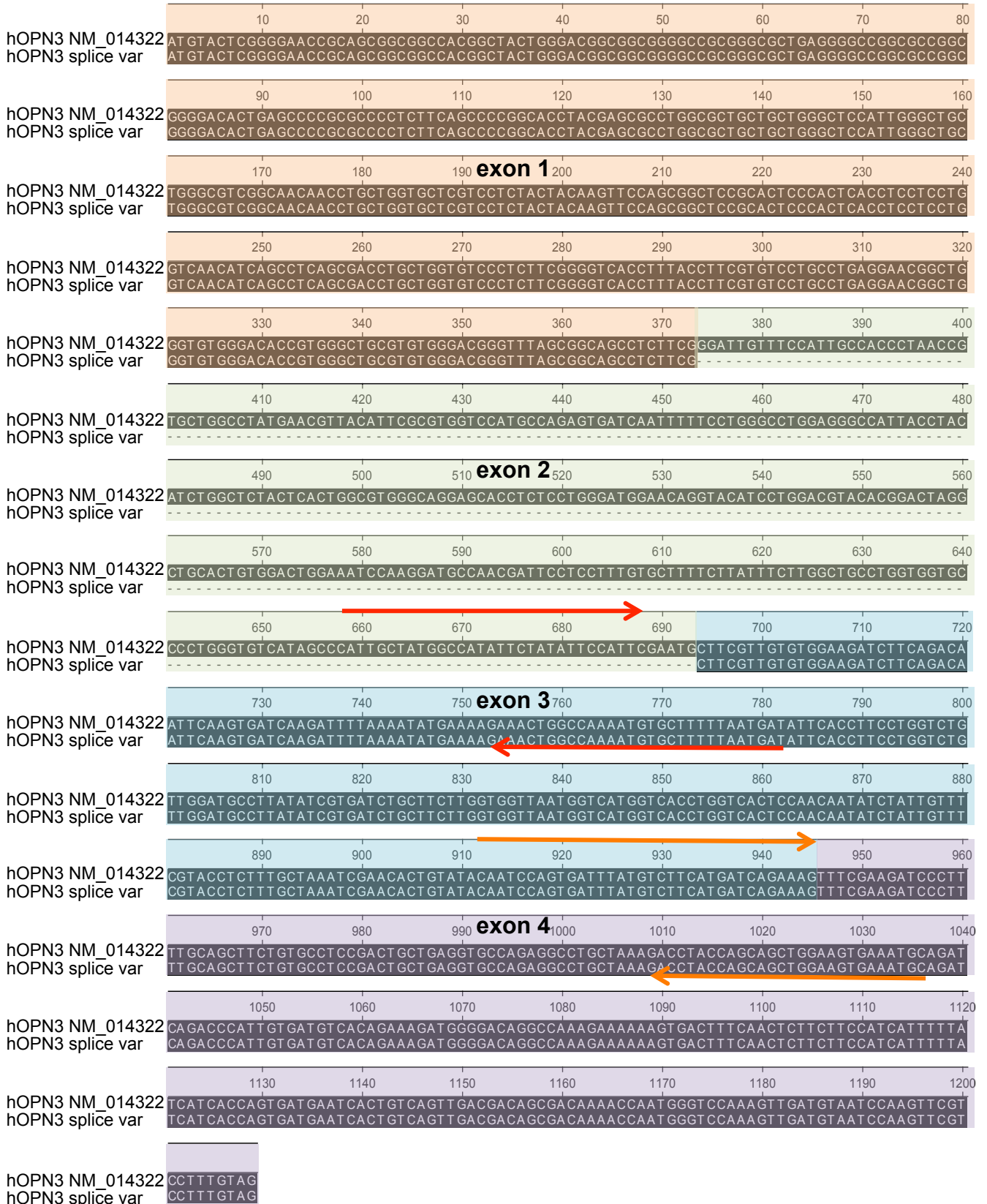


**Fig. S1.** Alignment of the human opsins cDNA surrounding the bases coding for the conserved retinal-binding lysine residue (red box).

