

Figure S9. Alignment of placental mammal AKA and AKB sequences. The alignment of the placental mammal AKA and AKB sequences used for the dN/dS analyses.

MATLAB multiple sequence alignment

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lcl|NM_198436.2 MDRSKENCISGPVKATAPVG-GPKRVLVTQQFPCQNPLPVNSGQAQRVLCPSNSSQRIPL 59
lcl|XM_01514873 MDRSKENCISGPVKAPAVG-GPKRVLVTQQFPCQNPLPANSQAQRVLCPSNSSQVRVPL 59
lcl|NM_00103802 MDRCKENCISGP-KTAVPLSDGPKRVPVAQQFSPQNVPVNSGQAQRVLCPTNSSQVRVPS 59
lcl|NM_00114250 MDRCKENCISGP-KTAVPLSDGPKRVPVAQQFSPQNVPVNSGQAQRVLCPTNSSQVRVPS 59
lcl|XM_00563519 MDKSKENCISGPKVTALGDGPKRVLVTQQFVPSQNPLSANSQAQRVLCPSNSSQVRVPP 60
lcl|XM_00398335 MDKSKENCISGPKVTIPLGDGPKRVPVTQQFVPSQNLLSANSQAQRVLCPSNSSQRIPL 60
lcl|XM_00567303 MDKCKENCISGL-KTTVPVGDGPKRVPVTQHFPQAHLPSANSQAQRVLCPSNSSQRLPL 59
lcl|XM_00148927 MDRSKENCISGPKVTIPLGDGPKRVPVTQQFVPSQNLLSANSQAQRVLCPSNSSQVRVPS 59
lcl|XM_00443024 MDRSKENCISGPKVTIPLGDGPKRVLVTQQFVPSQHPLSANSQAQRVLCPSNSSQVRVPP 60
lcl|XM_00827414 MERSKENCISGPIKAAALLGDGPKRVPVTQRFPSQNVPVNSGQAQRVLCPSNSSQVRVPS 60
lcl|XM_01452869 MDKSKENCISGLVKTIPSGDGPKRVLVTQQFVPSQYPLPANSQAQRVLCPSNSSQVRVPS 60
lcl|XM_00468690 MDKSKENCISGPKVTMPLRDGAKRVPVHQHAPSQSALPASSQAQRVLCPSN-SQRLPL 59
lcl|XM_00341990 MDKSKENCISGPKVTIPLGDGPKRVPVTQFPFSPQNPLSANSQAQRVLCPSNSSQVRVPS 60
lcl|XM_00432103 MDKCKENCISGP-KTTVPLGDGPKRVPVTQQFVPSQNVPVNSGQAQRVLCPSNSSQVRVPS 59
lcl|NM_004217.3 MAQKENS-----YWPWYGRQTAQPSGLSTLPQRLRKEPV 34
lcl|XM_01511855 MAQKENS-----YWPWYGRQTAQPSGLSTLPQRLRKEPV 34
lcl|NM_183084.2 MAQKENS-----YWPWYGRQTAQPSGLSTLPQRLRKEPV 34
lcl|XM_00401268 MAQKENS-----YWPWYGRQTAQPSGLSTLPQRLRKEAV 34
lcl|XM_844813.4 MTQKENS-----YWPWYGRQTAQPSGLSTLPQRLRKEAV 34
lcl|XM_00399619 MAQKENS-----YWPWYGRQTAQPSGLSTLPQRLRKEAV 34
lcl|NM_213919.2 MAQKENS-----YWPWYGRQTAQPSGLSTLPQRLRKEAV 34
lcl|XM_00150481 MTQKENS-----YWPWYGRQTAQPSGLSTLPQRLRKEAV 34
lcl|XM_00443309 MAQKENS-----YWPWYGRQTAQPSGLSTLPQRLRKEAV 34
lcl|XM_00827074 MAQKENS-----YWPWYGRQTAQPSGLSTLPQRLRKEAV 34
lcl|XM_00587878 MTQKENS-----YWPWYGRQTAQPSGLSTLPQRLRKEAV 34
