

Additional File 10. Best likelihood models and estimates of the proportion of adaptive substitutions across loci ($\bar{\alpha}$). Divergence was measured to the inferred ancestral sequence of the *P. chabaudi*-*P. vinckei* clade (*P. c. chabaudi* and *P. v.* subsp.) or the *P. berghei*-*P. yoelii* clade (*P. y. yoelii*). The best (highest Akaike weight) and secondary models are shown, with Akaike weights in brackets. Estimates of $\bar{\alpha}$ (and 95% CI) across loci were obtained from 1000 bootstraps on the results of model ii. Likelihood models: i) α is constrained to zero at all loci, i.e. no adaptive evolution; ii) α is a free-parameter common to all loci; and iii) α can take a different value at each locus.

taxa	dataset	best model	secondary model	$\bar{\alpha}$
<i>P. c. chabaudi</i>	all loci	iii (1.00)	-	0.640 (0.212; 0.874)
	w/out <i>cyspro</i>	ii (0.65)	i (0.33)	0.456 (0.061; 0.769)
<i>P. vinckei</i> subsp.	all loci	iii (0.97)	i (0.03)	0.165 (-0.120; 0.516)
	w/out <i>cyspro</i>	i (0.73)	ii (0.27)	0.279 (-0.067; 0.698)
<i>P. y. yoelii</i>	all loci	i (0.74)	ii (0.26)	-0.261 (-1.189; 0.516)
	w/out <i>cyspro</i>	i (0.70)	ii (0.30)	-0.524 (-1.939; 0.470)