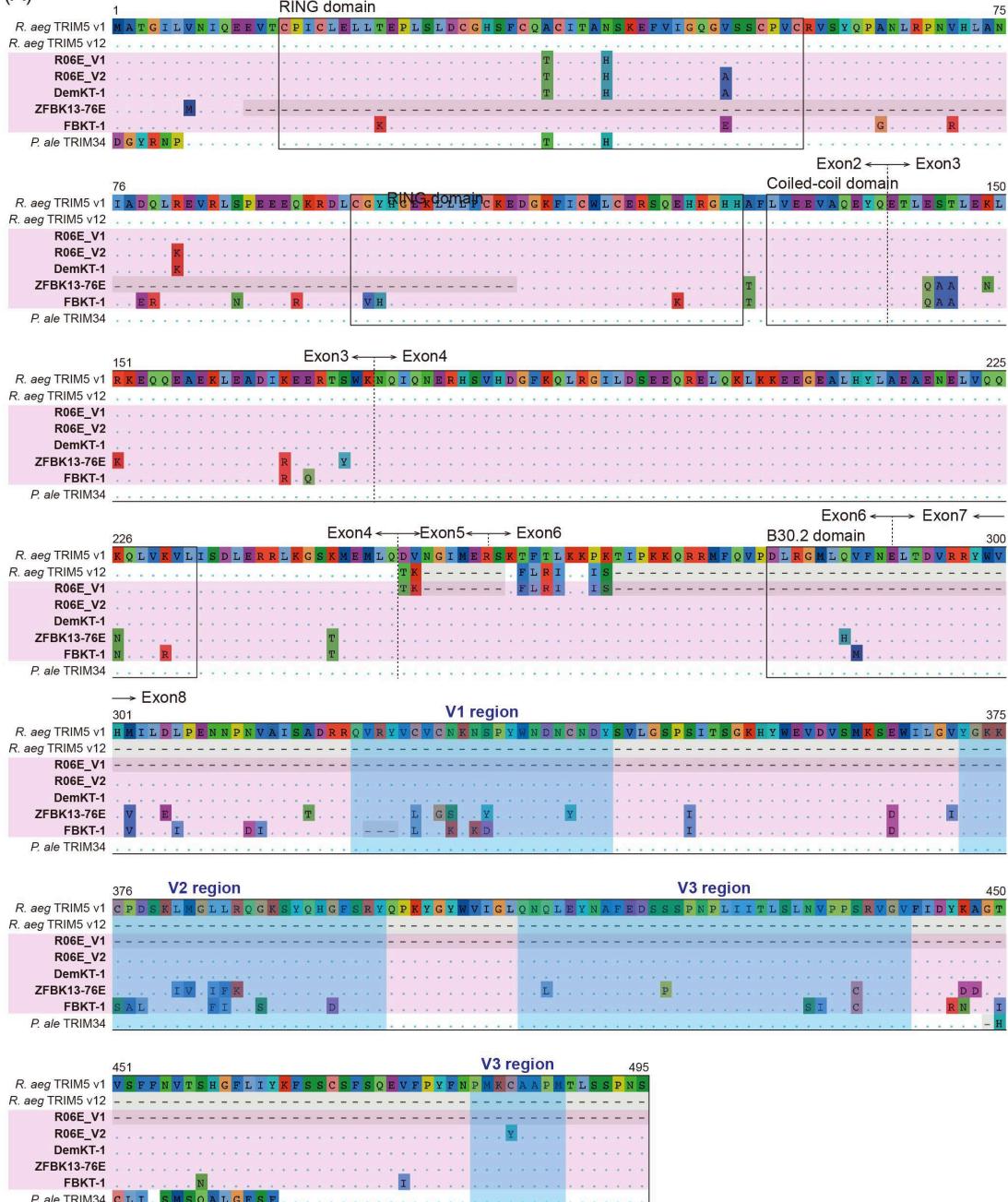


## 1 Supplemental information captions

(A)



