

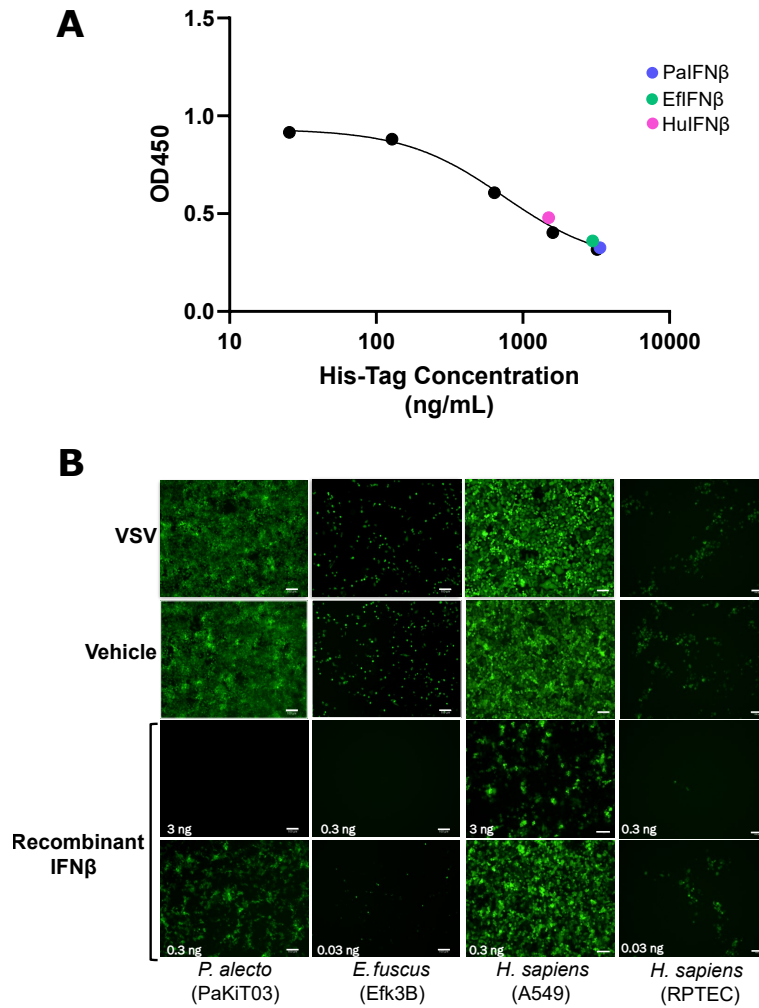
SUPPLEMENTARY MATERIALS FOR

Bat-specific adaptations in interferon signaling and GBP1 contribute to enhanced viral tolerance

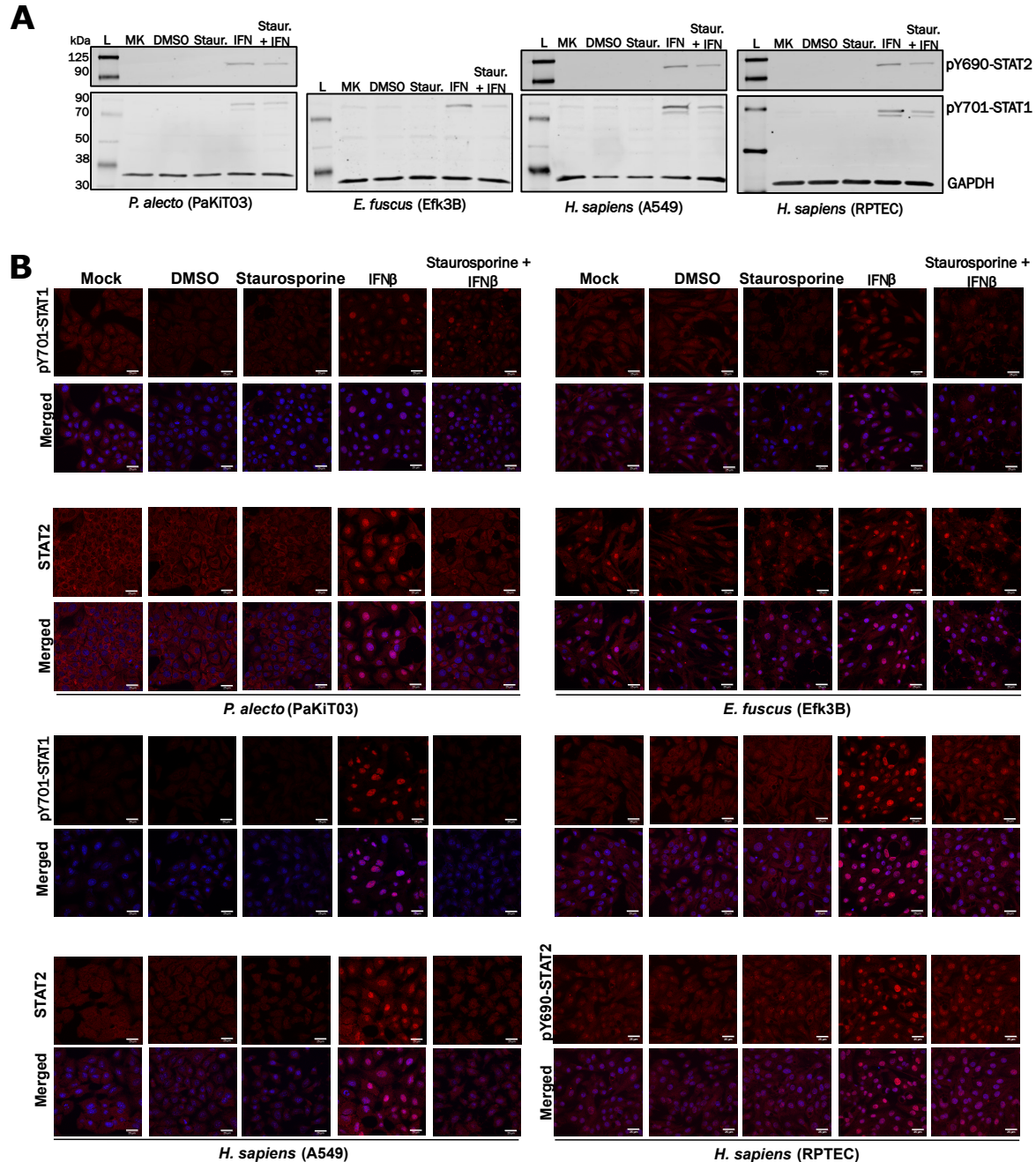
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The supplement contains: Supplementary Figures 1 to 17

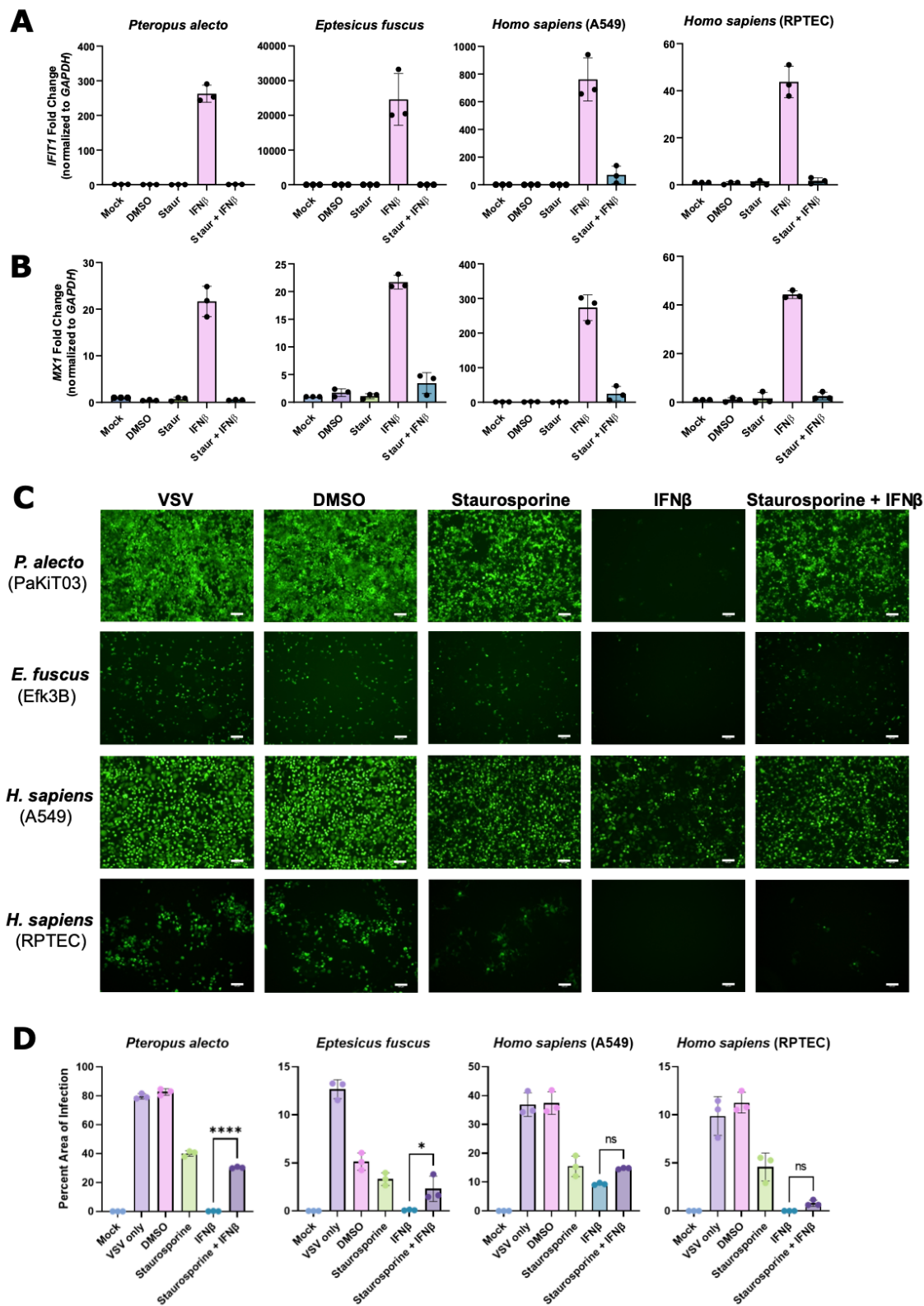
Supplementary Tables S1 to S7 are provided as sheets in a separate Excel file



Supplementary Figure 1. Generation of functional IFN β . (A) Stock concentrations for IFN β expressing a 6x-His tag for *P. alecto*, *E. fuscus* and humans were determined by a competitive ELISA. Black dots represent standards included in the commercial ELISA. (B) *P. alecto* (PaKiT03), *E. fuscus* (EfK3B), and human A549 and primary RPTEC cells were treated with the vehicle control or with serially diluted, species-matched IFN β for 6 hours prior to infection with VSV-GFP (MOI 0.1). Infection levels were assessed 16 hours post infection using fluorescent microscopy. The last dilution where 100% protection was observed was selected as 1 unit (i.e. 1U) of IFN β for each species. Scale bars = 100 μ M. Image is representative of 3 replicates.

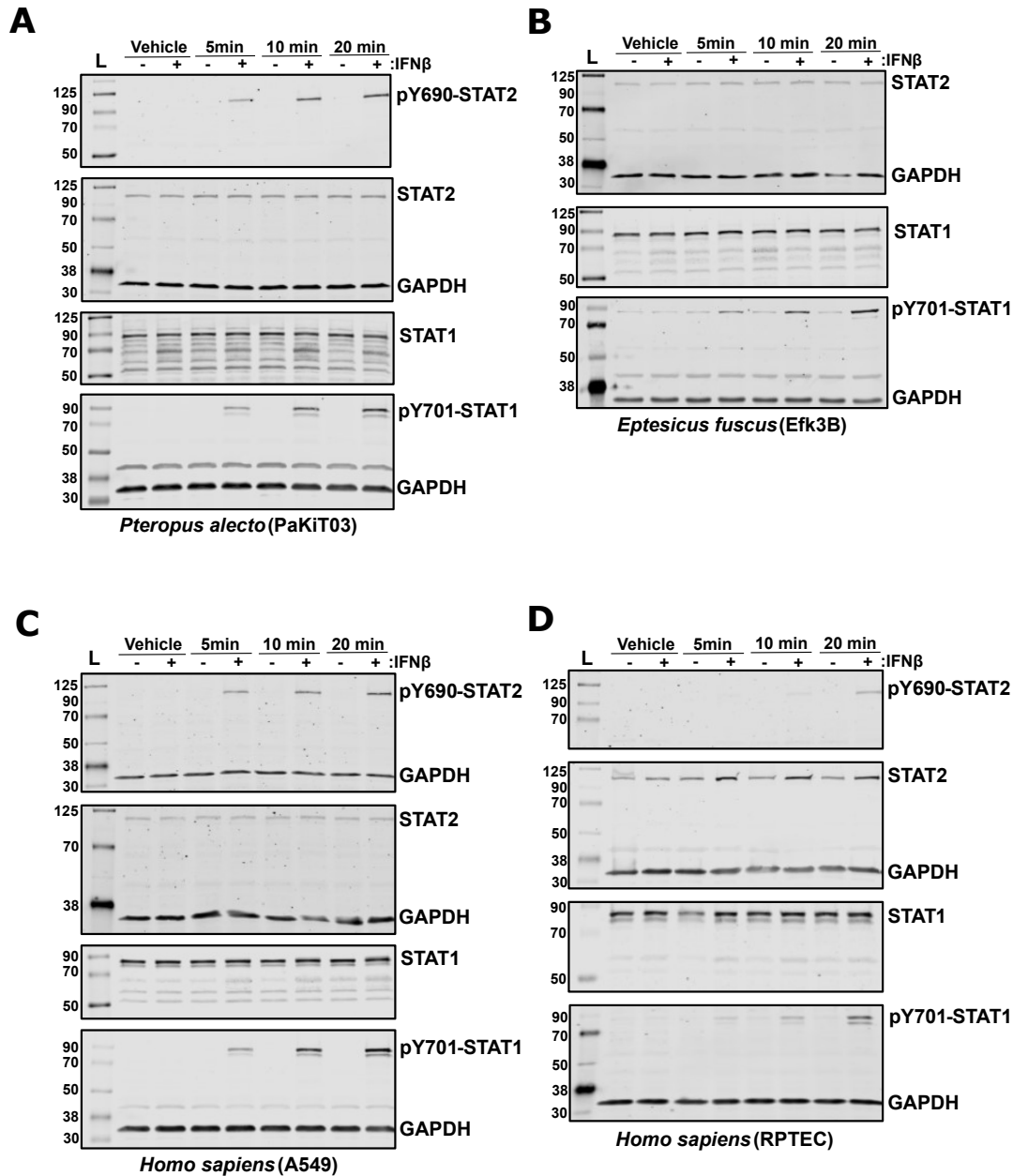


Supplementary Figure 2. Phosphorylation of STAT1 and STAT2 during bat IFN β signaling. *P. alecto* (PaKiT03), *E. fuscus* (EfK3B), and human (A549, RPTEC) cells were treated with Staurosporine (Staur; 500nM), species-matched IFN β (10 U/mL), or treated with both Staurosporine and IFN β for 4 hours. (A) Protein lysates from cells were harvested to evaluate the phosphorylation of STAT1 (pY701-STAT1) and STAT2 (pY690-STAT2). GAPDH was used as a loading control. Lane “L” represents molecular weight ladder (kDa). (B) Cells were fixed in 100% methanol and stained for pY701-STAT1, pY690-STAT2, STAT2, and/or DAPI. Nuclear translocation was visualized by confocal microscopy. Scale bars = 25 μ M. Image is representative of 3 replicates.



Supplementary Figure 3. Phosphorylation is required for IFN β -induced antiviral response. *P. alecto* (PaKiT03), *E. fuscus* (EfK3B), and human (A549, RPTEC) cells were

treated with Staurosporine (Staur; 500nM), species-matched IFN β (10 U/mL), or treated with both Staurosporine and IFN β for 4 hours. qRT-PCR was performed to evaluate the upregulation of *IFIT1* (**A**) and *MX1* (**B**) transcripts. (**C**) Following 4 hours of Staurosporine and/or IFN β treatment, cells were infected with VSV-GFP (MOI 0.1) for 16 hours. Viral replication was visualized using fluorescent microscopy, and (**D**) GFP signal was quantified using ImageJ to determine percent area of infection. Data are represented as mean \pm SD, n=3 replicates/time points (Ordinary one-way ANOVA).



Supplementary Figure 4. Full immunoblots for STAT1 and STAT2 phosphorylation. PaKiT03 (A), Efk3B (B), A549 (C), and RPTEC (D) cells were treated with vehicle or species matched IFN β (10 U/mL) for 5, 10, and 20 minutes. Total STAT1, STAT2, and phosphorylated STAT1 (pY701-STAT1) and STAT2 (pY690-STAT2) were assessed by immunoblotting. GAPDH was used as a loading control. Lane "L" represents molecular weight ladder (kDa).

P. alecto	1	MAQWEMLNQNDSPFQDQLHQLYTNSSLVPDIRQYLAVWIEDQNWQEAALGKDDSKANMLFFHFLDQLKYECCGRCSQDPEC	80
P. giganteus	1	MAQWEMLNQNDSPFQDQLHQLYTNSSLVPDIRQYLAVWIEDQNWQEAALGKDDSKANMLFFHFLDQLKYECCGRCSQDPEC	80
P. vampyrus	1	MAQWEMLNQNDSPFQDQLHQLYTNSSLVPDIRQYLAVWIEDQNWQEAALGKDDSKANMLFFHFLDQLKYECCGRCSQDPEC	80
P. rodricensis	1	MAQWEMLNQNDSPFQDQLHQLYTNSSLVPDIRQYLAVWIEDQNWQEAALGKDDSKANMLFFHFLDQLKYECCGRCSQDPEC	80
R. aegyptiacus	1	MAQWEMLNQNDSPFQDQLHQLYTNSSLVPDIRQYLAVWIEDQNWQEAALGNDSSKANMLFFHFLDQLKYECCGRCSQDPEC	80
R. ferrumequinum	1	MAQWEMLNQNDSPFQDQLHQLYTNSSLVPDIRQYLAVWIEDQNWQEAALGNDSSKANMLFFHFLDQLKYECCGRCSQDPEC	80
S. hondurensis	1	MAQWEMLNQNDSPFQDQLHQLYTNSSLPMDIRQYLAVWIEDQNWQEAALGNNSSQANMLFLHFSQDQNYECARCSQDPEC	80
A. jamaicensis	1	MAQWEMLNQNDSPFQDQLHQLYTNSSLPMDIRQYLAVWIEDQNWQEAALGNNSSQANMLFLHFSQDQNYECARCSQDPEC	80
P. discolor	1	MAQWEMLNQNDSPFQDQLHQLYTNSSLPMDIRQYLAVWIEDQNWQEAALRN-SYQANMLFLHFSQDQNYECARCSQDPEC	79
P. hasatus	1	MAQWEMLNQNDSPFQDQLHQLYTNSSLPMDIRQYLAVWIEDQNWQEAALRN-SYQANMLFLHFSQDQNYECARCSQDPEC	79
D. rotundus	1	MAQWEMLNQNDSPFQDQLHQLYTNSSLPMDIRQYLAVWIEDQNWQEAALGNNSSQANMLFLHFLDQNYECARCSQDPEC	80
E. fuscus	1	MAQWEMLNQNDSPFQDQLHQLYTNSSLVPDIRQYLAVWIEDQNWQEAALGSDNSQANMLCFHFLDQNYECARCSQDPEC	80
H. armiger	1	MAQWEMLNQNDSPFQDQLHQLYTNSSLVPDIRQYLAVWIEDQNWQEAALGSDSSKANMLFFHFLDQNYECGRCSQDPEC	80
M. molossus	1	MAQWEMLNQNDSPFQDQLHQLYTNSSLVPDIRQYLAVWIEDQNWQEAALGSDNSQANMLYLFHFLDQNYECARCSQDPEC	80
M. natalensis	1	MAQWEMLNQNDSPFQDQLHQLYTNSSLPMDIRQYLAVWIEDQNWQEAALGNDSSQANMLFFHFLDQNYECGRCSQDPEC	80
M. brandtii	1	MAQWEMLNQNDSPFQDQLHQLYTNSSLVPDIRQYLAVWIEDQNWQEAALGNDSSQANMLCFHFVQDQNYECARCSQDPEC	80
M. lucifugus	1	MAQWEMLNQNDSPFQDQLHQLYTNSSLVPDIRQYLAVWIEDQNWQEAALGNDSSQANMLCFHFVQDQNYECARCSQDPEC	80
M. myotis	1	MAQWEMLNQNDSPFQDQLHQLYTNSSLVPDIRQYLAVWIEDQNWQEAALGNDSSQANMLCFHFVQDQNYECARCSQDPEC	80
M. davidii	1	MAQWEMLNQNDSPFQDQLHQLYTNSSLVPDIRQYLAVWIEDQNWQEAALGNDSSQANMLCFHFVQDQNYECARCSQDPEC	80
P. kuhlii	1	MAQWEMLNQNDSPFQDQLHQLYTNSSLVPDIRQYLAVWIEDQNWQEAALGNDSSQANMLCFHFVQDQNYECARCSQDPEC	80
H. sapiens	1	MAQWEMLNQNDSPFQDQLHQLYTNSSLVPDIRQYLAVWIEDQNWQEAALGSDSSKANMLFFHFLDQNYECGRCSQDPEC	80

