

**Figure S10.** Alignment of placental mammal AKA and AKC sequences. The alignment of the placental mammal AKA and AKC sequences used for the dN/dS analyses.

MATLAB multiple sequence alignment

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1cl|NM_198436.2 MDRSKENCISGPVKATAPVG-GPKRVLVTQQFPCQNPLPVNSGQAQRVLCPSNSSQRIPL 59
1cl|XM_01514873 MDRSKENCISGPVKPAAPVG-GPKRVLVTQQFPCQNPLPANSQAQRVLCPSNSSQRVPL 59
1cl|NM_00103802 MDRCKENCISGP-KTAVPLSDGPKRVPVAQQFPSQNPVSVNSGQAQRVLCPTNSSQRVPS 59
1cl|NM_00114250 MDRCKENCISGP-KTAVPLSDGPKRVPVAQQFPSQNPVSVNSGQAQRVLCPTNSSQRVPS 59
1cl|XM_00563519 MDKSKENCIAAGPVKTAIALGDGPKRVLVTQQVPSQNPLSANSQAQRVLCPSNSSQRVPP 60
1cl|XM_00398335 MDKSKENCVAGPVKTTIPLGDGPKRVPVTQQFPSQNLLSANSQAQRVLCPSNSSQRIPS 60
1cl|XM_00567303 MDKCKENCISGL-KTTVPPGDGPKRVPVTHFPAQHPLSANSQAQRVLCPSNSSQRLPS 59
1cl|XM_00148927 MDRSKENCISGPVKTTVPLGDGPKRVPVTQQLP-QNLLSANSQAQRVLCPSNSSHRVPS 59
1cl|XM_00443024 MDRSKENCVAGPVKTTIPLGDGPKRVLVTQQFPSQHPLSANSQAQRVLCPSNSSHRAPT 60
1cl|XM_00827414 MERCKENCISGPIKAAALLGDGPKRVPVTQRFPSQNPVSACSGQAERVLCPNSSSQRVPS 60
1cl|XM_01452869 MDKSKENGISGLVKTTIPSGDGPKRVLVTQQFPSQYPLPANSQAQRVLCPSNSSQVPS 60
1cl|XM_00468690 MDKSKENCISGPVKTMVPLRDGAKRVPVHQHAPSQSALPASSQAQRVLCPSN-SQRLPS 59
1cl|XM_00341990 MDKSKENCISGPIKTTLLPLGDGPKRVPVTQFPFQNPVSVNSGQAQRVLCPSNSSQVPS 60
1cl|XM_00432103 MDKCKENCISGP-KTTVPLGDGPKRVPVTQQFPSQNPVSVNSGQAQRVLCPSNSSQRVPS 59
1cl|NM_00101587 MSS-----PR 5
1cl|XM_00109836 MSS-----PK 5
1cl|XM_00521979 MSH----- 3
1cl|XM_00401544 MSH----- 3
1cl|XM_00561607 MLS-----G 4
1cl|XM_00694080 MQS-----G 4
1cl|XM_02109730 ----- 0
1cl|XM_00150199 M----- 1
1cl|XM_00443911 M----- 1
1cl|XM_00824896 MQS----- 3
1cl|XM_01453723 MNP----- 3
1cl|XM_01273470 MKS----- 3
1cl|XM_00340664 MFT----- 3
1cl|XM_01992887 ----- 0

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1cl|XM_01514873 QAQKLVSSHK--LVQNQKQKQLQATSVPHVPSRPPSHTPKSKQPLPSAPENNPEEELASK 117
1cl|NM_00103802 QAQKLVSIQK--PVQTLKQKPPQAASAPRPVTRPPSNTQKSKQPQPPAPGNNPEKEVASK 117
1cl|NM_00114250 QAQKLVSIQK--PVQTLKQKPPQAASAPRPVTRPPSNTQKSKQPQPPAPGNNPEKEVASK 117
1cl|XM_00563519 QTQKLVSSHK--PAQNLKQKQLQATGVPRPASRLNNTQKSEQPSSAPGNNSEKELATK 118
