**1** Supplemental information captions



(B)	RING domain	
Consensus	MASGIL×NIKEEVTCPICLELLTEPLSLDCGH×FCQACITANNRESMI×Q×GESSCPVCR×SYQP×NLRPN×H×ANIVE×LREVKLSP×E	
Eptesicus	Q.	88
Miniopterus		88 90
YubKT-1	VEE	89
Tb1.Lu-v2 Tb1.Lu-v1		90
Tb1.Lu-v3		5
Myotis brandtii Myotis lucifugus	. T VV. M. K	89
Desmodus		90
Phyllostomus	.DVEKL.QNMSGI.KW.MKTAD.	90
Rosellus		89
<b>C</b>		-
Entesicus		178
Efk3b		178
Miniopterus	.LE.T	180
Tb1.Lu-v2	IN R. G.F	180
Tb1.Lu-v1	IN	180
Myotis brandtii		5 179
Myotis lucifugus		179
Desmodus Phyllostomus	Q_N	180
Rosettus		179
	Exon 4 ← → Exon 6	_
Consensus	× VQD × FK × LRGIL × SEEQKELQRL × KEE × × L × DLAQAESELAQQ × QLL × DLISDLEHRLQGS × VEMLQDVNGIM × RSKTFTL × KPK × ×	
Eptesicus	KSC.H	268
Miniopterus	KF. YYV.Q. D. E. GDN.D. V. G. T KS.IK.Q.I.R. EAL	200
YubKT-1	ER Y. EH E DT K. EE RDD. K	269
Tb1.Lu-v2 Tb1.Lu-v1	QCY.EK.TE.KK. GNI.NY.H.D.S.V.KPS.K.I.M QCY.EK.TE.KK. GNI.NY.H.D.S.V.K	270
Tb1.Lu-v3	E.K	80
Myotis brandtii Myotis lucifuqus	KS.LYY.Q.K.ATE.AAEN.D	269 269
Desmodus	QICK. VF.DT. KK.VRDI.HE.SV.S.V.R.	270
Phyllostomus	QIC.NDK.AADI.HE.SV.SLV.R.M.E.YT.K	270
Rosellus		-05
	Exon 6 $\leftarrow$ Exon 7 $\leftarrow$ Exon 8 B30.2 domain V1 region	
Consensus	Exon 6 - Exon 7 - Exon 8 B30.2 domain V1 region	
Consensus Eptesicus	Exon 6 ← → Exon 7 ← → Exon 8     B30.2 domain     V1 region       × KQR VFQ PDL × MLQ FNELTD RRYWVH × TLDPP × K N × IS · DRRQVR     D     VLGSP × ITS6KHYWEV       STI.ARWVVVVTD.S.IV.AKPAFYLRTLYLYQKGNYE.YGPA	358
Consensus Eptesicus Efk3b	Exon 7 ← → Exon 8       B30.2 domain       V1 region         KQR VFQ PDL       NLQ FNELTD       RRYWWH       TLDPP       K N × IS DRRQVR       D       VLGSP × ITS6KHYWEV         STI.A.RW.V.V.V.V.V.TD.S.IV.A       KPAFYLRTLYLYQKGNYE.YG       P       A         STI.A.RR.V.N.NV       V       TD.S.IV.A       KPVFYLRTLYLYQKGNYE.YG       P         STI.A.RW.V.       V       TD.S.IV.A       KPVFYLRTLYLYQKGNYE.YG       P	358 358
Consensus Eptesicus Efk3b Miniopterus YubKT-1	Exon 6         Exon 7         Exon 8         B30.2 domain         V1 region           KQR         VFQ         PL         NLQ         FNELTD         RRYWVH         TLDPP         K/N         IS         DRRQVR         D         VLGSP         ITS6KHYWEV           ST         I.A.         RR.V.         V         V         TD         S.IV.A.         KPAFYLRTLYLYQKGNYE.YG         P.         A           ST         I.A.         RR.V.         NV         V         TD         S.IV.A.         KPVFYLRTLYLYQKGNYE.YG         P.         A           SK.         T.IRA         RR.V.         NV         V         TD         S.IV.A.         KVLRWSTDTLP <endyq.cd< td="">         RF.         A           SK.         T.IRA         RR.V.         A.Q.         F.SLLKNDPDVA.LQ.         KVLRWSTDTLP<endyq.cd< td="">         RF.         I           PK.VR.         G.         RKV.PAC         A.V.         TD         LVI.A.WKPAFYLRKLFLYQKGDYE.YG         PM         PM</endyq.cd<></endyq.cd<>	358 358 358 359
Consensus Eptesicus Eft3b Miniopterus YubKT-1 Tb1.Lu-v2 Tb1.Lu-v2	Exon 6 ←→ Exon 7 ←→ Exon 8       B30.2 domain       V1 region         X       KQR VFQ × P       P       L       NLQ FNELTD × RYWYH × TLDPP × K × N × IS × DRRQVR       D × VLGSP × ITSGKHYWEV         ST. I. A.       RW. V. V. V. TD.S. IV. A.       KYPAFYLRTLYLQKGNYE.YG       P.       A         ST. I. A.       RW. V. V. V. TD.S. IV. A.       KYPAFYLRTLYLQKGNYE.YG       P.       A         ST. I. A.       R.V. NV. V. TD.S. IV. A.       KYPAFYLRTLYLQKGNYE.YG       P.       A         ST. I. A.       R.V. NV. V. TD.S. IV. A.       KYPAFYLRTLYLQKGNYE.YG       P.       A         SK. T. IRV.       K A.M. A.Q.       F. SLKNDPDVA.L.Q.       KVLRWSTDTLP = ENDYQ.CD.       RF.       I         PK. VR. G.       RKV.PAC.       A.       V.       TD.E.VI.A.WKL.       PAFYLRKLFLYQKGDYE.YG.       PM         SK. GRA. A.       KG. VL.       AQ.       V.       MH.S.VI.E.Q.       PVFPSRTLYLHLRDRYE.YG.       L	358 358 358 359 360
Consensus Eptesicus Eft3b Miniopterus YubKT-1 Tb1.Lu-v2 Tb1.Lu-v1 Tb1.Lu-v3	Exon 6	358 358 358 359 360 268 80
Consensus Eptesicus Efk3b Miniopterus YubKT-1 Tb1.Lu-v2 Tb1.Lu-v3 Myotis brandtii	Exon 6         Exon 7         Exon 8         B30.2 domain         V1 region           X         KQR VFQ × P         DL × MLQ × FNÉLTD × RRYWÝH × TLDPP × K × N × XIS × DRRQVR         D × VLGSP × ITSGKHYWEV           ST. I. A.         RW. V. V. V. TD.S. IV. A.         KYAFYLRTLYLYQKGNYE.YG. P. A           ST. I. A.         RR. V. NV. V. TD.S. IV. A.         KYAFYLRTLYLYQKGNYE.YG. P. A           SK. T. IRV.         K. A. M. A.Q. F. SLLKNDPDVA. L.Q.         KVLRWSTTDTLP-ENDYQ.CD. RF. I           PK. VR. G.         RKV.PAC. A. V. TD.E. VI. A. WK. PAFYLRKLFLYQKGDYE.YG. PM.         SK. GRA. A. KG. VL. AQ. V. MH.S. VI. E.Q.           PM. T. L.A.         RGV.EA.T. AEA. S.E.V. TN.SIIV. E.        LRRSRFSYLF-GGDNM.FGI. S.	358 358 359 360 268 80 357
Consensus Eptesicus Efk3b Miniopterus YubKT-1 Tb1.Lu-v2 Tb1.Lu-v3 Myotis lucifugus Desmodus	Exon 6         Exon 7         Exon 8         B30.2 domain         V1 region           X         KQR VFQ × P         D         × VLGSP × ITSGKHYWEV         D         × VLGSP × ITSGKHYWEV           ST. I. A.         RW. V. V. V. TD.S. IV. A.         KYAFYLRTLYLYQKGNYE.YG. P. A         KYAFYLRTLYLYQKGNYE.YG. P. A           ST. I. A.         RR. V. NV. V. TD.S. IV. A.         KYAFYLRTLYLYQKGNYE.YG. P. A           SK. T. IRV.         K- A.M. A.Q. F. SLLKNDPDVA. L.Q.         KVLRWSTTDTLP-ENDYQ.CD. RF. III           PK. VR. G.         RKV.PAC. A. V. TD.E.VI. A.MK. PAFYLRKLFLYQKGDYE.YG. PM. SK.GRA. A. KG. VL. AQ. V. MH.S.VI. E.Q. PVFPSRTLYLHLRDRYE.YG. L.           PM. T.L.A.         RGV.EA.T. AEA.S.E.V. TN.SIIV. E. LRRSRFSYLF-GGDMM.FGI. S.           PM. R. RA.         GG. V. V. H. V. TD.SYNV.E. SLELL           PM. R. RA         GG. V. V. H. V. TD.SYNV.E. SLELL	358 358 359 360 268 80 357 354 353