2

**(B)**

**RING domain**

Consensus	RING domain	
Eptesicus	MASGIL NIKEEVTCPICLELLTEPLSLDCGHxFQACITANNRESMIXQ	GESSCPVCRxSYQPxNLRPNxHxANIVE xLEVKLSPx
Efk3b	.....V.....	.....M.....T.....G--D.....I.....E.....R.V.....T.....Q.....
Miniopterus	.....V.E.	.....M.....T.....G--D.....I.....E.....R.V.....T.....Q.....
YubKT-1	.....VEE.....	.....S.....T.S.Q.....R.E.....IT.....EK.....R.V.S.....A.K.....NTE.....
Tb1.Lu-v2	.....E.E	.....G.S.....K.....R.E.....R.....TN.....EK.Q.....SWKLS.....T.QR.....TE.....
Tb1.Lu-v1	.....E.E	.....K.....S.....MG.E.....RH.....L.....G.....SR.L.....AI.....KK.....
Tb1.Lu-v3	.....	.....S.....MV.E.....RH.....L.....G.....SR.L.....AI.....KK.....
Myotis brandtii	.....T.VV.M.K.....	.....D.....M.....T.....C.....KST.....E.....QNV.K.....AF.F.....Q.....
Myotis lucifugus	.....M.M.....	.....M.....T.....G.I.G.....C.....I.....E.....R.V.....A.K.....K.....
Desmodus	.....D.E.....LKL.....	.....K.....C.T.....K.....TVSKER.....QS.....GI.Q.....Q.V.....T.....AN.....E.....
Phyllostomus	.....D.....LKL.....M.....	.....C.T.....YK.....VSEK.QN.....M.....S.....GI.K.....W.M.....KT.....A.....D.....
Rosettus	.....T.....V.Q.....	.....S.....SK.FV.G.....V.....A.....V.L.....ADQ.....R.....E.....

**B-box domain**

Consensus	B-box domain	
Eptesicus	EQKRLD <b>CV</b> xHGEKLLLFCKEDxKxICWLCCERSQEHRGHHT	FLMEEVAQEYKxEKLQAALDRRAEQQQAEKLxXDIxEERTS KxX1xNEK
Efk3b	.....Q.R.....E.I.....R.Q.....I.....	.....ED.LE.....K.DQ.E.....L.....
Miniopterus	.....Q.R.....E.I.....R.Q.....I.....	.....ED.LE.....K.DQ.E.....L.....
YubKT-1	.....L.ER.....E.I.....R.Q.....P.....I.....	.....N.....TV.....G.....EWGS.....R.Q.....W.NK.Q.....GN.....
Tb1.Lu-v2	.....R.H.....HF.E.HG.L.FV.....	.....KILVK.....A.....D.A.....GK.K.....K.W.GS.....RK.SN.RQNQVQK.R.....
Tb1.Lu-v1	.....IN.R.....G.F.....	.....K.....KW.D.WRA.....K.....W.DHLEK.S.....
Tb1.Lu-v3	.....IN.R.....G.F.....	.....K.....KW.D.WRA.....K.....W.DHLEK.S.....
Myotis brandtii	.....R.....Q.E.I.....R.C.....S.....PV.....N.....E.....	.....DD.LE.....K.DK.Q.....DL.....
Myotis lucifugus	.....S.H.....Q.E.I.....RD.....I.....	.....DD.LE.....K.DQ.EH.R.....
Desmodus	.....T.ER.....G.F.....	.....Q.N.....H.....EA.KK.....W.NLMQ.R.....
Phyllostomus	.....ER.....G.F.....	.....K.....EA.K.....G.W.NL.E.....R.....
Rosettus	.....GY.....G.F.....A.....V.....Q.T.EST.EK.K.....E.....	.....EA.K.....W.NQ.Q.....R.....