lcl|XM_00468461 MAQKENS-----YWPWYGRQTAQPSGLSTLPQRLRKEAV 34
lcl|XM_00341691 MAQKENS-----YWPWYGRQTAQPSGLSTLPQRLRKEAV 34
lcl|XM_01994424 MAQKENS-----YWPWYGRQTAQPSGLSTLPQRLRKEAV 34
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lcl|XM_01514873 QAQKLVSSSH--LVQNLKQKQLQATSVPHVPSRPPSHTPKSKQPLSAPENNPEELASK 117
lcl|NM_00103802 QAQKLVSISQK--PVQTLKQKPPQAASAPRPVTRPPSNTQKSKQPPAPGNNPEKEVASK 117
lcl|NM_00114250 QAQKLVSISQK--PVQTLKQKPPQAASAPRPVTRPPSNTQKSKQPPAPGNNPEKEVASK 117
lcl|XM_00563519 QTQKLVSSSH--PAQNLKQKQLQATGVPVPSRPLNNTQKSEQPSAPGNNSEKELATK 118
lcl|XM_00398335 QTQKLVSSSH--PVQNLKQKQLQATSVPSRPLNNTQKSEQPLSATGNNSEKELTTK 118
lcl|XM_00567303 HTQKLVSSSH--PVQNLKQKQSQATSGRPVPSRPLSNTQKSEQPPAPGNNPEKEAASK 117
lcl|XM_00148927 QAQKLVSSSH--PVQNLKQKQSQATSVPHVPSRPLNNTQKSEQPLSATGNNSEKELASK 117
lcl|XM_00443024 QAQKLVSSSH--PVQNLKQKQSQATSVPPVPSRPLNNTQKSEQPPAPGNNSEKERTSK 118
lcl|XM_00827414 QAQKLPAEK----PVQKLQAQAASVPRPVSKPPNNTPKSEQPPAPGNNPEKELTSN 116
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lcl|XM_00468690 QAQKLVSSSHKAVPNPNLQKQLQANNAPRAAPRLAGTPKSEPP-PSAPGNNSEKEQASK 118
lcl|XM_00341990 QAQKLVSSSH--PVQNLKQKQLQATGVPVPSRPLNNTQKSEQPPAPGNNSEKELASK 118
lcl|XM_00432103 QAQKLVSSSH--SVQPLKQKPTQAASAPRSVPSRPLSNTQKSEQPLSATGNNPEKEAASK 117
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lcl|XM_01511855 TPSALVLSMR-----SNVQPTAAPGQ---KVVENS 61
lcl|NM_183084.2 TPSALVLSMR-----SNAQPTAAPGQ---KVVENS 61
lcl|XM_00401268 IPSALVLSMR-----SNAQPTAAPGQ---KVVENS 61
lcl|XM_844813.4 TPSALVLSMR-----SNGQPTAAPGQ---KVVENS 61
lcl|XM_00399619 TPSALVLSMR-----SNTQPTAAPGQ---KVVENS 61
lcl|NM_213919.2 TPSALVLSMR-----SNTQPTAAPGQ---KVVENS 61
lcl|XM_00150481 TPSALVLSMR-----SNAQPTVALGQ---KVMENS 61
lcl|XM_00443309 TPSALVLSMR-----SNAQPTAALGQ---KVVENS 61
lcl|XM_00827074 TPSALVLLNR-----SNAPPTAVLGQ---KGMENS 61
lcl|XM_00587878 TPSSLVLSMR-----SNAQPTAAPGQ-----NS 57
lcl|XM_00468461 TPSALVLMNR-----SNTQPTAAPGQ---KVVENS 61
lcl|XM_00341691 TPSALVLSMR-----SNAQPTAAPGE---KMTENS 62
lcl|XM_01994424 TPSALVLSMR-----SNAQPTAALQ---KVVENS 61
