 1 (rod opsin), *RH2* = rhodopsin 2, *SWS2* = short-wavelength-sensitive 2, *SWS1* = short-wavelength-sensitive 1, *LWS* = long-wavelength-sensitive, *va* = vertebrate ancient opsin (outgroup), scalebar = substitution per site.