

Supplementary Figures and Tables



Fig S1. Parasitisation of the Greenland shark cornea. Representative photograph of the head and eye of a Greenland shark, *Somniosus microcephalus*, showing attachment of the copepod parasite, *Ommatokoita elongata*, to the cornea. This image was provided with permission for use by Ghislain Bardout from the Under the Pole expedition.

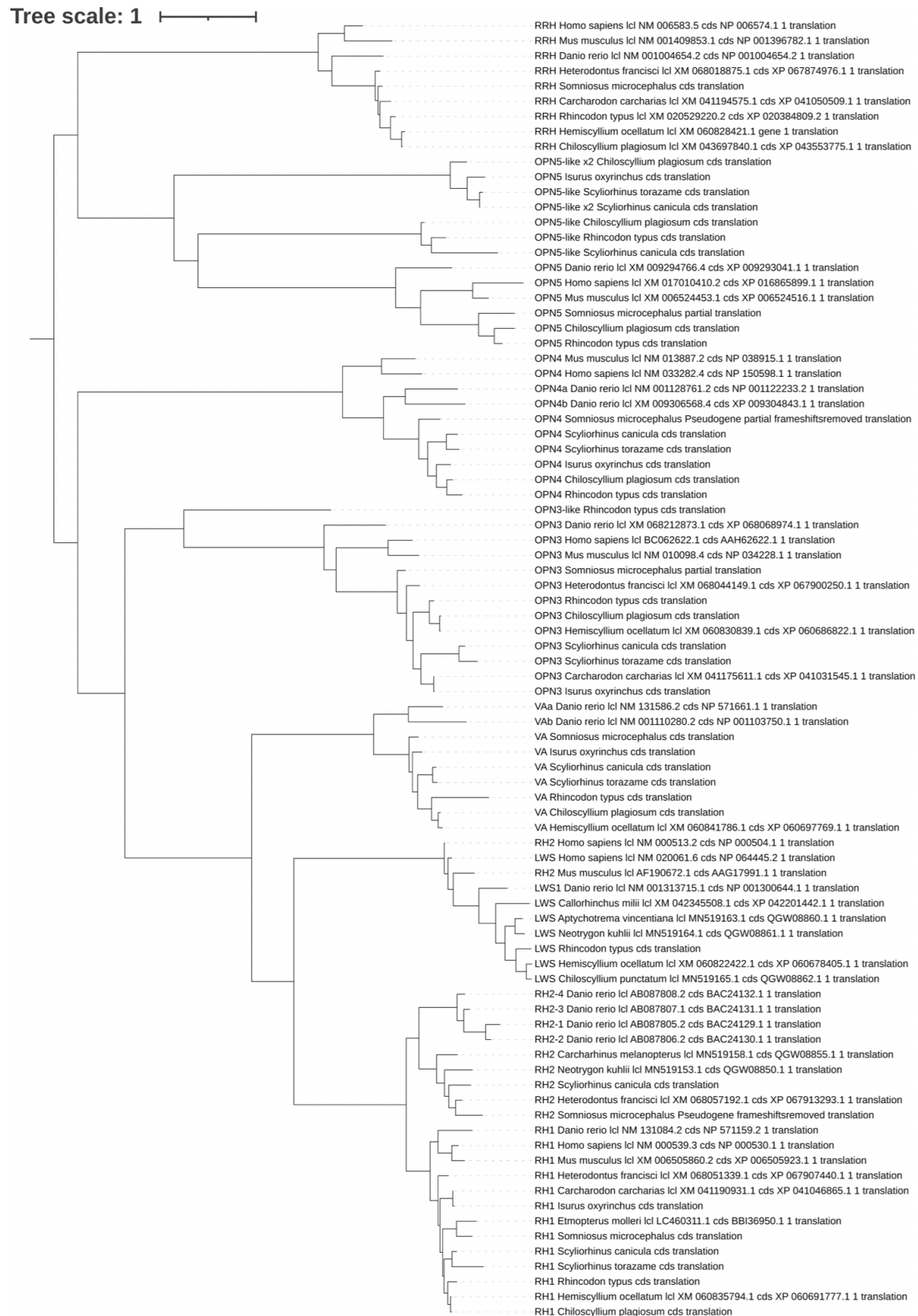


Fig S2. Opsin phylogeny. Gene tree with sequences from several shark species and outgroup species (*Danio rerio*, *Homo sapiens* and *Mus musculus*). The scale bar denotes substitutions per site.

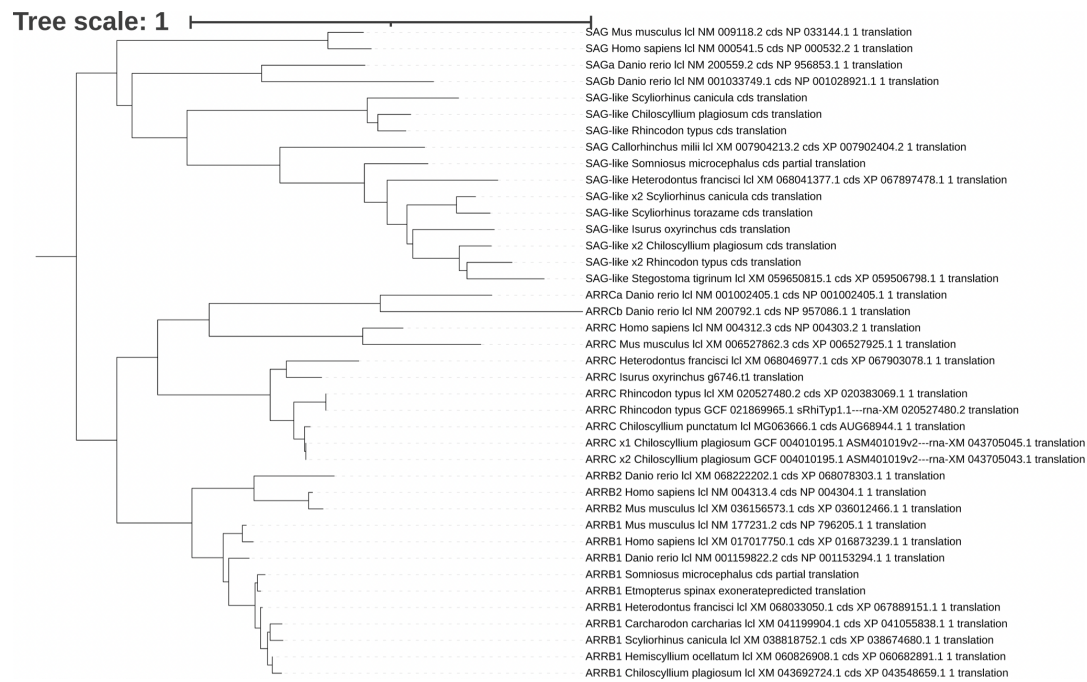


Fig S3. Arrestin phylogeny. Gene tree with sequences from several shark species and outgroup species (*Danio rerio*, *Homo sapiens* and *Mus musculus*). The scale bar denotes substitutions per site.

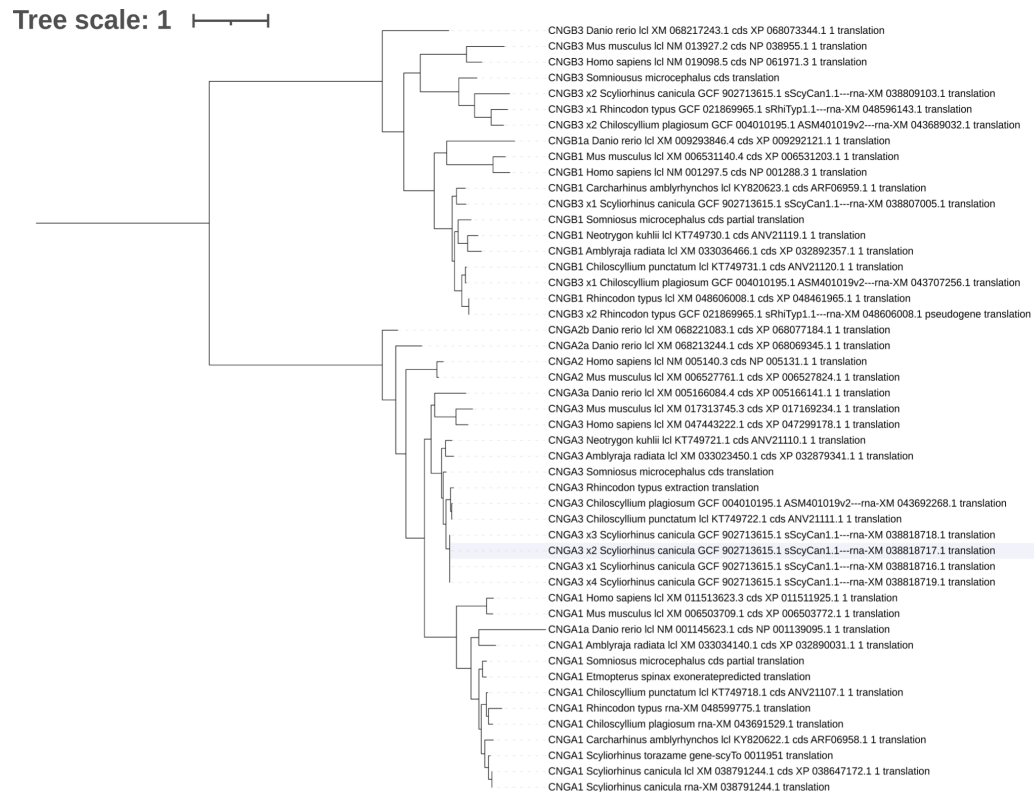


Fig S4. Cyclic nucleotide gated channel phylogeny. Gene tree with sequences from several shark species and outgroup species (*Danio rerio*, *Homo sapiens* and *Mus musculus*). The scale bar denotes substitutions per site.

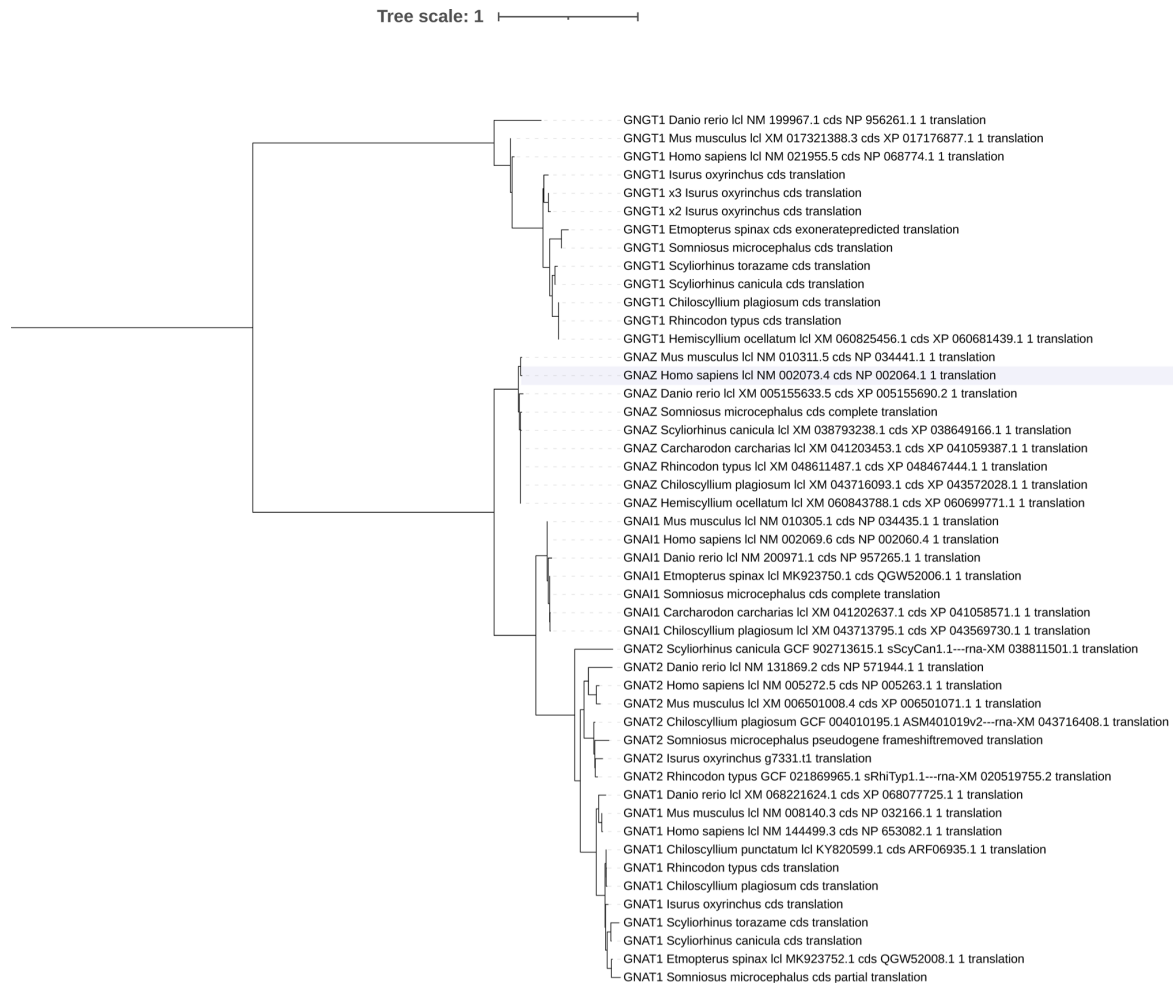


Fig S5. Transducin phylogeny. Gene tree with sequences from several shark species and outgroup species (*Danio rerio*, *Homo sapiens* and *Mus musculus*). The scale bar denotes substitutions per site.

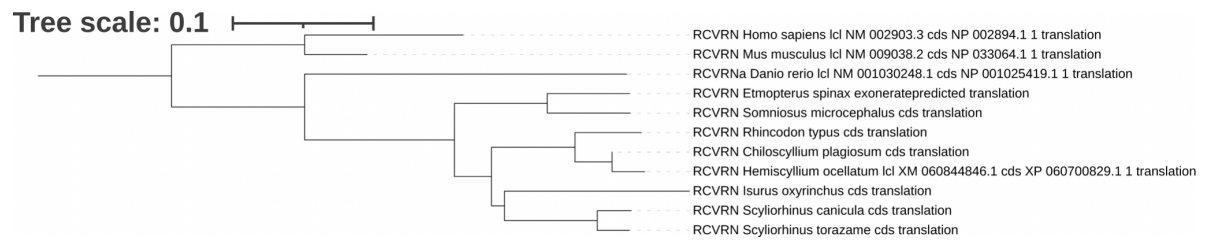


Fig S6. Recoverin phylogeny. Gene tree with sequences from several shark species and outgroup species (*Danio rerio*, *Homo sapiens* and *Mus musculus*). The scale bar denotes substitutions per site.

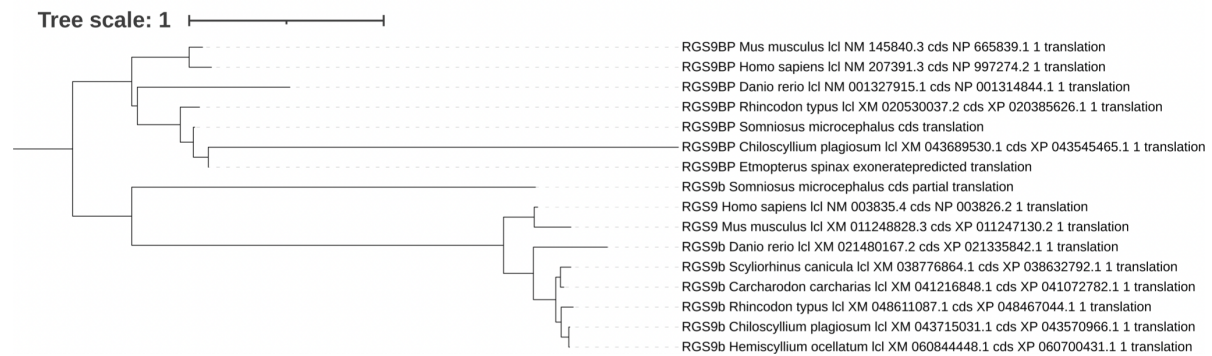


Fig S7. Regulator of G protein signalling 9 phylogeny. Gene tree with sequences from several shark species and outgroup species (*Danio rerio*, *Homo sapiens* and *Mus musculus*). The scale bar denotes substitutions per site.

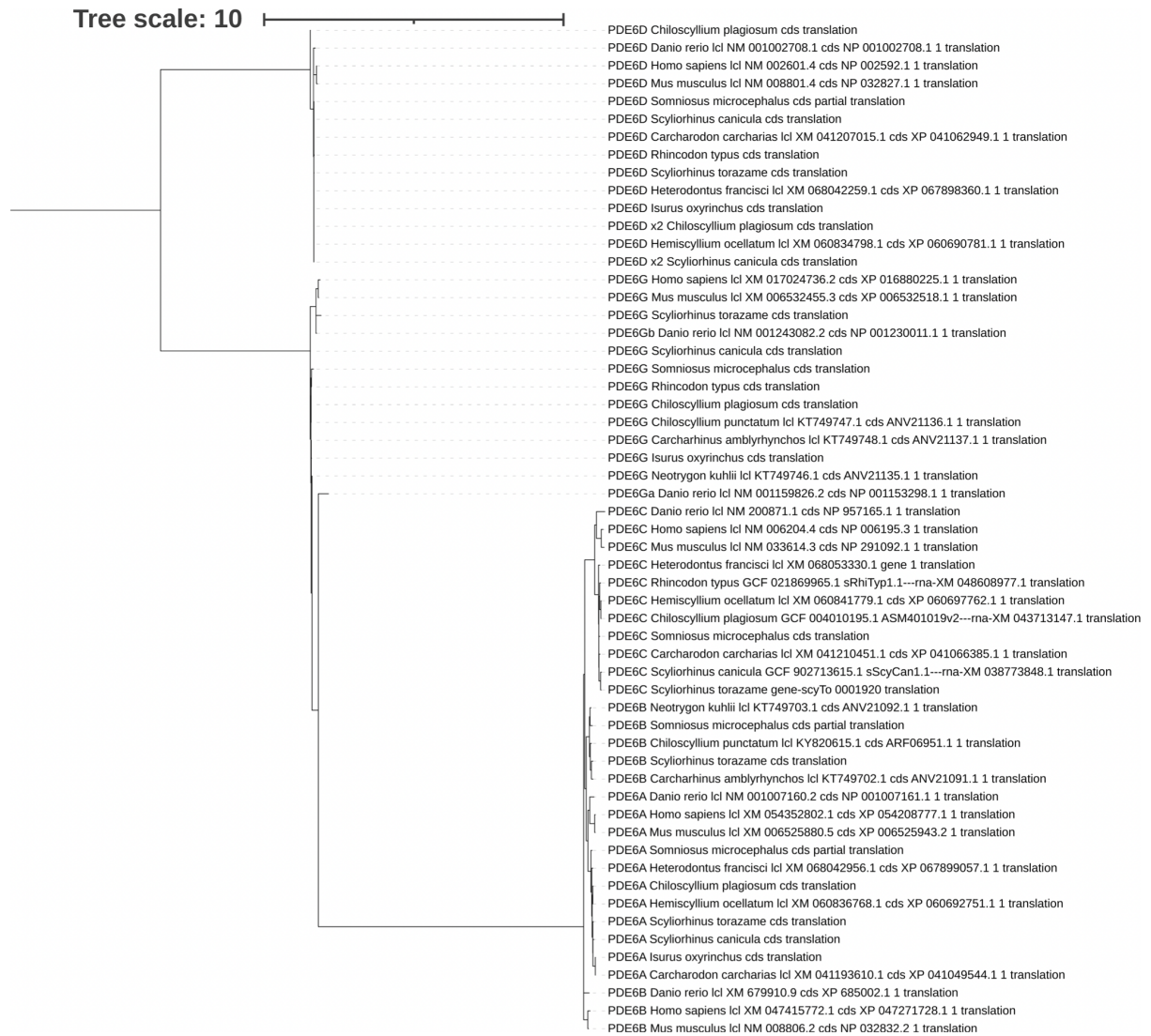


Fig S8. Phosphodiesterase phylogeny. Gene tree with sequences from several shark species and outgroup species (*Danio rerio*, *Homo sapiens* and *Mus musculus*). The scale bar denotes substitutions per site.

