

**Figure S2.** Alignment of placental mammal AK sequences. The alignment of the placental mammal AKA, AKB, and AKC sequences used for the dN/dS analyses.

MATLAB multiple sequence alignment

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lcl|NM_001038002 MDRCKENCISGP-KTAVPLSDGPKRVPVAQGFPSQNPVSVNSGQAQRVLCPTNSSQRIPL 59
lcl|NM_00114250 MDRCKENCISGP-KTAVPLSDGPKRVPVAQGFPSQNPVSVNSGQAQRVLCPTNSSQRIPL 59
lcl|XM_00563519 MDKSKENCISGPVKTAIALGDGPKRVLVTQQVPSQNPVSVNSGQAQRVLCPSNSSQRIPL 60
lcl|XM_00398335 MDKSKENCISGPVKTTIPLGDGPKRVPVTQGFPSQNPVSVNSGQAQRVLCPSNSSQRIPL 60
lcl|XM_00567303 MDKCKENCISGL-KTTVPPGDGPKRVPVTQHFPAQHLPSANSGQAQRVLCPSNSSQRIPL 59
lcl|XM_00148927 MDRSKENCISGPVKTTVPLGDGPKRVPVTQQLP-QNLLSANSGQAQRVLCPSNSSQRIPL 59
lcl|XM_00443024 MDRSKENCISGPVKTTIPLGDGPKRVLVTQGFPSQNPVSVNSGQAQRVLCPSNSSQRIPL 60
lcl|XM_00827414 MERSKENCISGPVKAALLGDGPKRVPVTQGFPSQNPVSVNSGQAQRVLCPSNSSQRIPL 60
lcl|XM_01452869 MDKSKENCISGLVKTIPSGDGPKRVLVTQGFPSQNPVSVNSGQAQRVLCPSNSSQRIPL 60
lcl|XM_00468690 MDKSKENCISGPVKTMVPLRDGAKRVPVHQHAPSQSALPASSGQAQRVLCPSNSSQRIPL 59
lcl|XM_00341990 MDKSKENCISGPVKTTLPLGDGPKRVPVTQGFPSQNPVSVNSGQAQRVLCPSNSSQRIPL 60
lcl|XM_00432103 MDKCKENCISGP-KTTVPLGDGPKRVPVTQGFPSQNPVSVNSGQAQRVLCPSNSSQRIPL 59
lcl|NM_004217.3 MAQKENSYPWPYGRQTAQSG-----LSTLPQRLRKEPV 34
lcl|XM_01511855 MAQKENAYPWPYGRQTAQSG-----LSTLPQRLRKEPV 34
lcl|NM_183084.2 MAQKENAYPWPYGRQTAQSG-----LNTLPQRLRKEPV 34
lcl|XM_00401268 MAQKENAYPWPYGRQTAQSG-----LNTLPQRLRKEAV 34
lcl|XM_844813.4 MTQKENAYPWPYGRQTTQPG-----LNTLPQRLRKDPA 34
lcl|XM_00399619 MAQKENAYPWPYGRQTTQPG-----LNTLPQRLRKEPA 34
lcl|NM_213919.2 MAQKENTYPWPYGRQTAQSG-----LNTLPQRLRKEAV 34
lcl|XM_00150481 MTQKENAYPWPYGRQTAQSG-----LNTLPQRLRKEPA 34
lcl|XM_00443309 MAQKENAYPWPYGRQTAQSG-----LNTLPQRLRKEPV 34
lcl|XM_00827074 MAQKENAYPWPYSRPTQSG-----LNTLPQRLRKEAA 34
lcl|XM_00587878 MTQKENAYPWPYGRQTAQSG-----LNTLPQRLRKEAV 34
lcl|XM_00468461 MAQKENAYPWPYGRQTAQSG-----LNTLPQRLRKEAV 34
lcl|XM_00341691 MAQKENAYPWPYGRQTAQSG-----LNTLPQRLRKEAV 34
lcl|XM_01994424 MAQKENAYPWPYGRQTAQSG-----LNTLPQRLRKEPV 34
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lcl|XM_00109836 MSSPKAAVLGKAAQ----- 14