P. alecto	81	LLLQHNLRKFCRDIQAFPPQGPQTQLAEMIFNLLLEEKRILIAQRAQLLEQGEVPVEVPVESQQ-PEIESRILELRVMMMEKL	159
P. giganteus	81	LLLQHNLRKFCRDIQAFPPQGPQTQLAEMIFNLLLEEKRILIAQRAQLLEQGEVPVEVPVESQQ-PEIESRILELRVMMMEKL	159
P. vampyrus	81	LLLQHNLRKFCRDIQAFPPQGPQTQLAEMIFNLLLEEKRILIAQRAQLLEQGEVPVEVPVESQQ-PEIESRILELRVMMMEKL	159
P. rodricensis	81	LLLQHNLRKFCRDIQAFPPQGPQTQLAEMIFNLLLEEKRILIAQRAQLLEQGEVPVEVPVESQQ-PEIESRILELRVMMMEKL	159
R. aegyptiacus	81	LLLQHNLRKFCRDIQAFPPQGPQTQLAEMIFNLLLEEKRILIAQRAQLLEQGEPALEVPVESQQ-PEIESRILELRVMMMEKL	159
R. ferrumequinum	81	LLLQHNLRKFCRDIQAFPPQGPQTQLAEMIFNLLLEEKRILIAQRAQLLEQGEPALEAPVESQQHEIESRILELRAMMEKL	160
S. hondurensis	81	LLLQHNLRKFCRDIQAFPPGGPIQLAEMIFNLLLEEKRILIAQRAQVEQEEPDQLQAPVESQQ-HEIESRILELRAMMEKL	159
A. jamaicensis	81	LLLQHNLRKFCRDIQAFPPGGPIQLAEMIFNLLLEEKRILIAQRAQVEQEEPDQLHAPVESQQ-HEIESRILELRAMMEKL	159
P. discolor	80	LLLQHNLRKFCRDIQAFPPGGPIQLAEMIFNLLLEEKRILIAQRAQVEQEEPDQLQAPVESQQ-HEIESRILELRAMMEKL	158
P. hasatus	80	LLLQHNLRKFCRDIQAFPPGGPIQLAEMIFNLLLEEKRILIAQRAQVEQEEPDQLQAPVESQQ-HEIESRILELRAMMEKL	158
D. rotundus	81	LLLQHNLRKFCRDIQAFPPGGPIQLAEMIFNLLLEEKRILIAQRAQVEQEEPDQLHAPVESQQ-HEIESRILELRAMMEKL	159
E. fuscus	81	LLLQHNLRKFCRDIQAFPPGGPIQLAEMIFNLLLEEKRILIAQRAQVEQEEPALEAPVESQQ-HEIESRILELRAMMEKL	159
H. armiger	81	LLLQHNLRKFCRDIQAFPPGGPIQLAEMIFNLLLEEKRILIAQRAQVEQEEPALEAPVESQQ-HEIESRILELRAMMEKL	159
M. molossus	81	LLLQHNLRKFCRDIQAFPPGGPIQLAEMIFNLLLEEKRILIAQRAQVEQEEPALEAPVESQQ-HEIESRILELRAMMEKL	159
M. natalensis	81	LLLQHNLRKFCRDIQAFPPGGPIQLAEMIFNLLLEEKRILIAQRAQVEQEEPALEAPVESQQ-HEIESRILELRAMMEKL	159
M. brandtii	81	LLLQHNLRKFCRDIQAFPPGGPIQLAEMIFNLLLEEKRILIAQRAQVEQEEPALEAPVESQQ-HEIESRILELRAMMEKL	159
M. lucifugus	81	LLLQHNLRKFCRDIQAFPPGGPIQLAEMIFNLLLEEKRILIAQRAQVEQEEPALEAPVESQQ-HEIESRILELRAMMEKL	159
M. myotis	81	LLLQHNLRKFCRDIQAFPPGGPIQLAEMIFNLLLEEKRILIAQRAQVEQEEPALEAPVESQQ-HEIESRILELRAMMEKL	159
M. davidii	81	LLLQHNLRKFCRDIQAFPPGGPIQLAEMIFNLLLEEKRILIAQRAQVEQEEPALEAPVESQQ-HEIESRILELRAMMEKL	159
P. kuhlii	81	LLLQHNLRKFCRDIQAFPPGGPIQLAEMIFNLLLEEKRILIAQRAQVEQEEPALEAPVESQQ-HEIESRILELRAMMEKL	159
H. sapiens	81	LLLQHNLRKFCRDIQAFPPGGPIQLAEMIFNLLLEEKRILIAQRAQLLEQGEVPVEVPVESQQ-HEIESRILELRAMMEKL	159

P. alecto	160	VKSISQLKDQDVFVCFRYKTS--VRTASLDPHQIRQQQLQETLNELDKRRKEVLDASKALLGLRTTLTELLPKLEEWK	237
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P. vampyrus	160	VKSISQLKDQDVFVCFRYKTHTLARTASLDPHQIRQQQLQETLNELDKRRKEVLDASKALLGLRTTLTELLPKLEEWK	239
P. rodricensis	160	VKSISQLKDQDVFVCFRYKTHTLARTASLDPHQIRQQQLQETLNELDKRRKEVLDASKALLGLRTTLTELLPKLEEWK	239
R. aegyptiacus	160	VKSISQLKDQDVFVCFRYKTHISVKTPTSLDPHQIRHQQLQETLNELDKRRKEVLDSSKALLGLRTTLTELLPKLEEWK	239
R. ferrumequinum	161	VKSISQLKDQDVFVCFRYNTQKSVRTPSLDPHQTRHQQLQETLNELDKRRKEVLDTSKALLGLRTTLTELLPKLEEWK	240
S. hondurensis	160	VKSISQLKDQDVFVCFRYKTQAPVRTASLDPHHTKQKQLQETLNELDKRRKEVLDSSRALLGLRTTLTELLPKLEEWK	239
A. jamaicensis	160	VKSISQLKDQDVFVCFRYKTQAPVRTASLDPHHTKQKQLQETLNELDKRRKEVLDSSRALLGLRTTLTELLPKLEEWK	239
P. discolor	159	VKSISQLKDQDVFVCFRYKTQAPVRTASLDPHHTKQKQLQETLNELDKRRKEVLDSSRALLGLRTTLTELLPKLEEWK	238
P. hasatus	159	VKSISQLKDQDVFVCFRYKTQAPVRTASLDPHHTKQKQLQETLNELDKRRKEVLDSSRALLGLRTTLTELLPKLEEWK	238
D. rotundus	160	VKSISQLKDQDVFVCFRYKTQAPVRTASLDPHHTQKQLQETLNELDKRRKEVLDSSRALLGLRTTLTELLPKLEEWK	239
E. fuscus	160	VKSISQLKDQDVFVCFRYKTQAPVRTASLDPHHTQKQLQETLNELDKRRKEVLDSSRALLGLRTTLTELLPKLEEWK	239
H. armiger	160	VKSISQLKDQDVFVCFRYKTQAPVRTASLDPHHTQKQLQETLNELDKRRKEVLDSSRALLGLRTTLTELLPKLEEWK	239
M. molossus	160	VKSISQLKDQDVFVCFRYKTQAPVRTASLDPHHTQKQLQETLNELDKRRKEVLDSSRALLGLRTTLTELLPKLEEWK	239
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M. brandtii	160	VKSISQLKDQDVFVCFRYKTQAPVRTASLDPHHTQKQLQETLNELDKRRKEVLDSSRALLGLRTTLTELLPKLEEWK	239
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P. kuhlii	160	VKSISQLKDQDVFVCFRYKTQAPVRTASLDPHHTQKQLQETLNELDKRRKEVLDSSRALLGLRTTLTELLPKLEEWK	239
H. sapiens	160	VKSISQLKDQDVFVCFRYKTQAPVRTASLDPHHTQKQLQETLNELDKRRKEVLDSSRALLGLRTTLTELLPKLEEWK	239

***Supplementary Figure 5 continues on next page**

P. alecto	238	VQQQKACIGSREDG--GLELSQLEKWFTDGAKLLFHLRQLLKKELKGLSHLVSYHHDPLTTGVDLR	EAQVTELLQRLLLR	315
P. giganteus	240	VQQQKACIGSREDG--GLELSQLEKWFTDGAKLLFHLRQLLKKELKGLSHLVSYHHDPLTTGVDLR	EAQVTELLQRLLLR	317
P. vampyrus	240	VQQQKACIGSREDG--GLELSQLEKWFTDGAKLLFHLRQLLKKELKGLSHLVSYHHDPLTTGVDLR	EAQVTELLQRLLLR	317
P. rodricensis	240	VQQQKACIGSREDG--GLELSQLEKWFTDGAKLLFHLRQLLKKELKGLSHLVSYHHDPLTTGVDLR	EAQVTELLQRLLLR	317
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S. hondurensis	240	AQQQKACIGAPTNGGLELELLQLLEKWFTDGAKLLFHLRQLLKKELKGLSLLVTYENDPLTKGVDMQEAQVMELLQRLLHRA	319	
A. jamaicensis	240	AQQQKACIGAPTNGGLELELLQLLEKWFTDGAKLLFHLRQLLKKELKGLSLLVTYENDPLTKGVDMQEAQVMELLQRLLHRA	319	
P. discolor	239	AQQQKACIGAPTNG--GLQLLQLEKWFTDGAKLLFHLRQLLKKELKGLSLLVTYENDPLTKGVDMQEAQVMELLQRLLHRA	316	
P. hasatus	239	AQQQKACIGAPTNG--GLQLLQLEKWFTDGAKLLFHLRQLLKKELKGLSLLVTYDNDPLTKGVDMQEAQVMELLQRLLHRA	316	
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H. armiger	240	VQQQKACIGAPVDG--GLELFQLEKWFTDGAKLLFHLRQLLKKELKGLSRLVSYQDDPLTKGVHLQEAQVTELLQRLLHRA	317	
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P. kuhlii	239	AQQQKACIGAPAEQ--GLELVQLEKWFTDGAKLLFHLRQLLKKELKGLS-HVSYDNDRLASGADQQQARATELLRHLLHRA	315	
H. sapiens	240	AQQQKACIRAPIDH--GLE--QLETWFTDGAKLLFHLRQLLKKELKGLSCLVSYQDDPLTKGVDLR	EAQVTELLQRLLHRA	315

P. alecto	316	FVVETQPCMPQTPHRPLILRTGSKFTVTRRLVRLQEGNETLTAEVFIDRNPLQSQGRKFNFILTSNRKTLTPEKGQSQG	395
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P. vampyrus	318	FVVETQPCMPQTPHRPLILRTGSKFTVTRRLVRLQEGNETLTAEVFIDRNPLQSQGRKFNFILTSNRKTLTPEKGQSQG	397
P. rodricensis	318	FVVETQPCMPQTPHRPLILRTGSKFTVTRRLVRLQEGNETLTAEVFIDRNPLQSQGRKFNFILTSNRKTLTPEKGQSQG	397
R. aegyptiacus	318	FVVETQPCMPQTPHRPLILRTGSKFTVTRRLVRLQEGNESLTAEVFIDRNSLQSQGRKFNFILTSNRKTLTPEKGQSQG	397
R. ferrumequinum	319	FVVETQPCMPQTPHRPLILRTGSKFTVTRRLVRLQEGNETLTAEVSIDRNPQSQGRKFNFILTSNQKTLTPEKGQSQG	398
S. hondurensis	320	FVVETQPCMPQTLHRPLILRTGSKFTVTRRLVRLQEGSESLTAEVFIDRNPQSQGRKFNFILTSNRKTLTPEKGQSQG	399
A. jamaicensis	320	FVVETQPCMPQTYHRPLILRTGSKFTVTRRLVRLQEGSESLTAEVFIDRNPQSQGRKFNFILTSNRKTLTPEKGQSQG	399
P. discolor	317	FVVETQPCMPQTPHRPLILRTGSKFTVTRRLVRLQEGSESLTAEVFIDRNPQSQGRKFNFILTSNQKTLTPEKGQSQG	396
P. hasatus	317	FVVETQPCMPQTPHRPLILRTGSKFTVTRRLVRLQEGSESLTAEVFIDRNPQSQGRKFNFILTSNRKTLTPEKGQSQG	396
D. rotundus	318	FVVETQPCMPQTPHRPLILRTGSKFTVTRRLVRLQEGSESLTAEVFIDRNPQSQGRKFNFILTSNQKTLTPEKGQSQG	397
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H. armiger	318	FVVENQPCMPQTPHRPLILRTGSKFTVTRRLVRLQEGNESLTAEVSIDRNPQSQGRKFNFILTSNQKTLTPEKGQSQG	397
M. molossus	317	FVVETQPCMPQTLHRPLILRTGSKFTVTRRLVRLQEGSESLTAEVFIDRNPQSQSFRKFNFILTSNQKTLTPEKGQSQG	396
M. natalensis	317	FVITETQPCMPQTPHRPLILRTGSKFTVTRRLVRLQEGSESLTAEVFIDRNPQSQGRKFNFILTSNQKTLTPEKGQSQG	396
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M. lucifugus	318	FVVETQPCMPQTPHRPLILRTGSKFTVTRRLVRLQEGSESLTAEVFIDKNPPQSQGRKFNFILTSNQKTLTPEKGQSQG	397
M. myotis	318	FVVETQPCMPQTPHRPLILRTGSKFTVTRRLVRLQEGSESLTAEVFIDKDPQSQGRKFNFILTSNQKTLTPEKGQSQG	397
M. davidii	318	FVVETQPCMPQTPHRPLILRTGTIKFTVTRRLVRLQEGSESLTAEVFIDKNPPQSQGRKFNFILTSNQKTLTPEKGQSQG	397
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H. sapiens	316	FVVETQPCMPQTPHRPLILKGTGSKFTVTRRLVRLQEGNESLTVESIDRNPQLQGRKFNFILTSNQKTLTPEKGQSQG	395

P. alecto	396	LIWDFS YLTLLVEQRSGSGSGKGNKGLLGVT EELHIISFTVKYTYQGLKQELKTD TLPVVIISNMNQLSIAWASVLWFNLL	475
P. giganteus	398	LIWDFS YLTLLVEQRSGSGSGKGNKGLLGVT EELHIISFTVKYTYQGLKQELKTD TLPVVIISNMNQLSIAWASVLWFNLL	477
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P. rodricensis	398	LIWDFS YLTLLVEQRSGSGSGKGNKGLLGVT EELHIISFTVKYTYQGLKQELKTD TLPVVIISNMNQLSIAWASVLWFNLL	477
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S. hondurensis	400	LIWDFRYLTLLTEQRSGSGSGKGSNKGLLGVT EELHIISFTVRYTYQGLKQELKTD TLPVVIISNTNQLSIAWASVLWFNLL	479
A. jamaicensis	400	LIWDFRYLTLLTEQRSGSGSGKGSNKGLLGVT EELHIISFTVRYTYQGLKQELKTD TLPVVIISNTNQLSIAWASVLWFNLL	479
P. discolor	397	LIWDFRYLTLLTEQRSGSGSGKGSNKGLLGVT EELHIISFTVKYTYQGLKQELKTD TLPVVIISNTNQLSIAWASVLWFNLL	476
P. hasatus	397	LIWDFRYLTLLTEQRSGSGSGKGSNKGLLGVT EELHIISFTVKYTYQGLKQELKTD TLPVVIISNTNQLSIAWASVLWFNLL	476
D. rotundus	398	LIWDFRYLTLLTEQRSGSGSGKGTNKSLLGVT EELHIISFTVKYTYQGLKQELKTD TLPVVIISNTNQLSIAWASVLWFNLL	477
E. fuscus	398	LIWDFGYLTLLVEQRSGSGSGKGSNKGLLGVT EELHIISFTVQYTYQGLKQELKAD TLPVVIISNTNQLSIAWASVLWFNLL	477
H. armiger	398	LIWDFGYLTLLVEQRSGSGSGKGSNKGLLGVT EELHIISITVKYTYQGLKQELKTD TLPVVIISNMNQLSIAWASVLWFNLL	477
M. molossus	397	LIWDFGYLTLLVEQRSGSGSGKGSNKGLLGVT EELHIISFTVKYTYQGLKQELKTD TLPVVIISNMNQLSIAWASVLWFNLL	476
M. natalensis	397	LIWDFGYLTLLVEQRSGSGSGKGSNKGLLGVT EELHIISFTVKYTYQGLKQELKTD TLPVVIISNMNQLSIAWASVLWFNLL	476
M. brandtii	398	LIWDFGYLTLLVEQRSGSGSGKGSNKGLLGVT EELHIISFTVRYTYQGLKQELKAD TLPVVIISNMNQLSIAWASVLWFNLL	477
M. lucifugus	398	LIWDFGYLTLLVEQRSGSGSGKGSNKGLLGVT EELHIISFTVRYTYQGLKQELKAD TLPVVIISNMNQLSIAWASVLWFNLL	477
M. myotis	398	LIWDFGYLTLLVEQRSGSGSGKGSNKGLLGVT EELHIISFTVRYTYQGLKQELKAD TLPVVIISNMNQLSIAWASVLWFNLL	477
M. davidii	398	LIWDFGYLTLLVEQRSGSGSGKGSNKGLLGVT EELHIISFTVRYTYQGLKQELKAD TLPVVIISNMNQLSIAWASVLWFNLL	477
P. kuhlii	396	LIWDFGYLTLLVEQRSGSGSGKGSNKGLLGVT EELHIISFTVRYTYQGLKQELKAD TLPVVIISNMNQLSIAWASVLWFNLL	475
H. sapiens	396	LIWDFGYLTLLVEQRSGSGSGKGSNKGLLGVT EELHIISFTVKYTYQGLKQELKTD TLPVVIISNMNQLSIAWASVLWFNLL	475

*Supplementary Figure 5 continues on next page

P. alecto	476	SSNPQNQQFFSSPPKAPWS	LLGPALSWQFL	SYVGRGLDQDQLNMLRDKLFEQKSKNED	ALLSWADFTKRESPPGKLPFWT	555
P. giganteus	478	SSNPQNQQFFSSPPKAPWS	LLGPALSWQFL	SYVGRGLDQDQLNMLRDKLFEQKSKNED	ALLSWADFTKRESPPGKLPFWT	557
P. vampyrus	478	SSNPQNQQFFSSPPKAPWS	LLGPALSWQFL	SYVGRGLDQDQLNMLRDKLFEQKSKNED	ALLSWADFTKRESPPGKLPFWT	557
P. rodricensis	478	SSNPQNQQFFSSPPKAPWS	LLGPALSWQFL	SYVGRGLDQDQLNMLRDKLFEQKSKNED	ALLSWADFTKRESPPGKLPFWT	557
R. aegyptiacus	478	SSNPQNQQFFSSPPKAPWS	LLGPALSWQFL	SYVGRGLDQDQLNMLRDKLFEQKSKNED	ALLSWADFTKRESPPGKLPFWT	557
R. ferrumequinum	479	TNPQNQQFFSSPPKAPWS	LLGPALSWQFL	SYVGRGLDQDQLSMLKDKLFGKNCRNE	ALLSWADFTKRESPPGKLPFWT	558
S. hondurensis	480	SSNPQNQQFFSSPPKAPWS	LLGPALSWQFL	SYVGRGLDQDQLSMLRDKLFGQNSGND	ALLSWADFTKRESPPGKLPFWT	559
A. jamaicensis	480	SSNPQNQQFFSSPPKAPWN	LLGPALSWQFSSYVGRGLDQDQLSMLRDKLFGQNSGNEGAVLSWAE	FTKRESPPGKLPFWT	559	
P. discolor	477	SSNPQNQLFFSSTPKAPWN	LLGPALSWQFSSYVGRGLDQDQLSMLRDKLFGQNSGNEGALLSWADFTKRESPPGKLPFWT	556		
P. hasatus	477	SSNPQNQLFFSSPPKAPWN	LLGPALSWQFSSYVGRGLDQDQLSMLRDKLFGQNSGNEGALLSWADFTKRESPPGKLPFWT	556		
D. rotundus	478	SSNPQNQQFFSSPPKAPWN	LLGPALSWQFSSYVGRGLDQDQLSMLKDKLFGQNSGNEGALLSWADFTKRESPPGKLPFWT	557		
E. fuscus	478	SSNPQNQQFFSSPPKAPWT	LLGPALSWQFSSYVGRGLDQDQLSMLKDKLFGQNSGNEGALLSWADFTKRESPPGKLPFWT	557		
H. armiger	478	TNPQNQQFFSSPPKAPWS	LLGPALSWQFL	SYVGRGLDQDQLSMLKDKLFGKNCRNE	ALLSWADFTKRESPPGKLPFWT	557
M. molossus	477	SSNPQNQQFFSSPPKAPWN	LLGPALSWQFSSYVGRGLDQDQLNMLRDKLFGQNSGNEGALLSWADFTKRESPPGKLPFWT	556		
M. natalensis	477	SSNPQNQQFFSSPPKAPWN	LLGPALSWQFSSYVGRGLDQDQLSMLKDKLFGQNSGNEGALLSWADFTKRESPPGKLPFWT	556		
M. brandtii	478	SSNPQNQQFFSSPPKAPWT	LLGPALSWQFSSYVGRGLDQDQLSMLKDKLFGQNSGNEGALLSWADFTKRESPPGKLPFWT	557		
M. lucifugus	478	SSNPQNQQFFSSPPKAPWT	LLGPALSWQFSSYVGRGLDQDQLSMLKDKLFGQNSGNEGALLSWADFTKRESPPGKLPFWT	557		
M. myotis	478	SSNPQNQQFFSSPPKAPWT	LLGPALSWQFSSYVGRGLDQDQLSMLKDKLFGQNSGNEGALLSWADFTKRESPPGKLPFWT	557		
M. davidii	478	SSNPQNQQFFSSPPKAPWT	LLGPALSWQFSSYVGRGLDQDQLSMLKDKLFGQNSGNEGALLSWADFTKRESPPGKLPFWT	557		
P. kuhlii	476	SSNPQNQQFFSSPPKAPWA	LLGPALSWQFSSYVGRGLDQDQLSMLKDKLFGQNSGSEGA	ALLSWADFTKRESPPGKLPFWT	555	
H. sapiens	476	SPNLPQNQQFFSSPPKAPWS	LLGPALSWQFSSYVGRGLDQDQLSMLRDKLFGQNCRTEDPL	ALLSWADFTKRESPPGKLPFWT	555	

