Supplemental Table S3.

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Summary of the mtDNA sequencing and microsatellite genotyping analyses from droppings for each of the *Myotis* spp. (ME: *Myotis emarginatus*, MC: *Myotis capaccinii* and MD: *Myotis daubentonii*). Cyt-b Seq: number of samples sequenced for mtDNA; Cyt-b Seq +: samples with a reliable Cyt-b sequence; M1 PCR+ > 50%: samples that passed the first multiplex M1 screening; M1-M3 R ≥ 0.95: samples reliably and completely genotyped at the three multiplex reactions; Recovered *R* ≥ 0.95: samples with a *R* < 0.95 at M2 and M3 and that were further amplified another four times at unreliable loci reaching the *R* ≥ 0.95; Total *R* ≥ 0.95: total number of reliable genotypes.

	mtDNA Sequencing		**Microsatellite Genotyping**			
	Cyt-b Seq	**Cyt- b Seq+**	**M1 PCR+ > 50%**	***M1,M2,M3* *R* ≥0.95**	**Recovered *R* ≥0.95**	**Total *R* ≥0.95**
ME	210	195	115	100	4	104
MC	50	25	15	8	2	10
MD	25	25	20	13	2	15
Total	285	245	150	121	8	129