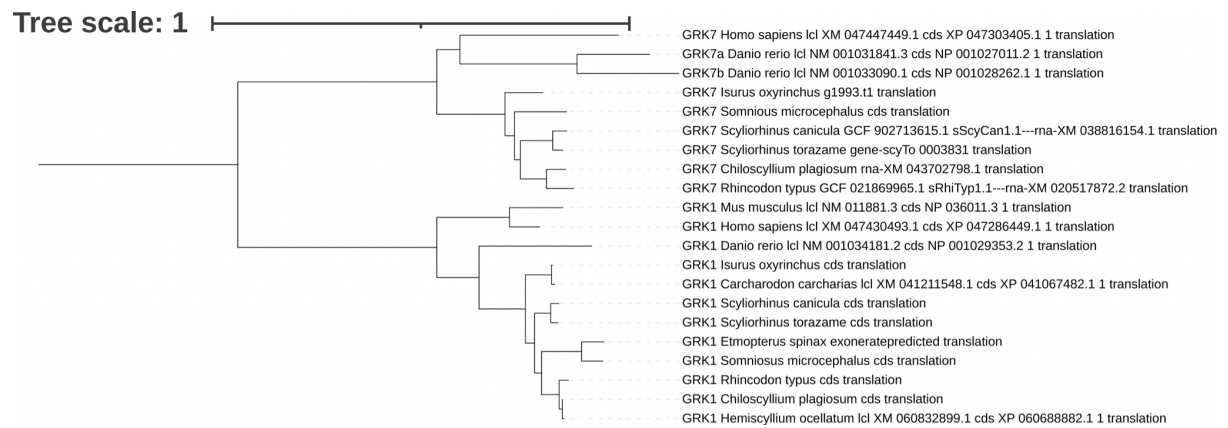


Fig S9. G-protein coupled receptor kinase phylogeny. Gene tree with sequences from several shark species and outgroup species (*Danio rerio*, *Homo sapiens* and *Mus musculus*). The scale bar denotes substitutions per site.

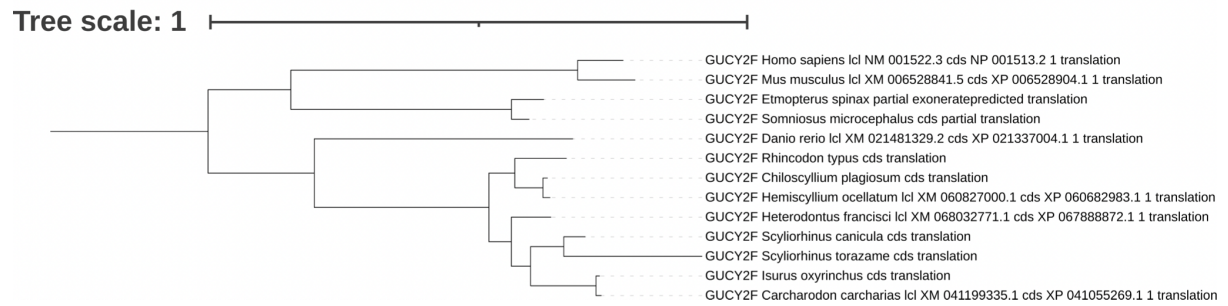


Fig S10. Guanylate cyclase 2F phylogeny. Gene tree with sequences from several shark species and outgroup species (*Danio rerio*, *Homo sapiens* and *Mus musculus*). The scale bar denotes substitutions per site.

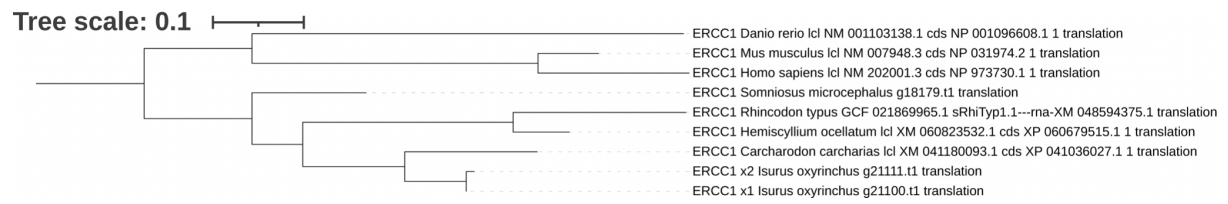


Fig S11. ERCC excision repair 1 phylogeny. Gene tree with sequences from several shark species and outgroup species (*Danio rerio*, *Homo sapiens* and *Mus musculus*). The scale bar denotes substitutions per site.

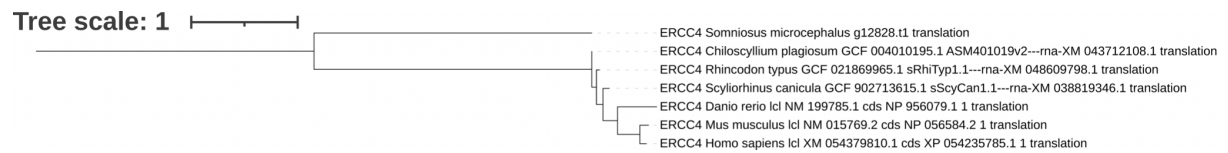


Fig S12. ERCC excision repair 4 phylogeny. Gene tree with sequences from several shark species and outgroup species (*Danio rerio*, *Homo sapiens* and *Mus musculus*). The scale bar denotes substitutions per site.

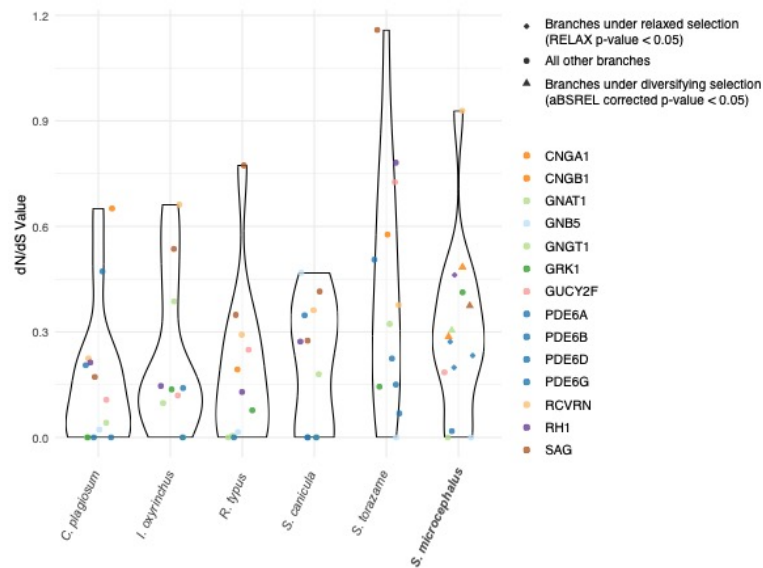


Fig S13. Distribution of dN/dS (ω) values of rod phototransduction genes in chondrichthyan species. Violin plots showing per-species distributions of ω ratios for genes involved in rod-based phototransduction, coloured by gene type. Source data are provided as a Source Data file.

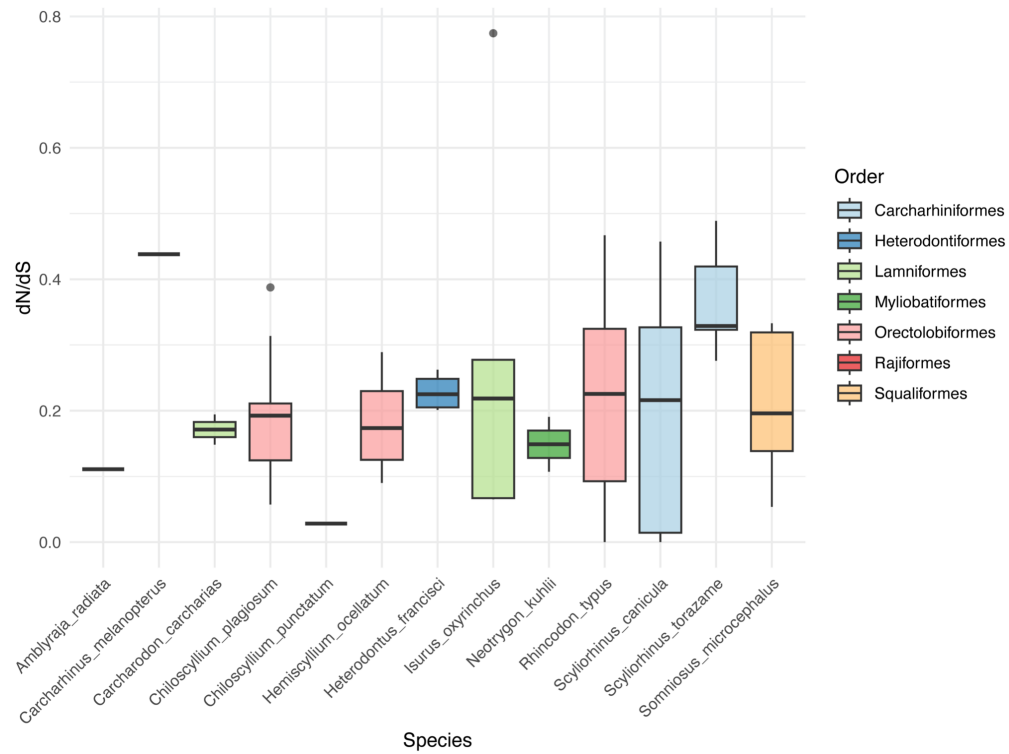


Fig S14. Distribution of dN/dS (ω) values of all retrieved cone and non-visual phototransduction genes in chondrichthyan species. Box-and-whisker plots showing per-species distributions of ω ratios for genes involved in cone-based and non-visual phototransduction, coloured by order. Source data are provided as a Source Data file.

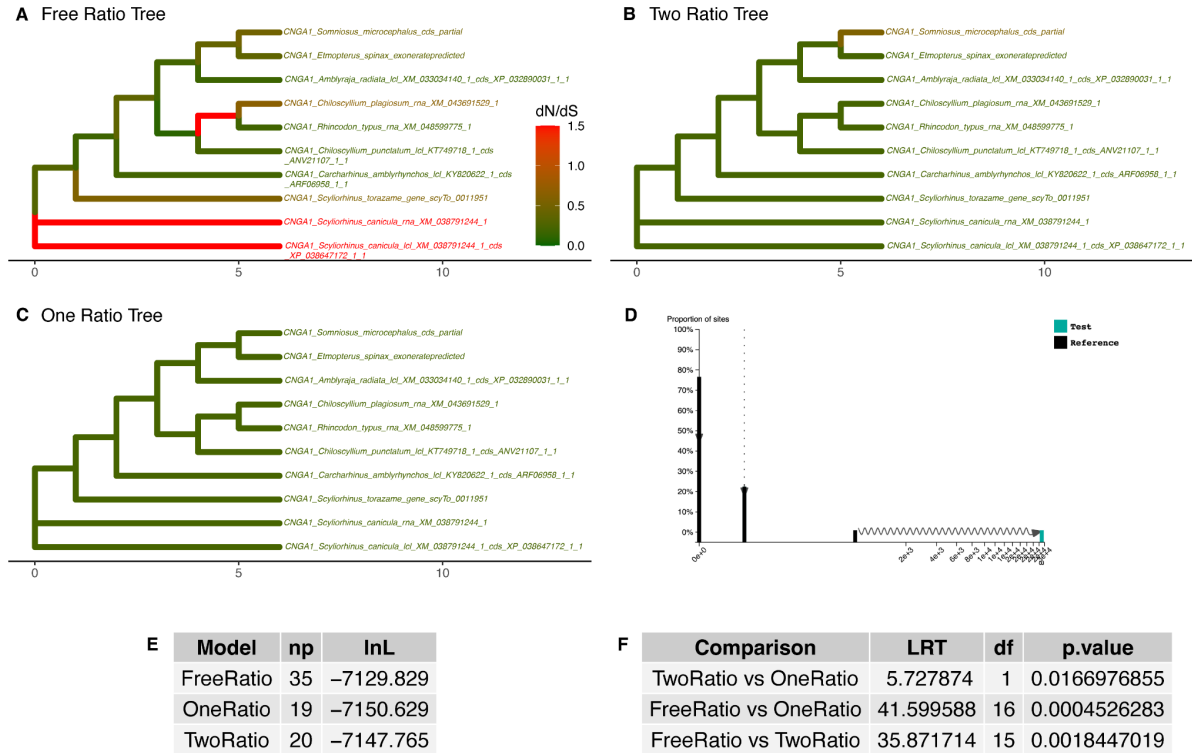


Fig S15. Selection analysis on chondrichthyan CNGA1 genes. PAML was used to compute the dN/dS ($= \omega$) per branch under four different models. **A**, Free-ratio model which fits one ω ratio per branch. **B**, Two-ratio model with one ω ratio for *Somniosus microcephalus* and one ω ratio for other shark species. **C**, One-ratio model with the same ω ratio for all shark species. **D**, RELAX ω distribution results under the RELAX alternative model, assigning *Somniosus microcephalus* as test branches and all other shark species as reference branches. **E**, Log-likelihood (lnL) and number of parameters (np) of each model. **F**, Log-likelihood ratio test (LRT) between each of the models, showing degrees of freedom (df) and statistical significance (p.value) for each comparison.

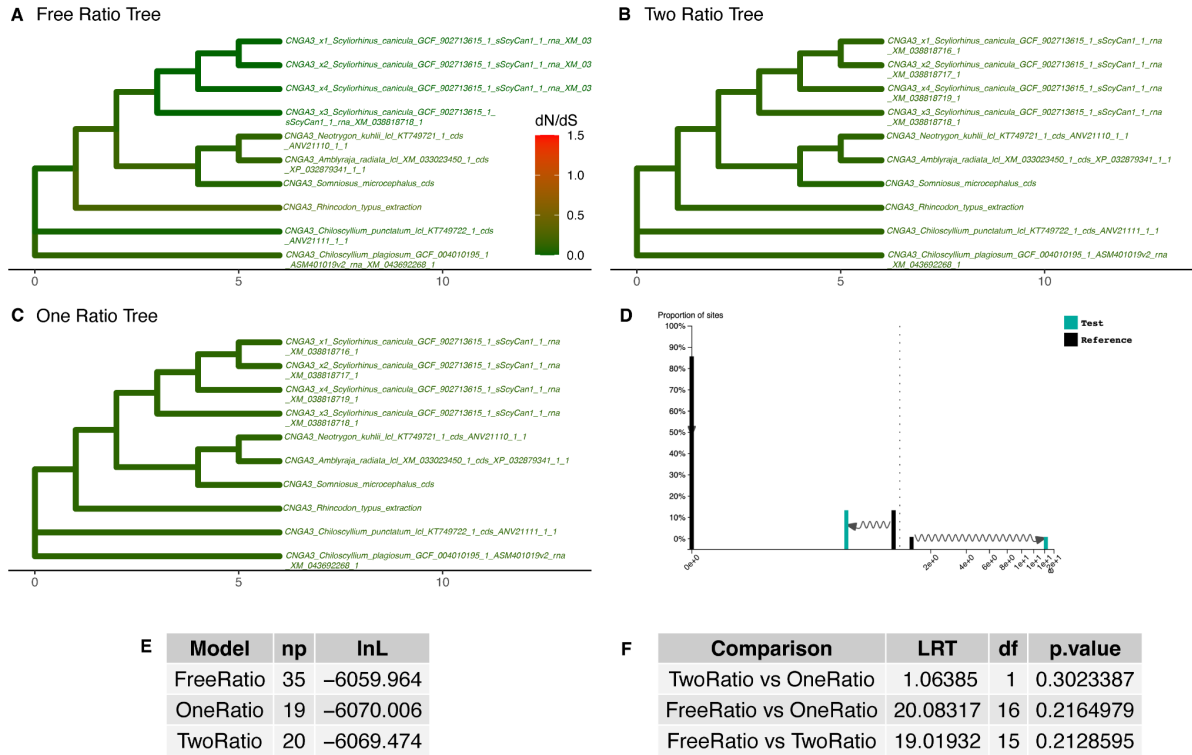


Fig S16. Selection analysis on chondrichthyan CNGA3 genes. PAML was used to compute the dN/dS ($= \omega$) per branch under four different models. **A**, Free-ratio model which fits one ω ratio per branch. **B**, Two-ratio model with one ω ratio for *Somniosus microcephalus* and one ω ratio for other shark species. **C**, One-ratio model with the same ω ratio for all shark species. **D**, RELAX ω distribution results under the RELAX alternative model, assigning *Somniosus microcephalus* as test branches and all other shark species as reference branches. **E**, Log-likelihood (lnL) and number of parameters (np) of each model. **F**, Log-likelihood ratio test (LRT) between each of the models, showing degrees of freedom (df) and statistical significance (p.value) for each comparison.

