Table S4A. Summary of positive selection in primate GBP2 (MEME, FEL, SLAC).

Model	Sites with evidence of positive selection (p-value)*
MEME	208 K (0.04)
	209 G (0.04)
	247 H (0.03)
	296 L (0.01)
	513 E (0.01)
	565 N (0.02)
	582 K (0.01)
	585 E (0.04)
	586 P (0.01)
FEL	**247 H (0.050)**
	582 K (0.033)
	585 E (0.033)
SLAC	No positively selected sites identified

Table S4B. Summary of positive selection in primate GBP2 using REL algorithm.

Sites with evidence of diversifying selection*	Posterior probability $\beta > \alpha$
H247	**0.98**
K582	**0.98**
E585	**0.99**

Table S4C. Summary of positive selection in primate GBP2 using FUBAR algorithm.

Sites with evidence of diversifying selection*	Posterior probability $\beta > \alpha$
M11	0.930
N161	0.925
E188	0.944
F234	0.926
A241	0.940
H247	**0.984**
E327	0.939
E334	0.924
G338	0.999
A549	0.909
L550	**0.936**
E564	0.905
K582	**0.989**
E585	**0.992**

*Amino acid positions shown are for human GBP2.