

**Figure S8.** Alignment of placental mammal AKB and AKC sequences. The alignment of the placental mammal AKB and AKC sequences used for the dN/dS analyses.

MATLAB multiple sequence alignment

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1cl|NM_004217.3 MAQKENSYPWPYGRQTAPSGSLSTLPQRVLRKEPVTSPALVMSRSNVQPTAAPGQ-KVME 59
1cl|XM_01511855 MAQKENAYPWPYGRQTAPSGSLSTLPQRVLRKEPVTSPALVMSRSNVQPTAAPGQ-KVVE 59
1cl|NM_183084.2 MAQKENAYPWPYGRQTAPGLNLTLPQRVLRKEPVTSPALVMSRSNAQPTAAPGQ-KVVE 59
1cl|XM_00401268 MAQKENAYPWPYGRQTAPGLNLTLPQRVLRKEAVIPSAVLMMSRSNAQPTAAPGQ-KVVE 59
1cl|XM_844813.4 MTQKENAYPWPYGRQTTPQGLNLTLPQRVLRKDPATPSALVMSRSNGQPTAAPGQ-KVVE 59
1cl|XM_00399619 MAQKENAYPWPYGRQTTPQGLNLTLPQRVLRKEPATPSALVMSRSNTQPTAAPGQ-KVVE 59
1cl|NM_213919.2 MAQKENTYPWPYGRQTAQSGNLNLTLPQRVLRKEAVTPSALVMSRSNTQPTAAPGQ-KVVE 59
1cl|XM_00150481 MTQKENAYPWPYGRQTAQSGNLNLTLPQRVLRKEPATPSALVMSRSNAQPTVALGQ-KVME 59
1cl|XM_00443309 MAQKENAYPWPYGRQTAQSGNLNLTLPQRVLRKEPVTSPALVMSRSNAQPTAALGQ-KVVE 59
1cl|XM_00827074 MAQKENAYPWPYSRPTPQSGNLNLTLPQRILRKEAATPSALVLLNRSNAPPTAVLGQ-KGME 59
1cl|XM_00587878 MTQKENAYPWPYGRQTAQCGNLNLTLPQRVLRKQDPTTSSLVMSRSNAQPTAAPGQ----- 55
1cl|XM_00468461 MAQKENAYPWPYGRQTAQSGNLNLTLPQRVLRKDPPTPSALVLMMSRSNTQPTAAPGQ-KVVE 59
1cl|XM_00341691 MAQKENAYPWPYGRQTAQSGNLNLTLPQRVFRKDLATPSALVMSRSNAQPTAAPGKKMTE 60
1cl|XM_01994424 MAQKENAYPWPYGRQTAQSGNLNLTLPQRVLRKEPVTSPALVMSRSNAQPTAAPLQ-KVVE 59
1cl|NM_00101587 MSSPRAVVQLGKA-----QPAGEELATANQTA----- 27
1cl|XM_00109836 MSSPKAAVQLGRA-----QPAGEAVTAANQTA----- 27
1cl|XM_00521979 MSHRGATARKAGG-----MQHAAAAGQ----- 21
1cl|XM_00401544 MSHRGATARKAGG-----MQPAAAAGQ----- 21
1cl|XM_00561607 MLSGSAQPAASE-----GEKTQEQSKDAAGH----- 25
1cl|XM_00694080 MQSGSVQPAEE-----EEQTRDQGTAAAGL----- 26
1cl|XM_02109730 MKSGSVQPAVA-----AAGQ----- 15
1cl|XM_00150199 MSLPEAVMKSG-----SVRPAPVPTAGQ----- 22
1cl|XM_00443911 MSLPRAVMKLG-----DVQSAGETAGQ----- 22
1cl|XM_00824896 MQS-----GSSQAAG----- 10
1cl|XM_01453723 MNPGLLSIIAE-----KKEPW----- 17
1cl|XM_01273470 MKS-----GDAQAAGAAGG----- 14
1cl|XM_00340664 MFTNVALSFARR-----EWKELAPTERAL----- 24
1cl|XM_01992887 MKSGSAQPAAV-----AGQ----- 14