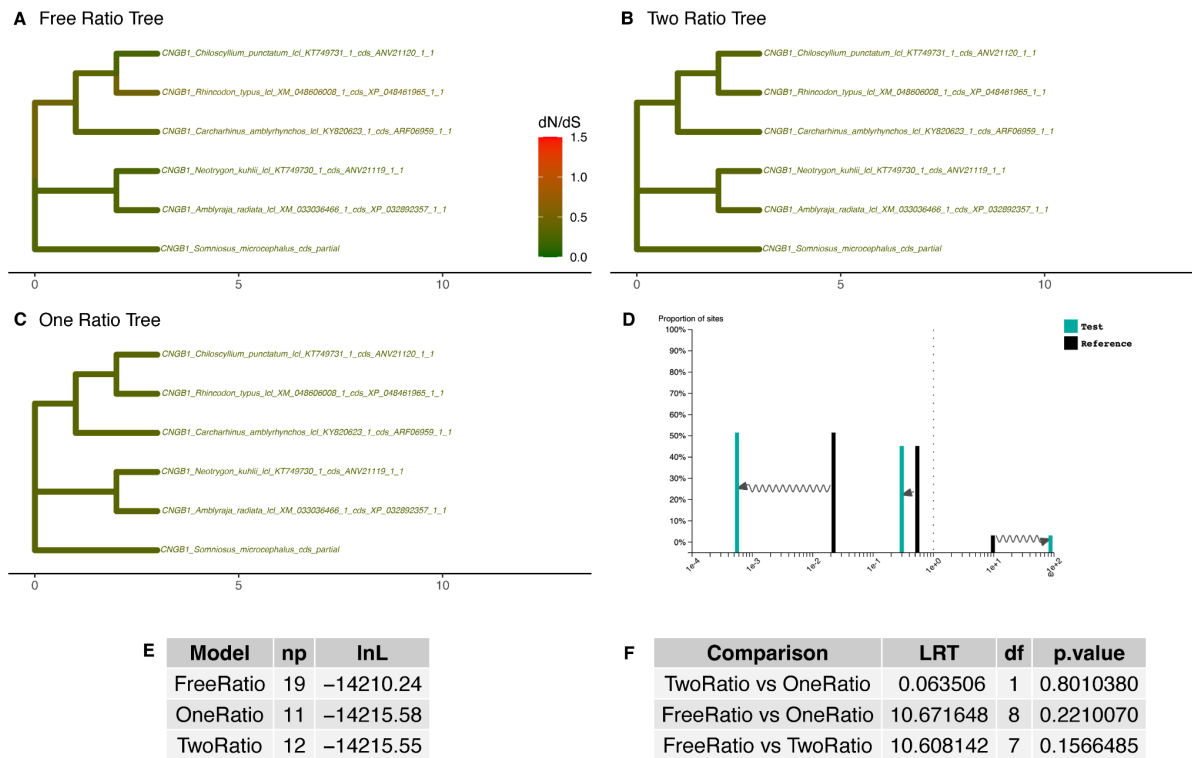


Fig S17. Selection analysis on chondrichthyan CNGB1 genes. PAML was used to compute the dN/dS ($= \omega$) per branch under four different models. **A**, Free-ratio model which fits one ω ratio per branch. **B**, Two-ratio model with one ω ratio for *Somniosus microcephalus* and one ω ratio for other shark species. **C**, One-ratio model with the same ω ratio for all shark species. **D**, RELAX ω distribution results under the RELAX alternative model, assigning *Somniosus microcephalus* as test branches and all other shark species as reference branches. **E**, Log-likelihood (lnL) and number of parameters (np) of each model. **F**, Log-likelihood ratio test (LRT) between each of the models, showing degrees of freedom (df) and statistical significance (p.value) for each comparison.

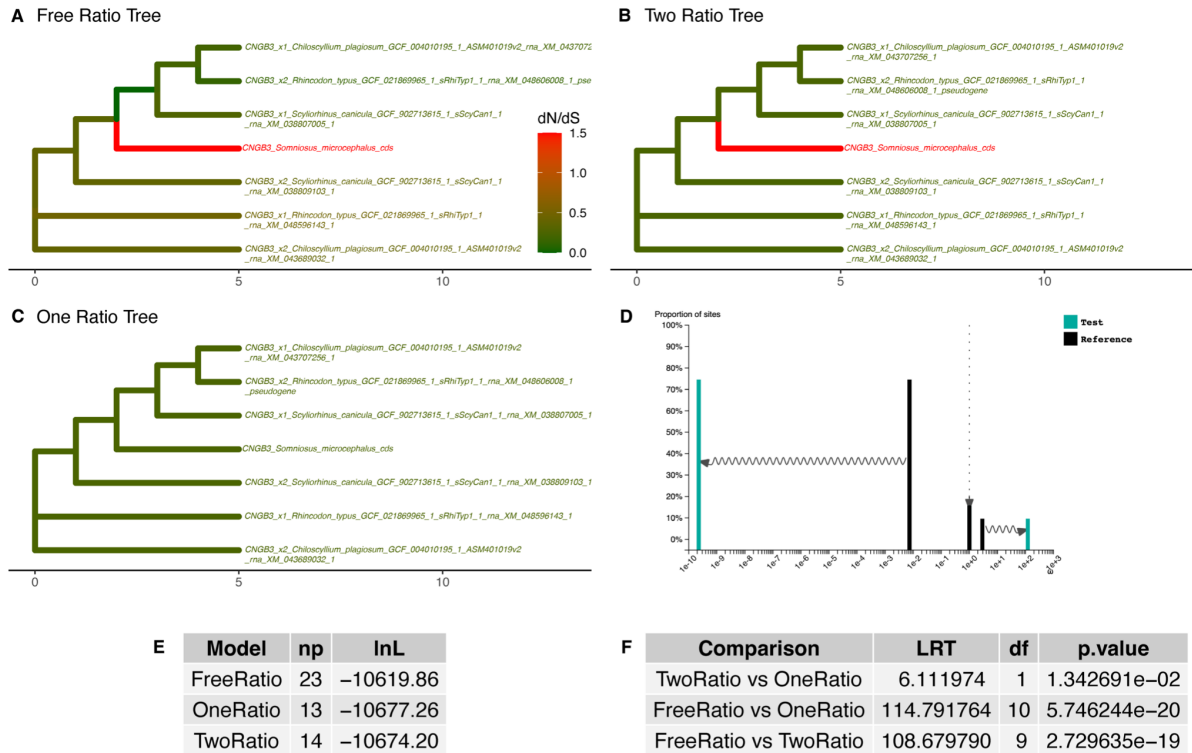


Fig S18. Selection analysis on chondrichthyan CNGB3 genes. PAML was used to compute the dN/dS ($= \omega$) per branch under four different models. **A**, Free-ratio model which fits one ω ratio per branch. **B**, Two-ratio model with one ω ratio for *Somniosus microcephalus* and one ω ratio for other shark species. **C**, One-ratio model with the same ω ratio for all shark species. **D**, RELAX ω distribution results under the RELAX alternative model, assigning *Somniosus microcephalus* as test branches and all other shark species as reference branches. **E**, Log-likelihood (lnL) and number of parameters (np) of each model. **F**, Log-likelihood ratio test (LRT) between each of the models, showing degrees of freedom (df) and statistical significance (p.value) for each comparison.

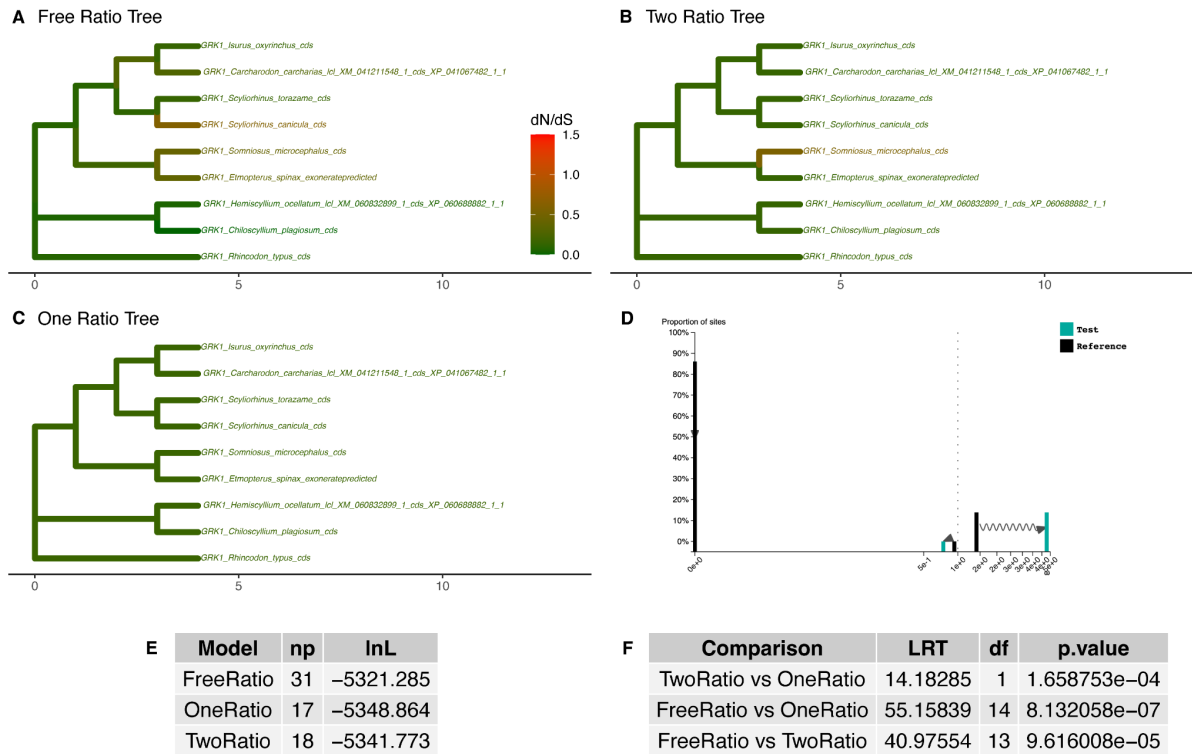


Fig S19. Selection analysis on chondrichthyan GRK1 genes. PAML was used to compute the dN/dS ($= \omega$) per branch under four different models. **A**, Free-ratio model which fits one ω ratio per branch. **B**, Two-ratio model with one ω ratio for *Somniosus microcephalus* and one ω ratio for other shark species. **C**, One-ratio model with the same ω ratio for all shark species. **D**, RELAX ω distribution results under the RELAX alternative model, assigning *Somniosus microcephalus* as test branches and all other shark species as reference branches. **E**, Log-likelihood (lnL) and number of parameters (np) of each model. **F**, Log-likelihood ratio test (LRT) between each of the models, showing degrees of freedom (df) and statistical significance (p.value) for each comparison.

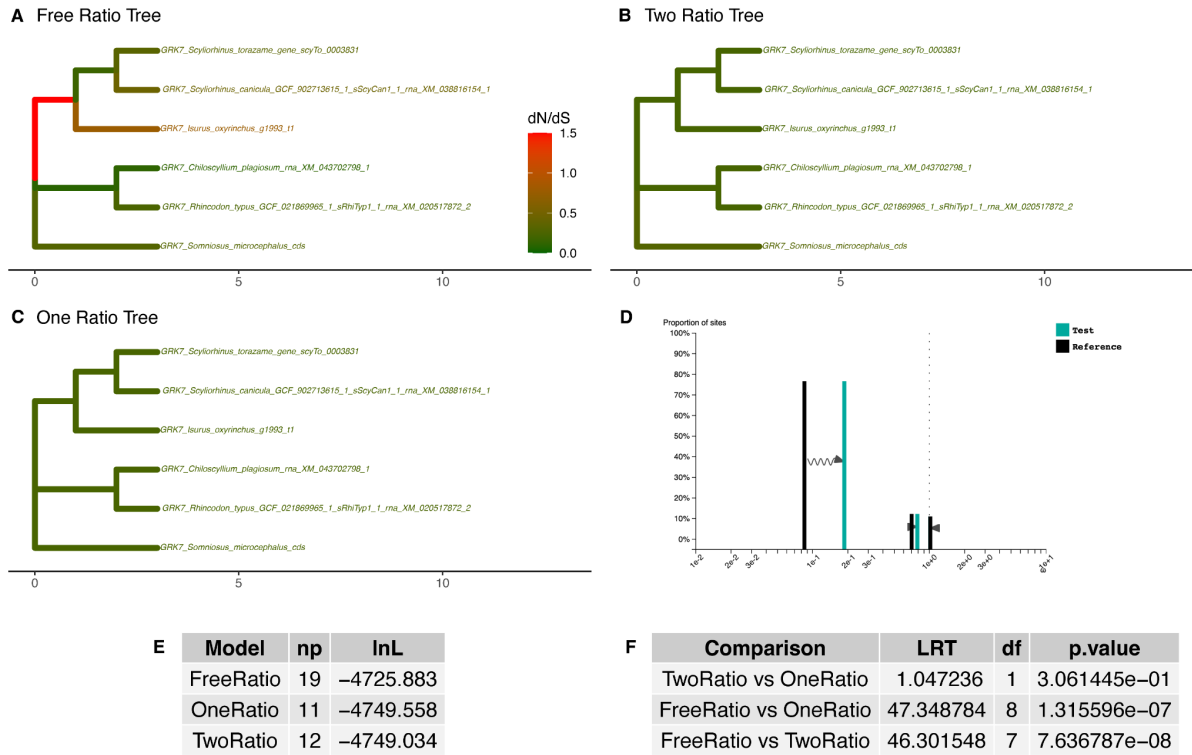


Fig S20. Selection analysis on chondrichthyan GRK7 genes. PAML was used to compute the dN/dS ($= \omega$) per branch under four different models. **A**, Free-ratio model which fits one ω ratio per branch. **B**, Two-ratio model with one ω ratio for *Somniosus microcephalus* and one ω ratio for other shark species. **C**, One-ratio model with the same ω ratio for all shark species. **D**, RELAX ω distribution results under the RELAX alternative model, assigning *Somniosus microcephalus* as test branches and all other shark species as reference branches. **E**, Log-likelihood (lnL) and number of parameters (np) of each model. **F**, Log-likelihood ratio test (LRT) between each of the models, showing degrees of freedom (df) and statistical significance (p.value) for each comparison.

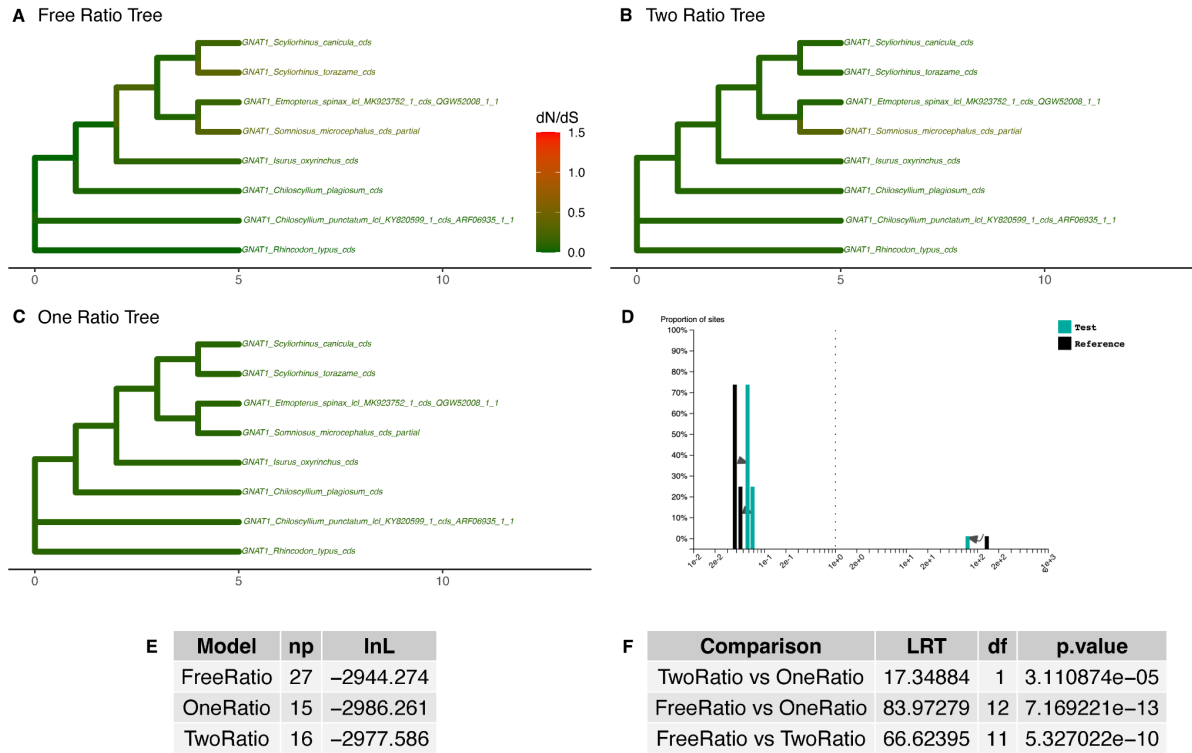


Fig S21. Selection analysis on chondrichthyan GNAT1 genes. PAML was used to compute the dN/dS ($= \omega$) per branch under four different models. **A**, Free-ratio model which fits one ω ratio per branch. **B**, Two-ratio model with one ω ratio for *Somniosus microcephalus* and one ω ratio for other shark species. **C**, One-ratio model with the same ω ratio for all shark species. **D**, RELAX ω distribution results under the RELAX alternative model, assigning *Somniosus microcephalus* as test branches and all other shark species as reference branches. **E**, Log-likelihood (lnL) and number of parameters (np) of each model. **F**, Log-likelihood ratio test (LRT) between each of the models, showing degrees of freedom (df) and statistical significance (p.value) for each comparison.

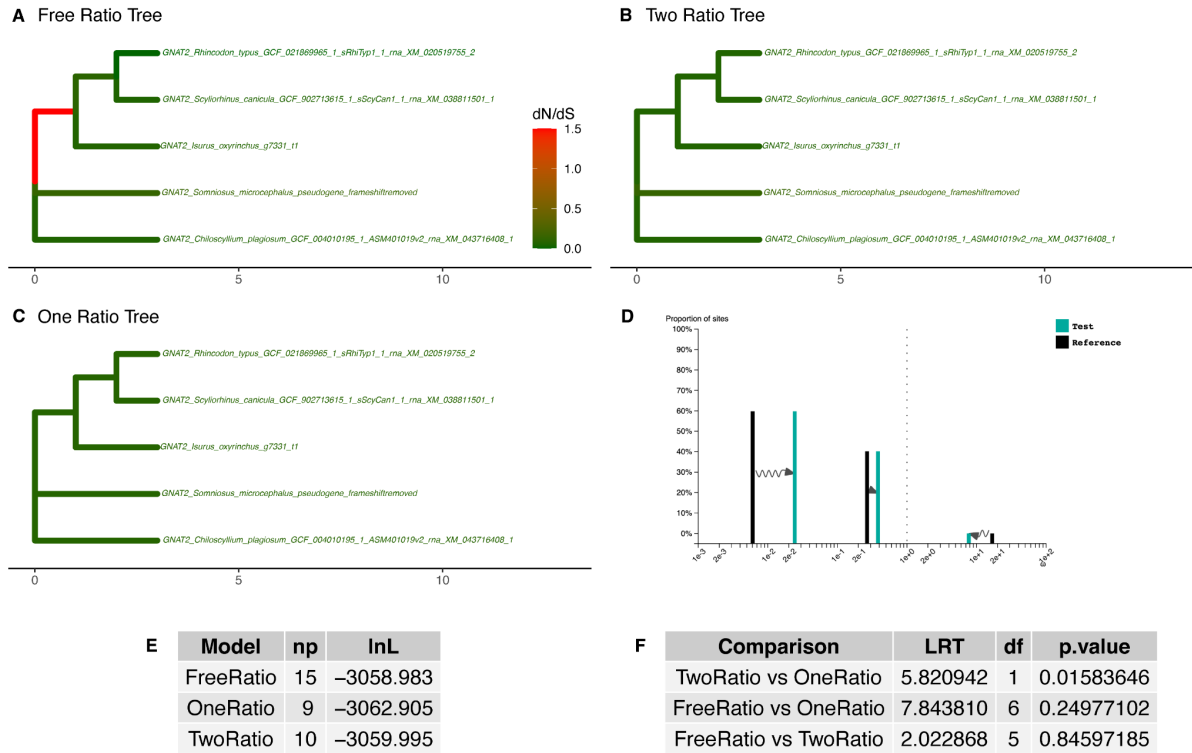


Fig S22. Selection analysis on chondrichthyan GNAT2 genes. PAML was used to compute the dN/dS ($= \omega$) per branch under four different models. **A**, Free-ratio model which fits one ω ratio per branch. **B**, Two-ratio model with one ω ratio for *Somniosus microcephalus* and one ω ratio for other shark species. **C**, One-ratio model with the same ω ratio for all shark species. **D**, RELAX ω distribution results under the RELAX alternative model, assigning *Somniosus microcephalus* as test branches and all other shark species as reference branches. **E**, Log-likelihood (lnL) and number of parameters (np) of each model. **F**, Log-likelihood ratio test (LRT) between each of the models, showing degrees of freedom (df) and statistical significance (p.value) for each comparison.