Consensus Eptesicus Efk3b Miniopterus YubKT-1 Tb1.Lu-v2 Tb1.Lu-v2 Tb1.Lu-v3 Myotis brandtii Myotis brandtii Myotis brandtii Desmodus Desmodus	Exon 6         Exon 7         Exon 8         B30.2 domain         V1 region           X         KQR VFQ × P         DL         MLQ         FNELTD         RRYWYH         TLDPP         XK × X × XS         DR         VLGSP × ITSGKHYWEV           ST.         I.         A.         RW.         V.         V         TD         S. IV. A.         KPAFYLRTLYLYQKGNYE.YG         P.         A           ST.         I.         A.         RW.         V.         V.         TD         S. IV. A.         KPAFYLRTLYLYQKGNYE.YG         P.         A           SK.         T. I. A.         RK.         V.         NV         TD         S. IV. A.         KPAFYLRTLYLYQKGNYE.YG         P.         A           SK.         T. IRV         K.         A.         RV         TD         S. VI. A.         KPAFYLRTLYLYQKGNYE.YG         P.         A           SK.         T. IRV         K.         A.         Q.         F. SLLKNDPDVA.L.Q.         KVLRWSTTDTLP-ENDYQ.CD.         RF.         IA           PK.         V.         A.         V.         TD E. VI. A. WK.RWSTTDTLP-ENDYQ.CD.         RF.         PM.           SK. GRA.A.         KG.         V.         AQ         MH.S. VI. E.Q.         PAFYLRKLFLYQKGDYE.YG.<	358 358 359 360 268 80 357 354 353 353
Consensus Eptesicus EftR3b Miniopterus YubKT-1 Tb1.Lu-v2 Tb1.Lu-v2 Tb1.Lu-v3 Myotis Jucifugus Desmodus Phyllostomus Rosettus	Exon 6         Exon 7         Exon 8         B30.2 domain         V1 region           X         KQR VFQ VP         DL         MLQ         FNELTD         RRYWYH         TLDPP         K N × XIS         DRRQVR         D         VLGSP         ITSGKHYWEV           ST.         I.         A.         RW         V         V         TD         S. IV. A.         KPAFYLRTLYLYQKGNYE.YG         P.         A           ST.         I.         A.         RW         V         V         TD         S. IV. A.         KPAFYLRTLYLYQKGNYE.YG         P.         A           SK.         T. I. A.         RK         V         NV         V         TD         S. IV. A.         KPAFYLRTLYLYQKGNYE.YG         P.         A           SK.         T.I.V.         K-         A.         M.         Y.         TD         S. IV. A.         KPAFYLRTLYLYQKGNYE.YG         P.         A           SK.         T.I.V.         K-         A.         M.         Q.         F.         SLLKNDPDVA         L.Q.         KVLRWSTTDTLP-ENDYQ.CD.         RF         A           SK.         GRA.         A.         Q.         V         MH.S.         VI.         E.         PAFYLRKLFLYQKGDYE.YG         PM	358 358 359 360 268 80 357 354 353 353 353
Consensus Eptesicus EftS3b Miniopterus YubKT-1 Tb1.Lu-v2 Tb1.Lu-v3 Myotis brandtii Myotis brandtii Myotis brandtii Myotis brandtii Rosettus	Exon 6 ← → Exon 7 ← → Exon 8         B30.2 domain         V1 region           X         KQR VFQ         POL<: NLQ : FNÉLTD         RRYWÝH / TLDPP         K × N × IS         DRRQVR         D         VLGSP : ITSGKHYWEV           ST. I. A.         RW. V. V. V. V. TD.S. IV. A.         KPAFYLRTLYLYQKGNYE.YG         P. A           ST. I. A.         RR. V. NV. V. TD.S. IV. A.         KPAFYLRTLYLYQKGNYE.YG         P. A           ST. I. A.         RR. V. NV. V. TD.S. IV. A.         KPAFYLRTLYLYQKGNYE.YG         P. A           SK. T. IRV.         K. A. M. A.Q.         F. SLLKNDPDVA.L.Q.         KVLRWSTDTLP = FNDYQ.CD.         RF	358 358 359 360 268 80 357 354 353 353 359
Consensus Eptesicus EftS3b Miniopterus YubKT-1 Tb1.Lu-v2 Tb1.Lu-v3 Myotis brandtii Myotis brandtii Myotis brandtii Myotis brandtii Ryslostomus Rosettus Consensus	Exon 6	358 358 359 360 268 80 357 354 353 353 359
Consensus Eptesicus ErR3b Miniopterus YubKT-1 Tb1.Lu-v1 Tb1.Lu-v1 Tb1.Lu-v3 Myotis brandtii Myotis brandtii Myotis brandtii Desmodus Phyliostomus Rosettus Consensus Eptesicus ErR3b	Exon 6 ←→ Exon 7 ←→ Exon 8       B30.2 domain       V1 region         XX       KQR VFQ P       P       LX       MLQ FNELTD       RRYWYH × TLDPP       X KN × XIS       D × VLGSP × ITSGKHYWEV         ST. I. A.       RW. V. V. V. TD.S. IV. A.       KPAFYLRTLYLQKGNYE.YG. P. A         ST. I. A.       RR. V. NV. V. TD.S. IV. A.       KPAFYLRTLYLQKGNYE.YG. P. A         SK. T. I.RV.       K. A.M. A.Q.       F.SLKNDPDVA.L.Q.       KVLRWSTDTLP-ENDYQ.CD. RF. I         PK. VR. G.       RKV.PAC. A.       V. TD.E. VI. A. WK. PAFYLRTLYLYQKGNYE.YG. PM.       SK         SK. GRA. A.       KG. VL. A.Q.       V. TD.E. VI. A. WK. PAFYLRTLYLQKGNYE.YG. PM.       SK         PM. T. L.A.       RGV.EA.T. AEA.S.E.V. TN.SIIV.E.       - LRRSRFSYLF-GGDNM.FGI. S.       SK         PM. R. RA.       GG. V. V. H. V. TD.SYNV.E.       SLPL YILDAVINFG.S.       SK         SKE. R. V.       NE. A. V. I.Q.SHD.Q.VA.A.       YEHHL DANKNASA.LV.       SK         SKE. R. V.       NE. A. V. I.Q.SHD.Q.VA.A.       YEHHL DANKNASA.LV.       SK         V2 region       V2 region       V3 region       V3 region         DVS' K×AW       LGVYG K PDS       Q       Q       Q       SV REYKAF DS       SS          TD.Y. V. V. C.       NMMDFVKQGKKR.HVC.QY. KY.       HS. V. D. D	358 358 359 360 268 80 357 354 353 353 359 442 442
