Table 1: Results of the evolutionary analyses for positively selected sites for Mx1 in bats. P-values were achieved by performing chi-squared tests on twice the difference of the computed log likelihood values of the models disallowing (M7) or allowing (M8) $dN/dS > 1$. The BEB column lists rapidly evolving sites with a $dN/dS > 1$ and a posterior probability > 0.95, determined by the Bayes Empirical Bayes implemented in `Codeml`. Amino acids refer to *Myotis daubentonii*. Note that INDELs and the stop codon were removed from the alignment prior to evolutionary analysis. Shown positions were mapped back to the **alignment with gaps**. Fragments arising from insignificant breakpoints (adjusted p-value > 0.1) are marked with an asterisk.

Region	**M7 vs M8** (χ^2)	**M7 vs M8** p-value	**% sites with** $\omega > 1$	**avg**(ω)	**M8 BEB** ($PP > 0.95/ > \mathbf{0.99}$)
F61					
full (aa 1–672)	82.85	< 0.001	8.06	2.75	L138; D141; R205; A209; S361; R433; **D436**; F439; **R443**; S559; **E562**; S569; **L570**; Q571; **Q572**; **T573**; S574; S575; A577; D578; **T581**
frag1* (aa 1–106)	17.01	< 0.001	38.07	1.92	**A16**; T17; D19; **P22**; **S25**; H26; P27; G31; G38; **L40**; E41; **L44**; **N46**; S47; Q51
frag2* (aa 107–201)	0.39	0.821	NA	NA	NA
frag3* (aa 202–672)	82.48	< 0.001	8.1	3.0	A209; D436; **R443**; E562; S569; **L570**; **Q572**; T573; S574; S575; D578; **T581**
F1X4					
full (aa 1–672)	76.34	< 0.001	7.05	2.79	R205; D436; F439; R443; E562; **L570**; **Q572**; T573; S574; S575; D578; T581
frag1* (aa 1–106)	20.33	< 0.001	31.04	2.12	**A16**; T17; **D19**; **P22**; **S25**; H26; P27; G31; G38; L40; E41; **L44**; **N46**; S47; Q51
frag2* (aa 107–201)	0.09	0.956	NA	NA	NA
frag3* (aa 202–672)	84.88	< 0.001	7.76	3.02	R205; D436; F439; R443; E562; **L570**; **Q572**; T573; **S574**; **S575**; D578; **T581**
F3X4					
full (aa 1–672)	101.39	< 0.001	6.26	3.45	R205; A209; S361; F439; R443; T494; A549; E562; S569; **L570**; **Q572**; T573; S574; **S575**; D578; **T581**
frag1* (aa 1–106)	24.05	< 0.001	21.3	2.76	**A16**; T17; D19; **P22**; A23; **S25**; H26; P27; **G31**; G38; L40; **L44**; N46
frag2* (aa 107–201)	0.19	0.908	NA	NA	NA
frag3* (aa 202–672)	112.69	< 0.001	6.59	3.83	**R205**; A209; **S361**; D436; F439; R443; T494; A549; E562; S569; **L570**; **Q572**; T573; **S574**; **S575**; D578; **T581**