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1cl|NM_004217.3 NSSGTPDILTRHFTIDDFEIGRPLGKGKFGNVYLAREKKSHFIVALKVLFKSQIEKEGVE 119
1cl|XM_01511855 NSSGTPNIMLRHFTIDDFEIGRPLGKGKFGNVYLAREKKSHFIVALKVLFKSQIEKEGVE 119
1cl|NM_183084.2 NSSGTPNIPKRSFTIDDFEIGRPLGKGKFGNVYLAREKKSHFIVALKVLFKSQIEKEGVE 119
1cl|XM_00401268 NSSGTLNIPKRSFTIDDFEIGRPLGKGKFGNVYLAREKKSHFIVALKVLFKSQIEKEGVE 119
1cl|XM_844813.4 NSSGIPNFSMRSFTIDDFEIGRPLGKGKFGNVYLAREKKSHFIVALKVLFKSQIEKEGVE 119
1cl|XM_00399619 NSSGTPNFSMRSFTIDDFEIGRPLGKGKFGNVYLAREKKSHFIVALKVLFKSQIEKEGVE 119
1cl|NM_213919.2 NSSGTPNFSTRSFTIDDFEIGRPLGKGKFGNVYLAREKKSHFIVALKVLFKSQIEKEGVE 119
1cl|XM_00150481 NSSGTPNLMRSFTIDDFEIGRPLGKGKFGNVYLAREKKSHFIVALKVLFKSQIEKEGVE 119
1cl|XM_00443309 NSSGTPNLMRSFTIDDFEIGRPLGKGKFGNVYLAREKKSHFIVALKVLFKSQIEKEGVE 119
1cl|XM_00827074 NSSGAPNF-TRPFTIDDFEIGRPLGKGKFGNVYLAREKKSHFIVALKVLFKSQIEKEGVE 118
1cl|XM_00587878 NSNGTPN-LMRSFTIDDFEIGRPLGKGKFGNVYLAREKKSRFIVALKVLFKSQIEKEGVE 114
1cl|XM_00468461 NSSGTPNLMRSFTIDDFEIGRPLGKGKFGNVYLAREKKSHFIVALKVLFKSQIEKEGVE 119
1cl|XM_00341691 NSSGTPSLMRPFTIDDFEIGRPLGKGKFGNVYLAREKKSHFIVALKVLFKSQIEKEGVE 120
1cl|XM_01994424 NNSRTPNFMSRSFTIDDFEIGRPLGKGKFGNVYLAREKKSHFIVALKVLFKSQIEKEGVE 119
1cl|NM_00101587 --QQPSSPAMRRLTVDDFEIGRPLGKGKFGNVYLARLKESHFIVALKVLFKSQIEKEGLE 85
1cl|XM_00109836 --QQPSSPAMRRLKIDDFEIGRPLGKGKFGNVYLARLKESHFIVALKVLFKSQIEKEGLE 85
1cl|XM_00521979 --TVPGAPTARRFTVDDFEIGRPLGKGKFGNVYLARLKKNHFIVALKVLFKSQIEKEGLE 79
1cl|XM_00401544 --SVPGAPAAARFTIDDFEIGRPLGKGKFGNVYLARLKKNHFIVALKVLFKSQIEKEGLE 79
1cl|XM_00561607 --VELSVPPGRRLTIDDFEIGRPLGKGKFGNVYLARLKESHFIVALKVLFKSQIEKEGLE 83
1cl|XM_00694080 --VELMPPVRRLTIDDFEIGRPLGKGKFGNVYLARLKESHFIVALKVLFKSQIEKEGLE 84
1cl|XM_02109730 --TVSNIPTGRRLTIDDFEIGRPLGKGKFGNVYLARLKESHFIVALKVLFKSQIEKEGLE 73
1cl|XM_00150199 --SQPGFPNVRHLTIDDFEIGRPLGKGKFGNVYLARLKESHFIVALKVLFKSQIEKEGLE 80
1cl|XM_00443911 --TQPSFTVRHFTIDDFEIGRPLGKGKFGNVYLARLKESHFIVALKVLFKSQIEKEGLE 80
1cl|XM_00824896 --PAQPSVPLRRLTIDDFEIGRPLGKGKFGNVYLARLKDSHFIVALKVLFKSQIEKEGME 68
1cl|XM_01453723 --PSSSPGSRSLTIDDFEIRCLPLGKGKFGNVYLARLRDSHFIVALKVLFKSQLEKEGME 75
1cl|XM_01273470 --PALPVATVRRLTIDDFEIGRPLGKGKFGNVYLARLRRESRFIVALKVLFKSQIEKEGLE 72
1cl|XM_00340664 --YGDVLLMERRLTIDDFEIGRPLGKGKFGNVYLARLQENHFLVALKVLFKSQIEKEGLE 82
1cl|XM_01992887 --TMPSIPTVRRLTIDDFEIGRPLGKGKFGNVYLARLKESHFIVALKVLFKSQIEKEGLE 72

