Table S1 Positive selection analyses for TRIM5 and TRIM22 of Order Chiroptera.

A) Amino acids under Positive Selection using five different methods

Gene	Teste of Selection for PAML[c]					Amino acids under Positive Selection				Total of sites
	lnL[a] M7	lnL[a] M8	2Δ lnL[b]	p-value	Sites	SLAC[d]	FEL[e]	MEME[e]	FUBAR[f]	
TRIM5	-18295,7	-18105,8	379,7	<0.001	7, 80, 99, 165, 182, 188, 191, 198, 212, 284, 297, 302, 321, 324, 325, 328, 331, 333, 337, 338, 344-359, 370, 379, 393, 395, 396, 403, 404, 406, 408-413, 415-419, 426, 428-433, 439, 441, 456, 464, 480, 482, 484-487, 496, 502, 549	4,185,212,226,284,297,298,327,348,350,352,373,379,410,413,432,456,487,502,549	4,55,74,98,151,159,168,185,191,212,226,233,253,264,284,289,297,298,327,348-350,352,373,379,393,405,410,413,416,427,430,432,456,475,487,502,547,549,553	4,5,6,8,11,15,16,17,18,19,22,55,72,82,159,168,185,191,205,212, 226,233,253,255,256, 264,284, 297,298,308,316,327,330,332,334,336-338,345,348-350,352,354,370,373,379,394,405,410-419, 426,428,431,432,442,443, 456,462,470,475,487,525,538,545,547,549,555,557	4,159,168,185,191,212,226,233,253,284,297,348-350,359,379,410,413,416,419,430,432,456,487,502,547,549	**31**
TRIM22	-13024,2	-12969,2	110,1	<0.001	4, 7, 10, 19, 37, 47-51, 54, 55, 64, 69, 72, 81, 82, 84, 87-89, 91, 93, 94, 99, 104-106, 118, 128, 133, 134, 155, 177, 186, 201, 205, 216, 219, 220, 222, 226, 243, 246, 248, 250, 252, 256, 259, 261, 275, 278, 281, 284, 288, 289, 293, 314, 320, 322, 329, 331, 332, 381, 385, 398, 409, 431, 451, 457, 468	7,19,69,94,215,283,352,409,431,453,457,505	4,7,19,51,69,128,215,261,283,284,332,338,352,382,385,399,409,431,453,475,505	4,7,13,19,29,37,42,51,52,69,70,91,104-107,175,205,208,215,218,219,221,227,258,261,266,269,283,284,293,306,311,314,327,332,346,352,370,385,399,409,431,453, 455,465,505,508,	7,19,20,37,49,51,55,64,69,215,222,243,256,259,261,284,288,293,332,352,385,407,409,431,453,457	**19**

a) lnL: log-likelihood scores.

b) 2ΔlnL: likelihood ratio test (LRT) to detect positive selection.