P. alecto	556	WLDKILDLVHDHLKDLWNDGRIMGFVSRSQERLLKKT	ISGTFLRLFSETSEGGITCSWVEHQDDDKVLIYSVQ	PFTKEV	635
P. giganteus	558	WLDKILDLVHDHLKDLWNDGRIMGFVSRSQERLLKKT	ISGTFLRLFSETSEGGITCSWVEHQDDDKVLIYSVQ	PFTKEV	637
P. vampyrus	558	WLDKILDLVHDHLKDLWNDGRIMGFVSRSQERLLKKT	ISGTFLRLFSETSEGGITCSWVEHQDDDKVLIYSVQ	PFTKEV	637
P. rodricensis	558	WLDKILDLVHDHLKDLWNDGRIMGFVSRSQERLLKKT	ISGTFLRLFSETSEGGITCSWVEHQDDDKVLIYSVQ	PFTKEV	637
R. aegyptiacus	558	WLDKILDLVHDHLKDLWNDGRIMGFVSRSQERLLKKT	ISGTFLRLFSETSEGGITCSWVEHQDDDKVLIYSVQ	PFTKEV	637
R. ferrumequinum	559	WLDKILDLVHDHLKDLWKDGRIMGFVSRSQERLLKKT	ISGTFLRLFSETSEGGITCSWVEHQDDDKVLIYSVQ	PFTKEV	638
S. hondurensis	560	WLDKILDLVHDHLKDLWKDGRIMGFVSRSQERLLKKT	ISGTFLRLFSETLEGGITCSWVEHQDDDKVLIYSVQ	PFTKEV	639
A. jamaicensis	560	WLDKILDLVHDHLKDLWKDGRIMGFVSRSQERLLKKT	ISGTFLRLFSETLEGGITCSWVEHQDDDKVLIYSVQ	PFTKEV	639
P. discolor	557	WLDKILDLVHDHLKDLWKDGRIMGFVSRSQERLLKKT	ISGTFLRLFSETLEGGITCSWVEHQDDDKVLIYSVQ	PFTKEV	636
P. hasatus	557	WLDKILDLVHDHLKDLWKDGRIMGFVSRSQERLLKKT	ISGTFLRLFSETLEGGITCSWVEHQDDDKVLIYSVQ	PFTKEV	636
D. rotundus	558	WLDKILDLVHDHLKDLWKDGRIMGFVSRSQERLLKKT	ISGTFLRLFSETSEGGITCSWVEHQDDDKVLIYSVQ	PFTKEV	637
E. fuscus	558	WLDKILDLVHDHLKDLWNDGRIMGFVSRSQERLLKKT	ISGTFLRLFSETSEGGITCSWVEHQDDDKVLIYSVQ	PFTKEV	637
H. armiger	558	WLDKILDLVHDHLKDLWNRGLIMGFVSRSQERLLKKT	ISGTFLRLFSETSEGGITCSWVEHQDDDKVLIYSVQ	PFTKEV	637
M. molossus	557	WLDKILDLVHDHLKDLWNDGRIMGFVSRSQERLLKKT	ISGTFLRLFSETSEGGITCSWVEHQDDDKVLIYSVQ	PFTKEV	636
M. natalensis	557	WLDKILDLVHDHLKDLWKDGRIMGFVSRSQERLLKKT	ISGTFLRLFSETSEGGITCSWVEHQDDDKVLIYSVQ	PFTKEV	636
M. brandtii	558	WLDKILDLVHEHLKDLWNDGRIMGFVSRSQERLLKKT	ISGTFLRLFSETSEGGITCSWVEHQDDDKVLIYSVQ	PFTKEV	637
M. lucifugus	558	WLDKILDLVHEHLKDLWNDGRIMGFVSRSQERLLKKT	ISGTFLRLFSETSEGGITCSWVEHQDDDKVLIYSVQ	PFTKEV	637
M. myotis	558	WLDKILDLVHEHLKDLWNDGRIMGFVSRSQERLLKKT	ISGTFLRLFSETSEGGITCSWVEHQDDDKVLIYSVQ	PFTKEV	637
M. davidii	558	WLDKILDLVHEHLKDLWNDGRIMGFVSRSQERLLKKT	ISGTFLRLFSETSEGGITCSWVEHQDDDKVLIYSVQ	PFTKEV	637
P. kuhlii	556	WLDKILELVHDHLKDLWNDGRIMGFVSRSQERLLKKT	ISGTFLRLFSETAEGGVTCWVEHQDDDKVLIYSVQ	PFTKEV	635
H. sapiens	556	WLDKILELVHDHLKDLWNDGRIMGFVSRSQERLLKKT	ISGTFLRLFSETSEGGITCSWVEHQDDDKVLIYSVQ	PFTKEV	635

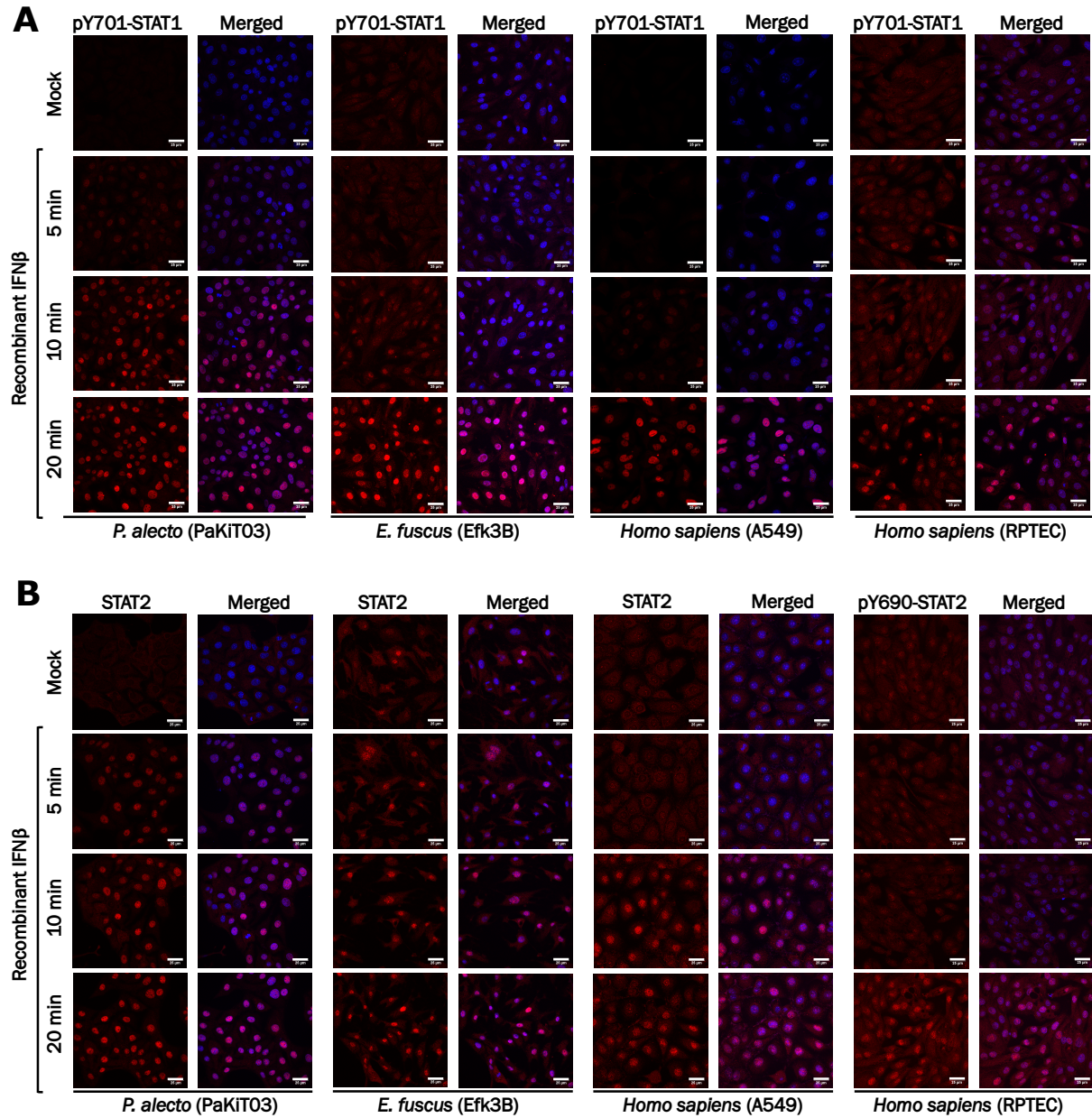
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P. giganteus	638	LQSLPLTKIIRHYQLLTEENIPENPLCF	FLYPRIPRDEAFGCYYEDKVNLE	ERRKYLKHKLIIVSNRQVDELQQLPEPNLE	717		
P. vampyrus	638	LQSLPLTKIIRHYQLLTEENIPENPLCF	FLYPRIPRDEAFGCYYEDKVNLE	ERRKYLKHKLIIVSNRQVDELQQLPEPNLE	717		
P. rodricensis	638	LQSLPLTKIIRHYQLLTEENIPENPLCF	FLYPRIPRDEAFGCYYEDKVNLE	ERRKYLKHKLIIVSNRQVDELQQLPEPNLE	717		
R. aegyptiacus	638	LQSLPLTKIIRHYQLLTEENIPENPLCF	FLYPRIPRDEAFGCYYEDKVNLE	ERRKYLKHKLIIVSNRQVDELQQLPEPNLE	717		
R. ferrumequinum	639	LQSLPLTKIIRHYQLLTEENIPENPLRFLYPR	IPRDEAFGCYYEDKVNLE	ERRKYLKHKLIIVSNRQVDELQQLPEPNLE	718		
S. hondurensis	640	LQSLPLTKIIRHYQLLTEENIPENPLRFLYPR	IPRDEAFGCYYEDKVNLE	ERRKYLKHKLIIVSNRQVDELQQLPEPNLE	719		
A. jamaicensis	640	LQSLPLTKIIRHYQLLTEENIPENPLRFLYPR	IPRDEAFGCYYEDKVNLE	ERRKYLKHKLIIVSNRQVDELQQLPEPNLE	719		
P. discolor	637	LQSLPLTKIIRHYQLFTEENIPENPLCF	FLYPRIPRDEAFGCYYEDKVNLE	ERRKYLKHKLIIVSNRQVDELQQLPEPNLE	716		
P. hasatus	637	LQSLPLTKIIRHYQLFTEENIPENPLCF	FLYPRIPRDEAFGCYYEDKVNLE	ERRKYLKHKLIIVSNRQVDELQQLPEPNLE	716		
D. rotundus	638	LQSLPLTKIIRHYQLFTEENIPENPLCF	FLYPRIPRDEAFGCYYEDKVNLE	ERRKYLKHKLIIVSNRQVDELQQLPEPNLE	717		
E. fuscus	638	LQSLPLTKIIRHYQLLTEENIPENPLRFLYPR	IPRDEAFGCYYEDKVNLE	ERRKYLKHKLIIVSNRQVDELQQLPEPNLE	717		
H. armiger	638	LQSLPLTKIIRHYQLLTEENIPENPLRFLYPR	IPRDEAFGCYYEDKVNLE	ERRKYLKHKLIIVSNRQVDELQQLPEPNLE	717		
M. molossus	637	LQSLPLTKIIRHYQLLTEENIPENPLCF	FLYPRIPRDEAFGCYYEDKVNLE	ERRKYLKHKLIIVSNRQVDELQQLPEPNLE	716		
M. natalensis	637	LQSLPLTKIIRHYQLLTEENIPENPLCF	FLYPRIPRDEAFGCYYEDKVNLE	ERRKYLKHKLIIVSNRQVDELQQLPEPNLE	716		
M. brandtii	638	LQSLPLTKIIRHYQLLTEENIPENPLRFLYPR	IPRDEAFGCYYEDKVNLE	ERRKYLKHKLIIVSNRQVDELQQLPEPNLE	717		
M. lucifugus	638	LQSLPLTKIIRHYQLLTEENIPENPLRFLYPR	IPRDEAFGCYYEDKVNLE	ERRKYLKHKLIIVSNRQVDELQQLPEPNLE	717		
M. myotis	638	LQSLPLTKIIRHYQLLTEENIPENPLRFLYPR	IPRDEAFGCYYEDKVNLE	ERRKYLKHKLIIVSNRQVDELQQLPEPNLE	717		
M. davidii	638	LQSLPLTKIIRHYQLLTEENIPENPLRFLYPR	IPRDEAFGCYYEDKVNLE	ERRKYLKHKLIIVSNRQVDELQQLPEPNLE	717		
P. kuhlii	636	LQSLPLTKIIRHYQLLTEENIPENPLRFLYPR	IPRDEAFGCYYEDKVNLE	ERRKYLKHKLIIVSNRQVDELQQLPEPNLE	715		
H. sapiens	636	LQSLPLTKIIRHYQLLTEENIPENPLRFLYPR	IPRDEAFGCYYEDKVNLE	ERRKYLKHKLIIVSNRQVDELQQLPEPNLE	715		

*Supplementary Figure 5 continues on next page

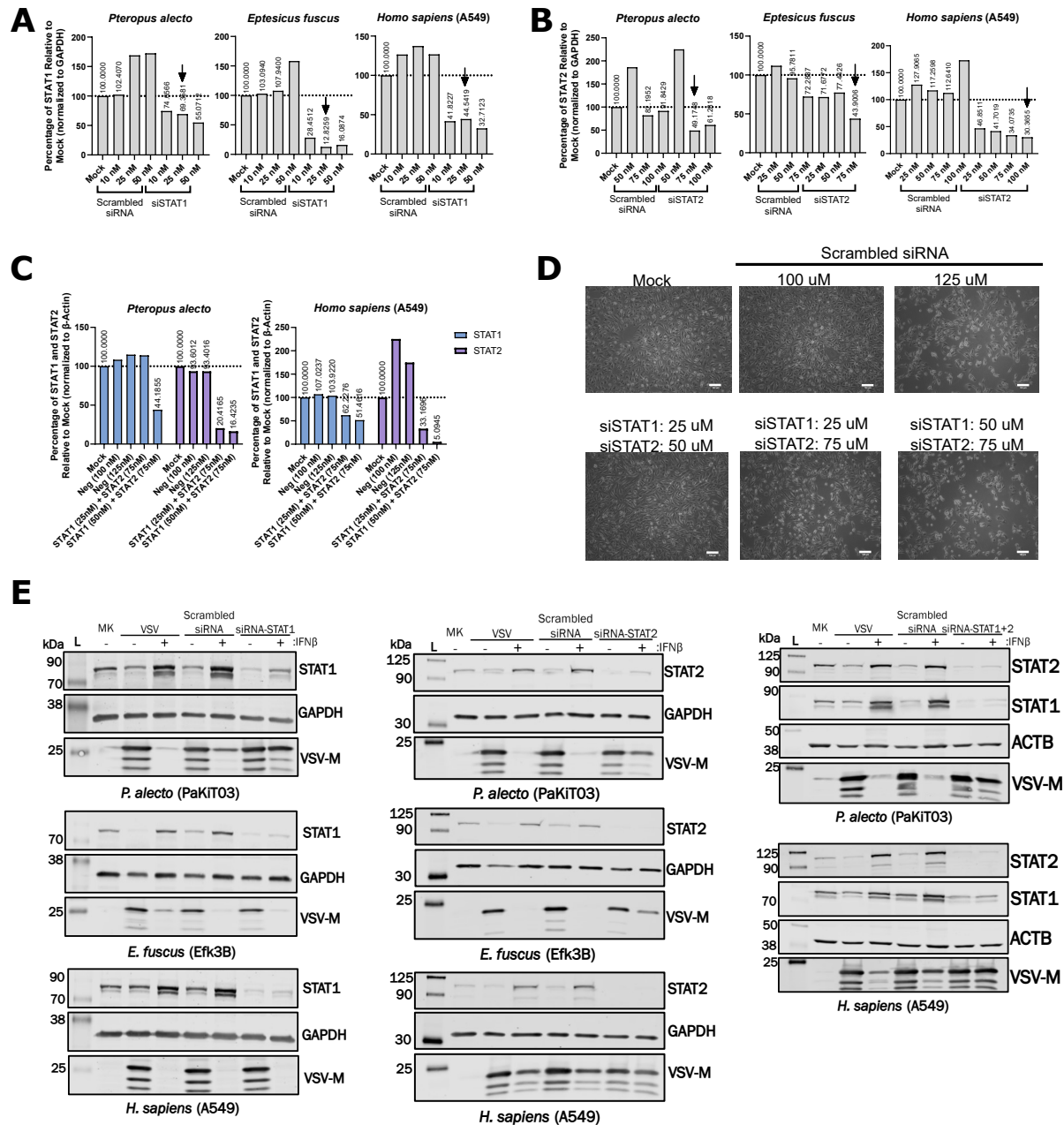
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P. giganteus	718	PEAESLELYPGLAEP	--EPGLGLELEPLLKAGLDLGPPLERMLEPTPG	---TVSQGMS	ELNLGPELKLEPI	LGPI	SQP	791
P. vampyrus	718	PEAESLELYPGLAEP	--EPGLGLELEPLLKAGLDLGPPLERMLEPTPG	---TVSQGMS	ELNLGPELKLEPI	LGPI	SQP	791
P. rodricensis	718	PEAESLELYPGLAEP	--EPGLGLELEPLLKAGLDLGPPLERMLEPTPG	---TVSQGMS	ELNLGPELKLEPI	LGPI	SQP	791
R. aegyptiacus	718	LEVESSELYPGLAEP	--DPGLGLELEPLLKAGLDLGPPLERMLEPTPG	---TVSQGMS	ELNLGPELKLEPI	LEPI	SQP	791
R. ferrumequinum	719	PEVESSELYPGLAEP	--EPGLGLELEPLLKAGLDLGPPLERMLEPTPG	---PTQSLPKP	NLGP	ELT	DP	779
S. hondurensis	720	PEVESLELSPGLAPGP	--EPGLGLELEPLLKAGLDLGPPLERMLEPTPG	---VVQEP	NLGP	ELT	DP	785
A. jamaicensis	720	PEVESLELSPGLAPGP	--EPGLGLELEPLLKAGLDLGPPLERMLEPTPG	---VVQEP	NLGP	ELT	DP	785
P. discolor	717	PEVESLELSPGLAPGP	--EPGLGLELEPLLKAGLDLGPPLERMLEPTPG	---TVREP	NLGP	ELT	DP	782
P. hasatus	717	PEVESLELSPGLAPGP	--EPGLGLELEPLLKAGLDLGPPLERMLEPTPG	---AVQEP	NLGP	ELT	DP	782
D. rotundus	718	PEVESLELSPGLAPGP	--EPGLGLELEPLLKAGLDLGPPLERMLEPTPG	---VEQEP	NLGP	ELT	DP	783
E. fuscus	718	PEVESLELSPGLAPGP	--EPGLGLELEPLLKAGLDLGPPLERMLEPTPG	---LDVVS	QRM	PD	LG	789
H. armiger	718	PEVESSELYPGLAEP	--EPGLGLELEPLLKAGLDLGPPLERMLEPTPG	---LTQ	RVP	KP	NL	782
M. molossus	717	PEVESLELSPGLAPGP	--EPGLGLELEPLLKAGLDLGPPLERMLEPTPG	---LGRVS	QSV	PE	NL	794
M. natalensis	717	LEEDPSLEPP	---GP	EPGLGLELEPLLKAGLDLGPPLERMLEPTPG	---FMSV	SLI	VE	790
M. brandtii	718	PEVEPLDLPGLAPGP	--ELGLDLELEPLLKAGLDLGP	---PLEP	---	ELE	LEPT	783
M. lucifugus	718	PEVEPLDLPGLAPGP	--ELGLDLELEPLLKAGLDLGP	---PLEP	---	ELE	LEPT	783
M. myotis	718	PEVEPLDLPGLAPGP	--ELGLDLELEPLLKAGLDLGP	---ALEP	---	ELE	LEPT	786
M. davidii	718	PEVEPLDLPGLAPGP	--ELGLDLELEPLLKAGLDLGP	---ALEP	---	ELE	LEPT	786
P. kuhlii	716	PEVESLELSPGLAPGP	--ELGLDLELEPLLKAGLDLGP	---	---	---	---	773
H. sapiens	716	PEVESLELSPGLAPGP	--ELGLDLELEPLLKAGLDLGP	---	---	---	---	785

P. alecto	790	VPE	--PD	--LPHDLEHLNTEEME	IFRNSM	NIED	IMPNGD	PLLAD	QNTV	DEAY	ILHPS	SHFHT	EG	PLIP	SDY	855
P. giganteus	792	VPE	--PD	--LPHDLEHLNTEEME	IFRNSM	NIED	IMPNGD	PLLAD	QNTV	DEAY	ILHPS	SHFHT	EG	PLIP	SDY	857
P. vampyrus	792	VPE	--PD	--LPHDLEHLNTEEME	IFRNSM	NIED	IMPNGD	PLLAD	QNTV	DEAY	ILHPS	SHFHT	EG	PLIP	SDY	857
P. rodricensis	792	VPE	--PD	--LPHDLEHLNTEEME	IFRNSM	NIED	IMPNGD	PLLAD	QNTV	DEAY	ILHPS	SHFHT	EG	PLIP	SDY	857
R. aegyptiacus	792	VPE	--PD	--LPHDLEHLNTEEME	IFRNSM	NIED	IMPNGD	PLLAD	QNTV	DEAY	ILHPS	SHFHT	EG	PLIP	SDY	857
R. ferrumequinum	780	VPEPE	EP	EP	EP	EP	EP	EP	EP	EP	EP	EP	EP	EP	EP	849
S. hondurensis	786	AP	EP	EP	EP	EP	EP	EP	EP	EP	EP	EP	EP	EP	EP	853
A. jamaicensis	786	AP	EP	EP	EP	EP	EP	EP	EP	EP	EP	EP	EP	EP	EP	853
P. discolor	783	AP	EP	EP	EP	EP	EP	EP	EP	EP	EP	EP	EP	EP	EP	850
P. hasatus	783	AP	EP	EP	EP	EP	EP	EP	EP	EP	EP	EP	EP	EP	EP	850
D. rotundus	784	AP	EP	EP	EP	EP	EP	EP	EP	EP	EP	EP	EP	EP	EP	851
E. fuscus	790	VPEPE	EP	EP	EP	EP	EP	EP	EP	EP	EP	EP	EP	EP	EP	857
H. armiger	783	VTE	EP	EP	EP	EP	EP	EP	EP	EP	EP	EP	EP	EP	EP	850
M. molossus	795	VPE	--PD	--LPHDLEHLNTEEME	IFRNSM	NIED	IMPNGD	PLLAG	QNTT	DEAY	IFHT	SHFY	AD	GPL	SP	860
M. natalensis	791	VPEPE	PD	--LPHDLEHLNTEEME	IFRNSM	NIED	IMPNGD	PLLAG	QNTT	DEAY	IFHT	SHFY	AD	GPL	SP	858
M. brandtii	784	VPEPEPE	PD	--LPHDLEHLNTEEME	IFRNSM	NIED	IMPNGD	PLLAG	QNTT	DEAY	IFHT	SHFY	AD	GPL	SP	852
M. lucifugus	784	VPEPEPE	PD	--LPHDLEHLNTEEME	IFRNSM	NIED	IMPNGD	PLLAG	QNTT	DEAY	IFHT	SHFY	AD	GPL	SP	852
M. myotis	787	VPEPEPE	PD	--LPHDLEHLNTEEME	IFRNSM	NIED	IMPNGD	PLLAG	QNTT	DEAY	IFHT	SHFY	AD	GPL	SP	855
M. davidii	787	VPEPEPE	PD	--LPHDLEHLNTEEME	IFRNSM	NIED	IMPNGD	PLLAG	QNTT	DEAY	IFHT	SHFY	AD	GPL	SP	853
P. kuhlii	774	MP	EA	EP	ES	DL	PH	DL	RHLN	TE	EME	IF	FN	---	---	840
H. sapiens	786	VPE	--PD	--LPHDLEHLNTEEME	IFRNSM	NIED	IMPNGD	PLLAG	QNTT	DEAY	IFHT	SHFY	AD	GPL	SP	851

Supplementary Figure 5. Bat STAT2 multiple sequence alignment. Grey boxes indicate identical residues. Purple box highlights region surrounding the tyrosine phosphorylation site in humans. ClustalW alignment was generated using MacVector software. Human sequence was included for comparison.