**Coiled-coil domain**

Consensus	Coiled-coil domain	
Eptesicus	XXVQDxFK LRGIL SEEQKELQRL KEEXXXL DLQAQAESELAQQ QLL DLISDLEHRLQGSxVEMLDQVNGIM RSKTFKL KPKxx	Exon 2 ←→ Exon 3
Efk3b	KS...C.H....A.....E.AAEN.D.....R.....RK.R.....T.....K.T.K.....Q....SL.....	Exon 3 ←→ Exon 4
Miniopterus	KS...C.Q....A.....E.AAEN.D.....R.....RK.R.....T.....K.T.K.....Q....SL.....	Exon 3 ←→ Exon 4
YubKT-1	KF...YYY.Q....D.....E.GDN.D.....R.....V.G.T.....T.....KS.IK.Q.I.R.EAL.....	Exon 3 ←→ Exon 4
Tb1.Lu-v2	ER...Y.EH.E..DT.....K.EE.RDD.K.....V.G.T.....TA.....IE.....K..TL.....	Exon 3 ←→ Exon 4
Tb1.Lu-v1	QC...Y.EK.T..E.K.....K.GNI.NY.H.....D.....S.V.K.....P.....S.K.I..M..NV.....	Exon 3 ←→ Exon 4
Tb1.Lu-v3	QC...Y.EK.T..E.K.....K.GNI.NY.H.....D.....S.V.K.....P.....S.K.I..M..--.....	Exon 3 ←→ Exon 4
Myotis brandtii	KS...Y.Q.K....A..T.....E.AAEN.D.....R.....RK.R.....A.....K.E.....K.RTL.....	Exon 3 ←→ Exon 4
Myotis lucifugus	KS.LYY.RE....AR.Q.....E.AAENHD.V.....KK.R.....A.....K.E.....K..TL.....	Exon 3 ←→ Exon 4
Desmodus	QI...C.K..VF.DT..K.....K.V.....RDI.H.E.S.....V.S.V.R.....E.....MRR.E.D.E.....K.S.PV.....	Exon 3 ←→ Exon 4
Phyllostomus	QI...C.N....D.....K.A.....ADI.H.E.S.....V.SLV.R.....M.E.Y.....T.K.....E.....K..TV.....	Exon 3 ←→ Exon 4
Rosettus	HS.H.G....Q....D..R.....K.K.....GEA.HY.E.N..V..K.VKV.....R..K.KM.....E.....K..TI.....	Exon 3 ←→ Exon 4

**B30.2 domain**

Consensus	B30.2 domain	
Eptesicus	XXKQRxVFQxPDLxxMLQxFNÉLTDxRRYWHTLDPPxKxNxxISxDRRQVR	Exon 4 ←→ Exon 5 ←→ Exon 6
Efk3b	ST...I..A..RW..V.....V.....V.....TD.S.IV.A.....KPAFYRLTLYQKGNEY.E.YG.....P.....A.....	Exon 4 ←→ Exon 5 ←→ Exon 6
Miniopterus	ST...I..A..RR..V.....V.....V.....TD.S.IV.A.....KPAFYRLTLYQKGNEY.E.YG.....P.....A.....	Exon 4 ←→ Exon 5 ←→ Exon 6
YubKT-1	SK...T.IRV.....K...A.M.....A.Q.....F.....SLLKNPDVA..L.Q.....KVLRWSTTDLTP:ENDYQ.CD.....RF.....I.....	Exon 4 ←→ Exon 5 ←→ Exon 6
Tb1.Lu-v2	PK...VR..G.....RKV.PAC.....A.....V.....TD.E.VI..A.WK.....PAFYRLKLFYQKGDY.E.YG.....PM.....	Exon 4 ←→ Exon 5 ←→ Exon 6
Tb1.Lu-v1	SK...GRA..A..KG...V.....AQ.....V.....MH.S.VI..E.Q.....PVFPSRTLYLHLRDRYE.YG.....L.....	Exon 4 ←→ Exon 5 ←→ Exon 6
Tb1.Lu-v3	-----	-----
Myotis brandtii	PM...T.L.A...RGV.EA.T..AEA.S.E.V.....TN.SIIV.E.....LRRSRFSYLF-GGDNM.FGI.....S.....	Exon 4 ←→ Exon 5 ←→ Exon 6
Myotis lucifugus	PM...R.RA...GG..V.....V.H.....V.....TD.SYNV.E.....SLPLL---YIAADKTNFG.....S.....	Exon 4 ←→ Exon 5 ←→ Exon 6
Desmodus	ST...R..A..SG..V.....V.....LI.....KN.Q.VA.A.....YEHHL---DANKNASA..LV.....	Exon 4 ←→ Exon 5 ←→ Exon 6
Phyllostomus	SKE..R..V..NE..A..V.....I.Q.SMD.Q.VA.A..M.....YEHHL---DANTKASA..LA.....	Exon 4 ←→ Exon 5 ←→ Exon 6
Rosettus	PK...RM..V..RG..V.....V.....MI..L.ENNP.VA.A.....YVCVCNKNSPYWNDNCN.YS.....S.....	Exon 4 ←→ Exon 5 ←→ Exon 6