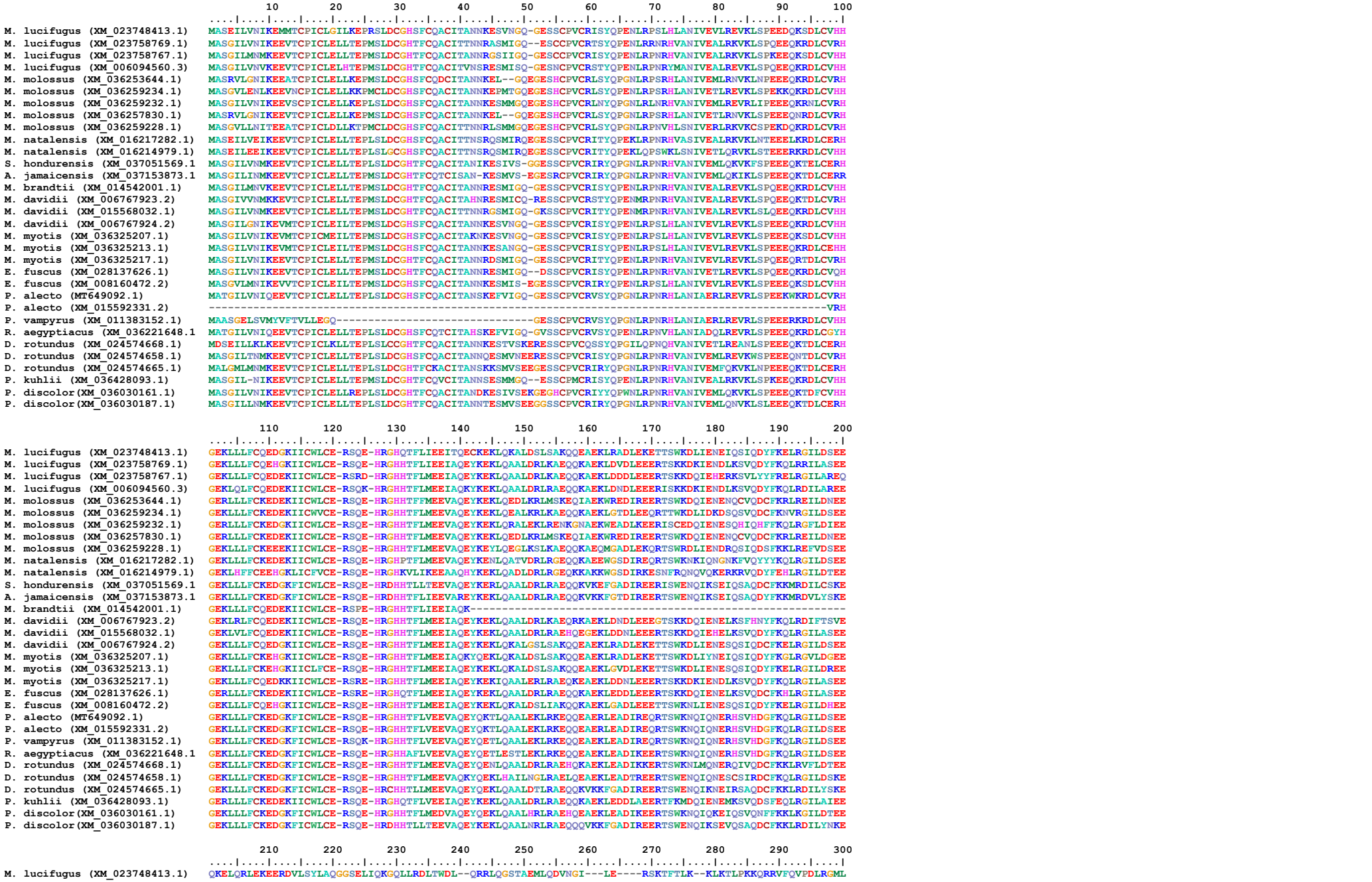
c) Codons with posterior probabilities >90% in the BEB analyses (*: P>95%; **: P>99%).

