

Table 1. Bat skin, oral, and gut microbiome sampling (n = count of 16S rRNA libraries retained post-filtering), total ASVs recovered by sample type, and parasite prevalence (n_p/n) of bat flies (Hippoboscoidea) and malarial parasites (Haemosporidia)

Host Taxonomy		16S rRNA Libraries (n)			Parasite Prevalence n_p/n (%)	
Family	Species	Skin	Oral	Gut	Hippoboscoidea	Haemosporidia
Hipposideridae	<i>Hipposideros caffer</i>	39	37	43	17/47 (36%)	0/47 (0%)
Miniopteridae	<i>Miniopterus africanus</i>	22	20	22	9/22 (41%)	11/22 (50%)
	<i>Miniopterus minor</i>	16	15	15	11/17 (65%)	11/17 (65%)
	<i>Miniopterus natalensis</i>	41	31	31	20/47 (43%)	21/47 (45%)
Pteropodidae	<i>Rousettus aegyptiacus</i>	34	33	32	19/39 (60%)	0/39 (0%)
	<i>Stenonycteris lanosus</i>	32	24	37	13/37 (35%)	0/37 (0%)
Rhinolophidae	<i>Rhinolophus clivosus acrotis</i>	32	25	21	19/32 (59%)	2/32 (6%)
	<i>Rhinolophus eloquens</i>	21	18	24	17/26 (65%)	0/26 (0%)
		5,77				
Total ASVs		29,270	3,361	1		