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1cl|NM_004217.3 HQLRREIEIQAHLHPNILRLYNYFYDRRIYLILEYAPRGELYKELQKSCTFDEQRTAT 179
1cl|XM_01511855 HQLRREIEIQAHLHPNILRLYNYFYDRRIYLILEYAPRGELYKELQKSRTFDEQRTAT 179
1cl|NM_183084.2 HQLRREIEIQAHLQHPNILRLYNYFYDRRIYLILEYAPRGELYKELQKSRTFDEQRTAT 179
1cl|XM_00401268 HQLRREIEIQAHLQHPNILRLYNYFYDRRIYLILEYAPRGELYKELQKSRTFDEQRTAT 179
1cl|XM_844813.4 HQLRREIEIQAHLQHPNILRLYNYFYDRRIYLILEYAPRGELYKELQKSHTFDEQRTAT 179
1cl|XM_00399619 HQLRREIEIQAHLQHPNILRLYNYFYDRRIYLILEYAPRGELYKELQKSRTFDEQRTAT 179
1cl|NM_213919.2 HQLRREIEIQAHLQHPNILRLYNYFYDRRIYLILEYAPRGELYKELQKCRTFDEQRTAT 179
1cl|XM_00150481 HQLRREIEIQAHLQHPNILRLYNYFYDRRIYLILEYAPRGELYKELQKSRTFDEQRTAT 179
1cl|XM_00443309 HQLRREIEIQAHLQHPNILRLYNYFYDRRIYLILEYAPRGELYKELQKSRTFDEQRTAT 179

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lcl|XM\_00150199 LPPEMIEGRTYNEKVDLWCIGVLCYELLVGNPPFESNSHNETYRRILKVDVRFPPSIPSG 260  
lcl|XM\_00443911 LPPEMIEGRTYNEKVDLWCIGVLCYELLVGNPPFESNSHNETYRRILKVDVRFPPSIPLG 260  
lcl|XM\_00824896 LPPEMIEGRTYDEKVDLWCIGVLCYELLVGNPPFESVSHNETYRRILKVDVKFPVTMSLG 248  
lcl|XM\_01453723 LPPEMVEQRTYSEMVDLWCIGVLCYELLVGNPPFKSSSYSETYRRILKVDVKFPPSIPLG 255  
lcl|XM\_01273470 LPPEMIEGRTYNEKVDLWCIGVLCYELLVGKPPFESSTHNETYRRILKVDVRFPPSVPLG 252  
lcl|XM\_00340664 LPPEMIEGRTYDERVDLWCIGVLCYELLVGNPPFESPSHTETYRRILKVDVRFPPSMPSG 262  
lcl|XM\_01992887 LPPEMIEGRTYNEKVDLWCIGVLCYELLVGNPPFESPSHNETYRRILQVDVRFPPSMPLG 252

