

**Table S1.** Field information for specimens used in this study.

<b>Species</b>	<b>Field Number</b>	<b>Locality</b>	<b>Date Captured</b>	<b>Sex</b>
<i>Carollia castanea</i>	LS084	La Selva, Costa Rica	Aug 4 2017	M
<i>Carollia sowelli</i>	LS073	La Selva, Costa Rica	Aug 4 2017	M
<i>Carollia perspicillata</i>	LS070	La Selva, Costa Rica	Aug 4 2017	M

**Table S2.** Number of intact olfactory receptor (OR) genes found within each olfactory receptor subfamily. Intact OR genes are genes with reading frames longer than 650bp that do not have a premature stop codon or frameshift mutation.

Species	Class I				Class II									Total
	51	52	55	56	1/3/7	2/13	4	5/8/9	6	10	11	12	14	
<i>Carollia castanea</i>	73	69	1	16	188	102	103	180	56	74	14	3	2	881
<i>Carollia sowellii</i>	75	69	1	24	261	127	99	200	62	73	22	1	2	1017
<i>Carollia perspicillata</i>	93	104	3	15	258	121	98	242	83	76	14	4	4	1115
Orthogroup count	75	84	1	13	236	117	116	210	66	77	19	3	3	1019

**Table S3.** Number of intact sequences for each olfactory receptor subfamily. Alignment length and percent identity was calculated from nucleotide alignments based on the transAlign algorithm. The model of evolution estimated for each alignment was determined by ModelOMatic v.1.01 and applied to each alignment for tree inference in IQtree. Data in this table refer to the alignment with the root, but with stop codons for all sequences removed.

<b>OR subfamily</b>	<b># sequences</b>	<b>Alignment Length (bp)</b>	<b>% pairwise identity</b>	<b>Model</b>
<i>Class I</i>				
OR 51	242	1,149	58.5	Codon F64+4dG
OR 52	243	1,212	58.5	Codon F64+4dG
OR 55	7	1,074	80.2	Codon F64+4dG
OR 56	56	1,095	79.2	Codon F64+4dG
<i>Class II</i>				
OR 1/3/7	708	1,242	64.9	Codon F3X4+4dG
OR 2/13	351	1,191	57.8	Codon F1X4+4dG
OR 4	301	1,263	63.0	Codon F64+4dG
OR 5/8/9	623	1,284	57.5	Codon F1X4+4dG
OR 6	202	1,194	59.6	Codon F64+4dG
OR 10	224	1,167	55.1	Codon F64+4dG
OR 11	51	1,128	64.8	Codon F64+4dG
OR 12	9	1,065	84.7	Codon F3X4+4dG
OR 14	9	1,104	77.9	Codon F3X4+4dG