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lcl|XM_01514873 QKNEESKKRQWALEDFEIGRPLGKGKFGNVYLAREKQSKFIALKVLFAQLEKAGVEHQ 177
lcl|NM_00103802 QKNEESKKRQWALEDFEIGRPLGKGKFGNVYLAREKQSKFIALKVLFAQLEKAGVEHQ 177
lcl|NM_00114250 QKNEESKKRQWALEDFEIGRPLGKGKFGNVYLAREKQSKFIALKVLFAQLEKAGVEHQ 177
lcl|XM_00563519 QKNEESKKRQWALEDFEIGRPLGKGKFGNVYLAREKQSKFIALKVLFAQLEKAGVEHQ 178
lcl|XM_00398335 QKNEESKKRQWALEDFEIGRPLGKGKFGNVYLAREKQSKFIALKVLFAQLEKAGVEHQ 178
lcl|XM_00567303 QKNEESKKRQWALEDFEIGRPLGKGKFGNVYLAREKQSKFIALKVLFTQLEKAGVEHQ 177

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lcllXM_00827412	QKNEESKKRQWLTLEDFIGRPLGKGKGFNVYLAREKQSKFITALKVLFKAQLEKAGVEHQ	176
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lcllXM_00432103	QKNEESKKRQWALDFEIGRPLGKGKGFNVYLAREKQSKFITALKVLFKAQLEKAGVEHQ	178
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lcllXM_01511855	SGTPNILMRHFTIDDFEIGRPLGKGKGFNVYLAREKKSHFIVALKVLFKSQIEKEGEVHQ	121
lcllNM_183084.2	SGTPNIPKRSFTIDDFEIGRPLGKGKGFNVYLAREKKSHFIVALKVLFKSQIEKEGEVHQ	1221
lcllXM_00401268	SGTLNIPKRSFTIDDFEIGRPLGKGKGFNVYLAREKKSHFIVALKVLFKSQIEKEGEVHQ	121
lcllXM_844813.4	SGIPNFSMRSFTIDDFEIGRPLGKGKGFNVYLAREKKSHFIVALKVLFKSQIEKEGEVHQ	121
lcllXM_00399619	SGTPNFSMRSFTIDDFEIGRPLGKGKGFNVYLAREKKSHFIVALKVLFKSQIEKEGEVHQ	121
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lcllXM_00827074	SGAPNF-TRPFTIDDFEIGRPLGKGKGFNVYLAREKKSHFIVALKVLFKSQIEKEGEVHQ	120
lcllXM_00587878	NGTPN-LMRSFTIDDFEIGRPLGKGKGFNVYLAREKKSRLFIVALKVLFKSQIEKEGEVHQ	116
lcllXM_00468461	SGTPNLLMRSFTIDDFEIGRPLGKGKGFNVYLAREKKSHFIVALKVLFKSQIEKEGEVHQ	1221
lcllXM_00341691	SGTPNSMLRPFITIDDFEIGRPLGKGKGFNVYLAREKKSHFIVALKVLFKSQIEKEGEVHQ	1221
lcllXM_01994424	SRTPNFSMRSFTIDDFEIGRPLGKGKGFNVYLAREKKSHFIVALKVLFKSQIEKEGEVHQ	121

lcl|XM_00401268 MEELADALTYCHAKKVIHRDIKPENLLGLRGELKIADFGWSVHAPSLRRKTCMCGTLDYL 240
lcl|XM_844813.4 MEELADALMYCHGKKVIHRDIKPENLLGLQGELKIADFGWSVHAPSLRRKTCMCGTLDYL 240
lcl|XM_00399619 MEELADALLYCHGKKVIHRDIKPENLLGLQGELKIADFGWSVHAPSLRRKTCMCGTLDYL 240
lcl|NM_213919.2 MEELADALIYCHGKKVIHRDIKPENLLGLQGELKIADFGWSVHAPSLRRKTCMCGTLDYL 240