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lcl|XM_00694080 MQSGSVQPAASEEE----- 14
lcl|XM_02109730 MKSGSVQPAASAAA----- 13
lcl|XM_00150199 MSLEAVMKSGSV----- 13
lcl|XM_00443911 MSLEAVMKSGSV----- 13
lcl|XM_00824896 MQS----- 3
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lcl|XM_01992887 MKSGSAQPAAVAG----- 13
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lcl|NM_001038002 QAKLVSIQK--PVQTLKQKPPQAASAPRPVTRPPSNTQKSKQPLSPAPENNPKEELASK 117
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lcl|XM_00567303 HTQLVSSHK--PVQNLKQKQSQATSGPRVPSRPLNNTQKSEQPLSPAGNNSEKELASK 117
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lcl|XM_00468461 TPSALVMNR-----SNTQPTAAPGQ---KVMENS 61
lcl|XM_00341691 TPSALVMSR-----SNAQPTAALGQ---KVMENS 62
lcl|XM_01994424 TPSALVMSR-----SNAQPTAALQ---KVMENS 61
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lcl|XM_00109836 -----PA-----GEAVTANQTA----- 27
lcl|XM_00521979 -----HAAAAGQ----- 21
lcl|XM_00401544 -----PAAAAGQ----- 21
lcl|XM_00561607 -----K-----TQEQSKDAAGH----- 25
lcl|XM_00694080 -----Q-----TRDQGTAAAGL----- 26
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lcl|XM\_01992887 -----Q----- 14

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lcl|NM\_00103802 QKNEESKKRQWALEDFEIGRPLGKGKFGNVYLAREKQSKFILALKVLFKAQLEKAGVEHQ 177  
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lcl|XM\_00398335 QKNEESKKRQWALEDFEIGRPLGKGKFGNVYLAREKQSKFILALKVLFKAQLEKAGVEHQ 178  
lcl|XM\_00567303 QKNEESKKRQWALEDFEIGRPLGKGKFGNVYLAREKQSKFILALKVLFKAQLEKAGVEHQ 177  
lcl|XM\_00148927 EKNEESKKRQWALEDFEIGRPLGKGKFGNVYLAREKQSKFILALKVLFKAQLEKAGVEHQ 177  
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lcl|XM\_01992887 TMPSIPTVRRLTIDDFEIGRPLGKGKFGNVYLARLKESHFIVALVKVLFKSQIEKEGLEHQ 74  
::\*: \* \*\*\*\*\* ..\*:\*:\*:\*:\*: \*::\*

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lclIMM_00150199	MEELADALTYCHEKKVHHRDIKPENLLGFRGEVKIADFGWSVHTPSLRRKTCGTL	DYL	201
lclIMM_00443911	MEELADALTYCHEKKVHHRDIKPENLLGFRGEVKIADFGWSVHTPSLRRKTCGTL	DYL	201
lclIMM_00824896	MEELADALTYCHGGKVHHRDIKPENLLGFRGEVKIADFGWSVHTPSLRRKTCGTL	DYL	189
lclIMM_01453723	MEELAHALAYCHENKVHHRDIKPENLLGLRGVEKIADFGWSVHTPSLRRKTCGTL	DYL	196
