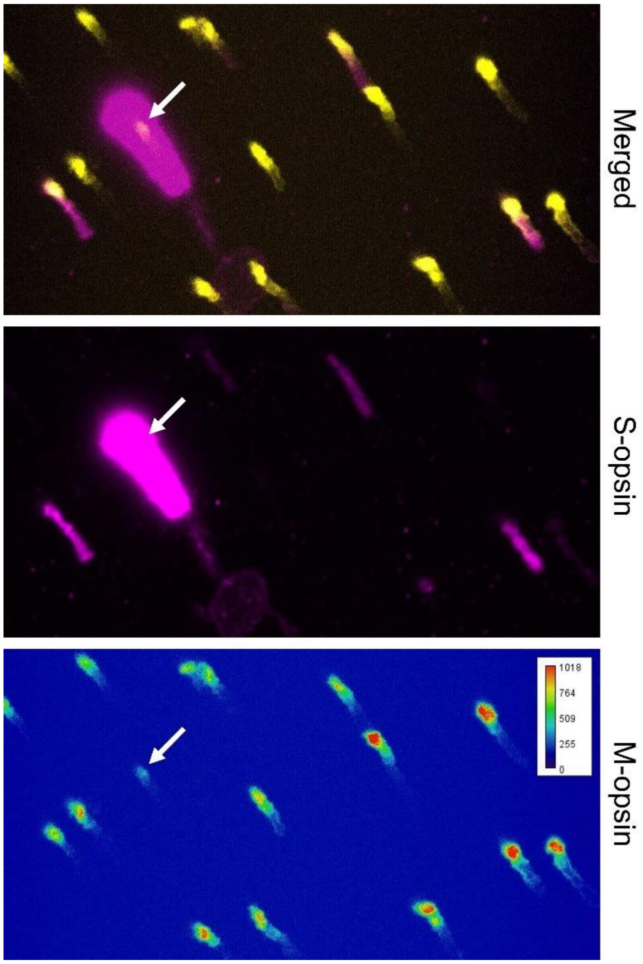
Supplement

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**
	Combined S-cone samples		Combined M-cone samples		
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



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.