Consensus Eptesicus ErR3b Miniopterus YubKT-1 Tb1.Lu-v1 Tb1.Lu-v3 Myotis brantlii Myotis brantlii Desmodus Phyllostomus Rosettus Consensus Eptesicus ErR3b Miniopterus	Exon 7 → Exon 8       B30.2 domain       V1 region         XX KQR VFQ P         DLX MLQ FNELTD RRYWYH TLDPP XK NN XIS DRRQVR         XK NN XIS DRRQVR         ST. I. A.       RW. V. V. V. TD.S. IV. A.       KPAFYLRTLYLQKGNYE.YG. P. A         ST. I. A.       RW. V. V. V. TD.S. IV. A.       KPAFYLRTLYLQKGNYE.YG. P. A         SK. GRA. A.         SK. GRA. A.       M. A.Q. F. SLLKNDPDVA. L.Q.       KVLRWSTDTLP-ENDYQ.CD. RF. II         PK. VR. G. RKV PAC. A. V. TD.E.VI. A.WK. PAFYLRKLFLQKGDYE.YG. PM.         SK. GRA. A.       KG. VL. AQ. V. TD.E.VI. A.WK. PAFYLRKLFLQKGDYE.YG. PM.         SK. GRA. A.       KG. VL. AQ. V. TD.E.VI. A.WK. PAFYLRKLFLQKGDYE.YG. PM.         PM. T. L.A.         RGV. PAC. A. V. TD.SIVV.E.         VPFPSRTLYLH.RDRYE.YG. PM.         SK.GRA. A.         KG.V. V. H. V. TD.SIVV.E.         VIENDEL OF PSRTLYLH.RDRYE.YG. PM.         ST.R. A. SG. V. V. H. V. TD.SIVV.E.         SIVENDEL OF PSRTLYLH.RDRYE.YG. PM.         SIVENDEL OF PSRTLYLH.RDRYE.YG. PM.         SIVENDEL OF PSRTLYLH.RDRYE.YG. PM.         SIVENDEL OF PSRTLYLH.RDRYE.YG. PM.         SIVENDE	358 358 358 359 360 268 80 357 354 353 353 359 442 442 442
Consensus Eptesicus Eft&3b Miniopterus YubKT-1 Tb1.Lu-v1 Tb1.Lu-v3 Myotis buarditus Desmodus Phyllostomus Rosettus Consensus Eptesicus Eft&3b Miniopterus YubKT-1 Tb1.Lu-v2	Exon 6 ← → Exon 7 ← → Exon 8       B30.2 domain       V1 region         X       KQR VFQ P       P       D       VLGSP×ITSGKHYWEV         ST. I. A.       RW. V. V. V. TD.S. IV. A.       KPAFYLRTLYLQKGNYE.YG. P. A         ST. I. A.       RR. V. NV. V. TD.S. IV. A.       KPAFYLRTLYLQKGNYE.YG. P. A         SK. GRA. A.       K. N. A. Q. F. SLLKNDPDVA. L.Q.       KVLRWSTDTLP-ENDYQ.CD. RF. I.I         PK. VR. G.       RKV.PAC. A. V. TD.E.VI. A. WK. PAFYLRTLYLQKGYE.YG. P. A         SK. GRA. A.       KG. V. V. TD.S. IV. A.       KPVFYLRTLYLQKGNYE.YG. P. A         PK. VR. G.       RKV.PAC. A. V. TD.E.VI. A. WK. PAFYLRTLYLQKGNYE.YG. P. A         SK. GRA. A.       KG. V. V. TD.S.IV. A.       KVLRWSTDTLP-ENDYQ.CD. RF. I.I         PK. VR. G.       RKV.PAC. A. V. TD.E.VI. A.WK. PAFYLRKLFLQKGDYE.YG. PM. S         SK. GRA. A.       KG. VL. AQ. V. MH.S. VI.E.Q. PVFPSRLVLIRDRYE.YG. L.         SK. GRA. A.       KG. V. V. H. V. TD.SIVV.E.       LRSRFSYLF-GGDNM.FGI. S.         ST. R. A.       SG. V. V. H. V. TD.SYNV.E.       SLPLLYIADKINFG. S.         ST. R. A.       SG. V. V. LI KN.Q. VA. A.       YEHHLDANKKASA. LV.         SKE. R. V.       NE. A. V. II.Q.SMD.Q. VA. A.       YEHHLDANKKASA. LA         PK. RM.V.       RG. V. V. V. MI.L.ENNP.VA. A.       YUVCVCKNSPWNDNCN.YS. S.         V2 region       V3 re	358 358 359 360 268 80 357 354 353 353 359 442 442 442 436 443 444
Consensus Eptesicus ER3b Miniopterus YubKT-1 Tb1.Lu-v2 Tb1.Lu-v3 Myotis brandtii Myotis lucifugus Desmodus Phyllostomus Rosettus Consensus Eptesicus ER3b Miniopterus YubKT-1 Tb1.Lu-v2	Exon 6	358 358 359 360 268 80 357 354 353 353 353 359 442 442 436 443 444 268
Consensus Eptesicus ER-3b Miniopterus YubKT-1 Tb1.Lu-v2 Tb1.Lu-v2 Tb1.Lu-v3 Myotis brandtii Myotis brandtii Myotis brandtii Myotis brandtii Phyllostomus Rosettus Consensus Eptesicus Eptesicus Eptesicus Eptesicus Tb1.Lu-v3 YubKT-1 Tb1.Lu-v3 Miniopterus YubKT-1 Tb1.Lu-v3	Exon 6	358 358 359 360 268 80 357 354 353 359 442 442 436 443 444 268 80 441
Consensus Eptesicus Eft&3b Miniopterus YubKT-1 Tb1.Lu-v1 Tb1.Lu-v3 Myotis brandtii Myotis bucifugus Phyllostomus Rosettus Consensus Eft&3b Miniopterus YubKT-1 Tb1.Lu-v1 Tb1.Lu-v3 Myotis brandtii Myotis brandtii Myotis brandtii Myotis brandtii	Exon 8 → Exon 7 → Exon 8         B30.2 domain         V1 region           X         KQR VFQ         PL         NLQ FNELTD         RRYWYH TLDPP         K         N:XIS         D         VLGSP ITS6KHYWEV           ST. I. A.         RW. V. V. V. V. TD.S. IV. A.         KPAFYLRTLYLQKGNYE.YG. P. A           ST. I. A.         RR. V. NV. V. TD.S. IV. A.         KPAFYLRTLYLQKGNYE.YG. P. A           SK. T. IRV.         K. A. M. A.Q.         F.SLKNDPDVA.L.Q.         KVURWSTDTLP-ENDYQ.CD. RF. I           PK. VR. G.         RKV. PAC.         A. W. V. TD.STIV.A.         KPAFYLRKLFLYQKGDYE.YG. P. A           SK. GRA.A.         KG. VL. AQ.         V. TD.S.IV.A.         KPVFYLRLLLYQKGVE.YG.P. A           PK. VR. G.         RKV. PAC.         A.         WKIRSTDTLP-ENDYQ.CD. RF. I         I           SK. GRA.A.         KG. VL. AQ.         V. TD.STIV.E.         PL         RIKKGPKEYKGINE.YG.           PM. T. L.A.         RGV.EA.T. AEA.S.E.V.         TN.SIIV.E.         LRRSRFSYLF-GGDDM.FGI.S.         ST           PM. R. RA.GG. V.         V. H. V. TD.SYNV.E.         SLPLIYILDKINFG.S.         ST         RA           SKE. R. V.         NE. A.         V. O. TO.SYNV.BONG.VA.A.         NYEHHLDANTKASA.LV.         SKE           PKRM.V.         YG.GONV.V.         MI.L.ENNP.VA.A.         YCVCNKN	358 358 359 360 268 80 357 354 353 353 353 353 355 359 442 442 436 443 444 268 80 441 438
Consensus Eptesicus Erk3b Miniopterus YubKT-1 Tb1.Lu-v1 Tb1.Lu-v1 Tb1.Lu-v1 Tb1.Lu-v3 Myotis brandtii Myotis brandtii Myotis brandtii Eptesicus Erk3b Miniopterus YubKT-1 Tb1.Lu-v2 Tb1.Lu-v3 Myotis brandtii Myotis brandtii Myotis brandtii Myotis brandtii	Exon 6 → Exon 7 → Exon 8         B30.2 domain         V1 region           XX         KQR VFQ P         P         D         VLGSP ITSGKHYMEV           ST. I. A.         RW. V. V. V. V. TD.S. IV. A.         KPAFYLRTLYLQKGNYE.YG. P. A           ST. I. A.         RW. V. V. V. TD.S. IV. A.         KPAFYLRTLYLQKGNYE.YG. P. A           SK. T. I.RV.         K. N. V. V. V. TD.S. IV. A.         KPAFYLRTLYLQKGNYE.YG. P. A           SK. T. I.RV.         K. A.M. A.Q.         F. SLLKNDPDVA.L.Q.         KVLRWSTTDTLP-ENDYQ.CD. RF. I           PK.VR. G.         RKV.PAC.         A.V. V. TD.E.VI.A. WKLRWSTTDTLP-ENDYQ.CD. RF. I         I           PMT.L.A.         RGV.PAC.         A.V. TD.E.VI.A. WKLRWSTTDTLP-ENDYQ.CD. RF. I         I           PM. R.R. GG.V.         V. TD.STIV.E.         LRRSRFSYLF-GGDDM.FGI.S.         S           ST. R. A.         SG.V.         V. TD.SYNV.E.         SLPLYIDADKINFG.S.         S           SKE. R.V.         N.B. A.V.         I.Q.SMD.Q.VA.A.         YUCHHLDANKASA.LA         KA           PKRM.V.         RG.V.         V. II.Q.SMD.Q.VA.A.         YUCKNSPYWNDNCN.YS.S.         S           V2 region         V2 region         V3 region         V3 region           V2 region         V3 region         V3 region           V2 v. V.C.         NMMD	358 358 359 360 268 80 268 80 357 354 353 353 353 353 359 442 442 436 443 444 268 80 441 438 421