1cl|XM_00398335 QTQKLVSSHK--PVQNLKQKQLQATSVPRSVSRPLNNTQKSEQPLPSATGNNSEKELTTK 118
1cl|XM_00567303 HTQKLVSSHK--PVQNLKQKQSQATSGPRPVSRPLSNTQQSEQPQAAPGNNPEKEAASK 117
1cl|XM_00148927 QAQKLVSSHK--PVQNLKQKQSQATSVPHVPRPLNNTQKSEQLPSPAGNNSEKELASK 117
1cl|XM_00443024 QAQKLVSSHR--PVQNLKQKQSQATSVPPPVSRLNSTQKSEQPSPAGNNSEKERTSK 118
1cl|XM_00827414 QAQKLLPAEK---PVQKLKQAQASVPRPVSKPPNNTPKSEQPPSAPGNNPEKELTSN 116
1cl|XM_01452869 KAQKLVSSHK--PVLNLKQKQLQATSGPCPVSRPLNNTQKSEQPQPPAPGNNSEKEVASK 118
1cl|XM_00468690 QAQKLVSSHKAVPNPNLKQKQLQANNAPRAAPRPLAGTPKSEPP-PSAPGNNSEKEQASK 118
1cl|XM_00341990 QAQKLVSSRK--PVQSQKQKPLQITTVPRPVSRPPNNTPKGEQAQPPASGNNSGKELASK 118
1cl|XM_00432103 QVQKLVSSQK--SVQPLKQKPTQAASAPRSVSRPLSNTQKSEQQLPAPGNNPEKEAASK 117
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1cl|XM_00109836 AAVQLGRAQP-----AGEAVTAANQTA 27
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1cl|XM_00401544 ----RGTARK-----AGGMQPAAGAAGQ 21
1cl|XM_00561607 SAQPASEGE-----KTQEYSKDAAGH 25
1cl|XM_00694080 SVQPAAEEEE-----QTRDQGTAAAGL 26
1cl|XM_02109730 -----MKS-----GSVQPAVAAAGQ 15
1cl|XM_00150199 -SLPEAVMKS-----GSVRPAVPTAGQ 22
1cl|XM_00443911 -SLPRAVMKL-----GDVQSAGETAGQ 22
1cl|XM_00824896 -----GSSQAAG 10
1cl|XM_01453723 -GFLLSI-----IAEKKEPW 17
1cl|XM_01273470 -----GDAQAAGAAGG 14

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 1cl|XM\_01992887 -----MKS-----GSAQPA-AVAGQ 14

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 1cl|XM\_01514873 QKNEESKKRQWALEDFEIGRPLGKGKFGNVYLAREKQSKFILALKVLFKAQLEKAGVEHQ 177  
 1cl|NM\_00103802 QKNEESKKRQWALEDFEIGRPLGKGKFGNVYLAREKQSKFILALKVLFKAQLEKAGVEHQ 177  
 1cl|NM\_00114250 QKNEESKKRQWALEDFEIGRPLGKGKFGNVYLAREKQSKFILALKVLFKAQLEKAGVEHQ 177  
 1cl|XM\_00563519 QKNEESKKRQWALEDFEIGRPLGKGKFGNVYLAREKQSKFILAIKVLFAQLEKAGVEHQ 178  
 1cl|XM\_00398335 QKNEESKKRQWALEDFEIGRPLGKGKFGNVYLAREKQSKFILALKVLFKAQLEKAGVEHQ 178  
 1cl|XM\_00567303 QKNEESKKRQWALEDFEIGRPLGKGKFGNVYLAREKQSKFILALKVLFKTQLEKAGVEHQ 177  
 1cl|XM\_00148927 EKNEESKKRQWALEDFEIGRPLGKGKFGNVYLAREKQSKFILALKVLFKAQLEKAGVEHQ 177  
 1cl|XM\_00443024 EKNEESKKRQWALEDFEIGRPLGKGKFGNVYLAREKQSKFILALKVLFKAQLEKAGVEHQ 178  