# OPN3 splice isoforms

A



**Fig. S2A.** Alignment of full-length OPN3 cDNA and the splice variant identified in HEMs and KERs.

# OPN3 splice isoforms

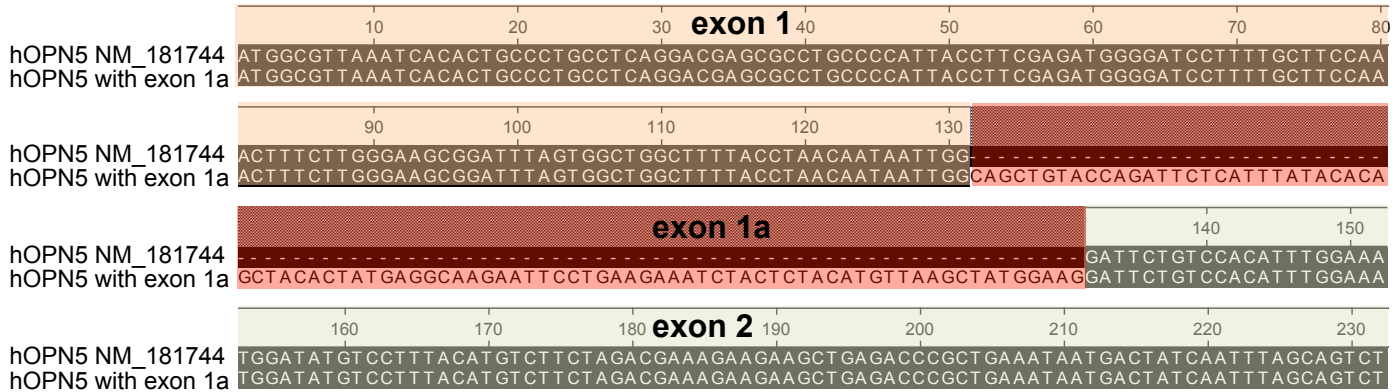
**B**



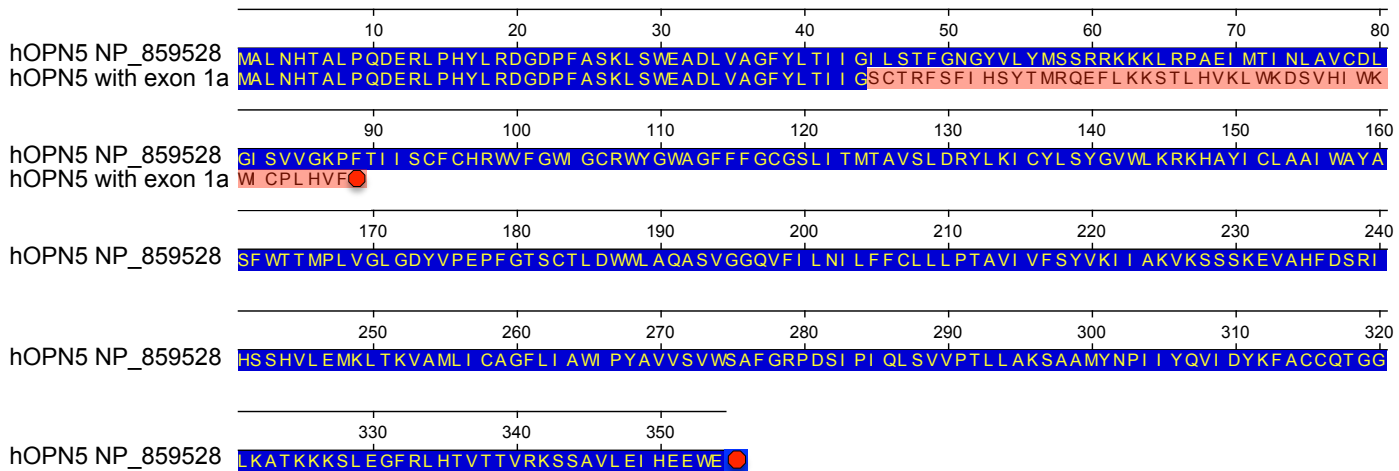
**Fig. S2B.** Alignment of full-length OPN3 protein and the protein predicted by the splice variant identified in HEMs and KERs.