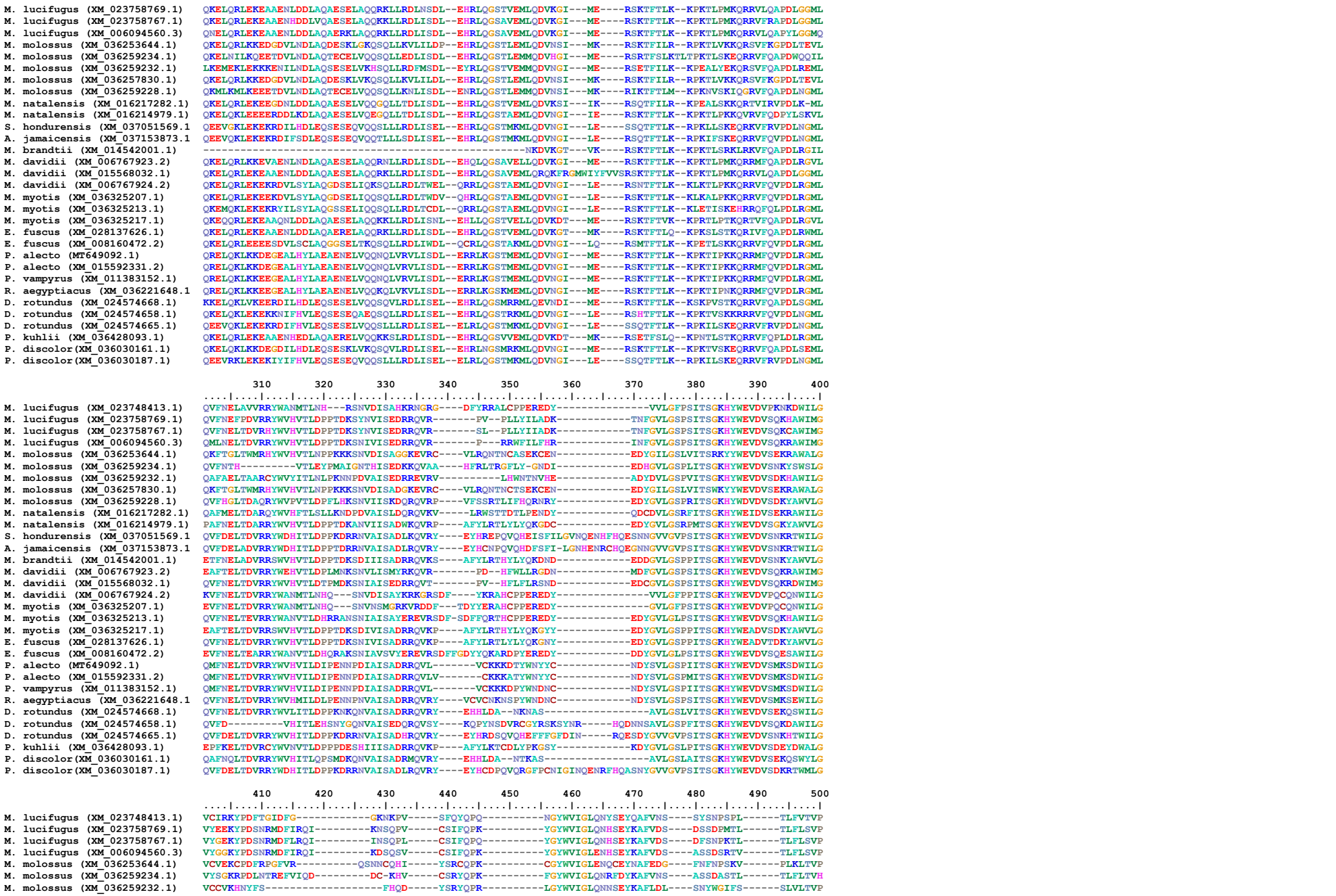
d) Codons with significance level <0.1

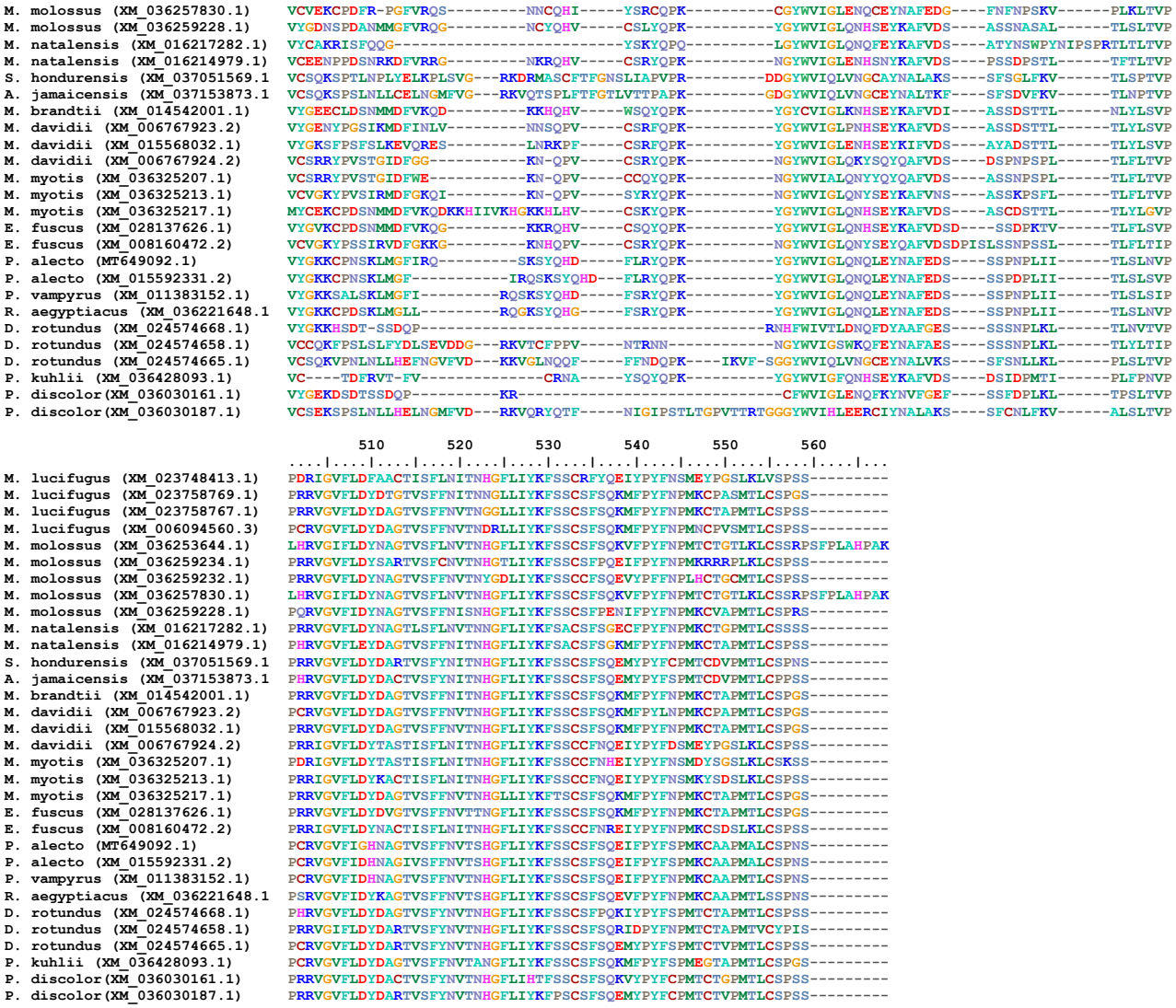
e) Codons with significance level <0.05

f) Codons with posterior probabilities >0.90

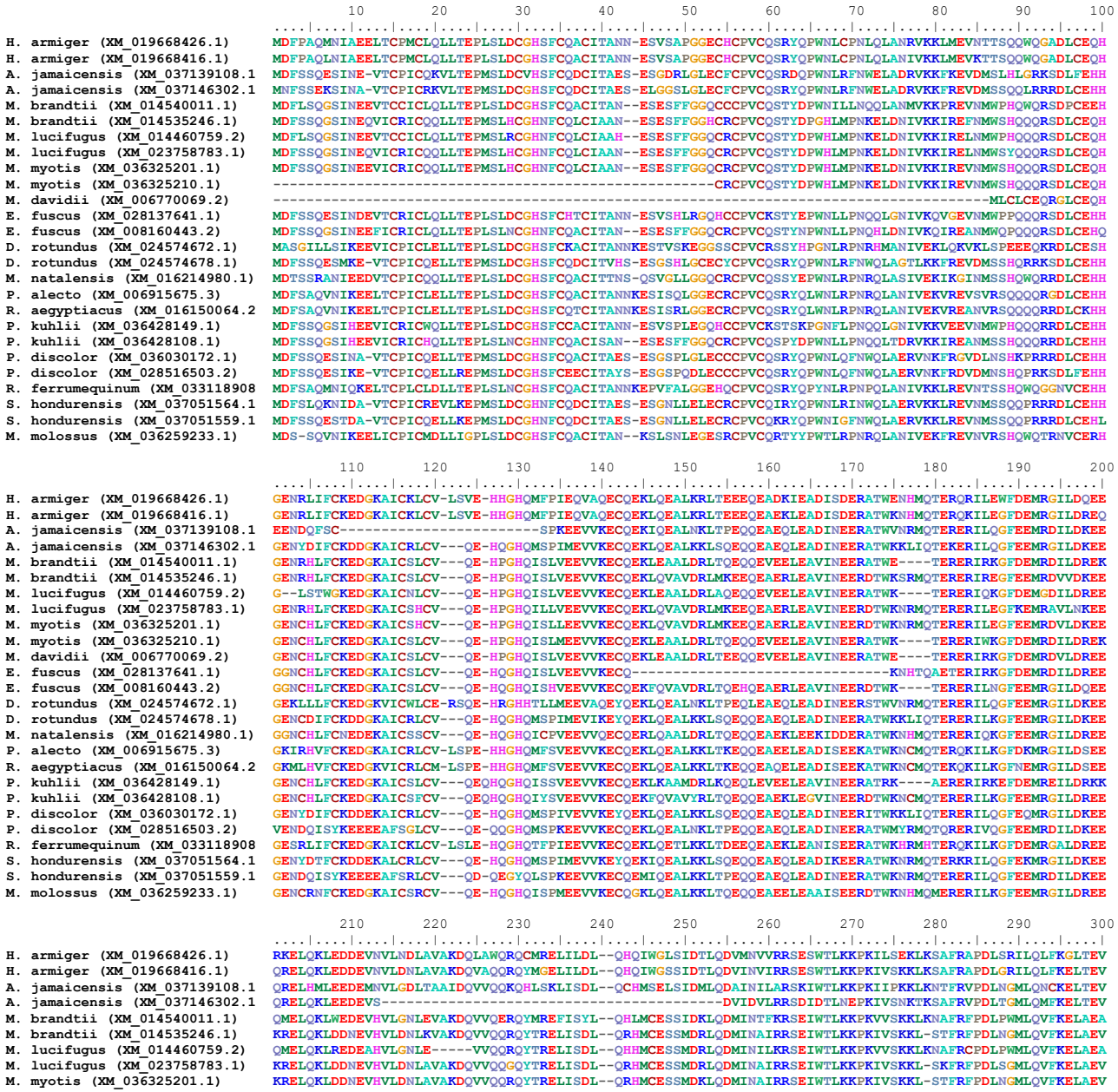
B) TRIM5 alignment used to infer codons under positive selection




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M. lucifugus (XM_023758767.1)
M. lucifugus (XM_006094560.3)
M. molossus (XM_036253644.1)
M. molossus (XM_036259234.1)
M. molossus (XM_036259232.1)
M. molossus (XM_036257830.1)
M. molossus (XM_036259228.1)
M. natalensis (XM_016217282.1)
M. natalensis (XM_016214979.1)
S. hondurensis (XM_037051569.1
A. jamaicensis (XM_037153873.1
M. brandtii (XM_014542001.1)
M. davidii (XM_006767923.2)
M. davidii (XM_015568032.1)
M. davidii (XM_006767924.2)
M. myotis (XM_036325207.1)
M. myotis (XM_036325213.1)
M. myotis (XM_036325217.1)
E. fuscus (XM_028137626.1)
E. fuscus (XM_008160472.2)
P. alecto (MT649092.1)
P. alecto (XM_015592331.2)
P. vampyrus (XM_011383152.1)
R. aegyptiacus (XM_036221648.1
D. rotundus (XM_024574668.1)
D. rotundus (XM_024574658.1)
D. rotundus (XM_024574665.1)
P. kuhlii (XM_036428093.1)
P. discolor(XM_036030161.1)
P. discolor(XM_036030187.1)
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340
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360
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380
390
400
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D. rotundus (XM_024574665.1)
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P. discolor(XM_036030187.1)
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480
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500
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M. natalensis (XM_016217282.1)
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D. rotundus (XM_024574658.1)
D. rotundus (XM_024574665.1)
P. kuhlii (XM_036428093.1)
P. discolor(XM_036030161.1)
P. discolor(XM_036030187.1)
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520
530
540
550
560