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lcl|NM\_004217.3 AQDLISKLLRHNPSERLPLAQVSAHPWVRANSRRVLPPSALQSV\* 345  
lcl|XM\_01511855 AQDLISKLLRHNPSERLPLAQVSAHPWVRANSRRVLPPSALQSV\* 345  
lcl|NM\_183084.2 AQDLIYKLLKHNPSERLPLAQVSAHPWVRTHSRRVLPPSAPQSV\* 345  
lcl|XM\_00401268 AQDLISKLLKHNPSERLPLAQVSAHPWVRANSRRVLPPSAPQSV\* 345  
lcl|XM\_844813.4 AQDLISKLLKHNPSERLPLSQVSAHPWVRANSRRMLPPSAVQAIP\* 345  
lcl|XM\_00399619 AQDLISKLLKHNPSERLPLAQVSAHPWVRANSRRVLPPSALQSV\* 345  
lcl|NM\_213919.2 AQDLISKLLKHNPSERLPLAQVSAHPWVRANSRRVLPPSAPQSV\* 345  
lcl|XM\_00150481 AQDLISKLLRHNPSERLPLAQVSAHPWVRANSRRVLPPSALQSV\* 345  
lcl|XM\_00443309 AQDLISKLLKHNPSERLPLAQVSAHPWVRANSRRVLPPSAPQSV\* 345  
lcl|XM\_00827074 AQDLISKLLRHNPSERLPLAQVSAHPWVRANSRRVLPPSAMQSV\* 344  
lcl|XM\_00587878 AQDLISKLLKHNPSERLPLAQVSAHPWVRANSRRVLPPSALQSVH\* 340  
lcl|XM\_00468461 AQDLITKLLKHNPSERLPLTQVSAHPWVRANSRRVLPPSALQSV\* 345  
lcl|XM\_00341691 AQDLISKLLKHNPSERLPLAQVSAHPWVRANSRRVLPPSALQSV\* 346  
lcl|XM\_01994424 AQDLISKLLKHNPSERLPLAQVAAHPWVRANSRRVLPPSALQSV\* 345  
lcl|NM\_00101587 ARDLISRLRLRYQPLERLPLAQILKHPWVQAHSRRVLPPCAQMAS\*- 310  
lcl|XM\_00109836 ARDLISKLLRYQPLERLPLAQILKHPWVQVHSRRVLPPCAQMAS\*- 310  
lcl|XM\_00521979 ARDLISKLLRFQPLERLPLVRVLEHPWIRAHSQRVLPSSVPMF\*- 304  
lcl|XM\_00401544 ARDLISKLLRFQPLERLPLVRVLEHPWIRAHSQRVLPSSVQRAF\*- 304  
lcl|XM\_00561607 AQDLVSKLLRYQPLERLPLAQIMEHPWVRANSRRVLPPSVQMAS\*- 308  
lcl|XM\_00694080 ARDLISKLLRYQPLERLPLSQILEHPWVRANSRRVPPSVQMD\*- 309  
lcl|XM\_02109730 AQDLISRLRLRYQPSDRLPLDQILEHPWVRANSRRVLPPSTQMVS\*- 298  
lcl|XM\_00150199 AKDLISKLLRYQPLERLPLDQILEHPWVRANSRRVLPPSAQMAS\*- 305  
lcl|XM\_00443911 AKDLISKLLRYQPLERLPLDQIMEHPWVRANSRRVLPPSAQMAS\*- 305  
lcl|XM\_00824896 ARDLISRLRLRYQPSERLPLAQILRHPWVQAHSRRVLPPCAHPAS\*- 293  
lcl|XM\_01453723 AQDLISKLLRYQPSERLPLAQVLQHPWVQAHSRRVGPPAPAS\*- 300  
lcl|XM\_01273470 AQDLISSLLRYQPSERLPLAQILQHPWVRMHSRRVLPPSAQVAS\*- 297  
lcl|XM\_00340664 AQDLISKLLRYQPFERLALAQVLEHPWVQAHSQRVLPSSAQMAS\*- 307  
lcl|XM\_01992887 AQDLISKLLRYQPSERLPLVQILEHPWVRANSRRVLPPSAQMVS\*- 297

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