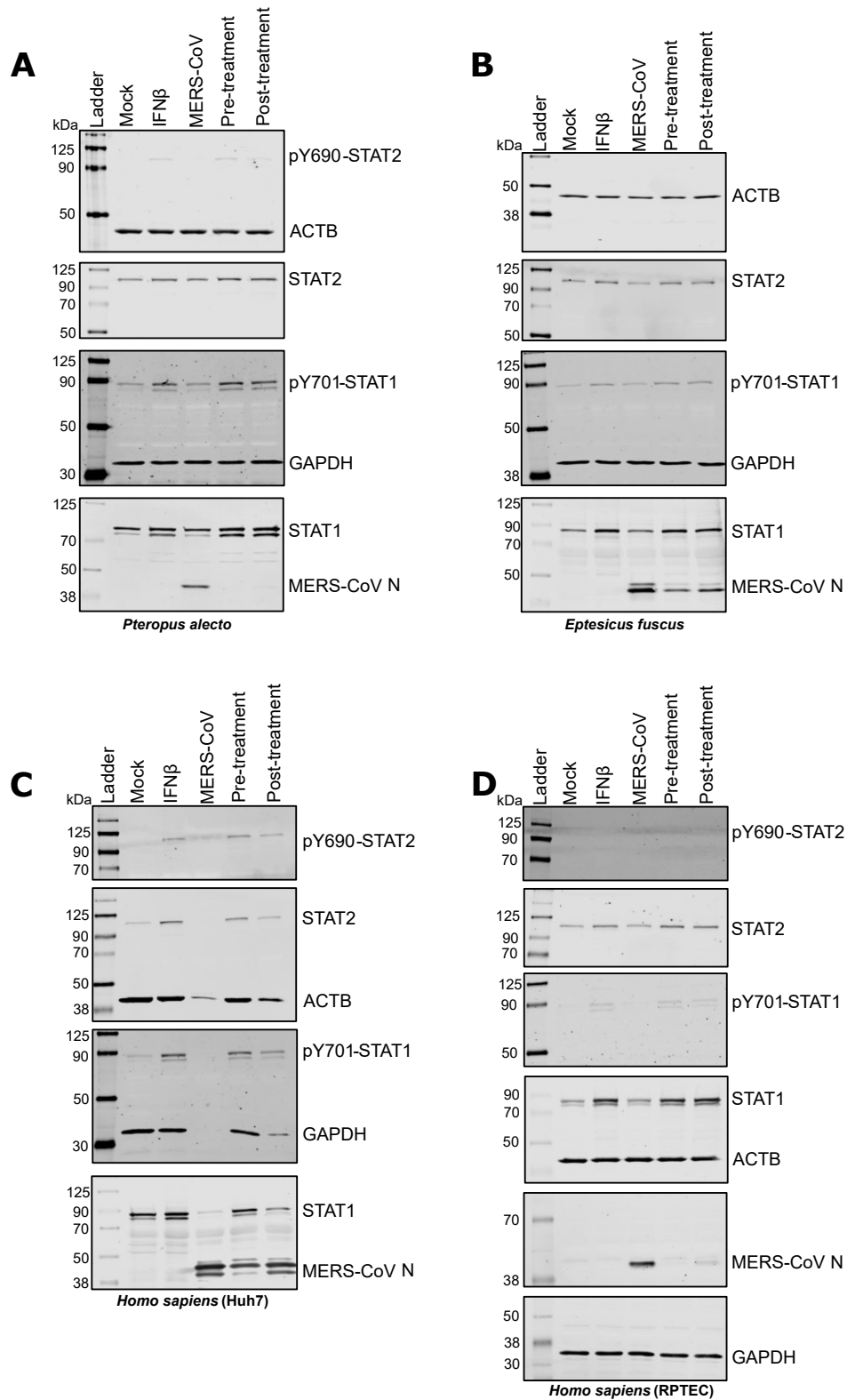


Supplementary Figure 6. Nuclear translocation of STAT1 and STAT2. *P. alecto* (PaKIT03), *E. fuscus* (EfK3B), and human A549 and RPTEC cells were treated for 5, 10, and 20 minutes with species matched IFN β (10 U/mL) or with the vehicle control. Cells were stained for pY701-STAT1 (**A**), pY690-STAT2 or STAT2 (**B**), and DAPI. Nuclear translocation of stained proteins was visualized by confocal microscopy. Scale bars = 25 μ m. Image is representative of 3 replicates.



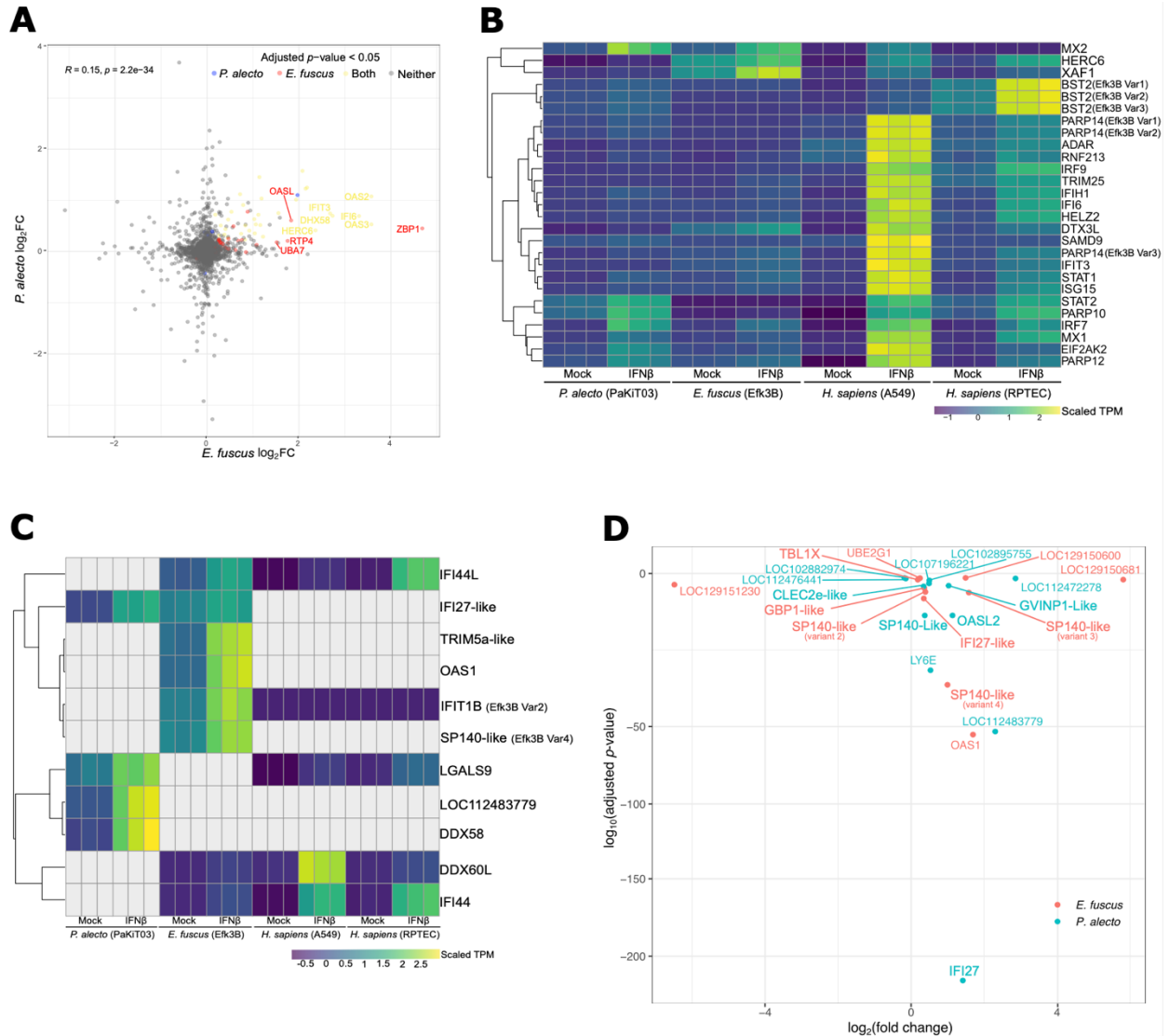
Supplementary Figure 7. siRNA-mediated knockdown of STAT1 and STAT2. *P. alecto* (PaKiT03), *E. fuscus* (EfK3B), and human A549 cells were transfected 4 hours post seeding with various concentrations of siRNA targeting STAT1 (A) and STAT2 (B) individually, and in combination to achieve a double knockdown (C). (A-C) Forty-eight hours later, protein lysates were harvested and STAT1, STAT2, GAPDH, and/or β -actin levels were quantified by immunoblotting. (D) Brightfield images of EfK3B cells transfected with siSTAT1 and siSTAT2 at concentrations where single knockdowns were achieved. Scale bars = 100 μ M. (E) PaKiT03, EfK3B, and human A549 cells were transfected with siRNA-STAT1 (25 nM), siRNA-STAT2 (75 nM), a combination of both siRNAs (STAT1, 25nM; STAT2, 75nM), or with the scrambled siRNA (control) 4 hours post

seeding cells. After 48 hours, cells were treated with species-matched IFN β (10 U/mL) for 6 hours, followed by infection with VSV-GFP (MOI 0.1) for 16 hours. Cell lysates were harvested and assessed by immunoblotting for VSV-M, GAPDH, β -actin, STAT1 and/or STAT2. Immunoblots are representative of 3 replicates.



Supplementary Figure 8. Full immunoblots of IFN β treatment and MERS-CoV infection. PaKiT03 (A), Efk3B (B), Huh7 (C), and RPTEC (D) cells were pretreated with

species-matched IFN β for 6 hours prior to infection with MERS-CoV or received IFN β treatment following infection with MERS-CoV (MOI 0.1) for 48 hours. Protein lysates were harvested and probed for total STAT1 and STAT2, pY701-STAT1, pY690-STAT2, MERS-CoV nucleoprotein (N), GAPDH, and β -actin by immunoblotting.



Supplementary Figure 9. Host transcriptional response to IFN β stimulation. (A) Function enrichment plot for differentially expressed genes (DEGs) in PaKiT03 and EfK3B cells. **(B)** Heatmap indicating the expression levels of the top 27 bat DEGs involved in the IFN β response in PaKiT03, EfK3B, A549, and RPTEC cells, ranked by p -value. *E. fuscus* transcript variants are indicated in brackets (i.e. var1) and are plotted against the transcript levels of a single variant that was detected in PaKiT03, A549, and RPTEC cells. **(C)** Heatmap indicating the expression levels of genes that do not exist in all four cell lines but were significantly differentially expressed in at least one cell line. ‘LOC’ symbol represents genes that do not have a published symbol and orthologs that have not yet been determined or named. **(D)** Top upregulated genes in PaKiT03 and EfK3B cells, orthologues for which were not clearly identifiable within the human genome or orthologous genes were not upregulated upon IFN β stimulation of human cells. Paralogs are indicated (i.e. var1). See **Supplementary Table S7** for the representative LOC symbol.

LOC103296399 1 ATGGAGCCCTGGGAGGTGCTCTACGATAATGAATCAGGAACACGTGGGGATAACATTTCACTACTCAGAGTTCTGGCTTC 80
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 H. sapiens IFIT1B 1 0

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 LOC103300075 1 - - - - - ATGAGTATGAATGCTGATGAAGATCAGATCCAA 33
 H. sapiens IFIT1B 1 - - - - - ATGAGTGAAGAATCTGATGAAAGCTTATTGAA 33

LOC103296399 160 GACAACCTTGTTCACCTGAGATGTCACCTTACCTGGAAGCTGCACATTGAAGACACTGAACTGCAAGATTTAGAAAAACAG 239
 LOC103300075 34 GCTAGGCTGGAACAGCTGAGATGTCACCTTACATGGAAGTTGACACATTGAAGACACTGAACTGCTGTATTAGAAAAACAG 113
 H. sapiens IFIT1B 34 GACAGCTGGAATTCAGCTGAGATGTCACCTTACATGGAAGTTGTTAATTGAAGCCCTGAAATCTGTATTAGAAAAACAG 113

LOC103296399 240 GGTCTTGGATCAGATTGAGTTCCTAGAGCACAACTTCAATGTGGGCATACACAACCTACTGGCCTATGTGAAACACCTGA 319
 LOC103300075 114 GGCTCTTGTATGCAATTGAGTTCCTAGACACAAAACTTCAATGTGGGCATACACAACCTACTGGCCTATGTGAAACACCTGA 193
 H. sapiens IFIT1B 114 GATCTGGAGAGAGATTCAGTTCTTCGACACCAAAATCAATGTGGGAATACACAACCTACTAGCCTATGTGAAACACCTGA 193

LOC103296399 320 ATGGCCAGAATCAGGAAGCCCTGGAGAGCTTGAAAGGAAGCTGAAGACTTAATGCAGGCAGGCACATCCGCCAGTCAGAC 399
 LOC103300075 194 ATGGCCAGAATCAGGAAGCCCTGAAGAGCTTGAAAGGAAGCTGAAGACTTAATGCAGGCAGGAACATGTTGCCAGTCAGAC 273
 H. sapiens IFIT1B 194 AAGGCCAGAATCAGGAAGCCCTGCTAGCTTGAAAGAGGCTGAAGACTTAATTCAGAAAGAACATGCCAACCAAGCAGAT 273

LOC103296399 400 GCGATAAAGCTGGTTACCTGGGGCAACTATGCCTGGCTGTATTACCACATGGACAGGCTGGCGGACGCCAGATTACCT 479
 LOC103300075 274 GCGATAAAGCTGGTTACCTGGGGCAACTATGCCTGGCTGTATTACCACATGGACAGGCTGGCGGACGCCAGATTACCT 353
 H. sapiens IFIT1B 274 ATTCAGAGTCTGGTTCACCTGGGGCAACTTTCCTGGCTGTATTACCACATGGCAGATTTGGCAAGACCCAGACTTACCT 353

LOC103296399 480 GGACAAGGTGGAGAGCACTTGCAAAAAGTTTCCAGCCCTCCTGCTACACAATGGAGTGGCCTGAGATGGACTGTAAAG 559
 LOC103300075 354 GGACAAGGTGGAGAGCACTTGCAAAAAGTTTCCAGCCCTCCTGCTACACAATGGAGTGGCCTGAGATGGACTGTGCCG 433
 H. sapiens IFIT1B 354 GGACAAGGTGGAGAAACACTTGCAGCAAGTTTGCAGATCTTCCCTCTATGAAGATGGAGTTCAGAGGCTGGACTGTGAGG 433

LOC103296399 560 AAGGATGGGCCTTGTGAAATGTGGAGGAAAGAATTACGAACGGCTAAAGCCTGCTTTGAGAAGGCTCTGGAAGTGGAC 639
 LOC103300075 434 AAGGATGGGCCTTGTGAAATGTGGAGGAAAGAATTATGAACGGGCTAAAGCCTGCTTTGAGAAGGCTCTGGAAGTGGAC 513
 H. sapiens IFIT1B 434 AAGGATGGGCCTTGGGAAGTGTGGTGGAAAGAATTATGAACGGGCTAAAGCCTGCTTTGAAGAAGGCTCTGGAAGTGGAC 513

LOC103296399 640 CCTGAAAACCTGAAATTCAGCACTGGGTATGCAATTTGTGTCTATCGTCTGGATGGCTTTAAACAAAACACCACCTCTCTCG 719
 LOC103300075 514 CCGTAAAACCTGAAATTCAGCACTGGGTATGCAATTTGTGTCTTTCGTCTGGATGGCTTTAAACAAAACACCACCTGTTTGA 593
 H. sapiens IFIT1B 514 CCGTAAAACCTGAAATTCATTACTGGGTACGCAATCACCCTCTATCCCTCTGGATAAATTTAACAACCAATCAGGAGGAA 593

LOC103296399 720 TAAGACATTTTGTGTGACAGCCCTTAAACCGGGCCATCAGGCTAAATCCAGGAGATGGGTATATTAAGTGTCTCTCTCGGCA 799
 LOC103300075 594 TGAGGCATTTTGTGTGACAGCCCTTAAACCGGGCCATCAGGCTAAATCCAGAGATGCATATTAAGGCTCTCTCTTGGTGTG 673
 H. sapiens IFIT1B 594 TAAGGCATTTTCTCTGCACTGCTTAAACAGAGTGTTCAGGCTAAATCCAGATGATGTATATATTAAGGCTCTCTCTTGGCT 673

LOC103296399 800 TGAAACTTCAGAAATATAGGACAACGAAGCTGAGGGAGAAAAGTACATTGAAGAAGCACTGGCCAACATGTCTTCGAGGCC 879
 LOC103300075 674 TGAAACTTCAGGAGATAGGACAAGGAAGCTGAGGGAGAAAAGTACATTGAAGAAGCACTGGCCAACATGTCTTCGAGAGCT 753
 H. sapiens IFIT1B 674 TGAACTTCAGGATGAGGACAAGGAAGCTGAGGAGAAAAGTACATTGAAGAAGCTGTGACCAAGTATATCTTCACAGGCC 753

LOC103296399 880 TATGTCCTTCGATATGCGGCCAAGTTTACCGAAAAGGGCTCTTTAGCTTAAAGCTCTTCAGCTCTTAAAAATGGCTTT 959
 LOC103300075 754 TATGTCCTTCGATATGCGGCCAAGTTTACCGAAAAGGGCTCTTTAGCTTAAAGCTCTTCAGCTCTTAAAAATGGCTTT 833
 H. sapiens IFIT1B 754 TATGTCCTTTCATATATGCAAGCAAGTTTATCGAAAGAAAAGGCTCTCTGAGTAAAGCTCTTCAGCTCTTAAAAATGGCTTT 833

LOC103296399 960 GCAGGCAACACCTTCTCTGCTCTCTGTCATCACCAGATAGGGCTTTGCTATAGAGCACAAAGTCCATAAAAATAACAAAG 1039
 LOC103300075 834 GCGGGCAACACCTTCTCTGCTCTCTGTCATCACCAGATAGGGCTTTGCTACAGATCACAAACATATCTTAATAAACAAAG 913
 H. sapiens IFIT1B 834 GGAGCAACACACCTCTCTGCTCTCTGTCATCACCAGATAGGGGCTTTGCTACAGGGCACAAATGATCCAAATCAAGGAAG 913

LOC103296399 1040 CTACAACTGGGAGCCTAGAGGACCGGATAGAGAAAATATCGACAGAATAACAAAATTAGCCATATCTCATTTTGAATTT 1119
 LOC103300075 914 CTTCAAACTGGGAGCCTAGAGGACCGGATAGAGAAAATATCGACAGAATAACAAAATTAGCCATATCTCATTTTGAATTT 993
 H. sapiens IFIT1B 914 CTACAACTGGGAGCCTAGAGGACCAAGATAGGAAACTGTTGACAGATTGGTTCAATTGGCTATATGCAATTTGAAAG 993

LOC103296399 1120 GCTGTGGAACAAAAGCCAACATTGGAAGTTGCTTATACACACCTAGCAGATATGTAATTCATTTGCAGGCAATAGCAGAAA 1199
 LOC103300075 994 GCTGTGGAACAAAAGCCAACATTGGAATTTGCTTATATACACCTAGCAGATATGTAATTCATTTGCAGGCAACATAGAAA 1073
 H. sapiens IFIT1B 994 ACTATTAATGTTAAAGGCAACATTGGAAGTGTGCTATGTTGACCTGGCTGAATCCTATGCAAGAAATAGGCCAGCAGCAAAA 1073

LOC103296399 1200 AGCTGAAGAGACTTATCAAAAAGTGTCTGTCATGAAATCAACTGAAGAAGAAAATAATGCAAGAGATATATTCCAGCAAG 1279
 LOC103300075 1074 AGCTGAAGAGACTTATCAAAAAGTGTCTGTCATGAAATCACTGAAGAAGAAAATAATGCAAGAGATATATTACCTGCTATG 1153
 H. sapiens IFIT1B 1074 GGCTGAGGACATTTTCAGAAAAGGTTTACGTCATGAAGATCTTTGAAGATCAGCTAAAGCAAGAGATTCATTACCACTACG 1153

LOC103296399 1280 GTCGATTTTCAGGAATTTAAAGGAAATCTGAAGTCGATGCAATTTATCTATTATTTAAAAAGCAATCAAAATAGAAAAAGCCA 1359
 LOC103300075 1154 GTCGATTTTCAGGAATTTCAAGGAAATCTGAAGTCGATGCAATTTATCTATTATTTAAAAAGCAATCAAAATTAAGAAAAAGCCA 1233
 H. sapiens IFIT1B 1154 GCCCTTTTCAGAAACATCTGGGAAATCTCAAGATAAAGCAATTACCTATTATTTAAAAAGGTTTGAAGAAATAGAAAAATG 1233

LOC103296399 1360 TCATCTGTAAAGAGACAGAAGTATCACTTCTCTGGAGAGAGTGGTTTTAAGGAAAACCTCAAAAGAAACCCAGTAGACATAGA 1439
 LOC103300075 1234 TC - - - - - CTAAGAGACAGAAGTATCAATCTCTGGAGAGAGTGGTTTTAAAGAAACCTCAAAAGAAACCCAGTAGACATAGA 1310
 H. sapiens IFIT1B 1234 TCCTATTCAGGGAAGAACTTCTCAATGCTTTAGAGAAATTTGGCTAAAGATGTATTCACCAAGATGTATCGGCTTGTGGA 1313

LOC103296399 1440 AAGCTTGAGCATCCTTGGGTTACCTACAAAATTGAAAGGAGAAAATGAATAAAGCCCTGGAGTACTATGAGCGGGCCCTGA 1519
 LOC103300075 1311 AAGCTTGAGCATCCTTGGGTTACCTACAAAATTGAAAGGAGAAAATGAATAAAGCCCTGGAGTACTATGAGCGGGCCCTGA 1390
 H. sapiens IFIT1B 1314 AAGTGTTCAGCTTCCTTGGGCTTATTCACAAAATTGAAAGGAGAAAATGAATGATGCTTTGCTGTCTATGAGAGGGGCTCTGA 1393

LOC103296399 1520 GGCTGGCTGCTGACTTTGAGAACCTGTGGGACACGCTCCTTAG 1563
 LOC103300075 1391 GGCTGGCTGCTGACTTTGAGAACCTGTGGGACACGCTCCTTAG 1434
 H. sapiens IFIT1B 1394 GGCTGGCTGCTGACCTT - - - GAACCTTATTTTAA 1425

Supplementary Figure 10. Gene alignment of *E. fuscus* and human *IFIT1B*. Grey boxes indicate identical residues. ClustalW alignment was generated using MacVector software. Two uncharacterized genes (LOC103296399 and LOC103300075) were identified to be orthologous to human *IFITB*.