 1cl|XM\_00827414 QKNEESKKRQWLEDFDIGRPLGKGKFGNVYLAREKQSKFILALKVLFKAQLEKAGVEHQ 176  
 1cl|XM\_01452869 QKNEESKK-QWLEDFEIGRPLGKGKFGNVYLAREKQSKFILALKVLFKAQLEKAGVEHQ 177  
 1cl|XM\_00468690 QKTEESKKRQWALEDFEIGRPLGKGKFGNVYLAREKQSKFILALKVLFKAQLEKAGVEHQ 178  
 1cl|XM\_00341990 QKNEESKKRQWALEDFEIGRPLGKGKFGNVYLAREKQSKFILALKVLFKAQLEKAGVEHQ 178  
 1cl|XM\_00432103 QKNEESKKRQWALEDFEIGRPLGKGKFGNVYLAREKQSKFILALKVLFKAQLEKAGVEHQ 177  
 1cl|NM\_00101587 QPSSPAMRRLTVDDFEIGRPLGKGKFGNVYLARLKESHFIVALKVLFSQIEKEGLEHQ 87  
 1cl|XM\_00109836 QPSSPAMRRLKIDDFEIGRPLGKGKFGNVYLARLKESHFIVALKVLFSQIEKEGLEHQ 87  
 1cl|XM\_00521979 TVPGAPTARRFTVDDFEIGRPLGKGKFGNVYLARLKKNHFIVALKVLFSQIEKEGLEHQ 81  
 1cl|XM\_00401544 SVPGAPAAARRFTIDDFEIGRPLGKGKFGNVYLARLKKNHFIVALKVLFSQIEKEGLEHQ 81  
 1cl|XM\_00561607 VELSVPPGRRLTIDDFEIGRPLGKGKFGNVYLARLKESHFIVALKVLFSQIEKEGLEHQ 85  
 1cl|XM\_00694080 VELGMPVRRLTIDDFEIGRPLGKGKFGNVYLARLKESHFIVALKVLFSQIEKEGLEHQ 86  
 1cl|XM\_02109730 TVSNIPTGRRLTIDDFEIGRPLGKGKFGNVYLARLKESHFIVALKVLFSQIEKEGLEHQ 75  
 1cl|XM\_00150199 SQPGFPNVRHLTIDDFEIGRPLGKGKFGNVYLARLKESHFIVALKVLFSQIEKEGLEHQ 82  
 1cl|XM\_00443911 TQPSFPTVRHFTIDDFEIGRPLGKGKFGNVYLARLKESHFIVALKVLFSQIEKEGLEHQ 82  
 1cl|XM\_00824896 PAQPSVPLRRLTIDDFEIGRPLGKGKFGNVYLARLKDSHFIVALKVLFSQIEKEGMEHQ 70  
 1cl|XM\_01453723 PSSPSPGSRSLTIDDFIRCLPLGKGKFGNVYLARLRDSHFIVALKVLFSQIEKEGMEHQ 77  
 1cl|XM\_01273470 PALPVATVRRLTIDDFEIGRPLGKGKFGNVYLARLRRESRFLVALKVLFSQIEKEGLEHQ 74  
 1cl|XM\_00340664 YGDVLLRRLTIDDFEIGRPLGKGKFGNVYLARLQENHFLVALKVLFSQIEKEGLEHQ 84  
 1cl|XM\_01992887 TMPSIPTVRRLTIDDFEIGRPLGKGKFGNVYLARLKESHFIVALKVLFSQIEKEGLEHQ 74

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 1cl|XM\_01514873 LRREVEIQSHLRHPNLRLYGYFHDATRVYLILEYAPLGTVYRELQKLSKFDEQRTAT-Y 236  
 1cl|NM\_00103802 LRREVEIQSHLRHPNLRLYGYFHDATRVYLILEYAPLGAVYRELQKLSKFDEQRTAT-Y 236  
 1cl|NM\_00114250 LRREIQSHLRHPNLRLYGYFHDATRVYLILEYAPLGAVYRELQKLSKFDEQRTAT-Y 236  
 1cl|XM\_00563519 LRREVEIQSHLRHPNLRLYGYFHDATRVYLILEYAPLGAVYRELQKLSKFDEQRTAT-Y 237  
 1cl|XM\_00398335 LRREVEIQSHLRHPNLRLYGYFHDATRVYLILEYAPLGAVYRELQKLSKFDEQRTAT-Y 237  
 1cl|XM\_00567303 LRREVEIQSHLRHPNLRLYGYFHDATRVYLILEYAPLGAVYRELQKLSKFDEQRTAT-Y 236  