Consensus Eptesicus Erk3b Miniopterus YubKT-1 Tb1.Lu-v1 Tb1.Lu-v1 Tb1.Lu-v3 Myotis brandtii Myotis brandtii Myotis brandtii Rosettus Consensus Eptesicus Erk3b Miniopterus YubKT-1 Tb1.Lu-v1 Tb1.Lu-v3 Hyubis brandtii Tb1.Lu-v3 Hyubis brandtii Ph.Lu-v3 Hyubis brandtii Rosettus Desmodus Phyliostomus Rosettus	Exon 6 → Exon 7 → Exon 8         B30.2 domain         V1 region           XX         KQR VFQ P         P         DL × MLQ FNELTD × RRYWYH × TLDPP × K×N××IS × DRRQVR         D × VLGSP×ITSGKHYWEV           ST. I. A.         RW. V. V. V. V. TD.S. IV. A.         KPAFYLRTLYLQKGNYE.YG. P. A           ST. I. A.         RR. V. NV. V. TD.S. IV. A.         KPAFYLRTLYLQKGNYE.YG. P. A           SK. T. I.RV.         K. A. M. A.Q.         F. SLLKNDPDVA.L.Q.         KVLRWSTTDTLP-ENDYQ.CD. RF. I           PK.VR. G.         RKV.PAC.         A.         V. TD.E.VI.A.         WKLRWSTTDTLP-ENDYQ.CD. RF. I           SK.GRA.A.         KG.VL. AQ.         V. TD.S.TV.A.         KPFYLRLLLUKKGDVE.YG. P. A           SK.GRA.A.         KG.VL.AQ.         V. TD.S.TV.A.         KPFYLRLLLUKKGDVE.YG. P. A           SK.GRA.A.         KG.VL.AQ.         V. TD.S.TV.A.         PFNKLKLLUKGDVE.YG. P. A           SK.GRA.A.         KG.VL.AQ.         V. TD.S.TV.A.         PFNKLKLLUKGDVE.YG. P. A           SKE.R.V.         N.H. A.Q. V. TD.STVV.E.         SLPLFYITADKINFGG.S.         S.           ST.R.A.         SG.V. V. H. V. TD.STVV.E.         SLPLFYITADKINFGG.S.         S.           SKE.R.V.V.         NE.A. V. H.H.LENNV.A.A.         YEHLYATADKINFG.S.         S.           V. RG.V.V.V.         MI.L.ENNV.A.A.         YEHLYATAKASA. <th>358 359 360 268 80 357 354 353 353 353 353 353 354 442 442 442 436 80 441 438 80 441 438 421 443</th>	358 359 360 268 80 357 354 353 353 353 353 353 354 442 442 442 436 80 441 438 80 441 438 421 443
Consensus Eptesicus Erk3b Miniopterus YubKT-1 Tb1.Lu-V1 Tb1.Lu-V3 Myotis brandtii Ayotis brandtii Desmodus Phyllostomus Rosettus Consensus Eptesicus Erk3b Miniopterus YubKT-1 Tb1.Lu-V3 Myotis brandtii Tb1.Lu-V3 Myotis brandtii Desmodus Phyllostomus Rosettus	Exon 6 → Exon 7 → Exon 8         B30.2 domain         V1 region           XX         KQR V FQ × P         D         VLGSP×ITS6KHYWEV           ST. I. A.         RW. V. V. V. V. TD.S. IV. A.         KPAFYLRTLYLQKGNYE.YG. P. A           ST. I. A.         RR. V. NV. V. TD.S. IV. A.         KPAFYLRTLYLQKGNYE.YG. P. A           SK. T. I. RV.         K. N. V. TD.S. IV. A.         KPAFYLRTLYLQKGNYE.YG. P. A           SK. T. I. RV.         K. A. M. A. Q. F. SLLKNDPDVA. L. Q.         KVLRWSTTDTLP-ENDYQ.CD. RF. II           PK. VR. G.         RKV.PAC. A. V. TD.E. VI. A. WK. PAFYLRKLFLYQKGDYE.YG. PM.         SK           SK. GRA. A.         KG. VL. AQ. V. TD.E. VI. A. WK. PAFYLRLFLYQKGDYE.YG. PM.         SK           PM. R. RA.         GG. V. V. TD.S. IV. A.         KPVFYLRKLFLYQKGDYE.YG. PM.           SK. GRA. A.         KG. VL. AQ. V. TD.E. VI. A.WK. PAFYLRKLFLYQKGDYE.YG.         PM.           PM. R. RA.         GG. V. V. H. V. TD.SIV.E.         LRSRFSYLF-GGDNM.FGIS.           ST. R. A.         SG. V. V. H. V. TD.SYNV.E.         SLPLICYILADKINFG.S.           ST. R. A.         SG. V. V. U. II. (SND Q.VA.A. M. YEHHL DANKNASA. LV.           SKE. R. V.         NE. A. V. O. MIL.ENP.VA.A.         YUVCVCKNSPYWNDNCN.YS. S.           VZ region         V3 region           V2 region         V3 region           V2 region	358 358 359 360 268 80 357 354 353 353 353 353 353 359 442 442 438 444 268 80 441 438 80 441 438 80
Consensus Eptesicus Erk3b Miniopterus YubKT-1 Tb1.Lu-V1 Tb1.Lu-V3 Myotis brandtii Myotis brandtii Ayotis brandtii Ayotis brandtii Erk3b Miniopterus YubKT-1 Tb1.Lu-V3 Myotis brandtii Myotis brand	Exon 6 ← → Exon 7 ← → Exon 8         B30.2 domain         V1 region           XX         KQR VFQ × P         P         DL × MLQ FNELTD × RRYWYH × TLDPP × K × N × XIS × DRRQVR         XX × XX	358 358 359 360 268 80 357 354 353 353 353 353 353 353 353 353 359 442 442 442 443 444 443
Consensus Eptesicus Entesicus Entesib Miniopterus YubKT-1 Tb1.Lu-v1 Tb1.Lu-v3 Myotis brantlii Desmodus Phyllostomus Rosettus Consensus Entesicus EftR3b Miniopterus YubKT-1 Tb1.Lu-v3 Myotis lucifugus Desmodus Phyllostomus Rosettus Consensus Eptesicus Eptesicus Eptesicus	Exon 8 → Exon 7 → Exon 8         B30.2 domain         V1 region           XX         KQR VFQ POL         NLQ FNELTD         RRYWYH TLDPP         KX W X IS         DR VLGSP         D         VLGSP         ITSGKHYWEV           ST. I. A.         RW. V. V. V. V. TD.S. IV. A.         KPAFYLRTLYLYQKGNYE.YG         P. A           ST. I. A.         RR. V. NV. V. TD.S. IV. A.         KPAFYLRTLYLYQKGNYE.YG         P. A           SK. T. IRV.         K. A. M. A.Q.         F. SLLKNDPDVA.L.Q.         KVLRWSTDTLP-ENDYQ.CD.         RF.         I           PK. VR. G.         RKV.PAC.         A. V. TD.S. IV. A.         KVLRWSTDTLP-ENDYQ.CD.         RF.         I           SK. GRA.A.         KGVL. AQ.         V. TD.STNV.E.         PVFPSRTLYLKLFLYQKGDYE.YG         PM.           SK. GRA.A.         KGV.EA.T. AEA.S.E.V.         TN SIIV.E.         PKVRKGVERKFFYLF         PGDMM.FGI.S.           PM. T.L.A.         RGV.EA.T. AEA.S.E.V.         TN SIIV.E.         -LRRSRFSYLF-GGDNM.FGI.S.         SS           ST. R. A. SG.V.         V.H. V.         TD SYNV.E.         SLPLIYILADKINFG.S.         SS           VZ region         V3 region         V3 region         V3 region           V2 region         V3 region         V3 region           VS KAW L6VYG K PDS         QS	358 358 359 268 80 357 353 353 353 353 353 355 442 442 442 442 443 444 268 80 441 438 80 441 438 421 443
