Table S3. GBP2 whole gene log likelihood scores and parameter estimates for four models of variable ω among sites assuming the f3X4 model of codon frequencies in PAML.

Site Model	**Parameter Estimates**	**Sites* with ω**>1**	**lnL**
M1: Neutral	(ω_0=0) f_0=0.735 (ω_1=1) f_1=0.265 branch ω (mean)=0.293	Not allowed	-5061.10
M2: Selection	(ω_0=0) f_0=0.732 (ω_1=1) f_1=0.248 **(ω_2=6.6) f_2=0.021** branch ω (mean)=0.421	**247 H 0.993** 575 W 0.976 **582 K 0.999** **585 E 1.000** 587 I 0.975	-5037.85
M7: β	p=0.01204 q=0.02377 branch ω (mean)=0.314	Not allowed	-5061.77
M8: β and ω	p=0.07563 q=0.18279 f_0=0.97860 **ω_1=6.5 (f_1=0.0214)** branch ω (mean)=0.426	241 P 0.969 **247 H 0.997** 575 W 0.991 **582 K 0.999** 583 S 0.979 584 L 0.978 **585 E 1.000** 587 I 0.993	-5038.30

*posterior probabilities >0.95 by Bayes Empirical Bayes (BEB) analysis

**ω=dN/dS

***Amino acid positions shown are for human GBP2.