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 1cl|XM\_00827414 LRREVEIQSHLRHPNLRLYGYFHDATRVYLILEYAPLGTVYRELQKLSKFDEQRTAT-Y 235  
 1cl|XM\_01452869 LRREVEIQSHLRHPNLRLYGYFHDATRVYLILEYAPLGTVYRELQKLSRFDEQRTAT-Y 236  
 1cl|XM\_00468690 LRREVEIQSHLRHPNLRLYGYFHDATRVYLILEYAPLGAVYRELQKLSKFDEQRTAT-Y 237  
 1cl|XM\_00341990 VRREVEIQSHLRHPNLRLYGYFHDATRVYLILEYAPLGTVYRELQKXSKFDEQRTAP\*Y 238  
 1cl|XM\_00432103 LRREVEIQSHLRHPNLRLYGYFHDATRVYLILEYAPLGAVYRELQKLSKFDEQRTAT-Y 236  
 1cl|NM\_00101587 LRREIEIQAHLQHPNLRLYNYFHDARRVYLILEYAPRGELYKELQKSEKLDEQRTAT-I 146  
 1cl|XM\_00109836 LRREIEIQAHLQHPNLRLYNYFHDARRVYLILEYAPRGELYKELQKSEKLDEQRTAT-I 146  
 1cl|XM\_00521979 LRREVEIQAHLQHPNLRLYNYFHDARRVYLILEYAPKGELYKALQRSHTFDEQRTAT-I 140  
 1cl|XM\_00401544 LRREVEIQAHLQHPNLRLYNYFHDARRVYLILEYAPKGELYKALQRSHTFDEQRTAT-I 140  
 1cl|XM\_00561607 LRREIEIQAHLQHPNLRLYNYFHDARRVYLILEYAPRGELYKELQKSHTLDEQRTAT-I 144  
 1cl|XM\_00694080 LRREIEIQAHLQHPNLRLYNYFHDARRVYLILEYAPRGELYKELQKSNTLDEQRTAT-I 145  
 1cl|XM\_02109730 LRREIEIQAHLQHPNLRLYNYFHDARRVYLILEYAPRGELYKELQKSHTLDEQRTAT-I 134  
 1cl|XM\_00150199 LRREIEIQAHLQHPNLRLYNYFHDARRVYLILEYAPRGELYKELQKSHTLDEQRTAT-I 141  
 1cl|XM\_00443911 LRREIEIQAHLQHPNLRLYNYFHDARRVYLILEYAPRGELYKELQKSHTLDEQRTAT-I 141  
 1cl|XM\_00824896 LRREIEIQAHLQHPNLRLYNYFHDARRVYLILEYAPRGELYKELQKCHTLDEQRTAT-I 129  
 1cl|XM\_01453723 LRREIEIQSHLRHPNLRHNYFHDARRVYLILEYAPRGELYKELQKSHTIDEQSTAT-I 136

lc| |XM\_01273470 LRREVEIQAHLRHPNILRLYNYFHDARRVYLILEYAPRGELYKELQNCHTLDEQRTAT-I 133  
lc| |XM\_00340664 LRREIEIQAHLQHPNILRLYNYFHDARRVYLILEYAPRGELYKELQKSHRLDEQRTAT-I 143  
lc| |XM\_01992887 LRREIEIQAHLQHPNILRLYNYFHDARRMYLILEYAPRGELYKELQKSHTLDEQRTAT-V 133  
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lc| |NM\_00114250 ITELANALSYCHSKRVIHRDIKPENLLGSAGELKIADFGWSVHAPSSRRTTLCGTDYL 296  
lc| |XM\_00563519 ITELADALSYCHSKRVIHRDIKPENLLGSAGELKIADFGWSVHAPSSRRTTLCGTDYL 297  
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lc| |XM\_00148927 ITELANALAYCHSKRVIHRDIKPENLLGSAGELKIADFGWSVHAPSSRRTTLCGTDYL 296  
lc| |XM\_00443024 ITELANALAYCHSKRVIHRDIKPENLLGSAGELKIADFGWSVHAPSSRRTTLCGTDYL 297  
lc| |XM\_00827414 ITELANALLYCHSKRVIHRDIKPENLLGSAGELKIADFGWSVHAPSSRRTTLCGTDYL 295  