C) TRIM22 alignment used to infer codons under positive selection




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R. aegyptiacus (XM_016150064.2
P. kuhlii (XM_036428149.1)
P. kuhlii (XM_036428108.1)
P. discolor (XM_036030172.1)
P. discolor (XM_028516503.2)
R. ferrumequinum (XM_033118908
S. hondurensis (XM_037051564.1
S. hondurensis (XM_037051559.1
M. molossus (XM_036259233.1)
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H. armiger (XM_019668416.1)
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A. jamaicensis (XM_037146302.1
M. brandtii (XM_014540011.1)
M. brandtii (XM_014535246.1)
M. lucifugus (XM_014460759.2)
M. lucifugus (XM_023758783.1)
M. myotis (XM_036325201.1)
M. myotis (XM_036325210.1)
M. davidii (XM_006770069.2)
E. fuscus (XM_028137641.1)
E. fuscus (XM_008160443.2)
D. rotundus (XM_024574672.1)
D. rotundus (XM_024574678.1)
M. natalensis (XM_016214980.1)
P. alecto (XM_006915675.3)
R. aegyptiacus (XM_016150064.2
P. kuhlii (XM_036428149.1)
P. kuhlii (XM_036428108.1)
P. discolor (XM_036030172.1)
P. discolor (XM_028516503.2)
R. ferrumequinum (XM_033118908
S. hondurensis (XM_037051564.1
S. hondurensis (XM_037051559.1
M. molossus (XM_036259233.1)
410 420 430 440 450 460 470 480 490 500
H. armiger (XM_019668426.1)
H. armiger (XM_019668416.1)
A. jamaicensis (XM_037139108.1
A. jamaicensis (XM_037146302.1
M. brandtii (XM_014540011.1)
M. brandtii (XM_014535246.1)
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M. myotis (XM_036325210.1)
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D. rotundus (XM_024574678.1)
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R. aegyptiacus (XM_016150064.2
P. kuhlii (XM_036428149.1)
P. kuhlii (XM_036428108.1)
P. discolor (XM_036030172.1)
P. discolor (XM_028516503.2)
R. ferrumequinum (XM_033118908
S. hondurensis (XM_037051564.1
S. hondurensis (XM_037051559.1
M. molossus (XM_036259233.1)
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H. armiger (XM_019668426.1)
H. armiger (XM_019668416.1)

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A. jamaicensis (XM_037139108.1  WNCPVPMTLCPPGS
A. jamaicensis (XM_037146302.1  WNCPVPMTLCPPGS
M. brandtii (XM_014540011.1)    WNCPAPMTLCPPSS
M. brandtii (XM_014535246.1)    WNCPVPMKLCPPSS
M. lucifugus (XM_014460759.2)   WNCPAPMILCPPSS
M. lucifugus (XM_023758783.1)   GNCPVPMKLCPPSS
M. myotis (XM_036325201.1)      WNCPVPMKLCPPSS
M. myotis (XM_036325210.1)      WNCPAPMTLCPPSS
M. davidii (XM_006770069.2)     WNCPAPMTLSPPSS
E. fuscus (XM_028137641.1)      CNCPAPLTLCPPSS
E. fuscus (XM_008160443.2)      WNCPVPMTLCPPSS
D. rotundus (XM_024574672.1)    WNCPVPMTLCPPGS
D. rotundus (XM_024574678.1)    WNCPVPMTLCPPGS
M. natalensis (XM_016214980.1)  WNCPVPMTLCPPSS
P. alecto (XM_006915675.3)      WNCLAPMTLCQPNS
R. aegyptiacus (XM_016150064.2  GNCPTPMTLCQPNS
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P. kuhlii (XM_036428108.1)      WNCPVPITLCPPSS
P. discolor (XM_036030172.1)    WNCPVPMTLCPPGS
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S. hondurensis (XM_037051564.1  WNCPVPMTLCPPGP
S. hondurensis (XM_037051559.1  WNCPVPMTLCPPGF
M. molossus (XM_036259233.1)    WNCPAPMTLCPPSS
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