P. alecto IFIT1 1 ATGAGTAA GAATGCTGATGAAGATCAGGTCAAAGATAGGCTGGAGCAATGAGATGTCACTTTACATGGAAGTTGCTAAT 80
 H. sapiens IFIT1 1 ATGAGTAA GAATGCTGATGATATCAGGTCAAAGATAGTCTGGAGCAATGAGATGTCACTTTACATGGAAGTTATCCAT 80

P. alecto IFIT1 81 CGAAGACACTGAAATTAACGATTAGAAAACAGGGTTTTCGATGAGATTGAATTCCTAGACATCAAATACACGTGGGAA 160
 H. sapiens IFIT1 81 TGATGACGATGAAATGCCGTGATTTAGAAAACAGAGTCTTGATCAGATTGAATTCCTAGACATCAAATACAGTGTGGGAA 160

P. alecto IFIT1 161 TTTACCAACCTACTGCCTATATTAAGCACCTGAAAGGCCAAATAGGAAGCCCTGAGAGCTTGAAGAAGCTGAAACC 240
 H. sapiens IFIT1 161 TACCAACCTACTAGCCTATGTGAAACACCTGAAAGGCCAAGATAGGAAGCCCTGAGAGCTTGAAGAAGCTGAAACC 240

P. alecto IFIT1 241 TTAATCAGCAAGAAGCTTACCAACCAATCGAACACAAAGAGCTGGTTACCTGGGGCAACTATGCCTGGCTGTATTACCA 320
 H. sapiens IFIT1 241 TTAATGCAAGGAAGAACATGACCAACCAAGCAATGTGAGGAGCTGGTTACCTGGGGCAACTATGCCTGGATGTATTACCA 320

P. alecto IFIT1 321 CATGGGCAGCTGGCGAGAAGTCCAGATTATCTGGACAAAGTGGAAACACTTGCAAGAAGCTTGCAGTCCCTCTCGCT 400
 H. sapiens IFIT1 321 CATGGGCAGACTGGCGAGAAGCCAGACTTATCTGGACAAAGTGGAAACACTTGCAAGAAGCTTCAATCCCTCTCGCT 400

P. alecto IFIT1 401 GTAGACTGGAGTGTCTGAGATGGACTGTGAGGAAGGATGGCCCTTGCTGAAATGTGGAGGAAAGAAATTCGAACGACGCC 480
 H. sapiens IFIT1 401 ATAGAAATGGAGTGTCCAGAAATGACTGTGAGGAAGGATGGCCCTTGCTGAAATGTGGAGGAAAGAAATTCGAACGAGGCC 480

P. alecto IFIT1 481 AAGGCCTGCTTTGAAAAGGCTCTGGAAGCGGACCCTGAAAACCTCGAATTCAACCTGGGTATGCGATCACTATGTTTCG 560
 H. sapiens IFIT1 481 AAGGCCTGCTTTGAAAAGGTGCTTGAAAGTGGACCCTGAAAACCTCGAATCCAGCGCTGGGTATGCGATCTGTGCTTATTCG 560

P. alecto IFIT1 561 TCTGGATAGCTTTTCAAAAGAAAGCGCAATTTAAAGAGCCATTTTCTCTACACCCCTAAAGCAGGCATCAAGCTTAAATC 640
 H. sapiens IFIT1 561 CTTGGATGCTTTTCAAAAGAAAGCAAAATTCACAGCCATTTTCTTTGCTTCCCTAAAGCAGGCTGTGCTTAAATC 640

P. alecto IFIT1 641 CCGAAGATGCATATATTAAGGCTCTCCTTGGCCTGAAGCTTCAGGATGAGGAACAAGCTGAGGACAAAAGTACATT 720
 H. sapiens IFIT1 641 CAGACAATGCATATATTAAGGCTCTCCTTGGCCTGAAGCTTCAGGATGAGGAACAAGCTGAGGACAAAAGTACATT 720

P. alecto IFIT1 721 GAAGAAGCACTGACCAAAATGTGCTGCAGACCTATGCTTTTCGTATGCAGCCATGTTTTACCGAAGAAAAGGCTCTGT 800
 H. sapiens IFIT1 721 GAAGAAGCTCTAGCCAAATGTGCTGCAGACCTATGCTTTTCGATATGCAGCCATGTTTTACCGAAGAAAAGGCTCTGT 800

P. alecto IFIT1 801 GGATAAAGCGCTTCAGCTCTTAAAAAAGCTTTGCGAGCAACACCCTCTTCTGCTTCTCATCACCAGATAGGGCTTT 880
 H. sapiens IFIT1 801 GGATAAAGCTCTTCAGTATTAATAAAAAGGCTTTGCGAGCAACACCCTCTTCTGCTTCTCATCACCAGATAGGGCTTT 880

P. alecto IFIT1 881 GCTACAGATCACAAATTCGTCAAATAAGAAAGCTGCAAAATGGCAGCCTAGAGGACAGATAGAGAAAAATGTAATAGA 960
 H. sapiens IFIT1 881 GCTACAGGACAAATTCATCAAAATCAAGGAGGCTACAAAAGGCAGCCTAGAGGACAGAACAGAGAAAAATGTAACAAA 960

P. alecto IFIT1 961 ATAAACAGATTAGCCATATTTCAATTTGAATTCAACCTGAACAAAAGCCACATTTGAGATTAGCTTACAAACACCTGGC 1040
 H. sapiens IFIT1 961 ATGATTAAGATCAGCCATATTTCAATTTGAATCTGCACTGGAACAAAAGCCACATTTGAGATTGGCTCATCTAGACCTGGC 1040

P. alecto IFIT1 1041 AGATATGTACATAGAAGCAGGCAACTATGAAAAAGCTGAAGACCTTATCAAAAAAGTGTATGCCTGAAAAACCTTTGACA 1120
 H. sapiens IFIT1 1041 AAGATATGTATATAGAAGCAGGCAACTACAGAAAAAGCTGAAGACATTTTCAAAAAATGTTATGCATGAAACCACTTTGCTAG 1120

P. alecto IFIT1 1121 AAGAAATTCGCAAGAAATATATTTCTACTATGGCCAAATTCAGGAATTTCAAAAGAAATCTGAATTCATGCAATTATC 1200
 H. sapiens IFIT1 1121 AAGAAACAATGCAAGACATACATTTCTACTATGGTGGTTTCAGGAATTTCAAAAGAAATCTGACCTCATGCAATTATC 1200

P. alecto IFIT1 1201 TATTATTTAAAAGCAATAAAAAATAGAAACCCAGTCATATTCAAGAGATAAAAGTATCAATCTTTTGAGAAATTGGTTTT 1280
 H. sapiens IFIT1 1201 CATTATTTAAAAGCTATAAAAAATAGAACAGGCATCATTAACAGGAGATAAAAGTATCAATCTTTTGAGAAATTGGTTTT 1280

P. alecto IFIT1 1281 AAGGAACTTCGGAGAAATGGATCAGACATAGAAAGCTTGAGCATCCTCGGGTTCATCTACAAATTGAAGGAGAAATAGA 1360
 H. sapiens IFIT1 1281 AAGGAACTTCGGAGAAAGGCATTAGATCTGAAAGCTTGAGCATCCTCGGGTTCATCTACAAATTGAAGGAAATATAGA 1360

P. alecto IFIT1 1361 ATGAAGCCTTGGAGTATTACGAGGAGGCCCTAAAGCTGGCTGCTGACTTTGAGAGCTTTGTGTGA 1425
 H. sapiens IFIT1 1361 ATGAAGCCTTGGAGTCTATGAGCGGCCCTGAGAGCTGGCTGCTGACTTTGAGAACCTCTGTGAGACAAGGTCCTTAG 1437

Supplementary Figure 11. Gene alignment of *P. alecto* and human *IFIT1*. Grey boxes indicate identical residues. ClustalW alignment was generated using MacVector software.

A

P. alecto IFIT1	1	MSKNAEDQVKDRLEQLRCHFTWKLLLETFEITDLENRVFDEIEFLDIKYNVGIHNLLAYIKHLKGONKEALESLKEAET	80
H. sapiens IFIT1	1	MSTNGEDHQVKDSLEQLRCHFTWELSLIDDEMPDLENRVLDQIEFLDTKYSVGIHNLLAYVKHLKGONEEALKSLKEAEN	80
P. alecto IFIT1	81	LIQQERTNQSNITKRLVTWGNYYAWLYYHMGSLGVEVQIYLDKVENTCKKLASPSCCRLECEPEMDCEEGWALLKCGGKNYERA	160
H. sapiens IFIT1	81	LMQEHHDNQANVRS LVTWGNFAWYMYHMGRLAEAQTYLDKVENTCKKLSPFVRYRMCEPEIDCEEGWALLKCGGKNYERA	160
P. alecto IFIT1	161	KACFEKALEADPENPEFNTGYAITMFRDLSFHKETQFKEAFSLHPLKQAIRLNPEDATYKALLGLKLQDVVEQAEGQKYI	240
H. sapiens IFIT1	161	KACFEKVLLEVDPENPESSAGYAISAYRLDGFKLATKNHKPFSLLPLRQAVRLNPDNGYIKVLLALKLQDEGQEAEGEKYI	240
P. alecto IFIT1	241	EEALTKMSSQTYVFRYAAMFYRRKGSVDKALQLLKTALQATPSSAF LHHQIGLCYRSQVVRQIKKTARWQPRGQDRENVNR	320
H. sapiens IFIT1	241	EEALANMSSQTYVFRYAAMFYRRKGSVDKALQLLKKALQETPTSVL LHHQIGLCYKACMIQIKKEATKQPRGQNRKLDK	320
P. alecto IFIT1	321	ITRLAIFHFEFTLKQKPTFEIAYKHLADMYIEAGNYEKAEEDTYQKVRRLKKLDKEVLQETIYYQQFOEFQRKSEIDAII	400
H. sapiens IFIT1	321	MIRSLAIFHFEFAVEKKPTFEVAHLDLARMYIEAGNHRKAEENFQKLLCMKPVVEETMDIHHEHYGRFOEFQRKSDVNAII	400
P. alecto IFIT1	401	YYLKAIKIENQSYSRDKSISLEKLVLRKLRRNGSDIESLSILGFIYKIKGEMNEALEYYEALKLAADFESFV	474
H. sapiens IFIT1	401	HYLKAIKIEQASLTDRDKSINSIKLVLRKLRRKALDLESLSILGFVYKLEGNMNEALEYYERALLRLAADFENSVRQGP	478

B

P. alecto IFIT3	1	MSEVS SSKNSLEKILPQLKCHFTWNLFQKDSLSHDLDRVRNQIEFLNTECKATTYNLLAYIKHLHQNEAALEYLQQAEE	80
H. sapiens IFIT3	1	MSEVT -KNSLEKILPQLKCHFTWNLFKEDSVSRDLDRVCNQIEFLNTEFKATMYNLLAYIKHLDDNNEAALECLRQAEE	79
P. alecto IFIT3	81	LIQRERTDQVEIRSLVTWGNYYAWYYHLGRFSEAQVYVDKVKHLCEKFSNPYSIECEPELDSEEGWTLQCGGKNERAKV	160
H. sapiens IFIT3	80	LIQQRHADAQAEIRSLVTWGNYYAWYYHLGRSLDAQIYVDKVKQTCKKFSNPYSIEYSELDCEEGWTLQKCGGKNERAKV	157
P. alecto IFIT3	161	CFEKALEEKKNPFESSGLAIAMYCLDDKPKQKCSVSVLQKAIELSPDNQYIKVLLALKLQKINKEAEGEPVIEALEKA	240
H. sapiens IFIT3	158	CFEKALEEKKNPFESSGLAIAMYHLDNHPEKQFSTDVLQKAIELSPDNQYIKVLLGLKLQKMNKEAEGEQFVEALEKS	237
P. alecto IFIT3	241	PCQTDILHSAAKFYQKKGDLDAKIELLKKALESMFNNSHLCYLISGICYTAKVRQIENTGYSNASWNRKEIEELSKYARDY	320
H. sapiens IFIT3	238	PCQTDVILRSAAKFYRRKGDLDAKIELFQRVLESTPNNGYLYHQIGCCYKAKVRQMONTGESEASGNKEMIEALKQYAMDY	317
P. alecto IFIT3	321	SEKAIIEKVLNPLNAYSDLAEP-LETECYQTA FNKELPNAEMKQFHQLSCNFOEYH GKSEDTPVQHYLKDLSISIKSTEKEK	399
H. sapiens IFIT3	318	SNKALEKGLNPLNAYSDLAEFLETECYQTFNKEVPDAEKQSHQRYCNLQKYNKGSEDTPVQHGLEGLSISKSTDKKE	397
P. alecto IFIT3	400	EKCQPQNVAAENQLPQNAPNSWYLOGLIHKKNGLYLQAAECFEKELGRLLRDSFSGTSSIFLPASELKEGSEEVGGGADSS	479
H. sapiens IFIT3	398	IKDQPQNVSENLQPQNAPNYWYLOGLIHKQNGDLLQAAKCYEKELGRLLRDAFSGTSSIFLPASELEDGSEEMGGGAVSS	477
P. alecto IFIT3	480	T L R E L P D P	487
H. sapiens IFIT3	478	S P R E L L S N S E Q L N	490

Supplementary Figure 12. Amino acid sequence comparison of human and *P. alecto* IFIT1 and IFIT3. Grey boxes indicate identical residues. ClustalW alignment was generated using MacVector software for IFIT1 (A) and IFIT3 (B).