**V1 region**

Consensus	V1 region	
Eptesicus	XXKQRxVFQxPDLxxMLQxFNÉLTDxRRYWHTLDPPxKxNxxISxDRRQVR	Exon 6 ←→ Exon 7 ←→ Exon 8
Efk3b	ST...I..A..RW..V.....V.....V.....TD.S.IV.A.....KPAFYRLTLYQKGNEY.E.YG.....P.....A.....	Exon 6 ←→ Exon 7 ←→ Exon 8
Miniopterus	ST...I..A..RR..V.....V.....V.....TD.S.IV.A.....KPAFYRLTLYQKGNEY.E.YG.....P.....A.....	Exon 6 ←→ Exon 7 ←→ Exon 8
YubKT-1	SK...T.IRV.....K...A.M.....A.Q.....F.....SLLKNPDVA..L.Q.....KVLRWSTTDLTP:ENDYQ.CD.....RF.....I.....	Exon 6 ←→ Exon 7 ←→ Exon 8
Tb1.Lu-v2	PK...VR..G.....RKV.PAC.....A.....V.....TD.E.VI..A.WK.....PAFYRLKLFYQKGDY.E.YG.....PM.....	Exon 6 ←→ Exon 7 ←→ Exon 8
Tb1.Lu-v1	SK...GRA..A..KG...V.....AQ.....V.....MH.S.VI..E.Q.....PVFPSRTLYLHLRDRYE.YG.....L.....	Exon 6 ←→ Exon 7 ←→ Exon 8
Tb1.Lu-v3	-----	-----
Myotis brandtii	PM...T.L.A...RGV.EA.T..AEA.S.E.V.....TN.SIIV.E.....LRRSRFSYLF-GGDNM.FGI.....S.....	Exon 6 ←→ Exon 7 ←→ Exon 8
Myotis lucifugus	PM...R.RA...GG..V.....V.H.....V.....TD.SYNV.E.....SLPLL---YIAADKTNFG.....S.....	Exon 6 ←→ Exon 7 ←→ Exon 8
Desmodus	ST...R..A..SG..V.....V.....LI.....KN.Q.VA.A.....YEHHL---DANKNASA..LV.....	Exon 6 ←→ Exon 7 ←→ Exon 8
Phyllostomus	SKE..R..V..NE..A..V.....I.Q.SMD.Q.VA.A..M.....YEHHL---DANTKASA..LA.....	Exon 6 ←→ Exon 7 ←→ Exon 8
Rosettus	PK...RM..V..RG..V.....V.....MI..L.ENNP.VA.A.....YVCVCNKNSPYWNDNCN.YS.....S.....	Exon 6 ←→ Exon 7 ←→ Exon 8