# OPN5 splice isoforms

**A**



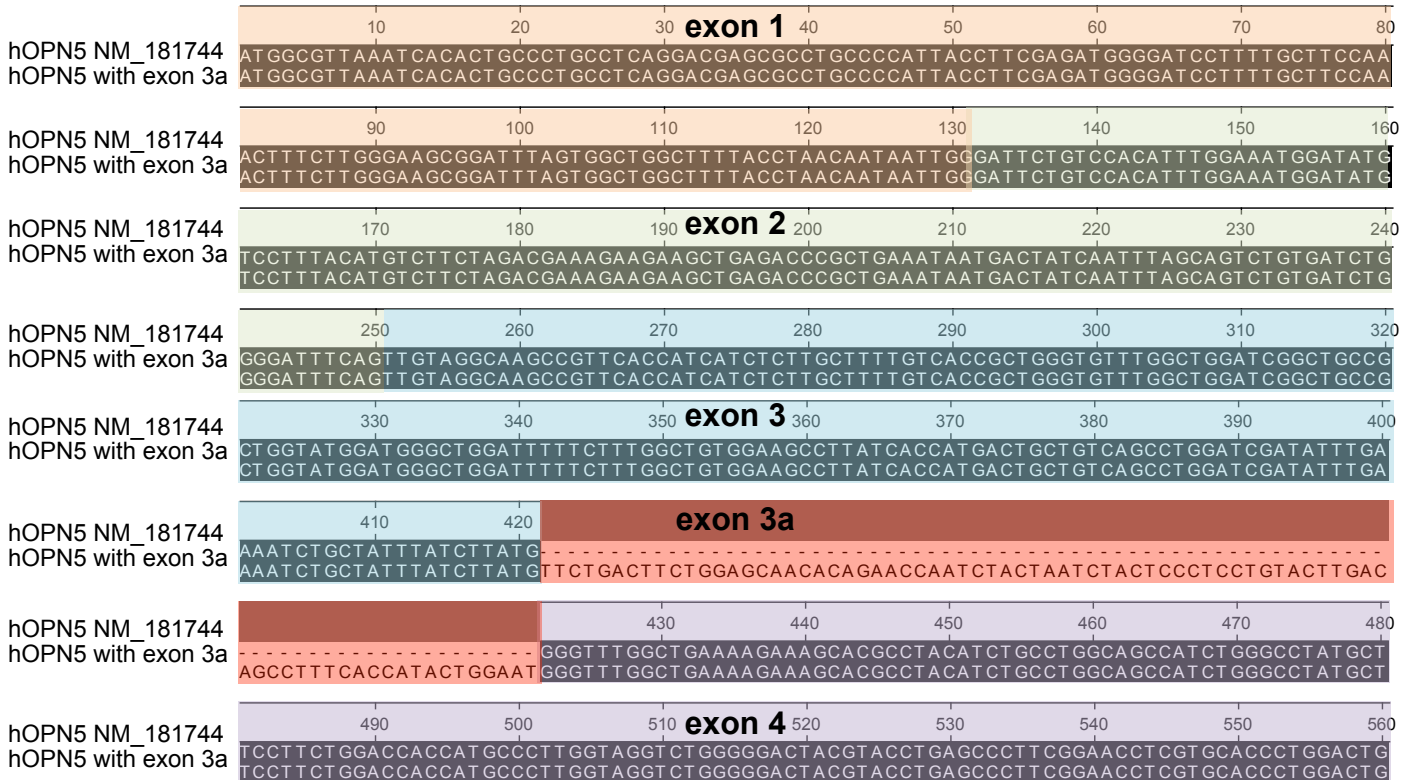
**B**



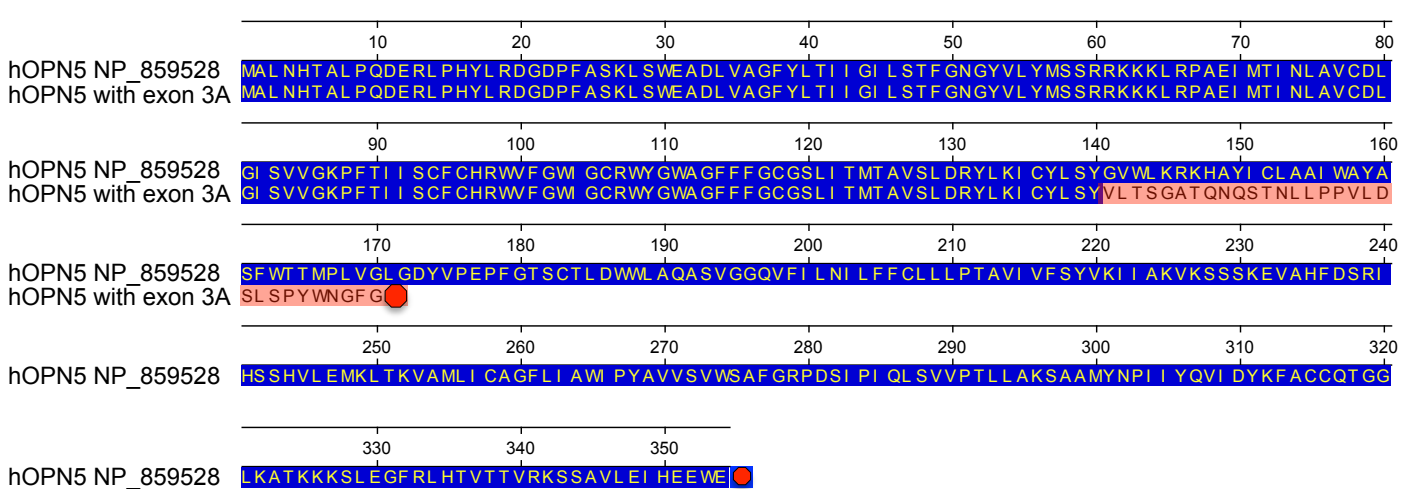
**Fig. S3A-B.** Alignment of cDNA and predicted protein of full-length OPN5 and the exon1 splice variants identified in HEMs and KERs.

