

Studying the microbiota of bats: accuracy of direct and indirect samplings

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Table S1. Description of GLMs used for the analysis of alpha-diversity. N gives the number of samples included in the analysis. Excreta refers to the sample type (faeces/urine). "Full model" gives the complete set of explanatory variables tested (and their interactions) included in the model. "Minimal model" gives the model containing only the significant variables and their interactions. All starting GLMs were simplified by backward stepwise elimination of non-significant terms ($p > 0.05$), to obtain the minimum adequate model. The χ^2 significant values given in the results are those obtained when the variable is deleted from the minimal model.

Analysis	Model nb.	N	Full model	Minimal model
Alpha-diversity between excreta samples	GLM ₁	35	Excreta*Session	Excreta
Alpha-diversity between sampling approaches in urine	GLM ₂	24	Sampling*Session	Session
Alpha-diversity between sampling approaches in faeces	GLM ₃	11	Sampling*Session	null

Figure S1. Results of LefSe analysis for urine (left) and faeces (right) samples. Phylotypes enriched in direct and indirect samplings are colored by green and red, respectively. Only phylotypes meeting a LDA significant threshold > 2 and $p > 0.05$ are shown.