Consensus Eptesicus EftS3b Miniopterus YubKT-1 Tb1.Lu-v1 Tb1.Lu-v3 Myotis brandtii Myotis brandtii Myotis brandtii Consensus Eptesicus EftS3b Miniopterus YubKT-1 Tb1.Lu-v3 Myotis brandtii Myotis Brandtii Miniopterus Brandtii Myotis Brandtii Myotis Brandtii Myotis Brandtii Myotis Brandtii Myotis Brandtii Myotis Brandtii Myotis Brandtii Miniopterus Brandtii Myotis Brandtii Myotis Bra	Exon 6         Exon 7         Exon 8         B30.2 domain         V1 region           VX         KQR_VFQ_PDL         NLQ_FNELTD_RRYWYH_TLDPP>         K N_XIS_DRRQVR         D_XVLGSP_ITSGKHYWEV           ST.         I. A.         RR         V.         V.         V.         TD.S. IV. A.         KPAFYLRTLYLYQKGNYE.YG         P.         A           ST.         I. A.         RR.V.         V.         V.         TD.S. IV. A.         KPAFYLRTLYLYQKGNYE.YG         P.         A           SK.         T.T.I. A.         RR.V.         N.V.         V.         TD.S. IV. A.         KPAFYLRTLYLYQKGNYE.YG         P.         A           SK.         G.         RKV.PAC         A.         Q.         TD.S. IV. A.         KVLRVSTDIP-ENDYQ.CD.         RF.         I           SK.         G.         RKV.PAC         A.         AQ         V.         TD.S.IV.A.         NEW KLEFVQKOVED.         RF.         I           SK.         G.RAV.PAC         A.         AQ         V.         TD.S.IV.A.         NEW KLEFVQKOVED.         RF.         I           PM.         R.K.S.         RA.         AQ         V.         TD.S.IV.A.         SPLI-STITLHLEDPYKYH.         RG.         SST.           PM.         T.L.A.<	358 358 359 268 80 357 353 353 353 353 353 354 442 442 442 442 442 442 443 444 443 444 443 441 443
Consensus Eptesicus Eft3b Miniopterus YubKT-1 Tb1.Lu-v1 Tb1.Lu-v3 Myotis brandtii Myotis lucifugus Desmodus Phyllostomus Rosettus Consensus Eptesicus Eft3b Miniopterus YubKT-1 Tb1.Lu-v3 Myotis brandtii Myotis brandtii Myotis brandtii Myotis brandtii Myotis brandtii Rosettus Consensus Eptesicus Eft3b Miniopterus YubKT-1	Exon 6 → Exon 7 → Exon 8         B30.2 domain         V1 region           X         KQR VFQ PDL MLQ FNELTD RRYWH TLDPP × K N × 15 DRRQV         D         VLGSP ITSGKHYWEV           ST. I. A.         RW V V V V V TD.S. IV A.         KPAFYLRTLYLYQKGNYE YG P. A           ST. I. A.         RW V V. V V TD.S. IV A.         KPAFYLRTLYLYQKGNYE YG P. A           SK. T. IRV         K. K. A. M. A.Q.         F. SLLKNDPDVA LQ V. KWSTDTD-PENDYQ CD. RF         T           SK. GRA.A.         KG. VL AQ         V TD.S. IV A.         KVLWSTDTD-PENDYQ CD. RF         T           SK. GRA.A.         KG. VL AQ         V TD.S. IV A.K.         PAFVLRTLFLVQKGNYE YG         PM           SK. GRA.A.         KG. VL AQ         V TD.S. IV A.K.         PAFVLRTLFLVQKGNYE YG         PM           SK. GRA.A.         KG. VL AQ         V TD.S. IV A.K.         PAFVLRTLFLVQKGNYE YG         PM           SK. GRA.A.         KG. VL AQ         V TD.S. IV A.K.         PAFVLRTLFLVQKGNYE YG         PM           SK. GRA.A.         SG V V H. V         TD.SYNV.E         SLPLLYILADKTBYEG         S.           ST.R. R.A.         SG V V H. V. I. KN.Q.VA.A.         YEHHL         DANKASA.LA         V.           PK. R.R.A.         SG V V V MI L ENNP.VA.A.         YUVCVCNKNSPWNDUCN YS         S.           VZ region	358 358 359 360 268 80 357 354 353 353 353 353 359 442 442 436 443 444 268 80 441 438 421 443
Consensus Eptesicus Erk3b Miniopterus YubKT-1 Tb1.Lu-V1 Tb1.Lu-V1 Tb1.Lu-V3 Myotis brandtii Myotis brandtii Ayotis brandtii Eptesicus Erk3b Miniopterus YubKT-1 Tb1.Lu-V3 Myotis brandtii Myotis brandtii Myotis brandtii Myotis brandtii Myotis brandtii Myotis brandtii Myotis brandtii Rosettus Erk3b Miniopterus Phyllostomus Rosettus Erk3b Miniopterus YubKT-1 Tb1.Lu-V3 Myotis brandtii Myotis brandtii Myotis brandtii Myotis brandtii Myotis brandtii Myotis brandtii Myotis brandtii Myotis brandtii Myotis brandtii Myotis brandtii Tb1.Lu-V3 Myotis brandtii Tb1.Lu-V3 Myotis brandtii Tb1.Lu-V3 Tb1.Lu-V3 Tb1.Lu-V3 Tb1.Lu-V3 Tb1.Lu-V3 Myotis brandtii Tb1.Lu-V3 Tb1.Lu-	Exon 6         Exon 7         Exon 8         B30.2 domain         V1 region           ST. I. A. RW. V. V. V. V. TD.S. IV. A. KPAFYLRTLYLYQKGNYE.YG. P. A.         N. KPAFYLRTLYLYQKGNYE.YG. P. A.           ST. I. A. RW. V. V. V. V. TD.S. IV. A. KPVFYLRTLYLYQKGNYE.YG. P. A.         SK. ST. I. A. RW. V. Y. V. TD.S. IV. A. KPVFYLRTLYLYQKGNYE.YG. P. A.           SK. J. I. A. RW. V. Y. V. V. TD.S. IV. A. KPVFYLRTLYLYQKGNYE.YG. P. A.         SK. ST. A. RW. K. A. M. A.Q. F. SLLKNDPVA. L.Q. KVLWSTDTLP-FNDVQ.CD. RF. I.           SK. GRA. A. KG. V. PAC. A. V. TD. S. IV. A. K. VARSTDTLP-FNDVG.CD. RF. I.         SK. GRA. A.           SK. GRA. A. KG. VL. AQ. V. MH.S.VI.E.Q. PVFPSRTLYLHENRYE.YG. L.         PM. SLEAR. S.E.V. TN.SIIV.ELRRSRFSYLF-GGDNM.FGI.S.           PM. R. RA. GG. V. V. H. V. TD.SYNV.E. SLPLLYIADKTNFG.S.         S.           ST. R. A. SG. V. V. H. V. TD. SYNV.E. SLPLLPANKNASA. LV.         SKE.R. V. NE A. V. T. Q. SMD.Q.VA. A. YEHHLDANKNASA. LV.           V2 region         V2 region         V3 region           V2 region         V3 region         V4 region           V2 region         V2 reg	358 358 359 360 268 80 357 354 353 353 353 353 359 442 442 436 443 444 268 80 441 438 421 443