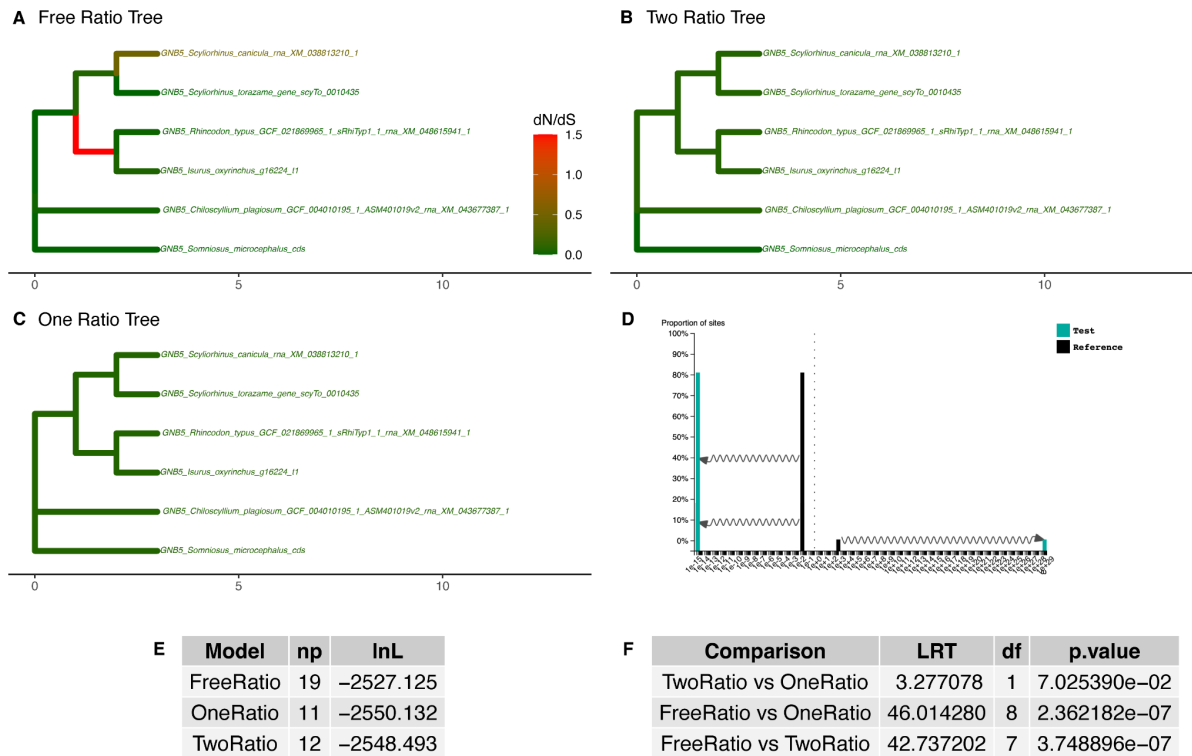


Fig S23. Selection analysis on chondrichthyan GNB5 genes. PAML was used to compute the dN/dS ($= \omega$) per branch under four different models. **A**, Free-ratio model which fits one ω ratio per branch. **B**, Two-ratio model with one ω ratio for *Somniosus microcephalus* and one ω ratio for other shark species. **C**, One-ratio model with the same ω ratio for all shark species. **D**, RELAX ω distribution results under the RELAX alternative model, assigning *Somniosus microcephalus* as test branches and all other shark species as reference branches. **E**, Log-likelihood (lnL) and number of parameters (np) of each model. **F**, Log-likelihood ratio test (LRT) between each of the models, showing degrees of freedom (df) and statistical significance (p.value) for each comparison.

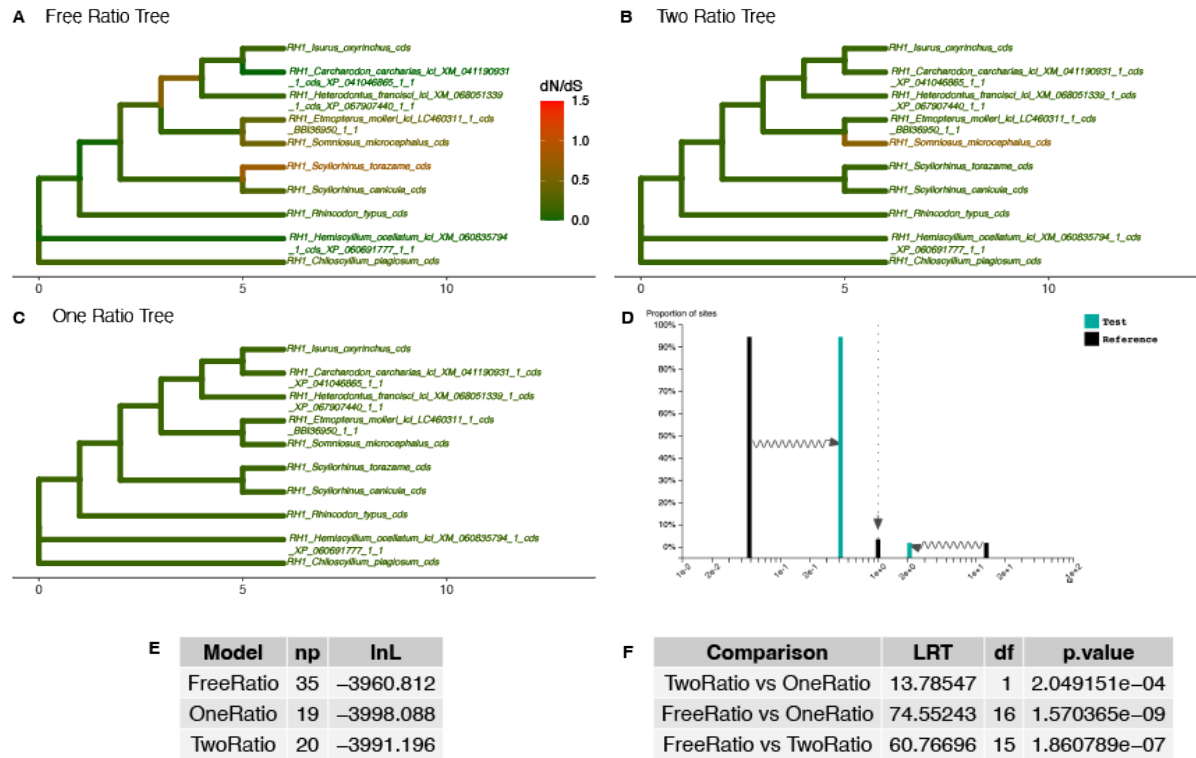


Fig S24. Selection analysis on chondrichthyan RH1 genes. PAML was used to compute the dN/dS ($= \omega$) per branch under four different models. **A**, Free-ratio model which fits one ω ratio per branch. **B**, Two-ratio model with one ω ratio for *Somniosus microcephalus* and one ω ratio for other shark species. **C**, One-ratio model with the same ω ratio for all shark species. **D**, RELAX ω distribution results under the RELAX alternative model, assigning *Somniosus microcephalus* as test branches and all other shark species as reference branches. **E**, Log-likelihood (lnL) and number of parameters (np) of each model. **F**, Log-likelihood ratio test (LRT) between each of the models, showing degrees of freedom (df) and statistical significance (p.value) for each comparison.

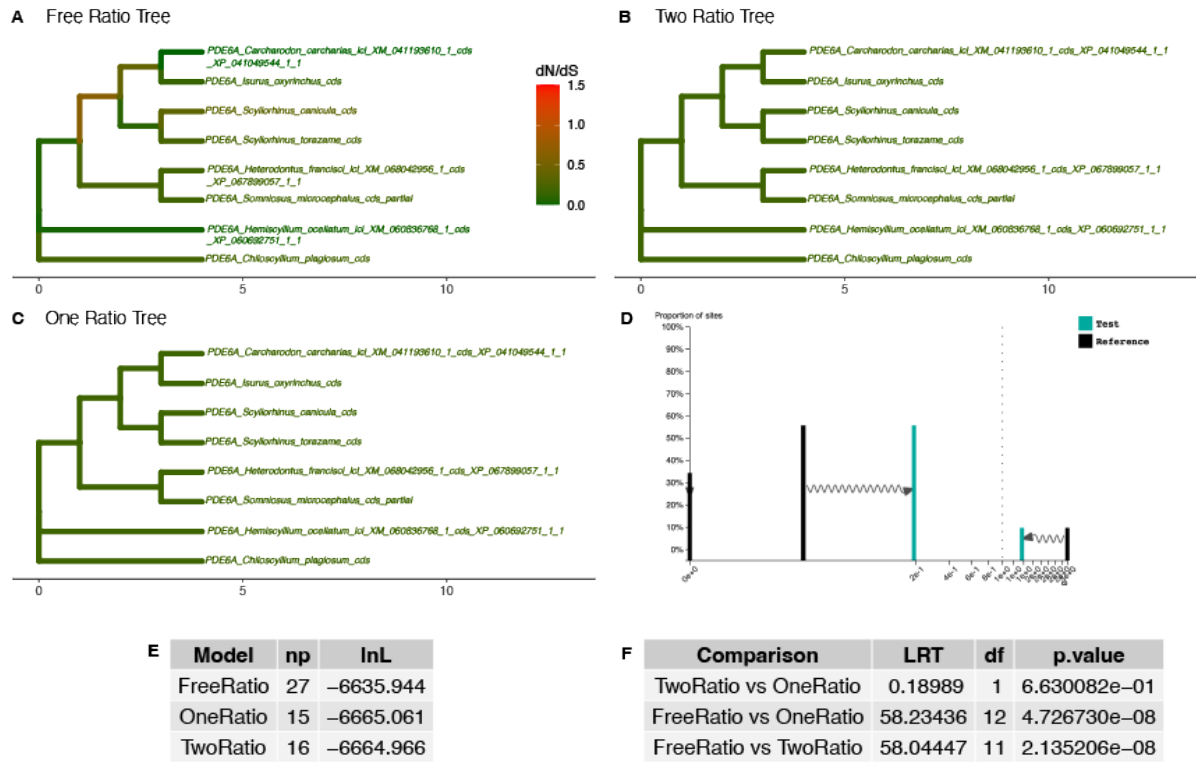


Fig S25. Selection analysis on chondrichthyan PDE6A genes. PAML was used to compute the dN/dS ($= \omega$) per branch under four different models. **A**, Free-ratio model which fits one ω ratio per branch. **B**, Two-ratio model with one ω ratio for *Somniosus microcephalus* and one ω ratio for other shark species. **C**, One-ratio model with the same ω ratio for all shark species. **D**, RELAX ω distribution results under the RELAX alternative model, assigning *Somniosus microcephalus* as test branches and all other shark species as reference branches. **E**, Log-likelihood (lnL) and number of parameters (np) of each model. **F**, Log-likelihood ratio test (LRT) between each of the models, showing degrees of freedom (df) and statistical significance (p.value) for each comparison.

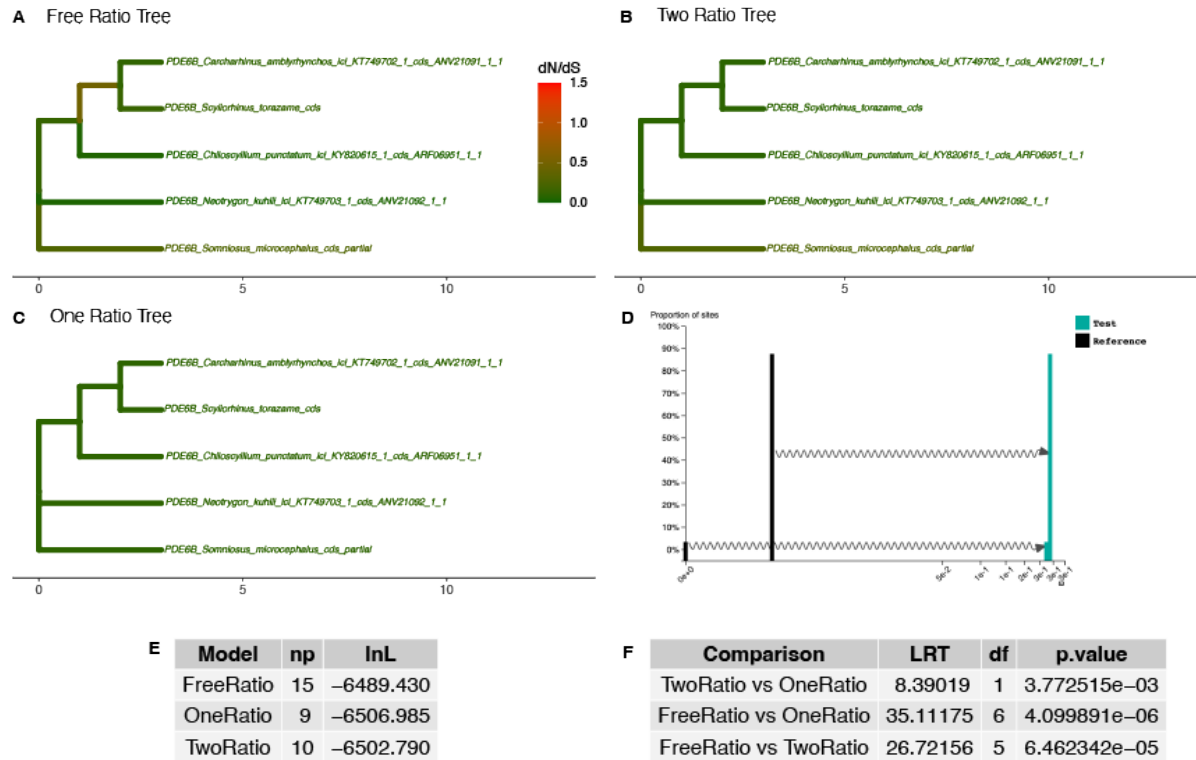


Fig S26. Selection analysis on chondrichthyan PDE6B genes. PAML was used to compute the dN/dS ($= \omega$) per branch under four different models. **A**, Free-ratio model which fits one ω ratio per branch. **B**, Two-ratio model with one ω ratio for *Somniosus microcephalus* and one ω ratio for other shark species. **C**, One-ratio model with the same ω ratio for all shark species. **D**, RELAX ω distribution results under the RELAX alternative model, assigning *Somniosus microcephalus* as test branches and all other shark species as reference branches. **E**, Log-likelihood (lnL) and number of parameters (np) of each model. **F**, Log-likelihood ratio test (LRT) between each of the models, showing degrees of freedom (df) and statistical significance (p.value) for each comparison.

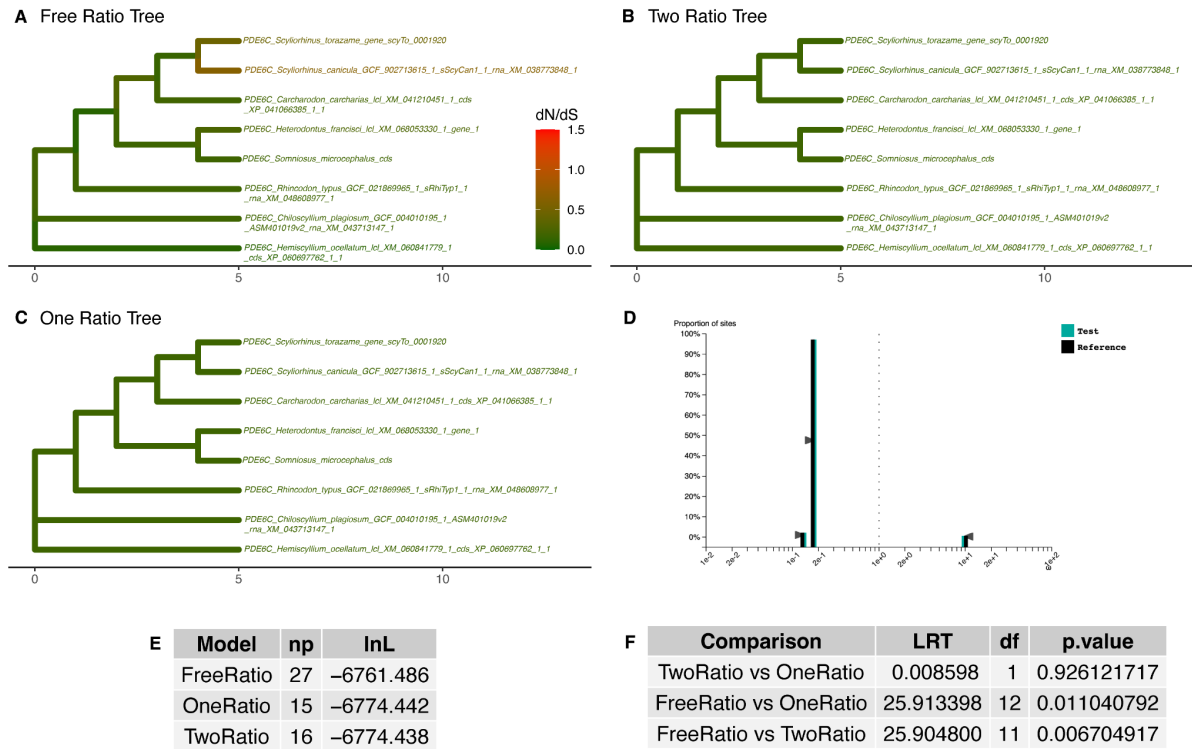


Fig S27. Selection analysis on chondrichthyan PDE6C genes. PAML was used to compute the dN/dS ($= \omega$) per branch under four different models. **A**, Free-ratio model which fits one ω ratio per branch. **B**, Two-ratio model with one ω ratio for *Somniosus microcephalus* and one ω ratio for other shark species. **C**, One-ratio model with the same ω ratio for all shark species. **D**, RELAX ω distribution results under the RELAX alternative model, assigning *Somniosus microcephalus* as test branches and all other shark species as reference branches. **E**, Log-likelihood (lnL) and number of parameters (np) of each model. **F**, Log-likelihood ratio test (LRT) between each of the models, showing degrees of freedom (df) and statistical significance (p.value) for each comparison.

