Supplementary Information

"Interacting Proteins on Human Spermatozoa: Adaptive Evolution of the Binding of Semenogelin I to EPPIN"

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Supplementary Table S1. Likelihood ratio test between different evolutionary models for *EPPIN* (A) and *SEMG1* (B).

Evolutionary model	Degrees of Freedom	LRT	P-value
(A) *EPPIN*			
M1a (null) vs M2a (positive)	2	0.2600	0.8781
M7 (null) vs M8 (positive)	2	0.3446	0.8418
(B) *SEMG1*			
M1a (null) vs M2a (positive)	2	14.0926	0.0009*
M7 (null) vs M8 (positive)	2	14.0950	0.0009*

Degree of freedom indicates the difference in the number of parameters between models; LRT (Log-likelihood ratio test) was calculated using the formula (-2[Log(null) – Log(positive)]) to compare the better fit model with the χ^2-distribution; P-value is the probability that two models should differ in log likelihood as much as that observed, given the degree of freedom. *$P<0.05$ was considered significant.