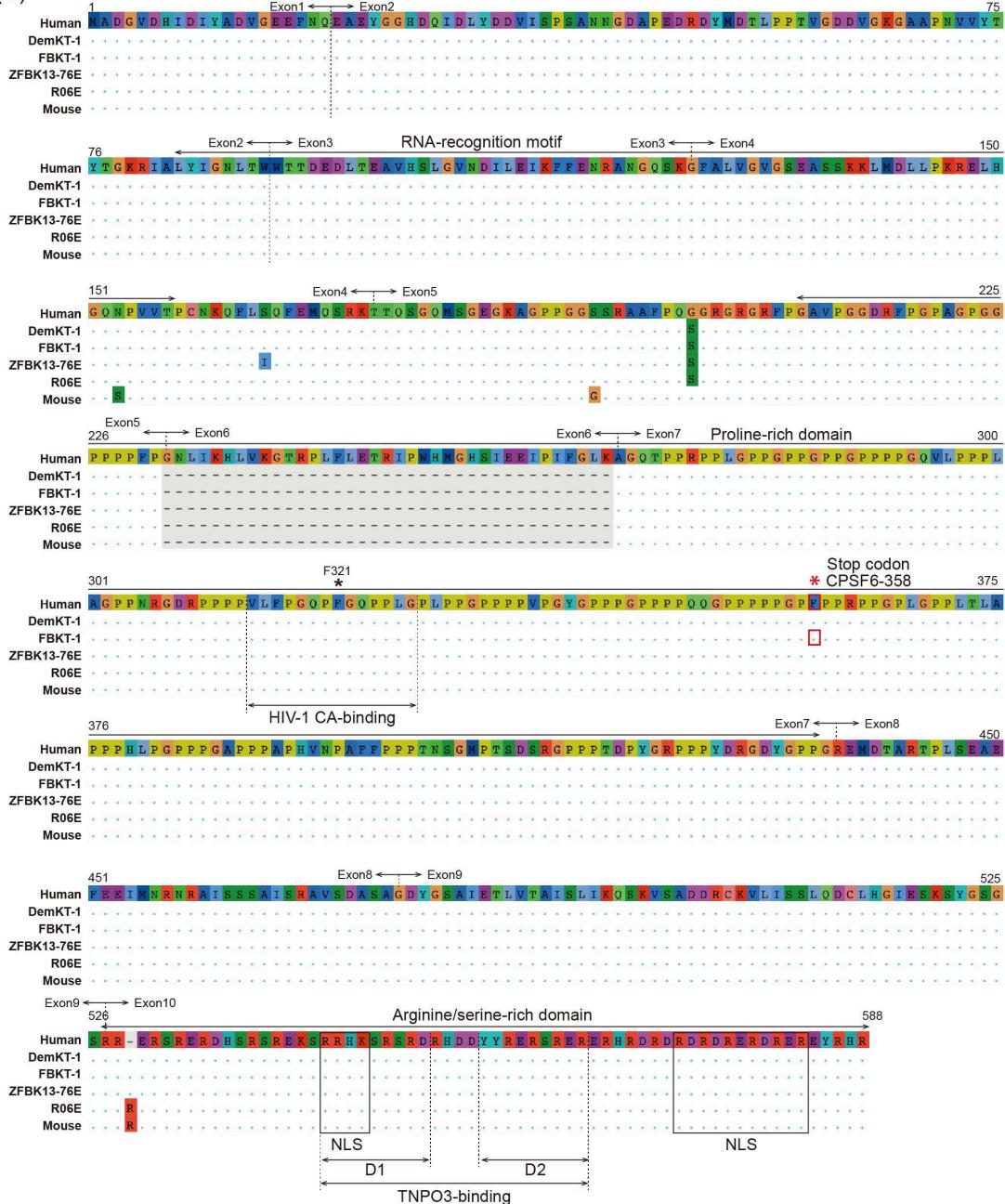
**V2 region**

Consensus	V2 region	
Eptesicus	DVS.KxAWxLGVYg.KxPDS.....Q.....S.....QPxGYWVIGLQNxxEYKAFxDS.xS.....P.....P.....xXxTLxLxVPPxRVGVF	V3 region
Efk3b	TD.Y.V....V.C....NMMDFVKQGKKR.HVC.QY..KY.....HS.....V.D.....D.....KTV.....F.S.....R.....	V3 region
Miniopterus	TD.Y.V....V.C....NMMDFLKQCKKH.HVC.QY..KY.....HS.....L.D.....D.....KTV.....F.S.....R.....	V3 region
YubKT-1	E.R.I..CA.R.....ISF.QGY.KY..QL.....QF.....V.ATYNSWPYNI.SPR.T.T..R.....	V3 region
Tb1.Lu-v2	E.Y.V....CEENP.G.NRKGFVRGRNNR.HVC.RY..RN.....E.HSK.....V.P.H.....SSTL.FT.T..H.....	V3 region
Tb1.Lu-v1	D.Y.V....DNC..NMMGFVRQGNNY.HVC.RY..KY.....HS.....V.A.S.....ASTL.S.T..HC.....	V3 region
Tb1.Lu-v3	-----	-----
Myotis brandtii	Q.R..IM....E.Y....KKMDFIROIKNS.PL.C.KF..KY....V.....NS.....V.A.D.....STTV.F.S.....R.....	V3 region
Myotis lucifugus	Q.C..IM....E.Y....NRMDFLQRQINS.PL.C..IF..QY.....HS.....V.DF.N.....KTL.F.S.....R.....	V3 region
Desmodus	E.Q.S..I....K.HS.T.....SD.RNHF.IVT.D.QFD.A..GE.S..N.....LKL.NVT..H.....	V3 region
Phyllostomus	E.Q.S..I....E.DS.T.....SD.KRCF..E.QFK.NV.GEFS.FD.....LKL.PS.T..R.....	V3 region
Rosettus	M.SE.I....K.C....KLMGLLRQGKSY.HGF.RY..KY.....QL..N..E..S..SPN.....LII..S..N..S.....	V3 region