lc| |XM\_01452869 ITEL TNALSYCHSKRVIHRDIKPENLLGSTGELKIADFGWSVHAPSSRRTTLCGTDYL 296  
lc| |XM\_00468690 ITELADALSYCHSKRVIHRDIKPENLLGSAGELKIADFGWSVHAPSSRRTTLCGTDYL 297  
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lc| |NM\_00101587 IEELADALTYCHDKKVIHRDIKPENLLGFRGEVKIADFGWSVHTPSLRRTMCGTDYL 206  
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lc| |XM\_00521979 IEELADALTYCHERKVIHRDIKPENLLGLMGEVKIADFGWSVHTPSLRRTTLCGTDYL 200  
lc| |XM\_00401544 IEELADALTYCHEKKVIHRDIKPENLLGLMGEVKIADFGWSVHTPSLRRTTLCGTDYL 200  
lc| |XM\_00561607 MEELADALTYCHEKKVIHRDIKPENLLGFRGEVKIADFGWSVHTPSLRRTMCGTDYL 204  
lc| |XM\_00694080 MEELADALTYCHEKKVIHRDIKPENLLGFRGEVKIADFGWSVHTPSLRRTMCGTDYL 205  
lc| |XM\_02109730 MEELADALTYCHEKKVIHRDIKPENLLGFRGEVKIADFGWSVHTPSLRRTMCGTDYL 194  
lc| |XM\_00150199 MEELADALTYCHEKKVIHRDIKPENLLGFRGEVKIADFGWSVHTPSLRRTMCGTDYL 201  
lc| |XM\_00443911 MEELADALTYCHEKKVIHRDIKPENLLGFRGEVKIADFGWSVHTPSLRRTMCGTDYL 201  
lc| |XM\_00824896 MEELADALTYCHGKVIHRDIKPENLLGFRGEVKIADFGWSVHTSLRRRTMCGTDYL 189  
lc| |XM\_01453723 MEELAHALAYCHENKVIHRDIKPENLLGLRGEVKIADFGWSVHTPSLRRTMCGTDYL 196  
lc| |XM\_01273470 IEELADALTYCHEKKVIHRDIKPENLLGYRGEVKIADFGWSVHTPSLRRTMCGTDYL 193  
lc| |XM\_00340664 MEELADALTYCHEKKVIHRDIKPENLLGLRGEVKIADFGWSVHTSLRRRTMCGTDYL 203  
lc| |XM\_01992887 MEELADALTYCHEKKVIHRDIKPENLLGFRGEVKIADFGWSVHTPSLRRTMCGTDYL 193  
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lc| |XM\_00827414 PPEMIEGRMHDEKVDLWSLGVLCYEFVLVGKPPFEANTYQETYRRISRVEFTFPDFVTEGA 355  
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lc| |XM\_00109836 PPEMIEGRTYDEKVDLWCIGVLCYELLVGYPPEFESTSHSETYRRILKVDVRFPLSMPLGA 266  
lc| |XM\_00521979 PPEMIEGRTYDEKVDLWCIGVLCYELLVGNPPFESASTSETYRRILKVDLRFPPSMSSGA 260  
lc| |XM\_00401544 PPEMIEGRTYDEKVDLWCIGVLCYELLVGNPPFESASTSETYRRILKVDLRFPPSMSSGA 260  
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lc| |XM\_00443911 PPEMIEGRTYNEKVDLWCIGVLCYELLVGNPPFESNSHNETYRRILKVDVRFPPSIPLGA 261  
lc| |XM\_00824896 PPEMIEGRTYDEKVDLWCIGVLCYELLVGNPPFESVSHNETYRRILKVDVRFVPTMSLGA 249

lcl | XM\_01453723 PPEMVEQRTYSEMVDLWCIGVLCYELLVGNPPFKSSSYSETYRRILKVDVKFPPSIPLGA 256  
