Table S4. Parameter estimates of ω ratios, log-likelihood scores and LRT statistics for the ependymin data under different branch-, site-, and branch-site models of codon evolution. (References provided in the Additional file 2: Additional_Text.pdf)

Model	Estimates of Parameters	ℓ [a]	LRT [b]	df [c]	p Value	PSS [d]
M0: $\omega_o = \omega_{FishBrain} = \omega_{FishTj} = \omega_{MERPs}$	$\omega_o = 0.155$	-27658.44				None
Postduplication and Postspeciation (PD-PS) Models [51]						
Mps$_1$: ω_b; $\omega_{MERPs(PD)} = \omega_{FishBrain(PD)} = \omega_{FishTj(PD)}$; $\omega_{MERPs(PS)} = \omega_{FishBrain(PS)} = \omega_{FishTj(PS)}$	$\omega_{(PD)} = 1.139$, $\omega_{(PS)} = 0.161$, $\omega_b = 0.056$	-27650.30	M0 vs. Mps$_1$	2	0.0003	
Mps$_2$: $\omega_b = \omega_{MERPs}$; $\omega_{FishBrain(PD)} = \omega_{FishTj(PD)}$; $\omega_{FishBrain(PS)} = \omega_{FishTj(PS)}$	$\omega_{(PD)} = 1.983$, $\omega_{(PS)} = 0.180$, $\omega_b = 0.114$	-27644.73	M0 vs. Mps$_2$	2	< 0.0001	
Paralog Models [51]						
Mp$_1$: ω_b; $\omega_{FishBrain}$; ω_{FishTj}; ω_{MERPs}	$\omega_{FishBrain} = 0.175$; $\omega_{FishTj} = 0.198$; $\omega_{MERPs} = 0.123$; $\omega_b = 0.057$	-27641.01	M0 vs. Mp$_1$	3	< 0.0001	
Mp$_2$: $\omega_b = \omega_{MERPs}$; $\omega_{FishBrain}$; ω_{FishTj}	$\omega_{FishBrain} = 0.175$; $\omega_{FishTj} = 0.198$; $\omega_{MERPs} = \omega_b = 0.114$	-27644.89	M0 vs. Mp$_2$	2	< 0.0001	
Mp$_3$: ω_b; ω_{MERPs}; $\omega_{Non\text{-}MERPs}$	$\omega_{MERPs} = 0.1221$; $\omega_{Non\text{-}MERPs} = 0.1793$; $\omega_b = 0.068$	-27644.35	M0 vs. Mp$_3$	2	< 0.0001	
Site - Models (Separate groups) [52-54]						
Model 0: One-ratio						
FishBrain (32 Taxa)	$\omega_o = 0.182$	-9390.26				
FishTj (12 Taxa)	$\omega_o = 0.195$	-6681.65				
MERPs (17 Taxa)	$\omega_o = 0.115$	-6147.06				
Basal (8 Taxa)	$\omega_o = 0.051$	-5050.18				

Model 3: Discrete (K = 3)

FishBrain (32 Taxa)	$\omega_o = 0.004$, $p_o = 0.099$, $\omega_1 = 0.114$, $p_1 = 0.498$, $\omega_2 = 0.414$, $(p_2 = 0.403)$	-9215.15	M0 vs. M3 (K =3)	4	< 0.0001	None
FishTj (12 Taxa)	$\omega_o = 0.014$, $p_o = 0.184$, $\omega_1 = 0.153$, $p_1 = 0.415$, $\omega_2 = 0.470$, $(p_2 = 0.402)$	-6530.63	M0 vs. M3 (K =3)	4	< 0.0001	None
MERPs (17 Taxa)	$\omega_o = 0.009$, $p_o = 0.331$, $\omega_1 = 0.090$, $p_1 = 0.418$, $\omega_2 = 0.482$, $(p_2 = 0.251)$	-5929.25	M0 vs. M3 (K =3)	4	< 0.0001	None
Basal (8 Taxa)	$\omega_o = 0.003$, $p_o = 0.120$, $\omega_1 = 0.059$, $p_1 = 0.757$, $\omega_2 = 0.382$, $(p_2 = 0.122)$	-4972.79	M0 vs. M3 (K =3)	4	< 0.0001	None

Site - Models (70 sequences dataset) [52-54]