P. alecto	1	MSKNADEQV	KDRLEQLRCHFTWKLLIEDTEIT	DLENRVFDEIEFLDI	KYNVGIHNLAYI	KHLKGQNK	EAL	ESLKEAE	T	80	
P. vampyrus	1	MSKNADEQV	KDRLEQLRCHFTWKLLIEDTEIT	DLENRVFDEIEFLDI	KYNVGIHNLAYI	KHLKGQNK	EAL	ESLKEAE	T	80	
R. aegyptiacus	1	MSKNADEQV	KDRLEQLRCHFTWKLLIEDTEIT	DLENRTFDEIEFLDI	KHNVGIHNLAYI	KHLKGQNK	EAL	ESLKEAE	T	80	
P. mesoamericanus	1	MSKSADQV	KDRLEQLRCHFTWKLVI	AEVPP	DLENRVFDEIEFLDTKFNV	AIHNLAYVKHL	LTGQNK	EAL	QSLKAAED	80	
R. ferrumequinum	1	MSKTTAEDK	IKDGLDQLRCHFTWKL	LIEDTEMT	DLENRVFDEIEFLDTKFNV	GIHNLAYVKHLKGQNK	EAL	ESLKEAE	T	80	
A. jamaicensis	1	MSENSEEDQ	LKDRLEQLRCHFTWKL	LIEDVEMT	DLENRIYNQIE	YLDTKFNVAI	HNLAYVKHLKGQNK	EAL	QSLKQAE	80	
S. hondurensis	1	MSKNS	SEEDQLKDRLEQLRCHFTWKL	LIEDVEIA	DLENRIYSQIE	FLDTKFNV	AIHNLAYVKHLKGQNK	EAL	QSLKQAE	80	
P. hastatus	1	MSKTS	SEEDQLKDRLEQLRCHFTWKL	LIEDVEIA	DLENRVFDEIEFLDTKFNV	SVHNLAYVKHLKGQNK	EAL	QSLKQAE	80		
P. discolor	1	MSKTS	KEDQLKDRLEQLRCHFTWKL	LIEDVEIA	DLENRVFDEIEFLDTKFNV	PTYNHNLAYVKHLKGQNK	EAL	QSLKQAE	80		
D. rotundus	1	MSKNA	SEEDQLKDRLEQLRCHFTWKL	LIEDVLS	DLENRVFDEIEFLDTKFNV	AIHNLAYVKHLKGQNK	EAL	QSLKQAE	80		
E. fuscus	1	MSMNADEQ	IQARLEQLRCHFTWKL	LIEDTELS	DLENRVFDEIEFLDTKFNV	GIHNLAYVKHLKGQNK	EAL	QSLKQAE	80		
M. brandtii	1	MSDELNDK	LIEDKLVQLRCHFTWKL	LIEDTEHL	DLENRV	LDQIEYLDNNFNVGIHNLAYVKHL	NGHNK	EAL	ESLKEAE	80	
M. molossus	1	MSKNADEQ	IKARLEQLRCHFTWKL	LIEDTELP	DLENRVFDEIEFLDTKFNV	GIHNLAYVKHLKGQNK	EAL	ESLKEAE	T	80	
M. natalensis	1	MGKNADEQ	IKARVEQLRCHFTWKL	LIEDTELL	DLENRVFDEIEFLDTKFNV	GIHNLAYVKHLKGQNK	EAL	QSLKEAE	H	80	
P. kuhlii	1	MSVNADEQ	VRAKLEQLRCHFTWKL	LIEDTVLS	DLENRVFDEIEFLDTKFNV	GIHNLAYVKHLKGQNK	EAL	QSLKEAE	D	80	
H. sapiens	1	MSTNGD	HDHVKDSLEQLRCHFTWKL	LIEDTEMP	DLENRV	LDQIEFLDTKYS	GIHNLAYVKHLKGQNK	EAL	ESLKEAE	N	80
P. alecto	81	LIQOERTN	QSNTRKRLVTWGNyawlyyhmgs	CEVQIYLDKVENTCKK	LASPS	CRLE	CEPMDCEE	GWALLKCGGK	NYERA	160	
P. vampyrus	81	LIQOERTN	QSNTRKRLVTWGNyawlyyhmgs	CEVQIYLDKVENTCKK	VASPS	CRLE	CEPMDCEE	GWALLKCGGK	NYERA	160	
R. aegyptiacus	81	LIQOERTN	QSNTRKRLVTWGNyawlyyhmgs	CEVQIYLDKVENTCKK	VASPS	CRLE	CEPMDCEE	GWALLKCGGK	NYERA	160	
P. mesoamericanus	81	LIQTEHARQ	SDVRRRLVTWGNyawlyyhmgs	CEVQIYLDKVENTCKK	QLASPS	CRLE	CEPMDCEE	GWALLKCGGK	NYERA	160	
R. ferrumequinum	81	LIQTEHARQ	SDVRRRLVTWGNyawlyyhmgs	CEVQIYLDKVENTCKK	QLASPS	CRLE	CEPMDCEE	GWALLKCGGK	NYERA	160	
A. jamaicensis	81	LSQTEHAGQ	SDVRRRLVTWGNyawlyyhmgs	CEVQIYLDKVENTCKK	QLASPS	CRLE	CEPMDCEE	GWALLKCGGK	NYERA	160	
S. hondurensis	81	LRQTEHVGQ	SEVRRRLVTWGNyawlyyhmgs	CEVQIYLDKVENTCKK	QLASPS	CRLE	CEPMDCEE	GWALLKCGGK	NYERA	160	
P. hastatus	81	LYQTEHODQ	AHVRRRLVTWGNyawlyyhmgs	CEVQIYLDKVENTCKK	QLASPS	CRLE	CEPMDCEE	GWALLKCGGK	NYERA	160	
P. discolor	81	LIQTEHODQ	AHVRRRLVTWGNyawlyyhmgs	CEVQIYLDKVENTCKK	QLASPS	CRLE	CEPMDCEE	GWALLKCGGK	NYERA	160	
D. rotundus	81	LIQTEHODQ	SEVRRRLVTWGNyawlyyhmgs	CEVQIYLDKVENTCKK	QLASPS	CRLE	CEPMDCEE	GWALLKCGGK	NYERA	160	
E. fuscus	81	LMQAEHAGQ	SDAIKLVTWGNyawlyyhmgs	CEVQIYLDKVENTCKK	QLASPS	CRLE	CEPMDCEE	GWALLKCGGK	NYERA	160	
M. brandtii	81	LMQAGHI	IPQSDAIKLVTWGNyawlyyhmgs	CEVQIYLDKVENTCKK	QLASPS	CRLE	CEPMDCEE	GWALLKCGGK	NYERA	160	
M. molossus	81	LIQTEHAGQ	SDVSLVNWGNyawlyyhmgs	CEVQIYLDKVENTCKK	QLASPS	CRLE	CEPMDCEE	GWALLKCGGK	NYERA	160	
M. natalensis	81	LMQAEHAGQ	SDVRLVNWGNyawlyyhmgs	CEVQIYLDKVENTCKK	QLASPS	CRLE	CEPMDCEE	GWALLKCGGK	NYERA	159	
P. kuhlii	81	LMQAEHAGQ	SDAIELVTWGNyawlyyhmgs	CEVQIYLDKVENTCKK	QLASPS	CRLE	CEPMDCEE	GWALLKCGGK	NYERA	160	
H. sapiens	81	LMQAEHAGQ	SDAIELVTWGNyawlyyhmgs	CEVQIYLDKVENTCKK	QLASPS	CRLE	CEPMDCEE	GWALLKCGGK	NYERA	160	
P. alecto	161	KACFEKALE	ADPENPEFNTGYAI	TMFRLDS	FFHKE	TFKEAF	SLHPLKQAI	RLNPEDAYIKALL	GLKLQDVGE	QAEQKYI	240
P. vampyrus	161	KACFEKALE	VDPENPEFNTGYAI	TMFRLDS	FFHKE	TFKEAF	SLHPLKQAI	RLNPEDAYIKALL	GLKLQDVGE	QAEQKYI	240
R. aegyptiacus	161	KACFEKALE	VDPENPEFNTGYAI	TMFRLDS	FFHKE	TFKEAF	SLHPLKQAI	RLNPEDAYIKALL	GLKLQDVGE	QAEQKYI	240
P. mesoamericanus	161	KACFEKALE	VDPENPEFNTGYAI	AVYRLDGF	FNKAS	TFKEAF	SLHPLKQAI	RLNPEDAYIKALL	GLKLQDVGE	QAEQKYI	240
R. ferrumequinum	161	KACFEKALE	VDPENPEFNTGYAI	AVYRLDGF	FNKAS	TFKEAF	SLHPLKQAI	RLNPEDAYIKALL	GLKLQDVGE	QAEQKYI	240
A. jamaicensis	161	KACFEKALE	VDPENPEFNTGYAI	AVYRLDGF	FNKAS	TFKEAF	SLHPLKQAI	RLNPEDAYIKALL	GLKLQDVGE	QAEQKYI	240
S. hondurensis	161	KACFEKALE	VDPENPEFNTGYAI	AVYRLDGF	FNKAS	TFKEAF	SLHPLKQAI	RLNPEDAYIKALL	GLKLQDVGE	QAEQKYI	240
P. hastatus	161	KACFEKALE	VDPENPEFNTGYAI	AVYRLDGF	FNKAS	TFKEAF	SLHPLKQAI	RLNPEDAYIKALL	GLKLQDVGE	QAEQKYI	240
P. discolor	161	KACFEKALE	VDPENPEFNTGYAI	AVYRLDGF	FNKAS	TFKEAF	SLHPLKQAI	RLNPEDAYIKALL	GLKLQDVGE	QAEQKYI	240
D. rotundus	161	KACFEKALE	VDPENPEFNTGYAI	AVYRLDGF	FNKAS	TFKEAF	SLHPLKQAI	RLNPEDAYIKALL	GLKLQDVGE	QAEQKYI	240
E. fuscus	161	KACFEKALE	VDPENPEFNTGYAI	AVYRLDGF	FNKAS	TFKEAF	SLHPLKQAI	RLNPEDAYIKALL	GLKLQDVGE	QAEQKYI	240
M. brandtii	161	KACFEKALE	VDPENPEFNTGYAI	AVYRLDGF	FNKAS	TFKEAF	SLHPLKQAI	RLNPEDAYIKALL	GLKLQDVGE	QAEQKYI	240
M. molossus	161	KACFEKALE	VDPENPEFNTGYAI	AVYRLDGF	FNKAS	TFKEAF	SLHPLKQAI	RLNPEDAYIKALL	GLKLQDVGE	QAEQKYI	240
M. natalensis	160	KACFEKALE	VDPENPEFNTGYAI	AVYRLDGF	FNKAS	TFKEAF	SLHPLKQAI	RLNPEDAYIKALL	GLKLQDVGE	QAEQKYI	239
P. kuhlii	161	KACFEKALE	VDPENPEFNTGYAI	AVYRLDGF	FNKAS	TFKEAF	SLHPLKQAI	RLNPEDAYIKALL	GLKLQDVGE	QAEQKYI	240
H. sapiens	161	KACFEKALE	VDPENPEFNTGYAI	AVYRLDGF	FNKAS	TFKEAF	SLHPLKQAI	RLNPEDAYIKALL	GLKLQDVGE	QAEQKYI	240
P. alecto	241	EEALTK	MSSTQYVFRYAAMFYRRKGSVDKALQLLK	TALQATPSSAFLHHQIGLCYRSQV	RIKKTAKWQPRGQDREN	VNR	320				
P. vampyrus	241	EEALTK	MSSTQYVFRYAAMFYRRKGSVDKALQLLK	TALQATPSSAFLHHQIGLCYRSQV	RIKKTAKWQPRGQDREN	VNR	320				
R. aegyptiacus	241	EEALTK	MSSTQYVFRYAAMFYRRKGSVDKALQLLK	TALQATPSSAFLHHQIGLCYRSQV	RIKKTAKWQPRGQDREN	VNR	320				
P. mesoamericanus	241	EEALTK	MSSTQYVFRYAAMFYRRKGSVDKALQLLK	TALQATPSSAFLHHQIGLCYRSQV	RIKKTAKWQPRGQDREN	VNR	320				
R. ferrumequinum	241	EEALTK	MSSTQYVFRYAAMFYRRKGSVDKALQLLK	TALQATPSSAFLHHQIGLCYRSQV	RIKKTAKWQPRGQDREN	VNR	320				
A. jamaicensis	241	EEALTK	MSSTQYVFRYAAMFYRRKGSVDKALQLLK	TALQATPSSAFLHHQIGLCYRSQV	RIKKTAKWQPRGQDREN	VNR	320				
S. hondurensis	241	EEALTK	MSSTQYVFRYAAMFYRRKGSVDKALQLLK	TALQATPSSAFLHHQIGLCYRSQV	RIKKTAKWQPRGQDREN	VNR	320				
P. hastatus	241	EEALTK	MSSTQYVFRYAAMFYRRKGSVDKALQLLK	TALQATPSSAFLHHQIGLCYRSQV	RIKKTAKWQPRGQDREN	VNR	320				
P. discolor	241	EEALTK	MSSTQYVFRYAAMFYRRKGSVDKALQLLK	TALQATPSSAFLHHQIGLCYRSQV	RIKKTAKWQPRGQDREN	VNR	320				
D. rotundus	241	EEALTK	MSSTQYVFRYAAMFYRRKGSVDKALQLLK	TALQATPSSAFLHHQIGLCYRSQV	RIKKTAKWQPRGQDREN	VNR	320				
E. fuscus	241	EEALTK	MSSTQYVFRYAAMFYRRKGSVDKALQLLK	TALQATPSSAFLHHQIGLCYRSQV	RIKKTAKWQPRGQDREN	VNR	320				
M. brandtii	241	EEALTK	MSSTQYVFRYAAMFYRRKGSVDKALQLLK	TALQATPSSAFLHHQIGLCYRSQV	RIKKTAKWQPRGQDREN	VNR	320				
M. molossus	240	EEALTK	MSSTQYVFRYAAMFYRRKGSVDKALQLLK	TALQATPSSAFLHHQIGLCYRSQV	RIKKTAKWQPRGQDREN	VNR	320				
M. natalensis	240	EEALTK	MSSTQYVFRYAAMFYRRKGSVDKALQLLK	TALQATPSSAFLHHQIGLCYRSQV	RIKKTAKWQPRGQDREN	VNR	320				
P. kuhlii	241	EEALTK	MSSTQYVFRYAAMFYRRKGSVDKALQLLK	TALQATPSSAFLHHQIGLCYRSQV	RIKKTAKWQPRGQDREN	VNR	320				
H. sapiens	241	EEALTK	MSSTQYVFRYAAMFYRRKGSVDKALQLLK	TALQATPSSAFLHHQIGLCYRSQV	RIKKTAKWQPRGQDREN	VNR	320				

*Supplementary Figure 13 continues on next page

P. alecto	321	ITRLAIFHFEFTLKQKPTFEIAYKHLADMYIEAGNYEKAEDTYQKVLRLKKLDKEVLQEIYFYVYGFQEFQKSEIDAI	400
P. vampyrus	321	ITRLAISHFEFTLKQKPTFEIAYIHLADMYIEAGNYEKAEDTYQKVLCLKKLDKEVLQEIYFYVYGRFQEFQKSEIDAI	400
P. aegyptiacus	321	IANLAISHFEFTLKQKPTFEIAYIHLADMYIEAGNYEKAEDTYQKVFMSKTLDDKDIQLDIYFHYGFQEFQKSESDAI	400
P. mesoamericanus	321	VTKLAISHLEFALEQKPTMEIAYIHLADMYSEAGNYSKAEDAYKTVLSMKSLEGEEKLQEIYFYVYGRFQEFQKSEDDAI	400
R. ferrumequinum	321	ITRLAISHFEFALEQKPTLEIAYKHLADMYIEAGNYGKAEDTYQKLLCLKSLEEBNLQEIYFYVYGRFQEFQKSEVDAI	400
A. jamaicensis	321	ITQLAISHFEFALEQKPTMEIAYVHLADMYIEAGNTRKAEDAYKTVFSMKSVEEEKLQEIYFYVYGRFQEFQKSEDAI	400
S. hondurensis	321	LVRMAICFEKKALELRPGEHMVYIDLAEYALGQHRLEAEDIFQKLLSMGIFHDHLHQNTHFRYGRFQEFQKSEVNAI	400
P. hastatus	321	ITKLAISHLEFALEQKPTMETAYVHLADMYIEAGNYRKAEDAYKTVFSMKSIEEEKLQDMYFHYGRFNEFHKKSEADA	400
P. discolor	321	ITKLAISHLEFALEQKPTMEIAYVHLADMYIEAGNYRKAEDAYKTVFSMKSIEEEKLQDMYFHYGRFNEFHKKSEADA	400
D. rotundus	321	ITKLAISHLEFALEQKPTMEIAYVHLADMYIEAGNYRKAEDAYKTVFSMKSLEEEKLQEIYFYVYGRFNEFHKKSEADA	400
E. fuscus	321	ITKLAISHFEFALEQKPTFEIAYIHLADMYVQAGNTRKAEDTYQKLLCMKSLKEENMQEIYFYVYGRFQEFQKSEVDAI	400
M. brandtii	321	KTKLAISHFEFAVEQKPTFEIAYMHLADMYSVAGNSRKAEDTYQKVFMSKSLKEEKIQEIYFYVYGRFQEFQKSEVDAI	400
M. molossus	321	ITRLAISHFEFALEQKPTFDIAYIHLADMYIEAGDYAKTDPLQYKVFMTPLDEKQLQELYLHHGRYQEFQKSEVSAMI	400
M. natalensis	320	ITRLAISHFEFALEQKPTFEVAYIHLADMYIEAGNYRKAEDAYQKLLSMKSLKEETLQEIYFYVYGRFQEFQKSEVNAI	399
P. kuhlii	321	ITKLAISHLEFAVEQKPTFDIAYLHLADMYIQAGSYRKAEDAYQKLLRVKSLKEETMQEIYFYVYGRFQEFQKSEVDAI	400
H. sapiens	321	MIRSAIFHFEFAVEKQKPTFEVHLDLARMYIEAGNHRKAEDENFQKLLCMKPVVEETMQDIHFHYGRFQEFQKSDVNAI	400

P. alecto	401	YYLKAIKIENQSYSRDKSISSELEKLVRLKLRNGSDIESLSILGFIYKLGEMNEALEYEEQALKLAADFFSFV	474
P. vampyrus	401	YYLKAIKIENQSYSRDKSISSELEKLVRLKLRNNSDIESLSILGFIYKLGEMNEALEYEEQALNLAADFFERF	473
R. aegyptiacus	401	YYLKAIKIENQSYSRDKSISSELEKLVRLKLRNNSDIESLRILRFIDKLGKEINEASFSDEKALKLAADFFSSVGLK	477
P. mesoamericanus	401	SYLKAITIEKPSFSRDKSLSALEKLVRLKLOTNEADIEQLSILGFVYKSRGEMNKALEYEEQALRLAAGF	470
R. ferrumequinum	401	YYLKSIEVAKPSFTRDKSISALEKLVRLKLRNNTSDIESLSILGFIHKLKGEINEALEYERARLSADVKNNSVGVDW	478
A. jamaicensis	401	YYLKAIKIENQSYSRDKSISALEKLVRLKLRNEADVESLSILGFVYKLGEMHEALGYERARLRAAGSENSVGVVP	478
S. hondurensis	401	YYLKAINKENSLFTSNESLRALKLVRLRRHRNGADIESLSILGFIHKKMGEMHEALECYEQALRLAAGSENSVGHVP	478
P. hastatus	401	YYLKAINKENSFTSNRSLSALEKLVRLKLRNEADVESLSILGFVCKLGEMHEALEWYERARKLAAGSENSVGHVP	478
P. discolor	401	YYLKAIKIEKSTFSRENSLSALEKLVRLKLRNGADIESLSILGFVYKLGEMHEALEWYERARLRAAGSENSVGRVP	478
D. rotundus	401	YYLKAIKIEKSTFSRENSLSALEKLVRLKLRNEADVESLSILGFVYKLGEMHEALEYERARLSLPGCWL	471
E. fuscus	401	YYLKAIKIEKPS-LRDRSINSLEHVVILKLRNPVDIESLSILGFTYKLGEMNKALEYERARLRAADFENPVGHAP	477
M. brandtii	401	YYLKAIKIEKPS-PRDRSISALEHVVILKLRNAEDMESLGILGFIYKLGKEINKALEYERARLRAAD	469
M. molossus	401	YYLKAIKIEKPTVYDRSISLEKLVRLKLRHRRNAEDIESLSILGFIYKLGEMNKALECYEQALRLANE	469
M. natalensis	400	YYLKIKINKLSIVREISIALEKLVRLKLRHRRNAEDMESLSILGLIYKLGEMNKALEYERARLRAAGFENSVDHVP	477
P. kuhlii	401	YYLKAIKIEKPSVYDRSISLEKLVRLKLRNNAEDIESLSILGFTYKLGEMNKALEYERARLRAANFESPVGHAP	478
H. sapiens	401	HYLKAIKIEKASLTRDKSINSLEKLVRLKLRKALDIESLSILGFVYKLEGNMNEALEYERARLRAADFENSVRQGP	478

Supplementary Figure 13. Multiple protein sequence alignment for bat IFIT1. Grey boxes indicate identical residues. ClustalW alignment was generated using MacVector software. Human sequence was included as a comparator. Black arrows indicate residues in human IFIT1 that are known to play a role in mRNA binding (R38, L46, W147, K151, E176 and Y218). Purple box highlights IFIT3 binding motif.

P. aleo	223	INKEAEGEPLV	I	EAL	EKAP	Q	T	D	L	LH	SA	AK	F	Y	K	K	G	D	L	K	A	I	E	L	L	K	A	L	E	S	M	P	N	S	H	L	C	Y	L	S	G	C	T	A	K	V	R	I	E	N	T	G	Y	S	N	302					
P. vampyrus	222	INKEAEGEPLV	I	EAL	EKAP	Q	T	D	L	LH	SA	AK	F	Y	K	K	G	D	L	K	A	I	E	L	L	K	A	L	E	S	M	P	N	S	H	L	C	Y	L	S	G	C	T	A	K	V	R	I	E	N	T	G	Y	S	N	301					
P. giganteus	222	INKEAEGEPLV	I	EAL	EKAP	Q	T	D	L	LH	SA	AK	F	Y	K	K	G	D	L	K	A	I	E	L	L	K	A	L	E	S	M	P	N	S	H	L	C	Y	L	S	G	C	T	A	K	V	R	I	E	N	T	G	Y	S	N	301					
R. aegyptiacus	222	INKEA K GEPLV	I	EAL	EKAP	Q	T	D	V	L	C	R	A	A	F	Y	R	K	G	D	L	K	A	I	E	L	L	K	A	L	E	S	M	P	N	S	Y	C	H	L	S	C	T	A	K	V	R	I	E	N	T	E	D	S	301						
R. ferrumequinum	222	IN K D TEGEPLV	I	EAL	EKAP	Q	T	D	V	L	H	N	A	A	F	Y	K	I	K	G	D	L	K	A	I	E	L	F	O	K	A	L	E	S	M	P	N	S	G	Y	I	C	H	A	R	C	E	R	K	A	Q	I	D	T	E	G	S	E	301		
R. sinicus	222	IN K T TEGEPLV	I	EAL	EKAP	R	O	T	D	V	L	H	N	A	A	F	Y	K	I	K	G	D	L	K	A	I	E	L	F	O	K	A	L	E	S	M	P	N	S	G	Y	I	C	H	A	R	C	E	R	K	A	Q	I	D	T	E	G	S	E	301	
A. jamaicensis	240	ANKEAEGEPLV	A	EAL	EKAP	Q	T	D	L	LH	SA	AK	F	Y	K	K	G	D	L	K	A	I	E	L	F	O	K	A	L	E	S	L	P	N	S	R	Y	I	C	Q	I	A	S	C	Y	R	A	K	A	Q	I	E	D	T	E	D	S	E	319		
S. hondurensis	224	VNKE G GEPLV	A	EAL	EKAP	H	O	T	D	V	L	H	SA	AK	F	Y	K	K	G	D	L	K	A	I	E	L	F	O	K	A	L	E	S	L	P	N	S	C	Y	I	C	Q	I	A	S	C	Y	R	A	K	E	Q	I	E	N	T	E	G	S	E	309
P. hastatus	230	INKEAEGEPLV	V	EAL	EKAP	Q	T	D	V	L	L	SA	AK	F	Y	K	K	G	D	L	K	A	I	E	L	F	O	K	A	L	E	S	L	P	N	S	Y	I	C	Q	I	A	S	C	Y	R	A	K	E	Q	I	E	N	T	E	G	S	E	303		
P. discolor	224	INKEAEGEPLV	V	EAL	EKAP	Q	T	D	V	L	L	SA	AK	F	Y	K	K	G	D	L	K	A	I	E	L	F	O	K	A	L	E	S	L	P	N	S	Y	I	C	Q	I	A	S	C	Y	R	A	K	E	Q	I	E	N	T	E	G	S	E	303		
D. rotundus	222	INKEAEGEPLV	G	EAL	EKAP	R	O	T	D	V	L	L	SA	AK	F	Y	K	K	G	D	L	K	A	I	E	L	F	O	K	A	L	E	S	L	P	N	S	Y	I	C	Q	I	A	S	C	Y	R	A	K	E	Q	I	E	N	T	E	G	S	E	301	
E. fuscus	222	MY E AE G EP L I	E	EAL	E R AP	Q	T	D	V	L	N	A	A	F	Y	R	K	K	G	D	L	K	A	I	E	L	L	K	A	L	E	S	L	P	N	S	N	I	C	R	O	I	A	C	C	R	A	K	E	Q	I	E	N	T	E	G	S	E	301		
M. brandtii	222	INKEAEG V LLI	E	EAL	EKAP	Q	T	D	V	L	L	SA	AK	F	Y	R	K	K	G	D	L	K	A	I	E	L	F	O	K	A	L	E	S	L	P	N	S	N	I	C	R	O	I	A	C	C	R	A	K	E	Q	I	E	N	T	E	G	S	E	301	
M. myotis	222	INKEAEGGLI	E	EAL	EKAP	Q	T	D	V	L	L	SA	AK	F	Y	R	K	K	G	D	L	K	A	I	E	L	F	O	K	A	L	E	S	L	P	N	S	N	I	C	R	O	I	A	C	C	R	A	K	E	Q	I	E	N	T	E	G	S	E	301	
M. davidii	222	INKEAEGGLI	E	EAL	EKAP	Q	T	D	V	L	L	SA	AK	F	Y	R	K	K	G	D	L	K	A	I	E	L	F	O	K	A	L	E	S	L	P	N	S	N	I	C	R	O	I	A	C	C	R	A	K	E	Q	I	E	N	T	E	G	S	E	301	
M. lucifugus	222	IN E AE G GLI	E	EAL	EKAP	Q	T	D	V	L	L	SA	AK	F	Y	R	K	K	G	D	L	K	A	I	E	L	F	O	K	A	L	E	S	L	P	N	S	N	I	C	R	O	I	A	C	C	R	A	K	E	Q	I	E	N	T	E	G	S	E	301	
M. molossus	222	TKKEA E GL W VI	E	EAL	E R AP	Q	R	D	V	L	L	SA	AK	F	Y	R	K	K	G	D	L	K	A	I	E	L	L	K	A	L	E	S	L	P	N	S	R	Y	L	C	H	L	I	A	C	H	Y	A	K	A	Q	I	D	T	E	D	S	E	301		
M. natalensis	222	TKHEAEGEPLV	V	EAL	EKAP	Q	T	D	V	L	L	SA	AK	F	Y	R	K	K	G	D	L	K	A	I	E	L	F	O	K	A	L	E	S	L	P	N	S	Y	I	C	R	O	I	A	C	C	R	A	K	E	Q	I	E	N	T	E	G	S	E	301	

