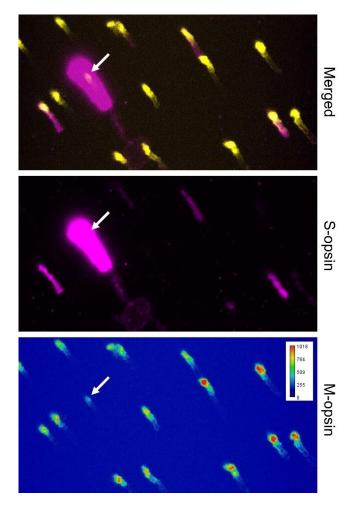
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Supplement

Table S1: Expression values (counts per million) of marker genes in S- and M-cone samples. Low number of marker genes from other cell types indicate little to no contamination. Cone genes were detected as expected.

Gene	Average expression in counts per million (cpm) after TMM (trimmed mean of M values) normalization				Expected cell type
I.	Combined S-cone samples		Combined M-	cone samples	1
Opn1sw	20681.26	± 6525.83	433.94	± 856.57	S-cones
Opn1mw	11.48	± 11.75	740.23	± 186.90	M-Cones
Cnga3	95.22	± 54.65	92.33	± 73.28	All cones
Cngb3	1618.16	± 457.70	1249.61	± 251.12	All cones
Gnat2	2837.57	± 929.58	3905.72	± 777.66	All cones
Grk7	400.83	± 195.09	460.50	± 126.99	All cones
Cnga1	5.28	± 12.86	14.23	± 37.66	Rods
Cngb1	112.44	± 61.80	25.05	± 20.40	Rods
Gnat1	0.00	± 0.00	0.02	± 0.06	Rods
Grk1	3.11	± 5.58	2.46	± 3.85	Rods
Rho	34.65	± 66.66	33.61	± 78.51	Rods
Gfap	0	± 0	0.00	± 0	Astrocytes
Vsx2	3.18	± 7.80	0.06	± 0.11	Bipolar cells
Rbpms	0.061	± 0.15	0.90	± 2.30	Ganglion cells
Pou4f2	0	± 0	0.00	± 0	Ganglion cells
Calb1	86.13	± 137.52	38.38	± 34.67	Horizontal cells
Vim	17.49	± 21.94	12.95	± 12.76	Müller Glia

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Suppl.Figure S1 This image shows a cone (arrow) that received a clear SCBC contact (not shown here) but was categorized as mixed cone, because its outer segment is S-opsin⁺ and M-opsin⁺. The strength of the M-opsin signal appears lower compared to surrounding M-opsin⁺ cones.