



Figure S2: Likelihood profile of λ s for bat models only ($N = 27$): (a) including the effects of hibernation season duration (standardized), body mass (standardized and log transformed) and interaction hibernation duration x body mass, (b) without interaction. logLik represent the likelihood value log-transformed. Lambda (λ) correspond to the relative effect of the phylogenetic tree on the linear model, ranging between 0 (covariation among species measurements is independent of co-ancestry) and 1 (covariance entirely explained by co-ancestry). Location of the maximum likelihood estimate of λ is symbolised by a red line, upper 95% CI is symbolized by a dashed red line. Note that the lower 95% CI can not be estimated.