lcl | XM\_01273470 PPEMIEGRTYNEKVDLWCIGVLCYELLVGKPPFESSHNETYRRILKVDVRFPPSVPLGA 253  
lcl | XM\_00340664 PPEMIEGRTYDERVDLWCIGVLCYELLVGNPPFESSHTETYRRILKVDVRFPPSMPSGA 263  
lcl | XM\_01992887 PPEMIEGRTYNEKVDLWCIGVLCYELLVGNPPFESSHNETYRRILQVDVRFPPSMPLGA 253  
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lcl | XM\_01514873 RDLISRLKHNPSQRPLKEVLEHPWITANSSKPSNCQNRVN\*----- 399  
lcl | NM\_00103802 RDLISRLKHNPSQRPTLKEVLEHPWIIANSKPSQCQKKESTSKQS\*-- 403  
lcl | NM\_00114250 RDLISRLKHNPSQRPTLKEVLEHPWITANSKPSQCQKKESTSKQS\*-- 403  
lcl | XM\_00563519 RDLISRLKHNPSQRPTLKDVLEHPWIMANSSKPSQKNDSTSKQS\* 406  
lcl | XM\_00398335 RDLISRLKHNPSQRPTLKEVLEHPWITANSKPSGSKSKESTGKQS\* 406  
lcl | XM\_00567303 RDLISRLKHNPSHRPTLKEVLEHPWITANSKPASSHKKESTSKQP\*-- 403  
lcl | XM\_00148927 RDLISRLKHNPSQRPTLKEVLEHPWITANSSKPSNSQKSKESTSKQP\* 405  
lcl | XM\_00443024 RDLISRLKHNPSQRPTLKEVLEHPWITANASKPSNSQKSKESTSKQS\* 406  
lcl | XM\_00827414 KDFISRLKHNPSHRPTLAEVLEHPWVKAKSSKPSCPDKEPASKQS\*- 403  
lcl | XM\_01452869 RDLISRLMHNPQNRLTLKEVLEHPWITANSSKPSQKSKESTSKQS\* 405  
lcl | XM\_00468690 RDLISRLKHNPSQRPTLKEVLEHPWITANSSKPPSSQKKNKESTSKQS\* 406  
lcl | XM\_00341990 RDLVSRLLKHNPSQRLTLKEVLEHPWITANSKKPPSSQNKKEPTSKQS\*- 406  
lcl | XM\_00432103 RDLISRLKHNPSQRPTLKEVLEHPWITANSKPSQKKESTSKQS\*-- 403  
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lcl | XM\_00561607 QDLVSKLLRYQPLERLPLAQIMEHPWVRAHSRRVLPPSVQMAS\*----- 308  
lcl | XM\_00694080 RDLISKLLRYQPLERLPLSQILEHPWVRAHSRRVPPSVQMDS\*----- 309  
lcl | XM\_02109730 QDLISRLRYQPSDRPLDQILEHPWVRAHSRRVLPPSTQMVS\*----- 298  
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lcl | XM\_00443911 KDLISKLLRYQPLERLPLDQIMEHPWVRAHSRRVLPPSAQMAS\*----- 305  
lcl | XM\_00824896 RDLISRLRYQPSERLPLAQILRHPWVQAHSRRVLPPCAHPAS\*----- 293  
lcl | XM\_01453723 QDLISKLLRYQPSERLLAQVLQHPWVQAHSRRVGGPPAPSAS\*----- 300  
lcl | XM\_01273470 QDLISSLLRYQPSERLPLAQILQHPWVRMHSRRVLPPSAQVAS\*----- 297  
lcl | XM\_00340664 QDLISKLLRYQPFERLALAQVLEHPWVQAHSQRVLPSPVQMAF\*----- 307  
lcl | XM\_01992887 QDLISKLLRYQPSERLPLVQILEHPWVRAHSRRVLPPSAQMVS\*----- 297  
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