lclIMM_01273470	IEELADALTYCHEKKVHHRDIKPENLLGYRGEVKIADFGWSVHTPSLRRKTCGTL	DYL	193
lclIMM_00340664	MEELADALTYCHEKKVHHRDIKPENLLGFRGEVKIADFGWSVHTPSLRRKTCGTL	DYL	203
lclIMM_01992887	MEELADALTYCHEKKVHHRDIKPENLLGFRGEVKIADFGWSVHTPSLRRKTCGTL	DYL	193

lclIXM\_00561607 PPEMIERRTYNEKVDLWCIGVLCYELLVGYPFESPSHNETYRRILKVDLRFPPSLPLGA 264  
lclIXM\_00694080 PPEMIERRTYNETVDLWCIGVLCYELLVGNPPFESHSHNETYRRILKVDIRFPPSIPLGA 265  
lclIXM\_02109730 PPEMIEGRTYNEKVDLWCIGVLCYELLVGNPPFESASHNETYRRILKVDVRFPPSLPLGA 254  
lclIXM\_00150199 PPEMIEGRTYNEKVDLWCIGVLCYELLVGNPPFESASHNETYRRILKVDVRFPPSIPLGA 261  
lclIXM\_00443911 PPEMIEGRTYNEKVDLWCIGVLCYELLVGNPPFESASHNETYRRILKVDVRFPPSIPLGA 261  
lclIXM\_00824896 PPEMIEGRTYDEKVDLWCIGVLCYELLVGNPPFESVSHNETYRRILKVDVRFPPSIPLGA 249  
lclIXM\_01453723 PPEMVEQRTYSEMDLWCIGVLCYELLVGNPPFESSYSETYRRILKVDVRFPPSIPLGA 256  
lclIXM\_01273470 PPEMIEGRTYNEKVDLWCIGVLCYELLVGKPPFESSHNETYRRILKVDVRFPPSVPLGA 253  
lclIXM\_00340664 PPEMIEGRTYDERVDLWCIGVLCYELLVGNPPFESSHTNETYRRILKVDVRFPPSMPSGA 263  
lclIXM\_01992887 PPEMIEGRTYNEKVDLWCIGVLCYELLVGNPPFESPSHNETYRRILQVDVRFPPSMPLGA 253  
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lclINM\_198436.2 RDLISRLLKHNPSSQRPMLEVLHPWITANSKPSNCQNKESASKQS\*- 404  
lclIXM\_01514873 RDLISRLLKHNPSSQRPMLEVLHPWITANSKPSNCQNRVN\*----- 399  
lclINM\_00103802 RDLISRLLKHNPSSQRPTLKEVLHPWITANSKPSQCKKESTSKQS\*- 403  
lclINM\_00114250 RDLISRLLKHNPSSQRPTLKEVLHPWITANSKPSQCKKESTSKQS\*- 403  
lclIXM\_00563519 RDLISRLLKHNPSSQRPTLKEVLHPWITANSKPSQCKKESTSKQS\* 406  
lclIXM\_00398335 RDLISRLLKHNPSSQRPTLKEVLHPWITANSKPSQCKKESTGKQS\* 406  
lclIXM\_00567303 RDLISRLLKHNPSSHRPTLKEVLHPWITANSKPASSHKESTSKQP\*- 403  
lclIXM\_00148927 RDLISRLLKHNPSSQRPTLKEVLHPWITANSKPSQCKKESTSKQP\* 405  
lclIXM\_00443024 RDLISRLLKHNPSSQRPTLKEVLHPWITANSKPSQCKKESTSKQS\* 406  
lclIXM\_00827414 KDFISRLLKHNPSSHRPTLAELHPWVWKAQSSKPSQCKKESTSKQS\*- 403  
lclIXM\_01452869 RDLISRLLKHNPSSQRPTLKEVLHPWITANSKPSQCKKESTSKQS\* 405  
lclIXM\_00468690 RDLISRLLKHNPSSQRPTLKEVLHPWITANSKPSQCKKESTSKQS\* 406  
lclIXM\_00341990 RDLISRLLKHNPSSQRPTLKEVLHPWITANSKPSQCKKESTSKQS\*- 406  
lclIXM\_00432103 RDLISRLLKHNPSSQRPTLKEVLHPWITANSKPSQCKKESTSKQS\*- 403  