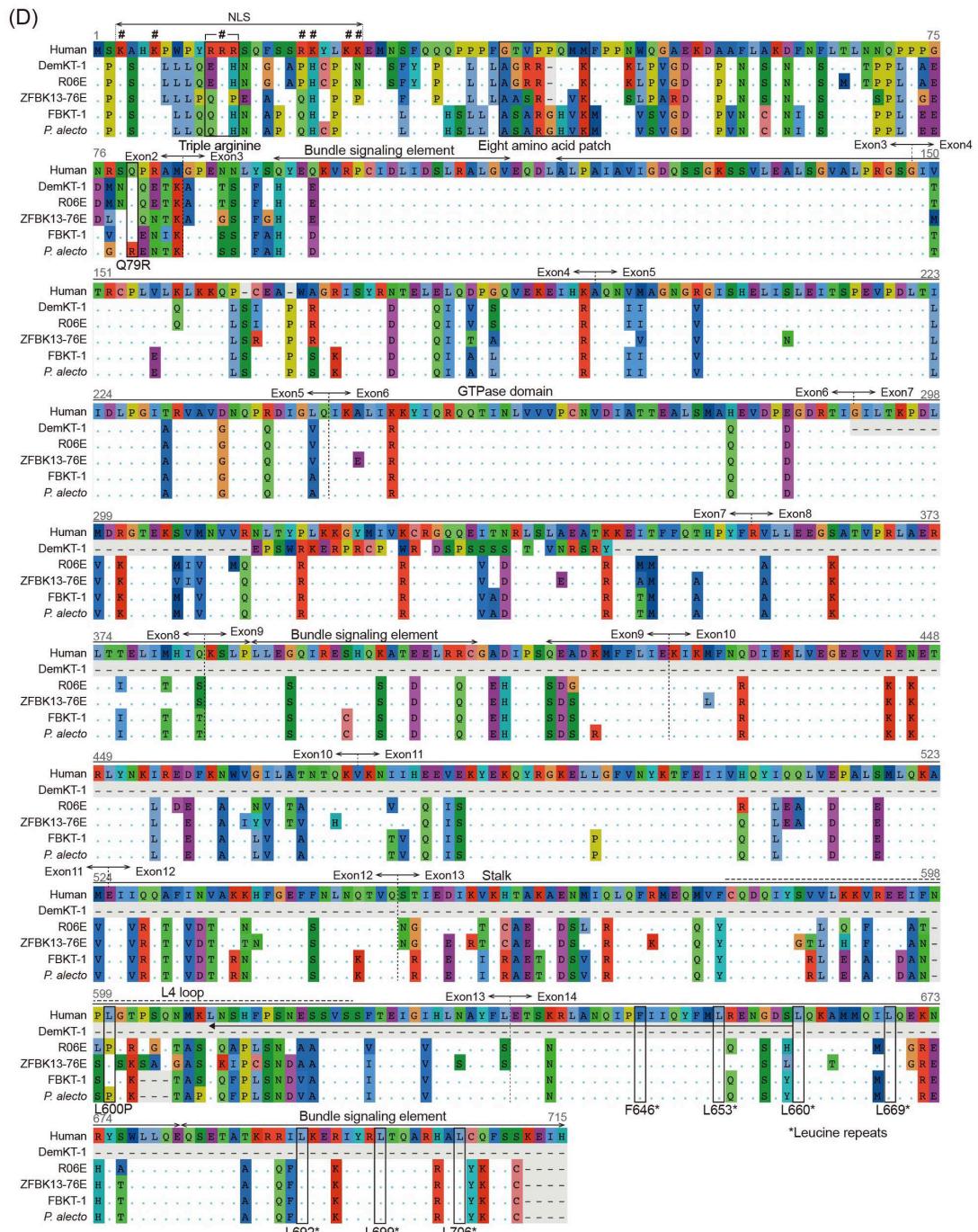
**V4 region**

Consensus	V4 region	
Eptesicus	LDYDAGTVSFFNTVxGFLIYKFSSCSFSQKxFPYFNPMK-----CTAPMTL-----CSPSS-----	Vector sequence
Efk3b	.....V.....TN.....M.....	.....G.....
Miniopterus	.....V.....TN.....M.....	.....G.....
YubKT-1	.....N..L.....N.....A.....GEC.....	.....S.....
Tb1.Lu-v2	.....E.....I.H.....A.....G.M.....	.....Vector sequence.....