# OPN5 splice isoforms

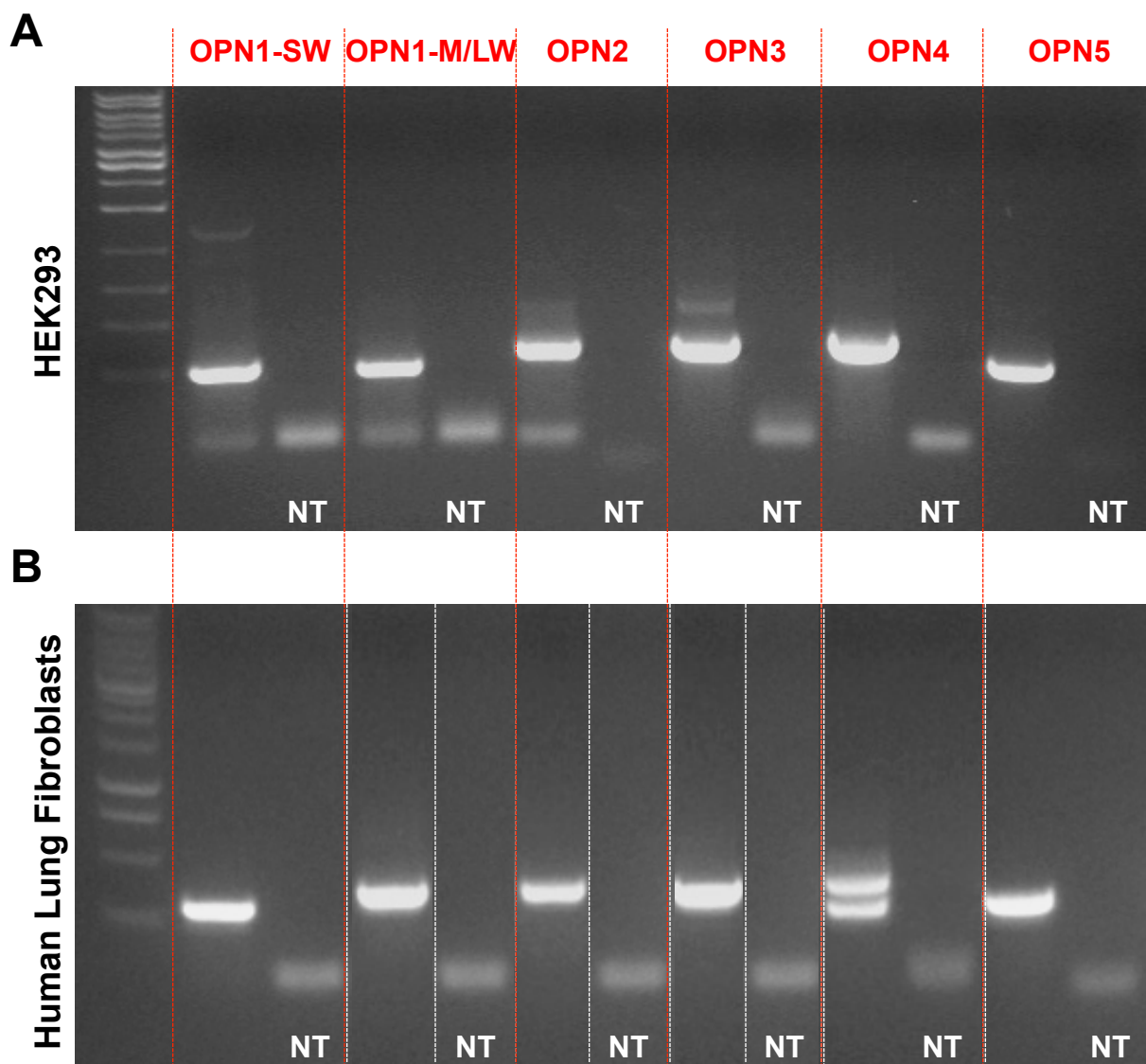
**C**



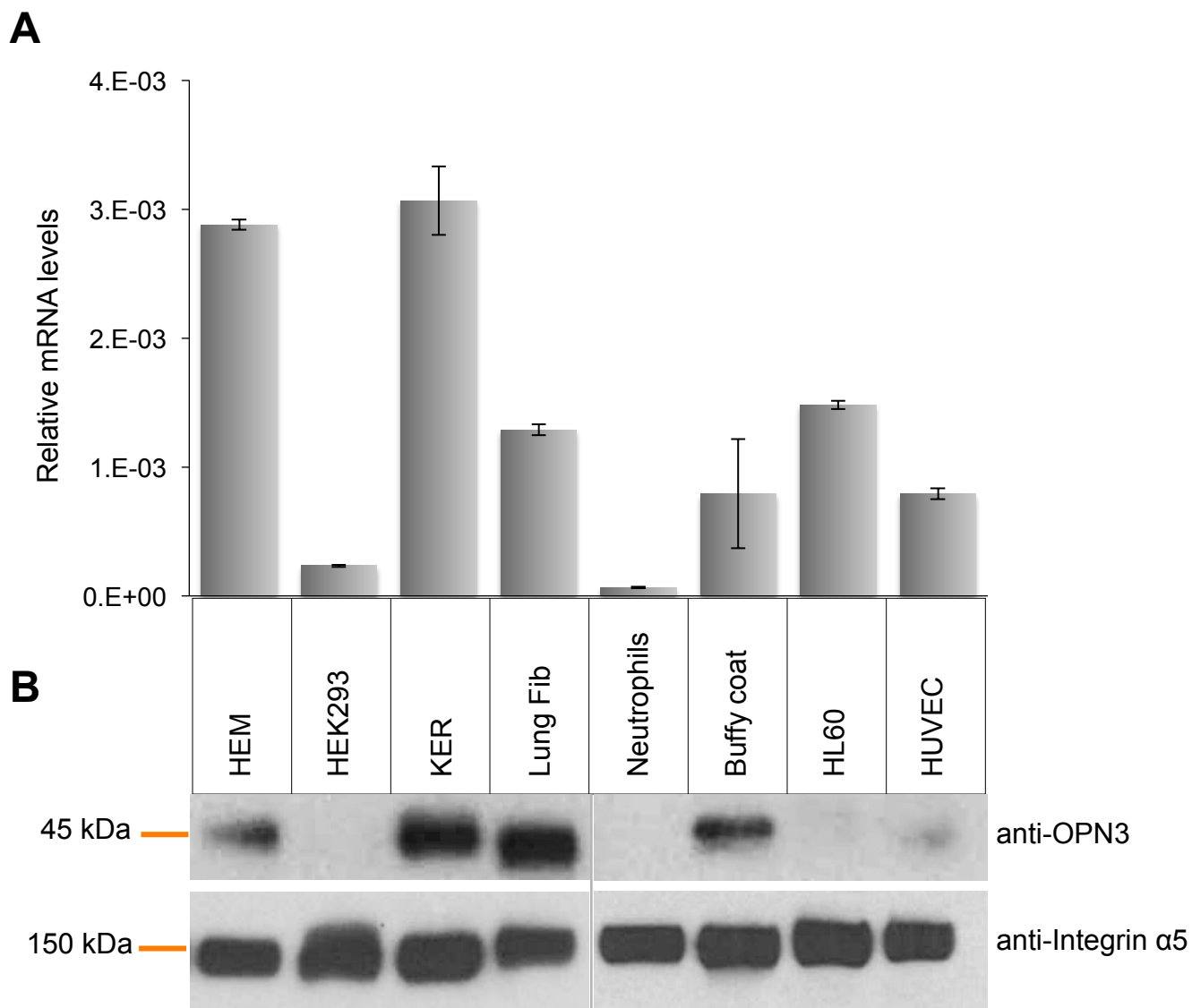
**D**



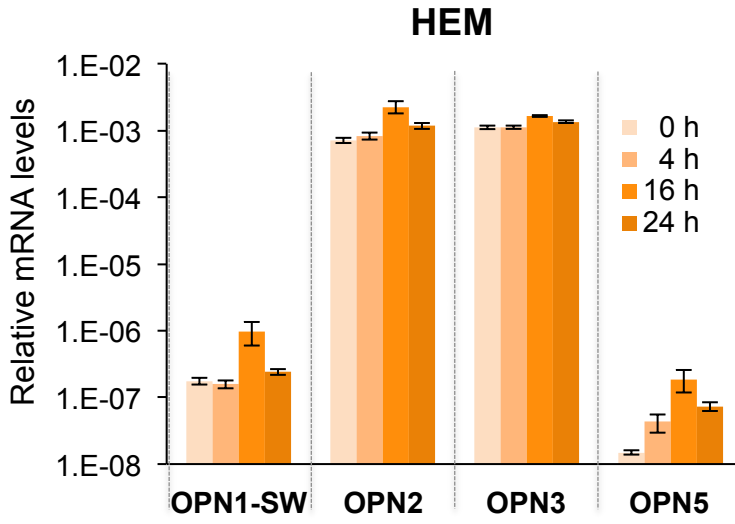
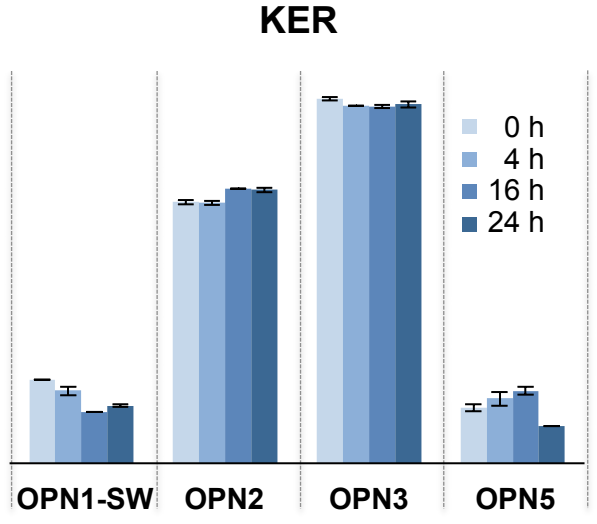
**Fig. S3C-D.** Alignment of cDNA and predicted protein of full-length OPN5 and the exon3 splice variants identified in HEMs and KERs.



**Figure S4.** RT-PCR screen for the region surrounding the retinal-binding site of human opsins in HEK293 cells and human lung fibroblasts.



**Figure S5.** qPCR and western blot analysis of OPN3 expression in different human cells.

**A****B**

**Figure S6.** Opsin expression levels in HEMs and KERs stimulated with UVR.