lcl|XM_00150481 MEELADALMYCHGKKVIHRDIKPENLLGLQGELKIADFGWSVHAPSLRRKTCMCGTLDYL 240
lcl|XM_00443309 MEELADALIYCHGKKVIHRDIKPENLLGLQGELKIADFGWSVHAPSLRRKTCMCGTLDYL 240
lcl|XM_00827074 MEELADALRYCHEKKVIHRDIKPENLLGLQGELKIADFGWSVHAPSLRRKTCMCGTLDYL 239
lcl|XM_00587878 MEELADALMYCHGKKVIHRDIKPENLLGLQGELKIADFGWSVHAPSLRRKTCMCGTLDYL 235
lcl|XM_00468461 MEELADALIYCHGKKVIHRDIKPENLLGLQGELKIADFGWSVHAPSLRRKTCMCGTLDYL 240
lcl|XM_00341691 MEELADALMYCHGKKVIHRDIKPENLLGLRGELKIADFGWSVHAPSLRRKTCMCGTLDYL 241
lcl|XM_01994424 MEELADALIYCHGKKVIHRDIKPENLLGLQGELKIADFGWSVHAPSLRRKTCMCGTLDYL 240
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lcl|NM_00103802 PPEMIEGRMHDEKVDLWSLGVLCYEFVGVKPPFEADTYQETYRRISRVEFTFPDCVPEGA 356
lcl|NM_00114250 PPEMIEGRMHDEKVDLWSLGVLCYEFVGVKPPFEADTYQETYRRISRVEFTFPDCVPEGA 356
lcl|XM_00563519 PPEMIEGRMHDEKVDLWSLGVLCYEFVGVKPPFEASTYQETYKRISRVEFTFPDFVPEGA 357
lcl|XM_00398335 PPEMIEGRMHDEKVDLWSLGVLCYEFVGVKPPFEASTYQETYKRISRVEFTFPDFVPEGA 357
lcl|XM_00567303 PPEMIEGRMHDEKVDLWSLGVLCYEFVGVKPPFEANTYQETYKRISRVEFTFPDFVPEGA 356
lcl|XM_00148927 PPEMIEGRMHDEKVDLWSLGVLCYEFVGVKPPFEASTYQETYKRISRVEFTFPDFVPEGA 356
lcl|XM_00443024 PPEMIEGRMHDEKVDLWSLGVLCYEFVGVKPPFEASTYQETYKRISRVEFTFPDFVPDGA 357
lcl|XM_00827414 PPEMIEGRMHDEKVDLWSLGVLCYEFVGVKPPFEANTYQETYRRISRVEFTFPDFVTEGA 355
lcl|XM_01452869 PPEMIEGRMHDEKVDLWSLGVLCYEFVGVKPPFEASTYQETYKRISRVEFTFPDFVREGA 356
lcl|XM_00468690 PPEMIEGRMHDEKVDLWSLGVLCYEFVGVKPPFEASTYQETYKRISRVEFTFPDFVPEGA 357
lcl|XM_00341990 PPEMIEGRMHDEKVDLWSLGVLCYEFVGVKPPFEASTYQETYNRISRVEFTFPDLVTVGA 358
lcl|XM_00432103 PPEMIEGRMHDEKVDLWSLGVLCYEFVGVKPPFEANTYQETYKRISRVEFTFPDFVPEGA 356
lcl|NM_004217.3 PPEMIEGRMHNEKVDLWCIGVLCYELLVGNPPFESASHNETYRRIVKVDLKFPASVPMGA 300
lcl|XM_01511855 PPEMIEGRTHNEKVDLWCIGVLCYELLVGNPPFESASHNETYRRIVKVDLKFPASVPTGA 300
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lcl|XM_00401268 PPEMIEGRTHNEKVDLWCIGVLCYELLVGNPPFESASHNETYRRIVKVDLKFPSPVPMGA 300
lcl|XM_844813.4 PPEMIEGRMHNEKVDLWCIGVLCYELLVGNPPFESASHNETYRRIVKVDLKFPSPVPTGA 300
lcl|XM_00399619 PPEMIEGRTHNEKVDLWCIGVLCYELLVGNPPFESASHNETYRRIVKVDLKFPASVPTGA 300