Consensus Eptesicus ER3b Miniopterus YubKT-1 Tb1.Lu-v1 Tb1.Lu-v3 Myotis brandtli Myotis brandtli Myotis brandtli Entsib Miniopterus YubKT-1 Tb1.Lu-v1 Tb1.Lu-v1 Tb1.Lu-v3 Myotis brandtli Myotis brandtli Myotis brandtli Bucituus Desmodus Phyllostomus Rosettus Consensus Entsib Miniopterus Phyllostomus Rosettus Entsib Miniopterus Phyllostomus Entsib Miniopterus Phyllostomus Entsib Miniopterus Phyllostomus Entsib Miniopterus YubKT-1 Tb1.Lu-v3 Entsib Miniopterus Phylostomus Entsib Miniopterus YubKT-1 Tb1.Lu-v3 Entsib Miniopterus YubKT-1 Tb1.Lu-v3 Myotis Lu-v3 Miniopterus Phylostomus Entsib Miniopterus Phylostomus Phylostomus Entsib Miniopterus Phylostomus Entsib Miniopterus Phylostomus Entsib Miniopterus Phylostomus Entsib Miniopterus Phylostomus Entsib Phylostomus Entsib Phylostomus Entsib Phylostomus Phylostomus Entsib Phylostomus Phylost	Exon 6         Exon 7         Exon 8         B30.2 domain         V1 region           VI cglon         VI cglon         VI cglon         VI cglon         VI cglon           Str. I. A.         RW. V. V. V. V. TD, S. IV. A.         KPAFYLRTLYLYQKGNYE, YG. P. A.         A           Str. I. A.         RR. V. NV. V. TD, S. IV. A.         KPAFYLRTLYLYQKGNYE, YG. P. A.         A           Str. I. A.         RR. V. A. M. A.Q. F. SLLKKDPDVA. L.Q.         KVLRWSTDTLP-ENDQ.CD. RF. I.         P           Sk. GRAV.A.         A.G. RVV.PAC. A. V. TD.E.V. I.A. WK. PAFYLRTLYLYQKGNYE, YG. P. A.         A           Sk. GRAV.A.A.         G. RVV.PAC. A. V. TD.E.V. I.A. WK. PAFYLRKLFLYGKGDYE, YG. P. M.         SK.GRAV.           PM. T.L.A.         RGV.EA.T. AEA.S.E.V. TN.SIIV.E.         -LRRSRFSYLF-GGDNM.FGI.S.         S.           PM. R.R.A.         GG. V. V.H. V. TD.STWV.E.         SLPLYIIADKTWFG.SS.         S.           Str. R. A.         SG.V. V.H. V. TD.STWV.E.         SLPLDANKKASA.LV.         SSS.S.           VZ region         VZ region         V3 region           VZ region         V3 region         V3 region           VZ region         V3 region         V3 region           VZ region         V3 region         V3 region           VV. V. C. NMMDFVKQGKKR HVC. QY. KY.         HS. V. D. D	358 358 359 360 268 80 357 354 433 353 359 442 436 443 444 268 80 441 438 421 443
Consensus Eptesicus Erk3b Miniopterus YubKT-1 Tb1.Lu-v1 Tb1.Lu-v3 Myotis brandtii Myotis lucitugus Desmodus Phyliostomus Rosettus Consensus Erk3b Miniopterus YubKT-1 Tb1.Lu-v1 Tb1.Lu-v3 Myotis brandtii Myotis brandtii Rosettus Consensus Erk3b Miniopterus Phyliostomus Rosettus Consensus Erk3b Miniopterus Phyliostomus Rosettus Consensus Erk3b Miniopterus Phyliostomus Rosettus Consensus Erk3b Miniopterus Phyliostomus Rosettus Consensus Erk3b Miniopterus YubKT-1 Tb1.Lu-v1 Tb1.Lu-v3 Myotis brandtii Tb1.Lu-v1 Tb1.Lu-v3 Myotis brandtii Tb1.Lu-v1 Tb1.Lu-v1 Tb1.Lu-v1 Tb1.Lu-v1 Myotis brandtii Dt1.Lu-v1 Tb1.Lu-v1 Myotis brandtii Dt1.Lu-v1 Tb1.Lu-v1 Myotis brandtii Dt1.Lu-v1 Tb1.Lu-v1 Tb1.Lu-v1 Tb1.Lu-v1 Myotis brandtii Dt1.Lu-v1 Tb1.Lu-v1 Myotis brandtii Dt1.Lu-v1 Tb1.Lu-v1 Myotis brandtii Dt1.Lu-v1 Myotis brandtii Dt1.Lu-v1 Tb1.Lu-v1 Myotis brandtii Dt1.Lu-v1 Dt1.	Exon 6 → Exon 7 → Exon 8         B30.2 domain         V1 region           Image: Constraint of the image o	358 358 359 360 268 80 357 354 433 353 359 442 436 443 444 268 80 441 438 421 443
Consensus Eptesicus Erk3b Miniopterus YubKT-1 Tb1.Lu-v1 Tb1.Lu-v3 Myotis brandtii Myotis brandtii Ayotis brandtii Ayotis brandtii Eptesicus Erk3b Miniopterus YubKT-1 Tb1.Lu-v3 Myotis brandtii Myotis brandtii Ayotis lucifugus Desmodus Erk3b Miniopterus YubKT-1 Tb1.Lu-v3 Myotis brandtii Myotis brandtii	Exon 6 → Exon 7 → Exon 8         B30.2 domain         V1 region           KQR VFQ         PL         NLQ FNELTD         RRWWITLDPP         K N         13         DRRQVR         D         VLGSP         TISGKHYWEV           ST. I. A.         RR. V V. V.         TD. S. IV. A         KPAFYLRTLYLYGKENYE VG P A           SK T. IRV.         K A. M. A.Q.         F. SLLKNOPDVA. L.Q.         KVLRWSTTDTLP-FNDVQ.CO RF T           PK. VR. G.         RKV. PAC V.         TD. S. IV. A         KPYFYLTLYLYGKENYE VG P A           SK KG. VL. A.Q.         V ML. A.W. K.WLRWSTTDTLP-FNDVQ.CO RF T         PK           PK. VR. G.         RKV. PAC A.Q.         V M.K. WLRWSTDTLP-FNDVQ.CO RF T           SK KG. V. A.Q. V M.S. IV. E.         -LRRSRFSYLF-GGDNM.FGI S.         S.           PM R. RA         SG. V. V. H. V. TD. STWV.E.         SLPLIYILADKINFG S.         S.           SKE. R. V NE. A V. LI KN.Q.VA.A.M. YEHHLDANKNASA.LV.         SKE.R. V NE. A V. II.Q.SMD.Q.VA.A.M. YEHHLDANKNASA.LV.         SKE.R. V N. MNGFVRQGKKH.HVC.QY KY HS. V. D. D KTV. F. S. R           TD.Y. V V. CNMMOFVRQGKKH.HVC.QY KY HS. V. D. D KTV. F. S. R         TD.Y. V V. C NMMOFVRQGKKH.HVC.QY KY HS. V. D. D KTV. F. S. R           TD.Y.	358 358 359 360 268 80 357 354 353 353 353 359 442 442 442 444 444 444 444 444 444 44
Consensus Eptesicus Erk3b Miniopterus YubKT-1 Tb1.Lu-v1 Tb1.Lu-v3 Myotis brandtii Myotis brandtii Ayotis brandtii Consensus Eptesicus Erk3b Miniopterus YubKT-1 Tb1.Lu-v3 Myotis brandtii Myotis brandtii Brandtii Brandtii Myotis brandtii Brandt	Exon 6 ←→ Exon 7 ←→ Exon 8         B30.2 domain         V1 region                KQR VFQ         PL         MQ         NLGSP ITS6KHYWEV         D         VLGSP ITS6KHYWEV           STI.A.         RR.V.NV.V.V.         TD.S.IV.A.         KPAFYLRTLYLYQKGNYE.YG.P.A.         A           SKT.ILYV.K-A.A.M.A.Q.F.SLLKNDPDVALQ.KVLWSTTDTLP-FNDVQ.CD.RFI         PM.         NKYLIYV.K-A.A.A.A.O.F.SLLKNDPDVALQ.KVLWSTTDTLP-FNDVQ.CD.RFI           PK.V.PR.G.B.RKV.PAC.AV.T.D.SIV.A.WK.PAFYLRTLYLQKGDVE.YG.PM.         SK.GRAA.A.KG.VLAQ.VV.MH.S.VI.E.Q.PVFPSRTLYLHLRORYE.YG.L.           PMR.R.A.SG.VLAQ.VV.MH.S.VI.E.Q.PVFPSRTLYLHLRORYE.YG.L.         SK.GRAA.A.KG.VLAAL.S.E.V.TN.SITV.ELRSRFSYLF-GGDM.FGI.S.           SKE.R.N.V.         V.ME.A.Y.N.V.E.NSIV.ESLPLLYIDAKINGG.S.         SS.S.S.S.S.S.S.S.S.S.S.S.S.S.S.S.S.S.S	358 358 359 360 268 80 357 354 353 353 359 442 442 442 444 444 444 444 444 444 44