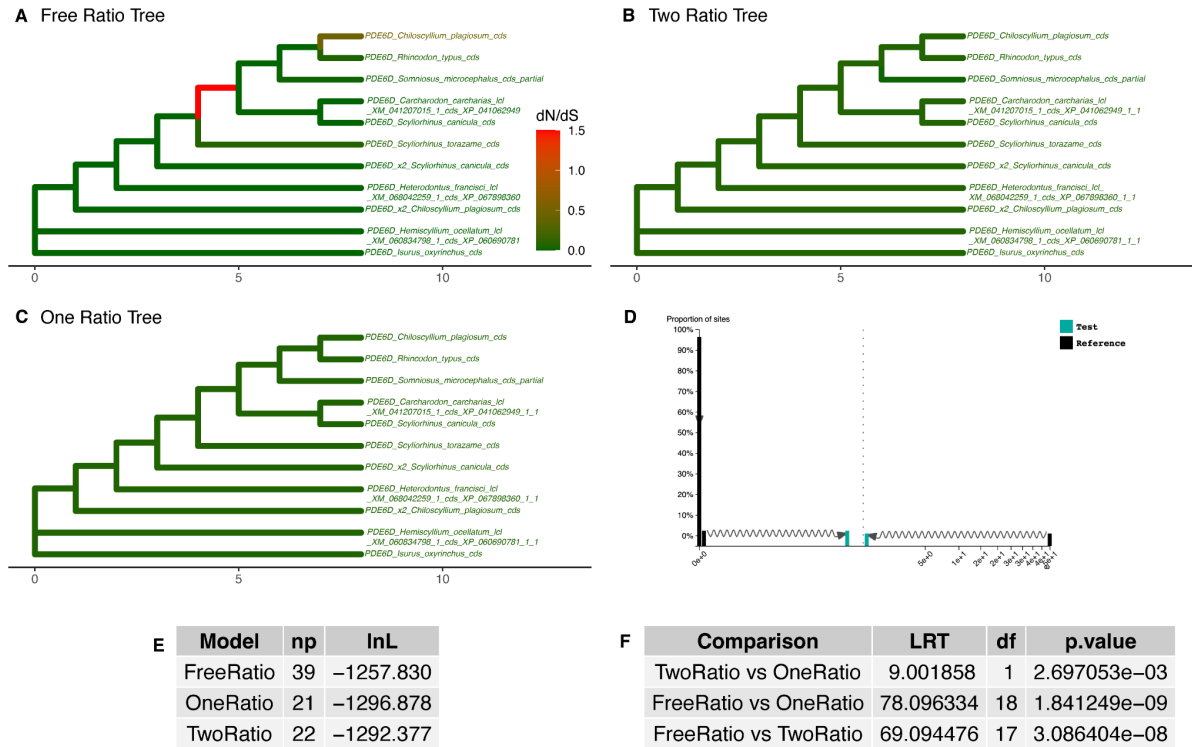


Fig S28. Selection analysis on chondrichthyan PDE6D genes. PAML was used to compute the dN/dS ($= \omega$) per branch under four different models. **A**, Free-ratio model which fits one ω ratio per branch. **B**, Two-ratio model with one ω ratio for *Somniosus microcephalus* and one ω ratio for other shark species. **C**, One-ratio model with the same ω ratio for all shark species. **D**, RELAX ω distribution results under the RELAX alternative model, assigning *Somniosus microcephalus* as test branches and all other shark species as reference branches. **E**, Log-likelihood (lnL) and number of parameters (np) of each model. **F**, Log-likelihood ratio test (LRT) between each of the models, showing degrees of freedom (df) and statistical significance (p.value) for each comparison.

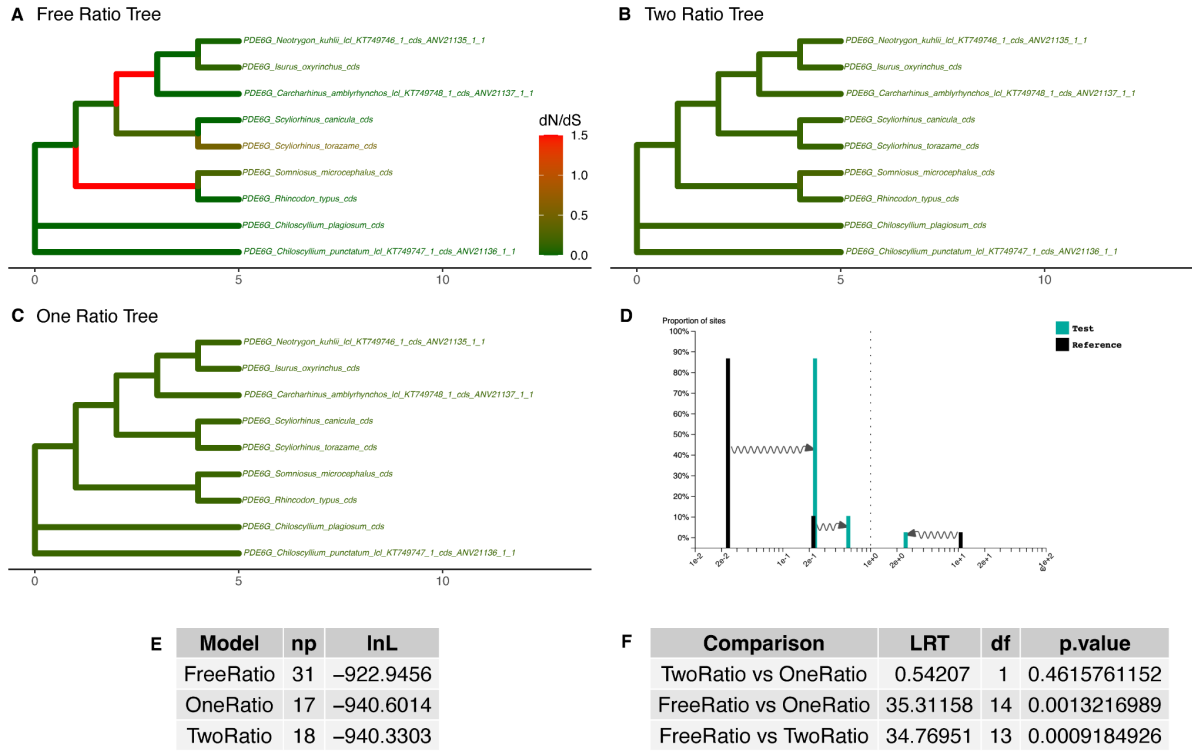


Fig S29. Selection analysis on chondrichthyan PDE6G genes. PAML was used to compute the dN/dS ($= \omega$) per branch under four different models. **A**, Free-ratio model which fits one ω ratio per branch. **B**, Two-ratio model with one ω ratio for *Somniosus microcephalus* and one ω ratio for other shark species. **C**, One-ratio model with the same ω ratio for all shark species. **D**, RELAX ω distribution results under the RELAX alternative model, assigning *Somniosus microcephalus* as test branches and all other shark species as reference branches. **E**, Log-likelihood (lnL) and number of parameters (np) of each model. **F**, Log-likelihood ratio test (LRT) between each of the models, showing degrees of freedom (df) and statistical significance (p.value) for each comparison.

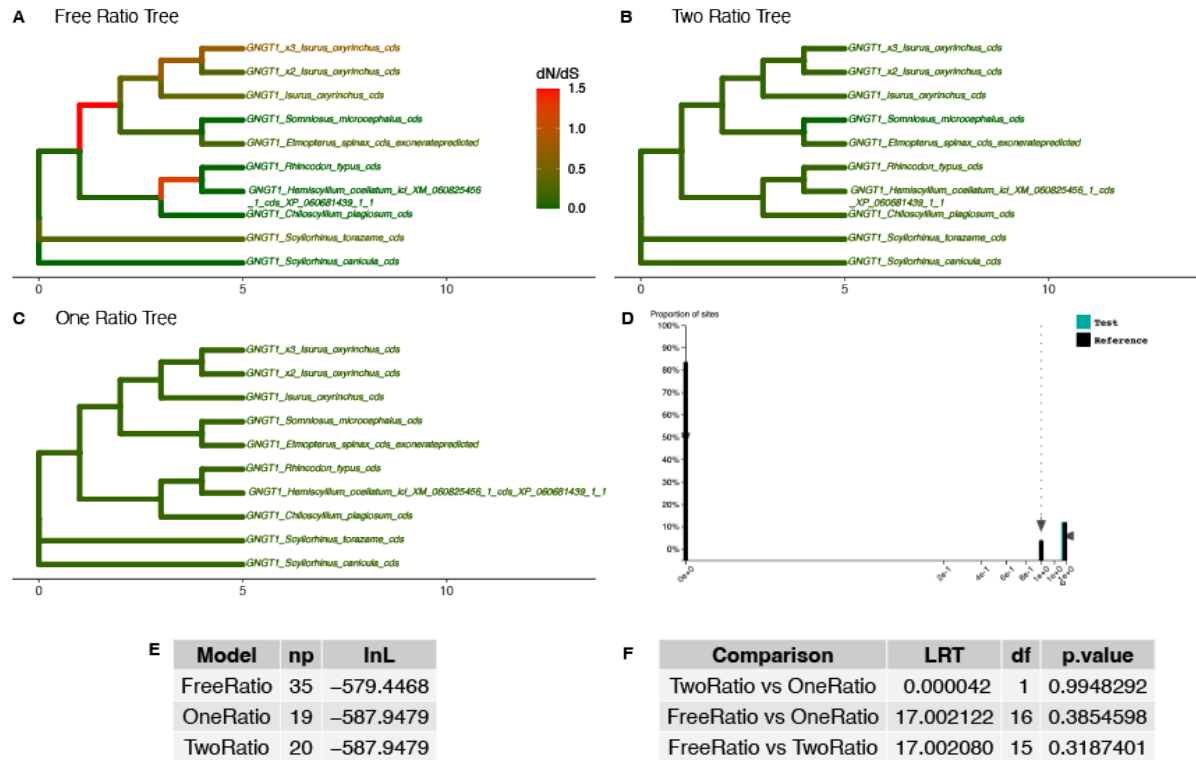


Fig S30. Selection analysis on chondrichthyan GNGT1 genes. PAML was used to compute the dN/dS ($= \omega$) per branch under four different models. **A**, Free-ratio model which fits one ω ratio per branch. **B**, Two-ratio model with one ω ratio for *Somniosus microcephalus* and one ω ratio for other shark species. **C**, One-ratio model with the same ω ratio for all shark species. **D**, RELAX ω distribution results under the RELAX alternative model, assigning *Somniosus microcephalus* as test branches and all other shark species as reference branches. **E**, Log-likelihood (lnL) and number of parameters (np) of each model. **F**, Log-likelihood ratio test (LRT) between each of the models, showing degrees of freedom (df) and statistical significance (p.value) for each comparison.

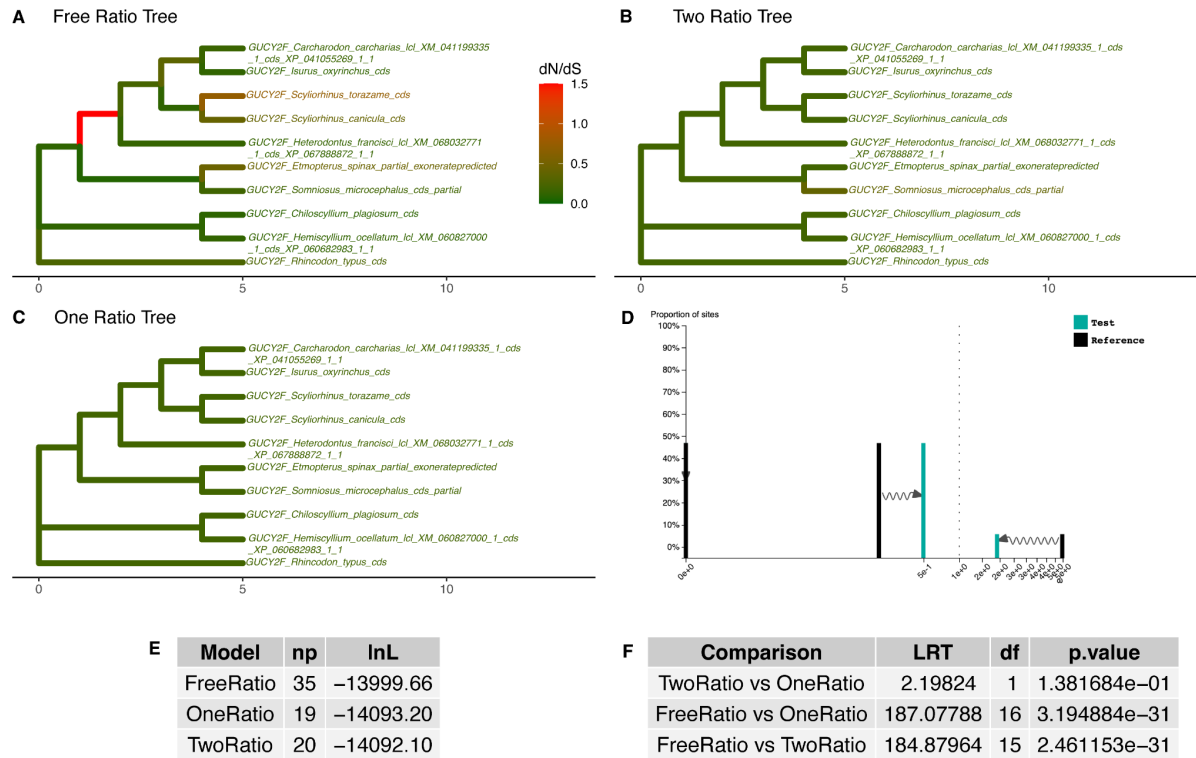


Fig S31. Selection analysis on chondrichthyan GUCY2F genes. PAML was used to compute the dN/dS ($= \omega$) per branch under four different models. **A**, Free-ratio model which fits one ω ratio per branch. **B**, Two-ratio model with one ω ratio for *Somniosus microcephalus* and one ω ratio for other shark species. **C**, One-ratio model with the same ω ratio for all shark species. **D**, RELAX ω distribution results under the RELAX alternative model, assigning *Somniosus microcephalus* as test branches and all other shark species as reference branches. **E**, Log-likelihood (lnL) and number of parameters (np) of each model. **F**, Log-likelihood ratio test (LRT) between each of the models, showing degrees of freedom (df) and statistical significance (p.value) for each comparison.

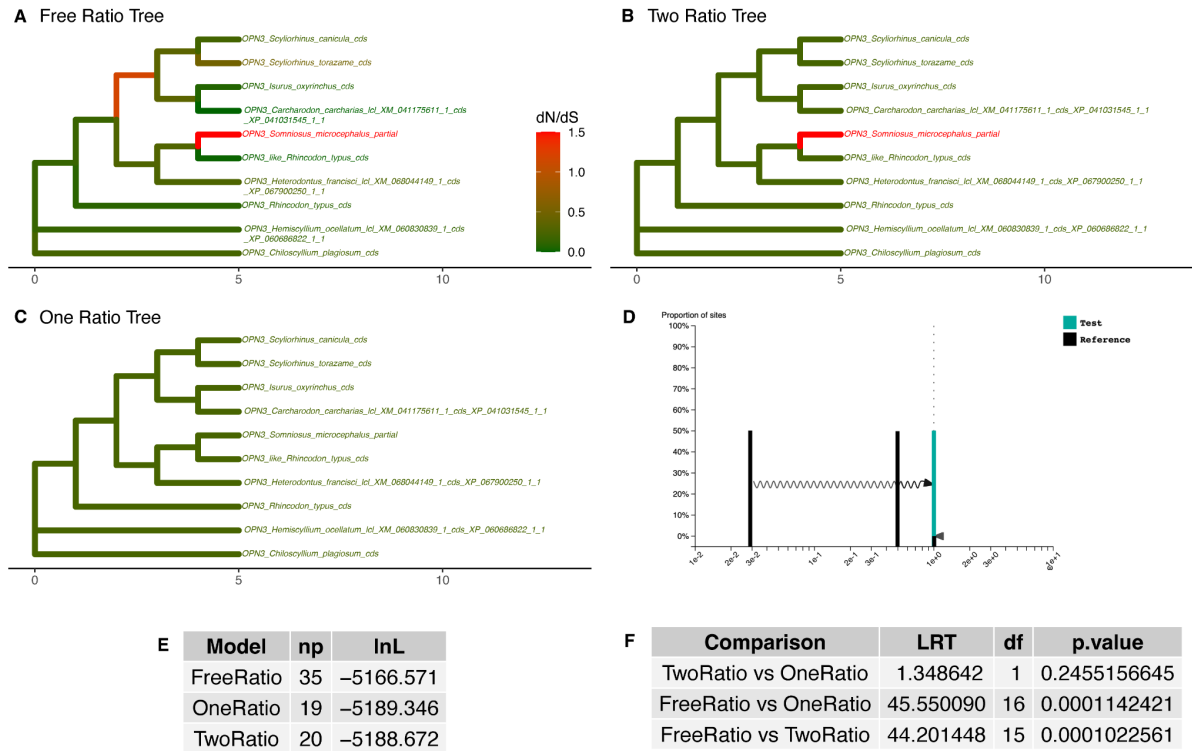


Fig S32. Selection analysis on chondrichthyan OPN3 genes. PAML was used to compute the dN/dS ($= \omega$) per branch under four different models. **A**, Free-ratio model which fits one ω ratio per branch. **B**, Two-ratio model with one ω ratio for *Somniosus microcephalus* and one ω ratio for other shark species. **C**, One-ratio model with the same ω ratio for all shark species. **D**, RELAX ω distribution results under the RELAX alternative model, assigning *Somniosus microcephalus* as test branches and all other shark species as reference branches. **E**, Log-likelihood (lnL) and number of parameters (np) of each model. **F**, Log-likelihood ratio test (LRT) between each of the models, showing degrees of freedom (df) and statistical significance (p.value) for each comparison.

