

SUPPLEMENTARY TABLE

Supplementary Table 1. Positive selected genes (PSGs) identified among 6 bat species through pairwise comparisons.

Ensembl Transcript ID	Gene Symbol	Ka	Ks	Ka/Ks	FDR
<i>Molossus molossus</i> versus <i>Pipistrellus kuhlii</i>					
ENST00000537690	<i>CCDC175</i>	0.3273	0.2503	1.31	0.0036
<i>Molossus molossus</i> versus <i>Phyllostomus discolor</i>					
ENST00000393316	<i>BCL2L15</i>	0.314	0.1867	1.682	0.0156
ENST00000618484	<i>BPIFA1</i>	0.5722	0.3442	1.662	0.0001
<i>Molossus molossus</i> versus <i>Rhinolophus ferrumequinum</i>					
ENST00000378186	<i>MS4A13</i>	0.33	0.1873	1.762	0.0274
ENST00000380232	<i>IFNB1</i>	0.4029	0.259	1.556	0.0424
ENST00000368051	<i>CD84</i>	0.2354	0.1565	1.504	0.03
ENST00000537690	<i>CCDC175</i>	0.2651	0.2173	1.22	0.0436
<i>Molossus molossus</i> versus <i>Rousettus aegyptiacus</i>					
ENST00000369102	<i>C1orf54</i>	0.2231	0.0985	2.264	0.0111
ENST00000537690	<i>CCDC175</i>	0.268	0.2173	1.233	0.0336
Ensembl Transcript ID	Gene Symbol	Ka	Ks	Ka/Ks	FDR
<i>Myotis myotis</i> versus <i>Phyllostomus discolor</i>					
NA					
<i>Myotis myotis</i> versus <i>Pipistrellus kuhlii</i>					
ENST00000391930	<i>IL20</i>	0.1981	0.0841	2.357	0.0061
ENST00000378186	<i>MS4A13</i>	0.1849	0.0831	2.226	0.0131
ENST00000546561	<i>TSPAN8</i>	0.2668	0.1396	1.911	0.0016
ENST00000389019	<i>SLCO6A1</i>	0.1507	0.0912	1.653	0.0159
ENST00000537690	<i>CCDC175</i>	0.1775	0.115	1.543	0.0013
ENST00000273352	<i>ADGRG7</i>	0.1874	0.1474	1.272	0.0477
<i>Myotis myotis</i> versus <i>Rhinolophus ferrumequinum</i>					
ENST00000372670	<i>WFDC6</i>	0.2698	0.1064	2.535	0.0304
ENST00000370350	<i>FATE1</i>	0.3787	0.2216	1.79	0.0074
ENST00000537690	<i>CCDC175</i>	0.321	0.2407	1.334	0.0014
<i>Myotis myotis</i> versus <i>Rousettus aegyptiacus</i>					
ENST00000445202	<i>PATE3</i>	0.2811	0.1345	2.091	0.0358
ENST00000381627	<i>RLN2</i>	0.3601	0.1987	1.812	0.0205
ENST00000370350	<i>FATE1</i>	0.3579	0.2039	1.755	0.0037
ENST00000537690	<i>CCDC175</i>	0.3025	0.2511	1.205	0.0439
Ensembl Transcript ID	Gene Symbol	Ka	Ks	Ka/Ks	FDR
<i>Phyllostomus discolor</i> versus <i>Pipistrellus kuhlii</i>					
ENST00000546561	<i>TSPAN8</i>	0.3542	0.2529	1.4	0.0373
<i>Phyllostomus discolor</i> versus <i>Rhinolophus ferrumequinum</i>					
ENST00000296739	<i>SPZ1</i>	0.2467	0.1614	1.528	0.0072
<i>Phyllostomus discolor</i> versus <i>Rousettus aegyptiacus</i>					
ENST00000371431	<i>AKAP19</i>	0.2644	0.1427	1.853	0.037
<i>Pipistrellus kuhlii</i> versus <i>Rhinolophus ferrumequinum</i>					
ENST00000378186	<i>MS4A13</i>	0.3606	0.1745	2.066	0.0023
ENST00000370250	<i>FATE1</i>	0.419	0.2327	1.801	0.0053
ENST00000537690	<i>CCDC175</i>	0.3427	0.2656	1.29	0.0047
<i>Pipistrellus kuhlii</i> versus <i>Rousettus aegyptiacus</i>					
NA					
<i>Rhinolophus ferrumequinum</i> versus <i>Rhinolophus ferrumequinum</i>					
ENST00000382208	<i>DEFB135</i>	0.3642	0.1551	2.349	0.0129

Genes that exhibited $Ka/Ks > 1$ and $FDR < 0.05$ (Fisher exact test) were considered positively selected genes.