Fig. S1 Amino acid alignments of pteropid megabat TRIM5α, CPSF6, and
Mx2/MxB, related to Figs. 1, 5, 7, and 8.

9 (A) Amino acid alignments of pteropid megabat TRIM5α, related to Fig. 5A.
10 Amino acid sequences of newly identified megabat cDNAs were predicted
11 computationally based on their nucleotide sequences and aligned with their

12 homologs of other pteropid megabats collected from the NCBI GenBank 13 database. Each dot represents an amino acid identical to the top sequence, 14 and each hyphen exhibits an amino acid deletion. The position numbering is 15 based on the positions of the top sequence. Exon boundaries predicted from 16 the NCBI database are shown with dotted lines. Newly identified sequences 17 are highlighted with a magenta background. The tripartite motif and the B30.2 18 domain are highlighted in boxes, and the variable regions in the B30.2 domain 19 are highlighted with a cyan background. Note that the new TRIM5 cDNAs from 20 four megabat cell lines contain the three characteristic domains, RING, B-box2, 21 and Coiled-coil domains, confirming that they are members of the TRIM family. 22 The TRIM5 $\alpha$  cDNA cloned from ZFBK13-76E is an exception, lacking the entire 23 RING domain and the amino-terminal half of the B-box2 domain, whose 24 structure is similar to the predicted TRIM34-like gene of P. vampyrus (LOC102888261, Accession # XM 015592331, Reference ASM32557v1). 25 26 From R06E cells, we successfully cloned two variants, R06E v1 and R06E v2. 27 The R06E v1 isoform was closely related to the predicted transcript variant 12 of 28 Rousettus TRIM5-like gene (Accession # XM 016150076). While the 29 nucleotide length of the R06E v1 was longer than that of the R06E v2 (1,578 bp 30 vs. 1,488 bp), the insertion of a premature stop codon makes the translation 31 product of the R06E v1 variant lose the carboxy-terminal half of the protein 32 including the entire B30.2 domain. (B) Amino acid alignments of microbat TRIM5 $\alpha$ , related to Figs. 5A and D. Names of the newly identified genes are 33

highlighted in red. Tb1.Lu-v1, -v2, and -v3 indicates Tb1.Lu TRIM5 $\alpha$  isoforms 1, 34 35 isoform 2, and isoform 3, respectively. Functional domains and the variable 36 regions in the B30.2 domain are highlighted with black boxes and a cyan 37 background, respectively. The consensus with a threshold of >50% homology 38 is shown at the top of the alignment; otherwise, shown as "X." Predicted exon 39 boundaries are shown based on the boundaries indicated for Rousettus 40 *aegyptiacus* TRIM5 $\alpha$  (Fig. S1). At the carboxy-terminal end, Tb1.Lu-v2 has an 41 additional 13 amino acid extension derived from the delivery MLV vector, likely a 42 result of a PCR or cloning error. This insertion of the vector sequence was 43 most likely caused by a single cytosine nucleotide deletion in the third codon of 44 the second-to-last serine (AGC). This deletion would result in the frameshift of 45 the last serine, changing the stop codon to a leucine with the addition of the 46 vector-derived sequence. (C) Amino acid alignments of pteropid megabat CPSF6, related to Figs. 5B and 7. Functional domains and predicted nuclear 47 localization signals (NLS) are as per the publication by Lee et al. (1). A black 48 49 box with an asterisk indicates the stop codon experimentally introduced in the 50 Proline-rich domain for truncation. Note that the new megabat CPSF6 include 51 three characteristic domains; the RNA-recognition motif, the Proline-rich (P-rich) 52 domain, and the Arginine/serine-rich (RS) domain with two NLS, confirming that 53 they are members of the CPSF6. The four megabat CPSF6 contain 37 amino 54 acids-deletions in the Proline-rich domain, similar to the human CPSF6 isoform 1 (2). Therefore, the megabat CPSF6 showed high similarities to both human 55

56 and mouse CPSF6 at an amino acid sequence level with a few lineage-specific 57 variabilities. (D) Amino acid alignments of pteropid megabat Mx2/MxB, related 58 to Figs. 5C and 8. A black box with an asterisk indicates a position of an amino acid substitution (Q79R and L600P) assessed in this study (Fig. 8). 59 The 60 arginine/lysin residues in the amino-terminal NLS, phenylalanine/leucine 61 residues in the carboxy-terminal leucine repeats, and the triple-arginine motif/the 62 8-amino acid segment in the amino-terminal region are highlighted with #, 63 asterisks with position numbers, and black boxes, respectively. Note that the newly identified pteropid bat Mx2 cDNAs contain three Bundle signaling 64 65 elements (BSEs), the GTPase domain, and the Stalk domain, suggesting that 66 they are close relatives to antiviral Mx proteins. The DemKT-1 Mx2 contains a 67 premature stop codon in the GTPase domain. (E) Amino acid alignment of 68 three variable regions in the B30.2 domain of primate and pteropid megabat 69 TRIM5 $\alpha$  and TRIM34 collected from the NCBI GenBank database.