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lcl|XM_00827074 PPEMIEGRTHNEKVDLWCIGVLCYELLVGNPPFESASHNETYRRIVKVDLKFPASVPAGA 299
lcl|XM_00587878 PPEMIEGRTHNEKVDLWCIGVLCYELLVGNPPFESASHNETYRRIVKVDLKFPSPVPAGA 295
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lcl|XM_00341691 PPEMIEGRMHNEKVDLWCIGVLCYELLVGNPPFESASHNETYRRIVKVDLKFPSPVPTGA 301
lcl|XM_01994424 PPEMIEGRTHNEKVDLWCIGVLCYELLVGNPPFESASHNETYRRIVKVDLKIPSPMPAGA 300
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lcl|NM_00103802 RDLISRLKHNPSQRPTLKEVLEHPWITANSKSPSSCQKKESTSKQS*- 403
lcl|NM_00114250 RDLISRLKHNPSQRPTLKEVLEHPWITANSKSPSSCQKKESTSKQS*- 403
lcl|XM_00563519 RDLISRLKHNPSQRPTLKDVLEHPWIMANSKSPSSQKNKDSTSKQS* 406
lcl|XM_00398335 RDLISRLKHNPSQRPTLKEVLEHPWITANSKSPSGSQKSKESTGKQS* 406
lcl|XM_00567303 RDLISRLKHNPSHRPTLKEVLEHPWITANSKPASSHKKESTSKQP*- 403
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lcl|XM_00443024 RDLISRLKHNPSQRPTLKEVLEHPWITANSKSPSNSQKSKESTSKQS* 406
lcl|XM_00827414 KDFISRLKHNPSHRPTLAEVLEHPWVKAHSSKSPSSCPDKEPASKQS*- 403
lcl|XM_01452869 RDLISRLLMHNPQRLTLKEVLEHPWITANSKSPSSQKSKESTSKQS* 405
lcl|XM_00468690 RDLISRLKHNPSQRPTLKEVLEHPWITANSKSPSSQKNKESTSKQS* 406
lcl|XM_00341990 RDLVSRLLKHNPSQRLTLKEVLEHPWITANSKPPSSQNKEPTSKQS*- 406
lcl|XM_00432103 RDLISRLKHNPSQRPTLKEVLEHPWITANSKSPSSQKKEASASKQS*- 403
lcl|NM_004217.3 QDLISKLLRHNPSERLPLAQVSAHPWVRANSRRVLPPSALQSV*- 345
lcl|XM_01511855 QDLISKLLRHNPSERLPLAQVSAHPWVRANSRRVLPPSALQSV*- 345
lcl|NM_183084.2 QDLISKLLKHNPSERLPLAQVSAHPWVRTHSRRVLPPSAPQSV*- 345
lcl|XM_00401268 QDLISKLLKHNPSERLPLAQVSAHPWVRANSRRVLPPSAPQSV*- 345
lcl|XM_844813.4 QDLISKLLKHNPSERLPLAQVSAHPWVRANSRRVLPPSAPQSV*- 345
lcl|XM_00399619 QDLISKLLKHNPSERLPLAQVSAHPWVRANSRRVLPPSALQSV*- 345
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lcl|XM_00468461 QDLITKLLKHNPSERLPLAQVSAHPWVRANSRRVLPPSALQSV*- 345
lcl|XM_00341691 QDLISKLLKHNPSERLPLAQVSAHPWVRANSRRVLPPSALQSV*- 346

1c1lXM_01994424 QDLISKLLKHNPSERLPLAQVAHPWVRAHSRRVLPPSALQSV*---- 345
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