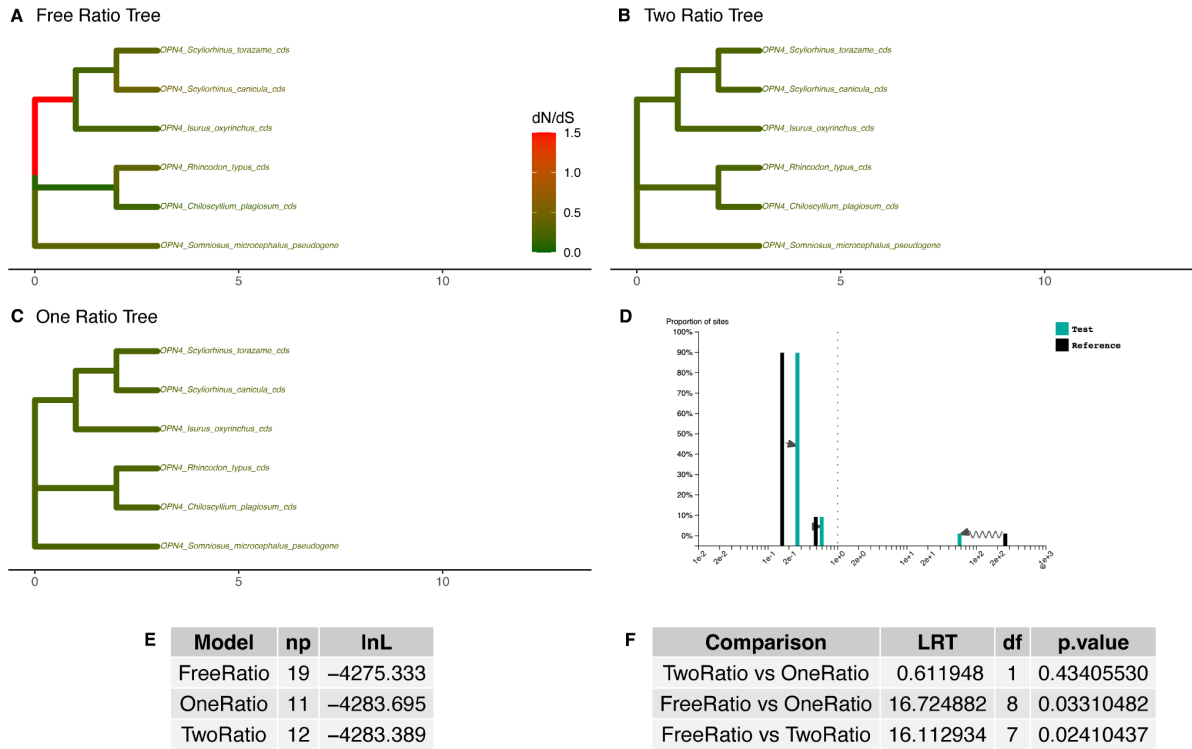


Fig S33. Selection analysis on chondrichthyan OPN4 genes. PAML was used to compute the dN/dS ($= \omega$) per branch under four different models. **A**, Free-ratio model which fits one ω ratio per branch. **B**, Two-ratio model with one ω ratio for *Somniosus microcephalus* and one ω ratio for other shark species. **C**, One-ratio model with the same ω ratio for all shark species. **D**, RELAX ω distribution results under the RELAX alternative model, assigning *Somniosus microcephalus* as test branches and all other shark species as reference branches. **E**, Log-likelihood (lnL) and number of parameters (np) of each model. **F**, Log-likelihood ratio test (LRT) between each of the models, showing degrees of freedom (df) and statistical significance (p.value) for each comparison.

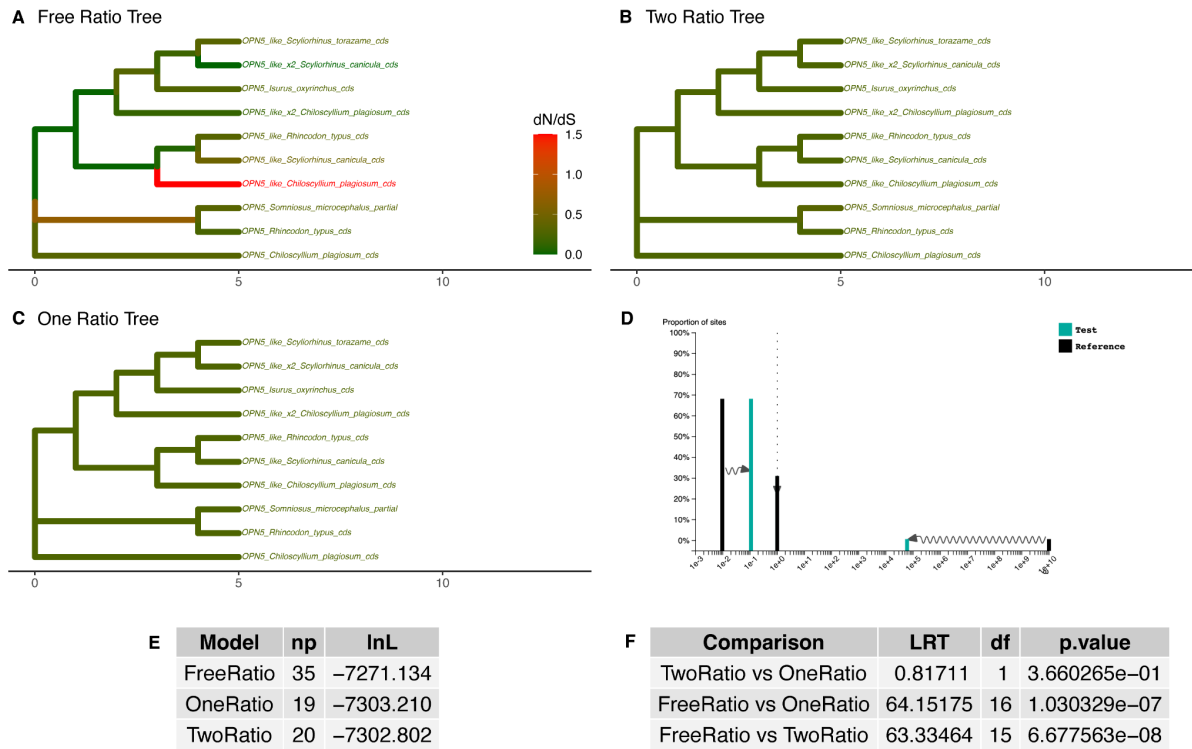


Fig S34. Selection analysis on chondrichthyan OPN5 genes. PAML was used to compute the dN/dS ($= \omega$) per branch under four different models. **A**, Free-ratio model which fits one ω ratio per branch. **B**, Two-ratio model with one ω ratio for *Somniosus microcephalus* and one ω ratio for other shark species. **C**, One-ratio model with the same ω ratio for all shark species. **D**, RELAX ω distribution results under the RELAX alternative model, assigning *Somniosus microcephalus* as test branches and all other shark species as reference branches. **E**, Log-likelihood (lnL) and number of parameters (np) of each model. **F**, Log-likelihood ratio test (LRT) between each of the models, showing degrees of freedom (df) and statistical significance (p.value) for each comparison.

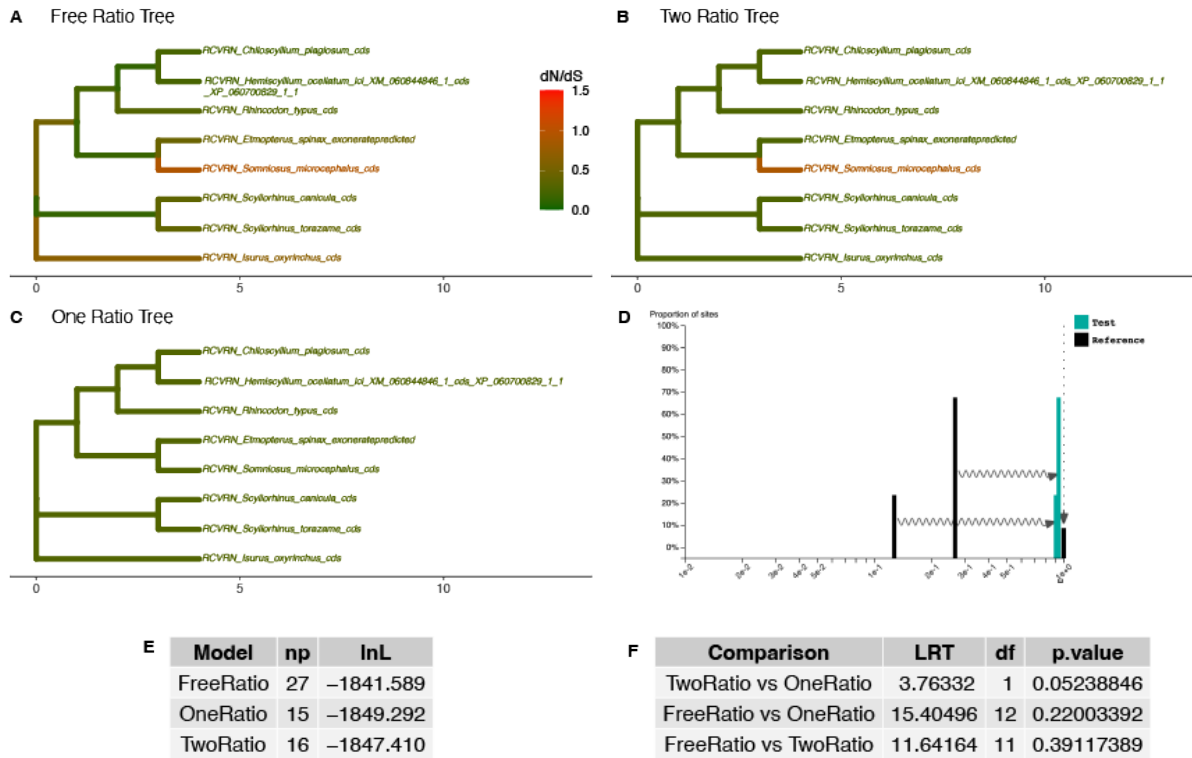


Fig S35. Selection analysis on chondrichthyan RCVRN genes. PAML was used to compute the dN/dS ($= \omega$) per branch under four different models. **A**, Free-ratio model which fits one ω ratio per branch. **B**, Two-ratio model with one ω ratio for *Somniosus microcephalus* and one ω ratio for other shark species. **C**, One-ratio model with the same ω ratio for all shark species. **D**, RELAX ω distribution results under the RELAX alternative model, assigning *Somniosus microcephalus* as test branches and all other shark species as reference branches. **E**, Log-likelihood (lnL) and number of parameters (np) of each model. **F**, Log-likelihood ratio test (LRT) between each of the models, showing degrees of freedom (df) and statistical significance (p.value) for each comparison.

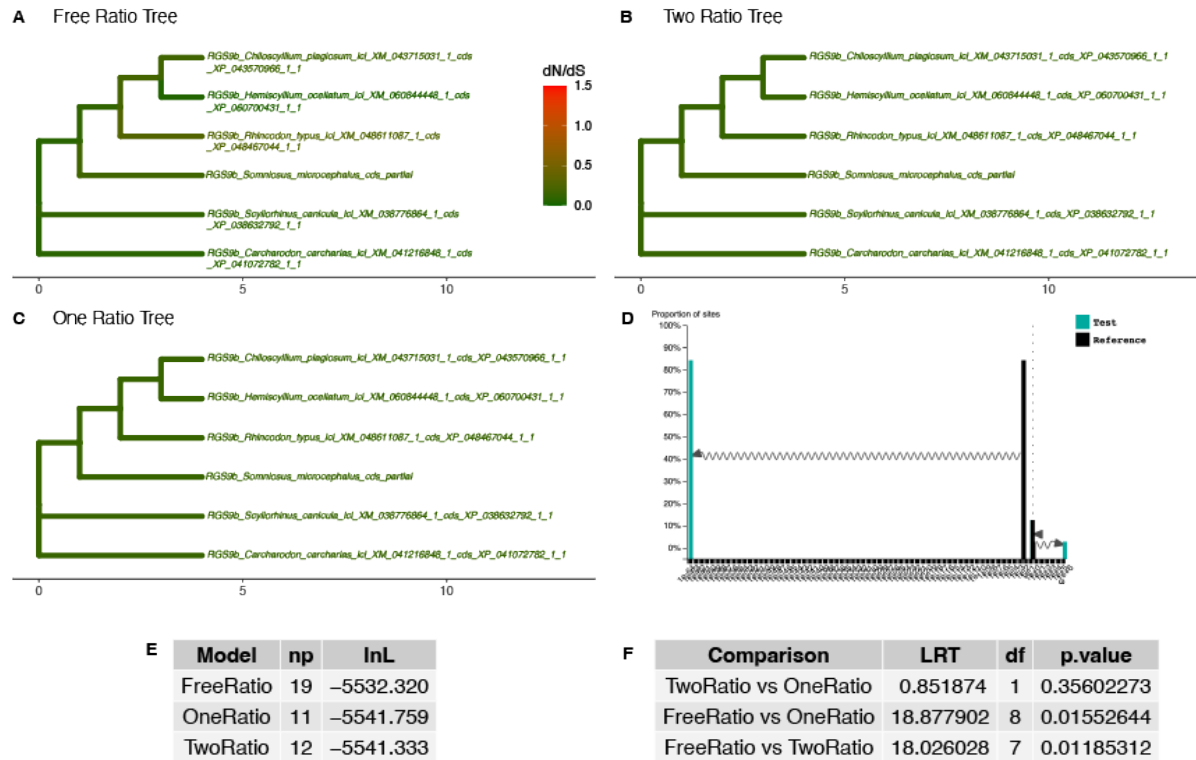


Fig S36. Selection analysis on chondrichthyan RGS9b genes. PAML was used to compute the dN/dS ($= \omega$) per branch under four different models. **A**, Free-ratio model which fits one ω ratio per branch. **B**, Two-ratio model with one ω ratio for *Sommiosus microcephalus* and one ω ratio for other shark species. **C**, One-ratio model with the same ω ratio for all shark species. **D**, RELAX ω distribution results under the RELAX alternative model, assigning *Sommiosus microcephalus* as test branches and all other shark species as reference branches. **E**, Log-likelihood (lnL) and number of parameters (np) of each model. **F**, Log-likelihood ratio test (LRT) between each of the models, showing degrees of freedom (df) and statistical significance (p.value) for each comparison.

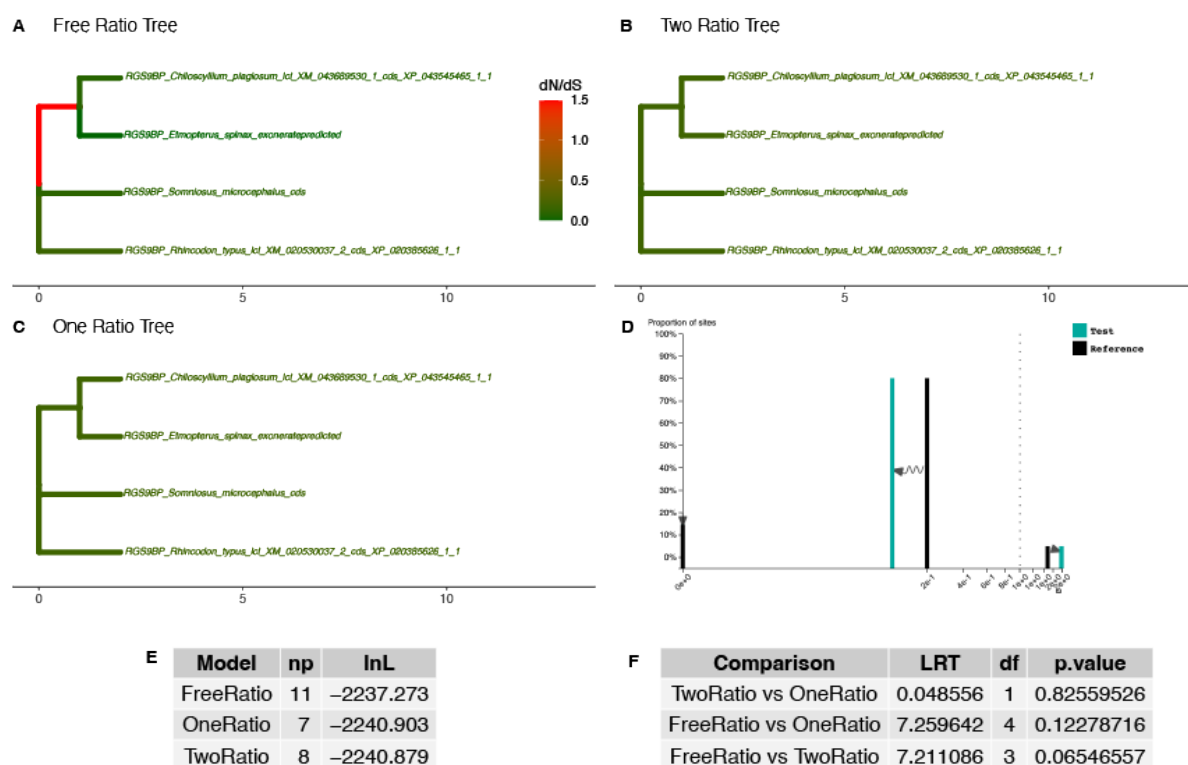


Fig S37. Selection analysis on chondrichthyan RGS9BP genes. PAML was used to compute the dN/dS ($= \omega$) per branch under four different models. **A**, Free-ratio model which fits one ω ratio per branch. **B**, Two-ratio model with one ω ratio for *Somniosus microcephalus* and one ω ratio for other shark species. **C**, One-ratio model with the same ω ratio for all shark species. **D**, RELAX ω distribution results under the RELAX alternative model, assigning *Somniosus microcephalus* as test branches and all other shark species as reference branches. **E**, Log-likelihood (lnL) and number of parameters (np) of each model. **F**, Log-likelihood ratio test (LRT) between each of the models, showing degrees of freedom (df) and statistical significance (p.value) for each comparison.

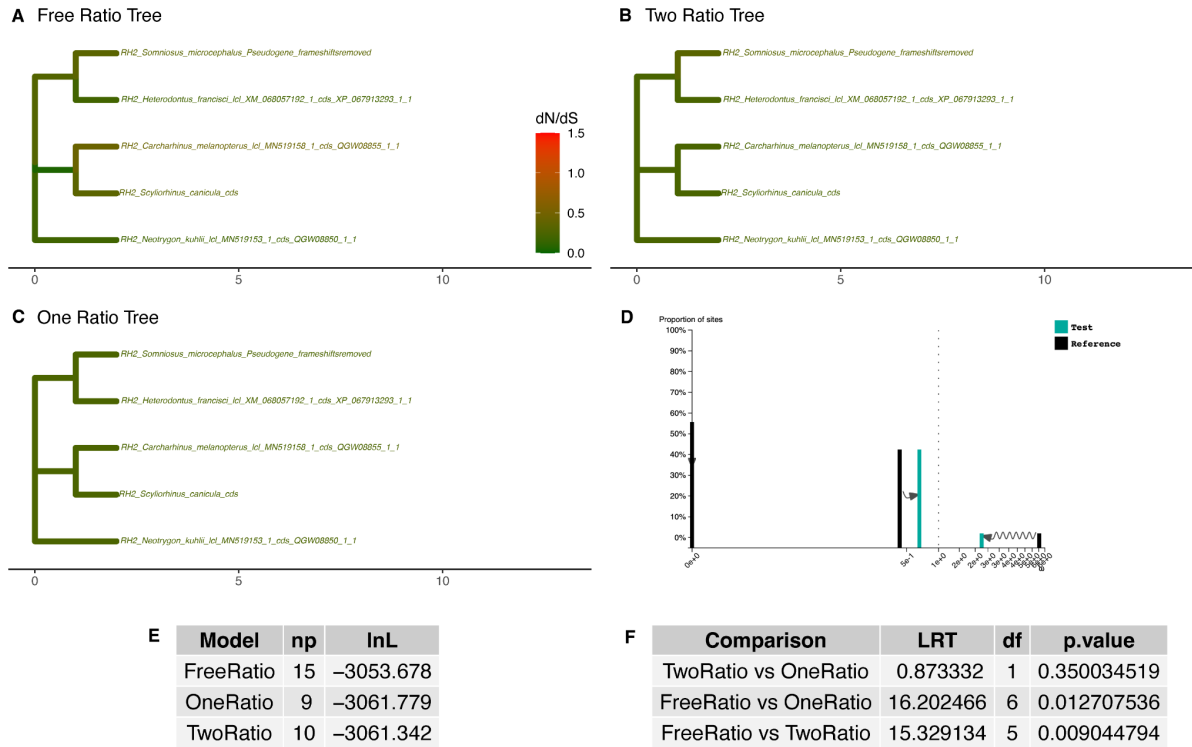


Fig S38. Selection analysis on chondrichthyan RH2 genes. PAML was used to compute the dN/dS ($= \omega$) per branch under four different models. **A**, Free-ratio model which fits one ω ratio per branch. **B**, Two-ratio model with one ω ratio for *Somniosus microcephalus* and one ω ratio for other shark species. **C**, One-ratio model with the same ω ratio for all shark species. **D**, RELAX ω distribution results under the RELAX alternative model, assigning *Somniosus microcephalus* as test branches and all other shark species as reference branches. **E**, Log-likelihood (lnL) and number of parameters (np) of each model. **F**, Log-likelihood ratio test (LRT) between each of the models, showing degrees of freedom (df) and statistical significance (p.value) for each comparison.