71 Table S1. GenBank accession numbers of the samples utilized for

72 constructing phylogenetic trees, calculating *dN/dS* ratios, and sequence

## analysis of megabat CPSF6 isoforms, related to Figs. 1A, 5, 7E, and 8D.

Mitochondrial cytochrome b (Fig 1A)	
Species	Accession number
Pteropus vampyrus	FJ561401
Pteropus alecto	KJ532406
Rousettus aegyptiacus	EU624124
Eonycteris spelaea	AB062476
Hipposideros armiger	EU434946
Cloeotis percivali	FJ457616
Rhinolophus sinicus	EU434941
Rhinolophus ferrumequinum	EU436673
Megaderma lyra	DQ888678
Rhinopoma microphyllum	KF874547
Nycteris leporinus	AF330802
Emballonura alecto	HQ693711
Phyllostomus hastatus	FJ155479
Desmodus rotundus	FJ155477
Mormoops megalophylla	AF330808
Pteronotus parnellii	AY604456

Noctilio albiventris	AF330806
Furipterus horrens	AY621004
Thyroptera tricolor	AY621005
Mystacina tuberculata	AY960981
Myotis (Cistugo) lesueuri	AY485687
Myotis lucifugus	AF376854
Myotis brandtii	AM261886
Myotis davidii	AB106591
Eptesicus fuscus	AF376835
Tadarida brasiliensis	JF489129
Natalus major	AY621021
Newly cloned bat restriction factor homologs (Fig 5)	
Sample name	Accession number
DemKT-1 TRIM5alpha	OP272517
EfK3B TRIM5alpha	OP272518
FBKT-1 TRIM5alpha	OP272519
R06E TRIM5alpha-v1	OP272520
R06E TRIM5alpha-v2	OP272521
Tb1Lu TRIM5alpha-v1	OP272522
Tb1Lu TRIM5alpha-v2	OP272523

Tb1Lu TRIM5alpha-v3	OP272524
YubKT-1 TRIM5alpha	OP272525
ZFBK13-76E TRIM5alpha	OP272526
DemKT-1 CPSF6	OP272527
FBKT-1 CPSF6	OP272528
R06E CPSF6	OP272529
ZFBK13-76E CPSF6	OP272530
DemKT-1 Mx2/MxB	OP272531
FBKT-1 Mx2/MxB	OP272532
R06E Mx2/MxB	OP272533
ZFBK13-76E Mx2/MxB	OP272534
Mammalian TRIM, Mx2 and CPSF6 (Fig 5)	
Sample name	Accession
Rousettus aegyptiacus TRIM5	XM_016150065
Homo TRIM5	NM_033034
Macaca TRIM5	NM_001032910
Bos TRIM5	DQ381151
Sus TRIM5	AK235927
Papio TRIM5	NM_001112632
Nomascus TRIM5	NM_001280113

Microcebus TRIM5	HQ413345
Ovis TRIM5	NM_001318072
Capra TRIM5	XM_005689800
Eptesicus fuscus TRIM5	XM_028137626
Callithrix TRIM5	XM_009007572
Saimiri TRIM5	XM_010334225
Rhinopithecus TRIM5	XM_010364548
Propithecus TRIM5	XM_012654429
Homo TRIM34	NM_021616
Rousettus aegyptiacus TRIM34	XM_016126824
Phyllostomus discolor TRIM34	XM_028515501
Myotis lucifugus TRIM34	XM_023758764
Eptesicus fuscus TRIM34	XM_008160439
Pteropus alecto TRIM34	XM_015592357
Pteropus vampyrus TRIM34	XM_011383134
Miniopterus natalensis TRIM34	XM_016215034
Homo TRIM7	NM_203293
Bos TRIM7	NM_001205446
Papio TRIM7	XM_003900656
Macaca TRIM7	XM_005558834
Homo TRIM26	NM_003449

Pan TRIM26	XM_003829748
Macaca TRIM26	NM_001114967
Bos TRIM26	XM_002697339
Homo TRIM39	BT007370
Gorilla TRIM39	XM_004043563
Homo TRIM47	NM_033452
Papio TRIM47	XM_003913451
Bos TRIM47	NM_001193197
Homo TRIM65	NM_173547
Macaca TRIM65	XM_028836809
Bos TRIM65	XM_027518688
Homo TRIM21	NM_003141
Macaca TRIM21	NM_001258045
Bos TRIM21	NM_182655
Homo TRIM22	NM_006074
Macaca TRIM22	EU124697
Canis TRIM22	XM_542402
Homo TRIM6	NM_001003818
Sus TRIM6	XM_021062360
Canis TRIM6	NM_001205190
Myotis davidii Mx2*	XM_006754321.2

Eptesicus fuscus Mx2*	XM_028151882.1
Miniopterus natalensis Mx2*	XM_016221319.1
Phyllostomus discolor Mx2*	XM_036017448.1
Desmodus rotundus Mx2*	XM_024559822.1
Rhinolophus ferrumequinum Mx2*	XM_033089263.1
Pteropus alecto Mx2*	XM_006916730.3
Bos taurus Mx2	XM_015473641.2
Ovis aries Mx2	XM_012175764.3
Macaca mulatta Mx2	NM_001079696.1
Cercocebus atys Mx2	XM_012037318.1
Papio anubis Mx2	XM_003895463.5
Homo sapiens Mx2	NM_002463.2
Pan troglodytes Mx2	XM_016938556.2
Gorilla gorilla Mx2	XM_019017898.2
Pongo abelii Mx2	XM_002830701.2
Saimiri boliviensis Mx2	XM_010338253.1
Callithrix jacchus Mx2	XM_035283249.1
Aotus nancymaae Mx2	XM_021669412.1
Miniopterus natalensis CPSF6	XM_016199385.1
Eptesicus fuscus CPSF6	XM_028156487.1
Rhinolophus ferrumequinum CPSF6	XM_033116537.1

Molossus molossus CPSF6	XM_036250921.1
Hipposideros armiger CPSF6	XM_019640530.1
Desmodus rotundus CPSF6	XM_024576197.1
Myotis myotis CPSF6	XM_036298067.1
Phyllostomus discolor CPSF6	XM_028531694.2
Rousettus aegyptiacus CPSF6	XM_016133567.2
Pteropus vampyrus CPSF6	XM_011374011.2
Homo sapiens CPSF6	NM_001300947.2
Mus musculus CPSF6	NM_001310609.1
Oryctolagus cuniculus CPSF6	XM_008256767.2
Felis catus CPSF6	XM_023257220.1
Sus scrofa CPSF6	XM_021090900.1
Ovis aries CPSF6	XM_027967466.1
Capra hircus CPSF6	XM_018047962.1
Bos taurus CPSF6	XM_005206464.4
Pan troglodytes CPSF6	XM_009425807.3
Gorilla gorilla CPSF6	XM_019038993.1
Pongo abelii CPSF6	XM_024256338.1
Papio Anubis CPSF6	XM_009181190.3
Macaca mulatta CPSF6	XM_015152234.2
Callithrix jacchus CPSF6	XM_009004183.2

Saimiri boliviensis CPSF6	XM_010338496.1
Aotus nancymaae CPSF6	XM_021665939.1
*: These samples were included in the ca	alculation of dN/dS ratio for Fig. 8
together with FBKT-1 and R06E Mx2 seque	nces.
SRA accession numbers (Fig. 7E)	
SRA accession number	
SRR2913598	
SRR2914059	
SRR2914282	
SRR2914295	
SRR2914359	
SRR2914360	
SRR2914366	
SRR2914368	
SRR2914369	
SRR2914370	
SRR2914371	
SRR2914372	
SRR7609226	
SRR7548028	

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SRR6453215
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SRR6453210
SRR6453214
SRR6453216
SRR6453213
SRR6453212

SRR6453208

SRR6453211

SRR7735101

SRR7735102

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