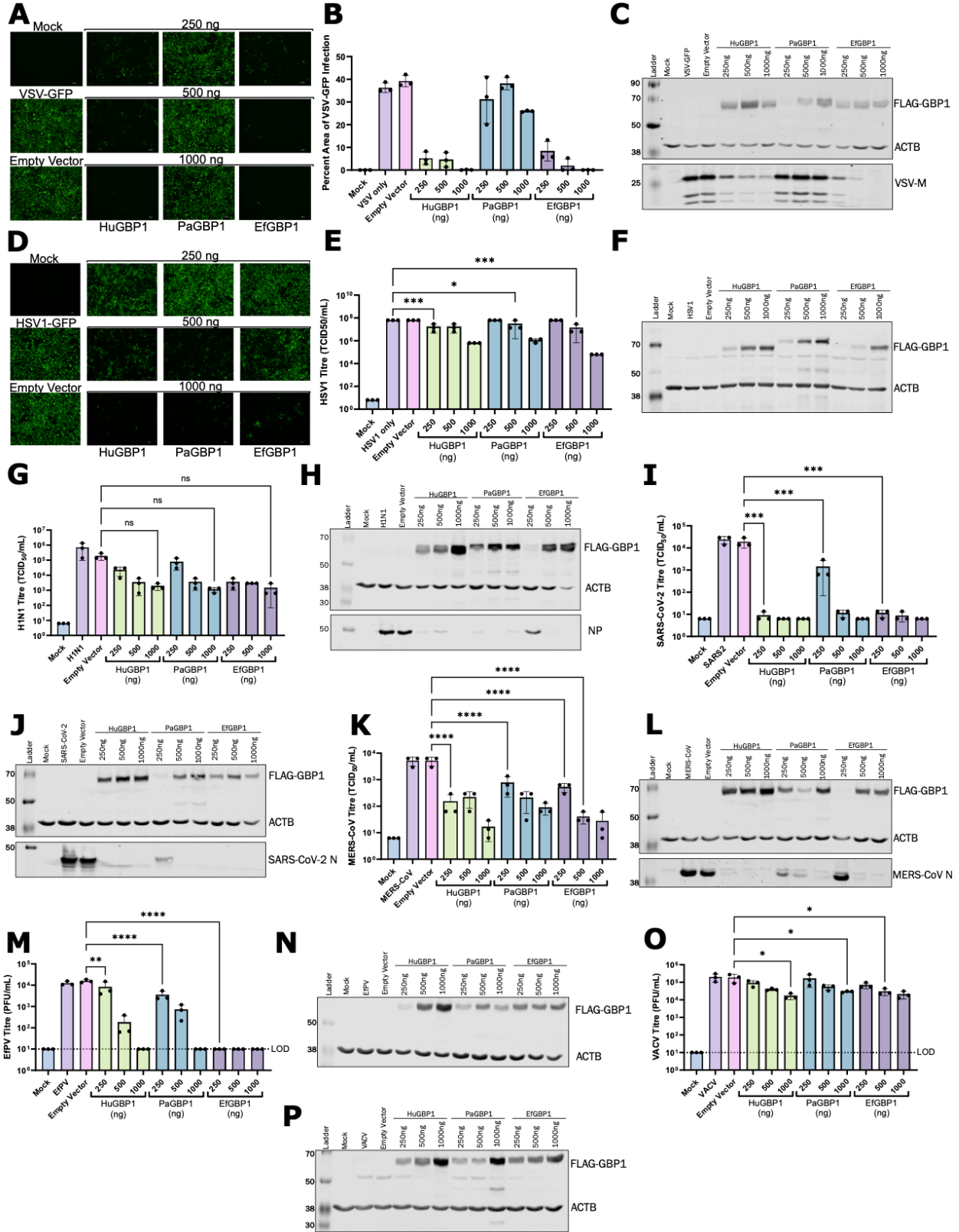
***Supplementary Figure 14 continues on next page**

P. alecto	303	ASWNREKIEELS	SKYARDYSEKAIEKVLNPLNAYSDLAEP-ET	ECYQTAFNKKLPNAEMKQFHQLSCNFQEYHGKSEDTVP	381			
P. vampyrus	302	ASWNREKIEELS	SKYARDYSEKAIEKVLNPLNAYSDLAEP-ET	ECYQTAFNKKLPNAEMKQFHQLSCNFQEYHGKSEDTVP	380			
P. giganteus	302	ASWNREKIEELS	SKYARDYSEKAIEKVLNPLNAYSDLAEP-ET	ECYQTAFNKKLPNAEMKQFHQLSCNFQEYHGKSEDTVP	380			
R. aegyptiacus	302	TSWNREKIEELS	SKYARDYAKKAIEKGNPLNAYFDLAEP-ET	ECYNTAFDEEXPDAATKQLHQLSCNFQEYLGKSEDTVP	380			
R. ferrumequinum	302	VSRRREKFEEL	RKYAMDYSKKAIEKGLSFLYAYSDLTELETE	CHPTAFNSSELPDTERKKLHQGGYNLQEHGTS	EDTVP	380		
R. sinicus	302	VSRRREKFEEL	SKYAMDYSKAMKGLSFLYAYSDLTEPEKE	CHPTAFNSRELPTNTERKKLHQGGYNLQEHGTS	EDTVP	380		
A. jamaicensis	320	TDNRREKIEEL	RKYARQYSNKAIEKGLDPLVYAYSDLTELETE	EECFET----	AFPKAEKKQFHQGGSNVQOYOGTSEDTSV	395		
S. hondurensis	304	ADNRREKIEEL	RKYAREYSNKAIEKGLNPIYAYSDLTELETE	EECFET----	AFQKVERKKQFHQGGSTFQEDDGTSEDTSV	379		
P. hastatus	310	ADNRREKIEEL	RKYARKYSNKAIEKGLNPIYAYSDLTELETE	EECFET----	AFPEASRKQFYOGYSNFOYOGKSEDTSV	385		
P. discolor	304	ADNRREKIEEL	RKYAREYSNKAIEKGLNPIYAYSDLTELETE	EECFET----	AFPEASRKQFYOGGSNFRQYOGKSEDTSV	379		
D. rotundus	302	ADNRREKIEEL	RKYARDYSNKAIEKGLNPIYAYSDLTELETE	EECFET----	TFREAERKKQFHQGGYNFRDYOGKSEDTSV	377		
E. fuscus	302	AGGNREKMEEL	RKSAMDYANKAIEKGLDPLVYAYSDLTELE	SEECYQT----	AFNKAERKKPLHQGGYNFQBNQKSEDTVP	377		
M. brandtii	302	AGGNREKMEEL	RKSAMDYSNKAIEKGLNPLVYAYSDLTELES	SEECYQT----	AFNKAERKKLHQGGYNFQBNQKSEDTVP	377		
M. myotis	302	AGGNREKMEEL	RKSAMDYSNKAIEKGLNPLVYAYSDLTELES	SEECYQT----	AFNKAERKKLHQGGYNFQBNQKSEDTVP	377		
M. davidii	302	ADGNREKMEEL	RKSAMDYSNKAIEKGLNPLVYAYSDLTELES	SEECYPT----	AFHEAERKKLHQGGYNFQBNQKSEDTVP	377		
M. lucifugus	302	AGGNREKMEEL	RKSAMDYSNKAIEKGLNPLVYAYSDLTELES	SEECYQT----	AFDKAERKKLHQGGYNFQBNQKSEDTVP	377		
M. molossus	302	APRNGEIEEL	RKQAMHYLKKAIEKGLNPLVYAYSDLTELETE	EECHOTPCSKELSEANRKPLPHYSYNFQBNHNGRSEDTVP	380			
M. natalensis	302	ARRRREKIEEL	RKYAMNYLKAYIEKGLNPLDYVSNFNDLETE	EYFOT----	VSNKAERKKQPHQGGYNFQBNHNGRSEDTVP	377		
H. sapiens	300	ASGNKEMTEAL	KQYAMDYSNKAIEKGLNPLNAYSDLAEPFLET	ECYQTPFNKEVFPDAEKQSSHQRVCNLRKYN	NGRSEDTAV	379		
P. alecto	382	QHHLKDL	SLISKSTEKEKEKCPQNV	VAENQLPQNA	PNNSWYLQGLTHKKNGYLLQAAEC	FEKELGRLLRD	SPSGISSIFLP	461
P. vampyrus	381	QHHLKDL	SLISKSTEKEKEKCPQNV	VAENQLPQNA	PNNSWYLQGLTHKKNGYLLQAAEC	FEKELGRLLRD	SPSGISSIFLP	460
P. giganteus	381	QHHLKDL	SLISKSTEKEKEKCPQNV	VAENQLPQNA	PNNSWYLQGLTHKKNGYLLQAAEC	FEKELGRLLRD	SPSGISSIFLP	460
R. aegyptiacus	381	QHHLKDL	SLISKSTEKEKEKCPQNV	VAENQLPQNA	PNNSWYLQGLTHKKNGYLLQAAEC	FEKELGRLLRD	SPSGISSIFLP	460
R. ferrumequinum	381	QHHLKDL	SLISKSTEKEKMKYQPN	AAENQLPQNA	PNNSWYLQGLTHKKNGYLLQAAEC	FEKELGRLLRD	SPSGISSIFLP	460
R. sinicus	381	QHHLKDL	SLISKSTEKEKMKYQPN	AAENQLPQNT	PNNSWYLQGLTHKKNGYLLQAAEC	FEKELGRLLRD	SPSGISSIFLP	460
A. jamaicensis	396	LHHLNLT	VNTKATEKEKAKYQPN	GAENQLPQNA	PNNSWYLQGLTHKKNGYLLQAAEC	FEKELGRLLRD	SPSGISSIFLP	470
S. hondurensis	380	LHHLNLT	VNTKATEKEKAKYQPN	GAENQLPQNA	PNNSWYLQGLTHKKNGYLLQAAEC	FEKELGRLLRD	SPSGISSIFLP	459
P. hastatus	386	LPHLNVL	PIPTKSTEKEKVKYQPN	GAENQLPQNA	PNNSWYLQGLTHKKNGYLLQAAEC	FEKELGRLLRD	SPSGISSIFLP	465
P. discolor	380	LPHLNVL	PIPTKSTEKEKVKYQPN	GAENQLPQNA	PNNSWYLQGLTHKKNGYLLQAAEC	FEKELGRLLRD	SPSGISSIFLP	459
D. rotundus	378	LHHLNVL	TIPTKSTEKEKVKYQPN	GAENQLPQNA	PNNSWYLQGLTHKKNGYLLQAAEC	FEKELGRLLRD	SPSGISSIFLP	457
E. fuscus	378	QHHL	-----STKST-----	ANGAERQLPR--	NSWYLQGLTHKKNGYLLQAAEC	FEKELGRLLRD	SPSGISSIFLP	440
M. brandtii	378	QHHL	-----STKST-----	ANGAERQLPR--	NSWYLQGLTHKKNGYLLQAAEC	FEKELGRLLRD	SPSGISSIFLP	440
M. myotis	378	QHHL	-----STKST-----	VNGAERQLPR--	NSWYLQGLTHKKNGYLLQAAEC	FEKELGRLLRD	SPSGISSIFLP	440
M. davidii	378	QHHL	-----STKST-----	ANGAERQLPR--	NSWYLQGLTHKKNGYLLQAAEC	FEKELGRLLRD	SPSGISSIFLP	440
M. lucifugus	378	QHHL	-----STKST-----	ANGAERQLPR--	NSWYLQGLTHKKNGYLLQAAEC	FEKELGRLLRD	SPSGISSIFLP	440
M. molossus	381	LHPLRTE	KEKLYQ-----PONGAENLPQ	TAQNDWYLQGLTHKKNGYLLQAAEC	FEKELGRLLRD	SPSGISSIFLP		452
M. natalensis	378	LHDLRA	TTISTLLST-----	ENGAENHLPQ	DAPNSWYLQGLTHKKNGYLLQAAEC	FEKELGRLLRD	SPSGISSIFLP	448
H. sapiens	380	QHHL	LEGSLISKSTDKKEIKDQPN	VSENLLPQNA	PNNSWYLQGLTHKKNGYLLQAAEC	FEKELGRLLRD	SPSGISSIFLP	459
P. alecto	462	ASELKE	-GSEEVGGAGDSST-LRELDPD					487
P. vampyrus	461	ASELKE	-GSEEVGGAGDSST-LRELDPD					486
P. giganteus	461	ASELKE	-GSEEVGGAGDSST-LRELDPD					486
R. aegyptiacus	461	AADLKE	-GSEEVGGAGDSSTSLRELPA					487
R. ferrumequinum	461	TSELEE	-GNERVGGAGDSST-LGEPLDS					486
R. sinicus	461	TSELEE	-GNERVGGAGDSST-LGEPLDS					487
A. jamaicensis	476	ASELEE	-GSAEVGGQTNGFP-LSELDPD	RAETEGRERE	GEGGAWNCHEGKKDGKAGVPQSELAD			537
S. hondurensis	460	TSELEE	-GCEEAGGGAGDSST-LSELDPD	RAETEGRERE	GEGGAWNCHEGKKDGKAGVPQSELAD			521
P. hastatus	466	ASELED	-GHAEVGGQTDGFP-LSELDPD	GAETEGRERE	GEGGAWNCHEGKKDGKAGVPQSELAD			527
P. discolor	460	ASELED	-GHAEVGGQTDGFP-LSELDPD	GAETEGRERE	GEGGAWNCHEGKKDGKAGVPQSELAD			521
D. rotundus	458	ASELEE	-GSAEVGGQTDSSP-LSELDPD	GAETEGRERE	GEGGAWNCHEGKKDGKAGVPQSELAD			519
E. fuscus	441	AEELAE	-GSAEVGGAGSSP-LSKLSD	PLADTEE				472
M. brandtii	441	AEELAE	-GSAEVGGAGSSP-LSKLSD	PLADTEE				472
M. myotis	441	AEELAE	-GSAEVGGAGSSP-LSKLSD	PLADTEE				472
M. davidii	441	AEELAE	-GSAEVGGAGSSP-LSKLSD	PLADTEE				472
M. lucifugus	441	AEELAE	-GSAEVGGAGSSP-LSKLSD	PLADTEE				472
M. molossus	453	ASELEE	-GSAEVGGAGAPV-SVKPLH					478
M. natalensis	449	ASELEE	-GSAEVGGAGAPV-SVKPLH					471
H. sapiens	460	ASELEE	-GSAEVGGAGAPV-SVKPLH					490

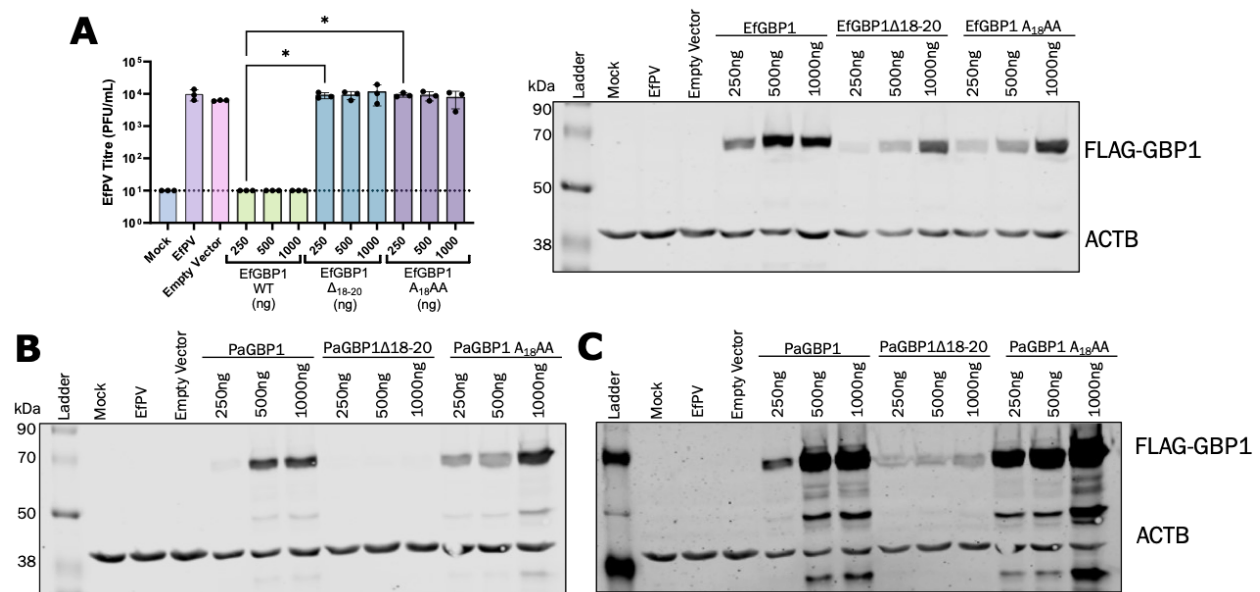
Supplementary Figure 14. Multiple protein sequence alignment for bat IFIT3. Grey boxes indicate identical residues. ClustalW alignment was generated using MacVector software. Human sequence was included as a comparator. Purple box highlights IFIT1 binding motif.

