Table S2

Estimated parameters under different codon substitution models for *OXTR*, *AVPR1a*, *AVPR1b*, and *AVPR2*.

	Model	*dN/dS*	Estimated parameters	*ℓ*	*p value*
AVPR1a	M1a: Nearly Neutral	0.2000	p_o=0.84972, (p_1=0.15028) (ω_o=0.05852), (ω_1=1.00000)	-10155.10	>0.999
	M2a: Selection	0.2000	p_o=0.84972, p_1=0.12155, (p_2=0.02873) (ω_o=0.05852), (ω_1=1.00000), ω_2=1.00000	-10155.10	
AVPR1b	M1a: Nearly Neutral	0.2104	p_o=0.85767, (p_1=0.14233) (ω_o=0.07939), (ω_1=1.00000)	-11068.99	0.4
	M2a: Selection	0.1247	p_o=0.85731, p_1=0.13855, (p_2=0.00414) (ω_o=0.07985), (ω_1=1.00000), ω_2=2.65042	-11068.11	
AVPR2	M1a: Nearly Neutral	0.1678	p_o=0.86382, (p_1=0.13618) (ω_o=0.03663), (ω_1=1.00000)	-5563.60	>0.999
	M2a: Selection	0.1678	p_o=0.86381, p_1=0.00588, (p_2=0.13030) (ω_o=0.03663), (ω_1=1.00000), ω_2=1.00000	-5563.60	
OXTR	M7: β	0.0617	[p=0.17515, q=2.45228]	-4316.14	>0.999
	M8: β & ω	0.0620	p_o=0.99688, (p_2 =0.00312), ω_2=1.00000	-4316.09	

p0 = proportion of sites where ω < 1, p1 = proportion of sites where ω = 1, and p2 = proportion of sites where ω > 1 (selection models only); ω0 < 1 (negative selection), ω1 ≅ 1 (neutral or relaxing selection), and ω2 >1 (positive selection). ℓ= Log likelihood values. Likelihood ratio tests were performed between neutral models (M1a- nearly neutral, and M7 - beta) and models that identify positive selection (M2a - selection, and M8, β & ω - beta +selection). The comparisons M1 vs M2 and M7 vs M8 had 2 degrees of freedom. Within parentheses: fixed parameters; within brackets: $^{\beta}$parameters p and q. dN/dS = non-synonymous/synonymous rate ratio.