lclINM\_004217.3 QDLISKLLRHNPSSERLPLAQVSAHPWVRANSRRVLPSSALQSV\*----- 345  
lclIXM\_01511855 QDLISKLLRHNPSSERLPLAQVSAHPWVRANSRRVLPSSALQSV\*----- 345  
lclINM\_183084.2 QDLISKLLRHNPSSERLPLAQVSAHPWVRANSRRVLPSSALQSV\*----- 345  
lclIXM\_00401268 QDLISKLLRHNPSSERLPLAQVSAHPWVRANSRRVLPSSALQSV\*----- 345  
lclIXM\_844813.4 QDLISKLLRHNPSSERLPLAQVSAHPWVRANSRRVLPSSALQSV\*----- 345  
lclIXM\_00399619 QDLISKLLRHNPSSERLPLAQVSAHPWVRANSRRVLPSSALQSV\*----- 345  
lclINM\_213919.2 QDLISKLLRHNPSSERLPLAQVSAHPWVRANSRRVLPSSALQSV\*----- 345  
lclIXM\_00150481 QDLISKLLRHNPSSERLPLAQVSAHPWVRANSRRVLPSSALQSV\*----- 345  
lclIXM\_00443309 QDLISKLLRHNPSSERLPLAQVSAHPWVRANSRRVLPSSALQSV\*----- 345  
lclIXM\_00827074 QDLISKLLRHNPSSERLPLAQVSAHPWVRANSRRVLPSSALQSV\*----- 344  
lclIXM\_00587878 QDLISKLLRHNPSSERLPLAQVSAHPWVRANSRRVLPSSALQSV\*----- 340  
lclIXM\_00468461 QDLISKLLRHNPSSERLPLAQVSAHPWVRANSRRVLPSSALQSV\*----- 345  
lclIXM\_00341691 QDLISKLLRHNPSSERLPLAQVSAHPWVRANSRRVLPSSALQSV\*----- 346  
lclIXM\_01994424 QDLISKLLRHNPSSERLPLAQVSAHPWVRANSRRVLPSSALQSV\*----- 345  
lclINM\_00101587 RDLISRLLRYQPLERLPLAQILKHPWVQAHSRRVLPSCAQMAS\*----- 310  
lclIXM\_00109836 RDLISKLLRYQPLERLPLAQILKHPWVQAHSRRVLPSCAQMAS\*----- 310  
lclIXM\_00521979 RDLISKLLRFQPLERLPLVRVLEHPWIRAHSSRRVLPSSVPMF\*----- 304  
lclIXM\_00401544 RDLISKLLRFQPLERLPLVRVLEHPWIRAHSSRRVLPSSVPMF\*----- 304  
lclIXM\_00561607 QDLVSKLLRYQPLERLPLAQIMEHPWVRANSRRVLPSSVQMAS\*----- 308  
lclIXM\_00694080 RDLISKLLRYQPLERLPLSQILEHPWVRANSRRVLPSSVQMAS\*----- 309  
lclIXM\_02109730 QDLISRLLRYQPSDRLLDQILEHPWVRANSRRVLPSTQMV\*----- 298  
lclIXM\_00150199 KDLISKLLRYQPLERLPLDQILEHPWVRANSRRVLPSSAQMAS\*----- 305  
lclIXM\_00443911 KDLISKLLRYQPLERLPLDQIMEHPWVRANSRRVLPSSAQMAS\*----- 305  
lclIXM\_00824896 RDLISRLLRYQPSERLPLAQILRHPWVQAHSRRVLPSCAHPAS\*----- 293  
lclIXM\_01453723 QDLISKLLRYQPSERLPLAQVLEHPWVQAHSRRVLPSCAHPAS\*----- 300  
lclIXM\_01273470 QDLISSLLRYQPSERLPLAQILQHPWVRANSRRVLPSCAHPAS\*----- 297  
lclIXM\_00340664 QDLISKLLRYQPFERLALAQVLEHPWVQAHSRRVLPSCAHPAS\*----- 307  
lclIXM\_01992887 QDLISKLLRYQPSERLPLVQILEHPWVRANSRRVLPSCAHPAS\*----- 297  
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