Pteropodidae	P. alecto	1	MSSETQMPGPVCLIENTENEITVNNKALILLSAITQPLVVVAIVGLYRTGKSYLMNKLAKKKGFSLGSTVQSHTKGIWM	80
	P. giganteus	1	MSSETQMPGPVCLIENTENEITVNNKALKILSAITQPLVVVAIVGLYRTGKSYLMNKLAKKKGFSLGSTVQSHTKGIWM	80
	P. vampyrus	1	MSSETQMPGPVCLIENTENEITVNNKALKILSAITQPLVVVAIVGLYRTGKSYLMNKLAKKKGFSLGSTVQSHTKGIWM	80
	P. mesoamericanus	1	MSSETQMPGPVCLIENTENEITVNNKALKILSAITQPLVVVAIVGLYRTGKSYLMNKLAKKKGFSLGSTVQSHTKGIWM	80
	S. hondurensis	1	MASETHMPGPVCLIENTENTQANPEALKILSAITQPLVVVAIVGLYRTGKSYLMNKLAKKKGFSLGSTVQSHTKGIWM	80
	A. jamaicensis	1	MSETHMHPVCLIENTNGKIAANPEALKILSAITQPLVVVAIVGLYRTGKSYLMNKLAKKKGFSLGSTVQSHTKGIWM	80
	P. discolor	1	MASETHMHPVCLIENTNGKIAANPEALKILSAITQPLVVVAIVGLYRTGKSYLMNKLAKKKGFSLGSTVQSHTKGIWM	80
	P. hastatus	1	MASETHMHPVCLIENTNGKIAANPEALKILSAITQPLVVVAIVGLYRTGKSYLMNKLAKKKGFSLGSTVQSHTKGIWM	80
	D. rotundus	1	MASETHMHPVCLIENTNGKIAANPEALKILSAITQPLVVVAIVGLYRTGKSYLMNKLAKKKGFSLGSTVQSHTKGIWM	80
	E. fuscus	1	MASDIQMPGPVCLIENTDTQANPEALKILSAITQPLVVVAIVGLYRTGKSYLMNKLAKKKGFSLGSTVQSHTKGIWM	80
Vespertilionidae	M. lucifugus	1	MASDIQMPGPVCLIENTDTQANPEALKILSAITQPLVVVAIVGLYRTGKSYLMNKLAKKKGFSLGSTVQSHTKGIWM	80
	M. myotis	1	MASDIQMPGPVCLIENTDTQANPEALKILSAITQPLVVVAIVGLYRTGKSYLMNKLAKKKGFSLGSTVQSHTKGIWM	80
	M. daubentonii	1	MASDIQMPGPVCLIENTDTQANPEALKILSAITQPLVVVAIVGLYRTGKSYLMNKLAKKKGFSLGSTVQSHTKGIWM	80
	P. kuhlii	1	MASDIQMPGPVCLIENTDTQANPEALKILSAITQPLVVVAIVGLYRTGKSYLMNKLAKKKGFSLGSTVQSHTKGIWM	80
Hominidae (outlier)	H. sapiens	1	MASDIQMPGPVCLIENTDTQANPEALKILSAITQPLVVVAIVGLYRTGKSYLMNKLAKKKGFSLGSTVQSHTKGIWM	80
Pteropodidae	P. alecto	81	WCVPHPKPDHTLVLLDTEG.GDVEKGDNQNDSWIFALAILLSSTFVYNSMGTINQAMDQLHYVTELDRIAKSSPDA	160
	P. giganteus	81	WCVPHPKPDHTLVLLDTEG.GDVEKGDNQNDSWIFALAILLSSTFVYNSMGTINQAMDQLHYVTELDRIAKSSPDA	160
	P. vampyrus	81	WCVPHPKPDHTLVLLDTEG.GDVEKGDNQNDSWIFALAILLSSTFVYNSMGTINQAMDQLHYVTELDRIAKSSPDA	160
	P. mesoamericanus	81	WCVPHPKPDHTLVLLDTEG.GDVEKGDNQNDSWIFALAILLSSTFVYNSMGTINQAMDQLHYVTELDRIAKSSPDA	160
	S. hondurensis	81	WCVPHPKPDHTLVLLDTEG.GDVEKGDNQNDSWIFALAILLSSTFVYNSMGTINQAMDQLHYVTELDRIAKSSPDA	160
	A. jamaicensis	81	WCVPHPKPDHTLVLLDTEG.GDVEKGDNQNDSWIFALAILLSSTFVYNSMGTINQAMDQLHYVTELDRIAKSSPDA	160
	P. discolor	81	WCVPHPKPDHTLVLLDTEG.GDVEKGDNQNDSWIFALAILLSSTFVYNSMGTINQAMDQLHYVTELDRIAKSSPDA	160
	P. hastatus	81	WCVPHPKPDHTLVLLDTEG.GDVEKGDNQNDSWIFALAILLSSTFVYNSMGTINQAMDQLHYVTELDRIAKSSPDA	160
	D. rotundus	81	WCVPHPKPDHTLVLLDTEG.GDVEKGDNQNDSWIFALAILLSSTFVYNSMGTINQAMDQLHYVTELDRIAKSSPDA	160
	E. fuscus	81	WCVPHPKPDHTLVLLDTEG.GDVEKGDNQNDSWIFALAILLSSTFVYNSMGTINQAMDQLHYVTELDRIAKSSPDA	160
Vespertilionidae	M. lucifugus	81	WCVPHPKPDHTLVLLDTEG.GDVEKGDNQNDSWIFALAILLSSTFVYNSMGTINQAMDQLHYVTELDRIAKSSPDA	160
	M. myotis	81	WCVPHPKPDHTLVLLDTEG.GDVEKGDNQNDSWIFALAILLSSTFVYNSMGTINQAMDQLHYVTELDRIAKSSPDA	160
	M. daubentonii	81	WCVPHPKPDHTLVLLDTEG.GDVEKGDNQNDSWIFALAILLSSTFVYNSMGTINQAMDQLHYVTELDRIAKSSPDA	160
	P. kuhlii	81	WCVPHPKPDHTLVLLDTEG.GDVEKGDNQNDSWIFALAILLSSTFVYNSMGTINQAMDQLHYVTELDRIAKSSPDA	160
Hominidae (outlier)	H. sapiens	81	WCVPHPKPDHTLVLLDTEG.GDVEKGDNQNDSWIFALAILLSSTFVYNSMGTINQAMDQLHYVTELDRIAKSSPDA	160
Pteropodidae	P. alecto	161	NE--DEDSADFSFFDFVWTLRDFSLLEADGGPISADEYLENSLKKKGTSPKDKNFNLPRLCIRKFFPKKCFIDFR	238
	P. giganteus	161	NE--DEDSADFSFFDFVWTLRDFSLLEADGGPISADEYLENSLKKKGTSPKDKNFNLPRLCIRKFFPKKCFIDFR	238
	P. vampyrus	161	NE--DEDSADFSFFDFVWTLRDFSLLEADGGPISADEYLENSLKKKGTSPKDKNFNLPRLCIRKFFPKKCFIDFR	238
	P. mesoamericanus	161	NE--VEDSTNHSFFDFVWTLRDFSLEADGGPISADEYLENSLKKKGTSPKDKNFNLPRLCIRKFFPKKCFIDFR	238
	S. hondurensis	161	NE--VEDSTNHSFFDFVWTLRDFSLEADGGPISADEYLENSLKKKGTSPKDKNFNLPRLCIRKFFPKKCFIDFR	238
	A. jamaicensis	161	NE--VEDSTNHSFFDFVWTLRDFSLEADGGPISADEYLENSLKKKGTSPKDKNFNLPRLCIRKFFPKKCFIDFR	238
	P. discolor	161	NE--VEDSTNHSFFDFVWTLRDFSLEADGGPISADEYLENSLKKKGTSPKDKNFNLPRLCIRKFFPKKCFIDFR	238
	P. hastatus	161	NE--VEDSTNHSFFDFVWTLRDFSLEADGGPISADEYLENSLKKKGTSPKDKNFNLPRLCIRKFFPKKCFIDFR	238
	D. rotundus	161	NE--VEDSTNHSFFDFVWTLRDFSLEADGGPISADEYLENSLKKKGTSPKDKNFNLPRLCIRKFFPKKCFIDFR	238
	E. fuscus	161	NE--VEDSTNHSFFDFVWTLRDFSLEADGGPISADEYLENSLKKKGTSPKDKNFNLPRLCIRKFFPKKCFIDFR	238
Vespertilionidae	M. lucifugus	161	NE--VEDSTNHSFFDFVWTLRDFSLEADGGPISADEYLENSLKKKGTSPKDKNFNLPRLCIRKFFPKKCFIDFR	238
	M. myotis	161	NE--VEDSTNHSFFDFVWTLRDFSLEADGGPISADEYLENSLKKKGTSPKDKNFNLPRLCIRKFFPKKCFIDFR	238
	M. daubentonii	161	NE--VEDSTNHSFFDFVWTLRDFSLEADGGPISADEYLENSLKKKGTSPKDKNFNLPRLCIRKFFPKKCFIDFR	238
	P. kuhlii	161	NE--VEDSTNHSFFDFVWTLRDFSLEADGGPISADEYLENSLKKKGTSPKDKNFNLPRLCIRKFFPKKCFIDFR	238
Hominidae (outlier)	H. sapiens	161	NE--VEDSTNHSFFDFVWTLRDFSLEADGGPISADEYLENSLKKKGTSPKDKNFNLPRLCIRKFFPKKCFIDFR	240
Pteropodidae	P. alecto	239	PTHKKLGOLETLNDELDFEFVQQAADFCSYIFHSKVKTLGGIQQVNGPRLSLVLTYYNAISSGDLPCMENAVLALA	318
	P. giganteus	239	PTHKKLGOLETLNDELDFEFVQQAADFCSYIFHSKVKTLGGIQQVNGPRLSLVLTYYNAISSGDLPCMENAVLALA	318
	P. vampyrus	239	PTHKKLGOLETLNDELDFEFVQQAADFCSYIFHSKVKTLGGIQQVNGPRLSLVLTYYNAISSGDLPCMENAVLALA	318
	P. mesoamericanus	239	PTHKKLGOLETLNDELDFEFVQQAADFCSYIFHSKVKTLGGIQQVNGPRLSLVLTYYNAISSGDLPCMENAVLALA	318
	S. hondurensis	239	PTHKKLGOLETLNDELDFEFVQQAADFCSYIFHSKVKTLGGIQQVNGPRLSLVLTYYNAISSGDLPCMENAVLALA	318
	A. jamaicensis	239	PTHKKLGOLETLNDELDFEFVQQAADFCSYIFHSKVKTLGGIQQVNGPRLSLVLTYYNAISSGDLPCMENAVLALA	318
	P. discolor	239	PTHKKLGOLETLNDELDFEFVQQAADFCSYIFHSKVKTLGGIQQVNGPRLSLVLTYYNAISSGDLPCMENAVLALA	318
	P. hastatus	239	PTHKKLGOLETLNDELDFEFVQQAADFCSYIFHSKVKTLGGIQQVNGPRLSLVLTYYNAISSGDLPCMENAVLALA	318
	D. rotundus	239	PTHKKLGOLETLNDELDFEFVQQAADFCSYIFHSKVKTLGGIQQVNGPRLSLVLTYYNAISSGDLPCMENAVLALA	318
	E. fuscus	239	PTHKKLGOLETLNDELDFEFVQQAADFCSYIFHSKVKTLGGIQQVNGPRLSLVLTYYNAISSGDLPCMENAVLALA	318
Vespertilionidae	M. lucifugus	239	PTHKKLGOLETLNDELDFEFVQQAADFCSYIFHSKVKTLGGIQQVNGPRLSLVLTYYNAISSGDLPCMENAVLALA	318
	M. myotis	239	PTHKKLGOLETLNDELDFEFVQQAADFCSYIFHSKVKTLGGIQQVNGPRLSLVLTYYNAISSGDLPCMENAVLALA	318
	M. daubentonii	239	PTHKKLGOLETLNDELDFEFVQQAADFCSYIFHSKVKTLGGIQQVNGPRLSLVLTYYNAISSGDLPCMENAVLALA	318
	P. kuhlii	239	PTHKKLGOLETLNDELDFEFVQQAADFCSYIFHSKVKTLGGIQQVNGPRLSLVLTYYNAISSGDLPCMENAVLALA	318
Hominidae (outlier)	H. sapiens	241	PTHKKLGOLETLNDELDFEFVQQAADFCSYIFHSKVKTLGGIQQVNGPRLSLVLTYYNAISSGDLPCMENAVLALA	320
Pteropodidae	P. alecto	319	QIENSAAYKKAIAHYDQOMAEKVLPTETLQELLDLHASEKEAIEVFINKSFKDVHILFQKELAAQLEKKRDDFKQNM	398
	P. giganteus	319	QIENSAAYKKAIAHYDQOMAEKVLPTETLQELLDLHASEKEAIEVFINKSFKDVHILFQKELAAQLEKKRDDFKQNM	398
	P. vampyrus	319	QIENSAAYKKAIAHYDQOMAEKVLPTETLQELLDLHASEKEAIEVFINKSFKDVHILFQKELAAQLEKKRDDFKQNM	398
	P. mesoamericanus	319	QIENSAAYKKAIAHYDQOMAEKVLPTETLQELLDLHASEKEAIEVFINKSFKDVHILFQKELAAQLEKKRDDFKQNM	398
	S. hondurensis	319	QIENSAAYKKAIAHYDQOMAEKVLPTETLQELLDLHASEKEAIEVFINKSFKDVHILFQKELAAQLEKKRDDFKQNM	398
	A. jamaicensis	319	QIENSAAYKKAIAHYDQOMAEKVLPTETLQELLDLHASEKEAIEVFINKSFKDVHILFQKELAAQLEKKRDDFKQNM	398
	P. discolor	319	QIENSAAYKKAIAHYDQOMAEKVLPTETLQELLDLHASEKEAIEVFINKSFKDVHILFQKELAAQLEKKRDDFKQNM	398
	P. hastatus	319	QIENSAAYKKAIAHYDQOMAEKVLPTETLQELLDLHASEKEAIEVFINKSFKDVHILFQKELAAQLEKKRDDFKQNM	398
	D. rotundus	319	QIENSAAYKKAIAHYDQOMAEKVLPTETLQELLDLHASEKEAIEVFINKSFKDVHILFQKELAAQLEKKRDDFKQNM	398
	E. fuscus	319	QIENSAAYKKAIAHYDQOMAEKVLPTETLQELLDLHASEKEAIEVFINKSFKDVHILFQKELAAQLEKKRDDFKQNM	398
Vespertilionidae	M. lucifugus	319	QIENSAAYKKAIAHYDQOMAEKVLPTETLQELLDLHASEKEAIEVFINKSFKDVHILFQKELAAQLEKKRDDFKQNM	398
	M. myotis	319	QIENSAAYKKAIAHYDQOMAEKVLPTETLQELLDLHASEKEAIEVFINKSFKDVHILFQKELAAQLEKKRDDFKQNM	398
	M. daubentonii	319	QIENSAAYKKAIAHYDQOMAEKVLPTETLQELLDLHASEKEAIEVFINKSFKDVHILFQKELAAQLEKKRDDFKQNM	398
	P. kuhlii	319	QIENSAAYKKAIAHYDQOMAEKVLPTETLQELLDLHASEKEAIEVFINKSFKDVHILFQKELAAQLEKKRDDFKQNM	398
Hominidae (outlier)	H. sapiens	321	QIENSAAYKKAIAHYDQOMAEKVLPTETLQELLDLHASEKEAIEVFINKSFKDVHILFQKELAAQLEKKRDDFKQNM	400
Pteropodidae	P. alecto	399	KASSDRCSALLKDIHFPLEEDIKQGIYSKPGGYLFIQKMLKKKYLOEPRKGIOSEELQTYLIESKESVDAILOTQD	478
	P. giganteus	399	KASSDRCSALLKDIHFPLEEDIKQGIYSKPGGYLFIQKMLKKKYLOEPRKGIOSEELQTYLIESKESVDAILOTQD	478
	P. vampyrus	399	KASSDRCSALLKDIHFPLEEDIKQGIYSKPGGYLFIQKMLKKKYLOEPRKGIOSEELQTYLIESKESVDAILOTQD	478
	P. mesoamericanus	399	KASSDRCSALLKDIHFPLEEDIKQGIYSKPGGYLFIQKMLKKKYLOEPRKGIOSEELQTYLIESKESVDAILOTQD	478
	S. hondurensis	399	KASSDRCSALLKDIHFPLEEDIKQGIYSKPGGYLFIQKMLKKKYLOEPRKGIOSEELQTYLIESKESVDAILOTQD	478
	A. jamaicensis	399	KASSDRCSALLKDIHFPLEEDIKQGIYSKPGGYLFIQKMLKKKYLOEPRKGIOSEELQTYLIESKESVDAILOTQD	478
	P. discolor	399	KASSDRCSALLKDIHFPLEEDIKQGIYSKPGGYLFIQKMLKKKYLOEPRKGIOSEELQTYLIESKESVDAILOTQD	478
	P. hastatus	399	KASSDRCSALLKDIHFPLEEDIKQGIYSKPGGYLFIQKMLKKKYLOEPRKGIOSEELQTYLIESKESVDAILOTQD	478
	D. rotundus	399	KASSDRCSALLKDIHFPLEEDIKQGIYSKPGGYLFIQKMLKKKYLOEPRKGIOSEELQTYLIESKESVDAILOTQD	478
	E. fuscus	399	KASSDRCSALLKDIHFPLEEDIKQGIYSKPGGYLFIQKMLKKKYLOEPRKGIOSEELQTYLIESKESVDAILOTQD	478
Vespertilionidae	M. lucifugus	399	KASSDRCSALLKDIHFPLEEDIKQGIYSKPGGYLFIQKMLKKKYLOEPRKGIOSEELQTYLIESKESVDAILOTQD	478
	M. myotis	399	KASSDRCSALLKDIHFPLEEDIKQGIYSKPGGYLFIQKMLKKKYLOEPRKGIOSEELQTYLIESKESVDAILOTQD	478
	M. daubentonii	399	KASSDRCSALLKDIHFPLEEDIKQGIYSKPGGYLFIQKMLKKKYLOEPRKGIOSEELQTYLIESKESVDAILOTQD	478
	P. kuhlii	399	KASSDRCSALLKDIHFPLEEDIKQGIYSKPGGYLFIQKMLKKKYLOEPRKGIOSEELQTYLIESKESVDAILOTQD	478
Hominidae (outlier)	H. sapiens	401	KASSDRCSALLKDIHFPLEEDIKQGIYSKPGGYLFIQKMLKKKYLOEPRKGIOSEELQTYLIESKESVDAILOTQD	480
Pteropodidae	P. alecto	479	SLTEKEKEIEVQRVKAESAEEAAKMLEEMQIKNOQMMQEKEKSHEHVHVKLTETKMAERAQLMAEQERTVALKLQEQSRL	558
	P. giganteus	479	SLTEKEKEIEVQRVKAESAEEAAKMLEEMQIKNOQMMQEKEKSHEHVHVKLTETKMAERAQLMAEQERTVALKLQEQSRL	558
	P. vampyrus	479	SLTEKEKEIEVQRVKAESAEEAAKMLEEMQIKNOQMMQEKEKSHEHVHVKLTETKMAERAQLMAEQERTVALKLQEQSRL	558
	P. mesoamericanus	479	SLTEKEKEIEVQRVKAESAEEAAKMLEEMQIKNOQMMQEKEKSHEHVHVKLTETKMAERAQLMAEQERTVALKLQEQSRL	558
	S. hondurensis	479	SLTEKEKEIEVQRVKAESAEEAAKMLEEMQIKNOQMMQEKEKSHEHVHVKLTETKMAERAQLMAEQERTVALKLQEQSRL	558
	A. jamaicensis	479	SLTEKEKEIEVQRVKAESAEEAAKMLEEMQIKNOQMMQEKEKSHEHVHVKLTETKMAERAQLMAEQERTVALKLQEQSRL	558
	P. discolor	479	SLTEKEKEIEVQRVKAESAEEAAKMLEEMQIKNOQMMQEKEKSHEHVHVKLTETKMAERAQLMAEQERTVALKLQEQSRL	558
	P. hastatus	479	SLTEKEKEIEVQRVKAESAEEAAKMLEEMQIKNOQMMQEKEKSHEHVHVKLTETKMAERAQLMAEQERTVALKLQEQSRL	558
	D. rotundus	479	SLTEKEKEIEVQRVKAESAEEAAKMLEEMQIKNOQMMQEKEKSHEHVHVKLTETKMAERAQLMAEQERTVALKLQEQSRL	558
	E. fuscus	479	SLTEKEKEIEVQRVKAESAEEAAKMLEEMQIKNOQMMQEKEKSHEHVHVKLTETKMAERAQLMAEQERTVALKLQEQSRL	558
Vespertilionidae	M. lucifugus	479	SLTEKEKEIEVQRVKAESAEEAAKMLEEMQIKNOQMMQEKEKSHEHVHVKLTETKMAERAQLMAEQERTVALKLQEQSRL	558
	M. myotis	479	SLTEKEKEIEVQRVKAESAEEAAKMLEEMQIKNOQMMQEKEKSHEHVHVKLTETKMAERAQLMAEQERTVALKLQEQSRL	558
	M. daubentonii	479	SLTEKEKEIEVQRVKAESAEEAAKMLEEMQIKNOQMMQEKEKSHEHVHVKLTETKMAERAQLMAEQERTVALKLQEQSRL	558
	P. kuhlii	479	SLTEKEKEIEVQRVKAESAEEAAKMLEEMQIKNOQMMQEKEKSHEHVHVKLTETKMAERAQLMAEQERTVALKLQEQSRL	558
Hominidae (outlier)	H. sapiens	481	SLTEKEKEIEVQRVKAESAEEAAKMLEEMQIKNOQMMQEKEKSHEHVHVKLTETKMAERAQLMAEQERTVALKLQEQSRL	560
Pteropodidae	P. alecto	559	LKEGFQNESRQIHNIEIKNSMERP--RSTLTLS	591
	P. giganteus	559	LKEGFQNESRQIHNIEIKNSMERP--RSTLTLS	591
	P. vampyrus	559	LKEGFQNESRQIHNIEIKNSMERP--RSTLTLS	591
	P. mesoamericanus	559	LKEGFQNESRQIHNIEIKNSMERP--RSTLTLS	591
	S. hondurensis	559	LKEGFQNESRQIHNIEIKNSMERP--RSTLTLS	591
	A. jamaicensis	559	LKEGFQNESRQIHNIEIKNSMERP--RSTLTLS	591
	P. discolor	559	LKEGFQNESRQIHNIEIKNSMERP--RSTLTLS	591
	P. hastatus	559	LKEGFQNESRQIHNIEIKNSMERP--RSTLTLS	591
	D. rotundus	559	LKEGFQNESRQIHNIEIKNSMERP--RSTLTLS	591
	E. fuscus	559	LKEGFQNESRQIHNIEIKNSMERP--RSTLTLS	591
Vespertilionidae	M. lucifugus	559	LKEGFQNESRQIHNIEIKNSMERP--RSTLTLS	591
	M. myotis	559	LKEGFQNESRQIHNIEIKNSMERP--RSTLTLS	591
	M. daubentonii	559	LKEGFQNESRQIHNIEIKNSMERP--RSTLTLS	591
	P. kuhlii	559	LKEGFQNESRQIHNIEIKNSMERP--RSTLTLS	591
Hominidae (outlier)	H. sapiens	561	LKEGFQNESRQIHNIEIKNSMERP--RSTLTLS	592

Supplementary Figure 15. Multiple protein sequence alignment for bat GBP1. Grey boxes indicate identical residues. The four conserved motifs within the GTP-binding domain (G1-G4) and the carboxy-terminal isoprenylation (CaaX) motif are marked in purple and teal boxes, respectively. Newly identified motif that plays a role in the antiviral activity of EfGBP1 against EfPV (AV1) is marked in green. ClustalW alignment was generated using MacVector software. Human sequence was included as a comparator.



Supplementary Figure 16. Antiviral activity of GBP1. A549-ACE2 cells were transfected with 250 to 1000ng of HuGBP1, PaGBP1, or EfGBP1 for 24 hours, followed by infection with VSV-GFP (MOI 0.01) (**A-C**), HSV1- GFP (MOI 0.01) (**D-F**), H1N1-PR8 (MOI 0.01) (**G-H**), SARS-CoV-2 (MOI 0.01) (**I-J**), MERS-CoV (MOI 0.1) (**K-L**), VACV (MOI 0.01) (**M-N**), or EfPV (MOI 0.01) (**O-P**). Immunofluorescent microscopy was performed for VSV-GFP to quantify virus replication. Supernatant for all other viruses was titrated by TCID₅₀ or plaque assay (n=3; One-way ANOVA, Tukey's multiple comparisons test). Immunoblotting was performed to confirm FLAG-GBP1 expression. β -actin was used as loading control. VSV-GFP, H1N1, SARS-CoV-2, and MERS-CoV infection was further validated by probing for virus-specific proteins in immunoblots.



Supplementary Figure 17. Mutagenesis of GBP1. (A) A549-ACE2 cells were transfected with 250 to 1000ng of EfGBP1 wildtype (WT), deletion (Δ_{18-20}), or substitution (A₁₈AA) variant for 24 hours, followed by infection with EfPV (MOI 0.01) for 48 hours. Supernatant was titrated by plaque assay (n=3; One-way ANOVA, Tukey's multiple comparisons test). Cell lysates were probed for FLAG-GBP1 and ACTB. All samples in Figures 4F, 4G and S17 were processed together and were derived from three independent biological replicates. (B) A549-ACE2 cells were transfected with 250 to 1000ng of WT, Δ_{18-20} , or A₁₈AA for PaGBP1 for 24 hours, followed by infection with EfPV (MOI 0.01) for 48 hours. Cell lysates were probed for FLAG-GBP1 and ACTB. (C) Overexposed image of (B) to demonstrate reduced expression of PaGBP1(Δ_{18-20}).