Model 0: one-ratio	$\omega_o = 0.155$	-27658.44				None
Model 1a: Nearly Neutral (K = 2)	$(\omega_o = 0.155)$, $p_o = 0.818$, $(\omega_1 = 1)$, $(p_1 = 0.182)$	-27729.28				Not Allowed
Model 3: Discrete (K = 2)	$\omega_o = 0.0834$, $p_o = 0.369$, $\omega_1 = 0.268$, $(p_1 = 0.631)$	-27471.28	M0 vs. M3 (K = 2)	2	< 0.0001	None
Model 3: Discrete (K = 3)	$\omega_o = 0.035$, $p_o = 0.121$, $\omega_1 = 0.137$, $p_1 = 0.430$, $\omega_2 = 0.320$, $(p_2 = 0.448)$	-27402.19	M0 vs. M3 (K = 3)	4	< 0.0001	None

Branch-Site Models (Testing PD branches for positive selection) [54-56]

PSS [d] for each lineage Prob ($\omega > 1$) using BEB inference

Model A:

FishBrain	$p_o = 0.396$, $p_1 = 0.087$, $(p_2 + p_3 = 0.517)$, $\omega_2 = \infty$	-27724.32	**51W** $(p = 0.975)$, **126Q** $(p = 0.951)$, **186 _** $(p = 0.952)$
FishTj	$p_o = 0.790$, $p_1 = 0.174$, $(p_2 + p_3 = 0.036)$, $\omega_2 = \infty$	-27726.70	**144S** $(p = 0.643)$
MERPs	$p_o = 0.587$, $p_1 = 0.127$, $(p_2 + p_3 = 0.285)$, $\omega_2 = \infty$	-27717.96	**86R** $(p = 0.964)$, **128W** $(p = 0.993)$, **196T** $(p = 0.972)$, **224S** $(p = 0.973)$, **231T** $(p = 0.952)$

Model B:

FishBrain	$p_o = 0.257$, $p_1 = 0.436$, $(p_2 + p_3 = 0.307)$, $\omega_o = 0.083$, $\omega_1 = 0.270$, $\omega_2 = $ **1.983**	-27466.48	MB vs. M3 (K = 2)	2	0.0083	Model B fits the data better than M3 (K=2)
FishTj	$p_o = 0.280$, $p_1 = 0.477$, $(p_2 + p_3 = 0.243)$, $\omega_o = 0.084$, $\omega_1 = 0.268$, $\omega_2 = $ **2.420**	-27471.28	MB vs. M3 (K = 2)	2	1.0	N.S.
MERPs	$p_o = 0.315$, $p_1 = 0.530$, $(p_2 + p_3 = 0.155)$, $\omega_o = 0.084$, $\omega_1 = 0.270$, $\omega_2 = $ **18.170**	-27469.29	MB vs. M3 (K = 2)	2	0.1372	N.S.

Branch-Site Tests of Positive Selection

			Branch-site TEST 1[e]		**Branch-site TEST 2[e]**	
FishBrain (MA with $\omega_2 = 1$ Fixed)	$p_o = 0.422$, $p_1 = 0.094$, $(p_2 + p_3 = 0.484)$, $\omega_o = 0.155$, $\omega_1 = 1$, $\omega_2 = 1$	-27725.91	MA vs. M1a df = 2	$p = 0.0071$	MA vs. MA $(\omega_2 = 1)$ df = 1	**$p = 0.0747$**
FishTj (MA with $\omega_2 = 1$ Fixed)	$p_o = 0.741$, $p_1 = 0.165$, $(p_2 + p_3 = 0.094)$, $\omega_o = 0.155$, $\omega_1 = 1$, $\omega_2 = 1$	-27729.28	MA vs. M1a df = 2	$p = 0.0763$	MA vs. MA $(\omega_2 = 1)$ df = 1	**$p = 0.0233$**
MERPs (MA with $\omega_2 = 1$ Fixed)	$p_o = 0.570$, $p_1 = 0.124$, $(p_2 + p_3 = 0.306)$, $\omega_o = 0.154$, $\omega_1 = 1$, $\omega_2 = 1$	-27725.42	MA vs. M1a df = 2	$p < 0.0001$	MA vs. MA $(\omega_2 = 1)$ df = 1	**$p = 0.0001$**

[a] ℓ, Log-likelihood scores.

[b] LRT, likelihood ratio test.

[c] df, Degrees of freedom.

[d] PSS, Positively Selected Sites. Sites potentially under positive selection are identified using the human ependymin sequence [Epdr_Homo] as the reference.

[e] TEST 1 and TEST 2 as defined in the Methods section of the main text [54-56]