Tb1.Lu-v1	.....N.....IS.H.....PK.I.....	.....LKITRGSGCGMCVS.....
Tb1.Lu-v3	-----	-----
Myotis brandtii	.....N.H.....VM.....	.....LQETRE.....SV.....
Myotis lucifugus	.....G.L.....M.....	.....LQETRE.....SV.....
Desmodus	.....Y..H.....HT.....	.....LQETRE.....SV.....
Phyllostomus	.....C..Y..H.....HT.....	.....LQETRE.....SV.....
Rosettus	I..K.....SH.....EV.....	.....A.....S..N.....

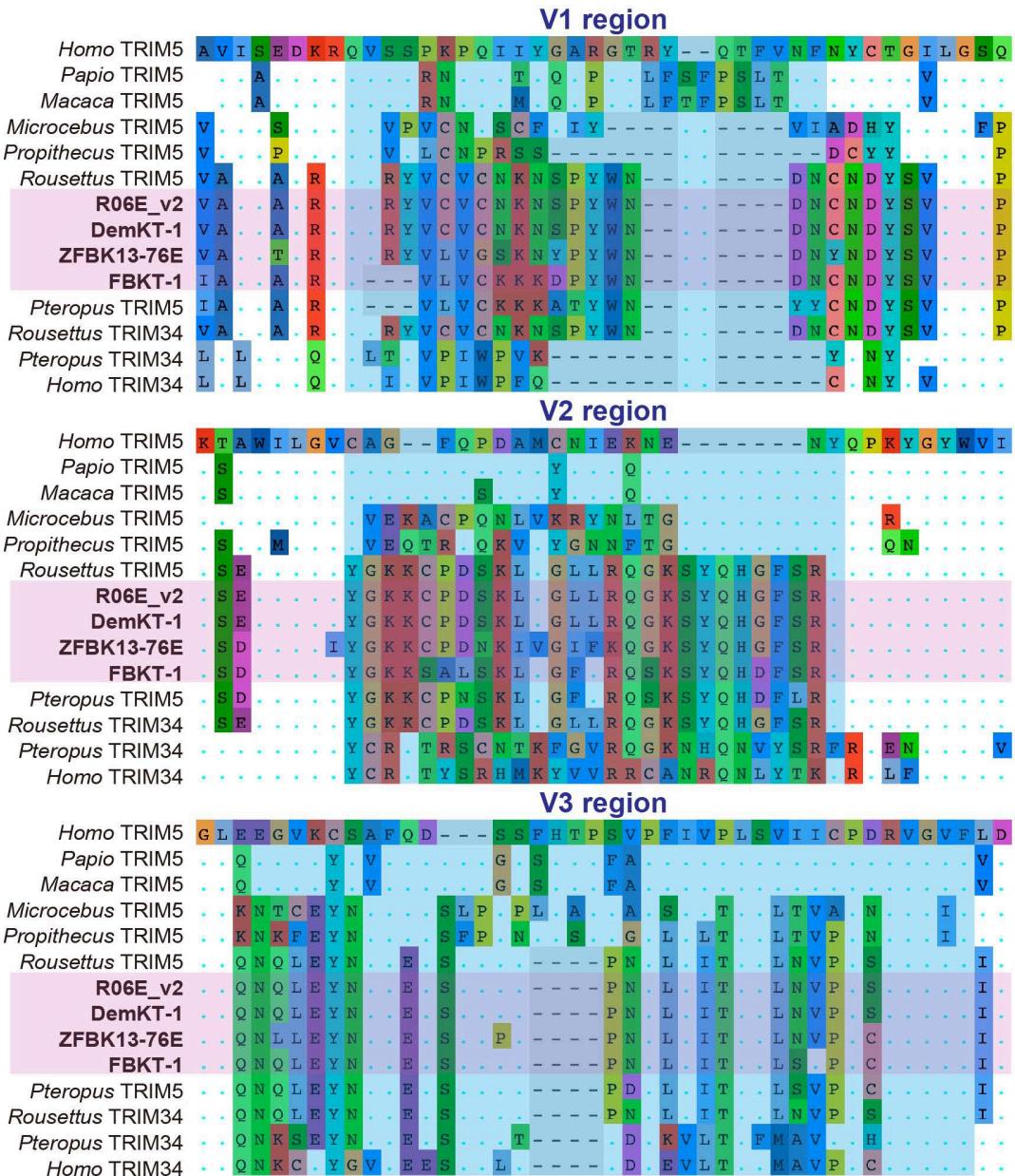
(C)