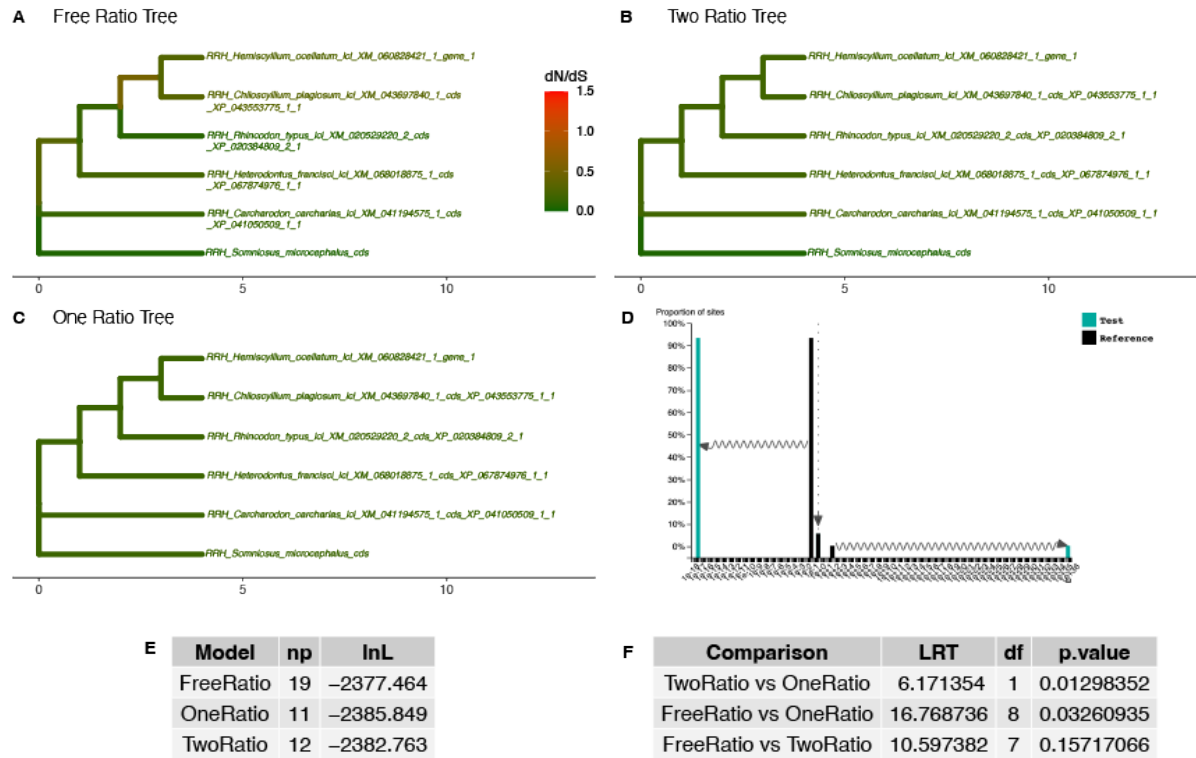


Fig S39. Selection analysis on chondrichthyan RRH genes. PAML was used to compute the dN/dS ($= \omega$) per branch under four different models. **A**, Free-ratio model which fits one ω ratio per branch. **B**, Two-ratio model with one ω ratio for *Somniosus microcephalus* and one ω ratio for other shark species. **C**, One-ratio model with the same ω ratio for all shark species. **D**, RELAX ω distribution results under the RELAX alternative model, assigning *Somniosus microcephalus* as test branches and all other shark species as reference branches. **E**, Log-likelihood (lnL) and number of parameters (np) of each model. **F**, Log-likelihood ratio test (LRT) between each of the models, showing degrees of freedom (df) and statistical significance (p.value) for each comparison.

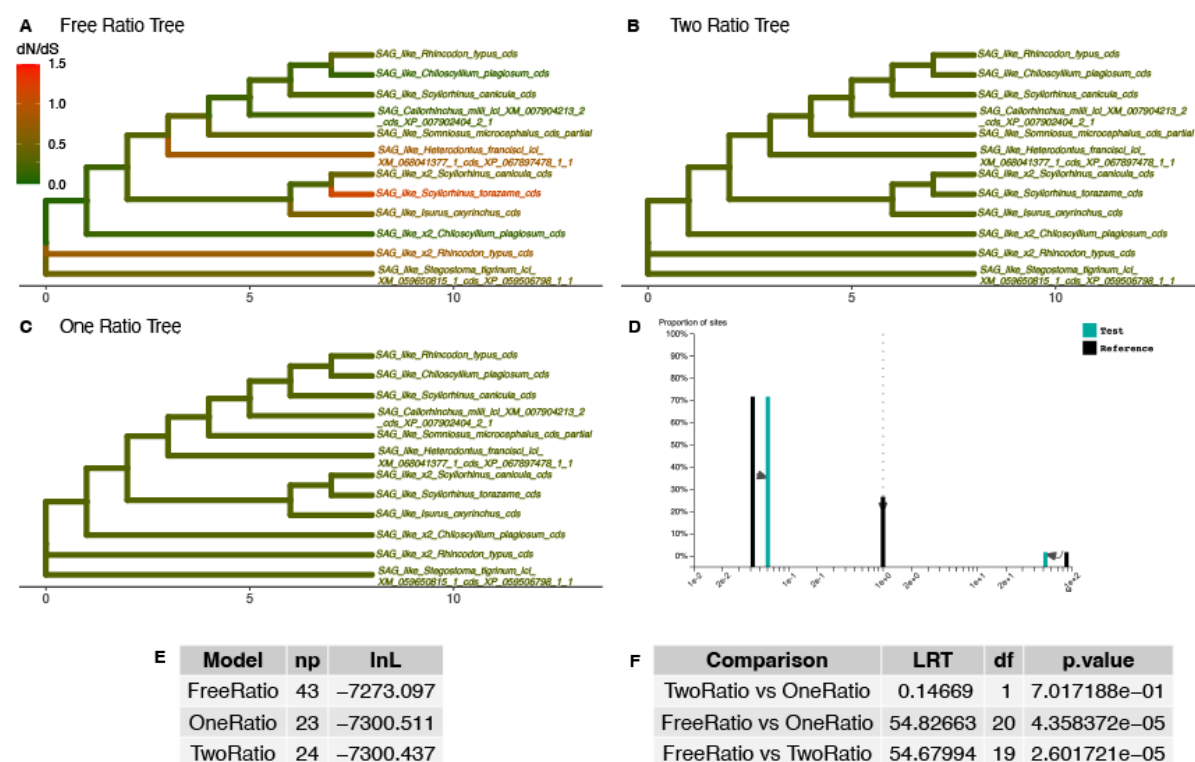


Fig S40. Selection analysis on chondrichthyan SAG genes. PAML was used to compute the dN/dS ($= \omega$) per branch under four different models. **A**, Free-ratio model which fits one ω ratio per branch. **B**, Two-ratio model with one ω ratio for *Sommiosus microcephalus* and one ω ratio for other shark species. **C**, One-ratio model with the same ω ratio for all shark species. **D**, RELAX ω distribution results under the RELAX alternative model, assigning *Sommiosus microcephalus* as test branches and all other shark species as reference branches. **E**, Log-likelihood (lnL) and number of parameters (np) of each model. **F**, Log-likelihood ratio test (LRT) between each of the models, showing degrees of freedom (df) and statistical significance (p.value) for each comparison.

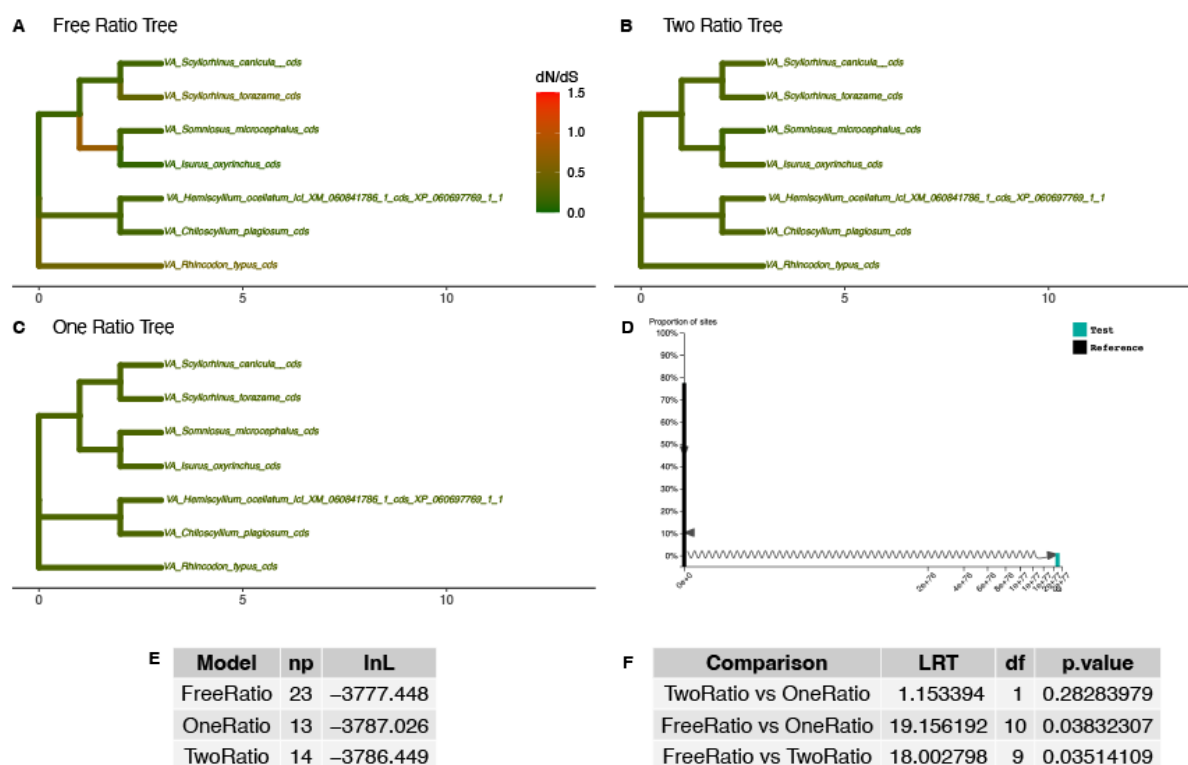


Fig S41. Selection analysis on chondrichthyan VA genes. PAML was used to compute the dN/dS ($= \omega$) per branch under four different models. **A**, Free-ratio model which fits one ω ratio per branch. **B**, Two-ratio model with one ω ratio for *Somniosus microcephalus* and one ω ratio for other shark species. **C**, One-ratio model with the same ω ratio for all shark species. **D**, RELAX ω distribution results under the RELAX alternative model, assigning *Somniosus microcephalus* as test branches and all other shark species as reference branches. **E**, Log-likelihood (lnL) and number of parameters (np) of each model. **F**, Log-likelihood ratio test (LRT) between each of the models, showing degrees of freedom (df) and statistical significance (p.value) for each comparison.

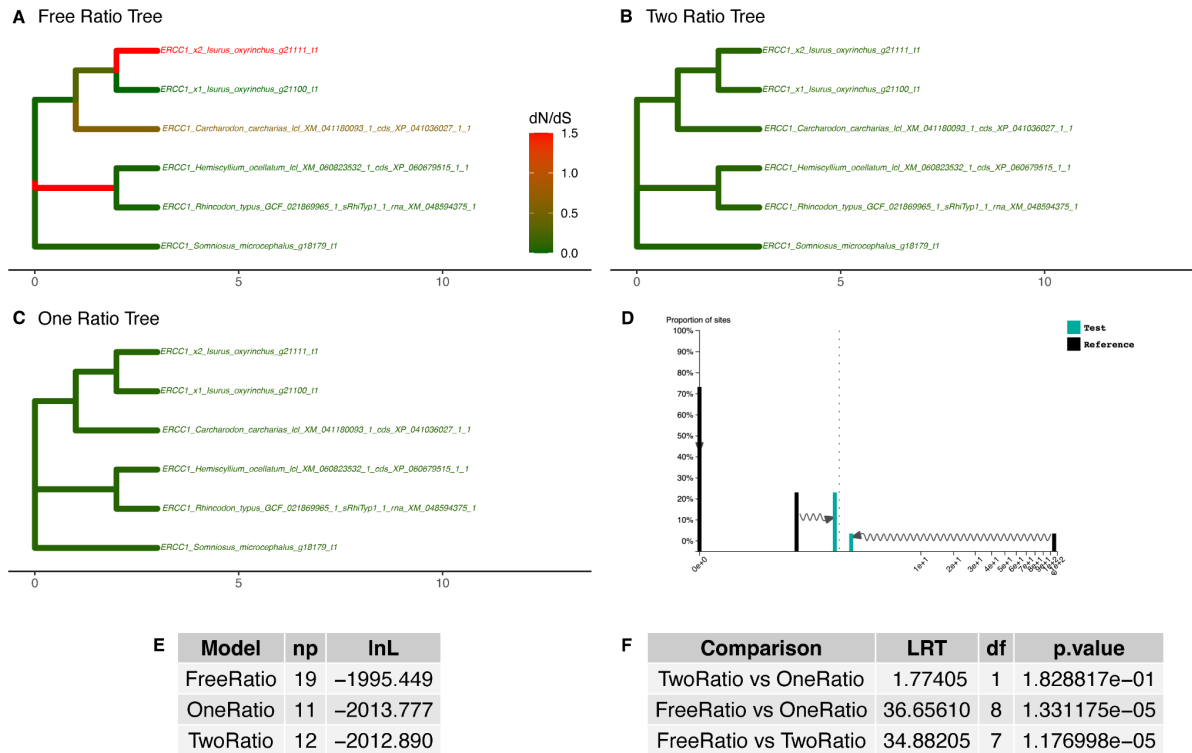


Fig S42. Selection analysis on chondrichthyan ERCC1 genes. PAML was used to compute the dN/dS ($= \omega$) per branch under four different models. **A**, Free-ratio model which fits one ω ratio per branch. **B**, Two-ratio model with one ω ratio for *Sommiosus microcephalus* and one ω ratio for other shark species. **C**, One-ratio model with the same ω ratio for all shark species. **D**, RELAX ω distribution results under the RELAX alternative model, assigning *Sommiosus microcephalus* as test branches and all other shark species as reference branches. **E**, Log-likelihood (lnL) and number of parameters (np) of each model. **F**, Log-likelihood ratio test (LRT) between each of the models, showing degrees of freedom (df) and statistical significance (p.value) for each comparison.

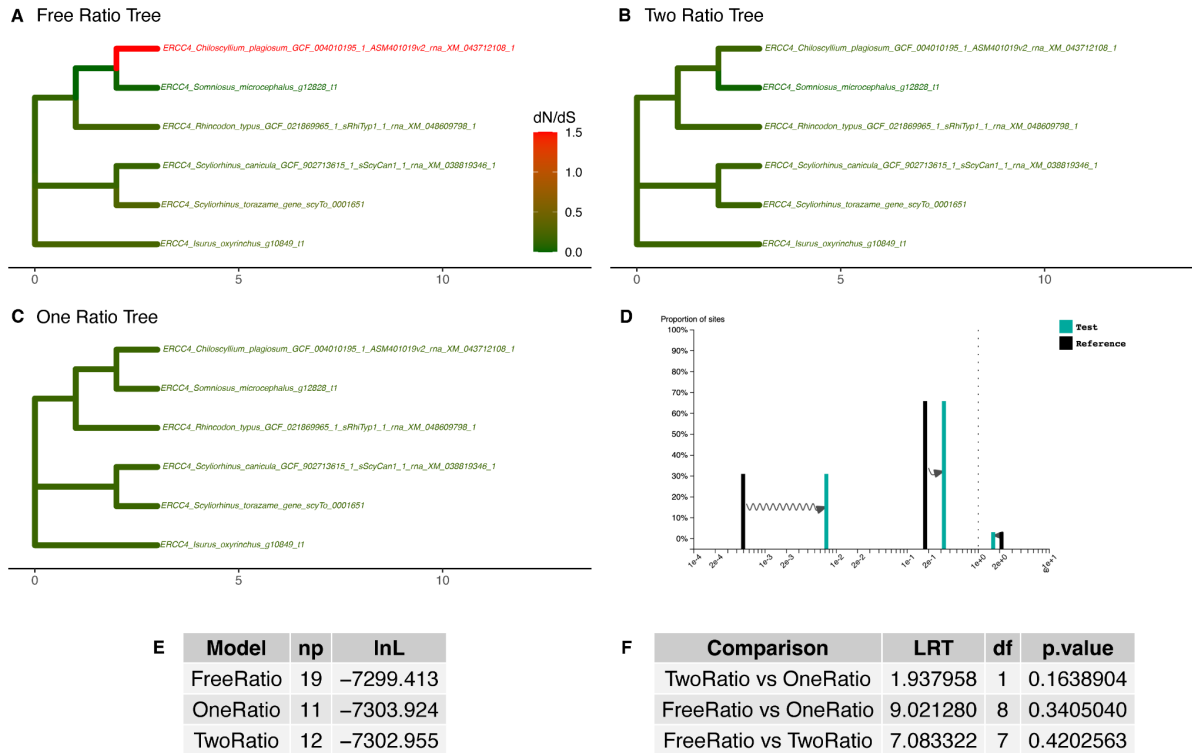


Fig S43. Selection analysis on chondrichthyan ERCC4 genes. PAML was used to compute the dN/dS ($= \omega$) per branch under four different models. **A**, Free-ratio model which fits one ω ratio per branch. **B**, Two-ratio model with one ω ratio for *Somniosus microcephalus* and one ω ratio for other shark species. **C**, One-ratio model with the same ω ratio for all shark species. **D**, RELAX ω distribution results under the RELAX alternative model, assigning *Somniosus microcephalus* as test branches and all other shark species as reference branches. **E**, Log-likelihood (lnL) and number of parameters (np) of each model. **F**, Log-likelihood ratio test (LRT) between each of the models, showing degrees of freedom (df) and statistical significance (p.value) for each comparison.

