More trees with your coffee? Diversity and habitat associations of terrestrial medium- and large-sized mammals in shade-grown coffee plantations of the highlands of Guatemala

SUPPORTING INFORMATION APPENDIX S1
CODE DESCRIPTION OF THE MULTI-SPECIES HIERARCHICAL ABUNDANCE MODEL

Description of parameter estimation procedures
We used hierarchical models simultaneously with software JAGS (Plummer, 2003) and R (R Development Core Team, 2011). We ran three parallel chains of length 400,000, after a burn-in of 200,000 iterations and a thinning rate of 200. Convergence was assessed using the Gelman-Rubin diagnostic where an estimate of $\hat{R} > 1.1$ indicates low convergence rates between chains (Brooks and Gelman, 1998; Kery, 2010).

We used standard uninformative prior distributions specified to have no influence on the posterior probability distributions. We set priors for log-scale parameters (i.e., covariate parameters used in the abundance model) as flat normal distributions with mean equal to zero and standard deviation equal to one hundred. We specified logit-scale parameters (i.e., covariate parameters used in the detection model) as t-distributions with $\sigma = 0.408$ and $\nu = 7.763$ as per Dorazio *et al.* (2011) such that back-transformed values assigned equal probability for all values between zero and one. We specified priors of standard deviation parameters as uniform distributions with equal probability between 0 and 100.

Literature cited

Brooks, S. P., Gelman, A. (1998) General methods for monitoring convergence of iterative simulations. *Journal of Computational and Graphical Statistics*, 7 (4), 434–455.

Dorazio, R. M., Gotelli, N. J., Ellison, A. M. (2011) Modern methods of estimating biodiversity from presence absence surveys. Pp. 277–302. *In*: O. Grillo, G. Venora (Eds.). *Biodiversity loss in a changing planet*. InTeck, Rijeka Croatia.
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Kery, M. (2010) *Introduction to WinBUGS for Ecologists: Bayesian approach to regression, ANOVA, mixed models and related analyses*. Academic Press, Burlington USA, 302 pp.
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Plummer, M. (2003) JAGS: A Program for Analysis of Bayesian Graphical Models Using Gibbs Sampling. *Proceedings of the 3rd International Workshop on Distributed Statistical Computing* (eds F. Leisch & A. Zeileis). Vienna, Austria, 1-10 pp.

R Development Core Team (2011) R: A language and environment for statistical computing. R Foundation for statistical computing, Vienna, Austria.

Model code run in JAGS. The symbol "#" precedes annotation remarks. Refer to Methods section of the main text for symbol equations and parameter definitions

```
# Priors
betmu[i] ~ dnorm(0,.1)                    #Abundance
bettau[i] ~ dgamma(.1,.1)                 #Precision parameter for abundance
phimu[i] ~ dt(0,0.4076321,7.63179)        #Detection probability
phitau[i] ~ dgamma(.1,.1)                 #Precision parameter for detection
                                 probability
bet1[i] ~ dnorm(betmu[1],bettau[1])       #Covariates on abundance
bet2[i] ~ dnorm(betmu[2],bettau[2])       #Covariates on detection probability

  for(i in 1:7){
  betmu[i] ~ dnorm(0,.1)
  bettau[i] ~ dgamma(.1,.1)
  }

  for(i in 1:8){
  phimu[i] ~ dt(0,0.4076321,7.63179)
  phitau[i] ~ dgamma(.1,.1)
  }

  for(i in 1:nsp){
  bet1[i] ~ dnorm(betmu[1],bettau[1])
  bet2[i] ~ dnorm(betmu[2],bettau[2])
  etc.
  phi1[i] ~ dnorm(phimu[1],phitau[1])
  phi2[i] ~ dnorm(phimu[2],phitau[2])
  etc.
  }

  for(i in 1:nsp){
  for(k in 1:nplot){
  N[i,k]~ dpois(lam[i,k])                  #Species-specific abundance per plot
  lam[i,k]<-exp(log.lam[i,k])*o[i]
  log.lam[i,k] <- bet1[i] + bet2[i]*landuse[k] + bet3[i]*road[k] + bet4[i]*pa[k]

  ymat[i,k]~dbin(p[i,k],5)
  p[i,k] <- 1-(1-r[i,k])^N[i,k]
  r[i,k] <- exp(logit.r [i,k])/(1+exp(logit.r[i,k]))
  logit.r[i,k]<-phi1[i] + phi2[i]*landuse[k] + phi3[i]*lure[k]
  }}

  R <- sum(o[])                            #Sum of number of species across all plots
  for(i in 1:nplot){
  rplot[i] <- sum(N[,i]>0)                 #Plot-specific estimate of species richness
  abund[k] <- sum(N[,k])
  }
```