4



(E)



6

7 **Fig. S1 Amino acid alignments of pteropid megabat TRIM5 $\alpha$ , CPSF6, and**8 **Mx2/MxB, related to Figs. 1, 5, 7, and 8.**9 (A) Amino acid alignments of pteropid megabat TRIM5 $\alpha$ , 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*  
25 (LOC102888261, Accession # XM\_015592331, Reference ASM32557v1).  
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  
33 TRIM5 $\alpha$ , related to Figs. 5A and D. Names of the newly identified genes are

34 highlighted in red. Tb1.Lu-v1, -v2, and -v3 indicates Tb1.Lu TRIM5 $\alpha$  isoforms 1,  
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  
47 CPSF6, related to Figs. 5B and 7. Functional domains and predicted nuclear  
48 localization signals (NLS) are as per the publication by Lee et al. (1). A black  
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  
55 1 (2). Therefore, the megabat CPSF6 showed high similarities to both human

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  
59 acid substitution (Q79R and L600P) assessed in this study (Fig. 8). The  
60 arginine/lysine 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  
64 newly identified pteropid bat Mx2 cDNAs contain three Bundle signaling  
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.

70

71 **Table S1. GenBank accession numbers of the samples utilized for**  
 72 **constructing phylogenetic trees, calculating dN/dS ratios, and sequence**  
 73 **analysis of megabat CPSF6 isoforms, related to Figs. 1A, 5, 7E, and 8D.**

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

<i>Noctilio albiventris</i>	AF330806
<i>Furipterus horrens</i>	AY621004
<i>Thyroptera tricolor</i>	AY621005
<i>Mystacinia tuberculata</i>	AY960981
<i>Myotis (Cistugo) lesueuri</i>	AY485687
<i>Myotis lucifugus</i>	AF376854
<i>Myotis brandtii</i>	AM261886
<i>Myotis davidii</i>	AB106591
<i>Eptesicus fuscus</i>	AF376835
<i>Tadarida brasiliensis</i>	JF489129
<i>Natalus major</i>	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
<i>Rousettus aegyptiacus</i> TRIM5	XM_016150065
<i>Homo</i> TRIM5	NM_033034
<i>Macaca</i> TRIM5	NM_001032910
<i>Bos</i> TRIM5	DQ381151
<i>Sus</i> TRIM5	AK235927
<i>Papio</i> TRIM5	NM_001112632
<i>Nomascus</i> TRIM5	NM_001280113

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

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

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

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

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

SRR7548029
SRR7548030
SRR7548031
SRR7548032
SRR7548033
SRR7548034
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SRR6453215
SRR6453209
SRR6453210
SRR6453214
SRR6453216
SRR6453213
SRR6453212

SRR6453208

SRR6453211

SRR7735101

SRR7735102

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