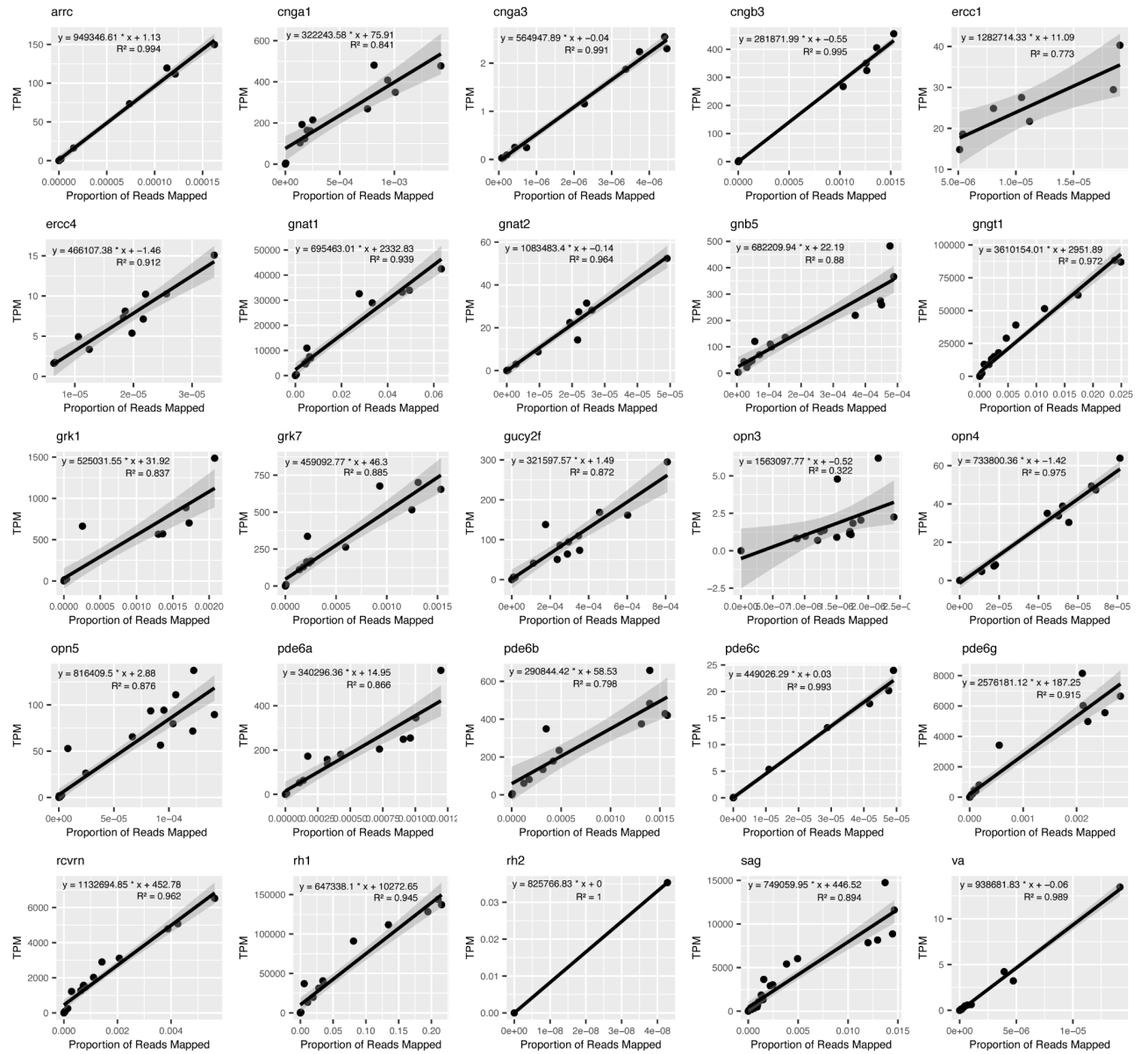


Fig S44. Per-gene correlations between measures of gene expression. For each gene analysed in this study, transcripts per-million (TPM) is plotted against the proportion of reads mapped to each gene in up to five shark species (*Scyliorhinus canicula*, *S. torazame*, *Isurus oxyrinchus*, *Rhincodon typus*, and *Chiloscyllium plagiosum*). The per-gene equations describing the linear regressions were used to extrapolate the TPM values for *Somniosus microcephalus* from the proportion of reads mapped. Source data are provided as a Source Data file.

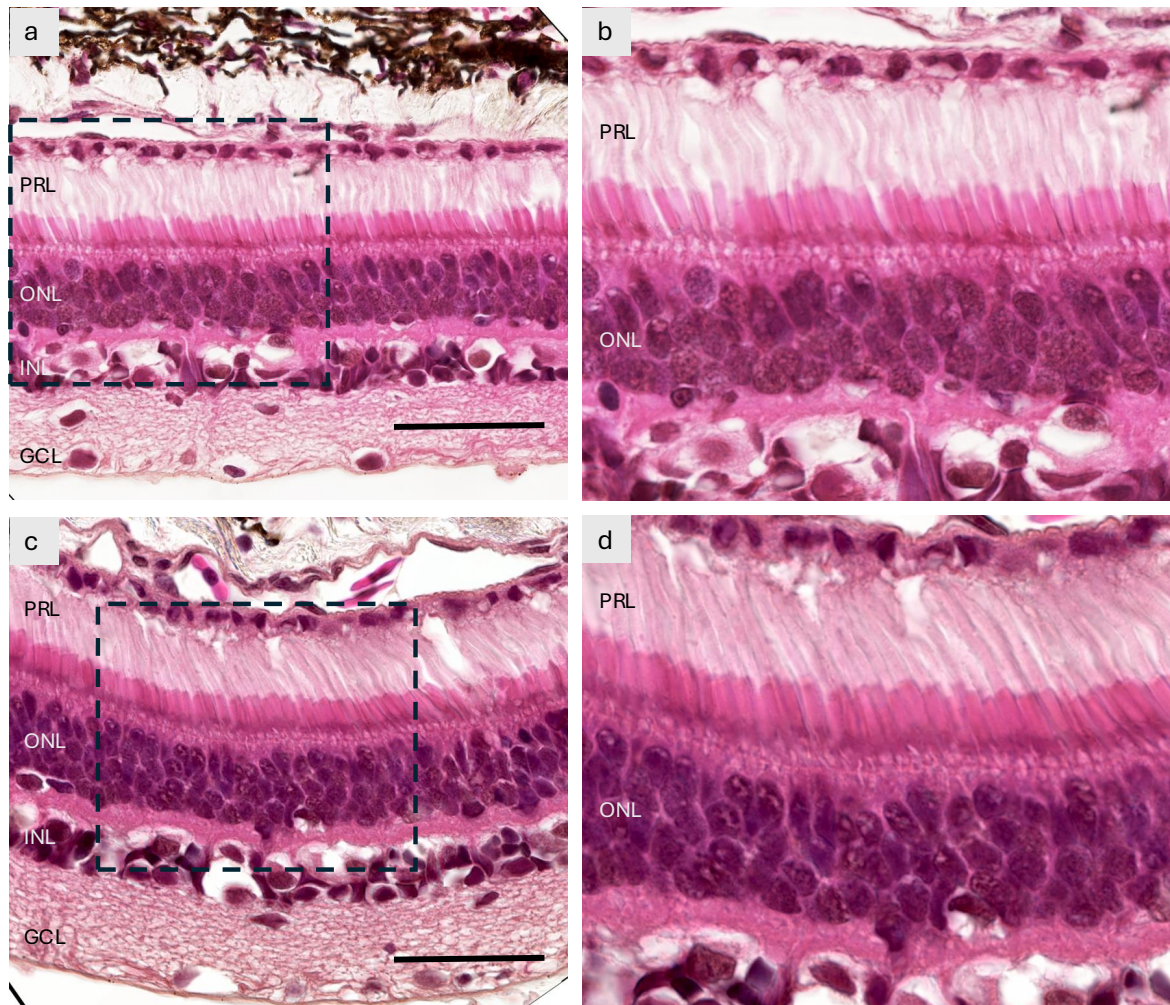


Fig S45. Structural integrity of the retina of the Greenland shark. Radial sections through the retina of *Somniosus microcephalus* showing all retinal layers (**a, c**) or zoomed images of the photoreceptor and inner nuclear layers (**b, d**). Dashed boxes represent the areas in panels a and c that are magnified in panels b and d, respectively. **Scale bars:** 50 μm . **Abbreviations:** PRL, photoreceptor layer; ONL, outer nuclear layer; INL, inner nuclear layer; GCL, ganglion cell layer.

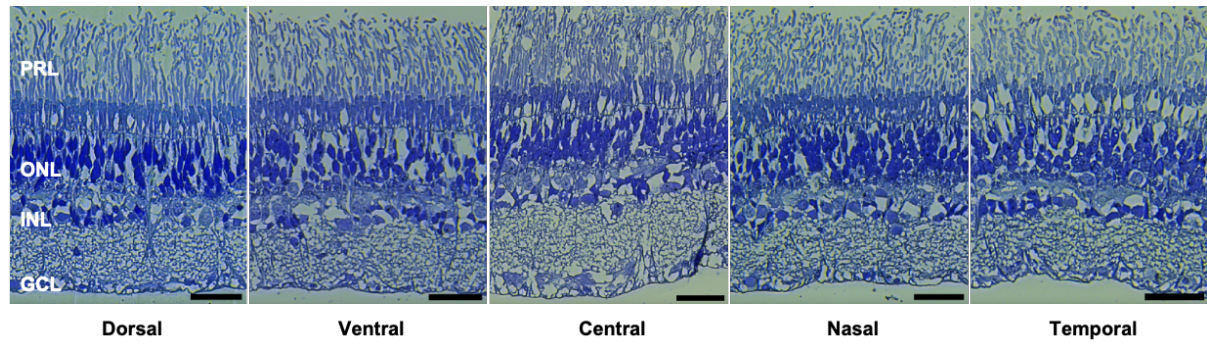


Fig S46. Retinal architecture in different regions of the Greenland shark retina.

Transverse sections through five regions of the retina of *Somniosus microcephalus*. Scale bars: 50 μm . **Abbreviations:** PRL, photoreceptor layer; RPE, retinal pigment epithelium; ONL, outer nuclear layer; INL, inner nuclear layer; GCL, ganglion cell layer.

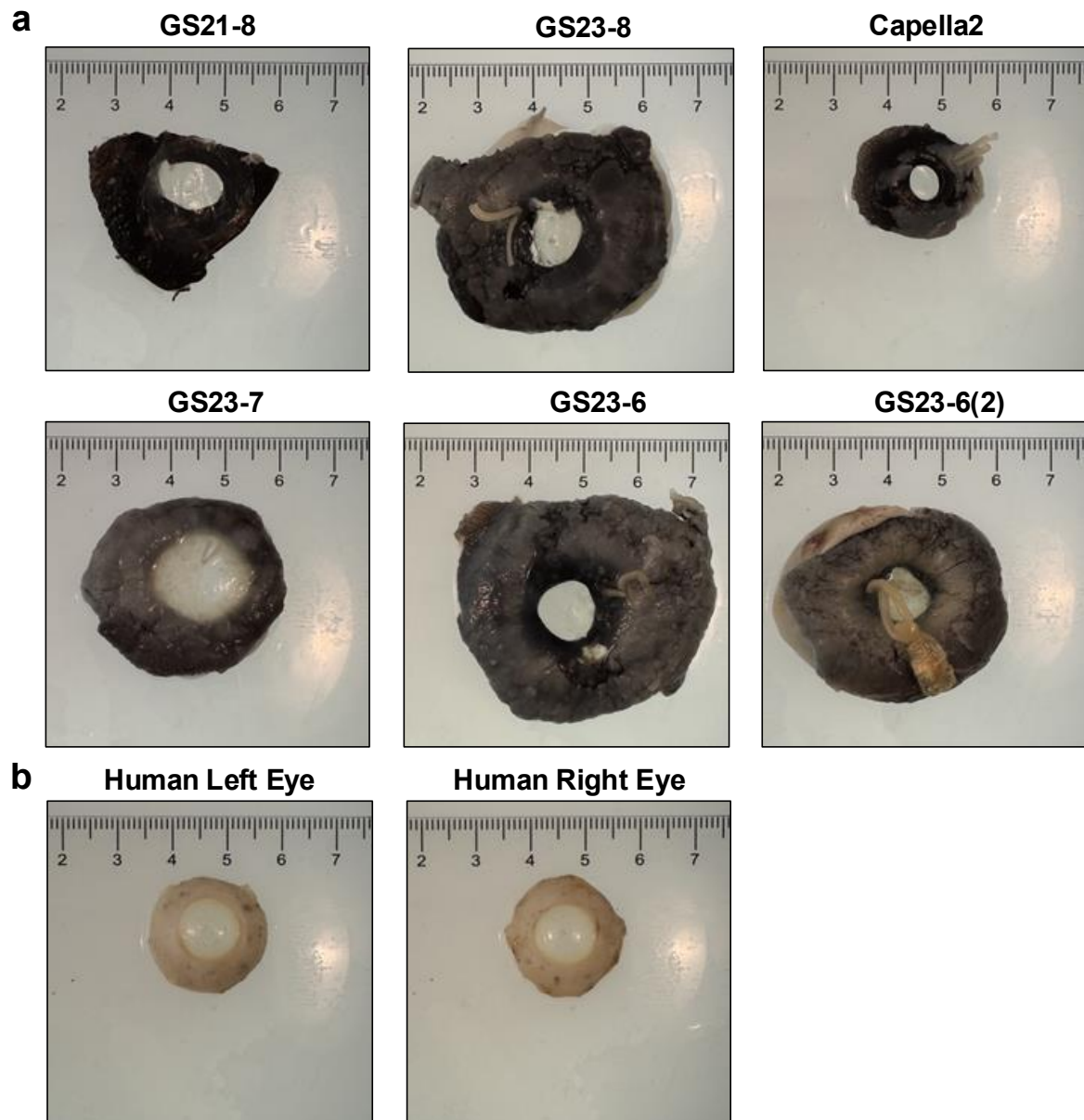


Fig S47. Corneas used in transmissivity experiment. Images of corneas from Greenland sharks (**a**) and humans (**b**) used to measure the transmission of light. All reference scales show units in centimetres.

Table S1. Details of specimens used in this study. All individuals were adult Greenland sharks (*Somniosus microcephalus*) collected off the coast of Greenland. M, male; F, female; n.a., not known.

Sex	TL (m)	Specimen ID	Depth of capture (m)	Estimated age (years)	Analyses
M	3.35	GS24_6	115	n.a.	Transcriptome
F	3.65	GS24_9	190	134 ± 20	Transcriptome
F	3.60	GS24_12	195	130 ± 19	Transcriptome
M	3.14	GS23_1	180	n.a.	Ultramicrotomy
F	3.31	GS23_6	292	110 ± 18	Ultramicrotomy, RNAscope, Chromatin staining, H&E staining, TUNEL assay, Corneal transmission (both left and right corneas)
F	3.54	GS24_4	214	126 ± 19	Ultramicrotomy
M	2.76	GS23_8	n.a.	n.a.	Corneal transmission
M	3.05	GShark21- 8	n.a.	n.a.	Corneal transmission, Lipidome
M	3.06	GS23-7	n.a.	n.a.	Genome, Lipidome, Corneal transmission
F	1.03	Capella 2	n.a.	<100	Corneal transmission

Table S2. Genomes and transcriptomes used in this study. All genomes are available from the NCBI Genome database and all transcriptomes are available from the Sequence Read Archive.

Species	Data type	Accession no.
<i>Somniosus microcephalus</i>	Genome	SRR32965274
	Transcriptome – retina (adult)	SRR32965277
	Transcriptome – retina (adult)	SRR32965276
	Transcriptome – retina (adult)	SRR32965275
<i>Scyliorhinus torazame</i>	Genome	GCA_003427355.1
	Transcriptome – retina (adult)	DRR111795
	Transcriptome – retina (adult)	DRR111817
<i>Scyliorhinus canicula</i>	Genome	GCF_902713615.1
	Transcriptome – retina (adult)	SRR12813952
	Transcriptome – retina (adult)	SRR12813953
	Transcriptome – retina (adult)	SRR12813954
	Transcriptome – retina (adult)	SRR12813957
	Transcriptome – retina (adult)	SRR12813958
<i>Rhincodon typus</i>	Genome	GCF_021869965.1
	Transcriptome – retina (juvenile)	SRR19140294
<i>Isurus oxyrinchus</i>	Genome	GCA_026770705.1
	Transcriptome – retina (juvenile)	SRR10998462
	Transcriptome – retina (juvenile)	SRR10998463

	Transcriptome – retina (juvenile)	SRR10998464
<i>Chiloscyllium plagiosum</i>	Genome	GCF_004010195.1
	Transcriptome – retina (adult)	SRR7539029
	Transcriptome – retina (adult)	SRR7539030
	Transcriptome – retina (adult)	SRR7539034
	Transcriptome – retina (adult)	SRR7539035
	Transcriptome – retina (adult)	SRR7539036
<i>Amblyraja radiata</i>	Genome	GCA_010909765.2
<i>Callorhinchus milii</i>	Genome	GCA_018977255.1
<i>Carcharodon carcharias</i>	Genome	GCA_017639515.1
<i>Chiloscyllium punctatum</i>	Genome	GCA_003427335.1
<i>Ginglymostoma cirratum</i>	Genome	GCA_024137785.1
<i>Hemiscyllium ocellatum</i>	Genome	GCA_020745735.1
<i>Leucoraja erinacea</i>	Genome	GCA_028641065.1
<i>Pristis pectinata</i>	Genome	GCA_009764475.2
<i>Raja brachyura</i>	Genome	GCA_963514005.1
<i>Sphyrna mokarran</i>	Genome	GCA_024679065.1
<i>Squalus acanthias</i>	Genome	GCA_030390025.1

Table S3. Assembly statistics for the Greenland shark genome. Statistics generated for a scaffold-level assembly using the *de novo* sequence assembler, ABySS.

Total number of scaffolds (n)	29940000
Number of sequences that are at least 500 bp long (n:500)	1175830
L50	191587
Length of shortest sequence (min)	500
N75	1623
N50	3383
N25	6343
Effective size (E-size)	4810
Length of longest sequence (max)	149844
Total length of all sequences in the assembly (sum)	2365000000
BUSCO complete (%)	14.2
BUSCO fragmented (%)	41.0
BUSCO missing (%)	44.8

Table S4. Corneal diameters. Diameters of corneal samples used for transmission experiments. Note that the specimen ID is matched to that given in Table S1.

Specimen ID	Corneal diameter (mm)
GS21-8	7.26
GS23-7	15.00
GS23-6	8.10
GS23-6(2)	6.53
GS23-8	7.90
Capella 2	5.00
Human (Left)	10.00
Human (Right)	10.00

Table S5. RNAscope probes. Details of probes used for RNAscope experiments.

RNAscope Probe	Catalog number
Smi-Rh1-C1	1595991-C1
Smi-Gad1-C2	1596161-C2
Smi-pkcalpha-C3	1595891-C3
Smi-Glula-C1	1595881-C1
Smi-RBPMS2-C2	1595851-C2
Smi-ELOVL2-C3	1596121-C3
Smi-Slc6a9-C	1596131-C3